University of Reading

Understanding fruit development in the cultivated cherry

A thesis submitted for the degree of Doctor of Philosophy

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September 2022

Abstract

The production of sweet cherry (*Prunus avium* L.) has increased constantly in the UK and worldwide, over the last 20 years. Sweet cherry fruit is appealing because of the bright colours, the balance between sweet and sour, the firmness, the juiciness and the good effects on human health, due to mainly the high content of anthocyanins, which are important antioxidants. The interest of growers is not limited just to an increase in production but also to obtain new varieties that can satisfy the market requirements. The study of the molecular and genetic factors involved in the developmental processes of the cherry fruit, can clear the way to the production of genome edited varieties that present specific and desirable traits. The objective of this study was to identify those factors that are responsible for the ovary to fruit transition, to identify potential targets that can be used for the creation of a seedless cherry and to start the setting up protocols for cherry *in vitro* propagation, regeneration and transformation. The application of gibberellin to unpollinated ovaries resulted in the triggering fruit set, without however being sufficient to complete the entire developmental process. Transcriptomic analysis of those samples, along with the pollinated controls, was used to map out an overview of the changes in gene expression during the first phases of fruit development. The focus was especially on hormones and transcription factors like the MADS-box genes, which are all known to be essential for the complex regulation of this process. *Pav_sc0000129.1_g.1480.1.mk* (*PavARF7*), *Pav_sc0000464.1_g350.1.mk* (*PavRGL2*), *Pav_sc0002327.1_g560.1.mk* and *Pav_sc0002393.1_g030.1.mk* (*PavAUX/IAA9*) were found to be downregulated in the open pollinated samples at the beginning of fruit development, potentially confirming their role as negative regulators of fruit development in sweet cherry as reported in other species like tomato. *In vitro* regeneration and propagation from seed tissues, such as embryo axes and cotyledons, resulted successful, while more effort will be needed to achieve the same results starting from somatic tissues like leaves.

Declaration

I confirm that this is my own work and that the use of all material from other sources has been properly and fully acknowledged.

Edoardo Vignati

Acknowledgements

First of all, I would like to thank Richard Harnden and Berry Gardens for funding and for giving me the opportunity to undertake this PhD project. Richard, in particular, for his enthusiasm, ideas and support not only on a professional level but especially on a human one. I really hope I have paid back, at least a little, all the investment in this project.

I am grateful to my supervisors, Dr Andrew J. Simkin at NIAB and Prof. Jim Dunwell, for their wisdom and support. Thank you especially for being always understanding and patience in those moments when I mostly needed it.

I would also like to thank Marzena Lipska, whose enthusiasm, passion and energy will always be impressed in my mind. Also, Marzena, thank you for introducing me to the magic world of cherries.

I want to also thank Prof. Mario Caccamo, who became part of this project in a challenging moment and made me find the light in the dark. I wish you the best of luck possible.

Thank you to all the people at NIAB EMR with whom I shared precious moments these last four years. I wish I could write down all the names, but then it would turn this part into a chapter. I have also found friends that I am sure will be part of my life after. Thank you to everyone for supporting me, and I hope I have been a good friend as much as you have been with me.

Un ringraziamento particolare alla mia famiglia, che anche se lontana mi ha sempre supportato, standomi vicino e spronandomi nei momenti di difficoltà. In questi quattro anni sono accaduti moltissimi avvenimenti ma sicuramente i più preziosi sono stati il vedere il mio nipotino Richi crescere ed essere un bambino speciale, e l'arrivo della Ludo, che sono sicuro è già una gemma preziosa come il suo fratellone. Infine un ricordo al mio grande amore Zoe, che è e sempre sarà nel mio cuore.

Un ringraziamento ai miei amici in Italia, che nonstante la distanza, non hanno mai mancato di farmi sentire ancora parte della loro vita, supportandomi e sopportandomi. Anche qui la lista di nomi sarebbe lunghissima, ma se stai leggendo questo, allora sicuramente fai parte delle persone a cui in questo momento sto pensando.

Thank you, Matteo, for not being just the other Italian PhD student and my flatmate, but also for becoming my friend. I cannot imagine sharing this experience with anyone else. I wish you all the best and good luck possible for your future.

Thank you, James, for becoming part of my life and supporting me in these last months, which I am sure were not easy for you. Now it is time to start a new chapter.

Finally, thank you to all the people that have been part of my life these last four years. I am so happy and grateful to have had the chance to meet you.

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Abbreviations

2,4-D: 2,4-Dichlorophenoxyacetic acid

ARF7: AUXIN REPONSE FACTOR 7

AUX/IAA9: AUXIN/INDOLE-3-ACETIC ACID 9

BLAST: Basic Local Alignment Search Tool

cDNA: Complementary Deoxyribonucleic Acid

CDS: Coding Sequence

CIM: Callus Induction Medium

DAT: Days After Treatment

DEGs: Differentially Expressed Genes

DNA: Deoxyribonucleic Acid

DOWN: Down-regulated DEGs

ERM: Embryo Rescue Medium

FM: Forcing Medium

GA: Gibberellins

GA_3: Gibberellic Acid 3

GAI: GIBBERELLIC ACID INSENSTIVE

GDR: Genome Database of Rosaceae

log2FC: Log2 Fold Change

mRNA: Messenger Ribonucleic Acid

MS: Murashige and Skoog

N.C.: Negative Control

NIAB EMR: National Institute of Agricultural Botany East Malling Research

O.P.: Open Pollinated

p-adj: p-value adjusted

QL: Quoirin and Lepoivre

RGA: REPRESSOR OF GA

RGL1: REPRTESSOR OF GA-like 1

RGL2: REPRESSOR OF GA-like 2

RNA: Ribonucleic Acid

RNA-Seq: Ribonucleic Acid Sequencing

SEM: Shoot Elongation Medium

SIM: Shoot Induction Medium

SPM: Shoot Propagation Medium

SRM: Shoot Regeneration Medium

UP: Up-regulated DEGs

WPM: Woody Plant Medium

Chapter 1: General Introduction

1.1 Background

The origin area of *Prunus avium* L. has been suggested to be Europe (Ukraine, in particular the areas close to the Black and Caspian seas) and central Asia (northern Iran and south to the Caucasian mountains) (De Candolle, 1886; Watkins, 1976; Faust & Suranyi, 1997; Webster, 1997). Commonly called sweet cherry, it is a deciduous tree, 15-32 m tall, with a trunk up to 1.5 m in circumference. It belongs to the Rosaceae family, which includes many plants such as rose (*Rosa* L.), apple (*Malus x domestica*), pear (*Pyrus* L.) peach (*Prunus persica*), strawberry (*Fragaria vesca* and *F. ananassa*) and raspberry (*Rubus* L.), that are very important economically. Young cherry trees show strong apical dominance with a straight trunk and symmetrical conical crown that becomes rounded to irregular on old trees. All parts of the plant, except for the ripe fruit, are slightly toxic, due to the presence of cyanogenic glycosides. The species has also become naturalised in North America and Australia since it is largely cultivated in these regions. Cherry production has seen a remarkable growth in the last few years. World-wide, cherry production has increased by 37%, between 2000 and 2020. In the UK, the increase in the same time period is even more significant since it is about 1300% (Fig. 1.1). This fact shows that growers are committing more resources to cherry production and a growing consumer interest is one of the drivers behind these increases.

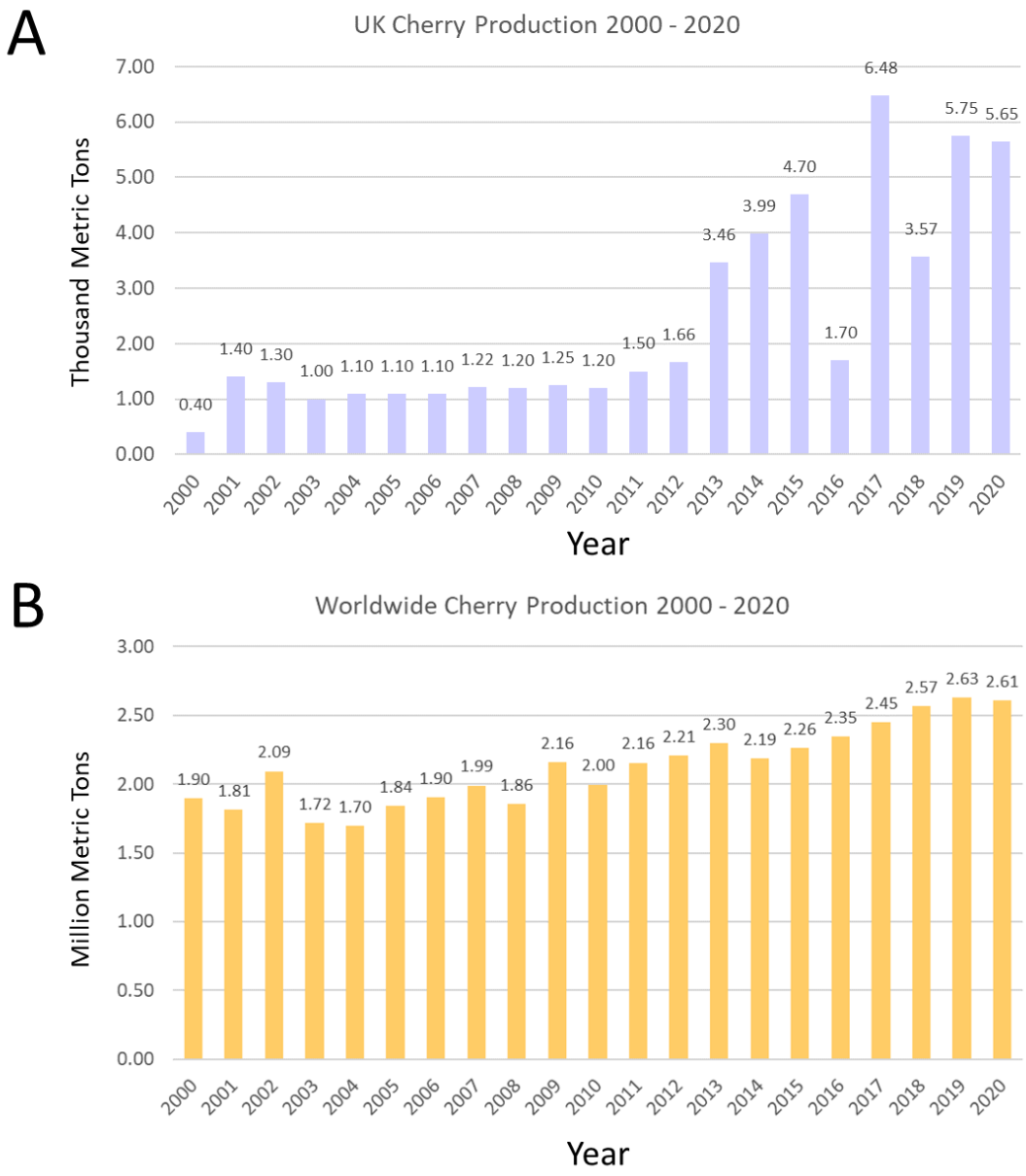


Figure 1.1: Graphical representation of UK (A) and worldwide (B) cherry production between 2000 and 2020. (A) All the values reported are official data, except for the 2009, which is a FAO estimation. (B) All the values are aggregates, which may include official, semi-official, estimated, or calculated data. Faostat, 2022.

The sweet cherry fruit is a non-climacteric drupe, 1-2 cm in diameter with an attractive appearance, due to its colour (bright red to dark purple) and pleasant intense flavour which is due to a combination of sugars (125-265 g/kg fresh weight) and organic acids (3.67-8.66 g/kg fresh weight) (Usenik *et al.,* 2008). The fruit are also high in fibre and contain a large range of bioactive compounds including polyphenols (~1500 mg/kg of fresh weight), anthocyanins, carotenoids and vitamins (Jakobek *et al.,* 2007; McCune *et al.,* 2011; Kelley *et al.,* 2018). Anthocyanins are responsible for the appealing red colour of cherries, that varies according to concentrations. In light-coloured cherries, anthocyanin concentration is a few mg in 100 g of fresh weight, while in dark purple cherries their concentration increases up to 700 mg in 100 g of fresh weight (Wang *et al.,* 1997). Cherries also contain high levels of minerals including magnesium (10 mg/100 g), potassium (200 mg/100 g), phosphorous (20 mg/100 g), and calcium (14 mg/100 g) (Ferretti *et al.,* 2010). Cherries are also a good source of tryptophan and serotonin (Cubero *et al.,* 2010; Garrido *et al.,* 2012). These data suggest that increasing cherry consumption could be beneficial to human health and quality of life of consumers (McCune *et al.,* 2011; Kelley *et al.,* 2018; Ferretti *et al.,* 2010; Bell *et al.,* 2014; Coelho *et al.,* 2015; Alba *et al.,* 2019).

Some of the most critical attributes desired by consumers include colour, firmness, sweetness and flavour intensity (Guyer *et al.,* 1993; Cliff *et al.,* 1996; Kappel *et al.,* 1996; Zheng *et al.,* 2016); however, consumers from different regions set different requirements for what is considered a good cherry. For example, in Norwegian, American and UK markets consumers prefer larger dark cherries (Lyngstad & Seske, 1995; Sekse & Lyngstad, 1996; Wermund & Fearne, 2000; Crisosto *et al.,* 2003). Growers and supermarkets often have a different set of criteria for evaluating cherry quality. Growers want cherries that are firm enough to resist damage during picking, processing, and transporting and easy to harvest (long peduncles), whilst supermarkets insist on a long shelf life.

However, cherry fruit contains a large stone and seed, the presence of which makes it a potential choking hazard for small children and inconvenient to eat 'on the move'. Identifying a means of generating a seedless, stoneless cherry has the potential of making the fruit even more attractive

to the consumer. Previous data has shown that seedless cultivars of fruit such as sweet orange (*Citrus sinensis*), grape (*Vitis vinifera*), and watermelon (*Citrullus lanatus*) have significantly increased consumer consumption (Pollak, 2001). The absence of the seeds/stone would also reduce processing costs, increasing profits, and for the consumer increases the potential of the fruit as a snacking product increasing consumer acceptance and consumption. A survey made at the Indonesian Citrus and Subtropical Fruits Research Institute (ICSFRI) in 2019 showed that seedlessness in *Citrus* species is one of the most important factors that influence the consumers' preferences (Budiyati *et al.,* 2021). Another survey conducted in Spain 2020, on what kind of information the consumers want to read on fruit packaging, showed again that for the *Citrus* species, the majority of consumers want to know if seeds are present or not. Regarding drupes, seedlessness is at the bottom of the list of factors checked, while the current main interest is on sweetness, taste intensity, firmness, and juiciness (Fernández-Serrano *et al.,* 2020). This is linked to the fact that seedless drupes are not available yet in supermarkets and thus there is no reason for consumers to look for this kind of information, as it happens with other seedless varieties such as *Citrus* species indeed, but also grapes and watermelon for example.

1.2 Aims and objectives

This project focused on providing insights about fruit development in the cultivated cherry. The understanding of the gene regulation that occurs during the first phases of fruit development, will be useful not only to comprehend better how drupe-type fruit development is regulated, but also will provide candidates for the production of a seedless cherry. Sweet cherry, unlike tomato, does not have a large collection of mutants that can be used to understand the function of specific genes during fruit development. Thus, the use of the CRISPR-Cas9 direct-site mutagenesis will be considered to study the identified candidate genes and to obtain a plant that produces seedless cherry fruits.

Chapter 2 consists of a collection of all the protocols tested *in vitro* to achieve shoot propagation and regeneration. This aspect of the project is important since it will be essential once cherry transformation using *Agrobacterium tumefaciens* is carried out.

In parallel, the role of hormones was investigated. In particular, the exogenous application of Gibberellic acid 3 (GA_3) to unpollinated 'Regina' ovaries was assessed as a possible means to trigger fruit set, i.e. promote the development of parthenocarpic cherry fruits (Chapter 3). The samples obtained from this field experiment were then used for the transcriptomic analysis (Chapter 4). In detail, RNA was extracted from pollinated and parthenocarpic putative whole fruits (GA_3-treated), along with their negative controls (unpollinated ovaries), and sequenced. The analysis and the comparison between the transcriptomes of these different samples, resulted in the identification and choice of four potential candidates as negative regulators of fruit development. The phylogenetic analysis of *Pav_sc0000129.1_g.1480.1.mk* (*PavARF7*), *Pav_sc0000464.1_g350.1.mk* (*PavRGL2*), *Pav_sc0002327.1_g560.1.mk* and *Pav_sc0002393.1_g030.1.mk* (*PavAUX/IAA9*) was conducted. The protein sequences of these genes were aligned to those of their respective orthologs in other plant species such as *Arabidopsis thaliana*, Solanaceae spp. and Rosaceae spp., to assess the conservation levels of the functional domains. Finally, plasmid vectors containing the codon-optimised CDS of these four candidate genes under a constitutive promoter, were assembled (Chapter 5).

The main findings and the general integration of all the different aspects analysed in this study, will be presented in the General discussion, together with the future perspectives (Chapter 6).

Chapter 2: *In vitro* tissue cultures of *Prunus avium*

2.1 Introduction

2.1.1 Background

Plant *in vitro* tissue culture consists of growing plants in aseptic conditions, providing nutrients, sugar and water through the optimised medium and controlling temperature and light type, intensity, and duration. In addition, different stimuli can be given to the plants by changing the type and the concentrations of different phytohormones.

The choice of the basal medium is critical for the success of the plant tissue culture establishment. MS basal medium (Murashige & Skoog, 1962) and its modifications are the most commonly used media in plant tissue cultures. In a meta-survey that included all the basal media used in the publications between 2011 and 2015, 82% of citations reported the usage of MS and MS-derived media (Herman, 2015). Basal medium contains macronutrient salts which provide nitrogen (N), phosphorus (P), sulphur (S), calcium (Ca) potassium (K), and magnesium (Mg), and micronutrient salts which provide boron (B), cobalt (Co), copper (Cu), iodine (I), manganese (Mn), molybdenum (Mo), and zinc (Zn). Vitamins (glycine, myo-inositol, nicotinic acid, pyridoxine HCl acid, and thiamine HCl) can be added to the basal formulation. Different plants may require basal media with different composition of nutrients. For example, basal media specific for woody plants, like Woody Plant Medium (WPM; Lloyd and McCown 1980) and Driver and Kuniyuki Woody plant medium (DKW; Driver and Kuniyuki 1984) have been developed. The usage of these media is reported in 6% of the citations surveyed by Herman (Herman, 2015).

The growth of plant tissues in culture can be stimulated by adding phytohormones to the medium. The response that is obtained, depends on which hormone/s are present and their concentration. The most important regulators are auxins and cytokinins. Higher concentrations of auxins promote root development while higher concentrations of cytokinins shoot

development. If the concentration ratio of those two hormones is close to 1 and the levels are medium-high (about 2 mg/l for auxin and 0.2 mg/l for cytokinins), the formation of a callus is promoted (Fig. 2.1) (Skoog & Miller, 1957). Not only the natural hormones, but also their synthetic forms can be used as growth regulators.

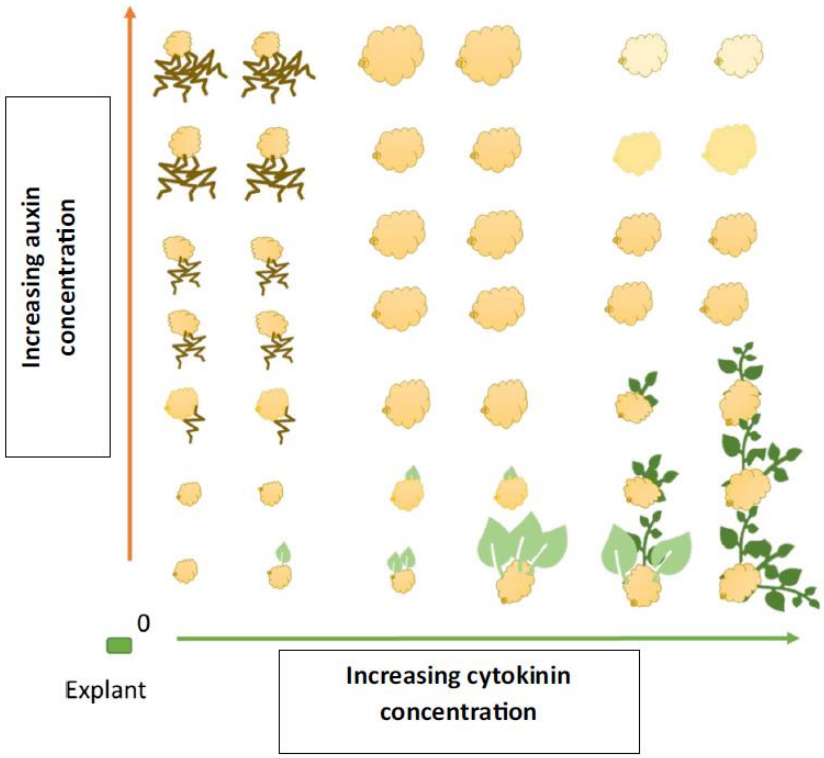


Figure 2.1: Illustration of the experiment conducted by Skoog & Miller, (1957) to show the effects of increasing concentrations of auxin and cytokinin on *Nicotiana tabacum* L. (tobacco) (Phillips & Garda, 2019).

The synthetic hormones, such as the synthetic auxins 2,4-dichlorophenoxyacetic acid (2,4-D) and picloram (PIC), have a higher potency in comparison to the natural hormone indole-3-acetic acid (IAA). Synthetic hormones such as cytokinin N6-benzyladenine (BA) can be cheaper and/or more stable than natural hormones. Gibberellic acid 3 (GA_3) is used to promote shoot elongation while its inhibitors, paclobutrazol (PBZ) and uniconazole (UNI) stimulate rooting in woody plants (Herman *et al.,* 2015).

2.1.2 Regeneration in sweet cherry

The *Prunus* genus includes species of high economic importance and, for this reason, research on *in vitro* regeneration and transformation of them is widespread. However, the majority of the *Prunus* species are recalcitrant in terms of their regeneration and transformation *in vitro*. In the literature there are several examples of successful protocols; those of note include apricot (*P. armeniaca* L.) (da Câmara Machado *et al.,* 1992), almond (*P. dulcis* Mill.) (Miguel & Oliveira, 1999), plum (*P. domestica* L.) (Mante *et al.,* 1991), and Japanese plum (*P. salicina*) (Tian *et al.,* 2007; Urtubia *et al.,* 2008). Sweet cherry (*Prunus avium*) is one of the most recalcitrant species along with peach (*Prunus persica*) (Song *et al.,* 2014). There are only a few examples of successful regeneration protocols from different types of explants in sweet cherry and they are summarised in Table 2.1.

Reference	Cultivar	Explant type	Basal media	Hormones	HEP*
Bhagwat & Lane, 2004	Lapins'	leaves from in vitro shoots	WPM	NAA + TDZ	71.40%
	Sweetheart'	leaves from in vitro shoots	WPM	NAA + TDZ	54%
Blando *et al.,* 2007	'Giorgia'	leaves from in vitro shoots	WPM	NAA + TDZ	25%
Canli & Tian, 2008	'Heidelfingen'	stored mature cotyledons	QL	IBA + TDZ	26.60%
	'Tehranivee'	stored mature cotyledons	QL	IBA + TDZ	23.30%
	'Sunburst'	stored mature cotyledons	QL	IBA + TDZ	53.30%
	'Vista'	stored mature cotyledons	QL	IBA + TDZ	70.00%
	'Vouge'	stored mature cotyledons	QL	IBA + TDZ	30%
Feeney *et al.* , 2007	'Bing'	callus from puntured shoots, stem section, shoot bases	WPM	BAP	100%
	'Lapis'	callus from puntured shoots, stem section, shoot bases	WPM	BAP	100%
	'Sweetheart'	callus from puntured shoots, stem section, shoot bases	WPM	BAP	100%
Matt & Jehle, 2005	'Giant Hardy Starking'	leaves and internode sections	DKW/WPM (1:1); QL	IBA + TDZ	8.3%; 27.8%
	'Kordia'	leaves and internode sections	DKW/WPM (1:1); QL	IBA + TDZ	11.1%; 25%
	'Regina'	leaves and internode sections	DKW/WPM (1:1); QL	IBA + TDZ	11.1%; 33.3%
	'Schneiders'	leaves and internode sections	DKW/WPM (1:1); QL	NAA/IBA + TDZ	16.7%; 50%
	'Sweetheart'	leaves and internode sections	DKW/WPM (1:1); QL	IBA + TDZ	10%; 41.7%
Tang *et al.,* 2002	'Burlat'	leaves from in vitro shoots	WPM	NAA + BAP	11.80%
	'Hedelfinger'	leaves from in vitro shoots	WPM	NAA + BAP	4.20%
	'Napoleon'	leaves from in vitro shoots	WPM	NAA + BAP	30.20%
	'Schneiders'	leaves from in vitro shoots	WPM	NAA + BAP	7.20%
Zong *et al.* , 2019	'Selah1'	leaves from in vitro shoots	WPM	IBA + TDZ	32.50%

Table 2.1: Summary of all the studies on sweet cherry (*Prunus avium* L.) regeneration. The higher efficiency percentage (HEP*) is reported. WPM: Woody Plant Medium (Lloyd and McCown 1980). DKW: Driver and Kuniyuki Woody plant medium (Driver and Kuniyuki 1984). QL: Quoirin and Lepoivre medium (Quoirin & Lepoivre, 1977). NAA: 1-naphthaleneacetic acid. IBA: indole-3-butyric acid. TDZ: thidiazuron. BAP: 6-benzylaminopurine.

Successful cherry transformation is even harder to accomplish. The transformation frequency reached by transforming 'Selah1's leaves was 1.2% (Zong *et al.,* 2019). When the explant used was Lapin and Bing's hypocotyls and epicotyls, the infection rate of *Agrobacterium tumefaciens*, after 7 days, was greater than 90% (Vergara *et al.,* 2021). However, the results shown are preliminary and the final transformation frequency was not indicated in this study.

The aim of this Chapter was to set up protocols for the propagation and regeneration using as explants, material from the varieties 'Merchant', 'Kordia' and 'Regina'. These three varieties, 'Regina' in particular, were used to conduct the field and transcriptomic experiments which are presented in Chapters 3 and 4. The final aim will be the transformation, using *Agrobacterium tumefaciens*, of this material kept in tissue culture, which will be sterile and controlled.

2.2 Materials and Methods

2.2.1 Plant material collection

All the plant material was collected from the cherry trees of the varieties 'Merchant', 'Kordia' and 'Regina' in the orchards at NIAB EMR (Kent) at different times of the year according to the type of explant. Mature cherry fruits were collected between the end of July ('Merchant' and 'Kordia') and the mid/end of August ('Regina') when the seed development was complete. Leaf material was collected between May and the end of June, while the sampling of shoots was conducted between December and February before bud dormancy was released. The shoots then were left in the cold store at 4°C for at least 4 weeks before being used.

2.2.2 Cherry stones extraction and cleaning

Open pollinated (O.P.) fruits were collected between the end of July and the first half of August 2019, according to the harvesting times of each variety ('Merchant' is the earliest while 'Regina' is the latest). Stones were divided from the fruit flesh, then they were washed with tap water to

remove the excess flesh. Thereafter, stones were left in a 1% pectinase solution (Sigma-Aldrich) overnight. Pectinase is an active pectolytic enzyme from *Aspergillus aculeatus* that hydrolyses pectin, which is one of the components of the plant cell wall. This step helps to clean further the flesh of the fruit from the stones, which has to be removed completely because it can be attacked by mould due to its high sugar content in the fruit flesh. The isolated stones were washed again with tap water to remove all the remaining flesh and to wash away the pectinase solution. The stones were then washed in a 10% bleach solution for 10 min to sterilise them and then rinsed in water before being left to dry completely. Sterile seeds were stored at 4°C until needed. In total, 926, 1551 and 1496 stones were collected from the varieties 'Merchant', 'Kordia' and 'Regina' respectively.

2.2.3 Embryo rescue

Stones were cracked to free the seed inside. Seed that were too shrivelled or empty were discarded. The sterilisation procedure was conducted in a laminar flow cabinet and consisted of soaking the seeds in 70% ethanol for 1 min, rinsing them with autoclaved distilled water and soaking them for at least 90 min on a shaker, in 10% Plant Preservative Mixture (PPM) solution. Seeds were then rinsed again and kept during all the time in autoclaved distilled water. The seed coat was removed, the embryo axis was excised from the cotyledons (see next paragraph) and placed in a vial, which contained the Embryo Rescue Medium (ERM). ERM was prepared using half-strength Murashige and Skoog (MS) salts supplemented with vitamins, 3.5%w/v sucrose, 0.5 mg/L IBA and 0.65%w/v agar. The pH was adjusted to 5.8. The ERM was autoclaved before being poured into the vials (10 ml ca.). The embryo rescue protocol used has been previously established at NIAB EMR (Lipska *et al.,* unpublished).

2.2.4 Shoot induction from cotyledons

The cotyledons excised during the embryo rescue procedure (see previous paragraph) were used as starting material for the shoot induction. Only the cotyledons that had a healthy appearance were used. A small portion of the distal area of the cotyledon was cut and discarded, while the remaining part was placed on the Shoot Induction Medium (SIM) with the adaxial sides up. The

SIM was prepared using full-strength Quoirin and Lepoivre salts (QL) supplemented with vitamins, 2.5%w/v sucrose, 0.51 mg/l IBA, 0.8 mg/l TDZ and 0.6%w/v agar. The pH was adjusted to 5.6. The SIM was autoclaved before being poured into sterile Petri dishes. For all the experiments, three biological replicates containing ten cotyledons each were made. The Petri dishes were covered with aluminium foil for 10 days at 23±1°C, before being left under direct light (light intensity: 68 umol m^{-2} s^{-1}; photoperiod: 16/8h light/dark). After about one month, the cluster of shoots and the clusters of buds were moved into jars containing Shoot Elongation Medium (SEM), which was prepared using full-strength Quoirin and Lepoivre salts (QL) supplemented with vitamins, 3%w/v sucrose, 0.1 mg/l IBA, 1.0 mg/l BAP and 0.6%w/v agar. The pH was adjusted to 5.6. The SEM was autoclaved before being poured into sterile autoclaved jars (50 ml ca.). After 4 weeks, the cluster of shoots or the single shoots were moved onto fresh SEM. This protocol was adjusted from the one reported by Canli *et al.,* (2008).

2.2.5 Forced explant preparation and propagation

The dormancy of the buds on the collected vernalized shoots was released to obtain forced shoots to propagate. Single shoots were put in tubes containing the Forcing Medium (FM). The bases of the shoots were first cut obliquely, to allow the flow of the FM from the base to the top. The FM was prepared using modified MS (half of the NH_4NO_3) with BAP 1.5 mg/L, IBA 0.01 mg/L, 0.1 mg/L GA_3, and 1% w/v sucrose. After adjusting the pH to 5.6 the medium was autoclaved before being used. The shoots were put in a growth chamber at 23±1°C and under direct light (light intensity: 68 umol m^{-2} s^{-1}; photoperiod: 16/8h light/dark) until the buds sprouted. Forced shoots were collected and the most external leaves and scales were removed. Then, the explants were sterilised by immersion in 10% v/v bleach solution for 10 minutes, followed by three washes with autoclaved distilled water for 5 minutes each. The shoots were then moved onto the Shoot Propagation Medium (SPM), which was prepared like the FM, but with 3% w/v sucrose and 0.6% w/v agar. The forced shoots were put in the growth chamber at 23±1°C and under direct light (light intensity: 68 umol m^{-2} s^{-1}; photoperiod: 16/8h light/dark).) and moved onto fresh PM every 30 days.

2.2.6 Callus induction from leaves

Young, light green leaves were collected from 'Merchant', 'Kordia' and 'Regina' trees in the orchard. They were cut in squares or rectangles of 0.5-2.0 cm side. Two washes with distilled water were done for 30 min each. Afterwards, they were sterilised with 10%v/v bleach and 0.01%v/v Tween20 solution on a shaker for 10 min, and then washed three times with autoclaved distilled water. Finally, a second round of sterilisation was conducted using 10% Plant Preservative Mixture (PPM) solution for one hour and half, followed by three washes with autoclaved distilled water. Leaves explants were put half with the adaxial side up, the other half with the abaxial side up, on the Callus Induction Medium (CIM), which was prepared using Woody Plant Medium (WPM) salts supplemented with vitamins, 3%w/v sucrose and 0.6%w/v agar. 2,4-D at different concentrations (0.05 – 0.5 – 5 mg/l) was added. The pH was adjusted to 5.6. The CIM was autoclaved before being poured into sterile Petri dishes. Explants were moved every four weeks onto fresh CIM.

2.2.7 Shoot induction from leaves

Expanded leaves with the midrib 1.5 – 2.0 cm long, were collected from the trees of all the three varieties in the orchard. Three washes with tap water were done for 60 min to remove the majority of the resin and other compounds from the external surface. Afterwards, they were sterilised with 10%v/v bleach and 0.01%v/v Tween20 solution on a shaker for 10 min and washed three times with autoclaved distilled water. Finally, a second round of sterilisation was conducted using 10% PPM solution for at least 90 min, followed by three washes with autoclaved distilled water. Four cuts, parallel to the midrib, were made before placing them on five different Shoot Regeneration Media (SRM) with the adaxial side up. All the SRM were prepared using the WPM salts supplemented with vitamins, 3%w/v sucrose and 0.6%w/v agar. The pH was adjusted to 5.6. The SRM was autoclaved before being poured in sterile autoclaved jars (50 ml ca.). Different hormones at different concentrations were added before autoclaving as reported in Table 2.2:

	IBA	NAA	2,4-D	BAP	TDZ
SRM1	1.0 mg/L			2.0 mg/L	
SRM2		0.1 mg/L			0.5 mg/L
SRM3	0.6 mg/L				1.0 mg/L
SRM4	0.5 mg/L				2.0 mg/L
SRM5			2.0 mg/L		2.0 mg/L

Table 2.2: Summary of the hormones used and their concentrations in the five Shoot Regeneration Media (SRM) tested. The red is used for auxins while the blue for cytokinins.

The jars were covered with aluminium foil for two weeks before being left under direct light (light intensity: 68 umol m^{-2} s^{-1}; photoperiod: 16/8h light/dark). Explants were moved onto fresh medium every 4 weeks. The protocol was adapted from Zong *et al.,* (2019).

2.2.8 Seed-derived shoots propagation

The shoots obtained from the embryo rescue and cotyledon induction (see paragraph5.2.2: Embryo rescue) were transferred to a Shoot Propagation Medium (SPM). This was prepared using the MS or QL salts (according to Zong *et al.*, 2019 and Canli *et al.,* 2008 respectively) supplemented with vitamins, 3% w/v sucrose, 0.1 mg/l IBA, 1.0 mg/l BAP and 0.6% w/v agar. The pH was adjusted to 5.6. The SEM was autoclaved before being poured in sterile autoclaved jars (50 ml ca.). Shoots were cut at node level, if present, increasing the number of segments to proliferate. They were transferred onto fresh medium every 8 weeks and left under direct light (16/8h light/dark photoperiod).

2.3 Results

2.3.1 Embryo rescue

The germination rate of the embryo axes was assessed four weeks after they were put on ERM. According to their appearance, the samples were divided into three categories:

- Emerging Leaves (Fig. 2.2): when the embryo axis had small leaves that were emerging at the level of the shoot apical meristem.
- Vigorous Phenotype (Fig. 2.3): with a vigorous growth or an obvious root development.
- No Changes: when the embryo axis had not shown any change from the initial state.

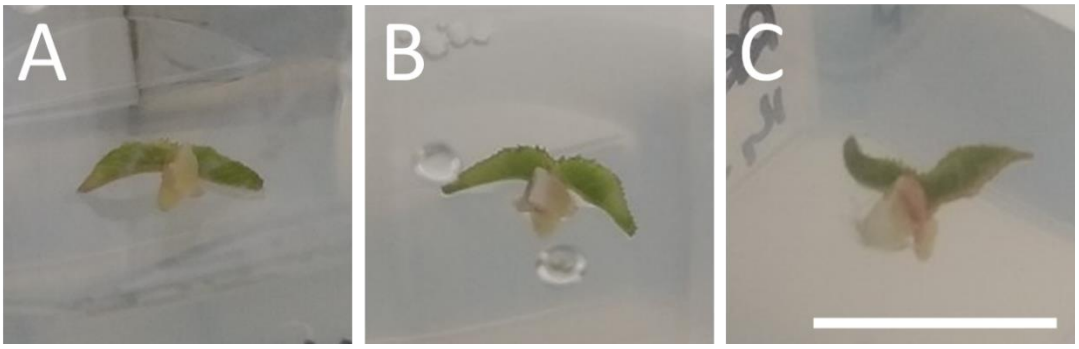


Figure 2.2: Embryo axes of 'Merchant' (A), 'Kordia' (B) and 'Regina' (C), after 4 weeks onto ERM, showing "Emerging Leaves" phenotype. Scale bar = 1 cm.

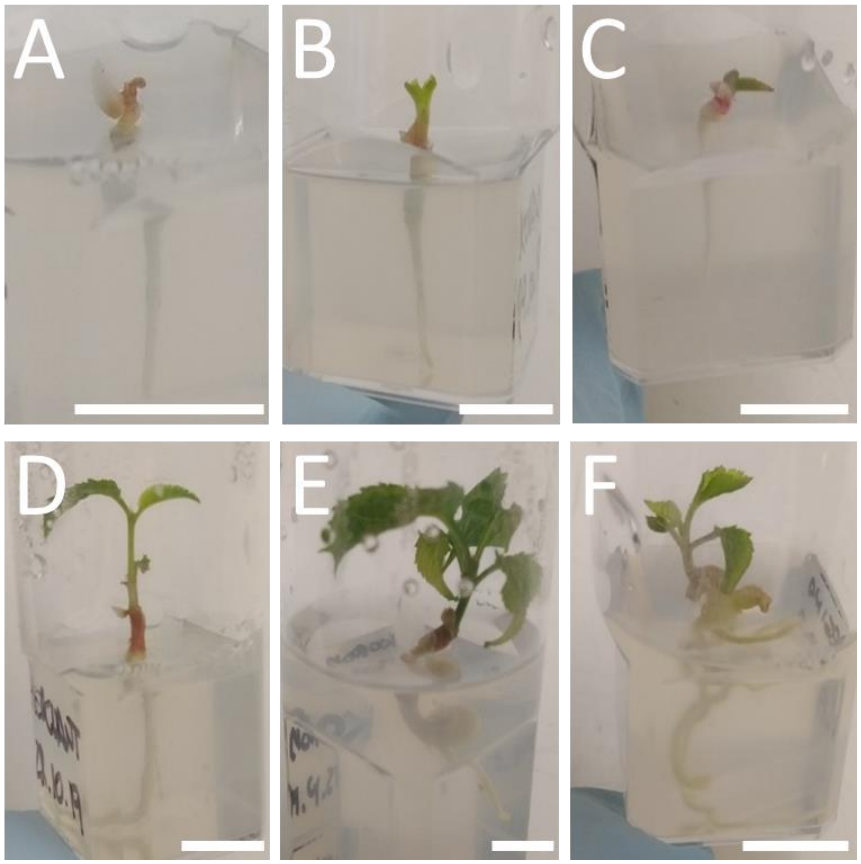


Figure 2.3: Embryo axes of 'Merchant' (A/D), 'Kordia' (B/E) and 'Regina' (C/F), after 4 weeks onto ERM, showing "Vigorous" phenotype. Scale bar = 1 cm.

Fig. 2.4 and Table 2.3 report the observations made on four replicates with 50 embryo axes each. In all the three varieties more than 50% of the embryo axes did not exhibit any change. The majority of the remaining embryo axes displayed an Emerging Leaves phenotype. No statistical difference was found between varieties, although 'Merchant' showed a higher percentage of axes with emerging leaves phenotype, and 'Regina' seemed the least responsive.

	'Merchant'			'Kordia'			'Regina'		
	Leaves	Vigorous	No Change	Leaves	Vigorous	No Change	Leaves	Vigorous	No Change
replicate 1	23 (46%)	0 (0%)	27 (54%)	9 (18%)	9 (18%)	32 (64%)	5 (10%)	1 (2%)	44 (88%)
replicate 2	14 (28%)	2 (4%)	34 (68%)	16 (32%)	7 (14%)	27 (54%)	17 (34%)	7 (14%)	26 (52%)
replicate 3	26 (52%)	2 (4%)	22 (44%)	17 (34%)	0 (0%)	33 (66%)	12 (24%)	2 (4%)	36 (72%)
replicate 4	17 (34%)	0 (0%)	33 (66%)	9 (18%)	0 (0%)	41 (82%)	7 (14%)	6 (12%)	37 (74%)

Table 2.3: Numbers of embryo axes showing the three different phenotypes identified for the four replicates after four weeks onto ERM. The percentages in brackets are calculated referring to the total number of embryo axes for each replicate (50).

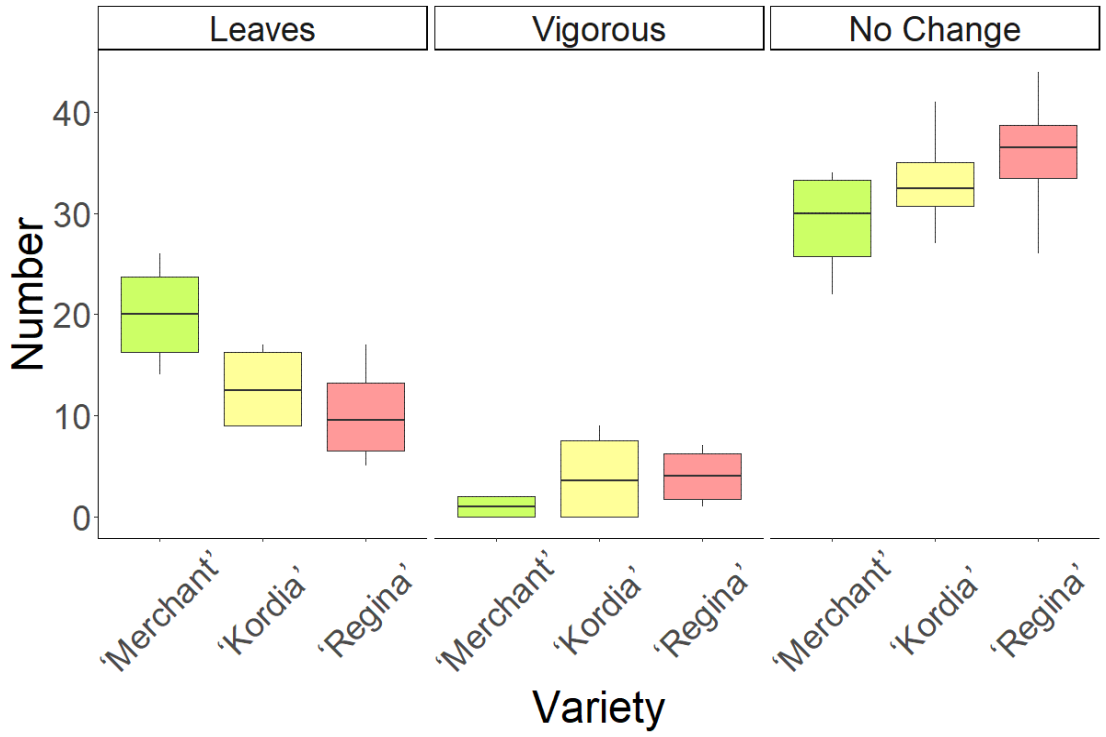


Figure 2.4: Boxplot of the three phenotypes observed in 'Merchant', 'Kordia' and 'Regina' embryo axes after being for four weeks onto ERM.

The 2-3 cm long shoots were moved onto Shoot Propagation Media (SPM) and sub-cultured onto fresh SPM every 8 weeks to give them time to grow (Fig. 2.5).

Figure 2.5: (A) 'Merchant', (B) 'Kordia' and (C) 'Regina' shoots onto SPM after six months. Scale bar = 5 cm.

2.3.2 Shoot induction from cotyledons

Shoot induction from cotyledons was observed after two weeks on SIM. 'Kordia' seemed the most responsive variety, although no significant difference was observed between the three varieties (Fig. 2.6; Table 2.4). As with the shoots obtained from the embryo axes, the ones induced from the cotyledons were put onto SPM and sub-cultured every 8 weeks (Fig. 2.7).

	'Merchant'	'Kordia'	'Regina'
replicate 1	0 (0%)	5 (16.67%)	1 (3.33%)
replicate 2	5 (16.67%)	10 (33.33%)	2 (6.67%)
replicate 3	5 (16.67%)	13 (43.33%)	4 (13.33%)
replicate 4	4 (13.33%)	10 (33.33%)	5 (16.67%)

Table 2.4: Numbers of shoot induced from the cotyledons of 'Merchant', 'Kordia' and 'Regina' onto SIM after two weeks. The percentages in brackets are calculated referring to the total number of cotyledons for each replicate (30).

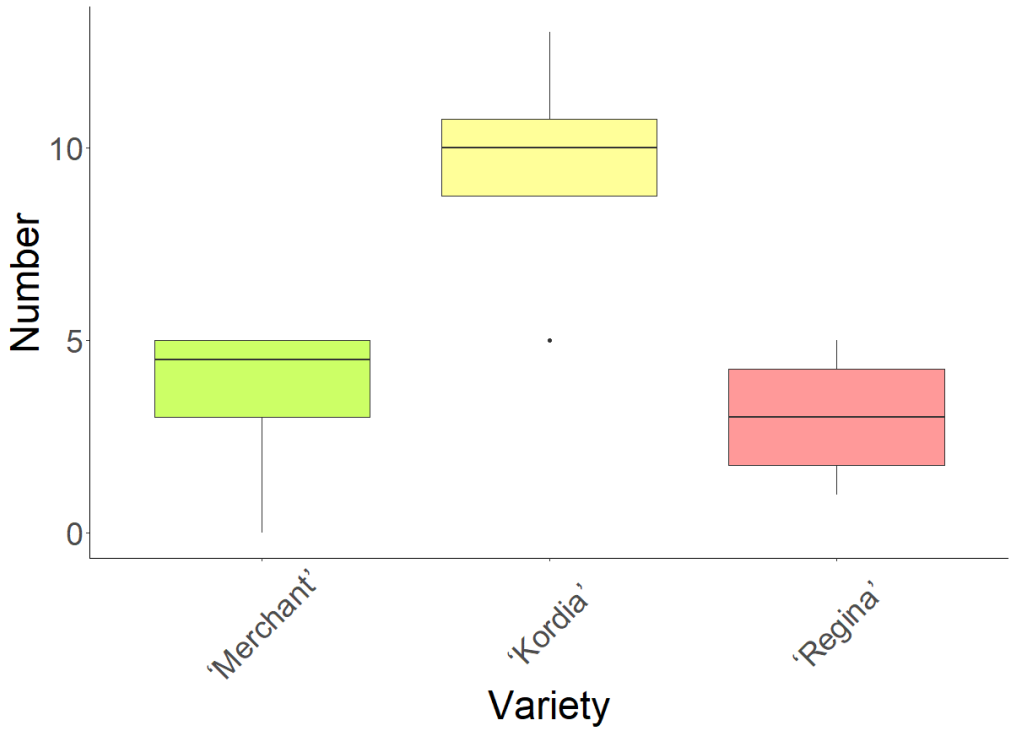


Figure 2.6: Boxplot of the shoot induced from cotyledons of 'Merchant', 'Kordia' and 'Regina' after being for two weeks onto SIM.

Figure 2.7: (A) 'Merchant', (B) 'Kordia' and (C) 'Regina' cotyledon-derived shoots onto SPM after six months. Scale bar = 5 cm.

2.3.3 Callus induction

After 2.5 weeks onto CIM, leaf explants presented callus formation in particular in the areas around the veins and the midrib (Fig. 2.8). No difference was observed between the explants with the abaxial or the adaxial surface directly in contact with the medium, or with the callus induction efficiency between the three different 2,4-D concentrations (Fig. 2.8; Table 2.5).

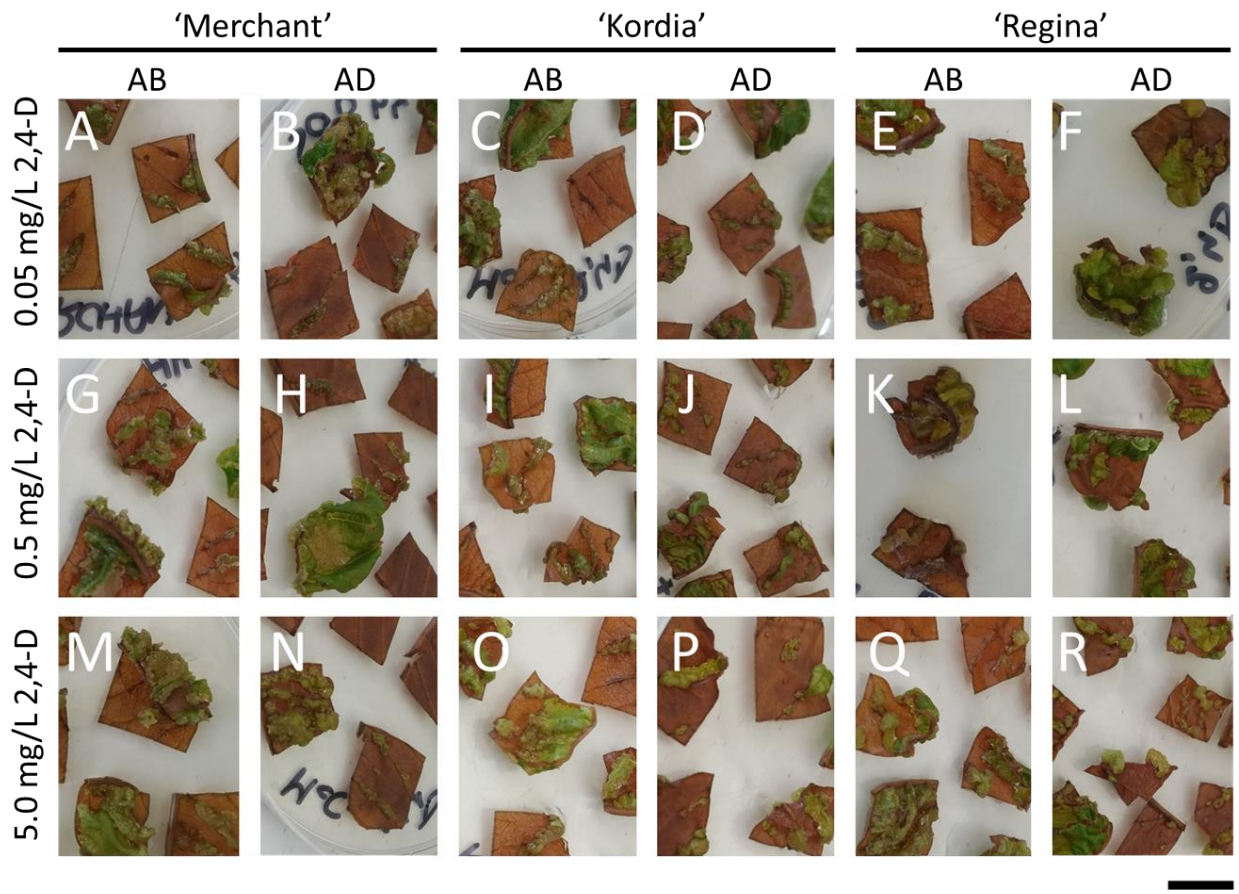


Figure 2.8: Leaf explants of 'Merchant', 'Kordia' and 'Regina' onto CIM at three different concentrations of 2,4-D (0.05, 0.5 and 5.0 mg/L) after 2.5 weeks. AB: abaxial. AD: adaxial. Scale bar: 1 cm.

2,4-D (mg/L)	Lamina side	'Merchant'	'Kordia'	'Regina'
0.05	AB	9/10	10/13	13/13
	AD	10/12	13/13	13/13
0.5	AB	8/12	10/12	12/12
	AD	6/12	12/13	12/12
5.0	AB	9/12	12/13	11/11
	AD	5/12	13/14	12/14

Table 2.5: Number of Calli on leaf explants of 'Merchant', 'Kordia' and 'Regina' after 2.5 weeks on CIM at three different concentrations of 2,4-D (0.05, 0.5 and 5.0 mg/L). AB: abaxial. AD: adaxial.

Once moved onto the SRM, the 2,4-D induced calli grew and became bigger; however, none of them produced any shoots. The calli induced by the CIM with 2,4-D 5 mg/L, seemed more responsive to the SRM (Fig. 2.9). However, callus proliferation and changing colour into dark brown were the only events observed (Fig. 2.9B;D;F).

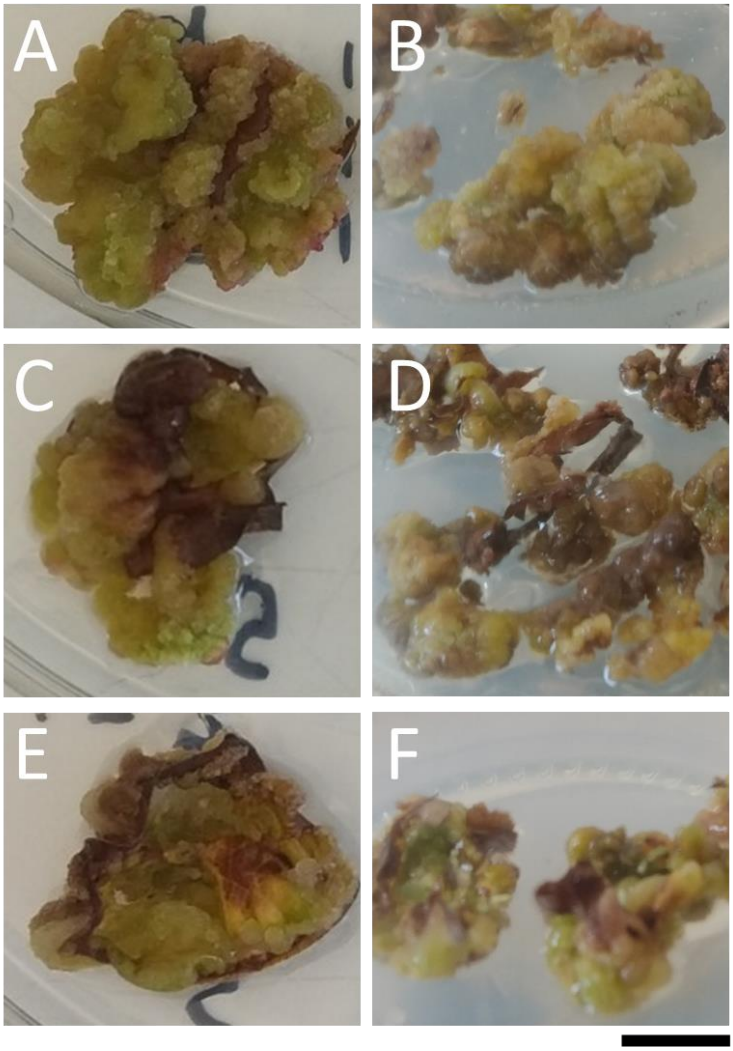


Figure 2.9: 2,4-D induced calli of 'Merchant' (A-B), 'Kordia' (C-D) and 'Regina' (E-F) onto SRM4 medium. Photos were taken after 10 days under light after two weeks of darkness (A/C/E) and after 44 days under light (B/D/F). Scale bar = 1 cm.

A similar result was obtained when small leaves were put directly onto the different five SRM. Fig. 2.10A-C shows the aspect of the leaves after two weeks in dark condition on SRM. As with the leaf explants on medium containing only 2,4-D, the formation of calli started at the level of the veins and midrib (Fig. 2.10A-C). After two months on shoot regeneration media, the calli became bigger; however, no shoot regeneration was observed (Fig. 2.10D-F).

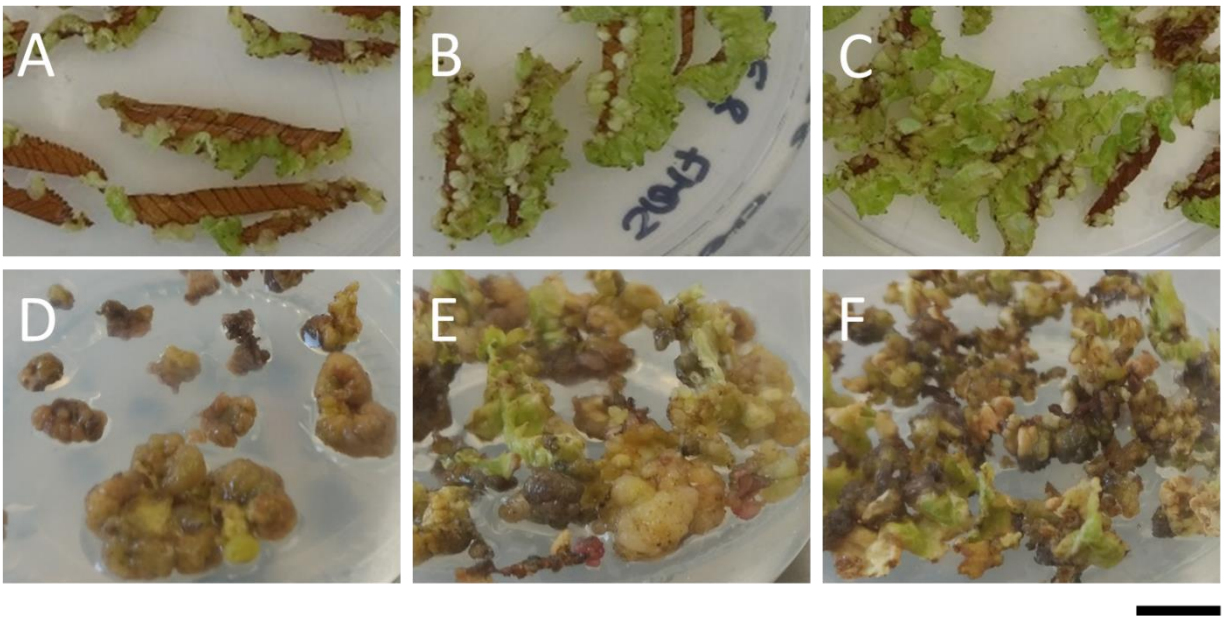


Figure 2.10: Photos of 'Merchant' (A), 'Kordia' (B) and 'Regina' (C) leaves after being for two weeks onto SRM7 in darkness, and of 'Merchant' (D), 'Kordia' (E) and 'Regina' (F) induced calli, onto SRM7 for two months. Scale bar = 1 cm.

2.3.4 Forced shoots

About 30-40% of the shoots were lost because of bacterial and/or mildew contaminations. After three weeks, the forced shoots moved onto SPM thrived (Fig. 2.11). Unfortunately, they all started to die at the same time after about four months. The leaves turned brown and abscised, and the shoots started to release compounds in the medium that turned brown from whitish. Sub-culturing the shoots did not stop this phenomenon and the same occurred when the experiment was repeated.

Figure 2.11: Forced shoots of 'Merchant' (A), 'Kordia' (B) and 'Regina' (C) after 50 days onto SPM. Scale bar = 1 cm.

2.4 Discussion

The manipulation *in vitro* of woody plants can be challenging and *Prunus avium* is one of the most recalcitrant species. First, the explant sampling presents immediate limitations. According to the explant type, only specific temporal windows are suitable. For example, the collection of shoots had to be done in winter when bud dormancy was established. Second, the sterilisation phase is crucial. Indeed, the approach used was aggressive, considering that the explants came from an orchard, which is definitely not an aseptic environment, but not too aggressive to kill the explants. Thus, great losses of plant material occurred, although the use of bleach, 10% for 10 minutes, showed good results. Finally, sweet cherry takes a significant amount of time to regenerate, and the efficiency is not high.

The results shown in this chapter are not exhaustive; however they represent a good foundation for the optimization of the regeneration and possibly transformation protocols in 'Merchant', 'Kordia' and 'Regina'. The protocol described by Matt & Jehle (2005) for 'Kordia', and 'Regina' was tested as well; however the high frequency of contamination and the complete absence of regeneration, resulted in the search for an alternative approach to achieve the objective. In fact, other attempts were done in addition to the ones reported; however all of them were completely unsuccessful. For example, all the approaches with leaf buds were not successful, due to also the high contamination rate observed already within the first days in tissue culture. Big green leaves

(1 month old), were tested as well, without any positive results. Neither the addition of FeEDDHA to the SPM helped the forced shoots which wilted, slower (a couple of weeks) than those on SPM without FeEDDHA, but still not able to propagate.The approaches reported are the ones that are the most promising, as mentioned above.

The embryo rescue protocol set up by Lipska *et al.,* (unpublished) at NIAB EMR, worked for the three sweet cherry varieties used, with a 20-40% efficiency (calculated considering only the Emerging leaves phenotype). This result is interesting considering that increasing auxin concentrations should promote root and not shoot development (Skoog & Miller, 1957). The embryo axes with vigorous phenotype developed a remarkably large root or even multiple roots (Fig. 2.3). The development of the shoot may be due to the fact that the plant material is not a callus, so undifferentiated and clustered cells, but embryo axes. Indeed, other examples in literature of embryo rescue done in other species such as *Vitis vinifera* reported the used of different phytohormones like IBA, NAA, IAA (auxins), GA_3 (gibberellins), BAP (cytokinin) and Abscisic acid (ABA) (Li *et al.,* 2015). In sweet cherry, 0.5 mg/L IBA in half-strength Murashige and Skoog (MS) medium is sufficient to promote shoot development.

In this study, it has been shown that the protocol set up by Canli *et al.* (2008), using mature cotyledons as plant material to induce shoot regeneration, works also for 'Merchant', 'Kordia' and 'Regina'. These three varieties were not included in the cited study (Table 2.1). 'Kordia' was the most responsive variety with a regeneration efficiency of 31.65% while the efficiency of regeneration in 'Regina' and 'Merchant' is less than observed in 'Kordia' (10% and 11.67% respectively). Shoots induced from cotyledons could be a good source of plant material to use for further experiments such as transformation; however, the ploidy of those shoots must be checked first. In fact, nuclei endoreplication may occur in the cotyledons cells which may originate tetraploid or octoploid shoots (Ellul *et al.,* 2003; Han *et al.,* 2004). These seed-derived shoots however present a limitation: they are the result of sexual reproduction, and since the majority of the cherry varieties are self-incompatible, it means that the genome of the mother is crossed with the genome of a different variety. This is not a disadvantage per se, but it may be

when the pure breed variety needs to be transformed. For this reason, shoot regeneration and propagation was attempted from vegetative tissues such as leaves and leaf buds. The forced shoots protocol shared by Dr Cristian Silvestri from the TUSCIA University (Viterbo, Italy; personal communication) in the first phases, was really promising. However, the forced shoots died after three months, not allowing the establishment of an *in vitro* population. Further studies will be needed to optimise the protocol to overcome the phenomenon and allow the shoots not only to survive but to proliferate. However, this protocol will still be useful to obtain leaves material to use for the regeneration and transformation protocol. The media used for shoot regeneration from leaves, reported in Zong *et al.* (2019), were tested but none of them was able to induce the formation of shoots from the leaf explants. Callus formation and development was observed, but it did not originate any shoots. Callus induction occurred also when the leaves were placed onto basal medium containing 2,4-D as growth regulator. In both cases, callus formation started from areas close to the ribs, confirming what was observed in sweet cherry by Zong *et al.* (2019), Bhagwat & Lane (2004) and Tang *et al.* (2002) and in sour cherry by Song & Sink (2005). These observations suggest at the level of the midrib and ribs there are some cells that can be induced and stimulated to proliferate and form a callus. The calli obtained by 2,4-D induction were moved onto the different SRM to assess if they were able to generate shoots but this attempt was also unsuccessful. The calli became bigger but did not develop any shoots.

Finally, although regeneration has not been achieved, the results shown in this study expand the knowledge already present in the literature about *in vitro* tissue culture in sweet cherry and can be the base of further works.

Chapter 3: Induced parthenocarpy in sweet cherry (*Prunus avium* L.) by GA_3 application

3.1 Introduction

3.1.1 Flower and fruit structure

The sweet cherry flower is hermaphroditic, meaning that both female and male reproductive organs are present. In fact, several stamens surround the single central pistil; stamens are the male reproductive organs, and they consist of anthers, where the pollen develops, on top of stalk-like filaments, the function of which is to allow nutrients and water to reach the anthers from the mother plant and to facilitate pollen dispersal (Scott *et al.,* 2004). The pistil or gynoecium is the female reproductive organ, which occupies the centre of the flower. In the external flower whorls, there are five white petals and five green sepals (Fig. 3.1). The majority of the sweet cherry cultivars are self-incompatible. Self-incompatibility (SI) of the inhibition of pollen tube growth, and this is controlled genetically by multiple allelic *S*-loci (Crane and Lawrence, 1929; Crane and Brown, 1937).

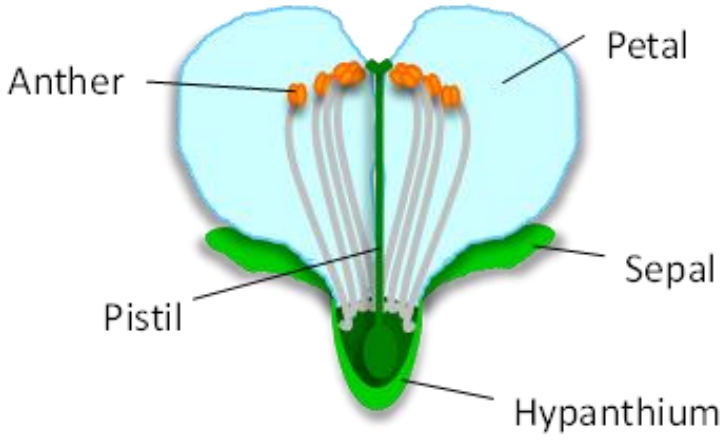


Figure 3.1: Schematic representation of sweet cherry flower.

Pollination success depends on both abiotic and biotic factors, and for this reason it often varies among years. Specifically, sweet cherries are insect pollinated with honeybees being the only pollinators reported to date (Godini *et al.*, 1998). Moreover, climatic conditions during anthesis have to be taken into consideration because a cloudy and rainy spring may reduce pollination success (Hedhly *et al.,* 2009).

After pollination and fertilisation occur, the pistil undergoes a series of changes that lead to the formation of the fruit. The sweet cherry fruit is a drupe, an indehiscent fruit of 1-2 cm in diameter (in some cultivars the diameter can be larger), that has an attractive appearance, due to its colour (often bright red to dark purple depending on the cultivar), and desirable intense flavour. Three parts can be identified in a drupe: the outer epicarp, or skin, the mesocarp that is the fleshy part of the fruit and a single central stone that is the lignified endocarp that surrounds the seed (Fig. 3.2).

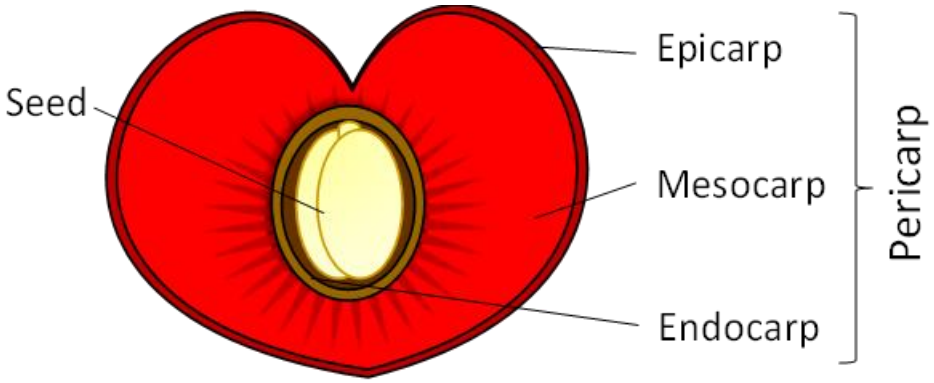


Figure 3.2: Schematic representation of the sweet cherry fruit (drupe).

3.1.2 Fruit development

Drupe development rate growth can be described by a double sigmoid curve, where three well marked stages can be identified (Fig. 3.3) (O Lilleland, 1933; O Lilleland, 1935; Tukey, 1934) The first period (stage I) is characterised by rapid development of the fruit tissues after fertilisation and it is followed by a period of delayed development (stage II). During the third and last period (stage III) the fruit develops rapidly to ripening.

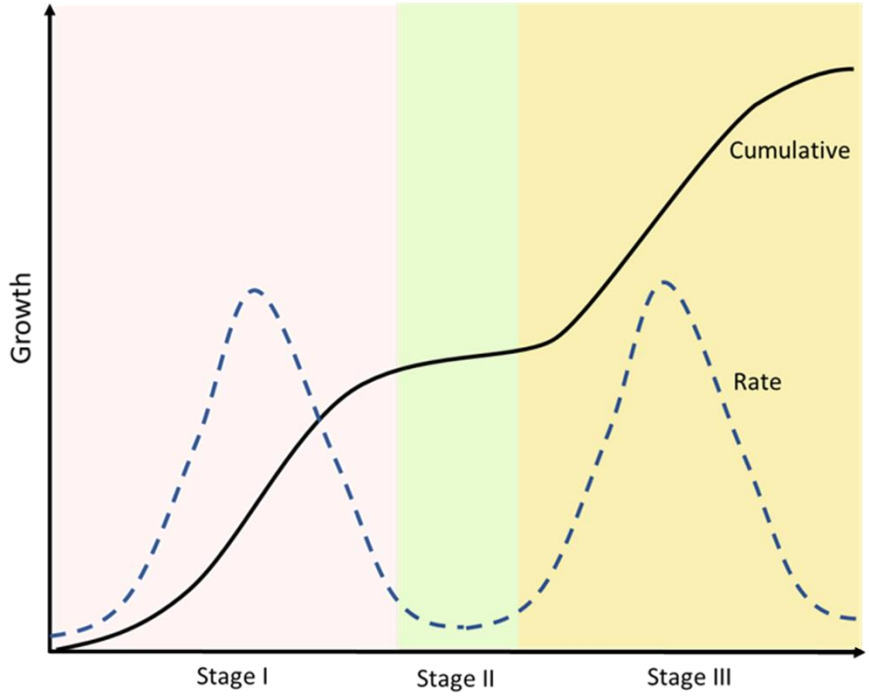


Figure 3.3: A double sigmoid growth curve representation. Cumulative and rate of growth are defined. After an initial exponential phase (Stage I) a second plateau phase occurs (Stage II), which is followed then by a second exponential phase (Stage III) until the complete ripening of the fruit. Developmental phases are allocated with respect to peaks and troughs in growth rate. Vignati *et al.,* 2022a.

Cherry varieties can be divided in early, mid and late ripening and all of them have a growth rate divided in these three stages. The duration of the stage I is very similar in all the varieties and is independent of the rate of growth and the size reached by the fruit during this period, while the duration of stage II is directly correlated with the rate of fruit ripening, being shorter in the earlier ripening varieties and longer in the later ones. Stage III continues till the fruit is ripe (Tukey *et al.,* 1934).

3.1.3 Epicarp development

The outer epidermis of the developing cherry fruit is constituted by a single row of cells that are covered externally by a cuticle, which is interrupted only by the presence of stomata (Fig. 3.4). During the pre-bloom period, the cells of the epidermis are already well differentiated, with an elongated shape and no hairs, and increase their size slowly, mainly in the radial direction (Fig. 3.4A). The mitotic activity is low since the increase of the number of cells is very low, while it is high during the first half of the stage I (Fig. 3.4B-D). The second half of stage I is characterised by an increase of cell size, both radially and tangentially. Moreover, during the second half of stage I the cuticle reaches its full thickness (Fig. 3.4D-E). No cell division is observed during stage II, which is characterised by slight tangential elongation of the cells and additional cell wall thickening (Fig. 3.4F-G). Lastly, during the last phase (stage III), a more than two-fold tangential enlargement of the cells occurs, with a decrease of the radial diameter and cuticle thickness, in order to accompany the large increase of the fruit surface area (Fig. 3.4G-I).

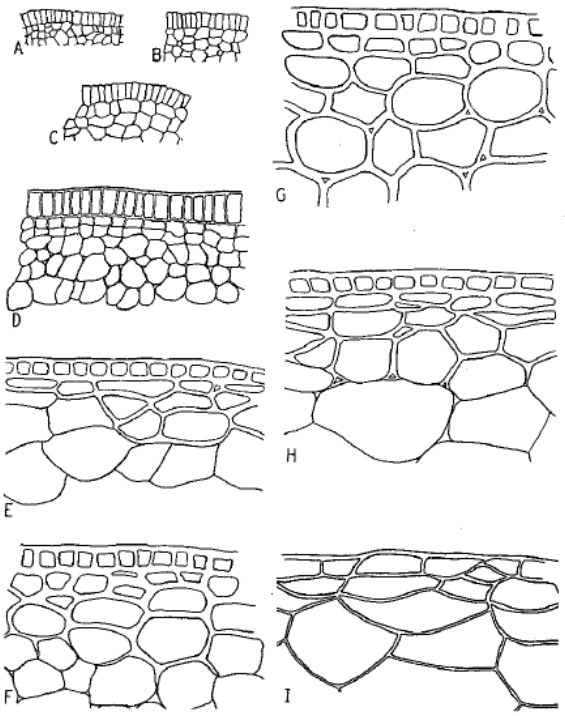


Figure 3.4: Camera lucida drawings of transverse sections x 163 showing epicarp and hypodermal layer development, 18 days before full bloom (A), 6 before full bloom (B), full bloom (C), 11 days after full bloom (D), 20 days after full bloom (E), 26 days after full bloom (F), 36 days after full bloom (G), 40 days after full bloom (H), fruit ripening, 57 days after fruit ripening (I). Adapted from Tukey and Young 1939.

Stomata are not uniformly distributed over the surface of the epicarp, being numerous near the apex and few near the stem end. The full differentiation of stomata can be found already during the pre-bloom period and the guard cells increase in size as the fruit develops, but at a lower rate than the epidermal cells. In the ripe fruit, the cells of the epidermis have a bright red colour due to the presence of the chromoplasts which are absent in the guard cells and in the cells that are immediately adjacent, developing a yellowish, straw-colour (Tukey & Young, 1939).

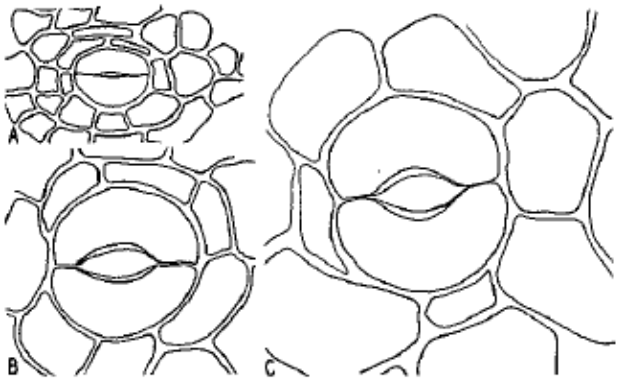


Figure 3.5: Camera lucida drawings of transverse sections x 480 showing stomatal guard cells and surrounding epidermal cells development at 18 days before full bloom (A), 20 days after full bloom (B) and at fruit ripening, 57 days after full bloom (C). Adapted Tukey *et al.,* 1939.

3.1.4 Fleshy mesocarp development

During the pre-bloom period the fleshy mesocarp is composed of almost isodiametric parenchymatous cells, which elongate according to a gradient tangentially to slight radially from the epidermis to the stony endocarp, respectively (Fig. 3.6A-B). The increase of tissue thickness, more than double, is due mostly to cell division. The first half of stage I is characterised by mitotic division of the cells, comprising an increase of about 20-30% in the number of cells from the epidermis to the stone, and no further divisions are observed after completion of this stage. The cells increase their diameter more than fourfold, mostly during the second half of stage I. Moreover, the differentiation of a hypodermal layer five or six cells thick, just under the epidermis, involves considerable thickening of the cells. The cells reach a little greater size than those of the epidermis and become tangentially elongated (Fig. 3.6C-E). On the other side, adjacent to the stone, a layer of small isodiametric cells, three or four cells wide, differentiates during the second half of the stage I (Fig. 3.6E-G). During stage II, some cell enlargement, less than 6%, occurs and intercellular spaces remain prominent. The cells just under the epidermis continue slowly to elongate tangentially, while limited cell division can be found in the thin layer of small cells adjacent to the stone; in other locations there is none. Stage III is also called “the final swell” (Fig. 3.6G-I) and during this period four parts of the fleshy mesocarp can be recognized (from the epidermis to the stony endocarp):

1. the hypodermal layer of collenchyma

2. the peripheral layer of thin-walled parenchyma, extending to a line just inside the ring of vascular bundles

3. the layer of radially elongated cells extending from this line nearly to the stone

4. The thin layer of small cells adjacent to the stone.

The transition from one part to the other is not precise, since there is a gradual transition from a tissue in which one cell type predominates to that in which another one is dominant. A gradient of cell elongation can be identified, from tangential in the hypodermal cells to radial in the ones close to the stone. The rapid enlargement of cells brings a decrease of the thickness of the cell walls and leads to the disappearance of the intercellular spaces that now are difficult to find (Tukey & Young, 1939).

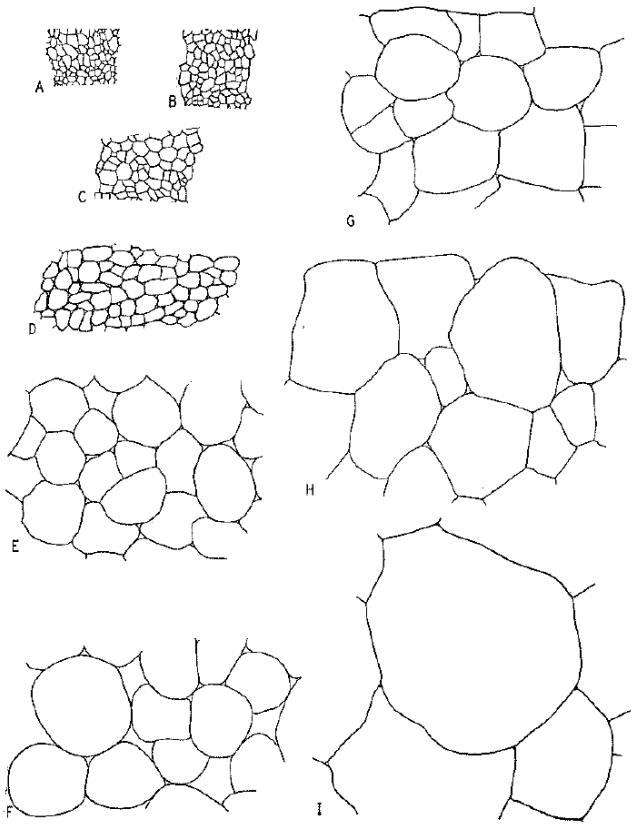


Figure 3.6: Camera lucida drawings of transverse sections x 163 showing fleshy mesocarp development, in region between hypodermal layer and ring of vascular bundles, at 18 days before full bloom (A), 6 days before bloom (B), full bloom (C), 11 days after full bloom (D), 20 days after full bloom (E), 26 days after full bloom (F), 36 days after full bloom (G), 40 days after full bloom (H) and fruit ripening, 57 days after full bloom (I). Adapted from Tuckey and Young 1939.

3.1.5 Development of the vasculature

The ventral and the dorsal capillary bundles do not go inside the stony endocarp, while the two bundles that supply the two ovules (in peach called “funicular bundles”), are at either side of the ventral suture and adjacent to the ovarian cavity. Pit bundles traversing the stony endocarp are not found in cherry, as instead it happens in peach. During the pre-bloom period the differentiation of a ring of vascular bundles, extending through the fleshy mesocarp, parallel to the central axis, occurs. However, the walls of xylem elements do not become sufficiently thickened to become conspicuous until about the full-bloom period. The number of bundles is fixed, so as the fruit develops the vasculature system extends progressively throughout the flesh, mostly by transverse divergence of small bundles from the main ones. At maturity a skeleton network of conductive tissue is formed (Fig 3.7) (Tukey & Young, 1939).

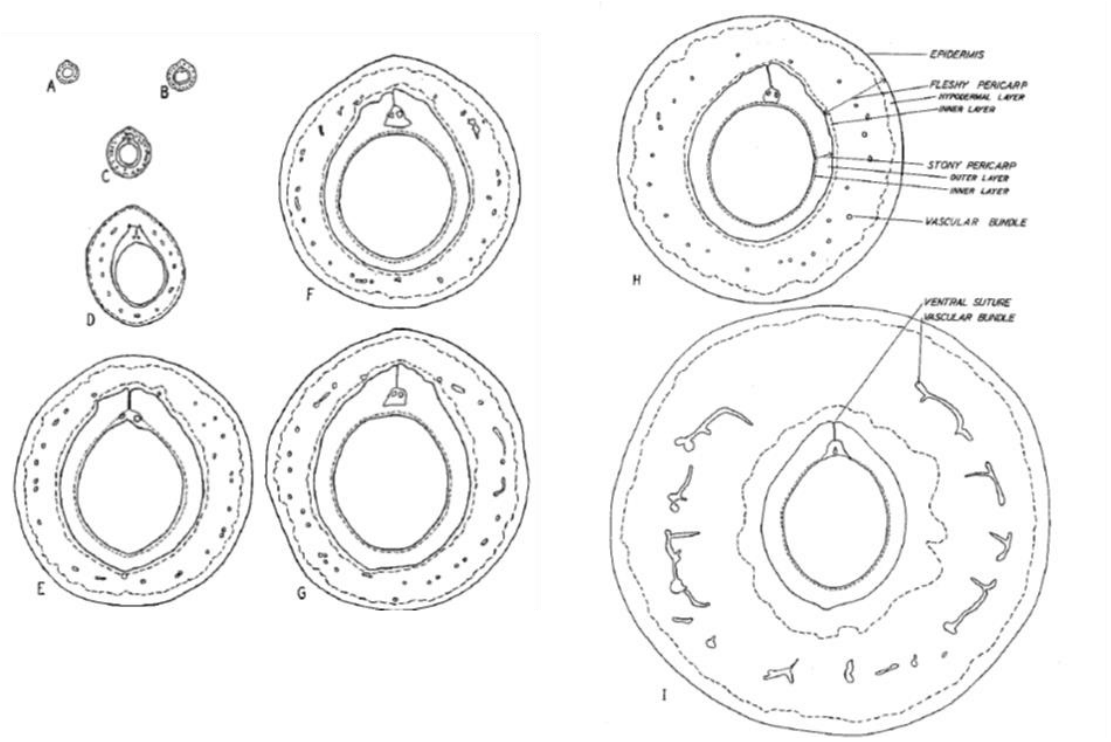


Figure 3.7: Development of the cherry fruit seen in transverse sections at 18 days before full bloom (A), 6 days before bloom (B), full bloom (C), 11 days after full bloom (D), 20 days after full bloom (E), 26 days after full bloom (F), 36 days after full bloom (G), 40 days after full bloom (H) and fruit ripening, 57 days after full bloom (I). Adapted from Tuckey and Young 1939.

3.1.6 Stony endocarp development

The innermost ovary wall comprises a single layer of cells, called the inner epidermis, and three or four layers of pericarp cells (Fig. 3.8A). These cells, which are destined to become part of the stony endocarp, are smaller than the other cells that are going to become the fleshy mesocarp, and this size difference persists to maturity. During the pre-bloom period, the inner epidermal cells elongate tangentially and divide transversally just before full bloom, to form with few adjacent pericarp cells, which have similar orientation and shape, a “hoop” that surrounds the ovary cavity (Fig. 3.8 B-C). The presence of this hoop is also reported in other species (Farmer, 1889; Winton, 1904). The group of cells that differentiate in the stony endocarp, does not give rise to the fleshy mesocarp and vice versa. Stage I is characterised by a large increase in both number and size of the inner layer cells (tangential elongation) and the outer layer cells (central radial elongation). No cell divisions are observed in the inner layer during the second half of stage I, while there is a greater increase of mitotic divisions and cell size in the outer layer. Cell walls become progressively thicker but do not harden significantly until the end of this stage, when the pit cannot be sectioned without special treatment (Fig. 3.8C-E). Thickening and hardening of the cell walls are the main events that occur during stage II, and no cell divisions are observed after the mid-point of this stage. Hardening does not occur uniformly in the stony endocarp, but begins near the apical end, at the hilum, and goes on downwards towards the chalaza, before including the whole endocarp at maturity. Although lignification occurs, cells are living and nuclei are abundant, even though the cellular lumen is frequently scarcely larger than the nucleus. At the end of stage II, the stony endocarp comprises 26-27 layers of very thick-walled lignified cells. This number of layers is the same as that present in the fleshy mesocarp, although the thickness is much less due to the very different destinies of the two tissues (Fig. 3.8E-G). During stage III there is a slight increase in hardness and brittleness, associated with a loss of moisture. It is possible to find occasional living cells with active nuclei (Fig. 3.8G-I) (Tukey & Young, 1939).

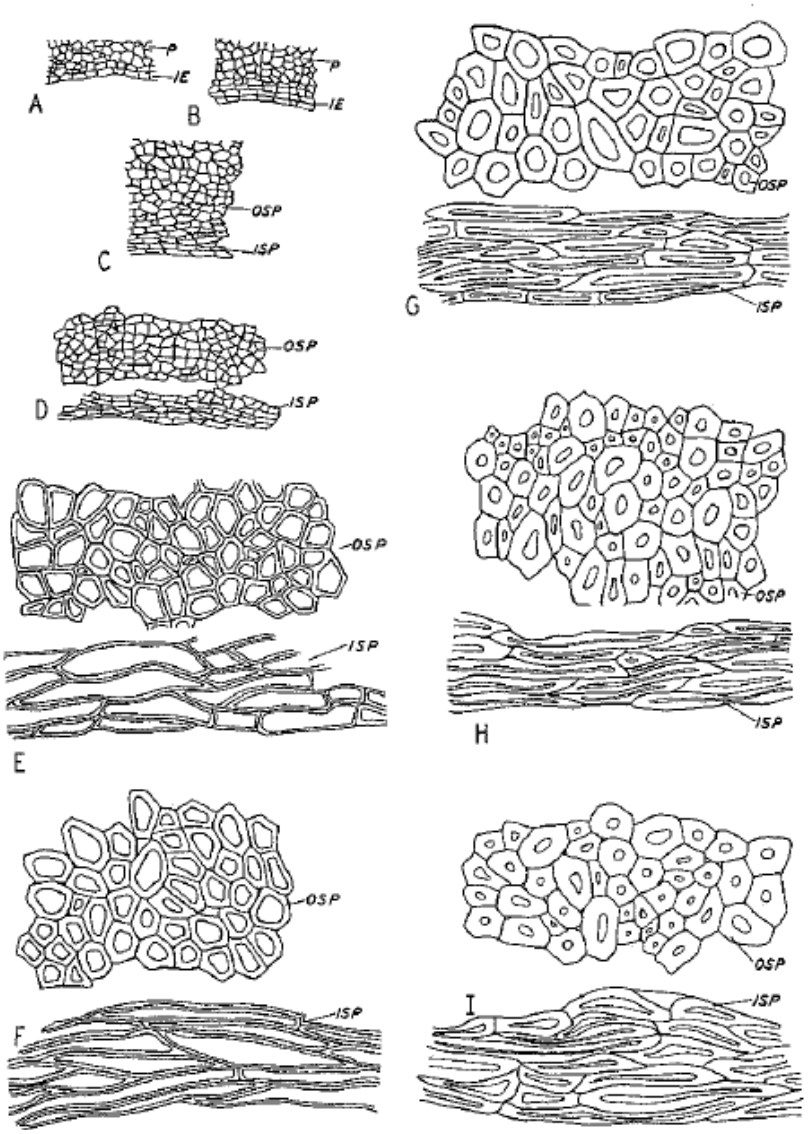


Figure 3.8: Camera lucida drawings of transverse sections x 163 showing stony endocarp development at 18 days before full bloom (A), 6 days before bloom (B), full bloom (C), 11 days after full bloom (D), 20 days after full bloom (E), 26 days after full bloom (F), 36 days after full bloom (G), 40 days after full bloom (H) and fruit ripening, 57 days after full bloom (I). p, pericarp; ie, inner epidermis; osp, outer stony pericarp (endocarp). Adapted from Tuckey and Young 1939.

3.1.7 Parthenocarpy and phytohormones

The production of a seeded fruit is not the only option that can be found in plants. Indeed, some plants can produce seedless fruits and one way is through parthenocarpy. Parthenocarpy (from Greek, “Virgin Fruit”) consists of the development of a fruit without the fertilisation of the ovule, which will develop into the seed. Parthenocarpy can be natural or induced artificially (Gustafson 1942). There are several examples of natural parthenocarpic fruits that can be found in horticultural crops such as tomato, pepper, cucumber, grapes, banana, oranges, pineapple, blackberry, kiwi, figs, etc. (Srivastava, 2002). Parthenocarpy is not only commercially interesting (seedless fruits are becoming more and more popular and preferred by consumers, and there is also a significant financial saving from the reduced cost of processing), but it is also a tool to study fruit development.

Parthenocarpy has a strong connection with phytohormones. Indeed, there are examples, such as in cucumber (*Cucumis sativus*) and fig (*Ficus carica* L.), where the ovaries that start fruit set through parthenocarpy, have a higher content of some endogenous phytohormones (Li *et al.,* 2014, Chai *et al.,* 2017, Su *et al.,* 2021).

Phytohormones have been one of the first tools used to study parthenocarpy and to produce parthenocarpic fruits. Indeed, the first published examples of exogenous application of phytohormones to pistils and developing fruits date back to the 1930s. Auxin was the first hormone identified, able to induce the parthenocarpic fruit development in citrus (Gustafson, 1939). Thereafter, this result has been confirmed in many other crops, using both natural and synthetic auxins such as 2,4-dicholophenoxyacetic acid (2,4-D) and naphthaleneacetic acid (NAA); for example in strawberry (Kang *et al.,* 2013; Nitsch, 1950), pear (Cong *et al.,* 2018), tomato (Serrani *et al.,* 2007a), cucumber (Wu *et al.,* 2016, Qian *et al.,* 2018), sweet chilli pepper (*Capsicum annuum* L.) (Kondo *et al.,* 2021), okra (Hossain *et al.,* 2021) and grape (Lu *et al.,* 2016). Auxin functions by promoting cell division, as observed in strawberry (Kang *et al.,* 2013). After auxin, gibberellins (GAs) have been used to induce parthenocarpic fruit development. GAs consist of a group of terpenoid molecules that control and regulate the development of vegetative and reproductive organs (Hedden *et al.,* 2012, Hedden *et al.,* 2016). In particular, GAs seem to play a

crucial role during fruit development, being positive modulators of several fruit-related features (Zang *et al.,* 2016, Garmendia *et al.,* 2019); the first examples reported in literature are in rose and apples (Davison, 1960; Prosser & Jackson, 1959). GA_1, GA_3, GA_4 and GA_7 are the bioactive GAs (Salazar-Cerezo *et al.,* 2018). However, not all the active GAs can induce parthenocarpy in all crops. For example, exogenous application of GA_3 can induce parthenocarpic fruit development in custard apple (dos Santos *et al.,* 2016), apple ("Honeycrisp" cultivar) (Galimba *et al.,* 2019), grape (Lu *et al.,* 1997, Or *et al.,* 2020), tomato (Gultom *et al.,* 2018), citrus (Mesejo *et al.,* 2016), loquat (Mesejo *et al.,* 2010, Reig *et al.,* 2011), and persimmon ("Rojo Brilliante") (Reig *et al.,* 2018). However, this does not occur in cucumber, for example, where GA_{4+7} application was needed (Qian *et al.,* 2018). The GA_{4+7} combination can also induce parthenocarpy in pear (Niu *et al.,* 2015, Liu *et al.,* 2018). Finally, GAs generate interest because they have been shown to induce parthenocarpy in the *Prunus* genus, in particular in peach (*P. persica*), almond (*P. dulce*), apricot (*P. armeniaca*) (Crane *et al.,* 1960), and many years later, in Chinese cherry (*P. pseudocerasus*) (Wen *et al.,* 2019). GAs have been selected to see if they have the same effect in sweet cherry cultivars (*P. avium*). In addition, auxin treatments are included because of their efficiency in inducing parthenocarpic fruit development in several crops, as mentioned above. In particular, auxin has been demonstrated to work upstream of GAs in many plant species such as Arabidopsis and pear (Cong *et al.,* 2018; Dorcey *et al.,* 2009). Finally, the crosstalk between the auxin and GA signalling pathways has been highlighted in tomato (Hu *et al.,* 2018).

Cytokinins (CKs) are another group of phytohormones that have a crucial role in development. The name of this group comes from "cytokinesis" because these molecules promote cell division ("cytokinesis") (El-Showk *et al.,* 2013). Exogenous application of CKs has been observed of being able to induce parthenocarpic fruit development in crops such as tomato (Ding *et al.,* 2013), pear (Cong *et al.,* 2020), fig (Chai *et al.,* 2019), grape (Lu *et al.,* 2016), cucumber (Qian *et al.,* 2018) and kiwi (Murakami *et al.,* 2020).

Brassinosteroids (BRs) and melatonin are able to induce parthenocarpy, although the cases reported in literature are much lower than the ones reported for the major hormones, auxins,

GAs and CKs. BRs, as suggested by the name, are steroid hormones involved in tissue growth and response to biotic and abiotic stress (Zhu *et al.,* 2013).

The application of the BR analogues 24-epibrassinolide and brassinolide, has been reported to promote parthenocarpic fruit development in cucumber and sweet apple (*Annona Squamosa* L.), respectively (Fu *et al.,* 2008, Mostafa *et al.,* 2018). Melatonin (N-acetyl-5-methoxytryptamine) is a hormone present both in animals and in plants. Indeed, it was discovered first in frogs, then in plants in 1955 (Sharif *et al.,* 2018, Arnao and Hernández-Ruiz 2020). In plants, melatonin is involved mostly in stress responses but also in several other processes such as senescence, plant growth and many others. It has a role also during flowering, fruit set and ripening (Arnao and Hernández-Ruiz 2020). So far, only one case of induced parthenocarpy by application of melatonin has been reported in the literature with the "Starkrimson" pear (*Pyrus communis* L.), by regulating the genes involved in the GA pathway (Liu *et al.,* 2018).

A negative regulator of fruit set is ethylene. This hormone has several functions, such as, tissue growth, fruit ripening and flower sex determination in watermelon and *Cucurbita pepo* species (Manzano *et al.,* 2014, Bakshi *et al.,* 2015, Schilling *et al.,* 2020). However, as mentioned, ethylene has a negative effect on fruit set. Application of the ethylene inhibitors 1-methylcyclopropene (1-MCP) and aminoethoxyvinylglycine (AVG) has been observed to induce parthenocarpy in tomato and zucchini, respectively (Martínez *et al.,* 2013, Shinozaki *et al.,* 2018). An additional proof of the negative role of ethylene has been obtained in tomato, where application of the ethylene precursor 1-aminocyclopropane-1-carboxylic acid (ACC), to ovaries suppressed fruit set (Shinozaki *et al.,* 2015).

3.1.8 Hormones applications in *Prunus* species

In 1960, Crane and collaborators showed that gibberellin (GA) treatment of different plants belonging to the *Prunus* genus is sufficient to initiate fruit set in some of them. Indeed, while *P. domestica* (plum) and *P. avium* (sweet cherry) did not produce any parthenocarpic fruit, *P. dulcis* (almond), *P. armeniaca* (apricot) and *P. persica* (peach) developed parthenocarpic fruits at a

frequency of 11.8%, 15.4% (500 ppm GA treatment) and 73.4%, respectively (50 ppm GA treatment applied twice) (Crane *et al.,* 1960).

Although the highest fruit set is reached in peach with the lowest concentration of GA, the highest concentration (500 ppm) led to a higher level of stone development and degree of sclerification, which is absent in the fruits treated with 50 ppm solution. The parthenocarpic peaches reached maturation about 10 days before the seeded ones (Crane *et al.,* 1960). It is likely that the failure to induce parthenocarpy in cherry was due to an incorrect concentration or use of an incorrect type of GA, because Wen and collaborators (2019) showed that treating emasculated *P. pseudocerasus* (Chinese cherry) pistils with 300 mg/L GA_3 solution was enough to trigger fruit set without pollination and the development of parthenocarpic fruit.

Despite all the examples of parthenocarpic fruit development induced by exogenous hormones application, in sweet cherry this result was not achieved yet. In this Chapter, the application of Gibberellic acid 3, mostly, was investigated, considering the results showed in Chinese cherry (Wen *et al.,* 2019). The induction of parthenocarpy was not studied *per se*, but also in order to obtain seedless material to use to research the genetic factors that play an essential role in this process (Chapter 4).

3.2 Materials and Methods

3.2.1 Plant material

Cherry trees of 'Merchant', 'Kordia' and 'Regina', which are early-, mid- and late-season varieties were used in the experiment carried on in 2019, while for the 2020 and 2021 experiments only 'Regina' was used. These varieties are also self-incompatible, which means that their ovules cannot be fertilised by the pollen produced from the same variety. Cherry flowers were emasculated before they reached the balloon stage and all the flower organs, except for the pistils, were removed. These experiments were performed in a cherry orchard situated in East Malling, Kent, United Kingdom.

3.2.2 Hormone solution preparation and treatments

The active forms of GA and auxin used in this study were the gibberellic acid 3 (GA_3) and the 2,4 Dichlorophenoxyacetic acid (2,4-D), as used in previous studies (Cong *et al.,* 2018; Wen *et al.,* 2019). 2,4-D treatment was conducted only in 2019, while the GA_3 treatments were conducted over all three years. In particular, 300 mg/L and 500 mg/L solutions were prepared because these concentrations of GA_3 have been demonstrated to be effective in inducing parthenocarpic fruit development in the Chinese cherry (Wen *et al.,* 2019). As reported in the datasheet of both the chemicals, Gibberellic Acid 3 (Sigma-Aldrich) and 2,4 Dichlorophenoxyacetic acid (Sigma-Aldrich), ethanol 70% (EtOH 70%) was used to solubilize the salts of both of the hormones. Before starting the experiments a solution of EtOH 70% was sprayed on emasculated pistils to assess if it could cause any damage to them. After confirmation that ethanol alone had no effect, all the solutions (GA_3 300 mg/L, GA_3 500 mg/L, 2,4-D 300 mg/L, 2,4-D 500 mg/L) were prepared, dispensed in four different sprayers and stored in the cold store at 4°C. A sprayer containing EtOH70% only was added as mock control. A Negative Control has been added as a further control in the experiments of 2020 and 2021.The last treatment included was hand-pollination (2019) or open pollination (2020 and 2021). Pollen from 'Kordia', stored in the cold store at 4°C from the previous spring, was used to hand-pollinate 'Merchant' pistils, while pollen from the 'Korvik' variety, collected during the same spring, was used to pollinate 'Kordia'. Pollen collection was made using

unopened flowers at the balloon stage, because at this stage pollen is mature and fertile. Anthers only were collected in a petri dish and they were left in a cabinet to dry before being stored at 4°C. Pollen is released by the dry anthers by shaking the petri dish.

3.2.3 Treatment procedures

Unopened flowers at the balloon stage were emasculated and only the pistils were left. Moreover, all the flowers that were at the wrong stage, either too young or already open, were removed from the branch as along with the flower buds. The emasculated flowers of each branch were treated in the same way, except for the ones used as the Negative Control, which remained untreated: sprayed with the mock solution (EtOH 70%), sprayed with one of the hormone solutions (GA_3 300 mg/L, GA_3 500 mg/L, 2,4-D 300 mg/L, 2,4-D 500 mg/L) or hand-pollinated. The treated branches were covered with pollination bags in order to prevent access by bees, which are the pollinators of the cherry flowers and could contaminate and confound the experiment. In the case of the open pollination, only the flowers at the balloon stage were left on the branch while all the other stages were discarded. Thus, all the remaining flowers reached the anthesis stage at the same time. Three biological replicates were made (indicated by the capital letters A, B and C); thus, every treatment was made three times, each one on three different trees. All the treatments, when possible, were performed on branches that were close to the others, in order to normalise as much as possible the microenvironment that surrounded the pistils. The summary of the treatments is reported in Table 3.1.

	2019			2020	2021
	'Merchant'	'Kordia'	'Regina'	'Regina'	'Regina'
Negative Control					
EtOH 70% (Mock Control)					
GA_3 300 mg/L					
GA_3 500 mg/L					
2,4-D 300 mg/L					
2,4-D 500 mg/L					
Hand-Pollinated (H.P.)					
Open-Pollinated (O.P.)					

Table 3.1: Summary of the treatments made on 'Merchant', 'Kordia' and 'Regina' from 2019 to 2021.

3.2.4 Sampling and storage

The treated pistils were checked every seven days after treatment (DAT). One pollination bag per time was removed in order to assess the condition of the ovaries and the developing fruits, and to collect some of them. Specifically, about 10 samples were collected for the molecular biology experiments, and about five samples for photography, which was used to measure the dimensional features. For the 2019 experiment, photographs were taken directly from the trees. Once all these actions were completed the branch was covered with the same pollination bag. This process was repeated for all the treatments to assess during the same day of the week. Collected samples were put in a falcon tube of 15 ml or 50 ml, previously cooled in liquid nitrogen. Collected ovaries and fruits for the molecular biology investigation were then frozen in liquid nitrogen and stored at -80°C while the ovaries and fruits used for measurements were kept in ice until the time of the photography.

3.2.5 Samples photo shooting, measurements, and statistical analysis

Ovaries and developing fruits were cut at the level of the suture line, i.e., the visible line that remains after the closure of the ovary. During the cherry flower development, the developing ovary produces semi-circular protuberances, which will then close (Quero-García *et al.,* 2017). It was decided to refer to the ovary/fruit wall where there was the suture line, as "dorsal", while

the opposite one as “ventral”. Five ovaries or fruits were photographed per treatment at every timepoint. Measurements of the dimensions were taken using the program ImageJ. Data were analysed in R, where all the graphs have been originated and the statistical analysis performed, using the Kruskal-Wallis test.

3.2.6 An overview of the three field experiments

Table 3.1 shows an overview of the different treatments present in the experiments conducted in 2019, 2020 and 2021. 2019 experiment was used as a preliminary test to check if exogenous application of hormones could induce parthenocarpy in *Prunus avium*. Since these experiments were conducted in an orchard, the weather played a crucial role. Indeed, in all the three years, modifications of the scheduled plan were required. In 2019, the treatments on ‘Merchant’ were severely reduced due to cold temperatures that did not allow emasculation when the trees were at their optimal stage. In 2020, the experiments were planned to be conducted on ‘Kordia’ and ‘Regina’; however, due to severe frost damage of ‘Kordia’, only ‘Regina’ was used. This change also caused a change in the pollinated control. Indeed, according to the observations from the cherry breeding program group at NIAB EMR, when ‘Regina’ is the mother, the hand pollination success rate is below 10%, which made hand-pollination unsuitable as a positive control (personal communication). For this reason, open pollination was chosen. Finally, in 2021 even ‘Regina’ was affected by the low temperatures, wind, and rain. Indeed, the government Met Office reported that April 2021 had the lowest average minimum temperatures since 1922. For this reason, hormone treatments could not be done for lack of usable flowers and only the Negative Control and the Open Pollination treatments were included.

3.3 Results

3.3.1 Exogenous application of gibberellins induces putative fruit development in sweet cherry

Unpollinated (Negative Control) and Mock-treated (EtOH70%) pistils remained small and green without starting the fruit set program (Fig. 3.9-13 A-B). From an external point of view no visible difference between these two treatments was observed. The application of EtOH70% to unpollinated pistils seems to have no evident effect on their survival. Indeed, at 42 Day After Treatment (DAT), no collection of unpollinated or mock-treated ovaries was possible because all the ovaries wilted and abscised from the branches. Interesting results were observed in the hormone-treated ovaries (Fig. 3.9-14 C-D). In particular, both the GA_3 treatments promote ovary enlargement already at 7 DAT (Fig. 3.9 C-D). The enlargement became more evident over time. Interestingly, these modifications were not caused by the presence of a developing seed since the developing fruits were empty inside (Fig. 3.10-13 C-D). In addition, already at 7 DAT slightly shrunk ovules were observed (Fig. 3.9 C-D). After this time, ovules aborted, remained as traces or disappeared completely. A difference in size was evident between the GA_3-treated ovaries and the unpollinated/mock-treated ones. However, at 28 DAT, GA_3-treated putative developing fruits started to wilt as well, by shrinking and accumulating red and purple pigments (Fig. 3.12 C-D). This phenomenon was observed in both the 300 mg/L and 500 mg/L treated samples. At 42 DAT the observations were stopped since the GA_3 ovaries were almost all dead (Fig. 3.14 C-D). Open pollinated ovaries started to increase their dimension already at 7 DAT, as the GA_3 treated ones, but while the latter ones wilted and died, the former ones continued the fruit development process (Fig. 3.9-14E). In these samples the lumen of the fruit was filled with the developing seed, which appeared pulpy at every time point. The wall of both the GA_3-treated putative developing fruits and the O.P. developing fruits showed a green and a white area at 14 DAT (Fig. 3.10E). This was the beginning of the differentiation of two different fruit components, the mesocarp and the endocarp respectively. In the O.P. samples, the endocarp development proceeded through time and lignification of this tissue was quite evident at 35 DAT, making the cutting in half of the fruit, harder to accomplish (Fig. 3.13E). The same endocarp developmental pattern was observed in

the GA_3-treated samples. However, it seemed that after the initial differentiation of this tissue, the normal development, with the subsequent lignification did not occur.

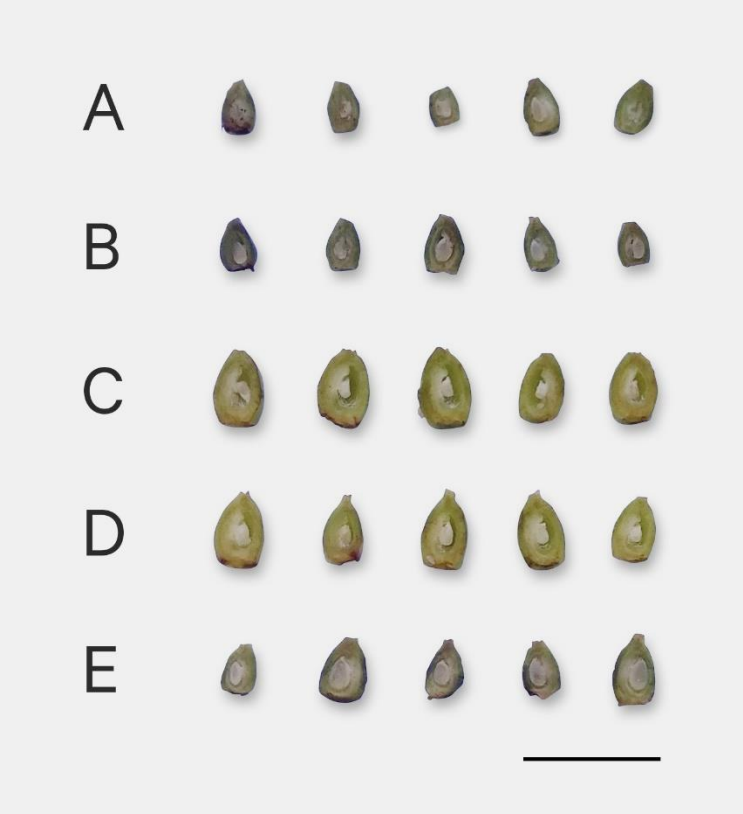


Figure 3.9: Panel that shows the unpollinated ovaries (N.C.) (A), EtOH70%-treated ovaries (B), 300 mg/L GA_3-treated (C), 500 mg/L GA_3-treated (D) ovaries and open pollinated (O.P.) (E) ovaries of 'Regina' 2020 at 7 DAT. Scale bars = 1cm. See Fig. S3.1 for the original photos.

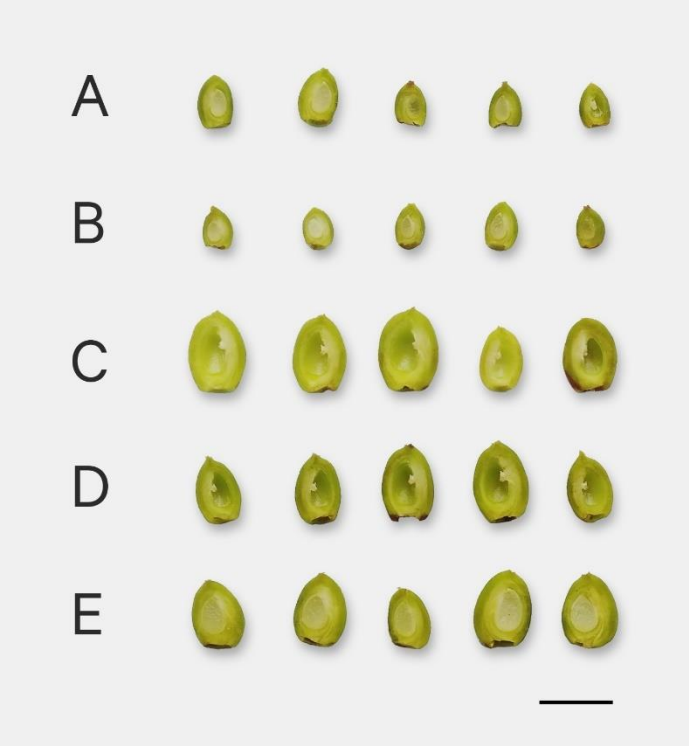


Figure 3.10: Panel that shows the unpollinated ovaries (N.C.) (A), EtOH70%-treated ovaries (B), 300 mg/L GA_3-treated (C), 500 mg/L GA_3-treated (D) ovaries and open pollinated (O.P.) (E) ovaries of 'Regina' 2020 at 14 DAT. Scale bars = 1cm. See Fig. S3.2 for the original photos.

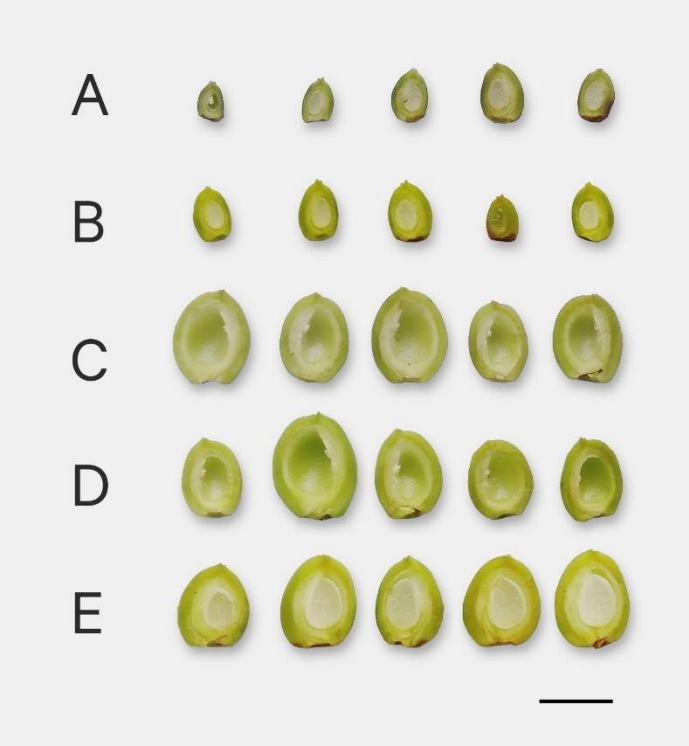


Figure 3.11: Panel that shows the unpollinated ovaries (N.C.) (A), EtOH70%-treated ovaries (B), 300 mg/L GA_3-treated (C), 500 mg/L GA_3-treated (D) ovaries and open pollinated (O.P.) (E) ovaries of 'Regina' 2020 at 21 DAT. Scale bars = 1cm. See Fig. S3.3 for the original photos.

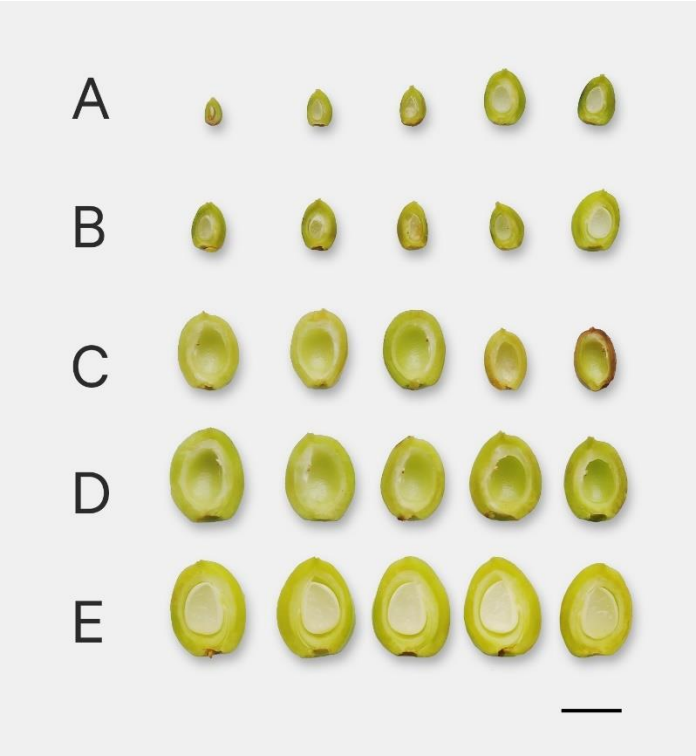


Figure 3.12: Panel that shows the unpollinated ovaries (N.C.) (A), EtOH70%-treated ovaries (B), 300 mg/L GA_3-treated (C), 500 mg/L GA_3-treated (D) ovaries and open pollinated (O.P.) (E) ovaries of 'Regina' 2020 at 28 DAT. Scale bars = 1cm. See Fig. S3.4 for the original photos.

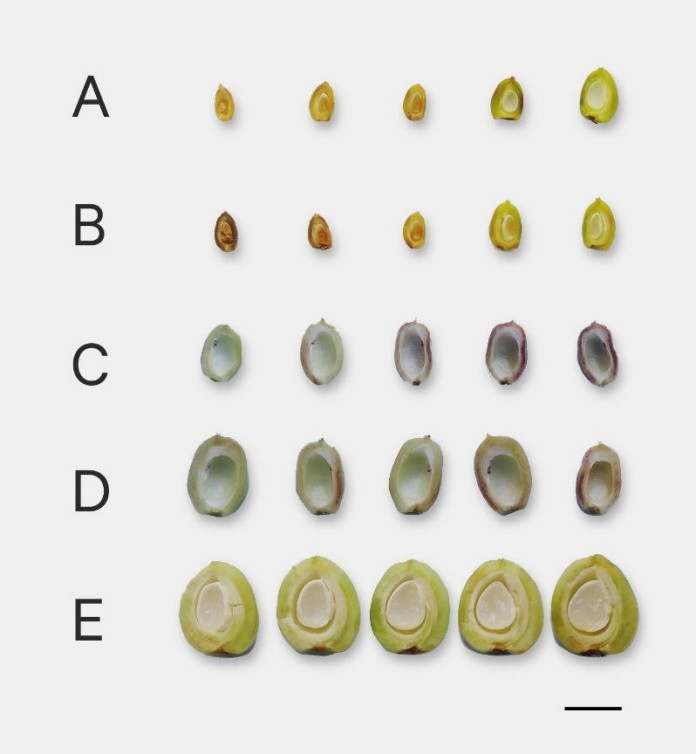


Figure 3.13: Panel that shows the unpollinated ovaries (N.C.) (A), EtOH70%-treated ovaries (B), 300 mg/L GA_3-treated (C), 500 mg/L GA_3-treated (D) ovaries and open pollinated (O.P.) (E) ovaries of 'Regina' 2020 at 35 DAT. Scale bars = 1cm. See Fig. S3.5 for the original photos.

Figure 3.14: Panel that shows the 300 mg/L GA_3-treated (A), 500 mg/L GA_3-treated (B) ovaries and open pollinated (O.P.) (C) ovaries of 'Regina' 2020 at 42 DAT. Scale bars = 1cm. See Fig. S3.6 for the original photos.

Finally, phenotypical changes were also observed in the pistils treated with 2,4-D (Fig. 3.15). In particular, 2,4-D treatments promoted an extension of the style but not an enlargement of the ovary, as GA_3 treatments did. In addition, 2,4-D treated ovaries were observed to degenerate and dry progressively over time until they were completely dead (Fig. 3.15C/H). Interestingly, ovary enlargement has been observed at a very low rate also in 'Kordia' and 'Regina' treated with 2,4-D solutions, starting from the 21 DAT time point (Fig. 3.15A-B, E-F). In this case, the ovaries were bigger than the drying ones, but smaller than the ones treated with GA_3 (Fig. 3.11 C-D). These ovaries also retained the long style, as observed in other 2,4-D treated pistils (Fig. 3.15A-B, E-F). Similarly, to what was observed in the GA_3 putative developing fruits, these enlarged ovaries were seedless as well (data not shown).

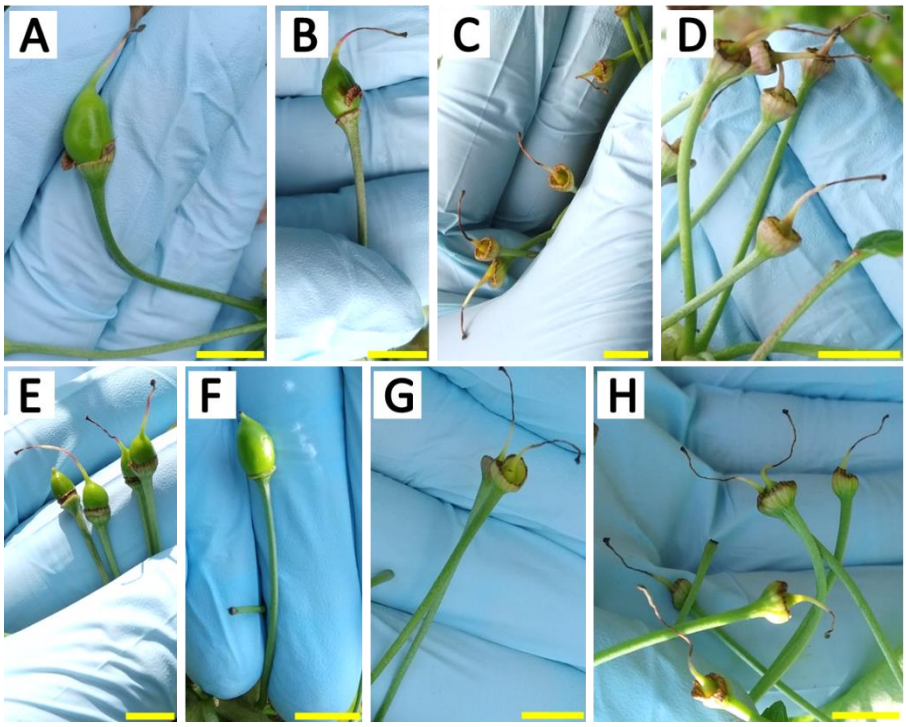


Figure 3.15: Panel that shows 'Kordia' 2019 ovaries treated with 2,4-D 300 mg/L (A/C) and 500 mg/L (B/D) and 'Regina' 2019 ovaries treated with 2,4-D 300 mg/L (E/G) and 500 mg/L (F/H) at 21DAT. Scale bars = 1cm

3.3.2 Initial development of GA_3-treated samples follows that observed in the Open pollinated samples.

Fig. 3.16A/C shows the curves obtained from the 2020 measurements of the developing fruits length and width, and in both cases, the O.P. curves are sigmoid. The same type of curve is obtained from the respective measurements in 2021 (Fig. 3.20A/C). The GA_3-treated samples show similar curves, however, only between 0 and 21 DAT, while after this timepoint a significant difference is visible: the O.P. 2020 curve continues with its exponential phase, while the GA_3-treated ones reach a plateau and then a decreasing phase (Fig. 3.16A/C). Indeed, between 7 and 21 DAT, there is no statistically significant difference between the O.P. and GA_3-treated samples, while at 28 DAT the difference starts being statistically significant (Fig. 3.16B/D). The two controls, the Negative control and the mock-treated one (EtOH70%), have an almost identical pattern. Indeed, their curves are more similar to a straight line, with a small slope (Fig. 3.16A/C).

This conclusion is confirmed also by the statistical analysis (Fig. 3.16B/D). The two controls remain also always statistically smaller compared to the GA_3-treated and the O.P. samples (Fig. 3.16B/D).

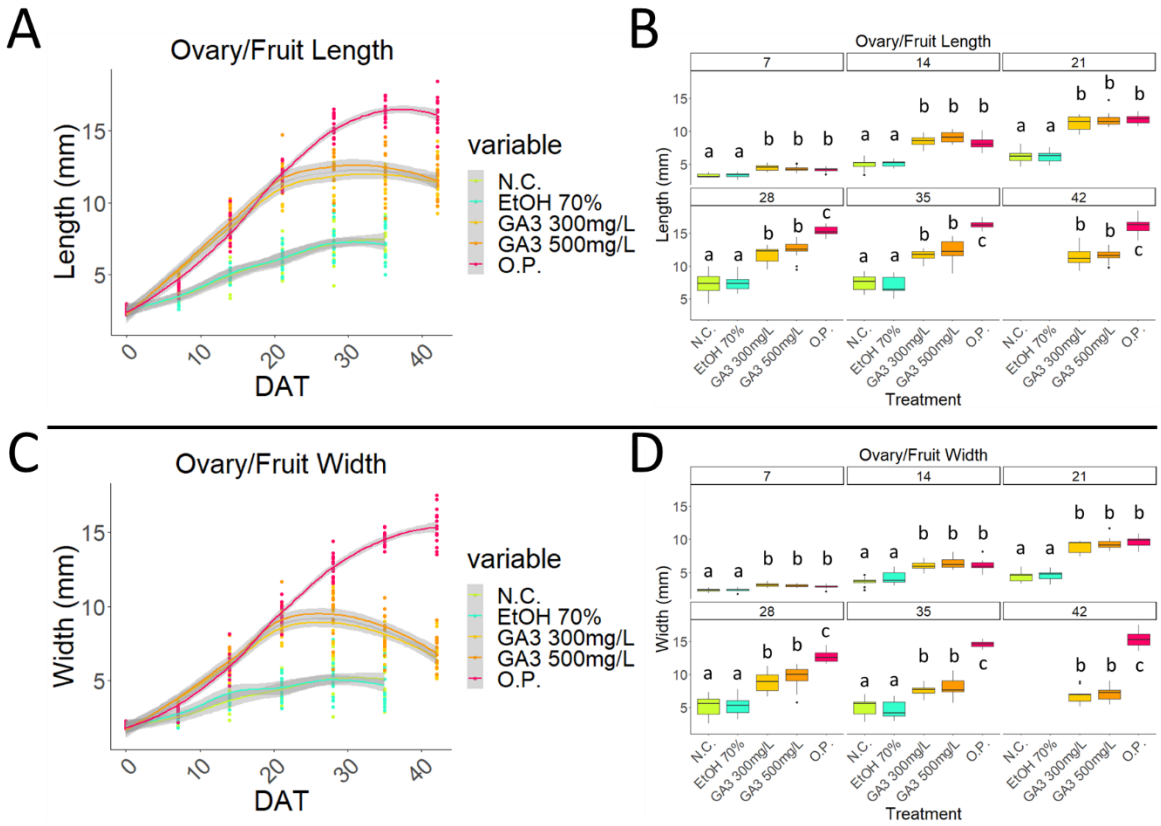


Figure 3.16: Graph that shows the curves obtained from the length measurements of all the five treatments from the beginning to the of the experiment (A). Boxplot graph of the length measurements (B). Graph that shows the curves obtained from the width measurements of all the five treatments from the beginning of the experiment (C). Boxplot graph of the width measurements (D). DAT: Days After Treatment.

The O.P. dorsal and ventral wall thickness curves appear to be similar to a stretched sigmoid that has not yet reached the plateau phase (Fig. 3.17A/C). Even when considering these dimensional parameters, a similarity in the pattern of the O.P. and the GA_3-treated curves can be observed in the first part of the experiment (0-21 DAT), while a difference comes after 21 DAT (Fig. 3.17A/C). Once again, the walls of the O.P. samples get thicker with time, while the ones of the GA_3-treated

ones, get thicker until timepoint 21 DAT, and then thinner. Interestingly, the GA_3-treatment curves suggest a more advanced thickness of the ventral wall compared to the O.P. one (Fig. 3.17C). However, a statistically significant difference is present only at time point 7 DAT, while between 14 and 28 DAT, all three treatments belong to the same group (Fig. 3.17B/D). Finally, again, at 35 DAT the O.P. samples are significantly thicker than the GA_3-treated ones (Fig. 3.17B/D).

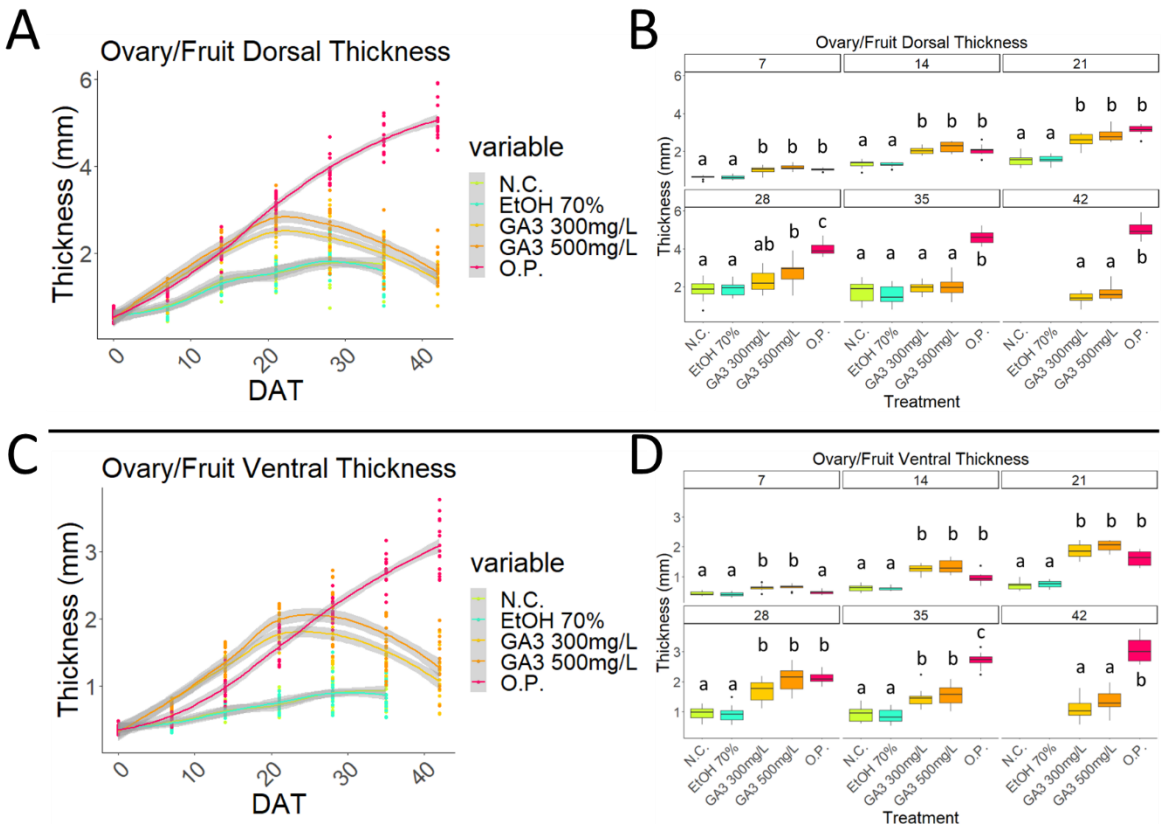


Figure 3.17: Graph that shows the curves obtained from the dorsal wall thickness measurements of all the five treatments from the beginning to the of the experiment (A). Boxplot graph of the dorsal wall thickness measurements (B). Graph that shows the curves obtained from the ventral wall thickness measurements of all the five treatments from the beginning to the of the experiment (C). Boxplot graph of the ventral wall thickness measurements (D). DAT: Days After Treatment.

The patterns of mesocarp and endocarp growth are quite similar if the dorsal and the ventral sides of the fruit are considered. Indeed, at the dorsal side, the thickness of both the mesocarp and the endocarp, are almost the same in the O.P. fruits and in the GA_3-treated putative fruits (Fig. 3.18A/C, Fig. 3.19A/C). However, the O.P. fruits get thicker than the GA_3-treated ones, whose mesocarp grows slightly before wilting and the endocarp degeneration is already visible at 28 DAT (Fig. 3.18, Fig. 3.19). On the contrary, both the ventral mesocarp and the dorsal and ventral endocarp of the GA_3-treated developing putative fruits are thicker than the O.P. developing fruits at 14 DAT (Fig. 3.18B/D, Fig. 3.19B/D). This difference is maintained in the ventral mesocarp until 28 DAT when no significant difference was observed (Fig. 3.18D), while at 21 DAT the dorsal mesocarp is significantly thicker in the O.P samples (Fig. 3.18B). The endocarp shows an interesting characteristic because for the first time a difference between the two dosages of GA_3 (300 mg/L and 500 mg/L) was observed (Fig. 3.19D). Indeed, while the putative fruits treated with 300 mg/L show a pattern coherent with that described for the dorsal endocarp, a significant growth of the ventral endocarp in the 500 mg/L treatment is visible at 14 and 21 DAT. The ventral endocarp is thicker even than the O.P. one at 14 DAT, while at 21 DAT the thickness of these two treatments is no longer significantly different (Fig. 3.19B/D).

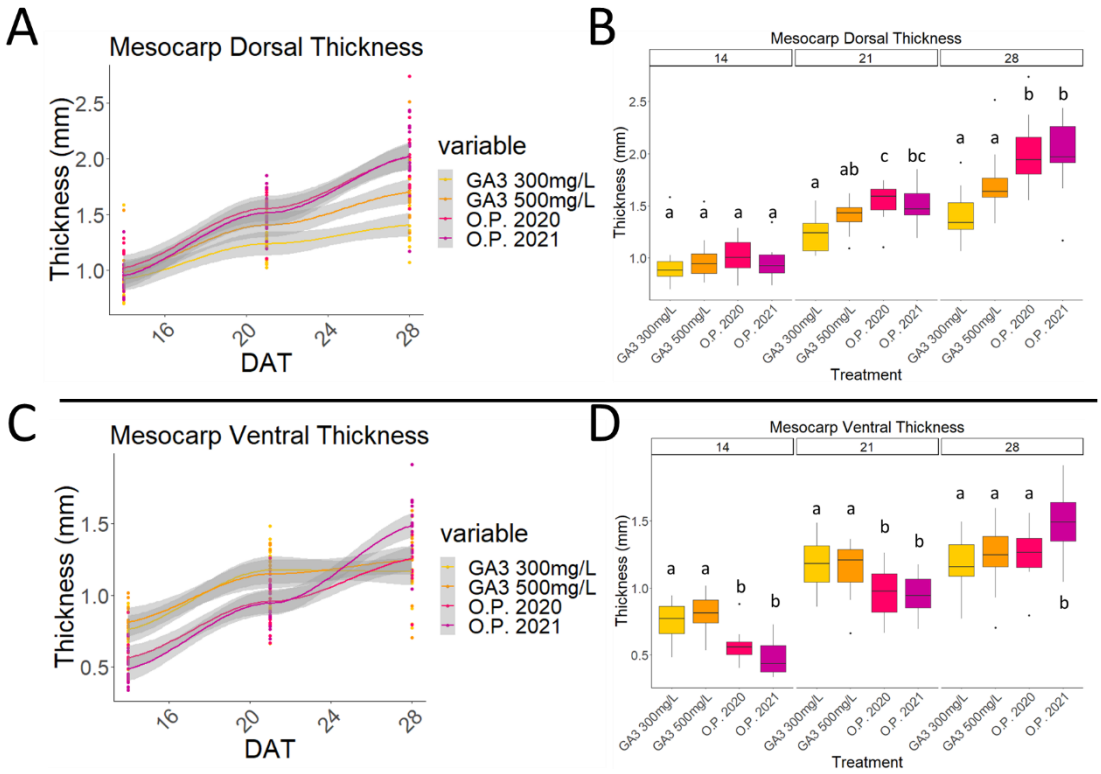


Figure 3.18: Graph that shows the curves obtained from the mesocarp dorsal thickness measurements of all the five treatments from the beginning to the of the experiment (A). Boxplot graph of the mesocarp dorsal thickness measurements (B). Graph that shows the curves obtained from the mesocarp ventral thickness measurements of all the five treatments from the beginning to the of the experiment (C). Boxplot graph of the mesocarp ventral thickness measurements (D). DAT: Days After Treatment.

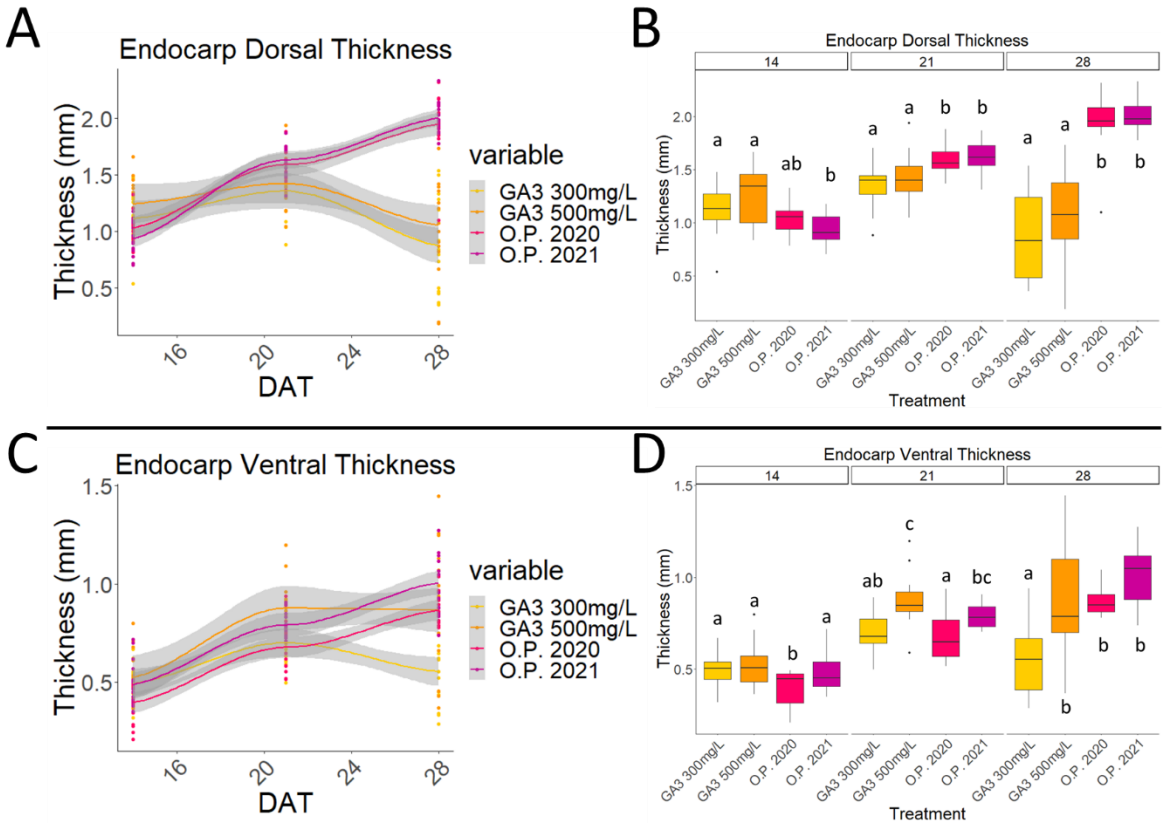


Figure 3.19: Graph that shows the curves obtained from the endocarp dorsal thickness measurements of all the five treatments from the beginning to the of the experiment (A). Boxplot graph of the endocarp dorsal thickness measurements (B). Graph that shows the curves obtained from the endocarp ventral thickness measurements of all the five treatments from the beginning to the of the experiment (C). Boxplot graph of the endocarp ventral thickness measurements (D). DAT: Days After Treatment.

3.3.3 Comparison of 'Regina' in 2020 and 2021

The patterns of the curves of the N.C. and the O.P. samples from 2020 and 2021 are very similar, although some differences can be observed, especially when N.C. 2020 is compared to N.C. 2021 (Fig. 3.20A/C and Fig. 3.21A/C). Indeed, in all the four dimensional parameters (length, width, dorsal and ventral thickness), the N.C. 2021 curve is always greater than the N.C. 2020 one. In some timepoints also this difference is significant. At time point 7, indeed, the N.C. 2021 values are always significantly greater than the N.C. 2020 ones (Fig. 3.20B/D, Fig. 3.21B/D). Interestingly, while in 2020 already at 7 DAT, a significant difference was observed between the N.C. and the O.P. samples, this difference is not maintained in 2021. From 14 DAT, a clear separation of the

O.P. 2020 and 2021 from the N.C. 2020 and 2021, can be observed. Finally, a small difference can be observed in the N.C 2021 samples, compared to the N.C. 2020 ones. Indeed, at 35 DAT and 28 DAT, the N.C. 2021 result in being slightly longer and thicker in the ventral wall respectively, than the N.C. 2020 unpollinated ovaries. This difference is not observed in any timepoint when O.P. 2020 and O.P. 2021 samples are compared (Fig. 3.20B/D, Fig. 3.21B/D).

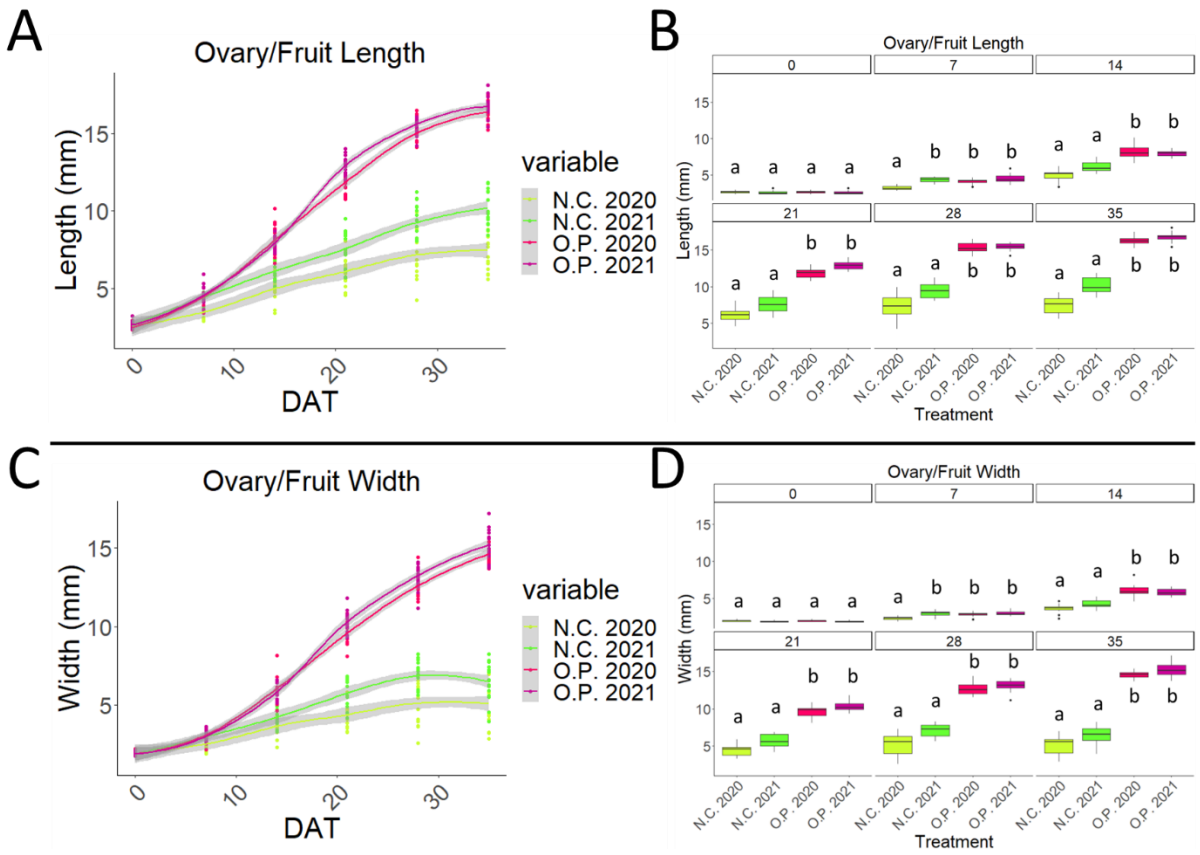


Figure 3.20: Comparison between 'Regina' 2020 and 'Regina 2021' N.C. and O.P. samples. (A) graph that shows the curves obtained from the length measurements of all the five treatments from the beginning to the of the experiment. (B) boxplot graph of the length measurements. (C) graph that shows the curves obtained from the width measurements of all the five treatments from the beginning to the of the experiment. (D) boxplot graph of the width measurements. DAT: Days After Treatment.

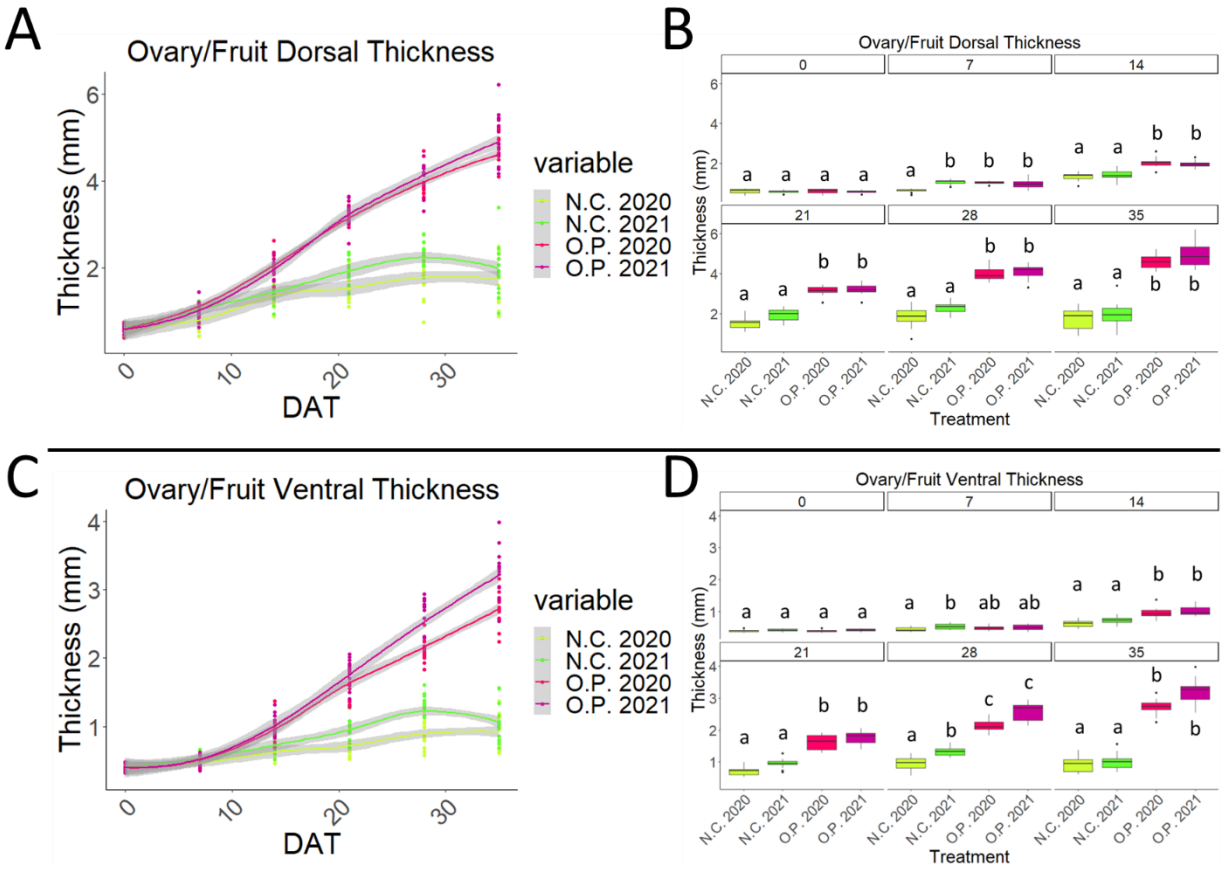


Figure 3.21: Comparison between 'Regina' 2020 and 'Regina' 2021 N.C. and O.P. samples. (A) graph that shows the curves obtained from the dorsal wall thickness measurements of all the five treatments from the beginning to the of the experiment. (B) boxplot graph of the dorsal wall thickness measurements. (C) graph that shows the curves obtained from the ventral wall thickness measurements of all the five treatments from the beginning to the of the experiment. (D) boxplot graph of the ventral wall thickness measurements. DAT: Days After Treatment.

3.4 Discussion and future work

Despite some technical and unforeseen issues that happened during these experiments, i.e. the low temperatures at the beginning of the spring, which significantly reduced the time window during which the emasculation and the treatments were possible to be done ('Merchant') in 2019, the severe frost damage of 'Kordia' flowers in 2020 and the cold temperature of April 2021 that affected 'Regina', interesting results were achieved. These results show that GA_3 treatment seems sufficient to initiate fruit set, while 2,4-D treatments do not appear to be able to promote fruit development without fertilisation. However, regarding the latter observation, the possibility that it was due to the high concentrations used cannot be ignored. It has previously been shown that 2,4-D can be used as herbicide, which makes the dosage used critical for the purpose of this experiment. The presence of enlarged seedless ovaries indicates the possibility that auxin can potentially initiate fruit set without fertilisation. It has been observed that the GA_3 treated ovaries develop into putative fruits but their development stops at some point. This may be explained by the fact that the lack of the developing seed causes a premature death of the fruit, because, as mentioned above, fruit and seed communicate during their development, in order to synchronise themselves. The developing seed indeed, constantly sends signals to the mother plant and only one application of exogenous hormones seems not enough to complete all the fruit development process.

However, despite the inability of completing the fruit development, it seems that GA_3 is involved in the fruit set initiation. The putative fruits have been observed to be quite similar to the O.P. ones, in the first phases of the experiment, before the wilting. It would be helpful to repeat these treatments, with multiple applications through time to check if this approach could lead to the mature parthenocarpic cherry fruit. This hypothesis was actually planned to be tested in the 2021 experiment; however, for the reasons mentioned above, it was not possible. This is a strategy that needs to be considered for future experiments.

A gene expression comparison between the GA_3 treated ovaries and the open-pollinated ones is required to check if they are developing into the same structures and if the same genetic pathways are activated.

The growth curves obtained from the measurements of the O.P. developing fruits (2020 and 2021) show a pattern coherent with what is reported in the literature. In particular, the length and the width curves display a sigmoid pattern. Drupe development follows a double sigmoid pattern, in which three phases are recognized. The observations in 'Regina' ended after a month and the first half of the double-sigmoid was obtained both in 2020 and 2021. This is consistent with the studies of Tukey and collaborators where they reported that phase I for the mid-season variety 'Montmorency' lasts 20-22 days (Tukey *et al.,* 1939). According to Tukey and Young (1934), during phase I the different tissues are established, and this is what was observed in 'Regina' as well. During phase II, the endocarp starts its lignification process and again this is coherent with the observations in this study. Phase II can be seen in the curves when the length and width curves are reaching the plateau (between 21 and 28 DAT). The endocarp starts to be quite hard at 28 DAT, which could be the first timepoint included in phase II. At 35 DAT, the lignification of the endocarp is quite visible. Thus, combining the curves obtained and the observations on the endocarp lignification, it is likely that the switch from phase I and phase II occurs between the timepoint 21 and 28 DAT. Timepoint 21 DAT seems crucial since it is when a difference appears in the growth curve patterns between O.P. and GA_3-treated samples. After 21 DAT indeed, the arrest of the growth of the GA_3-treated developing putative fruits begins. A plateau phase is present also in these curves, however, in this case this plateau could have a different meaning. Indeed, while in the O.P. the plateau phase is observed because the mitotic divisions are reduced, in favour of cell expansion, the plateau observed in GA_3-treatments curves is likely to be due to an arrest of the actual development.

These samples have been also used for RNAseq analysis (see Chapter 4). Transcriptomics analysis could help to understand if the GA_3 exogenous application triggers the fruit set programme in unpollinated ovaries.

Finally, when the experiments conducted in 2020 and 2021 are compared, a type of variation of the average values is observed. In particular, the 2021 unpollinated ovaries were bigger than the 2020 ones. Two explanations are possible. The first one is that, since the flower buds in 2021 opened significantly later than in 2020, the flower organs had more time to grow. The second

one is that the cold stress could have promoted a higher growth level of the 2021 ovaries. Biotic and abiotic stress have an impact on plants that may choose specific strategies to face them. It would be interesting to check if these observations were repeated another year, with a very extreme climate, and also with other types of stress such as drought and high salt concentration in the soil. Pollen cross contaminations can be excluded because new pollination bags were used and none of the unpollinated ovaries developed into fruit.

Chapter 4: Transcriptomic analysis of pollinated fruits and GA_3-treated putative fruits

4.1 Introduction

4.1.1 Flower development: the ABCDE and the Floral Quartet models

Flower organs are arranged in whorls namely sepals (most external; I whorl), petals (II whorl), stamens (III whorl) and carpel (most internal and IV whorl).The floral homeotic mutants, i.e. mutants with an altered floral organ identity, such as in *Arabidopsis thaliana* and *Anthirrinum majus* (snapdragon) have been studied and used to propose the ABC model of flower formation (Bowman *et al.,* 1991; Coen & Meyerowitz, 1991). ABC genes encode three different classes of MADS-domain transcription factors involved in the flower organ identity determination These factors work and interact to give the organ identity to sepals, petals, stamens, and carpel. Further studies showed the existence of other two classes: the D class, which is responsible for ovule identity and the E-class which has been proposed as another class of redundant floral organ identity genes (Theißen, 2001) (Fig. 4.1). This enhanced ABCDE model postulates that sepals are specified by A + E, petals by A+B+E, stamens by B+C+E, carpels by C+E and ovules by C+D+E (Fig. 4.1) (Goto *et al.,* 2001; Theißen, 2001; Theißen and Saedler, 2001; Theißen *et al.,* 2016). In addition, the floral quartet model (FQM) has been suggested to extend the ABCDE model (Theißen, 2001). According to the FQM, the factors form tetrameric complexes to carry out their functions, binding the DNA to activate or repress the expression of their target genes (Theißen, 2001) (Fig. 4.1). In particular, two MIKC-type MADS-box transcription factors belonging to the same class form a dimer, which can interact with another dimer of the same class or of a different class, to promote the development of a specific floral organ (Theißen & Saedler, 2001). The MIKC-type MADS-box transcription factors are composed of specific domains:

- MADS (M) domain: a DNA-binding domain, but it is also involved in the dimerization and in nuclear localization. It is the most conserved domain among the MADS-box transcription factors (Gramzow & Theißen, 2010)

- Intervening (I) domain: takes part in the selective formation of DNA-binding dimers. It shows only limited conservation (Kaufmann *et al.,* 2005)
- Keratin-like (K) domain: an essential element for dimerization and multimeric complex formation. This domain has a particular structural organisation of amphipathic helices in which the hydrophobic and charged residues are conserved and regularly spaced (Puranik *et al.,* 2014; Yang, Fanning, & Jack, 2003)
- C-terminal (C) domain: is somewhat variable. In some cases, it takes part in the transcriptional activation of the target genes or in the formation of multimeric complexes(Kaufmann *et al.,* 2005).

According to the FQM, MADS-box transcription factors form dimers which bind the DNA where the CArG boxes are present. The two dimers that are present in the tetramer recognize and bind two different CArG-boxes, which can also be far away in the DNA sequence, by looping the DNA and making them spatially close (Theißen, 2001; Theißen & Gramzow, 2016; Theißen & Saedler, 2001)

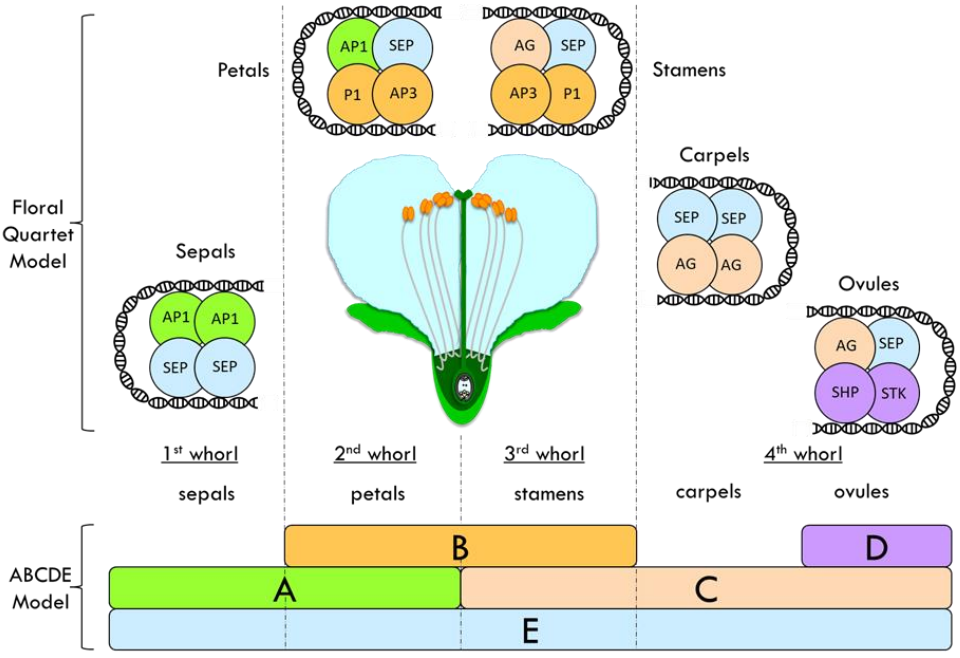


Figure 4.1: Floral quartet model (FQM) integrated to the ABCDE model proposed to explain the flower whorls identity determination in Arabidopsis thaliana. Class-A protein: APETALA1 (AP1); Class-B proteins: PISTILLATA (PI) and APETALA3 (AP3); Class-C protein: AGAMOUS (AG); Class-D proteins: SEEDSTICK (STK) and SHATTERPROOF (SHP); Class-E protein: SEPALLATA (SEP). Vignati *et al.,* 2022.

4.1.2 Fruit development

Fruit development is tightly controlled and regulated in order to produce the complex structure that bears the developing seed. There are several models used to explain this complicated process, however, the most widely used are the silique of *A. thaliana*, which is a dry fruit made by several distinct tissues, including the valves (seedpod walls), replum (middle ridge), septum, and valve margins (Roeder & Yanofsky, 2006). Tomato, *Solanum lycopersicum*, has become the primary model to study fleshy fruit development and ripening because of several advantages such as advanced molecular and genetics toolkits, mutants collection and ease of handling (Giovannoni, 2007).

Fleshy fruit development can be divided in two phases, early fruit development and ripening. In the majority of plant species, early fruit development comprises three phases: (1) fruit set, (2) cell division and (3) cell expansion (Fig. 4.2). In the first phase, the ovary either aborts or initiates the subsequent morphological changes that will lead to the formation of the fruit. The second phase is characterised by intense mitotic divisions of the cells, which remain small and compressed, entailing a small increase of the fruit size. However, the final fruit size is highly dependent on this phase since the number of cells is a very important determinant of the final dimensions. During the third and last phase, cells start to enlarge by as much as 100-fold, to reach the final fruit size. After these three phases, a green immature fruit is formed, which has the dimension of the mature fruit and starts the maturation process. During early fruit development, there is constant communication between the developing fruit and the developing seed. These signals can be hormones , such as auxin and gibberellins, produced in the endosperm or in the seed coat and are involved in the developmental synchronisation of all these different structures (Varoquaux *et al.,* 2000; Serrani *et al.,* 2008; Dorcey *et al.,* 2009). Fruits can be classified according to the tissue from which they originate:

- Botanical fruit: the fruit is derived from the ovary wall and examples include cherry, tomato, sugar apple (*Annona*) and peach (*Prunus persica*);
- Accessory fruit: the fruit develops from non-ovary tissues and examples are strawberry (from the receptacle that holds the ovaries) and apple (from the hypanthium).

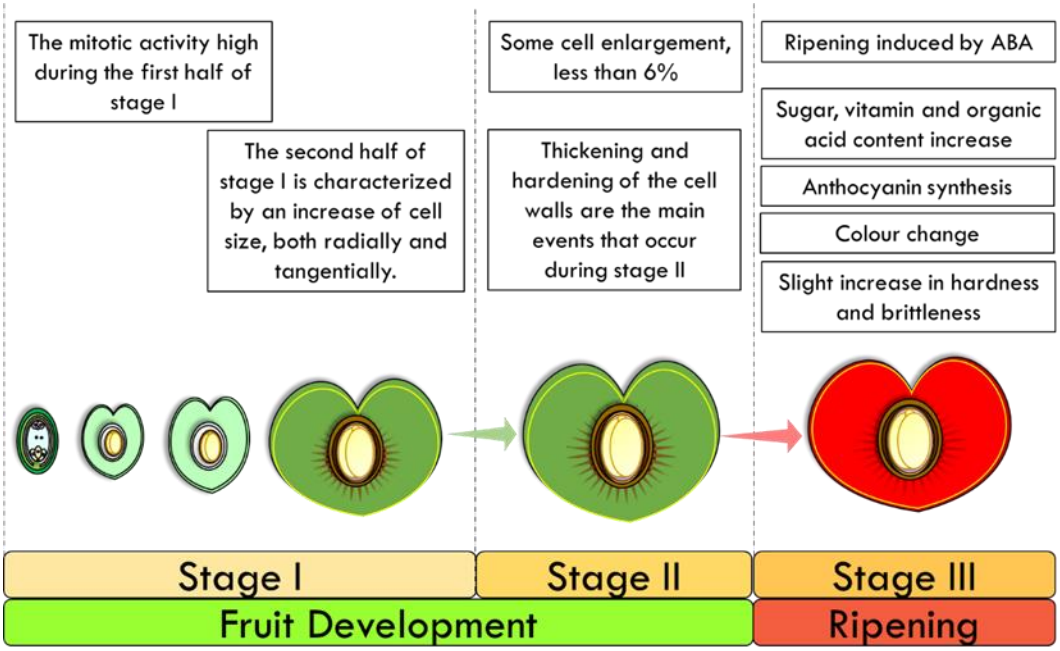


Figure 4.2: Fruit ripening in the cultivated cherry. After an initial exponential phase (Stage I) a plateau phase occurs (Stage II), which is followed then by a second exponential phase (Stage III) until the complete ripening of the fruit. Vignati *et al.,* 2022a.

4.1.3 Genetic control of fruit development

Fruit set is regulated through an extremely complex network. The three main ways to control and regulate the transition from ovary to fruit are through hormonal signals, genetics and epigenetics. Although epigenetic regulation is a very interesting and fascinating research field, with many relevant findings (Farinati *et al.,* 2017; Chachar *et al.,* 2022), this subject will not be included in this chapter. Very little is known about the hormonal control and the transcription factors responsible for sweet cherry fruit development, thus in this study the attention has been on these two aspects. In the next paragraph the focus will be on the MADS-box transcription factors because of their essential function during both flower (Paragraph 4.1.1) and fruit development. There are other transcription factors that are reported to contribute to the regulation of fruit set; these include the NAC superfamily, WRKY family, MYB and bHLH, which are also involved in other biological processes such as senescence, response to biotic and abiotic stress, metabolism, immunity (Ambawat *et al.,* 2013; Nuruzzaman *et al.,* 2013; Jiang *et al.,* 2017).

4.1.4 MADS-box transcription factors

The features of an organ are determined at a very early stage of the development. During the very first phases of development, many aspects of floral organs, such as ovary identity and size, and at least partially final fruit size and ripening are determined. Therefore, it is not surprising that some transcription factors involved in flower organ determination are also involved in fruit development.

The C-clade MADS-box transcription factor *AGAMOUS* (*AG*) is involved in stamen, carpel and ovule identity determination (Ma & dePamphilis , 2000). *AG* is expressed both in the stamens and in the carpels of peach. Moreover, more than one copy of *AGAMOUS* seems to be present in the peach genome. The *PpeAG* sequence present in GenBank (GenBank accession nos. AAU29513) was used for sequence alignment. *PpeAG* is also expressed at high levels in the mesocarp and the endocarp during fruit development (Tani *et al.,* 2009). In tomato, the down-regulation of *TOMATO AGAMOUS 1* (*TAG1*) by RNA interference (RNAi) not only causes flower defects, such as stamen with petalloid tissue, but leads to a loss of flower and fruit determinacy, producing flower-in-flower and fruit-in-fruit phenotypes (Pan *et al.,* 2010; Pnueli *et al.,* 1994). The important role of *AG* in both flower and fruit development has been reported in other species, such as strawberry (*Fragaria x ananassa*), cocoa (*Theobroma cacao* L.) and grape (*Vitis vinifera* L.), which produce different types of fruit (Boss *et al.,* 2001; Chaidamsari *et al.,* 2006; Rosin *et al.,* 2003). The tomato *SlAGAMOUS-LIKE6* (*SlAGL6*) gene is suggested to be a factor that inhibits ovary growth until pollination and fertilisation occur. It is highly expressed in the ovary at anthesis, and its expression level drops significantly after fruit set. Moreover, mutations of this gene result in facultative parthenocarpic fruit development, without any pleiotropic effect in the other vegetative and reproductive organs (Klap *et al.,* 2017; Takisawa *et al.,* 2018). A further MADS-box transcription factor that in tomato has been demonstrated to play an important function during both flower and fruit development is *MADS-BOX29* (*TM29*). It is an E-class gene (Fig. 4.1), and it has 68%, 63%, and 58% protein homology sequence with AtSEP1 (AGL2), AtSEP2 (AGL4), and AtSEP3 (AGL9), respectively. Indeed, it is highly expressed in all the flower whorls and when down-regulated, alterations in flower morphology occur. Moreover, down-regulation

of *TM29* resulted in the development of parthenocarpic fruits, suggesting that this gene has a negative regulatory effect on ovary growth before pollination (Ampomah-Dwamena *et al.,* 2002).

Another gene involved in the post-fertilisation differentiation of fruit tissues is *FRUITFULL* (*FUL*). This encodes a MADS-box transcription factor that negatively regulates the valve-margin identity genes in *A. thaliana (At)* (Liljegren *et al.,* 2004) and its expression is first observed in the carpel primordia during early flower development and later only in the valves regions. Targets of *AtFUL* are the *SHATTERPROOF1* (*SHP1*) and *SHATTERPROOF2* (*SHP2*) genes. The *AtSHP* genes also encode MADS-box transcription factors, which are necessary for the differentiation of the dehiscence zone, at the valve margin close to the replum, and for the lignification of the neighbouring cells. *AtSHP1* and *AtSHP2* are involved at the beginning of the genetic pathway that regulates the formation of the dehiscence zone (Liljegren *et al.,* 2000). These genes are also important in tomato fruit development. Indeed, a reduction of *SlFUL1* and *SlFUL2*, which are the homologs of *AtFUL*, greatly affects late fruit development, impacting on the ethylene-independent ripening process (Bemer *et al.,* 2012; Fujisawa *et al.,* 2014; Shima *et al.,* 2013). Moreover, knock-down of the tomato *SHP* orthologue, *TOMATO AGAMOUS-LIKE1* (*TAGL1*), affects both flower and fruit development, causing a loss of the style trichomes and a thinner fruit pericarp respectively (Vrebalov *et al.,* 2009), while its ectopic expression leads to the development of lycopene-rich fleshy sepals, supporting typical function of the C-type genes (Pan *et al.,* 2010; Pineda *et al.,* 2010). Finally, the combination of these mutant phenotypes and the gene expression patterns during fruit development also seem to support the model of a negative regulation of *TAGL1* by *SlFUL1* and *SlFUL2* in tomato, thus confirming the conservation of their roles and their regulatory interactions. This model is further supported by the results found in peach (*Prunus persica*).Whilst very little is known about the genetic regulation that occurs during the differentiation of the cherry fruit in all its components, many studies have been made in peach, which is emerging as a plant model for Rosaceous tree species, thanks to its small genome size of 300 Mb, which is slightly smaller than that of cherry (350 Mb) and about twice that of *A. thaliana* (135 Mb), and with a moderately short juvenile phase of 2-3 years. Peach, like cherry, belongs to the same clade of Rosids as Arabidopsis and they share anatomical and physiological

similarities regarding their flowers and fruits. In the peach genome, one putative *PpeFUL* ortholog gene and two copies of *PpeSHP* genes have been identified. Once aligned to the closest matching homologous protein sequences, both *PpeFUL* and *PpeSHP* showed the MADS domain are conserved, along with the conserved regions in the I and K domains, whilst the C-terminal domain was observed to be more divergent in both cases (Tani *et al.,* 2007). In addition, *PpeSHP* has been shown to maintain its typical function of C-type MADS-box transcription factor, since its overexpression in tomato promotes the formation of carpel-like fleshy and reddish sepals (Tadiello *et al.,* 2009). *PpeFUL* is expressed mostly in the mesocarp and in the exocarp, while its expression is very low in the endocarp. In contrast, *PpeSHP* gene expression is high in the endocarp but almost undetectable in the mesocarp and in the exocarp (Dardick *et al.,* 2010). Furthermore, peach cultivars with the split-pit phenotype, which is associated with a higher degree of lignification, show higher expression of *PpeSHP*. Interestingly the split-pit is a structure similar to the dehiscence zone of the dry fruits, where the important role of FUL and SHP in regulating lignin deposition, cell expansion and cell separation processes have been demonstrated (Fourquin & Ferrándiz, 2012; Heijmans *et al.,* 2012; Liljegren *et al.,* 2000; Tani *et al.,* 2007). Thus, all these results suggest that this regulatory pathway, where FUL is responsible for the inhibition of SHP, which in turn is upstream in the lignification pathway and seems to be conserved in dry and fleshy fruits, at least in the core eudicots.

Lastly, SHP1 and SHP2 are found to be associated with a D-class transcription factor, SEEDSTICK (STK). In Arabidopsis, *STK* is not only involved in the differentiation within the endocarp of the layer that will become lignified upon maturation but is also a master regulatory gene of ovule development, since ectopic expression of *STK* is sufficient to induce the formation of ectopic ovules (Favaro *et al.,* 2003). On the other hand, one of the most distinct phenotypes observed in the *stk* single mutant is the failure of the seed release from the mature fruit, due to a lack of lignification (Pinyopich *et al.,* 2003). In peach, one putative copy of the *STK* gene was identified and comparative analysis showed that it belongs to the D-lineage along with the other D-type MADS-box transcription factors and that the typical D lineage sequences at the C-terminus and the extension between the stop codon and the AG motif II are conserved (Tani *et al.,* 2009). *PpeSTK* expression is very high in the endocarp at the beginning of fruit development (at 29 Days

After Anthesis), and it decreases progressively during the next weeks (at 60 DAA it is not expressed anymore), while it remains low both in the exocarp and in the mesocarp (Dardick *et al.,* 2010). Therefore, it seems that there is a spatial regulation of gene expression during peach fruit development, and it could resemble the expression pattern observed in Arabidopsis. In conclusion, STK seems to be involved in the specification of the endocarp since another example is reported in the fruit of oil palm, where the natural *stk* mutant is almost stoneless (Singh *et al.,* 2013).

4.1.5 Hormonal signals and fruit development: Auxin

The most abundant auxin in higher plants is indole-3-acetic acid (IAA) the biosynthesis of which uses amino acid Tryptophan (Trp) as a precursor through a process that comprises two steps and is well conserved among higher plants (Mano and Nemoto 2012; Zhao, 2014). The first step of the pathway consists of the conversion of Trp into indole-3-pyruvate (IPA) by the TRYPTOPHAN AMINOTRANSFERASE OF ARABIDOPSIS (TAA) and TAA-related (TAR) families of amino transferases. Subsequently IPA is converted into IAA by the YUCCA family of flavin monooxygenases (Cao *et al.,* 2019). Both TAA/TAR and YUCCA families are characterised by several functionally redundant members. Alterations in the expression of one or more of these genes led to aberrant embryo phenotypes, due to defects of synthetised auxin (Stepanova *et al.,* 2008; Tao *et al.,* 2008; Stepanova *et al.,* 2011; Mashiguchi *et al.,* 2011; Zhao *et al.,* 2014; Brumos *et al.,* 2018). Notably, mutants in auxin biosynthesis show aberrant embryo phenotypes of the same type as those present in mutants in which the transport of auxin is affected.

Since auxin signalling is crucial for many developmental processes, its transport is highly regulated. Auxin transport is carried out by four classes of transporters: the PINFORMED (PIN) family, the PIN-LIKES (PILS) family, and the AUXIN1/LIKE-AUX (AUX/LAX) family the ATP-binding cassette family B (ABCB)-P-Glycoprotein (PGP) family. These transporters can be localised in the plasma membrane or in the endoplasmic reticulum, randomly or polarised to direct specifically the auxin flux (Kramer *et al.,* 2004, Zažímalová *et al.,* 2009). PIN proteins are the most important efflux carriers and they have been reported to play a crucial role also during fruit development.

Loss of PIN functionality leads to severe effects on embryo development, i.e. the level of aberration increases with the higher loss of PINs. For example, tomato ovaries have a high expression level of the *SlPIN4* gene, which decreases during fruit development. RNAi-mediated *SlPIN4* silencing causes the development of a parthenocarpic fruit, in addition to alterations in flower development. Mounet and collaborators suggest that *SlPIN4* has a crucial role in regulating auxin levels in tomato ovaries and in fruit set in tomato (Mounet at al., 2012).

Auxin regulates gene expression by causing the degradation of the AUXIN/INDOLE-3-ACETIC ACID (AUX/IAA)s, which are repressors bond to the AUXIN RESPONSE FACTORS (ARFs). Auxin binds the TRANSPORT INHIBITOR RESPONSE1 (TIR1) receptor, which promotes the polyubiquitination and degradation of the AUX/IAA proteins. Once freed from AUX/IAAs, ARFs can form homo or heterodimers and activate the transcription of the auxin response genes (Fig. 4.3) (Israeli *et al.,* 2020). The essential role of the AUX/IAAs and ARFs during fruit development is reported in many species including tomato (Goetz *et al.,* 2007; Hu *et al.,* 2018), eggplant (Du *et al.,* 2016), cucumber (Su *et al.,* 2021) and strawberry (Zhou *et al.,* 2021). In particular, the tomato ARF7 and AUX/IAA9, have not only been reported to be negative regulators of fruit set, but also seem to be involved in the crosstalk with the gibberellin signalling pathway (Hu *et al.,* 2018).

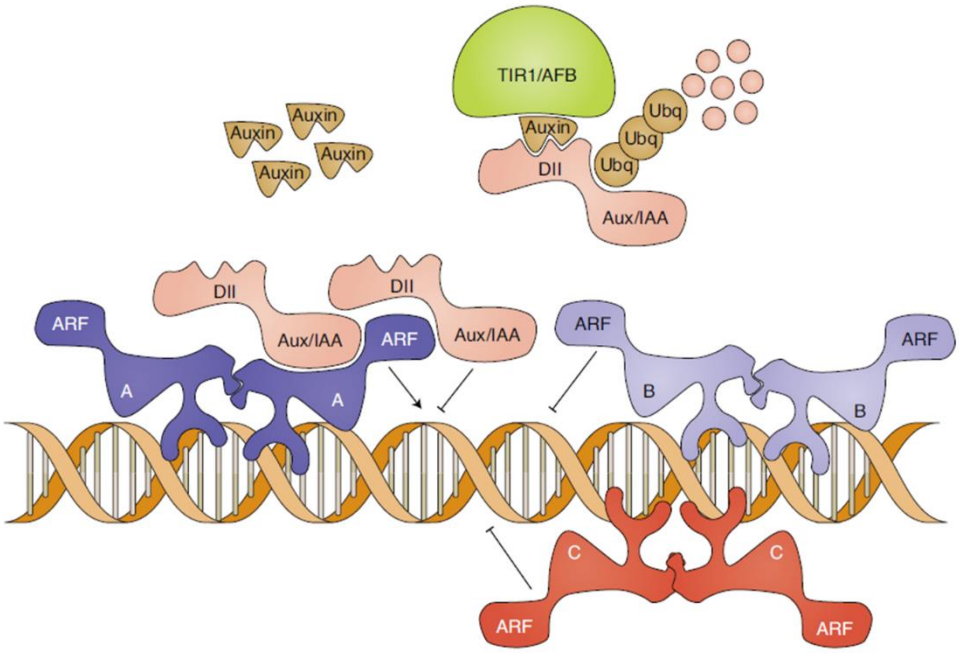


Figure 4.3: Illustration of the auxin signalling pathway. Three classes of ARFs have been identified: class-A includes mostly transcription activating ARFs, while classes-B & C are mainly transcriptional repressors. Only A-class ARFs are reported to interact with AUX/IAA proteins. Israeli *et al.,* 2020.

4.1.6 Hormonal signals and fruit development: Gibberellins

Gibberellins (GA) are tetracyclic diterpenoids that have a key function in seed and fruit development (Serrani *et al.,* 2007a; Serrani *et al.,* 2007b). The GA precursor is geranylgeranyl diphosphate, which is converted into ent-kaurene through a two-step reaction conducted by the ent-COPALYL DIPHOSPHATE SYNTHASE (CPS) and ent-KAURENE SYNTHASE (KS) enzymes. Ent-kaurene is then converted by ent-KAURENE OXIDASE (KO) and ent-KAURENOIC ACID OXIDASE (KAO) into GA_{12}. Finally, GA3-OXIDASES (GA3OX) GA13-OXIDASE (GA13OX) and GA20-OXIDASES (GA20OX) convert GA_{12} into the bioactive forms GA_1, GA_3, GA_4 and GA_7. GA homeostasis is maintained by GA2-OXIDASES (GA2OX) that converts the bioactive GA into their inactive forms (Hedden *et al.,* 2020). GA biosynthesis is linked to fruit set as is demonstrated, for example, in tomato and in pear, where the up-regulation of *SlGA20OX* and *PbGA20OX* respectively, led to an increase of the GA_4 levels and the formation of parthenocarpic fruits (Wang *et al.,* 2020).

Moreover, the down-regulation of *SlGA2OX* in tomato resulted in parthenocarpy associated with higher levels of GA_1 and GA_4 (Martínez-Bello *et al.,* 2015).

The GA signalling pathway is quite similar to the one described for auxin (Fig. 4.3). Indeed, GID1 (GA-INSENSITIVE DWARF1) is the GA receptor, and once bound to a molecule of GA, it promotes the degradation of the DELLA proteins. These proteins are negative regulators of GA signalling pathway. In tomato, a loss-of-function or down-regulation of *SlDELLA* led to the formation of parthenocarpic fruits, further confirming the crucial role of GA in fruit set (Martí *et al.,* 2007, Carrera *et al.,* 2012).

Gibberellins seem to be involved in the activation of the cell cycle in the ovary-wall cells. In fact, Mesejo *et al.,* (2016) compared the GAs levels and the gene expression in two different varieties of *Citrus*, Satsuma (*Citrus unshiu*) and Clementine (*Citrus clementina*), which are obligate and facultative parthenocarpic respectively. In Satsuma, the expression levels of *CYCA1;1*, which encodes a cyclin expressed during the G2 phase and controls the G2/M phases of the cell cycle (Fabian *et al.,* 2000), is higher than the one in Clementine. Interestingly in Satsuma there is a peak of *GA20OXIDASE2* (*GA20OX2*) expression just before the peak of *CYCA1;1* expression, while in Clementine this is delayed. Another GA biosynthetic enzyme encoding gene, *GA3OX2*, has a higher expression level in Satsuma than Clementine, during fruit development. Treatments with GA_3 caused an increase of GA_{20} and GA_1, which is the most important GA precursor in Satsuma ovaries. More importantly, a 132% increase of *CYCA1;1* expression has been observed six hours after treatment, and this effect is lost after two days. The treatment with paclobutrazol (PBZ), an inhibitor of GA biosynthesis, caused a decrease in *CYCA1;1* expression after six hours and this effect was maintained up to two days, proving once again that GAs influence the transcription rate of *CYCA1;1*. GA_3 enhances cell division, increasing the number of cell layers in the pericarp (effect lost at 15 Days After Treatment) while the opposite and expected effect has been observed after PBZ treatment. These effects on cell division and parthenocarpic fruit set upon GA_3 application have also been observed in Clementine (Mesejo *et al.,* 2016).

GAs have been shown to promote the transcriptional activation of many other genes that are involved in the fruit development. Transcriptome analysis of 'Dangshansuli' pear treated with GA_{4+7}, which induces parthenocarpic fruits, showed that 31 cyclins and 2 cyclin-dependent kinases (CDKs) were up-regulated at 3 DAT, while in the pollinated control this occurred at 9 DAT. Also, genes encoding expansins, enzymes involved in the modification of the cell wall, have been shown to be up-regulated in both the GA_{4+7} treated and pollinated ovaries. Briefly, 103 cell wall-related Differentially Expressed Genes (DEGs) have been identified between unpollinated and GA_{4+7} treated ovaries and 72 DEGs between unpollinated and pollinated ones at 3 DAT. Moreover, the number of differentially expressed transcription factors with similar expression patterns between GA_{4+7} and pollinated ovaries increases with time (32 at 3 DAT, 139 at 9 DAT and 329 at 14 DAT). These transcription factors belong mostly to the bHLH, MYB, NAC and WRKY families. The treatment with GA also influences the other hormonal pathways, since the treated ovaries showed a small but significant increase of IAA at 3 and 14 DAT, and a significant drop of abscisic acid (ABA). Indeed *PbARF5*, *PbARF6*, *PbARF18*, *PbARF19-like* and *Pb9-cis-epoxycarotenoid dioxygenase* (*NCED*) have been found to be down-regulated in both the GA_{4+7} treated and pollinated ovaries. Therefore, the model proposed by Liu and collaborators suggests that GA_{4+7} mimics the effect that pollination has in changing the hormones levels, causing a downstream change of expression of genes involved in different aspects of the transition from ovary to fruit (Liu *et al.,* 2018).

The role of auxins in fruit development from unfertilised ovules is well documented. It has been proposed that auxin can act as an alternative signal replacing pollination and fertilisation to initiate the fruit growth (Serrani *et al.,* 2008). Interestingly, 'Dangshansuli' pear emasculated pistils treated with the synthetic auxin 2,4-D, have been shown to produce parthenocarpic fruits, which are significantly smaller than the seeded fruits. Furthermore, ovaries treated simultaneously with 2,4-D and PBZ show a significant reduction of cortex thickness, cells division and cell expansion. Moreover, in the ovaries treated with 2,4-D, two pear cyclin-dependent kinases encoding genes, *Pbcyclin-dependent kinase B2;2* and, *Pbcyclin-dependent kinase B2;2-like*, and one expansin gene, *Pbexpansine-A10*, were up-regulated. In contrast, they were down-

regulated when co-application with PZB occurred. 2,4-D mostly induces the production of bioactive GA_4 (4-fold increase) and not GA_3, whose levels remain the same. Co-application of 2,4-D with PBZ, caused a drop of the GA_4 levels, while the GA_3 were not affected. The final evidence consists of the up-regulation of *PbGA20OX2-like* and *PbGA3OX-1*, involved in the production of GA_4, and the down-regulation of *PbGA2OX1-like* and *PbGA2OX2-like*, which converts the GA_4 precursors into an inactive form (Cong *et al.,* 2019). Furthermore, in tomato, auxin-induced parthenocarpic fruit development is mediated partially by GA, since co-application of auxin and PBZ causes a significant reduction in parthenocarpy (Serrani *et al.,* 2008). Auxin seems to act upstream of GA in the induction of fruit set, since auxin can trigger GA biosynthesis but not vice versa (Dorcey *et al.,* 2009).

4.1.7 Hormonal signals and fruit development: Ethylene

Ethylene is a gaseous hormone, involved in different processes such as fruit ripening, flower and leaf senescence and abscission, and germination (Yang and Hoffman 1984; Mattoo and Suttle 1991; Abeles *et al.,* 1992). However, it is also known to negatively influence fruit set. In tomato (Shinozaki *et al.,* 2015; Shinozaki *et al.,* 2018) and zucchini (Martínez *et al.,* 2013), the inhibition of ethylene biosynthesis resulted in parthenocarpic fruit development, while provision of an ethylene precursor, 1-aminocyclopropane-1-carboxylic acid (ACC), was shown to repress fruit set.

The ethylene biosynthetic pathway is a two-step process, starting with S-adenosyl-L-methionine (SAM). SAM is converted by ACC SYNTHASE (ACS) into 1-aminocyclopropane-1-carboxylic acid (ACC), which is subsequently converted into ethylene by ACC oxidase (ACO) (Argueso *et al.,* 2007). In tomato, lower expression of the ethylene biosynthesis genes has been found in the unpollinated ovaries of the parthenocarpic mutants *iaa9* and *pf1* (Shinozaki *et al.,* 2015; Clepet *et al.,* 2021). However, studies in zucchini (Martínez *et al.,* 2015), and in cucumber (Xin *et al.,* 2019), suggest that a certain level of ethylene is required at anthesis in the pollinated ovules for successful fruit set and development. Indeed, cell division has been proved to be negatively affected by the complete inhibition of ethylene biosynthesis (Xin *et al.,* 2019). This may explain why parthenocarpic fruits obtained following the applications of ethylene inhibitors to

unpollinated ovaries, or from mutants with ethylene biosynthesis negatively affected, are reported to be smaller than other parthenocarpic fruits with alterations in other pathways (Shinozaki *et al.,* 2015; Matsuo *et al.,* 2020).

Ethylene receptors, ETHYLENE RECEPTOR 1,2 (ETR1,2), ETHYLENE RESPONSE SENSOR (ERS1,2) and ETHYLENE INSENSITIVE 4 (EIN4), are transmembrane proteins mainly localised in the endoplasmic reticulum. Once bound to ethylene, these receptors are inactivated and can no longer activate the negative regulator CONSTITUTIVE TRIPLE RESPONSE1 (CTR1) kinase, allowing the downstream MAP kinases to start a signal cascade (Fig. 4.4). EIN2 is activated, resulting in the activation of EIN3/EIN3-LIKE (EIL) complex and the ETHYLENE RESPONSE FACTORS (ERFs). The abundance of ethylene receptors is tightly controlled by the ubiquitin-proteasome pathway, which is activated when the ethylene levels increase (Chen *et al.,* 2005). The importance of these genes during fruit set and parthenocarpy have been demonstrated in tomato (Shinozaki *et al.,* 2015), zucchini (Martínez *et al.,* 2015), cucumber (Wu *et al.,* 2016) and pear (Wang *et al.,* 2021).

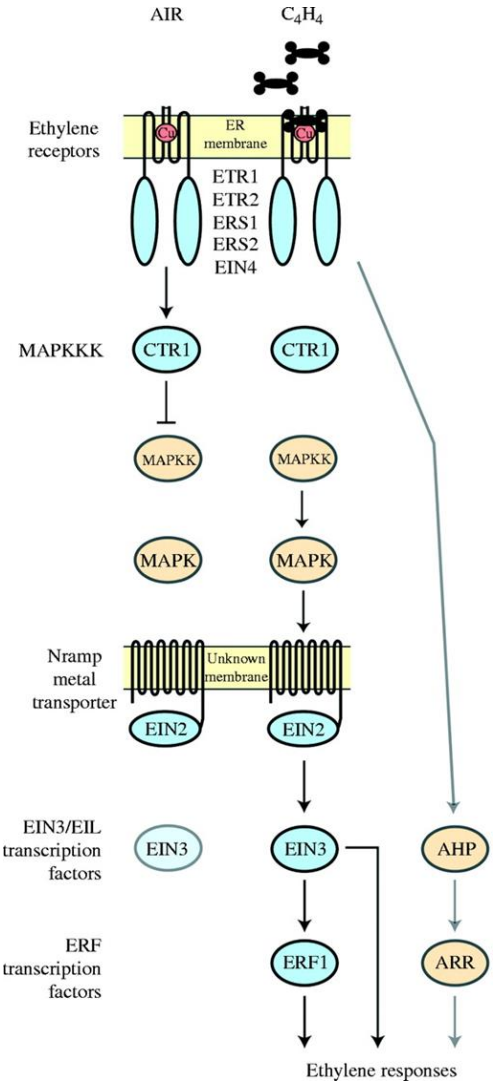


Figure 4.4: Schematic representation of the ethylene signalling pathway. When ethylene is not present the receptor activates CTR1, which inhibits the phosphorylation cascade promoted by the downstream Map kinases. When ethylene binds the receptor, CTR1 is not activated anymore, allowing the downstream MAPKKK to start the signal cascade. Chen *et al.,* 2005

4.1.8 Hormonal signals and fruit development: Abscisic acid

Abscisic acid (ABA) is an isoprenoid (terpenoid) hormone that is involved in several plant processes, such as response to biotic and abiotic stress (Zhu, 2002; Fujita *et al.,* 2006), seed development, dormancy, and germination (Finkelstein *et al.,* 2002), bud dormancy, flower differentiation and also fruit development and ripening (Forlani *et al.,* 2019; Cheng *et al.,* 2021; Fenn & Giovannoni, 2021).

The ABA biosynthetic pathway branches from the carotenoids pathway. The precursors for the formation of ABA are the epoxycarotenoids neoxanthin and violaxanthin, which are cleaved by a 9-cis-epoxycarotenoid dioxygenase (NCED) to form xanthoxin (Tan *et al.,* 2003). This compound is converted by a short chain dehydrogenase (SDR) into abscisic aldehyde, which is further converted into ABA by the enzyme ABSCISIC ACID OXIDASE (AAO) (Endo *et al.,* 2014). In tomato unpollinated ovaries, ABA biosynthetic genes have been found to be up-regulated and their expression decreases after fruit set. This suggests that ABA plays a role during fruit set. However, application of ABA or ABA inhibitors to unpollinated ovaries did not produce any visible effect, suggesting that ABA's role may be important in relation to the interactions with the other phytohormones (Virezen *et al.,* 2008; Nitsch *et al.,* 2009; Wang *et al.,* 2009).

Under non-stressed conditions, ABA levels are low and a specific E3 ligase polyubiquitinates not only the ABA receptors (PYR/PYL/RCAR), but also the protein kinases SnRK2s and the ABA-responsive factors, promoting their degradation. Moreover, the polyubiquitinated kinases SnRK2s are dephosphorylated by 2C-type protein phosphatases (PP2Cs), inhibiting their kinase activity. Under stress conditions, ABA levels increase in the cell, and it binds the ABA receptor (PYR/PYL/RCAR) that can bind the PP2C phosphatase. The SnRK2 kinase is no longer dephosphorylated and, in its phosphorylated form, can phosphorylate the ABA-responsive transcription factors (Fig. 4.5). Moreover, phosphorylation blocks the polyubiquitination from the E3 ligase and the subsequent degradation from the proteasome (Fujii *et al.,* 2009; Soon *et al.,* 2012; Dejonghe *et al.,* 2018; Sirko *et al.,* 2021). Investigation of the role of ABA in sweet cherry suggests that it plays an important role during flower development and early fruit development.

Indeed, peaks in ABA levels have been found in the cherry ovary at stage V and in developing fruits 7 days after full bloom (DAB) (Leng *et al.,* 2018). In the developing fruits, *PavNCED1* transcripts levels increase constantly, reaching a peak at about 7 DAB, when PaCYP707A2, which degrades ABA, is up-regulated. Genes that encode the ABA receptors PavPYL2 and PavPYL3, are highly expressed in the early fruit such as PavPP2C1, PavPP2C2, PavPPC3 and PavSnRK2.4 (Wang *et al.,* 2015; Leng *et al.,* 2018).

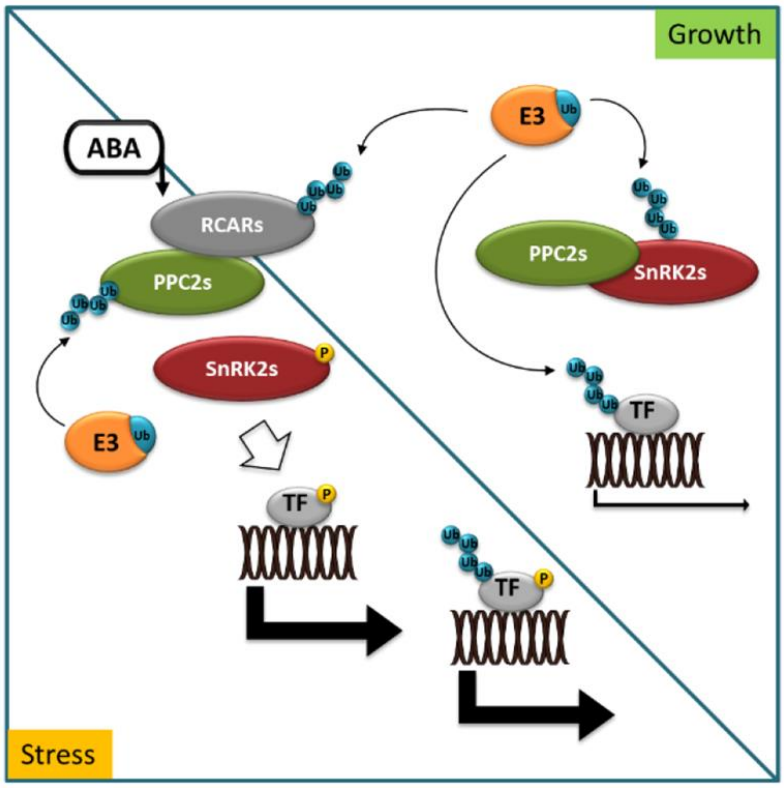


Figure 4.5: Schematic illustration of the ABA signalling pathway. Under non-stressed conditions (growth), PPC2s are free and de-phosphorylate SnRK2s, promoting their poly-ubiquitination, along with the ABA receptors (PYR/PYL/RCAR) and the ABA-responsive transcription factors (TF), by a specific E3 ligase. Under stressed conditions, ABA binds its receptors, which bind the PPC2 phosphatases, promoting their polyubiquitination by E3. SnRK2s are phosphorylated and can promote the ABA-responsive gene transcription, by phosphorylating TFs. Sirko *et al.,* 2021

4.1.9 Hormonal signals and fruit development: hormones crosstalk

Auxin and GA crosstalk has been investigated by Hu et al. (2018). Indeed, the tomato *entire* (*SlIAA9* loss of function), *SlARF7* RNAi and *procera* (*SlDELLA* loss of function) mutants show strong parthenocarpy. Also in tomato, auxin-induced parthenocarpic fruit development is mediated partially by GA, since co-application of auxin and PBZ causes a significant reduction in parthenocarpy (Serrani *et al.,* 2008). Moreover, bioactive GAs levels are high in the auxin-induced and *entire* parthenocarpic fruits because of the increased expression of GA biosynthetic genes and the repression of GA catabolism genes (Mignolli *et al.,* 2015; Serrani *et al.,* 2008). However, while IAA application promotes the formation of a parthenocarpic fruit by increasing the pericarp cell layers and enlarging the placenta, GAs-induced fruits have fewer cell layers but cells are larger. Parthenocarpic fruits induced by simultaneous application of IAA and GA display final size and cellular structure that are similar to the seeded ones. Through different types of experiments, such as Yeast two Hybrid (Y2H), Y3H, and co-immunoprecipitation, Hu and collaborators showed that SlARF7, an activator ARF, interacts with both SlAUX/IAA9 and SlDELLA, through different regions. In addition, ARF7 can form homodimers and heterodimers, but while the homodimerization is not affected by the interactions with SlDELLA or SlIAA9, a small reduction in heterodimerization is observed. The Luciferase assay demonstrated that while *GA20OX1*, *GA3OX1* and *GH3.2*, which encode auxin-amino acid conjugating enzymes that converts auxin to an inactive form, are repressed by SlARF7-SlAUX/IAA9 complex, they are induced by the SlDELLA-SlARF7 complex. Interestingly, SlDELLA seems to antagonise the SlARF7- SlAUX/IAA9 repressive effect on the target genes, such as *Expansin5* (*EXP5*) and the ethylene biosynthetic gene *ACC oxidase4* (*ACO4*) (Shinozaki *et al.,* 2015). As mentioned above, simultaneous application of auxin and GA produces the formation of a fruit with a structure similar to the seeded fruit, and this has been observed also in the *e pro* and *SlARF7i pro* double mutants, where both the pathways are affected. This can be explained by the fact that in tomato the crosstalk between GA and IAA, during the fruit set, occurs through DELLA, ARFs and IAA9 (Hu *et al.,* 2018) (Fig. 4.6). More recently, it has been proved this interaction occurs also in poplar to regulate gene expression in cambial development (Hu at al., 2022). These data and those highlighted by Sharif *et al.,* (2022)

demonstrate that synergistic and antagonistic crosstalk between hormones is essential for determining the fate of fruit set.

While auxin and gibberellins have a crucial role in fruit set, as mentioned above, ethylene and ABA also play a role in the regulation of fruit set, by acting mostly as negative regulators (Fig.4.6). In the model proposed by Shinozaki *et al.* (2015), ethylene has a negative impact on GA metabolism because it represses the expression of the GA biosynthetic gene *SlGA20OX3*, and promote the expression of *SlGA2OX* genes, along with the stabilisation of the SlDELLA proteins. Moreover, ethylene seems to have a positive effect on ABA synthesis because in the *Sletr1-1* mutant, a lower accumulation of ABA has been observed in unpollinated ovaries. The interaction between these two hormones has still to be clarified but another proof of it has been found in watermelon unpollinated ovules, where the overexpression of *ACS* and the accumulation of ABA are simultaneous (Chai *et al.,* 2017). In Shinozaki's model, the increase in the levels of auxin in the pollinated ovary, causes an increase in GA concentration and suppresses the accumulation of ethylene, resulting in a further positive effect on GA accumulation. Moreover, ABA concentration also decreases. More recently, in unpollinated ovaries of watermelon, the accumulation of ethylene and ABA is proposed to be responsible for an increase in the expression of fruit set negative regulators DELLA and AUX/IAA9 (Hu *et al.,* 2019). In the tomato mutant *Slrtr1-1* however, no changes in auxin levels have been observed, suggesting that only GA metabolism is affected by ethylene accumulation (Shinozaki *et al.,* 2015). Further studies are needed to clarify the interactions between these phytohormones, but it is also possible that different regulatory mechanisms are adopted in different species.

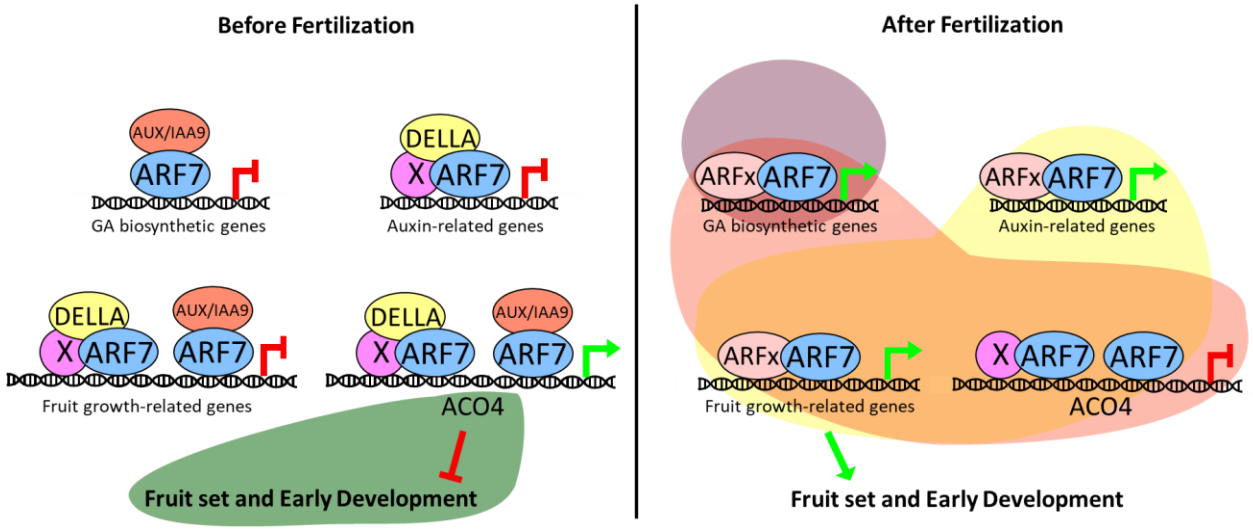


Figure 4.6: Proposed model by Hu *et al.,* (2018) of the crosstalk between auxin and GA signalling pathways during tomato fruit development. Before fertilisation, SlARF7 interacts with SlDELLA and SlAUX/IAA9, repressing the transcription of GA biosynthetic genes and the auxin-related ones. They also activate the transcription of ACO4, enhancing ethylene (green area) levels in the ovary which stays frozen. After fertilisation, auxin signal (purple circle) comes from the fertilised ovule, promoting the degradation of SlAUX/IAA9. Gibberellins (yellow area) are synthetised and promote the degradation of SlDELLA and a further accumulation of auxin (pink area). SlARF7 can interact with other SlARF proteins and promote fruit set. Vignati *et al.,* 2022b.

4.1.10 Cell cycle regulation and hormones

Cell proliferation is essential during organogenesis. In dividing cells, the cell cycle is divided into four distinct phases: G1, S, G2 and M. During Gap1 (G1) phase, the cell grows and prepares for the next phase, Synthesis (S). DNA is duplicated in phase S, and during the next phase, G2, the cells prepare itself for the M phase (mitosis) which results in the formation of two daughter cells (Inzé *et al.,* 2006). The transition from one phase to the next is highly controlled, and the most important and regulated checkpoints occur at the G1/S and G2/M transition boundaries. If the cell fails one of those checkpoints, the cycle will not proceed to the next phase (Menges *et al.,* 2005). This strict regulation is operated mainly by the complexes formed by Cyclins (CYC) and Cyclin-Dependent Kinases (CDK). Cell cycle is driven by the cyclic turnover of the different classes of CYC and by the phosphorylation status of the CDKs. The entry in this four-phased cycle is controlled by the CDKD/CYCH complex or by CDKF, which is positively regulated by CYCH (Shimotohno *et al.,* 2004). These factors activate CDKA/CYCD. The phosphorylation cascade carried out by the CDKA/CYCD complex, results in the CYCA transcriptional activation. At the G1/S checkpoint, CYCA replaces CYCD to form a complex with CDKA. CYCA/CDKA complex regulates the S phase. At the end of S phase, the CYCB/CDKB complex joins the CYCA/CDKA complex, and together they regulate the G2 and M phases. During the M phase, the degradation of CYCB, is needed to reach the end of this phase and end successfully the entire cycle (Dewitte & Murray, 2005). If, during the cycle something is wrong and the process must be stopped, CDKA is inhibited by the CDK-inhibitors (ICKs). P-type cyclins (CYCP) form a complex preferentially with CDKA and are linked to cell division and differentiation (Torres Acosta *et al.,* 2004).

Phytohormones play an active role in cell cycle regulation during organogenesis. Auxin promotes the expression of all the CYCs and CDKs while inhibiting the transcription of the ICKs. CYCB and CDKA are also positively regulated by Gibberellins, which have a negative effect on ICKs. In contrast, ABA promotes the expression of the ICKs (Shimotohno *et al.,* 2021).

Finally, as described above, during fruit development lots of different players have a critical role. The aim of this study was to analyse the gene expression in those players, in order to observe how fruit development is genetically controlled in sweet cherry, since there was not a study like

this. The ovaries and fruits obtained from the field experiment 'Regina' 2020 (Chapter 3), were used, allowing the comparison between the different types of samples. The focus was mostly on genes encoding for proteins that work on the hormone biosynthesis, de-activation, transport and signal transduction pathways, on cell cycle control like cyclins and CDKs and on transcription regulation.

4.2 Materials and Methods

4.2.1 Plant material

The developing cherry fruits and ovaries used for the transcriptomic analysis were collected from the field experiment conducted on the cultivar 'Regina' in 2020 and described in detail in the previous chapter (Chapter 3: 3.2 Materials and Methods). The samples were collected in falcon tubes and immediately frozen in liquid nitrogen and stored at -80°C.

4.2.2 RNA extraction and sequencing

Samples were ground using a mortar and pestle, both cooled with liquid nitrogen to avoid tissue oxidation, which is very quick in the case of cherry ovarian and fruit tissue, and RNA degradation. RNA was extracted with the RNAqueous™ Total RNA Isolation Kit (ThermoScientific), following the protocol reported on the datasheet. RNA quantity and purity was assessed using the Nanodrop (NanoDropTM 1000 Spectrophotometer) and the TapeStation System, to check RNA integrity. All the samples had an RIN integrity number higher than 8. RNA samples were sent to NOVOGENE UK Sequencing Centre (Cambridge, UK). The quality of the RNA was verified and the library created. Quality control results are reported in Table S4.1.

4.2.3 Differential gene expression analysis and GO analysis.

Transcripts were quantified using Kallisto (Bray *et al.,* 2016). The reference transcriptome was downloaded from the Genome Database for Rosaceae (GDR) (*Prunus_avium* v1.0.a1; Shirasawa

et al., 2017). DESeq2 was used to carry out differential expression analysis (Love *et al.,* 2014). From the GDR, the homology report of the *Prunus_avium* v1.0.a1 against Arabidopsis protein sequences was downloaded and used as reference. For the functional enrichment analysis, the web server g:Profiler was used (Uku *et al.,* 2019). Genes were considered to be statistically differentially expressed when the $|\log_2 FC|$ was higher than 1 and the p-value below 0.05. Heatmaps were normalised across features.

4.3 Results

4.3.1 The number of Diffentially Expressed Genes are treatments specific

Transcriptomic analysis can give a good overview of the genetic programs that are active or blocked in different samples. The focus is on the differentially expressed genes (DEGs) between subsequent timepoints within the same treatments. Table 4.1 and Fig. 4.7 show the number of DEGs in the first scenario: same treatment at subsequent timepoints. From timepoint 0 Days After Treatment (DAT) and 7 DAT, the first difference between treatments is observed. Indeed, the two controls show a number of DEGs (< 600) representing between 30-40% of those expressed in the GA_3-treated samples and in the open pollinated ones (O.P.) (1200-1700). Moreover, while the controls and the GA_3 300 mg/L-treated samples present a ratio between the genes that are up-regulated (UP) and down-regulated (DOWN) that is almost 1:1, GA_3 500mg/L-treated and, more evidently O.P., seem to demonstrate greater gene down-regulation (Table 4.1). In fact, in O.P. only 26% of the significantly differentially expressed genes are up-regulated. After 14 days, two interesting results can be observed. The first is that the GA_3-treated putative developing fruits have a number of DEGs (~2,300) approximately 40% higher than the O.P. developing fruits (1,336). Secondly, the UP:DOWN ratio observed at the previous time point, is reversed between the 7 DAT vs 14 DAT one. Indeed, now O.P. and the GA_3-treated samples exhibit a 1:1 ratio, while in the controls a higher number of down-regulated genes is observed. Comparing the 14 DAT vs 21 DAT times, the negative control (N.C.) shows a slight decrease of

number of DEGs, while in the mock control (EtOH 70%) there is a 10-fold decrease. These controls also present a further change in the UP:DOWN ratio. In fact, more genes are significantly up-regulated than down-regulated. In the other samples the 1:1 ratio is maintained. However, while the number of DEGs still increases in the GA_3-treated samples, in the O.P. it is reduced to almost the half of the one observed previously (from 1,336 to 601). In addition, although the UP:DOWN ratio is identical in these three samples, the GA_3-treated samples show a slight majority of up-regulated DEGs, while O.P. demonstrates the opposite. This difference in trends is also found in the later times, but in the opposite manner. At 28 DAT, while the number of DEGs in O.P. stays quite similar compared to the previous one, in all the other treatments a great increase can be observed. Indeed, an increase of about 300%, 4,700%, 250% and 270% occurs in the N.C., EtOH 70%, GA_3 300 mg/L and GA_3 500 mg/L respectively. Finally, the controls, such as the O.P. samples exhibit a higher number of UP DEGs (61.6%).

Treatment	0 DAT vs 7 DAT			7 DAT vs 14 DAT			14 DAT vs 21 DAT			21 DAT vs 28 DAT		
	UP	DOWN	TOTAL	UP	DOWN	TOTAL	UP	DOWN	TOTAL	UP	DOWN	TOTAL
N.C.	231 (41.8%)	322 (58.2%)	553	126 (18.4%)	560 (81.6%)	686	374 (77.8%)	107 (22.2%)	481	1,247 (77.9%)	354 (22.1%)	1,601
EtOH 70%	286 ((52.1%)	263 (47.9%)	549	234 (32.7%)	481 (67.3%)	715	53 (81.5%)	12 (18.5%)	65	1,646 (53.1%)	1,453 (46.9%)	3,099
GA3 300 mg/L	769 (44.7%)	950 (55.3%)	1,719	1,012 (42%)	1,397 (58%)	2,409	1,415 (53.4%)	1,233 (46.6%)	2,648	3,301 (48.4%)	3,519 (51.6%)	6,820
GA3 500 mg/L	615 (37.7%)	1,015 (62.3%)	1,630	1,025 (45.7%)	1,217 (54.3%)	2,242	1,607 (53.1%)	1,418 (46.9%)	3,025	3,756 (45.3%)	4,533 (54.7%)	8,289
O.P.	334 (26%)	951 (74%)	1,285	658 (49.3%)	678 (50.7%)	1,336	280 (46.6%)	321 (53.4%)	601	433 (61.6%)	270 (38.4%)	703

Table 4.1: Number of up-regulated, down-regulated, and total DEGs in each treatment at the four time periods. The percentages in relation to the total number is reported next to the number.

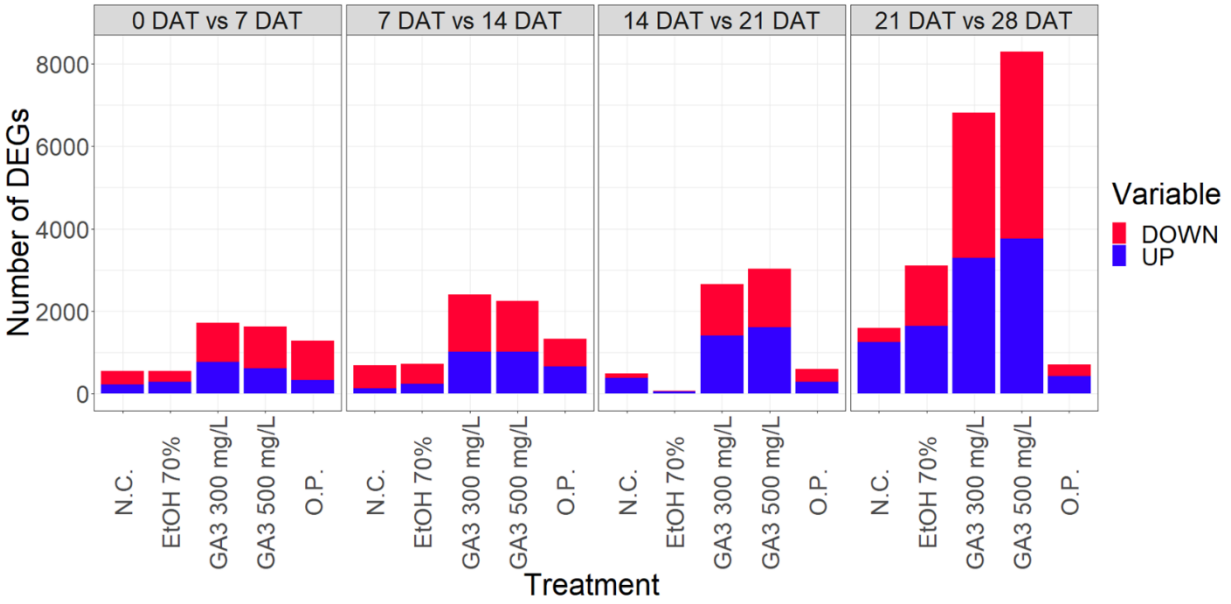


Figure 4.7: Histogram that shows the number of differentially expressed genes (DEGs) in each treatment at the four time periods. DEGs requirements are |log2FC| > 1 and p-adj. < 0.05. The later timepoint in each comparison is the frame to establish if the DEG is up-regulated (UP) or down-regulated (DOWN) compared to the previous timepoint.

The volcano plots of Fig. S4.1-5, show how gene expression differs between one timepoint compared to the previous one. The most significant and greatest changes of gene expression in the negative control occur mostly in the first 14 days (Fig. S4.1). The patterns of the EtOH 70% volcano plots are quite similar to the ones of the N.C. plots. For the mock treatment, the most evident and significant changes in gene expression occur during the two intervals 0 DAT vs 7 DAT and 7 DAT vs 14 DAT (Fig. S4.2). In the GA_3-treated samples, the magnitude of change of expression and its statistical significance is much broader than observed in the controls (Fig. S4.3-4). Moreover, the shapes of the corresponding plots of GA_3 300 mg/L and GA_3 500 mg/L are similar but also the order of the Log2 Fold Change and p-value ($-Log_{10}$*padj*) magnitudes are almost indistinguishable. Finally, the patterns of the O.P. plots seem to be a combination of the ones previously described for the controls and the GA_3-treated samples (Fig. S4.5). Indeed, in the first 14 days, the distribution of the values resembles that observed in the GA_3-treated samples, while between 14 DAT to 28 DAT, it resembles the pattern observed in the control plots (Fig. S4.1-5).

However, the evident difference between the O.P. plots and the control plots is that the O.P. plots present some genes whose expression changes are much greater and highly significant compared to controls (Fig. S4.1;2;6 C-D).

The different treatments share a certain number of DEGs at each timepoint and this number varies from timepoint to timepoint (Fig. 4.8-11). First, the number of genes that are significantly differentially expressed and in common between all the treatments is higher at the first two timepoints than the last two (Fig. 4.8-11). Indeed from 14 DAT there is a severe reduction of the shared DEGs percentage in all the treatments (Table 4.2). Between 0 DAT and 7 DAT, the percentage of shared DEGs in the controls is just below 50%, while for the GA_3-treated and O.P. it is approximately 15% and 20% respectively. In addition, in N.C. and EtOH 70%, more than half of the down-regulated DEGs are shared with all the other treatments (0 DAT vs 7 DAT), while already in the following interval (7 DAT vs 14 DAT) the percentage decreases markedly (from 57.8% and 70.7% to 17.3% and 20.2% respectively). This is not found once the up-regulated DEGs are taken into account (Table 4.1, Fig. 4.8-9).

A direct comparison between two treatments or groups of treatments can be made. The two controls treatments, N.C. and EtOH70%, although their overall results looked quite similar, show differences in the number of shared DEGs in the later stages (Fig. 4.10-11; S4.1-2; Table S4.2A). Indeed, until 14 DAT, the number of DEGs found in these two treatments are quite similar and even the ratios between the shared DEGs and the total amount at the first two timepoints are quite close. At 21 DAT instead, since the DEGs number is reduced about 10 times in EtOH 70 %, all the ratios in N.C. drop as well. Indeed, this observation can be applied for all the comparisons with made EtOH 70% at this timepoint. Interestingly, although in EtOH 70% there is such a small number of differentially expressed genes between 14 DAT and 21 DAT, only about a half of them are shared with the negative control (Fig. 4.10). At 28 DAT, the mock-treated samples exhibit a huge increase (about 4,700%) in the number of DEGs. At this timepoint instead, the N.C. shares the majority of its genes with EtOH 70% (about 75%), but not vice versa (about 38%) (Table S4.2A). Another interesting comparison is the one between the two GA_3-treated samples (Fig8-11; S4.6-13, Table S4.2). The percentage of shared DEGs in all the cases, up-regulated, down-

regulated and in combination, is always quite high. Indeed, it is never below 60%. However, at the last two timepoints, the percentages of shared DEGs in the GA_3 300 mg/L-treated samples are higher than found in the GA_3 500 mg/L samples (about 72% at 21 DAT and 86% at 28 DAT versus about 63% at 21 DAT and 71% at 28 DAT respectively). It means for example that at 28 DAT, GA_3 300 mg/L treated has about 955 DEGs that are not in common, much less than GA_3 500 mg/- treated, which has about 2,404 DEGs not shared with the GA_3 300 mg/L treated samples.

Other informative comparisons are those between the developing fruits, the seeded ones and the putative ones with their negative controls, N.C. and EtOH 70% respectively. While at 7 DAT, N.C. displays a high number of shared DEGs with O.P., in particular the down-regulated ones, in O.P. this occurs much less. Over time, both the treatments, especially the N.C., show an increase in the number of DEGs that are not shared. Indeed, at 28 DAT in N.C., the number of all DEGs that are not shared is three time higher than the one of O.P (1,470 vs 580), and the greater contribution comes from the up-regulated DEGs (1,163 vs 349). This may mean that at 28 DAT, in the N.C. aborting ovaries, there are pathways that are presumably much more activated than in the developing fruits or the number of activated pathways is higher. This is the opposite of what was observed at 7 DAT, when O.P. has a higher number of DEGs, especially down-regulated, than the negative control. This scenario is not exactly the same when the comparison is made between the GA_3-treated putative developing fruits and the mock-treated ovaries. Indeed, until 21 DAT, the pattern of decreasing in magnitude of the shared/overall DEGs ratios is quite similar to the one just described for O.P. and N.C., but at 28 DAT different results can be observed. At 28 DAT, that ratio increases instead of diminishing or being steady. In particular, EtOH 70% has about the 70% of its DEGs (total, up-regulated and down-regulated) shared with both the GA_3-treated samples. However, many more genes are activated and repressed at all the timepoints in the GA_3-treated samples (Table S4.2, Fig. 4.8-11; S4.6-13).

Treatment	0 DAT vs 7 DAT			7 DAT vs 14 DAT			14 DAT vs 21 DAT			21 DAT vs 28 DAT		
	UP	DOWN	TOTAL	UP	DOWN	TOTAL	UP	DOWN	TOTAL	UP	DOWN	TOTAL
N.C.	32.0%	57.8%	47.0%	30.2%	17.3%	20.4%	1.3%	2.8%	1.7%	4.8%	5.1%	5.0%
EtOH 70%	25.9%	70.7%	47.4%	16.2%	20.2%	19.6%	9.4%	25.0%	12.3%	3.6%	1.2%	2.6%
GA3 300 mg/L	9.6%	19.6%	15.1%	3.8%	6.9%	5.8%	0.4%	0.2%	0.3%	1.8%	0.5%	1.2%
GA3 500 mg/L	12.0%	18.3%	16.0%	3.7%	8.0%	6.2%	0.3%	0.2%	0.3%	1.6%	0.4%	1.0%
O.P.	22.2%	19.6%	20.2%	5.8%	14.3%	10.5%	1.8%	0.9%	1.3%	13.9%	6.7%	11.4%

Table 4.2: For each treatment, the percentage of the shared DEGs with all the other treatments is shown in relation to its own total number of DEGs.

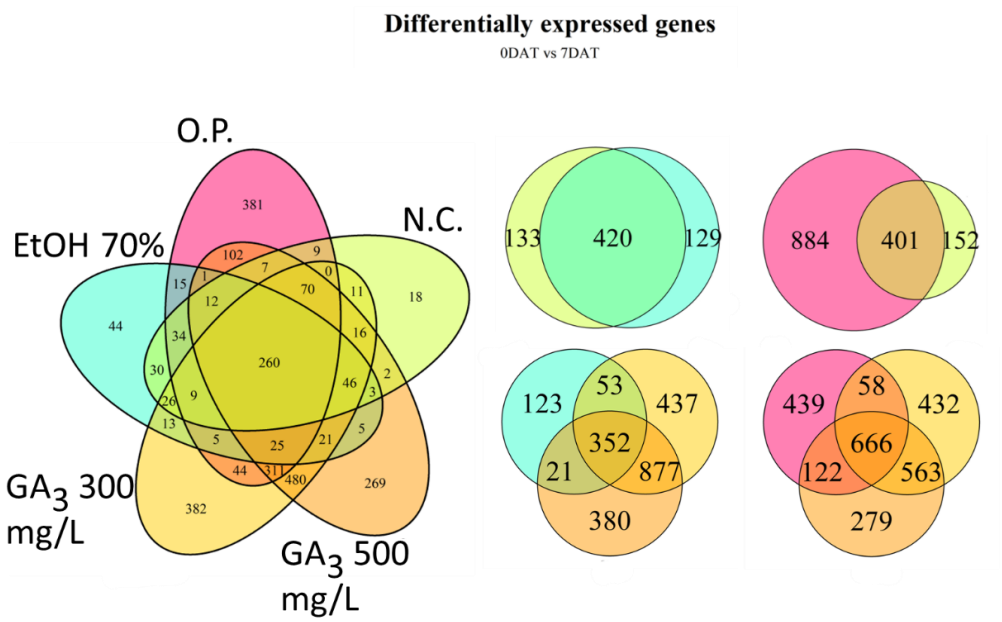


Figure 4.8: Venn diagrams of the significant DEGs (|log2FC| > 1 and p-adj. < 0.05) between 0 and 7 DAT. Green circle: Negative Control; light blue circle: EtOH 70%; orange circle: GA_3 300 mg/L; dark orange circle: GA_3 500 mg/L; magenta circle: open pollinated.

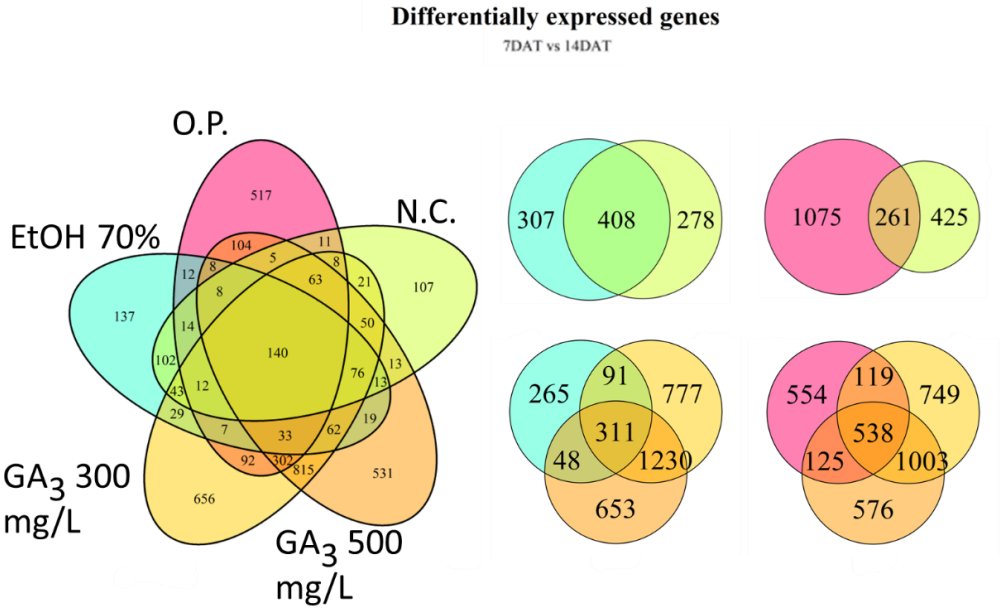


Figure 4.9: Venn diagrams of the significant DEGs (|log2FC| > 1 and p-adj. < 0.05) between 7 and 14 DAT. Green circle: Negative Control; light blue circle: EtOH 70%; orange circle: GA_3 300 mg/L; dark orange circle: GA_3 500 mg/L; magenta circle: open pollinated.

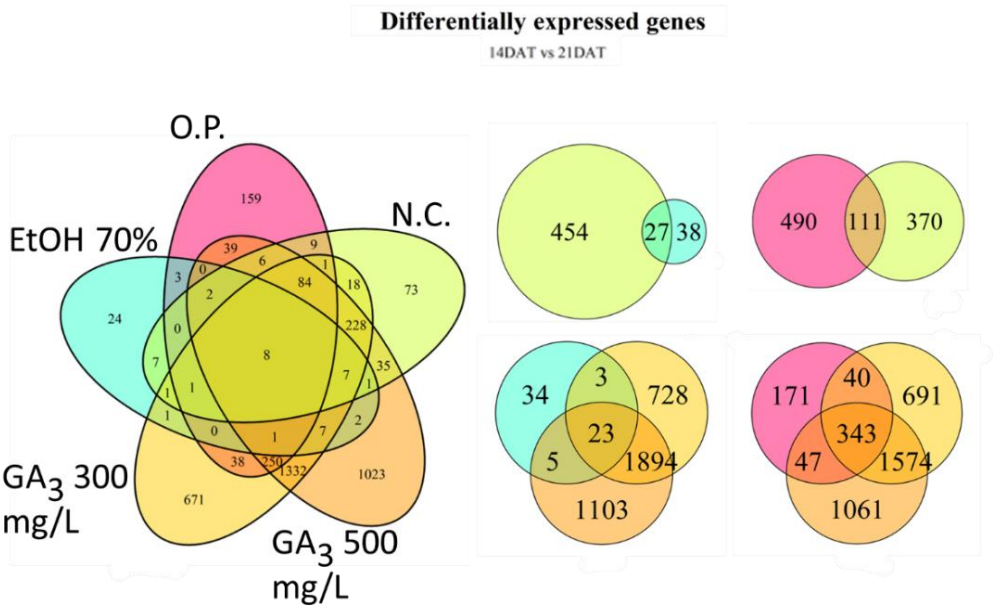


Figure 4.10: Venn diagrams of the significant DEGs (|log2FC| > 1 and p-adj. < 0.05) between 14 and 21 DAT. Green circle: Negative Control; light blue circle: EtOH 70%; orange circle: GA_3 300 mg/L; dark orange circle: GA_3 500 mg/L; magenta circle: open pollinated.

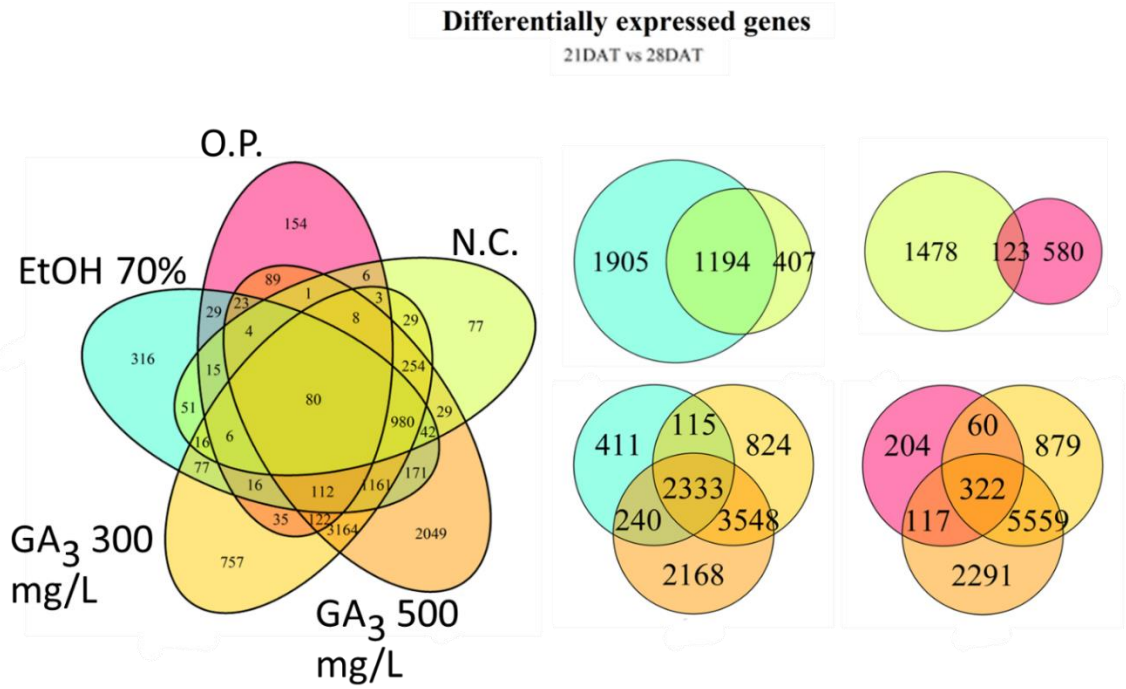


Figure 4.11: Venn diagrams of the significant DEGs (|log2FC| > 1 and p-adj. < 0.05) between 14 and 21 DAT. Green circle: Negative Control; light blue circle: EtOH 70%; orange circle: GA_3 300 mg/L; dark orange circle: GA_3 500 mg/L; magenta circle: open pollinated.

A final last interesting comparison is that between O.P. and the GA_3-treated samples. Since the beginning of the analysis, it is evident that O.P. has a higher number of DEGs shared than the other two treatments. The only exception is at 7 DAT, then about 50% of the down-regulated DEGs are common between the three treatments (Table S4.2; Fig. 4.8-11; S4.6-13). Interestingly, in the intersections O.P./N.C. and O.P./GA_3s, the number of differentially expressed genes at 28 DAT is at least half of the number found at 7 DAT, while in the intersections between the N.C. and the EtOH 70% and between the EtOH 70% and the GA_3s, it always increases, up to 10-fold (TableS4.2; Fig. 4.8-11; S4.6-13).

4.3.2 Pathways DEGs enrichment

Gene Ontology (GO) analysis was used to compare the differentially expressed genes of each treatment at a given timepoint in relation to the timepoint preceding it in order to identify those pathways that have an enriched number of DEGs. All the figures that show the output of this analysis are reported in the Supplementary Material (Fig. S4.14-24). The pathways that have been identified as being significantly enriched are related to response to stimulus, cell cycle, cell division, transcriptional regulation, cell wall, redox reactions, sugars metabolism, transport across the membrane and phosphorylating activity. The description below will focus on the response to hormones, and cell cycle and division.

4.3.3 Gene Ontology terms: response to hormones

A significant number of DEGs in all the treatments at 7 DAT, except for the GA_3 500 mg/L-treated samples, are present in GO terms related to hormones and stimuli (Fig. 4.12). In particular, the O.P. and the GA_3 300 mg/L-treated show a higher degree of significance and number of DEGs that belong to these pathways compared to the two controls. While the O.P. developing fruits seem to have significant changes in expression of genes in the auxin response pathway (response to auxin; GO:0009733), the GA_3 300 mg/L treated putative developing fruits seem more in the abscisic acid response pathway (response to abscisic acid; GO:0009738).

The list of genes that were associated with the GO term “response to hormone” (GO:0009725) has been identified; the majority of them were auxin and ABA response genes (Fig. 4.13; Table

S4.3). The auxin-related genes mostly belong to the SAUR-like auxin-responsive protein family and also ARFs and AUX/IAAs (see next paragraphs), while the ABA-related genes belong to the Major latex-like proteins (MLPs). The heatmap of Fig. 4.13 gives an overview of the gene expression of the DEGs that resulted associated with the GO terms reported in Fig. 4.12. More than 60% (14 out of 22) of the putative SAUR-protein encoding genes are significantly down-regulated at 7 DAT in the O.P. samples, while the putative *PavSAUR*-protein encoding gene (*Pav_sc0001105.1_g280.1.mk)*, is significantly up-regulated (log2FC = 2.010575, p-adj. = 0.0143), but no significant difference is observed when compared to the other treatments (Table S4.3). However, in the subsequent timepoints, the majority of these SAUR-protein encoding genes are significantly up-regulated. The controls keep the expression of those genes quite low. The GA_3-treated samples show a similar pattern to the pattern observed in the O.P., until 21 DAT, however the magnitude of the expression changes is not as great (Table S4.3). At 28 DAT, a significant and remarkable drop in SAUR-protein encoding genes expression occurs in those two GA_3-treated samples (for example *Pav_sc0007626.1_g030.1.br*: log2FC ~ 5 and p-adj. << 0.01; Table S4.3).

In contrast, at 7 DAT, the genes involved in the ABA response pathway, are upregulated (Fig. 4.13). The most significant upregulation occurs in the samples treated, with GA_3 300 mg/L. Gene expression in EtOH 70% and O.P. in most of the cases is lower than that observed in the two GA_3 treated samples. However, the O.P significantly expresses higher putative *PavMLP423* encoding genes (*Pav_sc0000174.1_g1430.1.br* and *Pav_sc0000174.1_g1620.1.br*) at 28 DAT ($log2FC_{O.P.\ vs\ ga3\text{-}treated\ at\ 28DAT}$ ~ 1 and p-adj. << 0.01 and $log2FC_{O.P.\ vs\ ga3\text{-}treated\ at\ 28DAT}$ ~ 7 and p-adj. << 0.01 respectively; Table S4.3), because they are severely down-regulated in the GA_3-treated putative fruits (log2FC ~ 2 and log2FC ~ 7 respectively, and p-adj. << 0.01; Table S4.3). The same can be observed when O.P. and N.C. are compared. This suggests that these two genes may play an important role in fruit development at later stages. Similarly, the expression of the putative *PavMLP423* encoding gene (*Pav_sc0000174.1_g1550.1.br*) is significantly higher in O.P. compared to N.C. at 21 (log2FC = 2.91 and p-adj. = 3.42E-05; Table S4.3) and 28 DAT (log2FC = 1.64 and p-adj. = 0.013; Table S4.3). In contrast, *Pav_sc0000890.1_g670.1.mk*, which putatively encodes for a C2HC zinc fingers superfamily protein is significantly more expressed in N.C than in

O.P. (log2FC = 2.92 and p-adj. = 4.75E-05; Table S4.3). The statistical significance of the difference in gene expression, between these two treatments is observed between 14 DAT to 28 DAT.

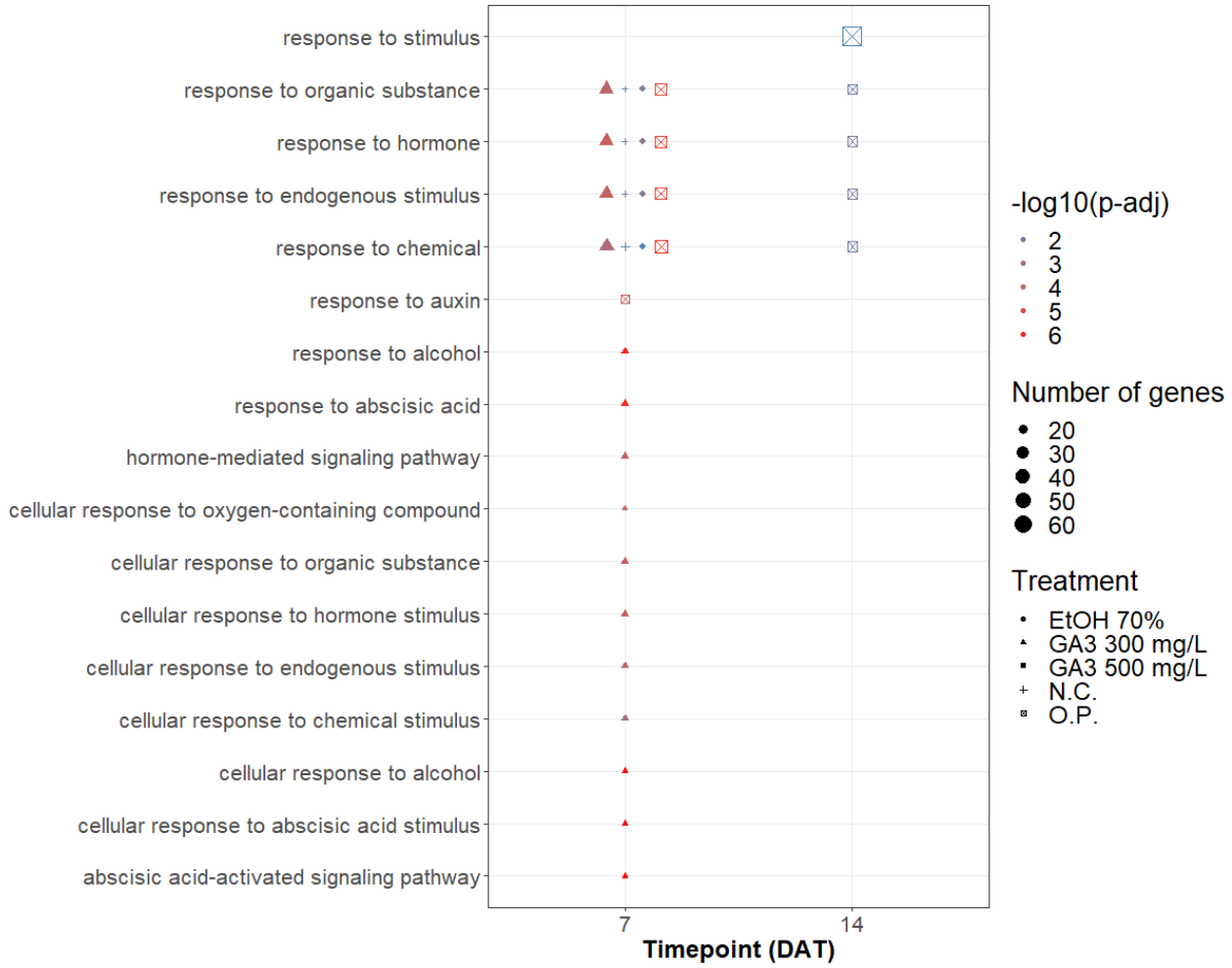


Figure 4.12: Dot plot that shows the pathways enriched according to the DEGs genes identified. The GO terms belong to the category "biological process" category and are all related to the response to hormones.

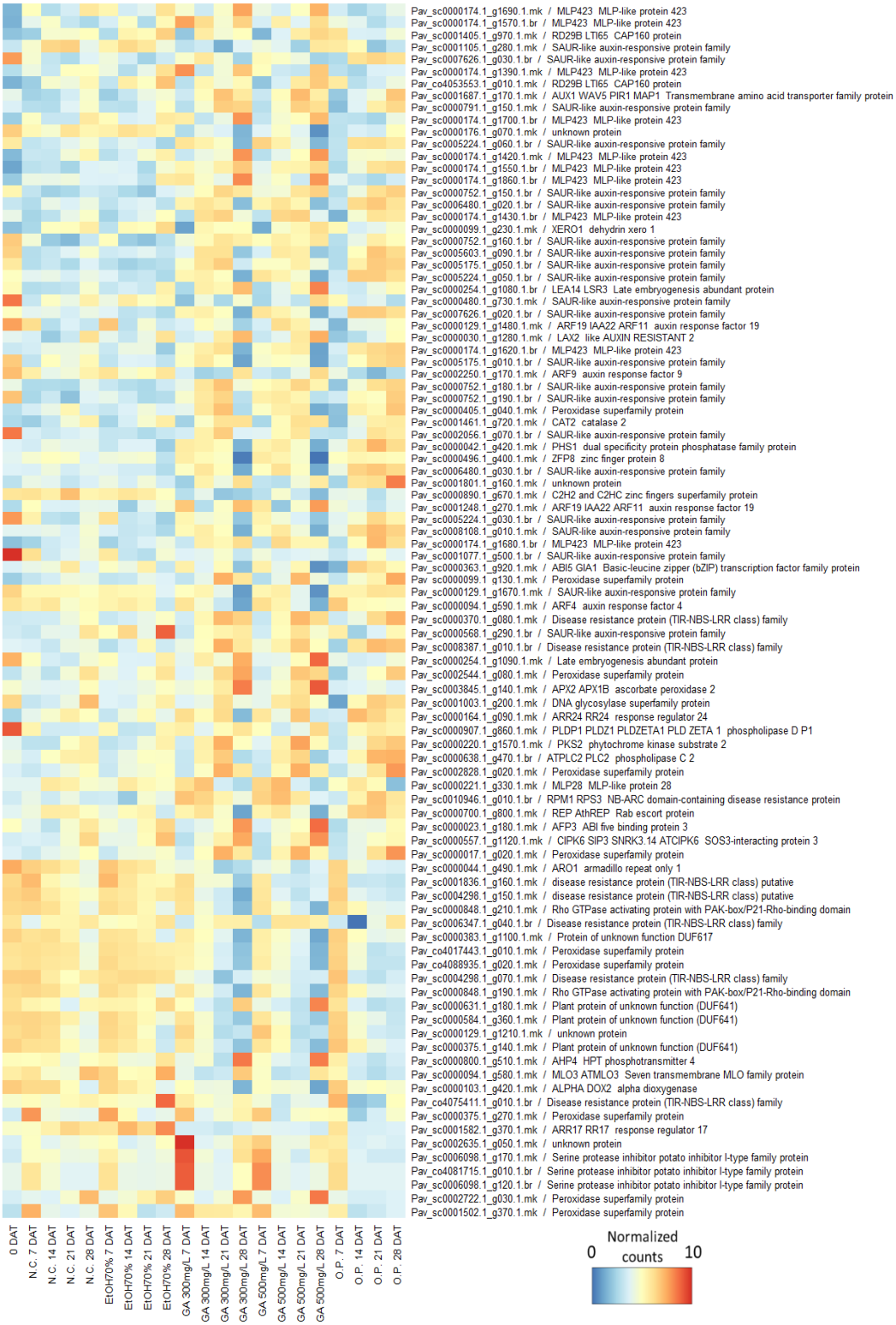


Figure 4.13: Heatmap of the genes associated with the GO categories related to response to hormones. Scale bar indicates the normalised gene counts.

4.3.4 Auxin: biosynthesis and signalling genes are differentially expressed

4.3.4.1 Auxin levels are regulated by auxin biosynthesis, conjugation and transport modulation

The expression profiles of the putative auxin biosynthetic genes are shown in Fig. 4.14. The putative *PavTAR2* gene (*Pav_sc0006018.1_g520.1.mk*) in the O.P. is constantly down-regulated, while in the other treatments after an initial down-regulation, at 14 DAT, start to increase its expression. Differential expression patterns were also found for genes of the *YUCCA* family. The putative *PavYUCCA4* gene (*Pav_sc0001258.1_g020.1.mk*) reaches a peak at 7 DAT in the O.P., although not significant, while the controls maintain a relatively constant level of expression and in the GA_3-treated, transcript levels are down-regulated. A continuous decrease of expression occurs at the subsequent timepoints in all the treatments. The levels of the putative *PavYUCCA6* gene (*Pav_sc0000800.1_g1260.1.mk*) stay low in the two controls through all the time. At 7 DAT the GA_3-treated samples have a peak of expression, followed by a significant decrease in transcript levels in the subsequent timepoints. The O.P. displays a peak in *PavYUCCA6* gene expression at 14 DAT, but expression levels are not as elevated as observed in the putative fruits at 7 DAT. At 21 DAT, *PavYUCCA6* transcript level is significantly higher ($1.1 < \log_2FC < 1.3$) in the O.P. than in all the other treatment, while at 28DAT the difference is significant only in relation to the GA_3-treated samples (log2FC ~ 4 and p-adj. << 0.01; Table S4.4). The putative *PavYUCCA10* gene (*Pav_sc0000848.1_g330.1.mk*), transcript level remains low in the N.C. and EtOH 70% controls. In contrast, a significative increase in transcript levels is observed at 14 DAT in GA_3-treated samples (log2FC ~ 2 and p-adj. << 0.01; Table S4.4), peaking at 21 DAT before significant down-regulation is observed (log2FC ~ 2.5 and p-adj. << 0.01; Table S4.4), while in the O.P. the levels continue to increase (Fig. 4.14; Table S4.4). The two putative genes that encodes for auxin receptor PavTIR1 (*Pav_sc0000848.1_g430.1.mk*; *Pav_sc0000598.1_g680.1.mk*) are highly expressed in the unpollinated ovaries at 0 DAT. They are down-regulated, non-significantly, in the GA_3-treated and O.P. samples, while in the controls the expression does not change at 7 DAT (Table S4.4). In all the treatments, especially the controls and the GA_3-treated, it is up-regulated, with the putative fruits showing a significant change of *Pav_sc0000848.1_g430.1.mk* expression levels at 14 DAT and 28 DAT (Table S4.4). Moreover, the O.P. expression of

Pav_sc0000848.1_g430.1.mk is statistically lower than the one in the GA_3-treated at 28 DAT (p-adj. < 0.05; Table S4.4). The O.P. at 28 DAT, reaches the same expression levels that were found at 0 DAT (Fig. 4.14).

Auxin homeostasis can be controlled by auxin conjugation made by the auxin-amido synthases encoded by the *GRETCHEN HAGEN 3* (*GH3*) genes. As the heatmap in Fig. 4.14 shows, *GH3* genes are expressed at all the timepoints in all treatments. However, some are differentially expressed. The putative *PavGH3.1* gene (*Pav_sc0000049.1_g070.1.mk*) shows a peak of expression at 21 DAT and 28 DAT in the O.P. samples while in the other treatments its expression is low at the beginning and then close to zero in the last two timepoints. A different expression pattern is observed for a second putative *PavGH3.1* gene (*Pav_sc0001422.1_g120.1.mk*). At 28 DAT the O.P. samples, the expression of *PavGH3.1* (*Pav_sc0001422.1_g120.1.mk*) is expressed at significantly lower levels than observed in all other treatments at the same timepoint (log2FC > 2; Table S4.4). O.P. indeed, is the only treatment that does not increase *PavGH3.1* (*Pav_sc0001422.1_g120.1.mk*) expression over the course of the experiment. The common feature between the two putative *PavGH3.1* genes is that in GA_3-treated at 7 DAT, both genes are up-regulated, significantly in the case of *PavGH3.1* (*Pav_sc0001422.1_g120.1.mk*) (log2FC ~ 2 and p-adj. < 0.01; Table S4.4). In contrast, the putative *PavGH3.10* gene (*Pav_sc0002360.1_g300.1.mk*) is expressed at a near constant level in all the treatments until 21 DAT, at which time it is down-regulated in all the samples except for the O.P. in which a small up-regulation is observed (Fig. 4.14; Table S4.4). The putative *PavGH3.6* gene (*Pav_sc0000269.1_g440.1.mk*) is not highly expressed in the unpollinated ovaries at 0 DAT, and its expression stays quite low in all the samples until 14 DAT. Indeed, a significant up-regulation in the controls and the GA_3-treated is observed at 28 DAT (log2FC ~ 2 and log2FC ~ 4 respectively, p-adj. < 0.01; Table S4.4), while in the open pollinated it is not expressed. Likewise, the expression levels of the putative *PavGH3.12 gene* (*Pav_sc0003065.1_g090.1.mk*) increase in the controls and the GA_3-treatment at later stages while its expression stays relatively steady in the O.P (Fig. 4.14) samples. The difference of expression between O.P. and the other treatments is significant at 28 DAT (log2FC ~ 1 and p-adj. <0.01; Table S4.4).

The putative *PavGH3.11* gene (*Pav_sc0000254.1_g140.1.mk*) is expressed at higher levels than the other *GH3* encoding genes, and is constantly up-regulated, especially by the putative fruits and the pollinated ones. At 28 DAT the greatest expression levels are observed in the putative fruits, followed by the pollinated ones and finally by the controls (Fig. 4.14).

Gene encoding PIN proteins play an important role in auxin transport. In the controls and the open pollinated samples, the expression levels of the *PIN* genes are elevated overall (Fig. 4.14). The putative *PavPIN2* gene (*Pav_sc0001181.1_g1180.1.mk*) is significantly down-regulated in the O.P. at 7 DAT (log2FC = 1.5 and p-adj. = 8.38E-10; Table S4.4). *PavPIN2* at 28 DAT is significantly lower in the O.P. in relation to the GA_3 300 mg/L-treated samples (log2FC ~ 0.57 and p-adj. = 0.018; Table S4.4). At 28 DAT, the putative *PavPIN5 encoding gene* (*Pav_sc0000744.1_g330.1.mk*) is more highly expressed in O.P. than in the N.C. (log2FC = 2 and p-adj. = 0.0013; Table S4.4). O.P. also has a higher expression of the putative *PavPIN4* gene (*Pav_sc0000103.1_g670.1.mk*; which is down-regulated at 7 DAT as well but not significantly; Table S4.4) and putative *PavPIN8* gene (*Pav_sc0000299.1_g150.1.mk*) compared to N.C. and the GA_3-treated samples (Table S4.4). The putative *PavPIN1* gene (*Pav_sc0001218.1_g170.1.mk*) is highly expressed at 0 DAT. At 7 DAT, a small non-significant up-regulation is observed in the O.P. samples only (Table S4.4). From 14 DAT, expression levels decrease over time, especially in the EtOH 70% and GA_3-treated samples, which at 28DAT show expression levels significantly lower than the levels observed in N.C. and O.P. (Fig. 4.14; Table S4.4).

Another important class of transporters are the AUXIN1/LIKE-AUX1 (AUX/LAX)s, which are major auxin influx carriers. The putative *PavAUX1* gene (*Pav_sc0001687.1_g170.1.mk*) is expressed at 0 DAT, then its expression levels are down-regulated in all treatments at 7 DAT (Fig. 4.14; Table S4.4). After 7 DAT, the O.P. samples show a constant up-regulation while in the putative developing fruits, expression reaches a peak at 21 DAT, and then down-regulation occurs at 28 DAT. Between 14 DAT and 21 DAT, the expression of *PavAUX1* in the GA_3-treated samples is significantly higher even than the one in O.P. (log2FC ~ 1.35 and p-adj. << 0.01; Table S4.4) which is already greater than the ones of the two controls, although not significantly (Table S4.4).

However, at 28 DAT, the highest expression is observed in the O.P. samples, and the difference of expression with N.C. is significant (log2FC = 1.14 and p-adj. << 0.01; Table S4.4). The two putative *PavLAX2* genes (*Pav_sc0000030.1_g1280.1.mk* and *Pav_sc0000373.1_g220.1.mk*) are up-regulated and down-regulated respectively. In both cases though, the most significant changes are observed in the GA_3-treated samples at 28 DAT (Table S4.4). When the expression levels are compared between the negative control and the O.P., between 14 DAT and 21 DAT, *PavLAX2* gene (*Pav_sc0000373.1_g220.1.mk*) is always higher in the controls, while the opposite occurs for *PavLAX2* genes (*Pav_sc0000030.1_g1280.1.mk*). However, at 28 DAT, for both genes the O.P. expression is significantly lower than observed in the negative control ($1 < log2FC < 2$ and p-adj. < 0.05; Table S4.4).

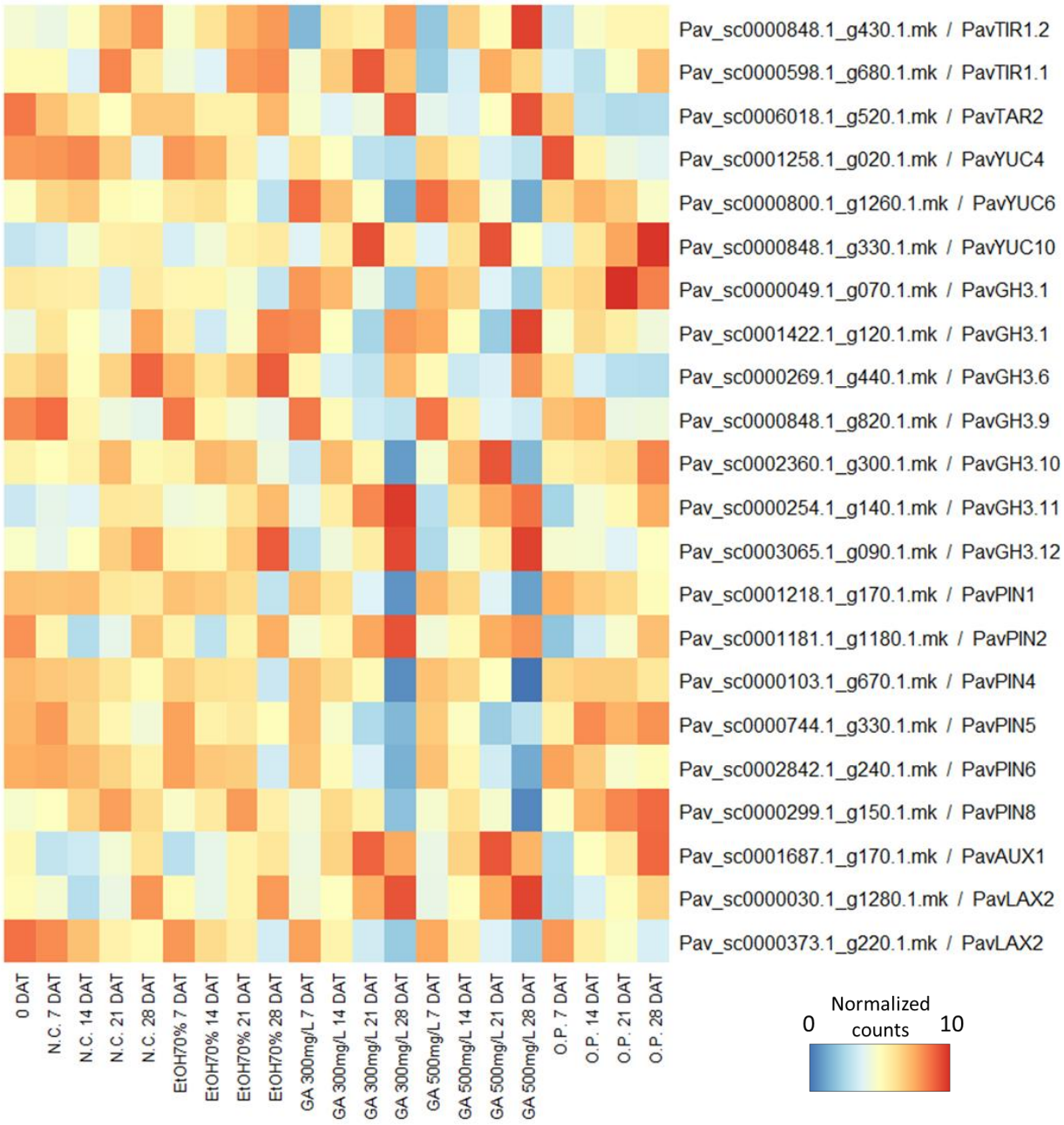


Figure 4.14: Heatmap of the putative cherry orthologs of the genes responsible of auxin biosynthesis, homeostasis regulation and transport. Scale bar indicates the normalised gene counts.

4.3.4.2 Auxin signalling pathway: the AUXIN RESPONSE FACTORS

The auxin signalling pathway is mediated by the *AUXIN RESPONSE FACTORS* (*ARFs*) and *AUXIN/INDOLE-3-ACETIC ACID* (*AUX/IAA*) gene family. The putative *PavARF1* (*Pav_sc0000848.1_g300.1.mk*), *PavARF3* (*Pav_sc0001900.1_g150.1.mk*), *PavARF4* (*Pav_sc0000094.1_g590.1.mk*), *PavARF10* (*Pav_sc0002446.1_g140.1.mk*), and *PavARF16* (*Pav_sc0000084.1_g430.1.mk*) are significantly down-regulated at 28 DAT in the GA_3-treated samples, despite the difference in the expression patterns (Table S4.5). In all the other timepoints, no other significant differences were observed between treatments, except for *ParARF10*, whose levels are higher in the O.P. than in the negative control at 28 DAT (log2FC = 0.68 and p-adj. = 0.045; Table S4.5) (Fig. 4.15). The opposite situation is observed when the putative *PavARF18* (*Pav_sc0000586.1_g230.1.mk*) and *PavARF19* (*Pav_sc0001248.1_g270.1.mk*) genes are considered. These genes are strongly up-regulated only in the GA_3-treated samples at the later stages, while no significant differences are observed between the other treatments (Table S4.5). The O.P. fruits exhibit a $log_2FC = 1.3$ and significant down-regulation of the putative *PavARF7* (*Pav_sc0000129.1_g1480.1.mk*) between 0 and 7 DAT. In the GA_3-treated samples, a significant down-regulation of the putative PavARF7 gene although to a lesser extent than observed in the O.P. samples (log2FC ~ 0.9 and p-adj. < 0.01; Table S4.5). At 7 DAT, the expression levels in the developing fruits/putative fruits are significantly lower (Log2FC ~ 1) than observed in the unpollinated controls (Table S4.5). The O.P. samples show a significant lower expression of *PavARF2* (*Pav_sc0000042.1_g450.1.mk*), *PavARF5* (*Pav_sc0001759.1_g010.1.br*; *Pav_sc0002080.1_g180.1.mk*; *Pav_sc0002826.1_g100.1.br*; *Pav_sc0003104.1_g030.1.br*; *Pav_sc0011314.1_g020.1.br*) and *PavARF9* (*Pav_sc0002250.1_g170.1.mk*) at the late stages (Fig. 4.15; Table S4.5). Finally, no significant differences in the expression profile of *PavARF6* (*Pav_sc0001345.1_g010.1.mk*; *Pav_sc0003135.1_g100.1.mk*), *PavARF8* (*Pav_sc0001314.1_g050.1.mk*), and *PavARF17* (*Pav_sc0000030.1_g880.1.mk*) have been observed in any samples regardless of the treatment (Table S4.5).

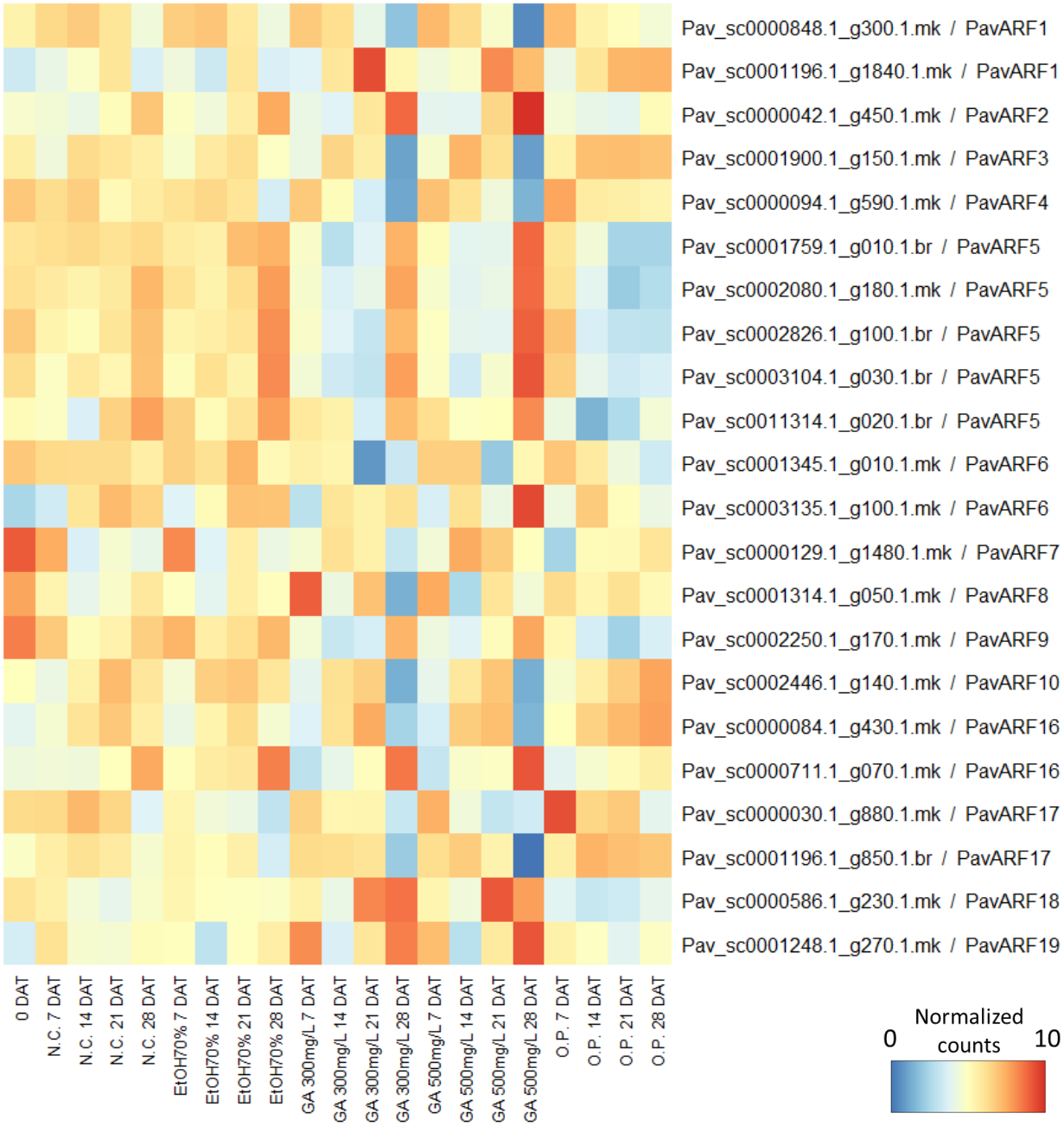


Figure 4.15: Heatmap of the putative cherry orthologs of the *AUXIN RESPONSE FACTORS* (*ARF*). Scale bar indicates the normalised gene counts.

4.3.4.3 Auxin signalling pathway: the AUX/IAA negative regulators

The expression of the *AUX/IAA* encoding genes show a wide difference between treatments, especially between the GA_3-treated and the open pollinated samples (Fig. 4.16). Among these, the putative *PavAUX/IAA14* (*Pav_sc0000998.1_g220.1.mk*) is one the most interesting. In fact, it is highly expressed at timepoint 0 DAT, and it is significantly and greatly down-regulated in all the treatments (in O.P. the log2FC = 8; Table S4.6). At 7 DAT, the level in the O.P. samples is significantly lower than the ones in the controls and GA_3-treated (Table S4.6). After timepoint 7, all the other samples demonstrate significant down-regulation of this gene and no difference between levels can be spotted. A great and significant down-regulation of the putative *PavAUX/IAA4* (*Pav_sc0000983.1_g280.1.mk*) can be observed in the O.P. at 7 DAT (log2FC = 2.49 and p-adj. = 1.62E-07; Table S4.6). The levels in O.P. are significantly lower than the levels in all the other treatments (Table S4.6). Its expression increases significantly at timepoint 14 DAT in O.P. (log2FC = 2.12 and p-adj. = 2.87E-05; Table S4.6), while the controls show a down-regulation (significant in EtOH 70 %; Table S4.6). The GA_3-treated samples instead, keep the expression quite high until 21 DAT, before it reduces significantly at 28 DAT (log2FC > 6 and p-adj. << 0.001; Table S4.6). Thus, at 28 DAT, the open pollinated samples have a significant and greater expression of putative *PavAUX/IAA4* (*Pav_sc0000983.1_g280.1.mk*) than all the other treatments (Table S4.6). A similar situation is present with the putative *PavAUX/IAA11* (*Pav_sc0002181.1_g160.1.mk*), *PavAUX/IAA17 (Pav_sc0000716.1_g230.1.mk*) and *PavAUX/IAA9* (*Pav_sc0002327.1_g560.1.mk*), where after an initial non-significant down-regulation at 7 DAT, expression increases in the O.P. samples over time (Fig. 4.16; Table S4.6). *PavAUX/IAA9* (*Pav_sc0002327.1_g560.1.mk*) is slightly up-regulated in treated samples at 7 DAT, although this change, like the down-regulation in O.P. is not statistically significant (Table S4.6). Finally, there are examples of genes highly expressed in the controls and GA_3-treated and poorly expressed in the O.P. at 28 DAT: *PavAUX/IAAX26* (*Pav_sc0000759.1_g050.1.mk*; *Pav_sc0000800.1_g500.1.mk*) and *PavAUX/IAA31* (*Pav_sc0000478.1_g250.1.mk*) (Fig. 4.16; Table S4.6).

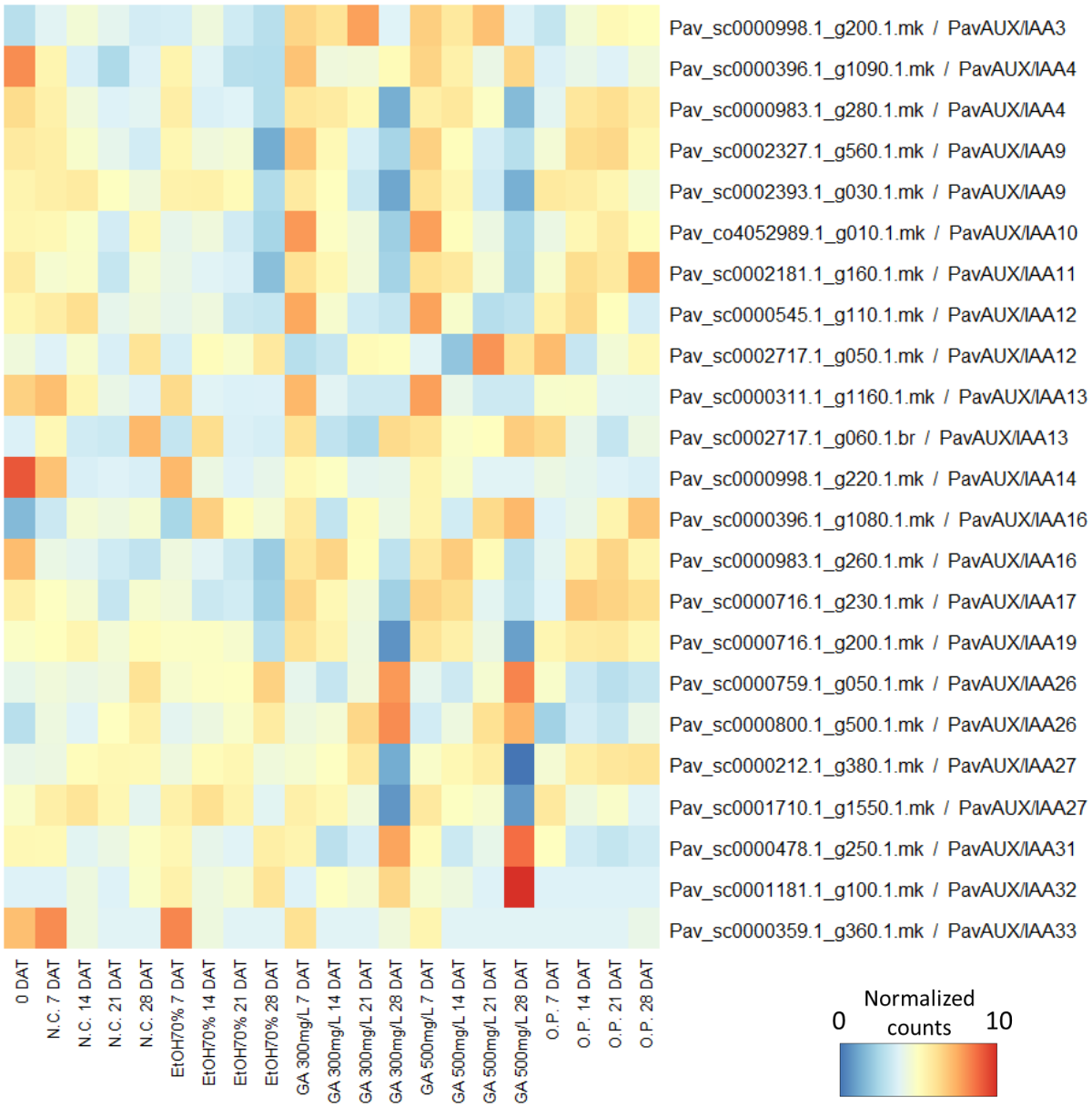


Figure 4.16: Heatmap of the putative cherry orthologs of the *AUXIN/INDOLE-3ACETIC ACID* (*AUX/IAA*) genes. Scale bar indicates the normalised gene counts.

4.3.5 Gibberellins-related genes do not exhibit a remarkable variation

In addition to auxin, gibberellins are essential signalling molecules for fruit development. The expression levels of the genes encoding the first enzymes in the biosynthetic process, the putative *PavCPS1* (*Pav_sc0000146.1_g580.1.mk*), are very low all the time. Its expression in the O.P. at 7 DAT, is higher than the one at 0 DAT, and the ones of all the other treatments, but this difference is not statistically significant (Fig. 4.17; Table S4.7). The putative *PavKS1* (*Pav_co4009519.1_g010.1.br*; *Pav_sc0005064.1_g030.1.mk*) is more expressed than *PavCPS1*, and the expression of *Pav_sc0005064.1_g030.1.mk* and *Pav_co4009519.1_g010.1.br* in the pollinated and treated ovaries becomes significantly higher than the one of their controls at 21 DAT and 28 DAT, respectively (log2FC ~ 2; Table S4.7). *PavATKO* (*Pav_sc0000890.1_g930.1.mk*) transcript levels in the controls remain almost always steady and before decreasing slightly at 28 DAT (Fig. 4.17). An evident difference can be observed in the GA_3-treated and in the O.P. samples instead. Indeed, it is significantly up-regulated in the developing fruits at 14 DAT (log2FC = 0.75 and p-adj. = 0.049; Table S4.7) but no significant difference with any other treatment has been found. At 28 DAT, there is a great drop of expression in the GA_3-treated samples (log2FC > 2 and p-adj. << 0.01; Table S4.7), while O.P. levels are significantly higher than the ones of all the other treatments (Table S4.7). The cherry ortholog of the *KAO* gene (*Pav_sc0000503.1_g830.1.mk*) is highly expressed at 0 DAT, but is down-regulated at later timepoints in all the treatments (Fig. 4.17). The greatest decrease in transcript number occurs in the O.P. samples whose levels from 21 DAT are significantly lower than the one of the other treatments (Table S4.7). When the focus is moved to the putative *PavGA20OX* encoding genes (*Pav_sc0000072.1_g640.1.mk*; *Pav_sc0001405.1_g250.1.mk*), no significant differences are found, except for the higher level in O.P. at 28 DAT of *Pav_sc0000072.1_g640.1.mk* compared to the GA_3-treated samples (log2FC ~ 1.5 and p-adj. << 0.01; Table S4.7). Finally, the last class of genes involved in gibberellin biosynthesis, the putative *PavGA3OX1* (*Pav_sc0000716.1_g300.1.mk*) and *PavGA3OX3 (Pav_sc0000704.1_g020.1.mk*) are strongly expressed at 0 DAT (Fig. 4.17). At 7 DAT, all the samples demonstrate reduced levels, especially the O.P. and GA_3-treated samples. In particular, levels of the putative *GA3OX3* in the O.P. samples are significantly lower than its negative control (log2FC = 5.08 and p-adj. = 0.03; Table S4.7; Fig. 4.17).

The putative GA inactivating genes *PavGA2OX2* (*Pav_sc0000095.1_g1110.1.mk*; *Pav_sc0003135.1_g610.1.mk*) and *Pav2OX8* (*Pav_sc0000410.1_g210.1.mk*; *Pav_sc0000910.1_g850.1.mk*) are always extremely low in the developing fruits at any timepoint (Fig. 4.17). The putative *PavGA2OX2* is significantly and extremely up-regulated at the later stages in the controls and the GA_3-treated putative fruits (Table S4.7). The up-regulation of *Pav_sc0000095.1_g1110.1.mk* in the aborting fruits is so great that their expression levels are significantly higher than their control, EtOH 70% (log2FC > 3 and p-adj. << 0.01; Table S4.7). On the contrary, *Pav2OX8* (*Pav_sc0000910.1_g850.1.mk*) is still expressed quite highly at 7 DAT, especially by the controls. Indeed, the log2FC between the N.C. and the O.P. is about 6.

The transcript levels of the putative orthologs encoding the GA receptor in cherry are quite high in all the treatments (Fig. 4.17). Already at 7 DAT the GA_3-treated are found to have significantly lower expression of the putative *PavGID1c* (*Pav_sc0000700.1_g870.1.mk*) (log2FC ~ 1.8 and p-adj. << 0.01; Table S4.7), while this is visible in the O.P. at 14 DAT (log2FC = 0.78 and p-adj. = 0.002; Table S4.7). *PavGID1c* levels in the developing pollinated and putative fruits remain low to the latest stages, while in the controls its expression is always almost quite the same (Fig. 4.17). In fact, the expression levels of the controls, already at 21 DAT is significantly higher than O.P. and GA_3-treated samples (Table S4.7). *PavGID1b* (*Pav_sc0000848.1_g080.1.mk*) is up-regulated in the GA_3-treated and controls from 21 DAT (Fig. 4.17; Table S4.7).

The signal transduction pathway of gibberellins is mediated by the negative regulators DELLA proteins. Two types of expression patterns of the putative *PavGAI* can be identified. Indeed, putative *PavGAI* (*Pav_sc0000704.1_g110.1.mk*) exhibit a strong up-regulation in the putative developing fruits already at 7 DAT (log2FC ~ 1.5 and p-adj. << 0.01; Table S4.7), but at 28 DAT, a significant drop occurs(log2FC > 1.5 and p-adj. << 0.01; Table S4.7). Similarly, also the putative *PavRGL2 gene* (*Pav_sc0000464.1_g350.1.mk*) is significantly up-regulated at 7 DAT in the GA_3-treated (log2FC ~ 0.7 and p-adj. < 0.01; Table S4.7), while it is non-significantly down-regulated in the O.P. samples (Table S4.7). Instead, the expression levels of the putative *PavGAI*

(Pav_sc0000221.1_g210.1.mk) increase significantly at 28 DAT only in the GA_3-treated samples (log2FC < 1 and p-adj. << 0.01; Table S4.7)and non-significantly in the EtOH 70% control, while in all the other treatments it stays quite low (Fig. 4.17). Finally, the putative cherry orthologs of *SLEEPY* (*SLY*) (*Pav_sc0000852.1_g250.1.mk*; *Pav_sc0000157.1_g290.1.mk*) are severely down-regulated in the GA_3-treated samples at 21 and mainly at 28 DAT (Table S4.7; Fig. 4.17).

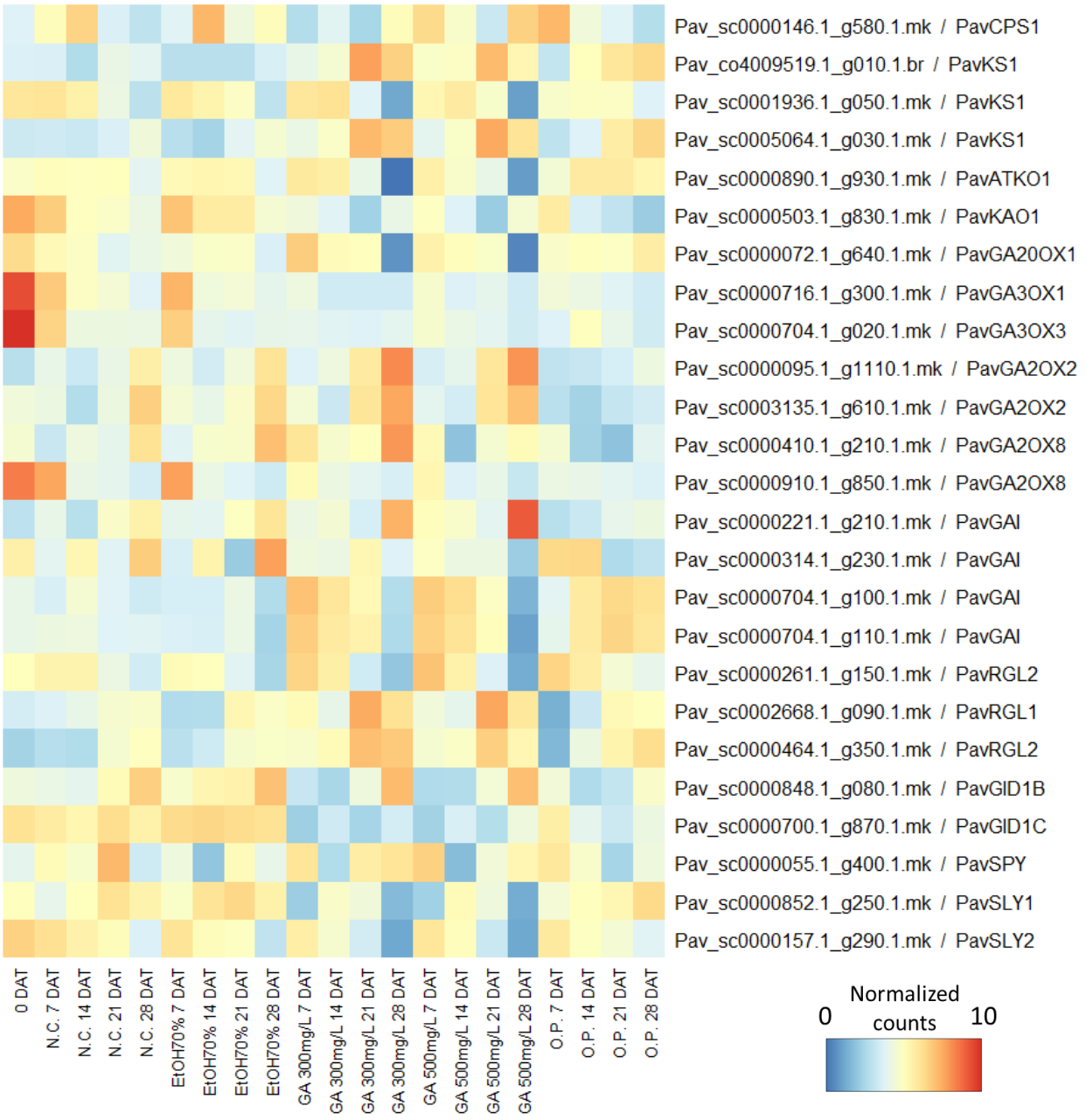


Figure 4.17: Heatmap of the putative cherry orthologs of the genes involved in GA biosynthesis, inactivation, and signal transduction. Scale bar indicates the normalised gene counts.

4.3.6 Ethylene-related genes are highly expressed in the aborting ovaries and putative fruits

Expression of the genes encoding the two key biosynthetic enzymes, ACC synthase (ACS) and ACC oxidase (ACO), has been analysed. The O.P. samples maintain the putative *PavACO1* (*Pav_sc0000813.1_g080.1.mk*; *Pav_sc0001073.1_g020.1.mk*) and *PavACO4* (*Pav_sc0002206.1_g310.1.mk*) transcript levels at a high level (Fig. 4.18). The controls and the GA_3-treated samples show significant up-regulation of these genes even more at 28 DAT, or even 21 DAT in the case of the putative *PavACO4* (GA_3-treated at 21DAT: log2FC > 4 and p-adj. << 0.01; Table S4.8). Instead, the level of expression of the putative *PavACS1* gene (*Pav_sc0000254.1_g1180.1.mk*) is remarkably lower than that of *PavACO*. A significant up-regulation occurs at 7 DAT in the GA_3-treated and O.P. developing fruits (log2FC > 3 and p-adj. < 0.05; Table S4.8); however, those levels are not significantly higher than those of the controls (Table S4.8). These levels are reduced in the subsequent timepoints, with no significant differences between treatments. The O.P. fruits also maintain a low level of expression of the putative *PavACS10* (*Pav_sc0002862.1_g330.1.mk*) and *PavACS12* (*Pav_sc0001928.1_g020.1.mk*) genes, while a significant up-regulation occurs in all the other treatments, as happens with putative *PavACO1* (Fig. 4.17; Table S4.8).

The open pollinated samples show a consistent up-regulation trend through time of the putative cherry ortholog of the *ETHYLENE RESPONSE SENSOR* 1 (*ERS1*; *Pav_sc0000130.1_g750.1.mk*), while a similar pattern is not observed in the other treatments (Fig. 4.17; Table S4.8). In fact, at 7 DAT the transcript levels are significantly lower in O.P. than in all the other treatments (log2FC < 1 and p-adj. < 0.05; Table S4.8), while at 28 DAT, it is the opposite (log2FC < 1 and p-adj. < 0.05; Table S4.8). The expression of all the other ethylene receptor genes stays lower in the open pollinated samples, while a slight up-regulation at 28 DAT occurs in the other treatments, especially the GA_3-treated ones. Indeed, the difference between the GA_3-treated and the O.P. samples is significant when putative *PavEIN1* (*Pav_sc0001323.1_g370.1.mk*), *PavETR2* (*Pav_sc0000729.1_g350.1.mk*), *PavEIN4* (ETHYLENE INSENSITIVE 4; *Pav_sc0000396.1_g730.1.mk*), and *PavEIL3* (*EIN3-Like*; *Pav_sc0005842.1_g070.1.mk*) are analysed. In particular, the expression of this latter gene is greatly higher in the GA_3- treated

samples at 28 DAT. The expression of putative *PavEIL3* and *PavERT2* are significantly lower in the O.P. than the negative control as well (log2FC < 1 and p-adj. < 0.05; Table S4.8). In the GA_3-treated samples two peaks of expression of the cherry ortholog of the negative regulator *PavCTR1* (*Pav_sc0000130.1_g780.1.mk*) have been observed at 14 DAT and 28 DAT. In the controls this gene is up-regulated at 28 DAT as well, while in the open pollinated the expression is significantly lower (log2FC > 1.7 and p-adj. << 0.001; Table S4.8; Fig. 4.18).

The same pattern can be found also when the putative *PavERFs* are analysed (Fig. 4.18; Table S4.8). Indeed, in the majority of the cases, while the expression levels in the O.P. samples are low all the time, with a couple of exceptions, in the GA_3-treated a significant up-regulation occurs at 28 DAT and sometimes also in the controls. Examples of the up-regulation that occurred in the aborting samples at 28 DAT are the putative *PavERF1* (*Pav_sc0000119.1_g160.1.mk*), *PavERF2* (*Pav_sc0001900.1_g290.1.mk*), *PavERF5* (*Pav_sc0000549.1_g1080.1.mk*), *PavERF7* (*Pav_sc0000241.1_g200.1.mk*), and *PavERF72* (*Pav_sc0000174.1_g1250.1.mk*) (Fig. 4.18; Table S4.8). In contrast, putative *PavERF4* (*Pav_sc0000975.1_g110.1.mk*) and *PavERF13* (*Pav_sc0001557.1_g150.1.mk*) are significantly more expressed in the O.P. at 28 DAT (log2FC > 1 and p-adj. < 0.01; Table S4.8). The putative cherry ortholog of *EIN3-binding F box protein 1* (*Pav_sc0001015.1_g080.1.mk*) is highly expressed at 0 DAT, then at 7 DAT a significant drop in expression occurs in all the treatments (Table S4.8). After this decrease, all the samples show up-regulation of the gene, with it reaching at 28 DAT, about the levels found at 0 DAT (Fig. 4.18).

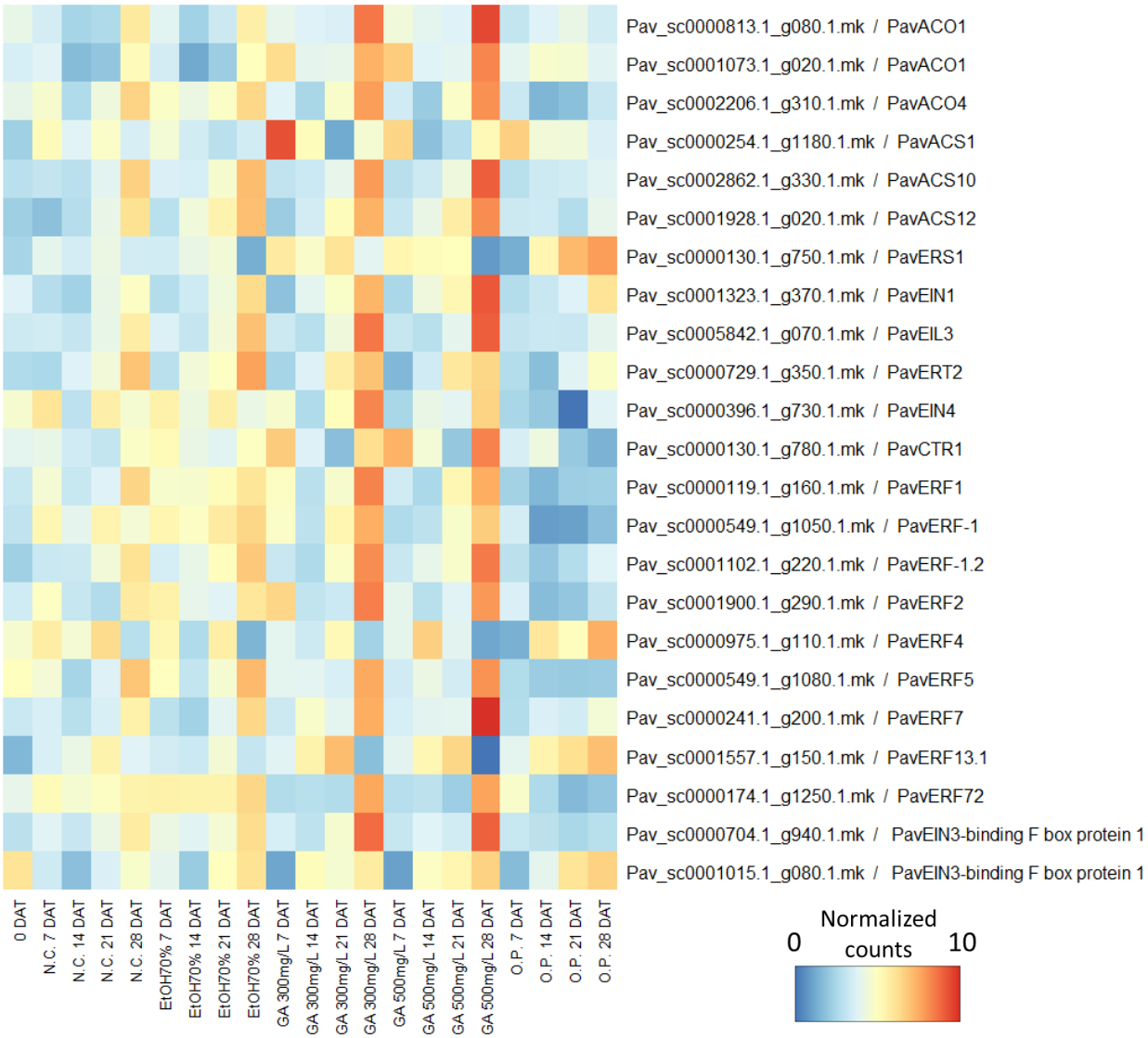


Figure 4.18: Heatmap of the putative cherry orthologs of the genes involved in ethylene biosynthesis, and signal transduction. Scale bar indicates the normalised gene counts.

4.3.7 Abscisic acid-related genes are differentially expressed during fruit set

Since the importance of ABA in fruit development has been already studied (Wang *et al.,* 2015; Leng *et al.,* 2018), ABA-related genes have been analysed. Both these studies were published before the release of the annotated cherry genome; the respective gene names have been identified by blasting the primer sequences to the cherry genome and obtaining the most significant result (lowest p-value and highest sequence identity). Putative *PavNCED1* (*Pav_sc0000095.1_g1080.1.mk*), is expressed at a low level in all the treatments and is significantly up-regulated only at 28 DAT in the $GA_3$300 mg/L-treated and O.P. samples (Fig. 4.19; Table S4.9). Thus, other putative cherry orthologs of *NCED* were searched and among these the ones found to be highly expressed at 0 DAT are putative *Pav NCED1* (*Pav_co4011289.1_g010.1.br; Pav_sc0000882.1_g260.1.mk; Pav_sc0007611.1_g010.1.mk*), putative *PavNCED4* (*Pav_sc0000354.1_g230.1.mk*) and putative *PavNCED5* (*Pav_sc0003135.1_g490.1.mk* (Fig. S4.25). All the putative *PavNCED1* genes are down-regulated at 28 DAT in all the treatments except for the O.P., which shows a higher expression (Fig. S4.25; Table S9).

Among the four putative *CYPA707* genes found by BLAST, only *PavCYPA707.2* (*Pav_sc0000563.1_g270.1.mk*) and *PavCYPA707.3* (*Pav_sc0000071.1_g720.1.mk*) show peaks of expression. In particular, *PavCYPA707.3* (*Pav_sc0000071.1_g720.1.mk*) is highly expressed at 0 DAT, then down-regulation occurs in all the samples until 21 DAT, when the GA_3-treated and the O.P. samples exhibit significant up-regulation (log2FC > 3 and p-adj. < 0.05; Table S4.9). However, only the O.P. samples keep the expression level significantly high at 28 DAT (Table S4.9). The GA_3-treated samples have a peak of expression of *PavCYPA707.2* (*Pav_sc0000563.1_g270.1.mk*) at 7 DAT (log2FC ~ 4.8 and p-adj. << 0.01; Table S4.9), which is followed by a decrease, while in the O.P. samples a peak has been reached at 28 DAT (Fig. 4.19; Table S4.9). The level of expression of the genes encoding the ABA receptors, *PavPYL2* (*Pav_sc0001341.1_g250.1.mk*), and *PavPYL3* (*Pav_sc0000591.1_g120.1.mk*) are high at 0 DAT, while the one of the putative *PavPYL1* (*Pav_sc0001335.1_g500.1.mk*) is overall lower. All the treatments are associated with an increase in the expression of these genes, and the greatest difference occurs in the GA_3-treated

samples (Table S4.9). All the putative *PavSnRK2* encoding genes are highly expressed. In particular, the putative *PavSnRK2.1* (*Pav_sc0001196.1_g350.1.mk*), *PavSnRK2.2* (*Pav_sc0000549.1_g120.1.mk*), *PavSnRK2.3* (*Pav_sc0000639.1_g120.1.mk*), and *PavSnRK2.6* (*Pav_sc0000257.1_g130.1.mk*) genes show further up-regulation over time in all the treatments (Fig. 4.19; Table S4.9). *PavSnRK2.1* (*Pav_sc0001196.1_g350.1.mk*) at 28 DAT is significantly higher in the developing fruits/ putative fruits, than in their controls (log2FC < 1 and p-adj. < 0.05; Table S4.9). All the treatments decrease the levels of the putative *PavSnRK2.5* (*Pav_sc0001242.1_g120.1.mk*) until 14 DAT, then the controls and GA_3-treated samples up-regulate it again (log2FC ~ 1 and p-adj. < 0.05; Table S4.9), while in the O.P. the levels stay low. The expression of the putative *PavSnRK2.4* (*Pav_sc0000908.1_g140.1.mk*) is high and remains at a consistent level in all the treatments (Fig. 4.19). Finally, the genes encoding PP2C have been analysed. All these are up-regulated overall, but some differences can be observed (Fig. 4.19; Table S4.9). The O.P. and GA_3-treated samples show significant down-regulation of the putative *PavPP2C5* (*Pav_sc0001335.1_g050.1.mk*) at 7 DAT($log2FC_{GA3}$ ~ 1.6; $log2FC_{OP}$ = 2.4 and p-adj. < 0.01; Table S4.9), but later the expression levels rise again significantly (Table S9). At 28 DAT, the putative fruits (GA_3-treated) are the ones that express this gene at the highest level. A similar trend can be observed also for the expression of the putative *PavPP2C4* (*Pav_sc0000554.1_g390.1.mk*) (Fig. 4.19; Table S4.9). The expression patterns observed for the putative *PavPP2C2* (*Pav_sc0000069.1_g410.1.mk*), *PavPP2C3* (*Pav_sc0002858.1_g200.1.mk*), and *PavPP2C6* (*Pav_sc0000212.1_g830.1.mk*) are very similar to the one just described for *PavPP2C4* and *PavPP2C5,* with the exception that the initial drop is not significant for any of the treatments (Fig. 4.19; Table S4.9). Moreover, the expression levels in O.P. of *PavPP2C2* are not significantly lower than the ones of the GA_3-treated samples. A slightly different pattern instead is the one of the putative *PavPP2C1* (*Pav_sc0000689.1_g440.1.mk*). Indeed, only the pollinated fruits and the putative ones show significantly increased levels over time (Table S4.9). The putative fruits reach their peak at 21 DAT before dropping at 28 DAT, while the levels in the O.P. at 28 DAT are significantly higher than all the others (log2FC < 1 and p-adj. < 0.05; Table S4.9; Fig. 4.19).

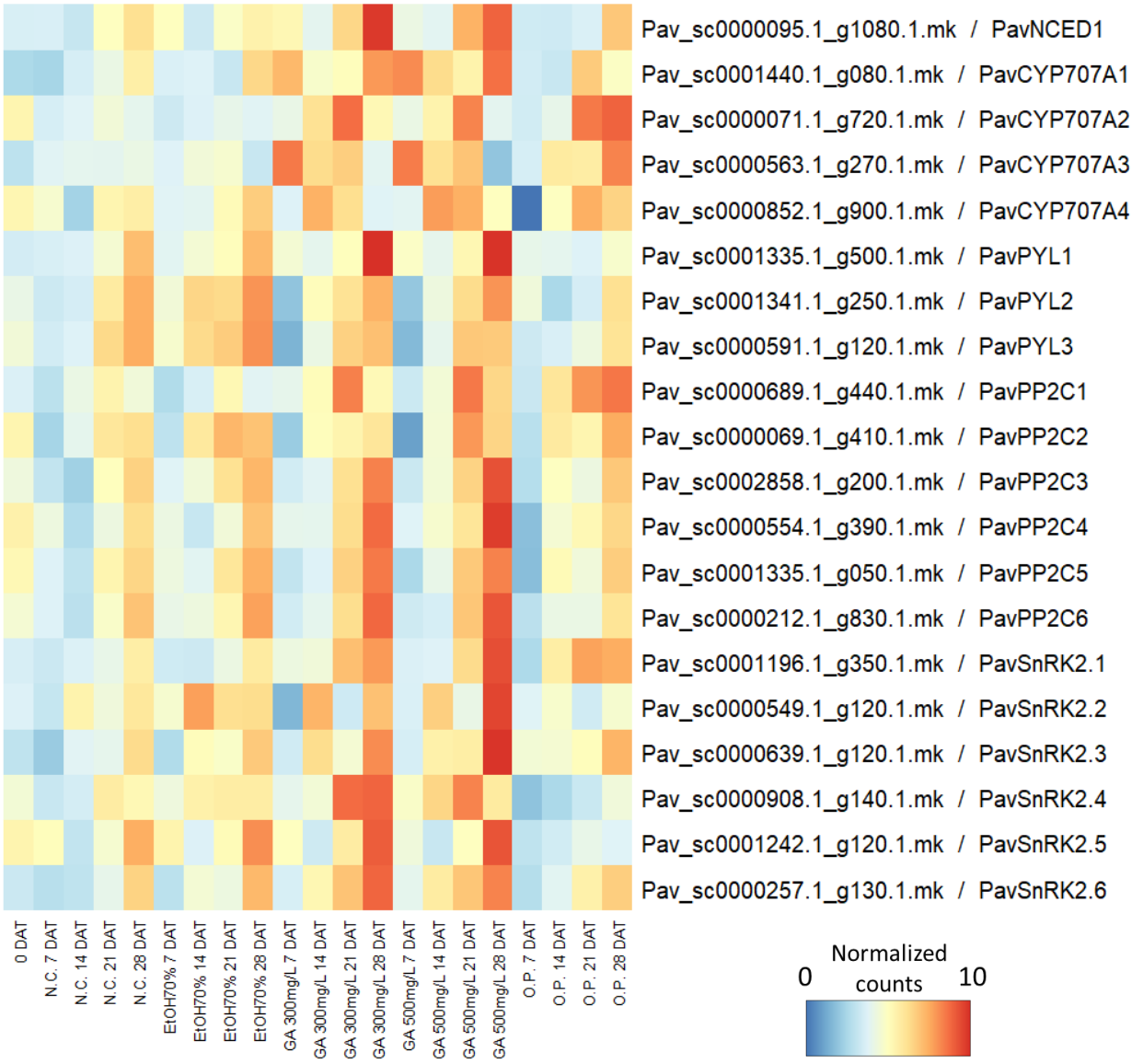


Figure 4.19: Heatmap of the putative cherry orthologs of the genes involved in ABA biosynthesis, inactivation, and signal transduction. Scale bar indicates the normalised gene counts.

4.3.8 GO terms: Cell cycle

The Gene Ontology analysis has also identified several GO terms that can be grouped together into the "cell cycle" (Fig. 4.20). At 14 DAT, only the GA_3-treated samples exhibit a significant enrichment of these pathways, while this happens as well in the O.P. samples at 21 DAT. The genes that are associated with these terms carry out different functions such as transcriptional regulation, DNA repair, cell wall biosynthesis, microtubule polymerization and movement, membrane transport and kinase activity. Moreover, the cyclins and the CKDs are found between these DEGs (Fig. 4.21-22).

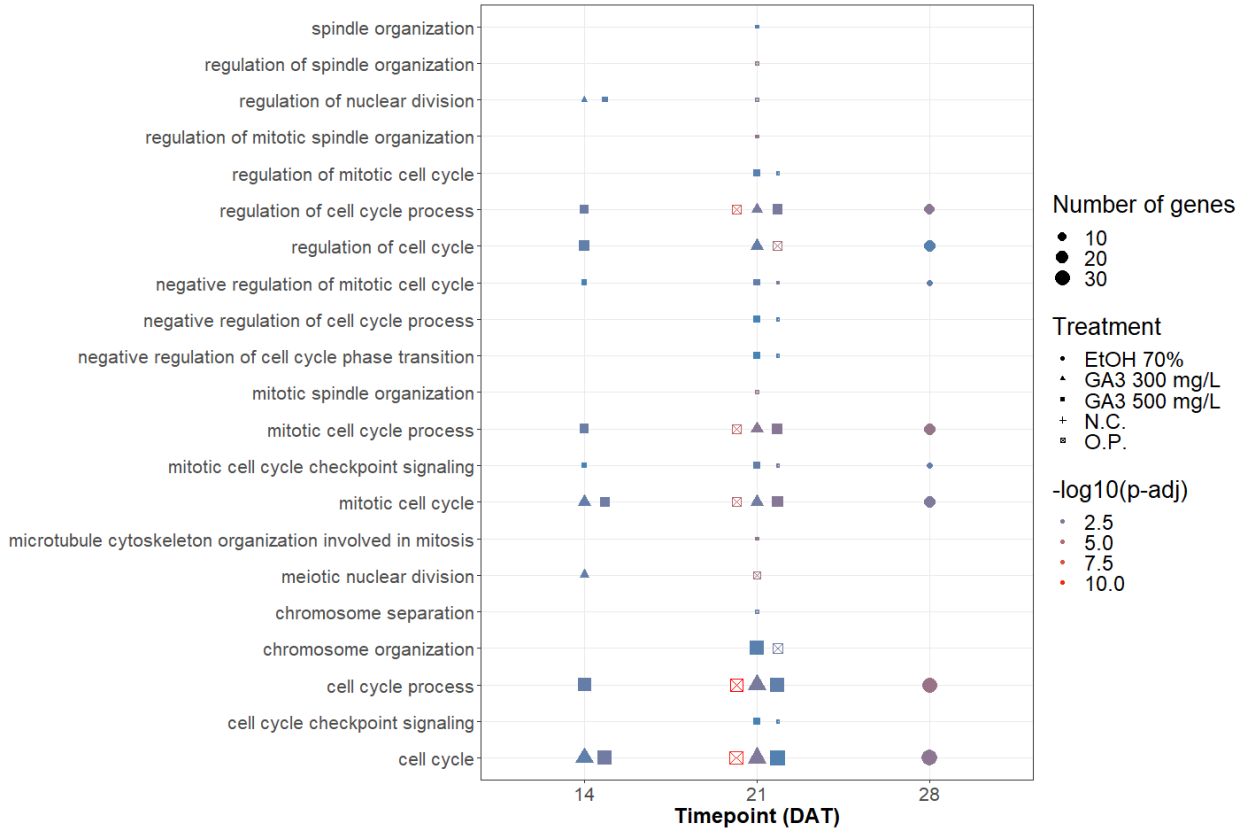


Figure 4.20: Dot plot that shows the pathways enriched of the DEGs genes identified. The GO terms belong to the category "biological process" category and are all related to the cell cycle progression and regulation.

4.3.8.1 Cell cycle regulators: Cyclins

A and B-type cyclins are progressively down-regulated from timepoint 0 to 28 DAT. In particular, the down-regulation is greater in the O.P. and mostly in the GA_3-treated samples (Fig. 4.21; Table S4.10). Indeed, at the latest stages, the expression levels in O.P. are significantly higher than the ones of the GA_3-treated, but lower than the ones in the negative control except for the putative *PavCYCB2;3* (*Pav_sc0000414.1_g160.1.mk*; *Pav_sc0002524.1_g040.1.mk*) and *PavCYCB3;1* (*Pav_sc0000497.1_g230.1.mk*), where significant difference between O.P. and N.C. is found at 21 DAT (log2FC ~ 1 and p-adj. < 0.05; Table S4.10) and not at 28 DAT (Table S4.10). D-type cyclins transcription patterns are more heterogeneous. The GA_3-treated samples always show a great down-regulation of them, apart from putative *PavCYCD2;1* (*Pav_sc0000257.1_g860.1.mk*), that is significantly up-regulated in these samples at 28 DAT (log2FC ~ 2 and p-adj. << 0.01; Table S4.10), reaching the expression levels observed in the controls, while in the O.P. it is significantly lower (log2FC ~ 1.7 and p-adj. << 0.01; Table S4.10). Expression of putative *PavCYCD4;2* (*Pav_sc0003894.1_g020.1.mk*) and *PavCYCD5;1* (*Pav_sc0005024.1_g060.1.mk*) is significantly higher in O.P. than all the other treatments at 28 DAT (Table S4.10). The O.P. samples also maintain a high level of expression of the putative *PavCYCH;1* (*Pav_sc0006080.1_g030.1.mk*), as do the GA_3-treated samples until 21 DAT, after which a significant drop of expression occurs (log2FC ~ 0.75 and p-adj. << 0.01; Table S4.10). This happens also to the controls, in which the down-regulation is not significant as the one of the treated putative fruits. A similar pattern of the one described for the putative *PavCYCD4;2* and *PavCYCD5;1* is found in the putative *PavCYCP1;1* (*Pav_sc0000146.1_g490.1.mk*) and *PavCYCP3;2* (*Pav_sc0000026.1_g130.1.mk*) (Fig. 4.21). In particular, this latter gene is greatly down-regulated at 28 DAT in the controls and GA_3-treated ($log2FC_{controls}$ ~ 2, $log2FC_{GA3\text{-}treated}$ > 6.69 and p-adj. << 0.01; Table S4.10). This down-regulation is not observed in the O.P., which has significantly higher expression levels compared to all the other treatments ($log2FC_{controls\ vs\ O.P.}$ ~ 3, $log2FC_{GA3\text{-}treated\ VS\ O.P.}$ > 7.4 and p-adj. << 0.01; Table S4.10). At 0 DAT, putative *PavCYCP4;1* (*Pav_sc0005664.1_g070.1.mk*) is quite high in expression but is down-regulated at 7 DAT in all the treatments, more greatly in the developing fruits and putative ones (log2FC > 3 and p-adj. << 0.01; Table S4.10). GA_3-treated samples also show a significant increase in the level of expression of this cyclin gene at 28 DAT (log2FC > 2 and

p-adj. << 0.01; Table S4.10), while in the controls the up-regulation is not significant (Fig. 4.21; Table S4.10).

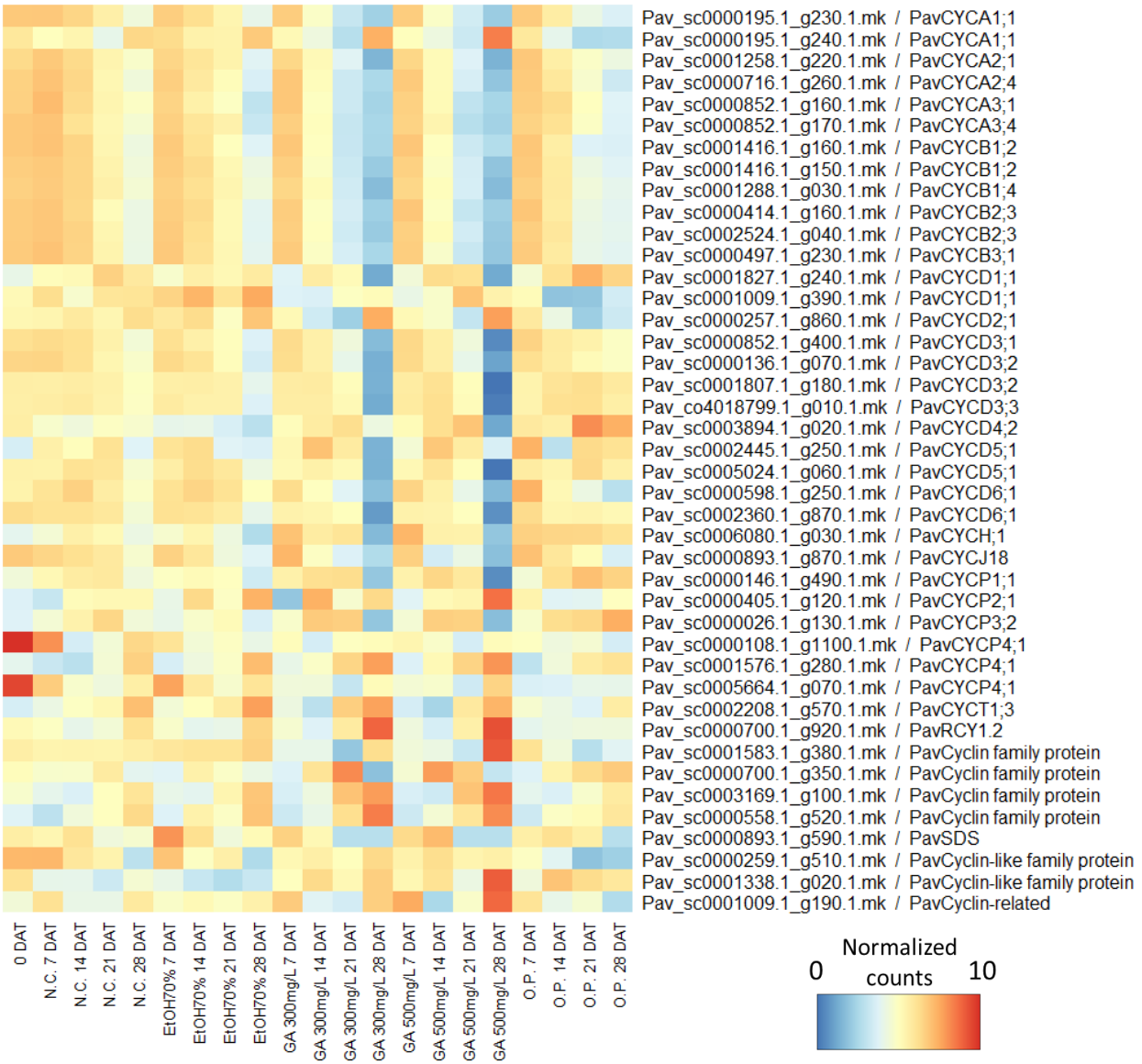


Figure 4.21: Heatmap of the putative cherry orthologs of the genes encoding for cyclins. Scale bar indicates the normalised gene counts.

4.3.8.2 Cell cycle regulators: CDKs and ICKs

At 0 DAT, the putative *PavCDKB1;2* (*Pav_sc0001699.1_g590.1.mk*) and *PavCDKB2;2* (*Pav_sc0000600.1_g680.1.mk*) genes are expressed. Then all the samples show down-regulation in their expression over time, especially the developing fruits and putative fruits ($Log2FC_{14\ vs\ 21\ DAT}$ are quite the same). At 21 DAT the controls have a significant higher expression compared to their fruit counterparts (log2FC > 1 and p-adj. << 0.01; Table S4.11) and the difference in expression developing fruits and putative fruits is significant as well (log2FC > 0.7 and p-adj. << 0.01; Table S4.11; Fig. 4.22). The pattern of the putative *PavCDKD1;1* (*Pav_sc0000103.1_g240.1.mk*) is really similar to the one just described for the putative *PavCDKB1;2* and *PavCDKB1;2*: however, no significant differences between treatments have been found. No significant changes or comparisons have been observed in the other CDKs (Table S4.11).

The putative *PavICK5* (*Pav_sc0000071.1_g860.1.mk*) seems to play an important role in fruit development since it is already significantly up-regulated in O.P. (log2FC = 3.1 and p-adj. = 1.76E-28; Table S4.11) and the GA_3-treated samples (log2FC > 1.57 and p-adj. << 0.01; Table S4.11) at 14 DAT when the levels are higher than in their controls (log2FC ~ 1.8 and p-adj. << 0.01; Table S4.11). However, at 28 DAT the GA_3-treated samples show reduced expression of this gene (log2FC ~ 1.3 and p-adj. << 0.01; Table S4.11). Thus at 28 DAT, the highest expression is observed in the O.P. fruits (Fig. 4.22; Table S4.11). The putative *PavICK6* (*Pav_sc0001963.1_g390.1.mk; Pav_sc0000022.1_g200.1.mk*) in the O.P. follows the opposite pattern of the one observed in the putative *PavICK5* (*Pav_sc0000071.1_g860.1.mk*). Indeed, its levels are significantly lower than the ones in the negative control at 14 DAT and 21 DAT respectively (log2FC ~ 0.7 and p-adj. << 0.01; Table S4.11). However, *Pav_sc0001963.1_g390.1.mk* in the open pollinated ovaries is significantly up-regulated at 7 DAT (log2FC = 0.54 and p-adj. = 0.027; Table S4.11), while in the GA_3 300mg/L-treated samples it is down-regulated (log2FC = 0.54 and p-adj. < 0.05; Table S4.11).

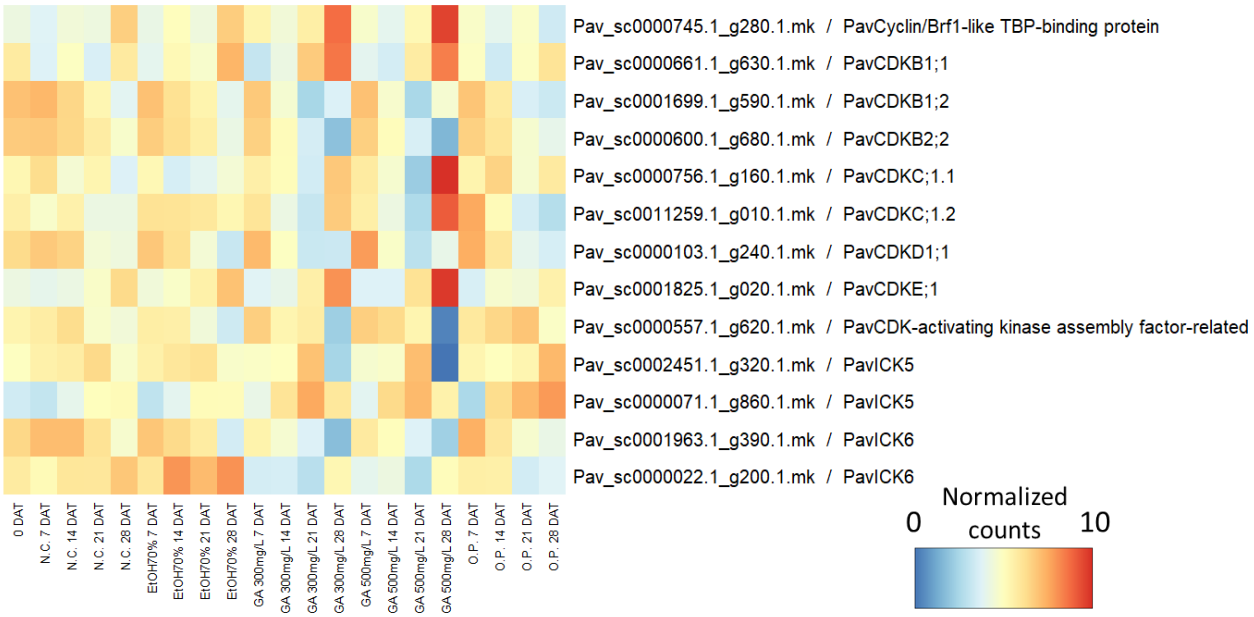


Figure 4.22: Heatmap of the putative cherry orthologs of the genes encoding for *CDK*s and *ICK*s. Scale bar indicates the normalised gene counts.

4.3.9 Frequency of transcription factor genes in the DEGs

The DEGs include genes encoding six of the major classes of transcription factor, MADS-box, MYB, NAC, WOX, WRKY and bHLH, which are known to be important for fruit development. In Fig. 4.23, the numbers of DEGs that belong to these categories, are shown. In the up-regulated DEGs it is evident that the major contribution is from bHLH, MYB, NAC and WRKY classes, while the MADS-box and WOX genes are smaller in number. When the down-regulated DEGs are analysed, the MYB and bHLH factors are overall about double the number in all the other classes. The GA_3-treated samples are the ones that always have a higher number of genes, which are mostly bHLH, MYB, NAC and WRKY factors. Interestingly, while the putative fruits show a higher number of genes differentially expressed that belong to these classes of transcription factors, in the pollinated developing fruits the number is much reduced, especially at the later stages. To understand better how the expression of the MADS-box and NAC encoding genes changes in these samples, a deeper analysis was conducted.

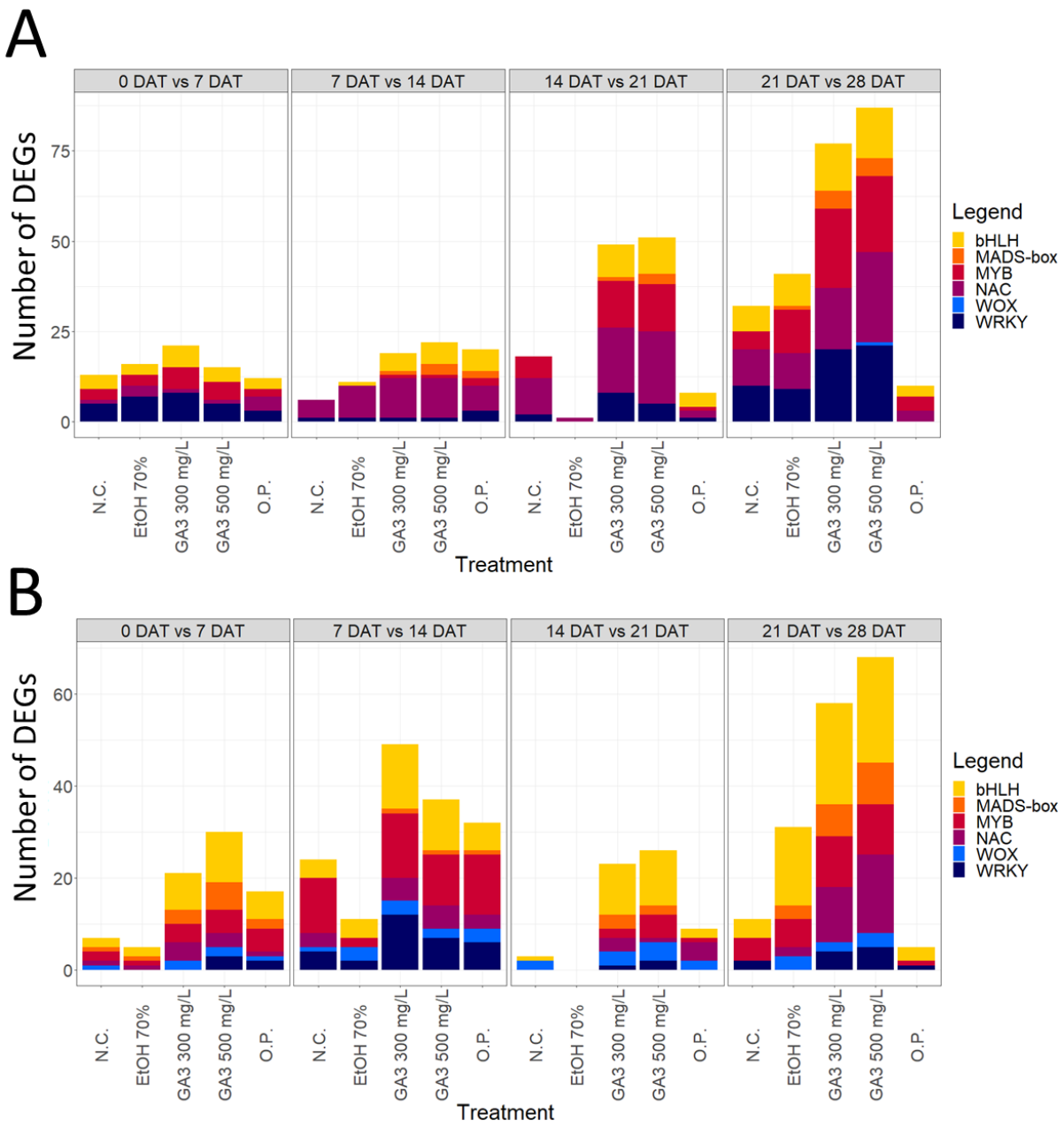


Figure 4.23: Histogram that shows the number of the differentially expressed genes (DEGs) that belong to the *MADS-box*, *MYB*, *NAC*, *WOX*, *WRKY* and *bHLH* gene families. DEGs requirements are |log2FC| > 1 and p-adj. < 0.05. (A) up-regulated DEGs; (B) downregulated DEGs. The later timepoint in each comparison is the basis used to establish if the DEG is up-regulated (UP) or downregulated (DOWN) compared to the previous timepoint.

4.3.10 *MADS-box* transcription factors and cherry fruit development

MADS-box transcription factors play an essential role in flower and fruit development, so for this reason their expression levels were investigated (Fig. 4.24; Table S4.12). The only gene that is significantly down-regulated at the early stages (14 DAT) in the O.P. compared the negative control (log2FC = 1.45 and p-adj. = 0.012; Table S4.12), is the putative *PavAGL3/SEP4* (*Pav_sc0001080.1_g900.1.mk*). Timepoint 0 DAT is when its expression is high, but over time it is gradually down-regulated in the controls, while the decreased expression in the O.P., and the GA_3-treated proceeds faster. The level in the O.P. fruits becomes even lower than the ones of the putative fruits, and at 28 DAT, the former exhibits the significantly lowest expression (log2FC > 1.1 and p-adj. < 0.01; Table S4.12). The other putative cherry orthologs of the *SEPALLATA* genes have been checked as well. As with the putative *PavAGL3/SEP4*, the putative *PavAGL9/SEP3* (*Pav_sc0000091.1_g150.1.mk*) is poorly expressed in the O.P. samples (Fig. 4.24). In all the other treatments, up-regulation of this gene occurs at 28 DAT, significantly in the GA_3-treated ones (log2FC > 1 and p-adj. << 0.01; Table S4.12). The putative *PavAGL9/SEP3* in O.P. at 28 DAT, presents a lower and significant expression (Table S4.12). The unpollinated ovaries at 0 DAT show a quite high expression of the putative *PavAGL4/SEP2* (*Pav_sc0000661.1_g410.1.mk*), which is significantly down-regulated at 7 DAT in all the treatments (log2FC < 1 and p-adj. < 0.01; Table S4.12). However, in the controls the down-regulation continues until 28 DAT, the open pollinated fruits keep its expression quite steady, by alternating non-significant up and down-regulation. The putative fruits instead exhibit a combined pattern, since until 14 DAT, they behave like the pollinated fruits, while after 14 DAT, like the controls (Fig. 4.24). At 28 DAT in fact, the O.P. presents significant higher levels, although not great, compared to all the other treatments (log2FC < 1 and p-adj. < 0.01; Table S4.12). *Pav_sc0001289.1_g020.1.mk*, a putative *PavAG* gene, is highly expressed in the unpollinated ovaries at 0 DAT, like the putative *PavAGL4/SEP2* and *PavAGL9/SEP3* (Fig. 4.24). However, after that timepoint, in the controls its levels decrease and remain low. The O.P. and GA_3-treated samples, which present low levels as well at 7 and 14 DAT, start to express this gene at a higher level at later stages. The GA_3-treated samples and O.P. show a significant increase (log2FC < 1 and p-adj. < 0.01; Table S4.12). *Pav_sc0003835.1_g220.1.mk* and *Pav_sc0000358.1_g630.1.mk* are both designated as putative *PavAGL1/SHP1* genes;

however, they display quite different patterns of expression. Indeed, *Pav_sc0003835.1_g220.1.mk* is highly expressed at 0 DAT, but is constantly down-regulated, especially in the controls and the GA_3-treated samples, while O.P. seems to reach a steady level (Fig. 4.24; Table S4.12). On the contrary, *Pav_sc0000358.1_g630.1.mk* is up-regulated over time and, again, the greatest changes are in the controls and hormone-treated samples, while in O.P. it remains at the same level (Fig. 4.24; Table S4.12). In the O.P. fruits, the putative *PavAGL7/AP1* (Pav_sc0000661.1_g360.1.mk) is up-regulated over time, significantly at 7 and 14 DAT (Table S4.12). The controls display the same trend, but the up-regulation is smaller and not significant (Table S4.12). The GA_3-treated samples reach the peak of expression at 21 DAT, then a significant drop is observed at 28 DAT (log2FC > 1.8 and p-adj. < 0.01; Table S4.12). Other significant differences between the O.P. and the other treatments at 28 DAT, are found in putative *PavAGL42* (*Pav_sc0001405.1_g300.1.mk*) and *PavAGL47* (Pav_sc0001060.1_g140.1.mk), which O.P. expresses significantly less these genes ($log2FC_{PavAGL42}$ ~ 1, $log2FC_{PavAGL47}$ ~ 3 and p-adj. < 0.01; Table S4.12). Finally, putative *PavAGL6* (*Pav_sc0000072.1_g670.1.mk*) and *PavAGL11/STK* (*Pav_sc0002136.1_g280.1.mk*), which are known to play a crucial role in fruit development, are significantly higher in the O.P. samples only when compared to the GA_3-treated ones at 21 ($log2FC_{PavAGL6}$ ~ 1 and p-adj. ~ 0.05 , $log2FC_{PavAGL11}$ > 1 and p-adj. < 0.01; Table S4.12) and 28 DAT ($log2FC_{PavAGL6}$ > 3, $log2FC_{PavAGL11}$ > 2 and p-adj. < 0.01; Table S4.12). The opposite happens with the expression of the putative *PavAGL8/FUL* (*Pav_sc0000358.1_g640.1.mk*) (Fig. 4.24; Table S4.12).

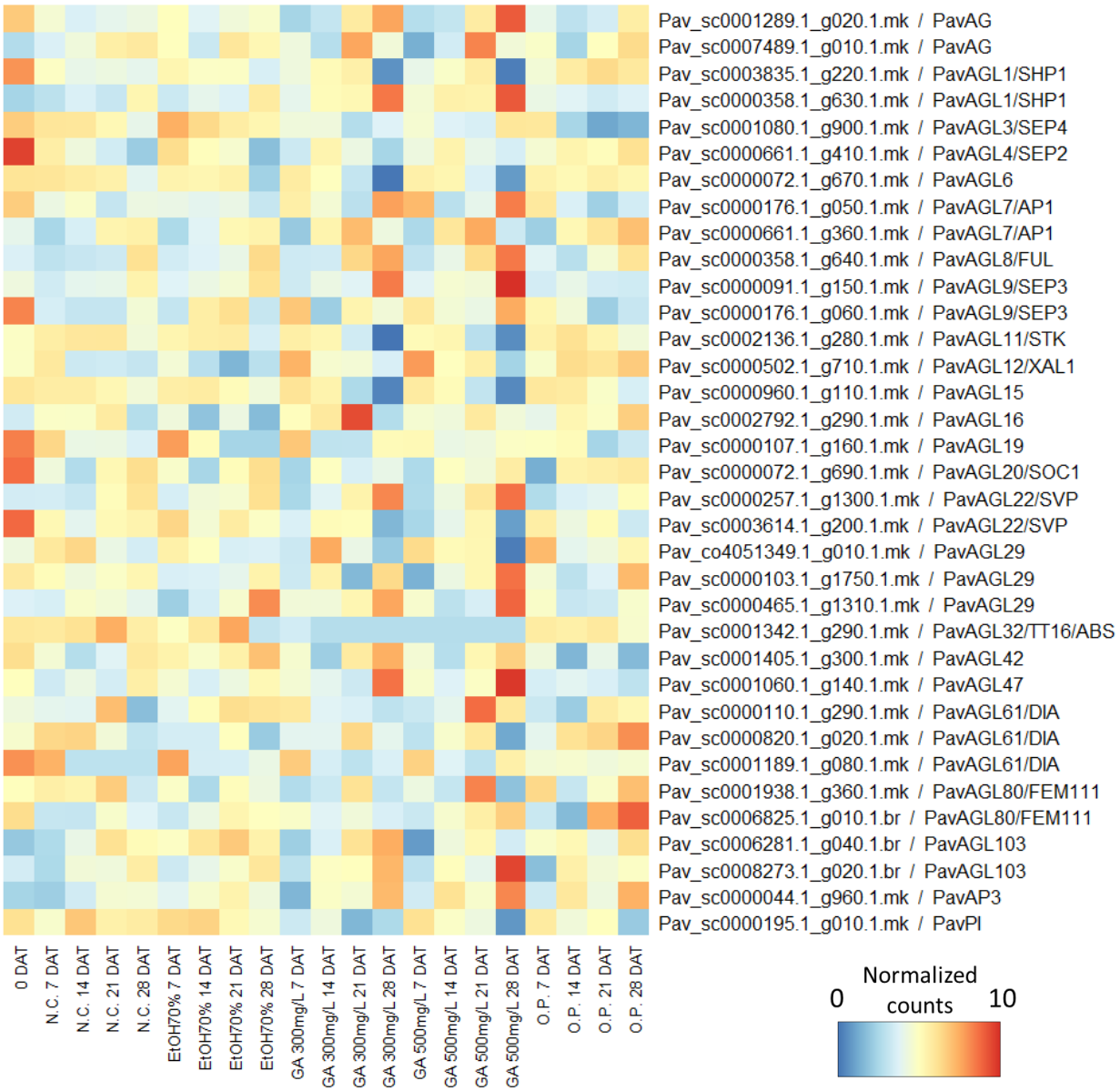


Figure 4.24: Heatmap of the putative cherry orthologs of the genes encoding for the *MADS-box* transcription factors. Scale bar indicates the normalised gene counts.

4.3.11 *NAC t*ranscription factor encoding genes are expressed mostly at later stages

The profile of expression of the putative NAC factors found in the cherry genome are shown in Fig. 4.25. Putative *PavANAC025* (*Pav_sc0002009.1_g210.1.mk*) is highly expressed at 0 DAT but in all the treatments a significant down-regulation is observed at 7 DAT. The magnitude of this change is greater in the O.P. (log2FC = 3.12 and p-adj. = 5.61E-15; Table S4.13) and GA_3-treated samples (log2FC ~ 2.3 and p-adj. << 0.01; Table S4.13), whose expression levels are significantly lower than that of their controls (log2FC ~ 1.3 and p-adj. < 0.01; Table S4.13). Moreover, from 14 DAT, the developing fruits (log2FC > 1 and p-adj. < 0.05; Table S4.13) and the putative developing fruits (log2FC = 1.74 and p-adj. = 0.00016; Table S4.13) show significant up-regulation in the expression of this gene, reversing the situation with their controls. At 28 DAT, the difference between O.P. and N.C. is significant (log2FC = 1.27 and p-adj. = 0.00196; Table S4.13). The putative *PavANAC043* (*Pav_sc0000586.1_g1000.1.mk*) and *PavANAC056* (*Pav_sc0000029.1_g090.1.mk*) at 0 DAT are poorly expressed, but from 14 DAT they start to be up-regulated in the pollinated and putative fruits (Fig. 4.25). The GA_3-treated samples present a further change. In fact, at 28 DAT, a down-regulation of these genes occurs, making the expression levels significantly lower than those in the O.P. samples, but higher than the ones in the mock-treated control (Table S4.13). A remarkably different scenario can be observed when putative *PavANAC022* (*Pav_sc0000095.1_g440.1.mk*), *PavANAC029* (*Pav_sc0000220.1_g1030.1.mk*), *PavANAC047* (*Pav_sc0001877.1_g160.1.mk*), *PavANAC072* (*Pav_sc0000029.1_g070.1.mk*), *PavANAC090* (*Pav_sc0000168.1_g110.1.mk*), *PavANAC100* (*Pav_sc0000484.1_g580.1.mk*; *Pav_sc0000877.1_g1000.1.mk*) are analysed. The expression levels of these genes are always low in the O.P. samples, while a remarkably higher expression can be found in all the other treatments, especially at 21 and 28 DAT (Fig. 4.25; Table S4.13).

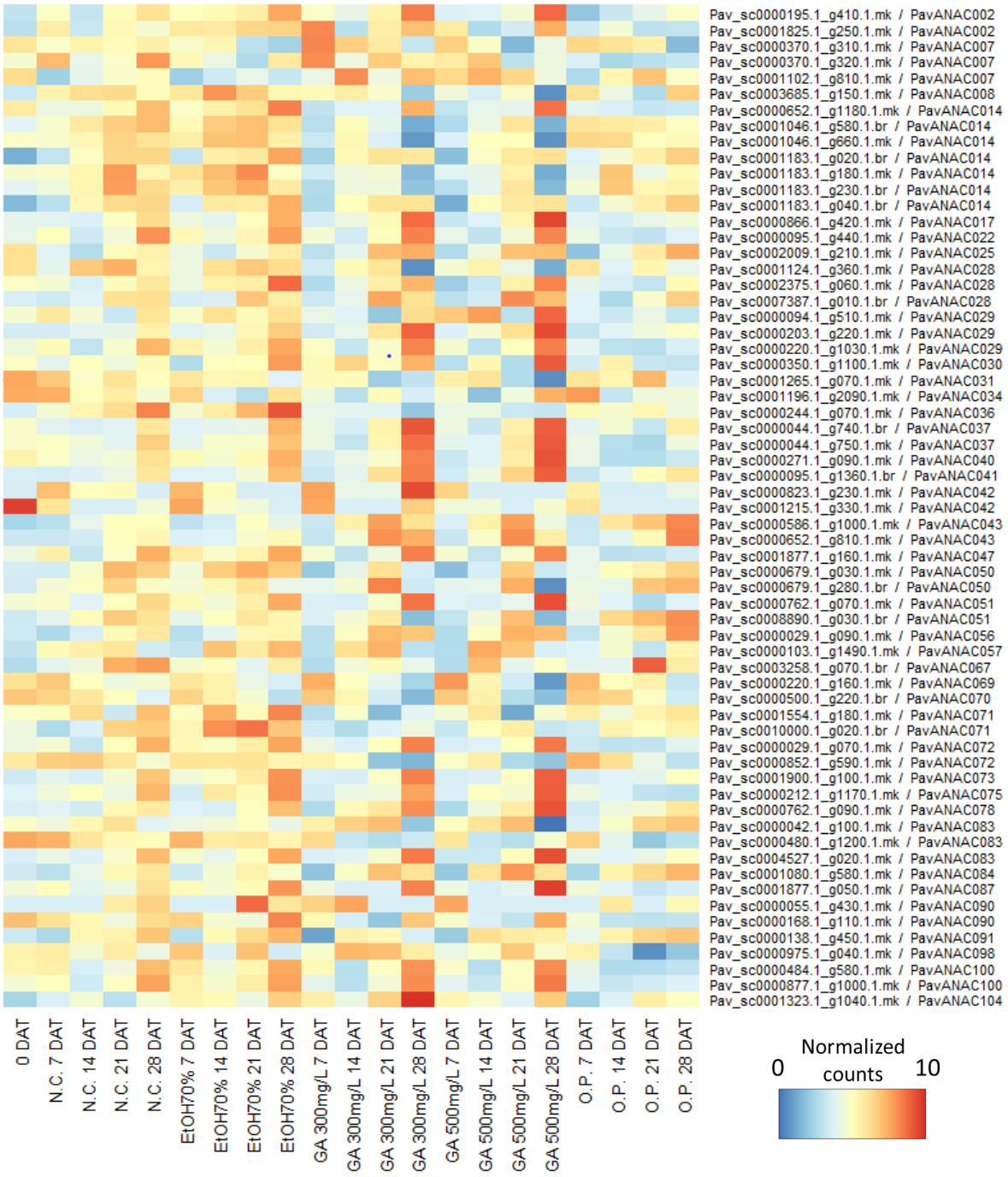


Figure 4.25: Heatmap of the putative cherry orthologs of the genes encoding for the *NAC* transcription factors. Scale bar indicates the normalised gene counts.

4.4 Discussion

Sweet cherry fruit development is still a relatively unexplored topic; thus, this transcriptomic analytic process can be a great tool to start understanding what happens in the pollinated and fertilised ovules of this species. A previous study using Chinese cherry (*Cerasus pseudocerasus*) (Wen *et al.,* 2019), lacked a positive control such as pollinated ovaries, an omission that did not allow a direct comparison between what it is happening in the GA_3-treated ovaries and the actual developing seeded fruit. The presence of the unpollinated and pollinated controls in the present study has helped to identify which pathways are active and repressed during fruit development and which pathways are activated by the applications of GA_3. Moreover, a direct comparison between these samples at the later stages, allowed the identification of differences between the fruits that continue to develop normally and those that are aborting.

First, the number of the significant differentially expressed genes (DEGs) in each treatment between two subsequent timepoints gives an idea of the changes that occur in the genetic programs of those samples. In fact, if in a sample a large number of genes are differentially expressed it is likely that some modifications are occurring, by activating or repressing pathways that before were silenced or not. At timepoints 7 and 14 DAT, it is evident that a genetic program has been activated in the pollinated and treated ovaries, since the number of DEGs increased approximately 2-fold compared to the controls (Fig. 4.7; Table 4.1). In addition, the difference in expression from 0 to 7 DAT is much greater and significant in these samples than in the controls, as is shown in the volcano plots (Fig. S4.1-5). The higher percentage of down-regulated genes from 0 to 7 DAT in the O.P., which are the ones mostly changed compared to the up-regulated genes (Fig. S4.5A), is consistent with the current hypothesis about fruit development: fruit development is blocked in the ovaries, and this repression is removed by a signal that comes from the fertilised ovule (Molesini *et al.,* 2020). Thus, the higher percentage of down-regulated genes could be explained by the removal of this blocking signal. In the GA_3-treated ovaries, this percentage is slightly lower, and it could be due to the lack of higher auxin levels signalling successful fertilisation. Moreover, there is a higher frequency of highly significantly and greatly up-regulated genes, which are not present in the pollinated ovaries. At 14 DAT, the increase of the number of DEGs in the pollinated and putative developing fruits may be the reflection of the

fruit set program activated, thus the ovary must undergo several morphological changes, such as an increase in cell number, cell expansion and cell differentiation. Additional evidence of this, could be found in the increase of the number of up-regulated DEGs, such as *SAUR-protein*, *bHLH*, *WRKY*, *NAC*, *WOX*, cell cycle regulators, protein kinases and transcriptional regulators encoding genes and genes that encodes for enzymes implicated in sugar metabolism and cell wall biosynthesis. In contrast, in the controls, the greatest and most significant changes are visible predominantly in the down-regulated DEGs, encoding for NAC, MYB transcription factors, SAUR-proteins and factors involved in metabolism. In the pollinated and treated ovaries this difference cannot be observed. At the later stages however, a notable difference between these two types of developing fruits is observed. The number of DEGs found in the pollinated fruits decreases between 14 DAT and 21 DAT and remains stable between 21 DAT and 28 DAT, suggesting that the fruit set program is set and proceeds. The putative developing fruits instead, increase their number of DEGs constantly until being about 10 times higher than the pollinated fruits. The plausible explanation is that the pollinated fruits have a program set that has been activated, while the treated putative fruits are undergoing a changing program. This is suggested also by the fact that in the treated putative fruits, the number of highly significantly and greatly changed DEGs is remarkably greater than that observed in the pollinated fruits. A great increase in the number of DEGs is observed in the controls, possibly due to the fact that these samples are aborting, and the increase in the transcript levels of genes involved in senescence and programmed cell death, significantly supports this hypothesis. The contrast between the magnitude of different levels of expression observed in the controls compared to the aborting putative fruits, may be explained by the fact that the controls have never changed their ovary identity, while the putative fruits have started the fruit set program. Thus, aborting as a developing fruit is not the same as an aborting unpollinated ovary. To test this hypothesis, it would be helpful to repeat all this experiment and add an aborting pollinated control, which however could be quite difficult to sample. The application of ethanol 70% shows a side effect on transcription regulation, even in the long-term. Indeed, in the last two timepoints, the percentages of DEGs that are shared by N.C. and EtOH 70%, becomes considerably lower. In particular at 28 DAT, it is indicative that only 38.5% of all DEGs in EtOH 70% are shared with the

unpollinated ovaries, while the EtOH 70% samples share about 80% of their DEGs with the GA_3-treated samples (Table S4.1). This is the opposite of what is observed between the negative control and the open pollinated, since at 28 DAT, the percentage of shared DEGs in relation to their total number of DEGs, is very low for both of them (7.7% N.C and 17.5% O.P.). The effect of ethanol application seems to last even a month later, and this is also a possible additional reason why the GA_3-treated samples at 28 DAT exhibit a greater number of DEGs. Finally, as hypothesised during the observations of the putative developing fruits at the time of sampling (Chapter 3), a dosage-dependent effect is likely to be present in the GA_3-treated samples. Indeed, although at 7 DAT more than 70% of DEGs are shared between the two treatments, a decrease in the number of shared DEGs and the increase of the total number of DEGs, could be evidence to support this hypothesis. At 28 DAT, GA_3 500 mg/L treated ovaries differentially express 1449 more genes than the other treatment.

As expected, when the GO terms enriched pathway analysis was conducted, one of the main areas that showed significant changes in gene expression related to the response to hormones. As described in the introduction of this chapter, hormones have an essential role in ovary to fruit transition. It is also not surprising that in addition to auxin, which is known to be the trigger hormone in most plant species, also factors related to ABA signalling resulted differentially expressed in cherry. Leng *et al.* (2018), previously observed an increase in the expression of different genes involved in ABA biosynthesis and signal transduction. As regards the genes involved in ABA biosynthesis and signalling (i.e *NCED1*), the results obtained are consistent with previous studies (Wang *et al.,* 2015; Leng *et al.,* 2018). The fact that the pollinated fruits are the only ones that continue to express the putative *PavNCED1* genes at 28 DAT, while in all the others a significant drop occurs, may support the importance of *NCED1* during cherry fruit development. The importance of ABA for the progression of fruit development seems supported also by the profiles of the factors involved in signal transduction. These factors were shown to be expressed at a continually increasing rate over time in the pollinated fruits. This trend, however, has also been observed in all the other treatments. Since ABA is involved in senescence, abortion, and abscission, it may be possible that it promotes these processes in the aborting samples (controls

and GA_3-treated samples), while it supports fruit development in O.P. samples. It is possible that the cells of the aborting samples increase all the signalling machinery to increase their sensitivity to ABA. Measuring the hormone contents in all these samples could be very useful, to check if there is a dosage-dependent effect of ABA during these phases. The work published by Teribia *et al.* (2016), shows the hormones profiles in the sweet cherry cultivar 'Prime Giant' from the stage "fully green and small sized" (called stage I in the article). ABA is shown to increase constantly in abundance over time. This is likely linked to the crucial role that ABA plays in the anthocyanin biosynthetic pathway during ripening (Teribia *et al.,* 2016; Ponce *et al.,* 2021). Wang *et al.,* (2016), demonstrated that MLP43 regulates positively ABA signalling, by binding directly SnRK2.6. The biological role of the MLP proteins is poorly understood; however, they have mainly been associated with plant defence and response to stress. For example, MLP423 and MLP423-like proteins in apple *(Malus domestica*) play an important role in defence from fungal infection and in abiotic stress responses (Zhu *et al.,* 2017). However, Ruperti *et al.* (2002), studied *PpeMLP1* gene in peach (*Prunus persica*) and observed a high expression of this gene in different organs of the plant including the fruitlet and the mesocarp. The model proposed is that *PpeMLP1* could be involved in the abscission process, but also, in mesocarp cell expansion (Ruperti at al., 2002). In other species, MLP genes have been reported to be induced after fruit set in cucumber (Suyama *et al.,* 1999), grape (Davies & Robinson, 2000), strawberry (Nam *et al.,* 1999) and melon, in which ethylene is reported to be the triggering agent (Aggelis *et al.,* 1999). Thus, a further analysis of the putative *PavMLP423* sequences could help to better understand the role of these genes in sweet cherry fruit development.

The role of auxins in the development of fruit from unfertilised ovules is well documented. It has been proposed that auxin can act as an alternative signal replacing pollination and fertilisation to initiate the fruit growth (Serrani *et al.,* 2008). In this study, auxin biosynthesis seems more regulated at the level of the *YUCCA* genes. Such genes show the greatest changes. During early fruit development, the genes responsible for auxin biosynthesis seem to be *PavYUCCA4* and *PavYUCCA6*, while at the later stages *PavYUCCA10* transcripts level increases. In the GA_3-treated samples, *PavYUCCA6* seems to compensate for the down-regulation of *PavYUCCA4*. It is possible

that the application of GA_3 can induce *PavYUCCA6*. Indeed, such an application appears to bypass the very initial part of the fruit program where auxin is the main player. This could also explain why *PavYUCCA10* in the treated samples reaches its peak of expression at 21 DAT, whereas this occurs at 28 DAT in the open pollinated samples, suggesting that GA_3 triggers the increase in *YUCCA10*. Moreover, the drop in expression of *PavYUCCA10* in the seedless putative fruits might provide further evidence that the fruit program has been activated, however, the lack of a seed, which constantly sends a signal, and the absence of this signal led to the abortion of these samples. The auxin receptor *TIR1-2* encoding genes, although slightly down-regulated at 7 DAT, are highly expressed.

The control of auxin homeostasis by the *GH3* genes seem to occur more in the later stages of fruit development rather than at the early ones. At these stages, it seems that the transport of auxin plays a crucial role in fruit set. *SlPIN4* for example is suggested to be involved in regulating auxin levels in tomato ovaries and in fruit set in tomato, since its down-regulation leads to parthenocarpic fruit development (Mounet at al., 2012). In cherry not only putative *PavPIN4*, but also *PavPIN2* and *PavPIN5*, along with the influx carrier gene *PavAUX1*, are down-regulated in the open pollinated fruits at 7 DAT. Auxin transporters thus, seem to be key factors during fruit set in sweet cherry. Another interesting result is found in the expression pattern of the *PavARFs* genes. The putative *PavARF7*, which is considered a negative regulator of fruit set, is significantly down-regulated at 7 DAT in both the open pollinated and the GA_3-treated samples. It is possible then that this gene has conserved its function in sweet cherry. The possible application of this result will be discussed in the next chapter (Chapter 5). In contrast, *PavARF8*, which is considered a negative regulator of fruit set, did not show any significant differential expression between the treatments. The role of this gene is still unclear because it is still not clear how it is linked to parthenocarpy. In eggplant, for example, the down-regulation of *SmARF8* via RNAi induces the development of parthenocarpic fruits, but the same happens when the same gene is overexpressed in Arabidopsis (Du *et al.,* 2016). Unlike *PavARF7*, *PavAUX/IAA9*, another gene reported to be a negative regulator of fruit set, is not significantly down-regulated at 7 DAT. It is less expressed in the pollinated fruits, but the difference in expression is not significant in relation to the previous timepoint or when compared to the expression in the negative control. It is

possible that this down-regulation is actually enough; however, further investigation is needed. *PavAUX/IAA9* will be treated as well in the next chapter (Chapter 5). A significant down-regulation at 7 DAT has been found in *PavAUX/IAA4,* which is expressed about 10 times less than *PavAUX/IAA9*, about 4 times less than *PavAUX/IAA14*, which does not seem fruit specific since it is down-regulated in all the treatments. The down-regulation of *PavAUX/IAA4* at 7 DAT seems consistent with what has been observed in strawberry. Indeed, *FveAUX/IAA4* transcript levels are higher in the receptacle before fertilisation and get significantly lower post fertilisation (Zhou *et al.,* 2021). *PavAUX/IAA17* has potentially maintained its function in cherry as well, since at the later stages it is significantly more expressed (Log_2FC ~ 2) in the developing fruits than in the aborting GA_3-treated putative fruits. This gene is reported to be involved in the control of fruit quality in tomato, since the mutant produces bigger and heavier fruits with a thicker pericarp (Su *et al.,* 2015).

The GA biosynthetic enzymes did not displayed significant differences between the treatments as it was observed with the auxin genes. Moreover, their levels were low. A further investigation may be needed to confirm if in the cherry genome there are other orthologs that have not been identified from the homology analysis, or it is possible that even a low expression of these genes is enough to have a significant effect. In the pollinated and treated ovaries at 7 and 14 DAT, the GA inactivating genes are kept down-regulated more strongly than in the controls. Moreover, *PavGA2OX2* is extremely up-regulated at 28 DAT in the aborting seedless fruits. In the controls, the up-regulation occurs as well, so the increase of expression of these genes, with the resulting diminishing of GA levels, may be linked to ovary and fruit abortion. Interestingly, the opposite scenario has been found with the GID1 receptors. The high expression of the *GID1*'s supports the hypothesis that low levels of GAs are enough to trigger fruit set. The application of gibberellin seems to trigger the up-regulation of the DELLA proteins in the ovaries. This could be the mechanism that the ovarian cells use to contrast the high sprayed GA_3 quantity. Since the unfertilised ovaries were provided with a high amount of Gibberellin, which promotes the DELLA degradation, it is possible that *DELLA protein* encoding genes are strongly up-regulated to balance this strong signal. Interestingly, the profile of the *PavRGL2*, which in the article of Wen

and collaborators in Chinese cherry (Wen at al., 2019), has been reported as ortholog of the tomato *SlDELLA*, is very similar to *PavAUX/IAA9*.

Finally, ethylene seems to retain its role in fruit abscission also in sweet cherry. The ethylene biosynthetic genes and the receptors are extremely up-regulated in the controls and the treated putative fruits at 28 DAT. In Chapter 3, it has been shown that ovary and fruit abscission started at 35 DAT and at 42 DAT, when the majority of them had fallen. Since the transcripts levels of these genes are quite high already at 0 DAT (anthesis), it is possible that even in sweet cherry, ethylene has an important role in fruit set and development, as reported in zucchini and cucumber (Martínez *et al.,* 2015; Xin *et al.,* 2019). Thus, at anthesis, and during fruit development, genes encoding proteins involved in ethylene biosynthesis and signalling are highly expressed, allowing the correct fruit program to proceed, while during ovary/fruit abortion and abscission, their levels become highly elevated. The higher production of ethylene is also promoted by the up-regulation of the transcription factor *PavANAC047* in the aborting samples, which binds to the ethylene biosynthetic gene promoters up-regulating their expression (Kim *et al.,* 2014). Thus, according to the ethylene dosage, the outcome is different. Finally, while most of the *PavERFs* are down-regulated in the open pollinated fruits, and highly up-regulated in the aborted fruits/ovaries, *PavERF4* displays the opposite pattern. In apple, *MdERF4*, has been shown to reduce ethylene levels by repressing *MdERF3,* which activates the transcription of *MdACS1* (Hu *et al.,* 2020). The negative role of *PavERF4* seems likely according to the results from the transcriptomic analysis. Indeed, the lack of a higher expression of these genes allows an increase in ethylene production in the aborting ovaries/fruits. *PavERF4* may have a future application in regards to early fruits abscission (June drop) in cherry.

One of the effects that hormones have is regulating the cell cycle and promoting or arresting cell division. Considering the types of samples that are analysed in this study, the finding that GO terms were associated with cell division and its regulation, was expected. The cyclins that seem to be involved in cell cycle progression in the open pollinated fruits are mostly the D-type cyclins (4;2 and 5;1), the H-type (H;1) and the P-type cyclins (P1;1 and P3;1). D-type and P-type cyclins

seem to have a major role at 21 and 28 DAT, since at 21 DAT, a significant increase in expression is observed. D-type cyclins are reported to be important during pollinated, natural parthenocarpic, and hormone-induced parthenocarpic fruit development in cucumber (Cui *et al.,* 2014), whilst P-type cyclins have been proposed to play a role in cell division and cell differentiation (Torres Acosta *et al.,* 2004). H-type cyclins instead are proposed to positively regulate CKD (Shimotohno *et al.,* 2004). CYCH;1 can interact with CDKD1;1, which is slightly up-regulated in the open pollinated and GA_3-treated ovaries at 7 DAT, although this up-regulation was not statistically significant. Finally, cell cycle progression inhibitors, *PavICK5* and *PavICK6*, are more highly expressed in the O.P. than in the other treatments. A possible explanation is that they are required to regulate cell division tightly in the developing tissues, and not in static tissues such as the unpollinated ovaries.

MADS-box transcription factors are known to be important in flower and fruit development. *SEPALLATA* genes and *AGAMOUS*, for example, are crucial for the correct development of flower whorls. In tomato, it has been shown that mutations in these genes cause alterations in flower organs and parthenocarpic flower development. Their expression is high in ovaries and decreases in the developing fruits. The observations on the putative cherry ortholog of the three *SEPALLATA* genes and of *AGAMOUS*, seem to confirm this conclusion. The cherry orthologous genes are highly expressed in the unpollinated ovaries and are down-regulated in the pollinated fruits, more significantly than in the controls. Moreover, since the hormone-treated samples in the first timepoint do not show a significant expression level compared to the pollinated controls, may be a further confirmation that the fruit set program has been started in these samples as well. Furthermore, *PavAGAMOUS (PavAG)*, is up-regulated again toward the end of the experimental temporal window as was previously seen in peach (Tani *et al.,* 2007). To further investigate the role of *PavAG* in mesocarp and endocarp development in cherry, later samples of later stages of development are needed. Other genes, however, do not show an expression pattern similar to their orthologs in other species. *PavAGL6* for example, is not highly expressed in the ovaries and more importantly, is not significantly down-regulated at the very beginning in the pollinated and treated ovaries. On the contrary, it is down-regulated after 20 days in all the aborting samples. A

further investigation may be needed since this gene has a great potential from an economic point of view, since its mutation in tomato results in parthenocarpic fruit development, without any other pleiotropic effects. Finally, the pollinated fruits seem to move toward tissue differentiation since the three MADS-box genes *PavSEEDSTICK* (*PavSTK)*, *PavSHATTERPROOF* (*PavSHP)* and *PavFRUITFULL* (*PavFUL)* are up-regulated. In peach, expression of *PpeSTK* and *PpeSHP* has been shown to be restricted to the endocarp area while expression of *PpeFUL* has been identified in the mesocarp. Thus, it is possible that the putative cherry orthologs have the same function considering that at 21 DAT the presence of the two tissues is visible (Chapter 3). A tissue specific expression analysis should be conducted, including also fruits at later stages, to confirm this conclusion. The up-regulation of *PavANAC056* in the pollinated fruits at 28 DAT, could represent further evidence that these tissues are differentiating, since this gene in purple-fleshed sweet potato, is associated with anthocyanin biosynthesis (Wei *et al.,* 2020). Finally, the in GA_3-treated samples, an up-regulation of *PavFUL* and *PavSHP* is observed, and this may be linked to the fact these samples are aborting. Indeed, these two genes are important for the lignification process, which occurs in these aborting fruits, especially at the level of the abscission zone (Merelo *et al.,* 2017).

In conclusion, this study gives an overview of early fruit development in sweet cherry, especially in relation to hormones and gene expression. The integration of these two approaches has helped to better understand the changes that occur in the developing fruits, and to identify the possible principal players. These data suggest that the fruit set program has been triggered in the GA_3-treated samples, which later abort, as is proven by the up-regulation also of transcription factors of the NAC, which are mostly down-regulated in the pollinated fruits. The information obtained from this analysis could be potentially the first step toward genetic improvement of sweet cherry varieties.

Chapter 5: Phylogenetic analysis of *PavARF7*, *PavAUX/IAA9* and *PavRGL2*, the potential candidate genes for the production of a seedless cherry

5.1 Introduction

5.1.1 The multiple advantages of fruit seedlessness

Seedless fruits are becoming more and more popular with consumers who prefer them to their seeded versions. Such fruits are much easier to process, thus reducing the costs for industry. There are two types of seedlessness: stenospermocarpy and parthenocarpy. The former term, refers to the formation of fruit with spontaneous or induced abortion of fertilised seeds (watermelon and grapes). Seed abortion can happen at different stages of development, so the final fruit may contain both aborted ovules and seed traces. Seedless watermelon and Ruby seedless grape are good examples of this type of seedlessness (Kihara, 1951; Mejia *et al.,* 2011). The latter term, parthenocarpy (from Greek "virgin fruit") refers to fruit set and development in the absence of fertilisation of the ovules (Picarella & Mazzucato, 2019; Sharif *et al.,* 2022). Natural parthenocarpy can be obligate in sterile species such as banana and pineapple, or facultative like the apple variety Rae Ime and the mandarin variety clementine (Yao *et al.,* 2001; Mesejo *et al.,* 2016). There are several advantages of parthenocarpy over stenospermocarpy; these include the absence of seeds and the absence of a need for pollination and pollinators.

Pollination, in particular, is a crucial aspect because it requires the presence of pollinators. Firstly, it is well known that sweet cherry pollination is mediated by insects, which are important for the production of a viable crop (Eeraerts *et al.,* 2020). Wild pollinators, including solitary bees, are essential to ensure sweet cherry yields (Eeraerts *et al.,* 2019); however, growers rely on commercial domesticated honeybees (*Apis mellifera*) for pollination at a cost up to 1000 euro per hectare, a considerable investment. The absence of the need for pollination also brings the potential for higher fruit yields and the absence of the seed/stone an increase in flesh content.

With no need for pollination, the significant costs of providing commercial domesticated honeybees to carry out this function would no longer be required, thus not only reducing production costs but also the reliance on the presence of wild bee populations and solitary bees, which also play a considerable role in fruit set. Furthermore, reliance on honeybees also comes with the drawback that they remain inactive under unfavourable weather conditions, such as at temperatures below 12°C or heavy rainfall, which can provide additional drawbacks to cherry production. Indeed, temperature, weather conditions and pollution and other factors have a strong impact on pollinators (Vanbergen *et al.,* 2013). Thus, the availability of plants that can produce fruits independently of pollination may play a surprisingly important role for cultivation considering the current climate change situation.

5.1.2 Strategies for the generation of seedless crops

Due to all the advantages linked to seedlessness, research has focused on the identification of those factors that are responsible for the generation of this trait. The aim is to apply this knowledge in different species in order to increase the range of available seedless crops.

A factor that has been reported to be linked to stenospermocarpy is the MADS-box transcription factor gene *AGL11/SEEDSTICK* (*AGL11/STK*). *STK/AGL11* is involved in the ovule identity determination (Theißen *et al.,* 2000) and is a master regulatory gene of seed development (Mizzotti *et al.,* 2014). Moreover, *STK/AGL11* has been reported to be expressed in the developing endocarp in peach, which makes this transcription factor an important element during multiple crucial pathways in sexual plant reproduction (Dardick *et al.,* 2010). The mutation of *STK/AGL11* in tomato and grape leads to the formation of stenospermocarpic fruits. *SlAGL11* is the *STK* homologue in tomato, it shares 81% similarity with the Arabidopsis gene, and it controls fruit and seed development, being expressed in the inner integuments of the ovule. *SlAGL11* has been silenced using an antisense construct and the lines produced did not exhibit any significant difference in fruit number, maturity achievement, final ripening colour and fruit size. Most of these lines were seedless, some had few seeds, smaller seeds, or ovule traces. The number of seeds was positively correlated to the expression level of *SlAGL11* in these lines (Ocarez & Mejía

2016). Further work by Huang *et al.* (2021) used CRISPR/Cas9 to silence *SlAGL11* and a second MADS-Box gene, *MBP3* in the same lines. This work resulted in the production of an all-flesh, seedless transgenic line with enhanced firmness and improved post-harvest storage; however, average fruit size was severely reduced.

VviAGL11 is the homologue of *STK* in grapevine and it starts to be highly expressed when the seed begins to develop, immediately after berry set (Mejía *et al.,* 2011). Comparing different seedless and seeded varieties of grapevine, it has been shown that the seeded ones had bigger berries and a higher expression of *VviAGL11* than the seedless ones. Seedless Ruby is a stenospermocarpic mutant that has a dominant mutation in *VviAGL11* since the heterozygous plants are seedless. The dominant phenotype is due to a single missense mutation (Arg197 to Leu197), which does not allow the formation of the correct transcriptional complex that is involved in activating all the genes necessary for the normal seed coat development and lignification, which is crucial for correct seed development, resulting in seed abortion (Ocarez & Mejía 2016; Royo *et al.,* 2018).

A much larger group of genes have been reported to cause parthenocarpic fruit development once mutated. Among these, other examples of MADS-box transcription factors can be found. In apple for example, the mutant Rae Ime has been reported to be parthenocarpic if not pollinated, while if it is pollinated it produces seeds with smaller embryos. Its flowers have no petals and stamens, in contrast to a wild type apple flower that has 5 and between 9 and 20 respectively. Its flowers have two whorls of five sepals and an increased number, up to 15 of styles and carpels, while the normal flower typically has 5.

There are other apple mutants, Spencer Seedless and Wellington Bloomless, which produce flowers with a similar phenotype of Rae Ime, and are parthenocarpic. This phenotype is similar to that observed in the Arabidopsis mutants *pi* and *ap3. PISTILLATA* (*PI*) and *APETALA3* (*AP3*) belong to the B-class MADS-box transcription factor genes and are involved in the identity determination of the petals, and stamens, with the A-class and C-class MADS-box transcription factors respectively (Thießen *et al.,* 2001). It has been observed that *MdPI*, which encodes a

protein with 64% identity to that encoded by *AtPI* and which has a similar expression pattern compared to Arabidopsis, in Rae Ime has a 9332 bp LRT-retrotransposon insertion that affects the function of this gene. The mutation of *MdPI* has also been found in Spencer Seedless and Wellington Bloomless (Yao *et al.,* 2001). Furthermore, co-suppression of *MdPI* in transgenic apple was also shown to result in parthenocarpy (see Tanaka & Wade, (2022) for review).

In tomato, the mutants of the E-class *SEPALLATA* ortholog, *MADS-BOX29* (*TM29*), and of *SlAGL6* (*AGAMOUS-like 6*) are obligate and facultative parthenocarpic respectively (Ampomah-Dwamena *et al.,* 2002; Klap *et al.,* 2017; Takisawa *et al.,* 2018). Down-regulation of TM29 through RNAi in tomato, leads to the production of a mutant with some flower defects, such as green and sterile anthers, and a pistil that develops a parthenocarpic fruit without pollination and fertilisation. The transgenic fruit are bigger than the wild type, although they remain green for a longer time before starting the maturation process. Moreover, ectopic shoot formation has been observed in the transgenic fruit, which become swollen and misshapen. The shoot produces in turn a new fruit from which a new ectopic shoot arises, and this cycle can be repeated three or four times (Ampomah-Dwamena *et al.,* 2002). While alterations in flower development and structure have been observed in *tm29* mutants, no pleiotropic effect in any other plant organs have been found when *SlAGL6* has been mutated (Klap *et al.,* 2017; Takisawa *et al.,* 2018).

Parthenocarpy can also be induced by altering the hormones homeostasis, regulation and signalling. A nice example of how manipulation of auxin homeostasis leads to parthenocarpic fruit development can be found in the eggplant mutant *pad-1*. The *PAD-1* gene encodes for an aminotransferase that has the function of converting the indole-3-pyruvic acid (IPyA), which is an intermediate in the auxin biosynthetic pathway, to tryptophan (Trp), that is the initial auxin precursor. Thus, as a consequence, the loss of function of this gene causes an increase of auxin levels in the unpollinated ovaries, which develop in parthenocarpic fruits. The same mutation has been generated in tomato (RNAi) and sweet pepper (EMS mutagenesis), resulting in parthenocarpic fruit development in both species (Matsuo *et al.,* 2020). Likewise, altering gibberellin homeostasis can induce parthenocarpy. Indeed, the silencing of the GA2-oxidases, which are responsible for the conversion of the active form of gibberellins into their inactive

forms, caused the development of parthenocarpic fruits in tomato, since in the unpollinated ovaries the gibberellin levels have been found to be higher than normal (Martínez-Bello *et al.,* 2015). Higher levels of auxin and/or gibberellins are perceived by the unpollinated ovary as positive signal consequent ovule fertilisation. An alternative strategy is to over-express auxin or gibberellin biosynthetic genes. For example, Wang *et al.* (2020), were able to induce parthenocarpic fruit development in tomato by over-expressing *PbGA20OX*, the pear ortholog of the gibberellins biosynthetic gene *GA20OX*. Moreover, the transient over-expression of *PbGA20OX* in the pear variety 'Dangshansu' resulted in the retention of unpollinated ovaries for longer than the wild type (Wang *et al.,* 2020). Sometimes it is even enough to alter the hormone transport to induce parthenocarpy. The mutation of the auxin efflux carrier encoding gene *PIN4* in tomato is one significant example. Auxin cannot diffuse freely from the site of its production to the neighbouring cell, since it is an acid, and it is limited by the difference of pH between the cytosol and the apoplast. For this reason, auxin is mainly transported through transmembrane carriers which can be tightly regulated in their copy-number and localisation. This results in specific directions of auxin fluxes (Zažímalová *et al.,* 2010). Mounet *et al.* (2012) reported the first example of parthenocarpic fruit development in tomato caused by the silencing of a PIN carrier.

The direct manipulation of hormone levels is not the only strategy. For example, the alteration of the players involved in signal transduction has been shown to be a successful approach to induce parthenocarpy. Indeed, in the unpollinated ovaries there are the negative regulators that are removed once the ovule fertilisation occurs, and the auxin and gibberellin levels increase. Thus, the removal of those negative regulators results in the initiation of the fruit set program even if pollination did not occur. Mutations in the *AUX/IAA* encoding genes are representative of this approach. In tomato, the knock-out mutants of *AUX/IAA9* encoding gene are parthenocarpic and in the *srl-1* parthenocarpic strawberry mutant, the suppression of *AUX/IAA4* has been observed (Wang *et al.,* 2005; Mazzucato *et al.,* 2015; Zhou *et al.,* 2021). Kim et al. (2020) proved that the silencing of *AUX/IAA9* in tomato mimics an increase of the auxin levels in the unpollinated ovaries and promotes the expression of auxin and gibberellins biosynthetic genes, which are activated during the fruit set (Kim *et al.,* 2020).

The AUXIN RESPONSE FACTORS 7 and 8 (ARF7 and 8) are also reported to be negative regulators of fruit set. The transcript levels of both genes are highly expressed in non-pollinated flowers and are down-regulated after pollination. Down-regulation of *SlARF7* in tomato resulted in the formation of parthenocarpic fruit and a significant reduction in the accumulation of GA compared to seeding fruit (de Jong *et al.,* 2009; de Jong *et al.,* 2011). Hu *et al.* (2018) reported that *SlARF7* RNAi lines also display a down-regulation of *SlARF5* and *SlARF8B,* which are both involved in fruit set regulation. In fact, the tomato *arf5* mutant also shows a parthenocarpic phenotype (Luo *et al.,* 2018). Similar results have been found with *ARF8* in tomato, eggplant and Arabidopsis. In Arabidopsis, *arf8* mutants display parthenocarpic siliques and the expression of the Arabidopsis mutant allele in tomato results in the production of seedless fruits (Goetz *et al.,* 2007; Goetz *et al.,* 2006; Du *et al.,* 2016). The eggplant RNAi *SmARF8* (*SmARF8i*) mutant also produces parthenocarpic fruits. Thus, different ARF proteins are involved in the regulation of fruit set exhibiting functional redundancy. In cucumber the major parthenocarpy-associated QTL (Parth 2.1) on chromosome 2 has been studied and among all the genes in this region, three are related to hormone signalling. Of particular note is *Csa2M068680*, which is the homolog of *AtARF19* (Wu *et al.,* 2016). The same outcome of the suppression of *AUX/IAA* encoding genes, is obtained when the targets are the *DELLA* encoding genes. The DELLA proteins have the same function as the AUX/IAA ones, in the gibberellin signalling pathway instead. Mutations in *SlDELLA* in tomato and *FveRGL1* in strawberry are both associated with parthenocarpic phenotype (Carrera *et al.,* 2012; Zhou *et al.,* 2021).

5.1.3 The protein domains of ARF, AUX/IAA and DELLA proteins

ARFs, AUX/IAAs and DELLAs are particularly interesting because they can interact, mediating the crosstalk between auxin and gibberellin signalling pathways that are the two most important for fruit set. The first evidence of this crosstalk was provided by Hu *et al.,* (2018) who demonstrated the interaction of SlARF7, SlAUX/IAA9 and SlDELLA (Hu *et al.,* 2018; see Figure 4.6, Chapter 4). Subsequently the interaction of FveARF7, FveAUX/IAA4 and FveRGL1 was demonstrated in strawberry fruit (Zhou *et al.,* 2021). In both studies, yeast two-hybrid experiments proved the interaction of the ARF proteins with both AUX/IAA and DELLA, through different domains.

The ARF7 and ARF8 proteins have three main domains (Fig. 5.1A). The B3 domain is at the N-terminal end and is responsible for the binding to the DNA at the level of the AuxRE (Auxin Responsive Elements) sequences. The mid domain is the activation domain (AD), which interacts with the DNA. Finally, the domain at the C-terminus is the PB1 domain, which is responsible for protein dimerization, that can occur with another ARF protein or with an AUX/IAA factor (Guilfoyle & Hagen, 2007). The AUX/IAA proteins have at their C-terminus, a PB1 domain, which contains a conserved "GDVP" motif, that is involved in electrostatic protein interactions, and a Nuclear Localisation Signal sequence (NLS). AUX/IAA proteins have two other important domains. Domain I is at the N-terminus and contains a LxLxL motif, which is an ethylene response factor (ERF)-associated amphiphilic repression (EAR) motif. The function of this domain is to bind TOPLESS, another transcriptional repressor. Domain II is a degron domain and is essential for the correct turnover of the AUX/IAA proteins. Specifically, it is involved in the binding with the TIR1/AFB proteins that promote degradation via the proteasome. In Domain II the "GWPPV" motif is conserved. A bipartite NLS is present in Domain II as well, that binds with the "KR" rate motif between Domain I and II (Fig. 5.1B) (Luo *et al.,* 2018).

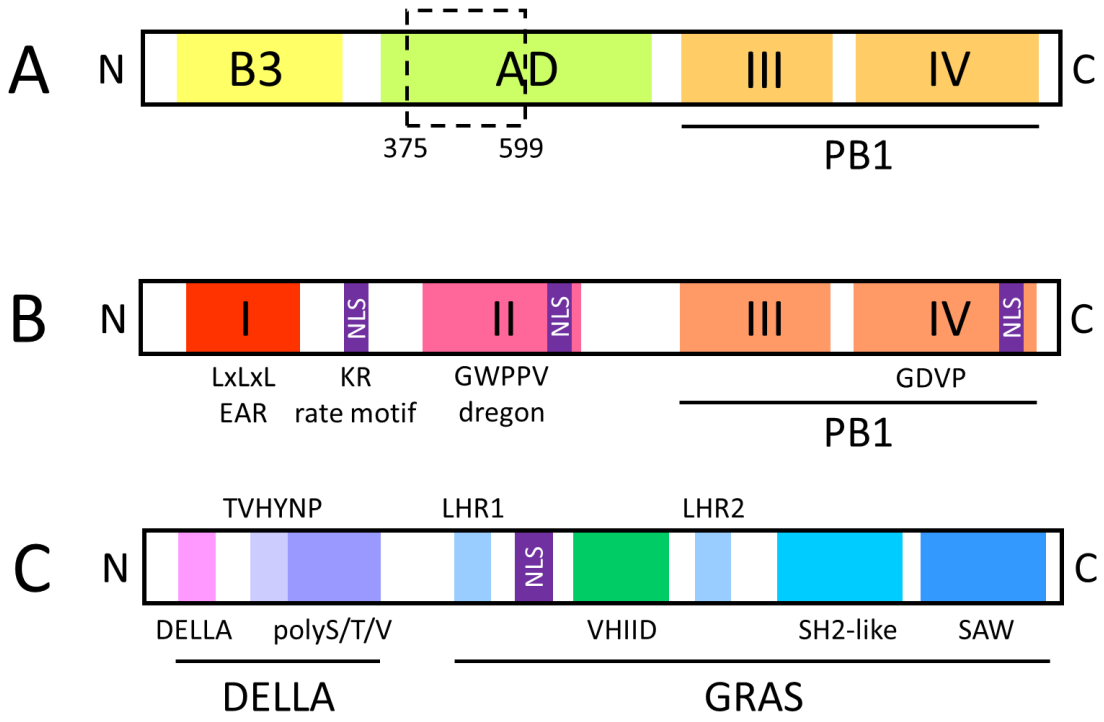


Figure 5.1: Schematic representation of the domains in ARF (A; Guilfoyle & Hagen, 2007), AUX/IAA (B; Luo *et al.,* 2018) and DELLA proteins (C; Xue *et al.,* 2022). The dashed box on ARF sequence represents the MR2 sequence in SlARF7 that is needed for the binding with SlDELLA (Hu *et al.,* 2018).

In the DELLA proteins, two big domains have been identified: the DELLA domain, which is the gibberellin responsive domain, and the GRAS domain, which is the functional domain (Fig. 5.1C). The DELLA domain at the N-terminal end, contains the "DELLA" and "VHYNP" motifs that are crucial for the binding with the gibberellin receptor GID1. In the DELLA domain, there are also polymeric Ser/Thr/Val (poly S/T/V) motifs, which may play a role in DELLA protein phosphorylation or glycosylation. The GRAS domain is at the C-terminus and contains six motifs: two "LHR" (leucine heptad repeats) motifs, that enclose one putative NLS and the conserved "VHIID" motif, and "SH2-like", and "SAW" motifs which are highly conserved. The GRAS domain is responsible for stabilising the DELLA domain interaction with GID1, and binding other regulatory elements, mostly thanks the two "LHR" motifs, repressing the gibberellins responsive genes (Xue *et al.,* 2022).

Thus, while ARF7 and AUX/IAA9 can interact through their C-terminal PB1 domains, Hu *et al.* (2018) showed that the interaction between ARF7 and DELLA occurs in a different part of the ARF7 sequence. Indeed, a yeast two-hybrid experiment has shown that the sequence that is involved in the binding with the DELLA protein is between residues 375 and 599, and it is mostly made by the N-terminal part of the AD domain (Fig. 5.1A) (Hu *et al.,* 2018).

5.1.4 Parthenocarpy as adaptive strategy adopted by Angiosperms

Natural parthenocarpy seems paradoxical, considering that the mother plant invests a high amount of energy to produce a fruit that does not contain a seed. However, the emergence of this trait in evolution, may have an adaptive reason. Picarella and Mazzucato (2019) were the first to investigate this question. In their review, they identified all the known examples of parthenocarpic species and reported the highest frequency (49.8%) occurred in the Rosidae, with six species in the Rosaceae. The Solanaceae family, which belongs to the Asteridae clade (13.8%), is also well represented, with nine species. The species were also subdivided into two groups according to the number of seeds contained in the fruit: monospermic (single seed) and plurispermic (multiple seeds). According to the model proposed, the reasons why natural parthenocarpy emerged in those two groups are different. Indeed, in the monospermic species, the driving force would have been the reduction of seed predation. In support of this hypothesis there are few examples. The parsnip webworms seem to prefer the seedless fruits, because they contain less furanocoumarins, so the seeded fruits are not attacked, or in *Pistacia terebinthus* L. the seedless fruits are not distinguishable from the seeded ones, decreasing the chances of a seeded fruit being picked by a predator (Zangerl *et al.,* 1991; Traveset, 1993). In plurispermic species instead, parthenocarpy, in particular facultative parthenocarpy, might have started to be used in those cases when not all the ovules were fertilised, resulting in a weak a signal to trigger fruit set, causing consequently ovary abortion and the loss of the ovules that were fertilised. This hypothesis is supported by the fact that a high number of dioecious species are parthenocarpic and their chances of high pollination rate is less frequent than that observed for the species with hermaphrodite flowers (Picarella & Mazzucato *et al.,* 2019).

5.1.5 Phylogenetic analysis of the Rosaceae family and *Prunus* genus

The Rosaceae family includes many species that are economically relevant such as apple, strawberry, peach, cherry, rose and others. It includes approximately 3,000 species which present different types of fruit structures: achene, drupe, drupelet, and pome. Conventionally, the type of fruit produced was used to divide this family in four subfamilies, but, more recently, phylogenetic analysis of the nuclear and plastid DNA has been used to understand the evolutionary history of this family. Thus, the three sub-families identified are Amygdaloideae, Dryadoideae, and Rosoideae (Potter *et al.,* 2002; Potter at al., 2007). The genus *Prunus* L. belongs to the Amygdaloideae sub-family and includes approximately 250-400 species, which produce a drupe type of fruit. As for the Rosaceae family, this genus is divided into three sub-groups based on the inflorescence architecture: deciduous solitary-flower (subg. *Prunus* and *Amygdalus*), deciduous corymbose (subg. *Cerasus*) and racemose (subg. *Padus*.). The species in the first two groups are diploid while those in the racemose group are polyploid. The evolutionary history of the *Prunus* genus has been investigated and presents some challenges due to the occurrence of allopolyploidy and hybridization. In particular, the racemose group has been the most studied group, and different models have been proposed in recent years about its evolutionary relationship with the other groups (Zhao *et al.,* 2016). For example, one phylogenetic study using both nuclear and plastid sequences suggests that the subg. *Prunus* + *Amygdalus* and the subg. *Cerasus* are sister clades, while the subg. *Padus* is a paraphyletic group (Fig. 5.2) (Hodel *et al.,* 2021). *Prunus avium* belongs to the *Cerasus* subgenus and its genome was published in 2017 (Shirasawa *et al.,* 2017). The estimated sweet cherry genome is about 350 Mb and the assembled genome PAV_10r covers 77.8% of it. Compared to other diploid *Prunus* species such as *P. armeniaca* (240 Mb), *P. dulcis* (240 Mb), *P. persica* (265 Mb) and *P. mume* (280 Mb), the cherry genome is about 100 Mb bigger (International, Peach Genome Initiative, (2013); Zhang *et al.,* 2012; Jiang *et al.,* 2019; Sánchez-Pérez *et al.,* 2019).

The comparison of the consensus genetic maps of cherry and peach also, showed a high level of chromosome synteny between those two species (Shirasawa *et al.,* 2017).

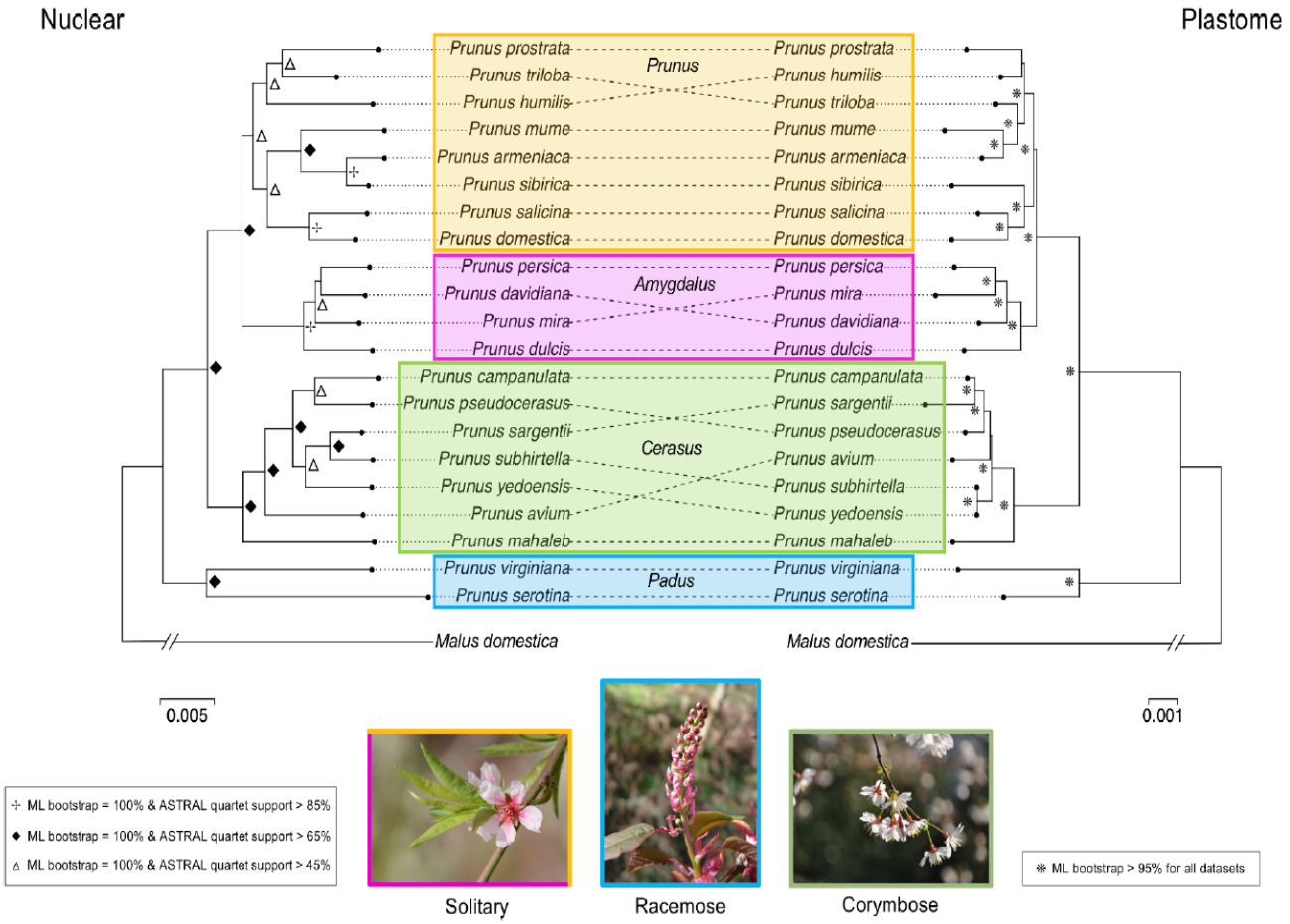


Figure 5.2: Phylogenetic trees obtained using nuclear markers and plastid sequences of 21 *Prunus* species. *Malus domestica* has been added as an outgroup. The bootstrap support is reported at the nodes by different symbols according to the significance. The three types of inflorescence architecture are shown in the photos. (Hodel *et al.,* 2021).

The aim of this Chapter was to investigate further *PavARF7*, PavAUX/*IAA9s* and *PavRGL2* since from the transcriptomic analysis (Chapter 4) those genes may be involved in blocking fruit set in sweet cherry. They could potentially be the targets of the CRIPSR-Cas9 direct site mutagenesis to obtain a parthenocarpic sweet cherry plant. A phylogenetic analysis of their transcript sequences and the alignment of their protein sequences to the ones of their orthologs in well characterized models like Arabidopsis and tomato, were conducted. Finally, the plasmids containing the coding sequence of these genes were assembled, in order to transform their corresponding tomato mutants. This was thought as a first step of the functional characterisation of these genes.

5.2 Materials and methods

5.2.1 Phylogenetic analysis of *PavARF7*, *PavAUX/IAA9*s and *PavRGL2*

Phylogenetic analysis was conducted using the cDNA sequences of all the putative cherry orthologs of *ARF*, *AUX/IAA* and *DELLA* genes. The corresponding orthologs in Arabidopsis, tomato, potato, sweet pepper, peach, almond and apple were added to this analysis. The Arabidopsis and tomato sequences were selected as references while the peach, almond, potato and sweet pepper were identified using BLAST. The sequences were aligned by MEGA 11 using MUSCLE as sequence alignment tool (Edgar, 2004; Tamura *et al.,* 2021) and the aligned sequences were used for the phylogenetic tree building process. The statistical method chosen was Maximum Likelihood and the test of Phylogeny was the Bootstrap method. The number of Bootstrap Replications was set at 1000.

5.2.2 Assessment of *PavARF7*, *PavAUX/IAA9*s and *PavRGL2* expression patterns

The gene count numbers of *PavARF7*, *PavAUX/IAA9*s and *PavRGL2* were checked from the transcriptomic data obtained in the experiment described in Chapter 4 (4.2 Materials and methods). Data were analysed using the DESeq2 package and graphs were constructed using ggplot2 (Love *et al.,* 2014).

5.2.3 Assessment of identity percentages between orthologs in different species

The percentage of identity (cDNA and protein sequence) and similarity (protein sequence only) of the selected genes were investigated. All the sequences were aligned using MEGA11 and the identity/similarity analysis was conducted using The Sequence Manipulation Suite (Stothard, 2000). The multiple alignment figures were generated using ESPript 3.0 (Robert *et al.,* 2014).

5.2.4 Golden Gate vector assembly

The vectors, that contain the codon-optimised CDS of *PavARF7*, *PavAUX/IAA9*s and *PavRGL2* genes under a constitutive promoter, were assembled using the Golden Gate technology (Engler *et al.,* 2009; Weber *et al.,* 2011). Codon optimisation was done to remove restriction sites

recognized by the restriction enzymes Bsa-HI and BbsI, used for the assembly. It consists of the change of the nucleotidic sequence, without altering the amino acid sequence. This is possible because the genetic code is degenerate: more codons or triplets encode for the same amino acid. Level-0 blocks of the four CDS with the correct adaptors were synthetized by NBS Biologicals (Huntingdon, UK). The other level-0 modules used in this phase were EC23002-(pL0VM-PU-FMV), which contains the constitutive promoter FMV (Richins *et al.,* 1987), and EC15320-(pL0VM-T-HSP18.2) which contains the HSP terminator (Hirai *et al.,* 2011). Bsa-HI and T4 ligase were the enzymes used for the level-one assembly reactions which resulted in the formation of the pFMV-CDS-tHSP cassette in the EC47811-(pl1v-r2-47811) backbone (Fig. 5.17-20A). This vector contains the Ampicillin resistance gene for the selection in *E. coli*. The four level-one modules were sent to Eurofins for sequencing using the L1M-R-FP and L1M-R-RP primers (Table 5.1), which anneal to the backbone just outside the assembled cassette. The level-two assembly was conducted with the same procedure, but in this case the restriction enzyme used was BbsI. The destination backbone vector chosen was EC50507-(pL2V-1-50507), which has a Kanamycin resistance gene for selection in *E. coli*. The other two level-one modules used were EC15529-(pL1M-R1-p35S-KAN-tNOS) (Fig. 5.3), which contains the Kanamycin/Neomycin resistance gene under constitutive 35S promoter (Amack and Antunes, 2020) for the selection in plant, and EC41744-(pL1M-ELE-2-41744) which provides the linker for the proper closure of the plasmid. All the four assembled level-two pLV2-(pFMV-CDS-HSP)-(p35S-KAN-Nos), shortened 60(EVX) pLV2-(pFMV-CDS-HSP)-KAN, vectors were sequenced using the primers reported in Table 5.1. These primers allowed the sequencing of the entire cassette, making it possible to control if any errors occurred during the assembly and that all the parts join as expected.

Primer Name	5'-3' Sequence
L1M-R-FP	CGGATAAACCTTTTCACGCCC
L1M-R-RP	GTACTGGGGTGGATGCAGTG
L2-FP	TGGCACATACAAATGGACGAACGG
L2-RP	CCACTCGATACAGGCAGCCCAT
pFMV F1	AAGGAATGGTGCAGAATTGTTAGGC
RGL2 F1	TCTTGGCTGCTTCTCAGGCTGG
RGL2 F2	ACTCACTTGAAGGCAGCTCTGG
ARF7 F1	AACAGCCTGCACTTAGCTCAAGC
ARF7 F2	TTGGATGCAAGCACTATTCAGC
AUX/IAA9.1 F1	AAGTCTCTACTGTCTCTGGTGG
AUX/IAA9.1 F2	AAGGTCAGCTTGGATGGTGCTCC
AUX/IAA9.2 F1	TTGACAGCTCCACGGTTTCGAGC
AUX/IAA9.2 F2	AAGGTCAGCATGGATGGTGCTCC
tHSP	TTGGCTTGTTGTGTTATGAATTTGTGGC
KANA	AACTGTTCGCCAGGCTCAAGG

Table 5.1: list of primers used for the sequencing

Figure 5.3: Plasmid map of the EC15529-(pL1M-R1-p35S-KAN-tNOS) level-one module used for the level-two modules assembly. The BbsI restriction sites are shown.

5.3 Results

5.3.1 Phylogenetic analysis of the putative *PavARFs* shows that *Pav_sc0000129.1_g.1480.1.mk* belongs to the *ARF7* clade.

Pav_sc0000129.1_g.1480.1.mk is expressed in unpollinated ovaries at anthesis and is significantly down-regulated at 7 DAT in the open pollinated and GA_3 ovaries (Fig. 5.4).

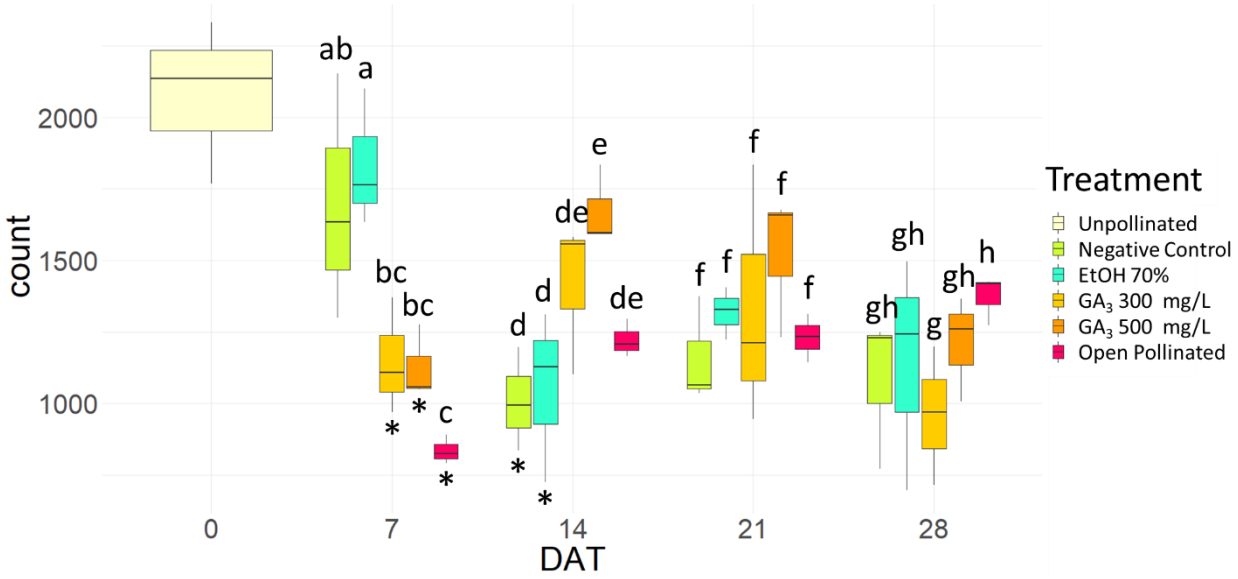


Figure 5.4: Boxplot shows the expression levels of *Pav_sc0000129.1_g.1480.1.mk* (*PavARF7*) in the five different treatments from timepoint 0 to 28 (DAT: Days After Treatment). The star means a significant difference in the expression levels compared to the previous timepoint, while the letters show the statistical difference between the treatments at the same timepoint.

To assess if *Pav_sc0000129.1_g.1480.1.mk* is the putative ortholog of *ARF7* in sweet cherry, a phylogenetic analysis was conducted. The phylogenetic tree reported in Fig. 5.5 was produced from the alignment of the cDNA sequences of all the putative *PavARFs* with the sequences of the ARF7 orthologs in *Arabidopsis thaliana (At)*, *Solanum lycopersicum (Sl)*, *Capsicum annuum (Ca)*, *Prunus persica (Ppe)*, *Prunus dulcis (Pdu)* and *Malus domestica (Md)*. *PpeARF7* and *PduARF7* group into a clade since both peach and almond belong to the *Amygdalus* sub-genus. Their clade is the most closely related to *PavARF7*. The three *Prunus* species form a monophyletic group as

well, which is most closely related to the apple ortholog. This clade includes all the taxa that belong to the Rosaceae family. This sub-tree structure is highly supported since the Bootstrap number is always greater than 90. Another highly supported clade contains the two species that belong to the Solanaceae family: tomato and sweet pepper. This clade is more closely related to Arabidopsis than the Rosaceae clade. However, this seems not to be statistically supported. All these clades are included into a unique bigger group, which is well supported.

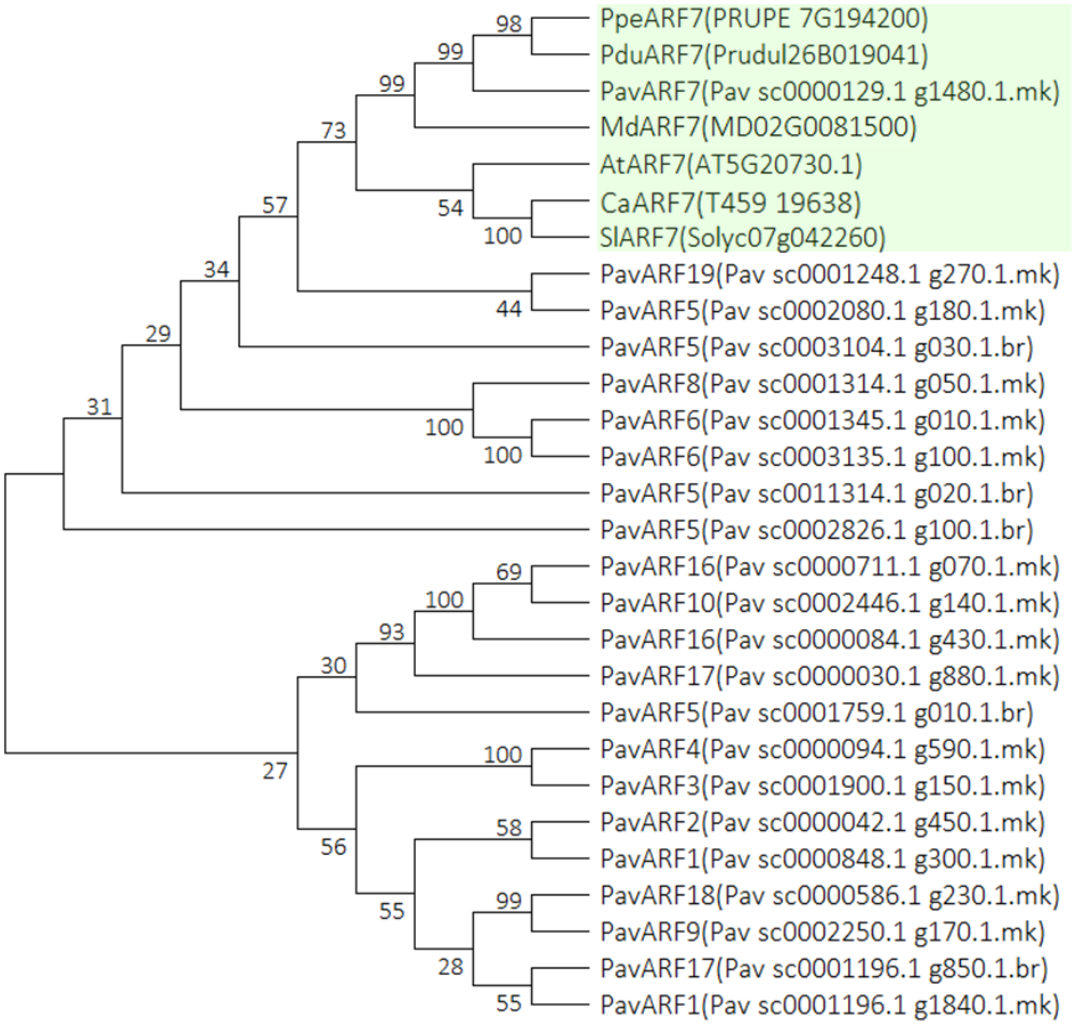


Figure 5.5: Phylogenetic tree obtained with the Maximum Likelihood method using cDNA sequences. The tree includes all the putative *ARF* cherry orthologs and the *ARF7* orthologs of Arabidopsis, tomato, sweet pepper, peach, almond and apple. The log likelihood is -84372.40. Numbers ate the nodes are the Bootstrap numbers that show the level of significance.

The number of exons is fairly consistent in all the species included in the analysis as well as their strand orientation (Table 5.2). Indeed, all these genes are on the reverse strand, with the exception of the *Amygdalus* clade, peach and almond, whose orthologs are reported on the forward strand. Despite this difference, the location of the three *Prunus* orthologs in the genome is conserved and is on chromosome 7. This location on chromosome 7 is found also in the two Solanaceae species while in Arabidopsis and apple, *AtARF7* and *MdARF7* are found in chromosome 5 and 2 respectively.

Gene	Symbol	cDNA length (nt)	Protein length (aa)	Number of exons	Strand	Chromosome
Pav_sc0000129.1_g1480.1.mk	PavARF7	3427	709	13	RV	7
AT5G20730.1	AtARF7	4341	1165	13	RV	5
Solyc07g042260	SlARF7	3832	930	15	RV	7
T459_19638	CaARF7	3333	1110	13	RV	7
PRUPE_7G194200	PpeARF7	5115	1168	14	FW	7
Prudul26B019041	PduARF7	6085	1168	14	FW	7
MD02G0081500	MdARF7	4627	1151	14	RV	2

Table 5.2: *ARF7* orthologs information about cDNA and protein sequence lengths, number of exons, orientation, and chromosome localisation. Data collected from Ensembl Plants.

Both the transcript and amino acid sequences of all the *ARF7* orthologs were aligned to assess the percentages identity (Table S5.1-2). The *PavARF7* cDNA sequence has the highest percentage identity with *PpeARF7*, about 62%, while with the other two taxa of the Rosaceae clade, it is slightly lower, approximately 53%. *PavARF7* is the ortholog that has the lower percentage identity within the Rosaceae clade, since the sequences in peach, almond and apple have a higher identity between themselves. This becomes even more evident when the amino acid sequences are aligned and compared. The percentages of identity and similarity between *PavARF7* and *PpeARF7* or *PduARF7* are about 60%, while between the two *Amygdalus* species it is more than 98%. These species also show higher identity and similarity levels with the *MdARF7* sequence. The two Solanaceae species share the higher identity of both the nucleotide and amino acid sequences, but some differences can be identified when compared to the Rosaceae clade. Indeed, while the comparison of *SlARF7* versus all the other species, displays an identity degree that is similar, *CaARF7* has higher percentages with the *Amygdalus* clade and *MdARF7*. This same observation can be made when *AtARF7* is considered in relation to the Rosaceae monophyletic group.

The three domains that characterise the ARF proteins are all well conserved in all the species (Fig. 5.6; Table S5.3-4-6), with an extremely high level of identity. However, an exception is present in regard to the B3 domain. For example, PavARF7 displays a much lower degree of identity (~40%) when aligned to the B3 domains of all the other ARF7 proteins (Fig. 5.6A; Table S5.3). This is due to the fact that PavARF7 sequence lacks the residues that are present from position 162 to 210 in all other sequences. All the other species are almost identical in this part of the domain (see Fig. 5.6A).

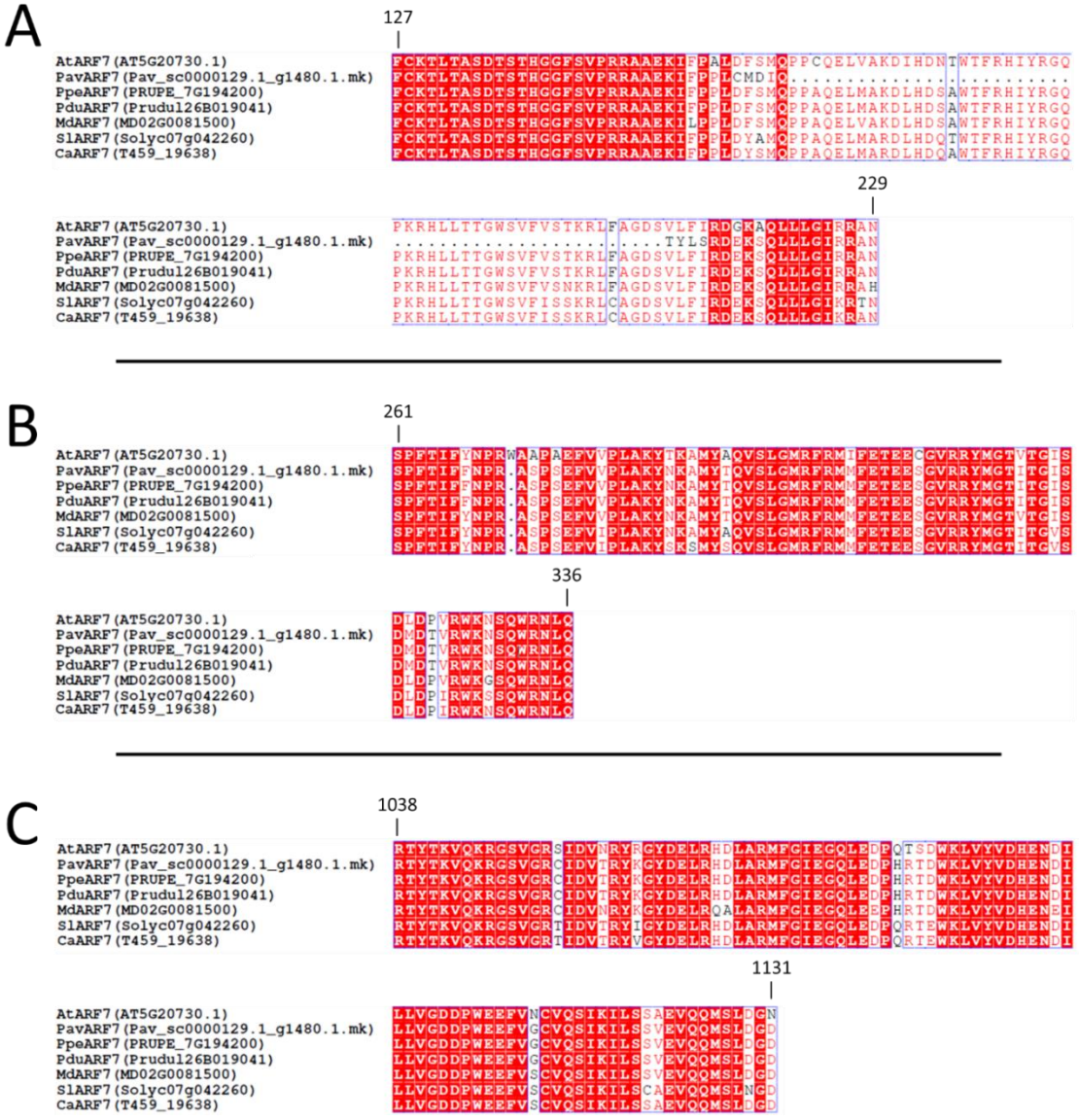


Figure 5.6: Multiple alignments of the ARF7 B3 domain. (A), AD domain (B) and PB1 domain (C). Red boxes indicate identical residues, the red letters have similar residues (same side chain category) while black letters denote different residues with side chains that belong to a different category.

The MR2 Domain, which is proposed in tomato to be involved in the interaction with DELLA proteins, is the least conserved (Fig. 5.7; Table S5.5). Its amino acid sequence identity percentage is high when species of the same families are compared, except for PavARF7. As observed with the B3 domain, PavARF7 protein lacks a large portion of this domain (from position 444). However, unlike the B3 domain, the sequences of the other species analysed exhibit a high level of variation and are not highly conserved. The tomato ortholog shows higher identity with CaARF7, then with the Rosaceae species, with the exception of PavARF7.

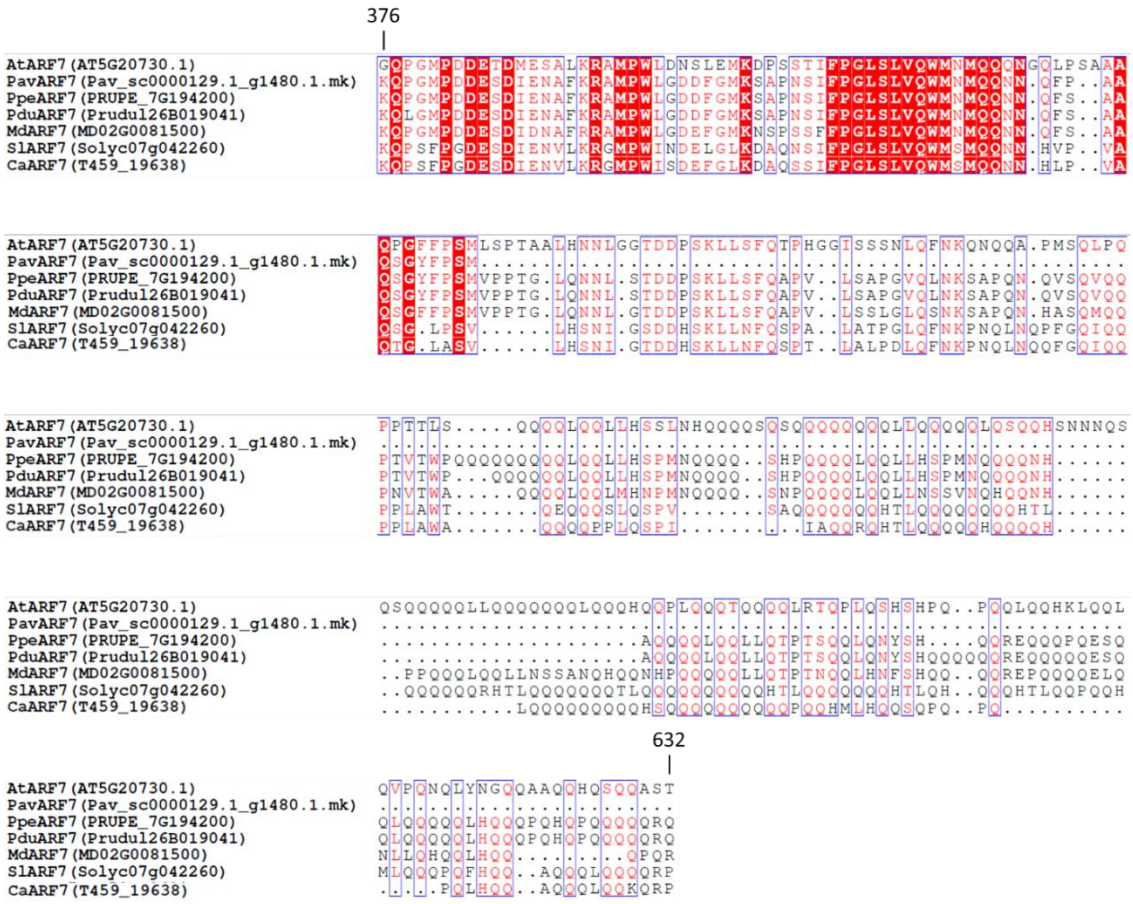


Figure 5.7: Multiple alignment of the ARF7 MR2 in tomato (Hu *et al.,* 2018). Red boxes indicate identical residues, the red letters have similar residues (same side chain category) while black letters denote different residues with side chains that belong to a different category.

5.3.2 Two putative *AUX/IAA9* genes in the *Prunus* species

Both *Pav_sc0002327.1_g560.1.mk* and *Pav_sc0002393.1_g030.1.mk* are highly expressed in the unpollinated ovaries at anthesis, with *Pav_sc0002327.1_g560.1.mk* counts that are two-fold higher than the ones of *Pav_sc0002393.1_g030.1.mk* (about 6.000 vs about 3.000) (Fig. 5.8). The two genes display slightly different patterns of expression. Both of the genes are down-regulated in the mock-control and in the GA_3-treated samples over time. However, *Pav_sc0002327.1_g560.1.mk* is slightly up-regulated at 7 DAT in the GA_3-treated ovaries, while in the pollinated ones it is down-regulated. In O.P. samples then, this gene is up-regulated, and its levels are higher than the ones in all the other treatments, while no difference is observed between O.P. and the negative control in relation to *Pav_sc0002393.1_g030.1.mk* expression.

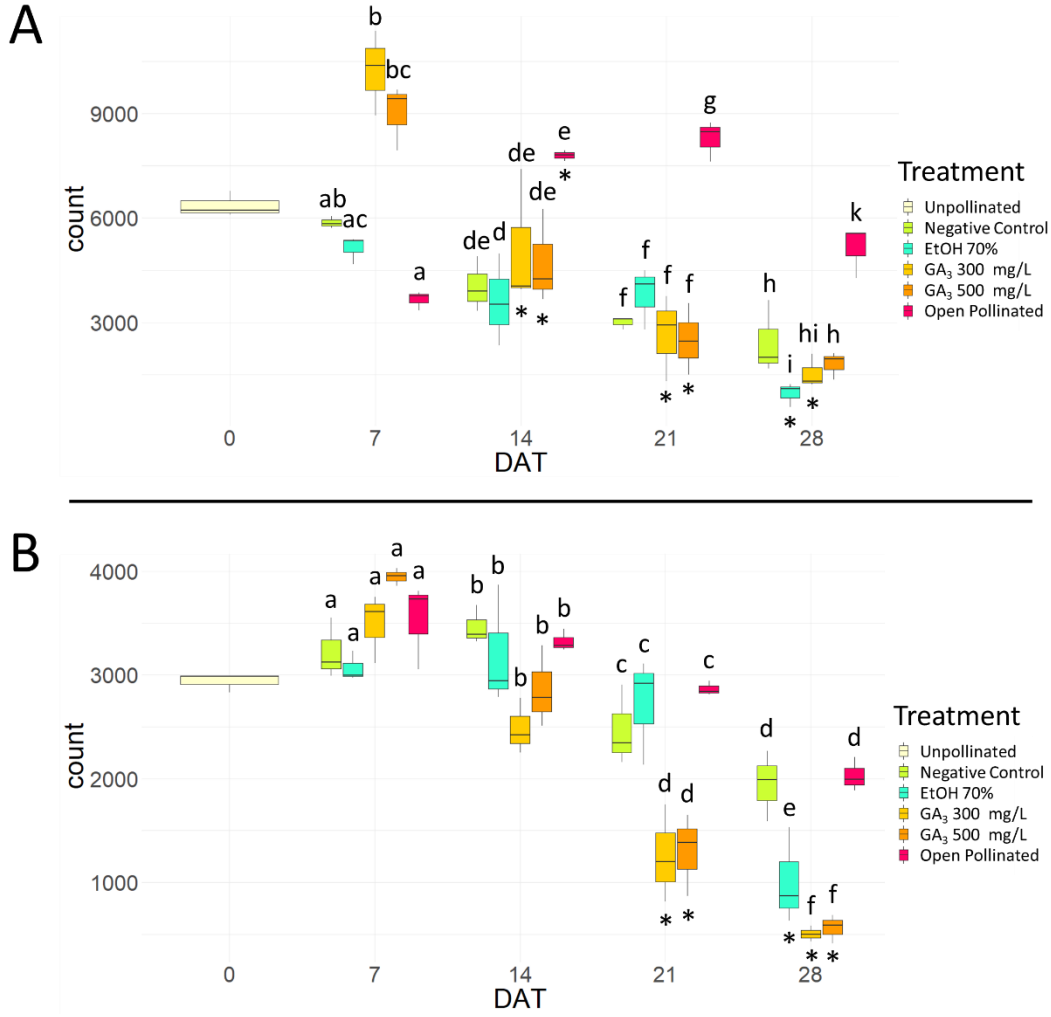


Figure 5.8: Boxplot that shows the expression levels of *Pav_sc0002327.1_g560.1.mk* (A) and *Pav_sc0002393.1_g030.1.mk* (B) in the five different treatments from timepoint 0 to 28 (DAT: Days After Treatment). The star denotes a significant difference in the expression levels compared to the previous timepoint, while the letters show the statistical difference between the treatments at the same timepoint.

All the putative *PavAUX/IAA* factor genes were included in a phylogenetic analysis. Once again, the same structure of the *Amygdalus* and Rosaceae monophyletic groups are observed (Fig. 5.9). *Pav_sc0002393.1_g030.1.mk* is in the clade with the orthologs identified in peach, almond and apple, that are reported as putative *AUX/IAA9* genes while the genes that are in the same clade as *Pav_sc0002327.1_g560.1.mk*, are reported to be putative *AUX/IAA8 /-like*. Interestingly, the Solanaceae *AUX/IAA9* clade is not closely related to *Pav_sc0002393.1_g030.1.mk*, which has higher similarity to the Arabidopsis clade. Indeed, the Solanaceae clade is significantly closer to the *Pav_sc0002327.1_g560.1.mk* clade and the putative orthologs of *AUX/IAA8*. *AtAUX/IAA8* however, is not included with this group but it is more closely related to *AtAUX/IAA9* and the Rosaceae *Pav_sc0002327.1_g560.1.mk* clade. The Solanaceae clade of *AUX/IAA8* is not closely related to either of those two groups. *PavAUX/IAA27* (*Pav_sc0001710.1_g1550.1.mk*) seems closely related to the clade which contains the Solanaceae orthologs of *AUX/IAA9* and the putative orthologs of *AUX/IAA8*. However, its branch is not supported since the Bootstrap number is low (19).

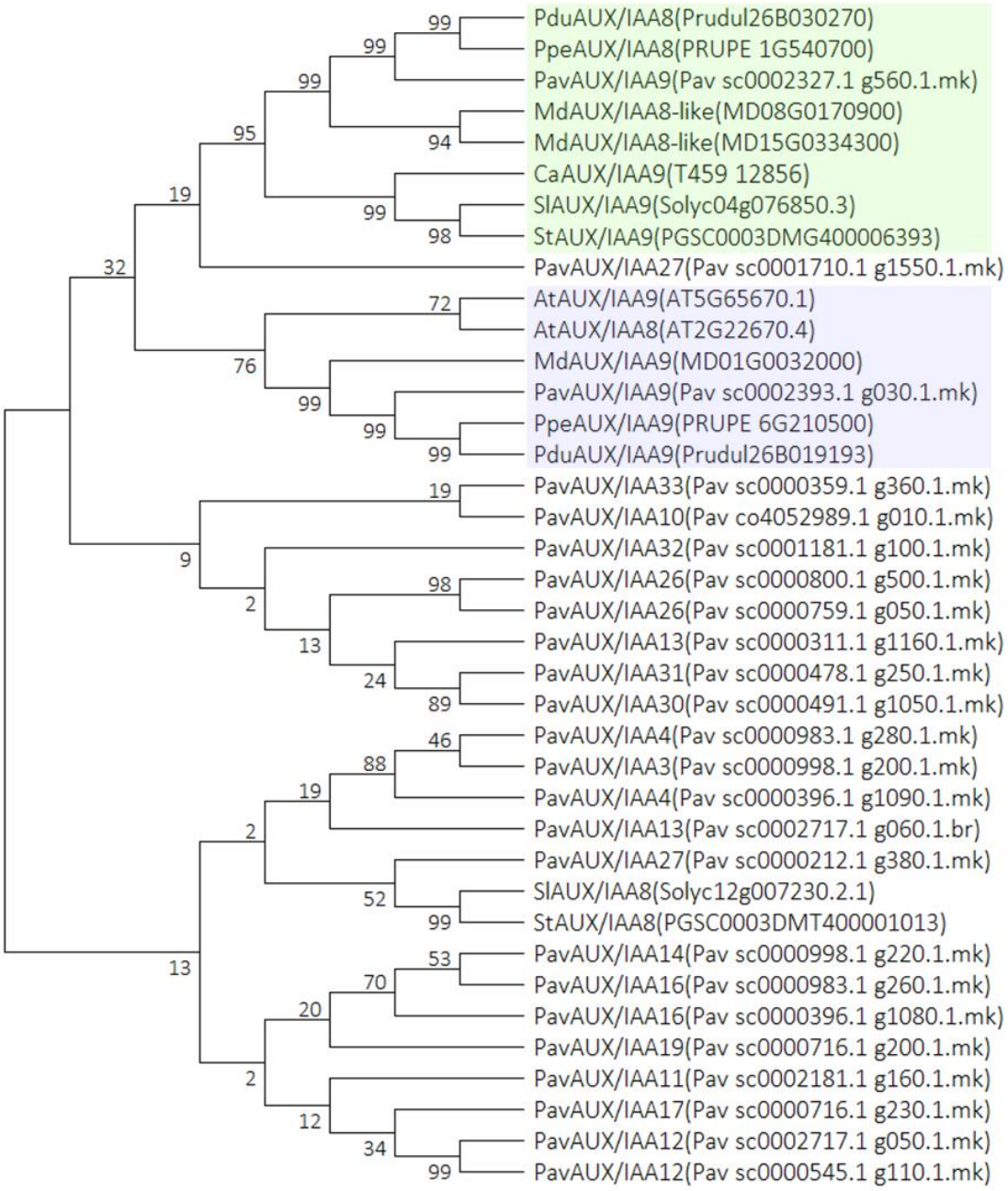


Figure 5.9: Phylogenetic tree obtained with the Maximum Likelihood method using cDNA sequences. The tree includes all the putative *AUX/IAA* cherry orthologs, the *AUX/IAA9* and the *AUX/IAA8* orthologs of Arabidopsis, tomato, sweet pepper, peach, almond and apple. The log likelihood is -53872.21. Numbers at the nodes are the Bootstrap numbers that show the level of significance.

Pav_sc0002327.1_g560.1.mk and *Pav_sc0002393.1_g030.1.mk* are located on two different chromosomes; chromosome 1 and 6 respectively (Table 5.3).The orthologs in peach and almond, that group in their respective clades, are found on the same chromosome. *Pav_sc0002393.1_g030.1.mk* is the only gene in its clade that is reported on the reverse strand. Two *MdAUX/IAA8-like* genes have been found on chromosome 8 (*MD08G0170900*) and 15 (*MD15G0334300*), while *MdAUX/IAA9* (*MD01G0032000*) ortholog are on chromosome 1. All the Solanaceae orthologs of *AUX/IAA9* genes are found on their respective chromosomes 4, while A*tAUX/IAA9* is on chromosome 5. The protein sequence length is consistent, and there is no evident difference in exon number. The two *MdAUX/IAA8-like* and *PavAUX/IAA9* (*Pav_sc0002393.1_g030.1.mk*) genes are the only ones reported to be on the reverse strand, while all the others are on the forward strand.

Gene	Symbol	cDNA length (nt)	Protein length (aa)	Number of exons	Strand	Chromosome
Pav_sc0002327.1_g560.1.mk	PavAUX/IAA9	2348	396	8	FW	1
AT5G65670	AtAUX/IAA9	1960	338	6	FW	5
Solyc04g076850	SlAUX/IAA9	1845	349	7	FW	4
PGSC0003DMT400016356	StAUX/IAA9	1764	349	7	FW	4
PHT84413	CaAUX/IAA9	1050	349	6	FW	4
PRUPE_1G540700	PpeAUX/IAA8	2822	397	5	FW	1
Prudul26B030270	PduAUX/IAA8	3331	397	5	FW	1
MD08G0170900	MdAUX/IAA8-like	2127	363	8	RV	8
MD15G0334300	MdAUX/IAA8-like	1980	363	8	RV	15
Pav_sc0002393.1_g030.1.mk	PavAUX/IAA9	1882	378	6	RV	6
PRUPE_6G210500	PpeAUX/IAA9	3455	378	5	FW	6
Prudul26B019193	PduAUX/IAA9	3214	378	5	FW	6
MD01G0032000	MdAUX/IAA9	2252	356	6	FW	1

Table 5.3: *AUX/IAA9* and *AUX/IAA8* orthologs information about cDNA and protein sequence lengths, number of exons, orientation, and chromosome localisation. Data collected from Ensembl Plants.

The coding sequences of *Pav_sc0002327.1_g560.1.mk* and *Pav_sc0002393.1_g030.1.mk* exhibit an identity percentage that is quite low (43.86%), while the protein sequences are identical and similar at 57.75% and 65.95% respectively (Table S5.7-8). Moreover, the amino acid sequences of the encoded proteins, compared to the ones of the taxa in their respective Rosaceae groups, are much more conserved than the nucleotide sequences. Cherry nucleotide sequences have a higher identity degree with the apple sequences; however this difference is not present when the amino acid sequences are compared. *Pav_sc0002393.1_g030.1.mk* shows a higher identity level to the Arabidopsis *AUX/IAA9* transcript and amino acid sequences than *Pav_sc0002327.1_g560.1.mk*. This observation cannot be applied when the cherry orthologs are compared to the Solanaceae ones since the difference in the percentages are low. The nucleotide and especially the amino acid sequences are highly conserved within the Solanaceae orthologs, which do not show great conservation level with *AtAUX/IAA9*.

The amino acid sequences of the domains that characterise this class of negative regulators, are extremely highly conserved among all the sequences analysed (Table S5.9-11). In Arabidopsis only, the "LxLxL" motif in Domain I has a Threonine (T) between the first and second Leucine (L), while all the other species have an Arginine (R) (Fig. 5.10). Threonine is a polar residue while Arginine is a basic residue (positively charged). Moreover, Pav_sc0002327.1_g560.1.mk, PpeAUX/IAA8 and PduAUX/IAA8 present an Aspartic acid (D) instead of a Glutamic acid (E) before the first leucine. These two residues are redundant since they are both negatively charged acid residues. All the sequences have the conserved "KR" rate motif, between Domain I and II (Fig. 5.9).

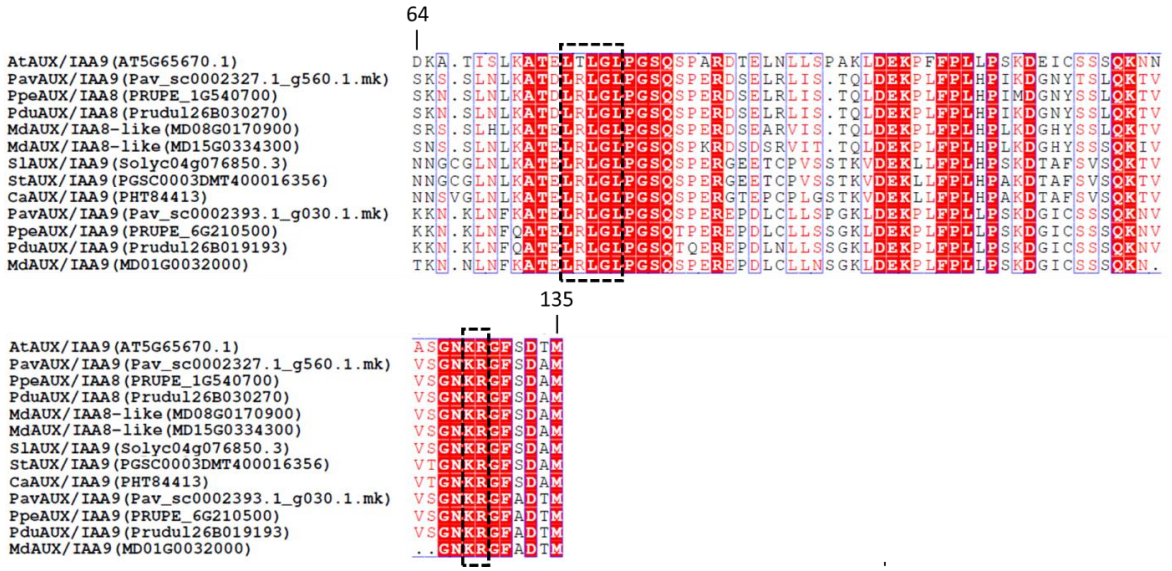


Figure 5.10: Multiple alignment of the region that contain the "LxLxL" EAR motif in Domain I and the "KR" rate motif between Domain I and II of the AUX/IAA protein sequences. Red boxes indicate identical residues, the red letters have similar residues (same side chain category) while black letters denote different residues with side chains that belong to a different category. The motifs are shown by the dashed line.

The “GWPPV” motif in Domain II is extremely well conserved. Indeed, although the last Valine (V) is substituted by an Isoleucine (I), in the Rosaceae and Solanaceae species, this substitution does not change the chemical-physical properties of the motif since both valine and isoleucine are hydrophobic side chain residues (Fig. 5.11; Table S5.10). Finally, the PB1 domain, which is at the C-terminus and contains the Domain III and IV, is also highly conserved (Fig. 5.11; Table S5.11). The “GDVP” motif is conserved in all the sequences (Fig. 5.11)

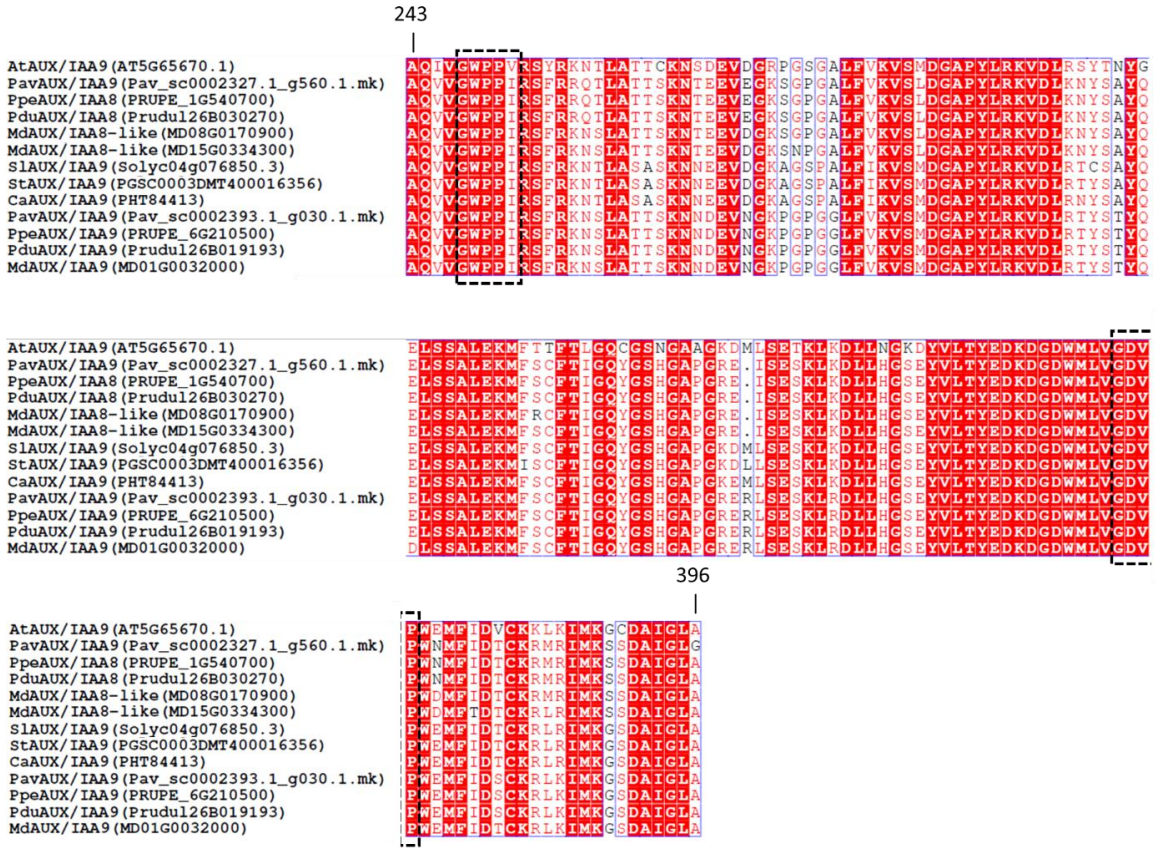


Figure 5.11: Multiple alignment of the region that contains Domain II (the “GWPPV” motif) and PB1 domain (“GDVP” motif) of the AUX/IAA protein sequences. Red boxes indicate identical residues, the red letters have similar residues (same side chain category) while black letters denote different residues with side chains that belong to a different category. The motifs are shown by the dashed line.

When the PB1 domain of AUX/IAA9 and ARF7 are aligned, a significant variation is observed, except for the "GDVP" motif, which also seems to be present in ARF7's PB1 domain (Fig. 5.12). In ARF7 the valine is replaced by an aspartic acid (D), and this substitution is present in all the ARF7 orthologs (Fig. 5.6; 5.12). The presence of an aspartic acid may be important for the interaction since it adds a negative charge to the domain.

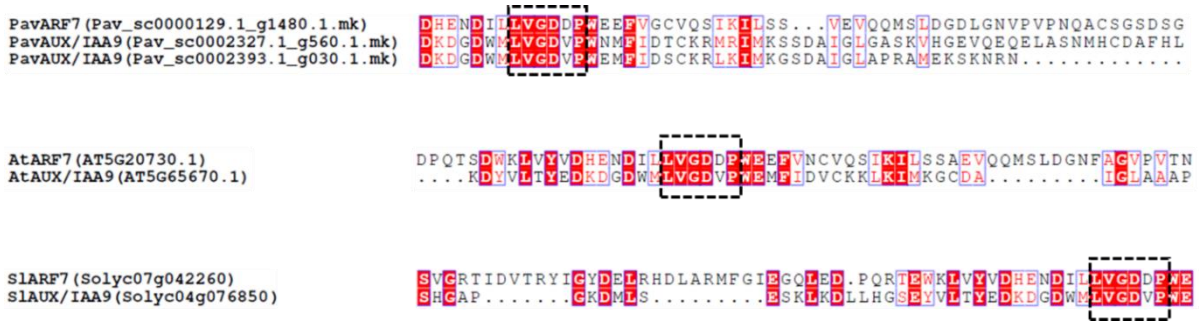


Figure 5.12: Multiple alignment of the PB1 domain with the focus on the region where the "GDVP" motif of the AUX/IAA protein sequences is present. Red boxes indicate identical residues, the red letters similar have residues (same side chain category) while black letters denote different residues with side chains that belong to a different category. The motifs are shown by the dashed line.

The fact that the two *PavAUX/IAA9* have been put in different clades with different peach, almond and apple orthologs in the phylogenetic tree, is supported by the residue substitutions. Examples can be found in position 277 (first residue of the PB1 domain), where all the taxa of the Rosaceae clade 2 (Fig. 5.9, blue clade) present a glycine (G), while all the other sequences have an alanine (A), or the opposite in position 284 where the sequences of the Rosaceae clade 1 (Fig. 5.8, green clade) have a leucine (L) instead of a methionine (M) (Fig. 5.11). When the entire PB1 sequence is checked, the number of cases where there is not a 100% identity is quite low (35 out of 103). The AtAUX/IAA9 sequence is the one that displays a higher number of non-equivalent residues substitutions (9 out of 19) (Fig. 5.11).

5.3.3 *PavRGL2* encodes for a DELLA protein without the "DELLA" motif

Pav_sc0000464.1_g350.1.mk encodes for a *RGL2* protein and it has been already reported in literature (Wen *et al.,* 2019) to be the ortholog of *SlDELLA*. It is highly expressed in the unpollinated ovaries at anthesis and only after pollination, at 7 DAT, its transcript levels get lower while in the other treatments they stay almost steady in the controls or significantly higher (in the GA_3-treated samples) (Fig. 5.13).

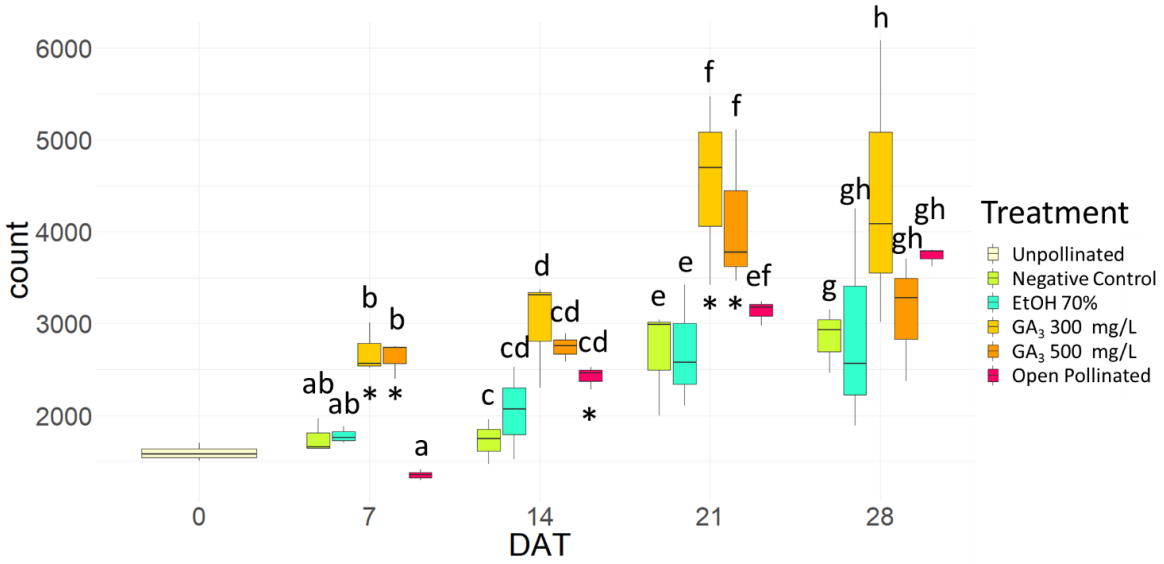


Figure 5.13: Boxplot that shows the expression levels of *Pav_sc0000464.1_g350.1.mk* (*PavRGL2*) in the five different treatments from timepoint 0 to 28 (DAT: Days After Treatment). The star denotes a significant difference in the expression levels compared to the previous timepoint, while the letters show the statistical difference between the treatments at the same timepoint.

To confirm the evolutionary close relationship between *Pav_sc0000464.1_g350.1.mk* and *SlDELLA* a phylogenetic analysis was conducted. All the cherry *RGL1*, *RGL2* and *GAI* sequences were used to identify their orthologs in peach, almond and apple, and those genes were used to build the phylogenetic tree. As shown in Fig. 5.14, four Rosaceae clades (*Amygdalus-Prunus*-Rosaceae) have been formed and the one that contains *PavRGL2* (*Pav_sc0000464.1_g350.1.mk*)

is closely related to the Solanaceae clade. The confidence of this correlation is well supported since the Bootstrap number is quite high (87).

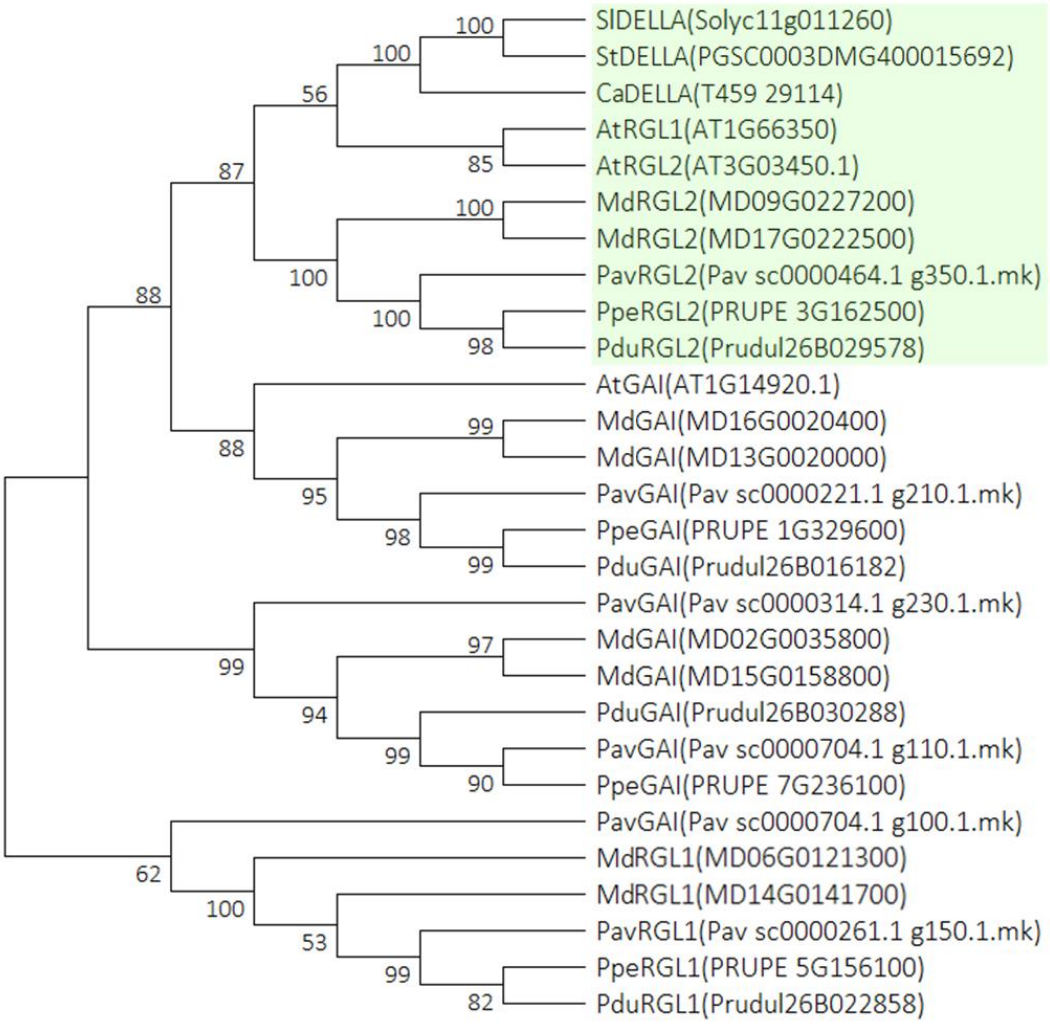


Figure 5.14: Phylogenetic tree obtained with the Maximum Likelihood method using cDNA sequences. The tree includes all the putative cherry, Arabidopsis, tomato, sweet pepper, peach, almond and apple *DELLA* orthologs. The log likelihood is -31300.45. Numbers at the nodes are the Bootstrap numbers that show the level of significance.

In the remaining discussion, the focus will be only on the clade that contains both *PavRGL2* (*Pav_sc0000464.1_g350.1.mk*) and *SlDELLA* (the green boxed clade in Fig. 5.13). All the genes contained in this group comprise one single exon and encode a protein between 511-596 amino

acids. The genes in cherry, Arabidopsis and tomato are on the reverse strand, while all the others are on the forward strand. In *Prunus,* the respective ortholog is on chromosome 3, while in the Solanaceae on chromosome 11 for tomato and potato, and chromosome 12 for sweet pepper. Apple has two orthologs of the *RGL2* gene that are closely related to *PavRGL2*, and one of them is on chromosome 9 (MD09G0227200), while the other in chromosome 17 (MD17G0222500) (Table 5.4).

Gene	Symbol	cDNA length (nt)	Protein length (aa)	Number of exons	Strand	Chromosome
Pav_sc0000464.1_g350.1.mk	PavRGL2	1596	531	1	RV	3
AT1G66350	AtRGL1	2082	511	1	FW	1
AT3G03450	AtRGL2	2316	547	1	RV	3
Solyc11g011260	SlDELLA	1767	588	1	RV	11
PGSC0003DMG400015692	StDELLA	2408	588	1	FW	11
T459_29114	CaDELLA	1791	596	1	FW	12
PRUPE_3G162500	PpeRGL2	2779	593	1	FW	3
Prudul26B029578	PduRGL2	2538	596	1	FW	3
MD09G0227200	MdRGL2	1743	580	1	FW	9
MD17G0222500	MdRGL2	1755	584	1	FW	17

Table 5.4: Information about cDNA and protein sequence lengths, number of exons, orientation, and chromosome localisation of the Arabidopsis, cherry, almond, peach, and apple *DELLA* orthologs that are closely related to the Solanaceae *DELLA* clade. Data collected from Ensembl Plants.

Within the Rosaceae clade, *PavRGL2* has a higher nucleotide identity level with the apple orthologs than with the other *Prunus* species (Table S5.12). However, when the amino acid sequences are compared, this observation is no longer maintained since the higher percentages are with peach and almond (Table S5.13). The peach and almond nucleotide and especially protein sequences are almost identical. The same higher identity can be observed within the Solanaceae clade. *AtRGL1* and *AtRGL2* show a quite consistent level of identity when compared to all the other transcript and protein sequences (Table S5.12-13).

DELLA proteins have two domains: a DELLA-domain at the N-terminus and a GRAS-domain at the C-terminus. PavRGL2 exhibits a quite lower conservation at the amino acid sequence of the DELLA domain (Table S5.14). This is mostly due to the fact that it lacks the “DELLA” motif (Fig. 5.15). All the other sequences contain this motif and AtRGL1 has a replacement of the alanine (A), with the

equivalent valine (V). These residues have indeed hydrophobic side chains. The "LExLE" motif instead is perfectly conserved in all the sequences and the "x" residue is a glutamine (Q). The Solanaceae species instead present a non-redundant substitution in the "VHYNP" motif. Indeed, all the three sequences have a lysine (K), which is positively charged, in the place of the tyrosine (Y), which is hydrophobic.

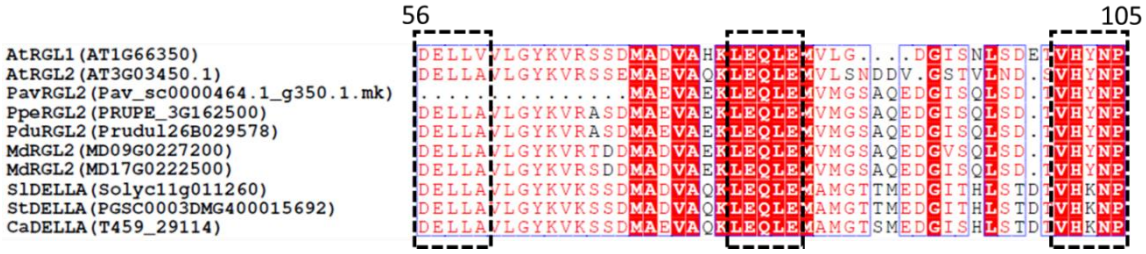


Figure 5.15: Multiple alignment of DELLA domains of the DELLA protein sequences. Red boxes indicate identical residues, the red letters have similar residues (same side chain category) while black letters for different residues with side chains that belong to a different category. The motifs are shown by the dashed line.

The GRAS domain is highly conserved among all the sequences, including PavRGL2 (Table S15). The two Leucine repeat regions (LHRI and LHRII), that enclose the "VHIID" motif, are quite conserved in all the sequences (Fig. 5.16). Indeed, the majority of the differences are made by similar residues, while the presence of non-similar residues is reduced and do not involve the conserved Leucine (L) residues. The "VHIID" motif is conserved in all the sequences and its sequence is "VHVID" (Fig. 5.16). Only CaDELLA has another valine (V) instead of the isoleucine (I), but both these residues have a hydrophobic side chain. The "LXXLL" motif in the SH2-like domain instead is not completely identical or similar among the sequences. Indeed, the Arabidopsis and the Solanaceae sequences have an arginine (R) as central residue while the *Prunus* species a proline (P) (Fig. 5.16). The two apple sequences do not have the same residue in this position. Indeed, MdRGL2 (MD09G0227200) has a glycine (G) while MdRGL2 (MD17G0222500) contains

an arginine as seen in the Arabidopsis and Solanaceae sequences. Finally, the SAW sub-domain is quite conserved among all the sequences analysed (Fig. 5.16).

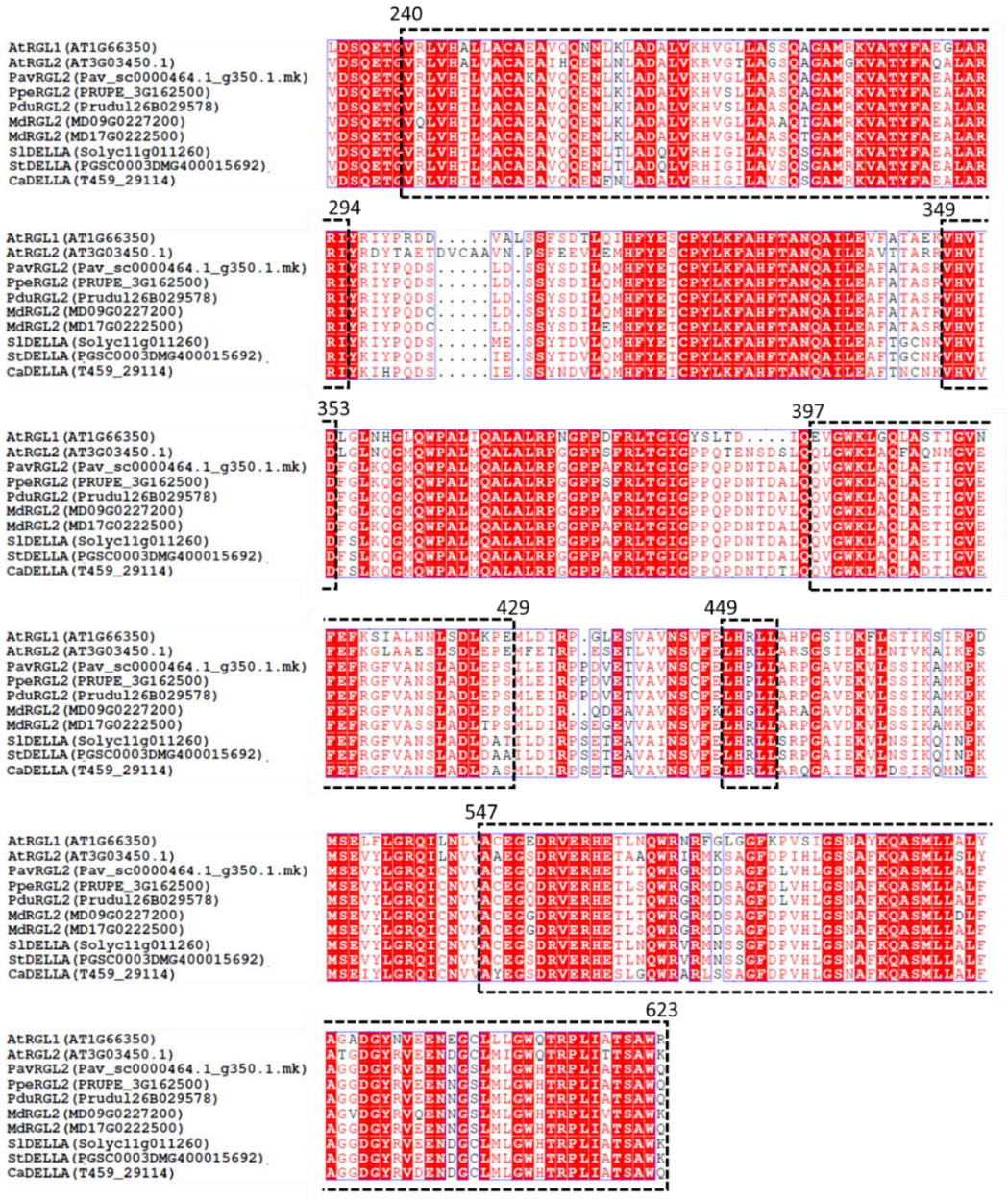


Figure 5.16: Multiple alignment of GRAS domains of the DELLA protein sequences. LHRI: 240-294; "VHIID" motif: 349-353; LHRII: 397-429; "LXXLL" motif (SH2-domain): 449-453; SAW domain: 547-623. Red boxes indicate identical residues, the red letters have similar residues (same side chain category) while black letters denote different residues with side chains that belong to a different category. The motifs are shown by the dashed line.

5.3.4 Assembly of vectors for *PavARF7*, *PavAUX/IAA9*s, and *PavRGL2* overexpression

After checking the phylogeneses and sequence conservation of *PavARF7*, *PavAUX/IAA9*s, and *PavRGL2* in relation to their well-studied orthologs in other species such as Arabidopsis and tomato, the next step would be to check their functionality. The chosen approach is to knock-in those genes in the tomato parthenocarpic mutants *ARF7i*, *entire* and *procera* respectively, and check if the overexpression of those genes can rescue the phenotype. The assembly of the four vectors has been done using the Golden Gate technology as described in the section Materials and Methods. Once assembled the level-one modules, the insertion sites were checked. In particular, the plasmids have been sent to sequencing with the L1M-R-FP and L1M-R-RP primers (Table 5.1, 5.2.4 Materials and Methods), which anneal to the pL1V-R2-47811 backbone sequence just close to the T-DNA right (RB) and left border (LB) respectively. Fig. 5.17-20 show the level-one plasmid maps obtained from an *in silico* assembly, which has been used as reference sequence to control the assembly sequencing. The alignment of the reference sequence and the sequenced one are shown as well. In particular, the junction regions between the backbone and the pFMV promoter, the pFMV promoter and the CDS of the genes, and the HSP terminator and the backbone are reported. All four plasmids have been assembled correctly as predicted, the final level-two modules cloning has been carried out.

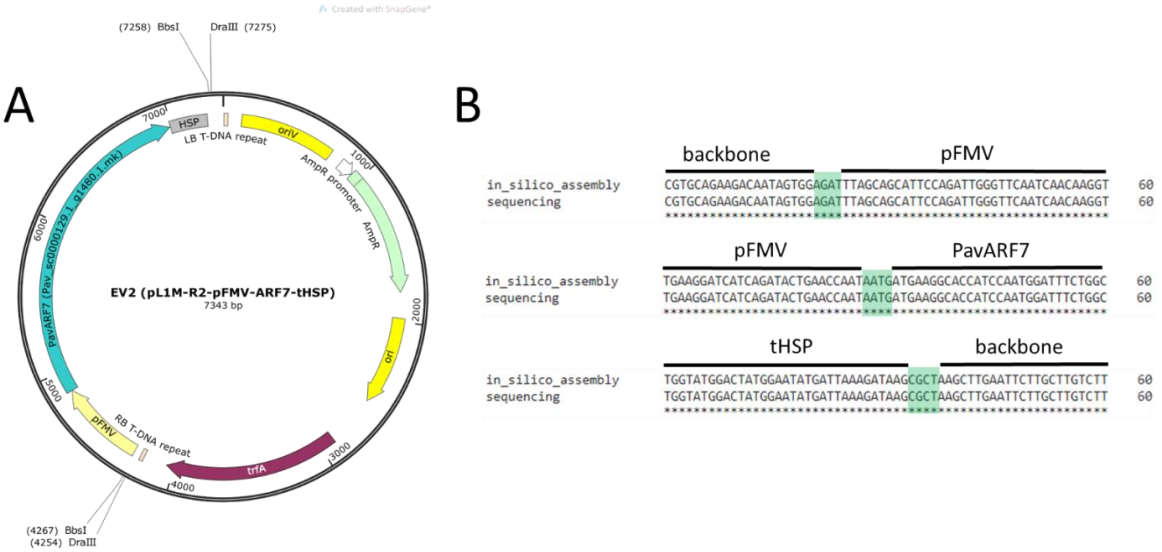


Figure 5.17: Level-one module containing the codon-optimised *PavARF7* (*Pav_sc0000129.1_g.1480.1.mk*) CDS sequence. (A) vector map of the in silico assembled level-one module. (B) Alignment of the reference sequence (in_silico_assembly) with the assembled sequenced vector. The green rectangles show the junction site after the digestion with Bsa-HI and the joining made by the T4 ligase

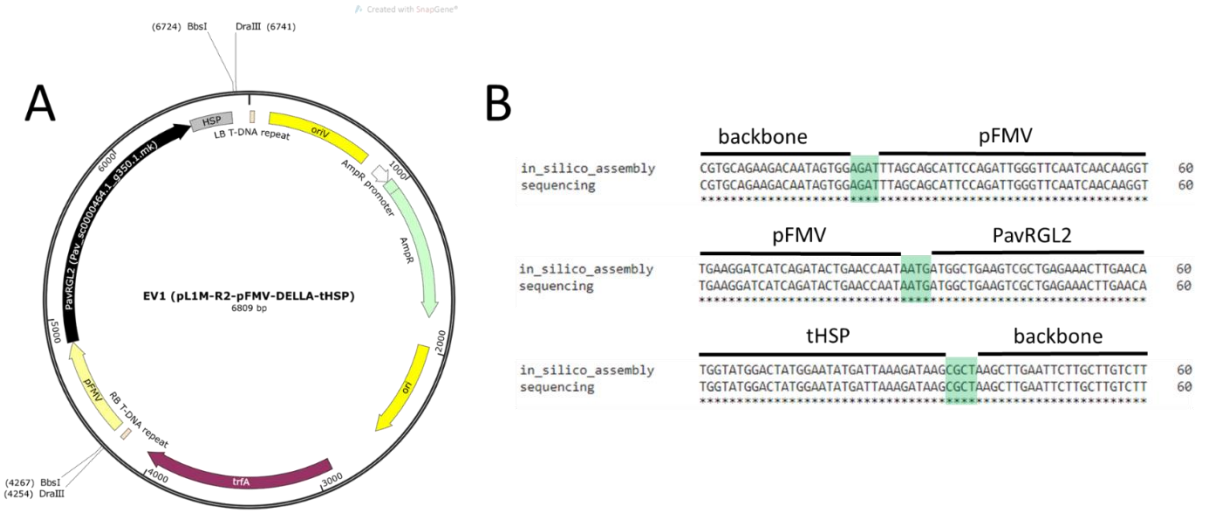


Figure 5.18: Level-one module containing the codon-optimised *PavRGL2* (*Pav_sc0000464.1_g350.1.mk*) CDS sequence. (A) vector map of the in silico assembled level-one module. (B) Alignment of the reference sequence (in_silico_assembly) with the assembled sequenced vector. The green rectangles show the junction site after the digestion with Bsa-HI and the ligation made by the T4 ligase.

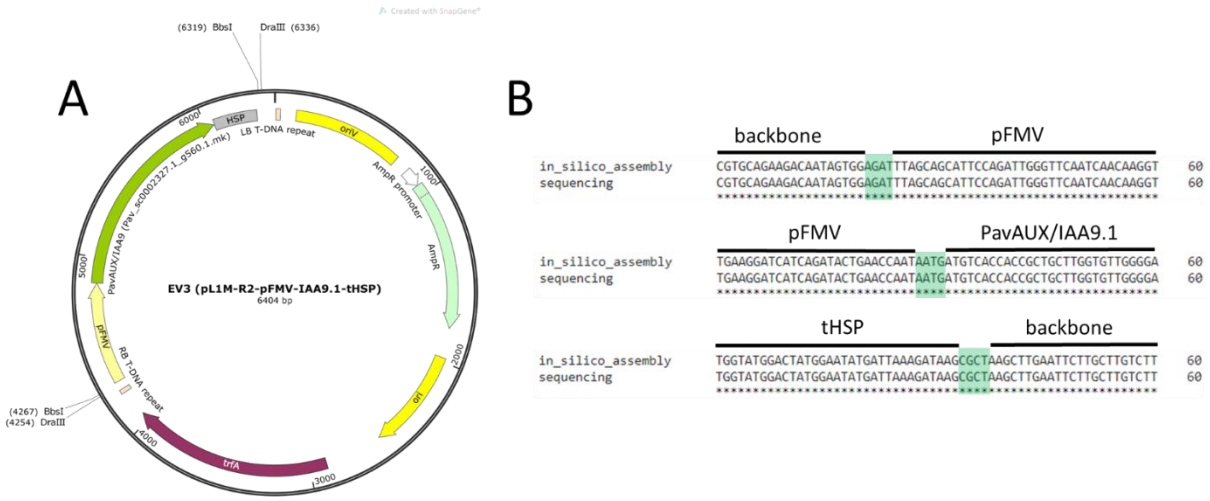


Figure 5.19: Level-one module containing the codon-optimised *PavAUX/IAA9* (*Pav_sc0002327.1_g560.1.mk*) CDS sequence. (A) vector map of the in silico assembled level-one module. (B) Alignment of the reference sequence (in_silico_assembly) with the assembled sequenced vector. The green rectangles show the junction site after the digestion with Bsa-HI and the ligation made by the T4 ligase.

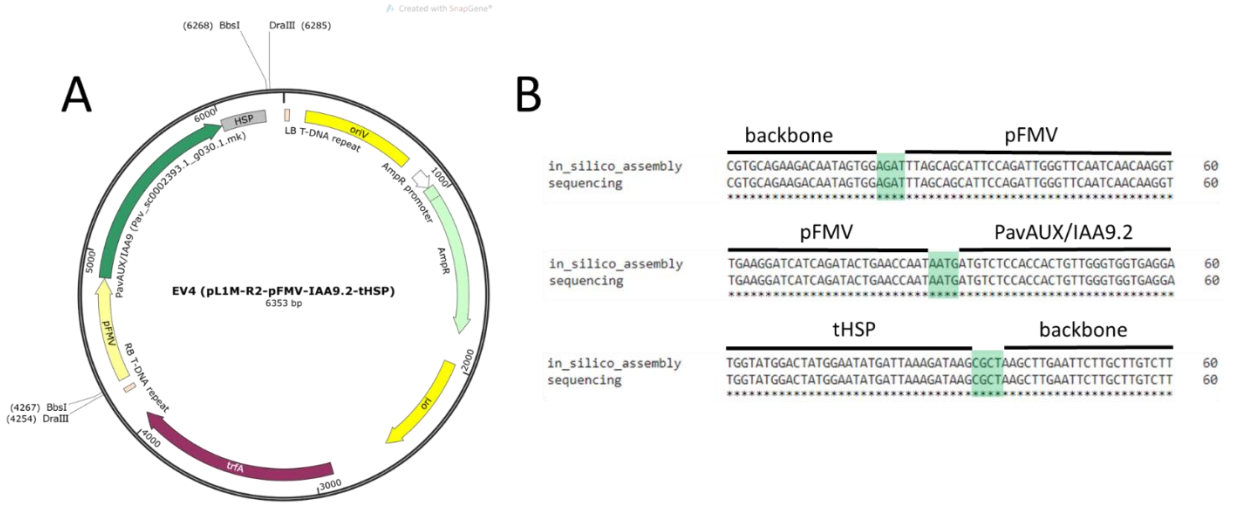
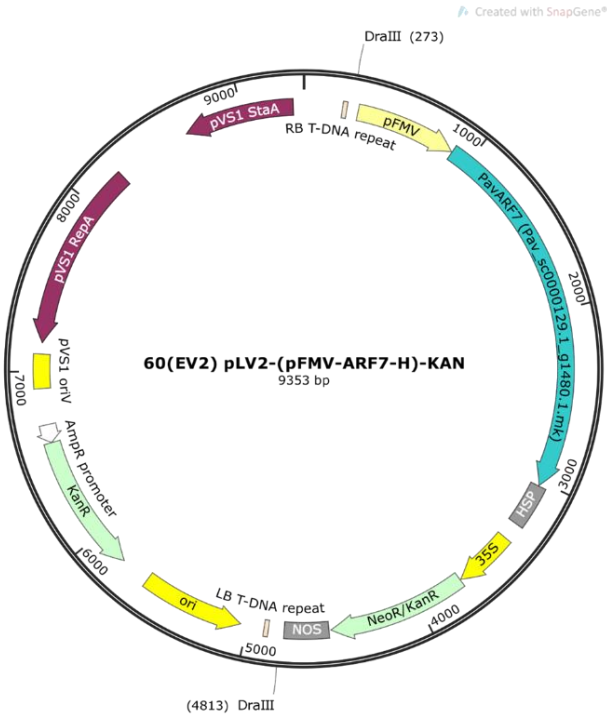


Figure 5.20: Level-one module containing the codon-optimised *PavAUX/IAA9* (*Pav_sc0002393.1_g030.1.mk*) CDS sequence. (A) vector map of the in silico assembled level-one module. (B) Alignment of the reference sequence (in-silico_assembly) with the assembled sequenced vector. The green rectangles show the junction site after the digestion with Bsa-HI and the ligation made by the T4 ligase.

Those level-one modules contain the pFMV-CDS-tHSP cassette that is the one that has to be moved to the level-two final vector as described in Materials and Methods paragraph 2.4. Within the RB-TDNA and LB T-DNA of those final vectors contain not only the pFMV-CDS-tHSP cassette, but also the p35S-KAN-tNOS one, which is needed for the transformed-plant selection. Indeed, the plants that will have this transgene inserted in their DNA will be able to survive after being grown on a medium containing kanamycin. For all four level-two vectors, the entire sequence contained between the RB T-DNA and the LB T-DNA has been sequenced. All the primer sequences used are reported in Table 1, in the Materials and Methods section. As for level-one modules, Fig. 5.21-24 show the vector map obtained from the *in silico* assembly, and all the junctions regions. All the parts of those cassettes assembled as predicted and the sequences have not displayed any mutations. Thus, all four 60(EVX) pLV2-(pFMV-CDS-tHSP)-KAN vectors are ready to be used to transform the corresponding seedlings of the tomato parthenocarpic mutants.

A



B

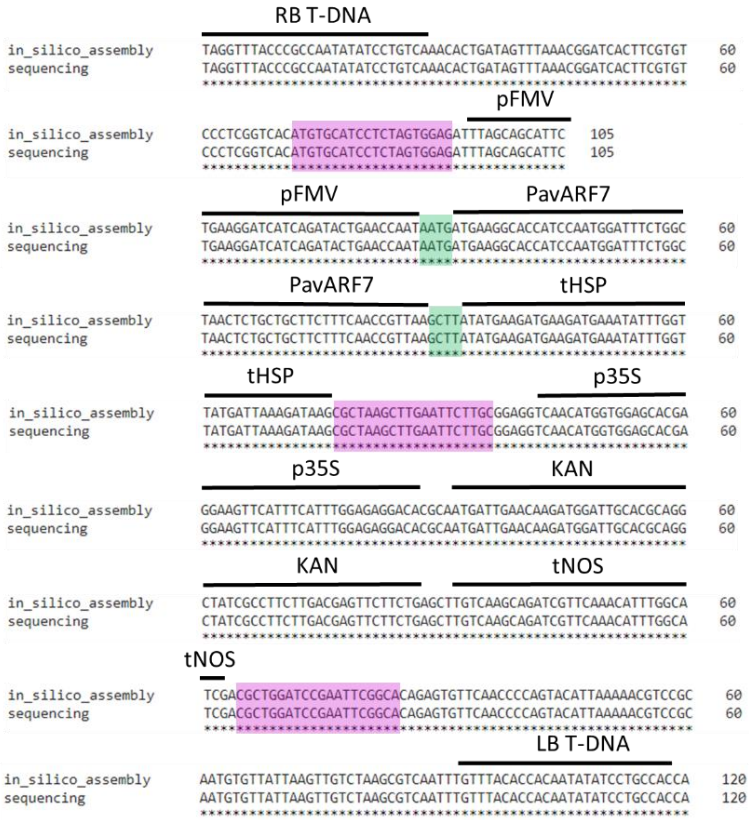


Figure 5.21: Level-two module containing the codon-optimised *PavARF7* (*Pav_sc0000129.1_g.1480.1.mk*) CDS sequence. (A) vector map of the in silico assembled level-one module. (B) Alignment of the reference sequence (in-silico assembly) with the assembled sequenced vector. The green and purple rectangles show the junction site after the digestion with Bsa-HI and BbsI respectively, and the ligation made by the T4 ligase.

A

B

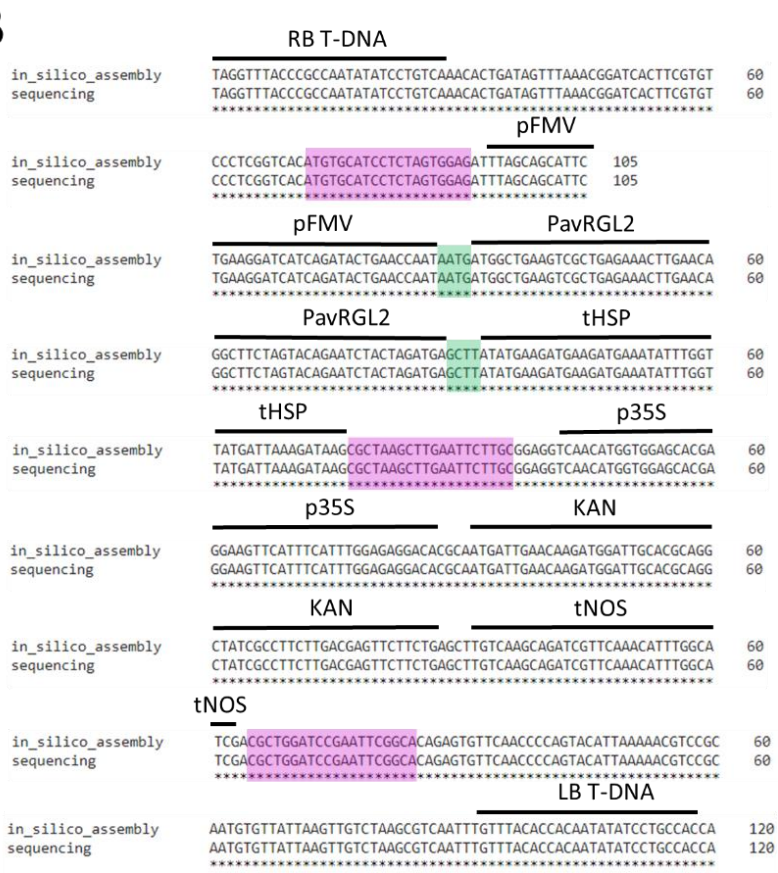


Figure 5.22: Level-two module containing the codon-optimised *PavRGL2* (*Pav_sc0000464.1_g350.1.mk*) CDS sequence. (A) vector map of the in silico assembled level-one module. (B) Alignment of the reference sequence (in_silico_assembly) with the assembled sequenced vector. The greed and purple rectangles show the junction site after the digestion with Bsa-HI and BbsI respectively, and the ligation made by the T4 ligase.

A

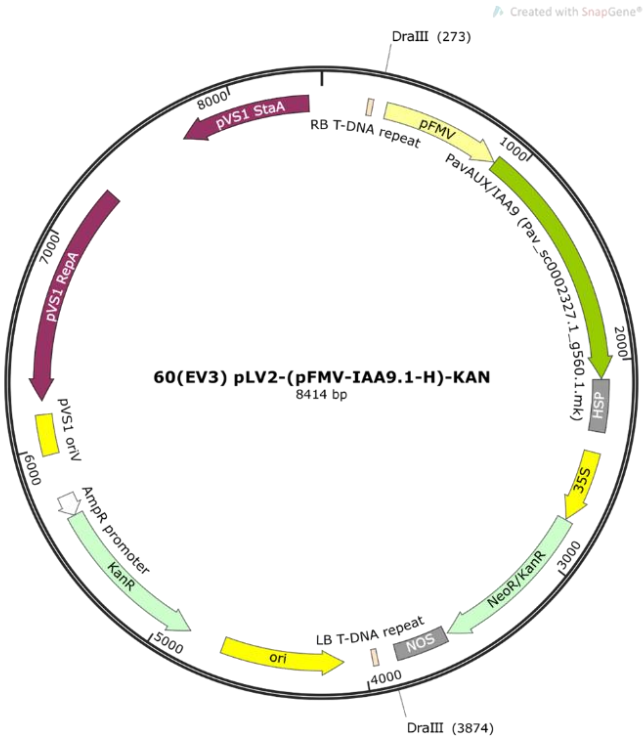


Figure 5.23: Level-one module containing the codon-optimised *PavAUX/IAA9* (*Pav_sc0002327.1_g560.1.mk*) CDS sequence. (A) vector map of the in silico assembled level-one module. (B) Alignment of the reference sequence (in_silico_assembly) with the assembled sequenced vector. The green and purple rectangles show the junction site after the digestion with Bsa-HI and BbsI respectively, and the joining made by the T4.

B

RB T-DNA

```
in_silico_assembly  TAGGTTTACCCGCCAATATATCCTGTCAAACACTGATAGTTTAAACGGATCACTTCGTGT  60
sequencing          TAGGTTTACCCGCCAATATATCCTGTCAAACACTGATAGTTTAAACGGATCACTTCGTGT  60
                    ************************************************************
```

pFMV

```
in_silico_assembly  CCCTCGGTCACATGTGCATCCTCTAGTGGAGATTTAGCAGCATTC  105
sequencing          CCCTCGGTCACATGTGCATCCTCTAGTGGAGATTTAGCAGCATTC  105
                    *********************************************
```

pFMV PavAUX/IAA9.1

```
in_silico_assembly  TGAAGGATCATCAGATACTGAACCAATAATGATGTCACCACCGCTGCTTGGTGTTGGGGA  60
sequencing          TGAAGGATCATCAGATACTGAACCAATAATGATGTCACCACCGCTGCTTGGTGTTGGGGA  60
                    ************************************************************
```

PavAUX/IAA9.1 tHSP

```
in_silico_assembly  AAGGCCTACAACCGCAGTAACCAGATAAGCTTATATGAAGATGAAGATGAAATATTTGGT  60
sequencing          AAGGCCTACAACCGCAGTAACCAGATAAGCTTATATGAAGATGAAGATGAAATATTTGGT  60
                    ************************************************************
```

tHSP p35S

```
in_silico_assembly  TATGATTAAAGATAAGCGCTAAGCTTGAATTCTTGCGGAGGTCAACATGGTGGAGCACGA  60
sequencing          TATGATTAAAGATAAGCGCTAAGCTTGAATTCTTGCGGAGGTCAACATGGTGGAGCACGA  60
                    ************************************************************
```

p35S KAN

```
in_silico_assembly  GGAAGTTCATTTCATTTGGAGAGGACACGCAATGATTGAACAAGATGGATTGCACGCAGG  60
sequencing          GGAAGTTCATTTCATTTGGAGAGGACACGCAATGATTGAACAAGATGGATTGCACGCAGG  60
                    ************************************************************
```

KAN tNOS

```
in_silico_assembly  CTATCGCCTTCTTGACGAGTTCTTCTGAGCTTGTCAAGCAGATCGTTCAAACATTTGGCA  60
sequencing          CTATCGCCTTCTTGACGAGTTCTTCTGAGCTTGTCAAGCAGATCGTTCAAACATTTGGCA  60
                    ************************************************************
```

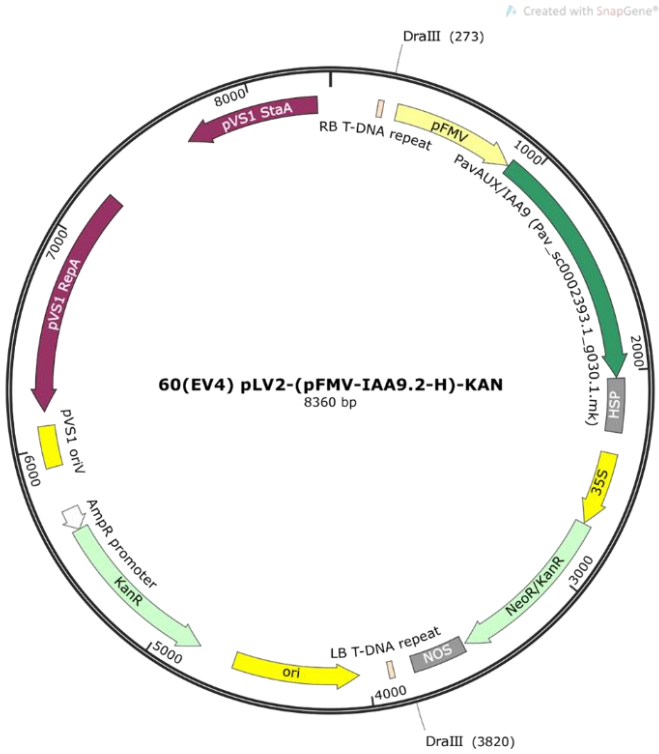
tNOS

```
in_silico_assembly  TCGACGCTGGATCCGAATTCGGCACAGAGTGTTCAACCCCAGTACATTAAAAACGTCCGC  60
sequencing          TCGACGCTGGATCCGAATTCGGCACAGAGTGTTCAACCCCAGTACATTAAAAACGTCCGC  60
                    ************************************************************
```

LB T-DNA

```
in_silico_assembly  AATGTGTTATTAAGTTGTCTAAGCGTCAATTTGTTTACACCACAATATATCCTGCCACCA  120
sequencing          AATGTGTTATTAAGTTGTCTAAGCGTCAATTTGTTTACACCACAATATATCCTGCCACCA  120
                    ************************************************************
```

A



B

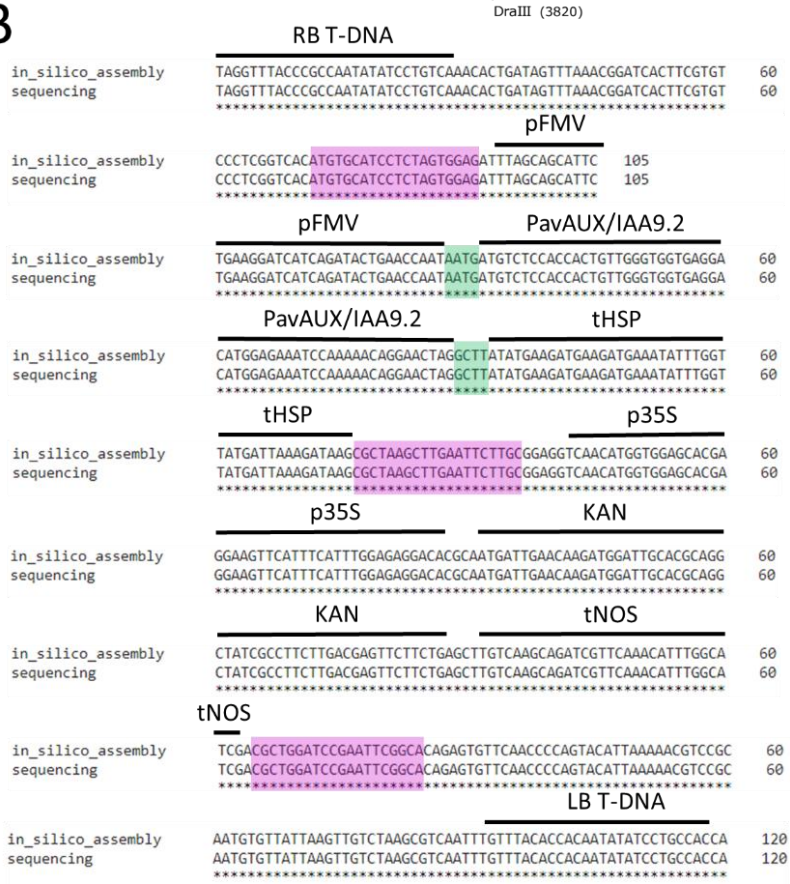


Figure 5.24: Level-one module containing the codon-optimised *PavAUX/IAA9* (*Pav_sc0002393.1_g030.1.mk*) CDS sequence. (A) vector map of the in silico assembled level-one module. (B) Alignment of the reference sequence (in_silico_assembly) with the assembled sequenced vector. The green and purple rectangles show the junction site after the digestion with Bsa-HI and BbsI respectively, and the joining made by the T4.

5.4 Discussion

Seedlessness has always been of interest to the agricultural industry due to the multiple advantages that it has. Breeding programs have been focused on the selection of seedless varieties that are more appealing to the consumers. In addition, in recent years, research has been trying to achieve the same results through direct-site mutagenesis. The knowledge acquired mainly from basic research about fruit development is tested and applied on commercially relevant crops. In this study, the species of interest is sweet cherry (*Prunus avium*). From the analysis of the transcriptome from fruits at the very early stages of development, three interesting candidates have been identified: the putative orthologs *PavARF7*, *PavAUX/IAA9* and *PavRGL2*. Those genes are good potential targets because in tomato the mutation of each of them results in parthenocarpic fruit development. In strawberry, the situation is similar although the members of these same families are different: *FveARF8*, *PavAUX/IAA4* and *PavRGL1* (Zhou *et al.,* 2021). This suggests a kind of conserved mechanism where the players may change according to the species. Moreover, these three genes are reported to be responsible for the crosstalk between the auxin and the gibberellin signalling pathways (Hu *et al.,* 2018).

A phylogenetic analysis has been conducted on *PavARF7*, *PavAUX/IAA9* (two putative orthologs) and *PavRGL2*, before moving to the functional characterisation. All the sweet cherry putative *ARFs*, *AUX/IAAs* and *DELLAs* orthologs have been included in the analysis to be sure that *Pav_sc0000129.1_g.1480.1.mk* (*PavARF7*), *Pav_sc0002327.1_g560.1.mk* and *Pav_sc0002393.1_g030.1.mk* (*PavAUX/IAA9*) and *Pav_sc0000464.1_g350.1.mk* (*PavRGL2*) were the actual orthologs and that none were potentially missed *a priori*. The phylogenetic trees of the *ARFs* confirmed the initial attribution of being *PavARF7* to *Pav_sc0000129.1_g.1480.1.mk. Pav_sc0000464.1_g350.1.mk* (*PavRGL2*) have been shown to be the *DELLA* protein encoding gene closely related to the Arabidopsis *AtRGL* proteins and, more importantly, to the tomato *SlDELLA*. The phylogenetic tree obtained from the alignment of the AUX/IAA sequences instead, revealed an interesting scenario. According to the tree, the two genes could potentially be PavAUX/IAA9, although *Pav_sc0002393.1_g030.1.mk* is in the clade with the Arabidopsis ortholog, and *Pav_sc0002327.1_g560.1.mk* with the Solanaceae orthologs. It is interesting that

the orthologs in peach, almond and apple of *Pav_sc0002327.1_g560.1.mk* are reported as AUX/IAA8 encoding genes. It is likely that an error was made when this description was attributed to those genes, considering that neither the Arabidopsis not the Solanaceae orthologs of *AUX/IAA8* were included in their clade. Thus, it may be possible that a duplication event occurred for this gene in the Rosaceae family. However, a further investigation may be needed to better understand the phylogenetic relationship between these two clades.

Despite the lower percentages of sequence identity in the cherry orthologs, compared to the other species in the study, the alignments have shown that the domains and motifs are quite conserved. However, PavARF7 and PavRGL2 in particular, exhibit some remarkable differences. Indeed, PavARF7 sequence lacks a large section of the B3 domain, that is involved in DNA binding, and also the MR2 sequence, which has been suggested by Hu *et al.* (2018) to interact with the DELLA protein. The PB1 domain that is responsible for protein dimerization with other ARFs or AUX/IAAs, on the contrary, is quite conserved. In particular, it is promising that the alignment of the PavARF7 and PavAUX/IAA9 PB1 domains are very similar to the domains found in species where this interaction has been already characterised and proved. An experiment that can be done in the future and would help to assess if PavARF7 can interact with both PavRGL2 and PavAUX/IAA9 is a yeast two-hybrid assay. PavRGL2's DELLA domain has been found to lack the "DELLA" motif, which is responsible, with the "VHYNP" motif, for the binding to GID1, the gibberellin receptor. The "VHYNP" motif is well conserved, which may be enough for the interaction with the gibberellins receptor. The only DELLA protein that has the "DELLA" motif is PavGAI (Pav_sc0000221.1_g210.1.mk), which is in the clade with the GAI orthologs of Arabidopsis. This clade also is a paraphyletic group of the clade where the DELLA orthologue PavRGL2 is contained.

Unfortunately, there is no collection of cherry mutants, like those for Arabidopsis or tomato, that can be used to study the functions of those genes. Therefore, direct site mutagenesis is the strategy that has to be used to obtain knock-out mutants of *PavARF7*, *PavRGL2* and *PavAUX/IAA9s*. However, two considerations need to be taken into account. First, *in vitro* cherry

regeneration and transformation are remarkably challenging because they have a low success rate and are time consuming (Vergara *et al.,* 2021). Second, the interest is in checking the phenotype at the flower and fruit level, and sweet cherry has a long juvenile phase (from 4 to 10 years) since it is a woody plant. This obstacle could be overcome by overexpressing a florigen gene such as *FLOWERING LOCUS-T* (*FT*). In fact, in plum (*Prunus domestica*), the overexpression of the poplar ortholog of *FT1* has significantly reduced the juvenile phase, allowing fruits to set just one year after seed germination (Srinivasan *et al.,* 2012). Thus, considering the high risk and the long waiting time before seeing the phenotype resulting from knocking-out those candidates from the cherry genome, a preliminary and faster strategy has been designed and started. As mentioned, tomato is the model plant for fleshy fruit development and there is a big collection of tomato mutants that can be used. In particular, the interest is in the parthenocarpic mutants *ARF7i*, *procera* (mutation in *SlDELLA*) and *entire* (mutation in *SlAUX/IAA9*). The seeds of the single mutants *ARF7i*, *procera (pro)* and *entire (e)*, and the double mutant *pro x e*, obtained from the crosses of two heterozygous parents have been provided by Prof. Tai-ping Sun's laboratory (Duke University, Durham, North Carolina, USA). These mutants will be used to assess if the cherry orthologs have the same function in *Prunus avium*. In fact, these cherry orthologs will be knocked-in in the genome of the parthenocarpic tomato mutants and the resulting phenotype will be checked. If the results were successful (the tomato plants will not be parthenocarpic anymore and will require flower pollination and ovules fertilisation), it would mean that it is likely that those genes take part in blocking of fruit set in unpollinated ovaries, and they are down-regulated shortly after pollination and fertilisation. This is already slightly suggested by the transcriptome analysis since all these genes, with the exception of *PavAUX/IAA9* (*Pav_sc0002393.1_g030.1.mk*), have been found to be down-regulated at 7 DAT. *PavAUX/IAA9* (*Pav_sc0002393.1_g030.1.mk*) has been included in this experiment since from the phylogenetic analysis, it aligned closely with the *AtAUX/IAA9* ortholog. The results from the knock-in experiment in tomato may help us understand if the two *PavAUX/IAA9* genes have different functions, or if both or neither, are involved in blocking fruit set. The down-regulation of *PavARF7* is especially remarkable in the open pollinated samples.

It has been shown that the assembly of the four vectors containing the codon-optimised coding sequences (CDS) under constitutive 35S promoter have been successful. Indeed, for each plasmid, the sequence of the entire cassette contained between the two T-DNA borders has been checked as well as the junction points. Future work will consist in the transformation of the parthenocarpic tomato mutants with these plasmids using *Agrobacterium tumefaciens*. If positive results are seen, the next step will be to knock-out those genes, in sweet cherry. The possibility of a parthenocarpic variety of sweet cherry is real, although ambitious and challenging. The study of the endocarp development could be combined, to understand which are the factors that are responsible for the stone differentiation and development. The generation of a cherry variety with no lignified endocarp is another critical aspect. The combination of the parthenocarpic and the endocarp absence traits is the ultimate challenge and goal that will be a revolution in the horticulture industry.

Chapter 6: General discussion

6.1 Key findings

Sweet cherry fruit development is still poorly investigated from a molecular point of view, while its physiology, nutritional properties and healthy effects on human beings have been more significantly studied. This is due to all the limitations that researchers have or had until a few years ago, when they tried to conduct molecular biology experiments using sweet cherry as a model. In Cherry, the availability of material is a limiting factor considering that *Prunus avium* is a deciduous plant and blooms only once a year and sample manipulation is challenging because sweet cherry ovaries and fruits contain many secondary metabolites that make the accomplishment of high-quality nucleic acids extraction more challenging. In contrast to Arabidopsis and tomato, there is no collection of sweet cherry mutants that can be used for studies of direct and reverse genetics. Thus, direct-site mutagenesis is a possible strategy, which, again, requires a consistent effort since sweet cherry is particularly recalcitrant toregeneration and transformation *in vitro* (Zong *et al.,* 2019; Vergara *et al.,* 2021). In this study, different approaches were tested to propagate and regenerate 'Merchant', 'Kordia' and 'Regina'. Successful results were achieved when the explants derived from the seed, i.e. embryo axes and cotyledons. However, the same was not observed when the explants were leaves, leaf buds, and shoots. Regenerated shoots from the seed are a good starting material, however more effort needs to be done in order to obtain regenerated shoots from somatic explants, making possible to transform a pure cultivar and not a mix of genotypes as it happens with the seed material. In fact, the majority of the sweet cherry cultivars are self-incompatible, which makes necessary the fusion of the gametes from two different cultivars to obtain a viable seed.The sweet cherry genome was published in 2017 and its annotation is not as good and precise as the annotation of the genomes of Arabidopsis and tomato, which are two of the most popular model species for plant molecular studies (Shirasawa *et al.,* 2017). The first study on transcriptomics in Chinese cherry (*Cerasus pseudocerasus*) was published in 2019 and it was conducted on unpollinated

ovaries treated with GA_3 (Wen *et al.,* 2019). However, that study presents a significant limitation which is the absence of pollinated fruits as positive controls.

In this study, it has been confirmed that one application of GA_3 to unpollinated ovaries, appears to be enough to initiate fruit set in *Prunus avium*, but not sufficient to complete the entire developmental process that would result in a fully formed seedless cherry. The treated and pollinated ovaries at the first stages of the experiment, not only looked quite similar macroscopically, but also showed similarities from a genetic point of view. In fact, in both the sample types, a higher number of differentially expressed genes was observed compared to their negative controls. Some differences were found as well, most likely due to the different activation timings of the hormonal signalling pathways. In fact, gibberellins signalling pathway has been proposed to be downstream and activated by the auxin signalling pathway (Serrani *et al.,* 2008; Hu *et al.,* 2018). Thus, the GA_3-treated samples lack all the changes in expression that the auxin signalling pathway produces. An example of this may be the much higher amount of downregulated DEGs compared to the upregulated DEGs in the pollinated samples, while this difference, although still present, is less strong in the GA_3-treated samples at 7 DAT. The higher percentage of downregulated DEGs also seems consistent with the current model for the ovary-fruit transition. According to this model, fruit development is frozen in the unpollinated ovary and once the fertilisation signal arrives, it is released, and the program can start.

After three weeks, a remarkable difference between the pollinated and the GA_3-treated samples became evident not only macroscopically, but also genetically. The abortion process initiation started to be visible at 21 DAT in few treated putative fruits, and this change was found also on the transcriptomics data. In fact, the number of DEGs in the aborting samples increased significantly at 21 DAT, and even more at 28 DAT, while in the open pollinated fruits it decreased and was much lower. Furthermore, the gene expression patterns shown in this study gives a clear visual representation of this change. In fact, for many genes, open pollinated and treated fruits showed similar expression patterns from 0 DAT to 14 DAT, however from 21 DAT, the expression pattern observed in the gibberellin treated fruits was more closely aligned with the expression

pattern of the controls, suggesting that at this point after treatment the fruit developmental program ceases in treated samples and it can no longer proceed due to the absence of further signals.

Interestingly, according to the observations of the open pollinated samples growth curves (length and width), the transition from phase I to phase II of fruit development occurs between 21 and 28 DAT. During phase II endocarp lignification occurs and this was observed in 'Regina' at 28 DAT. The expression levels of the putative genes *PavSTK*, *PavSHP* and *PavFUL,* seem to support this hypothesis. In peach, *PpeFUL* is responsible for the mesocarp differentiation, by restricting *PpeSHP* and *PpeSTK* in the endocarp, where they are involved in the activation of the lignin biosynthetic pathway (Dardick *et al.,* 2010). *PavSTK*, *PavSHP* snd *PavFUL* are up-regulated in the open pollinated fruits, however, they are also up-regulated in the aborting treated fruits and unpollinated ovaries. In this specific scenario, they may be involved in the lignification process due to abortion and abscission. Lignin is deposited in the abscission zone; thus, it is possible to explain the upregulation of these genes in the aborting samples (Merelo *et al.,* 2017). In addition, genes encoding factors involved in ethylene biosynthesis and signal transduction are up-regulated in the aborting samples, suggesting that ethylene is present at high concentration. Ethylene is a hormone involved in fruit abscission and it seems to retain this role also in sweet cherry.

Ethylene may also have an important role in fruit development considering that the transcript levels of the genes encoding for the ethylene biosynthetic enzymes were found to be highly expressed in the unpollinated ovaries at 0 DAT, suggesting that a basal quantity of this hormone is required. In zucchini and cucumber for example, it has been shown that ethylene inhibition has a negative effect on fruit development (Martínez *et al.,* 2015; Xin *et al.,* 2019). In the later stages of the aborting samples, ethylene levels may increase more, promoting abortion and abscission. In support of this is the fact that the putative genes *PavANAC047* and *PavERF4* have been observed to be significantly up- and down-regulated respectively, in those samples. These two genes have a complete opposite function. ANAC047 binds the ethylene biosynthetic gene

promoters up-regulating their expression (Kim *et al.,* 2014), while ERF4 represses the expression of *ERF3*, which has the same function of *ANAC047* (Hu *et al.,* 2020).

Like ethylene, ABA seems to have this dual role: support fruit development in the open pollinated fruits as already reported (Wang *et al.,* 2015; Leng *et al.,* 2018) and be involved in the abortion process of the unpollinated and GA_3-treated samples. Auxin and gibberellin are responsible for the successful development of the pollinated fruits. Auxin biosynthesis seems regulated mostly by the differential expression of the *YUCCA* encoding genes. In particular, *PavYUCCA4* and *PavYUCCA6*, at the first stages, and *PavYUCCA10* at later stages, are the genes that are suggested to take part in auxin biosynthesis. *PavYUCCA10* is especially interesting because in the pollinated fruits its expression reaches its peak at 28 DAT, while in the GA_3-treated putative fruits a peak at 21 DAT is observed, followed by a significant down-regulation. The expression of *PavYUCCA10*, may be dependent on the signal coming from the developing seed. In the open pollinated fruits, the signal is constant, so the development proceeds normally, while in the treated samples instead, the application of GA_3 is able to stimulate the expression of *PavYUCCA10* until 21 DAT but not beyond. *PavYUCCA10* transcript levels then decrease, and as a consequence, auxin level gets lower, resulting in fruit abortion. Once again, the time between 21 and 28 DAT is the critical moment when the paths of the pollinated and the GA_3-treated samples divide and go toward two different destinies. *PavYUCCA10* was shown to be up-regulated in a previous study in Chinese cherry (Wen *et al.,* 2019).

However, the expression patterns of the gibberellin biosynthetic genes did not show such a great difference between the developing fruits and their controls in this study. This may need further investigation, although it is possible that small changes of expression, and regulatory mechanisms at the level of translation, are enough to initiate a signalling cascade resulting in fruit development initiation. Importantly, transcript levels can give an idea, but they do not provide a definitive idea of the level of proteins encoded and present in the cells.

The expression patterns of *PavARF7*, *PavAUX/IAA9* and *PavRGL2* at 7 DAT, in the different samples were extremely interesting. In tomato, *SlARF7*, *SlAUX/IAA9* and *SlDELLA* are reported to be responsible for the crosstalk between auxin and gibberellins and the mutation of any of them results in parthenocarpic fruit development (Hu *et al.,* 2018). More recently this has been confirmed also in strawberry with *FveARF8*, *FveAUX/IAA4* and *FveRGA1* (Zhou *et al.,* 2021). In this study, all these genes were down-regulated at 7 DAT in the pollinated fruits. *PavARF7* is the only one that was significantly down-regulated, not only in O.P. but also in the GA_3-treated fruits. Instead, the levels of expression of *PavAUX/IAA* and *PavRGL2* in the pollinated fruits were lower compared to the levels at 0 DAT, however the drop was not statistically significant. In addition, these two genes were up-regulated in the GA_3-treated samples. The high GA concentration in the ovarian cells, upon external application, may have activated compensatory pathways to cushion the signal burst.

A phylogenetic analysis was conducted to assess that *PavARF7*, *PavAUX/IAA9* and *PavRGL2* were the orthologs of the genes in Arabidopsis and tomato. *PavAUX/IAA9* seems to have two copies in *Prunus* species, but only one was included on the clade of *SlAUX/IAA9*. However, the other copy was also included in the further steps, in order to check if the two *PavAUX/IAA9* encoding genes kept the same function in fruit development or only one of the two. Once aligned to their orthologs protein sequence in Arabidopsis, tomato, sweet pepper, potato, peach, almond and apple, the cherry genes exhibited reduced identity and similarity percentages, however, the majority of the functional motifs were perfectly conserved. The PavARF7 protein sequence lacked a portion of the N-terminal B3 domain and the MR2 sequence, identified in tomato to be the area responsible for the interaction with DELLA proteins (Hu *et al.,* 2018). PavRGL2 was shown to be missing the "DELLA" motif. Functional characterisation of these proteins is a crucial step. As mentioned above, sweet cherry is a challenging model and conducting direct-site mutagenesis is laborious, with efficiency percentages notably low. For this reason, a knock-in approach was chosen. Plasmid vectors, containing the four codon-optimised CDS under constitutive promoter, were assembled using the Golden Gate technology.

Finally, the addition of the mock control was really useful since it helped to demonstrate that application of 70% ethanol to unpollinated ovaries had long lasting effects on gene expression. This is evidence to definitely be considered when future experiments like the one conducted in this study, will be repeated.

This study is the first to give such a broad view of the cherry fruit transcriptomics, connecting not only the different hormonal pathways, but also transcription factors which are known to be important for fruit development in other well studied species. There is still a lot to do to expand the knowledge on the sweet cherry fruit development, but this study is definitely part of the foundation for the future studies.

6.2 Future perspectives

The transformation of the tomato mutants *ARF7 RNAi*, *entire* (*SlAUX/IAA9* knockout) and *procera* (*SlDELLA* knockout), with the vectors assembled, is an essential step to validate the function of the genes identified in sweet cherry. The observation of the knocked-in mutants' phenotypes will give a preliminary idea of the function of these four genes. Successful results, i.e. the restoration of the wild-type phenotype, will encourage site directed- mutagenesis in sweet cherry. Negative results will suggest trying other candidate genes such as *PavAUX/IAA4*.

Yeast two-hybrid assay is recommended because it will determine if PavARF7, PavAUX/IAA9 and PavRGL2 can interact as SlARF7, SlAUX/IAA9 and SlDELLA do in tomato or FveARF8, FveAUX/IAA4 and FveRGA1 do in strawberry. Proving the interaction of these three factors in cherry would add another piece to the final picture.

Finally, to prove that the cause of fruit abortion in the GA_3-treated samples, was the lack of constant hormonal signal, multiple applications over time will be very useful. This strategy was planned for Spring 2021, but due to severe frost damage and bad weather conditions, it could

not be carried out. The hormone content in all the different types of samples will also be extremely interesting to establish, in order to connect the expression levels of the different hormone biosynthetic genes to the actual concentration of them in the pollinated, treated and unpollinated samples.

The study to set up the *in vitro* regeneration and transformation protocols, using somatic explants, is crucial and needs to be considered. Different hormone concentrations, media and growth conditions should be tested.

Finally, the study of *PavSTK* should be considered since the mutation in this gene is reported to be linked to stenospermocarpy in grape and tomato. Moreover, *STK* may play an important role during endocarp development, thus, knocking it out may result also in the removal of the cherry stone, which is another critical aspect. To better understand which genes are responsible for the mesocarp and the endocarp differentiation and development in cherry, tissue specific transcriptomic analysis is required. The fruit-seed interaction and the stone development are unfortunately two different processes, which are regulated by different factors. The integration of the knowledge on these two processes, could lead to the obtaining of a cherry fruit completely pit-less. The removal of the seed and the stone from a drupe-type fruits would be a revolution, making these fruits even more appealing not only for the consumers but for the industry as well.

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Supplementary data

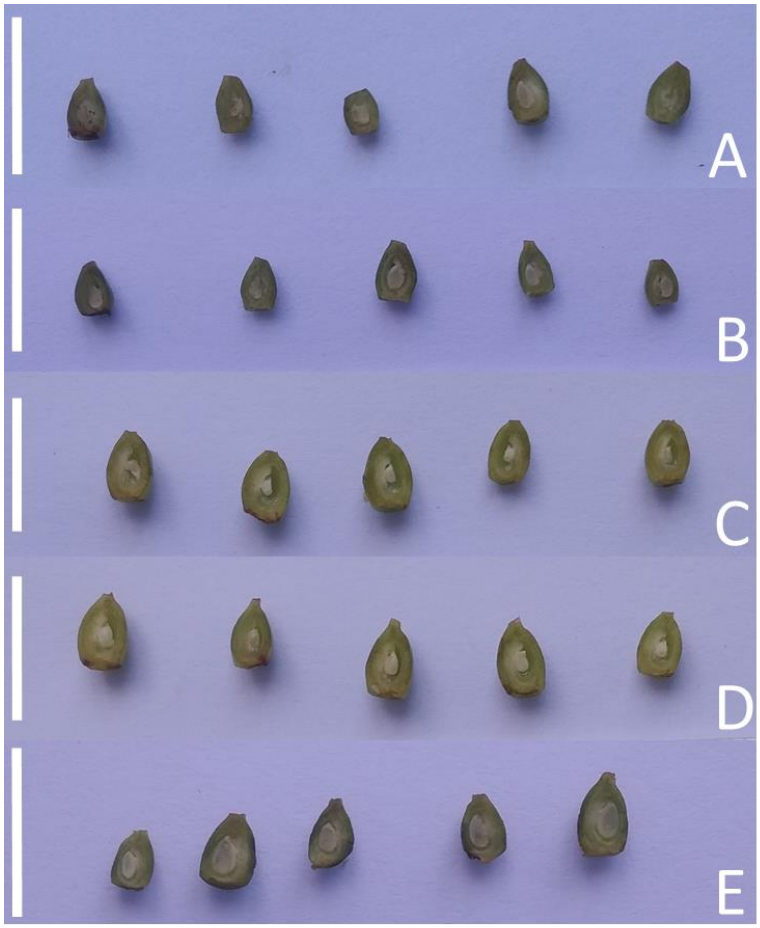

Figure S3.1: Panel with the original photos that show 'Regina' unpollinated ovaries (N.C.) (A), EtOH70%-treated ovaries (B), 300 mg/L GA_3- treated (C), 500 mg/L GA_3-treated (D) ovaries and open pollinated (O.P.) (E) ovaries at 7 DAT. Scale bars = 1cm.

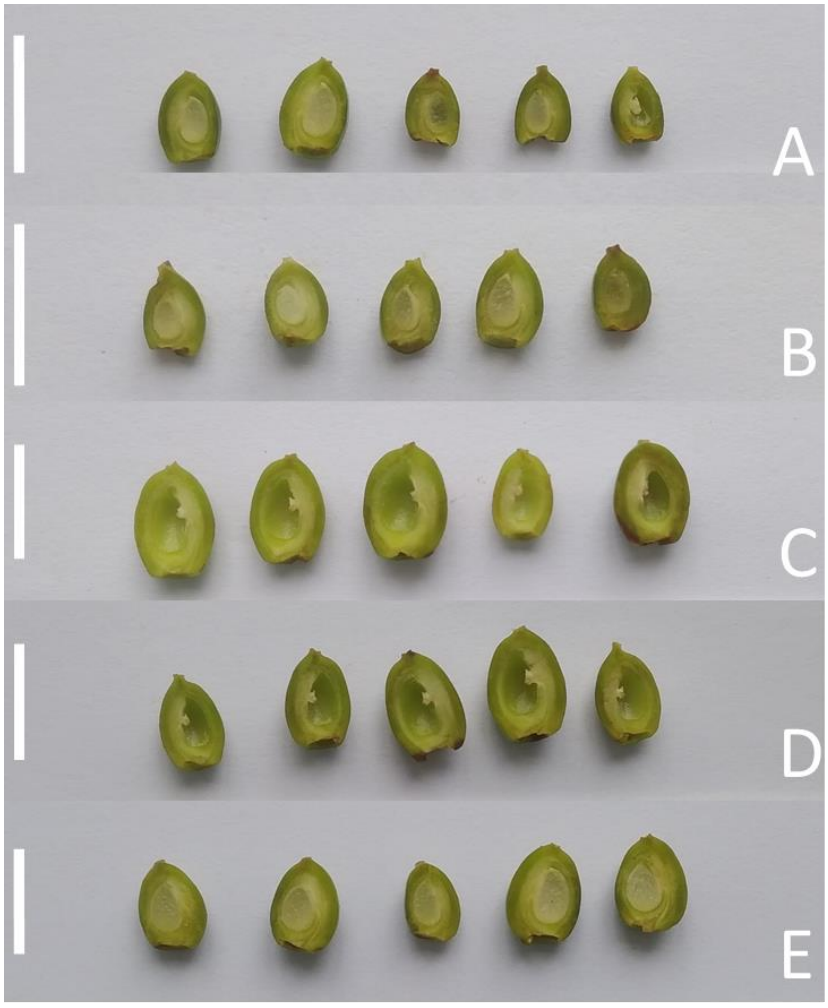

Figure S3.2: Panel with the original photos that show 'Regina' unpollinated ovaries (N.C.) (A), EtOH70%-treated ovaries (B), 300 mg/L GA_3- treated (C), 500 mg/L GA_3-treated (D) ovaries and open pollinated (O.P.) (E) ovaries at 14 DAT. Scale bars = 1cm.

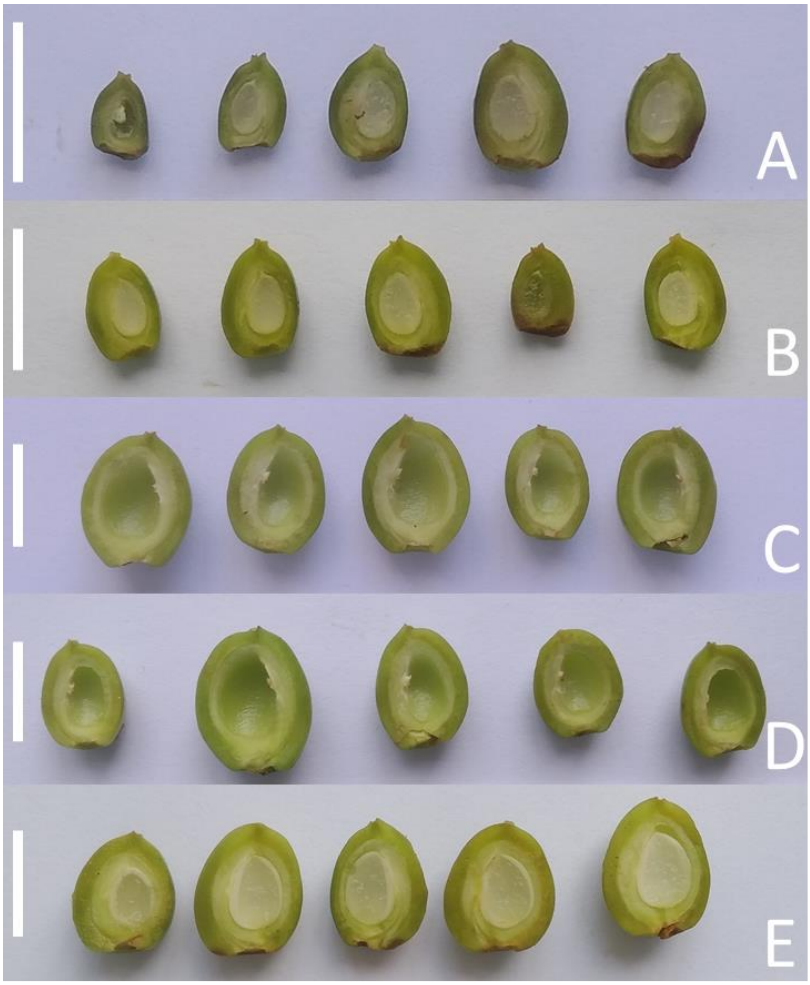

Figure S3.3: Panel with the original photos that show 'Regina' unpollinated ovaries (N.C.) (A), EtOH70%-treated ovaries (B), 300 mg/L GA_3- treated (C), 500 mg/L GA_3-treated (D) ovaries and open pollinated (O.P.) (E) ovaries at 21 DAT. Scale bars = 1cm.

Figure S3.4: Panel with the original photos that show 'Regina' unpollinated ovaries (N.C.) (A), EtOH70%-treated ovaries (B), 300 mg/L GA_3- treated (C), 500 mg/L GA_3-treated (D) ovaries and open pollinated (O.P.) (E) ovaries at 28 DAT. Scale bars = 1cm.

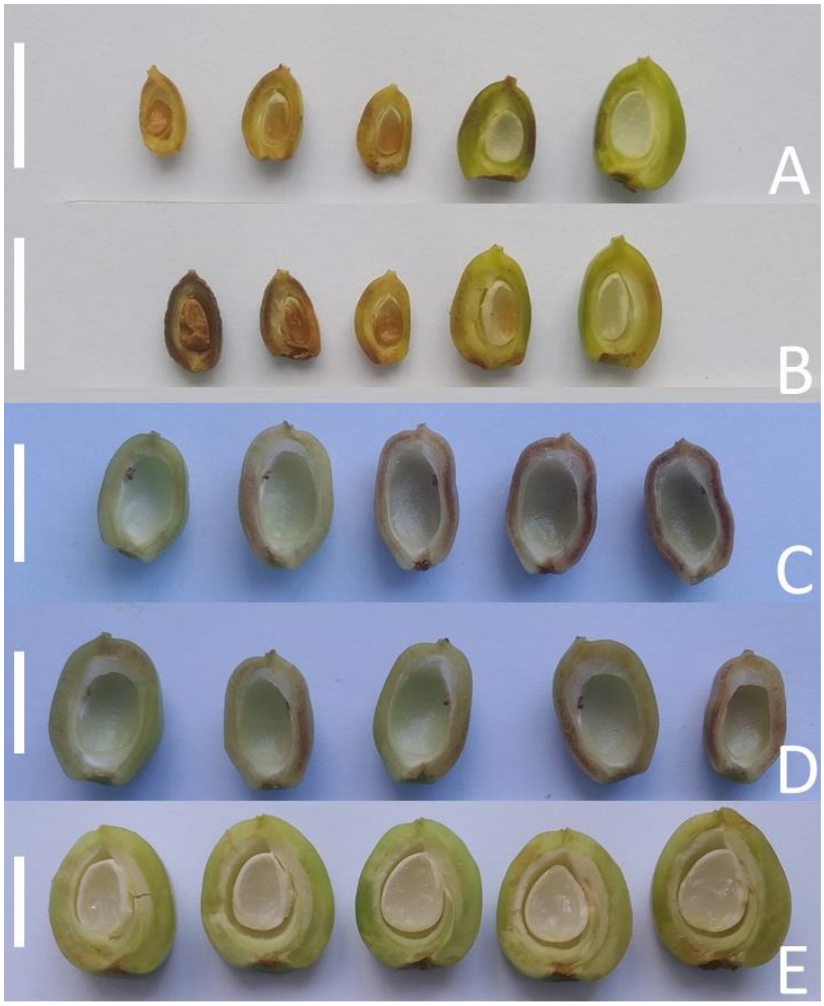

Figure S3.5: Panel with the original photos that show 'Regina' unpollinated ovaries (N.C.) (A), EtOH70%-treated ovaries (B), 300 mg/L GA_3- treated (C), 500 mg/L GA_3-treated (D) ovaries and open pollinated (O.P.) (E) ovaries at 35 DAT. Scale bars = 1cm.

Figure S3.6: Panel with the original photos that show 'Regina' 300 mg/L GA_3- treated (A), 500 mg/L GA_3-treated (B) ovaries and open pollinated (O.P.) (C) ovaries at 42 DAT. Scale bars = 1cm.

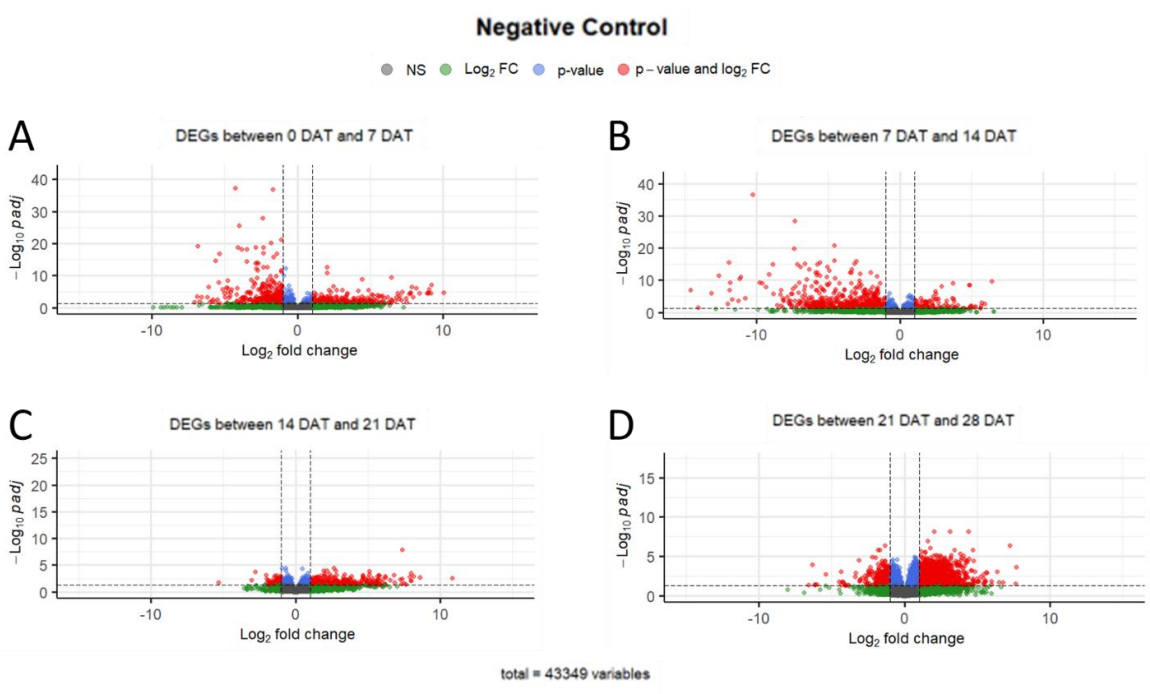

Figure S4.1: *V*olcano plot of all the DEGs in the negative control between 0 DAT and 7 DAT (A), 7 DAT and 14 DAT (B), 14 DAT and 21 DAT (C) and 21 and 28 DAT (D). The red dots are for the significantly (p-adj. < 0.05) DEGs with a |log2FC| > 1. The blue dots are for significantly (p-adj. < 0.05) DEGs but with a |log2FC| < 1. The green dots represent the non-statistically significant (p-adj. > 0.05) DEGs with |log2FC| > 1. The grey dots are for those genes that are neither statistically significant nor greatly changed in expression.

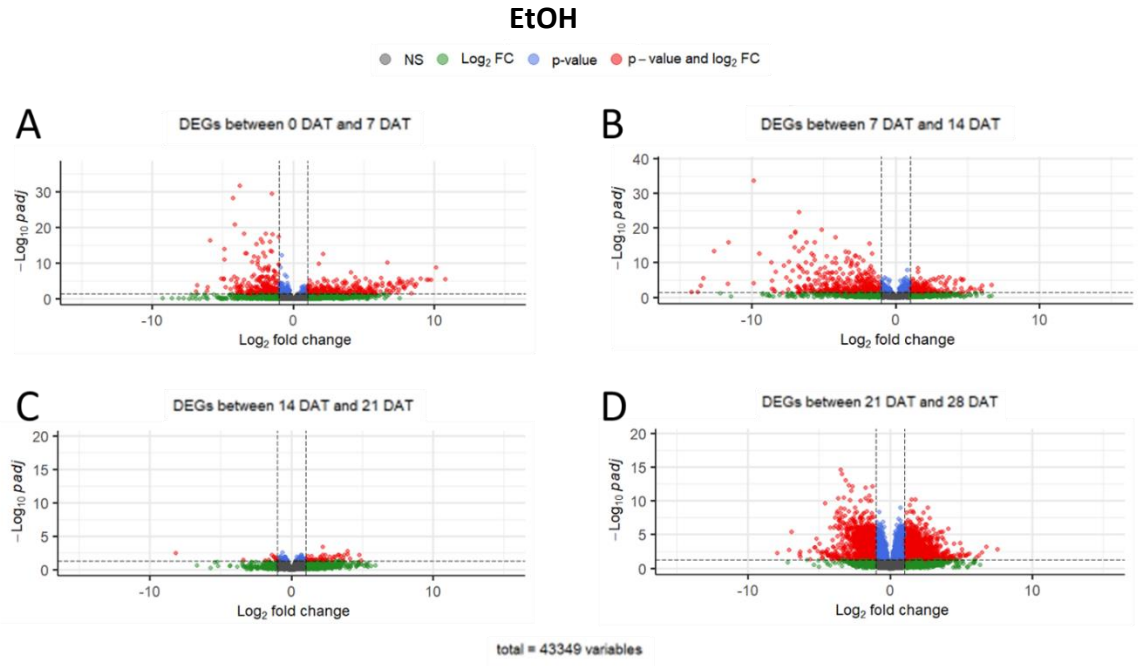

Figure S4.2: Volcano plot of all the DEGs in the mock treated ovaries (EtOH 70%) between 0 DAT and 7 DAT (A), 7 DAT and 14 DAT (B), 14 DAT and 21 DAT (C) and 21 and 28 DAT (D). The red dots are for the significantly (p-adj. < 0.05) DEGs with a |log2FC| > 1. The blue dots are for significantly (p-adj. < 0.05) DEGs but with a |log2FC| < 1. The green dots represent the non-statistically significant (p-adj. > 0.05) DEGs with |log2FC| > 1. The grey dots are for those genes that are neither statistically significant nor greatly changed in expression.

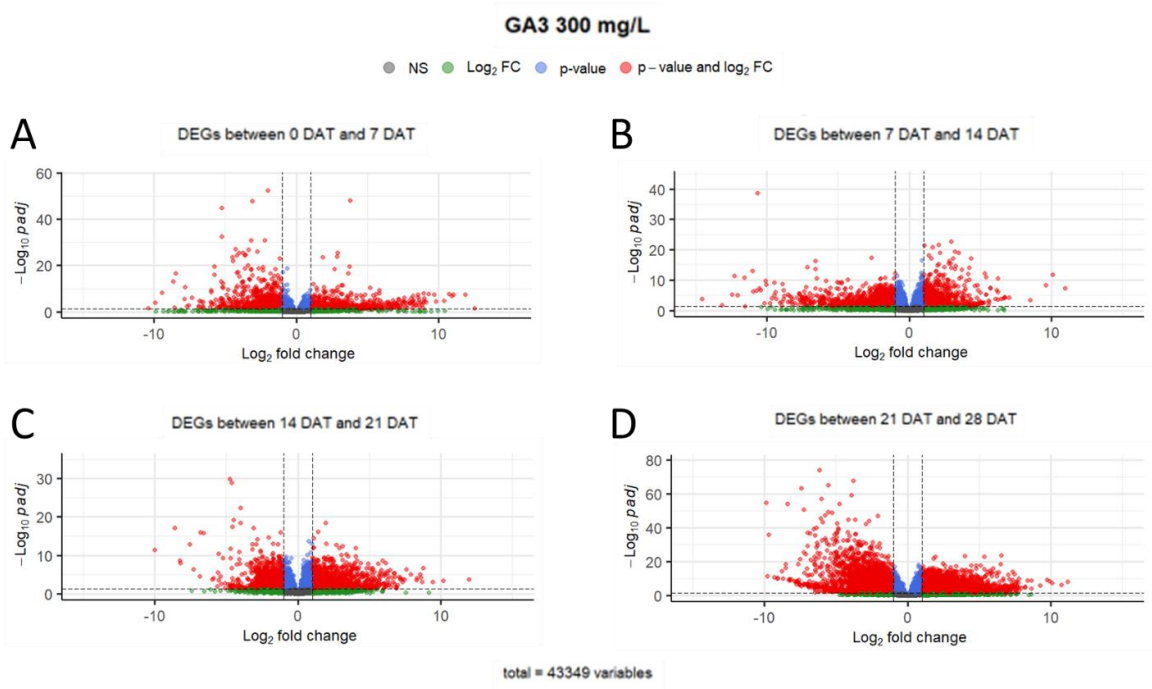

Figure S4.3: Volcano plot of all the DEGs in the ovaries treated with GA_3 300 mg/L, between 0 DAT and 7 DAT (A), 7 DAT and 14 DAT (B), 14 DAT and 21 DAT (C) and 21 and 28 DAT (D). The red dots are for the significantly (p-adj. < 0.05) DEGs with a |log2FC| > 1. The blue dots are for significantly (p-adj. < 0.05) DEGs but with a |log2FC| < 1. The green dots represent the non-statistically significant (p-adj. > 0.05) DEGs with |log2FC| > 1. The grey dots are for those genes that are neither statistically significant nor greatly changed in expression.

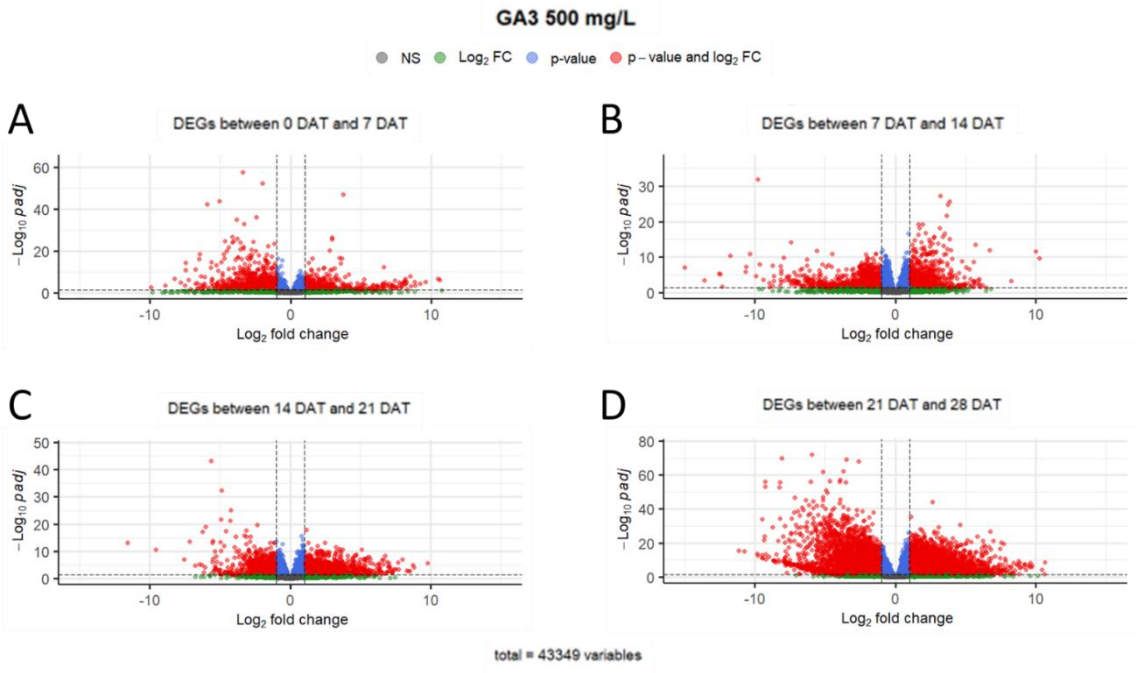

Figure S4.4: Volcano plot of all the DEGs in the ovaries treated with GA3 500 mg/L, between 0 DAT and 7 DAT (A), 7 DAT and 14 DAT (B), 14 DAT and 21 DAT (C) and 21 and 28 DAT (D). The red dots are for the significantly (p-adj. < 0.05) DEGs with a |log2FC| > 1. The blue dots are for significantly (p-adj. < 0.05) DEGs but with a |log2FC| < 1. The green dots represent the non-statistically significant (p-adj. > 0.05) DEGs with |log2FC| > 1. The grey dots are for those genes that are neither statistically significant nor greatly changed in expression.

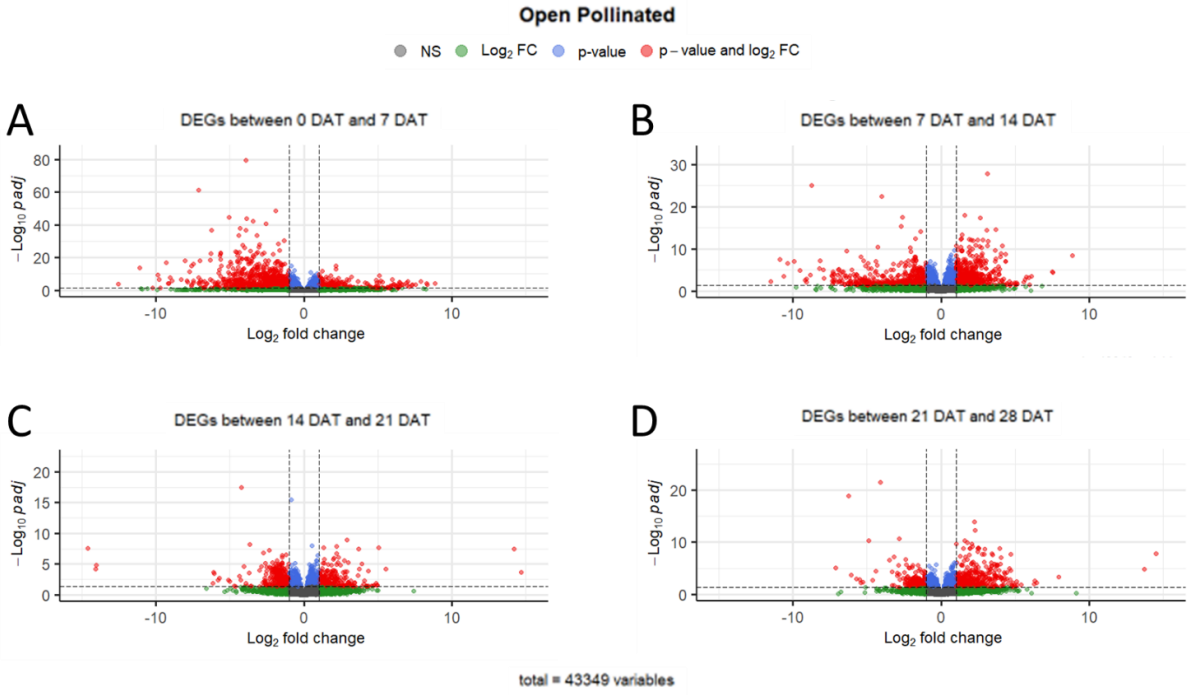

Figure S4.5: Volcano plot of all the DEGs in the pollinated ovaries between 0 DAT and 7 DAT (A), 7 DAT and 14 DAT (B), 14 DAT and 21 DAT (C) and 21 and 28 DAT (D). The red dots are for the significantly (p-adj. < 0.05) DEGs with a |log2FC| > 1. The blue dots are for significantly (p-adj. < 0.05) DEGs but with a |log2FC| < 1. The green dots represent the non-statistically significant (p-adj. > 0.05) DEGs with |log2FC| > 1. The grey dots are for those genes that are neither statistically significant nor greatly changed in expression.

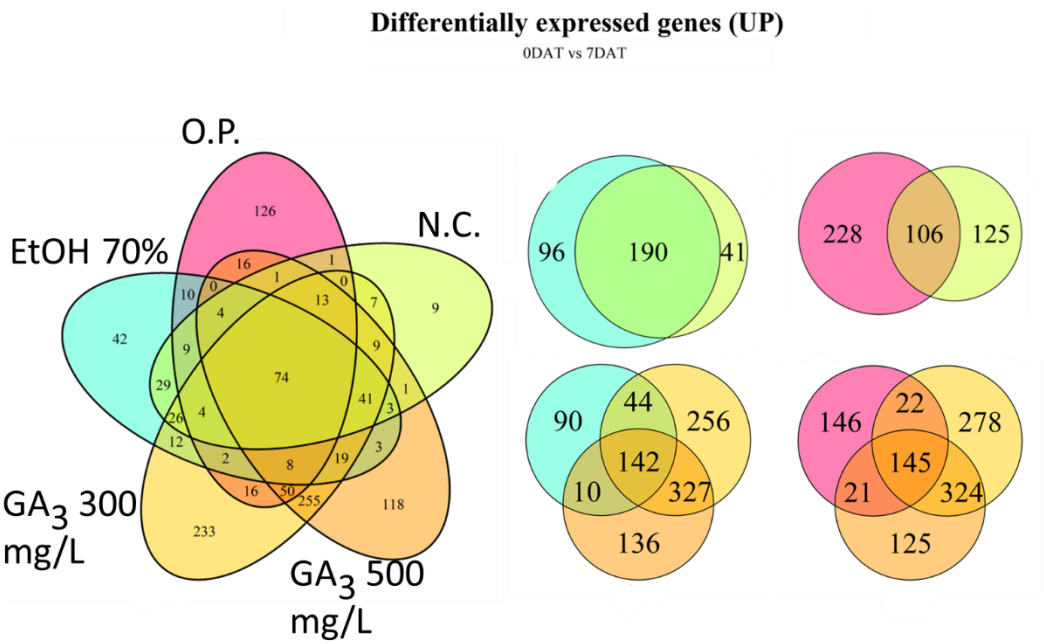

Figure S4.6: Venn diagrams of the significant upregulated DEGs (log2FC > 1 and p-adj. < 0.05) between 0 and 7 DAT. Green circle: Negative Control; light blue circle: EtOH 70%; orange circle: GA_3 300 mg/L; dark orange circle: GA_3 500 mg/L; magenta circle: open pollinated.

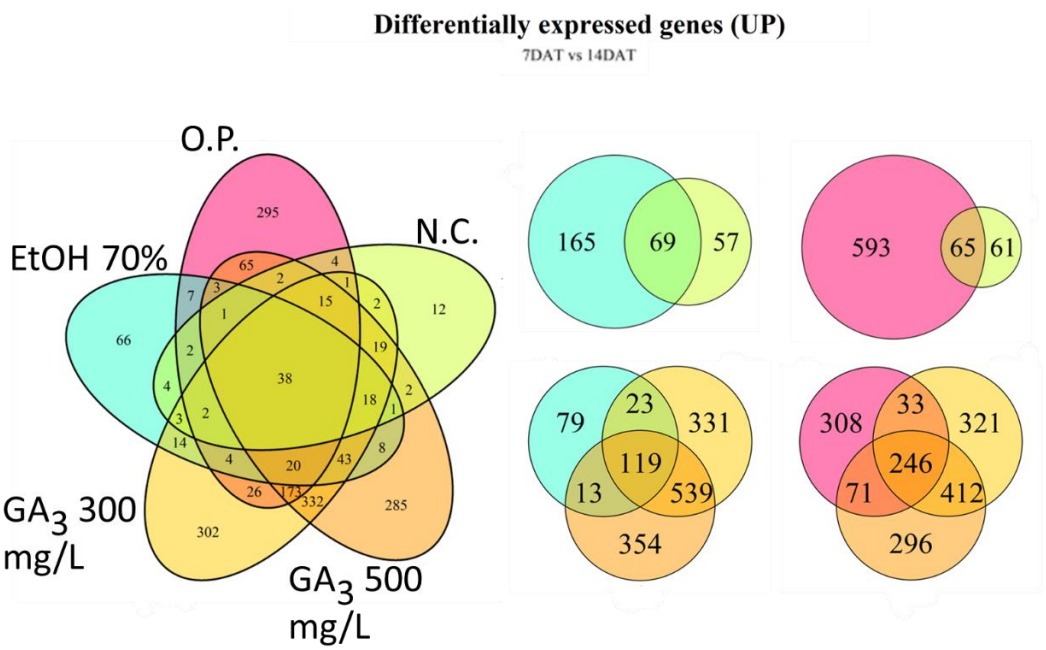

Figure S4.7: Venn diagrams of the significant upregulated DEGs (log2FC > 1 and p-adj. < 0.05) between 7 and 14 DAT. Green circle: Negative Control; light blue circle: EtOH 70%; orange circle: GA_3 300 mg/L; dark orange circle: GA_3 500 mg/L; magenta circle: open pollinated.

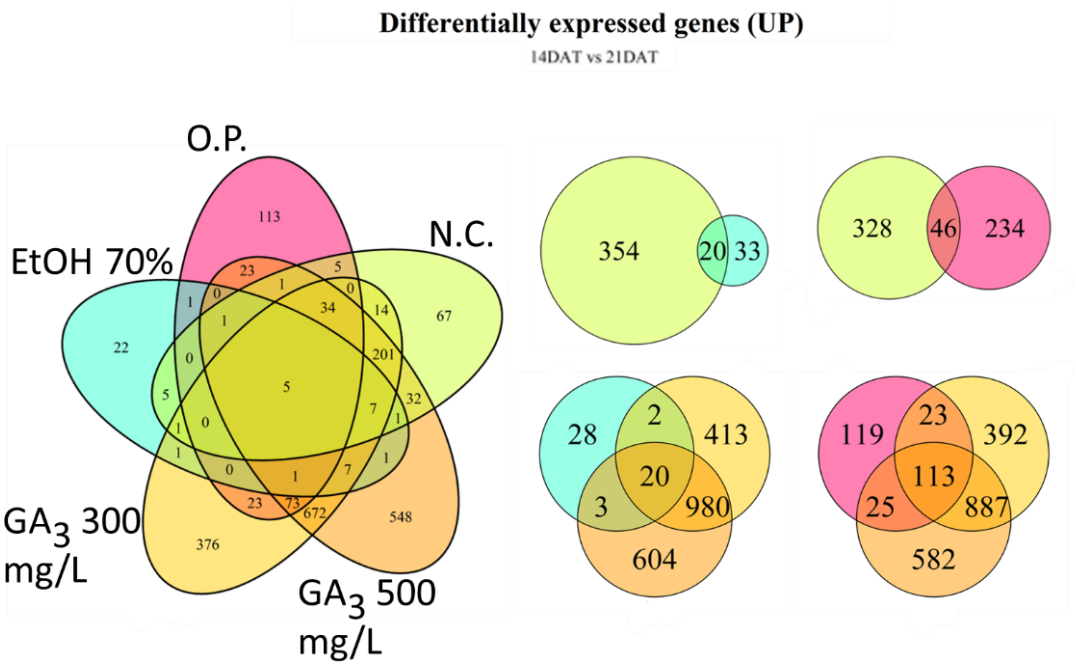

Figure S4.8: Venn diagrams of the significant upregulated DEGs (log2FC > 1 and p-adj. < 0.05) between 14 and 21 DAT. Green circle: Negative Control; light blue circle: EtOH 70%; orange circle: GA_3 300 mg/L; dark orange circle: GA_3 500 mg/L; magenta circle: open pollinated.

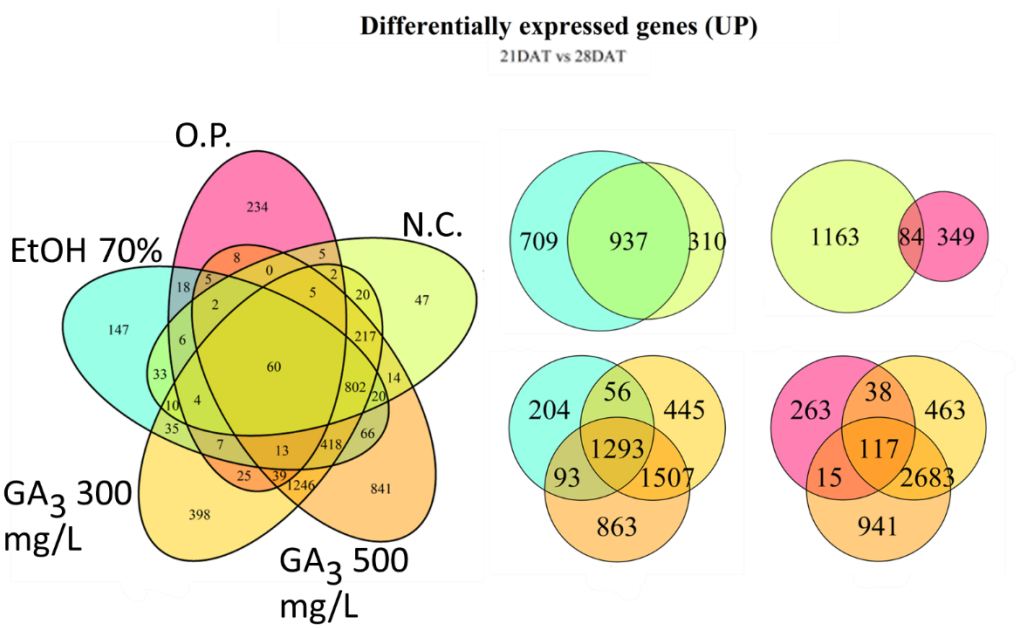

Figure S4.9: Venn diagrams of the significant upregulated DEGs (log2FC > 1 and p-adj. < 0.05) between 21 and 28 DAT. Green circle: Negative Control; light blue circle: EtOH 70%; orange circle: GA_3 300 mg/L; dark orange circle: GA_3 500 mg/L; magenta circle: open pollinated.

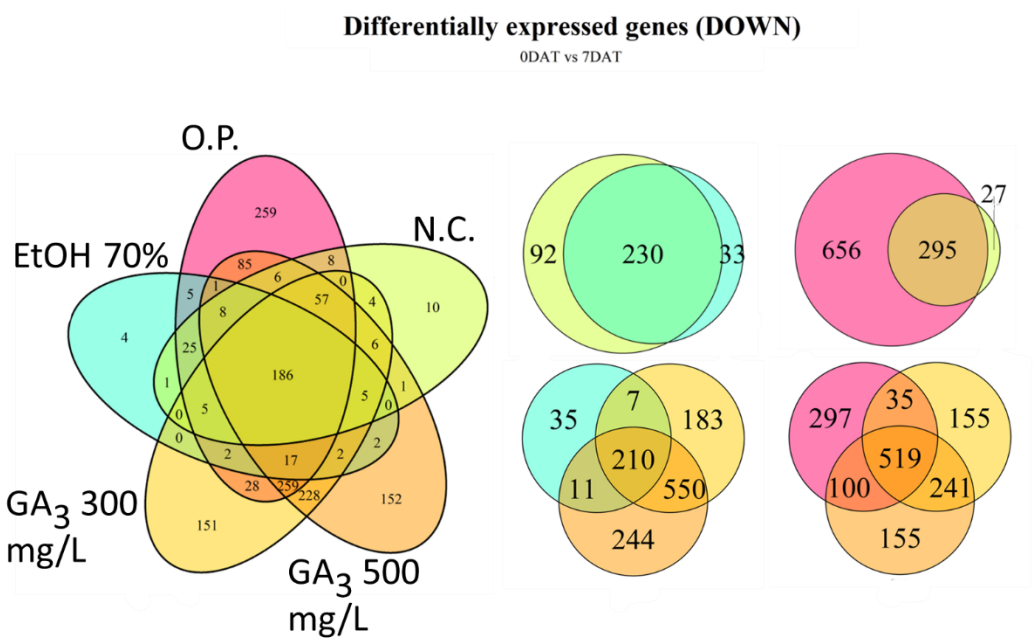

Figure S4.10: Venn diagrams of the significant downregulated DEGs (log2FC < -1 and p-adj. < 0.05) between 0 and 7 DAT. Green circle: Negative Control; light blue circle: EtOH 70%; orange circle: GA_3 300 mg/L; dark orange circle: GA_3 500 mg/L; magenta circle: open pollinated.

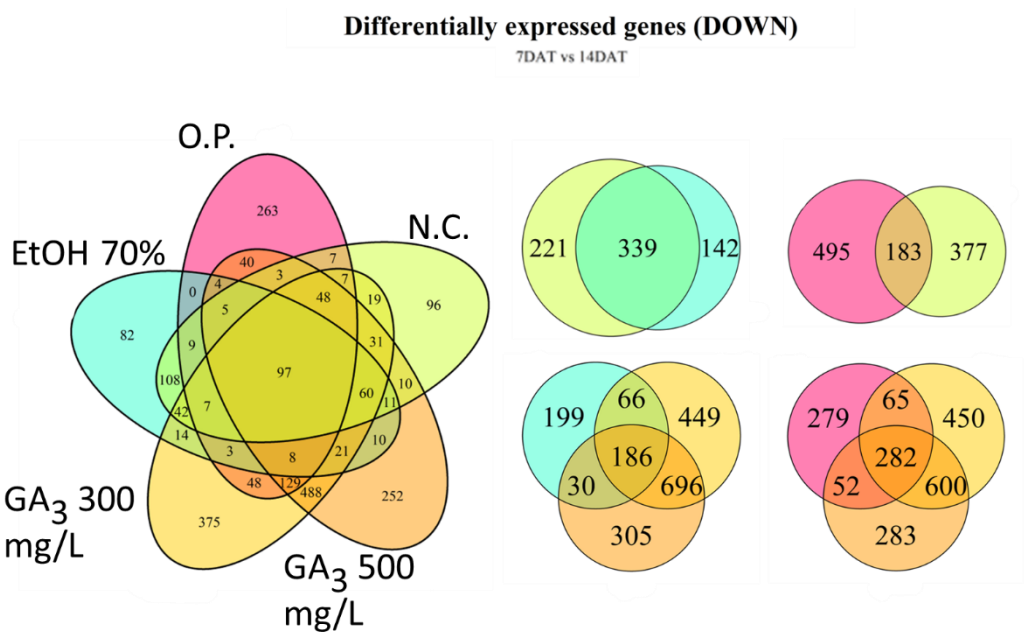

Figure S4.11: Venn diagrams of the significant downregulated DEGs (log2FC < -1 and p-adj. < 0.05) between 7 and 14 DAT. Green circle: Negative Control; light blue circle: EtOH 70%; orange circle: GA_3 300 mg/L; dark orange circle: GA_3 500 mg/L; magenta circle: open pollinated.

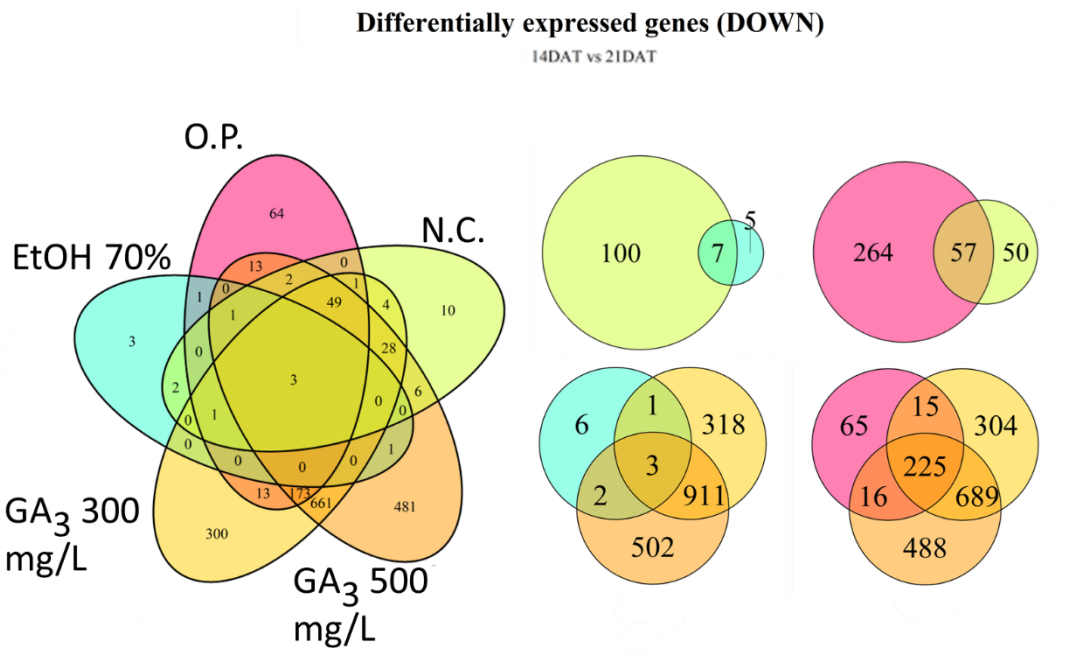

Figure S4.12: Venn diagrams of the significant downregulated DEGs (log2FC < -1 and p-adj. < 0.05) between 14 and 21 DAT. Green circle: Negative Control; light blue circle: EtOH 70%; orange circle: GA_3 300 mg/L; dark orange circle: GA_3 500 mg/L; magenta circle: open pollinated.

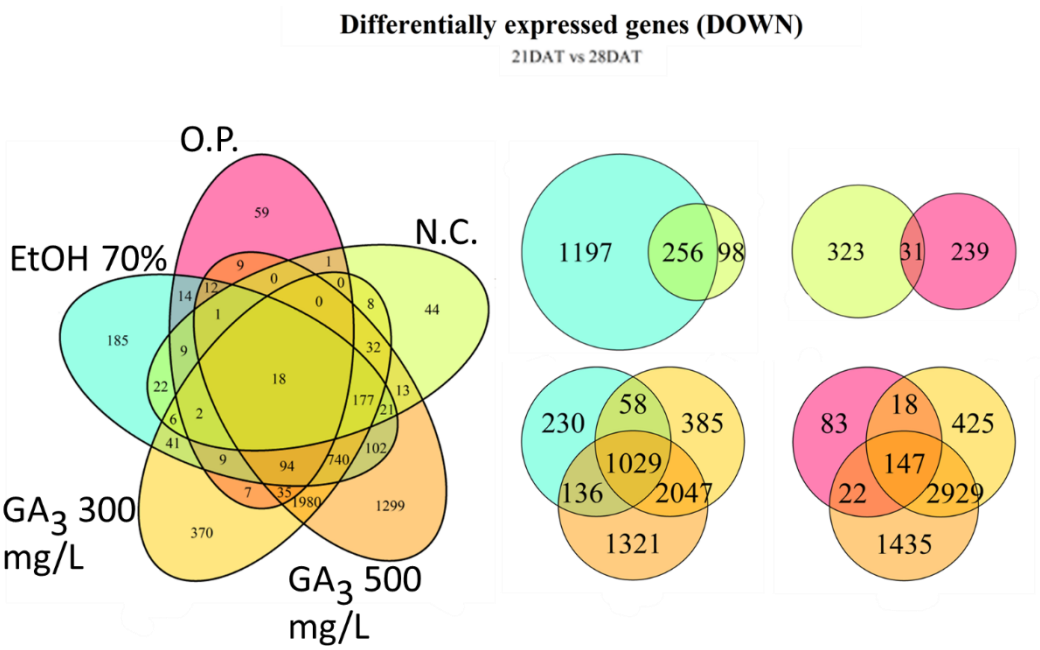

Figure S4.13: Venn diagrams of the significant downregulated DEGs (log2FC < -1 and p-adj. < 0.05) between 21 and 28 DAT. Green circle: Negative Control; light blue circle: EtOH 70%; orange circle: GA_3 300 mg/L; dark orange circle: GA_3 500 mg/L; magenta circle: open pollinated.

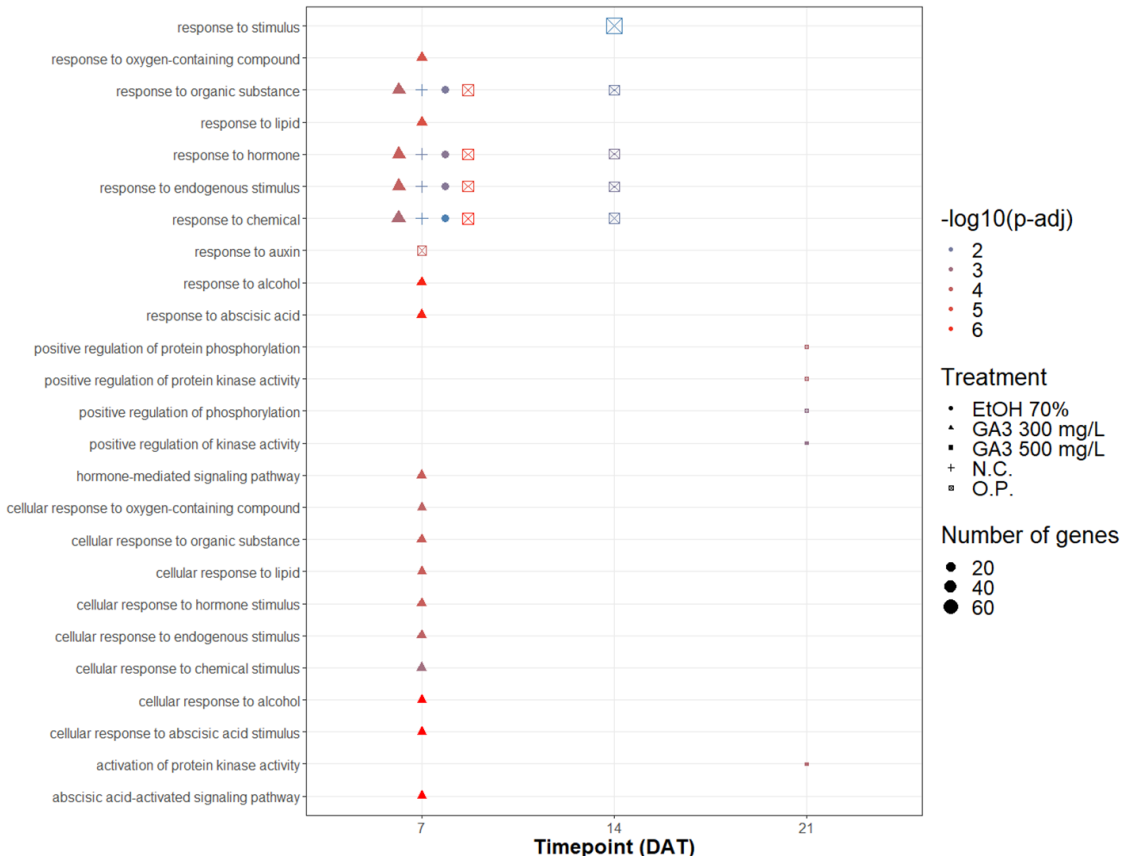

Figure S4.14: Dot plot that shows the pathways enriched according to the DEGs genes identified. The GO terms belong to the category "biological process" category and are all related to the response to hormones.

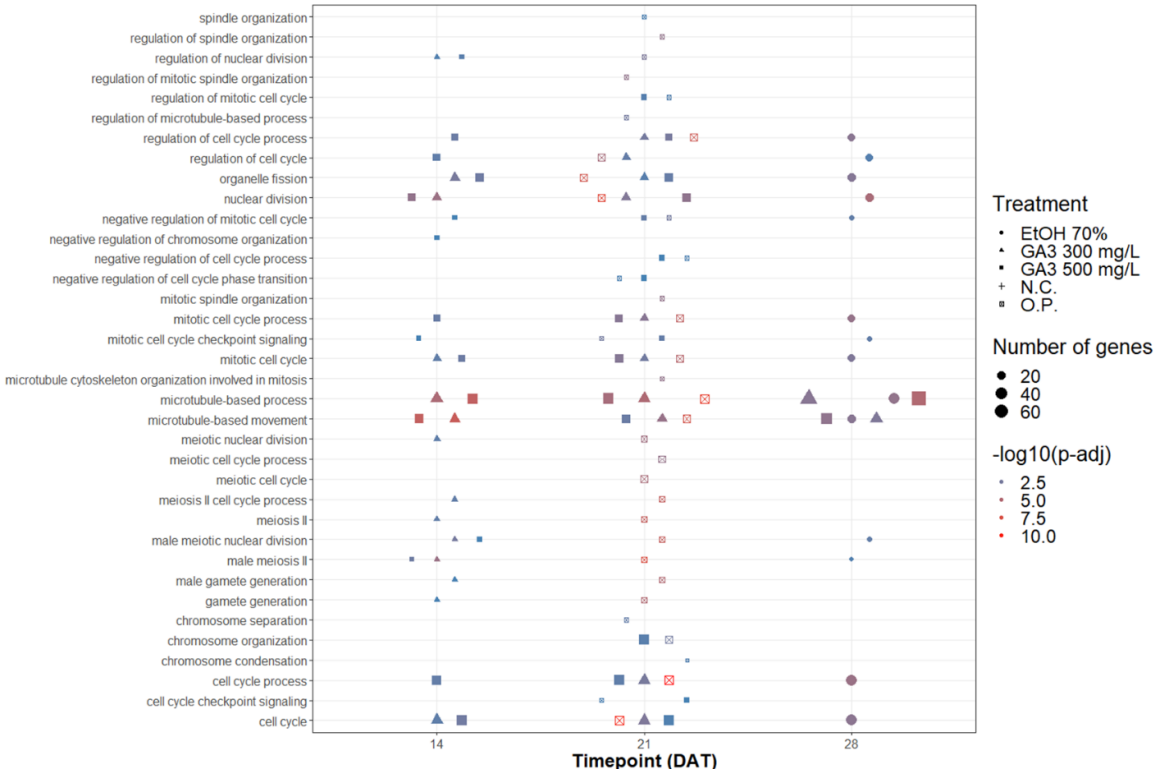

Figure S4.15: Dot plot that shows the pathways enriched according to the DEGs genes identified. The GO terms belong to the category “biological process” category and are all related to cell cycle and cell division.

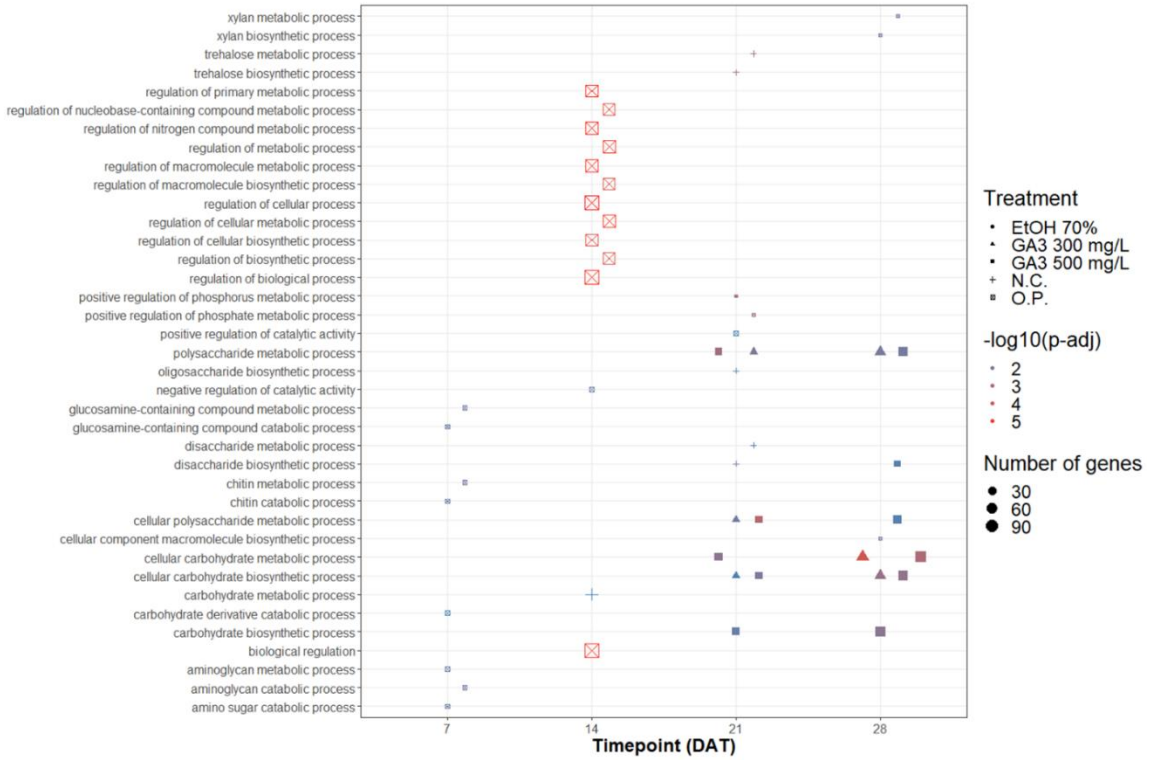

Figure S4.16: Dot plot that shows the pathways enriched according to the DEGs genes identified. The GO terms belong to the category “biological process” category and are all related to metabolic processes.

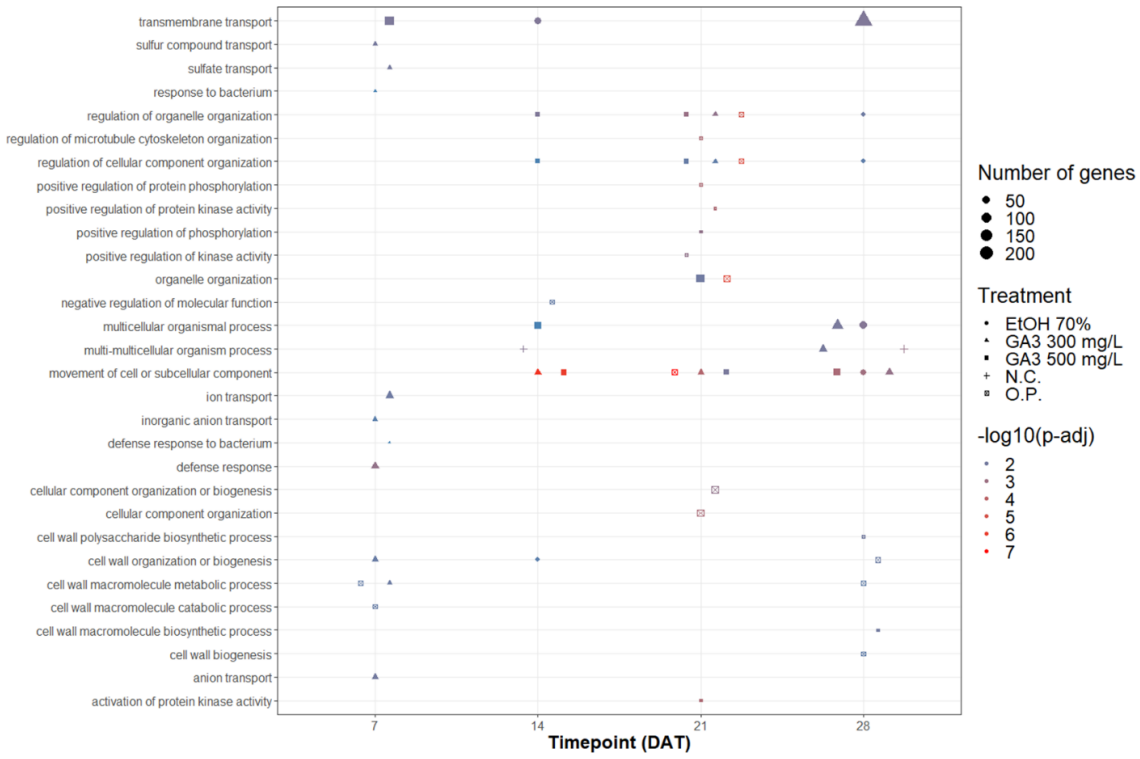

Figure S4.17: Dot plot that shows the pathways enriched according to the DEGs genes identified. The GO terms belong to the category "biological process" category and are all related to transmembrane transport, protein kinase activity and cell wall biosynthesis.

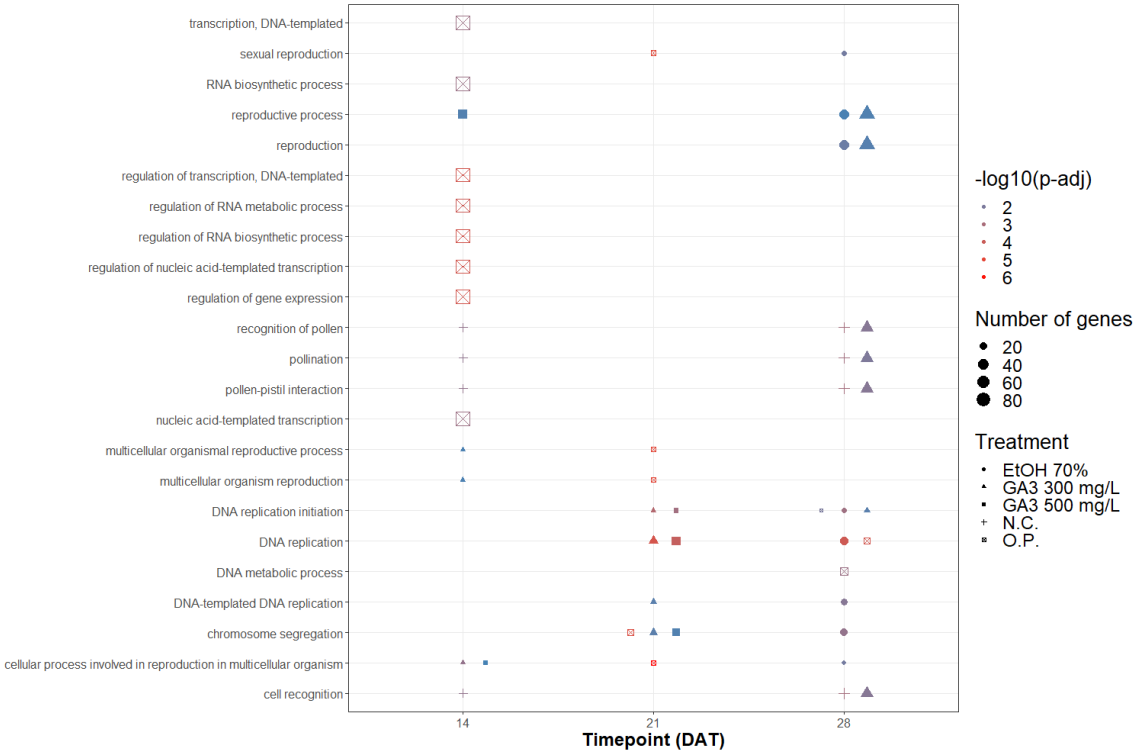

Figure S4.18: Dot plot that shows the pathways enriched according to the DEGs genes identified. The GO terms belong to the category "biological process" category and are all related to the regulation of DNA and RNA metabolic processes.

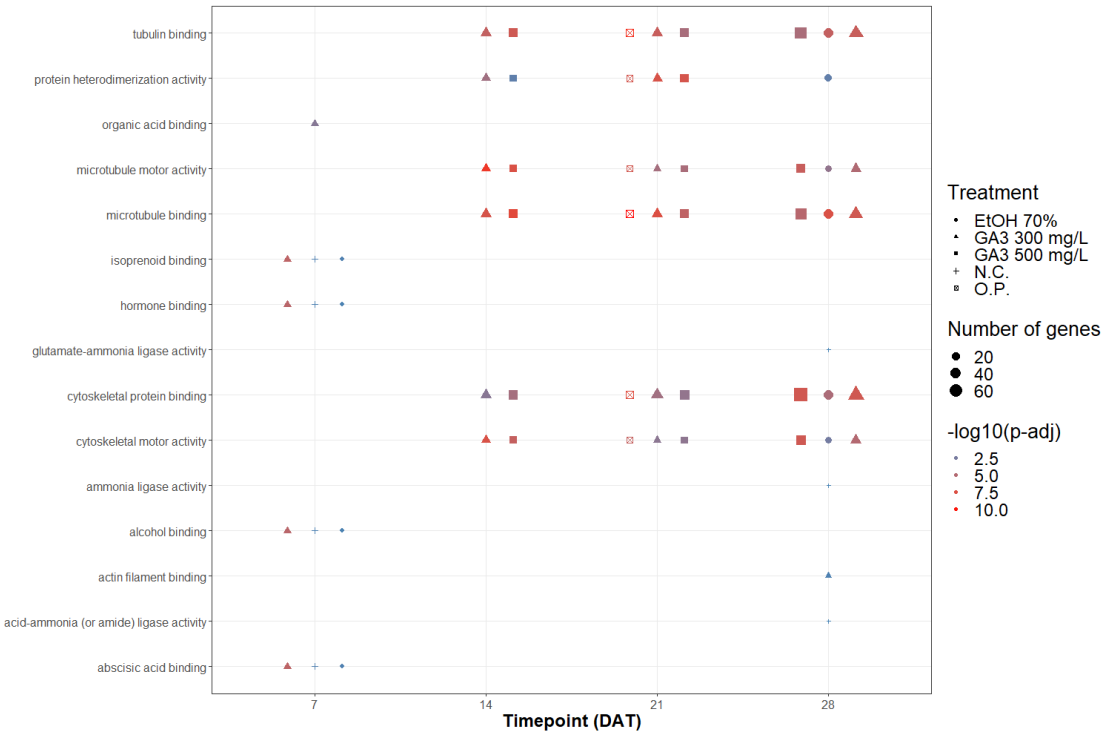

Figure S4.19: Dot plot that shows the pathways enriched according to the DEGs genes identified. The GO terms belong to the category “molecular function” category and are all related to binding activity.

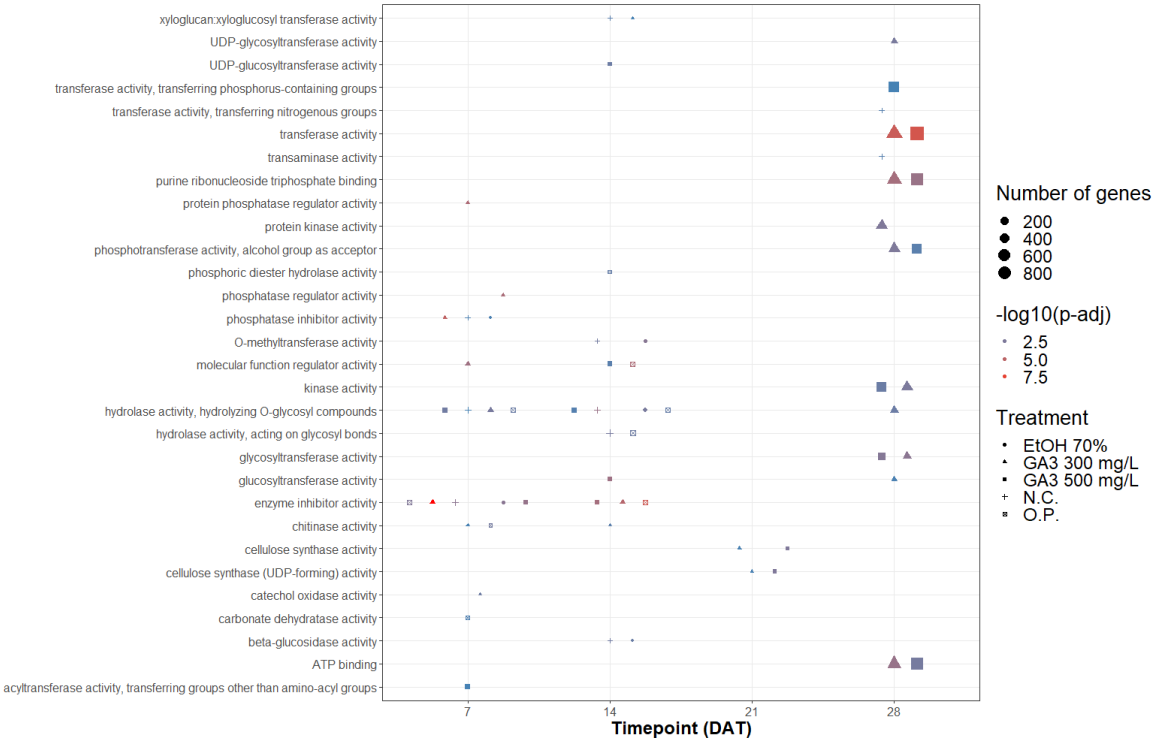

Figure S4.20: Dot plot that shows the pathways enriched according to the DEGs genes identified. The GO terms belong to the category “molecular function” category and are all related to different types of enzymatic activity.

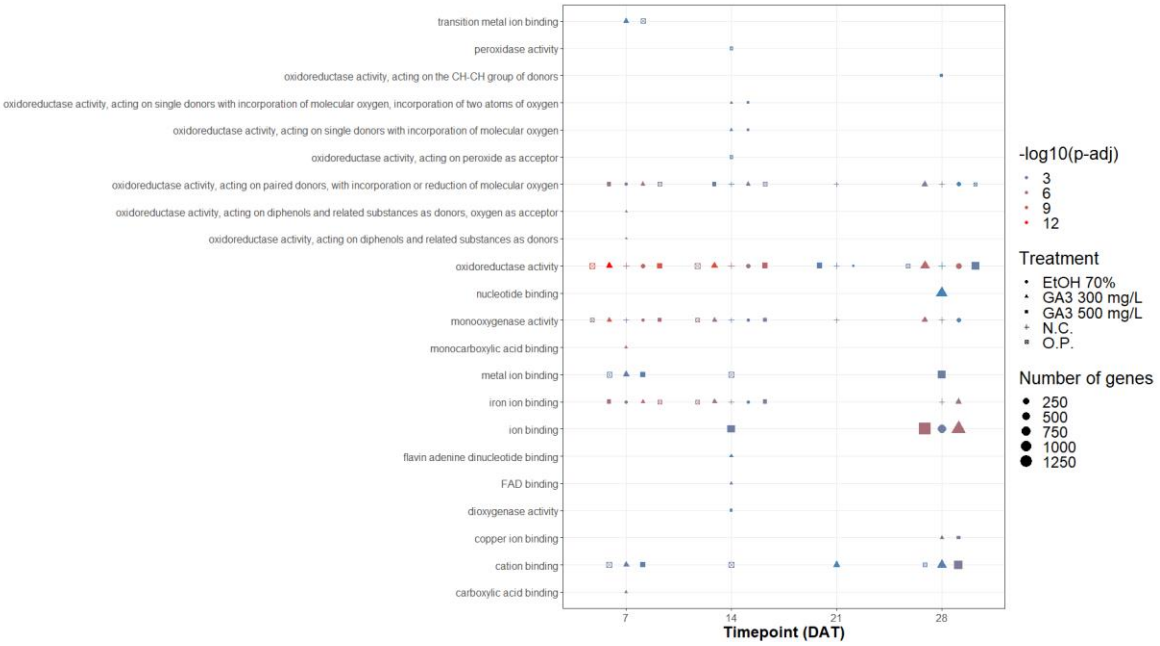

Figure S4.21: Dot plot that shows the pathways enriched according to the DEGs genes identified. The GO terms belong to the category "molecular function" category and are all related to oxidoreductase activity.

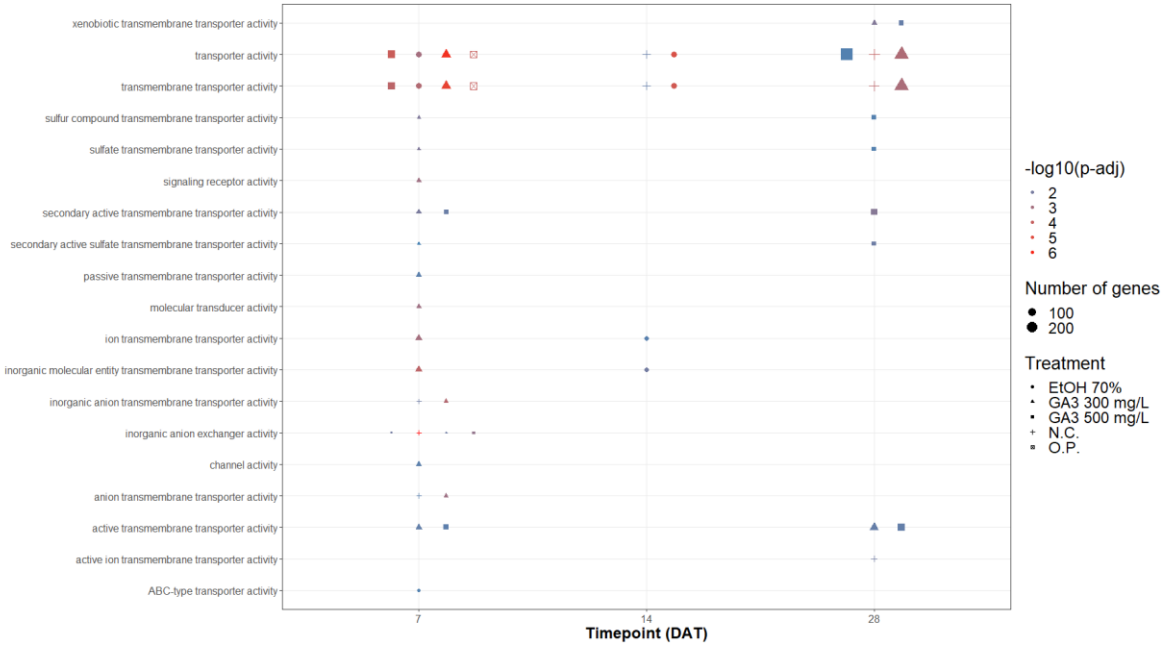

Figure S4.22: Dot plot that shows the pathways enriched according to the DEGs genes identified. The GO terms belong to the category "molecular function" category and are all related to transmembrane activity.

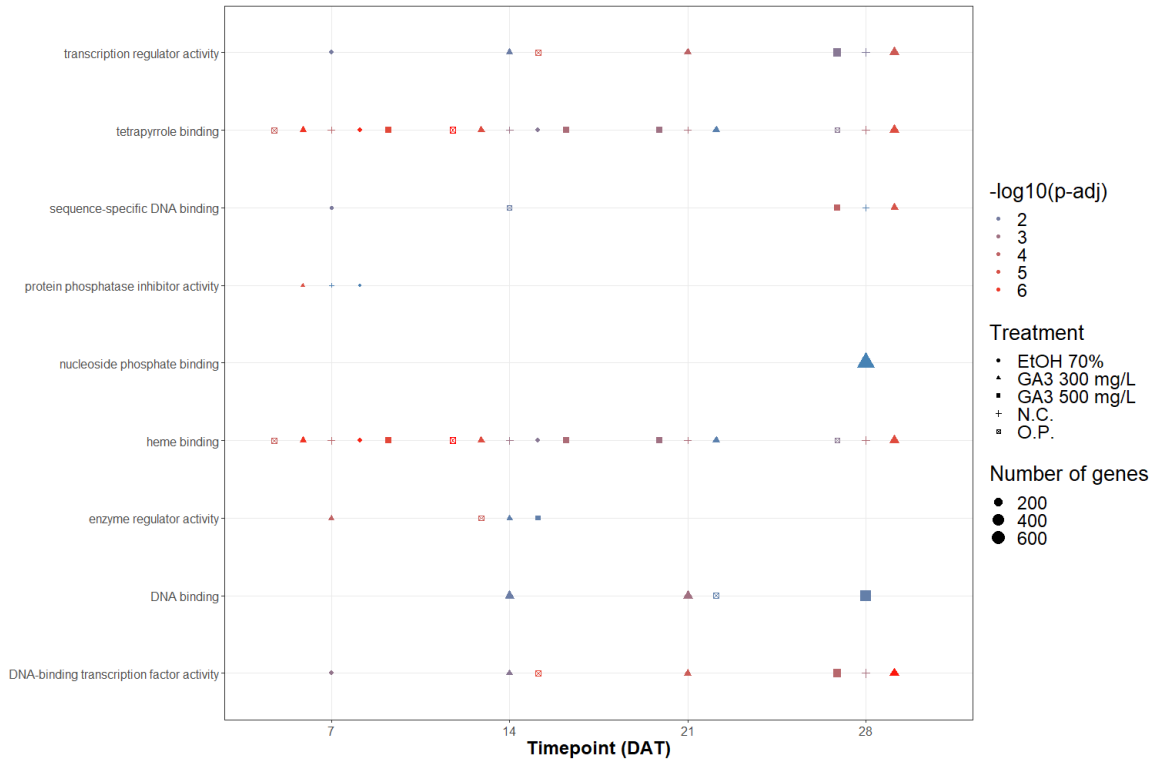

Figure S4.23: Dot plot that shows the pathways enriched according to the DEGs genes identified. The GO terms belong to the category “molecular function” category and are all related to nucleic acids activity and chlorophyll metabolic processes.

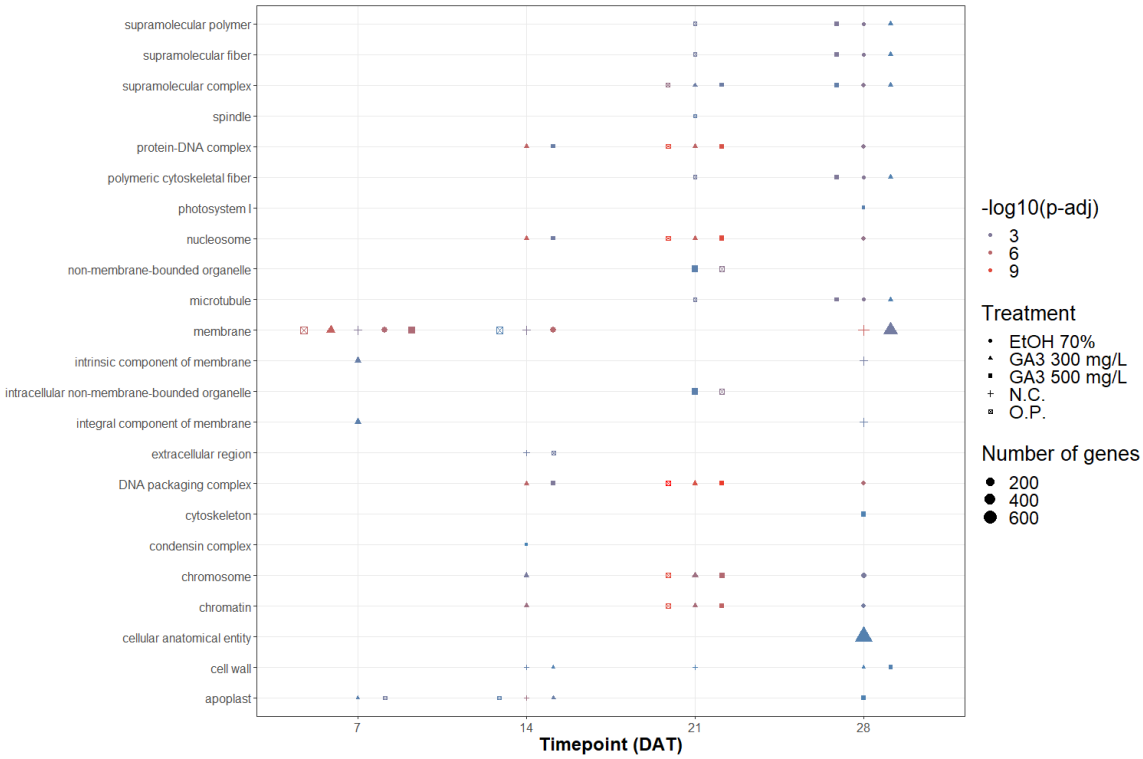

Figure S4.24: Dot plot that shows the pathways enriched according to the DEGs genes identified. The GO terms belong to the category “cellular compartment” category.

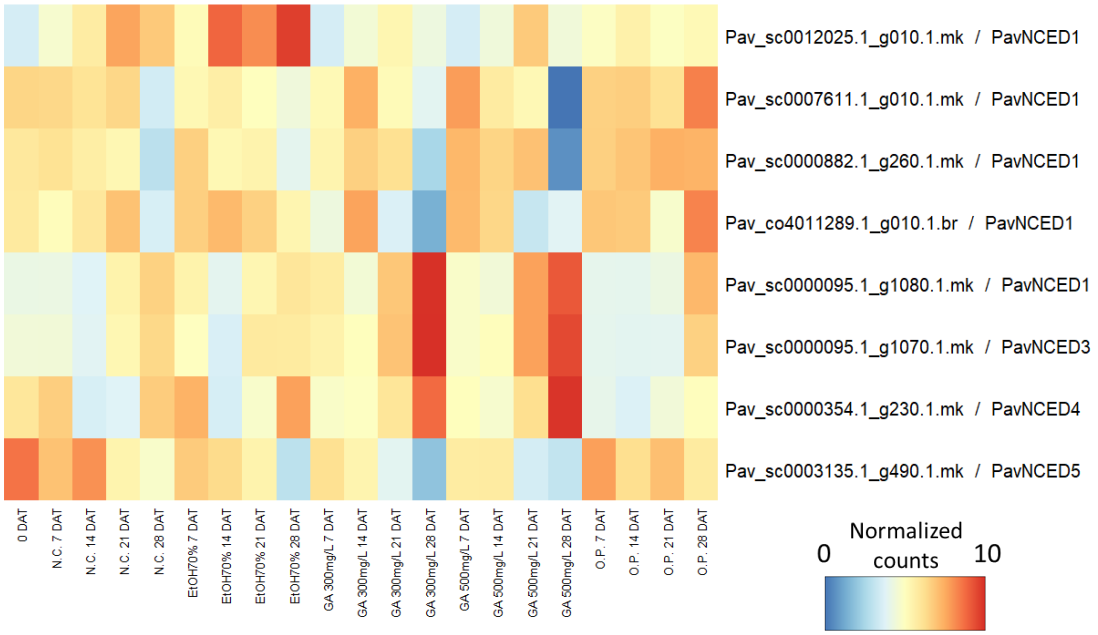

Figure S4.25: Heatmap of the putative cherry orthologs of the genes encoding for *NCED* (ABA biosynthesis). Scale bar indicates the normalised gene counts.

Table S4.1: quality check of all the RNA samples sequenced by NOVOGENE

Sample	Replicate	Raw reads	Raw data	Effective(%)	Error(%)	Q20(%)	Q30(%)	GC(%)
	A	47464936	7.12E+09	99.01	0.03	97.57	92.86	45.83
Unpollinat	B	41252656	6.19E+09	98.85	0.02	98.45	95.33	45.62
	C	45152328	6.77E+09	98.91	0.03	97.53	92.85	45.9
	A	46939100	7.04E+09	99	0.03	97.87	93.55	45.92
N.C. 7 DAT	B	42621590	6.39E+09	98.97	0.03	97.71	93.24	46.04
	C	40716324	6.11E+09	99.18	0.03	97.63	93.03	45.94
	A	46067506	6.91E+09	99.12	0.03	97.91	93.69	45.9
EtOH 70%	B	44757892	6.71E+09	98.96	0.03	97.62	93	46
	C	43304536	6.5E+09	98.91	0.03	97.79	93.43	46.1
	A	44317778	6.65E+09	98.48	0.03	97.8	93.42	46.05
GA3 300 m	B	43133688	6.47E+09	98.46	0.02	98.47	95.36	45.81
	C	43638982	6.55E+09	98.75	0.02	98.58	95.64	45.74
	A	43862026	6.58E+09	98.38	0.02	98.55	95.51	45.81
GA3 500 m	B	44408918	6.66E+09	98.66	0.03	97.8	93.41	46.1
	C	42812014	6.42E+09	98.47	0.02	98.5	95.44	45.91
	A	43600672	6.54E+09	98.92	0.03	97.75	93.29	45.93
O.P. 7 DAT	B	42482722	6.37E+09	98.91	0.02	98.47	95.34	45.83
	C	44755932	6.71E+09	98.72	0.02	98.39	95.12	45.62
	A	48560336	7.28E+09	98.87	0.03	97.72	93.22	45.96
N.C. 14 DA	B	42704916	6.41E+09	98.69	0.02	98.36	95.11	45.55
	C	41958074	6.29E+09	98.66	0.02	98.41	95.17	45.68
	A	42266932	6.34E+09	98.36	0.02	98.51	95.44	45.71
EtOH 70%	B	44086040	6.61E+09	98.56	0.02	98.5	95.5	45.5
	C	43209360	6.48E+09	98.65	0.02	98.43	95.24	45.57
	A	43686982	6.55E+09	99.06	0.03	97.61	93.03	46.05
GA3 300 m	B	45367398	6.81E+09	98.97	0.03	97.63	93.06	45.93
	C	44636434	6.7E+09	98.89	0.03	97.85	93.57	45.83
	A	43184464	6.48E+09	98.95	0.03	97.68	93.21	45.96
GA3 500 m	B	40733458	6.11E+09	99.01	0.03	97.63	93.07	45.98
	C	46398332	6.96E+09	98.89	0.03	97.5	93.08	46.02
	A	40089918	6.01E+09	98.76	0.03	97.9	93.71	45.91
O.P. 14 DA	B	42443480	6.37E+09	98.51	0.02	98.45	95.36	45.63
	C	41846338	6.28E+09	98.86	0.03	97.77	93.39	45.94
	A	42867292	6.43E+09	98.33	0.03	97.77	93.46	45.75
N.C. 21 DA	B	43715080	6.56E+09	98.53	0.03	97.84	93.56	45.69
	C	42550322	6.38E+09	98.6	0.03	97.85	93.55	45.72
	A	42065288	6.31E+09	97.91	0.03	97.78	93.4	45.91
EtOH 70%	B	43267398	6.49E+09	98.17	0.03	97.03	92.11	45.55
	C	43537122	6.53E+09	98.5	0.03	97.15	92.28	45.73
	A	41669972	6.25E+09	98.91	0.02	98.4	95.26	45.49
GA3 300 m	B	44527462	6.68E+09	98.73	0.02	98.46	95.33	45.49
	C	44244262	6.64E+09	98.65	0.02	98.45	95.32	45.63
	A	41117230	6.17E+09	98.03	0.02	98.52	95.57	45.41
GA3 500 m	B	39573452	5.94E+09	98.63	0.02	98.47	95.49	45.51
	C	42537490	6.38E+09	98.41	0.02	98.49	95.47	45.42
	A	41579270	6.24E+09	98.46	0.02	98.61	95.77	45.73
O.P. 21 DA	B	44918622	6.74E+09	98.79	0.02	98.49	95.5	45.57
	C	44365358	6.65E+09	98.77	0.02	98.55	95.58	45.72
	A	46169186	6.93E+09	98.55	0.02	98.48	95.4	45.47
N.C. 28 DA	B	45357620	6.8E+09	98.63	0.02	98.37	95.09	45.32
	C	45050584	6.76E+09	98.36	0.02	98.48	95.33	45.18
	A	40710394	6.11E+09	98.58	0.02	98.51	95.5	45.13
EtOH 70%	B	42716482	6.41E+09	98.45	0.02	98.5	95.5	45.28
	C	42276646	6.34E+09	98.32	0.02	98.46	95.36	45.04
	A	41558942	6.23E+09	98.64	0.02	98.51	95.48	45.16
GA3 300 m	B	42693152	6.4E+09	98.8	0.02	98.59	95.6	44.9
	C	40892222	6.13E+09	98.72	0.02	98.45	95.31	45.15
	A	42512438	6.38E+09	98.75	0.02	98.55	95.54	44.9
GA3 500 m	B	43632040	6.54E+09	98.68	0.02	98.46	95.3	44.75
	C	46902942	7.04E+09	98.62	0.02	98.46	95.37	44.97
	A	65063018	9.76E+09	98.81	0.03	97.67	93.23	45.7
O.P. 28 DA	B	43712356	6.56E+09	98.83	0.03	97.58	93	45.74
	C	44279484	6.64E+09	98.95	0.03	97.27	92.18	45.86

Table S4.2: for each intersection, it is shown the percentage of the shared DEGs with the other treatments of the intersection in relation to its own total number of DEGs. (A) N.C. ∩ EtOH 70%; (B) N.C. ∩ O.P.; (C) GA3 300 mg/L ∩ GA3 500 mg/L; (D) EtOH 70% ∩ GA3 300 mg/L; (E) EtOH 70% ∩ GA3 500 mg/L; (F) EtOH 70% ∩ GA3 300 mg/L ∩ GA3 500 mg/L; (G) O.P. ∩ GA3 300 mg/L; (H) O.P. ∩ GA3 500 mg/L; (I) O.P. ∩ GA3 300 mg/L ∩ GA3 500 mg/L.

Intersection	Treatment	0 DAT vs 7 DAT			7 DAT vs 14 DAT			14 DAT vs 21 DAT			21 DAT vs 28 DAT		
		UP	DOWN	TOTAL	UP	DOWN	TOTAL	UP	DOWN	TOTAL	UP	DOWN	TOTAL
A	N.C.	82.3%	71.4%	75.9%	54.8%	60.5%	59.5%	5.3%	6.5%	5.6%	75.1%	72.3%	74.6%
	EtOH 70%	66.4%	87.5%	76.5%	29.5%	70.5%	57.1%	37.7%	58.3%	41.5%	56.9%	17.6%	38.5%
B	N.C.	45.9%	91.6%	72.5%	51.6%	32.7%	38.0%	12.3%	53.3%	23.1%	6.7%	8.8%	7.7%
	O.P.	31.7%	31.0%	31.2%	9.9%	27.0%	19.5%	16.4%	17.8%	18.5%	19.4%	11.5%	17.5%
C	GA3 300 mg/L	61.4%	80.0%	71.5%	65.0%	63.1%	64.0%	70.7%	74.1%	72.4%	84.8%	87.4%	86.2%
	GA3 500 mg/L	76.7%	74.9%	75.4%	64.2%	72.5%	68.7%	62.2%	64.5%	63.4%	74.5%	67.9%	70.9%
D	EtOH 70%	63.6%	82.5%	74.1%	60.7%	52.4%	56.2%	41.5%	33.3%	40.0%	82.0%	74.8%	79.0%
	GA3 300 mg/L	23.7%	22.8%	23.7%	14.0%	18.0%	16.7%	1.6%	0.3%	1.0%	40.9%	30.9%	35.9%
E	EtOH 70%	53.1%	84.0%	67.9%	56.4%	44.9%	50.2%	43.4%	41.7%	43.1%	84.2%	80.2%	83.0%
	GA3 500 mg/L	24.7%	21.8%	22.9%	12.9%	17.7%	16.0%	1.4%	0.4%	0.9%	36.9%	25.7%	31.0%
F	EtOH 70%	49.7%	79.8%	64.1%	50.9%	38.7%	43.5%	37.7%	25.0%	35.4%	78.6%	70.8%	75.3%
	GA3 300 mg/L	18.5%	22.1%	20.5%	11.8%	13.3%	12.9%	1.4%	0.2%	0.9%	39.2%	29.2%	34.2%
	GA3 500 mg/L	23.1%	20.7%	21.6%	11.6%	15.3%	13.9%	1.2%	0.2%	0.8%	34.4%	22.7%	28.1%
G	O.P.	50.0%	58.3%	56.3%	42.4%	51.2%	49.2%	48.6%	74.8%	63.7%	35.8%	61.1%	54.3%
	GA3 300 mg/L	21.7%	58.3%	42.1%	27.6%	24.8%	27.3%	9.6%	19.5%	14.5%	4.7%	4.7%	5.6%
H	O.P.	49.7%	65.1%	61.3%	48.2%	49.3%	49.6%	49.3%	75.1%	64.9%	30.5%	62.6%	62.4%
	GA3 500 mg/L	27.0%	61.0%	48.3%	30.9%	27.4%	29.6%	8.6%	17.0%	12.9%	3.5%	3.7%	5.3%
I	O.P.	43.4%	54.6%	51.8%	37.4%	41.6%	40.3%	40.4%	70.1%	57.1%	27.0%	54.4%	45.8%
	GA3 300 mg/L	18.9%	54.6%	38.7%	24.3%	20.2%	22.3%	8.0%	18.2%	13.0%	3.5%	4.2%	4.7%
	GA3 500 mg/L	23.6%	51.1%	40.9%	24.0%	23.2%	24.0%	7.0%	15.9%	11.3%	3.1%	3.2%	3.9%

Table S4.3: Table with Log2FoldChange (log2FC) and p-value adjusted (p-adj) of the genes that belong to the GO categories related to response to hormones. The heatmap of these genes is showed in Fig. 4.13. Log2FC is calculated according to the following formula: expression level term1 - expression level term2.

Gene name	Gene description	N.C. 0 vs 7 DAT		EtOH 70% 0 vs 7 DAT		A3 300 mg/L 0 vs 7 DA		A3 500 mg/L 0 vs 7 DA		O.P. 0 vs 7 DAT		N.C. vs EtOH 7 DAT		C. vs GA3 300 mg/L 7 D	
		Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
Pav_sc0000174.1_g1690.1.mk	MLP423 MLP-like protein 423	-6.43777	4.14E-10	-6.64803	7.99E-11	-5.82262	1.23E-08	-5.22157	4.94E-07	-4.2509	8.46E-05	-0.21026	1	0.615154	0.796134
Pav_sc0000174.1_g1570.1.br	MLP423 MLP-like protein 423	-4.55028	0.241416	-4.18424	0.332165	-7.1444	0.002409	-4.58935	0.077411	-5.0023	0.070692	0.366039	1	-2.59412	0.409948
Pav_sc0001405.1_g970.1.mk	RD29B LTI65 CAP160 protein	-0.48465	0.933551	-1.19494	0.830896	-0.22383	0.922973	0.490322	0.81204	-5.10628	2.36E-05	-0.71029	1	0.260816	0.941259
Pav_sc0001105.1_g280.1.mk	SAUR-like auxin-responsive protein family	-1.20711	0.412894	-1.72732	0.111248	0.122869	0.93121	-0.93022	0.31967	-2.01058	0.01434	-0.52021	1	1.329979	0.252297
Pav_sc0007626.1_g030.1.br	SAUR-like auxin-responsive protein family	2.655777	0.012995	3.190264	0.001694	2.813314	0.002248	2.304027	0.0122	7.475129	2.25E-06	0.534487	1	0.157537	0.955159
Pav_sc0000174.1_g1390.1.mk	MLP423 MLP-like protein 423	-3.51535	0.431824	-4.05698	0.301666	-6.92499	0.00191	-4.54386	0.060869	-0.93727	0.860972	-0.54164	1	-3.40965	0.178606
Pav_co4053553.1_g010.1.mk	RD29B LTI65 CAP160 protein	-0.76707	0.861769	-1.95244	0.446165	-1.73527	0.251929	-0.45961	0.822592	-4.93753	3.04E-05	-1.18537	1	-0.9682	0.710082
Pav_sc0001687.1_g170.1.mk	AUX1 WAV5 PIR1 MAP1 Transmembrane amino acid transporter family protein	0.9595	0.048787	1.027048	0.02707	0.395307	0.421291	0.467352	0.306808	1.072572	0.006857	0.067548	1	-0.56419	0.353364
Pav_sc0000791.1_g150.1.mk	SAUR-like auxin-responsive protein family	1.371951	0.082204	1.219811	0.160168	1.385078	0.024694	1.48802	0.013157	3.880401	1.63E-10	-0.15214	1	0.013127	0.998867
Pav_sc0000174.1_g1700.1.br	MLP423 MLP-like protein 423	-4.21444	0.020312	-4.35815	0.014384	-4.89445	0.001065	-1.96947	0.296747	-1.61963	0.503349	-0.14371	1	-0.68	0.813341
Pav_sc0000176.1_g070.1.mk	unknown protein	0.62671	0.644718	0.495411	0.8475	1.79192	0.001034	1.265932	0.027488	1.649548	0.003473	-0.1313	1	1.16521	0.130215
Pav_sc0005224.1_g060.1.br	SAUR-like auxin-responsive protein family	3.34268	0.002716	2.829944	0.014317	-0.1761	0.914699	-0.64199	0.614455	3.50333	0.000518	-0.51274	1	-3.51878	0.002035
Pav_sc0000174.1_g1420.1.mk	MLP423 MLP-like protein 423	-1.49191	0.046571	-1.13433	0.228158	-1.48195	0.015235	-1.21437	0.052995	-1.30765	0.050765	0.357579	1	0.00996	0.999981
Pav_sc0000174.1_g1550.1.br	MLP423 MLP-like protein 423	-1.89639	0.128784	-2.74074	0.003763	-3.65145	3.53E-06	-2.73999	0.001047	-1.51932	0.169093	-0.84435	1	-1.75506	0.059329
Pav_sc0000174.1_g1860.1.br	MLP423 MLP-like protein 423	-4.80268	0.138632	-4.32933	0.232237	-6.00595	0.008009	-4.24019	0.086022	-3.8592	0.179494	0.473347	1	-1.20327	0.744725
Pav_sc0000752.1_g150.1.br	SAUR-like auxin-responsive protein family	1.606469	0.013826	1.546335	0.02019	0.882773	0.163634	0.697944	0.28627	1.781329	0.001491	-0.06013	1	-0.7237	0.447662
Pav_sc0006480.1_g020.1.br	SAUR-like auxin-responsive protein family	0.857988	0.761796	0.307384	0.993647	-2.98029	0.000399	-2.91539	0.000506	-0.14003	0.951391	-0.5506	1	-3.83828	6.44E-05
Pav_sc0000174.1_g1430.1.br	MLP423 MLP-like protein 423	1.342407	0.001001	1.337571	0.001074	1.10694	0.004145	0.919946	0.019778	2.073573	1.38E-09	-0.00484	1	-0.23547	0.787696
Pav_sc0000099.1_g230.1.mk	XERO1 dehydrin xero 1	-0.57913	0.739476	-1.01931	0.382947	0.74519	0.330867	0.563738	0.48118	-3.21018	6.73E-09	-0.44018	1	1.324319	0.119721
Pav_sc0000752.1_g160.1.br	SAUR-like auxin-responsive protein family	1.044496	0.499784	0.76971	0.763965	1.160164	0.177806	0.876998	0.325789	2.099146	0.009935	-0.27479	1	0.115668	0.957886
Pav_sc0005603.1_g090.1.br	SAUR-like auxin-responsive protein family	4.909716	5.32E-07	3.628807	6.24E-05	2.927441	0.000541	3.360099	6.47E-05	4.721228	1.55E-07	-1.28091	1	-1.98228	0.20356
Pav_sc0005175.1_g050.1.br	SAUR-like auxin-responsive protein family	2.104932	1.75E-05	2.005622	5.49E-05	0.680529	0.234336	0.687439	0.217205	2.176914	2E-06	-0.09931	1	-1.4244	0.018163
Pav_sc0005224.1_g050.1.br	SAUR-like auxin-responsive protein family	1.038105	0.624157	1.178939	0.584405	-0.30263	0.828669	-0.82033	0.443044	1.893966	0.077743	0.140834	1	-1.34073	0.32937
Pav_sc0000254.1_g1080.1.br	LEA14 LSR3 Late embryogenesis abundant protein	1.654315	0.018472	1.365906	0.090779	1.802009	0.002257	1.856636	0.001362	1.129863	0.109115	-0.28841	1	0.147695	0.924797
Pav_sc0000480.1_g730.1.mk	SAUR-like auxin-responsive protein family	4.165628	8.64E-07	2.9693	0.000712	5.998056	6.04E-10	4.862315	9.8E-09	2.179436	0.01179	-1.19633	1	1.832428	0.300701
Pav_sc0007626.1_g020.1.br	SAUR-like auxin-responsive protein family	1.038105	0.624157	1.178939	0.584405	-0.30263	0.828669	-0.82033	0.443044	1.893966	0.077743	0.140834	1	-1.34073	0.32937
Pav_sc0000129.1_g1480.1.mk	ARF19 IAA22 ARF11 auxin response factor 19	0.293334	0.704278	0.181523	0.945118	0.854959	0.003134	0.882998	0.001876	1.314196	7.02E-07	-0.11181	1	0.561625	0.175665
Pav_sc0000030.1_g1280.1.mk	LAX2 like AUXIN RESISTANT 2	0.414571	0.868659	-0.19068	0.99688	0.629633	0.503735	0.84772	0.319637	2.245502	0.001497	-0.60525	1	0.215062	0.909222
Pav_sc0000174.1_g1620.1.br	MLP423 MLP-like protein 423	-0.33995	0.882254	-0.00637	1	-1.97978	0.001223	-2.09832	0.000468	-0.50394	0.619751	0.333585	1	-1.63983	0.034629
Pav_sc0005175.1_g010.1.br	SAUR-like auxin-responsive protein family	3.323622	0.003478	3.049606	0.007937	1.364867	0.216876	1.521488	0.150164	2.895901	0.00489	-0.27402	1	-1.95876	0.202645
Pav_sc0002250.1_g170.1.mk	ARF9 auxin response factor 9	0.708602	0.23124	0.486945	0.597771	1.730248	4.92E-07	1.786856	1.69E-07	1.37352	0.000118	-0.22166	1	1.021646	0.027491
Pav_sc0000752.1_g180.1.br	SAUR-like auxin-responsive protein family	1.537282	0.150945	0.891802	0.609872	0.071	0.954783	-0.61108	0.456248	2.402914	0.003707	-0.64548	1	-1.46628	0.160177
Pav_sc0000752.1_g190.1.br	SAUR-like auxin-responsive protein family	3.0789	0.054616	1.775249	0.324951	1.079394	0.368904	0.773245	0.532993	2.499224	0.048991	-1.30365	1	-1.99951	0.316085
Pav_sc0000405.1_g040.1.mk	Peroxidase superfamily protein	-0.85988	0.751677	-0.35368	0.992592	-1.19741	0.292584	-1.91553	0.04404	0.114048	0.965428	0.5062	1	-0.33753	0.873448
Pav_sc0001461.1_g720.1.mk	CAT2 catalase 2	0.389505	0.721862	0.186611	0.980637	0.270271	0.633794	0.113222	0.865515	0.697724	0.156025	-0.20289	1	-0.11923	0.911051
Pav_sc0002056.1_g070.1.br	SAUR-like auxin-responsive protein family	4.568491	1.15E-05	4.93571	3.14E-06	4.767643	1.71E-06	4.169688	1.28E-05	5.458195	2.52E-07	0.367219	1	0.199152	0.953694
Pav_sc0000042.1_g420.1.mk	PHS1 dual specificity protein phosphatase family protein	0.146192	0.91428	0.319921	0.812217	-1.07777	0.000854	-0.92072	0.005044	-0.21788	0.705599	0.173729	1	-1.22396	0.000567
Pav_sc0000496.1_g400.1.mk	ZFP8 zinc finger protein 8	-0.53095	0.289508	-0.33049	0.724782	-1.23915	7.71E-06	-1.32136	1.24E-06	-0.75795	0.017171	0.200467	1	-0.7082	0.064409
Pav_sc0006480.1_g030.1.br	SAUR-like auxin-responsive protein family	0.0925	0.984833	-0.1429	1	-1.12852	0.210187	-1.22646	0.154343	-0.52319	0.700511	-0.2354	1	-1.22102	0.305712
Pav_sc0001801.1_g160.1.mk	unknown protein	-0.87433	0.578293	-0.96562	0.541052	0.503897	0.612374	-0.03516	0.982425	0.312643	0.823667	-0.09129	1	1.378229	0.167524
Pav_sc0000890.1_g670.1.mk	C2H2 and C2HC zinc fingers superfamily protein	-0.10289	0.975789	0.245944	0.990859	2.402922	0.001366	2.163098	0.003327	1.317094	0.115569	0.348831	1	2.505809	0.003532
Pav_sc0001248.1_g270.1.mk	ARF19 IAA22 ARF11 auxin response factor 19	-0.64328	0.09853	-0.36477	0.616673	-1.12989	2.39E-05	-0.94891	0.000542	-0.50114	0.150552	0.278504	1	-0.48661	0.245917
Pav_sc0005224.1_g030.1.br	SAUR-like auxin-responsive protein family	1.755574	0.193732	1.338246	0.451492	2.081948	0.024728	2.068065	0.023454	3.72558	2.91E-05	-0.41733	1	0.326373	0.887493
Pav_sc0008108.1_g010.1.mk	SAUR-like auxin-responsive protein family	-0.02188	1	0.296671	0.994317	-1.28463	0.226926	-1.23693	0.238686	-0.2836	0.885845	0.318549	1	-1.26275	0.387665
Pav_sc0000174.1_g1680.1.br	MLP423 MLP-like protein 423	-0.31512	0.718421	-0.29587	0.830896	-0.80158	0.014448	-0.6317	0.063371	-0.56374	0.148348	0.019254	1	-0.48646	0.323957
Pav_sc0001077.1_g500.1.br	SAUR-like auxin-responsive protein family	2.259358	0.163646	2.686414	0.062514	5.665901	6.16E-06	4.785503	3.49E-05	7.030295	6.55E-06	0.427056	1	3.406543	0.050042
Pav_sc0000363.1_g920.1.mk	ABI5 GIA1 Basic-leucine zipper (bZIP) transcription factor family protein	-0.106	0.914772	-0.26588	0.725019	-0.43007	0.109481	-0.44023	0.092309	0.466218	0.102589	-0.15988	1	-0.32407	0.414796
Pav_sc0000099.1_g130.1.mk	Peroxidase superfamily protein	-1.11926	0.540572	-1.0966	0.608146	-1.10534	0.280932	-0.78154	0.472914	-1.12669	0.329665	0.022662	1	0.013924	1
Pav_sc0000129.1_g1670.1.mk	SAUR-like auxin-responsive protein family	1.196081	0.091819	1.056483	0.181463	1.537093	0.003313	1.233184	0.021812	1.041203	0.089185	-0.1396	1	0.341012	0.767149
Pav_sc0000094.1_g590.1.mk	ARF4 auxin response factor 4	0.297374	0.826141	0.399063	0.824249	0.007909	0.996387	-0.11259	0.875244	-0.44336	0.482574	0.101689	1	-0.28946	0.751676

Pav_sc0000370.1_g080.1.mk	Disease resistance protein (TIR-NBS-LRR class) family	-0.03995	0.997264	0.424164	0.937454	-0.21629	0.831554	0.295665	0.76465	0.153034	0.914723	0.464111	1	-0.17634	0.915253
Pav_sc0000568.1_g290.1.br	SAUR-like auxin-responsive protein family	0.309234	0.959034	-1.28858	0.698402	0.353624	0.865209	0.191924	0.931077	-1.74582	0.213523	-1.59781	1	0.04439	0.995585
Pav_sc0008387.1_g010.1.br	Disease resistance protein (TIR-NBS-LRR class) family	0.207619	0.944858	0.728379	0.733097	-0.13515	0.900095	-0.22128	0.820976	0.891114	0.343907	0.52076	1	-0.34277	0.814311
Pav_sc0000254.1_g1090.1.mk	Late embryogenesis abundant protein	1.916325	0.122691	1.679926	0.228514	2.688162	0.002147	2.7267	0.001595	2.473849	0.00665	-0.2364	1	0.771837	0.661312
Pav_sc0002544.1_g080.1.mk	Peroxidase superfamily protein	-1.23699	0.327803	-1.36389	0.245954	-0.76654	0.410118	-0.32291	0.774322	0.819702	0.441057	-0.1269	1	0.470449	0.767565
Pav_sc0003845.1_g140.1.mk	APX2 APX1B ascorbate peroxidase 2	2.041004	0.643738	3.344486	0.384306	-0.18788	0.951294	2.654693	0.23101	5.176237	0.030679	1.303482	1	-2.22888	0.465853
Pav_sc0001003.1_g200.1.mk	DNA glycosylase superfamily protein	1.29434	0.046571	1.028452	0.190082	1.034984	0.063632	0.929154	0.096663	2.072351	1.61E-05	-0.26589	1	-0.25936	0.831762
Pav_sc0000164.1_g090.1.mk	ARR24 RR24 response regulator 24	-0.7104	0.417602	-0.3006	0.938612	-1.67248	0.000128	-1.5145	0.000599	-0.48973	0.473613	0.40979	1	-0.96209	0.119274
Pav_sc0000907.1_g860.1.mk	PLDP1 PLDZ1 PLDZETA1 PLD ZETA 1 phospholipase D P1	2.481759	3.3E-05	2.620659	9.16E-06	2.404972	2.27E-05	2.893482	1.49E-07	4.051215	3.35E-14	0.1389	1	-0.07679	0.966576
Pav_sc0000220.1_g1570.1.mk	PKS2 phytochrome kinase substrate 2	0.993104	0.378291	1.011008	0.383347	0.612307	0.435638	0.105398	0.921836	0.975639	0.214908	0.017903	1	-0.3808	0.791445
Pav_sc0000638.1_g470.1.br	ATPLC2 PLC2 phospholipase C 2	0.515335	0.643404	0.609846	0.574502	0.770377	0.134371	0.650211	0.213838	0.352784	0.637711	0.094511	1	0.255042	0.810377
Pav_sc0002828.1_g020.1.mk	Peroxidase superfamily protein	0.47447	0.718422	0.439481	0.836522	0.498354	0.421984	0.520423	0.383784	0.663374	0.309271	-0.03499	1	0.023884	0.991577
Pav_sc0000221.1_g330.1.mk	MLP28 MLP-like protein 28	-0.00316	1	-0.7007	0.568801	-2.81657	5.88E-10	-3.12136	2.84E-12	-1.4146	0.0084	-0.69754	1	-2.81341	8.92E-09
Pav_sc0010946.1_g010.1.br	RPM1 RPS3 NB-ARC domain-containing disease resistance protein	-0.39451	0.673447	-0.01663	1	-1.64423	8.42E-08	-1.53239	9.37E-07	0.052025	0.957001	0.377881	1	-1.24972	0.000244
Pav_sc0000700.1_g800.1.mk	REP AthREP Rab escort protein	-0.20907	0.895255	-0.10794	0.997635	-0.78989	0.078778	-0.8127	0.06299	-0.33934	0.612372	0.101127	1	-0.58082	0.374914
Pav_sc0000023.1_g180.1.mk	AFP3 ABI five binding protein 3	0.685857	0.42379	0.212587	0.979064	1.017272	0.030736	0.879572	0.065216	1.548457	0.000369	-0.47327	1	0.331415	0.724495
Pav_sc0000557.1_g1120.1.mk	CIPK6 SIP3 SNRK3.14 ATCIPK6 SOS3-interacting protein 3	-0.16778	0.931578	-0.59981	0.555681	0.57203	0.280045	0.566937	0.272243	0.449336	0.49509	-0.43203	1	0.73981	0.260552
Pav_sc0000017.1_g020.1.mk	Peroxidase superfamily protein	0.459545	0.673071	0.513242	0.663394	0.330217	0.572808	0.929083	0.039058	0.587238	0.306996	0.053697	1	-0.12933	0.909454
Pav_sc0000044.1_g490.1.mk	ARO1 armadillo repeat only 1	0.434978	0.209184	0.328286	0.485917	1.571693	2.72E-16	1.696193	6.47E-19	0.499753	0.04486	-0.10669	1	1.136715	1.89E-07
Pav_sc0001836.1_g160.1.mk	disease resistance protein (TIR-NBS-LRR class) putative	-0.25927	0.76382	-0.25858	0.862542	0.015834	0.982943	0.139146	0.761416	-0.0372	0.960966	0.00069	1	0.275106	0.638337
Pav_sc0004298.1_g150.1.mk	disease resistance protein (TIR-NBS-LRR class) putative	-0.10859	0.937342	0.127716	0.987006	0.111378	0.824972	0.206079	0.630788	-0.05955	0.934747	0.236304	1	0.219965	0.735923
Pav_sc0000848.1_g210.1.mk	Rho GTPase activating protein with PAK-box	-0.08685	0.966774	0.0716	1	0.321848	0.584665	0.301814	0.60645	0.023128	0.986798	0.158448	1	0.408696	0.615343
Pav_sc0006347.1_g040.1.br	Disease resistance protein (TIR-NBS-LRR class) family	0.540633	0.493439	0.292639	0.896086	0.717899	0.099234	0.829681	0.048318	0.689271	0.1463	-0.24799	1	0.177265	0.8594
Pav_sc0000383.1_g1100.1.mk	Protein of unknown function DUF617	0.299402	0.728292	0.294367	0.823318	0.58534	0.091213	0.639303	0.054211	-0.05233	0.945727	-0.00504	1	0.285938	0.642521
Pav_co4017443.1_g010.1.mk	Peroxidase superfamily protein	-0.08648	0.958468	-0.10636	0.994317	0.348473	0.424246	0.349398	0.409281	-0.28852	0.595124	-0.01988	1	0.434951	0.444359
Pav_co4088935.1_g020.1.mk	Peroxidase superfamily protein	-0.14383	0.902998	-0.26892	0.8475	0.324963	0.395421	0.208753	0.616983	-0.39131	0.343907	-0.12509	1	0.468792	0.313503
Pav_sc0004298.1_g070.1.mk	Disease resistance protein (TIR-NBS-LRR class) family	-0.03093	0.99207	0.166886	0.982874	0.788011	0.058118	0.762105	0.063425	-0.10934	0.891684	0.197821	1	0.818946	0.120001
Pav_sc0000848.1_g190.1.mk	Rho GTPase activating protein with PAK-box	-0.16811	0.941341	-0.03191	1	0.403848	0.547692	0.356179	0.598619	-0.20966	0.831183	0.136197	1	0.571954	0.507234
Pav_sc0000631.1_g180.1.mk	Plant protein of unknown function (DUF641)	0.427223	0.732065	0.387346	0.862542	0.703537	0.175533	1.146754	0.013267	0.057932	0.959598	-0.03988	1	0.276313	0.788492
Pav_sc0000584.1_g360.1.mk	Plant protein of unknown function (DUF641)	-0.03123	0.989791	-0.01826	1	0.294115	0.504359	0.357908	0.382464	-0.08692	0.90466	0.012961	1	0.325341	0.603807
Pav_sc0000129.1_g1210.1.mk	unknown protein	-0.14742	0.91747	-0.12435	0.990859	-0.15595	0.773481	-0.40583	0.320943	-0.262	0.643194	0.023064	1	-0.00854	0.998463
Pav_sc0000375.1_g140.1.mk	Plant protein of unknown function (DUF641)	0.384102	0.708735	0.335863	0.85714	0.694276	0.104726	0.590407	0.173535	-0.35326	0.550202	-0.04824	1	0.310174	0.693889
Pav_sc0000800.1_g510.1.mk	AHP4 HPT phosphotransmitter 4	0.031866	0.998194	-0.15936	0.999232	0.55132	0.565195	0.097998	0.937016	-0.37715	0.753355	-0.19123	1	0.519454	0.722241
Pav_sc0000094.1_g580.1.mk	MLO3 ATMLO3 Seven transmembrane MLO family protein	-0.26871	0.915063	-0.6455	0.754459	1.348291	0.048987	0.671127	0.385829	0.307508	0.79541	-0.37679	1	1.616998	0.043996
Pav_sc0000103.1_g420.1.mk	ALPHA DOX2 alpha dioxygenase	0.322322	0.876649	0.218513	0.989253	1.644307	0.004654	1.715047	0.002616	-0.01748	0.995994	-0.10381	1	1.321984	0.08621
Pav_co4075411.1_g010.1.br	Disease resistance protein (TIR-NBS-LRR class) family	-0.31231	0.954063	-0.37638	0.993615	-0.75683	0.613717	-0.45428	0.790913	-1.49236	0.271903	-0.06407	1	-0.44452	0.860597
Pav_sc0000375.1_g270.1.mk	Peroxidase superfamily protein	-4.87548	2.69E-06	-4.64921	1.1E-05	-3.88705	0.000179	-3.72293	0.00033	-2.10347	0.098379	0.226276	1	0.988434	0.636107
Pav_sc0001582.1_g370.1.mk	ARR17 RR17 response regulator 17	-0.08853	0.998153	-2.08273	0.55402	3.062562	0.141095	2.059084	0.304982	-1.92177	0.362648	-1.9942	1	3.151093	0.248906
Pav_sc0002635.1_g050.1.mk	unknown protein	-4.40807	0.322712	-5.07672	0.194725	-9.83872	3.56E-05	-7.23656	0.003733	-5.82208	0.038844	-0.66865	1	-5.43065	0.039353
Pav_sc0006098.1_g170.1.mk	Serine protease inhibitor potato inhibitor I-type family protein	-6.27407	0.031419	-8.62211	0.000495	-11.899	2.77E-08	-10.5986	1.14E-06	-8.85342	8.57E-05	-2.34804	1	-5.62488	0.010222
Pav_co4081715.1_g010.1.br	Serine protease inhibitor potato inhibitor I-type family protein	-5.20239	0.198801	-6.4613	0.055906	-8.41743	0.001032	-7.83155	0.002294	-6.35953	0.025856	-1.25891	1	-3.21505	0.348355
Pav_sc0006098.1_g120.1.br	Serine protease inhibitor potato inhibitor I-type family protein	-5.20239	0.198801	-6.4613	0.055906	-8.41743	0.001032	-7.83155	0.002294	-6.35954	0.025856	-1.25891	1	-3.21505	0.348356
Pav_sc0002722.1_g030.1.mk	Peroxidase superfamily protein	-18.5279	4.06E-10	-19.5134	1.76E-11	-21.2408	2.96E-14	-20.6776	1.64E-13	-19.0382	2.08E-11	-0.98552	1	-2.71294	0.631088
Pav_sc0001502.1_g370.1.mk	Peroxidase superfamily protein	-21.5866	7.24E-17	-21.1897	3.81E-16	-21.3717	7.2E-17	-21.3359	7.44E-17	-20.0282	7.13E-15	0.396804	1	0.21487	0.980733

C. vs GA3 500 mg/L 7 D		N.C. vs O.P. 7 DAT		70 % vs GA3 300 mg/L		70 % vs GA3 500 mg/L		tOH 70 % vs O.P. 7 DA		0 mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 7 D		3 500 mg/L vs O.P. 7 D		N.C. 7 vs 14 DAT		EtOH 70% 7 vs 14 DAT		A3 300 mg/L 7 vs 14 DA		A3 500 mg/L 7 vs 14 D	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
1.216205	0.430538	2.186869	0.149917	0.82541	0.593534	1.426461	0.258569	2.397124	0.084478	0.601051	1	1.571714	0.257733	0.970663	0.591347	3.437835	0.002452	2.3432	0.066306	1.641149	0.138048	0.903979	0.471753
-0.03907	0.994413	-0.45202	0.948278	-2.96016	0.22482	-0.40511	0.912492	-0.81806	0.872131	2.555045	1	2.142093	0.43663	-0.41295	0.934082	-0.63767	0.918098	-1.69867	0.591019	-0.4302	0.875888	-1.63241	0.481948
0.974971	0.649913	-4.62163	0.000896	0.97111	0.616564	1.685265	0.29051	-3.91134	0.007841	0.714155	1	-4.88245	0.000174	-5.5966	1.47E-05	-4.02886	0.004481	-4.06779	0.003443	-6.13103	1.67E-07	-2.99996	0.01928
0.276891	0.851669	-0.80347	0.649301	1.850185	0.037689	0.797097	0.4205	-0.28326	0.888685	-1.05309	1	-2.13344	0.012517	-1.08036	0.337882	-1.09163	0.407937	-0.66244	0.590994	-0.632	0.501083	0.30686	0.776943
-0.35175	0.848229	4.819352	0.025442	-0.37695	0.829901	-0.88624	0.504144	4.284865	0.059562	-0.50929	1	4.661814	0.016551	5.171102	0.007843	3.062723	0.062556	1.923712	0.243098	-1.54081	0.119466	0.371613	0.783647
-1.02851	0.746743	2.578077	0.580596	-2.86801	0.186829	-0.48688	0.880245	3.119713	0.370384	2.381134	1	5.987723	0.009859	3.606589	0.222873	2.117793	0.624129	4.080956	0.176888	5.997896	0.003369	2.630384	0.220426
0.307462	0.903299	-4.17046	0.002819	0.217171	0.927207	1.492835	0.344886	-2.98508	0.064006	1.275664	1	-3.20225	0.021375	-4.47792	0.000676	-3.66608	0.00988	-3.61045	0.008903	-3.89755	0.000972	-2.18627	0.095369
-0.49215	0.375464	0.113072	0.931753	-0.63174	0.186767	-0.5597	0.223973	0.045524	0.973365	0.072044	1	0.677264	0.159987	0.60522	0.266011	-0.15895	0.889885	-0.55284	0.309259	-0.94571	0.01144	-1.02927	0.005506
0.116069	0.927246	2.50845	0.000981	0.165267	0.880286	0.268209	0.780054	2.66059	0.000266	0.102942	1	2.495322	0.000513	2.392381	0.001437	0.328765	0.840905	0.189194	0.876152	-2.87159	5.74E-08	-3.06446	6.17E-09
2.244972	0.19716	2.594815	0.202323	-0.53629	0.799215	2.388679	0.111915	2.738522	0.13926	2.924972	1	3.274815	0.029417	0.349843	0.918107	2.205081	0.280926	1.73003	0.344647	2.497175	0.055942	-2.19364	0.111695
0.639221	0.438798	1.022838	0.246945	1.296509	0.044055	0.770521	0.25159	1.154138	0.136056	-0.52599	1	-0.14237	0.902657	0.383617	0.717304	0.217707	0.89576	-0.48875	0.587054	-0.68227	0.270262	-0.57024	0.377258
-3.98467	0.00019	0.160651	0.970659	-3.00605	0.005328	-3.47194	0.000695	0.673386	0.785464	-0.46589	1	3.679433	0.000503	4.145324	6.89E-05	-0.32805	0.927053	-0.91373	0.5785	0.205706	0.882459	0.793287	0.475472
0.27754	0.794252	0.184262	0.929993	-0.34762	0.711892	-0.08004	0.944596	-0.17332	0.920002	0.26758	1	0.174302	0.881331	-0.09328	0.95469	0.027455	0.994672	-0.76907	0.368743	-0.87261	0.166211	-0.99674	0.10633
-0.8436	0.44056	0.377071	0.877797	-0.91071	0.318391	0.000751	1	1.22142	0.288283	0.911463	1	2.132132	0.007597	1.220669	0.242801	-0.03374	0.995052	0.281998	0.84166	0.293006	0.753656	-1.05006	0.16005
1	1	0.943481	0.867003	-1.67662	0.499693	1	1	0.470133	0.930671	1.765758	1	2.146749	0.401086	0.380991	0.935751	0.181021	0.982108	0.210862	0.954725	0.327069	0.90024	-0.97961	0.676505
-0.90853	0.234133	0.174859	0.930731	-0.66356	0.382902	-0.84839	0.206859	0.234993	0.874408	-0.18483	1	0.898556	0.226447	1.083385	0.148932	0.675805	0.551344	0.443351	0.647277	-0.93313	0.106943	-0.20838	0.790436
-3.77337	8.13E-05	-0.99802	0.667069	-3.28767	0.000337	-3.22277	0.000407	-0.44742	0.845574	0.064902	1	2.840257	0.001614	2.775356	0.003054	-2.37128	0.040412	-1.12932	0.398465	-0.73442	0.436464	-0.69401	0.472792
-0.42246	0.466433	0.731166	0.226476	-0.23063	0.706332	-0.41763	0.399586	0.736001	0.187778	-0.18699	1	0.966633	0.027475	1.153627	0.007734	-0.46843	0.52166	-0.76694	0.120291	-2.79624	5.25E-17	-2.75728	1.65E-16
1.142867	0.158922	-2.63105	3.53E-05	1.764502	0.009832	1.58305	0.01918	-2.19087	0.000998	-0.18145	1	-3.95537	3.06E-12	-3.77392	3.18E-11	-2.45818	7.58E-05	-2.25886	0.000392	-4.21821	7.86E-15	-3.33974	2.21E-09
-0.1675	0.914307	1.054651	0.511294	0.390454	0.756258	0.107288	0.940882	1.329436	0.265764	-0.28317	1	0.938983	0.411276	1.222148	0.277049	1.575526	0.179476	1.691909	0.088138	-0.749	0.38943	-0.55873	0.546185
-1.54962	0.309176	-0.18849	0.96499	-0.70137	0.624038	-0.26871	0.878453	1.092421	0.588533	0.432658	1	1.793788	0.171411	1.361129	0.400086	-0.94359	0.711405	-0.24603	0.902049	-2.75874	0.000853	-2.73148	0.001355
-1.41749	0.014395	0.071982	0.971349	-1.32509	0.0175	-1.31818	0.014712	0.171292	0.904997	0.00691	1	1.496385	0.005559	1.489475	0.007937	-0.30825	0.814547	0.518517	0.52205	-0.9713	0.047324	-0.0829	0.912865
-1.85843	0.088909	0.855861	0.724795	-1.48157	0.176801	-1.99927	0.03925	0.715027	0.722875	-0.5177	1	2.196593	0.037577	2.714294	0.007874	-0.15707	0.964734	1.356358	0.340222	-0.51561	0.627971	0.346765	0.767082
0.202322	0.860184	-0.52445	0.732135	0.436103	0.627787	0.49073	0.548007	-0.23604	0.877097	0.054627	1	-0.67215	0.437152	-0.72677	0.435259	-0.14483	0.945542	-0.44933	0.654559	-2.53589	3.56E-06	-1.04765	0.090035
0.696687	0.68581	-1.98619	0.121151	3.028756	0.014688	1.893015	0.08675	-0.78986	0.636648	-1.13574	1	-3.81862	0.000801	-2.68288	0.0147	-1.80459	0.161688	-1.18838	0.325143	-3.1266	0.00363	-1.52122	0.149103
-1.85843	0.088909	0.855861	0.724795	-1.48157	0.176801	-1.99927	0.03925	0.715027	0.722875	-0.5177	1	2.196593	0.037577	2.714294	0.007874	-0.15707	0.964734	1.356358	0.340222	-0.51561	0.627971	0.346765	0.767082
0.589664	0.106966	1.020862	0.001306	0.673436	0.044588	0.701475	0.027603	1.132673	0.000163	0.028039	1	0.459237	0.226868	0.431198	0.304956	0.749718	0.033792	0.796611	0.015474	-0.29884	0.369233	-0.57125	0.053005
0.433149	0.725419	1.830931	0.044744	0.82031	0.391604	1.038397	0.221655	2.436179	0.001639	0.218087	1	1.615869	0.050741	1.397782	0.13223	1.672469	0.065651	0.334238	0.803288	-0.56979	0.50273	-0.83317	0.297256
-1.75836	0.014395	-0.16399	0.941778	-1.97341	0.003338	-2.09195	0.001231	-0.49758	0.698094	-0.11854	1	1.475836	0.038742	1.594374	0.030123	-0.97429	0.342469	-1.3282	0.085806	-1.2168	0.053973	-0.89877	0.179212
-1.80213	0.201284	-0.42772	0.910686	-1.68474	0.189958	-1.52812	0.216524	-0.1537	0.964176	0.156621	1	1.531034	0.2605	1.374414	0.376218	-2.01055	0.192548	-0.61725	0.744274	-1.16654	0.264518	-0.2561	0.857889
1.078254	0.013105	0.664918	0.277605	1.243303	0.001915	1.299911	0.000899	0.886575	0.069935	0.056608	1	-0.35673	0.536755	-0.41334	0.50376	0.737501	0.1707	0.669415	0.17514	0.628678	0.118249	0.257275	0.595952
-2.14837	0.009032	0.865632	0.687885	-0.8208	0.378844	-1.50289	0.045937	1.511112	0.224785	-0.68208	1	2.331914	0.008754	3.013998	0.000273	0.041763	0.993322	0.412652	0.757446	-1.52918	0.01442	-0.35476	0.66531
1	1	-0.57968	0.90399	1	1	1	1	0.723976	0.798617	-0.30615	1	1.41983	0.397037	1.72598	0.299556	-0.44454	0.92253	0.867953	0.678489	-0.55116	0.663968	-0.25548	0.858023
-1.05564	0.372453	0.97393	0.67836	-0.84373	0.508222	-1.56184	0.114637	0.467731	0.850128	-0.71812	1	1.311457	0.314126	2.029574	0.079477	-0.46495	0.836698	-0.71762	0.630002	-1.47339	0.061782	-0.55521	0.545248
-0.27628	0.68218	0.308219	0.775778	0.083659	0.911471	-0.07339	0.921889	0.511113	0.451843	-0.15705	1	0.427453	0.470468	0.584502	0.315015	-0.95902	0.058753	-1.24706	0.004117	-2.37767	2.12E-11	-2.45927	3.54E-12
-0.3988	0.85748	0.889703	0.804448	-0.16807	0.943113	-0.76602	0.658468	0.522485	0.876991	-0.59796	1	0.690551	0.765551	1.288507	0.540535	0.065932	0.991884	0.694356	0.772864	-2.85746	0.00731	-1.70428	0.125322
-1.06692	0.003404	-0.36407	0.624459	-1.39769	2.3E-05	-1.24065	0.00025	-0.5378	0.29125	0.157048	1	0.859897	0.019728	0.702849	0.092993	-0.47631	0.405206	-0.36163	0.475888	0.064582	0.898024	-0.16415	0.710869
-0.7904	0.022276	-0.22699	0.776701	-0.90867	0.00474	-0.99087	0.001264	-0.42746	0.37257	-0.0822	1	0.481207	0.204008	0.56341	0.146841	-0.27558	0.670847	-0.13824	0.806349	0.311048	0.353393	0.202672	0.585082
-1.31895	0.200109	-0.61569	0.771599	-0.98562	0.325953	-1.08356	0.239028	-0.3803	0.841074	-0.09794	1	0.605321	0.613866	0.703261	0.589322	-0.67218	0.707994	0.715544	0.586982	-1.23098	0.105625	-1.0325	0.190562
0.839169	0.412371	1.186975	0.314728	1.46952	0.075567	0.93046	0.270581	1.278266	0.211959	-0.53906	1	-0.19125	0.896697	0.347806	0.8168	0.231942	0.914331	0.627469	0.571555	-2.0837	0.001836	-0.08945	0.936909
2.265986	0.007015	1.419981	0.17133	2.156978	0.010382	1.917155	0.018536	1.07115	0.337565	-0.23982	1	-1.08583	0.316891	-0.846	0.504668	0.263525	0.894459	-0.28414	0.82709	-1.10014	0.19959	-1.31885	0.09808
-0.30563	0.47259	0.142135	0.874001	-0.76512	0.015017	-0.58413	0.066703	-0.13637	0.844944	0.180983	1	0.628748	0.056366	0.447766	0.261987	0.332729	0.543933	0.460832	0.239907	1.065474	5.4E-05	1.110133	2.79E-05
0.312491	0.857297	1.970006	0.168264	0.743702	0.5739	0.72982	0.555225	2.387335	0.051596	-0.01388	1	1.643632	0.184016	1.657515	0.213704	3.428228	0.004072	4.019445	0.000406	0.787813	0.478193	0.810765	0.469664
-1.21505	0.344319	-0.26172	0.935851	-1.5813	0.161036	-1.5336	0.14887	-0.58027	0.782915	0.047702	1	1.001033	0.441966	0.953331	0.516599	-0.19297	0.955478	0.623917	0.713943	-0.6714	0.51952	-0.63855	0.554002
-0.31658	0.517584	-0.24862	0.771599	-0.50571	0.203971	-0.33584	0.413358	-0.26788	0.676246	0.169877	1	0.237835	0.645734	0.067959	0.933471	-0.58951	0.208681	-0.45305	0.31339	-1.49452	1.42E-07	-2.03039	1.53E-13
1	1	4.770937	0.022047	2.979487	0.063646	1	1	4.343881	0.042437	-0.8804	1	1.364394	0.657687	2.244792	0.418312	4.259363	0.015865	5.250243	0.01162	-0.73639	0.707855	1.527337	0.421296
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0.337721	0.832494	-0.00743	1	-0.00874	0.996675	0.315058	0.82529	-0.03009	0.995783	0.323797	1	-0.02135	0.9938	-0.34515	0.854247	-0.52116	0.810334	-0.1763	0.921824	-1.49658	0.087899	-1.70392	0.046769
0.037102	0.976481	-0.15488	0.931575	0.48061	0.524469	0.176701	0.846047	-0.01528	0.99709	-0.30391	1	-0.49589	0.536335	-0.19198	0.872889	0.075836	0.971524	0.267406	0.783018	-0.46076	0.458651	-0.43123	0.499038
-0.40996	0.532861	-0.74073	0.28878	-0.39115	0.520527	-0.51165	0.33356	-0.84242	0.161779	-0.1205	1	-0.45127	0.471499	-0.33077	0.66932	-0.24317	0.827307	-0.2102	0.789911	0.893037	0.036075	0.414046	0.404735

0.335612	0.769765	0.192981	0.930731	-0.64045	0.475703	-0.1285	0.918167	-0.27113	0.872131	0.511954
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0.810375	0.5615	0.557523	0.829505	1.008236	0.40025	1.046774	0.345588	0.793923	0.647845	0.038538
0.914076	0.387675	2.056689	0.021637	0.59735	0.577197	1.040978	0.234125	2.183591	0.009472	0.443628
0.613689	0.876662	3.135233	0.492384	-3.53236	0.161585	-0.68979	0.863819	1.831751	0.73069	2.842569
-0.36519	0.672095	0.778012	0.411474	0.006532	0.995684	-0.0993	0.918167	1.043899	0.149247	-0.10583
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-0.88771	0.308054	-0.01747	0.997441	-0.3987	0.686446	-0.90561	0.223519	-0.03537	0.991746	-0.50691
0.134876	0.878417	-0.16255	0.918664	0.160531	0.842735	0.040365	0.964195	-0.25706	0.809613	-0.12017
0.045953	0.967089	0.188904	0.910539	0.058873	0.949074	0.080942	0.930052	0.223893	0.852877	0.022069
-3.1182	3.64E-11	-1.41144	0.026868	-2.11586	2.87E-05	-2.42066	1.06E-06	-0.71389	0.391923	-0.30479
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-0.60363	0.286165	-0.13027	0.929196	-0.68195	0.179011	-0.70476	0.1365	-0.2314	0.810212	-0.02281
0.193714	0.815851	0.8626	0.214934	0.804685	0.142112	0.666985	0.211141	1.33587	0.01004	-0.1377
0.734718	0.208822	0.617117	0.467739	1.17184	0.016633	1.166748	0.013905	1.049147	0.066277	-0.00509
0.469538	0.47222	0.127693	0.930945	-0.18302	0.80326	0.415841	0.468821	0.073996	0.95666	0.598866
1.261216	2.63E-09	0.064776	0.932927	1.243407	4.13E-09	1.367907	2.69E-11	0.171467	0.711877	0.124501
0.398418	0.352741	0.222069	0.785317	0.274417	0.523514	0.397728	0.277887	0.22138	0.727813	0.123311
0.314666	0.501716	0.049035	0.96499	-0.01634	0.978984	0.078362	0.889657	-0.18727	0.78873	0.094701
0.388662	0.561732	0.109975	0.942605	0.250248	0.713198	0.230213	0.721188	-0.04847	0.974059	-0.02003
0.289048	0.679189	0.148637	0.916201	0.42526	0.440743	0.537042	0.278843	0.396632	0.599814	0.111782
0.339901	0.473153	-0.35173	0.609383	0.290973	0.518364	0.344936	0.391172	-0.34669	0.540879	0.053963
0.435876	0.372676	-0.20205	0.841603	0.454832	0.303389	0.455757	0.269419	-0.18216	0.821589	0.000925
0.352582	0.429214	-0.24748	0.755705	0.593881	0.098994	0.477672	0.177567	-0.12239	0.87454	-0.11621
0.79304	0.101303	-0.0784	0.95256	0.621125	0.198739	0.595219	0.193876	-0.27622	0.72896	-0.02591
0.524285	0.482568	-0.04156	0.983804	0.435757	0.542178	0.388088	0.572827	-0.17775	0.895303	-0.04767
0.719531	0.24899	-0.36929	0.756	0.31619	0.648571	0.759408	0.156282	-0.32941	0.730591	0.443218
0.389134	0.428172	-0.0557	0.962918	0.31238	0.509991	0.376173	0.372001	-0.06866	0.946139	0.063793
-0.25841	0.644144	-0.11459	0.924374	-0.0316	0.961964	-0.28147	0.544625	-0.13765	0.875406	-0.24987
0.206305	0.763187	-0.73736	0.208852	0.358414	0.517001	0.254545	0.650622	-0.68912	0.220873	-0.10387
0.066131	0.966015	-0.40902	0.832578	0.710683	0.460126	0.257361	0.817965	-0.21779	0.904997	-0.45332
0.939833	0.273755	0.576215	0.708447	1.993791	0.003609	1.316626	0.05807	0.953008	0.323124	-0.67716
1.392725	0.046532	-0.3398	0.843324	1.425793	0.030408	1.496534	0.017383	-0.23599	0.87331	0.070741
1	1	-1.18005	0.580312	1	1	1	1	-1.11599	0.526665	0.302548
1.152551	0.475444	2.772014	0.043347	0.762158	0.640538	0.926275	0.52607	2.545738	0.068929	0.164117
2.147615	0.376754	-1.83323	0.571875	5.145295	0.009707	4.141817	0.021205	0.160968	0.974945	-1.00348
-2.82849	0.345549	-1.41401	0.81612	-4.76201	0.047114	-2.15984	0.422937	-0.74536	0.897688	2.602162
-4.32453	0.057737	-2.57935	0.481858	-3.27684	0.150005	-1.97649	0.406925	-0.23131	0.970403	1.300354
-2.62916	0.410283	-1.15715	0.862621	-1.95613	0.528255	-1.37025	0.66583	0.101766	0.992838	0.585885
-2.62916	0.410284	-1.15715	0.862621	-1.95613	0.528255	-1.37025	0.66583	0.101766	0.992838	0.585885
-2.14976	0.658243	-0.51039	0.961758	-1.72742	0.705044	-1.16424	0.806532	0.475135	0.958747	0.563183
0.25068	0.966015	1.558339	0.841078	-0.18193	0.971867	-0.14612	0.976689	1.161535	0.858603	0.03581

1	0.369323	0.73445	-0.14263	0.931911	-0.21462	0.910707	-0.793	0.391302	-3.08732	4.15E-10	-3.48333	1.67E-11
1	-2.09944	0.138303	-1.93774	0.206222	-0.90248	0.752815	-0.92124	0.563128	-1.64764	0.188499	-1.5118	0.227427
1	1.026268	0.256109	1.112391	0.237889	0.295683	0.874529	-0.49555	0.666525	-0.43121	0.547822	-0.55184	0.419268
1	-0.21431	0.908405	-0.25285	0.904333	1.153344	0.476429	1.08776	0.404457	-2.00883	0.022181	-0.08963	0.95162
1	1.586241	0.065488	1.142613	0.271435	1.353681	0.209148	0.400136	0.760924	-0.55956	0.523858	-1.17335	0.127077
1	5.364113	0.03023	2.521544	0.525027	1.358416	0.807978	-1.33149	0.727982	-0.2389	0.926589	-2.94534	0.147321
1	1.037367	0.095453	1.143197	0.07587	-0.21233	0.890326	-0.08579	0.936151	-0.39235	0.528757	-0.70684	0.208087
1	1.182752	0.01923	1.024766	0.067145	-0.28135	0.808495	-0.53128	0.438333	0.477304	0.350704	0.555887	0.268287
1	1.646243	0.018628	1.157734	0.169096	1.724401	0.019705	2.001297	0.003906	1.426507	0.021098	1.258601	0.050032
1	0.363332	0.743916	0.870242	0.345064	0.025267	0.995738	-0.43728	0.685402	-2.00791	0.000292	-1.44308	0.010769
1	-0.41759	0.551322	-0.29743	0.734739	-1.06316	0.066128	-0.66268	0.300755	-1.82854	1.27E-05	-1.78103	2.3E-05
1	0.16502	0.862298	0.142951	0.901887	-0.43664	0.684146	-1.21366	0.029751	-1.74652	8.67E-05	-2.12304	1.16E-06
1	1.401971	0.010843	1.706763	0.001411	-2.48435	2.31E-07	-1.67177	0.001926	-0.78867	0.133189	-0.76193	0.150571
1	1.696255	1.64E-07	1.584418	2.62E-06	0.409087	0.572517	0.759477	0.163893	0.175713	0.636343	-0.16509	0.666344
1	0.450551	0.449102	0.473365	0.466275	-0.74247	0.220869	-0.55428	0.34639	-0.33539	0.482179	-0.30656	0.535696
1	0.531185	0.412178	0.668886	0.303319	0.579581	0.478759	0.158304	0.859817	-0.39514	0.456018	-0.66742	0.165051
1	-0.12269	0.890008	-0.1176	0.911073	0.141648	0.919664	-0.06156	0.946663	-1.48768	0.000312	-1.62075	7.76E-05
1	0.257021	0.729287	-0.34185	0.666053	-0.74655	0.252901	-1.25487	0.007348	-1.6042	4.1E-05	-2.60714	4.19E-12
1	-1.07194	5.78E-07	-1.19644	1.25E-08	0.16304	0.764395	0.297037	0.355199	-0.16696	0.541247	-0.2281	0.383711
1	-0.05304	0.934716	-0.17635	0.769371	0.564568	0.200957	0.308129	0.507234	0.525671	0.094015	0.79199	0.007811
1	-0.17093	0.752416	-0.26563	0.624642	0.319765	0.616636	0.048777	0.939352	0.836817	0.005148	0.820771	0.006421
1	-0.29872	0.673992	-0.27869	0.73345	0.235446	0.836698	0.295744	0.685402	1.31791	0.001237	1.332622	0.001094
1	-0.02863	0.978143	-0.14041	0.886999	-0.37395	0.654691	-0.06402	0.935409	-0.40763	0.375977	-0.83917	0.037139
1	-0.63767	0.090502	-0.69163	0.078202	-0.1065	0.913164	0.089698	0.888306	0.454904	0.1836	0.578576	0.078814
1	-0.637	0.126439	-0.63792	0.1552	0.112559	0.915977	0.148195	0.820465	0.486845	0.183454	0.601218	0.088134
1	-0.71627	0.03829	-0.60006	0.125153	0.175968	0.823202	0.279531	0.561689	0.385601	0.245901	0.680288	0.023704
1	-0.89735	0.042943	-0.87144	0.065812	0.337216	0.688553	-0.1188	0.876088	0.197233	0.707855	0.112575	0.847311
1	-0.61351	0.38079	-0.56584	0.475202	0.204178	0.889863	0.363025	0.66503	1.533755	0.001215	1.523531	0.001323
1	-0.6456	0.289497	-1.08882	0.04847	0.147106	0.919015	0.028086	0.977506	0.795047	0.101249	0.417173	0.459438
1	-0.38104	0.42696	-0.44483	0.375535	0.11311	0.913164	0.333272	0.520655	1.063168	0.000768	1.036077	0.001097
1	-0.10605	0.874285	0.143824	0.845762	0.189296	0.836698	0.306081	0.582469	1.324311	8.78E-05	1.202928	0.000305
1	-1.04754	0.013446	-0.94367	0.039674	0.069193	0.96243	0.37563	0.537873	1.544317	3.55E-05	1.015148	0.008422
1	-0.92847	0.324699	-0.47515	0.706268	-0.17658	0.93986	0.649008	0.551452	-0.39685	0.660775	0.851408	0.299725
1	-1.04078	0.209133	-0.36362	0.773357	1.07256	0.268353	1.149531	0.152314	1.240471	0.089695	2.03113	0.002638
1	-1.66178	0.008339	-1.73252	0.007381	-0.04331	0.988449	0.568322	0.530746	0.823341	0.194916	0.4065	0.582748
1	1	1	1	1	0.261361	0.94674	0.303581	0.890836	0.110827	0.947513	1.015232	0.4759
1	1.78358	0.194324	1.619463	0.292784	3.615325	0.001625	2.465909	0.057734	3.346631	0.001107	3.990877	8.02E-05
1	-4.98433	0.01256	-3.98085	0.045658	-1.31579	0.703076	-0.99916	0.693996	0.055859	0.993391	0.019374	1
1	4.016643	0.107724	1.414481	0.718099	2.583554	0.611089	5.080768	0.119331	8.836298	0.00018	4.331572	0.057857
1	3.045535	0.198916	1.745181	0.584178	0.27111	0.971524	2.900657	0.266416	5.350034	0.00281	5.821317	0.001405
1	2.057898	0.531244	1.472014	0.718816	2.843518	0.508081	5.5994	0.068946	6.954433	0.00249	6.842367	0.004659
1	2.057898	0.531244	1.472014	0.718816	2.843518	0.508081	5.5994	0.068946	6.954433	0.00249	6.842367	0.004659
1	2.202557	0.640739	1.639374	0.778705	2.501661	0.740149	-2.55198	0.584732	5.146463	0.11794	4.511783	0.183016
1	1.34347	0.773542	1.30766	0.811822	2.542336	0.653428	-0.29949	0.954766	0.379602	0.926906	2.471972	0.425315

O.P. 7 vs 14 DAT		N.C. vs EtOH 14 DAT		. vs GA3 300 mg/L 14		. vs GA3 500 mg/L 14		N.C. vs O.P. 14 DAT		40 % vs GA3 300 mg/L		40 % vs GA3 500 mg/L		OH 140 % vs O.P. 14 D		mg/L vs GA3 500 mg/L		300 mg/L vs O.P. 14		500 mg/L vs O.P. 14		N.C. 14 vs 21 DAT	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
1.7959	0.143092	-1.30489	0.815883	-1.18153	0.429365	-1.31765	0.363745	0.544934	0.851547	0.123359	0.953944	-0.01276	1	1.849825	0.14831	-0.13612	1	1.726466	0.355254	1.862584	0.322073	-1.74313	0.204169
0.574828	0.857238	-0.69496	0.970348	-2.38665	0.353973	-1.03382	0.761985	0.760472	0.891575	-1.69169	0.529958	-0.33885	0.93067	1.455435	0.610937	1.352833	1	3.147121	0.350519	1.794288	0.708012	1	1
2.871129	0.040575	-0.74922	0.926755	-1.84136	0.272561	2.003869	0.218774	2.278356	0.237302	-1.09214	0.56282	2.75309	0.057043	3.027578	0.035288	3.845228	0.268145	4.119715	0.010426	0.274488	0.95271	0.956822	0.632671
0.424987	0.704058	-0.09101	1	1.78961	0.038915	1.675382	0.056133	0.713153	0.65983	1.880625	0.023307	1.766396	0.035985	0.804167	0.434484	-0.11423	1	-1.07646	0.472401	-0.96223	0.550276	-0.13042	0.931979
-6.11216	0.00033	-0.60452	0.964652	-4.446	0.000425	-3.04286	0.035808	-4.35553	0.002328	-3.84148	0.000919	-2.43834	0.070153	-3.75101	0.001888	1.403139	1	0.090469	0.98223	-1.31267	0.483393	1	1
1.804956	0.615206	1.421528	0.927961	0.470456	0.925485	-0.51592	0.917703	2.26524	0.674481	-0.95107	0.835697	-1.93745	0.60273	0.843712	0.86018	-0.98638	1	1.794784	0.796806	2.781161	0.60252	1	1
3.061558	0.020654	-1.12975	0.875223	-1.19967	0.511176	1.787266	0.269305	2.55718	0.142049	-0.06993	0.98133	2.917014	0.031167	3.686929	0.005359	2.986941	1	3.756855	0.020325	0.769914	0.835849	0.811904	0.683125
-0.96572	0.01769	-0.32634	0.885519	-1.35095	0.000404	-1.36247	0.000341	-0.6937	0.222965	-1.02461	0.01125	-1.03613	0.010236	-0.36736	0.490907	-0.01151	1	0.657252	0.316294	0.668766	0.322073	-0.48324	0.359737
-4.13469	2.13E-11	-0.29171	0.948192	-3.18722	3.92E-09	-3.27715	8.68E-10	-1.95501	0.00412	-2.89551	9.7E-08	-2.98544	3.04E-08	-1.66329	0.008522	-0.08993	1	1.232219	0.164292	1.322147	0.124698	-2.01705	0.003357
0.199872	0.941644	-0.61876	0.950042	-0.38791	0.886879	-2.15375	0.184608	0.589606	0.883841	0.230853	0.926394	-1.53499	0.373376	1.208365	0.538548	-1.76584	1	0.977512	0.794021	2.743355	0.211988	-0.26485	0.920732
-0.31077	0.70557	-0.83776	0.727813	0.265228	0.795685	-0.14872	0.902326	0.494359	0.684884	1.102987	0.082152	0.689038	0.351154	1.332117	0.031809	-0.41395	1	0.229131	0.895693	0.643079	0.595899	-0.60191	0.448719
-3.8946	0.000105	-1.09841	0.854711	-2.98502	0.004032	-2.86333	0.006291	-3.4059	0.002428	-1.88662	0.083796	-1.76493	0.116623	-2.30749	0.029274	0.121689	1	-0.42088	0.882589	-0.54257	0.847725	-0.98637	0.510178
-1.46954	0.018636	-0.43895	0.902903	-0.8901	0.238316	-0.74665	0.353373	-1.31273	0.098099	-0.45115	0.612912	-0.3077	0.755237	-0.87378	0.235849	0.14345	1	-0.42263	0.784133	-0.56608	0.688417	-1.18407	0.107902
-1.6098	0.048525	-0.52861	0.905403	-1.42832	0.09337	-1.85992	0.016665	-1.19899	0.286022	-0.89971	0.329481	-1.33131	0.104266	-0.67038	0.499264	-0.4316	1	0.229325	0.922082	0.66093	0.692171	0.678714	0.558991
0.246776	0.945715	0.503188	0.980058	-1.05722	0.722393	-0.59814	0.86837	1.009235	0.836609	-1.56041	0.544085	-1.10133	0.704802	0.506048	0.882354	0.459079	1	2.066456	0.60857	1.607377	0.73104	1	1
-1.06762	0.09664	-0.29259	0.944486	-2.33264	2.38E-05	-1.79271	0.002353	-1.56856	0.028588	-2.04005	0.0003	-1.50012	0.012974	-1.27598	0.04781	0.539925	1	0.764071	0.478917	0.224146	0.906243	-0.18802	0.864344
-3.65796	7.24E-06	0.691364	0.889829	-2.20142	0.012362	-2.0961	0.018762	-2.2847	0.023593	-2.89278	0.000507	-2.78747	0.000904	-2.97606	0.000502	0.105317	1	-0.08328	0.981439	-0.1886	0.946672	0.650511	0.621758
-2.46081	7.24E-13	-0.30334	0.896829	-2.56327	5.13E-14	-2.71131	9.27E-16	-1.26121	0.004483	-2.25993	9.31E-11	-2.40796	2.43E-12	-0.95786	0.024608	-0.14803	1	1.302065	0.005158	1.450098	0.001082	-0.85979	0.068966
1.612317	0.013883	-0.24086	0.96826	-0.43572	0.668293	0.261303	0.831351	1.439444	0.080078	-0.19485	0.86252	0.502168	0.595294	1.680308	0.012809	0.697019	1	1.87516	0.020792	1.178141	0.265779	-0.03662	0.980865
-0.84439	0.405094	-0.1584	0.990632	-2.20886	0.009892	-2.30176	0.00628	-1.36527	0.279383	-2.05046	0.015346	-2.14335	0.010467	-1.20686	0.234451	-0.09289	1	0.843595	0.618214	0.936489	0.556596	0.474002	0.755436
-3.27492	0.001214	-0.58334	0.924305	-3.79742	1.78E-05	-3.33751	0.000258	-2.51981	0.030198	-3.21408	0.00027	-2.75416	0.002497	-1.93647	0.057438	0.459917	1	1.277612	0.403671	0.817695	0.68458	-0.96099	0.490225
-2.01368	2.72E-05	0.727458	0.763423	-2.08746	9.58E-06	-1.19214	0.030332	-1.63345	0.003971	-2.81491	8.62E-10	-1.9196	0.000118	-2.3609	1.58E-06	0.895315	1	0.454009	0.699372	-0.44131	0.715142	0.421979	0.585753
-3.2726	0.00025	1.654266	0.67243	-1.69927	0.096416	-1.35459	0.218356	-2.25966	0.036432	-3.35353	0.000433	-3.00886	0.002089	-3.91393	4.2E-05	0.344674	1	-0.5604	0.802802	-0.90507	0.633261	0.765822	0.585192
0.145394	0.88553	-0.59291	0.867713	-2.24337	0.000124	-0.70049	0.402094	-0.23423	0.890325	-1.65046	0.008065	-0.10759	0.930614	0.358681	0.696516	1.542874	0.949198	2.009142	0.00527	0.466268	0.773777	-0.02778	0.985976
1.598488	0.114196	-0.58012	0.91012	0.51042	0.727565	0.980056	0.430482	1.416884	0.315074	1.090542	0.323246	1.560179	0.127408	1.997007	0.045084	0.469636	1	0.906465	0.675255	0.436829	0.885526	0.560355	0.683923
-3.2726	0.00025	1.654266	0.67243	-1.69927	0.096416	-1.35459	0.218356	-2.25966	0.036432	-3.35353	0.000433	-3.00886	0.002089	-3.91393	4.2E-05	0.344674	1	-0.5604	0.802802	-0.90507	0.633261	0.765822	0.585192
-0.5481	0.095377	-0.06492	0.98484	-0.48693	0.178707	-0.73131	0.021777	-0.27695	0.653357	-0.42201	0.24833	-0.66639	0.037253	-0.21204	0.623906	-0.24438	1	0.209974	0.782809	0.454351	0.402206	-0.19955	0.667902
-0.87482	0.319158	-1.94348	0.213805	-2.0272	0.007161	-2.07249	0.005409	-0.71636	0.624557	-0.08372	0.953657	-0.12901	0.930614	1.227119	0.152552	-0.04529	1	1.31084	0.266189	1.356133	0.25865	-1.49295	0.091756
-2.97013	2.63E-07	-0.02033	1	-1.88234	0.00353	-1.68285	0.011222	-2.15983	0.001946	-1.86201	0.003589	-1.66252	0.011308	-2.1395	0.000849	0.19949	1	-0.27749	0.885518	-0.47698	0.778773	-0.01848	0.991871
-1.58717	0.186062	1.119277	0.844957	-1.11475	0.397409	-0.04769	0.988305	-0.00435	1	-2.23402	0.037125	-1.16697	0.386744	-1.12362	0.396392	1.067059	1	1.110401	0.590003	0.043342	0.994103	0.66504	0.66923
0.828958	0.047399	-0.28974	0.899469	0.912823	0.032959	0.598028	0.214189	0.756375	0.163908	1.202566	0.002002	0.887771	0.032817	1.046118	0.011101	-0.3148	1	-0.15645	0.898132	0.158347	0.904248	-0.20307	0.753334
-2.6736	0.00098	-0.27459	0.971034	-3.03723	6.1E-06	-2.54489	0.000289	-1.84974	0.042971	-2.76264	3.1E-05	-2.2703	0.001144	-1.57514	0.047118	0.492342	1	1.187493	0.251773	0.695151	0.628566	0.040605	0.984153
-1.5316	0.282159	0.008838	1	-2.10613	0.129867	-2.1166	0.127071	1	1	-2.11497	0.114311	-2.12544	0.116446	-1.67558	0.257949	-0.01048	1	1	1	1	1	1	1
-2.54687	0.006951	0.253525	0.975383	-1.34596	0.145467	-1.1459	0.243217	-1.10799	0.386589	-1.59949	0.068992	-1.39943	0.131999	-1.36152	0.149856	0.200063	1	0.237971	0.921983	0.037908	0.992714	1	1
-2.13176	5.66E-09	-0.49093	0.818689	-1.53788	8.81E-05	-1.77653	3.26E-06	-0.86452	0.115531	-1.04695	0.013794	-1.2856	0.001595	-0.37358	0.50472	-0.23865	1	0.673363	0.333172	0.912017	0.137157	-1.23922	0.008372
-1.60983	0.28803	0.995642	0.898614	-2.72424	0.020124	-2.16902	0.087654	-0.78606	0.775846	-3.71988	0.002231	-3.16466	0.012979	-1.7817	0.258653	0.555226	1	1.938182	0.251773	1.382956	0.511226	-0.1559	0.949658
-0.92635	0.006938	0.288407	0.879787	-0.68307	0.076314	-0.75475	0.042711	-0.8141	0.055125	-0.97148	0.004545	-1.04316	0.001979	-1.10251	0.001337	-0.07168	1	-0.13103	0.900211	-0.05935	0.960956	0.162046	0.77892
-0.2957	0.433459	0.337805	0.839453	-0.12157	0.83027	-0.31215	0.467159	-0.24712	0.706267	-0.45938	0.205321	-0.64996	0.049201	-0.58492	0.089396	-0.19058	1	-0.12554	0.890637	0.065037	0.950786	0.145548	0.777184
-1.98669	0.010363	1.15233	0.75268	-1.77981	0.030376	-1.67927	0.044089	-1.9302	0.037149	-2.93214	0.000125	-2.8316	0.000235	-3.08253	8.42E-05	0.100539	1	-0.15039	0.952618	-0.25093	0.920381	1.003264	0.356798
-2.37736	0.000549	0.304236	0.957919	-0.93741	0.300041	0.517776	0.650182	-1.42233	0.134725	-1.24165	0.122295	0.213539	0.869451	-1.72656	0.022213	1.455189	1	-0.48491	0.785392	-1.9401	0.04421	0.370038	0.755142
-0.13634	0.91666	-0.19884	0.977767	1.142147	0.195705	0.683616	0.503454	1.020118	0.383937	1.340985	0.096962	0.882454	0.327979	1.218956	0.146471	-0.45853	1	-0.12203	0.962094	0.336502	0.887482	-0.73754	0.431789
0.150524	0.722746	0.406607	0.759639	0.246132	0.576495	0.471774	0.185774	-0.04007	0.97229	-0.16048	0.729149	0.065166	0.909689	-0.44668	0.207651	0.225641	1	-0.2862	0.675255	-0.51184	0.306473	0.025005	0.970525
-0.86669	0.506743	0.173888	0.9991	-2.31404	0.074175	-2.30497	0.075028	-2.32492	0.133677	-2.48793	0.049469	-2.47886	0.052291	-2.4988	0.052762	0.009069	1	-0.01087	1	-0.01994	1	0.90048	0.69103
-1.97465	0.040611	1.135436	0.830395	-1.74118	0.096416	-1.66063	0.118562	-2.0434	0.079532	-2.87662	0.002574	-2.79607	0.003621	-3.17883	0.000966	0.080551	1	-0.30222	0.917191	-0.38277	0.893799	0.652616	0.660471
-1.35617	5.02E-06	0.155718	0.946235	-1.39147	2.71E-06	-1.75746	5.83E-10	-1.01528	0.005038	-1.54718	1.09E-07	-1.91318	7.25E-12	-1.171	0.000262	-0.366	1	0.376182	0.569069	0.742178	0.112311	-0.1292	0.820986
-1.42832	0.574096	1.417936	0.914765	-1.58921	0.509568	-0.20588	0.966112	-0.91675	0.840004	-3.00714	0.206334	-1.62382	0.617645	-2.33468	0.380368	1.383326	1	0.672463	0.884085	-0.71086	0.902537	1	1
-1.14087	3.78E-07	0.032249	0.9999	0.122446	0.779185	0.07728	0.878845	-0.50435	0.13243	0.090197	0.833046	0.045032	0.928524	-0.5366	0.048659	-0.04517	1	-0.62679	0.06825	-0.58163	0.109645	-0.3374	0.297409
-1.9568	0.032617	0.367522	0.960026	-0.9615	0.420707	-0.84505	0.501022	-1.44307	0.265177	-1.32903	0.198945	-1.21257	0.259995	-1.81059	0.060402	0.116456	1	-0.48157	0.843804	-0.59802	0.803448	-1.05034	0.369383
0.002548	1	0.051972	1	-0.19558	0.849563	-0.46997	0.560603	-0.22817	0.878794	-0.24755	0.780868	-0.52194	0.486926	-0.28014	0.736301	-0.27439	1	-0.03259	0.991971	0.241802	0.888734	0.075911	0.945144
1.028873	0.023115	0.134651	0.975344	0.846738	0.091166	0.247251	0.741529	0.531303	0.488516	0.712087	0.161183	0.1126	0.890581	0.396652	0.504081	-0.59949	1	-0.31543	0.774752	0.284052	0.815705	0.764418	0.158198

-1.89029	0.001358	-0.11427	0.989519	-3.04904	1.04E-09	-2.93309	5.01E-09	-1.48268	0.036392	-2.93477	3.69E-09	-2.81883	2E-08	-1.36842	0.028041	0.115947	1	1.566359	0.016134	1.450412	0.039882	-1.6428	0.012636
2.754067	0.044209	-1.61658	0.693295	-0.70077	0.692283	-0.72663	0.684887	1.601498	0.494792	0.915801	0.523381	0.889945	0.542405	3.218073	0.01776	-0.02586	1	2.302271	0.274044	2.328128	0.286651	1	1
-1.87013	0.00548	-0.27047	0.965347	-1.06966	0.164705	-1.27642	0.075136	-1.48232	0.062241	-0.79919	0.308724	-1.00595	0.167565	-1.21185	0.078275	-0.20676	1	-0.41266	0.774471	-0.2059	0.913482	-0.67013	0.465479
0.568253	0.652785	-0.30198	0.97309	-2.39033	0.012065	-0.4326	0.79554	-0.02757	0.998296	-2.08835	0.030612	-0.13061	0.945041	0.274416	0.862644	1.957739	1	2.362767	0.059477	0.405028	0.891326	0.159841	0.929421
-1.79978	0.02084	-1.08045	0.740305	-1.4428	0.093767	-1.61295	0.051904	-1.09677	0.356195	-0.36235	0.765757	-0.5325	0.637962	-0.01633	0.994764	-0.17015	1	0.346023	0.875021	0.516176	0.802427	-1.99733	0.021144
-1.92881	0.570945	-1.38642	0.917586	-3.82619	0.119812	-3.69006	0.139551	-0.15199	0.991778	-2.43977	0.284548	-2.30364	0.326595	1.234432	0.716125	0.136132	1	3.674204	0.283148	3.538072	0.334145	-1.38011	0.694447
-1.60658	0.002084	-0.13934	0.980079	-0.43937	0.581476	-0.85969	0.178525	-0.61623	0.518647	-0.30003	0.716538	-0.72035	0.273844	-0.47689	0.508454	-0.42032	1	-0.17686	0.919809	0.243456	0.885798	-0.23679	0.79643
-1.54315	0.00058	0.159863	0.97138	-0.20343	0.810222	0.033138	0.980203	-1.04113	0.079368	-0.36329	0.591516	-0.12672	0.883535	-1.201	0.014278	0.23657	1	-0.8377	0.258289	-1.07427	0.112311	-0.42651	0.519052
-1.43776	0.03503	0.415796	0.918394	-0.37468	0.735745	-0.05408	0.976061	-1.59271	0.04712	-0.79048	0.361762	-0.46987	0.649837	-2.0085	0.003036	0.320603	1	-1.21803	0.234062	-1.53863	0.105718	0.050389	0.974615
-1.3678	0.040783	-0.44464	0.908326	-2.41397	3.24E-05	-2.35606	5.47E-05	-1.41053	0.081312	-1.96933	0.000865	-1.91141	0.001333	-0.96589	0.190065	0.057914	1	1.003441	0.296159	0.945527	0.359025	-1.88733	0.007835
-1.27897	0.006301	0.494985	0.851588	-0.51034	0.419803	-0.58299	0.337804	-0.37836	0.70551	-1.00533	0.0431	-1.07798	0.027646	-0.87335	0.097888	-0.07265	1	0.131981	0.931682	0.204634	0.890553	-0.54686	0.380475
-1.21748	0.016939	-0.81201	0.66727	-1.28599	0.011122	-1.64044	0.000492	-0.59193	0.49244	-0.47398	0.468285	-0.82843	0.136762	0.220077	0.775751	-0.35445	1	0.694061	0.431701	1.048509	0.151322	-0.74265	0.234822
-1.12899	0.039281	0.115038	0.984156	-1.11774	0.048817	-1.39579	0.008003	-0.05608	0.979745	-1.23277	0.021449	-1.51082	0.003146	-0.17112	0.845452	-0.27805	1	1.061654	0.171096	1.339704	0.060826	0.382521	0.621911
-1.08387	0.002628	0.728271	0.657628	-1.4831	4.18E-06	-1.71206	3.78E-08	-1.04643	0.011844	-2.21137	1.89E-10	-2.44033	5.41E-13	-1.7747	4.25E-06	-0.22897	1	0.43667	0.459975	0.665637	0.1612	-0.49492	0.310564
-1.05501	0.01292	0.28931	0.905403	-0.17374	0.819376	-0.16773	0.831351	-0.44281	0.564447	-0.46305	0.39134	-0.45704	0.407619	-0.73212	0.124574	0.006013	1	-0.26907	0.802572	-0.27508	0.807411	0.016771	0.98785
-1.05144	0.030294	-0.89455	0.562494	-0.64331	0.273194	-1.05329	0.036212	-0.76842	0.262164	0.251238	0.728234	-0.15874	0.844414	0.126122	0.876319	-0.40998	1	-0.12512	0.935455	0.284863	0.827926	-1.06775	0.049722
-1.04264	0.026901	-0.63524	0.75268	-0.88952	0.083973	-1.02768	0.036818	-0.56717	0.46636	-0.25428	0.718056	-0.39244	0.541106	0.068067	0.940108	-0.13816	1	0.322348	0.777432	0.460512	0.650301	-1.05423	0.047302
-1.0341	0.022923	-0.45462	0.853386	-0.98698	0.035317	-1.39106	0.000935	-0.15986	0.893718	-0.53236	0.326016	-0.93644	0.041665	0.294762	0.637263	-0.40408	1	0.827117	0.223271	1.231198	0.028789	-0.38785	0.530218
1.02826	9.28E-07	0.027306	1	0.806714	0.000278	0.870077	6.59E-05	0.929996	6.59E-05	0.779408	0.000496	0.842771	0.000134	0.90269	6.48E-05	0.063364	1	0.123283	0.851926	0.059919	0.940784	0.281561	0.358707
1.047651	0.000534	-0.25575	0.885519	0.236209	0.625347	0.625839	0.078836	0.705153	0.082245	0.491958	0.177983	0.881589	0.005394	0.960902	0.00294	0.38963	1	0.468944	0.405153	0.079314	0.943171	0.2021	0.678218
1.06166	0.000532	-0.03468	1	0.737017	0.033574	0.815672	0.014664	0.790931	0.044288	0.771701	0.020358	0.850356	0.009099	0.825615	0.014419	0.078655	1	0.053914	0.960832	-0.02474	0.986725	0.275475	0.549059
1.070786	0.018093	0.218747	0.941208	1.49116	0.000505	1.485838	0.000515	0.945315	0.102714	1.272414	0.004068	1.267092	0.004301	0.726569	0.16033	-0.00532	1	-0.54585	0.534235	-0.54052	0.54813	0.833447	0.121477
1.127063	0.029478	0.061935	0.99434	0.143589	0.846462	-0.17617	0.801441	1.649652	0.001395	0.081654	0.909617	-0.23811	0.694413	1.587717	0.00102	-0.31976	1	1.506063	0.010389	1.825823	0.000438	-0.03618	0.966272
1.127477	0.000282	0.191162	0.921338	0.847342	0.012722	1.024977	0.001506	0.882248	0.024226	0.65618	0.067086	0.833815	0.013612	0.691085	0.054762	0.177635	1	0.034906	0.979905	-0.14273	0.894527	0.535951	0.185868
1.273937	0.000115	0.015755	1	0.809237	0.033574	0.924534	0.010884	0.959333	0.021941	0.793482	0.032516	0.90878	0.011457	0.943578	0.010043	0.115297	1	0.150096	0.887536	0.034798	0.981219	0.122927	0.844211
1.323941	3.63E-06	-0.02153	1	0.678425	0.048915	0.856902	0.007281	0.900493	0.012793	0.699952	0.034434	0.878429	0.005209	0.922019	0.00413	0.178477	1	0.222068	0.779195	0.043591	0.970675	0.102075	0.854535
1.353352	0.000536	-0.25819	0.912752	0.678962	0.158663	0.568399	0.261993	0.937732	0.072878	0.937154	0.026064	0.826591	0.058479	1.195924	0.004457	-0.11056	1	0.25877	0.822329	0.369333	0.716637	0.26194	0.66907
1.371847	0.007779	0.295044	0.925111	1.901531	9.64E-05	1.843638	0.000166	1.126112	0.089681	1.606487	0.001481	1.548594	0.002374	0.831068	0.16855	-0.05789	1	-0.77542	0.392841	-0.71753	0.459964	0.980792	0.114916
1.465736	0.001687	-0.1589	0.971998	0.924255	0.091377	0.989598	0.065727	0.949339	0.14675	1.083151	0.032383	1.148495	0.022115	1.108236	0.032752	0.065343	1	0.025085	0.994396	-0.04026	0.986071	0.927598	0.110228
1.486196	2.13E-06	0.233123	0.908529	1.275399	9.38E-05	1.312101	5.07E-05	1.317389	0.000195	1.042276	0.002191	1.078978	0.001429	1.084266	0.001935	0.036702	1	0.04199	0.974601	0.005288	1	0.595955	0.160797
1.544244	8.71E-06	0.139849	0.966132	1.126479	0.002681	0.755222	0.066461	1.240363	0.003212	0.98663	0.01046	0.615373	0.153029	1.100514	0.005239	-0.37126	1	0.113884	0.931669	0.485141	0.537833	1.228924	0.003886
1.56192	2.69E-05	0.258198	0.915401	1.785298	2.76E-06	1.15226	0.005133	0.755366	0.178659	1.5271	0.000116	0.894062	0.040805	0.497167	0.328842	-0.63304	1	-1.02993	0.082226	-0.39689	0.675968	1.055851	0.024152
1.704184	0.034529	0.63436	0.875223	0.299189	0.813355	1.094121	0.231824	1.471746	0.168188	-0.33517	0.775847	0.459761	0.702816	0.837387	0.419696	0.794932	1	1.172558	0.397683	0.377626	0.885798	0.808872	0.407226
1.864265	0.007675	-0.29982	0.948368	1.784909	0.01814	1.898403	0.011615	1.36792	0.152171	2.084731	0.003332	2.198226	0.002101	1.667742	0.025795	0.113495	1	-0.41699	0.843858	-0.53048	0.800067	0.176832	0.884402
2.081074	0.000265	0.507822	0.878077	2.188634	0.000142	1.842534	0.001968	1.784583	0.009845	1.680812	0.00574	1.334712	0.037772	1.276761	0.053312	-0.3461	1	-0.40405	0.800409	-0.05795	0.981574	1.262022	0.078185
3.566227	0.030981	-0.02185	1	1	1	0.611902	0.782926	1	1	-0.5732	0.74131	0.63375	0.754753	1	1	1.206953	1	1	1	1	1	1	1
3.953966	0.000265	-0.92314	0.884131	0.71974	0.688562	1.528103	0.284496	3.110656	0.022461	1.64288	0.21798	2.451243	0.040961	4.033796	0.000363	0.808363	1	2.390916	0.167298	1.582553	0.468619	0.224992	0.916566
4.584913	0.01222	-1.67757	0.84512	4.522742	0.024298	3.482779	0.070438	4.067469	0.077206	6.200316	0.000644	5.160353	0.002268	5.745043	0.001506	-1.03996	1	-0.45527	0.949053	0.58469	0.930323	-1.19931	0.598429
5.717392	0.038635	1.828568	0.917586	0.822093	0.885633	-1.08047	0.831198	1.71983	0.809526	-1.00648	0.847815	-2.90904	0.435707	0	1	-1.90257	1	0.897737	0.928916	2.800301	0.65334	1	1
5.88514	0.005828	0.281505	0.997273	-0.54596	0.886442	1.225677	0.713743	3.034681	0.382908	-0.82747	0.797994	0.944172	0.775537	2.753176	0.30578	1.771638	1	3.580641	0.313777	1.809004	0.740351	1.480364	0.622404
7.235651	0.007974	1.496968	0.927961	0.895867	0.856475	1.369686	0.772776	3.234984	0.522964	-0.6011	0.906674	-0.12728	0.988207	1.738016	0.700591	0.473819	1	2.339117	0.745907	1.865298	0.826211	3.337833	0.376879
7.235651	0.007974	1.496968	0.927961	0.895868	0.856475	1.369686	0.772776	3.234984	0.522964	-0.6011	0.906674	-0.12728	0.988207	1.738016	0.700591	0.473819	1	2.339117	0.745907	1.865298	0.826211	3.337833	0.376879
18.78001	1.4E-10	-6.03916	0.590392	-0.06814	0.997604	-0.13964	0.99111	15.76797	5.88E-06	5.971024	0.099441	5.899527	0.107478	21.80713	2.32E-14	-0.0715	1	15.83611	7.99E-06	15.9076	1.04E-05	-7.63344	0.043097
19.94639	4.7E-14	-2.44503	0.875223	-1.94786	0.644415	0.180316	0.981803	18.96239	7.89E-12	0.497161	0.919408	2.625341	0.484712	21.40742	3.65E-16	2.12818	1	20.91025	5.95E-15	18.78207	1.67E-11	1	1

tOH 70% 14 vs 21 DAT		3 300 mg/L 14 vs 21 D		3 500 mg/L 14 vs 21 D		O.P. 14 vs 21 DAT		N.C. vs EtOH 21 DAT		. vs GA3 300 mg/L 21		. vs GA3 500 mg/L 21		N.C. vs O.P. 21 DAT		10 % vs GA3 300 mg/L		10 % vs GA3 500 mg/L		OH 210 % vs O.P. 21 D		mg/L vs GA3 500 mg/	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
-1.22415	0.536486	-2.26073	0.027285	-2.18399	0.030501	-1.16689	0.472491	-0.78592	1	-1.69913	0.12487	-1.75851	0.118836	1.121167	0.395695	-0.91322	0.463085	-0.97259	0.444032	1.907083	0.083591	-0.05938	1
1	1	1.839059	0.378251	1.895761	0.36881	1.478331	0.690331	1.994525	1	-0.90163	0.731256	0.507905	0.868	1.884763	0.49284	-2.89616	0.198272	-1.48662	0.590755	-0.10976	0.980879	1.409535	1
1.181453	0.655036	2.959903	0.017601	-2.47098	0.048786	0.077987	0.986411	-0.52459	1	0.161722	0.941013	-1.42393	0.346748	1.399521	0.383349	0.686312	0.685819	-0.89934	0.588847	1.924112	0.170609	-1.58566	1
0.128832	0.949469	2.393595	0.002644	1.348454	0.089256	2.634407	0.002014	0.168234	1	4.313622	3.71E-09	3.154253	1.15E-05	3.477977	2.54E-06	4.145389	1.5E-08	2.986019	3.76E-05	3.309743	7.29E-06	-1.15937	1
3.325261	0.301448	1.544281	0.110936	0.514149	0.671241	-0.30315	0.874621	0.92031	1	-4.70215	0.005565	-4.32914	0.014376	-6.45911	8.62E-05	-5.62246	0.000575	-5.24945	0.001939	-7.37942	3.71E-06	0.373007	1
1	1	-4.13599	0.052769	-0.15499	0.964171	-3.18481	0.34874	2.716747	1	0.858041	0.713285	3.852669	0.05559	3.604009	0.078555	-1.85871	0.372568	1.135922	0.674446	0.887262	0.744643	2.994628	1
1.298659	0.591229	1.680673	0.196575	-2.64898	0.026341	-0.55748	0.823433	-0.64299	1	-0.33091	0.859523	-1.67362	0.230393	1.1878	0.457163	0.312088	0.865499	-1.03063	0.503543	1.830793	0.177789	-1.34272	1
-0.64625	0.330267	-1.0852	0.002627	-1.13985	0.00127	-0.34287	0.58133	-0.48935	1	-1.95291	6.62E-09	-2.01907	2.04E-09	-0.55333	0.213078	-1.46356	2.33E-05	-1.52972	1.05E-05	-0.06398	0.916663	-0.06616	1
-1.55541	0.068673	-2.7383	7.76E-08	-2.37524	3.13E-06	-2.46364	1.4E-05	0.169929	1	-3.90847	9.58E-16	-3.63533	1.55E-13	-2.4016	5.33E-06	-4.0784	4.26E-17	-3.80526	7.38E-15	-2.57153	7.55E-07	0.273137	1
-0.69323	0.815999	-1.45	0.304023	-0.32425	0.842415	1.286878	0.639721	-1.04714	1	-1.57305	0.283274	-2.21314	0.11128	2.141337	0.245188	-0.52592	0.762898	-1.16601	0.446802	3.188472	0.042771	-0.64009	1
0.310292	0.809067	0.154937	0.835269	0.518525	0.394835	0.100652	0.943851	0.074447	1	1.022079	0.076377	0.971718	0.104077	1.196925	0.041934	0.947632	0.100859	0.897271	0.137924	1.122477	0.050416	-0.05036	1
0.32789	0.896557	0.715894	0.509316	0.840363	0.417055	-0.03909	0.99313	0.215851	1	-1.28276	0.230976	-1.0366	0.368935	-2.45862	0.011344	-1.49861	0.145494	-1.25245	0.26015	-2.67447	0.004293	0.246158	1
-0.95665	0.353592	-0.58367	0.371085	-1.20704	0.033772	-0.02493	0.99313	-0.21153	1	-0.28971	0.714628	-0.76963	0.248323	-0.15359	0.877923	-0.07818	0.936178	-0.5581	0.432996	0.057936	0.955928	-0.47992	1
1.095997	0.42141	-0.55309	0.483076	0.045094	0.968197	-1.03193	0.276116	-0.11133	1	-2.66012	0.000105	-2.49354	0.000385	-2.90963	3.42E-05	-2.54879	0.000186	-2.38221	0.000679	-2.79831	5.1E-05	0.166577	1
1	1	0.911165	0.671289	1.014046	0.633599	2.525291	0.477449	2.560661	1	-0.35399	0.900849	0.207973	0.946857	3.326595	0.207302	-2.91465	0.211913	-2.35269	0.359949	0.765933	0.839492	0.561961	1
0.545648	0.655997	-0.66943	0.252303	-0.93982	0.085631	-1.22499	0.066652	0.441076	1	-2.81405	1.84E-08	-2.54451	5.92E-07	-2.60554	6.12E-07	-3.25513	8.82E-11	-2.98559	4.44E-09	-3.04662	4.44E-09	0.269541	1
-0.21071	0.926204	0.434686	0.657892	0.341122	0.729965	-0.41518	0.78518	-0.16985	1	-2.41724	0.002357	-2.40549	0.002954	-3.35039	1.84E-05	-2.24739	0.004535	-2.23564	0.005891	-3.18054	3.81E-05	0.011752	1
-0.41343	0.580413	-0.26623	0.55554	-0.12696	0.795425	-1.15538	0.006056	0.143012	1	-1.96971	6.29E-09	-1.97847	6.15E-09	-1.5568	1.68E-05	-2.11272	3.29E-10	-2.12148	3.39E-10	-1.69981	1.55E-06	-0.00876	1
0.216699	0.889704	0.499848	0.484705	-0.64395	0.335316	-0.41597	0.703783	0.01245	1	0.100747	0.920906	-0.34603	0.68344	1.060086	0.124892	0.088297	0.931287	-0.35848	0.668836	1.047635	0.114509	-0.44678	1
0.410542	0.842622	-0.07197	0.952275	0.365278	0.685587	-0.7369	0.540909	-0.22186	1	-2.75483	0.000391	-2.41048	0.003047	-2.57617	0.00167	-2.53297	0.000927	-2.18862	0.006709	-2.3543	0.003099	0.344351	1
-0.67051	0.741305	0.044568	0.974694	-0.14593	0.89848	-1.67488	0.108103	-0.29286	1	-2.79187	0.000627	-2.52244	0.002888	-3.2337	9.43E-05	-2.499	0.002093	-2.22958	0.008758	-2.94084	0.000297	0.269424	1
-0.19409	0.881634	-0.29085	0.612489	-0.6909	0.162275	-0.71749	0.27829	0.111389	1	-2.80028	1.14E-10	-2.30502	2.43E-07	-2.77291	5.99E-10	-2.91167	1.98E-11	-2.41641	5.7E-08	-2.8843	1.03E-10	0.495265	1
-0.54665	0.817299	0.51108	0.612654	0.438893	0.667819	0.027046	0.997126	0.341799	1	-1.95401	0.031508	-1.68152	0.081229	-2.99844	0.000512	-2.29581	0.01002	-2.02332	0.031952	-3.34024	9.74E-05	0.272486	1
0.445855	0.731943	0.618656	0.344363	-0.87656	0.14653	-0.68733	0.438541	-0.11927	1	-1.59693	0.005453	-1.54928	0.008478	-0.89378	0.191684	-1.47766	0.010197	-1.43001	0.016012	-0.77451	0.245528	0.047654	1
0.47394	0.806217	2.304262	0.019024	0.854592	0.410566	-0.50248	0.772272	-0.66654	1	2.254327	0.025911	1.274294	0.224114	0.354047	0.801064	2.920864	0.001939	1.940831	0.03919	1.020584	0.305451	-0.98003	1
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-0.32203	0.566896	0.08749	0.820264	0.137716	0.697077	-0.00973	0.996949	-0.1874	1	-0.19989	0.588721	-0.39404	0.229699	-0.08714	0.857758	-0.01249	0.983005	-0.20664	0.581438	0.10026	0.810688	-0.19415	1
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0.517468	0.770496	-0.5025	0.465797	-0.68577	0.291225	-1.14797	0.157314	0.202272	1	-3.58034	7.77E-09	-3.27127	2.27E-07	-3.03831	4.05E-06	-3.78261	2.06E-09	-3.47354	6.49E-08	-3.24058	1.11E-06	0.309071	1
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1	1	-0.27871	0.839538	-0.63363	0.590286	-1.33697	0.519248	-0.21768	1	-0.5782	0.670479	-0.95897	0.442818	0.66581	0.676077	-0.36052	0.804421	-0.74129	0.56579	0.883489	0.518557	-0.38077	1
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0.568083	0.554112	4.013737	3.13E-19	4.266812	5.83E-22	0.848971	0.201166	0.300599	1	2.513481	4.94E-08	2.488505	8.55E-08	0.410369	0.541926	2.212882	2.17E-06	2.187906	3.63E-06	0.10977	0.887328	-0.02498	1
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0.182559	0.697568	1.186622	7.13E-09	0.788714	0.000152	0.361625	0.235024	-0.0717	1	1.711775	1.05E-18	1.377231	3.14E-12	1.01006	1.21E-06	1.783471	2.26E-20	1.448927	1.47E-13	1.081757	1.3E-07	-0.33454	1
0.140676	0.845402	0.025201	0.960278	0.02849	0.952559	-0.04378	0.957551	-0.31717	1	0.05931	0.902194	0.452229	0.184608	0.45927	0.19436	0.376483	0.264635	0.769402	0.01127	0.776443	0.010268	0.39292	1
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0.175531	0.825452	0.8037	0.015121	0.582185	0.086314	1.048086	0.004977	0.068358	1	1.49001	1.11E-06	1.383792	8.2E-06	1.884492	1.03E-09	1.421651	3.45E-06	1.315433	2.57E-05	1.816133	3.71E-09	-0.10622	1
0.092873	0.904693	0.784949	0.007282	0.668934	0.022731	0.95615	0.003976	-0.03073	1	1.3613	5.6E-07	1.423762	1.71E-07	1.754569	1.74E-10	1.392028	2.65E-07	1.45449	8.12E-08	1.785297	6.16E-11	0.062462	1
-0.06272	0.950532	0.858758	0.04143	0.305771	0.507854	0.187727	0.823557	-0.58285	1	1.27578	0.001245	0.61223	0.166507	0.863519	0.045154	1.858629	4.18E-07	1.195079	0.001581	1.446368	0.000126	-0.66355	1
0.69138	0.441972	1.313464	0.006905	1.543247	0.001095	1.35034	0.018163	0.005632	1	2.234203	8.02E-07	2.406093	1.08E-07	1.49566	0.00248	2.228571	7.62E-07	2.400461	1.08E-07	1.490028	0.002042	0.17189	1
0.202893	0.852573	0.598539	0.250572	0.388723	0.476253	0.57893	0.423726	-0.8836	1	0.595196	0.278483	0.450723	0.449618	0.600671	0.306964	1.478797	0.00092	1.334324	0.003826	1.484272	0.001205	-0.14447	1
0.588841	0.303897	1.213443	0.000105	1.158265	0.00019	0.399409	0.419324	0.226009	1	1.892887	1.19E-10	1.874411	2.25E-10	1.120842	0.000532	1.666878	1.95E-08	1.648402	3.56E-08	0.894834	0.006335	-0.01848	1
0.929866	0.084396	2.198588	9.07E-07	2.451865	1.25E-08	1.195948	0.015157	-0.15921	1	2.096143	2.16E-06	1.978163	7.99E-06	1.207387	0.005192	2.255352	2.15E-07	2.137372	9.03E-07	1.366596	0.000885	-0.11798	1
0.656263	0.336911	1.868948	1.94E-05	2.966117	2.64E-11	1.464142	0.0008	-0.14139	1	2.598395	2.1E-10	3.062526	2.4E-12	1.163656	0.005371	2.739785	1.5E-11	3.203916	1.38E-13	1.305046	0.001094	0.464131	1
-0.05837	0.979961	2.005427	0.01504	0.233692	0.821487	0.705444	0.644422	-0.23288	1	1.495744	0.10127	0.518941	0.608258	1.368319	0.15525	1.728628	0.045725	0.751825	0.414037	1.601203	0.068329	-0.9768	1
-0.17853	0.910774	-0.59543	0.474009	-0.79355	0.311138	0.699743	0.565773	-0.65519	1	1.012647	0.164378	0.928022	0.221233	1.890831	0.009525	1.667836	0.009436	1.58321	0.017192	2.546019	0.000148	-0.08463	1
0.592495	0.607008	-0.06419	0.945379	0.125531	0.874681	-0.37083	0.724678	-0.16171	1	0.862423	0.17598	0.706042	0.298459	0.151729	0.878667	1.024128	0.091437	0.867748	0.182187	0.313434	0.69071	-0.15638	1
1	1	0.698058	0.595304	-0.35212	0.832141	1	1	0.240732	1	0.401318	0.803336	0.558093	0.728033	2.415559	0.182145	0.160587	0.931827	0.317362	0.857735	2.174828	0.220564	0.156775	1
1.245189	0.543809	-1.12523	0.344523	-1.93413	0.070932	-2.22678	0.109123	0.097057	1	-0.63048	0.655545	-0.63102	0.664976	0.658884	0.671828	-0.72754	0.593472	-0.72807	0.605529	0.561828	0.702822	-0.00054	1
0.704834	0.841537	2.354553	0.364135	0.464787	0.852177	0.909476	0.837338	0.226569	1	8.076603	2.32E-05	5.146875	0.002053	6.176253	0.001235	7.850034	3.89E-05	4.920306	0.003357	5.949684	0.001539	-2.92973	1
-2.82199	0.590989	-3.10675	0.264342	-0.05386	0.993168	-0.9477	0.880414	1.636008	1	0.344778	0.923149	1.495101	0.61989	3.401566	0.265192	-1.29123	0.66808	-0.14091	0.974592	1.765559	0.612771	1.150324	1
2.068375	0.600493	2.832316	0.173411	4.601255	0.052192	2.859766	0.456156	0.869516	1	0.805991	0.779572	4.346568	0.094157	4.414082	0.097179	-0.06352	0.990129	3.477052	0.209407	3.544567	0.192722	3.540577	1
0.870528	0.908027	2.350358	0.466423	1.793957	0.597115	0	1	-0.97034	1	0	1	0	1	0	1	0.87873	0.839919	0.796148	0.86136	0.863662	0.847229	0	1
0.870529	0.908028	2.350358	0.466423	1.793957	0.597115	0	1	-0.97034	1	0	1	0	1	0	1	0.87873	0.839919	0.796148	0.86136	0.863662	0.847229	0	1
-2.40131	0.688766	-6.90856	0.023918	-6.53531	0.030552	0	1	-0.80704	1	0.65673	0.882555	0.958491	0.821136	23.39319	5.89E-17	1.463765	0.70022	1.765527	0.641688	24.20022	3.88E-18	0.301762	1
21.46634	1.85E-15	0.751763	0.828765	-0.21343	0.960018	-15.7292	8.54E-07	17.85353	1.59E-09	-2.36388	0.462892	-1.20089	0.754633	2.06546	0.615445	-20.2174	4.96E-15	-19.0544	3.76E-13	-15.7881	1.04E-07	1.162989	1

3 300 mg/L vs O.P. 21		3 500 mg/L vs O.P. 21		N.C. 21 vs 28 DAT		EtOH 70% 21 vs 28 DAT		3 300 mg/L 21 vs 28 D		3 500 mg/L 21 vs 28 D		O.P. 21 vs 28 DAT		N.C. vs EtOH 28 DAT		. vs GA3 300 mg/L 28		. vs GA3 500 mg/L 28		N.C. vs O.P. 28 DAT		30 % vs GA3 300 mg/L	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
2.820301	0.008403	2.879677	0.006207	-3.12167	0.003251	-2.44322	0.013348	-2.98849	0.000909	-2.54096	0.004622	-1.56171	0.258664	-0.10747	0.965095	-1.56596	0.116002	-1.17781	0.233427	2.681127	0.00632	-1.45848	0.176534
2.786393	0.234557	1.376858	0.604063	2.38465	0.349892	-3.51216	0.082545	-1.11551	0.560167	-2.01236	0.273802	-1.82362	0.571712	1	1	-4.40179	0.025517	-3.88911	0.044886	-2.3235	0.32887	-0.4995	0.847607
1.237799	0.422381	2.823455	0.032258	-0.26065	0.896719	-2.50946	0.042348	-1.14514	0.357827	-1.50255	0.207081	-1.09637	0.580117	-2.77341	0.115453	-0.72277	0.609159	-2.66583	0.01978	0.5638	0.733692	2.050634	0.116285
-0.83565	0.421377	0.323724	0.771628	1.668305	0.03844	1.45057	0.049578	-2.38058	0.001144	-2.84744	1.9E-05	-0.90915	0.431556	-0.0495	0.978434	0.264734	0.773131	-1.36149	0.050008	0.900518	0.287121	0.314236	0.757052
-1.75697	0.082349	-2.12997	0.031569	-3.26722	0.09496	-3.52986	0.051171	5.170213	0.000654	4.721646	0.001801	0.17647	0.921613	1	1	3.735288	0.02513	3.659728	0.023693	-3.01542	0.001902	3.077621	0.104654
2.745968	0.19337	-0.24866	0.940259	1.559237	0.462563	-3.15724	0.070509	-1.05911	0.546381	-3.95561	0.019295	-0.05561	0.996899	1	1	-1.76031	0.319623	-1.66218	0.327257	1.989166	0.33829	0.239423	0.925559
1.518706	0.286621	2.861423	0.023967	-0.80218	0.614075	-2.4138	0.042356	-0.96917	0.425483	-1.26164	0.278311	-0.9983	0.607707	-2.25462	0.208129	-0.49791	0.725893	-2.13309	0.056886	0.991678	0.489562	1.756717	0.169717
1.399579	0.000174	1.46574	7.54E-05	-0.68075	0.100356	-0.14282	0.750511	0.530501	0.13082	0.832591	0.011987	-1.26573	0.00162	0.048578	0.957504	-0.74166	0.036175	-0.50573	0.156623	-1.13831	0.001222	-0.79024	0.033725
1.506875	0.008261	1.233738	0.031521	-1.33191	0.024822	-1.68696	0.001565	0.450296	0.411367	0.522242	0.327444	-0.9633	0.175411	-0.18512	0.869657	-2.12627	1.48E-05	-1.78118	0.000232	-2.03299	6.32E-05	-1.94114	0.00013
3.714388	0.018865	4.354481	0.004229	-3.53297	0.007077	-2.09892	0.085312	-2.86875	0.008278	-1.49168	0.18961	-3.71812	0.035403	0.386912	0.875144	-0.90883	0.480029	-0.17186	0.905099	1.956192	0.120017	-1.29574	0.330994
0.174845	0.828816	0.225206	0.763878	0.308576	0.673399	0.165031	0.803844	0.673246	0.201968	1.332019	0.006564	-0.75546	0.31561	-0.0691	0.958676	1.386749	0.006274	1.995161	3.76E-05	0.132893	0.864048	1.455847	0.005839
-1.17586	0.269281	-1.42201	0.157726	-0.83446	0.482056	1.245425	0.261359	6.966001	3.1E-06	6.660059	6.39E-06	0.433078	0.785609	2.295738	0.114735	6.517703	2.32E-05	6.457919	1.73E-05	-1.19108	0.233504	4.221965	0.015149
0.136112	0.87737	0.616032	0.355494	-0.92153	0.156276	-0.78067	0.185213	-2.84447	9.79E-09	-2.29407	3.08E-06	0.184693	0.869769	-0.07067	0.959794	-2.21264	1.6E-05	-2.14217	1.91E-05	0.952632	0.109446	-2.14198	4.69E-05
-0.24952	0.794937	-0.41609	0.626429	-1.35436	0.101005	-1.81501	0.010552	-0.6073	0.355671	-0.52991	0.426682	-0.08762	0.95359	-0.57197	0.640511	-1.91306	0.00223	-1.66909	0.006781	-1.64289	0.013224	-1.34109	0.048053
3.680582	0.136915	3.118621	0.212886	0.436568	0.875038	-3.98533	0.050999	-2.62104	0.095723	-3.08366	0.048246	-2.68071	0.406741	1	1	-3.4116	0.037603	-3.31226	0.037532	0.209315	0.943161	-1.55035	0.412129
0.208509	0.785251	-0.06103	0.945199	-0.74171	0.263906	-1.43089	0.009838	0.35805	0.513855	-0.55591	0.280084	-0.27446	0.7672	-0.2481	0.81877	-1.71429	0.000561	-2.35871	6.24E-07	-2.1383	2.05E-05	-1.46619	0.005171
-0.93315	0.313671	-0.9449	0.290725	-0.80379	0.431019	0.451355	0.649024	7.546575	1.42E-07	7.457352	1.29E-07	0.658601	0.596071	1.085291	0.426105	5.933123	7.2E-05	5.855652	5.8E-05	-1.888	0.015766	4.847832	0.002322
0.412912	0.358698	0.421673	0.330828	-0.56292	0.191817	-0.83351	0.023045	1.578161	1.37E-06	2.081472	7.3E-11	0.193195	0.767826	-0.12758	0.867659	0.171368	0.695197	0.665917	0.056546	-0.80069	0.031755	0.298949	0.502951
0.959338	0.160893	1.406119	0.027401	-0.65222	0.375876	-1.3147	0.02705	-0.66835	0.257982	-0.98774	0.076527	-0.73214	0.398968	-0.65004	0.526287	0.084617	0.91529	-0.68156	0.251084	0.980157	0.122436	0.734653	0.27008
0.178665	0.8727	-0.16569	0.880887	-1.37421	0.147212	-0.70143	0.448376	0.271194	0.737033	-0.60602	0.403515	0.280785	0.836507	0.450918	0.763101	-1.10943	0.140017	-1.64229	0.016561	-0.92117	0.268019	-1.56035	0.047584
-0.44183	0.685614	-0.71126	0.463962	-1.20022	0.234867	0.782107	0.436312	7.238725	5.21E-07	6.086269	2.88E-06	0.493242	0.714996	1.689464	0.205863	5.647079	0.000182	4.764047	0.000405	-1.54024	0.064833	3.957616	0.017861
0.027371	0.97446	-0.46789	0.397217	-0.80687	0.149346	-0.14761	0.812756	2.316468	3.85E-08	1.014735	0.017786	0.125225	0.894871	0.77065	0.319632	0.323054	0.555833	-0.48341	0.315866	-1.84082	3.02E-05	-0.4476	0.447194
-1.04443	0.275336	-1.31692	0.143903	-0.90347	0.413228	0.488416	0.682367	6.896651	1.98E-06	6.564381	4.67E-06	0.323656	0.828064	1.733688	0.234909	5.846115	0.00011	5.786331	8.53E-05	-1.77131	0.034074	4.112427	0.015213
0.703154	0.305023	0.655499	0.328227	-1.15444	0.070231	-1.78502	0.001398	-1.1997	0.023126	-2.38946	1.55E-06	-0.57151	0.516716	-0.74985	0.422857	-1.6422	0.002032	-2.7843	2.96E-08	-0.31086	0.675762	-0.89235	0.143283
-1.90028	0.083072	-0.92025	0.397528	-1.23222	0.195914	-0.22982	0.820445	-2.67257	0.002463	-2.99923	0.0001	1.618436	0.19767	0.335863	0.835289	0.813981	0.347488	-0.49271	0.562283	3.204707	0.000212	0.478118	0.650037
-1.04443	0.275336	-1.31692	0.143903	-0.90347	0.413228	0.488416	0.682367	6.896651	1.98E-06	6.564381	4.67E-06	0.323656	0.828064	1.733688	0.234909	5.846115	0.00011	5.786331	8.53E-05	-1.77131	0.034074	4.112427	0.015213
0.112749	0.782741	0.306901	0.352463	0.097753	0.814004	0.203995	0.520948	0.470375	0.07611	0.329912	0.224018	-0.15747	0.746709	-0.08116	0.892403	0.172729	0.588761	-0.16189	0.591268	-0.34236	0.274321	0.253891	0.444039
2.21864	0.001748	2.269738	0.001199	-3.44126	1.45E-06	-2.12732	0.001403	-1.47153	0.019244	-1.69054	0.005737	-1.27017	0.154806	0.0677	0.967732	-0.88687	0.201545	-1.15698	0.073404	1.53312	0.025052	-0.95457	0.197857
-0.27392	0.748698	-0.77238	0.259812	-0.31565	0.704195	2.152106	0.000239	6.822742	1.78E-37	7.19907	1.29E-38	-0.25081	0.818888	2.324098	0.000647	4.502057	1.39E-16	5.376849	8.89E-22	-2.84541	2.62E-07	2.177958	0.00025
-0.74761	0.522189	-0.84609	0.444857	-0.86202	0.466641	0.343094	0.78372	6.42347	1.84E-05	6.265199	2.29E-05	-0.17902	0.923161	1.627441	0.286237	6.367212	3.56E-05	6.307428	2.69E-05	-0.98288	0.340953	4.739771	0.004807
0.601783	0.160572	1.605012	1.59E-05	-0.49751	0.245316	-0.42461	0.269399	-1.74983	5.56E-08	-0.84419	0.009695	-0.62448	0.213299	-0.25999	0.694228	-0.31886	0.4109	-0.41645	0.242974	1.408269	4E-05	-0.05887	0.915611
0.542029	0.458486	0.232958	0.776627	-1.52383	0.050394	-1.0278	0.186865	1.833965	0.000912	0.72706	0.207185	-0.21824	0.845034	0.698302	0.543618	-0.22254	0.779059	-1.02038	0.0873	-1.73272	0.003426	-0.92085	0.211012
1.081808	0.346263	0.416039	0.760042	-1.45548	0.406735	-0.19927	0.917615	2.523996	0.023164	1.83064	0.115954	1	1	1	1	0.533811	0.734771	0.506223	0.732746	-1.98518	0.060602	-0.30201	0.889314
1.093271	0.164587	0.40711	0.662247	1.580366	0.071877	0.536179	0.557439	2.413969	0.000855	4.336055	0.000532	-1.004	0.29324	1	1	-0.10833	0.929024	2.499915	0.071207	-2.43303	0.000964	0.252504	0.842635
0.455378	0.326554	0.560015	0.197999	-0.91466	0.029453	-0.94042	0.013214	-0.09667	0.830931	0.091784	0.841161	-0.15416	0.831637	-0.14781	0.849866	-0.63267	0.097127	-0.54885	0.140961	-0.23478	0.631982	-0.48485	0.255668
0.591256	0.63078	0.072459	0.965197	-0.32436	0.846853	-0.39904	0.816944	3.35851	0.000413	3.451448	0.000803	0.329733	0.852442	1.285683	0.540063	0.344058	0.810021	0.955793	0.454057	-2.09346	0.039498	-0.94163	0.544275
-1.11158	0.000657	-1.2308	0.000124	-0.01979	0.973044	0.759156	0.016371	1.988389	1.65E-12	1.948798	2.44E-12	0.546808	0.195175	0.902315	0.030198	1.396391	1.6E-06	1.476021	2.16E-07	-1.15677	0.000116	0.494076	0.154355
-0.26084	0.46807	-0.34304	0.30046	0.728397	0.019105	1.166156	3.67E-05	3.59987	8.49E-37	3.715722	3.31E-37	0.107475	0.843125	0.543897	0.219821	2.817624	1.95E-22	3.015674	1.9E-24	-0.93561	0.000639	2.273727	2.28E-14
-1.28457	0.09905	-1.40208	0.062368	-0.58678	0.563015	0.072584	0.947543	7.220934	2.64E-07	7.04364	3.54E-07	0.347088	0.776109	0.768274	0.581071	5.932847	5.04E-05	5.873063	3.84E-05	-2.22557	0.001353	5.164573	0.000839
-1.13248	0.126636	-1.06604	0.143716	-0.16518	0.875348	0.718806	0.317895	-1.0914	0.079029	-0.88956	0.155954	-1.10323	0.201089	0.202437	0.888319	-1.54653	0.013595	-1.41113	0.021393	-2.69084	1.17E-05	-1.74896	0.007284
-0.46749	0.693465	0.413654	0.697567	0.883933	0.243954	0.460931	0.540962	0.191526	0.864326	1.201475	0.171071	-1.0466	0.329408	0.347571	0.786616	2.692154	0.000532	2.820955	0.000299	0.986532	0.178395	2.344583	0.004729
0.511778	0.095143	0.472015	0.118736	-0.1263	0.747239	-0.19909	0.521507	-0.60901	0.015087	-0.8793	0.000253	-0.24253	0.582019	-0.17166	0.738957	-0.81349	0.001343	-1.04402	1.63E-05	0.064769	0.87145	-0.64183	0.018571
-1.34804	0.181608	-2.19465	0.023643	-2.81339	0.03963	3.105591	0.07735	5.846024	8.89E-05	4.939636	0.001006	0.855001	0.521418	4.485876	0.046892	5.126403	0.00104	5.066619	0.00085	-1.21266	0.227311	0.640527	0.838476
-1.5188	0.102008	-1.79749	0.044149	-1.21821	0.248552	-0.30084	0.801005	6.86965	2.61E-06	6.531176	6.18E-06	0.456514	0.748106	1.363801	0.348607	6.336438	2.7E-05	6.276654	2.02E-05	-1.5955	0.064765	4.972637	0.002231
-1.09694	0.000319	-1.07601	0.000393	-0.51704	0.132738	-0.38879	0.221489	-0.51285	0.068547	-0.0456	0.90287	0.56744	0.143052	0.134212	0.822858	-0.98588	0.000354	-0.53957	0.056717	-1.00253	0.000438	-1.12009	6.59E-05
-0.00472	1	-2.07447	0.231012	-1.21862	0.518516	-4.28945	0.018891	3.205404	0.062087	-0.87954	0.623396	1.440272	0.484556	1	1	2.574911	0.170343	0.559716	0.732466	0.805059	0.657102	2.847867	0.149291
-0.2122	0.468667	-0.17136	0.560815	0.442134	0.088879	0.524249	0.022681	0.621386	0.003286	1.025885	4.5E-07	0.198621	0.595634	0.127498	0.774916	0.355969	0.126883	0.719633	0.000634	-0.27899	0.28434	0.228471	0.399804
2.393121	0.005187	2.037585	0.017912	0.001401	1	0.214314	0.833107	0.579295	0.492295	2.222239	0.002184	-2.47245	0.007862	0.489493	0.750601	-3.30825	7.41E-06	-1.30977	0.091584	-3.96688	1.34E-07	-3.79774	3.12E-07
-1.86195	0.000336	-1.96361	0.000131	0.173848	0.817651	1.282434	0.010638	4.292574	5.68E-15	5.07725	5.46E-16	0.063711	0.956413	1.085023	0.14412	5.069236	1.11E-20	5.955575	1.68E-21	-1.02157	0.047678	3.984213	1.05E-12
-1.07404	0.014137	-0.68333	0.132123	-0.27031	0.621961	1.16452	0.003685	1.365782	0.000245	1.525586	2.69E-05	0.117065	0.88871	1.009608	0.075466	2.537752	3.58E-12	2.306843	1.91E-10	0.214991	0.687195	1.528144	8.96E-05

0.963998	0.056105	0.975145	0.047692	-0.96245	0.076736	-1.11384	0.024164	0.606435	0.172711	1.025242	0.013866	-1.13832	0.039935	0.236448	0.801816	-2.1233	4.84E-07	-1.71564	4.2E-05	-2.90406	9.69E-12	-2.35975	3.63E-08
1.244011	0.324643	1.624783	0.160511	-0.85817	0.491593	-2.0764	0.026757	-0.41083	0.700886	0.77157	0.450693	-1.19837	0.439275	1	1	-0.13086	0.918118	0.670763	0.527083	0.325602	0.808741	1.305051	0.197494
0.109967	0.887625	-0.15092	0.837785	-0.01037	0.993737	1.053885	0.089401	0.572034	0.267345	0.452173	0.405097	0.105448	0.918409	0.563138	0.614553	-0.81217	0.155686	-0.67114	0.239289	-1.16879	0.031811	-1.3753	0.026689
0.719877	0.51207	1.304611	0.173239	-1.21621	0.228876	-2.10504	0.012125	-2.38896	0.001849	-3.59084	1.1E-06	-0.63552	0.655065	-1.31325	0.329032	-2.27699	0.004184	-4.06361	5.04E-08	0.196323	0.875255	-0.96375	0.313271
1.679499	0.025772	2.052821	0.004593	-1.29509	0.099061	-1.19781	0.091792	-0.98642	0.140914	0.506929	0.479377	-1.67522	0.050065	-0.25713	0.857077	-1.49999	0.024521	-0.37996	0.613359	-0.50929	0.554123	-1.24286	0.087387
3.9483	0.023768	4.739708	0.004784	-3.03485	0.116663	-2.72088	0.107047	-3.37959	0.013835	-2.72693	0.04733	3.041573	0.315532	-0.19551	0.959093	-5.07913	0.000263	-5.21788	0.000112	5.290328	0.010114	-4.88362	0.0007
-0.12872	0.867401	-0.14857	0.838584	-1.35187	0.010839	-0.52303	0.329054	0.716812	0.131107	0.500663	0.305193	0.140177	0.890452	0.590121	0.479538	1.255281	0.007105	1.058987	0.021016	0.549931	0.329131	0.665159	0.22054
-0.06826	0.924166	0.22357	0.697878	0.229384	0.703234	0.37018	0.445459	2.071102	1.65E-07	1.541804	6.46E-05	0.352949	0.61608	0.33835	0.668958	1.563195	0.000154	0.742071	0.076712	-0.22321	0.694869	1.224845	0.005641
-0.53717	0.470784	-1.36337	0.032778	-0.10964	0.914605	-2.15632	0.0003	-0.68299	0.239863	-1.74818	0.001013	0.302911	0.771395	-1.82588	0.017145	-2.04524	0.00025	-2.28423	2.25E-05	-1.59651	0.007339	-0.21936	0.787126
0.741183	0.225658	0.905028	0.116426	-0.55395	0.407692	-0.93481	0.092085	1.667234	0.000532	1.470276	0.001921	-0.30014	0.74225	-0.00556	0.996105	0.374189	0.537097	0.013386	0.991297	-0.852	0.129066	0.379751	0.571519
-0.36753	0.503373	-0.51903	0.298213	-0.07451	0.915857	0.043957	0.939319	2.922976	2.68E-14	3.339451	3.32E-18	-0.06896	0.942342	0.57427	0.418019	2.155476	4.64E-08	2.723451	2.83E-12	-1.204	0.003983	1.581206	0.000144
1.164983	0.01397	1.161766	0.012993	-0.73729	0.154877	-0.38187	0.446403	1.111418	0.00602	1.561814	6.51E-05	-1.57032	0.001149	0.13817	0.885805	-0.97037	0.023262	-0.51676	0.244604	-2.48713	1.25E-09	-1.10854	0.012504
-2.10311	3.21E-05	-2.07814	3.82E-05	0.994511	0.066129	0.471321	0.375696	1.704037	0.001223	2.40129	1.59E-05	6.264699	1.37E-19	-0.22259	0.81859	3.223007	1.9E-10	3.895284	7.52E-13	5.680558	1.23E-16	3.445597	1.24E-11
-0.63022	0.051272	-0.39679	0.230626	0.496247	0.233535	0.226027	0.558162	0.410986	0.208248	1.046436	0.00081	0.428331	0.279123	-0.45043	0.45576	-0.62218	0.084486	-0.22016	0.594885	-1.23505	8.87E-05	-0.17175	0.715232
-0.88877	0.034353	-1.14418	0.004647	0.340462	0.491593	1.145752	0.003576	2.429802	1.64E-09	1.930124	9.58E-07	0.524881	0.331072	0.89944	0.118164	2.410821	3.42E-09	2.166554	4.38E-08	-0.38287	0.396415	1.511381	0.00073
0.487752	0.35052	0.632063	0.192383	-0.86722	0.069062	-0.79535	0.065402	-2.14569	1.16E-08	-2.39445	8.6E-11	-0.69217	0.234457	-0.35553	0.643194	-1.42427	0.000288	-1.81734	1.46E-06	0.517002	0.281492	-1.06874	0.011275
0.754652	0.111532	0.844956	0.063466	-1.73818	9.29E-05	-1.72156	2.64E-05	-1.72177	3.97E-06	-2.03884	2.42E-08	-0.36311	0.594302	-0.39428	0.597611	-0.89999	0.025894	-1.30736	0.000567	1.213326	0.003014	-0.50571	0.282844
1.141702	0.006085	1.048047	0.011648	-0.69643	0.126443	-0.36625	0.407045	1.272169	0.00033	1.869609	5.71E-08	-1.59111	0.000125	0.272571	0.711894	-0.91306	0.015823	-0.22197	0.605709	-2.63464	2.43E-13	-1.18564	0.002067
-0.70171	0.002138	-0.36717	0.129351	0.743522	0.001064	0.594885	0.004879	-0.26707	0.21783	-0.44717	0.025623	0.055173	0.902871	-0.22033	0.558997	0.701178	0.000532	0.186534	0.403536	0.321711	0.169262	0.921512	5.21E-06
0.39996	0.251605	0.007041	0.99256	0.134696	0.748497	0.118103	0.739421	0.749733	0.006505	-0.14737	0.649568	0.086487	0.886981	-0.33377	0.504161	0.674347	0.019422	0.170168	0.59593	0.411061	0.203693	1.008113	0.00043
-0.01584	0.977979	-0.17166	0.668239	0.175543	0.666103	-0.18743	0.584737	0.811128	0.003674	-0.32891	0.267224	0.110747	0.84787	-0.41765	0.388954	1.338092	1.27E-06	0.353878	0.233967	0.621872	0.040927	1.75574	1.3E-10
-0.67173	0.163125	-0.61267	0.197865	1.137303	0.010396	1.270489	0.001758	2.039997	4.6E-07	2.311065	1.11E-08	0.2371	0.744835	0.180265	0.829612	2.82278	1.71E-12	3.034793	5.02E-14	0.348156	0.489562	2.642515	9.15E-11
0.342847	0.469884	0.474439	0.270692	-0.09796	0.858684	-0.23571	0.570235	-0.04725	0.92084	0.076508	0.866671	-0.44204	0.411634	-0.11437	0.879902	0.036197	0.943681	0.028361	0.955858	-0.01575	0.98319	0.150564	0.76826
0.030197	0.957925	-0.07339	0.881019	1.013294	0.001918	1.297287	2.33E-05	2.036449	2.62E-10	2.232012	1.71E-11	-0.1795	0.744434	0.314348	0.577334	2.010833	6.39E-10	2.309979	4.54E-12	-0.17491	0.668675	1.696484	5.6E-07
0.394482	0.321679	0.5007	0.177446	0.953863	0.006139	0.125421	0.753188	1.017017	0.00071	1.249203	2.03E-05	-0.18674	0.745693	-0.76008	0.099751	1.553163	2.11E-07	1.679132	1.06E-08	0.743884	0.024156	2.313247	2.79E-15
0.393269	0.262084	0.330807	0.344114	0.865101	0.00517	0.077196	0.831292	1.068826	7.23E-05	1.167712	1.15E-05	0.006121	0.999933	-0.81863	0.031334	1.565025	5.31E-09	1.726373	6.86E-11	0.895589	0.001611	2.383657	8.66E-20
-0.41226	0.432207	0.251289	0.635524	-0.2848	0.555543	0.147379	0.739611	-0.68122	0.089674	-0.03916	0.944548	-0.26162	0.702178	-0.15068	0.838985	0.879351	0.018681	0.857862	0.018464	0.886694	0.019172	1.030026	0.007586
-0.73854	0.192082	-0.91043	0.089905	1.126432	0.032026	1.530658	0.001162	3.029047	4.67E-09	2.33434	1.99E-06	0.340636	0.677661	0.409858	0.637868	4.136818	3.99E-16	3.614001	7.95E-14	0.709864	0.17635	3.726961	6.36E-13
0.005475	0.999624	0.149948	0.830108	-1.0503	0.031115	-0.88217	0.042005	-2.58554	9.93E-11	-3.18561	2.32E-16	-0.16613	0.856762	-0.71547	0.289873	-0.94005	0.023173	-1.68459	1.02E-05	1.484842	0.000593	-0.22457	0.688665
-0.77204	0.028263	-0.75357	0.029642	1.017694	0.002696	0.675096	0.03531	0.785982	0.009779	0.718509	0.017312	0.721599	0.075374	-0.11659	0.861017	1.661175	1.78E-08	1.575226	5.99E-08	0.824747	0.009908	1.777765	2.24E-09
-0.88876	0.122307	-0.77078	0.17378	0.650277	0.146235	1.676607	7.66E-05	-0.53316	0.331281	-0.34436	0.551581	0.253014	0.753841	0.867121	0.206824	0.912702	0.049268	0.983528	0.030546	0.810124	0.074592	0.045581	0.957946
-1.43474	0.00317	-1.89887	0.000148	1.085269	0.011298	2.847474	7.19E-11	4.184607	0.000412	5.500372	3.2E-05	0.879155	0.118504	1.620815	0.00434	5.697734	1.3E-06	7.47763	1.01E-08	0.957542	0.028719	4.076919	0.001358
-0.12743	0.936542	0.849378	0.410445	-0.55194	0.529193	-1.11132	0.093237	-4.14371	2.24E-09	-3.17933	1.14E-07	-0.77483	0.564578	-0.79227	0.458546	-2.09602	0.000237	-2.10845	0.000145	1.145426	0.131086	-1.30375	0.031507
0.878183	0.309194	0.962809	0.241859	-2.00201	0.001492	-1.65243	0.004204	-3.00041	7.3E-08	-2.14119	0.000141	-0.64861	0.573503	-0.30561	0.784564	0.01425	0.991838	0.788845	0.170486	3.244233	2.81E-08	0.319857	0.670291
-0.71069	0.294275	-0.55431	0.416575	1.327616	0.032922	1.314413	0.019463	3.057772	2.12E-07	5.188152	7.9E-11	0.352469	0.714996	-0.17491	0.887526	2.592578	2.23E-05	4.566578	2.08E-08	-0.82342	0.183479	2.767488	8.33E-06
1	1	1	1	1	1	-1.98785	0.037253	-0.50069	0.682696	0.428261	0.775967	1	1	1	1	0.103872	0.942282	1.189603	0.339277	0.308562	0.83162	1.647741	0.108722
1.289364	0.301143	1.2899	0.284236	-0.08572	0.963326	-0.09235	0.947642	-1.21213	0.232906	-2.46103	0.008288	-1.19918	0.436811	0.090425	0.971846	-1.75689	0.085865	-3.00633	0.001317	-0.45458	0.744802	-1.84732	0.087996
-1.90035	0.532749	1.029378	0.713032	0.524638	0.802432	-1.34647	0.387564	-2.84603	0.194896	1.491739	0.512591	-0.77334	0.846281	-1.64454	0.496268	4.705933	0.003995	6.113976	0.00077	4.878274	0.002668	6.350473	9.96E-05
3.056789	0.306187	1.906465	0.560875	0.546828	0.867434	-2.28666	0.33523	-3.23152	0.096923	-3.2478	0.111753	1.102074	0.835856	1	1	-3.43357	0.091284	-2.29952	0.264377	3.956813	0.137322	-2.23609	0.327326
3.608091	0.188588	0	1	-0.84893	0.752809	-1.94687	0.354357	-5.47273	0.001434	-7.54791	0.000184	0	1	-0.22842	0.960201	-3.81781	0.028775	-2.35241	0.188379	5.421217	0.018884	-3.58938	0.054493
0	1	0	1	0	1	-1.13947	0.738622	-4.13782	0.093772	-2.35103	0.403038	0	1	-2.06584	0.687767	-4.18546	0.104925	-2.48125	0.382595	0	1	-2.11962	0.478107
0	1	0	1	0	1	-1.13947	0.738622	-4.13782	0.093772	-2.35103	0.403038	0	1	-2.06584	0.687767	-4.18546	0.104925	-2.48125	0.382595	0	1	-2.11962	0.478107
22.73646	6.26E-16	22.4347	2.15E-15	-2.74553	0.42297	-1.38113	0.672645	-3.96914	0.132006	-5.26687	0.036907	-16.7687	1.15E-07	0.55736	0.927035	-0.56688	0.87374	-1.56285	0.596342	9.370027	0.000673	-1.12424	0.763814
4.429338	0.166845	3.266349	0.321232	-0.20548	0.965342	-15.9428	1.45E-07	0.017157	1	-0.76444	0.796128	-2.04568	0.667651	1	1	-2.14124	0.443061	-1.75985	0.5173	0.225257	0.960567	-4.25744	0.155202

80 % vs GA3 500 mg/L		OH 280 % vs O.P. 28 D		mg/L vs GA3 500 mg/L		300 mg/L vs O.P. 28		500 mg/L vs O.P. 28	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
-1.07033	0.302143	2.788601	0.002761	0.38815	0.835546	4.247085	1.2E-06	3.858935	8.43E-06
0.013177	1	1.578784	0.429897	1	1	2.078284	0.24748	1.565606	0.379383
0.107575	0.9473	3.337206	0.003768	-1.94306	0.258426	1.286572	0.291861	3.229632	0.003036
-1.31199	0.068346	0.95002	0.219319	-1.62623	0.098445	0.635784	0.408726	2.262009	0.000535
3.002061	0.089889	-3.67309	0.000293	1	1	-6.75071	3.41E-06	-6.67515	3.28E-06
0.337554	0.868589	3.988898	0.019315	1	1	3.749475	0.022457	3.651344	0.023466
0.121535	0.936586	3.246301	0.003376	-1.63518	0.338677	1.489584	0.194992	3.124766	0.002881
-0.55431	0.128489	-1.18689	0.000416	0.235929	0.706842	-0.39665	0.270398	-0.63258	0.057029
-1.59606	0.001448	-1.84786	0.000174	0.345084	0.707548	0.093279	0.885778	-0.2518	0.645088
-0.55877	0.676885	1.569279	0.196432	0.736972	0.713864	2.865021	0.00751	2.128049	0.04803
2.064259	3.04E-05	0.201991	0.754375	0.608412	0.457004	-1.25386	0.010326	-1.86227	8.1E-05
4.162181	0.01174	-3.48681	0.000148	0	1	-7.70878	1.43E-07	-7.649	1.25E-07
-2.0715	5.64E-05	1.023298	0.063563	0.070477	0.958012	3.165274	9.05E-11	3.094797	1.44E-10
-1.09712	0.093382	-1.07092	0.10214	0.243967	0.843221	0.270165	0.702302	0.026199	0.977999
-1.45102	0.398389	2.070556	0.247208	1	1	3.62091	0.020422	3.521571	0.021561
-2.11061	1.36E-05	-1.8902	9.9E-05	-0.64442	0.402975	-0.424	0.428458	0.220413	0.681293
4.770361	0.001844	-2.97329	5.91E-05	-0.07747	0.993128	-7.82112	3.1E-08	-7.74365	2.89E-08
0.793499	0.024856	-0.67311	0.062194	0.49455	0.355221	-0.97205	0.003399	-1.4666	4.49E-06
-0.03152	0.969498	1.630192	0.003462	-0.76617	0.379541	0.89554	0.113865	1.661714	0.001584
-2.09321	0.003253	-1.37209	0.066561	-0.53286	0.656492	0.188256	0.82189	0.721119	0.291248
3.074583	0.037191	-3.2297	4.42E-05	-0.88303	0.817239	-7.18732	4.5E-07	-6.30428	9.06E-07
-1.25406	0.00649	-2.61147	1.05E-09	-0.80647	0.234069	-2.16387	2.06E-07	-1.35741	0.00098
4.052643	0.011825	-3.505	3.15E-05	0	1	-7.61742	8.5E-08	-7.55764	7.48E-08
-2.03445	9.75E-05	0.438999	0.487486	-1.1421	0.136002	1.331345	0.010099	2.47345	4.84E-07
-0.82858	0.321536	2.868844	0.000682	-1.30669	0.251085	2.390726	0.004332	3.697421	2.67E-06
4.052643	0.011825	-3.505	3.15E-05	0	1	-7.61742	8.5E-08	-7.55764	7.48E-08
-0.08072	0.811988	-0.2612	0.385494	-0.33462	0.418956	-0.51509	0.047667	-0.18048	0.513275
-1.22468	0.064911	1.46542	0.02461	-0.27011	0.832378	2.419993	5.51E-05	2.690102	4.9E-06
3.052751	2.12E-07	-5.16951	1.04E-22	0.874793	0.374402	-7.34747	1.09E-43	-8.22226	1.19E-50
4.679987	0.003637	-2.61033	0.003724	1	1	-7.3501	5.32E-07	-7.29031	4.71E-07
-0.15646	0.706342	1.668263	3.27E-07	-0.09759	0.895898	1.727132	5.18E-08	1.82472	5.38E-09
-1.71868	0.00521	-2.43103	2.72E-05	-0.79783	0.38747	-1.51018	0.006541	-0.71234	0.201477
-0.3296	0.853386	-2.821	0.012881	1	1	-2.51899	0.021468	-2.4914	0.020959
2.860752	0.041269	-2.0722	0.00316	1	1	-2.3247	0.001166	-4.93295	5.29E-05
-0.40104	0.316644	-0.08697	0.861565	0.083816	0.9216	0.397884	0.29598	0.314068	0.398964
-0.32989	0.841416	-3.37915	0.001504	1	1	-2.43752	0.012063	-3.04926	0.002991
0.573706	0.069917	-2.05908	3.41E-13	0.07963	0.908305	-2.55316	2.55E-20	-2.63279	7.67E-22
2.471777	3.24E-16	-1.47951	1.13E-08	0.19805	0.772654	-3.75324	2.2E-40	-3.95128	1.46E-42
5.10479	0.000642	-2.99385	1.34E-05	0	1	-8.15842	3.03E-09	-8.09863	2.54E-09
-1.61357	0.010059	-2.89328	1.03E-06	0.135394	0.925647	-1.14432	0.057796	-1.27971	0.028322
2.473384	0.002501	0.638961	0.388488	0.1288	0.957802	-1.70562	0.031016	-1.83442	0.021036
-0.87236	0.000523	0.236432	0.425915	-0.23053	0.594653	0.878264	0.000277	1.10879	2.41E-06
0.580743	0.826971	-5.69854	0.000177	1	1	-6.33907	1.43E-05	-6.27928	1.32E-05
4.912853	0.001693	-2.9593	0.000282	0	1	-7.93194	2.92E-08	-7.87215	2.51E-08
-0.67378	0.018505	-1.13674	2.79E-05	0.44631	0.290935	-0.01666	0.970868	-0.46296	0.090449
0.832673	0.606366	1.078015	0.482976	1	1	-1.76985	0.357494	0.245342	0.887173
0.592135	0.007206	-0.40649	0.07447	0.363664	0.268023	-0.63496	0.002308	-0.99863	6.99E-07
-1.79927	0.020286	-4.45637	7.76E-10	1.998479	0.057514	-0.65863	0.426757	-2.65711	0.000177
4.870552	2.49E-14	-2.1066	4.36E-06	0.886339	0.468472	-6.09081	5.33E-30	-6.97715	9.63E-30
1.297235	0.000723	-0.79462	0.045069	-0.23091	0.758509	-2.32276	1.02E-10	-2.09185	3.83E-09

-1.95209	5.4E-06	-3.14051	4.92E-14	0.40766	0.574816	-0.78076	0.067826	-1.18842	0.003394
2.106674	0.023704	1.761514	0.051156	1	1	0.456463	0.660979	-0.34516	0.744987
-1.23427	0.039931	-1.73192	0.001511	1	1	-0.35662	0.511799	-0.49765	0.327969
-2.75036	0.00041	1.509571	0.069603	-1.78661	0.111787	2.473318	0.001063	4.259931	4.56E-09
-0.12283	0.887623	-0.25216	0.766549	1.120029	0.248616	0.990699	0.135087	-0.12933	0.867909
-5.02237	0.000304	5.485838	0.004869	-0.13875	0.970514	10.36946	7.3E-09	10.50821	2.91E-09
0.468865	0.368008	-0.04019	0.956448	-0.19629	0.832484	-0.70535	0.1344	-0.50906	0.278308
0.403721	0.389038	-0.56156	0.207902	-0.82112	0.189702	-1.78641	5.54E-06	-0.96528	0.014027
-0.45835	0.46869	0.229366	0.746207	-0.23899	0.827466	0.448725	0.457442	0.687718	0.211178
0.018948	0.98216	-0.84644	0.107825	-0.3608	0.69716	-1.22619	0.011929	-0.86538	0.075039
2.149181	9.03E-08	-1.77826	4.67E-06	0.567975	0.395046	-3.35947	6.96E-19	-3.92745	4.44E-25
-0.65493	0.14348	-2.6253	3.38E-11	0.453614	0.505116	-1.51676	0.000108	-1.97037	2.67E-07
4.117875	5.32E-14	5.903148	1.83E-18	0.672277	0.527604	2.457551	0.000729	1.785274	0.01976
0.230272	0.581919	-0.78462	0.009947	0.402017	0.482937	-0.61288	0.042653	-1.01489	0.000901
1.267113	0.003234	-1.28231	0.000489	-0.24427	0.792746	-2.79369	1.3E-12	-2.54943	2.52E-11
-1.46181	0.000187	0.872536	0.033951	-0.39307	0.554071	1.941276	1.79E-07	2.334346	1.67E-10
-0.91308	0.023202	1.607608	2.55E-05	-0.40737	0.531932	2.113314	7.75E-09	2.520687	2.54E-12
-0.49454	0.225054	-2.90721	1.07E-16	0.691095	0.208407	-1.72158	5.9E-07	-2.41267	1.05E-12
0.406868	0.054189	0.542045	0.007889	-0.51464	0.072566	-0.37947	0.063693	0.135177	0.531506
0.503934	0.084467	0.744827	0.007259	-0.50418	0.236128	-0.26329	0.392069	0.240893	0.407272
0.771527	0.006216	1.03952	0.000136	-0.98421	0.008864	-0.71622	0.010161	0.267993	0.355797
2.854528	3.14E-12	0.167891	0.738855	0.212013	0.818969	-2.47462	3.77E-10	-2.68664	1.31E-11
0.142728	0.74682	0.09862	0.826141	-0.00784	0.996269	-0.05194	0.909753	-0.04411	0.918055
1.99563	7.22E-09	-0.48926	0.125796	0.299146	0.673127	-2.18575	4.44E-12	-2.48489	2.17E-14
2.439216	5.06E-17	1.503968	3.25E-07	0.125969	0.844559	-0.80928	0.007335	-0.93525	0.001495
2.545005	2.22E-22	1.714221	5.01E-11	0.161348	0.771958	-0.66944	0.015275	-0.83078	0.001966
1.008537	0.006415	1.037369	0.003351	-0.02149	0.987869	0.007343	0.997559	0.028832	0.95479
3.204143	8.85E-11	0.300006	0.588961	-0.52282	0.617089	-3.42696	1.28E-11	-2.90414	1.3E-09
-0.96911	0.016814	2.200316	4.26E-08	-0.74454	0.205941	2.42489	4.8E-10	3.16943	8.63E-17
1.691816	9.54E-09	0.941336	0.001708	-0.08595	0.902924	-0.83643	0.005121	-0.75048	0.011052
0.116407	0.857205	-0.057	0.933605	0.070826	0.956304	-0.10258	0.863506	-0.1734	0.747188
5.856815	1.83E-05	-0.66327	0.186177	1.779896	0.555214	-4.74019	3.96E-05	-6.52009	3.8E-07
-1.31618	0.021326	1.937694	0.002724	1	1	3.241446	3.85E-08	3.253878	2.38E-08
1.094451	0.055593	3.54984	2.88E-10	0.774595	0.367209	3.229983	4.8E-09	2.455389	1.02E-05
4.741487	9.85E-09	-0.64851	0.276757	1.974	0.136633	-3.416	3.31E-09	-5.39	8.04E-12
2.733472	0.013667	1.85243	0.041153	1	1	0.204689	0.872444	-0.88104	0.470023
-3.09675	0.001273	-0.545	0.651463	-1.24943	0.409779	1.302317	0.192483	2.551752	0.005314
7.758516	2.26E-05	6.522815	1.59E-05	1.408043	0.71599	0.172342	0.94726	-1.2357	0.573379
-1.10205	0.629081	5.154288	0.028978	1	1	7.390381	0.000622	6.256336	0.003761
-2.12399	0.25587	5.649641	0.009504	1.465394	0.612429	9.239024	3.83E-06	7.77363	9.55E-05
-0.41541	0.902614	2.161339	0.485841	1	1	4.28096	0.078751	2.576748	0.334604
-0.41541	0.902614	2.161339	0.485841	1	1	4.28096	0.078751	2.576748	0.334604
-2.12022	0.47368	8.812667	0.000908	-0.99597	0.849379	9.936908	9.2E-05	10.93288	1.16E-05
-3.87605	0.16796	-1.89095	0.555248	1	1	2.366497	0.359246	1.985106	0.428275

Table S4.4: Table with Log2FoldChange (log2FC) and p-value adjusted (p-adj) of the genes that are involved in auxin biosynthesis, conjugation and transport. The heatmap of these genes is showed in Fig. 4.14. Log2FC is calculated according to the following formula: expression level term1 - expression level term2.

Gene name	Gene description	N.C. 0 vs 7 DAT		EtOH 70% 0 vs 7 DAT		A3 300 mg/L 0 vs 7 DA		A3 500 mg/L 0 vs 7 DA		O.P. 0 vs 7 DAT		N.C. vs EtOH 7 DAT		. vs GA3 300 mg/L 7 D		. vs GA3 500 mg/L 7 D		N.C. vs O.P. 7 DAT		70 % vs GA3
		Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
Pav_sc0000848.1_g430.1.mk	PavTIR1	0.046869	0.959034	-0.02039	1	0.372711	0.068123	0.315907	0.12852	0.184424	0.518033	-0.06726	1	0.325842	0.242163	0.269037	0.305102	0.137555	0.789507	0.393101
Pav_sc0000598.1_g680.1.mk	PavTIR1	0.005162	1	0.069902	0.98318	0.042668	0.874312	0.241146	0.184368	0.14167	0.575121	0.064739	1	0.037506	0.929306	0.235983	0.288069	0.136507	0.74245	-0.02723
Pav_sc0006018.1_g520.1.mk	PavTAR2	0.565607	0.538296	0.59345	0.54254	1.467235	0.000502	1.750784	1.91E-05	0.666885	0.223583	0.027843	1	0.901628	0.13688	1.185177	0.021184	0.101278	0.947177	0.873785
Pav_sc0001258.1_g020.1.mk	PavYUC4	-0.0829	0.980808	-0.04198	1	1.334794	0.043812	0.96789	0.161951	-0.93204	0.228155	0.040922	1	1.417693	0.085759	1.050789	0.198654	-0.84914	0.466006	1.376771
Pav_sc0000800.1_g1260.1.mk	PavYUC6	-1.24062	0.049114	-0.80524	0.393177	-2.90159	2.59E-11	-2.94296	1.04E-11	-1.1762	0.030842	0.435372	1	-1.66098	0.002324	-1.70234	0.001269	0.064417	0.972905	-2.09635
Pav_sc0000848.1_g330.1.mk	PavYUC10	-0.3066	0.899036	-0.41272	0.936705	-0.62835	0.432927	-0.56005	0.48337	-0.41794	0.69803	-0.10612	1	-0.32175	0.82469	-0.25345	0.828145	-0.11134	0.960552	-0.21564
Pav_sc0000049.1_g070.1.mk	PavGH3.1	0.050327	0.998356	0.526769	0.980637	-1.71979	0.184316	-1.37425	0.305581	-0.22598	0.932281	0.476442	1	-1.77012	0.304256	-1.42457	0.382002	-0.2763	0.944991	-2.24656
Pav_sc0001422.1_g120.1.mk	PavGH3.1	-1.02732	0.511309	-0.82967	0.721191	-2.19543	0.003079	-1.96199	0.008668	-0.3101	0.836252	0.197645	1	-1.16811	0.304867	-0.93467	0.386491	0.717217	0.698443	-1.36576
Pav_sc0000269.1_g440.1.mk	PavGH3.6	-0.49564	0.858495	-0.83777	0.770741	0.816343	0.440275	0.915959	0.358471	0.098674	0.961977	-0.34213	1	1.311983	0.291393	1.4116	0.191167	0.594315	0.791512	1.654113
Pav_sc0000848.1_g820.1.mk	PavGH3.9	-0.63329	0.783069	-0.28484	0.990859	-0.2288	0.861109	-0.29245	0.81295	0.857945	0.457485	0.34845	1	0.404486	0.824843	0.340837	0.812365	1.491234	0.2215	0.056036
Pav_sc0002360.1_g300.1.mk	PavGH3.10	0.148247	0.936723	0.020667	1	0.713496	0.139661	0.273346	0.640146	0.003075	1	-0.12758	1	0.565249	0.42903	0.125099	0.877448	-0.14517	0.920057	0.692829
Pav_sc0000254.1_g140.1.mk	PavGH3.11	-0.23883	0.793704	-0.32415	0.748151	-0.19837	0.648657	0.090145	0.859212	0.229267	0.653607	-0.08532	1	0.040455	0.964303	0.328973	0.473096	0.468095	0.397821	0.125778
Pav_sc0003065.1_g090.1.mk	PavGH3.12	0.199491	0.806682	-0.14967	0.961236	0.50061	0.08914	0.580718	0.03755	0.039482	0.952243	-0.34916	1	0.301119	0.525072	0.381227	0.311486	-0.16001	0.839163	0.650279
Pav_sc0001218.1_g170.1.mk	PavPIN1	0.065178	0.985084	0.050535	1	0.027561	0.984907	-0.14855	0.878787	-0.32059	0.761351	-0.01464	1	-0.03762	0.985896	-0.21373	0.846102	-0.38576	0.813809	-0.02297
Pav_sc0001181.1_g1180.1.mk	PavPIN2	0.603895	0.120079	0.615027	0.111803	0.850678	0.001851	0.862164	0.001362	1.500255	8.38E-10	0.011132	1	0.246784	0.649772	0.258269	0.550276	0.896361	0.004383	0.235651
Pav_sc0000103.1_g670.1.mk	PavPIN4	0.302401	0.894251	0.412656	0.925649	0.035487	0.979193	0.129583	0.901139	0.58999	0.512126	0.110255	1	-0.26691	0.851647	-0.17282	0.880365	0.287589	0.87903	-0.37717
Pav_sc0000744.1_g330.1.mk	PavPIN5	-0.32681	0.903803	-0.23989	0.993242	0.065715	0.96175	0.262738	0.809752	0.908361	0.33965	0.086927	1	0.392528	0.804833	0.589552	0.592754	1.235174	0.271854	0.305601
Pav_sc0002842.1_g240.1.mk	PavPIN6	-0.11972	0.956736	-0.23989	0.971917	0.433995	0.465944	0.417205	0.47474	-0.22433	0.796659	-0.12017	1	0.55371	0.477394	0.53692	0.42511	-0.10462	0.94845	0.673881
Pav_sc0000299.1_g150.1.mk	PavPIN8	-0.07763	0.959371	-0.01784	1	0.076438	0.893356	-0.0057	0.996689	-0.07125	0.924606	0.059789	1	0.154065	0.842789	0.071925	0.9145	0.00638	0.998826	0.094276
Pav_sc0001687.1_g170.1.mk	PavAUX1	0.9595	0.048787	1.027048	0.02707	0.395307	0.421291	0.467352	0.306808	1.072572	0.006857	0.067548	1	-0.56419	0.353364	-0.49215	0.375464	0.113072	0.931753	-0.63174
Pav_sc0000030.1_g1280.1.mk	PavLAX2	0.414571	0.868659	-0.19068	0.99688	0.629633	0.503735	0.84772	0.319637	2.245502	0.001497	-0.60525	1	0.215062	0.909222	0.433149	0.725419	1.830931	0.044744	0.82031
Pav_sc0000373.1_g220.1.mk	PavLAX2	0.405486	0.837444	0.623676	0.770741	0.777575	0.290716	0.950406	0.163798	0.545644	0.567077	0.218191	1	0.37209	0.786291	0.544921	0.570562	0.140159	0.948278	0.153899

3 300 mg/L	70 % vs GA3 500 mg/L		tOH 70 % vs O.P. 7 DA		0 mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 7 D		3 500 mg/L vs O.P. 7 D		N.C. 7 vs 14 DAT		EtOH 70% 7 vs 14 DAT		A3 300 mg/L 7 vs 14 DA		A3 500 mg/L 7 vs 14 D		O.P. 7 vs 14 DAT		N.C. vs EtOH 14 DAT		. vs GA3 30
p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
0.075443	0.336297	0.119767	0.204815	0.551908	-0.0568	1	-0.18829	0.505209	-0.13148	0.711543	-0.10435	0.835009	-0.22144	0.429777	-0.55986	0.001821	-0.59776	0.000798	-0.21914	0.350362	-0.18436	0.868884	-0.12967
0.929104	0.171244	0.406925	0.071768	0.857451	0.198478	1	0.099002	0.719286	-0.09948	0.751468	0.099557	0.807739	0.030326	0.92702	-0.16838	0.353725	-0.11192	0.580904	0.047109	0.856837	-0.00449	1	-0.23044
0.092289	1.157334	0.015024	0.073434	0.956803	0.283549	1	-0.80035	0.138831	-1.0839	0.039674	0.339684	0.740149	0.466416	0.48185	0.394206	0.45455	0.10312	0.880005	1.518357	0.000612	0.154576	0.971034	0.956151
0.056942	1.009867	0.160609	-0.89007	0.3547	-0.3669	1	-2.26684	0.000294	-1.89993	0.004842	-0.17617	0.930377	0.225587	0.851554	1.244183	0.067393	0.970924	0.15795	2.89338	9.39E-07	0.442674	0.903446	2.838041
1.85E-05	-2.13771	1.04E-05	-0.37095	0.72094	-0.04136	1	1.725393	0.000589	1.766758	0.000565	-0.27855	0.829926	-0.2188	0.81769	1.18924	0.01312	1.099172	0.023522	-0.7285	0.211008	0.495119	0.864575	-0.19319
0.843186	-0.14733	0.897437	-0.00522	1	0.068304	1	0.210418	0.860551	0.142113	0.926639	-1.06605	0.26201	-0.7609	0.399451	-1.61181	0.00642	-2.04749	0.000372	-1.83814	0.00322	0.199026	0.97428	-0.86752
0.09396	-1.90102	0.145994	-0.75275	0.762148	0.345546	1	1.493817	0.334603	1.148271	0.54233	0.048763	0.995139	-0.33738	0.884338	0.144339	0.936628	0.576248	0.700883	-0.33743	0.853369	0.090296	1	-1.67454
0.130172	-1.13232	0.198546	0.519572	0.748745	0.233439	1	1.885328	0.024074	1.651889	0.075089	0.557381	0.756788	1.108354	0.288612	1.795926	0.013869	1.393017	0.067573	-0.90115	0.327546	0.748618	0.864732	0.070434
0.087169	1.753729	0.054108	0.936444	0.519755	0.099617	1	-0.71767	0.570783	-0.81729	0.553871	1.535239	0.200781	0.756157	0.562256	1.549232	0.06631	1.849771	0.024328	2.314613	0.006721	-1.12121	0.773408	1.325977
0.971311	-0.00761	0.996689	1.142784	0.366649	-0.06365	1	1.086748	0.310591	1.150397	0.312737	2.960122	0.000327	3.042059	0.000256	3.284652	1.88E-05	2.778643	0.000289	-0.21105	0.872713	0.430386	0.941287	0.729016
0.1929	0.252679	0.683657	-0.01759	0.993926	-0.44015	1	-0.71042	0.193554	-0.27027	0.738333	-0.17634	0.883502	-0.5685	0.320343	-1.18167	0.00353	-0.7499	0.077102	-0.10154	0.884454	-0.51974	0.798398	-0.44008
0.808635	0.414296	0.26187	0.553418	0.216223	0.288518	1	0.42764	0.300948	0.139122	0.832799	0.065105	0.954144	-0.06755	0.915515	-0.46259	0.152224	-0.89026	0.002256	-0.59271	0.082549	-0.21798	0.905901	-0.48724
0.031893	0.730387	0.011071	0.189151	0.737071	0.080108	1	-0.46113	0.171506	-0.54124	0.118447	-0.24203	0.67869	-0.00972	0.988505	-0.39694	0.165567	-0.54715	0.043125	0.017731	0.974843	-0.11684	0.957026	0.146211
0.984641	-0.19908	0.841227	-0.37112	0.772702	-0.17611	1	-0.34815	0.726433	-0.17204	0.899065	-0.11378	0.957473	0.099865	0.934154	0.589535	0.37235	0.641387	0.328124	0.577597	0.432934	0.199003	0.972736	0.665699
0.559808	0.247137	0.508183	0.885229	0.004382	0.011485	1	0.649577	0.041857	0.638092	0.059708	0.694295	0.04189	0.573377	0.099485	-0.19466	0.567785	-0.18169	0.605968	-0.37152	0.268291	-0.10979	0.967475	-0.64217
0.685163	-0.28307	0.760306	0.177334	0.918104	0.094095	1	0.554503	0.540668	0.460408	0.672539	0.131124	0.952345	0.50474	0.601792	0.699978	0.290193	0.501719	0.48403	-0.20666	0.830149	0.483871	0.889829	0.30194
0.794826	0.502625	0.608206	1.148247	0.278297	0.197023	1	0.842646	0.394723	0.645623	0.591072	0.695486	0.634307	1.140984	0.226483	1.213551	0.093757	1.112054	0.134085	-1.40256	0.068988	0.532425	0.899469	0.910594
0.24457	0.657091	0.228371	0.015552	0.996339	-0.01679	1	-0.65833	0.280679	-0.64154	0.33915	0.341571	0.755397	0.830122	0.163651	1.885295	9.68E-06	1.64494	0.000141	0.90156	0.076316	0.36838	0.891517	2.097434
0.873418	0.012136	0.984424	-0.05341	0.958539	-0.08214	1	-0.14768	0.806237	-0.06554	0.937508	-0.45928	0.397973	-0.30501	0.548967	-0.55593	0.096078	-0.41403	0.243212	-0.6816	0.049224	0.21406	0.912664	0.057424
0.186767	-0.5597	0.223973	0.045524	0.973365	0.072044	1	0.677264	0.159987	0.60522	0.266011	-0.15895	0.889885	-0.55284	0.309259	-0.94571	0.01144	-1.02927	0.005506	-0.96572	0.01769	-0.32634	0.885519	-1.35095
0.391604	1.038397	0.221655	2.436179	0.001639	0.218087	1	1.615869	0.050741	1.397782	0.13223	1.672469	0.065651	0.334238	0.803288	-0.56979	0.50273	-0.83317	0.297256	-0.87482	0.319158	-1.94348	0.213805	-2.0272
0.891221	0.32673	0.723517	-0.07803	0.968892	0.172831	1	-0.23193	0.839544	-0.40476	0.726959	1.039777	0.273936	1.270013	0.098165	2.023456	0.000529	1.902853	0.001242	2.212724	0.000257	0.448427	0.903446	1.355769

0 mg/L 14	. vs GA3 500 mg/L 14		N.C. vs O.P. 14 DAT		40 % vs GA3 300 mg/L		40 % vs GA3 500 mg/L		OH 140 % vs O.P. 14 D		mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 14		3 500 mg/L vs O.P. 14		N.C. 14 vs 21 DAT		tOH 70% 14 vs 21 DA		3 300 mg/L 14 vs 21 D		3 500 mg/L
p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
0.673273	-0.22437	0.391483	0.022757	0.977455	0.054685	0.87315	-0.04002	0.914841	0.207115	0.410177	-0.0947	1	0.15243	0.751516	0.24713	0.516775	-0.26936	0.282953	-0.14749	0.712774	0.051814	0.836599	0.198183
0.26707	0.02451	0.949965	0.084059	0.845217	-0.22594	0.263829	0.029002	0.930614	0.088551	0.72433	0.254946	1	0.314495	0.229299	0.059549	0.914726	-0.37701	0.051024	-0.35096	0.170124	-0.19651	0.247011	-0.32867
0.060309	0.948613	0.062051	1.279951	0.019828	0.801575	0.122197	0.794038	0.13115	1.125376	0.023211	-0.00754	1	0.3238	0.788792	0.331338	0.795981	0.440579	0.485062	0.054135	0.9653	-0.23689	0.667885	-0.65149
4.36E-06	2.197878	0.000484	2.220401	0.001775	2.395367	0.000211	1.755204	0.008455	1.777727	0.009455	-0.64016	1	-0.61764	0.710698	0.022522	0.996043	1.102868	0.157963	1.473381	0.12649	3.012083	0.001118	2.000912
0.839841	-0.32462	0.697614	-0.38554	0.733139	-0.68831	0.271372	-0.81974	0.169179	-0.88066	0.133661	-0.13143	1	-0.19235	0.901837	-0.06092	0.977047	1.278515	0.030922	0.675409	0.456885	1.623104	0.000461	1.857871
0.273184	-1.23489	0.080151	-0.88343	0.382958	-1.06655	0.136146	-1.43392	0.030157	-1.08246	0.135528	-0.36737	1	-0.01591	1	0.351462	0.848881	-0.69913	0.413511	-0.81253	0.46685	-2.50569	5.43E-06	-2.09755
0.247487	-0.89709	0.618015	-0.6625	0.818179	-1.76484	0.198716	-0.98739	0.552917	-0.7528	0.658125	0.777455	1	1.012044	0.716759	0.23459	0.953526	2.756706	0.052395	0.931309	0.697383	2.812731	0.009925	2.526677
0.969887	-0.09904	0.958807	-0.74132	0.629495	-0.67818	0.528459	-0.84765	0.408393	-1.48993	0.085181	-0.16947	1	-0.81175	0.630692	-0.64228	0.735993	0.398193	0.755436	-0.7761	0.598625	1.425668	0.056861	1.818553
0.200136	1.726132	0.07185	1.373689	0.280383	2.447188	0.003925	2.847343	0.000581	2.4949	0.004318	0.400155	1	0.047712	0.992986	-0.35244	0.900927	-1.35833	0.200593	-0.76835	0.645238	0.507139	0.611578	-0.78221
0.582634	0.159358	0.936447	-1.67994	0.139153	0.29863	0.847809	-0.27103	0.863247	-2.11033	0.019755	-0.56966	1	-2.40896	0.032955	-1.8393	0.147126	2.126017	0.064298	1.395924	0.397999	4.110287	0.004998	2.992508
0.442157	-0.44846	0.437013	-0.07037	0.962678	0.079659	0.91586	0.071277	0.930676	0.449372	0.404436	-0.00838	1	0.369713	0.710642	0.378096	0.704035	-0.45975	0.41928	0.137699	0.89034	0.474219	0.28003	-0.60803
0.201697	-0.6264	0.075856	-0.18972	0.80413	-0.26927	0.540609	-0.40842	0.29729	0.028262	0.967348	-0.13915	1	0.297528	0.682339	0.43668	0.458563	-0.59032	0.122489	-0.43098	0.431834	-0.77978	0.007072	-0.43399
0.752507	0.076112	0.893493	0.099757	0.89441	0.263052	0.475581	0.192953	0.63825	0.216598	0.568534	-0.0701	1	-0.04645	0.960832	0.023645	0.985091	-0.45134	0.180081	-0.38456	0.410129	-0.39362	0.149499	-0.30491
0.411718	0.541442	0.53538	0.305613	0.842775	0.466696	0.587927	0.34244	0.718849	0.10661	0.925768	-0.12426	1	-0.36009	0.824946	-0.23583	0.90479	0.900658	0.236304	0.327701	0.805886	2.055632	0.000144	2.186386
0.040102	-0.61771	0.049383	-0.16945	0.808902	-0.53239	0.095077	-0.50793	0.11982	-0.05967	0.909644	0.024463	1	0.472724	0.320286	0.448261	0.380915	-0.34214	0.371856	-0.61602	0.162406	-0.55726	0.041739	-0.56763
0.779114	0.197776	0.872447	-0.0502	0.988154	-0.18193	0.866606	-0.28609	0.778965	-0.53407	0.525242	-0.10416	1	-0.35214	0.836216	-0.24798	0.902368	0.606728	0.480462	0.027197	0.988218	0.922097	0.132868	1.254792
0.334772	1.00612	0.271922	-0.86287	0.488516	0.378169	0.741257	0.473695	0.673305	-1.3953	0.081948	0.095526	1	-1.77347	0.079298	-1.86899	0.062552	0.764687	0.441698	-0.07615	0.97107	1.930182	0.007038	2.3419
1.57E-06	1.840289	3.82E-05	0.45537	0.628621	1.729054	0.000149	1.471908	0.001709	0.086989	0.9229	-0.25715	1	-1.64207	0.002936	-1.38492	0.024339	0.486923	0.456148	0.071428	0.954043	1.498567	0.000971	2.257034
0.930949	0.117177	0.853975	-0.21594	0.77175	-0.15664	0.765568	-0.09688	0.868932	-0.43	0.278488	0.059753	1	-0.27336	0.724449	-0.33311	0.639942	-0.32128	0.464556	-0.55701	0.293115	0.22397	0.54668	0.433169
0.000404	-1.36247	0.000341	-0.6937	0.222965	-1.02461	0.01125	-1.03613	0.010236	-0.36736	0.490907	-0.01151	1	0.657252	0.316294	0.668766	0.322073	-0.48324	0.359737	-0.64625	0.330267	-1.0852	0.002627	-1.13985
0.007161	-2.07249	0.005409	-0.71636	0.624557	-0.08372	0.953657	-0.12901	0.930614	1.227119	0.152552	-0.04529	1	1.31084	0.266189	1.356133	0.25865	-1.49295	0.091756	-0.79571	0.560855	-2.32235	0.000459	-2.32816
0.056353	1.407997	0.04421	1.313105	0.125474	0.907342	0.243189	0.95957	0.212465	0.864678	0.273455	0.052228	1	-0.04266	0.990178	-0.09489	0.968203	1.288853	0.093194	0.858148	0.445862	2.663234	2.71E-05	2.293959

14 vs 21 D	O.P. 14 vs 21 DAT		N.C. vs EtOH 21 DAT		. vs GA3 300 mg/L 21		. vs GA3 500 mg/L 21		N.C. vs O.P. 21 DAT		10 % vs GA3 300 mg/L		10 % vs GA3 500 mg/L		OH 210 % vs O.P. 21 D		mg/L vs GA3 500 mg/		300 mg/L vs O.P. 21		500 mg/L vs O.P. 21		N.C. 21 v
p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
0.324288	-0.07324	0.851679	-0.06248	1	0.191506	0.382119	0.243175	0.254417	0.218886	0.340643	0.253985	0.213863	0.305654	0.133165	0.281365	0.169193	0.051669	1	0.027379	0.928026	-0.02429	0.934318	-0.15738
0.033771	-0.15774	0.533881	0.021556	1	-0.04994	0.830472	0.072845	0.747245	0.303321	0.079518	-0.07149	0.740918	0.051289	0.828445	0.281765	0.094011	0.122782	1	0.353258	0.034181	0.230476	0.182393	0.213369
0.150859	0.164833	0.867243	-0.23187	1	0.27868	0.627211	-0.14345	0.826115	1.004205	0.034981	0.510548	0.305065	0.088417	0.898274	1.236074	0.005089	-0.42213	1	0.725526	0.146748	1.147657	0.012596	-0.75772
0.005095	1.346661	0.138755	0.813186	1	4.747256	2.18E-08	3.095922	4.43E-06	2.464194	0.00021	3.934069	6.4E-06	2.282736	0.001519	1.651007	0.019394	-1.65133	1	-2.28306	0.030103	-0.63173	0.514396	3.133845
4.27E-05	0.421585	0.603161	-0.10799	1	0.151402	0.837955	0.254735	0.714635	-1.24247	0.014043	0.259389	0.696643	0.362722	0.572749	-1.13448	0.022626	0.103333	1	-1.39387	0.005581	-1.4972	0.002487	0.149348
0.000144	-1.28537	0.081286	0.085626	1	-2.67408	6.74E-07	-2.63331	1.19E-06	-1.46967	0.017529	-2.7597	2.46E-07	-2.71894	4.57E-07	-1.5553	0.008824	0.040763	1	1.204408	0.05802	1.163645	0.061195	-0.147
0.021243	-2.83129	0.029876	-1.7351	1	-1.61852	0.212014	-1.12712	0.438046	-6.2505	2.93E-09	0.116582	0.953701	0.607982	0.701207	-4.5154	1.72E-05	0.491401	1	-4.63198	2.3E-05	-5.12338	2.5E-06	-2.84199
0.010754	0.403752	0.773783	-0.42567	1	1.097909	0.177759	1.321325	0.101653	-0.73576	0.440683	1.523582	0.042686	1.746997	0.020563	-0.31008	0.766414	0.223416	1	-1.83367	0.01766	-2.05708	0.006363	-2.19353
0.387875	0.772827	0.567252	-0.53123	1	3.19145	2.2E-05	2.302254	0.003966	3.50485	5.86E-06	3.722682	4.01E-07	2.833485	0.000213	4.036081	8.86E-08	-0.8892	1	0.3134	0.791332	1.202596	0.182645	-2.35025
0.003581	4.056676	2.58E-05	-0.29971	1	2.713286	0.10242	1.02585	0.48332	0.250718	0.892236	3.012993	0.058282	1.325556	0.325783	0.550425	0.697675	-1.68744	1	-2.46257	0.162684	-0.77513	0.604487	0.255579
0.125414	-0.11987	0.894458	0.077711	1	0.493891	0.281085	-0.59674	0.166912	0.269509	0.634064	0.41618	0.37503	-0.67445	0.110295	0.191799	0.729437	-1.09063	1	-0.22438	0.681376	0.866253	0.033886	0.551207
0.159269	-0.21341	0.687576	-0.05864	1	-0.67671	0.025063	-0.47007	0.155493	0.187195	0.666083	-0.61807	0.040988	-0.41143	0.227259	0.245835	0.514297	0.206634	1	0.863903	0.004757	0.657269	0.03434	0.037512
0.273594	0.200753	0.661794	-0.05007	1	0.203931	0.529063	0.222541	0.4982	0.751845	0.004185	0.254	0.403173	0.27261	0.380573	0.801915	0.001546	0.01861	1	0.547915	0.050224	0.529304	0.053877	-0.30298
3.99E-05	0.305886	0.780588	-0.37395	1	1.820672	0.000881	1.82717	0.000994	-0.28916	0.738974	2.194626	3.39E-05	2.201124	3.91E-05	0.084795	0.928594	0.006498	1	-2.10983	0.000219	-2.11633	0.000196	0.155847
0.033901	-0.3205	0.43769	-0.38366	1	-0.85729	0.000982	-0.8432	0.001455	-0.14781	0.717583	-0.47363	0.098408	-0.45954	0.123499	0.235853	0.488575	0.014094	1	0.709482	0.012288	0.695388	0.013103	-0.72725
0.029169	0.006745	1	-0.09566	1	0.61731	0.374897	0.845841	0.203748	-0.65018	0.380403	0.71297	0.285196	0.941501	0.148658	-0.55452	0.438773	0.228531	1	-1.26749	0.043302	-1.49602	0.013282	0.73585
0.001121	0.450166	0.711063	-0.30842	1	2.07609	0.003713	2.583334	0.000372	-1.17739	0.128824	2.384505	0.000571	2.891749	4.39E-05	-0.86898	0.267984	0.507244	1	-3.25348	4.67E-06	-3.76073	1.7E-07	0.532224
4.5E-07	2.113206	5.77E-06	-0.04711	1	3.109078	6.66E-14	3.610399	1.26E-17	2.081652	1.44E-06	3.156193	2.1E-14	3.657514	3.84E-18	2.128767	6.39E-07	0.501321	1	-1.02743	0.045864	-1.52875	0.002073	1.068431
0.195836	-0.22603	0.667714	-0.02167	1	0.602677	0.06025	0.87163	0.005135	-0.12068	0.802661	0.624342	0.046901	0.893295	0.003803	-0.09902	0.8215	0.268952	1	-0.72336	0.025772	-0.99231	0.001649	0.384059
0.00127	-0.34287	0.58133	-0.48935	1	-1.95291	6.62E-09	-2.01907	2.04E-09	-0.55333	0.213078	-1.46356	2.33E-05	-1.52972	1.05E-05	-0.06398	0.916663	-0.06616	1	1.399579	0.000174	1.46574	7.54E-05	-0.68075
0.000374	-1.41455	0.112593	-1.24625	1	-2.85661	8.85E-06	-2.9077	6.55E-06	-0.63797	0.491807	-1.61036	0.020838	-1.66146	0.019409	0.608279	0.485926	-0.0511	1	2.21864	0.001748	2.269738	0.001199	-3.44126
0.000238	0.859568	0.339468	0.017722	1	2.730149	1.21E-05	2.413103	0.000124	0.88382	0.235187	2.712428	1.3E-05	2.395381	0.000139	0.866098	0.219488	-0.31705	1	-1.84633	0.009587	-1.52928	0.029756	0.551413

s 28 DAT	EtOH 70% 21 vs 28 DAT		A3 300 mg/L 21 vs 28 D		A3 500 mg/L 21 vs 28 D		O.P. 21 vs 28 DAT		N.C. vs EtOH 28 DAT		. vs GA3 300 mg/L 28		. vs GA3 500 mg/L 28		N.C. vs O.P. 28 DAT		80 % vs GA3 300 mg/L		80 % vs GA3 500 mg/L		OH 280 % vs O.P. 28 D		mg/L vs GA
p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
0.4929	-0.07605	0.72833	-0.32895	0.05162	-0.6068	0.000133	0.000362	1	0.018854	0.966298	0.019939	0.934952	-0.20624	0.248425	0.376632	0.039493	0.001085	1	-0.22509	0.219581	0.357778	0.039877	-0.22618
0.238761	-0.03667	0.84835	0.164797	0.280484	0.07572	0.649287	-0.19134	0.387618	-0.22848	0.351214	-0.09851	0.5718	-0.0648	0.705691	-0.10139	0.597163	0.12997	0.481272	0.163676	0.307481	0.127089	0.446971	0.033706
0.109479	-0.80283	0.055217	-1.90459	2.79E-07	-1.51067	3.6E-05	-0.0182	0.991946	-0.27697	0.717728	-0.86819	0.028258	-0.8964	0.018896	1.74373	1.45E-05	-0.59122	0.185046	-0.61943	0.130115	2.020703	1.44E-07	-0.02821
2.98E-05	1.965153	0.004459	0.562583	0.707982	1.453769	0.147452	0.586924	0.63838	-0.35551	0.821886	2.175994	0.069919	1.415846	0.16692	-0.08273	0.949486	2.5315	0.041357	1.771352	0.082925	0.272779	0.775495	-0.76015
0.838371	1.775793	0.000239	3.934185	1.79E-13	4.062864	1.59E-13	1.562789	0.00331	1.518459	0.015613	3.93624	2.21E-13	4.168252	5.56E-14	0.170973	0.799587	2.417781	3.22E-05	2.649793	6.8E-06	-1.34749	0.003743	0.232012
0.871956	-0.22688	0.749604	2.18071	2.21E-05	3.003064	2.36E-09	-1.57635	0.020187	0.005741	0.996402	-0.34637	0.601627	0.516747	0.385161	-2.89902	5.51E-08	-0.35211	0.632716	0.511006	0.409935	-2.90476	1.88E-08	0.863117
0.019683	1.238036	0.307137	4.490146	0.000923	3.28296	0.007995	1.287928	0.410971	2.344929	0.150951	5.713621	2.87E-05	4.997835	3.67E-05	-2.12057	0.055911	3.368692	0.028214	2.652906	0.047814	-4.4655	8.84E-06	-0.71579
0.003769	-1.95668	0.005257	-3.84514	1.17E-09	-4.33724	3.02E-12	0.552317	0.641737	-0.18883	0.903329	-0.5537	0.480298	-0.82238	0.24449	2.01009	0.00388	-0.36487	0.696181	-0.63356	0.401797	2.198916	0.000847	-0.26869
0.004636	-1.82137	0.018654	-3.77071	7.05E-08	-3.65841	9.03E-08	0.146227	0.933441	-0.00236	0.999602	1.770989	0.017552	0.994092	0.195201	6.001322	4.51E-17	1.773345	0.02418	0.996448	0.208961	6.003678	1.15E-17	-0.7769
0.873654	0.409504	0.737722	1.428176	0.500066	0.692768	0.660078	-0.12972	0.956577	-0.14578	0.955165	3.885883	0.016023	1.463039	0.287906	-0.13458	0.934257	4.031664	0.017315	1.60882	0.255534	0.011203	1	-2.42284
0.231961	0.79474	0.048888	1.217154	0.002671	2.23935	2.84E-09	-0.55248	0.302389	0.321244	0.665205	1.159838	0.005841	1.0914	0.007713	-0.83417	0.03282	0.838594	0.077191	0.770156	0.085286	-1.15542	0.001699	-0.06844
0.939779	-0.34312	0.269045	-0.45493	0.0987	-0.30047	0.292917	-0.5914	0.112959	-0.43927	0.344032	-1.16915	9.32E-06	-0.80806	0.002188	-0.44171	0.15711	-0.72988	0.010939	-0.36879	0.210966	-0.00244	1	0.361089
0.314573	-0.61299	0.012272	-0.93608	2.57E-05	-0.99667	5.27E-06	-0.2998	0.425001	-0.36008	0.367881	-0.42917	0.079327	-0.47114	0.043284	0.755028	0.001785	-0.06909	0.846723	-0.11107	0.696647	1.115105	6.84E-07	-0.04198
0.85501	2.757726	5.05E-07	3.902041	4.19E-11	3.080376	1.72E-08	1.08668	0.132762	2.227925	0.000446	5.566867	8.43E-22	4.751699	1.5E-18	0.641674	0.308539	3.338942	5.64E-08	2.523774	1.13E-05	-1.58625	0.002528	-0.81517
0.010733	-0.48437	0.071688	-0.44287	0.077577	-0.12159	0.673648	-0.58056	0.081982	-0.14078	0.783573	-0.57291	0.024206	-0.23754	0.379974	-0.00111	1	-0.43212	0.12489	-0.09676	0.757314	0.139669	0.651039	0.335367
0.28537	2.542326	5.94E-06	4.842624	2.16E-18	5.478573	3.07E-20	0.744048	0.363183	1.710816	0.020489	4.724084	1.69E-17	5.588564	6.73E-21	-0.64198	0.324904	3.013268	2.7E-07	3.877747	3.28E-10	-2.3528	6.53E-06	0.86448
0.549286	0.190797	0.821101	0.171662	0.852118	-1.09717	0.136054	-0.36846	0.749557	-0.64984	0.589664	1.715528	0.015944	0.953939	0.174376	-2.07808	0.001345	2.36537	0.000869	1.603781	0.018285	-1.42824	0.025772	-0.76159
0.026511	3.502897	2.29E-15	5.172005	1.31E-07	5.198227	7E-06	-0.4533	0.517236	2.387351	1.03E-06	7.212651	9.42E-14	7.740195	1.48E-11	0.559919	0.262009	4.8253	2.57E-06	5.352844	8.07E-06	-1.82743	2.1E-05	0.527544
0.28039	0.54992	0.071011	1.124273	0.00031	1.378411	3.42E-05	-0.14582	0.776962	0.144196	0.811481	1.342892	1.86E-05	1.865981	1.11E-08	-0.65056	0.027748	1.198696	0.000276	1.721785	3.37E-07	-0.79476	0.00437	0.523089
0.100356	-0.14282	0.750511	0.530501	0.13082	0.832591	0.011987	-1.26573	0.00162	0.048578	0.957504	-0.74166	0.036175	-0.50573	0.156623	-1.13831	0.001222	-0.79024	0.033725	-0.55431	0.128489	-1.18689	0.000416	0.235929
1.45E-06	-2.12732	0.001403	-1.47153	0.019244	-1.69054	0.005737	-1.27017	0.154806	0.0677	0.967732	-0.88687	0.201545	-1.15698	0.073404	1.53312	0.025052	-0.95457	0.197857	-1.22468	0.064911	1.46542	0.02461	-0.27011
0.47249	2.494187	9.45E-05	3.690579	0.003603	2.938565	0.002285	1.756076	0.025096	1.960495	0.020186	5.869315	2.19E-06	4.800255	2.4E-07	2.088483	0.000891	3.90882	0.003972	2.839759	0.005223	0.127987	0.890867	-1.06906

A3 500 mg/	3 300 mg/L vs O.P. 28		3 500 mg/L vs O.P. 28	
p-adj	Log2FC	p-adj	Log2FC	p-adj
0.390886	0.356693	0.031552	0.582871	0.000208
0.9217	-0.00288	0.997333	-0.03659	0.826911
0.980694	2.61192	1.59E-12	2.64013	4.76E-13
0.76083	-2.25872	0.044674	-1.49857	0.117816
0.87449	-3.76527	1.07E-12	-3.99728	2.16E-13
0.295335	-2.55265	4.1E-07	-3.41577	6.05E-12
0.821619	-7.83419	1.47E-09	-7.11841	8.74E-10
0.842193	2.563788	4.62E-05	2.832474	4.53E-06
0.517813	4.230333	9.2E-10	5.00723	1.75E-13
0.386909	-4.02046	0.008289	-1.59762	0.21051
0.952423	-1.99401	1.58E-07	-1.92557	2.95E-07
0.394501	0.727435	0.005347	0.366346	0.174974
0.941132	1.184195	5.58E-08	1.226172	1.21E-08
0.452923	-4.92519	1.71E-17	-4.11003	1.52E-14
0.386979	0.571793	0.018349	0.236426	0.354046
0.433321	-5.36607	1.06E-22	-6.23055	3.23E-26
0.52449	-3.79361	2.74E-09	-3.03202	6.12E-07
0.871398	-6.65273	3.34E-12	-7.18028	1.76E-10
0.378254	-1.99345	9.08E-12	-2.51654	6.92E-16
0.706842	-0.39665	0.270398	-0.63258	0.057029
0.832378	2.419993	5.51E-05	2.690102	4.9E-06
0.695979	-3.78083	0.002406	-2.71177	0.00453

Table S4.5: Table with Log2FoldChange (log2FC) and p-value adjusted (p-adj) of the genes that encode for AUXIN RESPONSE FACTORS (ARFs). The heatmap of these genes is showed in Fig. 4.15. Log2FC is calculated according to the following formula: expression level term1 - expression level term2.

Gene name	Gene description	N.C. 0 vs 7 DAT		EtOH 70% 0 vs 7 DAT		A3 300 mg/L 0 vs 7 DA		A3 500 mg/L 0 vs 7 DA		O.P. 0 vs 7 DAT		N.C. vs EtOH 7 DAT		C. vs GA3 300 mg/L 7 D		C. vs GA3 500 mg/L 7 D		N.C. vs O.P. 7 DAT		70 % vs GA3 300 mg/L	
		Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
Pav_sc0000848.1_g300.1.mk	PavARF1	-0.28397	0.60145	-0.38007	0.384238	-0.42389	0.100978	-0.55254	0.020404	-0.52147	0.045204	-0.0961	1	-0.13992	0.790788	-0.26856	0.434227	-0.2375	0.666462	-0.04382	0.920795
Pav_sc0001196.1_g1840.1.mk	PavARF1	-0.06705	0.884873	-0.08499	0.931387	-0.04428	0.829081	-0.10546	0.518585	-0.07649	0.730174	-0.01795	1	0.022769	0.947226	-0.03842	0.873025	-0.00944	0.985722	0.040718	0.854
Pav_sc0000042.1_g450.1.mk	PavARF2	0.07534	0.948229	-0.07966	0.993647	0.188189	0.569813	0.272095	0.354749	0.071499	0.890103	-0.155	1	0.112849	0.843718	0.196755	0.615448	-0.00384	1	0.267848	0.41431
Pav_sc0001900.1_g150.1.mk	PavARF3	0.499105	0.35635	0.367531	0.65894	0.533633	0.116257	0.358504	0.326166	0.01503	0.989143	-0.13157	1	0.034528	0.969891	-0.1406	0.798514	-0.48408	0.36694	0.166102	0.737299
Pav_sc0000094.1_g590.1.mk	PavARF4	0.297374	0.826141	0.399063	0.824249	0.007909	0.996387	-0.11259	0.875244	-0.44336	0.482574	0.101689	1	-0.28946	0.751676	-0.40996	0.532861	-0.74073	0.28878	-0.39115	0.520527
Pav_sc0001759.1_g010.1.br	PavARF5	-0.11809	0.968094	0.091905	1	0.552145	0.495899	0.369255	0.670105	-0.00429	1	0.209997	1	0.670237	0.540085	0.487347	0.622849	0.113798	0.958571	0.460241	0.616941
Pav_sc0002080.1_g180.1.mk	PavARF5	0.201173	0.899166	0.025473	1	0.756398	0.095424	0.746804	0.092811	0.004949	1	-0.1757	1	0.555225	0.408918	0.545631	0.350064	-0.19622	0.880298	0.730925	0.14548
Pav_sc0002826.1_g100.1.br	PavARF5	0.593047	0.624157	0.595938	0.680998	0.923029	0.107694	0.840471	0.14114	-0.09717	0.933641	0.002891	1	0.329982	0.777786	0.247424	0.793449	-0.69022	0.490177	0.327091	0.69022
Pav_sc0003104.1_g030.1.br	PavARF5	0.649916	0.714173	0.541484	0.877178	0.873095	0.275076	0.68918	0.401062	-0.18334	0.894014	-0.10843	1	0.223179	0.899307	0.039264	0.981491	-0.83326	0.539834	0.33161	0.770643
Pav_sc0011314.1_g020.1.br	PavARF5	0.795789	0.854199	-0.47053	0.987022	0.095454	0.969571	-0.04437	0.987898	1.397514	0.503357	-1.26632	1	-0.70033	0.81614	1	1	0.601725	0.903979	1	1
Pav_sc0001345.1_g010.1.mk	PavARF6	0.059238	0.924854	0.031183	1	0.145794	0.438623	0.012862	0.964708	-0.00197	1	-0.02806	1	0.086556	0.793826	-0.04638	0.868776	-0.0612	0.900368	0.114611	0.596258
Pav_sc0003135.1_g100.1.mk	PavARF6	-0.13083	0.843738	-0.19013	0.823318	-0.07107	0.829965	-0.17945	0.490567	-0.26896	0.326984	-0.05931	1	0.059756	0.911807	-0.04862	0.90364	-0.13813	0.806071	0.119065	0.711172
Pav_sc0000129.1_g1480.1.mk	PavARF7	0.293334	0.704278	0.181523	0.945118	0.854959	0.003134	0.882998	0.001876	1.314196	7.02E-07	-0.11181	1	0.561625	0.175665	0.589664	0.106966	1.020862	0.001306	0.673436	0.044588
Pav_sc0001314.1_g050.1.mk	PavARF8	0.166747	0.399135	0.197611	0.25268	-0.11044	0.416463	-0.00941	0.964708	0.095693	0.566035	0.030865	1	-0.27718	0.036844	-0.17616	0.215206	-0.07105	0.814459	-0.30805	0.008061
Pav_sc0002250.1_g170.1.mk	PavARF9	0.708602	0.23124	0.486945	0.597771	1.730248	4.92E-07	1.786856	1.69E-07	1.37352	0.000118	-0.22166	1	1.021646	0.027491	1.078254	0.013105	0.664918	0.277605	1.243303	0.001915
Pav_sc0002446.1_g140.1.mk	PavARF10	0.357986	0.697025	0.224657	0.939341	0.448038	0.289317	0.41139	0.326787	0.145715	0.834815	-0.13333	1	0.090052	0.921678	0.053404	0.943504	-0.21227	0.836342	0.22338	0.682578
Pav_sc0000084.1_g430.1.mk	PavARF16	-0.18672	0.87359	-0.08778	0.99688	0.051831	0.929992	0.093677	0.864793	-0.322	0.518277	0.098934	1	0.238549	0.731012	0.280395	0.593804	-0.13528	0.902562	0.139615	0.804242
Pav_sc0000711.1_g070.1.mk	PavARF16	-0.03284	0.981483	-0.18771	0.906159	0.335868	0.264253	0.287313	0.345548	0.107561	0.829028	-0.15487	1	0.368713	0.353222	0.320158	0.377261	0.140406	0.85391	0.523582	0.075977
Pav_sc0000030.1_g880.1.mk	PavARF17	-0.00197	1	0.096828	0.961236	-0.044	0.878805	-0.12795	0.577418	-0.31172	0.124709	0.098797	1	-0.04203	0.925097	-0.12598	0.65532	-0.30976	0.247623	-0.14082	0.573499
Pav_sc0001196.1_g850.1.br	PavARF17	-0.42703	0.497426	-0.31223	0.773974	-0.72084	0.023187	-0.61903	0.054677	-0.40013	0.337492	0.114797	1	-0.29381	0.611401	-0.192	0.713055	0.0269	0.982309	-0.4086	0.301576
Pav_sc0000586.1_g230.1.mk	PavARF18	0.13166	0.940282	0.178302	0.980637	0.123688	0.844685	0.165588	0.778369	0.592595	0.22535	0.046642	1	-0.00797	0.998998	0.033928	0.969134	0.460935	0.572106	-0.05461	0.940126
Pav_sc0001248.1_g270.1.mk	PavARF19	-0.64328	0.09853	-0.36477	0.616673	-1.12989	2.39E-05	-0.94891	0.000542	-0.50114	0.150552	0.278504	1	-0.48661	0.245917	-0.30563	0.47259	0.142135	0.874001	-0.76512	0.015017

70 % vs GA3 500 mg/L		tOH 70 % vs O.P. 7 DA		0 mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 7 D		3 500 mg/L vs O.P. 7 D		N.C. 7 vs 14 DAT		EtOH 70% 7 vs 14 DAT		A3 300 mg/L 7 vs 14 DA		A3 500 mg/L 7 vs 14 D		O.P. 7 vs 14 DAT		N.C. vs EtOH 14 DAT		. vs GA3 300 mg/L 14	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
-0.17247	0.59771	-0.1414	0.78821	-0.12865	1	-0.09758	0.820932	0.031064	0.960306	-0.12866	0.835634	-0.09215	0.839373	0.193137	0.485166	0.286385	0.267306	0.487535	0.057545	-0.05959	0.982396	0.181875	0.622602
-0.02047	0.93101	0.008506	0.987509	-0.06119	1	-0.03221	0.901126	0.028973	0.925917	-0.07104	0.828617	0.072445	0.74487	-0.17838	0.183454	-0.01648	0.934458	-0.15684	0.304189	0.125534	0.864027	-0.08457	0.679691
0.351754	0.222969	0.151158	0.780499	0.083905	1	-0.11669	0.788874	-0.2006	0.640349	0.121668	0.853056	0.157112	0.707242	0.16389	0.58329	0.031985	0.934105	0.156059	0.646674	-0.11956	0.945412	0.155072	0.70245
-0.00903	0.987982	-0.3525	0.513427	-0.17513	1	-0.5186	0.177709	-0.34347	0.481376	-0.79606	0.029957	-0.48561	0.245185	-0.89146	0.002189	-1.03734	0.000286	-0.60517	0.07376	0.178871	0.925845	-0.06088	0.924799
-0.51165	0.33356	-0.84242	0.161779	-0.1205	1	-0.45127	0.471499	-0.33077	0.66932	-0.24317	0.827307	-0.2102	0.789911	0.893037	0.036075	0.414046	0.404735	1.028873	0.023115	0.134651	0.975344	0.846738	0.091166
0.27735	0.774271	-0.0962	0.959101	-0.18289	1	-0.55644	0.554959	-0.37355	0.755187	-0.0637	0.981237	0.070627	0.954725	1.03271	0.136839	0.578325	0.440523	0.610604	0.438562	0.344327	0.927961	1.766651	0.010059
0.721331	0.126783	-0.02052	0.992626	-0.00959	1	-0.75145	0.138027	-0.74185	0.176375	0.156558	0.899573	0.309129	0.654415	0.528955	0.240385	0.393938	0.413902	1.140405	0.00752	-0.02313	1	0.927622	0.047248
0.244533	0.766023	-0.69311	0.403105	-0.08256	1	-1.0202	0.100908	-0.93764	0.171315	0.186804	0.907711	-0.08718	0.935409	0.430348	0.512503	0.513592	0.425648	1.616955	0.003147	-0.2711	0.937967	0.573526	0.459353
0.147696	0.90564	-0.72482	0.536169	-0.18391	1	-1.05644	0.217297	-0.87252	0.380255	-0.56135	0.708121	-0.55324	0.600523	0.67001	0.424668	0.8213	0.308127	1.108303	0.149237	-0.10032	0.995765	1.45454	0.07159
1	1	1.868048	0.40073	-0.13982	1	1	1	1	1	0.718593	0.860863	0.848303	0.669792	0.082442	0.970105	0.793796	0.630293	2.811209	0.227926	-1.13661	0.891999	1	1
-0.01832	0.948039	-0.03315	0.937524	-0.13293	1	-0.14776	0.497461	-0.01483	0.97181	-0.00626	0.995201	0.031004	0.919631	0.008533	0.975012	0.008098	0.977331	0.116427	0.551285	0.009207	1	0.101346	0.669713
0.010685	0.978808	-0.07882	0.879675	-0.10838	1	-0.19789	0.515769	-0.08951	0.838169	-0.39969	0.163616	-0.2288	0.45142	-0.46164	0.020933	-0.36271	0.081653	-0.36909	0.106317	0.111577	0.932894	-0.0022	1
0.701475	0.027603	1.132673	0.000163	0.028039	1	0.459237	0.226868	0.431198	0.304956	0.749718	0.033792	0.796611	0.015474	-0.29884	0.369233	-0.57125	0.053005	-0.5481	0.095377	-0.06492	0.98484	-0.48693	0.178707
-0.20702	0.085557	-0.10192	0.619686	0.101024	1	0.206129	0.110427	0.105106	0.558988	0.08151	0.749735	0.051124	0.798067	0.347985	0.000539	0.380397	0.000139	0.06535	0.66709	0.000479	1	-0.01071	0.967179
1.299911	0.000899	0.886575	0.069935	0.056608	1	-0.35673	0.536755	-0.41334	0.50376	0.737501	0.1707	0.669415	0.17514	0.628678	0.118249	0.257275	0.595952	0.828958	0.047399	-0.28974	0.899469	0.912823	0.032959
0.186733	0.724665	-0.07894	0.938382	-0.03665	1	-0.30232	0.577849	-0.26567	0.680469	-0.56012	0.320145	-0.91362	0.022946	-1.0326	0.001953	-0.77496	0.025502	-0.40787	0.347831	-0.48683	0.763423	-0.38243	0.438801
0.181461	0.71476	-0.23421	0.739147	0.041846	1	-0.37383	0.432022	-0.41567	0.413342	-0.46134	0.418813	-0.36578	0.459919	-0.70516	0.03132	-0.88498	0.005305	-0.44072	0.262952	0.194498	0.924305	-0.00527	0.999219
0.475027	0.095484	0.295275	0.50409	-0.04856	1	-0.22831	0.55426	-0.17975	0.704773	0.005478	0.998685	-0.2231	0.579633	-0.26814	0.347217	-0.42418	0.10633	-0.18269	0.595803	-0.38344	0.714247	0.095098	0.846282
-0.22478	0.278813	-0.40855	0.062139	-0.08395	1	-0.26773	0.223307	-0.18378	0.504668	-0.10346	0.811856	0.052797	0.878532	0.148626	0.460603	0.318306	0.068978	0.288531	0.138831	0.255057	0.732925	0.210061	0.369193
-0.3068	0.438935	-0.0879	0.921501	0.101804	1	0.320706	0.476722	0.218902	0.70183	-0.17735	0.823248	0.29499	0.540457	-0.09019	0.835165	-0.35	0.306591	-0.81369	0.010321	0.587141	0.590392	-0.20665	0.679487
-0.01271	0.986113	0.414294	0.554716	0.041901	1	0.468908	0.387736	0.427007	0.489147	0.249197	0.79597	0.062382	0.937105	0.35877	0.421181	0.272487	0.569595	0.193506	0.737092	-0.14017	0.970201	0.101601	0.89778
-0.58413	0.066703	-0.13637	0.844944	0.180983	1	0.628748	0.056366	0.447766	0.261987	0.332729	0.543933	0.460832	0.239907	1.065474	5.4E-05	1.110133	2.79E-05	0.150524	0.722746	0.406607	0.759639	0.246132	0.576495

. vs GA3 500 mg/L 14		N.C. vs O.P. 14 DAT		40 % vs GA3 300 mg/L		40 % vs GA3 500 mg/L		OH 140 % vs O.P. 14 D		mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 14		3 500 mg/L vs O.P. 14		N.C. 14 vs 21 DAT		EtOH 70% 14 vs 21 DA		3 300 mg/L 14 vs 21 D		3 500 mg/L 14 vs 21 D	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
0.146477	0.71498	0.37869	0.297111	0.241462	0.451385	0.206065	0.545438	0.438278	0.111123	-0.0354	1	0.196816	0.73788	0.232213	0.675566	0.222882	0.512002	0.327831	0.434864	0.667629	0.002674	0.486594	0.031624
0.016143	0.960223	-0.09524	0.741452	-0.21011	0.15771	-0.10939	0.552802	-0.22077	0.139125	0.100717	1	-0.01067	0.985102	-0.11138	0.722429	-0.10577	0.572333	-0.23222	0.271256	-0.30077	0.011964	-0.30212	0.010489
0.107072	0.820346	0.030549	0.976166	0.274627	0.399395	0.226627	0.517595	0.150105	0.684899	-0.048	1	-0.12452	0.863458	-0.07652	0.929187	-0.3921	0.213166	-0.52398	0.174683	-0.87941	8.33E-05	-1.07296	8.89E-07
-0.38188	0.357864	-0.29318	0.645856	-0.23975	0.599518	-0.56076	0.11649	-0.47206	0.210055	-0.32101	1	-0.23231	0.768626	0.0887	0.933205	0.104705	0.851241	-0.15941	0.820869	0.306589	0.361288	0.460522	0.133585
0.247251	0.741529	0.531303	0.488516	0.712087	0.161183	0.1126	0.890581	0.396652	0.504081	-0.59949	1	-0.31543	0.774752	0.284052	0.815705	0.764418	0.158198	0.204549	0.840031	0.819344	0.053743	1.028117	0.010896
1.129375	0.133222	0.788106	0.469259	1.422323	0.048103	0.785048	0.344514	0.443779	0.62883	-0.63728	1	-0.97854	0.426753	-0.34127	0.864334	0.1279	0.913345	-0.6096	0.608792	-0.62056	0.408543	-0.24417	0.761545
0.783011	0.109589	0.787624	0.183552	0.95075	0.034434	0.806139	0.08975	0.810752	0.089684	-0.14461	1	-0.14	0.921168	0.004613	1	-0.2251	0.746367	-0.42988	0.591229	-0.29151	0.545506	-0.28239	0.548787
0.574213	0.466757	0.739932	0.437221	0.844623	0.195957	0.845309	0.202865	1.011029	0.11772	0.000686	1	0.166406	0.932112	0.16572	0.933205	-0.43558	0.574564	-0.22567	0.854067	0.420679	0.533958	-0.01662	0.988984
1.421915	0.079219	0.836398	0.489431	1.554863	0.042069	1.522238	0.049824	0.936721	0.269066	-0.03262	1	-0.61814	0.734454	-0.58552	0.762512	0.354953	0.74802	0.20244	0.902144	0.165611	0.874821	-0.81562	0.28209
-0.76495	0.776058	1	1	-0.19987	0.932833	0.371661	0.881264	1	1	0.571534	1	1	1	1	1	1	1	1	1	1.487563	0.372929	-0.04768	0.986154
-0.03202	0.924597	0.061481	0.882523	0.092139	0.688418	-0.04123	0.881729	0.052275	0.836948	-0.13337	1	-0.03986	0.937552	0.093502	0.82567	-0.00567	0.988889	-0.12945	0.668504	0.550521	4.68E-05	0.531286	7.18E-05
-0.01165	0.98523	-0.10754	0.841253	-0.11378	0.727042	-0.12323	0.708487	-0.21911	0.419194	-0.00945	1	-0.10533	0.860456	-0.09588	0.885526	-0.17575	0.559661	-0.26747	0.470858	0.080231	0.755975	0.261967	0.210302
-0.73131	0.021777	-0.27695	0.653357	-0.42201	0.24833	-0.66639	0.037253	-0.21204	0.623906	-0.24438	1	0.209974	0.782809	0.454351	0.402206	-0.19955	0.667902	-0.32203	0.566896	0.08749	0.820264	0.137716	0.697077
0.122728	0.416089	-0.08721	0.715506	-0.01119	0.959678	0.122249	0.402855	-0.08769	0.567046	0.133436	1	-0.07651	0.784709	-0.20994	0.232047	-0.05644	0.756884	-0.12271	0.543904	-0.19148	0.073826	-0.26263	0.009385
0.598028	0.214189	0.756375	0.163908	1.202566	0.002002	0.887771	0.032817	1.046118	0.011101	-0.3148	1	-0.15645	0.898132	0.158347	0.904248	-0.20307	0.753334	-0.24623	0.770308	-0.18244	0.705518	-0.87087	0.016516
-0.16144	0.807987	-0.06003	0.962476	0.104403	0.868772	0.32539	0.518521	0.426805	0.347619	0.220986	1	0.322402	0.703798	0.101415	0.933205	-0.69772	0.108071	-0.10586	0.905943	-0.08156	0.863652	-0.42921	0.237354
-0.14325	0.821651	-0.11467	0.904382	-0.19977	0.698911	-0.33775	0.462541	-0.30916	0.495948	-0.13798	1	-0.10939	0.921512	0.028584	0.985213	-0.20099	0.704545	-0.24953	0.723083	-0.37472	0.285622	-0.11518	0.7786
-0.1095	0.82347	-0.04776	0.957575	0.478541	0.096585	0.273938	0.429392	0.335681	0.294407	-0.2046	1	-0.14286	0.843305	0.061742	0.944273	-0.15961	0.692053	-0.01008	0.989796	-0.24491	0.379279	-0.01551	0.970591
0.295789	0.158153	0.082238	0.861507	-0.045	0.886796	0.040732	0.904544	-0.17282	0.459072	0.085728	1	-0.12782	0.772922	-0.21355	0.550452	0.072004	0.81269	0.037438	0.934734	-0.01422	0.959962	0.128333	0.511215
-0.36465	0.387508	-0.60944	0.154	-0.79379	0.014014	-0.95179	0.0022	-1.19658	0.000101	-0.15801	1	-0.40279	0.500225	-0.24479	0.763097	0.215764	0.652961	-0.27799	0.657409	0.168757	0.648295	0.593334	0.044916
0.057218	0.951701	0.405244	0.595067	0.241775	0.688418	0.197392	0.758538	0.545418	0.260125	-0.04438	1	0.303643	0.760445	0.348026	0.716637	0.148602	0.832557	0.020332	0.986602	-1.10134	0.002187	-1.33648	0.000128
0.471774	0.185774	-0.04007	0.97229	-0.16048	0.729149	0.065166	0.909689	-0.44668	0.207651	0.225641	1	-0.2862	0.675255	-0.51184	0.306473	0.025005	0.970525	-0.48048	0.333021	-0.55191	0.051813	-0.73779	0.006291

O.P. 14 vs 21 DAT		N.C. vs EtOH 21 DAT		. vs GA3 300 mg/L 21 D		. vs GA3 500 mg/L 21 D		N.C. vs O.P. 21 DAT		10 % vs GA3 300 mg/L		10 % vs GA3 500 mg/L		OH 210 % vs O.P. 21 D		mg/L vs GA3 500 mg/L		300 mg/L vs O.P. 21 D		500 mg/L vs O.P. 21		N.C. 21 vs 28 DAT	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
0.165201	0.686876	0.045361	1	0.626622	0.005791	0.410188	0.103176	0.321009	0.24336	0.58126	0.010552	0.364827	0.155431	0.275648	0.30282	-0.21643	1	-0.30561	0.252926	-0.08918	0.779569	0.52076	0.034906
-0.10806	0.597365	-0.00092	1	-0.27958	0.02389	-0.18021	0.191808	-0.09753	0.560946	-0.27865	0.022391	-0.17929	0.195145	-0.09661	0.536334	0.099366	1	0.182043	0.184426	0.082677	0.590322	0.213326	0.11639
0.06233	0.909507	-0.25143	1	-0.33223	0.208781	-0.57379	0.017863	0.484982	0.060787	-0.0808	0.814066	-0.32235	0.235444	0.736415	0.001471	-0.24155	1	0.817215	0.000612	1.05877	4.3E-06	-0.75327	0.001963
-0.00063	1	-0.08525	1	0.141009	0.734906	-0.02607	0.96163	-0.39852	0.269663	0.226256	0.547095	0.059179	0.902294	-0.31327	0.379938	-0.16708	1	-0.53953	0.09905	-0.37245	0.268011	0.155515	0.70106
0.060735	0.95706	-0.42522	1	0.901664	0.036152	0.51095	0.299588	-0.17238	0.79832	1.326882	0.000844	0.936169	0.030283	0.252839	0.65316	-0.39071	1	-1.07404	0.014137	-0.68333	0.132123	-0.27031	0.621961
1.259295	0.147155	-0.39317	1	1.018193	0.124391	0.757302	0.288194	1.919501	0.003569	1.411365	0.020513	1.150473	0.074771	2.312673	0.000203	-0.26089	1	0.901308	0.245847	1.1622	0.106246	-0.27438	0.736294
0.94853	0.055536	-0.22791	1	0.861214	0.037837	0.725719	0.098831	1.961252	2.17E-07	1.089122	0.005479	0.953627	0.020452	2.18916	3.71E-09	-0.1355	1	1.100038	0.00914	1.235533	0.002659	-0.78794	0.072139
0.40894	0.695445	-0.06119	1	1.429784	0.008084	0.993172	0.082122	1.58445	0.004718	1.490972	0.004763	1.054361	0.059336	1.645638	0.002391	-0.43661	1	0.154666	0.864503	0.591278	0.382055	-0.5925	0.305158
0.629639	0.598839	-0.25284	1	1.265198	0.091956	0.251343	0.798907	1.111084	0.168183	1.518034	0.032277	0.504179	0.551526	1.36392	0.061403	-1.01386	1	-0.15411	0.895362	0.859741	0.284626	-0.80267	0.279292
1	1	0.077363	1	1.948757	0.226818	0.985044	0.537936	2.631047	0.156493	1.871394	0.246403	0.907681	0.57691	2.553684	0.153089	-0.96371	1	1	1	1	1	1	1
0.176031	0.411254	-0.11458	1	0.657533	4.75E-07	0.504931	0.000216	0.243179	0.135282	0.772112	1.63E-09	0.61951	2.59E-06	0.357758	0.013434	-0.1526	1	-0.41435	0.00521	-0.26175	0.088175	0.08446	0.658253
0.254682	0.382353	0.019856	1	0.253775	0.261966	0.426061	0.040531	0.322892	0.156745	0.233918	0.302865	0.406205	0.051506	0.303036	0.168499	0.172287	1	0.069117	0.810707	-0.10317	0.690332	0.088432	0.749998
-0.00973	0.996949	-0.1874	1	-0.19989	0.588721	-0.39404	0.229699	-0.08714	0.857758	-0.01249	0.983005	-0.20664	0.581438	0.10026	0.810688	-0.19415	1	0.112749	0.782741	0.306901	0.352463	0.097753	0.814004
-0.05438	0.790084	-0.06579	1	-0.14575	0.212557	-0.08347	0.537933	-0.08515	0.551786	-0.07996	0.543228	-0.01768	0.917753	-0.01937	0.908848	0.062283	1	0.060595	0.666715	-0.00169	0.99592	-0.06978	0.609638
0.575791	0.286255	-0.3329	1	0.933458	0.012728	-0.06977	0.908791	1.535241	2.47E-05	1.266357	0.000318	0.263128	0.589227	1.86814	1E-07	-1.00323	1	0.601783	0.160572	1.605012	1.59E-05	-0.49751	0.245316
-0.43983	0.380671	0.105032	1	0.233737	0.59731	0.107074	0.83697	0.197861	0.695529	0.128706	0.792682	0.002042	1	0.09283	0.858006	-0.12666	1	-0.03588	0.951653	0.090787	0.856189	0.484143	0.217511
-0.17306	0.779113	0.145956	1	-0.179	0.675465	-0.05744	0.913788	-0.08674	0.875115	-0.32496	0.386635	-0.2034	0.637217	-0.2327	0.574805	0.121563	1	0.092263	0.846742	-0.0293	0.958139	0.34218	0.373421
-0.12198	0.80179	-0.23391	1	0.009802	0.986267	0.034599	0.934068	-0.01014	0.987377	0.243713	0.401186	0.26851	0.363505	0.223776	0.46055	0.024797	1	-0.01994	0.963652	-0.04473	0.905174	-0.66985	0.00885
-0.03028	0.9447	0.220491	1	0.123834	0.563346	0.352118	0.047881	-0.02005	0.952335	-0.09666	0.664357	0.131627	0.547066	-0.24054	0.201519	0.228284	1	-0.14388	0.491933	-0.37217	0.03491	0.287262	0.124209
0.143619	0.808886	0.093384	1	-0.25365	0.494402	0.012919	0.984413	-0.68158	0.031682	-0.34704	0.312517	-0.08046	0.86136	-0.77496	0.009726	0.266571	1	-0.42793	0.206483	-0.6945	0.025396	0.49734	0.13837
-0.04752	0.963652	-0.26844	1	-1.14834	0.001398	-1.42787	4.54E-05	0.209118	0.71122	-0.87989	0.018045	-1.15942	0.001349	0.477563	0.270299	-0.27953	1	1.357456	0.000295	1.636987	7.54E-06	-0.20768	0.681592
0.246068	0.602005	-0.09887	1	-0.33078	0.306934	-0.29102	0.3954	0.180993	0.656914	-0.23191	0.501512	-0.19215	0.604642	0.279866	0.410218	0.039762	1	0.511778	0.095143	0.472015	0.118736	-0.1263	0.747239

tOH 70% 21 vs 28 DA		3 300 mg/L 21 vs 28 D		3 500 mg/L 21 vs 28 D		O.P. 21 vs 28 DAT		N.C. vs EtOH 28 DAT		. vs GA3 300 mg/L 28		. vs GA3 500 mg/L 28		N.C. vs O.P. 28 DAT		30 % vs GA3 300 mg/L		30 % vs GA3 500 mg/L		OH 280 % vs O.P. 28 D		mg/L vs GA3 500 mg/	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
0.46992	0.037318	0.585235	0.005792	1.288971	3.11E-10	0.177614	0.633996	-0.00548	0.990878	0.691097	0.001385	1.178399	1.55E-08	-0.02214	0.953166	0.696576	0.001934	1.183878	2.52E-08	-0.01666	0.961148	0.487302	0.13367
0.185322	0.133906	0.322977	0.003011	0.085987	0.48745	-0.00674	0.985424	-0.02893	0.913113	-0.16993	0.163303	-0.30755	0.005184	-0.3176	0.006803	-0.141	0.29937	-0.27862	0.014968	-0.28868	0.010732	-0.13762	0.443964
-0.74016	0.001042	-1.20003	3.62E-09	-1.37819	4.82E-12	-0.49269	0.094181	-0.23832	0.551365	-0.77899	0.000251	-1.19871	3.42E-09	0.745562	0.000763	-0.54066	0.019345	-0.96038	4.33E-06	0.983886	2.32E-06	-0.41972	0.184346
0.437633	0.147193	1.741607	1.2E-11	2.02819	9.34E-16	0.062194	0.91859	0.196871	0.7164	1.727101	2.38E-11	1.846607	4.69E-13	-0.49184	0.110062	1.530229	7.14E-09	1.649736	2.17E-10	-0.68871	0.012693	0.119506	0.827689
1.16452	0.003685	1.365782	0.000245	1.525586	2.69E-05	0.117065	0.88871	1.009608	0.075466	2.537752	3.58E-12	2.306843	1.91E-10	0.214991	0.687195	1.528144	8.96E-05	1.297235	0.000723	-0.79462	0.045069	-0.23091	0.758509
-0.13228	0.853079	-1.60789	0.003126	-1.8446	0.000396	-0.05737	0.974384	-0.25107	0.825699	-0.31532	0.63252	-0.81292	0.138693	2.136509	0.000326	-0.06425	0.943356	-0.56185	0.342652	2.387582	2.37E-05	-0.4976	0.579794
-0.78869	0.045075	-1.91045	3.65E-08	-2.2457	3.93E-11	-0.30808	0.640553	-0.22867	0.758635	-0.2613	0.553677	-0.73205	0.047215	2.441107	1.38E-11	-0.03263	0.960899	-0.50338	0.205492	2.669772	2.3E-14	-0.47075	0.414082
-0.8163	0.092993	-2.02734	1.76E-05	-2.2304	4.61E-07	0.02104	0.99365	-0.28499	0.747665	-0.00506	1	-0.64473	0.158418	2.197988	8.1E-06	0.279938	0.64424	-0.35973	0.476817	2.482983	1.32E-07	-0.63967	0.352207
-0.97769	0.117729	-2.46374	4.43E-05	-1.87496	0.000749	-0.19571	0.893923	-0.42785	0.698822	-0.39587	0.560548	-0.82095	0.158767	1.718045	0.007085	0.031984	0.976939	-0.39309	0.548935	2.1459	0.000285	-0.42507	0.671009
-0.63568	0.608402	-2.8364	0.027206	-1.79094	0.111983	1	1	1	1	-0.14093	0.91717	-0.05919	0.968211	2.162963	0.087381	-0.32932	0.822362	-0.24758	0.845648	1.974568	0.10455	1	1
0.23631	0.098231	-0.30294	0.020436	-0.38044	0.002546	0.116865	0.609614	0.037272	0.902919	0.270135	0.048407	0.040027	0.806215	0.275584	0.055639	0.232863	0.118659	0.002755	0.992417	0.238312	0.085126	-0.23011	0.242194
-0.01036	0.969407	-0.14315	0.475096	-0.79577	2.54E-06	0.115988	0.729062	-0.07894	0.839915	0.022193	0.932621	-0.45815	0.010108	0.350447	0.082712	0.10113	0.68967	-0.37921	0.04258	0.429385	0.020206	-0.48034	0.055541
0.203995	0.520948	0.470375	0.07611	0.329912	0.224018	-0.15747	0.746709	-0.08116	0.892403	0.172729	0.588761	-0.16189	0.591268	-0.34236	0.274321	0.253891	0.444039	-0.08072	0.811988	-0.2612	0.385494	-0.33462	0.418956
0.03851	0.759254	0.395331	1.53E-05	0.105179	0.29926	0.067174	0.700808	0.042499	0.836989	0.319359	0.000813	0.09149	0.382374	0.051798	0.700844	0.27686	0.006157	0.048991	0.67655	0.009299	0.950589	-0.22787	0.094577
-0.42461	0.269399	-1.74983	5.56E-08	-0.84419	0.009695	-0.62448	0.213299	-0.25999	0.694228	-0.31886	0.4109	-0.41645	0.242974	1.408269	4E-05	-0.05887	0.915611	-0.15646	0.706342	1.668263	3.27E-07	-0.09759	0.895898
0.325526	0.372435	2.070583	3.21E-12	2.332801	1.66E-15	-0.39395	0.421028	-0.05359	0.946048	1.820178	1.6E-09	1.955733	4.8E-11	-0.68023	0.045542	1.873763	7.85E-10	2.009318	2.38E-11	-0.62665	0.053239	0.135555	0.834232
0.295471	0.391459	1.410646	5.34E-07	1.512634	5.81E-08	-0.14905	0.789344	0.099247	0.881517	0.889464	0.00293	1.113014	0.00011	-0.57797	0.074299	0.790216	0.012971	1.013767	0.000678	-0.67722	0.023587	0.223551	0.685644
-0.60689	0.009793	-0.90862	1.96E-05	-1.05994	3.64E-07	-0.12268	0.773712	-0.17095	0.697035	-0.22897	0.367331	-0.35549	0.122081	0.537033	0.025169	-0.05802	0.868326	-0.18454	0.473012	0.707984	0.001346	-0.12652	0.766681
0.129364	0.489447	0.207807	0.202578	-0.02844	0.890813	0.290809	0.181264	0.062592	0.853735	0.044379	0.83524	0.036419	0.855306	-0.0165	0.952157	-0.01821	0.945744	-0.02617	0.901978	-0.0791	0.68524	-0.00796	0.989708
1.065828	0.000211	2.083584	1.67E-15	2.90307	1.77E-27	0.080367	0.893732	0.661872	0.11727	1.332592	9.33E-07	2.418649	3.54E-19	-1.09855	6.79E-05	0.67072	0.028384	1.756778	3.14E-10	-1.76043	1.71E-11	1.086058	0.004526
0.023407	0.963113	-0.26403	0.483062	0.345739	0.339688	-0.21214	0.740667	-0.03736	0.967039	-1.20469	0.00035	-0.87445	0.009329	0.204654	0.667705	-1.16733	0.000839	-0.83709	0.016205	0.242011	0.560076	0.330239	0.563372
-0.19909	0.521507	-0.60901	0.015087	-0.8793	0.000253	-0.24253	0.582019	-0.17166	0.738957	-0.81349	0.001343	-1.04402	1.63E-05	0.064769	0.87145	-0.64183	0.018571	-0.87236	0.000523	0.236432	0.425915	-0.23053	0.594653

300 mg/L vs O.P. 28		500 mg/L vs O.P. 28	
Log2FC	p-adj	Log2FC	p-adj
-0.71323	0.000537	-1.20054	3.28E-09
-0.14768	0.204133	-0.01005	0.945233
1.524549	2.33E-14	1.944269	5.38E-23
-2.21894	1.44E-18	-2.33845	7.43E-21
-2.32276	1.02E-10	-2.09185	3.83E-09
2.451833	7.92E-06	2.949432	3.29E-08
2.702404	2.27E-15	3.173156	3.85E-21
2.203045	2.21E-06	2.842717	2.59E-10
2.113915	0.000241	2.53899	5.34E-06
2.303892	0.041987	2.22215	0.046224
0.00545	0.983379	0.235557	0.065827
0.328255	0.070098	0.808593	1.32E-06
-0.51509	0.047667	-0.18048	0.513275
-0.26756	0.003815	-0.03969	0.709432
1.727132	5.18E-08	1.82472	5.38E-09
-2.50041	1.09E-17	-2.63597	8.5E-20
-1.46743	1.18E-07	-1.69099	7.38E-10
0.766	0.000299	0.892522	1.63E-05
-0.06088	0.74145	-0.05292	0.764858
-2.43115	3.81E-21	-3.5172	1.72E-40
1.409342	1.12E-05	1.079103	0.00078
0.878264	0.000277	1.10879	2.41E-06

Table S4.6: Table with Log2FoldChange (log2FC) and p-value adjusted (p-adj) of the genes that encode for AUXIN/INDOLE-3ACETIC ACID (AUX/IAA). The heatmap of these genes is showed in Fig. 4.16. Log2FC is calculated according to the following formula: expression level term1 - expression level term2.

Gene name	Gene description	N.C. 0 vs 7 DAT		EtOH 70% 0 vs 7 DAT		A3 300 mg/L 0 vs 7 DA		A3 500 mg/L 0 vs 7 DA		O.P. 0 vs 7 DAT		N.C. vs EtOH 7 DAT		. vs GA3 300 mg/L 7 D		. vs GA3 500 mg/L 7 D		N.C. vs O.P. 7 DAT		70 % vs GA3
		Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
Pav_sc0000998.1_g200.1.mk	PavAUX/IAA3	-0.42573	0.729413	-0.31104	0.924897	-1.55398	0.000272	-1.57321	0.000199	-0.11223	0.910298	0.11469	1	-1.12825	0.041936	-1.14749	0.027146	0.313494	0.798815	-1.24294
Pav_sc0000396.1_g1090.1.mk	PavAUX/IAA4	0.972787	0.060891	0.967872	0.063817	0.420864	0.408862	0.563012	0.220961	1.601559	1.83E-05	-0.00492	1	-0.55192	0.396178	-0.40978	0.501532	0.628772	0.381653	-0.54701
Pav_sc0000983.1_g280.1.mk	PavAUX/IAA4	0.709495	0.496407	0.642157	0.620145	0.383955	0.580556	0.666141	0.260454	2.486369	1.62E-07	-0.06734	1	-0.32554	0.770099	-0.04335	0.970377	1.776874	0.002491	-0.2582
Pav_sc0002327.1_g560.1.mk	PavAUX/IAA9	0.11653	0.950893	0.310343	0.886102	-0.68551	0.109089	-0.50254	0.264159	0.800405	0.0703	0.193813	1	-0.80204	0.129958	-0.61907	0.230519	0.683876	0.272305	-0.99585
Pav_sc0002393.1_g030.1.mk	PavAUX/IAA9	-0.13398	0.90194	-0.06232	0.999982	-0.24963	0.494791	-0.42625	0.171054	-0.26602	0.529076	0.071657	1	-0.11566	0.863633	-0.29227	0.484096	-0.13204	0.880356	-0.18731
Pav_co4052989.1_g010.1.mk	PavAUX/IAA10	0.050227	0.992152	0.92641	0.516721	-1.42427	0.022846	-1.35509	0.029512	0.80112	0.37351	0.876183	1	-1.4745	0.056663	-1.40532	0.055665	0.750893	0.593399	-2.35068
Pav_sc0002181.1_g160.1.mk	PavAUX/IAA11	0.694396	0.692985	0.987544	0.485917	-0.18144	0.872133	-0.21325	0.844875	0.650988	0.523641	0.293147	1	-0.87583	0.429994	-0.90764	0.337763	-0.04341	0.98848	-1.16898
Pav_sc0000545.1_g110.1.mk	PavAUX/IAA12	-0.12204	0.932973	0.36041	0.730135	-0.65808	0.0568	-0.70199	0.035268	-0.04937	0.951391	0.482446	1	-0.53605	0.263697	-0.57996	0.164256	0.07267	0.949332	-1.01849
Pav_sc0002717.1_g050.1.mk	PavAUX/IAA12	0.25453	0.927626	0.356479	0.963928	0.659994	0.443125	0.364793	0.692441	-0.96084	0.178198	0.10195	1	0.405465	0.794066	0.110264	0.937145	-1.21537	0.164847	0.303515
Pav_sc0000311.1_g1160.1.mk	PavAUX/IAA13	-0.34423	0.959371	0.288143	1	-0.40752	0.862669	-0.79414	0.69432	2.032334	0.331862	0.632371	1	-0.06329	0.992609	1	1	2.376562	0.387863	1
Pav_sc0002717.1_g060.1.br	PavAUX/IAA13	-0.30774	0.858495	0.092587	1	-0.36594	0.601165	-0.42224	0.520664	-0.44083	0.57918	0.400325	1	-0.0582	0.968585	-0.1145	0.907889	-0.13309	0.939422	-0.45852
Pav_sc0000998.1_g220.1.mk	PavAUX/IAA14	2.363785	0.020495	1.803389	0.150708	5.146832	4.78E-11	4.836634	6.6E-10	8.034807	1.02E-18	-0.5604	1	2.783048	0.006804	2.472849	0.016215	5.671023	3.47E-08	3.343443
Pav_sc0000396.1_g1080.1.mk	PavAUX/IAA16	-0.23305	0.72445	-0.11722	0.977045	-0.60963	0.013845	-0.55166	0.026739	-0.29966	0.37295	0.115831	1	-0.37658	0.310567	-0.31861	0.355647	-0.06661	0.937445	-0.49241
Pav_sc0000983.1_g260.1.mk	PavAUX/IAA16	1.882493	1.66E-10	1.779282	2.43E-09	0.701939	0.042368	0.749138	0.025224	2.051446	3.82E-13	-0.10321	1	-1.18055	0.000818	-1.13336	0.001314	0.168953	0.868591	-1.07734
Pav_sc0000716.1_g230.1.mk	PavAUX/IAA17	0.372364	0.862943	0.639468	0.773974	-0.48316	0.573655	-0.52536	0.520441	1.010936	0.200479	0.267104	1	-0.85552	0.400128	-0.89772	0.302269	0.638572	0.667494	-1.12262
Pav_sc0000716.1_g200.1.mk	PavAUX/IAA19	-0.25417	0.944973	-0.03959	1	-1.80957	0.026418	-1.76028	0.028941	-0.72543	0.548126	0.214581	1	-1.5554	0.156601	-1.50611	0.130007	-0.47125	0.838555	-1.76998
Pav_sc0000759.1_g050.1.mk	PavAUX/IAA26	-0.23321	0.879207	-0.41949	0.79469	0.049682	0.949656	0.03349	0.968723	-0.481	0.428496	-0.18628	1	0.282895	0.758328	0.266704	0.712915	-0.24779	0.843978	0.469176
Pav_sc0000800.1_g500.1.mk	PavAUX/IAA26	-0.8779	0.179423	-0.67165	0.443304	-0.89974	0.054688	-0.42079	0.447556	0.321402	0.667402	0.206246	1	-0.02185	0.991098	0.457106	0.485262	1.199297	0.026436	-0.22809
Pav_sc0000212.1_g380.1.mk	PavAUX/IAA27	-0.07007	0.980955	-0.1103	1	-0.25447	0.747594	-0.35326	0.620062	-0.23835	0.812403	-0.04023	1	-0.18441	0.88791	-0.2832	0.756103	-0.16828	0.92702	-0.14417
Pav_sc0001710.1_g1550.1.mk	PavAUX/IAA27	-0.27181	0.742737	-0.25504	0.862542	-0.2665	0.494827	-0.36165	0.304051	-0.3549	0.393091	0.016771	1	0.005317	0.999377	-0.08983	0.874576	-0.08309	0.935851	-0.01145
Pav_sc0000478.1_g250.1.mk	PavAUX/IAA31	-0.01374	1	-0.04035	1	-0.12092	0.893917	0.093095	0.921811	0.169701	0.878141	-0.02662	1	-0.10718	0.940041	0.106834	0.92117	0.18344	0.920603	-0.08057
Pav_sc0001181.1_g100.1.mk	PavAUX/IAA32	1	1	1	1	1	1	1	1	1	1	-3.1873	1	1	1	1	1	1	1	1
Pav_sc0000359.1_g360.1.mk	PavAUX/IAA33	-1.25709	0.935157	-1.06874	0.994317	0.969922	0.868118	1.938312	0.703224	6.327222	0.174968	0.188353	1	2.227011	0.769376	1	1	7.584312	0.172674	1

3 300 mg/L	70 % vs GA3 500 mg/L		tOH 70 % vs O.P. 7 DA		0 mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 7 D		3 500 mg/L vs O.P. 7 D		N.C. 7 vs 14 DAT		EtOH 70% 7 vs 14 DAT		A3 300 mg/L 7 vs 14 DA		A3 500 mg/L 7 vs 14 D		O.P. 7 vs 14 DAT		N.C. vs EtOH 14 DAT		. vs GA3 30
p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
0.010382	-1.26218	0.007338	0.198804	0.858241	-0.01924	1	1.441744	0.001834	1.46098	0.002188	-0.27942	0.805302	-0.35284	0.631294	0.228618	0.689757	0.2888	0.605298	-0.59834	0.265717	0.041271	1	-0.62021
0.292081	-0.40486	0.437874	0.633687	0.311037	0.142148	1	1.180695	0.00629	1.038547	0.027766	0.653238	0.310842	0.551779	0.33623	0.935907	0.018039	0.150096	0.790106	-0.15171	0.812584	-0.10637	0.981547	-0.26925
0.758801	0.023983	0.981065	1.844212	0.001147	0.282186	1	2.102414	6.2E-05	1.820229	0.001177	1.203078	0.071921	2.163049	3.95E-05	0.095282	0.902498	-0.34515	0.590486	-2.11772	2.87E-05	0.892634	0.683581	-1.43334
0.021109	-0.81289	0.058709	0.490063	0.451854	0.182966	1	1.485916	0.000113	1.30295	0.001465	0.540156	0.423747	0.507001	0.361789	0.995095	0.007668	0.934257	0.013288	-1.09347	0.005994	0.160658	0.964525	-0.3471
0.660447	-0.36393	0.28142	-0.2037	0.72896	-0.17661	1	-0.01639	0.982142	0.160225	0.772067	-0.10294	0.903627	-0.06092	0.916759	0.491815	0.085332	0.465607	0.108119	0.087939	0.845117	0.113681	0.965347	0.479105
0.000309	-2.2815	0.000439	-0.12529	0.951453	0.069177	1	2.225389	0.000501	2.156211	0.001177	0.311882	0.857477	-0.29652	0.816283	1.713361	0.003437	1.538858	0.009573	-0.7534	0.353989	0.26778	0.964886	-0.07302
0.156577	-1.20079	0.118614	-0.33656	0.836019	-0.03181	1	0.832425	0.378617	0.864234	0.398893	-0.10617	0.968284	0.114309	0.935069	0.475178	0.562091	0.173206	0.861014	-0.92153	0.251332	0.513626	0.899469	-0.29449
0.00361	-1.0624	0.001618	-0.40978	0.468613	-0.04391	1	0.608717	0.120276	0.652627	0.112478	-0.15048	0.866544	-0.12969	0.842765	0.837257	0.007531	0.884996	0.004597	-0.26821	0.531841	0.503241	0.708856	0.451695
0.795062	0.008314	0.995265	-1.31732	0.102629	-0.2952	1	-1.62083	0.020202	-1.32563	0.075667	-0.25448	0.892487	-0.47132	0.655179	-0.17393	0.864585	0.651357	0.45155	1.469137	0.026675	-0.1149	0.989451	0.486014
1	1	1	1.744191	0.529042	-0.38662	1	1	1	1	1	1.787938	0.519104	3.59009	0.145143	4.212459	0.023355	4.554725	0.012937	-0.10743	0.975422	2.434523	0.80589	1
0.527844	-0.51483	0.432779	-0.53342	0.5674	-0.0563	1	-0.07489	0.944371	-0.01859	0.990873	0.392046	0.745694	-0.46482	0.564008	0.487432	0.410301	0.229741	0.735271	0.421741	0.525926	-0.45654	0.875223	0.037187
0.000281	3.033244	0.000972	6.231418	6.05E-10	-0.3102	1	2.887975	0.018091	3.198174	0.009147	9.611481	7.69E-10	6.263402	9.25E-11	0.697919	0.540201	1.460369	0.150888	0.921908	0.641438	-3.90847	0.461709	-6.13051
0.084242	-0.43444	0.117383	-0.18244	0.718107	0.057978	1	0.309972	0.358601	0.251994	0.529871	-0.19168	0.735984	-0.61845	0.027886	0.36087	0.161452	0.239196	0.395892	-0.05832	0.88716	-0.31093	0.800566	0.175966
0.001931	-1.03014	0.002688	0.272164	0.682377	0.047199	1	1.349508	3.08E-05	1.302308	8.3E-05	0.129647	0.89458	0.304031	0.56356	-0.30976	0.413589	-0.5099	0.139582	-1.03389	0.001763	0.071173	0.985677	-1.61996
0.141828	-1.16483	0.102206	0.371468	0.79659	-0.0422	1	1.494092	0.037157	1.536292	0.039929	0.190629	0.925753	0.635042	0.514502	0.650918	0.360863	0.137544	0.884948	-1.67659	0.010285	0.711517	0.842421	-0.39523
0.049819	-1.72069	0.046568	-0.68583	0.656209	0.049286	1	1.084143	0.306014	1.034857	0.380485	-0.47424	0.812156	-0.09464	0.953825	0.916361	0.290615	0.686448	0.460107	-0.61701	0.555749	0.594181	0.899469	-0.16479
0.413617	0.452984	0.403425	-0.06151	0.963407	-0.01619	1	-0.53068	0.371699	-0.51449	0.435091	0.163023	0.897746	-0.16966	0.837578	0.61035	0.178651	0.483908	0.310645	1.043135	0.020086	-0.51896	0.817632	0.730222
0.747734	0.250861	0.697829	0.993051	0.089595	0.478954	1	1.221145	0.010895	0.742191	0.219956	0.267636	0.808212	-0.21868	0.78363	-0.15098	0.800372	-0.47607	0.334943	-0.71422	0.163	-0.28007	0.917586	-0.44047
0.877376	-0.24297	0.76267	-0.12805	0.932025	-0.09879	1	0.016124	0.993144	0.114917	0.928936	-0.43879	0.708653	-0.42973	0.60911	-0.16386	0.822302	-0.24743	0.722271	-0.57072	0.378615	-0.03118	1	0.090524
0.985143	-0.1066	0.831591	-0.09986	0.903358	-0.09515	1	-0.08841	0.879192	0.006742	0.994054	-0.1507	0.85101	-0.24577	0.610549	0.079718	0.851863	0.312709	0.356948	0.502494	0.139364	-0.07829	0.981004	0.235736
0.935374	0.133449	0.889691	0.210055	0.876324	0.214014	1	0.29062	0.753641	0.076606	0.958124	1.042332	0.179476	0.96209	0.172754	2.04596	0.000102	1.518442	0.004863	1.324037	0.02616	-0.10686	0.989451	0.896447
1	1	1	1	1	-1.91659	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	-0.06249	1	1
1	1	1	7.395959	0.165317	0.968391	1	5.357301	0.29104	4.38891	0.467122	5.216055	0.397765	5.043163	0.325161	5.357333	0.18636	4.336655	0.310717	0	1	0.015461	1	2.368289

0 mg/L 14	. vs GA3 500 mg/L 14		N.C. vs O.P. 14 DAT		40 % vs GA3 300 mg/L		40 % vs GA3 500 mg/L		OH 140 % vs O.P. 14 D		mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 14		3 500 mg/L vs O.P. 14		N.C. 14 vs 21 DAT		tOH 70% 14 vs 21 DA		3 300 mg/L 14 vs 21 D		3 500 mg/L
p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
0.283261	-0.57927	0.330146	-0.00542	1	-0.66148	0.227156	-0.62054	0.269862	-0.04669	0.962007	0.040946	1	0.614789	0.47278	0.573842	0.524653	0.165481	0.8389	0.412986	0.65021	-0.66348	0.142858	-0.41698
0.6859	-0.91292	0.044062	-0.17618	0.877572	-0.16288	0.814988	-0.80654	0.080545	-0.06981	0.931318	-0.64366	1	0.093075	0.947781	0.736737	0.286509	0.376321	0.526082	0.395375	0.62655	-0.04606	0.94123	0.674389
0.009367	-1.59158	0.002783	-1.54392	0.012387	-2.32597	5.07E-06	-2.48421	7.61E-07	-2.43655	3.42E-06	-0.15824	1	-0.11058	0.951453	0.047659	0.983481	0.829937	0.246486	-0.33262	0.791897	0.493367	0.385838	1.018263
0.553022	-0.22497	0.739708	-0.94975	0.054294	-0.50776	0.305921	-0.38563	0.48185	-1.1104	0.007071	0.122128	1	-0.60264	0.384356	-0.72477	0.268336	0.433317	0.42715	-0.07204	0.944257	0.953163	0.009962	0.919177
0.160295	0.276284	0.499818	0.058841	0.951189	0.365425	0.305921	0.162603	0.722125	-0.05484	0.919257	-0.20282	1	-0.42026	0.408188	-0.21744	0.772976	0.487146	0.170516	0.233442	0.687979	0.98613	0.000131	1.137692
0.961659	-0.17834	0.895697	-0.31439	0.856377	-0.3408	0.747057	-0.44612	0.661928	-0.58217	0.520082	-0.10533	1	-0.24137	0.905472	-0.13605	0.952069	1.095337	0.22018	0.80366	0.540286	0.103591	0.911536	0.631768
0.816296	-0.62827	0.53513	-0.85877	0.470517	-0.80811	0.365045	-1.14189	0.156879	-1.37239	0.074958	-0.33378	1	-0.56428	0.737716	-0.2305	0.921245	0.939861	0.298079	0.073013	0.97107	0.47852	0.541777	0.71687
0.291054	0.455523	0.287103	-0.04506	0.97229	-0.05155	0.935376	-0.04772	0.946571	-0.5483	0.165456	0.003829	1	-0.49676	0.404512	-0.50058	0.41479	0.653609	0.110228	0.382619	0.550286	0.368741	0.314274	0.627201
0.63973	1.016098	0.264921	0.508245	0.735048	0.600911	0.511024	1.130995	0.18338	0.623142	0.485564	0.530084	1	0.022231	0.999388	-0.50785	0.809692	1	1	0.120676	0.939971	-0.79741	0.245942	-2.15088
1	2.31688	0.38782	1	1	-0.07329	0.990083	-0.11764	0.985445	1	1	-0.04435	1	1	1	1	1	1	1	1	1	1.80125	0.512853	1.768819
0.979608	-0.27681	0.761998	-0.1034	0.954367	0.493726	0.488322	0.179731	0.840873	0.353142	0.636734	-0.314	1	-0.14058	0.937901	0.173411	0.92195	0.053571	0.96285	0.473024	0.644128	0.125271	0.863363	-0.01617
0.000435	-5.67826	0.001495	-3.01855	0.332848	-2.22204	0.08013	-1.76979	0.205186	0.889923	0.680051	0.452252	1	3.111964	0.106841	2.659712	0.204715	-1.02806	0.800131	2.860743	0.377861	3.522012	0.00839	3.568819
0.650677	0.11227	0.807692	0.066744	0.929082	0.486901	0.076186	0.423205	0.141369	0.377679	0.205918	-0.0637	1	-0.10922	0.883647	-0.04553	0.958462	0.030646	0.952621	0.220006	0.657409	-0.26271	0.319307	-0.39049
1.15E-07	-1.7729	2.98E-09	-0.99459	0.010576	-1.69113	2.21E-08	-1.84407	5.1E-10	-1.06576	0.001928	-0.15294	1	0.625373	0.242841	0.778313	0.112311	0.377638	0.417562	0.380992	0.543904	0.906321	0.003377	0.972552
0.708035	-0.95081	0.234008	-1.22864	0.168265	-1.10675	0.133186	-1.66232	0.012005	-1.94016	0.003381	-0.55557	1	-0.83341	0.498312	-0.27784	0.894403	0.767426	0.376879	-0.16441	0.919411	0.403981	0.585529	1.109156
0.920476	-0.34542	0.820356	-0.61402	0.732454	-0.75897	0.489492	-0.9396	0.370048	-1.2082	0.211238	-0.18063	1	-0.44922	0.841577	-0.2686	0.921245	1.159424	0.261423	0.275847	0.888216	1.325389	0.093698	1.603522
0.161227	0.587588	0.291099	0.632323	0.359127	1.249183	0.00421	1.106549	0.013573	1.151284	0.011658	-0.14263	1	-0.0979	0.947702	0.044734	0.980556	-0.15706	0.839402	-0.08465	0.940596	-1.07751	0.007741	-1.17653
0.481649	-0.2866	0.696087	0.217443	0.854734	-0.1604	0.833174	-0.00654	0.998961	0.497508	0.387244	0.153866	1	0.657911	0.406516	0.504045	0.591143	-0.66026	0.243864	-0.31991	0.733134	-1.10762	0.006699	-1.09919
0.933877	-0.09185	0.940284	-0.30022	0.821064	0.1217	0.90008	-0.06067	0.95865	-0.26904	0.742391	-0.18237	1	-0.39074	0.769471	-0.20837	0.905	-0.10233	0.919844	-0.08388	0.951772	-0.51413	0.366923	-0.2331
0.614853	0.373578	0.354069	0.570106	0.179349	0.31403	0.438725	0.451872	0.21713	0.6484	0.052367	0.137842	1	0.33437	0.60863	0.196527	0.816827	0.232564	0.608712	0.25775	0.67524	0.28936	0.378921	0.081029
0.222552	0.582943	0.485582	0.465145	0.714218	1.003304	0.14183	0.6898	0.365407	0.572002	0.459995	-0.3135	1	-0.4313	0.780605	-0.1178	0.955033	-0.22681	0.819447	0.204568	0.882296	-0.57116	0.384818	-0.83016
1	1	1	1	1	1	1	1	1	1	1	0.913382	1	1	1	1	1	1	1	1	1	1	1	1
0.722176	2.316002	0.733735	1	1	2.352828	0.704035	2.300541	0.7207	2.259243	0.708513	0	1	1	1	1	1	1	1	1	1	0	1	0

14 vs 21 D	O.P. 14 vs 21 DAT		N.C. vs EtOH 21 DAT		. vs GA3 300 mg/L 21		. vs GA3 500 mg/L 21		N.C. vs O.P. 21 DAT		10 % vs GA3 300 mg/L		10 % vs GA3 500 mg/L		OH 210 % vs O.P. 21 D		mg/L vs GA3 500 mg/		300 mg/L vs O.P. 21		500 mg/L vs O.P. 21		N.C. 21 v
p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
0.382905	-0.28781	0.712809	0.288777	1	-1.44917	0.000412	-1.16173	0.007562	-0.45871	0.412163	-1.73795	1.33E-05	-1.4505	0.000482	-0.74749	0.113635	0.287448	1	0.99046	0.030752	0.703012	0.133624	0.22357
0.091191	0.129454	0.881458	-0.08732	1	-0.69163	0.102326	-0.61485	0.165749	-0.42305	0.406329	-0.60432	0.158706	-0.52753	0.248143	-0.33573	0.501713	0.076786	1	0.268588	0.603558	0.191802	0.71405	-0.43357
0.041273	-0.24115	0.807333	-0.26992	1	-1.76991	0.000394	-1.40325	0.008574	-2.61501	6.91E-08	-1.49998	0.002854	-1.13333	0.038502	-2.34508	1.24E-06	0.366653	1	-0.8451	0.126635	-1.21175	0.020494	-0.20831
0.011892	-0.08683	0.924351	-0.3447	1	0.172745	0.744362	0.260887	0.603851	-1.46989	5.57E-05	0.517443	0.21762	0.605585	0.149876	-1.12519	0.002422	0.088142	1	-1.64264	8.75E-06	-1.73078	2.39E-06	0.298724
6.38E-06	0.213942	0.650363	-0.14002	1	0.97809	0.000136	0.92683	0.000387	-0.21436	0.567369	1.118113	7.89E-06	1.066853	2.74E-05	-0.07434	0.857389	-0.05126	1	-1.19245	7.8E-06	-1.14119	2.02E-05	0.343468
0.377673	-0.33895	0.772861	-0.0239	1	-1.06476	0.148831	-0.64191	0.460776	-1.74868	0.01025	-1.04087	0.154203	-0.61802	0.477321	-1.72478	0.009232	0.422851	1	-0.68392	0.354194	-1.10677	0.106339	-1.43095
0.316128	0.222262	0.875947	-0.35322	1	-0.75583	0.327268	-0.85126	0.268161	-1.57637	0.023241	-0.4026	0.641167	-0.49804	0.561213	-1.22315	0.08166	-0.09543	1	-0.82054	0.285383	-0.72511	0.338053	-0.8276
0.061952	0.380793	0.429833	0.23225	1	0.166826	0.714209	0.429114	0.27518	-0.31788	0.45577	-0.06542	0.901139	0.196864	0.674182	-0.55013	0.125106	0.262288	1	-0.4847	0.193142	-0.74699	0.032697	-0.08378
0.000494	-0.66143	0.51923	-0.40055	1	-0.71773	0.313477	-1.54111	0.008378	-0.55952	0.498099	-0.31717	0.689408	-1.14056	0.050991	-0.15897	0.86068	-0.82338	1	0.158208	0.859794	0.98159	0.100543	-0.99613
0.510775	1	1	2.194965	1	3.07913	0.190827	3.002348	0.21541	1.18049	0.687368	0.884166	0.803406	0.807383	0.827528	-1.01448	0.760359	0	1	1	1	1	1	1
0.987756	0.20337	0.852316	-0.03709	1	0.108887	0.896131	-0.34655	0.605576	0.046403	0.965764	0.145972	0.849875	-0.30946	0.64921	0.083488	0.921595	-0.45543	1	-0.06248	0.94528	0.392948	0.53146	-0.67279
0.018715	1.882954	0.541961	-0.01967	1	-1.58044	0.528169	-1.08138	0.717874	-0.10754	0.984831	-1.56077	0.529601	-1.06171	0.720948	-0.08787	0.986123	0.499058	1	1.472906	0.563083	0.973848	0.73073	0.908086
0.106055	-0.19237	0.638794	-0.12157	1	-0.11739	0.719542	-0.30886	0.261568	-0.15627	0.647609	0.004181	0.99638	-0.18729	0.538829	-0.03469	0.930422	-0.19147	1	-0.03888	0.919131	0.152593	0.612624	-0.03575
0.001302	-0.61666	0.137947	0.074527	1	-1.09128	0.000363	-1.17798	0.000115	-1.98889	1.16E-11	-1.1658	0.000112	-1.25251	3.33E-05	-2.06342	1.27E-12	-0.08671	1	-0.89761	0.006689	-0.8109	0.014122	0.213806
0.072203	0.12733	0.933863	-0.22032	1	-0.75868	0.283366	-0.60908	0.424383	-1.86874	0.002452	-0.53836	0.473588	-0.38876	0.639995	-1.64843	0.007228	0.1496	1	-1.11007	0.099081	-1.25967	0.051462	-0.86812
0.033464	-0.13741	0.945263	-0.2894	1	0.001171	1	0.098677	0.940313	-1.91085	0.016899	0.290567	0.791543	0.388074	0.718775	-1.62145	0.041912	0.097506	1	-1.91202	0.017302	-2.00952	0.010748	-0.77771
0.002843	0.307954	0.673812	-0.44656	1	-0.19024	0.743115	-0.43188	0.394184	1.097332	0.010396	0.256324	0.635512	0.01468	0.987355	1.543892	0.000102	-0.24164	1	1.287568	0.002381	1.529213	0.000206	-1.28052
0.006463	0.177337	0.843218	0.060285	1	-0.88783	0.039388	-0.72553	0.114312	1.05504	0.017656	-0.94811	0.023971	-0.78582	0.080933	0.994755	0.022344	0.162291	1	1.942866	2.34E-06	1.780575	1.88E-05	-0.39461
0.710531	-0.15096	0.893983	-0.01272	1	-0.32127	0.62932	-0.22261	0.762058	-0.34885	0.628054	-0.30855	0.640915	-0.20989	0.774964	-0.33612	0.615455	0.098662	1	-0.02757	0.976139	-0.12624	0.865321	0.008481
0.834714	-0.14633	0.798152	-0.05311	1	0.292531	0.399533	0.222043	0.557667	0.191211	0.647766	0.34564	0.297653	0.275151	0.44496	0.244319	0.505027	-0.07049	1	-0.10132	0.810707	-0.03083	0.950014	0.452985
0.151293	0.255739	0.830662	0.324524	1	0.552102	0.401677	-0.02041	0.987186	0.947697	0.138788	0.227578	0.771864	-0.34493	0.639589	0.623173	0.354492	-0.57251	1	0.395595	0.599269	0.968105	0.110904	-0.56939
1	1	1	-1.87091	1	1	1	1	1	1	1	1	1	1	1	1	1	1.744468	1	1	1	1	1	1
1	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0

s 28 DAT	EtOH 70% 21 vs 28 DAT		3 300 mg/L 21 vs 28 D		3 500 mg/L 21 vs 28 D		O.P. 21 vs 28 DAT		N.C. vs EtOH 28 DAT		. vs GA3 300 mg/L 28		. vs GA3 500 mg/L 28		N.C. vs O.P. 28 DAT		30 % vs GA3 300 mg/L		30 % vs GA3 500 mg/L		OH 280 % vs O.P. 28 D		mg/L vs GA
p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
0.707607	0.242688	0.631844	1.230758	0.001302	1.270475	0.000781	0.101719	0.908907	0.307896	0.698095	-0.44199	0.327124	-0.11482	0.818429	-0.58057	0.214144	-0.74988	0.096454	-0.42272	0.350646	-0.88846	0.030751	0.327166
0.361715	-0.05856	0.908971	-0.37255	0.336841	-0.88818	0.010941	-0.26371	0.687111	0.287684	0.686302	-0.63062	0.100188	-1.06946	0.002273	-0.25318	0.601614	-0.9183	0.017654	-1.35714	0.00013	-0.54087	0.167977	-0.43884
0.789159	1.383517	0.014908	6.864525	5.53E-09	5.410663	3.69E-10	0.553547	0.444393	1.321897	0.106268	5.302924	1.47E-05	4.215715	2.24E-06	-1.85315	0.00012	3.981027	0.002567	2.893818	0.002641	-3.17505	1.69E-10	-1.08721
0.532567	1.992342	2.77E-08	0.783946	0.022114	0.473736	0.182564	0.689983	0.153334	1.348921	0.00179	0.657967	0.070537	0.435899	0.234124	-1.07863	0.002591	-0.69095	0.073076	-0.91302	0.009127	-2.42755	1.49E-13	-0.22207
0.283103	1.43059	3.07E-08	1.322529	3.1E-08	1.214635	2.5E-07	0.498039	0.152682	0.9471	0.002644	1.957151	1.04E-16	1.797998	1.95E-14	-0.05979	0.878825	1.010051	7.25E-05	0.850898	0.000695	-1.00689	3.33E-05	-0.15915
0.046181	0.276998	0.755692	1.800697	0.009803	1.456795	0.045789	0.458925	0.642167	1.68405	0.074965	2.166882	0.002007	2.245832	0.001222	0.141193	0.872881	0.482832	0.64352	0.561782	0.540174	-1.54286	0.017634	0.07895
0.286705	0.323471	0.675254	1.227577	0.043457	0.942369	0.124493	-0.94605	0.288155	0.797845	0.461534	1.299346	0.038822	0.918708	0.14402	-1.69482	0.007209	0.501501	0.527092	0.120863	0.881122	-2.49267	1.94E-05	-0.38064
0.866412	0.04511	0.91813	0.151084	0.683751	-0.06595	0.875225	0.509481	0.242947	0.361145	0.518638	0.401694	0.243565	0.446946	0.1738	0.275389	0.477526	0.040549	0.9398	0.085801	0.837672	-0.08576	0.838295	0.045252
0.134535	-0.39582	0.542712	0.205868	0.76204	0.631771	0.234843	-0.10876	0.928824	1	1	0.484275	0.445432	0.086797	0.899412	0.327854	0.638644	0.284508	0.718231	-0.11297	0.873521	0.128087	0.858855	1
1	-0.22073	0.945368	0	1	0	1	1	1	1	1	0.491539	0.87448	0.431756	0.882345	-1.21874	0.669352	0.681697	0.842945	0.621913	0.831242	-1.02858	0.691713	1
0.23782	-0.04697	0.944349	-0.66627	0.176621	-0.38143	0.443203	-0.33372	0.692279	0.588737	0.470304	0.115405	0.851806	-0.05519	0.927002	0.385473	0.4986	-0.47333	0.421466	-0.64392	0.203014	-0.20326	0.731866	-0.17059
0.776001	-2.45446	0.199925	-0.79499	0.641553	-0.3223	0.89328	1.121094	0.773243	-3.38222	0.222149	-3.28352	0.075199	-2.31177	0.264452	0	1	0.098704	0.968464	1.070452	0.571064	3.487692	0.049129	0.971747
0.926369	0.056951	0.844772	0.103561	0.684244	-0.14204	0.559806	-0.21296	0.562234	-0.02887	0.960121	0.021918	0.945546	-0.41515	0.057781	-0.33348	0.184969	0.050791	0.883442	-0.38628	0.090088	-0.3046	0.198425	-0.43707
0.616233	0.408515	0.227338	1.312299	3.24E-06	1.515806	4.44E-08	0.684947	0.081041	0.269236	0.639883	0.007218	0.993103	0.124015	0.731188	-1.51775	2.2E-07	-0.26202	0.500615	-0.14522	0.696099	-1.78698	2.74E-10	0.116797
0.220662	-0.15235	0.839798	1.283224	0.021543	0.478907	0.434468	0.192491	0.873279	0.495454	0.647465	1.392664	0.015354	0.737947	0.213993	-0.80813	0.221536	0.89721	0.168433	0.242493	0.730027	-1.30359	0.023281	-0.65472
0.402698	1.588191	0.033646	6.566806	8.9E-21	5.594728	1.27E-16	0.754322	0.512418	2.076506	0.035324	7.345689	7.98E-26	6.471117	1.11E-21	-0.37881	0.701363	5.269182	2.32E-13	4.394611	2.89E-10	-2.45532	0.000355	-0.87457
0.002762	-1.16552	0.003284	-2.28948	1.17E-10	-2.32705	2.81E-11	-0.23093	0.744434	-0.33156	0.649738	-1.1992	0.001449	-1.47841	4.13E-05	2.146916	9.24E-09	-0.86763	0.034614	-1.14685	0.00235	2.478481	5.68E-12	-0.27922
0.44417	-0.60564	0.154285	-0.9143	0.014503	-0.59493	0.122778	-0.57371	0.330429	-0.15074	0.857495	-1.40751	0.00017	-0.92585	0.013979	0.875942	0.035512	-1.25677	0.001329	-0.77511	0.04999	1.026685	0.008034	0.481662
0.994178	0.409575	0.458351	1.838203	2.92E-05	2.417913	1.77E-08	-0.05766	0.96007	0.388371	0.664984	1.508451	0.001014	2.186823	5.72E-07	-0.41498	0.485893	1.120079	0.024366	1.798451	7.06E-05	-0.80335	0.101225	0.678372
0.168477	0.480345	0.097672	1.036298	4.79E-05	1.18652	2.07E-06	0.307586	0.47149	-0.02575	0.970819	0.875844	0.000979	0.955577	0.000199	0.045811	0.917024	0.901592	0.001014	0.981326	0.000194	0.071559	0.843269	0.079734
0.36941	-1.51258	0.002855	-3.02715	3.33E-11	-3.15914	4.65E-13	-0.24199	0.814747	-0.61867	0.465557	-1.90566	2.74E-05	-2.61017	1.96E-09	1.27509	0.015781	-1.28699	0.008025	-1.9915	7.59E-06	1.893759	7.67E-05	-0.70451
1	1	1	-2.35509	0.652999	-6.44767	0.164063	1	1	1	1	-1.67568	0.774775	-4.02379	0.407561	1	1	1	1	1	1	3.87112	0.472382	1
1	0	1	-2.6761	0.492602	0	1	1	1	1	1	-2.71956	0.515802	0	1	-0.85887	0.880223	-2.52677	0.58886	0	1	-0.66608	0.897761	1

A3 500 mg/	3 300 mg/L vs O.P. 28		3 500 mg/L vs O.P. 28	
p-adj	Log2FC	p-adj	Log2FC	p-adj
0.642437	-0.13858	0.771311	-0.46574	0.248292
0.444012	0.377431	0.326505	0.816271	0.017952
0.685238	-7.15608	6.76E-10	-6.06887	9.6E-13
0.730419	-1.7366	7E-08	-1.51453	2.12E-06
0.740535	-2.01694	5.09E-18	-1.85779	7.68E-16
0.972742	-2.02569	0.002693	-2.10464	0.001884
0.740051	-2.99417	1.14E-07	-2.61353	2.87E-06
0.956359	-0.12631	0.732693	-0.17156	0.61545
1	-0.15642	0.818698	0.241057	0.682262
1	-1.71028	0.447515	-1.6505	0.440743
0.858066	0.270068	0.603029	0.44066	0.344236
0.756024	3.388988	0.051739	2.417241	0.215715
0.165278	-0.35539	0.10458	0.081674	0.736796
0.850125	-1.52497	3.49E-08	-1.64176	1.9E-09
0.471942	-2.2008	3.38E-05	-1.54608	0.003646
0.495036	-7.7245	8.54E-29	-6.84993	1.23E-24
0.68029	3.346114	7.51E-22	3.625329	7.85E-26
0.421661	2.283454	1.28E-10	1.801792	3.48E-07
0.342011	-1.92343	9.16E-06	-2.6018	8.57E-10
0.892482	-0.83003	0.001145	-0.90977	0.000277
0.304941	3.180748	1.57E-12	3.885256	1.39E-18
1	4.325278	0.379946	6.673389	0.13618
1	1.860688	0.643968	-0.33242	0.943658

Table S4.7: Table with Log2FoldChange (log2FC) and p-value adjusted (p-adj) of the genes involved in GA biosynthesis, inactivation, and signal transduction. The heatmap of these genes is showed in Fig. 4.17. Log2FC is calculated according to the following formula: expression level term1 - expression level term2.

Gene name	Gene description	N.C. 0 vs 7 DAT		EtOH 70% 0 vs 7 DAT		A3 300 mg/L 0 vs 7 DA		A3 500 mg/L 0 vs 7 DA		O.P. 0 vs 7 DAT		N.C. vs EtOH 7 DAT		C. vs GA3 300 mg/L 7 D		C. vs GA3 500 mg/L 7 D		N.C. vs O.P. 7 DAT		70 % vs GA3 300 mg/L	
		Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
Pav_sc0000146.1_g580.1.mk	PavCPS1	-1.04103	0.831415	-0.29407	1	0.95129	0.74048	-1.90103	0.262197	-2.48608	0.151574	0.746965	1	1	1	1	1	1	1	1	1
Pav_co4009519.1_g010.1.br	PavKS1	0.001017	1	1.640141	0.820886	-0.39924	0.856138	-1.11983	0.490906	1.621072	0.545653	1.639124	1	-0.40025	0.909452	1	1	1.620054	0.70823	-2.03938	0.366504
Pav_sc0001936.1_g050.1.mk	PavKS1	-0.02284	0.998194	0.03061	1	-0.0063	0.998106	0.285206	0.685867	0.503048	0.497715	0.053449	1	0.016539	0.995737	0.308046	0.715414	0.525888	0.641601	-0.03691	0.9695
Pav_sc0005064.1_g030.1.mk	PavKS1	0.077623	0.990629	1.40448	0.51866	-1.29849	0.147432	-1.05758	0.257755	0.358964	0.838201	1.326857	1	-1.37611	0.244603	-1.1352	0.31518	0.281341	0.928592	-2.70297	0.008542
Pav_sc0000890.1_g930.1.mk	PavATKO1	-0.14538	0.922459	-0.24541	0.922714	-0.60008	0.126223	-0.46189	0.258497	0.175408	0.79421	-0.10003	1	-0.4547	0.433049	-0.31651	0.564239	0.320786	0.718	-0.35468	0.465168
Pav_sc0000503.1_g830.1.mk	PavKAO1	0.418614	0.707664	0.340082	0.882013	1.723642	1.22E-05	1.381017	0.000664	0.936027	0.045331	-0.07853	1	1.305029	0.007455	0.962403	0.061253	0.517413	0.559847	1.38356	0.002071
Pav_sc0000072.1_g640.1.mk	PavGA20OX1	0.318803	0.748594	0.529013	0.480061	-0.10981	0.847997	0.216249	0.664486	0.438134	0.376068	0.21021	1	-0.42861	0.474764	-0.10255	0.881683	0.119331	0.926237	-0.63882	0.140331
Pav_sc0000716.1_g300.1.mk	PavGA3OX1	1.705826	0.584511	1.39301	0.775287	5.158127	0.000813	4.630563	0.001737	4.556558	0.002466	-0.31282	1	3.452302	0.108206	1	1	2.850733	0.226347	3.765117	0.03815
Pav_sc0000704.1_g020.1.mk	PavGA3OX3	2.407396	0.155393	2.39223	0.16285	6.559678	5.13E-05	5.198795	7.3E-05	7.483816	1.67E-05	-0.01517	1	4.152281	0.064164	1	1	5.07642	0.031027	1	1
Pav_sc0000095.1_g1110.1.mk	PavGA2OX2	-2.4596	0.071328	-2.7528	0.028879	-1.90323	0.098057	-1.47861	0.215807	-0.3853	0.858092	-0.2932	1	0.556365	0.815453	0.980991	0.538855	2.074301	0.178498	0.849567	0.572319
Pav_sc0003135.1_g610.1.mk	PavGA2OX2	-0.2327	0.969672	-0.33764	0.996723	-0.08454	0.975431	0.637389	0.730703	2.822251	0.055573	-0.10495	1	0.14816	0.967986	0.870085	0.67679	3.054947	0.080506	0.253105	0.913437
Pav_sc0000410.1_g210.1.mk	PavGA2OX8	0.961929	0.760386	0.49	0.980637	-0.78525	0.551913	-0.4343	0.775667	-0.11344	0.964107	-0.47193	1	-1.74718	0.275609	1	1	-1.07537	0.686901	-1.27525	0.333853
Pav_sc0000910.1_g850.1.mk	PavGA2OX8	0.643453	0.903075	0.399666	0.99497	4.144896	0.002096	3.844158	0.004263	6.218628	1.21E-06	-0.24379	1	3.501443	0.040169	3.200705	0.051945	5.575175	0.000127	3.745229	0.01292
Pav_sc0000221.1_g210.1.mk	PavGAI	-0.18529	0.722952	-0.17225	0.841605	-0.21386	0.370689	-0.36452	0.075276	0.021427	0.964226	0.013035	1	-0.02858	0.95839	-0.17924	0.547309	0.206712	0.63369	-0.04161	0.908028
Pav_sc0000314.1_g230.1.mk	PavGAI	0.513479	0.84281	0.637576	0.886488	0.474059	0.677802	0.222633	0.861576	-0.37979	0.784592	0.124097	1	-0.03942	0.991617	-0.29085	0.849668	-0.89327	0.594434	-0.16352	0.915888
Pav_sc0000704.1_g100.1.mk	PavGAI	0.290044	0.853319	0.350792	0.905155	-1.46887	0.000841	-1.34523	0.002343	0.144442	0.883162	0.060749	1	-1.75892	0.000244	-1.63528	0.000776	-0.1456	0.929993	-1.81967	7.72E-05
Pav_sc0000704.1_g110.1.mk	PavGAI	-0.10274	0.959371	0.244031	0.960576	-1.5381	0.000124	-1.51499	0.000145	0.049227	0.962622	0.346773	1	-1.43536	0.002014	-1.41225	0.001916	0.151969	0.917103	-1.78213	1.96E-05
Pav_sc0000261.1_g150.1.mk	PavRGL1	-0.23165	0.824882	-0.06238	1	-0.83035	0.013693	-1.08626	0.000598	-0.83919	0.016347	0.169272	1	-0.59869	0.209166	-0.8546	0.026494	-0.60753	0.238519	-0.76796	0.041825
Pav_sc0002668.1_g090.1.mk	PavRGL1	-0.24969	0.94515	0.434327	0.968063	-0.79679	0.41188	-0.46855	0.667341	1.340922	0.215568	0.684016	1	-0.5471	0.730614	-0.21887	0.881683	1.59061	0.226816	-1.23112	0.206411
Pav_sc0000464.1_g350.1.mk	PavRGL2	-0.13586	0.902366	-0.15918	0.962866	-0.75882	0.007761	-0.72049	0.011276	0.237318	0.600707	-0.02332	1	-0.62296	0.099309	-0.58463	0.097676	0.373174	0.512151	-0.59964	0.069247
Pav_sc0000848.1_g080.1.mk	PavGID1B	0.092884	0.984855	-0.32103	0.989253	1.081057	0.268408	1.59937	0.065451	-0.08807	0.965428	-0.41392	1	0.988173	0.478311	1.506486	0.154353	-0.18095	0.949815	1.402089	0.163148
Pav_sc0000700.1_g870.1.mk	PavGID1C	0.183815	0.818313	-0.09838	0.989253	1.845357	3.08E-17	1.789686	2.96E-16	0.241044	0.538048	-0.2822	1	1.661542	7.82E-13	1.605871	6.89E-12	0.057229	0.949257	1.943742	2.28E-18
Pav_sc0000055.1_g400.1.mk	PavSPY	-0.06977	0.853138	-0.02525	0.999941	-0.13516	0.32345	-0.17815	0.153172	-0.12249	0.45252	0.044519	1	-0.06539	0.797268	-0.10837	0.529995	-0.05271	0.881909	-0.10991	0.484485
Pav_sc0000852.1_g250.1.mk	PavSLY1	0.483622	0.112225	0.112288	0.973817	1.403507	2.09E-13	1.3443	2.43E-12	0.238155	0.457851	-0.37133	1	0.919886	5.21E-05	0.860679	0.000169	-0.24547	0.611736	1.29122	3.13E-10
Pav_sc0000157.1_g290.1.mk	PavSLY2	0.445476	0.76308	0.550696	0.744709	1.065414	0.054527	0.738357	0.210032	0.828395	0.202503	0.105221	1	0.619938	0.48289	0.292882	0.74732	0.38292	0.784435	0.514717	0.477429

70 % vs GA3 500 mg/L		tOH 70 % vs O.P. 7 DA		0 mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 7 D		3 500 mg/L vs O.P. 7 D		N.C. 7 vs 14 DAT		EtOH 70% 7 vs 14 DAT		A3 300 mg/L 7 vs 14 DA		A3 500 mg/L 7 vs 14 D		O.P. 7 vs 14 DAT		N.C. vs EtOH 14 DAT		. vs GA3 300 mg/L 14	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
1	1	1	1	-2.85232	1	1	1	1	1	-1.1659	0.676805	1	1	-0.54922	0.844595	1.239772	0.436888	1	1	-0.23237	0.988699	1	1
1	1	-0.01907	1	-0.72059	1	2.020308	0.405415	2.740899	0.227319	2.577101	0.442631	0.026949	0.99714	-0.53084	0.749026	-0.16908	0.924604	-3.05773	0.097486	-0.91103	0.963215	-3.5082	0.105824
0.254596	0.734269	0.472438	0.6201	0.291507	1	0.509349	0.489624	0.217842	0.841796	0.178183	0.905242	0.181447	0.851392	-0.17483	0.793549	-0.22075	0.744167	-0.03792	0.970733	0.056714	1	-0.33647	0.670907
-2.46206	0.016423	-1.04552	0.58178	0.24091	1	1.657449	0.092797	1.416539	0.211193	0.167335	0.958811	1.391494	0.521877	-0.8532	0.275593	-1.16333	0.123559	-1.00533	0.338307	2.551016	0.577272	-2.39664	0.003182
-0.21648	0.673867	0.420814	0.492371	0.138196	1	0.77549	0.057449	0.637294	0.173505	0.040734	0.979507	-0.09896	0.889435	0.112685	0.818884	0.509122	0.177184	-0.75495	0.049053	-0.23972	0.91203	-0.38275	0.440386
1.040935	0.02308	0.595945	0.379677	-0.34263	1	-0.78762	0.130648	-0.44499	0.524785	0.951301	0.082843	0.523412	0.393374	0.328458	0.526897	0.712365	0.113435	1.251418	0.004379	-0.50642	0.82846	0.682186	0.205033
-0.31276	0.523084	-0.09088	0.931853	0.326057	1	0.547942	0.23663	0.221885	0.752095	0.115312	0.919923	-0.06788	0.927866	0.448777	0.245001	0.122401	0.811058	-0.05623	0.93335	0.027014	1	-0.09515	0.898185
1	1	3.163548	0.12852	-0.52756	1	-0.60157	0.854155	-0.074	0.988931	2.707606	0.226129	3.580332	0.056131	3.219419	0.164742	2.72989	0.242332	0.852488	0.746441	0.55991	0.97309	3.964114	0.114195
1	1	5.091586	0.025279	-1.36088	1	0.924138	0.82654	2.285021	0.4842	3.255089	0.093343	3.251428	0.07231	0.037709	0.997715	0.753038	0.753782	-3.15269	0.16675	-0.01883	1	0.934902	0.791791
1.274192	0.316065	2.367502	0.084262	0.424625	1	1.517936	0.271113	1.09331	0.523558	1.254707	0.515202	1.176429	0.444547	-1.01973	0.387011	-1.15987	0.31847	-0.32581	0.847588	-0.37148	0.970429	-1.71807	0.178448
0.975031	0.572486	3.159893	0.058965	0.721926	1	2.906788	0.054871	2.184862	0.224826	3.385583	0.033792	0.153246	0.953206	1.776781	0.191519	0.798468	0.622544	1.273833	0.507227	-3.33728	0.270704	-1.46064	0.441995
1	1	-0.60344	0.801089	0.350943	1	0.671804	0.675809	0.320861	0.889393	-0.79737	0.76687	-0.54263	0.773923	0.751015	0.519822	2.203546	0.07536	1.163896	0.408599	-0.21719	0.985677	-0.19879	0.926187
3.444492	0.01952	5.818962	4.1E-05	-0.30074	1	2.073733	0.271614	2.37447	0.221826	5.19385	0.000231	5.255912	0.00016	1.480037	0.351204	4.284674	0.004324	0.252658	0.924507	-0.18173	1	-0.21237	0.945829
-0.19227	0.439627	0.193677	0.592951	-0.15066	1	0.235291	0.38517	0.38595	0.11791	0.200973	0.609984	-0.0339	0.932185	-0.04654	0.868296	0.060432	0.827082	-0.06941	0.820783	-0.22184	0.831272	-0.27609	0.266828
-0.41494	0.735645	-1.01737	0.434028	-0.25143	1	-0.85385	0.444701	-0.60243	0.654537	-0.37104	0.865603	-0.43931	0.76065	-0.05097	0.97295	0.243136	0.834237	0.118122	0.929658	0.055831	1	0.280656	0.856045
-1.69603	0.000269	-0.20635	0.859725	0.123642	1	1.613316	0.000469	1.489674	0.002279	-0.51082	0.581577	0.058399	0.953141	0.398557	0.442225	0.198552	0.742938	-1.02305	0.039258	0.629963	0.775457	-0.84955	0.113782
-1.75903	2.58E-05	-0.1948	0.850418	0.023106	1	1.587328	0.00017	1.564222	0.000291	-0.06273	0.970443	0.039729	0.96298	0.492342	0.290372	0.337898	0.506733	-1.06292	0.016379	0.449236	0.855644	-0.88028	0.070392
-1.02388	0.00292	-0.7768	0.068896	-0.25591	1	-0.00884	0.993508	0.247071	0.680954	-0.0091	0.997284	0.04174	0.952259	0.485356	0.165575	0.777748	0.015765	0.47057	0.226591	0.22011	0.9154	-0.10424	0.874081
-0.90288	0.359773	0.906595	0.574114	0.328236	1	2.137711	0.021694	1.809475	0.086221	-0.05772	0.988297	-0.11935	0.943213	0.406106	0.676048	0.10074	0.933908	-1.38778	0.160854	0.622392	0.891999	-0.08327	0.96336
-0.56131	0.077281	0.396495	0.390269	0.038329	1	0.996134	0.000546	0.957805	0.001415	0.022425	0.987479	-0.19549	0.685402	-0.15073	0.679205	-0.06336	0.881673	-0.84183	0.003467	-0.24123	0.884131	-0.79612	0.007617
1.920403	0.031685	0.232962	0.921908	0.518314	1	-1.16913	0.285176	-1.68744	0.104419	0.160859	0.957473	-0.64536	0.632393	0.132599	0.917398	-0.36665	0.742792	1.666582	0.06539	-1.22013	0.732925	0.959913	0.398514
1.88807	7.81E-17	0.339429	0.422541	-0.05567	1	-1.60431	5.04E-12	-1.54864	3.18E-11	0.134339	0.845861	-0.09003	0.859817	-0.55782	0.028977	-0.61659	0.014311	0.777143	0.002741	-0.50657	0.566225	0.969386	0.000108
-0.15289	0.257219	-0.09723	0.659633	-0.04299	1	0.012677	0.9615	0.055662	0.812204	0.008604	0.988086	0.12896	0.442941	0.217357	0.056492	0.314001	0.003644	0.069709	0.66083	0.164876	0.744002	0.143366	0.344693
1.232013	2.02E-09	0.125868	0.80448	-0.05921	1	-1.16535	1.59E-08	-1.10615	1.48E-07	-0.48708	0.092094	-0.64091	0.008184	-1.28115	5.56E-11	-1.39613	5.48E-13	-0.23212	0.402301	-0.52517	0.324093	0.125817	0.740299
0.187661	0.830102	0.277699	0.821288	-0.32706	1	-0.23702	0.802058	0.090038	0.947719	0.740044	0.405658	1.172025	0.062001	1.140619	0.028069	1.018207	0.053041	1.091875	0.05637	0.537202	0.858968	1.020513	0.098456

. vs GA3 500 mg/L 14		N.C. vs O.P. 14 DAT		40 % vs GA3 300 mg/L		40 % vs GA3 500 mg/L		OH 140 % vs O.P. 14 D		mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 14		3 500 mg/L vs O.P. 14		N.C. 14 vs 21 DAT		EtOH 70% 14 vs 21 DA		3 300 mg/L 14 vs 21 D		3 500 mg/L 14 vs 21 D	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
1	1	1	1	1	1	1.778051	0.295168	1	1	-1.06333	1	1	1	1	1	1	1	1	1	1.397475	0.570356	1.479737	0.460372
-3.86703	0.061806	-4.01477	0.096834	-2.59717	0.2013	-2.956	0.128846	-3.10375	0.107335	-0.35883	1	-0.50658	0.887165	-0.14775	0.973785	1	1	1	1	-2.6517	0.009631	-1.9382	0.05777
-0.09088	0.937787	0.309786	0.803555	-0.39318	0.587934	-0.1476	0.871405	0.253071	0.750457	0.245587	1	0.646254	0.5119	0.400667	0.763737	0.622261	0.367807	0.156618	0.901649	1.229038	0.01197	0.492979	0.362124
-2.46586	0.002091	-0.89133	0.58578	-4.94766	4.36E-05	-5.01688	3.22E-05	-3.44234	0.01271	-0.06922	1	1.505314	0.200783	1.574536	0.17303	-0.68446	0.590422	-3.65616	0.042414	-2.38789	0.0001	-2.52936	2.71E-05
0.151881	0.825443	-0.4749	0.428856	-0.14303	0.812637	0.391604	0.417207	-0.23518	0.653694	0.534633	1	-0.09215	0.939348	-0.62678	0.304289	-0.05482	0.939768	0.032715	0.975146	0.876109	0.00948	0.347427	0.363824
0.723468	0.171651	0.817531	0.18706	1.188606	0.007579	1.229888	0.005456	1.323951	0.003424	0.041282	1	0.135345	0.927324	0.094063	0.952069	0.074542	0.930415	0.070925	0.949895	0.867847	0.0474	0.982776	0.02118
-0.09547	0.903804	-0.05221	0.971438	-0.12216	0.8504	-0.12248	0.85255	-0.07922	0.908213	-0.00032	1	0.042937	0.977435	0.043256	0.978601	0.31841	0.562539	-0.0339	0.975157	-0.00038	1	0.109467	0.817688
2.947021	0.284917	0.995614	0.823689	3.404204	0.191155	2.387111	0.41957	0.435704	0.895025	-1.01709	1	-2.9685	0.493132	-1.95141	0.725341	1	1	1	1	0	1	-1.00443	0.732478
0.289348	0.946055	1	1	0.953729	0.769326	0.308175	0.933488	-1.31253	0.559255	-0.64555	1	1	1	1	1	1	1	1	1	0.802697	0.785387	0.477012	0.857207
-1.43359	0.288584	0.493784	0.863749	-1.34659	0.30889	-1.06211	0.463063	0.865264	0.559121	0.284477	1	2.211853	0.169269	1.927376	0.274806	-1.5411	0.256735	-1.83492	0.296277	-3.41801	0.00032	-3.49496	0.000193
-1.71703	0.342594	0.943198	0.797939	1.87664	0.231705	1.620252	0.325804	4.28048	0.004173	-0.25639	1	2.40384	0.332876	2.660228	0.275987	-4.0302	0.008698	-0.88384	0.743208	-4.22326	0.000299	-3.5149	0.002576
1.604686	0.332658	0.885897	0.731336	0.0184	0.996938	1.821875	0.231725	1.103085	0.470961	1.803475	1	1.084686	0.687078	-0.71879	0.859485	1	1	1	1	-0.45289	0.714627	-1.77621	0.156287
2.291529	0.265081	0.633983	0.878071	-0.03065	0.99516	2.473254	0.204025	0.815708	0.718504	2.503899	1	0.846353	0.838902	-1.65755	0.657613	0.349843	0.900553	1.066997	0.738788	1.559199	0.341527	-1.64837	0.34011
-0.31978	0.176721	-0.06367	0.909868	-0.05424	0.876971	-0.09794	0.760694	0.15817	0.564795	-0.04369	1	0.212414	0.618214	0.256107	0.50653	-0.32846	0.181841	-0.14128	0.735111	0.16788	0.437793	0.133197	0.541733
0.323331	0.836456	-0.40411	0.836867	0.224825	0.876217	0.267501	0.852843	-0.45994	0.689221	0.042676	1	-0.68477	0.723596	-0.72744	0.704035	1	1	1	1	-0.31689	0.75584	0.030666	0.984978
-0.92591	0.075892	-0.65783	0.381133	-1.47951	0.001393	-1.55587	0.00069	-1.2878	0.008984	-0.07636	1	0.191714	0.889834	0.268076	0.84066	0.497568	0.449543	-0.41587	0.66557	0.422166	0.398849	0.684369	0.131107
-1.01162	0.029555	-0.84822	0.151217	-1.32952	0.001874	-1.46086	0.000503	-1.29746	0.003525	-0.13134	1	0.032063	0.987795	0.163401	0.909446	0.344974	0.589458	-0.35684	0.686569	0.191601	0.71571	0.538556	0.215221
-0.06776	0.930514	-0.12787	0.891575	-0.32435	0.482889	-0.28787	0.554479	-0.34797	0.435174	0.03648	1	-0.02363	0.988955	-0.06011	0.960136	0.712868	0.082758	0.665369	0.228008	1.26001	4.56E-05	1.051248	0.00067
-0.0604	0.977349	0.260554	0.908519	-0.70566	0.528519	-0.6828	0.552681	-0.36184	0.780381	0.02287	1	0.343827	0.886474	0.320958	0.902967	-0.39484	0.757441	-1.13676	0.407203	-1.49321	0.040406	-1.46502	0.041068
-0.67041	0.032601	-0.49108	0.247436	-0.55489	0.084318	-0.42918	0.219171	-0.24985	0.530247	0.125706	1	0.305039	0.632877	0.179333	0.827456	-0.63428	0.065967	-0.40703	0.419795	-0.59744	0.030175	-0.58601	0.030728
0.978981	0.387515	1.324769	0.297111	2.180043	0.011246	2.199112	0.010469	2.544899	0.003107	0.019069	1	0.364856	0.885518	0.345787	0.90079	-1.17942	0.276029	-0.46945	0.80194	-2.10808	0.006851	-1.77884	0.022807
0.854946	0.000879	0.700032	0.027073	1.475952	1.85E-10	1.361512	5.4E-09	1.206599	1.17E-06	-0.11444	1	-0.26935	0.647383	-0.15491	0.839247	-0.37892	0.261106	0.091303	0.886948	0.469479	0.067719	0.423966	0.096781
0.197024	0.151352	0.008394	0.989546	-0.02151	0.919337	0.032148	0.879919	-0.15648	0.272144	0.053658	1	-0.13497	0.573339	-0.18863	0.352699	-0.15611	0.296038	-0.19413	0.314407	-0.18883	0.097103	-0.17454	0.123927
-0.04837	0.924188	0.00949	0.995706	0.650983	0.003884	0.476797	0.051128	0.534656	0.027502	-0.17419	1	-0.11633	0.857685	0.057859	0.941025	-0.54225	0.039033	-0.16553	0.727271	0.165234	0.515831	0.392521	0.069053
0.571045	0.442782	0.734751	0.403454	0.483311	0.519325	0.033843	0.980916	0.197549	0.82667	-0.44947	1	-0.28576	0.853431	0.163706	0.930077	0.540051	0.468753	0.130974	0.924315	1.536691	0.002665	2.288895	3.61E-06

O.P. 14 vs 21 DAT		N.C. vs EtOH 21 DAT		. vs GA3 300 mg/L 21 D		. vs GA3 500 mg/L 21 D		N.C. vs O.P. 21 DAT		10 % vs GA3 300 mg/L		10 % vs GA3 500 mg/L		OH 210 % vs O.P. 21 D		mg/L vs GA3 500 mg/L		300 mg/L vs O.P. 21 D		500 mg/L vs O.P. 21		N.C. 21 vs 28 DAT	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
1	1	-0.82891	1	1.798725	0.459775	0.81766	0.760304	1	1	2.627634	0.211036	1.646569	0.447354	0.73784	0.725459	-0.98107	1	1	1	1	1	1	1
-0.90951	0.601895	2.411676	1	-2.81479	0.00646	-2.46012	0.023721	-1.57917	0.215409	-5.22646	0.000368	-4.87179	0.001288	-3.99085	0.012135	0.354671	1	1.235611	0.264673	0.880941	0.442258	0.311481	0.864769
0.033299	0.984661	-0.40893	1	0.270308	0.698456	-0.22016	0.763939	-0.27918	0.709103	0.679237	0.228828	0.188765	0.795528	0.129752	0.862483	-0.49047	1	-0.54948	0.36717	-0.05901	0.942483	0.648891	0.292517
-2.45333	0.001416	-0.42068	1	-4.10007	7.51E-11	-4.31076	8.56E-12	-2.6602	0.000135	-3.67939	2.09E-09	-3.89008	2.49E-10	-2.23952	0.000999	-0.21069	1	1.439867	0.033884	1.650559	0.011876	-1.25666	0.126681
-0.01457	0.99343	-0.15219	1	0.548172	0.14602	0.554123	0.15036	-0.43466	0.30037	0.700365	0.047934	0.706316	0.052691	-0.28246	0.514996	0.005951	1	-0.98283	0.005743	-0.98878	0.004908	0.634808	0.095188
0.333885	0.656964	-0.51004	1	1.475491	0.000282	1.631702	6.1E-05	1.076874	0.014912	1.985528	2.89E-07	2.141739	3.91E-08	1.586911	8.82E-05	0.156211	1	-0.39862	0.461225	-0.55483	0.264116	0.30865	0.564639
0.009663	0.999764	-0.32529	1	-0.41393	0.328898	-0.30441	0.518863	-0.36096	0.44681	-0.08864	0.869964	0.020885	0.975384	-0.03566	0.956103	0.109526	1	0.052978	0.928157	-0.05655	0.920401	-0.11886	0.826004
1.024724	0.798324	-0.42438	1	3.343271	0.144599	1.409891	0.587936	1.487638	0.589912	3.767647	0.082122	1.834268	0.445924	1.912014	0.417192	-1.93338	1	-1.85563	0.531309	0.077747	0.987579	1.579423	0.529187
1	1	0.976386	1	1.783157	0.478475	0.811919	0.769521	0.87029	0.770236	0.806771	0.80236	-0.16447	0.965322	-0.1061	0.980594	-0.97124	1	-0.91287	0.772322	0.058371	0.990809	0.323208	0.908348
-0.73396	0.684345	-0.6653	1	-3.59498	0.000132	-3.38745	0.000412	1.30092	0.289664	-2.92967	0.002306	-2.72215	0.006274	1.966224	0.064635	0.207528	1	4.895898	4.12E-07	4.68837	1.52E-06	-2.11129	0.051332
-1.90359	0.355328	-0.19093	1	-1.65371	0.220747	-1.20173	0.419847	3.069806	0.019217	-1.46278	0.285445	-1.01081	0.508718	3.260732	0.009477	0.451973	1	4.72351	0.000143	4.271537	0.000632	-1.74071	0.207375
0.699993	0.779537	0.057552	1	-0.13919	0.931063	0.340966	0.817376	2.098383	0.116305	-0.19674	0.894653	0.283413	0.851314	2.04083	0.114056	0.480153	1	2.23757	0.083758	1.757417	0.188982	-0.55206	0.655369
0.709394	0.812693	0.535429	1	0.996986	0.604514	0.293317	0.900378	0.993534	0.639554	0.461557	0.833621	-0.24211	0.919648	0.458105	0.838742	-0.70367	1	-0.00345	1	0.700218	0.725225	1.791295	0.328958
-0.1331	0.69022	-0.03467	1	0.220251	0.311607	0.141876	0.563333	0.131682	0.620789	0.254919	0.2221	0.176544	0.448607	0.166351	0.476629	-0.07837	1	-0.08857	0.73434	-0.01019	0.978055	-0.13587	0.572385
1.332047	0.237071	0.526348	1	-0.63242	0.527177	-0.24218	0.847424	0.331754	0.81448	-1.15877	0.213511	-0.76853	0.479031	-0.19459	0.890869	0.390234	1	0.964173	0.330593	0.573939	0.598455	-1.27247	0.132842
-0.31872	0.680438	-0.28348	1	-0.92495	0.047254	-0.73911	0.140032	-1.47412	0.000857	-0.64147	0.190873	-0.45563	0.406646	-1.19064	0.007153	0.185841	1	-0.54917	0.283738	-0.73501	0.12264	0.207668	0.748161
-0.43213	0.506217	-0.25258	1	-1.03366	0.012093	-0.81804	0.063199	-1.62532	4.24E-05	-0.78108	0.067719	-0.56546	0.231994	-1.37274	0.000588	0.215618	1	-0.59167	0.205171	-0.80728	0.063289	-0.03828	0.957114
0.630083	0.135685	0.172611	1	0.442904	0.237049	0.270622	0.526512	-0.21065	0.658043	0.270293	0.512769	0.098011	0.846776	-0.38326	0.319549	-0.17228	1	-0.65355	0.068349	-0.48127	0.186093	0.416726	0.283995
-0.79653	0.499902	-0.11953	1	-1.18165	0.124203	-1.13058	0.15443	-0.14113	0.915451	-1.06212	0.169614	-1.01105	0.21302	-0.02161	0.990744	0.051066	1	1.040513	0.197705	0.989447	0.211904	0.06529	0.958531
-0.36988	0.356118	-0.01399	1	-0.75929	0.005051	-0.62215	0.030061	-0.22668	0.548038	-0.7453	0.005515	-0.60816	0.033637	-0.2127	0.549069	0.137139	1	0.532601	0.075803	0.395462	0.194664	-0.08877	0.827492
-0.42828	0.782882	-0.51016	1	0.031258	0.986417	0.379561	0.741696	2.075907	0.012176	0.541416	0.598872	0.889718	0.353808	2.586065	0.000899	0.348302	1	2.044649	0.014438	1.696347	0.043359	-1.23788	0.171561
0.312266	0.40246	-0.03634	1	1.817784	1.44E-16	1.657831	9.17E-14	1.391217	1.57E-09	1.854128	2.36E-17	1.694175	1.74E-14	1.427562	4.19E-10	-0.15995	1	-0.42657	0.125166	-0.26661	0.359604	0.332194	0.253984
0.143772	0.374099	0.126851	1	0.110642	0.397939	0.178591	0.142466	0.308276	0.005926	-0.01621	0.929355	0.051741	0.741052	0.181425	0.131932	0.067949	1	0.197634	0.102777	0.129684	0.303222	0.247881	0.034989
-0.14456	0.70697	-0.14844	1	0.833301	2.91E-05	0.886402	8.44E-06	0.407184	0.087143	0.981744	4.49E-07	1.034846	1.06E-07	0.555628	0.009982	0.053101	1	-0.42612	0.067115	-0.47922	0.032837	0.307102	0.212965
0.467475	0.585318	0.128125	1	2.017153	4.06E-05	2.319889	2.37E-06	0.662175	0.291716	1.889029	0.000133	2.191764	9.53E-06	0.53405	0.388064	0.302736	1	-1.35498	0.014942	-1.65771	0.002315	1.695278	0.001648

EtOH 70% 21 vs 28 DAT		A3 300 mg/L 21 vs 28 D		A3 500 mg/L 21 vs 28 D		O.P. 21 vs 28 DAT		N.C. vs EtOH 28 DAT		. vs GA3 300 mg/L 28 D		. vs GA3 500 mg/L 28 D		N.C. vs O.P. 28 DAT		80 % vs GA3 300 mg/L		80 % vs GA3 500 mg/L		OH 280 % vs O.P. 28 D		mg/L vs GA3 500 mg/	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
1	1	-2.90257	0.103901	-2.87697	0.06163	1	1	1	1	-1.44342	0.391351	-2.39888	0.092705	0.684302	0.791845	0.144772	0.946502	-0.81069	0.564123	2.272491	0.184021	1	1
-1.5416	0.410125	0.772621	0.416017	1.536456	0.102991	-0.35057	0.847437	1	1	-2.35365	0.025102	-1.23514	0.283848	-2.24123	0.042827	-2.91224	0.01426	-1.79373	0.149908	-2.79982	0.012727	1	1
0.96704	0.058924	1.51724	0.006365	2.098612	0.000106	0.541695	0.466012	-0.09078	0.942815	1.138656	0.059524	1.229556	0.037645	-0.38637	0.543224	1.229437	0.054176	1.320337	0.029809	-0.29559	0.621685	0.0909	0.956771
-1.05122	0.147967	0.330635	0.618054	1.18938	0.03795	-0.70439	0.451777	-0.21525	0.880466	-2.51278	2.24E-05	-1.86473	0.001702	-2.10794	0.000696	-2.29753	0.000175	-1.64948	0.007479	-1.89269	0.001622	0.648053	0.496246
0.733419	0.029558	2.809768	1.09E-16	1.982164	4.75E-10	0.247552	0.65654	-0.05358	0.947316	2.723132	1.13E-15	1.901479	3.97E-09	-0.82191	0.014299	2.776713	5.54E-16	1.955061	2.57E-09	-0.76833	0.016984	-0.82165	0.138588
0.607535	0.149454	-1.29412	0.000696	-1.49747	6.69E-05	0.527047	0.395494	-0.21115	0.790825	-0.12728	0.806014	-0.17442	0.70389	1.295272	0.001425	0.083872	0.892488	0.036733	0.946225	1.506424	8.68E-05	-0.04714	0.963789
0.410251	0.292209	1.259784	0.000551	1.385556	0.000228	-0.23094	0.692279	0.203814	0.772413	0.964706	0.013201	1.200004	0.001963	-0.47304	0.215393	0.760891	0.080858	0.99619	0.015988	-0.67685	0.051119	0.235298	0.783762
1.77858	0.393775	0	1	1.450395	0.546178	2.004569	0.588235	1	1	1.340648	0.612056	1.280864	0.606025	1.912785	0.491917	1.565867	0.582089	1.506083	0.55231	2.138004	0.38677	1	1
-1.17489	0.586622	-1.31019	0.569749	1.453175	0.520996	1	1	1	1	0.149762	0.957242	1.941885	0.349427	2.573806	0.260606	0.671473	0.794702	2.463596	0.226391	3.095517	0.12063	1	1
-2.40619	0.012631	-2.42754	0.006411	-2.40324	0.006209	-1.27892	0.364643	-0.96021	0.574881	-3.91124	1.07E-05	-3.67941	2.32E-05	2.13329	0.030806	-2.95103	0.001715	-2.7192	0.002858	3.093499	0.000589	0.231829	0.911759
-1.79664	0.138682	-1.21677	0.297293	-0.72049	0.559094	-0.72509	0.737579	-0.24686	0.925232	-1.12976	0.365087	-0.18151	0.899153	4.085423	0.000343	-0.88291	0.535369	0.065348	0.967952	4.332282	7.02E-05	0.948253	0.617636
-1.08218	0.259834	-1.25843	0.143655	-0.34874	0.756336	-1.29393	0.474438	1	1	-0.84556	0.362224	0.544289	0.590862	1.356518	0.19295	-0.37299	0.748815	1.016853	0.292538	1.829082	0.046357	1	1
2.778316	0.145209	1.107088	0.524236	4.543657	0.011097	0.469017	0.878791	1.52245	0.66188	0.312779	0.888707	3.045678	0.123623	-0.32874	0.888108	-1.20967	0.634181	1.523229	0.547151	-1.85119	0.358121	2.732899	0.378266
-0.17549	0.382775	-0.66577	4.62E-05	-0.883	2.87E-08	-0.03807	0.920712	-0.07428	0.840467	-0.30965	0.08739	-0.60525	0.000229	0.229483	0.262028	-0.23537	0.246074	-0.53097	0.00185	0.303762	0.094038	-0.2956	0.247197
-1.75506	0.026111	0.660723	0.432618	0.901348	0.328201	-0.10296	0.959028	1	1	1.300778	0.096545	1.931637	0.017691	1.501268	0.055702	1.257018	0.137423	1.887877	0.02537	1.457508	0.050551	1	1
0.783476	0.091775	1.313078	0.00143	2.264523	1.8E-07	0.146282	0.86081	0.292328	0.737882	0.180463	0.748934	1.317748	0.00446	-1.53551	0.000247	-0.11187	0.872967	1.02542	0.038333	-1.82784	6.23E-06	1.137285	0.096285
0.883404	0.028264	1.551365	1.59E-05	2.279084	1E-10	0.333259	0.611426	0.669106	0.291259	0.555989	0.176063	1.499326	3.8E-05	-1.25378	0.001206	-0.11312	0.847088	0.83022	0.035007	-1.92289	1.1E-07	0.943337	0.077988
0.905833	0.005378	0.904887	0.003482	1.454388	1.69E-06	0.323104	0.513389	0.661718	0.183541	0.931065	0.003518	1.308284	2.49E-05	-0.30427	0.424837	0.269347	0.522861	0.646566	0.061407	-0.96599	0.001631	0.377219	0.491856
0.016644	0.989206	0.624942	0.375354	0.711716	0.303106	0.031392	0.990619	-0.16817	0.915636	-0.622	0.419106	-0.48416	0.523753	-0.17503	0.865848	-0.45382	0.61105	-0.31598	0.701444	-0.00686	1	0.137839	0.931328
-0.10126	0.760001	0.043789	0.893531	0.401667	0.114811	-0.25484	0.547944	-0.02647	0.968224	-0.62672	0.014596	-0.13171	0.655224	-0.39275	0.179018	-0.60025	0.027593	-0.10523	0.739822	-0.36628	0.18176	0.495017	0.180728
-1.26712	0.113537	-1.73593	0.015764	-1.94126	0.005678	-1.54855	0.125578	-0.53939	0.708146	-0.46679	0.600896	-0.32381	0.709585	1.765241	0.024353	0.072608	0.954883	0.215584	0.820171	2.304636	0.001426	0.142976	0.935805
0.099132	0.739445	-0.50884	0.025866	-0.77768	0.000346	-0.43912	0.175854	-0.26941	0.51879	0.976752	1.21E-05	0.547959	0.015562	0.619907	0.01044	1.246158	2.03E-08	0.817365	0.000291	0.889313	6.51E-05	-0.42879	0.205941
0.049751	0.701254	-0.04561	0.702553	-0.06249	0.587474	-0.12084	0.453078	-0.07128	0.7235	-0.18285	0.087997	-0.13178	0.21949	-0.06044	0.664175	-0.11157	0.373617	-0.0605	0.621794	0.010835	0.944706	0.051074	0.799162
0.452961	0.030044	1.353743	3.62E-13	1.494701	4.46E-16	-0.52092	0.040292	-0.00258	0.995502	1.879941	1.21E-24	2.074001	6.95E-30	-0.42084	0.050017	1.882526	2.09E-24	2.076586	1.08E-29	-0.41826	0.038977	0.19406	0.566752
2.810468	6.26E-08	7.601312	1.41E-08	7.238793	4.45E-08	0.910145	0.180917	1.243315	0.11106	7.923187	5.06E-09	7.863403	3.88E-09	-0.12296	0.872151	6.679873	2.02E-06	6.620089	1.61E-06	-1.36627	0.007753	0	1

300 mg/L vs O.P. 28		500 mg/L vs O.P. 28	
Log2FC	p-adj	Log2FC	p-adj
2.127719	0.201326	3.083181	0.038426
0.112418	0.925481	-1.00609	0.295326
-1.52503	0.005274	-1.61593	0.003157
0.404842	0.53319	-0.24321	0.708006
-3.54504	9.37E-27	-2.72339	2.16E-18
1.422552	0.000147	1.46969	6.7E-05
-1.43774	4.55E-05	-1.67304	3.67E-06
0	1	0	1
2.424044	0.255603	0	1
6.044527	9.35E-13	5.812698	3.71E-12
5.215187	6.02E-07	4.266934	4.12E-05
2.202077	0.010218	0.812229	0.406513
-0.64152	0.72826	-3.37442	0.06646
0.539132	0.000962	0.83473	1.2E-07
0.20049	0.84236	-0.43037	0.655832
-1.71597	1.56E-05	-2.85326	1.51E-11
-1.80977	2.86E-07	-2.75311	2.44E-15
-1.23534	3.35E-05	-1.61256	6.25E-08
0.446962	0.547507	0.309123	0.671702
0.233969	0.391239	-0.26105	0.31071
2.232028	0.001363	2.089051	0.002414
-0.35685	0.126461	0.071949	0.783402
0.122406	0.247532	0.071332	0.504117
-2.30078	4.15E-37	-2.49484	1.7E-43
-8.04615	1.04E-09	-7.98636	8.71E-10

Table S4.8: Table with Log2FoldChange (log2FC) and p-value adjusted (p-adj) of the genes involved in ethylene biosynthesis, and signal transduction. The heatmap of these genes is showed in Fig. 4.18. Log2FC is calculated according to the following formula: expression level term1 - expression level term2.

Gene name	Gene description	N.C. 0 vs 7 DAT		EtOH 70% 0 vs 7 DAT		A3 300 mg/L 0 vs 7 DA		A3 500 mg/L 0 vs 7 DA		O.P. 0 vs 7 DAT		N.C. vs EtOH 7 DAT		C. vs GA3 300 mg/L 7 D		C. vs GA3 500 mg/L 7 D		N.C. vs O.P. 7 DAT	
		Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
Pav_sc0000813.1_g080.1.mk	PavACO1	0.17223	0.83572	0.061281	0.999232	0.007383	0.992733	-0.10157	0.799862	0.283458	0.446316	-0.11095	1	-0.16485	0.768307	-0.2738	0.476854	0.111229	0.894371
Pav_sc0001073.1_g020.1.mk	PavACO1	-0.03394	0.96966	0.014446	1	-0.39217	0.036614	-0.46421	0.009146	-0.05718	0.87837	0.048383	1	-0.35823	0.148425	-0.43027	0.042979	-0.02324	0.972813
Pav_sc0002206.1_g310.1.mk	PavACO4	-0.8256	0.735033	-0.9986	0.704857	0.358418	0.798826	0.890399	0.414785	0.958767	0.453466	-0.173	1	1.184018	0.409734	1.715999	0.122661	1.784368	0.166023
Pav_sc0000254.1_g1180.1.mk	PavACS1	-2.3271	0.40919	-1.96958	0.600226	-4.63262	0.000968	-3.20413	0.035295	-3.3484	0.038055	0.357518	1	-2.30553	0.118286	1	1	-1.02131	0.71633
Pav_sc0002862.1_g330.1.mk	PavACS10	-0.14376	0.953856	-0.5411	0.74355	-0.0956	0.915043	0.026883	0.981023	0.044874	0.971775	-0.39734	1	0.048153	0.976638	0.17064	0.860184	0.188631	0.914178
Pav_sc0001928.1_g020.1.mk	PavACS12	0.0968	0.929223	-0.13212	0.969115	0.015909	0.977279	-0.21537	0.495255	-0.22929	0.542437	-0.22892	1	-0.08089	0.898965	-0.31217	0.378141	-0.32609	0.509286
Pav_sc0000130.1_g750.1.mk	PavERS1	-0.19422	0.33945	-0.12338	0.749281	-0.41535	0.000186	-0.37269	0.000893	0.128897	0.44737	0.070834	1	-0.22113	0.180837	-0.17847	0.258785	0.323115	0.023871
Pav_sc0001323.1_g370.1.mk	PavEIN1	0.117325	0.727627	0.120466	0.801337	0.199673	0.151104	0.128414	0.398016	0.116388	0.534866	0.003141	1	0.082349	0.757056	0.01109	0.968216	-0.00094	1
Pav_sc0005842.1_g070.1.mk	PavEIL3	-0.04677	0.976168	-0.15818	0.973817	-0.00519	0.996918	0.043223	0.939459	0.077622	0.910108	-0.11141	1	0.041582	0.963387	0.089992	0.879993	0.124391	0.904506
Pav_sc0000729.1_g350.1.mk	PavERT2	0.027966	0.989435	-0.07878	0.99688	0.056297	0.913052	0.301862	0.408217	-0.03663	0.960477	-0.10674	1	0.02833	0.97621	0.273896	0.549264	-0.0646	0.949982
Pav_sc0000396.1_g730.1.mk	PavEIN4	-0.1288	0.887576	-0.07434	0.994498	0.004801	0.996301	0.215779	0.495305	0.233539	0.533877	0.054468	1	0.133604	0.813707	0.344581	0.314622	0.362342	0.425066
Pav_sc0000130.1_g780.1.mk	CTR1	-0.07513	0.970485	-0.58892	0.505244	-1.30726	0.00105	-1.59497	3.03E-05	0.198129	0.801995	-0.51379	1	-1.23213	0.009486	-1.51984	0.000398	0.273259	0.814611
Pav_sc0000119.1_g160.1.mk	PavERF1	-1.88091	0.721762	-1.94421	0.785688	-2.22324	0.352367	-0.42912	0.901139	0.804159	0.845521	-0.0633	1	-0.34233	0.94692	1.451787	0.645023	2.685069	0.496053
Pav_sc0000549.1_g1050.1.mk	PavERF-1	-0.9413	0.568945	-0.97264	0.594281	-0.74417	0.437536	0.190722	0.879188	-0.17558	0.917258	-0.03134	1	0.197131	0.919621	1.132024	0.264941	0.765719	0.65969
Pav_sc0001102.1_g220.1.mk	PavERF-1	-0.85516	0.606874	-1.06683	0.466896	-0.8722	0.314402	-0.96744	0.240321	-0.63521	0.570118	-0.21167	1	-0.01704	0.998577	-0.11228	0.93975	0.219946	0.929993
Pav_sc0001900.1_g290.1.mk	PavERF2	-1.27633	0.378308	-1.67781	0.14688	-2.31451	0.003397	-0.49217	0.666124	-0.22488	0.897355	-0.40148	1	-1.03818	0.422049	0.78416	0.520162	1.051449	0.511903
Pav_sc0000975.1_g110.1.mk	PavERF4	-0.28355	0.85131	-0.1926	0.984752	0.198536	0.782316	0.194396	0.781059	0.941678	0.070256	0.09095	1	0.482083	0.553902	0.477943	0.482875	1.225225	0.029141
Pav_sc0000549.1_g1080.1.mk	PavERF5	0.285029	0.934009	-0.0149	1	0.694429	0.496166	1.080374	0.225298	1.668553	0.05738	-0.29993	1	0.409399	0.819886	0.795344	0.497862	1.383523	0.268113
Pav_sc0000241.1_g200.1.mk	PavERF7	-0.10123	0.948447	0.108279	0.993647	0.000387	1	-0.09084	0.866754	0.171638	0.777042	0.209509	1	0.101617	0.905333	0.010391	0.991741	0.272868	0.747242
Pav_sc0001557.1_g150.1.mk	PavERF13	-1.73498	0.035602	-1.66408	0.053052	-1.9617	0.003103	-1.98051	0.002455	-2.02213	0.002414	0.070901	1	-0.22672	0.87468	-0.24553	0.821025	-0.28715	0.875508
Pav_sc0000174.1_g1250.1.mk	PavEBP	-0.47991	0.661915	-0.64848	0.485455	0.59641	0.254895	0.558015	0.281614	-0.2924	0.700737	-0.16857	1	1.076323	0.055704	1.037928	0.050522	0.187508	0.896871
Pav_sc0000704.1_g940.1.mk	EIN3-binding F box protein 1	-0.34633	0.846432	-0.48303	0.844563	-0.23422	0.785171	-0.11637	0.901854	-0.1084	0.931945	-0.1367	1	0.112109	0.939056	0.229958	0.818473	0.237935	0.891865
Pav_sc0001015.1_g080.1.mk	EIN3-binding F box protein 1	0.666159	0.125528	0.515956	0.360586	1.227568	2.29E-05	1.249683	1.4E-05	1.089848	0.000234	-0.1502	1	0.561409	0.211171	0.583524	0.142162	0.423689	0.484146

70 % vs GA3 300 mg/L		70 % vs GA3 500 mg/L		tOH 70 % vs O.P. 7 DA		0 mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 7 D		3 500 mg/L vs O.P. 7 D		N.C. 7 vs 14 DAT		EtOH 70% 7 vs 14 DAT		A3 300 mg/L 7 vs 14 DA		A3 500 mg/L 7 vs 14 D		O.P. 7 vs 14 DAT		N.C. vs EtOH 14 DAT	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
-0.0539	0.910787	-0.16285	0.663645	0.222177	0.661255	-0.10895	1	0.276075	0.46335	0.385029	0.292958	0.291592	0.560364	0.413584	0.237623	0.092774	0.792594	0.146834	0.659765	-0.19113	0.584777	0.011044	1
-0.40661	0.047195	-0.47865	0.0123	-0.07162	0.875605	-0.07204	1	0.334991	0.123288	0.407029	0.060612	0.269505	0.362609	0.290059	0.230971	0.322894	0.076672	0.430339	0.013442	-0.10999	0.663521	0.068937	0.96826
1.357017	0.218668	1.888998	0.05253	1.957366	0.094977	0.531981	1	0.600349	0.681412	0.068368	0.979969	2.746178	0.004233	0.591605	0.693526	1.767382	0.045883	1.74621	0.048635	2.491059	0.006052	-2.32757	0.239153
1	1	1	1	-1.37882	0.484361	1.428491	1	1.284219	0.375825	-0.14427	0.95971	1.173012	0.673075	1.236148	0.571213	2.304306	0.033226	4.620032	0.008628	0.994218	0.494731	0.420653	0.97793
0.445498	0.539231	0.567985	0.373784	0.585975	0.510901	0.122487	1	0.140477	0.890212	0.01799	0.990899	0.159428	0.922135	0.06606	0.950212	-0.1613	0.821203	-0.31657	0.624757	-0.33782	0.631439	-0.49071	0.87145
0.14803	0.701476	-0.08325	0.843407	-0.09717	0.876324	-0.23128	1	-0.2452	0.503847	-0.01392	0.986376	-0.21704	0.692426	-0.39337	0.231951	-0.29841	0.268891	-0.21721	0.451287	-0.01709	0.973325	-0.40525	0.67387
-0.29196	0.025096	-0.24931	0.053002	0.252281	0.111293	0.042655	1	0.544244	1.03E-06	0.501589	1.47E-05	0.054211	0.866365	-0.10496	0.573259	0.128869	0.32022	0.044677	0.783092	-0.49187	7.99E-06	-0.08834	0.899469
0.079207	0.678097	0.007948	0.973313	-0.00408	0.996503	-0.07126	1	-0.08329	0.684818	-0.01203	0.972335	0.036523	0.928047	-0.09557	0.638509	-0.21858	0.083689	-0.20077	0.118893	-0.06129	0.738842	-0.12895	0.858968
0.152989	0.766314	0.201399	0.653346	0.235798	0.713091	0.04841	1	0.082809	0.895873	0.034399	0.968366	0.102522	0.915381	0.197674	0.711765	0.204371	0.595258	0.130039	0.762143	-0.05156	0.927143	-0.01625	1
0.135072	0.784072	0.380638	0.288275	0.042142	0.96365	0.245566	1	-0.09293	0.87083	-0.3385	0.468329	-0.38073	0.470154	-0.50255	0.191783	-0.38175	0.229292	-0.60159	0.040733	0.302555	0.416016	-0.22856	0.895628
0.079136	0.855365	0.290114	0.343361	0.307875	0.460799	0.210978	1	0.228739	0.539695	0.017761	0.981748	0.29726	0.517528	0.102636	0.829003	0.19817	0.498053	-0.20473	0.489622	0.031755	0.945748	-0.14016	0.927961
-0.71835	0.150293	-1.00605	0.022959	0.787047	0.178217	-0.28771	1	1.505393	0.000269	1.793101	9.48E-06	0.356152	0.70104	0.493188	0.413255	1.448784	0.000145	1.339491	0.000488	-0.37183	0.484564	-0.37675	0.875223
-0.27904	0.938059	1.515083	0.567427	2.748366	0.39751	1.79412	1	3.027403	0.246421	1.233282	0.756234	2.038545	0.609353	-0.02999	0.996451	2.911223	0.168136	1.392197	0.58911	3.506562	0.233553	-2.13183	0.850472
0.228469	0.863056	1.163362	0.183067	0.797057	0.559691	0.934893	1	0.568588	0.635533	-0.3663	0.815538	0.534736	0.767295	0.191159	0.900119	0.602973	0.49587	-0.18844	0.864599	1.126689	0.199721	-0.37492	0.94167
0.194627	0.87959	0.099389	0.941502	0.431617	0.787305	-0.09524	1	0.23699	0.86319	0.332227	0.825785	-0.13378	0.959741	-0.57204	0.622106	0.557805	0.511643	-0.55788	0.515982	0.862893	0.326744	-0.64993	0.875223
-0.6367	0.579411	1.185639	0.206581	1.452928	0.209971	1.822342	1	2.089631	0.017169	0.267289	0.886854	1.504988	0.198844	1.156468	0.296041	2.539637	0.000766	1.017828	0.25774	2.024652	0.027352	-0.75	0.875223
0.391133	0.550672	0.386994	0.528466	1.134276	0.047276	-0.00414	1	0.743143	0.199443	0.747282	0.231901	0.31335	0.777516	0.659225	0.299424	-0.21775	0.716347	-0.76096	0.1074	-1.31612	0.004639	0.436825	0.872658
0.709328	0.521463	1.095273	0.238349	1.683452	0.109319	0.385945	1	0.974124	0.371491	0.588179	0.680757	1.549235	0.156973	1.128628	0.29831	0.060763	0.964596	-0.57265	0.550772	0.403946	0.727426	-0.72054	0.875223
-0.10789	0.851467	-0.19912	0.678244	0.063359	0.949201	-0.09123	1	0.171251	0.767416	0.262477	0.652315	0.233515	0.767809	0.197358	0.731657	-0.49389	0.151877	-0.13457	0.765795	-0.30037	0.474759	0.173352	0.936603
-0.29762	0.757141	-0.31643	0.718415	-0.35806	0.783907	-0.01881	1	-0.06043	0.964339	-0.04162	0.981748	-0.43922	0.748994	0.016931	0.990999	-0.98182	0.088077	-0.87823	0.138511	-0.9234	0.149791	0.527052	0.875223
1.24489	0.00972	1.206496	0.010573	0.356075	0.690552	-0.03839	1	-0.88882	0.092435	-0.85042	0.138807	0.236535	0.841033	0.013974	0.990042	-0.03191	0.968044	-0.08587	0.899515	0.944035	0.049843	-0.39113	0.875223
0.248805	0.784873	0.366654	0.637345	0.374631	0.749089	0.117849	1	0.125826	0.911489	0.007977	0.996899	0.230798	0.882829	0.116058	0.918425	0.188853	0.800719	-0.2869	0.688606	0.099524	0.917057	-0.25144	0.949761
0.711612	0.045579	0.733727	0.029942	0.573892	0.200513	0.022115	1	-0.13772	0.808324	-0.15983	0.80331	0.39585	0.481369	0.448863	0.3009	-1.08333	0.000174	-1.01754	0.000473	-0.58324	0.092628	-0.09719	0.975344

. vs GA3 300 mg/L 14		L vs GA3 500 mg/L 14		N.C. vs O.P. 14 DAT		40 % vs GA3 300 mg/L		40 % vs GA3 500 mg/L		OH 140 % vs O.P. 14 D		mg/L vs GA3 500 mg/		300 mg/L vs O.P. 14		500 mg/L vs O.P. 14		N.C. 14 vs 21 DAT		EtOH 70% 14 vs 21 DAT		3 300 mg/L 14 vs 21 D	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
-0.36367	0.276939	-0.41856	0.189813	-0.37149	0.38483	-0.37471	0.241916	-0.4296	0.164426	-0.38254	0.232054	-0.05489	1	-0.00783	0.999838	0.047065	0.959935	-0.07324	0.880514	-0.27088	0.587491	0.013365	0.975582
-0.30484	0.16465	-0.26944	0.235645	-0.40273	0.089681	-0.37378	0.061505	-0.33837	0.102353	-0.47167	0.01466	0.035406	1	-0.09789	0.85037	-0.1333	0.785985	-0.03397	0.923056	-0.13168	0.734445	-0.01472	0.960105
0.205223	0.910547	0.716031	0.605674	1.529248	0.247376	2.532794	0.005288	3.043603	0.000517	3.85682	8.85E-06	0.510809	1	1.324026	0.412155	0.813217	0.706743	-2.83785	0.005541	-1.41127	0.357307	-4.13249	1.97E-07
-1.17423	0.538209	2.569986	0.309757	1	1	-1.59489	0.371263	2.149333	0.425521	-1.62075	0.357326	3.744218	1	1	1	1	1	1	1	1	1	4.670839	0.007744
-0.27258	0.759282	-0.30536	0.72842	-0.30862	0.808143	0.218134	0.799947	0.185351	0.838036	0.182091	0.836029	-0.03278	1	-0.03604	0.988987	-0.00326	1	-0.76866	0.246486	-0.85416	0.326511	-0.56022	0.306246
-0.16226	0.6859	-0.31234	0.341069	-0.12613	0.847901	0.242994	0.469168	0.09291	0.827711	0.279118	0.383404	-0.15008	1	0.036125	0.966059	0.186208	0.778774	-0.30542	0.357198	-0.1958	0.696599	-0.35329	0.157544
-0.14647	0.353871	-0.18801	0.193339	-0.22297	0.180107	-0.05814	0.76227	-0.09967	0.562073	-0.13463	0.379247	-0.04154	1	-0.0765	0.809563	-0.03496	0.931802	-0.09181	0.605634	-0.03924	0.893487	-0.15956	0.188394
-0.17275	0.281068	-0.2262	0.124796	-0.09875	0.721875	-0.0438	0.840618	-0.09725	0.602212	0.030195	0.8931	-0.05345	1	0.073998	0.831621	0.127449	0.65345	-0.21441	0.172298	-0.1169	0.63719	-0.1065	0.441994
0.143431	0.801691	0.117509	0.851447	-0.02969	0.98424	0.159686	0.75317	0.133763	0.803638	-0.01343	0.986039	-0.02592	1	-0.17312	0.847143	-0.14719	0.885092	-0.41924	0.312494	-0.55302	0.293089	-0.71839	0.015968
0.027311	0.969887	0.053044	0.938577	0.618688	0.124811	0.255874	0.541761	0.281607	0.498115	0.847251	0.006541	0.025733	1	0.591377	0.206687	0.565644	0.245341	-0.22641	0.61158	-0.22828	0.709262	-0.66514	0.0175
0.034513	0.949406	-0.15741	0.707785	0.096837	0.889946	0.17467	0.642721	-0.01725	0.978293	0.236994	0.485587	-0.19192	1	0.062324	0.941182	0.254245	0.656207	-0.2682	0.440731	-0.14127	0.800862	-0.27044	0.310862
-0.1395	0.863029	-0.5365	0.331126	-0.45472	0.564742	0.23725	0.717855	-0.15975	0.825845	-0.07797	0.922849	-0.397	1	-0.31522	0.768626	0.081784	0.9558	0.111952	0.886272	0.018476	0.988437	0.931884	0.020355
0.530344	0.900042	0.805439	0.846491	4.153086	0.26177	2.662173	0.293765	2.937268	0.244659	6.284915	0.015327	0.275095	1	3.622742	0.433555	3.347647	0.503566	-1.9806	0.478159	-1.63673	0.672614	-4.1468	0.031696
0.265368	0.856045	0.408851	0.759091	1.357672	0.216896	0.640283	0.554796	0.783767	0.45047	1.732587	0.037856	0.143483	1	1.092304	0.437263	0.94882	0.540234	-0.63176	0.57102	-0.43279	0.798437	-1.52348	0.037062
0.674536	0.521471	-0.53638	0.638807	1.216615	0.26177	1.324468	0.105261	0.11355	0.937706	1.866546	0.01587	-1.21092	1	0.542079	0.769471	1.752997	0.09936	-0.82178	0.405333	-0.94088	0.463885	-2.47183	0.000157
-0.00353	1	0.296999	0.857833	1.571113	0.214459	0.746466	0.517745	1.046998	0.325218	2.321112	0.011658	0.300532	1	1.574646	0.269857	1.274113	0.440176	0.466315	0.735715	-0.1542	0.942664	-0.66697	0.470145
-0.04901	0.963767	-0.59637	0.32644	-0.40424	0.681362	-0.48584	0.432777	-1.0332	0.037534	-0.84107	0.116172	-0.54736	1	-0.35523	0.761504	0.192131	0.900191	-0.48312	0.454518	-0.74217	0.346101	-0.1436	0.808996
-1.07907	0.290134	-1.32654	0.164882	0.238234	0.918995	-0.35854	0.784349	-0.60601	0.608137	0.958769	0.344063	-0.24747	1	1.317307	0.323344	1.564779	0.2132	-1.30409	0.192328	-1.22838	0.366785	-0.23034	0.821888
-0.62579	0.104902	-0.3577	0.441583	-0.26102	0.722796	-0.79914	0.022182	-0.53105	0.180727	-0.43437	0.297396	0.268094	1	0.364776	0.611278	0.096683	0.932364	-0.22592	0.66116	-0.51017	0.372602	0.262041	0.480767
-0.76932	0.286342	-0.68454	0.366107	-0.77134	0.408824	-1.29637	0.035654	-1.21159	0.056625	-1.29839	0.040541	0.084781	1	-0.00202	1	-0.0868	0.966428	-0.86655	0.228024	-0.85624	0.399664	-0.89982	0.09399
0.807879	0.127845	0.715524	0.191586	0.895007	0.146597	1.199007	0.009401	1.106653	0.018935	1.286136	0.006056	-0.09235	1	0.087129	0.954741	0.179483	0.90479	-0.13691	0.868044	0.000347	1	-0.2781	0.594823
0.070165	0.954473	-0.28774	0.767092	0.106662	0.955065	0.3216	0.707514	-0.0363	0.979763	0.358097	0.659353	-0.3579	1	0.036497	0.99032	0.3944	0.792673	-0.45743	0.572638	-0.3016	0.80872	-1.25647	0.015867
-0.91777	0.004316	-0.82987	0.011814	-0.5554	0.225448	-0.82058	0.011781	-0.73268	0.028998	-0.45821	0.235414	0.0879	1	0.362365	0.587293	0.274465	0.722738	-0.47733	0.240113	-0.71186	0.137303	0.208264	0.565475

3 500 mg/L	14 vs 21 D	O.P. 14 vs 21 DAT		N.C. vs EtOH 21 DAT		. vs GA3 300 mg/L 21		L vs GA3 500 mg/L 21		N.C. vs O.P. 21 DAT		10 % vs GA3 300 mg/L		10 % vs GA3 500 mg/L		OH 210 % vs O.P. 21 D		mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 21		500 mg/L vs O.P. 21	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
0.040654	0.908735	-0.11021	0.832113	-0.18659	1	-0.27706	0.348473	-0.30467	0.303933	-0.40846	0.157872	-0.09047	0.803577	-0.11807	0.741242	-0.22187	0.478769	-0.0276	1	-0.1314	0.700643	-0.1038	0.761552
-0.0284	0.908019	0.012774	0.983184	-0.02877	1	-0.28559	0.129979	-0.26386	0.178298	-0.35598	0.061269	-0.25682	0.177003	-0.23509	0.241282	-0.32722	0.078093	0.021732	1	-0.0704	0.776337	-0.09213	0.685427
-4.58451	4.74E-09	-0.39201	0.823433	-0.90099	1	-1.08942	0.267915	-1.03063	0.310489	3.975094	8.75E-07	-0.18843	0.886913	-0.12964	0.92823	4.876083	4.91E-10	0.05879	1	5.06451	2.1E-10	5.00572	3.64E-10
-1.60289	0.488267	1	1	1.782292	1	4.565404	0.011092	2.035894	0.227856	0.388052	0.846074	2.783113	0.195395	0.253602	0.926419	-1.39424	0.416113	-2.52951	1	-4.17735	0.031584	-1.64784	0.340926
-0.82848	0.098712	-0.07805	0.953295	-0.57621	1	-0.06414	0.939925	-0.36518	0.572358	0.381989	0.576915	0.512067	0.375982	0.211028	0.766211	0.958197	0.066497	-0.30104	1	0.44613	0.464748	0.747169	0.167559
-0.36107	0.136768	0.131947	0.774981	-0.29564	1	-0.21013	0.467945	-0.36799	0.161328	0.31123	0.282508	0.085504	0.800935	-0.07236	0.839282	0.606868	0.011094	-0.15786	1	0.521364	0.040458	0.679223	0.004966
-0.00016	1	-0.22395	0.125357	-0.03577	1	-0.21422	0.073007	-0.09636	0.50932	-0.3551	0.001685	-0.17845	0.143762	-0.06059	0.702806	-0.31933	0.004447	0.117855	1	-0.14089	0.286808	-0.25874	0.02866
-0.11496	0.388049	-0.05539	0.820614	-0.03144	1	-0.06484	0.68936	-0.12675	0.385904	0.060271	0.743817	-0.0334	0.85167	-0.09531	0.536555	0.091708	0.552536	-0.06191	1	0.125111	0.387603	0.187023	0.153359
-0.49497	0.109224	0.004658	1	-0.15004	1	-0.15572	0.704813	0.04178	0.935281	0.394213	0.28287	-0.00568	0.995821	0.191819	0.637294	0.544252	0.09303	0.197503	1	0.549936	0.096452	0.352433	0.307226
-0.73074	0.007362	-0.65132	0.064116	-0.23044	1	-0.41142	0.189479	-0.45129	0.151681	0.193774	0.633692	-0.18098	0.62184	-0.22085	0.544008	0.42421	0.179669	-0.03987	1	0.605194	0.046582	0.645063	0.029063
0.060651	0.851812	0.214606	0.597335	-0.01323	1	0.032272	0.937294	0.171441	0.588649	0.579641	0.02245	0.045505	0.903846	0.184674	0.551848	0.592874	0.01537	0.139169	1	0.547369	0.033234	0.4082	0.118001
1.168208	0.002355	1.078219	0.023114	-0.47023	1	0.680431	0.119974	0.519754	0.271718	0.511549	0.303927	1.150657	0.003264	0.989981	0.016051	0.981776	0.016966	-0.16068	1	-0.16888	0.770452	-0.00821	0.993761
-3.73681	0.056084	-1.88414	0.688769	-1.78796	1	-1.63586	0.466655	-0.95077	0.713949	4.24955	0.083652	0.152103	0.964137	0.83719	0.747092	6.037511	0.005989	0.685087	1	5.885408	0.010427	5.200321	0.023643
-0.98907	0.196151	-0.00742	1	-0.17595	1	-0.62635	0.486272	0.051545	0.969616	1.982016	0.008258	-0.45041	0.634536	0.227491	0.837013	2.157963	0.002713	0.677897	1	2.608369	0.000363	1.930472	0.010214
-0.81262	0.271751	-0.64912	0.575544	-0.76903	1	-0.97551	0.202702	-0.52722	0.556721	1.38928	0.06714	-0.20648	0.837471	0.24181	0.814751	2.15831	0.001404	0.448287	1	2.364787	0.000685	1.9165	0.006774
-1.42778	0.074061	-0.40692	0.817559	-1.37052	1	-1.13682	0.202167	-1.5971	0.059606	0.697878	0.539249	0.233696	0.838717	-0.22658	0.849644	2.068393	0.01235	-0.46028	1	1.834697	0.036336	2.294976	0.006014
0.773365	0.083988	0.268724	0.744054	0.177776	1	0.290514	0.616819	0.660118	0.187239	0.347608	0.569542	0.112738	0.867144	0.482342	0.366925	0.169833	0.792427	0.369604	1	0.057095	0.938665	-0.31251	0.572864
0.247498	0.802729	0.043197	0.988074	-0.64482	1	-0.00532	1	0.225048	0.847407	1.585525	0.055618	0.639499	0.492867	0.869864	0.336061	2.230342	0.00296	0.230366	1	1.590844	0.052158	1.360478	0.095371
-0.00407	0.998301	0.073461	0.924157	-0.1109	1	-0.13783	0.759353	-0.13585	0.77013	0.038364	0.952299	-0.02693	0.963728	-0.02495	0.965322	0.149264	0.739708	0.001979	1	0.176197	0.682845	0.174218	0.67431
-0.66708	0.232072	-0.43815	0.626789	0.537359	1	-0.80259	0.157988	-0.48508	0.45948	-0.34294	0.649695	-1.33995	0.009666	-1.02243	0.070602	-0.88029	0.128717	0.317515	1	0.459655	0.471514	0.14214	0.851539
0.151122	0.785772	0.42201	0.544939	-0.25387	1	0.666685	0.158214	1.003556	0.02414	1.453928	0.000638	0.920556	0.035236	1.257427	0.002993	1.707799	3.07E-05	0.336871	1	0.787243	0.095666	0.450372	0.368412
0.176279	0.797761	0.160142	0.892172	-0.0956	1	-0.72887	0.217973	0.345971	0.626021	0.724234	0.254907	-0.63327	0.293012	0.441573	0.510752	0.819836	0.161304	1.074843	1	1.453106	0.008025	0.378263	0.565927
-0.06535	0.874918	-0.49427	0.233773	-0.33172	1	-0.23217	0.546725	-0.41789	0.228957	-0.57234	0.088302	0.099551	0.821398	-0.08617	0.852971	-0.24061	0.533656	-0.18572	1	-0.34017	0.343034	-0.15445	0.69668

N.C. 21 vs 28 DAT		tOH 70% 21 vs 28 DA		3 300 mg/L 21 vs 28 D		3 500 mg/L 21 vs 28 D		O.P. 21 vs 28 DAT		N.C. vs EtOH 28 DAT		. vs GA3 300 mg/L 28 I		vs GA3 500 mg/L 28 I		N.C. vs O.P. 28 DAT		30 % vs GA3 300 mg/L		30 % vs GA3 500 mg/L		OH 280 % vs O.P. 28 D	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
-0.96173	0.000188	-0.69206	0.004028	-1.47031	8.31E-12	-1.61205	2.5E-14	0.204011	0.610518	0.083077	0.871269	-0.78564	0.000525	-0.95499	1.17E-05	0.757276	0.001341	-0.86872	0.000173	-1.03807	2.83E-06	0.674199	0.003205
-0.4398	0.016908	-0.41975	0.012513	-0.51146	0.000859	-0.62103	3.21E-05	0.108061	0.71079	-0.00872	0.982887	-0.35725	0.02902	-0.44509	0.004152	0.191876	0.321868	-0.34853	0.045669	-0.43637	0.006442	0.200599	0.25717
-2.56613	0.00397	-1.88362	0.023916	-2.94797	8.37E-05	-3.35874	4.73E-06	-1.9215	0.066457	-0.21848	0.905347	-1.47126	0.075122	-1.82324	0.019182	4.619717	2.44E-09	-1.25277	0.166098	-1.60476	0.048514	4.838199	9.7E-11
1.43376	0.365417	-0.78374	0.648694	-4.32188	0.008844	-2.21024	0.108584	1	1	1	1	-1.19023	0.413058	-1.60811	0.21614	-0.88725	0.59309	-0.75502	0.653123	-1.1729	0.385995	-0.45204	0.774831
-1.9864	9.29E-05	-1.64594	0.00045	-2.62996	5.04E-10	-2.99212	5.67E-13	-0.26545	0.753663	-0.23575	0.801816	-0.7077	0.142898	-1.3709	0.001633	2.102935	2.82E-06	-0.47195	0.398031	-1.13516	0.012539	2.338681	5.79E-08
-0.45718	0.074024	-0.37116	0.112074	-0.48374	0.022781	-0.48861	0.018915	-0.28582	0.397963	-0.20962	0.602859	-0.2367	0.325281	-0.39942	0.064003	0.482591	0.037892	-0.02708	0.939911	-0.1898	0.436239	0.69221	0.00107
0.096511	0.497114	0.379395	0.000508	0.231973	0.025122	0.505848	2.58E-07	-0.07394	0.693512	0.247115	0.123803	-0.07875	0.529192	0.312976	0.002286	-0.52556	3.16E-07	-0.32587	0.002861	0.065861	0.604666	-0.77267	4.99E-15
-0.08697	0.572047	-0.23046	0.050337	-0.30789	0.003895	-0.4512	1.09E-05	-0.27167	0.060975	-0.17493	0.350827	-0.28577	0.01004	-0.49099	2.25E-06	-0.12443	0.354737	-0.11084	0.419736	-0.31605	0.003971	0.050496	0.717356
-0.61521	0.059195	-1.00958	0.0004	-1.5959	5.22E-10	-1.978	4.54E-15	-0.30314	0.502852	-0.54442	0.21737	-1.13642	1.87E-05	-1.32101	2.83E-07	0.706278	0.015488	-0.592	0.047184	-0.77659	0.004396	1.250696	2.12E-06
-0.77817	0.00839	-0.80189	0.002924	-0.37477	0.160579	-0.17493	0.545867	-0.30648	0.461445	-0.25416	0.60179	-0.00802	0.989325	0.151952	0.609397	0.66546	0.015113	0.246135	0.449666	0.40611	0.139384	0.919619	0.000267
0.102788	0.761546	0.145262	0.593885	-0.30728	0.178196	-0.2901	0.202519	-0.38774	0.223533	0.029241	0.960161	-0.3778	0.105541	-0.22145	0.353629	0.089114	0.784326	-0.40704	0.100012	-0.25069	0.306905	0.059873	0.8414
-0.8848	0.04045	-0.42499	0.315751	-2.35314	1.12E-11	-2.95683	2.72E-18	0.329874	0.612765	-0.01042	0.990044	-0.78792	0.036975	-1.55228	7.49E-06	1.726218	2.89E-06	-0.7775	0.053218	-1.54185	1.39E-05	1.736639	1.07E-06
-1.80492	0.417553	-0.56461	0.797578	-1.26261	0.492469	-1.52672	0.393595	-1.2912	0.744838	-0.54765	0.885381	-1.09354	0.58696	-0.67257	0.736135	4.763277	0.012213	-0.5459	0.828668	-0.12493	0.957937	5.310923	0.002933
0.244734	0.817283	-0.43385	0.598589	-0.30699	0.694228	-0.71793	0.305885	-0.3694	0.772009	-0.85453	0.474906	-1.17808	0.093889	-0.91111	0.191101	1.367884	0.063161	-0.32355	0.733386	-0.05658	0.952196	2.222415	0.000707
-1.24093	0.101169	-1.18035	0.083124	-1.76351	0.003759	-2.54285	1.46E-05	-0.91131	0.344756	-0.70845	0.539642	-1.49809	0.019063	-1.82914	0.002638	1.7189	0.009574	-0.78964	0.292705	-1.12069	0.088182	2.427348	7.16E-05
-2.70845	0.000881	-1.46488	0.05368	-3.11093	3.38E-06	-2.33357	0.000461	-1.12053	0.327059	-0.12695	0.943041	-1.5393	0.032164	-1.22222	0.085823	2.285792	0.00199	-1.41236	0.067477	-1.09527	0.141214	2.412738	0.000609
0.961734	0.044138	1.152258	0.006912	0.72203	0.078891	0.789016	0.049821	-0.6792	0.25125	0.3683	0.637824	0.05081	0.93107	0.4874	0.260284	-1.29332	0.002014	-0.31749	0.550815	0.1191	0.821763	-1.66162	2.4E-05
-2.11405	0.007475	-1.47869	0.046219	-2.42459	0.000255	-2.85097	1.07E-05	-0.04594	0.983397	-0.00946	0.995301	-0.31586	0.72022	-0.51188	0.511532	3.653633	1.04E-07	-0.30639	0.760269	-0.50241	0.535841	3.663097	3.54E-08
-0.74041	0.028984	-0.83731	0.005994	-1.28727	2.85E-06	-2.00215	7.24E-14	-0.3478	0.455023	-0.2078	0.717728	-0.68469	0.020811	-1.3976	3.15E-07	0.43097	0.204327	-0.47689	0.150591	-1.1898	2.43E-05	0.638769	0.032405
1.073359	0.071152	1.112114	0.049576	3.015304	8.42E-09	5.841356	2.56E-09	-0.44701	0.58004	0.576114	0.566226	1.139354	0.058819	4.282922	2.57E-05	-1.86331	0.000188	0.563241	0.456559	3.706808	0.000503	-2.43942	8E-07
-0.31826	0.563731	-0.47793	0.290684	-1.91152	2.75E-07	-2.25041	6.73E-10	-0.15273	0.851565	-0.41354	0.575055	-0.92657	0.021395	-0.92859	0.017197	1.619457	4.53E-05	-0.51303	0.2746	-0.51505	0.230549	2.032995	7.19E-08
-0.59856	0.341691	-0.61878	0.26116	-0.95926	0.046716	-2.20258	9.67E-07	-0.11353	0.917028	-0.11582	0.919039	-1.08957	0.027752	-1.25805	0.007789	1.209268	0.019101	-0.97375	0.068283	-1.14222	0.020106	1.325092	0.00629
-0.25488	0.500446	-0.28026	0.388513	-0.33354	0.253408	-0.35876	0.209202	-0.13693	0.798882	-0.35711	0.4738	-0.31084	0.317838	-0.52177	0.061989	-0.45439	0.152063	0.046268	0.919904	-0.16466	0.620615	-0.09728	0.789922

mg/L vs GA3 500 mg/		300 mg/L vs O.P. 28		3 500 mg/L vs O.P. 28	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
-0.16935	0.680061	1.542917	3.59E-13	1.712265	2.85E-16
-0.08784	0.774129	0.549124	0.000274	0.636969	1.59E-05
-0.35199	0.821971	6.090973	4.37E-17	6.442961	2.34E-19
1	1	0.302978	0.831433	0.720857	0.543649
-0.6632	0.338028	2.810633	1.54E-11	3.473837	2.67E-17
-0.16272	0.670486	0.719289	0.000427	0.882014	9.11E-06
0.39173	0.00389	-0.4468	4.66E-06	-0.83853	2.06E-18
-0.20522	0.204913	0.161336	0.149739	0.366551	0.000338
-0.18459	0.711318	1.842698	3.32E-13	2.027287	4.57E-16
0.159976	0.741018	0.673484	0.00697	0.513509	0.039874
0.156351	0.695626	0.466912	0.03069	0.310561	0.154926
-0.76436	0.145075	2.514135	1.9E-13	3.278493	1.78E-22
0.42097	0.911586	5.856819	0.000587	5.435849	0.001258
0.266966	0.842251	2.545964	4.99E-05	2.278999	0.000249
-0.33105	0.785816	3.216986	3.69E-08	3.548038	7.11E-10
0.317086	0.818634	3.825096	7.81E-09	3.50801	9.19E-08
0.436591	0.513106	-1.34413	0.000488	-1.78072	2.1E-06
-0.19602	0.898294	3.969492	7.33E-10	4.16551	5.74E-11
-0.71291	0.077365	1.115661	4.42E-05	1.828566	5.11E-12
3.143567	0.034178	-3.00266	5.89E-09	-6.14623	2.2E-10
-0.00202	1	2.546028	2.92E-12	2.548048	1.5E-12
-0.16847	0.866332	2.298839	3.3E-07	2.467313	2.66E-08
-0.21093	0.66899	-0.14355	0.651113	0.067382	0.834625

Table S4.9: Table with Log2FoldChange (log2FC) and p-value adjusted (p-adj) of the genes involved in ABA biosynthesis, inactivation, and signal transduction. The heatmap of these genes is showed in Fig. 4.19. Log2FC is calculated according to the following formula: expression level term1 - expression level term2.

Gene name	Gene description	N.C. 0 vs 7 DAT		EtOH 70% 0 vs 7 DAT		A3 300 mg/L 0 vs 7 DA		A3 500 mg/L 0 vs 7 DA		O.P. 0 vs 7 DAT		N.C. vs EtOH 7 DAT		. vs GA3 300 mg/L 7 D		. vs GA3 500 mg/L 7 D		N.C. vs O.P. 7 DAT		70 % vs GA3 300 mg/L	
		Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
Pav_sc0012025.1_g010.1.mk	NCED1	-3.28046	0.520865	-3.40907	0.519146	0	1	0	1	-2.86028	0.414366	-0.12862	1	3.230057	0.417197	1	1	0.420177	0.95633	1	1
Pav_sc0007611.1_g010.1.mk	NCED1	0.0032	1	0.155472	0.939078	0.168418	0.618678	-0.15963	0.63197	-0.03133	0.959145	0.152272	1	0.165218	0.750819	-0.16283	0.686227	-0.03453	0.970294	0.012945	0.978828
Pav_sc0000882.1_g260.1.mk	NCED1	-0.02165	0.978788	-0.07916	0.973582	0.047348	0.851257	-0.16227	0.386335	-0.08029	0.776496	-0.05751	1	0.068998	0.848635	-0.14062	0.553575	-0.05864	0.910539	0.126506	0.570615
Pav_co4011289.1_g010.1.br	NCED1	0.063453	0.967857	-0.10608	0.993647	0.199068	0.66804	-0.10598	0.838057	-0.10456	0.876913	-0.16953	1	0.135615	0.862256	-0.16943	0.764901	-0.16802	0.864062	0.305148	0.501599
Pav_sc0000095.1_g1080.1.mk	NCED1	0.037238	1	-1.37786	0.633046	-1.65953	0.19412	-0.58851	0.720491	0.239803	0.926674	-1.4151	1	-1.69677	0.321666	-0.62575	0.750653	0.202565	0.960601	-0.28167	0.887398
Pav_sc0000095.1_g1070.1.mk	NCED3	-0.15591	0.980242	-0.61478	0.965607	-1.2049	0.384177	-0.35823	0.844435	0.786171	0.697772	-0.45887	1	-1.04899	0.615343	-0.20231	0.931199	0.942083	0.760492	-0.59012	0.73704
Pav_sc0000354.1_g230.1.mk	NCED4	-0.55996	0.778826	-0.94387	0.537069	0.773246	0.360006	0.627579	0.468926	1.228307	0.134059	-0.38391	1	1.333207	0.164831	1.187539	0.184283	1.788267	0.036875	1.717114	0.024694
Pav_sc0003135.1_g490.1.mk	NCED5	1.053118	0.482254	1.16888	0.416294	1.640622	0.036132	1.929274	0.009656	0.571192	0.639545	0.115761	1	0.587504	0.698677	0.876156	0.424964	-0.48193	0.820225	0.471743	0.684294
Pav_sc0001440.1_g080.1.mk	CYP707A1	0.321434	0.952914	-0.94409	0.839759	-3.26932	0.000811	-3.76327	6.39E-05	-0.77876	0.65978	-1.26553	1	-3.59075	0.001494	-4.08471	0.000119	-1.1002	0.667755	-2.32522	0.030039
Pav_sc0000563.1_g270.1.mk	CYP707A2	-1.04688	0.77042	-1.08827	0.854862	-4.80077	2.5E-05	-4.75232	2.9E-05	-0.82162	0.703231	-0.0414	1	-3.7539	0.005323	-3.70545	0.004611	0.225255	0.958658	-3.7125	0.003486
Pav_sc0000071.1_g720.1.mk	CYP707A3	2.760202	0.188115	3.065581	0.114055	1.48918	0.390501	1.64693	0.316593	2.962498	0.060145	0.305379	1	-1.27102	0.638216	-1.11327	0.62176	0.202297	0.970117	-1.5764	0.400805
Pav_sc0000852.1_g900.1.mk	CYP707A4	0.171043	0.954097	0.518221	0.870457	0.525476	0.522351	0.474308	0.564556	1.927796	0.002486	0.347178	1	0.354433	0.800944	0.303264	0.783561	1.756753	0.024552	0.007255	0.996108
Pav_sc0001341.1_g250.1.mk	PYL1	0.404806	0.794695	-0.1289	0.998574	1.002761	0.076576	1.038219	0.058907	-0.10109	0.934378	-0.53371	1	0.597956	0.508524	0.633413	0.403914	-0.50589	0.691589	1.131663	0.061173
Pav_sc0001335.1_g500.1.mk	PYL2	-0.06149	0.981965	-0.21592	0.980766	-0.56749	0.325545	-0.71754	0.176069	-0.32965	0.682905	-0.15443	1	-0.506	0.549749	-0.65605	0.319499	-0.26817	0.850124	-0.35157	0.617062
Pav_sc0000591.1_g120.1.mk	PYL3	0.406771	0.67807	-0.06661	1	1.156307	0.002248	1.081025	0.004225	0.433695	0.43008	-0.47338	1	0.749537	0.1667	0.674255	0.180247	0.026924	0.987169	1.222922	0.002886
Pav_sc0000689.1_g440.1.mk	PavPP2C1	0.124221	0.773819	0.159562	0.742739	-0.06915	0.765224	0.045678	0.851749	0.068394	0.813562	0.035341	1	-0.19337	0.431723	-0.07854	0.764985	-0.05583	0.91367	-0.22872	0.220487
Pav_sc0000069.1_g410.1.mk	PavPP2C2	0.308485	0.089454	0.249063	0.256163	0.328454	0.018358	0.436793	0.000814	0.258524	0.104092	-0.05942	1	0.019969	0.958816	0.128308	0.542403	-0.04996	0.914701	0.079391	0.712026
Pav_sc0002858.1_g200.1.mk	PavPP2C3	0.690498	0.529556	0.299363	0.960576	0.495965	0.461171	0.576193	0.360831	0.788227	0.236327	-0.39114	1	-0.19453	0.881088	-0.11431	0.914112	0.097728	0.958581	0.196602	0.826669
Pav_sc0000554.1_g390.1.mk	PavPP2C4	0.69376	0.321373	0.725354	0.287677	0.842021	0.052653	0.973403	0.018639	2.103161	5.34E-09	0.031594	1	0.14826	0.885105	0.279643	0.681828	1.409401	0.001508	0.116667	0.873096
Pav_sc0001335.1_g050.1.mk	PavPP2C5	0.992721	0.237508	0.621054	0.677204	1.40185	0.008811	1.8234	0.000317	2.404906	6.3E-07	-0.37167	1	0.409128	0.708062	0.830679	0.247901	1.412185	0.034802	0.780795	0.244866
Pav_sc0000212.1_g830.1.mk	PavPP2C6	0.50767	0.531726	0.26301	0.927465	0.662807	0.120229	0.702159	0.0879	0.982421	0.015173	-0.24466	1	0.155137	0.868463	0.19449	0.774377	0.474751	0.555485	0.399797	0.448146
Pav_sc0001196.1_g350.1.mk	PavSnRK2.1	0.045871	0.935157	0.027197	1	-0.1223	0.452323	-0.02715	0.901631	0.144081	0.423058	-0.01867	1	-0.16817	0.415263	-0.07302	0.739018	0.09821	0.770856	-0.1495	0.372369
Pav_sc0000549.1_g120.1.mk	PavSnRK2.2	0.080742	0.952566	-0.1443	0.973817	0.310127	0.374324	-0.00274	0.999268	-0.01831	0.981569	-0.22504	1	0.229385	0.686171	-0.08348	0.876662	-0.09905	0.918664	0.454422	0.189958
Pav_sc0000639.1_g120.1.mk	PavSnRK2.3	0.329878	0.807175	0.125272	0.995231	-0.15994	0.823425	-0.21185	0.747988	-0.58095	0.329095	-0.20461	1	-0.48982	0.527873	-0.54172	0.39712	-0.91083	0.154738	-0.28521	0.67596
Pav_sc0000908.1_g140.1.mk	PavSnRK2.4	0.198332	0.86363	0.024973	1	0.070552	0.90395	-0.05731	0.924114	0.391085	0.410447	-0.17336	1	-0.12778	0.878346	-0.25565	0.641841	0.192753	0.847468	0.045578	0.942892
Pav_sc0001242.1_g120.1.mk	PavSnRK2.5	0.150905	0.928907	-0.01463	1	0.201978	0.727941	0.461403	0.314231	1.10473	0.004914	-0.16553	1	0.051073	0.964127	0.310498	0.617697	0.953825	0.055834	0.216604	0.725564
Pav_sc0000257.1_g130.1.mk	PavSnRK2.6	0.133416	0.85395	0.111222	0.973817	-0.08904	0.794994	-0.22748	0.387838	0.147024	0.692369	-0.02219	1	-0.22245	0.572434	-0.36089	0.205185	0.013608	0.989083	-0.20026	0.512751

70 % vs GA3 500 mg/L		tOH 70 % vs O.P. 7 DA		0 mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 7 D		3 500 mg/L vs O.P. 7 D		N.C. 7 vs 14 DAT		EtOH 70% 7 vs 14 DAT		A3 300 mg/L 7 vs 14 DA		A3 500 mg/L 7 vs 14 D		O.P. 7 vs 14 DAT		N.C. vs EtOH 14 DAT		. vs GA3 300 mg/L 14	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
1	1	0.548794	0.927901	0	1	-2.80988	0.428747	-2.76307	0.484002	-0.69662	0.910759	-3.72231	0.123789	-1.83932	0.568281	-2.45427	0.402601	-0.67423	0.843639	-3.1543	0.665461	2.087356	0.534513
-0.3151	0.282821	-0.1868	0.708011	-0.32805	1	-0.19975	0.597967	0.128297	0.793651	0.057517	0.946474	-0.04069	0.935409	-0.32324	0.216245	0.25087	0.365979	-0.01108	0.982407	0.054064	0.984583	-0.21554	0.55292
-0.08311	0.716251	-0.00114	1	-0.20962	1	-0.12764	0.591503	0.081975	0.79207	0.039753	0.940709	0.132303	0.590994	-0.13162	0.463334	0.0934	0.632418	-0.03797	0.882197	0.035042	0.984041	-0.10237	0.682284
9.97E-05	1	0.001517	1	-0.30505	1	-0.30363	0.533471	0.001418	1	-0.04684	0.971085	-0.00578	0.99581	-0.41623	0.233424	0.025543	0.963401	0.010291	0.98828	-0.12847	0.966132	-0.23377	0.647271
0.789356	0.612667	1.617666	0.365084	1.071028	1	1.899338	0.175645	0.82831	0.691458	0.590589	0.848427	1.385659	0.392003	1.301974	0.285518	-0.05908	0.978762	0.143426	0.947847	-0.62003	0.934832	-0.98539	0.571208
0.25655	0.899769	1.400948	0.482941	0.846673	1	1.991071	0.163695	1.144397	0.559162	1.10562	0.663827	0.964802	0.596396	0.469456	0.746932	-0.50317	0.736821	0.105346	0.965718	-0.59968	0.94167	-1.68515	0.259415
1.571447	0.035312	2.172175	0.004261	-0.14567	1	0.45506	0.691441	0.600728	0.613245	2.229698	0.002321	2.435092	0.00049	-0.05409	0.963933	0.221908	0.8199	0.383464	0.701033	-0.17851	0.981547	-0.95058	0.288399
0.760395	0.431036	-0.59769	0.691825	0.288652	1	-1.06943	0.281683	-1.35808	0.17015	-0.71208	0.656106	0.034667	0.984328	0.590816	0.508518	0.032011	0.984041	1.034211	0.243573	0.862504	0.831172	1.890395	0.019856
-2.81918	0.004706	0.16533	0.957995	-0.49395	1	2.490552	0.019101	2.984507	0.004122	-1.34874	0.492673	-0.67886	0.681753	1.452657	0.13385	0.952987	0.355583	0.094348	0.963223	-0.59564	0.920099	-0.78935	0.601384
-3.66405	0.00307	0.26665	0.941309	0.048449	1	3.97915	0.001208	3.930701	0.002036	-0.20786	0.964973	-1.1458	0.542544	1.019284	0.453348	1.561049	0.216788	-2.07705	0.127575	-0.97933	0.889829	-2.52675	0.062533
-1.41865	0.432524	-0.10308	0.986296	0.15775	1	1.473319	0.472566	1.315569	0.580907	-0.72331	0.847562	-0.69824	0.787369	-2.64618	0.058155	-1.9291	0.194914	-1.29909	0.468864	0.330449	0.983328	-3.19389	0.039347
-0.04391	0.970893	1.409575	0.101825	-0.05117	1	1.40232	0.060634	1.453489	0.063762	0.728489	0.538824	-0.11138	0.930512	-1.15208	0.06527	-1.23854	0.044134	-1.83446	0.005134	-0.4927	0.894989	-1.52613	0.023937
1.16712	0.041455	0.027815	0.991774	0.035457	1	-1.10385	0.071614	-1.13931	0.079111	-0.10015	0.958811	-1.03908	0.113971	-1.48481	0.002821	-1.15842	0.024445	0.877369	0.141491	-1.47263	0.156474	-0.78671	0.234546
-0.50162	0.405308	-0.11373	0.93347	-0.15005	1	0.237831	0.777957	0.387882	0.642488	-0.05483	0.979562	-0.37141	0.632756	0.274854	0.645894	0.421383	0.449747	0.057736	0.949124	-0.47102	0.864575	-0.17632	0.848322
1.14764	0.004604	0.500309	0.432622	-0.07528	1	-0.72261	0.12298	-0.64733	0.21621	-0.14583	0.899617	-0.75428	0.12144	-1.03883	0.004851	-0.90948	0.015621	-0.10096	0.873733	-1.08184	0.156474	-0.14346	0.848024
-0.11388	0.582497	-0.09117	0.785251	0.114831	1	0.137548	0.542789	0.022716	0.955344	-0.2212	0.375018	-0.17045	0.44362	-0.16492	0.321016	-0.18478	0.260475	-0.45153	0.002684	0.086091	0.927235	-0.13709	0.538536
0.18773	0.249628	0.009461	0.987002	0.108339	1	-0.06993	0.77187	-0.17827	0.384381	-0.17242	0.484362	-0.32082	0.046421	-0.29529	0.02798	-0.34854	0.008081	-0.30847	0.034432	-0.20781	0.70936	-0.1029	0.632746
0.27683	0.723843	0.488863	0.625211	0.080228	1	0.292262	0.74748	0.212033	0.852523	0.371682	0.767809	-0.55957	0.478664	-0.27629	0.680074	-0.68076	0.229379	-1.14098	0.042587	-1.32239	0.260933	-0.84251	0.19373
0.248049	0.679106	1.377807	0.001851	0.131383	1	1.261141	0.003497	1.129758	0.01492	0.903854	0.090782	0.469889	0.439718	-0.03714	0.957487	-0.50934	0.255448	-1.56496	6.69E-05	-0.40237	0.86782	-0.79273	0.099036
1.202346	0.039658	1.783852	0.002167	0.421551	1	1.003057	0.125703	0.581506	0.504668	0.359041	0.783317	0.157897	0.883134	-0.38425	0.551183	-1.09293	0.040326	-2.3868	1.68E-06	-0.57281	0.853386	-0.33416	0.707764
0.43915	0.359593	0.719411	0.191106	0.039353	1	0.319614	0.592804	0.280261	0.69328	0.464726	0.516127	-0.17806	0.804644	-0.36738	0.406447	-0.10048	0.858283	-0.76723	0.070334	-0.88745	0.377039	-0.67697	0.145649
-0.05435	0.78647	0.116884	0.632879	0.095145	1	0.26638	0.072349	0.171235	0.362314	-0.07168	0.827446	-0.00496	0.987288	-0.01619	0.936432	-0.00456	0.987539	-0.48554	5.96E-05	0.048043	0.968531	-0.11268	0.554154
0.141555	0.740221	0.125986	0.854909	-0.31287	1	-0.32844	0.411276	-0.01557	0.986646	-0.35991	0.478008	-0.48357	0.190584	-0.87158	0.000985	-0.44361	0.131742	-0.13687	0.74436	-0.3487	0.804737	-0.28228	0.485344
-0.33712	0.582099	-0.70622	0.295213	-0.0519	1	-0.42101	0.525487	-0.3691	0.635078	-0.66196	0.367214	-0.99294	0.061478	-1.12235	0.008302	-0.78009	0.084427	-0.02947	0.974604	-0.53559	0.818689	-0.95021	0.058556
-0.08229	0.893527	0.366112	0.548952	-0.12787	1	0.320533	0.526806	0.448399	0.37338	-0.08854	0.93964	-0.2216	0.699222	-0.07982	0.871007	-0.24076	0.563602	-0.10524	0.846536	-0.30642	0.875223	-0.11906	0.8564
0.476029	0.31608	1.119356	0.012467	0.259425	1	0.902752	0.041037	0.643327	0.223797	0.93527	0.051592	0.758906	0.121167	0.743224	0.057413	0.552602	0.182766	-0.18768	0.746605	-0.3419	0.875223	-0.14097	0.852012
-0.3387	0.177427	0.035802	0.957995	-0.13844	1	0.236062	0.453185	0.374501	0.198228	-0.09757	0.871991	-0.52514	0.036022	-0.51343	0.012601	-0.50442	0.014145	-0.32683	0.195529	-0.44976	0.461709	-0.63832	0.003463

. vs GA3 500 mg/L 14		N.C. vs O.P. 14 DAT		40 % vs GA3 300 mg/L		40 % vs GA3 500 mg/L		OH 140 % vs O.P. 14 D		mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 14		3 500 mg/L vs O.P. 14		N.C. 14 vs 21 DAT		EtOH 70% 14 vs 21 DA		3 300 mg/L 14 vs 21 D		3 500 mg/L 14 vs 21 D	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
1.425608	0.687853	1	1	5.24166	0.024959	4.579912	0.040502	3.596874	0.105978	-0.66175	1	1	1	1	1	1	1	1	1	-1.88648	0.464582	-2.36078	0.280324
0.030525	0.961266	-0.10313	0.879995	-0.2696	0.405368	-0.02354	0.967616	-0.15719	0.667103	0.246061	1	0.11241	0.876816	-0.13365	0.858067	-0.03769	0.939472	0.09213	0.878549	0.302076	0.239482	0.064171	0.840942
-0.08697	0.745675	-0.13637	0.679594	-0.13741	0.52901	-0.12201	0.596934	-0.17141	0.396803	0.015399	1	-0.034	0.949053	-0.04939	0.926067	0.032865	0.912391	-0.02279	0.955356	0.050985	0.79717	-0.06541	0.725708
-0.09705	0.88555	-0.11088	0.905985	-0.1053	0.853911	0.031421	0.966798	0.017588	0.981469	0.136724	1	0.12289	0.903598	-0.01383	0.994325	-0.11386	0.845894	0.065925	0.938208	0.407229	0.231716	0.37827	0.265187
-1.27541	0.426548	-0.2446	0.951189	-0.36536	0.856146	-0.65538	0.721401	0.375433	0.85097	-0.29003	1	0.74079	0.812458	1.030816	0.712368	-2.19925	0.117242	-1.71307	0.379809	-2.77624	0.007895	-3.14871	0.001819
-1.8111	0.212822	-0.05819	0.994697	-1.08547	0.492965	-1.21142	0.436496	0.541492	0.783925	-0.12595	1	1.626961	0.469993	1.752911	0.423127	-2.14401	0.137868	-2.05774	0.271593	-2.19727	0.035578	-2.79924	0.004755
-0.82025	0.385911	-0.05797	0.988154	-0.77207	0.400994	-0.64174	0.515362	0.120547	0.929683	0.130328	1	0.892613	0.5119	0.762284	0.614545	-0.17738	0.893466	-1.0755	0.368381	-0.89132	0.213946	-1.25721	0.058934
1.620242	0.056004	1.26436	0.263141	1.027892	0.27879	0.757739	0.472381	0.401856	0.730479	-0.27015	1	-0.62604	0.739634	-0.35588	0.884656	1.776329	0.048224	0.666986	0.664932	1.23353	0.110439	1.864222	0.009742
-1.78298	0.114577	0.342892	0.90743	-0.19371	0.913807	-1.18733	0.330442	0.938537	0.494817	-0.99362	1	1.132244	0.600565	2.125869	0.158498	-0.40001	0.820059	0.949012	0.633694	-0.23794	0.850906	0.508203	0.640348
-1.93654	0.187236	-1.64393	0.412957	-1.54742	0.301889	-0.9572	0.587151	-0.6646	0.715178	0.590214	1	0.882818	0.769471	0.292604	0.943541	-0.04533	0.989316	-0.03353	0.993646	0.033634	0.988293	-0.54381	0.700174
-2.31906	0.172583	-0.37348	0.930668	-3.52434	0.016342	-2.64951	0.097889	-0.70393	0.750298	0.874833	1	2.820408	0.19769	1.945575	0.470561	-0.79911	0.727771	-0.76585	0.809923	-2.86692	0.03258	-3.26171	0.011866
-1.66377	0.01104	-0.80619	0.458491	-1.03344	0.154387	-1.17107	0.097934	-0.3135	0.749542	-0.13763	1	0.719942	0.582517	0.857574	0.472236	-0.93296	0.251376	-0.37688	0.785203	0.319503	0.667436	0.064086	0.943215
-0.42486	0.603795	0.471625	0.674527	0.685928	0.303078	1.047771	0.077317	1.944259	0.000236	0.361843	1	1.258331	0.105604	0.896488	0.329856	-1.10495	0.084933	-0.04278	0.979763	-0.57202	0.31022	-0.99811	0.047739
-0.17984	0.85046	-0.15561	0.911313	0.294703	0.690526	0.291181	0.702816	0.315416	0.655449	-0.00352	1	0.020713	0.996279	0.024235	0.992714	-0.60367	0.346517	-0.39203	0.688766	-0.70065	0.148044	-0.68815	0.147791
-0.08939	0.91799	0.071796	0.958681	0.938373	0.022306	0.992444	0.01446	1.153634	0.004382	0.054071	1	0.215261	0.845469	0.16119	0.901101	-1.02623	0.024152	-0.16684	0.855671	-1.03501	0.004334	-1.15161	0.001127
-0.04212	0.894697	-0.28616	0.178029	-0.22318	0.223394	-0.12821	0.55913	-0.37225	0.022433	0.094968	1	-0.14907	0.673767	-0.24404	0.363574	-0.21137	0.285072	-0.27637	0.269982	-0.53079	0.000106	-0.66049	7.68E-07
-0.04781	0.860851	-0.18601	0.41728	0.104912	0.60436	0.160005	0.379018	0.021803	0.937027	0.055093	1	-0.08311	0.827472	-0.1382	0.660808	-0.21491	0.222508	-0.14505	0.577339	-0.04164	0.814534	-0.37804	0.00258
-1.16674	0.0456	-1.41494	0.027224	0.479879	0.516244	0.155642	0.870791	-0.09255	0.928551	-0.32424	1	-0.57243	0.61922	-0.24819	0.883055	-1.46633	0.016885	-0.85014	0.345093	-1.26229	0.011024	-1.28028	0.008669
-1.13356	0.008218	-1.05941	0.037884	-0.39036	0.495662	-0.73118	0.12736	-0.65704	0.186404	-0.34082	1	-0.26667	0.811024	0.074146	0.960047	-0.94067	0.056804	-0.62843	0.380131	-1.27268	0.000781	-0.78685	0.045701
-0.62129	0.401343	-1.33365	0.046119	0.238646	0.789959	-0.04848	0.969922	-0.76084	0.250025	-0.28713	1	-0.99949	0.246771	-0.71236	0.499258	-1.45258	0.020404	-1.32365	0.092803	-2.05395	2.16E-05	-2.01606	2.5E-05
-0.37071	0.514106	-0.75721	0.16131	0.210474	0.73301	0.516732	0.293239	0.130239	0.845452	0.306258	1	-0.08024	0.952618	-0.38649	0.666918	-1.14682	0.010588	-0.5974	0.372602	-1.40262	6.78E-05	-2.21256	6E-11
-0.0059	0.989252	-0.31565	0.047048	-0.16072	0.32365	-0.05394	0.805283	-0.36369	0.006599	0.106779	1	-0.20297	0.354873	-0.30975	0.097413	-0.07202	0.730791	-0.14248	0.551304	-0.4172	0.000337	-0.4155	0.000313
-0.16718	0.730402	0.123986	0.875459	0.066414	0.898778	0.181516	0.684825	0.472683	0.159783	0.115102	1	0.406269	0.438984	0.291168	0.651313	0.163954	0.722058	0.23051	0.69265	0.601177	0.027297	0.360723	0.210919
-0.65986	0.239643	-0.27834	0.798432	-0.41462	0.504218	-0.12427	0.880745	0.257245	0.703984	0.29035	1	0.671865	0.399549	0.381515	0.73104	-0.05762	0.950719	0.151944	0.889782	0.666897	0.138897	-0.03164	0.964281
-0.40787	0.376237	0.176051	0.844218	0.187356	0.728093	-0.10145	0.870224	0.482471	0.251027	-0.2888	1	0.295115	0.723051	0.583916	0.322073	-0.32343	0.505235	-0.02027	0.985553	-0.66907	0.04262	-0.29927	0.413543
-0.07217	0.937276	-0.16912	0.877201	0.200923	0.749432	0.269726	0.657261	0.172775	0.786329	0.068803	1	-0.02815	0.988619	-0.09695	0.943541	-0.78984	0.099156	-0.73722	0.253299	-1.21221	0.000737	-0.82511	0.025482
-0.76774	0.000211	-0.21565	0.620184	-0.18855	0.528519	-0.31798	0.216383	0.234113	0.405933	-0.12943	1	0.422664	0.210897	0.552092	0.069913	-0.2822	0.327345	0.100966	0.839874	-0.47831	0.016246	-0.32989	0.108649

O.P. 14 vs 21 DAT		N.C. vs EtOH 21 DAT		. vs GA3 300 mg/L 21 D		. vs GA3 500 mg/L 21 D		N.C. vs O.P. 21 DAT		10 % vs GA3 300 mg/L		10 % vs GA3 500 mg/L		OH 210 % vs O.P. 21 D		mg/L vs GA3 500 mg/L		300 mg/L vs O.P. 21 D		500 mg/L vs O.P. 21		N.C. 21 vs 28 DAT	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
1	1	-0.94673	1	1.720989	0.446793	0.584941	0.829579	2.488679	0.294731	2.667718	0.185624	1.53167	0.495935	3.435409	0.097608	-1.13605	1	0.767691	0.792228	1.903738	0.411215	0.549824	0.836129
0.083707	0.87122	0.183887	1	0.124232	0.701214	0.132387	0.690064	0.018273	0.971429	-0.05965	0.86989	-0.0515	0.892205	-0.16561	0.596849	0.008156	1	-0.10596	0.751802	-0.11411	0.72004	0.379609	0.160061
-0.05495	0.863817	-0.02061	1	-0.08425	0.673954	-0.18525	0.289468	-0.22418	0.201044	-0.06364	0.760825	-0.16464	0.358686	-0.20357	0.227681	-0.101	1	-0.13993	0.444464	-0.03893	0.858633	0.282523	0.084271
0.227005	0.685341	0.05131	1	0.287312	0.455157	0.395076	0.285567	0.229978	0.601805	0.236001	0.553146	0.343766	0.367213	0.178667	0.677676	0.107764	1	-0.05733	0.90963	-0.1651	0.691409	0.367461	0.325635
-0.58078	0.789473	-0.13385	1	-1.56238	0.181341	-2.22488	0.045405	1.373866	0.29961	-1.42853	0.224658	-2.09102	0.061711	1.507717	0.216557	-0.66249	1	2.936249	0.008547	3.598742	0.000834	-0.79096	0.559313
-0.21377	0.945602	-0.51341	1	-1.73841	0.117081	-2.46633	0.019424	1.872053	0.142113	-1.225	0.294931	-1.95292	0.073585	2.385461	0.038654	-0.72792	1	3.610462	0.001219	4.338385	6.36E-05	-0.92109	0.473362
-0.56199	0.623381	-1.07663	1	-1.66451	0.012666	-1.90007	0.004079	-0.44258	0.646052	-0.58789	0.468455	-0.82344	0.292449	0.634052	0.437842	-0.23556	1	1.221939	0.093972	1.457497	0.036624	-2.21485	0.001261
-0.56837	0.654732	-0.24684	1	1.347596	0.087041	1.708135	0.02758	-1.08034	0.210489	1.594436	0.033911	1.954974	0.009115	-0.8335	0.330068	0.360539	1	-2.42794	0.001183	-2.78848	0.000157	0.337179	0.742722
-2.37918	0.035692	0.753372	1	-0.62729	0.60396	-0.87477	0.44983	-1.63628	0.110663	-1.38066	0.18856	-1.62814	0.120194	-2.38965	0.012079	-0.24748	1	-1.00899	0.345425	-0.76151	0.48235	-1.05147	0.337606
-0.00718	1	-0.96754	1	-2.44779	0.039921	-2.43503	0.045548	-1.60579	0.248605	-1.48026	0.249395	-1.46749	0.270145	-0.63825	0.68536	0.012767	1	0.842008	0.565709	0.829241	0.558997	-0.2492	0.893093
-5.52731	7.33E-05	0.363708	1	-5.2617	2.4E-05	-4.78166	0.000177	-5.10168	8.98E-05	-5.62541	4.93E-06	-5.14537	4.36E-05	-5.46539	1.76E-05	0.480042	1	0.16002	0.944597	-0.32002	0.87206	-0.36828	0.855847
-0.74859	0.397393	0.06338	1	-0.27368	0.743468	-0.66672	0.351386	-0.62182	0.418386	-0.33706	0.67095	-0.7301	0.297181	-0.6852	0.327004	-0.39305	1	-0.34815	0.663348	0.044902	0.966243	-0.21301	0.80467
-0.45734	0.589864	-0.41047	1	-0.25378	0.716192	-0.31803	0.644512	1.11923	0.040385	0.156694	0.833112	0.092444	0.910408	1.529699	0.00217	-0.06425	1	1.373005	0.009349	1.437256	0.00555	-0.72803	0.2122
0.124452	0.906857	-0.25938	1	-0.2733	0.654333	-0.26432	0.676873	0.572516	0.313452	-0.01392	0.990164	-0.00493	0.99969	0.8319	0.092218	0.008985	1	0.845819	0.093236	0.836834	0.088802	-1.25526	0.008525
-0.25644	0.701986	-0.22244	1	-0.15224	0.776999	-0.21477	0.678873	0.84159	0.035442	0.0702	0.905118	0.007673	0.995035	1.064032	0.004099	-0.06253	1	0.993832	0.010853	1.056359	0.005678	-0.39106	0.387085
-0.32315	0.071797	0.021087	1	-0.45651	0.001003	-0.49124	0.000402	-0.39794	0.007382	-0.4776	0.000492	-0.51233	0.000196	-0.41903	0.003436	-0.03473	1	0.058568	0.776261	0.0933	0.612321	0.165042	0.340339
0.044461	0.877261	-0.13794	1	0.070377	0.694163	-0.21093	0.150503	0.073368	0.710423	0.208319	0.142015	-0.07299	0.689725	0.21131	0.145656	-0.28131	1	0.00299	0.994868	0.284295	0.039974	-0.01724	0.937528
0.353341	0.696474	-0.7062	1	-0.63846	0.27078	-0.98069	0.071052	0.404739	0.561156	0.067738	0.937002	-0.27449	0.697006	1.110935	0.033919	-0.34223	1	1.043197	0.055911	1.385428	0.007559	-0.81951	0.149465
-0.40785	0.520343	-0.09014	1	-1.12475	0.003716	-0.97974	0.015727	-0.52659	0.274306	-1.03461	0.007831	-0.8896	0.030272	-0.43645	0.353598	0.145014	1	0.598163	0.180639	0.453149	0.318667	-1.14898	0.005424
0.49429	0.557331	-0.44388	1	-0.93554	0.086039	-1.18477	0.025881	0.613215	0.34029	-0.49166	0.422677	-0.74089	0.205305	1.057094	0.050372	-0.24923	1	1.548757	0.003331	1.797989	0.000469	-0.71333	0.229954
-0.00832	1	-0.33802	1	-0.93278	0.012471	-1.43645	3.94E-05	0.381288	0.43211	-0.59475	0.137635	-1.09843	0.002706	0.719311	0.069418	-0.50368	1	1.314065	0.000454	1.817742	3.99E-07	-1.23947	0.001261
-0.31965	0.026715	-0.02241	1	-0.45786	6.32E-05	-0.34937	0.004088	-0.56327	1.03E-06	-0.43545	0.000147	-0.32696	0.007693	-0.54086	2.55E-06	0.108484	1	-0.10542	0.48971	-0.2139	0.103709	-0.23882	0.074798
0.199435	0.680505	-0.28214	1	0.15494	0.673135	0.029588	0.951169	0.159468	0.694233	0.437081	0.135914	0.311728	0.339795	0.441609	0.141483	-0.12535	1	0.004528	0.997406	0.12988	0.721315	-0.2858	0.386714
-0.18355	0.837431	-0.32602	1	-0.22569	0.699588	-0.63387	0.19214	-0.40427	0.476213	0.100333	0.878749	-0.30785	0.585932	-0.07825	0.910837	-0.40818	1	-0.17858	0.769378	0.229603	0.681664	-0.98175	0.032646
-0.09931	0.892172	-0.00327	1	-0.46471	0.202516	-0.38371	0.323659	0.400167	0.323751	-0.46145	0.200836	-0.38044	0.328509	0.403434	0.287697	0.081002	1	0.864879	0.011303	0.783878	0.021265	0.078231	0.877549
-0.31078	0.633161	-0.28928	1	-0.56334	0.173998	-0.10745	0.853859	0.309931	0.546975	-0.27406	0.564941	0.181833	0.732819	0.599212	0.148659	0.455897	1	0.873275	0.028693	0.417379	0.335508	-1.25131	0.001209
-0.50513	0.04154	-0.0666	1	-0.83442	8.63E-06	-0.81544	1.69E-05	-0.43858	0.048055	-0.76782	4.61E-05	-0.74884	9.32E-05	-0.37198	0.090387	0.018987	1	0.395846	0.070161	0.376859	0.079558	-0.7224	0.0006

tOH 70% 21 vs 28 DAT		3 300 mg/L 21 vs 28 D		3 500 mg/L 21 vs 28 D		O.P. 21 vs 28 DAT		N.C. vs EtOH 28 DAT		. vs GA3 300 mg/L 28		. vs GA3 500 mg/L 28		N.C. vs O.P. 28 DAT		30 % vs GA3 300 mg/L		30 % vs GA3 500 mg/L		OH 280 % vs O.P. 28 D		mg/L vs GA3 500 mg/	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
-0.53529	0.798651	1.493692	0.514409	2.070106	0.300399	1	1	1	1	2.664857	0.224552	2.105223	0.299554	1.306566	0.567009	4.696698	0.027107	4.137064	0.03002	3.338407	0.05643	1	1
0.091661	0.751051	0.187783	0.447542	0.612346	0.006129	-0.28559	0.389583	-0.10406	0.827752	-0.06759	0.826015	0.365124	0.130169	-0.64693	0.0043	0.036467	0.922884	0.469185	0.05307	-0.54287	0.013937	0.432719	0.21745
0.169308	0.279464	0.368698	0.005847	0.702228	3.94E-08	0.00825	0.985347	-0.13383	0.606339	0.001924	0.999284	0.234453	0.09695	-0.49846	0.000335	0.135753	0.432635	0.368282	0.00813	-0.36463	0.007958	0.232529	0.260891
0.151315	0.68052	0.324539	0.303978	-0.0448	0.910224	-0.38102	0.390308	-0.16484	0.783025	0.244389	0.483432	-0.01718	0.970401	-0.51851	0.109525	0.409226	0.241702	0.147653	0.680969	-0.35367	0.268688	-0.26157	0.613968
-0.2023	0.879476	-1.91771	0.045296	-0.46283	0.677732	-2.61249	0.040355	0.454808	0.826476	-2.68913	0.005353	-1.89674	0.050111	-0.44766	0.746996	-3.14394	0.001517	-2.35155	0.01641	-0.90247	0.421108	0.792385	0.636214
0.216478	0.867256	-1.89082	0.040098	-0.61673	0.550526	-2.9293	0.021641	0.624161	0.743772	-2.70814	0.003591	-2.16197	0.018894	-0.13616	0.931899	-3.3323	0.000462	-2.78613	0.002936	-0.76032	0.498153	0.546168	0.755689
-1.9507	0.002177	-1.85814	0.001566	-2.25523	7.91E-05	-0.41309	0.711417	-0.81247	0.45372	-1.3078	0.037276	-1.94046	0.000936	1.359186	0.03986	-0.49533	0.530553	-1.12798	0.075866	2.17166	0.000268	-0.63266	0.5281
2.108846	0.00333	2.124878	0.003562	0.258174	0.764923	0.908924	0.376007	1.524827	0.15915	3.135296	1.49E-05	1.62913	0.018126	-0.5086	0.569051	1.610468	0.053147	0.104303	0.913915	-2.03343	0.002904	-1.50617	0.178105
-2.3706	0.00915	-1.82146	0.025057	-2.34662	0.002508	1.087323	0.39328	-0.56575	0.730229	-1.39728	0.105512	-2.16992	0.006061	0.502515	0.66081	-0.83152	0.408816	-1.60417	0.054395	1.068268	0.241604	-0.77264	0.56385
0.353803	0.801569	2.431878	0.021014	4.441833	4.81E-05	-1.81939	0.225622	-0.36453	0.879636	0.233285	0.876137	2.256007	0.057714	-3.17598	0.003726	0.597819	0.692072	2.620541	0.029673	-2.81144	0.007756	2.022722	0.252478
0.217324	0.900105	2.328006	0.058527	3.849286	0.000965	-0.34251	0.899715	0.949315	0.696844	-2.56542	0.044114	-0.56409	0.69878	-5.07591	4.01E-05	-3.51473	0.006626	-1.51341	0.266011	-6.02522	3.49E-07	2.001322	0.278274
-0.92959	0.120249	0.663288	0.255951	0.698986	0.21847	0.265754	0.801486	-0.65321	0.509053	0.602617	0.33435	0.245266	0.707784	-0.14306	0.865837	1.255826	0.035947	0.898475	0.12221	0.510144	0.417047	-0.35735	0.730371
-0.55895	0.2948	-0.43262	0.391351	-0.63918	0.179456	-1.22818	0.041698	-0.24139	0.802671	0.04163	0.952955	-0.22918	0.673958	0.619076	0.264174	0.283025	0.656831	0.012217	0.98892	0.860471	0.078054	-0.27081	0.760121
-1.00432	0.023014	-2.35425	1.72E-09	-2.2577	4.61E-09	-0.50861	0.450356	-0.00845	0.993518	-1.3723	0.000819	-1.26677	0.001577	1.31916	0.002221	-1.36386	0.001349	-1.25832	0.002296	1.327606	0.001291	0.105535	0.911091
-0.45479	0.241559	-0.08418	0.845276	0.079518	0.856761	-0.68784	0.151381	-0.28618	0.666396	0.154634	0.723947	0.255808	0.507114	0.544805	0.167445	0.440812	0.280916	0.541985	0.136811	0.830983	0.016932	0.101173	0.892482
0.201719	0.17304	0.485808	0.000129	0.323852	0.011697	-0.09381	0.69774	0.057763	0.840024	-0.13574	0.370859	-0.33243	0.011095	-0.65679	6.12E-07	-0.19351	0.214779	-0.39019	0.003353	-0.71456	1.76E-08	-0.19669	0.337981
0.032206	0.842252	-0.08221	0.547159	0.151181	0.228355	-0.21785	0.206625	-0.08849	0.710638	0.005411	0.981199	-0.0425	0.77443	-0.12724	0.396745	0.093904	0.553793	0.04599	0.763909	-0.03874	0.809218	-0.04791	0.845559
-0.71099	0.166752	-1.25686	0.005257	-1.2872	0.003662	-1.34577	0.021229	-0.59768	0.47324	-1.07581	0.023039	-1.44839	0.001193	-0.12153	0.865845	-0.47813	0.406478	-0.85071	0.078919	0.476151	0.368473	-0.37258	0.646486
-1.41648	0.00018	-1.58363	4.07E-06	-2.05005	1.01E-09	-0.66003	0.203098	-0.35764	0.602859	-1.5594	9.73E-06	-1.88081	3.63E-08	-0.03763	0.953593	-1.20176	0.001251	-1.52317	1.56E-05	0.320006	0.451042	-0.32141	0.607162
-1.03949	0.038411	-1.10119	0.017281	-0.72423	0.12726	-1.46262	0.012394	-0.77004	0.333442	-1.3234	0.005012	-1.19567	0.009539	-0.13608	0.850958	-0.55336	0.332386	-0.42563	0.426136	0.633963	0.219505	0.127731	0.902843
-1.34911	0.000148	-1.42298	1.11E-05	-1.1257	0.000488	-1.06949	0.011676	-0.44767	0.465235	-1.1163	0.000974	-1.32269	4.76E-05	0.551266	0.160459	-0.66863	0.07808	-0.87503	0.011139	0.998932	0.003309	-0.2064	0.749138
-0.25245	0.035223	-0.13823	0.241527	-0.49612	2.08E-06	0.035792	0.883244	-0.03604	0.888876	-0.35727	0.00137	-0.60667	8.42E-09	-0.28866	0.015251	-0.32123	0.006384	-0.57064	1.15E-07	-0.25263	0.02795	-0.24941	0.118785
-0.01641	0.964511	-0.66482	0.006419	-0.86456	0.000247	-0.18855	0.674696	-0.01275	0.983906	-0.22407	0.440768	-0.54917	0.027252	0.25672	0.412036	-0.21132	0.51362	-0.53642	0.036903	0.269473	0.342753	-0.3251	0.407576
-0.95042	0.022284	-1.5677	2.64E-05	-1.64686	6.91E-06	-0.85562	0.111615	-0.29469	0.703506	-0.81164	0.046006	-1.29899	0.000572	-0.27814	0.596539	-0.51695	0.267464	-1.00429	0.011176	0.016554	0.983257	-0.48735	0.431466
-0.04027	0.924765	-0.16193	0.639626	0.362001	0.245967	-0.17391	0.757276	-0.12177	0.852189	-0.70487	0.021289	-0.09994	0.786269	0.148029	0.730159	-0.5831	0.080367	0.021828	0.959778	0.269799	0.440256	0.604928	0.164098
-1.37906	0.000113	-1.4233	1.25E-05	-1.97217	5.3E-10	0.148051	0.831207	-0.41702	0.504161	-0.73533	0.037891	-0.8283	0.014329	1.709296	5.54E-07	-0.31831	0.466183	-0.41128	0.276478	2.126318	7.83E-11	-0.09297	0.903085
-0.84538	1.24E-05	-0.54838	0.001891	-0.4018	0.025002	-0.31969	0.231132	-0.18958	0.58148	-0.6604	0.00024	-0.49484	0.005797	-0.03587	0.903892	-0.47082	0.015418	-0.30526	0.115901	0.153716	0.476009	0.165558	0.595744

300 mg/L vs O.P. 28		500 mg/L vs O.P. 28	
Log2FC	p-adj	Log2FC	p-adj
-1.35829	0.556401	-0.79866	0.71168
-0.57934	0.006698	-1.01206	1.56E-06
-0.50038	0.00011	-0.73291	6.36E-09
-0.7629	0.007006	-0.50132	0.077458
2.241467	0.016537	1.449082	0.12554
2.571976	0.003878	2.025808	0.022851
2.666987	2.82E-06	3.299644	3.36E-09
-3.64389	1.34E-07	-2.13773	0.001027
1.899792	0.017519	2.672433	0.000455
-3.40926	0.000755	-5.43198	3.84E-07
-2.51049	0.03789	-4.51182	7.76E-05
-0.74568	0.190741	-0.38833	0.501634
0.577446	0.233198	0.848254	0.059996
2.691461	2.74E-12	2.585926	1.1E-11
0.390171	0.279402	0.288998	0.415712
-0.52105	3.02E-05	-0.32436	0.010235
-0.13265	0.300417	-0.08473	0.505715
0.954279	0.036459	1.326858	0.002331
1.521769	7.64E-06	1.843175	3.19E-08
1.187327	0.009002	1.059596	0.018319
1.667561	1.54E-07	1.873958	2.1E-09
0.068607	0.588733	0.318013	0.002575
0.480794	0.052916	0.80589	0.000568
0.533501	0.186754	1.020847	0.00596
0.852898	0.002982	0.24797	0.426126
2.44463	1.38E-14	2.537596	5.88E-16
0.624534	0.000299	0.458975	0.00832

Table S4.10: Table with Log2FoldChange (log2FC) and p-value adjusted (p-adj) of the genes that encode for Cyclins (CYC). The heatmap of these genes is showed in Fig. 4.21. Log2FC is calculated according to the following formula: expression level term1 - expression level term2.

Gene name	Gene description	N.C. 0 vs 7 DAT		EtOH 70% 0 vs 7 DAT		A3 300 mg/L 0 vs 7 DA		A3 500 mg/L 0 vs 7 DA		O.P. 0 vs 7 DAT		N.C. vs EtOH 7 DAT		C. vs GA3 300 mg/L 7 D		C. vs GA3 500 mg/L 7 D		N.C. vs O.P. 7 DAT		70 % vs GA3 300 mg/L	
		Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
Pav_sc0000195.1_g230.1.mk	PavCYCA1;1	-0.00512	1	0.137075	0.995079	0.108918	0.892757	0.120952	0.877738	0.081849	0.942092	0.142198	1	0.114041	0.92619	0.126075	0.889637	0.086972	0.958658	-0.02816	0.975563
Pav_sc0000195.1_g240.1.mk	PavCYCA1;1	0.267228	0.739476	-0.12661	0.982891	0.192094	0.63788	0.24798	0.509206	0.009936	0.994914	-0.39384	1	-0.07513	0.920597	-0.01925	0.978131	-0.25729	0.724948	0.318707	0.41431
Pav_sc0001258.1_g220.1.mk	PavCYCA2;1	-0.50498	0.615658	-0.13234	0.994317	-0.09934	0.892972	-0.13306	0.848955	-0.52092	0.381699	0.372642	1	0.405642	0.617254	0.371922	0.581234	-0.01594	0.99559	0.033001	0.968856
Pav_sc0000716.1_g260.1.mk	PavCYCA2;4	-0.25917	0.789627	-0.04657	1	-0.20337	0.666253	-0.16198	0.740592	-0.12582	0.85011	0.2126	1	0.055797	0.950907	0.09719	0.876662	0.133351	0.903442	-0.1568	0.774784
Pav_sc0000852.1_g160.1.mk	PavCYCA3;1	-0.43272	0.728292	0.053627	1	-0.22546	0.745205	-0.02082	0.983792	-0.06571	0.953918	0.486346	1	0.207255	0.847421	0.411899	0.562373	0.367008	0.759271	-0.27909	0.694156
Pav_sc0000852.1_g170.1.mk	PavCYCA3;4	-0.08876	0.959371	0.131055	0.992026	0.101103	0.870016	0.183796	0.738387	0.193737	0.777325	0.21981	1	0.189859	0.825694	0.272551	0.65427	0.282492	0.774509	-0.02995	0.966973
Pav_sc0001416.1_g160.1.mk	PavCYCB1;2	-0.12511	0.952229	0.035306	1	-0.05139	0.948456	-0.06656	0.931413	-0.03985	0.970227	0.16042	1	0.073724	0.950403	0.058558	0.950418	0.085261	0.95633	-0.0867	0.914031
Pav_sc0001416.1_g150.1.mk	PavCYCB1;2	-0.09708	0.959371	-0.0287	1	0.017297	0.986832	0.083718	0.905752	-0.09282	0.919271	0.068385	1	0.114381	0.915537	0.180803	0.806035	0.004267	1	0.045996	0.952302
Pav_sc0001288.1_g030.1.mk	PavCYCB1;4	-0.17072	0.933915	0.016822	1	0.187132	0.801711	0.185687	0.797739	-0.0136	0.996332	0.187538	1	0.357848	0.707899	0.356403	0.638712	0.157114	0.923629	0.17031	0.833425
Pav_sc0000414.1_g160.1.mk	PavCYCB2;3	-0.10201	0.95239	0.031994	1	0.005436	0.997293	-0.13233	0.811953	-0.12894	0.859042	0.134006	1	0.107448	0.907971	-0.03032	0.970051	-0.02693	0.985639	-0.02656	0.969504
Pav_sc0002524.1_g040.1.mk	PavCYCB2;3	-0.11395	0.952229	-0.01886	1	0.050415	0.945474	0.086214	0.899974	0.064592	0.946868	0.095092	1	0.164363	0.863625	0.200162	0.774476	0.17854	0.888085	0.069272	0.926012
Pav_sc0000497.1_g230.1.mk	PavCYCB3;1	-0.16515	0.915063	-0.02824	1	-0.00874	0.994965	0.063247	0.926121	0.015374	0.992258	0.136904	1	0.156404	0.865809	0.228394	0.727977	0.180521	0.880344	0.0195	0.9794
Pav_sc0001827.1_g240.1.mk	PavCYCD1;1	-0.40098	0.847719	-0.23191	0.990859	0.123774	0.911367	-0.14705	0.892694	-0.17315	0.898955	0.169069	1	0.52475	0.678106	0.253923	0.829397	0.227829	0.916764	0.355681	0.725607
Pav_sc0001009.1_g390.1.mk	PavCYCD1;1	-0.39714	0.842449	-0.49047	0.886488	0.548817	0.497762	0.376915	0.663674	-0.0433	0.979144	-0.09333	1	0.945962	0.315139	0.77406	0.381334	0.353843	0.845616	1.039291	0.168412
Pav_sc0000257.1_g860.1.mk	PavCYCD2;1	-0.03049	0.992152	-0.21705	0.960576	-0.00641	0.996918	0.015395	0.986548	-0.21855	0.745366	-0.18656	1	0.024081	0.986048	0.045884	0.956541	-0.18806	0.872853	0.21064	0.726805
Pav_sc0000852.1_g400.1.mk	PavCYCD3;1	-0.12825	0.95432	-0.00255	1	-0.12323	0.873738	-0.20187	0.776061	-0.29669	0.711806	0.125695	1	0.005014	1	-0.07362	0.939638	-0.16844	0.915847	-0.12068	0.885447
Pav_sc0000136.1_g070.1.mk	PavCYCD3;2	-0.04148	0.990092	0.09937	0.999982	0.175313	0.809878	0.068949	0.932616	0.223043	0.795413	0.140852	1	0.216795	0.838767	0.110431	0.901717	0.264525	0.843978	0.075943	0.929355
Pav_sc0001807.1_g180.1.mk	PavCYCD3;2	0.033204	0.99207	0.023373	1	-0.04873	0.947942	-0.07639	0.913299	0.161602	0.840703	-0.00983	1	-0.08194	0.940041	-0.1096	0.888055	0.128398	0.928132	-0.07211	0.92432
Pav_co4018799.1_g010.1.mk	PavCYCD3;3	-0.08173	0.969862	-0.13612	0.994317	-0.05112	0.950124	-0.1298	0.858096	0.116135	0.903532	-0.05439	1	0.030611	0.984745	-0.04807	0.961918	0.197867	0.889128	0.084998	0.917562
Pav_sc0003894.1_g020.1.mk	PavCYCD4;2	0.254039	0.761145	0.412557	0.521407	0.142452	0.749523	0.117388	0.79597	-0.04255	0.953197	0.158519	1	-0.11159	0.878326	-0.13665	0.795033	-0.29659	0.666971	-0.27011	0.518602
Pav_sc0002445.1_g250.1.mk	PavCYCD5;1	-0.64613	0.562731	-0.78149	0.421586	-0.58055	0.358553	-0.35865	0.618128	-1.12135	0.038055	-0.13537	1	0.06558	0.962426	0.28748	0.737003	-0.47522	0.654859	0.200946	0.802023
Pav_sc0005024.1_g060.1.mk	PavCYCD5;1	0.025645	0.993061	-0.1003	0.994317	0.257332	0.565281	0.210362	0.646615	-0.18296	0.756333	-0.12595	1	0.231687	0.737032	0.184717	0.748203	-0.2086	0.82253	0.357635	0.420902
Pav_sc0000598.1_g250.1.mk	PavCYCD6;1	-0.53805	0.630082	-0.59537	0.615012	-0.74926	0.157312	-0.9727	0.046048	-1.69382	0.000125	-0.05732	1	-0.21121	0.848196	-0.43465	0.547296	-1.15577	0.053214	-0.15389	0.851467
Pav_sc0002360.1_g870.1.mk	PavCYCD6;1	0.234549	0.83572	0.195151	0.963354	1.015468	0.003551	0.99114	0.004087	-0.02165	0.983265	-0.0394	1	0.780919	0.094889	0.756591	0.081125	-0.2562	0.788058	0.820317	0.040954
Pav_sc0006080.1_g030.1.mk	PavCYCH;1	-0.1116	0.810632	-0.13498	0.840818	-0.5786	3.53E-05	-0.64202	2.51E-06	-0.50643	0.000425	-0.02338	1	-0.46701	0.005771	-0.53042	0.000776	-0.39483	0.033404	-0.44363	0.00573
Pav_sc0000893.1_g870.1.mk	PavCYCJ18	0.120245	0.968168	0.124565	1	-0.28384	0.763335	0.094733	0.93188	-0.11946	0.933276	0.004321	1	-0.40408	0.760473	-0.02551	0.988444	-0.23971	0.908645	-0.4084	0.661941
Pav_sc0000146.1_g490.1.mk	PavCYCP1;1	-0.48943	0.611998	-0.28476	0.92549	-0.67536	0.144735	-0.63724	0.165244	-0.05875	0.954732	0.20467	1	-0.18593	0.848421	-0.1478	0.85042	0.430689	0.648456	-0.3906	0.500151
Pav_sc0000405.1_g120.1.mk	PavCYCP2;1	0.201464	0.922306	-0.16949	0.992756	0.658474	0.266266	-0.05247	0.954916	-0.62738	0.329888	-0.37096	1	0.45701	0.637668	-0.25394	0.767813	-0.82884	0.292808	0.827966	0.173171
Pav_sc0000026.1_g130.1.mk	PavCYCP3;2	-1.1576	0.436586	-0.71701	0.828769	-1.3961	0.099999	-1.01952	0.256082	-1.35629	0.144825	0.440595	1	-0.2385	0.903571	0.138084	0.930675	-0.19869	0.941039	-0.6791	0.529564
Pav_sc0000108.1_g1100.1.mk	PavCYCP4;1	1.397818	0.917892	2.432186	0.909062	3.910391	0.34799	2.476291	0.576668	3.21925	0.524258	1.034368	1	1	1	1	1	1	1	1	1
Pav_sc0001576.1_g280.1.mk	PavCYCP4;1	0.88811	0.557038	0.420053	0.950196	-0.13793	0.907791	0.344141	0.736336	1.308066	0.112778	-0.46806	1	-1.02604	0.341445	-0.54397	0.631023	0.419956	0.840584	-0.55798	0.578919
Pav_sc0005664.1_g070.1.mk	PavCYCP4;1	1.853831	0.04287	1.253871	0.332625	3.757303	1.79E-08	3.66345	4.17E-08	4.598373	1.87E-12	-0.59996	1	1.903472	0.041936	1.809618	0.04226	2.744541	0.000732	2.503432	0.001457
Pav_sc0002208.1_g570.1.mk	PavCYCT1;3	-0.08604	0.811315	-0.12635	0.730615	-0.10181	0.509041	-0.00896	0.970029	-0.1489	0.349803	-0.04031	1	-0.01576	0.962778	0.077076	0.697427	-0.06286	0.857872	0.024547	0.90991
Pav_sc0000700.1_g920.1.mk	PavRCY1.2	0.05989	0.933637	0.090967	0.962866	0.108908	0.633864	0.156659	0.443803	0.236634	0.265434	0.031077	1	0.049017	0.908958	0.096769	0.731715	0.176744	0.62669	0.01794	0.953569
Pav_sc0001583.1_g380.1.mk	PavCyclin family	0.024583	0.965154	-0.02389	1	0.13762	0.338934	0.098952	0.515994	-0.04701	0.841034	-0.04847	1	0.113037	0.609981	0.074369	0.710222	-0.07159	0.832707	0.161507	0.28399
Pav_sc0000700.1_g350.1.mk	PavCyclin family	-0.01782	1	0.546097	0.950184	0.66591	0.591691	0.25607	0.860016	0.675181	0.652434	0.563913	1	0.683726	0.713384	0.273886	0.870753	0.692997	0.773776	0.119813	0.945531
Pav_sc0003169.1_g100.1.mk	PavCyclin family	0.184082	0.61342	0.163252	0.750562	0.294046	0.082558	0.28482	0.087949	0.18847	0.382601	-0.02083	1	0.109964	0.73691	0.100738	0.702492	0.004388	0.997169	0.130794	0.562913
Pav_sc0000558.1_g520.1.mk	PavCyclin family	0.185739	0.691904	0.014061	1	0.104391	0.690983	0.088043	0.742503	0.099098	0.761351	-0.17168	1	-0.08135	0.848796	-0.0977	0.7586	-0.08664	0.87903	0.09033	0.76067
Pav_sc0000893.1_g590.1.mk	PavSDS	1	1	1	1	1	1	1	1	1	1	-1.5457	1	1	1	1	1	1	1	1	1
Pav_sc0000259.1_g510.1.mk	PavCyclin-like fa	-0.00257	1	0.058806	1	0.447644	0.2115	0.391792	0.278905	0.527898	0.163978	0.061371	1	0.450209	0.354176	0.394357	0.372676	0.530464	0.299048	0.388838	0.335444
Pav_sc0001338.1_g020.1.mk	PavCyclin-like fa	0.246956	0.373506	0.235851	0.444524	0.12855	0.532767	0.087933	0.690393	0.204687	0.325526	-0.01111	1	-0.11841	0.708928	-0.15902	0.494305	-0.04227	0.937445	-0.1073	0.646383
Pav_sc0001009.1_g190.1.mk	PavCyclin-relate	-0.15344	0.658205	-0.0286	1	-0.21291	0.184125	-0.2917	0.045459	-0.15482	0.443853	0.124841	1	-0.05946	0.860462	-0.13825	0.515674	-0.00137	1	-0.1843	0.30909

70 % vs GA3 500 mg/L		tOH 70 % vs O.P. 7 DA		0 mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 7 D		3 500 mg/L vs O.P. 7 D		N.C. 7 vs 14 DAT		EtOH 70% 7 vs 14 DAT		A3 300 mg/L 7 vs 14 DA		A3 500 mg/L 7 vs 14 D		O.P. 7 vs 14 DAT		N.C. vs EtOH 14 DAT		. vs GA3 300 mg/L 14	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
-0.01612	0.985829	-0.05523	0.973213	0.012034	1	-0.02707	0.98272	-0.0391	0.978058	0.344007	0.761687	0.501457	0.483408	2.18065	3.28E-07	2.153859	4.76E-07	1.176277	0.01731	0.299649	0.917586	1.950684	1.54E-05
0.374593	0.288043	0.136549	0.845593	0.055885	1	-0.18216	0.70989	-0.23804	0.643217	-0.12751	0.87657	0.216014	0.654559	0.294185	0.376713	0.237637	0.501727	0.560614	0.084996	-0.05031	0.992858	0.346565	0.390343
-0.00072	0.999964	-0.38858	0.641512	-0.03372	1	-0.42158	0.510565	-0.38786	0.597045	0.46704	0.585481	0.492527	0.441895	1.406418	0.000537	1.456459	0.000326	1.329685	0.002121	0.398129	0.875223	1.345021	0.002352
-0.11541	0.836371	-0.07925	0.933373	0.041394	1	0.077554	0.909237	0.036161	0.968366	0.342594	0.610522	0.495973	0.27599	1.287907	2.25E-05	1.198292	9.83E-05	0.596395	0.107976	0.365979	0.84689	1.00111	0.003373
-0.07445	0.930923	-0.11934	0.927744	0.204644	1	0.159753	0.854386	-0.04489	0.97216	0.613406	0.446906	0.765437	0.210903	1.609054	0.000166	1.171661	0.008377	0.278704	0.666704	0.638377	0.763423	1.202904	0.014882
0.052741	0.940871	0.062682	0.956803	0.082692	1	0.092633	0.903094	0.009941	0.993121	0.578722	0.337447	0.479382	0.370747	1.281463	0.000291	0.915087	0.012825	0.308969	0.528864	0.12047	0.97428	0.8926	0.035371
-0.10186	0.897302	-0.07516	0.9549	-0.01517	1	0.011537	0.993508	0.026703	0.984938	0.377257	0.693486	0.519808	0.410561	1.715424	1.68E-05	1.745177	1.3E-05	1.047197	0.022111	0.302971	0.908326	1.411891	0.001319
0.112418	0.877695	-0.06412	0.959101	0.066422	1	-0.11011	0.893527	-0.17654	0.840932	0.279255	0.777975	0.364477	0.57446	1.861293	4.44E-07	1.795159	1.24E-06	0.975554	0.023462	0.153607	0.969211	1.696419	1.26E-05
0.168865	0.829226	-0.03042	0.988322	-0.00144	1	-0.20073	0.813938	-0.19929	0.843066	0.314949	0.783317	0.504356	0.474909	1.65853	0.000131	1.788844	3.4E-05	1.00373	0.04743	0.376946	0.889829	1.701428	0.000201
-0.16433	0.765763	-0.16093	0.852877	-0.13777	1	-0.13438	0.839046	0.003392	0.999273	0.318169	0.683883	0.242859	0.687096	1.460889	8.11E-06	1.612209	6.65E-07	0.919635	0.013258	0.058696	0.993801	1.250168	0.000418
0.105071	0.883136	0.083449	0.944106	0.035799	1	0.014177	0.992039	-0.02162	0.987094	0.25938	0.79184	0.434256	0.465989	1.675407	3.76E-06	1.466455	6.78E-05	0.681768	0.129847	0.269968	0.91192	1.580391	3.49E-05
0.09149	0.895986	0.043617	0.973962	0.071991	1	0.024117	0.980237	-0.04787	0.963686	0.358226	0.663321	0.553754	0.29831	1.743291	6.82E-07	1.802013	2.89E-07	0.859646	0.037676	0.332432	0.878777	1.541469	3.49E-05
0.084854	0.944649	0.05876	0.979857	-0.27083	1	-0.29692	0.796059	-0.02609	0.989883	-0.07344	0.979295	-0.41395	0.701924	-0.7472	0.284278	-0.70132	0.324742	-0.63302	0.428371	-0.17144	0.980079	-0.14901	0.908764
0.86739	0.236883	0.447173	0.730047	-0.1719	1	-0.59212	0.522005	-0.42022	0.716017	0.500344	0.721705	-0.54438	0.578956	0.042546	0.96946	-0.31262	0.702105	1.249951	0.067197	-1.13805	0.611348	0.488164	0.615461
0.232443	0.673208	-0.00151	1	0.021803	1	-0.21215	0.746199	-0.23395	0.748684	-0.20264	0.839857	-0.2516	0.691865	0.807233	0.035309	0.215385	0.663251	0.656436	0.129609	-0.23552	0.917586	1.03395	0.01121
-0.19932	0.786487	-0.29413	0.774418	-0.07864	1	-0.17345	0.841188	-0.09482	0.935157	0.096584	0.955287	0.446831	0.538415	0.568956	0.261896	0.603571	0.231506	0.623841	0.260897	0.475942	0.858968	0.477386	0.471669
-0.03042	0.972188	0.123674	0.924202	-0.10636	1	0.04773	0.964187	0.154095	0.882445	0.283436	0.80537	0.254514	0.754014	0.683909	0.154224	0.689024	0.152144	0.447379	0.438067	0.111929	0.982892	0.617268	0.300525
-0.09976	0.892235	0.138229	0.90015	-0.02766	1	0.210337	0.767593	0.237994	0.763746	-0.07746	0.958718	-0.02839	0.973505	-0.05636	0.929855	-0.31744	0.514747	-0.48412	0.32605	0.039242	1	-0.06084	0.94451
0.006318	0.994181	0.252254	0.803826	-0.07868	1	0.167257	0.839046	0.245936	0.779311	-0.08468	0.958796	0.216122	0.790162	-0.0752	0.911964	-0.36252	0.493396	-0.56392	0.290246	0.246414	0.929508	0.040093	0.970969
-0.29517	0.438383	-0.45511	0.315725	-0.02506	1	-0.18501	0.705963	-0.15994	0.785544	0.06415	0.952345	-0.03817	0.950728	-0.17813	0.626411	-0.25958	0.450934	0.05613	0.912777	0.056194	0.989451	-0.35387	0.378615
0.422846	0.516577	-0.33986	0.715639	0.2219	1	-0.5408	0.411276	-0.7627	0.246468	0.137021	0.931049	-0.05913	0.950758	-0.44126	0.412624	-0.64976	0.211945	1.356228	0.011331	-0.33152	0.90723	-0.5127	0.431045
0.310665	0.470963	-0.08265	0.930444	-0.04697	1	-0.44029	0.323962	-0.39332	0.439657	-0.51354	0.327437	-0.51183	0.247262	-0.29457	0.441795	-0.64977	0.047613	0.245883	0.577646	-0.12424	0.96826	0.450653	0.288229
-0.37733	0.55282	-1.09845	0.067596	-0.22344	1	-0.94456	0.08757	-0.72112	0.269491	-0.56741	0.513018	-0.34361	0.660826	1.229065	0.006643	0.890429	0.060275	1.895752	2E-05	0.166476	0.970429	1.585262	0.000723
0.795989	0.039011	-0.2168	0.782581	-0.02433	1	-1.03712	0.005684	-1.01279	0.01004	0.00354	1	0.051016	0.944279	0.12706	0.792431	0.062148	0.908563	1.165012	0.000811	0.008077	1	0.904438	0.017163
-0.50704	0.000916	-0.37145	0.046022	-0.06342	1	0.072177	0.783635	0.135593	0.590952	-0.20424	0.436008	-0.15238	0.507234	0.232373	0.133874	0.338153	0.020062	0.019019	0.945639	0.028473	0.989451	-0.03039	0.92233
-0.02983	0.980501	-0.24403	0.875966	0.378572	1	0.164379	0.893527	-0.21419	0.879338	0.187714	0.926389	0.341836	0.761562	1.35584	0.034669	2.103241	0.002701	0.551409	0.496673	0.158442	0.982396	0.764042	0.401656
-0.35247	0.525906	0.226019	0.814701	0.038122	1	0.616614	0.255068	0.578492	0.336327	-0.29522	0.767245	-0.17912	0.820132	-0.41746	0.371142	-0.55805	0.209513	-0.99446	0.022343	0.320772	0.896829	-0.30817	0.637842
0.117017	0.894133	-0.45788	0.612312	-0.71095	1	-1.28585	0.017398	-0.5749	0.437981	-0.73265	0.354552	-0.78159	0.214996	-2.02934	4.49E-06	-0.5096	0.349576	0.561396	0.340989	-0.41989	0.875223	-0.83967	0.132151
-0.30251	0.807488	-0.63928	0.670792	0.376585	1	0.039814	0.984512	-0.33677	0.835804	-1.02179	0.436008	-0.65567	0.590994	-2.03057	0.004209	-2.35294	0.000809	-1.53934	0.058704	0.80672	0.851588	-1.24727	0.168344
1	1	1	1	-1.4341	1	1	1	1	1	5.433759	0.361874	1	1	2.845891	0.519822	1.119976	0.817326	1	1	-2.4305	0.917383	1	1
-0.07591	0.954395	0.888013	0.451636	0.482068	1	1.445992	0.079435	0.963925	0.35272	0.353439	0.852828	-1.43807	0.087574	-0.92532	0.20529	-1.75916	0.007627	-1.79897	0.013332	-2.25957	0.060479	-2.30479	0.000884
2.409579	0.001861	3.344501	8.4E-06	-0.09385	1	0.841069	0.453185	0.934923	0.433612	1.717975	0.072297	1.020069	0.3288	0.000305	1	-0.14175	0.9032	-0.15825	0.90689	-1.29787	0.657628	0.185802	0.906329
0.117388	0.437544	-0.02255	0.948768	0.09284	1	-0.0471	0.826339	-0.13994	0.441865	-0.10658	0.670791	-0.08167	0.672789	0.191936	0.11711	0.164815	0.201297	0.049922	0.779284	-0.0154	0.9991	0.28275	0.027571
0.065692	0.804878	0.145667	0.646763	0.047751	1	0.127726	0.621378	0.079975	0.815539	0.155753	0.656319	0.129944	0.62733	0.167735	0.36539	0.167267	0.37379	-0.04892	0.8525	0.005268	1	0.060999	0.848024
0.122839	0.414056	-0.02312	0.947883	-0.03867	1	-0.18463	0.2229	-0.14596	0.419915	-0.01562	0.973735	-0.03668	0.876088	0.004973	0.984101	0.031335	0.856361	0.159854	0.25429	-0.06953	0.924222	0.133627	0.414535
-0.29003	0.854169	0.129084	0.964709	-0.40984	1	0.009271	0.998889	0.419111	0.830293	0.017987	0.998968	-0.59559	0.692971	-1.13641	0.238851	-1.26355	0.160585	-0.97656	0.383744	-0.04967	1	-0.47067	0.747588
0.121568	0.5716	0.025219	0.958747	-0.00923	1	-0.10558	0.683448	-0.09635	0.750079	0.094504	0.810633	0.028652	0.928373	-0.18201	0.290112	0.073108	0.72972	0.094378	0.670084	-0.08668	0.930139	-0.16655	0.449531
0.073983	0.79884	0.085037	0.845574	-0.01635	1	-0.00529	0.993324	0.011054	0.985052	-0.34355	0.181663	-0.40632	0.056358	-0.18277	0.36966	-0.25262	0.189776	-0.33556	0.093323	-0.23445	0.784955	0.079436	0.810575
1	1	1	1	0.21817	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	-0.73829	0.968195	1	1
0.332986	0.397453	0.469093	0.336091	-0.05585	1	0.080255	0.90168	0.136106	0.841796	0.29651	0.6517	0.45379	0.292039	-0.08133	0.856254	-0.19146	0.630293	0.26242	0.533789	0.218651	0.908326	0.072366	0.909976
-0.14792	0.465213	-0.03116	0.946994	-0.04062	1	0.076137	0.782361	0.116755	0.680134	-0.0036	0.998152	0.104444	0.691573	-0.16057	0.357471	-0.09205	0.64175	-0.30995	0.068921	0.096943	0.918747	-0.27537	0.139045
-0.26309	0.09506	-0.12621	0.644578	-0.07879	1	0.058088	0.821748	0.136879	0.558994	0.176542	0.490472	-0.05681	0.835191	0.263946	0.063978	0.472324	0.000337	0.187686	0.265911	-0.10851	0.897724	0.027943	0.925028

. vs GA3 500 mg/L 14		N.C. vs O.P. 14 DAT		40 % vs GA3 300 mg/L		40 % vs GA3 500 mg/L		DH 140 % vs O.P. 14 D		mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 14		3 500 mg/L vs O.P. 14		N.C. 14 vs 21 DAT		EtOH 70% 14 vs 21 DA		3 300 mg/L 14 vs 21 D		3 500 mg/L 14 vs 21 D	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
1.935927	1.83E-05	0.919242	0.168188	1.651035	0.000432	1.636278	0.000495	0.619594	0.303197	-0.01476	1	-1.03144	0.158435	-1.01668	0.167342	1.044489	0.068496	0.932642	0.228308	2.113321	1.79E-06	1.854557	2.53E-05
0.345902	0.392688	0.430835	0.369276	0.396879	0.283099	0.396216	0.289015	0.481149	0.174646	-0.00066	1	0.08427	0.932712	0.084933	0.933243	0.393285	0.315457	-0.02521	0.978166	0.455482	0.134712	0.29846	0.347864
1.361341	0.001939	0.846707	0.164488	0.946892	0.047281	0.963212	0.043783	0.448578	0.440853	0.01632	1	-0.49831	0.600001	-0.51463	0.578715	1.117843	0.02896	0.600178	0.439846	1.576607	0.000144	1.833848	8.03E-06
0.952889	0.005736	0.387152	0.525569	0.635131	0.094439	0.58691	0.133997	0.021173	0.978187	-0.04822	1	-0.61396	0.261393	-0.56574	0.337205	0.846661	0.031367	0.572209	0.31415	1.379697	1.02E-05	1.248509	5.86E-05
0.970154	0.065014	0.032306	0.990064	0.564527	0.351385	0.331777	0.642581	-0.60607	0.299822	-0.23275	1	-1.1706	0.075994	-0.93785	0.200169	0.812457	0.163538	0.408054	0.667773	1.459581	0.000944	1.995822	3.67E-06
0.608916	0.194964	0.012739	0.997834	0.77213	0.072596	0.488446	0.322272	-0.10773	0.872478	-0.28368	1	-0.87986	0.126418	-0.59618	0.395957	0.680374	0.155186	0.326207	0.676536	1.699086	1.16E-05	2.50193	2.28E-10
1.426478	0.001116	0.755202	0.241631	1.10892	0.016355	1.123507	0.014889	0.452231	0.43824	0.014587	1	-0.65669	0.411708	-0.67128	0.412975	1.057362	0.041496	0.996683	0.139	1.755491	2.91E-05	1.671127	6.2E-05
1.696706	1.26E-05	0.700566	0.250759	1.542812	0.000104	1.5431	0.000105	0.54696	0.289947	0.000288	1	-0.99585	0.09917	-0.99614	0.100189	1.076809	0.025477	1.033997	0.084396	1.684941	8.59E-06	1.53429	4.61E-05
1.830298	4.95E-05	0.845895	0.214634	1.324483	0.006147	1.453352	0.002211	0.468949	0.459024	0.12887	1	-0.85553	0.266313	-0.9844	0.179064	1.164504	0.036454	0.934411	0.224561	2.37672	4.64E-08	2.173448	5.62E-07
1.26372	0.000347	0.574538	0.297343	1.191472	0.00088	1.205025	0.000761	0.515842	0.245778	0.013552	1	-0.67563	0.249615	-0.68918	0.249682	1.06933	0.01057	0.919451	0.078332	1.205033	0.000429	1.586132	2.54E-06
1.407237	0.000319	0.600928	0.341723	1.310423	0.000993	1.137269	0.005475	0.33096	0.556251	-0.17315	1	-0.97946	0.093712	-0.80631	0.203905	1.166747	0.011848	0.923907	0.12649	1.552438	2.85E-05	1.705795	3.02E-06
1.672182	6.07E-06	0.681941	0.229509	1.209037	0.00212	1.33975	0.000546	0.349509	0.514387	0.130712	1	-0.85953	0.153347	-0.99024	0.085204	1.028626	0.02403	0.800002	0.203383	1.376972	0.000276	1.719564	6.09E-06
-0.37396	0.732723	-0.33175	0.842941	0.022431	0.988765	-0.20251	0.860502	-0.16031	0.888459	-0.22495	1	-0.18274	0.93224	0.042208	0.989307	-0.49042	0.611894	0.13107	0.937627	0.145506	0.865424	0.060343	0.949319
-0.03891	0.982568	1.10345	0.2285	1.626216	0.011673	1.099144	0.127163	2.241501	0.000355	-0.52707	1	0.615286	0.675747	1.142357	0.279401	-0.41281	0.671827	0.697068	0.546806	-0.57841	0.398057	-0.74853	0.240224
0.463905	0.36958	0.671008	0.234803	1.269468	0.000901	0.699423	0.11126	0.906526	0.030532	-0.57004	1	-0.36294	0.699372	0.207103	0.861692	0.171492	0.795741	0.60224	0.356898	0.489647	0.249739	0.65164	0.091086
0.433364	0.53332	0.358818	0.735394	0.001444	1	-0.04258	0.969731	-0.11712	0.889052	-0.04402	1	-0.11857	0.940913	-0.07455	0.966131	0.551066	0.390086	0.422342	0.655853	0.940476	0.038652	0.989699	0.025403
0.516019	0.418677	0.428468	0.653453	0.505338	0.408237	0.404089	0.540459	0.316539	0.638086	-0.10125	1	-0.1888	0.892456	-0.08755	0.957308	0.781562	0.178384	0.80866	0.296277	1.275742	0.003071	1.457244	0.000524
-0.34958	0.570492	-0.27827	0.773394	-0.10009	0.893198	-0.38882	0.498079	-0.31751	0.58283	-0.28874	1	-0.21742	0.853431	0.071314	0.960956	0.142383	0.846457	0.076483	0.94352	0.461728	0.284943	0.807153	0.037078
-0.32591	0.649137	-0.28138	0.79575	-0.20632	0.780243	-0.57233	0.316762	-0.52779	0.35808	-0.36601	1	-0.32147	0.777024	0.044535	0.981219	0.290915	0.67861	-0.00181	1	0.382652	0.440427	0.830154	0.052161
-0.46038	0.207108	-0.30461	0.600658	-0.41006	0.266062	-0.51657	0.134186	-0.36081	0.34292	-0.10651	1	0.049253	0.961368	0.155766	0.862689	-0.13176	0.799871	0.140208	0.841791	-0.11165	0.763425	-0.22511	0.484807
-0.4993	0.454355	0.743985	0.406337	-0.18119	0.815401	-0.16779	0.836051	1.0755	0.07081	0.013401	1	1.256687	0.101591	1.243286	0.109845	-0.29972	0.690589	0.721948	0.409812	0.326367	0.545054	0.325877	0.539762
0.048482	0.950986	0.550817	0.265177	0.574893	0.128813	0.172723	0.747594	0.675058	0.068107	-0.40217	1	0.100165	0.928336	0.502335	0.408894	0.118116	0.841488	0.259203	0.701337	0.226404	0.554636	0.713562	0.022267
1.023191	0.053164	1.307393	0.022461	1.418786	0.003016	0.856716	0.116826	1.140918	0.027382	-0.56207	1	-0.27787	0.836567	0.284202	0.839247	0.905215	0.120509	0.319094	0.756242	1.01508	0.031104	1.33544	0.002619
0.815199	0.037587	0.905274	0.040009	0.896361	0.016101	0.807121	0.035219	0.897196	0.019215	-0.08924	1	0.000836	1	0.090075	0.942822	0.220457	0.695882	0.419493	0.524418	0.427186	0.254368	0.513532	0.148845
0.011969	0.976737	-0.17157	0.534302	-0.05887	0.81759	-0.0165	0.96167	-0.20004	0.289023	0.042363	1	-0.14118	0.693259	-0.18354	0.553029	0.063328	0.810253	0.207291	0.441314	-0.05891	0.754815	-0.02662	0.896701
1.890015	0.017398	0.12399	0.955175	0.6056	0.521464	1.731573	0.031487	-0.03445	0.981927	1.125974	1	-0.64005	0.688612	-1.76603	0.112311	0.196129	0.868155	0.938899	0.443144	0.915541	0.248496	-0.61379	0.490056
-0.41063	0.494978	-0.26855	0.789419	-0.62894	0.208887	-0.73141	0.130214	-0.58933	0.251363	-0.10247	1	0.039612	0.982659	0.14208	0.921245	-0.0661	0.936884	0.041758	0.972911	-0.00939	0.992367	0.24925	0.600307
-0.03089	0.981963	0.465209	0.637065	-0.41978	0.522972	0.389005	0.576194	0.885104	0.111971	0.808786	1	1.304884	0.043675	0.496099	0.652764	-0.02732	0.981012	0.497554	0.581828	0.955316	0.036728	-0.10559	0.865532
-1.19306	0.190725	-0.71623	0.63857	-2.05399	0.007606	-1.99978	0.009908	-1.52295	0.071881	0.054214	1	0.531041	0.77953	0.476827	0.821895	-0.91355	0.363899	-0.69883	0.644448	0.124682	0.905441	0.140077	0.88756
1	1	1	1	1	1	-0.80481	0.908491	1	1	-3.16002	1	1	1	1	1	1	1	1	1	-2.5073	0.565693	2.995089	0.461781
-2.65657	6.97E-05	-1.73245	0.048461	-0.04522	0.975735	-0.397	0.719077	0.527118	0.590301	-0.35178	1	0.572342	0.735967	0.92412	0.49292	-1.92326	0.018465	-0.15136	0.932788	-1.61836	0.011947	-1.24697	0.056084
-0.0501	0.981803	0.868316	0.54849	1.483669	0.081121	1.247765	0.165032	2.166183	0.00755	-0.2359	1	0.682514	0.718678	0.918418	0.573662	0.330367	0.805451	1.31842	0.30255	1.297458	0.100975	1.288707	0.093044
0.348468	0.003942	0.093636	0.717393	0.298154	0.01572	0.363872	0.002304	0.10904	0.496903	0.065719	1	-0.18911	0.360567	-0.25483	0.168332	-0.05736	0.769	-0.11079	0.627226	-0.51643	8.92E-07	-0.47777	7.12E-06
0.108282	0.694383	-0.02793	0.962498	0.055731	0.847899	0.103014	0.695806	-0.0332	0.91537	0.047283	1	-0.08893	0.852093	-0.13621	0.748468	-0.08557	0.757304	-0.02161	0.96128	-0.40313	0.009544	-0.40562	0.008167
0.121321	0.476735	0.103878	0.682861	0.203158	0.139927	0.190852	0.179789	0.173409	0.23515	-0.01231	1	-0.02975	0.941126	-0.01744	0.968729	-0.00486	0.98785	-0.00025	1	0.195422	0.101789	0.089221	0.499828
-1.00765	0.375153	-0.30155	0.903456	-0.421	0.761745	-0.95798	0.391292	-0.25189	0.867507	-0.53698	1	0.169114	0.953262	0.706092	0.73631	1	1	0.194448	0.932268	-0.64874	0.485678	0.427884	0.659241
0.079342	0.780236	0.004262	0.999012	-0.07987	0.752843	0.166024	0.442952	0.090944	0.704513	0.245892	1	0.170812	0.622686	-0.07508	0.882606	-0.37439	0.043779	-0.40968	0.065538	-0.72556	1.77E-07	-0.96896	8.32E-13
-0.00676	0.992973	-0.07865	0.875459	0.313884	0.129331	0.227686	0.323835	0.1558	0.530696	-0.0862	1	-0.15808	0.71851	-0.07189	0.90479	-0.10762	0.709284	0.146862	0.690169	-0.45455	0.007041	-0.31363	0.071372
1	1	1	1	1	1	1	1	1	1	-1.10051	1	1	1	1	1	1	1	1	1	1	1	1	1
-0.09361	0.885134	0.496374	0.319128	-0.14629	0.780857	-0.31226	0.478878	0.277723	0.535371	-0.16598	1	0.424008	0.49518	0.589985	0.272727	0.092093	0.874696	-0.14879	0.840987	0.101973	0.80301	0.172427	0.639441
-0.24747	0.197553	-0.34862	0.08817	-0.37232	0.024837	-0.34441	0.042849	-0.44556	0.006669	0.0279	1	-0.07324	0.874442	-0.10114	0.818418	0.087899	0.733433	0.059972	0.874514	0.130798	0.452721	0.217571	0.165247
0.157531	0.43108	0.009771	0.990407	0.136455	0.487178	0.266042	0.104063	0.118283	0.553558	0.129587	1	-0.01817	0.973196	-0.14776	0.650454	0.007301	0.983525	0.043132	0.904074	0.03701	0.844535	-0.21315	0.134768

O.P. 14 vs 21 DAT		N.C. vs EtOH 21 DAT		. vs GA3 300 mg/L 21 I		. vs GA3 500 mg/L 21 I		N.C. vs O.P. 21 DAT		10 % vs GA3 300 mg/L		10 % vs GA3 500 mg/L		OH 210 % vs O.P. 21 D		mg/L vs GA3 500 mg/L		300 mg/L vs O.P. 21		500 mg/L vs O.P. 21		N.C. 21 vs 28 DAT	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
1.77411	0.000265	0.187802	1	3.019516	5.75E-13	2.745995	7.44E-11	1.648863	0.000282	2.831714	1.61E-11	2.558193	1.57E-09	1.461061	0.00129	-0.27352	1	-1.37065	0.005481	-1.09713	0.027265	1.245584	0.01027
0.443141	0.279158	-0.46881	1	0.408763	0.207376	0.251078	0.4982	0.480692	0.149674	0.877571	0.001444	0.719886	0.013385	0.9495	0.000719	-0.15768	1	0.071929	0.872967	0.229614	0.525111	-0.77293	0.009258
0.955284	0.070203	-0.11954	1	1.803785	7.76E-06	2.077346	2.66E-07	0.684148	0.166667	1.923321	1.32E-06	2.196883	4.01E-08	0.803684	0.077462	0.273562	1	-1.11964	0.015395	-1.3932	0.002024	0.705098	0.141039
0.916807	0.014207	0.091527	1	1.534146	4.32E-07	1.354736	1.17E-05	0.457298	0.242305	1.44262	2.2E-06	1.263209	5.24E-05	0.365771	0.343485	-0.17941	1	-1.07685	0.001624	-0.89744	0.009082	0.608436	0.090314
1.081271	0.046072	0.233974	1	1.850027	1.42E-05	2.153519	4.17E-07	0.301121	0.642341	1.616053	0.00019	1.919545	8.9E-06	0.067147	0.928911	0.303491	1	-1.54891	0.00091	-1.8524	5.81E-05	0.218728	0.725046
1.009802	0.020976	-0.2337	1	1.911312	3.21E-07	2.430472	4.59E-10	0.342167	0.498094	2.145008	5.21E-09	2.664169	5.02E-12	0.575864	0.169317	0.519161	1	-1.56914	0.000153	-2.08831	8.58E-07	0.460078	0.304748
1.886456	2.66E-05	0.242291	1	2.110019	1.7E-07	2.040243	5.61E-07	1.584296	0.00021	1.867728	4.99E-06	1.797952	1.48E-05	1.342005	0.001824	-0.06978	1	-0.52572	0.330844	-0.45595	0.395404	0.902024	0.053509
1.639166	7.42E-05	0.110795	1	2.304551	1.48E-10	2.154188	2.98E-09	1.262924	0.001532	2.193756	1.17E-09	2.043393	2.11E-08	1.152129	0.003571	-0.15036	1	-1.04163	0.014321	-0.89126	0.035931	0.999339	0.017917
1.789344	0.000195	0.146852	1	2.913644	2.68E-12	2.839242	1.34E-11	1.470734	0.001328	2.766792	3.25E-11	2.69239	1.5E-10	1.323882	0.003614	-0.0744	1	-1.44291	0.002968	-1.36851	0.004577	1.193505	0.013445
1.283827	0.000658	-0.09118	1	1.385871	3.28E-05	1.780522	6.87E-08	0.789034	0.038097	1.477054	7.27E-06	1.871706	1.13E-08	0.880218	0.014209	0.394652	1	-0.59684	0.139133	-0.99149	0.008669	0.756374	0.048214
1.757561	9.66E-06	0.027127	1	1.966082	3.05E-08	1.946284	5.36E-08	1.191742	0.002373	1.938955	4.66E-08	1.919157	8.12E-08	1.164615	0.002437	-0.0198	1	-0.77434	0.072779	-0.75454	0.073962	1.017012	0.013264
1.652786	3.44E-05	0.103807	1	1.889815	1.37E-07	2.36312	8.36E-11	1.306101	0.000669	1.786008	7.11E-07	2.259313	6.11E-10	1.202293	0.001587	0.473305	1	-0.58371	0.206426	-1.05702	0.014073	1.130761	0.004825
-0.42243	0.699867	0.45005	1	0.486918	0.531342	0.176809	0.852802	-0.26376	0.787711	0.036868	0.975898	-0.27324	0.756896	-0.71381	0.32104	-0.31011	1	-0.75068	0.297581	-0.44057	0.56457	0.207336	0.816975
0.040039	0.985167	-0.02818	1	0.322565	0.690601	-0.37463	0.64406	1.556298	0.012914	0.35074	0.657289	-0.34646	0.673149	1.584473	0.008854	-0.6972	1	1.233733	0.058315	1.930929	0.001469	-0.02216	0.985541
0.878223	0.066441	0.195231	1	1.352105	0.000182	0.944054	0.014279	1.377739	0.000238	1.156875	0.001697	0.748823	0.063376	1.182509	0.001729	-0.40805	1	0.025634	0.972152	0.433686	0.339539	-0.41817	0.336245
0.206632	0.822571	0.347218	1	0.866796	0.067952	0.871997	0.072698	0.014384	0.991329	0.519578	0.318874	0.524779	0.33003	-0.33283	0.570353	0.005201	1	-0.85241	0.083764	-0.85761	0.073962	0.800869	0.109524
0.559609	0.39524	0.139028	1	1.111448	0.012867	1.191701	0.008052	0.206516	0.766389	0.972421	0.031298	1.052673	0.021417	0.067488	0.927342	0.080253	1	-0.90493	0.060858	-0.98519	0.035186	0.60487	0.241376
-0.15265	0.85444	-0.02666	1	0.258501	0.615042	0.315189	0.535149	-0.5733	0.21663	0.28516	0.566824	0.341848	0.490739	-0.54664	0.216564	0.056688	1	-0.8318	0.048293	-0.88849	0.029935	0.465215	0.317178
-0.02954	0.984086	-0.04631	1	0.131829	0.838518	0.213327	0.727768	-0.60184	0.241086	0.178138	0.768066	0.259636	0.657147	-0.55553	0.258999	0.081497	1	-0.73367	0.122033	-0.81516	0.073762	0.38771	0.46649
-0.62386	0.074246	0.328166	1	-0.33376	0.311526	-0.55373	0.068393	-0.79671	0.005547	-0.66192	0.020998	-0.88189	0.001506	-1.12488	3.19E-05	-0.21997	1	-0.46296	0.137616	-0.24298	0.470774	0.052296	0.909297
-1.10383	0.085167	0.690155	1	0.113388	0.874432	0.126298	0.860713	-0.06012	0.946698	-0.57677	0.304795	-0.56386	0.338678	-0.75027	0.161273	0.01291	1	-0.17351	0.793446	-0.18642	0.76924	0.694229	0.212608
-0.77702	0.041544	0.016846	1	0.55894	0.100819	0.643928	0.058259	-0.34432	0.391503	0.542094	0.108762	0.627083	0.065255	-0.36117	0.3291	0.084988	1	-0.90326	0.005919	-0.98825	0.002176	1.033092	0.001795
1.003015	0.086477	-0.41965	1	1.695127	0.000113	1.453416	0.001377	1.405193	0.002679	2.114772	5.9E-07	1.873061	1.47E-05	1.824838	3.58E-05	-0.24171	1	-0.28993	0.64869	-0.04822	0.952708	0.826244	0.104619
-0.0778	0.926107	0.207114	1	1.111167	0.000698	1.108274	0.000851	0.607015	0.115857	0.904054	0.007123	0.90116	0.008999	0.399901	0.319729	-0.00289	1	-0.50415	0.194942	-0.50126	0.186117	1.703247	1.44E-06
0.005706	0.994573	0.172436	1	-0.15263	0.376103	-0.07798	0.70329	-0.22919	0.172685	-0.32507	0.026935	-0.25041	0.119156	-0.40163	0.005594	0.074655	1	-0.07656	0.696982	-0.15122	0.369936	0.194999	0.252304
0.477963	0.67422	0.901211	1	1.483454	0.043257	1.080098	0.157422	0.405823	0.665277	0.582243	0.532676	0.178887	0.873882	-0.49539	0.577168	-0.40336	1	-1.07763	0.188964	-0.67427	0.415824	0.575763	0.474314
-0.46246	0.449246	0.428627	1	-0.25146	0.634026	-0.09529	0.881448	-0.66492	0.146474	-0.68009	0.109401	-0.52392	0.259324	-1.09354	0.006146	0.156171	1	-0.41346	0.392711	-0.56963	0.197999	0.780042	0.075092
-0.0093	1	0.104975	1	0.142957	0.837008	-0.10916	0.881597	0.483229	0.422893	0.037982	0.964848	-0.21414	0.744276	0.378254	0.525209	-0.25212	1	0.340272	0.574233	0.59239	0.259517	-0.09219	0.899697
-0.17135	0.920076	1.021438	1	-0.20904	0.846877	-0.13943	0.904743	0.02597	0.989905	-1.23048	0.105675	-1.16087	0.145974	-0.99547	0.220564	0.069609	1	0.23501	0.821848	0.165401	0.876652	2.165945	0.004135
1	1	-0.04594	1	-0.16535	0.983298	2.17702	0.663703	1	1	-0.11942	0.988008	2.222956	0.653289	-0.26878	0.967411	2.342372	1	1	1	1	1	1	1
-1.43458	0.080689	-0.48766	1	-1.99989	0.001562	-1.98027	0.002104	-1.24377	0.088488	-1.51223	0.020998	-1.49261	0.026858	-0.75611	0.325795	0.019619	1	0.756124	0.326785	0.736504	0.325967	-2.11434	0.001764
-0.35499	0.815847	-0.30981	1	1.152893	0.170487	0.908238	0.312488	0.182958	0.889771	1.462707	0.063712	1.218052	0.147962	0.492772	0.617539	-0.24466	1	-0.96994	0.277821	-0.72528	0.421661	-1.31913	0.103729
0.072378	0.731692	-0.06884	1	-0.17632	0.144567	-0.07194	0.633613	0.223371	0.07356	-0.10749	0.414495	-0.00311	0.990959	0.292206	0.010257	0.104378	1	0.399692	0.000424	0.295314	0.011923	-0.23293	0.050968
-0.02338	0.95692	0.069232	1	-0.25656	0.13612	-0.21177	0.248449	0.034264	0.904321	-0.32579	0.044687	-0.281	0.104171	-0.03497	0.888777	0.044789	1	0.29082	0.094353	0.246031	0.156801	-0.32069	0.063206
0.149275	0.377334	-0.06492	1	0.333911	0.002806	0.215404	0.083041	0.258014	0.035541	0.39883	0.000218	0.280323	0.016323	0.322933	0.00454	-0.11851	1	-0.0759	0.618346	0.04261	0.789141	-0.01541	0.93499
-0.21555	0.909248	0.328685	1	-0.93551	0.314017	-0.39586	0.734601	-0.3332	0.800937	-1.2642	0.150583	-0.72454	0.489291	-0.66188	0.532954	0.539652	1	0.602313	0.5534	0.062661	0.965336	0.777307	0.468484
-0.29457	0.135346	-0.12198	1	-0.51772	0.00026	-0.51523	0.000325	0.084077	0.709651	-0.39574	0.006854	-0.39325	0.008907	0.206054	0.227635	0.002488	1	0.601793	5.15E-05	0.599306	5.24E-05	-0.2748	0.096373
-0.06728	0.855724	0.020032	1	-0.2675	0.15613	-0.21277	0.2943	-0.03831	0.9022	-0.28753	0.116706	-0.2328	0.241695	-0.05834	0.818594	0.054727	1	0.229191	0.248838	0.174464	0.387653	-0.30311	0.111673
1	1	-0.03259	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1
0.489383	0.282826	-0.02223	1	0.082245	0.861875	-0.01328	0.984406	0.893664	0.005849	0.104477	0.814066	0.008955	0.990193	0.915896	0.003582	-0.09552	1	0.811419	0.015469	0.906941	0.005432	0.635503	0.062065
0.077527	0.791676	0.069016	1	-0.23247	0.160223	-0.1178	0.549043	-0.35899	0.02384	-0.30149	0.052284	-0.18682	0.293474	-0.428	0.004171	0.114674	1	-0.12651	0.502366	-0.24119	0.14162	-0.16158	0.373918
-0.05125	0.862964	-0.07268	1	0.057652	0.769456	-0.06292	0.752894	-0.04878	0.830044	0.130333	0.429068	0.00976	0.968389	0.023905	0.914834	-0.12057	1	-0.10643	0.544755	0.014145	0.952048	-0.15943	0.327405

EtOH 70% 21 vs 28 DAT		3 300 mg/L 21 vs 28 D		3 500 mg/L 21 vs 28 D		O.P. 21 vs 28 DAT		N.C. vs EtOH 28 DAT		. vs GA3 300 mg/L 28		. vs GA3 500 mg/L 28		N.C. vs O.P. 28 DAT		30 % vs GA3 300 mg/L		30 % vs GA3 500 mg/L		OH 280 % vs O.P. 28 D		mg/L vs GA3 500 mg/	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
1.702339	0.000128	1.54749	0.000977	2.127971	5.22E-06	0.814529	0.184462	0.644558	0.388954	3.321422	1.22E-13	3.628383	2.01E-15	1.217808	0.007138	2.676865	7.7E-09	2.983825	2.05E-10	0.573251	0.231459	0.306961	0.765332
-0.36942	0.200639	-1.42634	8.65E-09	-1.55911	1.17E-10	-0.02368	0.975038	-0.0653	0.914495	-0.24464	0.408127	-0.5351	0.036972	1.229948	2.47E-06	-0.17935	0.601947	-0.4698	0.080478	1.295246	2.65E-07	-0.29046	0.484745
1.960626	2.76E-06	6.218113	7.9E-08	5.324513	3.07E-08	0.7087	0.21527	1.135992	0.052364	7.3168	2.96E-10	6.696761	3.32E-12	0.68775	0.128622	6.180808	2.52E-07	5.560769	1.95E-08	-0.44824	0.334671	-0.62004	0.843523
1.222406	0.000119	0.694122	0.033086	1.402402	9.59E-06	1.099816	0.002371	0.705498	0.138217	1.619833	1.58E-07	2.148702	5.52E-12	0.948678	0.002882	0.914335	0.007809	1.443204	1.15E-05	0.243181	0.513242	0.528869	0.326956
1.906107	1.78E-05	1.055496	0.019328	0.704505	0.13193	1.16865	0.028856	1.921352	0.000129	2.686795	2.39E-10	2.639295	3.19E-10	1.251042	0.00409	0.765443	0.147448	0.717943	0.145379	-0.67031	0.151086	-0.0475	0.970576
2.14315	4.69E-08	0.946745	0.042527	0.634921	0.221968	1.066023	0.020414	1.449376	0.002934	2.397979	1.53E-08	2.605316	1.94E-09	0.948113	0.01459	0.948603	0.068722	1.15594	0.020154	-0.50126	0.256425	0.207337	0.849746
1.208429	0.004104	0.949921	0.037541	0.751883	0.097037	0.075447	0.93661	0.548696	0.44596	2.157916	5.18E-07	1.890102	5.76E-06	0.757719	0.094794	1.609219	0.000456	1.341405	0.002498	0.209023	0.686406	-0.26781	0.772093
1.152374	0.002629	1.539902	4.64E-05	1.933692	2.49E-07	0.528014	0.347137	0.26383	0.717518	2.845114	9.71E-15	3.08854	6.51E-17	0.791599	0.049759	2.581284	5.34E-12	2.82471	5.67E-14	0.527768	0.190028	0.243427	0.763425
1.318555	0.002787	3.987229	3.61E-10	3.755171	2.9E-10	0.6421	0.317015	0.271903	0.751108	5.707368	3.99E-20	5.400908	3.95E-20	0.919329	0.048294	5.435466	5.62E-18	5.129005	6.74E-18	0.647426	0.161037	-0.30646	0.856846
1.124167	0.000976	1.201513	0.000491	0.886666	0.012411	0.286264	0.619178	0.276611	0.665407	1.83101	7.36E-08	1.910814	1.42E-08	0.318925	0.444008	1.554399	1.15E-05	1.634204	2.77E-06	0.042314	0.93275	0.079804	0.930924
1.402327	0.000175	1.516691	4.18E-05	1.587599	1.47E-05	0.212587	0.752694	0.412443	0.534959	2.465761	1.1E-11	2.516872	3.28E-12	0.387317	0.38603	2.053318	4.51E-08	2.104429	1.56E-08	-0.02513	0.966782	0.051111	0.962463
1.344709	0.000325	1.451377	0.000449	1.738362	0.00015	0.268053	0.686021	0.317756	0.652652	2.210431	4.77E-08	2.970722	1.57E-11	0.443393	0.315216	1.892675	7.53E-06	2.652966	5.16E-09	0.125637	0.796931	0.760291	0.344092
-0.25292	0.729613	1.481413	0.007864	0.947476	0.095247	0.31552	0.766839	-0.0102	0.994022	1.760995	0.001938	0.916948	0.115425	-0.15558	0.858043	1.771196	0.002709	0.927149	0.122523	-0.14538	0.850087	-0.84405	0.339538
-0.8336	0.170084	-0.0553	0.944105	0.089809	0.901934	-0.58414	0.525279	-0.83961	0.373017	0.289419	0.673389	-0.26266	0.683936	0.99431	0.108174	1.129032	0.06182	0.576948	0.345743	1.833923	0.000675	-0.55208	0.546162
-0.86855	0.014025	-2.191	2.24E-11	-1.83176	9.43E-09	-0.47866	0.38714	-0.25514	0.696587	-0.42072	0.251813	-0.46953	0.176579	1.317256	0.000135	-0.16558	0.725833	-0.21438	0.588249	1.5724	1.63E-06	-0.0488	0.953269
1.117522	0.010428	2.258783	9.81E-09	2.736551	1.89E-12	0.514287	0.431888	0.663871	0.349703	2.32471	5.65E-09	2.80768	8.22E-13	-0.2722	0.62854	1.660839	7.7E-05	2.143808	1.17E-07	-0.93607	0.027632	0.482969	0.482832
1.589753	0.000207	3.138632	1.13E-13	3.662876	7.99E-17	0.290242	0.69539	1.12391	0.062517	3.64521	3.59E-18	4.249707	3.25E-22	-0.10811	0.864741	2.521299	9.47E-09	3.125796	4.82E-12	-1.23202	0.002626	0.604497	0.461526
1.156031	0.002113	3.004447	1.06E-18	4.086468	2.04E-32	0.336747	0.585195	0.664157	0.266681	2.797733	2.78E-16	3.936443	5.06E-30	-0.70177	0.078543	2.133577	1.58E-09	3.272286	1.25E-20	-1.36593	9.56E-05	1.138709	0.027229
1.316894	0.001403	2.99383	1.61E-15	4.032289	3.83E-26	0.457658	0.468621	0.882875	0.153259	2.737949	4.83E-13	3.857905	7.79E-24	-0.53189	0.256322	1.855074	3.2E-06	2.97503	3.13E-14	-1.41476	0.000246	1.119956	0.057452
0.197819	0.547545	0.421656	0.118727	1.410926	2.61E-08	0.173617	0.710295	0.473688	0.289873	0.035605	0.925877	0.804901	0.002661	-0.67539	0.013933	-0.43808	0.159487	0.331212	0.285811	-1.14908	6.51E-06	0.769296	0.043996
0.057458	0.933772	1.531441	0.005056	0.343432	0.510365	0.040564	0.970178	0.053384	0.967039	0.950599	0.125133	-0.2245	0.698121	-0.71378	0.159775	0.897215	0.189739	-0.27788	0.647028	-0.76717	0.112811	1	1
1.432834	3.92E-06	3.81399	2.48E-25	5.067217	2.56E-25	0.64101	0.104477	0.416588	0.439663	3.339838	2.1E-19	4.678053	1.64E-21	-0.7364	0.019416	2.92325	1.55E-14	4.261465	1.43E-17	-1.15299	7.57E-05	1.338215	0.114848
0.922838	0.039947	2.731709	5.27E-08	3.560248	4.08E-11	1.57927	0.003351	-0.32305	0.699493	3.600591	3.64E-13	4.18742	7.87E-15	2.158219	1.29E-06	3.923643	2.7E-15	4.510471	7.57E-17	2.48127	6.13E-09	0.586829	0.604567
2.080276	8.74E-11	6.047041	8.27E-58	6.007766	7.36E-57	0.240481	0.669372	0.584143	0.267325	5.454961	6.19E-47	5.412793	4.6E-46	-0.85575	0.010198	4.870818	5.36E-37	4.82865	2.77E-36	-1.4399	2.34E-06	-0.04217	0.97669
0.305911	0.036088	0.84879	7.81E-11	0.696086	7.6E-08	0.065367	0.798882	0.283348	0.197529	0.501159	0.000281	0.42311	0.00182	-0.35883	0.010904	0.217811	0.186254	0.139762	0.383581	-0.64217	8.04E-07	-0.07805	0.781161
0.433658	0.609276	0.4042	0.659884	2.19686	0.026386	1.188071	0.210199	0.759106	0.537772	1.311891	0.096835	2.701194	0.005339	1.01813	0.188186	0.552785	0.600284	1.942088	0.069772	0.259025	0.783003	1	1
0.937773	0.016043	2.29026	4.58E-11	3.24621	8.6E-21	0.266676	0.687303	0.586358	0.352328	1.258758	0.000612	2.370879	1.97E-11	-1.17828	0.001857	0.672401	0.109997	1.784522	1.09E-06	-1.76464	5.91E-07	1.112121	0.030438
-0.92023	0.038638	-0.63349	0.145608	-0.9948	0.013613	-0.38504	0.603564	-0.72307	0.299357	-0.39835	0.409472	-1.01177	0.013479	0.190375	0.753772	0.324722	0.549544	-0.2887	0.55214	0.913443	0.032704	-0.61342	0.338195
1.93883	0.006905	6.693681	5.8E-13	8.712183	2.53E-10	-0.94754	0.338516	0.794323	0.533241	4.318695	8.98E-06	6.406807	6.38E-06	-3.08752	3.21E-06	3.524373	0.000615	5.612484	0.000138	-3.88184	1.96E-09	2.088111	0.428612
1	1	-1.28866	0.729967	-3.67046	0.285407	1	1	1	1	0.794508	0.84784	0.755079	0.842808	4.65126	0.220524	-2.63693	0.534918	-2.67636	0.478857	1.219818	0.789659	1	1
-2.07	0.000919	-1.15932	0.052361	-1.53111	0.007674	-0.30423	0.791195	-0.44333	0.705811	-1.04488	0.098224	-1.39705	0.017871	0.566336	0.45632	-0.60155	0.419825	-0.95372	0.13206	1.009662	0.112118	-0.35217	0.756825
-1.28142	0.077584	-2.22957	0.000863	-2.98522	3.17E-06	0.052577	0.978637	-0.2721	0.850071	0.242452	0.783168	-0.75785	0.285046	1.554668	0.032768	0.514557	0.556509	-0.48575	0.532259	1.826772	0.006976	-1.0003	0.327248
-0.27507	0.00962	-0.14982	0.157428	-0.19775	0.055145	-0.27326	0.041323	-0.11097	0.550286	-0.0932	0.430673	-0.03676	0.769627	0.183042	0.105724	0.017765	0.916191	0.074209	0.540311	0.29401	0.003426	0.056444	0.780409
-0.49264	0.001158	-0.60737	9.45E-06	-0.73413	4.56E-08	-0.00409	0.997559	-0.10271	0.720666	-0.54323	0.000125	-0.62521	4.96E-06	0.350869	0.02402	-0.44052	0.003316	-0.52249	0.000233	0.453582	0.001578	-0.08197	0.76605
-0.05241	0.696901	-0.42524	2.38E-05	-0.56011	9.92E-09	-0.10063	0.576082	-0.10192	0.607211	-0.07592	0.547839	-0.3293	0.001161	0.172796	0.150084	0.025999	0.876432	-0.22738	0.035156	0.274711	0.009359	-0.25338	0.087413
-0.25951	0.80112	2.347068	0.0052	1.696604	0.047889	-0.16567	0.91934	1	1	0.634252	0.564992	0.523439	0.618157	-1.27617	0.153634	1.342381	0.193904	1.231568	0.19724	-0.56804	0.526275	1	1
-0.40654	0.004698	-0.23309	0.093545	-0.44635	0.000565	-0.29135	0.125956	-0.25372	0.264466	-0.476	0.000433	-0.68677	1.02E-07	0.067531	0.730849	-0.22228	0.157079	-0.43305	0.001435	0.321252	0.02161	-0.21077	0.311668
-0.44771	0.006819	-0.47205	0.001879	-0.47145	0.001686	-0.16073	0.542861	-0.12457	0.685993	-0.43644	0.005635	-0.38111	0.013924	0.104074	0.624669	-0.31187	0.073165	-0.25654	0.123906	0.228647	0.179673	0.055331	0.865137
1	1	0	1	0	1	1	1	1	1	1.376054	0.622774	1.31627	0.616479	1	1	1	1	1	1	2.757109	0.251563	1	1
0.653878	0.033491	-0.34706	0.243086	-0.03222	0.93767	-0.08807	0.894149	-0.00386	0.995516	-0.90032	0.00173	-0.681	0.018448	0.170095	0.67913	-0.89646	0.002965	-0.67714	0.024323	0.173953	0.636081	0.219321	0.666754
-0.07204	0.684605	-0.2046	0.151428	-0.58898	4.99E-06	0.048788	0.866964	0.158557	0.534453	-0.2755	0.056052	-0.5452	3.31E-05	-0.14862	0.384221	-0.43405	0.002486	-0.70376	1.16E-07	-0.30718	0.030438	-0.26971	0.182546
-0.06108	0.70639	-0.30277	0.015378	-0.37824	0.001668	0.183407	0.337017	0.025671	0.933019	-0.08569	0.574353	-0.28173	0.024187	0.294061	0.029808	-0.11136	0.494721	-0.3074	0.016585	0.26839	0.039425	-0.19604	0.309697

300 mg/L vs O.P. 28		500 mg/L vs O.P. 28	
Log2FC	p-adj	Log2FC	p-adj
-2.10361	3.08E-06	-2.41057	1.33E-07
1.474591	1.45E-09	1.765051	1.57E-13
-6.62905	5.9E-09	-6.00901	2.09E-10
-0.67115	0.037187	-1.20002	0.000143
-1.43575	0.000869	-1.38825	0.001108
-1.44987	0.000792	-1.6572	0.000168
-1.4002	0.001137	-1.13238	0.007277
-2.05352	2.14E-08	-2.29694	4.04E-10
-4.78804	1.28E-14	-4.48158	1.62E-14
-1.51209	5.81E-06	-1.59189	1.6E-06
-2.07844	6.65E-09	-2.12956	2.22E-09
-1.76704	9.61E-06	-2.52733	6.55E-09
-1.91657	0.000391	-1.07253	0.05032
0.704891	0.218126	1.256975	0.016693
1.737979	4.37E-08	1.786784	1.19E-08
-2.59691	1.98E-11	-3.07988	1.04E-15
-3.75332	1.56E-19	-4.35782	8.54E-24
-3.4995	2.01E-25	-4.63821	5.71E-42
-3.26984	1.22E-18	-4.38979	3.76E-31
-0.71099	0.004914	-1.48029	3.03E-09
-1.66438	0.001643	-0.48928	0.293777
-4.07624	2.68E-29	-5.41446	3.19E-29
-1.44237	0.00618	-2.0292	0.000271
-6.31071	2.99E-63	-6.26855	3.07E-62
-0.85998	2.02E-11	-0.78194	7.26E-10
-0.29376	0.753789	-1.68306	0.093544
-2.43704	1.17E-12	-3.54916	5.59E-25
0.58872	0.173097	1.202144	0.002169
-7.40621	6.04E-16	-9.49432	3.06E-12
3.856752	0.260883	3.896181	0.236514
1.611212	0.005038	1.963385	0.000429
1.312216	0.051174	2.312518	0.000232
0.276245	0.005098	0.219801	0.026599
0.894101	2.49E-11	0.976075	1.52E-13
0.248712	0.0154	0.502092	2.05E-07
-1.91043	0.024685	-1.79961	0.030006
0.543536	2.45E-05	0.754305	1.83E-09
0.540517	0.000274	0.485186	0.000994
0	1	0	1
1.070416	8.92E-05	0.851095	0.002031
0.126875	0.395595	0.39658	0.002223
0.379747	0.00171	0.575788	7.57E-07

Table S4.11: Table with Log2FoldChange (log2FC) and p-value adjusted (p-adj) of the genes that encode for Cyclin-dependent kinases (CDK) and CDK-inhibitors (ICK). The heatmap of these genes is showed in Fig. 4.22. Log2FC is calculated according to the following formula: expression level term1 - expression level term2.

Gene name	Gene description	N.C. 0 vs 7 DAT		EtOH 70% 0 vs 7 DAT		A3 300 mg/L 0 vs 7 DA		A3 500 mg/L 0 vs 7 DA		O.P. 0 vs 7 DAT		N.C. vs EtOH 7 DAT		C. vs GA3 300 mg/L 7 D		C. vs GA3 500 mg/L 7 D	
		Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
Pav_sc0000745.1_g280.1.mk	PavCyclin/Brf1-like TBP-binding protein	0.06388	0.856546	0.016826	1	-0.15239	0.203934	-0.06806	0.638911	-0.0659	0.717218	-0.04705	1	-0.21627	0.12962	-0.13194	0.38141
Pav_sc0000661.1_g630.1.mk	PavCDKB1;1	0.603445	0.309494	0.520443	0.462519	0.787652	0.034986	0.537044	0.169604	0.261434	0.641473	-0.083	1	0.184207	0.831762	-0.0664	0.930604
Pav_sc0001699.1_g590.1.mk	PavCDKB1;2	-0.12757	0.941341	0.004728	1	0.111715	0.858273	-0.00352	0.999289	0.04883	0.959294	0.132297	1	0.239283	0.771818	0.124049	0.863369
Pav_sc0000600.1_g680.1.mk	PavCDKB2;2	-0.07046	0.97671	0.03482	1	0.160527	0.835629	0.147784	0.847328	0.17438	0.856432	0.105282	1	0.230988	0.834987	0.218245	0.797101
Pav_sc0000756.1_g160.1.mk	PavCDKC;1.1	-0.06741	0.900993	0.009034	1	-0.02504	0.919467	-0.04944	0.822961	-0.00708	0.988634	0.076439	1	0.042365	0.907691	0.017961	0.953079
Pav_sc0011259.1_g010.1.mk	PavCDKC;1.2	0.08337	0.906711	-0.04705	0.997635	-0.04837	0.87322	-0.01831	0.958194	-0.19677	0.45027	-0.13042	1	-0.13174	0.726601	-0.10168	0.748985
Pav_sc0000103.1_g240.1.mk	PavCDKD1;1	-0.06982	0.909	-0.07554	0.976451	-0.13114	0.522641	-0.23358	0.176176	-0.17328	0.432464	-0.00571	1	-0.06132	0.871258	-0.16376	0.476854
Pav_sc0001825.1_g020.1.mk	PavCDKE;1	0.041903	0.954268	-0.03139	1	0.069214	0.768853	0.081333	0.711883	0.113837	0.648254	-0.07329	1	0.027311	0.947343	0.03943	0.893455
Pav_sc0000557.1_g620.1.mk	PavCDK-activating kinase assembly factor-related	-0.06732	0.934067	-0.06083	0.993647	-0.29655	0.149825	-0.28844	0.154886	-0.10874	0.739085	0.006493	1	-0.22923	0.452837	-0.22112	0.405007
Pav_sc0002451.1_g320.1.mk	PavICK5	-0.34117	0.75567	-0.34163	0.8475	0.075552	0.911515	0.196486	0.732194	-0.24682	0.712853	-0.00046	1	0.416724	0.544205	0.537658	0.318402
Pav_sc0000071.1_g860.1.mk	PavICK5	0.26818	0.787567	0.350939	0.758995	-0.67092	0.059152	-0.42845	0.269798	0.73235	0.056163	0.082759	1	-0.9391	0.018329	-0.69663	0.093936
Pav_sc0001963.1_g390.1.mk	PavICK6	-0.3796	0.32606	-0.25445	0.705586	0.538989	0.020908	0.341239	0.178353	-0.53758	0.026763	0.125148	1	0.918586	8.03E-05	0.720836	0.003458
Pav_sc0000022.1_g200.1.mk	PavICK6	0.122474	0.921075	-0.03899	1	0.49671	0.131905	0.385998	0.258762	0.02845	0.968705	-0.16146	1	0.374236	0.44669	0.263524	0.567665

N.C. vs O.P. 7 DAT		70 % vs GA3 300 mg/L		70 % vs GA3 500 mg/L		tOH 70 % vs O.P. 7 DA		0 mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 7 D		3 500 mg/L vs O.P. 7 D		N.C. 7 vs 14 DAT		EtOH 70% 7 vs 14 DAT		A3 300 mg/L 7 vs 14 DA		3 500 mg/L 7 vs 14 D		O.P. 7 vs 14 DAT	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
-0.12978	0.552163	-0.16921	0.186707	-0.08489	0.549737	-0.08273	0.695541	0.084326	1	0.086485	0.591508	0.00216	0.994692	-0.09196	0.691508	-0.12885	0.393374	0.131438	0.245281	0.108373	0.367631	0.098897	0.459766
-0.34201	0.69501	0.26721	0.624828	0.016601	0.98139	-0.25901	0.727001	-0.25061	1	-0.52622	0.271444	-0.27561	0.668626	-0.36302	0.620168	-0.36862	0.488625	-0.34438	0.415487	0.134829	0.793486	0.432972	0.327069
0.176399	0.88231	0.106987	0.874308	-0.00825	0.99081	0.044102	0.973409	-0.11523	1	-0.06288	0.938142	0.05235	0.958763	0.425288	0.564324	0.448566	0.420818	1.282908	0.000284	1.356869	0.000119	0.673909	0.114442
0.244842	0.865741	0.125706	0.883333	0.112963	0.89664	0.13956	0.918104	-0.01274	1	0.013854	0.993324	0.026597	0.986376	0.448362	0.659454	0.584405	0.396547	1.90598	1.11E-05	1.936806	8.11E-06	0.793162	0.142746
0.060329	0.894371	-0.03407	0.894264	-0.05848	0.793506	-0.01611	0.973703	-0.0244	1	0.017963	0.954714	0.042367	0.897351	0.111098	0.73182	0.109716	0.633282	0.046116	0.812818	0.103793	0.545668	-0.08932	0.647467
-0.28014	0.381858	-0.00132	0.997545	0.028744	0.933094	-0.14972	0.677089	0.030068	1	-0.1484	0.597112	-0.17847	0.555449	-0.08244	0.869839	-0.02457	0.94749	0.192137	0.347339	0.155803	0.47195	0.225768	0.303945
-0.10346	0.809841	-0.0556	0.835955	-0.15804	0.423822	-0.09775	0.774178	-0.10244	1	-0.04214	0.891964	0.060298	0.859133	0.023759	0.968863	0.082374	0.766458	0.342131	0.02566	0.459965	0.001795	0.227838	0.210276
0.071934	0.880344	0.100599	0.663934	0.112718	0.592824	0.145222	0.614018	0.012119	1	0.044623	0.880552	0.032504	0.932559	-0.04379	0.929705	-0.08819	0.740056	-0.03503	0.87519	0.015029	0.951938	-0.19686	0.279697
-0.04142	0.948811	-0.23573	0.319218	-0.22761	0.309138	-0.04791	0.927697	0.008112	1	0.187813	0.485854	0.179701	0.557411	-0.13282	0.763243	0.015565	0.966989	0.2997	0.114673	0.065515	0.798572	-0.13238	0.59551
0.094352	0.944701	0.417186	0.426257	0.53812	0.244581	0.094814	0.932025	0.120934	1	-0.32237	0.591792	-0.44331	0.469948	-0.12558	0.916785	-0.26533	0.683401	-0.08479	0.88326	-0.12767	0.81741	0.203758	0.720695
0.46417	0.490157	-1.02186	0.004537	-0.77939	0.03297	0.381411	0.534723	0.242461	1	1.403266	2.27E-05	1.160805	0.001127	-0.85994	0.031865	-0.8562	0.02642	-1.5793	5.99E-08	-2.04698	6.23E-13	-3.12058	1.76E-28
-0.15799	0.797136	0.793438	0.000749	0.595688	0.013833	-0.28314	0.452305	-0.19775	1	-1.07657	5.12E-07	-0.87882	0.000106	0.003105	1	0.260969	0.435477	0.500662	0.027218	0.435683	0.059164	0.827041	0.000148
-0.09402	0.927545	0.535696	0.131654	0.424985	0.223973	0.067436	0.936203	-0.11071	1	-0.46826	0.216602	-0.35755	0.433406	-0.17548	0.814547	-0.48882	0.208993	-0.02086	0.96867	-0.0718	0.870083	0.006033	0.9929

N.C. vs EtOH 14 DAT		. vs GA3 300 mg/L 14		. vs GA3 500 mg/L 14		N.C. vs O.P. 14 DAT		40 % vs GA3 300 mg/L		40 % vs GA3 500 mg/L		OH 140 % vs O.P. 14 D		mg/L vs GA3 500 mg/		300 mg/L vs O.P. 14		500 mg/L vs O.P. 14		N.C. 14 vs 21 DAT		tOH 70% 14 vs 21 DA	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
-0.08394	0.889829	0.00713	0.980956	0.068391	0.698128	0.061075	0.818042	0.09107	0.542416	0.152331	0.242399	0.145015	0.270157	0.061261	1	0.053945	0.862597	-0.00732	0.988606	0.012444	0.955123	0.090112	0.675026
-0.0886	0.981953	0.202848	0.734641	0.431452	0.377968	0.453985	0.474987	0.291447	0.566929	0.520051	0.24188	0.542583	0.219562	0.228604	1	0.251137	0.796055	0.022533	0.990165	0.377442	0.451977	0.139797	0.867044
0.155575	0.965076	1.096903	0.005614	1.05563	0.008003	0.42502	0.55393	0.941328	0.019928	0.900055	0.027968	0.269445	0.629437	-0.04127	1	-0.67188	0.287611	-0.63061	0.354222	0.678638	0.156348	0.43802	0.539594
0.241325	0.94091	1.688606	0.000297	1.70669	0.000243	0.589642	0.486173	1.447281	0.002643	1.465365	0.002323	0.348317	0.615071	0.018084	1	-1.09896	0.123437	-1.11705	0.114884	0.907357	0.125673	0.711836	0.394021
0.075057	0.935493	-0.02262	0.939651	0.010657	0.978296	-0.14009	0.619962	-0.09767	0.647966	-0.0644	0.788157	-0.21515	0.210982	0.033273	1	-0.11747	0.736499	-0.15075	0.632583	-0.06189	0.801142	-0.02438	0.947805
-0.07255	0.966132	0.142834	0.617404	0.136567	0.641576	0.028067	0.967369	0.215383	0.368767	0.209117	0.394186	0.100616	0.719904	-0.00627	1	-0.11477	0.821533	-0.1085	0.841837	0.126662	0.656036	0.026624	0.95573
0.0529	0.972736	0.257056	0.179839	0.272446	0.149167	0.100618	0.791412	0.204156	0.30492	0.219546	0.264442	0.047718	0.861389	0.01539	1	-0.15644	0.673591	-0.17183	0.619997	0.301498	0.119436	0.249288	0.356988
-0.11769	0.896503	0.036071	0.907637	0.098247	0.700239	-0.08114	0.836867	0.15376	0.458823	0.215937	0.255623	0.03655	0.894851	0.062176	1	-0.11721	0.763845	-0.17939	0.576888	-0.11007	0.637896	-0.13427	0.663729
0.154874	0.884131	0.203283	0.427573	-0.02279	0.961338	-0.04098	0.946038	0.048409	0.885602	-0.17766	0.494932	-0.19586	0.422705	-0.22607	1	-0.24426	0.49518	-0.01819	0.981254	0.36784	0.105673	0.276704	0.395697
-0.14021	0.970201	0.457509	0.39034	0.535567	0.287388	0.42369	0.566187	0.59772	0.199769	0.675777	0.137549	0.563901	0.239399	0.078057	1	-0.03382	0.984819	-0.11188	0.933205	-0.3761	0.493239	-0.10197	0.916133
0.086492	0.98122	-1.65846	2.84E-08	-1.88368	7.73E-11	-1.79647	3.61E-09	-1.74495	3.36E-09	-1.97017	7.72E-12	-1.88297	1.9E-10	-0.22522	1	-0.13802	0.888847	0.087203	0.938485	-0.7868	0.043863	-0.96552	0.037356
0.383011	0.665461	1.416143	1.96E-12	1.153414	3.15E-08	0.665948	0.012678	1.033132	1.45E-06	0.770402	0.000678	0.282936	0.332225	-0.26273	1	-0.7502	0.007118	-0.48747	0.169001	0.545801	0.042616	0.340094	0.393733
-0.4748	0.683581	0.528857	0.135681	0.367203	0.35754	0.087491	0.921028	1.003656	0.000575	0.842001	0.005288	0.562289	0.097649	-0.16165	1	-0.44137	0.413705	-0.27971	0.691811	0.001501	1	0.177966	0.784506

3 300 mg/L 14 vs 21 D		3 500 mg/L 14 vs 21 D		O.P. 14 vs 21 DAT		N.C. vs EtOH 21 DAT		. vs GA3 300 mg/L 21		. vs GA3 500 mg/L 21		N.C. vs O.P. 21 DAT		10 % vs GA3 300 mg/L		10 % vs GA3 500 mg/L		OH 210 % vs O.P. 21 D		mg/L vs GA3 500 mg/		300 mg/L vs O.P. 21
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
-0.1475	0.170873	-0.17099	0.100603	-0.10552	0.519171	-0.00627	1	-0.15282	0.170661	-0.11504	0.345831	-0.05689	0.708567	-0.14655	0.186937	-0.10877	0.377207	-0.05062	0.721841	0.037778	1	0.095931	0.441831
-0.71856	0.031776	-0.65984	0.057248	-0.4394	0.402104	-0.32624	1	-0.89315	0.007621	-0.60583	0.108191	-0.36285	0.419322	-0.56691	0.10536	-0.27958	0.514751	-0.03661	0.952014	0.287327	1	0.530301	0.152001
1.335797	0.000164	1.355236	0.000108	1.259609	0.00172	-0.08504	1	1.754062	2.28E-07	1.732228	4.02E-07	1.00599	0.008437	1.839106	4.53E-08	1.817272	8.24E-08	1.091034	0.002898	-0.02183	1	-0.74807	0.065845
2.045902	2.56E-06	2.083866	1.36E-06	1.671315	0.000699	0.045804	1	2.827151	8.44E-12	2.883199	4.22E-12	1.3536	0.00384	2.781347	1.66E-11	2.837395	8.66E-12	1.307796	0.004367	0.056048	1	-1.47355	0.002005
0.119733	0.44787	0.168835	0.247737	0.148315	0.484664	0.112567	1	0.159003	0.315839	0.241377	0.106682	0.070111	0.73557	0.046437	0.8149	0.128811	0.44847	-0.04246	0.835082	0.082374	1	-0.08889	0.622547
0.098857	0.65602	0.15844	0.431267	0.182549	0.521541	-0.17259	1	0.115029	0.623581	0.168345	0.452549	0.083954	0.762573	0.287616	0.130167	0.340933	0.073737	0.256541	0.19756	0.053317	1	-0.03107	0.913859
0.239986	0.137144	0.273345	0.07934	0.28915	0.148057	0.000689	1	0.195544	0.266644	0.244293	0.15587	0.088269	0.699033	0.194854	0.262699	0.243603	0.157704	0.08758	0.675767	0.048749	1	-0.10727	0.595248
-0.28439	0.056719	-0.44971	0.001211	0.038026	0.911834	-0.14189	1	-0.13825	0.436755	-0.24139	0.136891	0.066956	0.772143	0.003639	0.992651	-0.0995	0.60989	0.208845	0.205624	-0.10314	1	0.205206	0.221227
-0.08175	0.722248	0.207474	0.282018	-0.10845	0.741828	0.063738	1	-0.24631	0.222431	-0.18316	0.410016	-0.51727	0.004305	-0.31005	0.103541	-0.24689	0.23388	-0.58101	0.000865	0.063153	1	-0.27096	0.17612
-1.20857	0.000695	-1.29491	0.000223	-0.20987	0.772444	0.13392	1	-0.37495	0.398176	-0.38324	0.400423	0.589926	0.173897	-0.50887	0.217335	-0.51716	0.224377	0.456006	0.293239	-0.00829	1	0.964878	0.01333
-1.19173	4.82E-05	-0.62547	0.042717	-0.76457	0.041207	-0.09222	1	-2.06338	7.92E-14	-1.72234	8.63E-10	-1.77424	6.77E-10	-1.97116	9.26E-13	-1.63012	7.4E-09	-1.68201	4.82E-09	0.341037	1	0.289143	0.449691
0.519969	0.021099	0.755133	0.000398	0.720686	0.00324	0.177304	1	1.390311	3.14E-12	1.362746	1.2E-11	0.840833	9.88E-05	1.213007	1.63E-09	1.185442	5.18E-09	0.663529	0.002501	-0.02756	1	-0.54948	0.022047
0.123009	0.74286	0.347139	0.264283	0.47466	0.228698	-0.29833	1	0.650365	0.026727	0.712841	0.01552	0.560649	0.077382	0.948699	0.000476	1.011174	0.000217	0.858983	0.0023	0.062475	1	-0.08972	0.835044

3 500 mg/L vs O.P. 21		N.C. 21 vs 28 DAT		EtOH 70% 21 vs 28 DAT		3 300 mg/L 21 vs 28 D		3 500 mg/L 21 vs 28 D		O.P. 21 vs 28 DAT		N.C. vs EtOH 28 DAT		. vs GA3 300 mg/L 28		l. vs GA3 500 mg/L 28		N.C. vs O.P. 28 DAT		30 % vs GA3 300 mg/L		30 % vs GA3 500 mg/L	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
0.058153	0.659128	-0.28503	0.006565	-0.30128	0.001873	-0.4017	4.63E-06	-0.54479	2.15E-10	0.177683	0.179609	-0.02252	0.917262	-0.26948	0.003406	-0.3748	1.74E-05	0.405829	1.14E-05	-0.24696	0.011636	-0.35227	9.63E-05
0.242974	0.564095	-0.63035	0.093067	-0.70443	0.028484	-0.51771	0.08057	-0.7912	0.006046	-0.35099	0.473896	-0.40033	0.449836	-0.78052	0.009077	-0.76668	0.008585	-0.08349	0.856262	-0.38019	0.276031	-0.36635	0.255547
-0.72624	0.06813	0.802161	0.045011	0.8705	0.015224	-0.91115	0.006674	-1.36255	2.31E-05	0.236121	0.706435	-0.0167	0.984295	0.04075	0.934408	-0.43248	0.230068	0.439951	0.283716	0.057455	0.919602	-0.41578	0.268283
-1.5296	0.001164	1.086645	0.027551	1.954926	9.49E-06	2.941342	4.82E-11	3.545138	3.38E-14	0.900527	0.126619	0.914085	0.177068	4.681848	6.1E-27	5.341691	4.9E-31	1.167482	0.009308	3.767764	2.73E-17	4.427607	3.77E-21
-0.17127	0.267126	0.136907	0.408592	-0.05917	0.714432	-0.28708	0.020352	-0.59287	3.62E-07	-0.09351	0.676263	-0.08351	0.739895	-0.26498	0.040892	-0.48839	4.11E-05	-0.16031	0.284536	-0.18148	0.216489	-0.40489	0.001098
-0.08439	0.724655	0.003227	0.993638	0.053574	0.804004	-0.40486	0.0119	-0.67406	1.1E-05	0.076287	0.811764	-0.12224	0.703751	-0.29305	0.089795	-0.50895	0.001211	0.157014	0.447554	-0.17081	0.401229	-0.3867	0.019844
-0.15602	0.390265	0.038897	0.867286	0.184536	0.25151	-0.00547	0.984853	-0.18251	0.221269	0.066483	0.809106	0.146328	0.581954	0.151179	0.351672	0.022889	0.902503	0.115855	0.527984	0.004851	0.99078	-0.12344	0.456548
0.308346	0.045836	-0.30481	0.05464	-0.26928	0.061952	-0.45981	0.000346	-0.66834	7.18E-08	-0.19261	0.345478	-0.10636	0.68498	-0.29326	0.033332	-0.60493	1.66E-06	0.179152	0.26115	-0.18689	0.236687	-0.49856	0.000139
-0.33412	0.078911	0.027085	0.926703	0.255721	0.171296	0.831961	2.51E-07	1.194114	1.98E-13	0.488549	0.016996	0.292374	0.300055	0.558568	0.001054	0.983874	2.91E-09	-0.05581	0.82366	0.266194	0.1872	0.6915	7.55E-05
0.973165	0.011344	0.840963	0.036223	0.759745	0.038821	2.615887	4.31E-15	4.630546	5.86E-34	-1.04718	0.013546	0.052702	0.953723	1.399972	7.29E-05	3.406344	1.74E-18	-1.29822	0.000179	1.34727	0.000223	3.353642	1.36E-17
-0.05189	0.914146	-0.12872	0.775198	0.015528	0.971472	1.326614	9.22E-07	1.322154	7.57E-07	-0.4873	0.237806	0.052022	0.943355	-0.60805	0.04164	-0.27147	0.389738	-2.13282	1.37E-14	-0.66007	0.035303	-0.3235	0.315311
-0.52191	0.028026	0.812698	0.000387	1.359488	1.05E-10	1.167478	2.96E-08	0.838395	5.01E-05	0.304217	0.329408	0.724094	0.008519	1.745091	2.4E-17	1.388443	8.31E-12	0.332351	0.161951	1.020998	4.18E-06	0.664349	0.002625
-0.15219	0.688648	-0.19151	0.606663	-0.19529	0.53708	-0.50319	0.05923	-0.54235	0.038419	-0.07361	0.899976	-0.30212	0.526375	0.338682	0.242218	0.361999	0.189352	0.678549	0.014744	0.640804	0.023072	0.66412	0.012516

OH 280 % vs O.P. 28 D		mg/L vs GA3 500 mg/		300 mg/L vs O.P. 28		500 mg/L vs O.P. 28	
Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj
0.42835	1.68E-06	-0.10532	0.480838	0.675309	3.95E-15	0.780624	2.95E-20
0.316835	0.344146	0.013845	0.989892	0.697027	0.014656	0.683182	0.015096
0.456655	0.225003	-0.47323	0.373646	0.399201	0.267424	0.872432	0.007119
0.253397	0.630803	0.659843	0.447717	-3.51437	1.11E-15	-4.17421	1.21E-19
-0.0768	0.616584	-0.22341	0.228801	0.104678	0.443548	0.328088	0.005451
0.279255	0.107326	-0.21589	0.398449	0.450067	0.004233	0.665959	1.01E-05
-0.03047	0.877997	-0.12829	0.60971	-0.03532	0.843322	0.092966	0.539045
0.285515	0.038654	-0.31167	0.099192	0.472407	0.00019	0.784078	1.41E-10
-0.34818	0.044514	0.425306	0.099075	-0.61438	0.000146	-1.03968	1.1E-10
-1.35092	4.95E-05	2.006371	0.0001	-2.69819	2.59E-16	-4.70457	1.96E-35
-2.18484	7.67E-16	0.336576	0.46715	-1.52477	9.36E-09	-1.86134	1.19E-12
-0.39174	0.076323	-0.35665	0.313634	-1.41274	6.15E-12	-1.05609	1.5E-07
0.98067	0.000121	0.023316	0.975544	0.339867	0.21583	0.31655	0.234616

Table S4.12: Table with Log2FoldChange (log2FC) and p-value adjusted (p-adj) of the genes that encode for MADS-box transcription factors. The heatmap of these genes is showed in Fig. 4.24. Log2FC is calculated according to the following formula: expression level term1 - expression level term2.

Gene name	Gene description	N.C. 0 vs 7 DAT		EtOH 70% 0 vs 7 DAT		A3 300 mg/L 0 vs 7 DA		A3 500 mg/L 0 vs 7 DA		O.P. 0 vs 7 DAT		N.C. vs EtOH 7 DAT		. vs GA3 300 mg/L 7 D		. vs GA3 500 mg/L 7 D		N.C. vs O.P. 7 DAT		70 % vs GA3
		Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
Pav_sc0001289.1_g020.1.mk	PavAG	0.336988	8.87E-05	0.263436	0.005719	0.659838	1.97E-19	0.601093	3.42E-16	0.409313	1.1E-07	-0.07355	1	0.322849	0.000499	0.264104	0.0064	0.072325	0.74697	0.396402
Pav_sc0007489.1_g010.1.mk	PavAG	-0.176	0.932666	-0.46846	0.773692	-0.24261	0.73073	0.344022	0.600958	-0.44531	0.52483	-0.29245	1	-0.0666	0.960586	0.520027	0.467698	-0.26931	0.842848	0.225849
Pav_sc0003835.1_g220.1.mk	PavAGL1/SHP1	0.765927	9E-05	0.656041	0.001638	0.936183	1.21E-07	1.019611	4.58E-09	0.878146	7.25E-07	-0.10989	1	0.170256	0.660603	0.253684	0.366487	0.112219	0.848476	0.280142
Pav_sc0000358.1_g630.1.mk	PavAGL1/SHP1	-0.13686	0.84701	-0.2305	0.742344	-0.41087	0.078778	-0.55821	0.00929	-0.46094	0.057284	-0.09364	1	-0.27401	0.443266	-0.42135	0.118891	-0.32408	0.406261	-0.18037
Pav_sc0001080.1_g900.1.mk	PavAGL3/SEP4	0.267858	0.854017	-0.26096	0.949644	0.826207	0.093937	0.822518	0.088805	0.298391	0.689532	-0.52882	1	0.558349	0.466305	0.55466	0.400854	0.030533	0.987292	1.087171
Pav_sc0000661.1_g410.1.mk	PavAGL4/SEP2	0.526607	0.000194	0.434839	0.004488	0.84598	3.39E-12	0.724118	5.13E-09	0.671992	6.82E-08	-0.09177	1	0.319373	0.084754	0.197511	0.311542	0.145385	0.655021	0.411141
Pav_sc0000072.1_g670.1.mk	PavAGL6	-0.02096	1	0.314093	0.968063	0.182489	0.849132	0.275578	0.751115	0.191636	0.874794	0.335048	1	0.203445	0.89049	0.296533	0.772973	0.212591	0.915376	-0.1316
Pav_sc0000176.1_g050.1.mk	PavAGL7/AP1	1.638998	0.72445	1.94584	0.714227	0.617974	0.813671	-0.2918	0.916979	0.651757	0.841491	0.306842	1	-1.02102	0.795876	1	1	-0.98724	0.849658	1
Pav_sc0000661.1_g360.1.mk	PavAGL7/AP1	1.283873	0.068083	1.197498	0.106559	1.562839	0.003899	1.208209	0.02942	1.473951	0.00862	-0.08638	1	0.278966	0.831762	-0.07566	0.950372	0.190078	0.921956	0.365342
Pav_sc0000358.1_g640.1.mk	PavAGL8/FUL	0.178905	0.738625	0.057596	0.994786	0.075519	0.807989	0.147986	0.565793	-0.05278	0.898977	-0.12131	1	-0.10339	0.81653	-0.03092	0.939546	-0.23169	0.571875	0.017923
Pav_sc0000091.1_g150.1.mk	PavAGL9/SEP3	0.202412	0.735033	0.120372	0.963354	0.210949	0.448601	0.096236	0.769451	0.186738	0.58381	-0.08204	1	0.008537	0.994209	-0.10618	0.78246	-0.01567	0.985898	0.090577
Pav_sc0000176.1_g060.1.mk	PavAGL9/SEP3	3.011325	0.503778	1	1	1	1	1	1	1.403167	0.660109	0.96712	1	1	1	1	1	1	1	1
Pav_sc0002136.1_g280.1.mk	PavAGL11/STK	-0.48238	0.540092	-0.32133	0.856662	-0.45642	0.305838	-0.17655	0.748564	-0.40195	0.451642	0.161046	1	0.025954	0.984447	0.305828	0.603047	0.080425	0.950453	-0.13509
Pav_sc0000502.1_g710.1.mk	PavAGL12/XAL1	-1.41025	0.654879	0.203607	1	-1.91454	0.184372	-1.95576	0.163848	-0.02952	0.999535	1.613851	1	-0.50429	0.857674	1	1	1.380728	0.626841	1
Pav_sc0000960.1_g110.1.mk	PavAGL15	0.135754	0.921397	0.160108	0.976451	-0.03729	0.950887	0.091174	0.866202	0.040418	0.960681	0.024354	1	-0.17304	0.818072	-0.04458	0.950418	-0.09534	0.931704	-0.1974
Pav_sc0002792.1_g290.1.mk	PavAGL16	-0.3806	0.794892	-0.2925	0.954897	-0.40089	0.542763	-0.27591	0.696022	-0.14555	0.889551	0.088099	1	-0.02028	0.993417	0.104691	0.916528	0.235056	0.87903	-0.10838
Pav_sc0000107.1_g160.1.mk	PavAGL19	1.157411	0.758439	0.301176	0.999232	0.820749	0.660154	2.167758	0.165546	1.949615	0.2804	-0.85623	1	1	1	1	1	1	1	1
Pav_sc0000072.1_g690.1.mk	PavAGL20/SOC1	1.174735	0.003654	1.086323	0.009952	1.723641	3.69E-07	1.669224	9.18E-07	2.037133	5.6E-10	-0.08841	1	0.548905	0.352983	0.494489	0.353733	0.862398	0.091889	0.637318
Pav_sc0000257.1_g1300.1.mk	PavAGL22/SVP	-0.01111	1	-0.07375	1	0.79094	0.296173	0.677004	0.375496	0.52355	0.59387	-0.06264	1	0.802053	0.442298	0.688116	0.458513	0.534663	0.736339	0.864691
Pav_sc0003614.1_g200.1.mk	PavAGL22/SVP	1.120205	0.394977	0.742517	0.757302	1.523426	0.048075	2.307693	0.001521	0.865847	0.382042	-0.37769	1	0.403221	0.813405	1.187489	0.250045	-0.25436	0.919029	0.780909
Pav_co4051349.1_g010.1.mk	PavAGL29	-0.36822	0.790989	-0.29636	0.942132	0.159961	0.84025	-0.43788	0.459483	-0.67098	0.267462	0.071861	1	0.528178	0.526075	-0.06967	0.943616	-0.30277	0.813615	0.456318
Pav_sc0000103.1_g1750.1.mk	PavAGL29	0.161842	0.947377	0.578045	0.730117	0.648494	0.319448	1.420483	0.016474	0.355048	0.691793	0.416203	1	0.486652	0.645392	1.258641	0.085674	0.193205	0.915551	0.070449
Pav_sc0000465.1_g1310.1.mk	PavAGL29	0.443194	0.950893	2.733383	0.519169	-0.0559	0.987825	-0.28177	0.907591	-0.39634	0.891809	2.290189	1	-0.49909	0.895066	1	1	-0.83953	0.843807	1
Pav_sc0001342.1_g290.1.mk	PavAGL32/TT16/ABS	0.349317	0.973255	0.682888	0.993647	3.279454	0.206091	6.398925	0.013343	0.303377	0.953918	0.333571	1	2.930137	0.429213	6.049608	0.050503	-0.04594	0.998598	2.596567
Pav_sc0001405.1_g300.1.mk	PavAGL42	0.327529	0.527645	0.163085	0.93419	0.314002	0.286871	0.333401	0.239902	0.344386	0.287971	-0.16444	1	-0.01353	0.989751	0.005872	0.993597	0.016857	0.987693	0.150917
Pav_sc0001060.1_g140.1.mk	PavAGL47	0.958274	0.425719	0.222042	0.990859	0.199534	0.840899	0.16158	0.873218	0.84153	0.315515	-0.73623	1	-0.75874	0.483296	-0.79669	0.384504	-0.11674	0.960554	-0.02251
Pav_sc0000110.1_g290.1.mk	PavAGL61/DIA	0.26368	0.975951	0.340869	1	-0.59853	0.822239	0.948173	0.729086	0.999507	0.768732	0.077189	1	1	1	1	1	1	1	1
Pav_sc0000820.1_g020.1.mk	PavAGL61/DIA	-0.94277	0.762925	-0.12014	1	0.478755	0.807816	1.260904	0.46496	0.291149	0.91296	0.822626	1	1.421525	0.465853	1	1	1.233919	0.621699	1
Pav_sc0001189.1_g080.1.mk	PavAGL61/DIA	0.315826	0.974269	0.124114	1	0.857157	0.787106	1.023422	0.729997	1.863226	0.557908	-0.19171	1	1	1	1	1	1	1	1
Pav_sc0001938.1_g360.1.mk	PavAGL80/FEM111	-0.15053	0.946229	0.042222	1	0.624735	0.300816	0.22239	0.761728	-0.36941	0.627903	0.192747	1	0.77526	0.304867	0.372915	0.635773	-0.21889	0.881677	0.582513
Pav_sc0006825.1_g010.1.br	PavAGL80/FEM111	1	1	1	1	1	1	1	1	1	1	0.073987	1	1	1	1	1	1	1	1
Pav_sc0006281.1_g040.1.br	PavAGL103	-0.96832	0.843705	-2.27455	0.389935	-0.34627	0.899702	1.829092	0.477299	-2.16996	0.230507	-1.30622	1	0.622056	0.859472	1	1	-1.20164	0.702323	1.928276
Pav_sc0008273.1_g020.1.br	PavAGL103	0.159951	0.837444	0.028388	1	0.100322	0.79334	0.094523	0.801204	0.3136	0.341955	-0.13156	1	-0.05963	0.924671	-0.06543	0.888964	0.153649	0.826757	0.071934
Pav_sc0000044.1_g960.1.mk	PavAP3	-0.05791	0.97671	-0.32818	0.859703	0.172923	0.783828	-0.24019	0.655774	-0.26622	0.68125	-0.27028	1	0.23083	0.797333	-0.18228	0.789678	-0.20831	0.856095	0.501106
Pav_sc0000195.1_g010.1.mk	PavPI	0.93412	0.753097	-0.24582	0.997635	2.311263	0.098987	0.146388	0.933917	0.206548	0.926784	-1.17994	1	1.377143	0.570451	1	1	-0.72757	0.804667	1

3 300 mg/L	70 % vs GA3 500 mg/L		tOH 70 % vs O.P. 7 DA		0 mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 7 D		3 500 mg/L vs O.P. 7 D		N.C. 7 vs 14 DAT		EtOH 70% 7 vs 14 DAT		A3 300 mg/L 7 vs 14 DA		A3 500 mg/L 7 vs 14 D		O.P. 7 vs 14 DAT		N.C. vs EtOH 14 DAT		. vs GA3 30
p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
2.76E-06	0.337657	0.000114	0.145878	0.260357	-0.05875	1	-0.25052	0.00751	-0.19178	0.075664	0.135238	0.337837	0.176878	0.101751	-0.10534	0.27269	-0.04275	0.713915	0.169123	0.080457	-0.03191	0.970201	0.08227
0.764405	0.812478	0.133725	0.023141	0.992109	0.586628	1	-0.20271	0.80773	-0.78934	0.222855	-0.12637	0.93524	0.447831	0.529977	0.108645	0.873691	-0.46879	0.403138	0.517899	0.375383	0.281752	0.919928	0.168416
0.263569	0.36357	0.102822	0.222106	0.524045	0.083428	1	-0.05804	0.880577	-0.14146	0.699972	0.234715	0.527216	0.178004	0.570271	-0.25127	0.240385	-0.21945	0.322635	-0.30566	0.180514	-0.1666	0.88522	-0.31573
0.563198	-0.32771	0.194019	-0.23045	0.556925	-0.14734	1	-0.05007	0.910965	0.097262	0.832569	-0.18005	0.713453	-0.19157	0.578422	-0.29982	0.191888	-0.25411	0.286355	0.095729	0.77027	-0.10516	0.946529	-0.39378
0.030251	1.083482	0.025053	0.559355	0.435977	-0.00369	1	-0.52782	0.415688	-0.52413	0.467242	0.007532	0.99999	0.344094	0.622763	0.079445	0.912889	0.374908	0.521333	1.431931	0.004315	-0.19226	0.956823	0.630262
0.00684	0.289279	0.064091	0.237153	0.25874	-0.12186	1	-0.17399	0.378607	-0.05213	0.868604	0.186117	0.456585	0.186079	0.352634	-0.28783	0.040549	-0.17125	0.270056	-0.11509	0.53488	-0.09181	0.916571	-0.15457
0.903401	-0.03852	0.972617	-0.12246	0.944334	0.093088	1	0.009146	0.996831	-0.08394	0.958124	0.187172	0.919058	0.052132	0.964875	0.428474	0.543441	0.100562	0.910596	0.220895	0.809588	0.200008	0.972736	0.444747
1	1	1	-1.29408	0.72931	-0.90978	1	1	1	1	1	-0.66349	0.899994	0.328937	0.934328	1.298031	0.544673	4.380146	0.041088	1.210267	0.621953	1.299271	0.90723	1
0.671055	0.010712	0.992273	0.276454	0.836019	-0.35463	1	-0.08889	0.941744	0.265742	0.820986	-1.07871	0.155966	-1.1886	0.069149	-2.64984	4.74E-08	-2.55989	1.04E-07	-2.34291	3.66E-06	-0.19626	0.969836	-1.29217
0.961695	0.09039	0.763391	-0.11038	0.804296	0.072468	1	-0.1283	0.691512	-0.20077	0.528564	-0.07664	0.893237	-0.10579	0.76065	-0.01274	0.970574	-0.27941	0.176429	0.26682	0.246015	-0.15046	0.897208	-0.03948
0.805063	-0.02414	0.954001	0.066366	0.91419	-0.11471	1	-0.02421	0.962127	0.090502	0.847113	-0.13333	0.808088	-0.10758	0.787212	-0.19037	0.451003	-0.15859	0.551668	-0.14422	0.630354	-0.05628	0.981547	-0.0485
1	1	1	1	1	0.152042	1	1	1	1	1	1.018318	0.895252	1	1	4.074196	0.091519	0.359465	0.905263	1	1	-2.2608	0.874391	1
0.833253	0.144782	0.810384	-0.08062	0.941309	0.279874	1	0.054471	0.945354	-0.2254	0.752562	-0.14571	0.893462	-0.15394	0.829003	0.163526	0.739132	-0.12468	0.811347	-0.36686	0.432414	0.152819	0.964513	0.335194
1	1	1	-0.23312	0.956866	-0.04122	1	1	1	1	1	2.643876	0.215207	1.98394	0.461783	2.052348	0.12368	1.7577	0.189501	-1.0671	0.530716	0.953916	0.942997	1
0.699013	-0.06893	0.909033	-0.11969	0.89019	0.128461	1	0.077705	0.90843	-0.05076	0.955048	-0.00078	1	-0.05417	0.935957	0.299139	0.432195	0.338636	0.372007	0.057059	0.922768	-0.02904	1	0.126874
0.90526	0.016592	0.985922	0.146956	0.916849	0.124975	1	0.25534	0.768196	0.130364	0.911111	0.071823	0.970835	0.537137	0.471522	-0.17266	0.796422	-0.11502	0.875103	-0.28798	0.681185	0.553414	0.844343	-0.26477
1	1	1	1	1	1.347009	1	1	1	1	1	1.84406	0.518288	1	1	4.319629	0.026435	0.692101	0.752027	1	1	-0.74196	0.949761	1
0.166712	0.582901	0.185444	0.950811	0.042897	-0.05442	1	0.313493	0.596287	0.367909	0.566456	0.477444	0.483853	0.58199	0.258645	-0.70953	0.06282	-0.64539	0.096505	-1.17355	0.00192	0.016134	1	-0.63807
0.281764	0.750755	0.33011	0.597301	0.610742	-0.11394	1	-0.26739	0.821599	-0.15345	0.921807	0.091858	0.969608	-0.7232	0.39945	-1.19489	0.057293	-1.27859	0.037307	-0.67032	0.385755	-0.8777	0.732999	-0.48469
0.435701	1.565177	0.064169	0.12333	0.95659	0.784268	1	-0.65758	0.558558	-1.44185	0.14777	0.455139	0.808174	0.54037	0.657424	-0.35757	0.713406	-0.75736	0.399986	0.587091	0.548676	-0.29246	0.967475	-0.40949
0.495025	-0.14153	0.861104	-0.37463	0.682211	-0.59784	1	-0.83094	0.152168	-0.2331	0.804184	-0.11252	0.945187	0.170533	0.85211	-0.89272	0.059676	0.0662	0.927765	0.749192	0.166555	0.354912	0.897724	-0.25202
0.946623	0.842438	0.245042	-0.223	0.872812	0.771989	1	-0.29345	0.761686	-1.06544	0.180913	0.268653	0.850185	0.090294	0.936756	-0.59043	0.328692	-1.06407	0.084377	0.485819	0.509476	0.237844	0.957492	-0.37243
1	1	1	-3.12972	0.279625	-0.22587	1	-0.34044	0.903323	-0.11457	0.977709	-0.91271	0.798761	-2.22866	0.453928	0.013634	1	1.997112	0.313393	1.484765	0.463233	0.974237	0.911581	0.427249
0.388122	5.716037	0.043589	-0.37951	0.953439	3.119471	1	-2.97608	0.3331	-6.09555	0.047907	-0.31341	0.970285	-0.94043	0.815248	3.205574	0.278661	0	1	-0.1769	0.966377	-0.29345	0.998606	6.449122
0.693952	0.170316	0.629029	0.181301	0.727101	0.019399	1	0.030384	0.957656	0.010985	0.989142	0.333252	0.455829	0.141186	0.746014	0.45547	0.078426	0.339932	0.215738	0.566057	0.041207	-0.35651	0.756209	0.108691
0.985822	-0.06046	0.959141	0.619488	0.603171	-0.03795	1	0.641996	0.491954	0.67995	0.505243	-0.51509	0.726965	0.540309	0.591499	0.385758	0.620338	0.472273	0.537178	-0.27559	0.779477	0.319163	0.941287	0.142105
1	1	1	1	1	1.546699	1	1	1	1	1	-0.12364	0.988716	1	1	0.879835	0.684936	-0.69145	0.79498	1	1	-0.82036	0.942403	1
1	1	1	0.411293	0.899209	0.782149	1	-0.18761	0.944922	-0.96976	0.709916	-0.05354	0.99266	0.914929	0.661131	-0.00241	1	-1.33555	0.398246	-1.06846	0.464476	1.791091	0.719429	1.472652
1	1	1	1	1	0.166266	1	1	1	1	1	5.419075	0.094259	1	1	3.834402	0.141094	2.694628	0.308855	1	1	-1.01855	0.971034	1
0.382502	0.180169	0.823812	-0.41164	0.654366	-0.40234	1	-0.99415	0.089626	-0.5918	0.420794	0.073268	0.968284	0.516746	0.493719	-0.21007	0.762581	0.134067	0.855028	0.840015	0.130225	0.636225	0.790667	0.491923
1	1	1	1	1	0.83983	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	-1.49429	0.936603	1
0.264162	1	1	0.104581	0.980802	2.175361	1	-1.8237	0.326095	-3.99906	0.083489	-0.75891	0.819375	-1.0776	0.536925	-1.62897	0.280998	-3.77946	0.042751	-0.31602	0.867752	-1.62491	0.756351	-0.24801
0.866493	0.066135	0.878835	0.285212	0.50155	-0.0058	1	0.213278	0.568994	0.219077	0.600691	-0.34962	0.386994	-0.18032	0.649007	-0.38773	0.118565	-0.38624	0.122885	-0.70576	0.003879	0.037744	0.995168	-0.09773
0.318391	0.087993	0.898065	0.061964	0.956889	-0.41311	1	-0.43914	0.433985	-0.02603	0.982448	-0.20819	0.83545	-0.18402	0.78132	-0.71937	0.0641	-0.5276	0.175675	-0.46657	0.287986	-0.24611	0.912752	-0.28036
1	1	1	0.452366	0.848459	-2.16488	1	-2.10472	0.196553	0.06016	0.985272	-1.20052	0.543066	-0.00846	0.997996	-1.06014	0.516306	0.598487	0.657376	1.016495	0.473739	0.012119	1	1.517526

0 mg/L 14	. vs GA3 500 mg/L 14		N.C. vs O.P. 14 DAT		40 % vs GA3 300 mg/L		40 % vs GA3 500 mg/L		OH 140 % vs O.P. 14 D		mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 14		3 500 mg/L vs O.P. 14		N.C. 14 vs 21 DAT		tOH 70% 14 vs 21 DA		3 300 mg/L 14 vs 21 D		3 500 mg/L
p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
0.521944	0.086117	0.501022	0.106211	0.502272	0.114183	0.305029	0.118029	0.289671	0.138123	0.19484	0.003847	1	0.023941	0.936727	0.020094	0.947154	-0.05648	0.683125	-0.09128	0.587	-0.41036	1.53E-07	-0.40361
0.851203	0.177608	0.84781	0.374961	0.721483	-0.11334	0.896053	-0.10414	0.910634	0.093209	0.91956	0.009192	1	0.206545	0.887536	0.197353	0.90234	-0.12343	0.884401	-0.46931	0.599334	-0.71	0.125299	-0.77509
0.197873	-0.20049	0.484809	-0.42816	0.106571	-0.14913	0.614646	-0.03389	0.932872	-0.26156	0.295757	0.115242	1	-0.11243	0.841577	-0.22767	0.589944	-0.01877	0.966553	0.003636	0.997289	-0.11236	0.633627	-0.20958
0.125566	-0.49541	0.038249	-0.04831	0.946067	-0.28862	0.290629	-0.39025	0.120046	0.056855	0.883645	-0.10163	1	0.345471	0.355613	0.447103	0.186364	0.121076	0.73631	0.095006	0.853209	-0.04333	0.884884	0.015167
0.288229	0.922036	0.089495	1.454932	0.012074	0.822522	0.115591	1.114296	0.025374	1.647192	0.00102	0.291774	1	0.82467	0.347006	0.532897	0.653976	0.271338	0.70696	0.269699	0.78322	0.806651	0.115799	0.00292
0.433217	-0.15986	0.417622	-0.15582	0.560711	-0.06276	0.790831	-0.06805	0.77427	-0.06401	0.780039	-0.00529	1	-0.00125	1	0.004042	0.997641	0.129202	0.530193	0.054891	0.873153	0.153414	0.313576	0.187117
0.630987	0.209923	0.85771	0.246314	0.881207	0.244739	0.806714	0.009915	0.998411	0.046305	0.972425	-0.23482	1	-0.19843	0.920536	0.03639	0.990031	0.009131	0.996121	-0.07615	0.961502	1.056236	0.075985	0.975887
1	3.112836	0.272187	1	1	-0.35877	0.921374	1.813566	0.603458	1	1	2.172338	1	1	1	1	1	1	1	1	1	2.140763	0.393988	-2.02578
0.023691	-1.55685	0.003725	-1.07412	0.139183	-1.09591	0.059775	-1.36058	0.013014	-0.87786	0.162077	-0.26468	1	0.218047	0.891018	0.482725	0.699441	-1.21576	0.053714	-0.90341	0.310619	-1.0941	0.02858	-1.06809
0.922555	-0.23369	0.378249	0.111775	0.82194	0.110978	0.718419	-0.08323	0.803097	0.262235	0.284362	-0.19421	1	0.151257	0.76143	0.345464	0.300542	-0.02222	0.957049	-0.10699	0.809413	-0.82159	2.68E-06	-0.6071
0.91397	-0.13143	0.724646	-0.02656	0.976792	0.007784	0.988765	-0.07515	0.846923	0.029727	0.947381	-0.08294	1	0.021943	0.981628	0.104878	0.879649	-0.02526	0.95666	-0.07245	0.894335	0.072457	0.796184	-0.01147
1	1	1	1	1	1	1	1	1	1	1	-3.56269	1	1	1	1	1	1	1	1	1	1	1	1
0.545759	0.326866	0.561084	-0.14072	0.892225	0.182375	0.765606	0.174047	0.781475	-0.29354	0.578482	-0.00833	1	-0.47591	0.517997	-0.46758	0.53615	-0.00433	0.997756	-0.06108	0.950602	1.042864	0.002634	1.387994
1	-1.43169	0.526264	1	1	-2.04973	0.392123	-2.3856	0.293927	1	1	-0.33587	1	1	1	1	1	1	1	1	1	-0.39134	0.828582	-0.39577
0.842421	0.294832	0.557141	-0.0375	0.979241	0.155913	0.776487	0.32387	0.488846	-0.00846	0.993039	0.167958	1	-0.16437	0.867069	-0.33233	0.66788	0.21379	0.683125	0.342272	0.593935	1.525474	1.74E-06	1.194856
0.75562	-0.08215	0.943834	-0.12475	0.936028	-0.81818	0.1605	-0.63557	0.321278	-0.67816	0.275986	0.182615	1	0.140023	0.932367	-0.04259	0.985226	-0.2201	0.798533	-0.4525	0.652942	-0.7198	0.146499	-0.20129
1	1	1	1	1	1	1	0.600351	0.832494	1	1	-2.28052	1	1	1	1	1	1	1	1	1	-0.08666	0.984592	-1.14436
0.166412	-0.62834	0.172702	-0.7886	0.12604	-0.6542	0.136734	-0.64447	0.14923	-0.80473	0.056787	0.00973	1	-0.15053	0.89786	-0.16026	0.89849	-0.72235	0.123577	-0.70244	0.263324	0.366177	0.376197	0.13159
0.603706	-0.68233	0.413307	-0.22751	0.893723	0.393011	0.66108	0.19537	0.852447	0.650188	0.405678	-0.19764	1	0.257177	0.888593	0.454819	0.777504	-1.21499	0.092931	-0.15903	0.913303	-1.03235	0.07338	-1.09928
0.749951	-0.02501	0.994535	-0.12241	0.965016	-0.11704	0.933687	0.267443	0.840873	0.17005	0.902347	0.384478	1	0.287086	0.902431	-0.09739	0.97457	-0.50654	0.663073	-0.37879	0.821832	0.042661	0.972803	-0.42808
0.746333	0.109053	0.915172	0.558944	0.518239	-0.60693	0.29912	-0.24586	0.750348	0.204032	0.797288	0.361075	1	0.810966	0.304327	0.449891	0.693082	0.534288	0.411619	0.321978	0.762218	0.755408	0.110447	0.10822
0.658367	-0.07408	0.956083	0.410372	0.756192	-0.61027	0.3922	-0.31193	0.728894	0.172527	0.864533	0.298345	1	0.7828	0.461085	0.484455	0.737741	-0.04018	0.974798	-0.07042	0.962918	1.159417	0.043715	-0.1786
0.873281	2.184855	0.353792	1	1	-0.54699	0.833016	1.210619	0.67838	0.583707	0.840996	1.757606	1	1	1	1	1	1	1	1	1	-0.99059	0.515712	-1.40958
0.02117	6.396835	0.022303	0.090576	0.995706	6.742569	0.012574	6.690282	0.013519	0.384023	0.926384	0	1	-6.35855	0.091143	-6.30626	0.09936	1	1	-0.84232	0.867276	0	1	0
0.821905	0.012553	0.988305	0.249663	0.641378	0.465201	0.110151	0.369062	0.240384	0.606172	0.032192	-0.09614	1	0.140971	0.853587	0.23711	0.711898	-0.18431	0.63757	-0.16325	0.766735	-0.66733	0.005169	-0.50161
0.913072	0.190665	0.884932	0.122756	0.955175	-0.17706	0.87899	-0.1285	0.920229	-0.19641	0.861598	0.04856	1	-0.01935	0.999792	-0.06791	0.980501	0.444895	0.655866	-0.40068	0.77563	0.273171	0.736885	-0.57813
1	1	1	1	1	1	1	0.937033	0.733197	1	1	-0.02459	1	1	1	1	1	1	1	1	1	0.231613	0.93242	-2.07227
0.338868	0.921662	0.581334	1	1	-0.31844	0.896053	-0.86943	0.65918	-1.57209	0.307671	-0.55099	1	1	1	1	1	1	1	1	1	-2.11096	0.059311	-0.67229
1	1	1	1	1	1	1	-0.9983	0.840021	1	1	-0.97351	1	1	1	1	1	1	1	1	1	0.879903	0.814267	1.776629
0.485018	0.433715	0.55901	0.547858	0.559394	-0.1443	0.875849	-0.20251	0.819971	-0.08837	0.931175	-0.05821	1	0.055935	0.979567	0.114143	0.949406	-0.2774	0.713825	-0.58786	0.523687	-0.73515	0.140776	-1.10614
1	1	1	1	1	1	1	1	1	1	1	-1.01546	1	1	1	1	1	1	1	1	1	1	1	1
0.921687	-0.22313	0.937787	-0.75874	0.79473	1.376905	0.355657	1.401777	0.351707	0.866168	0.588915	0.024872	1	-0.51074	0.887536	-0.53561	0.889114	1	1	1	1	-0.97062	0.454891	-0.60937
0.827344	-0.10205	0.824468	-0.20249	0.693676	-0.13548	0.718419	-0.13979	0.717515	-0.24023	0.451845	-0.00431	1	-0.10476	0.884959	-0.10044	0.899117	0.012651	0.983076	-0.08477	0.885638	-0.00315	0.997617	0.167574
0.625583	-0.5017	0.283468	-0.46669	0.459312	-0.03425	0.963936	-0.25559	0.640044	-0.22058	0.683114	-0.22134	1	-0.18634	0.858369	0.035009	0.981254	-0.21566	0.718129	-0.1476	0.863206	0.085009	0.862654	0.265619
0.275387	1.011274	0.496857	1	1	1.505407	0.264715	0.999155	0.487903	1.477323	0.276278	-0.50625	1	1	1	1	1	1	1	1	1	2.879746	0.11785	0.621834

14 vs 21 D	O.P. 14 vs 21 DAT		N.C. vs EtOH 21 DAT		. vs GA3 300 mg/L 21		. vs GA3 500 mg/L 21		N.C. vs O.P. 21 DAT		10 % vs GA3 300 mg/L		10 % vs GA3 500 mg/L		OH 210 % vs O.P. 21 D		mg/L vs GA3 500 mg/		300 mg/L vs O.P. 21		500 mg/L vs O.P. 21		N.C. 21 v
p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
2.12E-07	-0.08037	0.566042	-0.06671	1	-0.27161	0.000741	-0.26101	0.001528	0.082323	0.458546	-0.2049	0.014224	-0.1943	0.024957	0.149035	0.103017	0.010597	1	0.353934	2.09E-05	0.343337	3.68E-05	-0.03568
0.083086	-0.51157	0.470109	-0.06413	1	-0.41816	0.423281	-0.47406	0.36264	-0.01318	0.991969	-0.35403	0.508728	-0.40993	0.443076	0.05095	0.947629	-0.0559	1	0.40498	0.451406	0.460881	0.360828	-0.12482
0.31482	-0.15719	0.633776	-0.14419	1	-0.40932	0.038087	-0.39129	0.054556	-0.56657	0.003401	-0.26513	0.211843	-0.2471	0.267207	-0.42238	0.032802	0.018022	1	-0.15726	0.513257	-0.17528	0.441572	0.035776
0.965128	0.106833	0.794914	-0.13123	1	-0.55819	0.006962	-0.60132	0.00374	-0.06255	0.86125	-0.42696	0.046187	-0.47009	0.029724	0.068682	0.825131	-0.04313	1	0.495638	0.02509	0.538769	0.012632	-0.60163
1	0.839424	0.302027	-0.1939	1	1.165576	0.016612	0.653618	0.218099	2.023018	0.000106	1.359474	0.003363	0.847517	0.088209	2.216917	1.12E-05	-0.51196	1	0.857443	0.18493	1.3694	0.017819	0.423482
0.194249	0.045847	0.877538	-0.16612	1	-0.13036	0.432718	-0.10194	0.571891	-0.23917	0.12222	0.035759	0.863061	0.064173	0.742971	-0.07305	0.699095	0.028414	1	-0.10881	0.530025	-0.13723	0.393611	0.163151
0.09558	-0.17132	0.892583	0.114726	1	1.491852	0.009487	1.176679	0.054079	0.06586	0.954122	1.377127	0.016903	1.061953	0.087788	-0.04887	0.9622	-0.31517	1	-1.42599	0.019182	-1.11082	0.068836	1.026641
0.419613	1	1	-1.34131	1	0.800372	0.824226	-1.19383	0.684899	1.750104	0.607099	2.141678	0.41522	0.147473	0.965275	3.09141	0.213989	-1.99421	1	1	1	1	1	1
0.029692	-0.56604	0.467033	0.116086	1	-1.17051	0.021103	-1.40918	0.004652	-0.42441	0.534294	-1.2866	0.009022	-1.52527	0.001795	-0.5405	0.367065	-0.23867	1	0.746102	0.185526	0.98477	0.062177	-0.07501
0.000599	-0.4643	0.04009	-0.23523	1	-0.83885	1.01E-06	-0.81857	2.26E-06	-0.3303	0.119173	-0.60362	0.000709	-0.58334	0.001379	-0.09508	0.717049	0.020285	1	0.508547	0.009185	0.488262	0.011623	-0.77867
0.975408	0.144097	0.702059	-0.10347	1	0.04922	0.882555	-0.11764	0.688379	0.142804	0.636354	0.152691	0.567948	-0.01417	0.970705	0.246275	0.31792	-0.16686	1	0.093584	0.751744	0.260444	0.273527	-0.32442
1	1	1	-2.70041	1	-2.59594	0.342081	-1.09296	0.768517	1	1	0.104467	0.977818	1	1	3.554445	0.166162	1.502981	1	1	1	1	1	1
3.3E-05	0.433355	0.423065	0.096075	1	1.382392	3.55E-05	1.719194	1.49E-07	0.29697	0.544441	1.286317	0.00013	1.623119	8.04E-07	0.200895	0.683485	0.336802	1	-1.08542	0.00322	-1.42222	6.23E-05	0.858189
0.815121	1	1	2.829246	1	-1.43321	0.421164	-1.77351	0.302502	-2.03208	0.237207	-4.26246	0.02368	-4.60276	0.014867	-4.86132	0.008741	-0.3403	1	1	1	1	1	1
0.000197	0.51347	0.253081	0.099443	1	1.438558	5.36E-06	1.275898	7.28E-05	0.26218	0.557209	1.339115	2.6E-05	1.176455	0.000315	0.162736	0.721045	-0.16266	1	-1.17638	0.000778	-1.01372	0.003786	0.444735
0.735994	0.102948	0.93065	0.321005	1	-0.76447	0.134249	-0.06334	0.938177	0.198298	0.795986	-1.08548	0.021824	-0.38435	0.529694	-0.12271	0.865904	0.701133	1	0.962773	0.059079	0.26164	0.672871	0.632686
0.516961	1	1	3.149901	1	2.110938	0.385578	-1.22728	0.535525	1	1	-1.03896	0.75527	-4.37718	0.030851	0	1	-3.33822	1	1	1	1	1	1
0.779196	-0.04341	0.965539	0.036046	1	0.450458	0.283253	0.225601	0.650025	-0.10966	0.85945	0.414411	0.325736	0.189554	0.71005	-0.14571	0.781413	-0.22486	1	-0.56012	0.171793	-0.33526	0.439687	-0.28611
0.047344	-0.21056	0.867245	0.17825	1	-0.30205	0.685637	-0.56663	0.402486	0.776912	0.25444	-0.4803	0.479485	-0.74488	0.241995	0.598662	0.379129	-0.26457	1	1.078965	0.079655	1.343539	0.021807	-0.60335
0.623468	-0.25135	0.872956	-0.1647	1	0.139712	0.903601	0.05345	0.967237	0.132782	0.919005	0.304415	0.760583	0.218152	0.84075	0.297485	0.769812	-0.08626	1	-0.00693	1	0.079332	0.947335	0.019452
0.860247	-0.14006	0.895247	0.142602	1	-0.0309	0.974627	-0.31702	0.607681	-0.1154	0.888656	-0.1735	0.800276	-0.45962	0.425194	-0.25801	0.690696	-0.28611	1	-0.0845	0.910209	0.201612	0.747828	0.126992
0.792159	-0.42674	0.661482	0.207599	1	0.827169	0.195498	-0.21251	0.780011	0.023809	0.985617	0.619569	0.36382	-0.42011	0.534846	-0.18379	0.814518	-1.03968	1	-0.80336	0.228933	0.236317	0.738681	-0.23937
0.49115	1	1	-0.18343	1	-0.84429	0.60993	0.494326	0.816791	0.894544	0.680385	-0.66086	0.696248	0.677754	0.732622	1.077973	0.569012	1.338618	1	1.738836	0.296129	0.400219	0.86101	-0.27578
1	-0.18077	0.977847	-0.04824	1	7.448508	0.002075	7.371726	0.002773	0.997334	0.752556	7.496744	0.001744	7.419962	0.002457	1.045569	0.712477	0	1	-6.45117	0.013877	-6.37439	0.013767	1.030323
0.039162	-0.50852	0.113052	-0.33545	1	-0.37433	0.1582	-0.30474	0.284395	-0.07454	0.857905	-0.03888	0.920062	0.03071	0.941018	0.26091	0.36443	0.069587	1	0.299787	0.290755	0.2302	0.424791	-0.38789
0.393808	0.236874	0.860766	-0.52641	1	-0.02962	0.983623	-0.83236	0.241041	-0.08526	0.946303	0.496791	0.522404	-0.30595	0.716214	0.441146	0.586946	-0.80274	1	-0.05565	0.960767	0.747096	0.285703	-1.23077
0.21416	1	1	0.567627	1	1.791337	0.35353	-0.53713	0.80266	1	1	1.22371	0.563313	-1.10476	0.563355	0.233652	0.92781	-2.32847	1	1	1	1	1	1
0.60211	1	1	-0.40075	1	-1.67995	0.135299	-0.79228	0.578634	-1.00339	0.477108	-1.2792	0.256656	-0.39153	0.801232	-0.60264	0.667741	0.887675	1	0.676566	0.590094	-0.21111	0.890491	0.467016
0.574338	1	1	-0.97599	1	0	1	0	1	1	1	0.883082	0.828297	0.8063	0.850724	-1.57182	0.652366	0	1	1	1	1	1	1
0.014373	-0.40888	0.625391	0.325771	1	0.034174	0.970293	-0.39502	0.481035	0.416386	0.49729	-0.2916	0.625421	-0.72079	0.150436	0.090615	0.903088	-0.4292	1	0.382212	0.513438	0.811409	0.097468	0.763018
1	1	1	-0.57269	1	1	1	1	1	1	1	1	1	1	1	1	1	-0.16057	1	1	1	1	1	1
0.662446	0.807978	0.697728	-0.50697	1	0.018747	0.997351	0.404866	0.804852	1.286606	0.373906	0.525715	0.716465	0.911834	0.50579	1.793574	0.15106	0.386119	1	1.267859	0.354194	0.88174	0.540657	0.304565
0.533714	0.207182	0.590019	-0.05968	1	-0.11353	0.721504	0.052878	0.887003	-0.00796	0.990457	-0.05386	0.878648	0.112555	0.732044	0.051721	0.886505	0.166412	1	0.105577	0.744357	-0.06083	0.858881	-0.24574
0.510207	0.311285	0.597618	-0.17805	1	0.020316	0.978372	-0.02042	0.976511	0.060255	0.92679	0.198366	0.669682	0.157631	0.754146	0.238306	0.607223	-0.04073	1	0.03994	0.948731	0.080674	0.881287	0.0176
0.656003	1	1	0.358244	1	3.789922	0.029561	1.025757	0.45922	0.259854	0.882788	3.431678	0.052688	0.667514	0.665429	-0.09839	0.95806	-2.76416	1	-3.53007	0.058007	-0.7659	0.592574	-0.03642

s 28 DAT	EtOH 70% 21 vs 28 DAT		3 300 mg/L 21 vs 28 D		3 500 mg/L 21 vs 28 D		O.P. 21 vs 28 DAT		N.C. vs EtOH 28 DAT		. vs GA3 300 mg/L 28		. vs GA3 500 mg/L 28		N.C. vs O.P. 28 DAT		30 % vs GA3 300 mg/L		30 % vs GA3 500 mg/L		OH 280 % vs O.P. 28 D		mg/L vs GA
p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
0.765648	-0.04465	0.648289	-0.27475	0.000195	-0.50689	9.75E-13	-0.33361	0.000125	-0.07568	0.606339	-0.51068	2.19E-12	-0.73223	5.47E-25	-0.21561	0.007805	-0.435	5.76E-09	-0.65655	6.3E-20	-0.13992	0.085586	-0.22154
0.848654	0.127649	0.812675	0.593361	0.164437	0.670378	0.108104	-0.18056	0.818396	0.188342	0.8279	0.300024	0.547037	0.32114	0.493447	-0.06892	0.916067	0.111682	0.865217	0.132799	0.808315	-0.25726	0.600627	0.021116
0.907392	0.333429	0.080972	1.258177	3.16E-14	1.36593	7.74E-17	0.129462	0.682079	0.153463	0.652125	0.813085	2.26E-06	0.938861	2.18E-08	-0.47289	0.010762	0.659622	0.000249	0.785398	5.58E-06	-0.62635	0.000271	0.125776
0.005754	-0.5643	0.004934	-0.86331	1.75E-06	-0.97564	3.61E-08	-0.07758	0.843254	-0.0939	0.816084	-0.81987	9.84E-06	-0.97534	5.7E-08	0.461493	0.024649	-0.72597	0.000161	-0.88144	1.71E-06	0.555397	0.003616	-0.15547
0.446693	0.163553	0.756989	-0.50632	0.318184	-0.9264	0.027996	-0.20224	0.859791	-0.45383	0.560012	0.23577	0.674024	-0.69626	0.10652	1.397295	0.005134	0.689598	0.176074	-0.24243	0.626238	1.851123	5.33E-05	-0.93203
0.317736	0.36727	0.005514	0.262521	0.037806	0.083625	0.556772	-0.13855	0.496088	0.038001	0.896204	-0.03099	0.859978	-0.18147	0.171174	-0.54088	1.75E-05	-0.06899	0.700203	-0.21947	0.102091	-0.57888	1.77E-06	-0.15048
0.105091	1.83201	0.001084	2.743751	7.52E-06	2.210833	7.91E-05	0.198242	0.853468	0.920095	0.313727	3.208962	2.01E-07	2.360871	2.99E-05	-0.76254	0.216851	2.288868	0.00056	1.440777	0.019278	-1.68263	0.001563	-0.84809
1	1.147582	0.634656	-4.76252	0.011136	-3.8519	0.011203	1	1	1	1	-2.29132	0.162562	-3.3749	0.023333	1.759792	0.466044	-3.76843	0.058072	-4.85201	0.006947	0.282691	0.929817	1
0.927185	-0.14756	0.810298	1.820043	3.73E-05	2.855041	5.5E-11	-0.64233	0.358497	0.04354	0.971402	0.724541	0.148554	1.520871	0.000875	-0.99173	0.047735	0.681001	0.212341	1.477331	0.00174	-1.03527	0.02792	0.79633
5.93E-05	-0.61539	0.000596	-0.32702	0.057816	-0.60956	0.000163	-0.40242	0.081041	-0.07195	0.846336	-0.3872	0.02803	-0.64946	7.32E-05	0.045948	0.862987	-0.31525	0.102705	-0.57751	0.000659	0.117901	0.570586	-0.26225
0.174167	-0.3513	0.094369	-1.05791	5.24E-09	-1.18341	2.79E-11	0.014367	0.979561	-0.13035	0.736727	-0.68427	0.000308	-0.97663	7.14E-08	0.481593	0.019227	-0.55392	0.006029	-0.84628	5.55E-06	0.611944	0.00131	-0.29236
1	1	1	1.155791	0.616776	-3.23925	0.098306	1	1	1	1	0.13871	0.967957	-2.75335	0.147592	1.623087	0.584449	-1.21171	0.712726	1	1	0.27267	0.942289	1
0.024921	1.2108	0.000414	2.154659	4.97E-12	1.510992	1.07E-06	0.579869	0.22069	0.448687	0.443958	2.678862	4.62E-18	2.371997	1.49E-14	0.018651	0.978345	2.230175	1.66E-12	1.92331	1.13E-09	-0.43004	0.237324	-0.30686
1	-3.02378	0.135556	0.934654	0.539379	3.086614	0.068447	1	1	1	1	-0.85848	0.66023	0.953178	0.666717	-2.89381	0.055687	-0.30402	0.900603	1.50764	0.47754	-2.33935	0.088527	1
0.240808	0.343395	0.325476	1.802401	5.87E-06	1.896588	1.09E-06	0.681629	0.103533	-0.0019	0.99825	2.796223	3.05E-13	2.727751	6.88E-13	0.499074	0.159029	2.798121	5.6E-13	2.729648	1.37E-12	0.500971	0.13115	-0.06847
0.256422	0.595716	0.236184	1.282923	0.002515	0.252406	0.614391	-0.38912	0.606468	0.284036	0.753325	-0.11424	0.852247	-0.44362	0.355326	-0.82351	0.091938	-0.39827	0.490029	-0.72766	0.125008	-1.10754	0.013193	-0.32938
1	1	1	-2.89774	0.124912	0.949483	0.55786	1	1	1	1	-2.02654	0.288704	-1.51754	0.439466	0.082889	0.985622	-3.7127	0.069177	-3.20369	0.111264	-1.60327	0.514329	1
0.534141	-0.3535	0.362681	-0.34855	0.333198	-0.4048	0.245197	-0.0453	0.956207	-0.03134	0.971402	0.388013	0.298956	0.106912	0.795038	0.131151	0.79095	0.419354	0.295685	0.138254	0.741067	0.162493	0.698587	-0.2811
0.359544	-0.90528	0.100862	-1.45779	0.002496	-1.39257	0.003319	-0.76697	0.326657	-0.12368	0.916423	-1.1565	0.022327	-1.35585	0.004958	0.613286	0.314461	-1.03281	0.058341	-1.23216	0.013947	0.736969	0.177098	-0.19935
0.990023	0.393921	0.633134	1.545455	0.032698	1.983237	0.006388	0.480235	0.690837	0.209766	0.889559	1.665715	0.024832	2.017234	0.006235	0.593565	0.486419	1.455949	0.072476	1.807468	0.019512	0.383799	0.642992	0.351519
0.858088	-0.00471	0.997145	0.30291	0.554209	1.273648	0.006312	-0.17207	0.841523	0.010897	0.991176	0.145016	0.813158	0.82964	0.099367	-0.41447	0.441896	0.134118	0.850156	0.818743	0.119049	-0.42537	0.39081	0.684625
0.736291	-0.36324	0.536077	-1.22958	0.018635	-0.79163	0.085307	-0.71406	0.300787	0.083728	0.944014	-0.16304	0.79517	-0.76477	0.100454	-0.45088	0.424277	-0.24677	0.715634	-0.8485	0.078476	-0.53461	0.294575	1
0.893967	-2.43518	0.034484	-1.34142	0.225445	-3.30075	0.003757	1	1	1	1	-1.90993	0.100188	-2.53064	0.017896	0.069188	0.977563	0.432888	0.763116	-0.18782	0.884157	2.412008	0.028551	1
0.713364	6.384811	0.007904	0	1	0	1	1.391063	0.68539	1	1	5.994985	0.009742	5.935202	0.008347	1.358074	0.592331	0.688733	0.868326	0.628949	0.856186	-3.94818	0.107975	1
0.153239	-0.26123	0.29712	-0.30255	0.186509	-0.25211	0.280716	0.483707	0.124384	-0.20879	0.613398	-0.28899	0.230664	-0.16896	0.4959	0.797057	0.000518	-0.0802	0.80739	0.039831	0.893231	1.005845	3.32E-06	0.12003
0.061768	-0.51972	0.41927	-2.77502	6.22E-08	-2.13133	1.2E-05	0.363082	0.741242	0.184635	0.876918	-1.57387	0.001987	-1.73292	0.000406	1.508587	0.011286	-1.7585	0.000889	-1.91755	0.000155	1.323952	0.022858	-0.15905
1	1	1	-0.30944	0.885471	1.273292	0.402192	1	1	1	1	-2.26123	0.308492	-3.00697	0.127142	-3.19144	0.131229	1.389812	0.478729	0.644072	0.717973	0.459606	0.800514	1
0.784413	1.907708	0.183555	1.930467	0.06634	2.575071	0.075661	1	1	1	1	-0.2165	0.895715	1.315777	0.435258	-2.10661	0.057186	-1.25645	0.476779	0.275835	0.903516	-3.14655	0.011868	1
1	1	1	-1.37999	0.639776	-3.63226	0.115245	1	1	1	1	-1.42345	0.653108	-3.75251	0.110139	-3.88832	0.126467	1.634702	0.596832	-0.69435	0.789052	-0.83017	0.743886	1
0.148428	0.173868	0.759546	0.789308	0.085696	1.575387	0.000368	-0.54756	0.399485	-0.26338	0.773793	0.060464	0.929131	0.417346	0.442197	-0.8942	0.057371	0.323842	0.60276	0.680725	0.195602	-0.63082	0.168987	0.356883
1	1	1	1	1	-0.86488	0.751316	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
0.851149	0.829483	0.484891	-1.05199	0.309452	0.572934	0.644813	-1.34147	0.410951	1	1	-1.33781	0.210844	0.673235	0.58382	-0.35943	0.808751	-1.35576	0.244663	0.655284	0.611946	-0.37738	0.772593	1
0.373122	-0.21714	0.377795	-0.40668	0.054537	-0.97999	5.69E-07	-0.07075	0.87646	-0.03107	0.955363	-0.27447	0.234087	-0.68137	0.000662	0.167036	0.54341	-0.2434	0.34427	-0.6503	0.001718	0.19811	0.415381	-0.4069
0.978848	0.222838	0.577506	-0.52416	0.113519	-0.67322	0.03314	-0.60126	0.175175	0.027187	0.974165	-0.52145	0.131942	-0.71124	0.025541	-0.55861	0.111724	-0.54864	0.143671	-0.73843	0.026636	-0.58579	0.078646	-0.18979
0.985513	0.36476	0.781243	-2.31568	0.194547	3.261007	0.042217	1	1	1	1	1.510656	0.227772	4.32318	0.004564	2.47072	0.069878	0.751237	0.645341	3.563761	0.030276	1.711301	0.226563	1

A3 500 mg/	3 300 mg/L vs O.P. 28		3 500 mg/L vs O.P. 28	
p-adj	Log2FC	p-adj	Log2FC	p-adj
0.032974	0.295079	4.68E-05	0.516623	1.76E-13
0.989708	-0.36894	0.410519	-0.39006	0.361682
0.701628	-1.28597	4.06E-15	-1.41175	3.1E-18
0.641789	1.281364	4.17E-13	1.436832	1.65E-16
0.144565	1.161525	0.016895	2.093556	1.67E-06
0.461294	-0.50989	1.73E-05	-0.35941	0.002517
0.44313	-3.9715	1.76E-11	-3.12341	7.84E-09
1	4.051116	0.021612	5.134696	0.00226
0.266431	-1.71627	8.75E-05	-2.5126	6.35E-09
0.315891	0.433153	0.009179	0.695407	1.2E-05
0.319366	1.165861	6.21E-11	1.458222	9.89E-17
1	1.484377	0.571403	4.376436	0.027719
0.590939	-2.66021	3.99E-18	-2.35335	7.95E-15
1	-2.03533	0.121483	-3.84699	0.015997
0.956302	-2.29715	1.84E-09	-2.22868	3.43E-09
0.680061	-0.70927	0.110966	-0.37989	0.401548
1	2.109428	0.235651	1.600424	0.380112
0.630704	-0.25686	0.486575	0.024239	0.957174
0.840484	1.769783	0.000176	1.969133	2.03E-05
0.829299	-1.07215	0.152741	-1.42367	0.054086
0.38824	-0.55948	0.226993	-1.24411	0.006467
1	-0.28784	0.577531	0.31389	0.496833
1	1.979119	0.069893	2.599823	0.011273
1	-4.63691	0.042463	-4.57713	0.040209
0.780362	1.086044	2.53E-07	0.966014	4.39E-06
0.880353	3.082455	1.58E-09	3.241506	1.19E-10
1	-0.93021	0.594831	-0.18447	0.917993
1	-1.89011	0.068837	-3.42239	0.01153
1	-2.46487	0.298683	-0.13582	0.958969
0.698081	-0.95466	0.029746	-1.31154	0.003042
1	-2.30509	0.36977	1	1
1	0.978378	0.342061	-1.03267	0.340632
0.183327	0.441507	0.032886	0.848409	1.07E-05
0.754621	-0.03716	0.930114	0.152633	0.647073
1	0.960064	0.545283	-1.85246	0.305261

Table S4.13: Table with Log2FoldChange (log2FC) and p-value adjusted (p-adj) of the genes that encode for NAC transcription factors. The heatmap of these genes is showed in Fig. 4.25. Log2FC is calculated according to the following formula: expression level term1 - expression level term2.

Gene name	Gene description	N.C. 0 vs 7 DAT		EtOH 70% 0 vs 7 DAT		A3 300 mg/L 0 vs 7 DA		A3 500 mg/L 0 vs 7 DA		O.P. 0 vs 7 DAT		N.C. vs EtOH 7 DAT		C. vs GA3 300 mg/L 7 D		C. vs GA3 500 mg/L 7 D		N.C. vs O.P. 7 DAT		70 % vs GA3
		Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
Pav_sc0000195.1_g410.1.mk	PavANAC002	-1.03065	0.333165	-1.07954	0.303669	-0.93411	0.185386	-0.31968	0.724699	0.58858	0.533877	-0.04888	1	0.09654	0.956391	0.710974	0.431276	1.619234	0.036788	0.145424
Pav_sc0001825.1_g250.1.mk	PavANAC002	-1.24991	0.471669	-1.36237	0.420634	-2.18036	0.014026	-1.21181	0.225153	-0.2104	0.914194	-0.11245	1	-0.93045	0.547985	0.038104	0.986888	1.039511	0.573161	-0.818
Pav_sc0000370.1_g310.1.mk	PavANAC007	0.303146	0.905303	0.327467	0.974915	-0.5837	0.473151	-0.11041	0.922816	-0.10702	0.945232	0.024321	1	-0.88685	0.385086	-0.41356	0.708293	-0.41016	0.826617	-0.91117
Pav_sc0000370.1_g320.1.mk	PavANAC007	-1.23343	0.527176	-0.34111	0.992756	-1.36943	0.19279	-0.4562	0.750744	0.558014	0.775075	0.892319	1	-0.136	0.953694	1	1	1.791445	0.246945	1
Pav_sc0001102.1_g810.1.mk	PavANAC007	2.254286	0.453952	2.290164	0.468972	0.493953	0.806104	0.103663	0.965947	1.863906	0.344174	0.035878	1	-1.76033	0.520837	1	1	-0.39038	0.948811	1
Pav_sc0003685.1_g150.1.mk	PavANAC008	-0.25882	0.583247	-0.32166	0.433969	-0.23829	0.35508	-0.14697	0.607032	-0.34507	0.181069	-0.06285	1	0.02053	0.975242	0.111849	0.760717	-0.08625	0.901056	0.083376
Pav_sc0000652.1_g1180.1.mk	PavANAC014	0.418942	0.321373	0.261945	0.744217	0.739388	0.002293	0.74459	0.001848	0.503543	0.074631	-0.157	1	0.320446	0.430681	0.325648	0.351333	0.084601	0.92135	0.477444
Pav_sc0001046.1_g580.1.br	PavANAC014	-0.59205	0.832882	-0.99918	0.688294	0.973887	0.391312	1.321046	0.206544	-1.53783	0.135969	-0.40713	1	1.565941	0.231781	1.913101	0.091043	-0.94578	0.611736	1.973072
Pav_sc0001046.1_g660.1.mk	PavANAC014	0.187921	0.96414	-0.84151	0.80646	1.415065	0.151283	1.098632	0.283539	-1.45333	0.175997	-1.02943	1	1.227144	0.379435	0.910711	0.48747	-1.64125	0.221652	2.256574
Pav_sc0001183.1_g020.1.br	PavANAC014	-1.16259	0.001057	-1.21735	0.00047	-0.73303	0.043931	-0.34688	0.427908	-1.61416	5.71E-08	-0.05477	1	0.429559	0.419558	0.815705	0.037909	-0.45157	0.444496	0.484327
Pav_sc0001183.1_g180.1.mk	PavANAC014	-0.12526	0.971099	-1.14647	0.390485	0.811019	0.359654	0.509608	0.599915	0.39221	0.763328	-1.02121	1	0.936283	0.426733	0.634872	0.571319	0.517474	0.79127	1.957492
Pav_sc0001183.1_g230.1.br	PavANAC014	-0.46471	0.824068	-1.68886	0.040747	1.396189	0.049204	1.273225	0.072838	-0.65022	0.515932	-1.22415	1	1.860899	0.019903	1.737935	0.025595	-0.18551	0.935851	3.085046
Pav_sc0001183.1_g040.1.br	PavANAC014	-0.90703	0.114906	-1.32094	0.002602	-0.6718	0.159084	0.169445	0.810657	-1.15845	0.005557	-0.41391	1	0.235228	0.791431	1.076474	0.031649	-0.25142	0.816983	0.649138
Pav_sc0000866.1_g420.1.mk	PavANAC017	0.035365	0.971931	-0.11195	0.968063	0.163886	0.561673	0.293568	0.216774	0.039754	0.934805	-0.14732	1	0.128521	0.779156	0.258203	0.391609	0.004389	0.998826	0.27584
Pav_sc0000095.1_g440.1.mk	PavANAC022	-1.74687	0.731653	-2.08731	0.707371	-0.95088	0.735921	-0.10419	0.979577	-0.47764	0.90638	-0.34045	1	0.795985	0.857119	1.642677	0.571319	1.269228	0.802103	1.136433
Pav_sc0002009.1_g210.1.mk	PavANAC025	1.526476	0.0014	1.342223	0.008283	2.286152	2.58E-08	2.5332	4.55E-10	3.123932	5.61E-15	-0.18425	1	0.759676	0.27566	1.006724	0.080519	1.597456	0.002202	0.943929
Pav_sc0001124.1_g360.1.mk	PavANAC028	0.367	0.693083	0.293436	0.876049	0.49992	0.234959	0.27665	0.558382	-0.01295	0.99395	-0.07356	1	0.13292	0.884162	-0.09035	0.89848	-0.37995	0.637669	0.206484
Pav_sc0002375.1_g060.1.mk	PavANAC028	0.054632	0.963958	0.127022	0.974915	0.491864	0.074605	0.583402	0.025605	0.178861	0.677029	0.072391	1	0.437233	0.243773	0.52877	0.096234	0.124229	0.876184	0.364842
Pav_sc0007387.1_g010.1.br	PavANAC028	0.04096	0.970057	0.007594	1	0.055015	0.883557	0.113969	0.727602	-0.03321	0.951549	-0.03337	1	0.014055	0.986086	0.073009	0.863369	-0.07417	0.924145	0.04742
Pav_sc0000094.1_g510.1.mk	PavANAC029	-1.25895	0.792712	1	1	1	1	1	1	0.581642	0.888992	0.293121	1	1	1	1	1	1	1	1
Pav_sc0000203.1_g220.1.mk	PavANAC029	0.007197	1	-0.54937	0.863883	0.109271	0.924171	-0.20823	0.84219	0.430258	0.703231	-0.55657	1	0.102074	0.956391	-0.21543	0.861428	0.42306	0.820342	0.658642
Pav_sc0000220.1_g1030.1.mk	PavANAC029	-1.43303	0.687976	-2.27431	0.367159	-1.10302	0.553522	-0.47238	0.82985	0.324134	0.917126	-0.84128	1	0.330009	0.926874	0.96065	0.674587	1.757168	0.533885	1.171285
Pav_sc0000350.1_g1100.1.mk	PavANAC030	0.42454	0.909477	1.199652	0.658288	-0.18874	0.905183	1.224459	0.306268	0.829	0.589297	0.775112	1	-0.61328	0.761941	0.799919	0.635207	0.404459	0.903307	-1.38839
Pav_sc0001265.1_g070.1.mk	PavANAC031	0.308086	0.937265	0.813131	0.835502	1.224593	0.267451	0.961745	0.390487	0.705778	0.626595	0.505045	1	0.916507	0.601569	1	1	0.397692	0.891865	0.411461
Pav_sc0001196.1_g2090.1.mk	PavANAC034	0.037606	0.997768	0.25012	0.989084	0.866717	0.277041	0.823113	0.294872	-0.07367	0.962379	0.212514	1	0.82911	0.460648	0.785506	0.422672	-0.11128	0.960601	0.616596
Pav_sc0000244.1_g070.1.mk	PavANAC036	-0.96412	0.714173	-0.79565	0.88225	-0.48766	0.746607	-0.48977	0.740075	-1.22835	0.359568	0.168472	1	0.476461	0.833513	0.474358	0.782503	-0.26423	0.935851	0.307988
Pav_sc0000044.1_g740.1.br	PavANAC037	0.471096	0.820795	0.573427	0.862222	0.179725	0.86991	0.281919	0.780928	0.472386	0.674006	0.102331	1	-0.29137	0.857119	-0.18918	0.883598	0.00129	1	-0.3937
Pav_sc0000044.1_g750.1.mk	PavANAC037	-0.09558	0.973817	0.464934	0.895845	0.295132	0.744136	0.457975	0.566546	0.275002	0.810726	0.560517	1	0.390715	0.761428	0.553558	0.550421	0.370585	0.828273	-0.1698
Pav_sc0000271.1_g090.1.mk	PavANAC040	0.261209	0.748594	0.122477	0.984752	0.804141	0.00727	0.895374	0.002172	0.526157	0.135504	-0.13873	1	0.542932	0.212157	0.634165	0.091449	0.264948	0.724461	0.681664
Pav_sc0000095.1_g1360.1.br	PavANAC041	0.041498	0.986999	-0.14506	0.990859	0.289874	0.596837	0.190761	0.747483	0.347184	0.580574	-0.18655	1	0.248376	0.777775	0.149263	0.842963	0.305686	0.774211	0.434931
Pav_sc0000823.1_g230.1.mk	PavANAC042	-4.73506	0.43297	-4.82508	0.439267	-5.36533	0.124566	-4.40722	0.222756	-3.8186	0.389698	-0.09002	1	1	1	1	1	1	1	1
Pav_sc0001215.1_g330.1.mk	PavANAC042	1	1	1	1	1	1	1	1	1	1	-0.98418	1	1	1	1	1	1	1	1
Pav_sc0000586.1_g1000.1.mk	PavANAC043	-2.38311	0.502595	-1.98385	0.7034	-3.21877	0.077639	-4.13259	0.012969	-3.44411	0.071494	0.399258	1	-0.83566	0.744136	-1.74948	0.274871	-1.06101	0.724948	-1.23492
Pav_sc0000652.1_g810.1.mk	PavANAC043	-0.0405	1	-1.60981	0.694573	0.149703	0.959765	-0.2526	0.924275	-0.18041	0.961529	-1.56931	1	0.190204	0.96656	-0.21209	0.947596	-0.13991	0.980493	1.759515
Pav_sc0001877.1_g160.1.mk	PavANAC047	-2.20471	0.365695	-2.39581	0.303042	-0.71174	0.730189	-0.59763	0.775643	0.086207	0.982938	-0.1911	1	1.492971	0.535956	1.607084	0.421425	2.290919	0.316449	1.684071
Pav_sc0000679.1_g030.1.mk	PavANAC050	0.046811	0.986999	-0.37087	0.869696	0.581968	0.268489	0.700578	0.152638	-0.20821	0.805868	-0.41768	1	0.535157	0.474685	0.653767	0.280772	-0.25502	0.84543	0.95284
Pav_sc0000679.1_g280.1.br	PavANAC050	-0.43092	0.810632	-0.41717	0.91624	-0.32913	0.702271	-0.21279	0.81878	-0.31146	0.773295	0.01375	1	0.101795	0.948728	0.218133	0.843248	0.119463	0.953522	0.088045
Pav_sc0000762.1_g070.1.mk	PavANAC051	-0.05937	0.959371	-0.16914	0.927507	0.218965	0.500367	0.184526	0.578137	0.041745	0.944692	-0.10977	1	0.278331	0.518737	0.243892	0.517584	0.101112	0.902562	0.388106
Pav_sc0008890.1_g030.1.br	PavANAC051	-0.54817	0.635266	-0.67871	0.51454	-0.3849	0.558343	0.233579	0.755771	-0.58078	0.385554	-0.13054	1	0.163272	0.892838	0.781749	0.23211	-0.03261	0.987267	0.293812
Pav_sc0000029.1_g090.1.mk	PavANAC056	1.451989	0.068643	1.036931	0.300004	0.808744	0.237963	1.178704	0.063425	0.526459	0.550886	-0.41506	1	-0.64324	0.580494	-0.27328	0.821077	-0.92553	0.419742	-0.22819
Pav_sc0000103.1_g1490.1.mk	PavANAC057	-0.78623	0.637229	-0.28928	0.987022	0.067415	0.963581	0.1635	0.899909	-0.39777	0.756993	0.496953	1	0.853644	0.469689	0.949728	0.337179	0.388463	0.843856	0.356691
Pav_sc0003258.1_g070.1.br	PavANAC067	1	1	1	1	1	1	1	1	1	1	-1.38163	1	1	1	1	1	1	1	1
Pav_sc0000220.1_g160.1.mk	PavANAC069	-0.25958	0.706141	0.063683	0.999176	-0.4775	0.090379	-0.6394	0.013069	-0.37169	0.27078	0.323265	1	-0.21792	0.664218	-0.37981	0.272999	-0.11211	0.891865	-0.54118
Pav_sc0000500.1_g220.1.br	PavANAC070	0.086814	0.944	0.096392	0.990859	0.034115	0.944369	0.105913	0.79597	0.040921	0.949916	0.009578	1	-0.0527	0.941259	0.019099	0.975598	-0.04589	0.961353	-0.06228
Pav_sc0001554.1_g180.1.mk	PavANAC071	-0.10329	0.978488	-0.03195	1	0.88983	0.320506	0.056427	0.969311	-0.3629	0.790605	0.07134	1	0.993115	0.40662	0.159713	0.914112	-0.25962	0.916771	0.921776
Pav_sc0010000.1_g020.1.br	PavANAC071	3.291646	0.601586	-1.39689	0.954089	1.363222	0.729511	2.272353	0.52135	1.372051	0.77629	-4.68854	1	-1.92842	0.759469	1	1	-1.9196	0.815123	1
Pav_sc0000029.1_g070.1.mk	PavANAC072	-0.4895	0.909	-1.30713	0.652492	-0.02096	0.996301	0.88901	0.529425	1.117331	0.484882	-0.81763	1	0.468538	0.857674	1.378507	0.372768	1.606828	0.417109	1.286165
Pav_sc0000852.1_g590.1.mk	PavANAC072	-0.18883	0.868832	-0.04549	1	0.044763	0.940524	0.207368	0.650946	-0.33515	0.487467	0.143342	1	0.233592	0.733856	0.396198	0.405176	-0.14632	0.888851	0.090251
Pav_sc0001900.1_g100.1.mk	PavANAC073	-0.5596	0.715031	-1.30388	0.088711	-0.24579	0.786453	-0.22962	0.796251	-0.13644	0.915134	-0.74428	1	0.313808	0.811332	0.329979	0.738969	0.423163	0.782958	1.058085
Pav_sc0000212.1_g1170.1.mk	PavANAC075	-0.16177	0.891263	0.073117	0.999642	0.066271	0.904394	0.023585	0.970949	-0.13871	0.821692	0.234885	1	0.228039	0.728858	0.185353	0.734662	0.023059	0.98573	-0.00685

Pav_sc0000762.1_g090.1.mk	PavANAC078	-0.0567	0.930943	-0.02566	1	0.199424	0.257007	0.200414	0.241785	0.038934	0.903874	0.031042	1	0.256126	0.240297	0.257115	0.185799	0.095635	0.820342	0.225084
Pav_sc0000042.1_g100.1.mk	PavANAC083	0.211413	0.880985	0.235515	0.951596	-0.24501	0.650832	-0.00875	0.994349	0.466873	0.396946	0.024102	1	-0.45642	0.48739	-0.22017	0.746709	0.25546	0.821777	-0.48053
Pav_sc0000480.1_g1200.1.mk	PavANAC083	0.14439	0.954063	0.159261	0.994317	0.628695	0.319663	0.841635	0.143958	0.499677	0.525232	0.014871	1	0.484305	0.627321	0.697245	0.343517	0.355287	0.804718	0.469434
Pav_sc0004527.1_g020.1.mk	PavANAC083	-0.50453	0.735811	-0.89908	0.359256	0.010747	0.996126	0.283533	0.720376	-0.38604	0.671742	-0.39455	1	0.515275	0.613983	0.788061	0.288625	0.118484	0.949982	0.909823
Pav_sc0001080.1_g580.1.mk	PavANAC084	0.240467	0.853319	0.022955	1	0.698822	0.105216	0.637161	0.13873	0.349802	0.563529	-0.21751	1	0.458355	0.495234	0.396694	0.503214	0.109335	0.935851	0.675868
Pav_sc0001877.1_g050.1.mk	PavANAC087	-0.5911	0.766892	-1.00693	0.495067	0.071743	0.957294	0.178854	0.879074	0.021176	0.995994	-0.41583	1	0.662841	0.615343	0.769952	0.456359	0.612274	0.729548	1.078672
Pav_sc0000055.1_g430.1.mk	PavANAC090	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1
Pav_sc0000168.1_g110.1.mk	PavANAC090	0.63548	0.78801	0.211363	0.99688	1.25852	0.171177	1.451489	0.097553	1.784178	0.05109	-0.42412	1	0.623041	0.708578	0.816009	0.511689	1.148698	0.467034	1.047157
Pav_sc0000138.1_g450.1.mk	PavANAC091	0.159814	0.887326	0.102859	0.993615	0.452162	0.197738	0.241118	0.547924	-0.15079	0.793013	-0.05696	1	0.292348	0.611759	0.081304	0.889996	-0.3106	0.661178	0.349303
Pav_sc0000975.1_g040.1.mk	PavANAC098	-0.12245	0.980242	-0.4547	0.973817	0.157618	0.921317	0.430034	0.752947	-0.07199	0.974341	-0.33225	1	0.280068	0.905333	0.552484	0.724657	0.050465	0.990243	0.612321
Pav_sc0000484.1_g580.1.mk	PavANAC100	-0.39496	0.959034	-0.84051	0.969936	0.3468	0.898947	1.032055	0.637139	1.644453	0.479809	-0.44554	1	0.741763	0.841172	1.427018	0.561327	2.039416	0.52318	1.187307
Pav_sc0000877.1_g1000.1.mk	PavANAC100	-0.80987	0.870379	-1.57649	0.713408	0.886594	0.661088	1.192426	0.515986	1.042494	0.658929	-0.76662	1	1.696467	0.479733	2.002299	0.306822	1.852366	0.512956	2.463086
Pav_sc0001323.1_g1040.1.mk	PavANAC104	-0.89316	0.94084	1	1	1	1	1	1	0.017426	1	-0.9751	1	1	1	1	1	1	1	1

3 300 mg/L	70 % vs GA3 500 mg/L		tOH 70 % vs O.P. 7 DA		0 mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 7 D		3 500 mg/L vs O.P. 7 D		N.C. 7 vs 14 DAT		EtOH 70% 7 vs 14 DAT		A3 300 mg/L 7 vs 14 DA		A3 500 mg/L 7 vs 14 D		O.P. 7 vs 14 DAT		N.C. vs EtOH 14 DAT		. vs GA3 30
p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
0.898097	0.759858	0.315364	1.668118	0.024086	0.614433	1	1.522694	0.028536	0.90826	0.305893	0.975652	0.32463	-0.04931	0.969071	0.242948	0.77159	-0.09439	0.922022	-0.68039	0.381538	-1.07385	0.656768	-0.63616
0.504871	0.150555	0.925719	1.151962	0.423143	0.968553	1	1.96996	0.04897	1.001407	0.468236	1.006778	0.547665	-0.30847	0.858808	2.072198	0.014718	1.234162	0.187358	-0.48584	0.70189	-1.4277	0.682713	0.134972
0.259586	-0.43788	0.637934	-0.43448	0.758418	0.473289	1	0.476683	0.63248	0.003394	1	-0.10648	0.967325	-0.16188	0.903657	0.388227	0.616066	0.392062	0.637644	0.09964	0.932186	-0.03108	1	-0.39214
1	1	1	0.899127	0.655959	0.913229	1	1.927447	0.099885	1.014219	0.553385	1.380971	0.36952	0.569354	0.742879	1.349718	0.16444	-0.48802	0.677488	0.536266	0.767911	0.080702	1	-0.16725
1	1	1	-0.42626	0.932025	-0.39029	1	1	1	1	1	-1.47964	0.665027	-0.96196	0.739786	-1.14932	0.414072	-0.51415	0.754882	-1.29104	0.506486	0.553565	0.967473	1
0.81332	0.174696	0.535431	-0.02341	0.974059	0.09132	1	-0.10678	0.77187	-0.1981	0.574977	-0.106	0.849639	-0.28899	0.319755	-0.04819	0.875134	0.104557	0.70776	0.218694	0.403889	-0.24584	0.82846	0.078339
0.102661	0.482645	0.081345	0.241598	0.604599	0.005201	1	-0.23585	0.52548	-0.24105	0.561831	-0.01517	0.990625	-0.24383	0.522798	-0.20559	0.480492	-0.26836	0.337422	0.085215	0.829897	-0.38566	0.693295	0.130034
0.05518	2.320231	0.017523	-0.53865	0.773572	0.34716	1	-2.51172	0.008797	-2.85888	0.003431	-0.8023	0.662419	-1.2789	0.27051	-1.84871	0.037893	-1.5303	0.109587	0.194647	0.892366	-0.88373	0.855928	0.519534
0.020427	1.940141	0.042765	-0.61182	0.742664	-0.31643	1	-2.86839	0.001489	-2.55196	0.00841	-0.69645	0.730328	-1.55584	0.170459	-2.15426	0.010973	-1.33419	0.148689	0.1055	0.949636	-1.88882	0.427557	-0.23066
0.232987	0.870473	0.014274	-0.3968	0.449449	0.386146	1	-0.88113	0.01142	-1.26727	0.000128	-1.15994	0.000184	-1.54425	4.33E-08	-1.84794	2.21E-11	-1.92637	1.18E-11	-0.47537	0.181308	-0.43908	0.735723	-0.25845
0.012493	1.656081	0.033469	1.538683	0.110522	-0.30141	1	-0.41881	0.734835	-0.1174	0.951439	-0.37159	0.84633	-1.08246	0.269791	-0.63613	0.446877	-0.14176	0.897101	-1.8507	0.012911	-1.73208	0.301903	0.671744
2.02E-06	2.962082	5.38E-06	1.038638	0.311126	-0.12296	1	-2.04641	0.003704	-1.92344	0.0099	-1.02552	0.346224	-1.67448	0.029267	-1.83944	0.003927	-1.38217	0.037896	-2.31636	0.00035	-1.87311	0.156474	1.046981
0.169238	1.490383	0.000484	0.162493	0.860349	0.841245	1	-0.48665	0.370653	-1.32789	0.003554	-1.46438	4.47E-05	-1.36724	9.04E-05	-1.54397	6.2E-06	-2.43005	1.1E-11	-0.77419	0.052005	-0.31677	0.874391	0.15564
0.302932	0.405522	0.082107	0.151708	0.727757	0.129682	1	-0.12413	0.727792	-0.25381	0.43186	0.081729	0.894111	0.101334	0.790162	-0.27984	0.210056	-0.19265	0.430824	0.125845	0.670083	-0.12771	0.919777	-0.23304
0.687917	1.983126	0.399135	1.609676	0.655285	0.846692	1	0.473243	0.901312	-0.37345	0.937037	5.246647	0.061073	0.87476	0.796694	3.796479	0.077784	5.352872	0.021931	3.823767	0.135153	-4.71234	0.461709	-0.65418
0.081767	1.190978	0.017564	1.78171	0.000272	0.247049	1	0.837781	0.161183	0.590732	0.429866	0.966737	0.126305	0.606851	0.35635	-0.93605	0.043782	-1.28939	0.003846	-1.73518	0.000158	-0.54414	0.831172	-1.14311
0.720899	-0.01679	0.981089	-0.30639	0.660219	-0.22327	1	-0.51287	0.283277	-0.2896	0.64608	-0.49503	0.422432	-0.31818	0.574254	-0.33668	0.421181	-0.16268	0.737698	0.436348	0.319118	0.103281	0.977767	0.291271
0.260784	0.456379	0.11808	0.051839	0.946139	0.091537	1	-0.313	0.383471	-0.40454	0.257785	0.214374	0.708671	-0.29597	0.427416	-0.35457	0.195057	-0.24914	0.404887	0.098905	0.803024	-0.43795	0.656768	-0.13171
0.908779	0.106374	0.755907	-0.04081	0.951453	0.058954	1	-0.08823	0.829141	-0.14718	0.724882	-0.07874	0.907711	-0.03896	0.931959	-0.16152	0.545037	-0.09299	0.761922	0.216728	0.443204	0.006418	1	-0.06873
1	1	1	1	1	-1.7787	1	1	1	1	1	1.334172	0.71763	1	1	0.6045	0.826245	-0.75842	0.631878	1	1	-1.46774	0.875223	1
0.459023	0.341138	0.723843	0.979629	0.337489	-0.3175	1	0.320987	0.784481	0.63849	0.56125	-0.58818	0.675122	-0.36862	0.742813	-0.81058	0.248422	-0.95515	0.158628	-0.81832	0.301488	-0.33701	0.936603	-0.12032
0.556225	1.801925	0.279666	2.598444	0.185891	0.63064	1	1.427159	0.482974	0.796519	0.770826	3.857775	0.015342	0.831754	0.730191	3.337163	0.013119	3.098159	0.023282	2.419676	0.124851	-3.8673	0.168441	-0.1906
0.273362	0.024807	0.990353	-0.37065	0.896855	1.413197	1	1.017738	0.470975	-0.39546	0.86727	-0.50682	0.839074	-1.38723	0.319157	-0.57703	0.59665	-1.43854	0.181024	-1.18946	0.307516	-0.1053	1	-0.68349
0.800178	1	1	-0.10735	0.973703	-0.26285	1	-0.51881	0.757497	-0.25597	0.908701	1.129738	0.526386	0.396553	0.82951	0.105665	0.948789	-0.20669	0.885084	0.460867	0.748096	-0.22814	0.983928	-0.10757
0.520113	0.572992	0.528589	-0.32379	0.829179	-0.0436	1	-0.94039	0.289992	-0.89678	0.364841	0.647914	0.638028	0.886679	0.369664	0.534359	0.549492	1.026263	0.22768	1.402068	0.070038	0.45128	0.917586	0.715555
0.857034	0.305885	0.857037	-0.4327	0.852877	-0.0021	1	-0.74069	0.62881	-0.73859	0.672419	-0.63396	0.783679	-0.77066	0.617479	0.08362	0.960523	-0.12673	0.934924	0.34905	0.816875	0.031778	1	1.194042
0.711002	-0.29151	0.786151	-0.10104	0.962544	0.102193	1	0.292661	0.811985	0.190467	0.904301	0.208292	0.925311	-0.12568	0.927866	0.407226	0.631607	0.4847	0.571771	-0.3856	0.68897	-0.23164	0.972736	-0.09244
0.875478	-0.00696	0.995935	-0.18993	0.911396	0.162843	1	-0.02013	0.992663	-0.18297	0.897545	0.305853	0.846658	-0.43033	0.667958	0.76465	0.264038	0.115622	0.902976	0.954941	0.197351	-0.17566	0.977638	0.849512
0.046771	0.772897	0.017077	0.40368	0.400267	0.091233	1	-0.27798	0.546541	-0.36922	0.436799	0.23716	0.728445	0.184993	0.713254	-0.27949	0.428405	-0.2441	0.513271	0.588721	0.088594	-0.1909	0.917586	0.02628
0.417006	0.335818	0.528983	0.492241	0.467058	-0.09911	1	0.05731	0.947741	0.156423	0.860132	-0.15553	0.893462	0.032167	0.967945	-0.60225	0.148599	-0.70829	0.077757	-0.5629	0.231223	0.001146	1	-0.19834
1	1	1	1	1	0.958109	1	1	1	1	1	1.993546	0.78077	1	1	4.388029	0.19093	4.343834	0.202959	1	1	-0.0752	1	1
1	1	1	1	1	3.176003	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	-1.85348	0.965076	1
0.476992	-2.14874	0.119869	-1.46027	0.496759	-0.91382	1	-0.22534	0.925047	0.688475	0.745038	-2.44738	0.114086	-1.88056	0.259611	-3.78083	0.000138	-2.82908	0.004049	-3.91482	0.000117	0.966084	0.875223	-2.16912
0.345518	1.357217	0.450732	1.429401	0.579025	-0.4023	1	-0.33011	0.916391	0.072184	0.988305	-0.88429	0.807384	-0.25767	0.923995	-3.73791	0.005007	-3.97269	0.001847	-2.0371	0.20567	-0.94269	0.905279	-2.66342
0.345614	1.798185	0.276022	2.482019	0.210665	0.114113	1	0.797948	0.73561	0.683835	0.810696	4.800584	0.000896	0.98651	0.666525	4.037103	0.002768	3.493176	0.010384	3.567136	0.018151	-4.00518	0.156474	0.72949
0.06241	1.07145	0.025202	0.162662	0.888397	0.11861	1	-0.79018	0.146853	-0.90879	0.104309	-0.55215	0.492662	-1.27552	0.00819	-0.79328	0.078599	-0.69957	0.131782	-0.41598	0.458422	-1.14106	0.239153	0.294021
0.936198	0.204382	0.836303	0.105713	0.952332	0.116337	1	0.017668	0.993321	-0.09867	0.949381	-0.17989	0.922137	-0.29517	0.7783	-0.12708	0.883098	-0.15399	0.857169	0.046523	0.96867	-0.10153	0.992339	0.154607
0.206813	0.353666	0.2285	0.210886	0.665104	-0.03444	1	-0.17722	0.66207	-0.14278	0.771124	0.237892	0.653046	0.168531	0.687558	0.022576	0.957328	0.045719	0.904304	0.142667	0.688445	-0.17914	0.903446	0.063015
0.686129	0.912289	0.096823	0.097935	0.944334	0.618477	1	-0.19588	0.82233	-0.81435	0.222873	-0.86908	0.186292	-0.6216	0.333919	-0.68046	0.168182	-1.13161	0.017144	-1.73113	5.86E-05	0.116939	0.981004	0.351887
0.830208	0.141773	0.902389	-0.51047	0.668677	0.36996	1	-0.28229	0.793139	-0.65225	0.513816	-1.81585	0.006704	-1.91753	0.001469	-2.82589	1.68E-08	-3.16985	6.7E-10	-2.21809	2.35E-05	-0.51674	0.871823	-1.65329
0.766045	0.452775	0.670281	-0.10849	0.959364	0.096084	1	-0.46518	0.698931	-0.56126	0.668236	-0.06838	0.980703	-0.89829	0.322633	-1.19403	0.08889	-1.6698	0.011248	-0.19287	0.860233	-0.33296	0.932727	-0.27201
1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.001563	1	1
0.071275	-0.70308	0.010229	-0.43537	0.260383	-0.1619	1	0.105812	0.821139	0.267707	0.51458	0.700609	0.02467	0.16946	0.710573	0.919427	0.000175	0.921485	0.000147	0.796704	0.003009	-0.20788	0.897724	0.0009
0.898356	0.009521	0.984758	-0.05547	0.944334	0.071797	1	0.006806	0.993508	-0.06499	0.919091	0.290779	0.581121	0.436237	0.220228	0.403867	0.148464	0.303993	0.305923	0.065849	0.881654	0.155037	0.925845	0.06039
0.33796	0.088373	0.949739	-0.33096	0.851399	-0.8334	1	-1.25273	0.173812	-0.41933	0.770451	-0.50224	0.774654	-0.97468	0.340333	-1.05691	0.17803	-0.56271	0.522537	0.520788	0.598949	-0.4011	0.928366	0.438441
1	1	1	2.768941	0.545137	0.909131	1	0.008829	1	-0.9003	0.894575	-1.77311	0.810633	-1.93948	0.582182	1.937709	0.588415	-3.18886	0.282369	-2.69018	0.398349	-4.8549	0.582662	1.782397
0.370092	2.196135	0.069108	2.424456	0.09106	0.90997	1	1.13829	0.473501	0.228321	0.933811	2.019659	0.200673	0.06566	0.977767	0.736398	0.579115	-0.71551	0.599348	0.626766	0.687336	-2.77163	0.255034	-0.81472
0.878387	0.252856	0.576996	-0.28967	0.647709	0.162605	1	-0.37992	0.413352	-0.54252	0.224744	-0.03245	0.982625	-0.01978	0.977767	0.142276	0.745941	-0.16422	0.707161	0.240479	0.587416	0.156013	0.948192	0.408316
0.121803	1.074256	0.094299	1.167439	0.137385	0.016171	1	0.109354	0.928031	0.093184	0.951596	0.370199	0.795928	-0.23951	0.826788	0.086123	0.923287	-0.07299	0.936046	-0.25903	0.765379	-1.35399	0.324093	0.029732
0.992133	-0.04953	0.934684	-0.21183	0.75719	-0.04269	1	-0.20498	0.698632	-0.16229	0.803213	-0.16959	0.837788	-0.65524	0.086414	-0.19572	0.620349	-0.33867	0.34238	0.126243	0.796462	-0.25076	0.889829	0.201912

0.225439	0.226073	0.194533	0.064594	0.860349	0.00099	1	-0.16049	0.457785	-0.16148	0.500504	0.070645	0.862136	0.004384	0.990688	-0.52702	0.000125	-0.37185	0.009741	-0.19219	0.281903	-0.03522	0.983301	-0.34154
0.338472	-0.24427	0.66583	0.231358	0.799426	0.236256	1	0.711883	0.136958	0.475627	0.436827	-0.35498	0.671888	-0.03097	0.969573	-0.43847	0.285578	-0.45283	0.281765	-0.40728	0.415612	0.348109	0.875223	-0.53991
0.526746	0.682374	0.281467	0.340416	0.764397	0.21294	1	-0.12902	0.904194	-0.34196	0.731322	0.713762	0.435503	0.736315	0.315731	1.78012	0.000483	1.574689	0.002499	1.434438	0.009837	0.037424	1	1.550663
0.169418	1.182609	0.046826	0.513032	0.619953	0.272786	1	-0.39679	0.652095	-0.66958	0.421881	0.457139	0.708653	0.400902	0.657959	-0.20885	0.776663	-0.02755	0.980181	0.288741	0.716512	-0.45078	0.887319	-0.15072
0.157482	0.614206	0.178037	0.326847	0.673275	-0.06166	1	-0.34902	0.560917	-0.28736	0.691828	-0.65457	0.275946	-0.72853	0.14206	-1.43432	6.59E-05	-2.04102	3.51E-09	-1.37682	0.000257	-0.29147	0.899469	-0.32139
0.213982	1.185782	0.138026	1.028104	0.349133	0.107111	1	-0.05057	0.975828	-0.15768	0.927729	1.121827	0.315155	0.768772	0.459626	0.846596	0.276923	0.668913	0.418706	0.663539	0.461911	-0.76889	0.850472	0.38761
1	1	1	1	1	-0.83616	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1
0.31901	1.240126	0.194019	1.572815	0.175363	0.192969	1	0.525658	0.706638	0.332689	0.856624	0.431621	0.841764	1.532685	0.145143	1.578842	0.072899	1.229958	0.183015	1.638318	0.108458	0.676947	0.889829	1.770262
0.391651	0.138259	0.772026	-0.25365	0.674923	-0.21104	1	-0.60295	0.098245	-0.39191	0.394749	-0.57552	0.188112	-0.55932	0.152314	-0.90436	0.001686	-0.82802	0.004369	-0.2819	0.466484	-0.04075	0.9991	-0.03649
0.649281	0.884737	0.44964	0.382718	0.860387	0.272416	1	-0.2296	0.90168	-0.50202	0.783923	0.268871	0.926466	0.91338	0.508752	-0.73877	0.480324	-0.28001	0.833002	0.908753	0.443437	0.312256	0.972736	-0.72757
0.610205	1.872561	0.337191	2.484959	0.307195	0.685255	1	1.297652	0.59727	0.612398	0.860895	3.854348	0.049267	1.51487	0.539199	4.946497	0.001212	5.178279	0.000957	5.282553	0.002281	-2.78502	0.654106	1.833912
0.153264	2.768918	0.080697	2.618986	0.19781	0.305832	1	0.1559	0.962494	-0.14993	0.970169	3.060198	0.105893	0.28891	0.921938	3.106797	0.034487	1.621994	0.317702	1.918583	0.269028	-3.53791	0.286586	1.743066
1	1	1	1	1	-0.61762	1	1	1	1	1	-0.93228	0.892617	1	1	-0.54399	0.855444	0.558081	0.854853	1	1	-0.59447	0.978899	1

0 mg/L 14	. vs GA3 500 mg/L 14		N.C. vs O.P. 14 DAT		40 % vs GA3 300 mg/L		40 % vs GA3 500 mg/L		OH 140 % vs O.P. 14 D		mg/L vs GA3 500 mg/		3 300 mg/L vs O.P. 14		3 500 mg/L vs O.P. 14		N.C. 14 vs 21 DAT		tOH 70% 14 vs 21 DA		3 300 mg/L 14 vs 21 D		3 500 mg/L
p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
0.470819	-0.35907	0.739303	-0.03681	0.992669	0.437685	0.640659	0.714784	0.388884	1.037042	0.160879	0.277099	1	0.599357	0.683499	0.322258	0.867767	-1.0388	0.186903	-0.30639	0.831917	-1.20491	0.046029	-0.54937
0.943466	0.265488	0.884625	-0.45311	0.845217	1.56267	0.122682	1.693186	0.091217	0.974588	0.397731	0.130516	1	-0.58808	0.801549	-0.7186	0.753778	-0.80411	0.527883	-0.03525	0.989634	-2.08818	0.012311	-0.30073
0.716795	0.084984	0.959904	-0.20404	0.916324	-0.36106	0.723056	0.116061	0.931248	-0.17297	0.881757	0.477124	1	0.188097	0.931338	-0.28903	0.894527	0.151964	0.905161	0.853962	0.500618	0.187585	0.823645	1.220826
0.936699	-1.09176	0.403698	1	1	-0.24796	0.894605	-1.17246	0.34904	0.866038	0.606485	-0.92451	1	1	1	1	1	1	1	1	1	-0.78805	0.460978	1.763344
1	-1.18513	0.524582	1	1	-1.98358	0.215771	-1.7387	0.308414	1	1	0.24488	1	1	1	1	1	1	1	1	1	1.196438	0.379279	0.30838
0.845859	0.322406	0.218356	0.238438	0.538908	0.324177	0.193655	0.568244	0.00871	0.484277	0.035417	0.244067	1	0.1601	0.767092	-0.08397	0.905925	-0.01889	0.968596	0.157894	0.72078	0.105781	0.678302	-0.14995
0.765305	0.072467	0.890039	0.184991	0.747179	0.515692	0.061015	0.458125	0.109899	0.570648	0.037321	-0.05757	1	0.054956	0.949053	0.112524	0.889309	-0.25205	0.473891	-0.18571	0.726572	0.002343	1	-0.04937
0.717368	1.1851	0.290754	0.051166	0.992152	1.403268	0.160794	2.068835	0.024026	0.934901	0.400535	0.665566	1	-0.46837	0.848688	-1.13393	0.511877	-0.54924	0.681561	-0.16673	0.940261	0.644739	0.517062	-1.24489
0.897308	0.272976	0.88039	-0.83929	0.641682	1.658158	0.095476	2.161792	0.01999	1.049522	0.353479	0.503634	1	-0.60864	0.79159	-1.11227	0.531201	-0.99809	0.41225	0.363344	0.862633	1.761682	0.039722	0.081408
0.569401	0.049274	0.94495	0.232998	0.735394	0.180633	0.697582	0.488356	0.174214	0.67208	0.044461	0.307723	1	0.491448	0.343892	0.183724	0.837487	-0.90729	0.008351	-0.16485	0.807472	-0.45786	0.128495	-0.6181
0.524916	0.864705	0.377968	-0.96163	0.428977	2.403825	0.000722	2.596785	0.000209	0.770452	0.415838	0.192961	1	-1.63337	0.130053	-1.82633	0.080192	-1.53307	0.07984	-0.10972	0.954045	-0.21606	0.817699	-0.91107
0.208239	1.381282	0.070438	-1.47635	0.094841	2.92009	3.29E-06	3.254391	1.14E-07	0.396758	0.695885	0.334301	1	-2.52333	0.00076	-2.85763	4.27E-05	-2.31967	0.00227	-0.19536	0.908631	-0.03573	0.974694	-1.87637
0.806127	0.110807	0.876296	0.438772	0.477747	0.472411	0.272652	0.427578	0.339181	0.755543	0.051299	-0.04483	1	0.283132	0.750607	0.327965	0.697358	-0.53671	0.2205	0.08157	0.926777	-0.5654	0.100935	-0.39432
0.420485	-0.01617	0.977894	0.048506	0.943673	-0.10533	0.755529	0.111541	0.745474	0.176219	0.548629	0.216871	1	0.281549	0.485278	0.064678	0.930077	-0.47975	0.053714	-0.39099	0.255663	-0.35891	0.081344	-0.66199
0.896318	1.748903	0.699044	-0.15365	0.992502	4.058153	0.090514	6.461239	0.008588	4.558683	0.07386	2.403086	1	0.500531	0.953065	-1.90256	0.800007	-5.65105	0.032452	-1.95557	0.576858	-5.92926	0.002548	-7.08722
0.024695	-1.24941	0.011118	-1.10446	0.066573	-0.59897	0.310337	-0.70527	0.211764	-0.56032	0.349142	-0.10629	1	0.038655	0.985269	0.144949	0.928645	-1.73218	0.000993	-0.91734	0.224561	-1.96556	1.5E-06	-1.77639
0.59251	0.241997	0.679636	0.551421	0.327502	0.18799	0.742248	0.138716	0.823486	0.448139	0.332293	-0.04927	1	0.260149	0.780687	0.309424	0.734967	-0.14708	0.81093	-0.12668	0.884387	-0.15768	0.722414	0.232822
0.769467	0.065259	0.90774	0.00876	0.997799	0.306241	0.355482	0.503212	0.081923	0.446713	0.137091	0.196971	1	0.140472	0.848507	-0.0565	0.950289	-0.32951	0.335227	-0.07227	0.910126	-0.30995	0.246706	-0.49439
0.875697	0.058759	0.902276	0.221296	0.624635	-0.07515	0.847911	0.05234	0.904391	0.214877	0.4821	0.127488	1	0.290025	0.509739	0.162537	0.792012	-0.40915	0.136154	-0.55995	0.08053	-0.60789	0.003109	-0.83068
1	1	1	1	1	1	1	1	1	1	1	-3.14161	1	1	1	1	1	1	1	1	1	1	1	1
0.928554	-0.5824	0.542238	0.192924	0.919783	0.216688	0.847629	-0.24539	0.825597	0.529932	0.558943	-0.46208	1	0.313244	0.869893	0.775323	0.560554	-0.05743	0.968729	-0.94366	0.394021	-1.95011	0.000835	-1.53095
0.950867	0.201034	0.953008	0.319069	0.945447	3.676693	0.011228	4.06833	0.004244	4.186366	0.004174	0.391637	1	0.509672	0.911566	0.118035	0.986071	-4.73781	0.002871	-1.88743	0.445762	-4.86224	0.000136	-5.31139
0.623435	-0.1318	0.952402	-0.27818	0.917721	-0.57819	0.670749	-0.0265	0.994003	-0.17288	0.921164	0.551692	1	0.405308	0.877643	-0.14638	0.965331	1	1	-0.127	0.956876	0.755818	0.453952	1.626894
0.963833	-0.68277	0.670883	-0.27118	0.929611	0.120574	0.951207	-0.45463	0.779456	-0.04304	0.985897	-0.5752	1	-0.16361	0.962094	0.411591	0.898732	1	1	1	1	1.361791	0.274854	2.092045
0.496744	1.163855	0.231824	0.642876	0.682357	0.264276	0.842212	0.712576	0.534618	0.191597	0.887912	0.4483	1	-0.07268	0.983054	-0.52098	0.82386	1	1	0.216193	0.909718	-0.72815	0.36477	-1.04471
0.357457	0.981593	0.477167	0.718782	0.740929	1.162264	0.355239	0.949815	0.480676	0.687004	0.621611	-0.21245	1	-0.47526	0.869893	-0.26281	0.938461	-0.3827	0.818169	-1.79839	0.236225	0.084676	0.957865	0.945188
0.951934	0.087231	0.961338	-0.5926	0.685	0.139207	0.913543	0.318874	0.787124	-0.36096	0.727685	0.179668	1	-0.50017	0.773289	-0.67983	0.671745	-0.09981	0.944099	-0.088	0.961309	-0.96843	0.156268	-1.25944
0.296305	0.363328	0.728951	1.019673	0.295573	1.025173	0.162225	0.538988	0.537578	1.195334	0.102243	-0.48618	1	0.170161	0.940431	0.656345	0.660004	0.266924	0.801061	-0.01419	0.994927	-1.42781	0.015501	-1.25836
0.972044	0.152905	0.779594	0.616509	0.154	0.217179	0.629694	0.343805	0.396017	0.807408	0.015155	0.126625	1	0.590229	0.243873	0.463603	0.429348	-0.12544	0.811836	-0.28453	0.624237	-0.22009	0.522113	-0.76579
0.775762	-0.4035	0.47318	-0.10168	0.933875	-0.19949	0.754202	-0.40464	0.454052	-0.10283	0.884318	-0.20516	1	0.09666	0.941787	0.301816	0.773777	-0.3593	0.524854	-0.51733	0.461723	-1.62353	2.56E-06	-1.54818
1	1	1	1	1	1	1	2.753328	0.567252	1	1	0.913913	1	1	1	1	1	1	1	1	1	-0.08652	0.990787	0
1	1	1	1	1	1	1	1	1	1	1	-1.01528	1	1	1	1	1	1	1	1	1	1	1	1
0.058627	-2.13118	0.063707	-2.52845	0.045772	-3.1352	0.002843	-3.09726	0.003328	-3.49453	0.00098	0.037936	1	-0.35933	0.911228	-0.39727	0.90479	-1.41187	0.293709	-2.28873	0.163342	-2.26941	0.0158	-2.2989
0.073013	-3.30049	0.0168	-1.29272	0.630156	-1.72073	0.275292	-2.3578	0.101178	-0.35003	0.878671	-0.63707	1	1.370692	0.618214	2.007767	0.371334	-3.71732	0.012986	-2.12305	0.322413	-5.15508	2.24E-06	-4.41555
0.777731	0.299676	0.928933	1.057471	0.75796	4.734665	0.000808	4.304851	0.002546	5.062646	0.000536	-0.42981	1	0.327981	0.94938	0.757795	0.869727	-4.60154	0.004248	-1.39761	0.600626	-5.0948	9.09E-05	-4.94346
0.682914	0.506343	0.411181	-0.11885	0.93006	1.435079	0.001104	1.6474	0.000123	1.022206	0.035557	0.212322	1	-0.41287	0.699372	-0.62519	0.462198	-1.00088	0.059574	-0.08184	0.943928	-0.86153	0.046273	-1.29416
0.895678	0.244026	0.827978	0.345874	0.812965	0.256135	0.79188	0.345554	0.712684	0.447401	0.592681	0.089419	1	0.191267	0.922082	0.101848	0.962223	-0.55352	0.500254	-0.30281	0.816675	-1.35219	0.013172	-1.21046
0.902942	0.051719	0.929115	0.005886	0.99968	0.242151	0.481388	0.230855	0.516498	0.185022	0.607802	-0.0113	1	-0.05713	0.947256	-0.04583	0.959259	-0.31472	0.348067	-0.29411	0.524336	-0.32506	0.209553	-0.14135
0.618139	0.51922	0.41034	-0.89466	0.139231	0.234948	0.747281	0.402281	0.540213	-1.0116	0.037796	0.167334	1	-1.24655	0.036776	-1.41388	0.01256	-1.18681	0.020478	-0.66667	0.387888	-0.8697	0.046987	-1.83388
0.002005	-1.62729	0.002383	-1.32777	0.046145	-1.13655	0.04623	-1.11055	0.055022	-0.81103	0.205445	0.026005	1	0.32552	0.818656	0.299515	0.846876	-1.98112	0.000862	-1.56485	0.034121	-2.47063	4.27E-08	-2.75002
0.813214	-0.65169	0.447731	0.263971	0.885107	0.060956	0.960986	-0.31873	0.742776	0.596935	0.493682	-0.37968	1	0.535979	0.738248	0.91566	0.440971	1	1	0.263325	0.855083	-0.3116	0.671818	0.2896
1	1	1	1	1	1	1	1	1	1	1	-1.79361	1	1	1	1	1	1	1	1	1	1	1	1
1	-0.15894	0.735648	-0.01601	0.992669	0.208784	0.606314	0.048947	0.929864	0.191872	0.632589	-0.15984	1	-0.01691	0.991971	0.142926	0.867379	0.27224	0.493804	0.535945	0.242264	0.385053	0.191281	0.760168
0.913053	0.032313	0.962724	-0.27082	0.608598	-0.09465	0.840818	-0.12272	0.787905	-0.42586	0.187689	-0.02808	1	-0.33121	0.541458	-0.30314	0.598057	0.319628	0.384852	0.303142	0.550036	0.658978	0.010888	0.978659
0.718931	0.099239	0.95591	0.76341	0.591315	0.839538	0.37849	0.500336	0.655602	1.164507	0.184988	-0.3392	1	0.32497	0.884392	0.664172	0.708968	1.245876	0.180614	0.848888	0.528979	1.547382	0.03411	2.231238
0.718353	-2.43504	0.525276	1	1	6.6373	0.016635	2.419859	0.429607	2.018237	0.510015	-4.21744	1	1	1	1	1	1	1	1	1	-2.88919	0.338671	-0.17517
0.636649	-1.35666	0.355564	0.213935	0.955065	1.956903	0.118078	1.414968	0.311637	2.985561	0.009905	-0.54194	1	1.028658	0.693632	1.570593	0.446473	-3.08099	0.01598	-1.1956	0.563973	-2.93781	0.003973	-2.21323
0.357478	0.264423	0.606099	0.126602	0.89086	0.252303	0.606847	0.10841	0.854994	-0.02941	0.968611	-0.14389	1	-0.28171	0.732855	-0.13782	0.900767	0.156739	0.781502	-0.01764	0.986382	0.640848	0.050951	0.665593
0.987476	-0.11321	0.932741	-0.20607	0.900803	1.383722	0.023307	1.24078	0.049156	1.14792	0.077886	-0.14294	1	-0.2358	0.893396	-0.09286	0.965376	-1.01581	0.158911	-0.84651	0.398004	-1.28761	0.018982	-1.14077
0.695305	0.016272	0.987351	0.318895	0.61107	0.452672	0.236945	0.267032	0.553617	0.569655	0.12011	-0.18564	1	0.116983	0.908892	0.302623	0.685398	0.20298	0.681561	0.18185	0.792688	-0.04245	0.927908	0.07625

0.039358	-0.18538	0.356145	-0.1672	0.549929	-0.30632	0.064684	-0.15016	0.471389	-0.13198	0.525182	0.156162	1	0.174344	0.581207	0.018182	0.977047	-0.37639	0.032452	-0.29909	0.222503	-0.17459	0.267989	-0.2945
0.259177	-0.31801	0.583593	0.203157	0.841183	-0.88802	0.029764	-0.66612	0.138859	-0.14495	0.828697	0.2219	1	0.74307	0.224046	0.52117	0.492632	-0.32292	0.559531	-0.18514	0.839874	-0.17225	0.704247	-0.36762
0.006645	1.558172	0.006203	1.075963	0.152925	1.51324	0.007533	1.520748	0.007387	1.038539	0.09694	0.007509	1	-0.4747	0.734454	-0.48221	0.732884	0.378508	0.64576	-0.08165	0.954043	0.407969	0.541731	0.326125
0.890327	0.303376	0.750582	-0.04991	0.984988	0.30007	0.72894	0.754161	0.270474	0.400871	0.612035	0.454091	1	0.100802	0.958335	-0.35329	0.819157	-0.93087	0.177116	-0.70347	0.474847	-0.75918	0.175139	-1.53158
0.588493	-0.98976	0.016628	-0.61292	0.306263	-0.02992	0.971663	-0.69829	0.11939	-0.32145	0.555145	-0.66837	1	-0.29153	0.768626	0.376841	0.677703	-0.51526	0.31894	-0.34629	0.659035	-1.06199	0.003218	-0.77698
0.754796	0.317038	0.816106	0.153986	0.948648	1.156495	0.168908	1.085924	0.209845	0.922871	0.305305	-0.07057	1	-0.23362	0.922082	-0.16305	0.947524	-0.36596	0.759863	-0.56089	0.698581	-0.09253	0.93155	-0.39819
1	1	1	1	1	1	1	1	1	1	1	3.134851	1	1	1	1	1	1	1	1	1	1	1	1
0.074587	1.614346	0.110512	2.355395	0.03453	1.093315	0.333305	0.937399	0.432284	1.678448	0.115034	-0.15592	1	0.585133	0.823196	0.741049	0.76719	0.922803	0.430544	0.136491	0.95177	2.587645	0.023178	0.766263
0.958439	-0.17119	0.746484	-0.01698	0.992703	0.004256	0.998496	-0.13044	0.802364	0.023765	0.972726	-0.1347	1	0.019509	0.991551	0.154206	0.871759	-0.0253	0.971954	-0.17811	0.793224	0.064302	0.877507	0.089207
0.595684	0.0036	1	0.690347	0.753162	-1.03983	0.383071	-0.30866	0.85255	0.37809	0.813283	0.731174	1	1.417921	0.394217	0.686747	0.792012	-0.36034	0.822868	-0.95817	0.57953	-0.05401	0.970839	-0.57767
0.42095	2.750949	0.182044	3.46762	0.151478	4.618934	0.005653	5.53597	0.000862	6.252642	0.000342	0.917037	1	1.633708	0.700672	0.716672	0.906524	-3.54312	0.066022	-1.74819	0.561198	-6.69118	5.37E-06	-6.99976
0.398492	0.564095	0.846362	0.710751	0.858051	5.280973	0.000287	4.102003	0.005538	4.248659	0.005217	-1.17897	1	-1.03231	0.796911	0.146656	0.981254	-3.65649	0.030177	-1.38398	0.620745	-5.67697	2.45E-05	-4.95604
1	1	1	1	1	1	1	1	1	1	1	0.484448	1	1	1	1	1	1	1	1	1	1	1	1

14 vs 21 D	O.P. 14 vs 21 DAT		N.C. vs EtOH 21 DAT		. vs GA3 300 mg/L 21		. vs GA3 500 mg/L 21		N.C. vs O.P. 21 DAT		10 % vs GA3 300 mg/L		10 % vs GA3 500 mg/L		OH 210 % vs O.P. 21 D		mg/L vs GA3 500 mg/		300 mg/L vs O.P. 21		500 mg/L vs O.P. 21		N.C. 21 v
p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
0.41299	-0.47274	0.651272	-0.34144	1	-0.80228	0.233846	0.13036	0.892371	0.529246	0.509859	-0.46084	0.538207	0.471799	0.539743	0.870685	0.194472	0.932636	1	1.331522	0.036839	0.398886	0.598537	-0.61712
0.784328	0.687776	0.640204	-0.65884	1	-1.14909	0.22852	0.768867	0.474238	1.038778	0.323775	-0.49025	0.661437	1.427707	0.126533	1.697618	0.057825	1.917959	1	2.187869	0.013783	0.269911	0.823356	0.254651
0.098181	0.171992	0.905747	0.670921	1	-0.35652	0.677501	1.153846	0.152006	-0.18402	0.866746	-1.02744	0.156366	0.482925	0.634641	-0.85494	0.271001	1.510366	1	0.172504	0.858512	-1.33786	0.082463	-0.29575
0.08759	1	1	1.351311	1	-0.68003	0.555444	0.946864	0.481561	0.462131	0.76639	-2.03134	0.066473	-0.40445	0.823566	-0.88918	0.54566	1.62689	1	1.142156	0.311036	-0.48473	0.745763	-1.01954
0.842609	1	1	0.978861	1	0.218593	0.915916	-0.42459	0.814933	-0.59826	0.742761	-0.76027	0.672758	-1.40345	0.374707	-1.57712	0.293826	-0.64318	1	1	1	1	1	1
0.526727	0.198611	0.551075	-0.06906	1	0.203007	0.403037	0.191342	0.451474	0.455937	0.036575	0.272064	0.228931	0.260399	0.269453	0.524994	0.010408	-0.01167	1	0.252929	0.291763	0.264595	0.250746	0.152635
0.881725	0.137477	0.765015	-0.31932	1	0.384426	0.141472	0.275145	0.337625	0.574517	0.023353	0.703743	0.00229	0.594462	0.01461	0.893834	0.000102	-0.10928	1	0.190091	0.53206	0.299373	0.270496	-0.59286
0.150792	0.10147	0.964088	-0.50123	1	1.713514	0.047214	0.489457	0.663703	0.701878	0.528655	2.214741	0.006328	0.990684	0.30318	1.203105	0.188766	-1.22406	1	-1.01164	0.304068	0.212421	0.86101	-0.48429
0.950869	1.231921	0.305431	-0.52738	1	2.529114	0.002115	1.352474	0.152577	1.390717	0.153831	3.056496	0.000119	1.879855	0.032576	1.918099	0.028112	-1.17664	1	-1.1384	0.245289	0.038244	0.983291	0.061622
0.030362	-0.63906	0.078847	0.303356	1	0.190982	0.607827	0.338461	0.318669	0.501225	0.120774	-0.11237	0.782813	0.035104	0.943676	0.197869	0.601406	0.147479	1	0.310244	0.366928	0.162765	0.663079	-0.0136
0.215728	1.753082	0.03473	-0.30873	1	1.988754	0.003299	1.486708	0.041404	2.324527	0.000726	2.297481	0.000464	1.795435	0.010148	2.633254	7.33E-05	-0.50205	1	0.335772	0.728034	0.837819	0.289325	1.458523
0.002264	1.645695	0.032149	0.251198	1	3.330925	9.56E-09	1.824586	0.00445	2.489014	6.84E-05	3.079727	1.32E-07	1.573388	0.016615	2.237817	0.000329	-1.50634	1	-0.84191	0.260561	0.664429	0.376801	1.18964
0.272064	-0.59704	0.187893	0.301509	1	0.126948	0.788171	0.253201	0.553466	0.378437	0.359923	-0.17456	0.694978	-0.04831	0.931066	0.076928	0.881274	0.126252	1	0.251489	0.550914	0.125236	0.784557	-0.09234
0.000467	-0.21786	0.492983	-0.03895	1	-0.1122	0.67621	-0.19841	0.42255	0.310395	0.185629	-0.07325	0.799907	-0.15946	0.534869	0.349348	0.107946	-0.0862	1	0.422599	0.050447	0.508804	0.014154	-0.54213
0.001068	1.857431	0.689574	-1.01686	1	-0.9324	0.698029	0.312727	0.915868	7.354825	0.001268	0.084463	0.980866	1.32959	0.563355	8.371688	0.000136	1.245127	1	8.287225	0.000295	7.042098	0.002418	-3.32731
1.28E-05	-1.14696	0.028142	0.2707	1	-1.3765	0.001004	-1.29362	0.00266	-0.51924	0.342684	-1.6472	5.12E-05	-1.56432	0.000165	-0.78994	0.094531	0.082879	1	0.857253	0.069667	0.774374	0.097386	-0.3457
0.574127	-0.30798	0.603007	0.123682	1	0.280669	0.511678	0.621899	0.100275	0.390518	0.365057	0.156987	0.740875	0.498218	0.209293	0.266836	0.546029	0.341231	1	0.109849	0.829778	-0.23138	0.60394	0.398731
0.043791	0.12375	0.802113	-0.18071	1	-0.11215	0.744172	-0.09962	0.783359	0.462018	0.094216	0.068562	0.850707	0.081086	0.826659	0.642729	0.009726	0.012525	1	0.574167	0.029088	0.561642	0.030149	-0.18911
2.82E-05	-0.39587	0.166216	-0.14438	1	-0.26747	0.269703	-0.36277	0.118622	0.234574	0.387587	-0.12308	0.658935	-0.21839	0.395179	0.378955	0.098045	-0.0953	1	0.502039	0.025732	0.597344	0.005937	-0.02252
1	1	1	-1.81515	1	1.76018	0.519551	0.718812	0.826394	1	1	3.575327	0.067999	1	1	1.13257	0.58318	-1.04137	1	1	1	1	1	1
0.009155	-0.58105	0.570503	-1.22324	1	-2.013	0.000545	-2.05592	0.00046	-0.3307	0.722976	-0.78977	0.245247	-0.83268	0.231053	0.892536	0.19333	-0.04292	1	1.682302	0.007857	1.725221	0.005588	-1.45844
2.26E-05	0.387644	0.901138	-1.01692	1	-0.31503	0.881838	-0.37254	0.858399	5.444524	2.97E-05	0.701885	0.698715	0.644377	0.733964	6.461443	3.08E-07	-0.05751	1	5.759558	1.55E-05	5.817066	1.18E-05	-2.69852
0.116017	1.212902	0.382725	-0.57845	1	-0.27383	0.842007	1.14894	0.352328	0.588564	0.678133	0.304625	0.812713	1.727393	0.116779	1.167017	0.283944	1.422768	1	0.862392	0.467011	-0.56038	0.688804	-0.43089
0.070274	-1.12117	0.408564	0.583603	1	2.174612	0.057198	2.329662	0.053782	-0.47196	0.716501	1.591009	0.198023	1.746059	0.183915	-1.05556	0.314595	0.15505	1	-2.64657	0.020384	-2.80162	0.0163	0.789329
0.193275	-0.55501	0.65856	0.881118	1	0.201053	0.839246	0.332794	0.727501	0.30151	0.772957	-0.68007	0.421637	-0.54832	0.556198	-0.57961	0.523733	0.131741	1	0.100458	0.928219	-0.03128	0.983077	0.315505
0.386716	-0.40491	0.833121	-1.38391	1	1.661416	0.094456	2.309478	0.01934	0.696569	0.582275	3.04533	0.000496	3.693393	3.4E-05	2.080484	0.024525	0.648063	1	-0.96485	0.398287	-1.61291	0.124927	-1.11824
0.053057	0.910621	0.355537	-0.21983	1	-0.96105	0.175704	-1.0724	0.130319	0.417831	0.680886	-0.74122	0.310847	-0.85257	0.243768	0.637663	0.448293	-0.11135	1	1.378881	0.055534	1.490228	0.032339	-1.27693
0.026669	0.156691	0.920415	-0.45678	1	-0.84522	0.186665	-1.16196	0.056704	0.90944	0.223324	-0.38844	0.594649	-0.70518	0.285943	1.366217	0.03306	-0.31674	1	1.754658	0.005743	2.0714	0.000722	-1.57229
0.005778	-0.0199	0.98594	-0.34999	1	-0.06838	0.880679	-0.48745	0.119802	0.722046	0.022286	0.281618	0.405718	-0.13746	0.730299	1.07204	0.000172	-0.41908	1	0.790422	0.0117	1.209499	3.46E-05	-0.68189
5.67E-06	-0.85707	0.063055	-0.15689	1	-1.46257	1.81E-05	-1.59238	2.67E-06	-0.59946	0.162904	-1.30568	0.000147	-1.43549	2.78E-05	-0.44257	0.306103	-0.12981	1	0.863114	0.025674	0.992922	0.008059	-1.21046
1	1	1	2.832635	1	1.793375	0.672512	2.681174	0.509117	1	1	-1.03926	0.833157	0	1	0	1	0.8878	1	1	1	1	1	1
1	1	1	-0.97396	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1
0.012809	-1.10342	0.448343	0.089226	1	-3.02665	0.000961	-3.01821	0.001177	-2.21999	0.029015	-3.11588	0.000601	-3.10744	0.000759	-2.30922	0.018155	0.008444	1	0.806661	0.49688	0.798217	0.487558	-0.06683
4.72E-05	-2.71886	0.066042	0.651583	1	-4.10118	0.000184	-3.99872	0.000322	-0.29427	0.885589	-4.75276	9.37E-06	-4.6503	1.87E-05	-0.94585	0.527652	0.102458	1	3.806911	0.001228	3.704453	0.001567	-0.57568
0.000108	-0.44131	0.891352	-0.80124	1	0.236227	0.914382	-0.04224	0.990736	5.217698	9.43E-05	1.037471	0.532882	0.759	0.678277	6.018942	3.29E-06	-0.27847	1	4.981472	0.000303	5.259942	0.000114	-3.2156
0.00139	-0.14109	0.880355	-0.22202	1	0.433369	0.395733	0.213064	0.725628	0.74093	0.124374	0.655388	0.155577	0.435083	0.403808	0.962949	0.028532	-0.22031	1	0.307561	0.578423	0.527867	0.273838	0.219614
0.026738	-1.03307	0.162137	0.14919	1	-0.64406	0.31156	-0.41291	0.566823	-0.13367	0.890831	-0.79325	0.18774	-0.5621	0.403861	-0.28286	0.712477	0.231147	1	0.510394	0.449405	0.279246	0.698076	0.563032
0.626573	0.308205	0.387597	-0.15852	1	0.052677	0.890874	0.225088	0.456582	0.628814	0.011842	0.211202	0.471213	0.383612	0.152117	0.787339	0.000791	0.17241	1	0.576136	0.023828	0.403726	0.122295	-0.38365
4.36E-06	-0.50789	0.416216	0.637077	1	0.668992	0.143638	-0.12785	0.840844	-0.21574	0.731777	0.031915	0.968368	-0.76493	0.09136	-0.85282	0.0521	-0.79684	1	-0.88474	0.049746	-0.08789	0.888168	0.535453
5.84E-10	-1.55342	0.004356	-0.10047	1	-2.14281	1.49E-06	-2.39619	5.68E-08	-0.90007	0.099644	-2.04233	4.52E-06	-2.29572	2.11E-07	-0.7996	0.135426	-0.25338	1	1.242735	0.014111	1.496119	0.002245	-0.77334
0.68596	0.50797	0.674575	-0.01164	1	-0.52561	0.467037	-0.30409	0.719374	0.829943	0.308054	-0.51397	0.47482	-0.29245	0.728835	0.84158	0.269441	0.221522	1	1.355552	0.053407	1.13403	0.110032	0.738938
1	1	1	2.43795	1	1	1	1	1	1	1	1	1	1	1	1	1	0.812498	1	1	1	1	1	1
0.004524	-0.23331	0.60126	0.055822	1	0.113713	0.776671	0.328991	0.333289	-0.52156	0.079063	0.057892	0.894661	0.273169	0.441627	-0.57738	0.039833	0.215278	1	-0.63527	0.028262	-0.85055	0.002648	-0.13148
7.98E-05	0.571291	0.077318	0.13855	1	0.399739	0.169205	0.691344	0.010271	-0.01916	0.973279	0.261189	0.40669	0.552794	0.049093	-0.15771	0.656326	0.291605	1	-0.4189	0.157175	-0.7105	0.009667	0.335908
0.001376	-0.42438	0.747761	-0.79809	1	0.739947	0.401146	1.0846	0.200885	-0.90684	0.298709	1.538032	0.037871	1.882686	0.011639	-0.10876	0.926037	0.344653	1	-1.64679	0.033633	-1.99144	0.008708	-1.88435
0.96167	1	1	-1.75446	1	2.312838	0.400336	0.809416	0.804819	1.61426	0.608045	4.0673	0.088614	2.563879	0.315681	3.368723	0.170005	-1.50342	1	-0.69858	0.844855	0.804844	0.798656	-0.82101
0.03292	-0.08842	0.979593	-0.88624	1	-0.67155	0.628296	-0.4889	0.748806	3.206508	0.002468	0.214692	0.896077	0.39734	0.797978	4.092748	4.62E-05	0.182648	1	3.878056	0.000231	3.695408	0.000449	-2.80218
0.037078	0.44516	0.333441	-0.01837	1	0.892424	0.004872	0.773277	0.019684	0.415023	0.28788	0.910791	0.003546	0.791644	0.015743	0.433389	0.23353	-0.11915	1	-0.4774	0.194271	-0.35825	0.338314	0.327028
0.037282	-0.17977	0.883134	-1.18469	1	-0.24206	0.756713	-0.23817	0.767894	0.629974	0.367243	0.942628	0.106947	0.946523	0.117883	1.814663	0.000746	0.003895	1	0.872035	0.159306	0.86814	0.151075	-2.04955
0.852464	0.182224	0.757233	-0.27189	1	-0.04352	0.933641	-0.11046	0.809804	0.298138	0.463214	0.228371	0.550285	0.161432	0.703109	0.570028	0.082273	-0.06694	1	0.341657	0.355241	0.408596	0.239389	-0.80166

0.038614	-0.06393	0.829883	0.042081	1	-0.13975	0.420597	-0.1035	0.585684	0.145257	0.43909	-0.18183	0.264075	-0.14558	0.409411	0.103176	0.583798	0.03625	1	0.285002	0.067782	0.248753	0.108583	-0.12786
0.352885	-0.67916	0.164741	0.485886	1	-0.38925	0.356478	-0.36272	0.412142	-0.15308	0.791072	-0.87513	0.015797	-0.84861	0.02354	-0.63897	0.107535	0.026526	1	0.236163	0.61677	0.209636	0.650678	0.780792
0.629966	1.399713	0.041207	-0.42274	1	1.580124	0.002895	1.505789	0.005664	2.097168	0.000122	2.002861	7.22E-05	1.928527	0.000177	2.519905	1.47E-06	-0.07433	1	0.517044	0.477841	0.591378	0.38874	0.029484
0.002174	-0.33423	0.728873	-0.22338	1	0.020978	0.986267	-0.29733	0.683559	0.546728	0.421484	0.244359	0.737136	-0.07395	0.933671	0.770109	0.190828	-0.31831	1	0.52575	0.411473	0.844059	0.140041	-2.06124
0.034062	-0.43549	0.444065	-0.1225	1	-0.86812	0.021588	-1.25148	0.000462	-0.53315	0.230494	-0.74562	0.05165	-1.12898	0.001889	-0.41065	0.352512	-0.38337	1	0.334966	0.466629	0.718331	0.068197	-0.30743
0.634879	0.746825	0.501036	-0.96381	1	0.661038	0.428111	0.284813	0.777743	1.266774	0.105481	1.624848	0.01735	1.248623	0.090388	2.230584	0.000992	-0.37623	1	0.605736	0.491815	0.981961	0.207498	-2.07785
1	1	1	-2.75499	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1
0.460371	0.168891	0.946382	-0.10936	1	3.435104	0.001554	1.457805	0.141368	1.601483	0.112853	3.544468	0.000927	1.56717	0.106678	1.710847	0.072677	-1.9773	1	-1.83362	0.166302	0.143677	0.924455	-1.54887
0.818721	-0.21459	0.680144	-0.19356	1	0.053104	0.912917	-0.05669	0.906066	-0.20628	0.620735	0.246667	0.495849	0.136875	0.743817	-0.01272	0.984107	-0.10979	1	-0.25938	0.476911	-0.14959	0.697567	-0.30516
0.574127	0.688445	0.697611	-0.28557	1	-0.42124	0.720101	-0.21373	0.875062	1.739133	0.102793	-0.13567	0.921472	0.071845	0.962967	2.024708	0.039771	0.20751	1	2.160373	0.031824	1.952862	0.051598	0.564389
2.85E-06	-0.79107	0.824857	-0.99009	1	-1.31415	0.489791	-0.70568	0.750982	6.219673	6.99E-05	-0.32406	0.89213	0.284408	0.908239	7.209765	1.91E-06	0.608463	1	7.53382	1.55E-06	6.925356	1.2E-05	-3.02239
0.000149	-0.75517	0.784109	-1.2654	1	-0.27741	0.900096	-0.73545	0.701557	3.612072	0.01196	0.987984	0.569462	0.529951	0.791237	4.87747	0.000261	-0.45803	1	3.889486	0.006702	4.34752	0.001925	-3.74811
1	1	1	-0.60989	1	-2.65841	0.284956	-1.2065	0.706947	1	1	-2.04852	0.392584	1	1	-0.54674	0.868231	1.451908	1	1	1	1	1	1

s 28 DAT	EtOH 70% 21 vs 28 DA	3 300 mg/L 21 vs 28 D	3 500 mg/L 21 vs 28 D	O.P. 21 vs 28 DAT	N.C. vs EtOH 28 DAT	. vs GA3 300 mg/L 28	. vs GA3 500 mg/L 28	N.C. vs O.P. 28 DAT	80 % vs GA3 300 mg/L	80 % vs GA3 500 mg/L	OH 280 % vs O.P. 28 D	mg/L vs GA
p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC	p-adj	Log2FC
0.393415	-1.18731	0.041925	-0.95625	0.083068	-2.11664	3.55E-05	-0.39428	0.692244	-0.91163	0.322851	-1.14141	0.043311	-1.36916	0.010621	0.752082	0.246105	-0.22977	0.773164	-0.45752	0.465211	1.663716	0.002127	-0.22775
0.841143	-0.24596	0.811666	0.209903	0.829407	-1.99434	0.007711	-0.07484	0.971469	-1.15945	0.39134	-1.19384	0.153177	-1.48012	0.058699	0.709284	0.478272	-0.03439	0.98458	-0.32068	0.741426	1.868731	0.018106	-0.28628
0.738721	0.258015	0.770436	0.672598	0.310143	-1.04179	0.135815	1.279504	0.15479	1.224685	0.243367	0.611827	0.388688	0.407801	0.559898	1.391237	0.045149	-0.61286	0.480741	-0.81688	0.269799	0.166552	0.86269	1
0.331271	-1.65027	0.133562	0.445712	0.650608	-0.64376	0.5863	1	1	1	1	0.785225	0.411935	1.32264	0.155917	1.943557	0.04803	0.064641	0.968323	0.602056	0.590426	1.222973	0.240391	1
1	0.802997	0.665084	-1.04742	0.391592	0.596454	0.658564	1	1	1	1	-0.98709	0.446325	0.01361	1	0.39417	0.825812	-2.61069	0.087097	-1.60999	0.314509	-1.22943	0.460885	1
0.554805	0.179653	0.411113	0.262816	0.182373	0.483672	0.008805	-0.48423	0.046855	-0.04204	0.925101	0.313187	0.121235	0.522379	0.005059	-0.18093	0.439367	0.355227	0.094472	0.564418	0.003142	-0.13889	0.531758	0.209191
0.019516	-0.58938	0.010586	-1.03248	6.53E-07	-1.27159	3.7E-10	-0.03482	0.947294	-0.31583	0.409699	-0.05519	0.855221	-0.40358	0.068751	1.132562	1.86E-07	0.260645	0.327293	-0.08775	0.749797	1.448394	3.58E-12	-0.34839
0.655373	0.419952	0.656165	3.321447	0.000674	4.095076	3.95E-06	0.541901	0.695065	0.40301	0.79504	5.519246	7.68E-09	5.068818	1.21E-08	1.728063	0.033652	5.116236	1.66E-07	4.665808	3.09E-07	1.325053	0.097693	-0.45043
0.967177	0.716265	0.4367	3.315355	1.86E-05	4.485838	2.76E-09	-0.20633	0.9054	0.127262	0.948445	5.782847	3.12E-14	5.77669	2.28E-14	1.122761	0.218671	5.655586	1.93E-13	5.649428	1.56E-13	0.995499	0.247183	-0.00616
0.979995	-0.98366	0.000282	0.123271	0.691188	-0.1636	0.583926	-0.62437	0.074861	-0.66671	0.08585	0.327852	0.260868	0.188461	0.526895	-0.10955	0.774943	0.994559	0.000167	0.855168	0.000975	0.557159	0.03687	-0.13939
0.052125	1.634877	0.014629	1.832094	0.003479	2.852643	2.6E-06	-0.62311	0.564339	-0.13237	0.931466	2.362325	0.000195	2.880827	2.94E-06	0.242897	0.798308	2.494699	0.000119	3.013201	1.57E-06	0.375271	0.632367	0.518502
0.093698	1.524983	0.01447	2.469117	1.43E-05	4.419942	1.54E-15	-0.15131	0.909391	0.586541	0.600449	4.610403	1.36E-16	5.054888	8.53E-20	1.148067	0.081052	4.023861	1.36E-12	4.468347	2.09E-15	0.561526	0.412211	0.444486
0.84959	-0.95004	0.002242	-0.01007	0.988079	-0.11777	0.749307	-0.63979	0.120906	-0.55619	0.253757	0.209217	0.56529	0.227764	0.503321	-0.16902	0.682199	0.765411	0.016643	0.783959	0.00975	0.387175	0.231964	0.018548
0.009316	-0.91504	1.23E-06	-1.32806	4.31E-15	-1.5218	6.21E-20	-0.13731	0.679058	-0.41185	0.143178	-0.89813	2.3E-07	-1.17808	2.49E-12	0.715222	0.000103	-0.48628	0.010704	-0.76622	1.16E-05	1.127076	7.36E-11	-0.27994
0.084558	-2.40211	0.180271	-2.5721	0.117508	-3.72453	0.017629	-3.84147	0.215896	-0.09166	0.982537	-0.17719	0.93973	-0.0845	0.974327	6.840666	6.29E-05	-0.08553	0.979301	0.007163	1	6.932325	2.47E-05	0.092693
0.534358	-0.69684	0.114684	-0.20035	0.665074	-0.03201	0.959681	-1.10096	0.030584	-0.08043	0.934583	-1.23114	0.00198	-0.97993	0.012893	-1.2745	0.001961	-1.15071	0.005987	-0.89949	0.028107	-1.19407	0.002599	0.251217
0.326324	0.092793	0.824706	0.825556	0.012407	0.572677	0.098234	0.248667	0.663309	-0.18226	0.780645	0.707494	0.042785	0.795846	0.018392	0.240455	0.571132	0.88975	0.012793	0.978101	0.004151	0.42271	0.229286	0.088351
0.5443	-0.64654	0.005507	-0.42653	0.058255	-0.61366	0.004314	-0.48405	0.121534	-0.63814	0.044636	-0.34957	0.146569	-0.52417	0.017809	0.16708	0.574531	0.288571	0.277154	0.113972	0.673818	0.805223	0.000213	-0.1746
0.949772	0.193677	0.397345	0.244976	0.232344	0.178009	0.39586	-0.32724	0.250239	0.07182	0.868262	3.42E-05	1	-0.16224	0.454805	-0.07014	0.809418	-0.07179	0.808073	-0.23406	0.280158	-0.14196	0.543885	-0.16227
1	1	1	-3.8836	0.024335	-4.32042	0.006864	1	1	1	1	-0.25327	0.886453	-1.73146	0.15036	2.014171	0.301373	0.531127	0.765149	1	1	2.798564	0.092212	1
0.025506	-1.22216	0.038794	-2.19509	2.73E-05	-2.68056	1.56E-07	-0.3818	0.710764	-0.98696	0.285045	-2.74966	2.13E-07	-3.27805	2.08E-10	0.745941	0.261559	-1.7627	0.001875	-2.29109	1.8E-05	1.732899	0.001616	-0.52839
0.064501	-2.07757	0.123022	-3.86392	0.001071	-3.94587	0.000676	-1.79074	0.343591	-0.39596	0.88808	-1.48043	0.27691	-1.61989	0.209249	6.352306	1.76E-07	-1.08447	0.490328	-1.22392	0.37519	6.748269	8.89E-09	-0.13946
0.729204	-0.94986	0.282374	-1.2089	0.140574	-3.43608	4.35E-05	-0.25957	0.895913	1	1	-1.05184	0.223246	-1.85625	0.01486	0.759888	0.482534	0.045577	0.975416	-0.75883	0.363608	1.857305	0.025719	1
0.496296	1.024103	0.364831	-0.20592	0.894738	2.78975	0.096013	2.319414	0.058832	1	1	1.17936	0.329761	4.330083	0.004365	1.058123	0.382689	0.360983	0.83764	3.511706	0.033678	0.239746	0.871029	1
0.731021	-0.97396	0.172688	0.209132	0.793598	-0.92666	0.135608	-0.01499	0.998941	1	1	0.09468	0.918856	-0.90937	0.147939	-0.02899	0.983518	0.50303	0.549472	-0.50102	0.4645	0.379364	0.609358	1
0.286976	-0.02329	0.986571	1.440626	0.155885	-0.09435	0.946521	0.686215	0.650439	-0.28897	0.872987	4.220283	4.64E-06	3.333365	8.74E-05	2.501025	0.004101	4.509249	1.3E-06	3.622332	2.89E-05	2.789991	0.000696	-0.88692
0.065739	-1.58148	0.008357	-1.72258	0.001148	-1.48614	0.00485	-1.4901	0.064163	-0.52438	0.614214	-1.40669	0.010355	-1.2816	0.017274	0.204665	0.806449	-0.88231	0.151147	-0.75722	0.193101	0.729048	0.22946	0.125091
0.008101	-1.18223	0.029729	-1.6371	0.000715	-1.43805	0.002538	-1.18608	0.134555	-0.06672	0.959794	-0.91002	0.080111	-1.02772	0.037486	1.295655	0.017947	-0.84331	0.133665	-0.961	0.061407	1.362373	0.008486	-0.1177
0.023031	-0.80769	0.00232	-1.41175	5.12E-09	-1.32858	1.32E-08	-0.22093	0.657124	-0.47579	0.251706	-0.79823	0.0014	-1.13414	1.61E-06	1.183006	7.37E-06	-0.32245	0.27845	-0.65835	0.00842	1.658792	2.74E-11	-0.3359
0.001446	-1.67811	1.39E-06	-1.28925	3.89E-05	-1.59859	1.63E-07	-0.61603	0.197376	-0.62454	0.25324	-1.54137	1.29E-06	-1.98051	1.27E-10	-0.00503	0.998718	-0.91682	0.007979	-1.35597	2.13E-05	0.619513	0.074368	-0.43914
1	1	1	-6.47142	0.018265	0	1	1	1	1	1	-7.47947	0.007651	0	1	-0.85823	0.857137	-7.28667	0.013541	0	1	-0.66544	0.877424	1
1	1	1	1	1	-1.36328	0.785948	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
0.968795	1.111999	0.281879	0.962763	0.298439	2.864165	0.000585	-1.25163	0.342678	1.268055	0.422215	-1.99706	0.02661	-0.08721	0.944114	-3.40479	0.00012	-3.26512	0.000313	-1.35527	0.162301	-4.67284	4.39E-08	1.909846
0.720604	-1.16582	0.350867	-0.24466	0.854899	1.743124	0.101854	-4.02549	0.001169	0.061447	0.982418	-3.77015	0.000318	-1.67991	0.126244	-3.74407	0.000568	-3.8316	0.00038	-1.74136	0.123101	-3.80552	0.000255	2.090237
0.022468	-2.44347	0.061793	-4.63713	6.07E-05	-3.91919	0.000653	-1.47803	0.470551	-0.02911	0.991586	-1.1853	0.393798	-0.74583	0.59236	6.955265	9.19E-09	-1.15619	0.45096	-0.71672	0.623158	6.984376	2.43E-09	0.439473
0.705869	0.300306	0.526756	0.994626	0.009626	1.382779	0.000188	-0.44644	0.478515	-0.14133	0.871269	1.208381	0.002001	1.376229	0.000259	0.074879	0.906141	1.349708	0.000745	1.517556	7.74E-05	0.216205	0.656636	0.167848
0.405065	0.484828	0.424021	1.664077	0.000842	2.786152	7.17E-08	-0.15366	0.889094	0.070987	0.958727	0.456984	0.455803	1.810207	0.000844	-0.85036	0.142558	0.385997	0.580552	1.73922	0.001961	-0.92134	0.086558	1.353223
0.155849	-0.56768	0.014091	-0.99589	1.61E-06	-1.36092	1.99E-11	-0.28322	0.41242	-0.34256	0.364282	-0.55957	0.011737	-0.75219	0.000349	0.729239	0.001248	-0.21701	0.429839	-0.40963	0.073243	1.071798	3.65E-07	-0.19262
0.275367	0.324966	0.490832	3.244828	2.31E-12	4.563752	3.37E-20	-0.54078	0.344831	0.426589	0.556941	3.378367	2.87E-13	3.900448	8.96E-15	-1.29197	0.000917	2.951778	5.7E-10	3.473859	1.45E-11	-1.71856	3.59E-06	0.522081
0.162267	-0.30238	0.586477	0.322391	0.513086	0.300572	0.543099	-2.07577	2E-05	0.370479	0.669661	-1.04708	0.021096	-1.32228	0.002133	-2.20251	5.32E-07	-1.41756	0.002081	-1.69276	0.000104	-2.57299	1.21E-09	-0.2752
0.338705	-0.30234	0.661159	0.812282	0.17873	1.049359	0.095889	-0.78581	0.408099	1	1	-0.45226	0.55169	0.006335	1	-0.69481	0.34081	0.600653	0.411912	1.059252	0.109493	0.358112	0.591842	1
1	1	1	1	1	-1.63287	0.623187	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
0.728589	0.2071	0.514206	0.676843	0.016353	1.149163	0.000153	0.995514	0.000704	0.394399	0.380309	0.922034	0.00098	1.609633	5.13E-08	0.605432	0.02961	0.527635	0.107992	1.215233	0.000117	0.211032	0.508698	0.687599
0.276813	0.560334	0.031138	0.741399	0.002586	0.34455	0.189448	0.484823	0.152008	0.362977	0.398144	0.80523	0.001368	0.699986	0.004491	0.129756	0.706423	0.442254	0.12736	0.337009	0.22562	-0.23322	0.413032	-0.10524
0.01116	-1.79328	0.007446	-1.27798	0.058835	-1.66565	0.011796	-0.2026	0.885005	-0.70702	0.543661	1.346312	0.044789	1.303297	0.044926	0.774906	0.316126	2.053333	0.002051	2.010317	0.001737	1.481927	0.022476	-0.04302
0.787382	1.177621	0.627573	-1.1727	0.639955	2.873186	0.246047	1	1	1	1	1.961141	0.398119	4.503609	0.056405	1.785038	0.484973	1.716976	0.513042	4.259444	0.083126	1.540873	0.516056	1
0.011293	-2.02084	0.050873	-3.15492	0.000661	-3.50252	0.000111	-1.19698	0.434276	-0.1049	0.967039	-1.02428	0.347794	-1.18924	0.243982	4.811708	4.92E-07	-0.91939	0.450348	-1.08434	0.311107	4.916606	1.01E-07	-0.16496
0.398937	0.070331	0.858504	0.111517	0.76204	-0.05771	0.883377	0.282355	0.576979	-0.27506	0.623662	0.676914	0.028499	0.388536	0.218006	0.37035	0.298326	0.951977	0.002171	0.6636	0.030199	0.645413	0.033353	-0.28838
0.000304	-1.74551	0.000899	-3.0561	1.1E-10	-3.68504	2.22E-15	-0.90805	0.211465	-0.88065	0.29759	-1.24861	0.014748	-1.87365	9.84E-05	1.771469	0.000598	-0.36795	0.581496	-0.993	0.057517	2.652122	3.87E-08	-0.62505
0.010542	-0.72902	0.010701	-0.82835	0.001965	-1.07538	3E-05	0.02208	0.978307	-0.19925	0.705811	-0.07021	0.850348	-0.38418	0.17105	1.121879	5.59E-05	0.129045	0.740101	-0.18493	0.561454	1.321133	6.42E-07	-0.31397

0.473551	-0.4374	0.001469	-0.47196	0.000176	-0.75575	5.23E-10	-0.292	0.104477	-0.26745	0.207403	-0.48384	0.000183	-0.73139	3.11E-09	-0.01887	0.932501	-0.21639	0.150679	-0.46393	0.000338	0.248579	0.071467	-0.24755
0.053872	0.325525	0.434791	1.956109	2.82E-08	3.029961	8.13E-14	-0.15221	0.812003	0.03062	0.973466	0.786071	0.050932	1.88645	1.05E-05	-1.08608	0.001939	0.755451	0.081747	1.85583	2.57E-05	-1.1167	0.000946	1.100378
0.975265	0.229545	0.706005	-0.63555	0.243908	-1.21633	0.013426	-0.663	0.430073	-0.22268	0.826939	0.915087	0.079087	0.259974	0.644316	1.40468	0.006653	1.137763	0.033809	0.48265	0.376281	1.627356	0.000806	-0.65511
0.000135	-2.04474	4.23E-05	-3.08234	7.78E-12	-3.37089	2.67E-14	-0.58347	0.446713	-0.20688	0.841412	-1.00013	0.044667	-1.60698	0.000504	2.024499	2.75E-05	-0.79324	0.14889	-1.4001	0.003531	2.231383	1.38E-06	-0.60685
0.510953	0.366834	0.358641	0.465255	0.190785	0.818731	0.013203	-0.3955	0.469945	0.551765	0.345838	-0.09543	0.837968	-0.12532	0.763617	-0.62122	0.10541	-0.6472	0.091706	-0.67708	0.057412	-1.17299	0.000475	-0.02989
0.002948	-2.57258	5.26E-05	-4.76669	2.1E-16	-5.41134	1.95E-21	-0.41199	0.730255	-1.45853	0.117059	-2.0278	0.000788	-3.04868	1.12E-07	2.932638	2.53E-06	-0.56927	0.461853	-1.59014	0.009541	4.39117	1.16E-13	-1.02087
1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
0.077953	-2.68071	0.000411	-5.51254	8.24E-09	-4.3275	4.06E-09	-0.28954	0.87632	-1.24121	0.297385	-0.52857	0.536377	-1.32083	0.066308	2.860805	0.000308	0.712635	0.422211	-0.07962	0.934437	4.102014	2.88E-08	-0.79225
0.390158	-0.21249	0.513799	0.303485	0.292629	-0.05636	0.872357	-0.07068	0.905828	-0.10089	0.865679	0.661751	0.016181	0.192111	0.529115	0.028201	0.952967	0.762637	0.007286	0.292997	0.329655	0.129087	0.703945	-0.46964
0.625739	0.88306	0.347093	0.276582	0.774101	0.667902	0.457263	-0.18849	0.928838	0.033096	0.987055	-0.70905	0.456266	-0.11022	0.922228	0.986255	0.353058	-0.74214	0.481192	-0.14331	0.900138	0.953159	0.335476	1
0.070694	-2.46518	0.108245	-2.7006	0.054704	-3.52795	0.009104	-1.1014	0.68707	-0.43288	0.892698	-0.99235	0.555757	-1.21124	0.433738	8.140661	8.57E-09	-0.55947	0.786808	-0.77836	0.646672	8.573538	3.43E-10	-0.21889
0.008832	-2.1715	0.11293	-3.57915	0.003183	-3.4543	0.003929	-0.62811	0.801	0.311215	0.916005	-0.10845	0.954826	-0.44164	0.772564	6.732073	6.39E-08	-0.41967	0.82508	-0.75286	0.615306	6.420859	1.05E-07	-0.33319
1	1	1	-0.41098	0.844848	-1.32037	0.514739	1	1	1	1	-2.01811	0.318341	-1.47559	0.469528	-0.34129	0.911752	-1.24751	0.586256	1	1	0.429305	0.864078	1

A3 500 mg/	B 300 mg/L vs O.P. 28		B 500 mg/L vs O.P. 28	
p-adj	Log2FC	p-adj	Log2FC	p-adj
0.834288	1.893488	0.000248	2.121239	2.77E-05
0.858066	1.903124	0.011687	2.189407	0.002813
1	0.77941	0.273546	0.983436	0.137152
1	1.158332	0.253621	0.620917	0.57016
1	1.381258	0.247014	0.38056	0.785801
0.509251	-0.49411	0.006577	-0.7033	6.85E-05
0.292323	1.187749	5.82E-09	1.536141	1.77E-14
0.849467	-3.79118	6.78E-05	-3.34075	0.000173
1	-4.66009	6.44E-10	-4.65393	4.53E-10
0.788231	-0.4374	0.098649	-0.29801	0.261262
0.657224	-2.11943	0.000543	-2.63793	1.19E-05
0.685155	-3.46234	4.41E-10	-3.90682	1.2E-12
0.985769	-0.37824	0.226592	-0.39678	0.186783
0.304644	1.613356	4.45E-22	1.893301	1.79E-30
0.986621	7.017855	1.03E-05	6.925162	1.03E-05
0.735076	-0.04336	0.936832	-0.29457	0.479236
0.915515	-0.46704	0.180483	-0.55539	0.098258
0.659647	0.516652	0.018238	0.691251	0.000987
0.637908	-0.07018	0.763875	0.092095	0.665837
1	2.267437	0.176699	3.745632	0.010891
0.565279	3.495599	8.88E-12	4.02399	1.58E-15
0.966061	7.832738	5.56E-12	7.972194	1.22E-12
1	1.811728	0.024257	2.61614	0.000521
1	-0.12124	0.938894	-3.27196	0.034717
1	-0.12367	0.882322	0.880385	0.136889
0.61554	-1.71926	0.077819	-0.83234	0.37743
0.921033	1.611359	0.001957	1.486268	0.003981
0.918326	2.205679	3.81E-06	2.323375	7.57E-07
0.384608	1.98124	2.47E-16	2.317143	1.65E-22
0.389487	1.536337	5.81E-07	1.975482	5.31E-11
1	6.621232	0.014447	-0.33178	0.931949
1	3.869249	0.354913	1	1
0.131119	-1.40773	0.10913	-3.31758	4.82E-05
0.177452	0.026075	0.994439	-2.06416	0.044027
0.860637	8.140566	7.51E-13	7.701093	6.79E-12
0.831801	-1.1335	0.002556	-1.30135	0.000392
0.092772	-1.30734	0.009253	-2.66056	2.08E-07
0.610099	1.288806	2.46E-10	1.481425	1.5E-13
0.630585	-4.67034	1.67E-25	-5.19242	2.65E-26
0.739719	-1.15543	0.006682	-0.88023	0.038557
1	-0.24254	0.728265	-0.70114	0.275329
1	-1.07298	0.752352	1	1
0.16349	-0.3166	0.302778	-1.0042	0.000845
0.842267	-0.67547	0.005655	-0.57023	0.018468
0.983948	-0.57141	0.419128	-0.52839	0.43423
1	-0.1761	0.953966	-2.71857	0.257812
0.944895	5.835992	6.2E-11	6.000948	9.71E-12
0.575865	-0.30656	0.342922	-0.01819	0.966039
0.432482	3.020075	1.03E-10	3.645124	2.35E-15
0.471392	1.192088	5.02E-06	1.506059	3.14E-09

0.200331	0.464965	0.000186	0.712512	3.39E-09
0.103109	-1.87215	7.07E-08	-2.97253	1.22E-13
0.406857	0.489593	0.374246	1.144706	0.016999
0.423219	3.024626	1.03E-11	3.63148	1.16E-16
0.975709	-0.52579	0.129602	-0.4959	0.141343
0.260212	4.960439	6.12E-18	5.981313	5.68E-26
1	-1.47492	0.843374	1	1
0.490951	3.389378	3.27E-06	4.181631	3.93E-09
0.245517	-0.63355	0.016207	-0.16391	0.567842
1	1.695302	0.045987	1.096471	0.214339
0.950348	9.133012	5.82E-12	9.351899	9.31E-13
0.905058	6.840527	5.04E-09	7.173717	5.18E-10
1	1.676818	0.372042	1.1343	0.548474

Table S5.1: Identity percentages between the cDNA sequences.

	PavARF7	*AtARF7*	*SlARF7*	*CaARF7*	*PpeARF7*	*PduARF7*	*MdARF7*
PavARF7		40.63%	37.94%	34.54%	62.46%	52.54%	53.33%
AtARF7	40.63%		49.75%	48.15%	52.86%	44.92%	51.71%
SlARF7	37.94%	49.75%		81.02%	51.22%	43.30%	51.98%
CaARF7	34.54%	48.15%	81.02%		46.87%	39.63%	50.02%
PpeARF7	62.46%	52.86%	51.22%	46.87%		83.12%	71.18%
PduARF7	52.54%	44.92%	43.30%	39.63%	83.12%		60.68%
MdARF7	53.33%	51.71%	51.98%	50.02%	71.18%	60.68%	

Table S5.2: Identity and similarity percentages of the aminoacidic sequences. The similarity percentage is reported in brackets.

	PavARF7	AtARF7	SlARF7	CaARF7	PpeARF7	PduARF7	MdARF7
PavARF7		45.2% (49.62%)	48.3% (52.14%)	49.42% (53.53%)	59.76% (59.76%)	59.5% (59.5%)	53.52% (55.32%)
AtARF7	45.2% (49.62%)		59.83% (68.79%)	58.88% (66.75%)	61.36% (68.66%)	61.22% (68.53%)	59.64% (67.08%)
SlARF7	48.3% (52.14%)	59.83% (68.79%)		87.79% (90.16%)	66.16% (72.96%)	66.3% (73.11%)	63.76% (71.46%)
CaARF7	49.42% (53.53%)	58.88% (66.75%)	87.79% (90.16%)		65.31% (72.08%)	65.51% (72.29%)	63.17% (70.62%)
PpeARF7	59.76% (59.76%)	61.36% (68.66%)	66.16% (72.96%)	65.31% (72.08%)		98.89% (98.89%)	83.61% (86.13%)
PduARF7	59.5% (59.5%)	61.22% (68.53%)	66.3% (73.11%)	65.51% (72.29%)	98.89% (98.89%)		83.67% (86.2%)
MdARF7	53.52% (55.32%)	59.64% (67.08%)	63.76% (71.46%)	63.17% (70.62%)	83.61% (86.13%)	83.67% (86.2%)	

Table S5.3: Identity and similarity percentages of the aminoacidic sequences of B3 domain. The similarity percentage is reported in brackets.

	PavARF7	AtARF7	SlARF7	CaARF7	PpeARF7	PduARF7	MdARF7
PavARF7		41.75% (41.75%)	42.72% (43.69%)	43.69% (44.66%)	44.66% (44.66%)	44.66% (44.66%)	42.72% (42.72%)
AtARF7	41.75% (41.75%)		85.44% (92.23%)	86.41% (93.2%)	92.23% (93.2%)	92.23% (93.2%)	90.29% (91.26%)
SlARF7	42.72% (43.69%)	85.44% (92.23%)		97.09% (97.09%)	90.29% (95.15%)	90.29% (95.15%)	87.38% (91.26%)
CaARF7	43.69% (44.66%)	86.41% (93.2%)	97.09% (97.09%)		93.2% (98.06%)	93.2% (98.06%)	90.29% (94.17%)
PpeARF7	44.66% (44.66%)	92.23% (93.2%)	90.29% (95.15%)	93.2% (98.06%)		100% (100%)	96.12% (96.12%)
PduARF7	44.66% (44.66%)	92.23% (93.2%)	90.29% (95.15%)	93.2% (98.06%)	100% (100%)		96.12% (96.12%)
MdARF7	42.72% (42.72%)	90.29% (91.26%)	87.38% (91.26%)	90.29% (94.17%)	96.12% (96.12%)	96.12% (96.12%)	

Table S5.4: Identity and similarity percentages of the aminoacidic sequences of Activation domain (AD). The similarity percentage is reported in brackets.

	PavARF7	AtARF7	SlARF7	CaARF7	PpeARF7	PduARF7	MdARF7
PavARF7		85.53% (88.16%)	89.33% (94.67%)	88% (94.67%)	100% (100%)	100% (100%)	93.33% (96%)
AtARF7	85.53% (88.16%)		85.53% (90.79%)	84.21% (90.79%)	85.53% (88.16%)	85.53% (88.16%)	89.47% (89.47%)
SlARF7	89.33% (94.67%)	85.53% (90.79%)		94.67% (94.67%)	89.33% (94.67%)	89.33% (94.67%)	92% (97.33%)
CaARF7	88% (94.67%)	84.21% (90.79%)	94.67% (94.67%)		88% (94.67%)	88% (94.67%)	89.33% (96%)
PpeARF7	100% (100%)	85.53% (88.16%)	89.33% (94.67%)	88% (94.67%)		100% (100%)	93.33% (96%)
PduARF7	100% (100%)	85.53% (88.16%)	89.33% (94.67%)	88% (94.67%)	100% (100%)		93.33% (96%)
MdARF7	93.33% (96%)	89.47% (89.47%)	92% (97.33%)	89.33% (96%)	93.33% (96%)	93.33% (96%)	

Table S5.5: Identity and similarity percentages of the aminoacidic sequences of the MR2 sequence (Hu et al., 2018). The similarity percentage is reported in brackets.

	PavARF7	AtARF7	SlARF7	CaARF7	PpeARF7	PduARF7	MdARF7
PavARF7		17.97% (19.92%)	19.91% (22.12%)	21.61% (24.62%)	28.7% (28.7%)	28.13% (28.13%)	24.35% (26.09%)
AtARF7	17.97% (19.92%)		44.36% (53.31%)	40.86% (46.3%)	45.98% (52.11%)	46.15% (52.31%)	47.27% (54.3%)
SlARF7	19.91% (22.12%)	44.36% (53.31%)		69.33% (72%)	44.9% (51.43%)	45.49% (52.05%)	42.86% (52.1%)
CaARF7	21.61% (24.62%)	40.86% (46.3%)	69.33% (72%)		42.37% (48.31%)	42.55% (48.51%)	40.76% (47.9%)
PpeARF7	28.7% (28.7%)	45.98% (52.11%)	44.9% (51.43%)	42.37% (48.31%)		96.04% (96.04%)	68.85% (72.13%)
PduARF7	28.13% (28.13%)	46.15% (52.31%)	45.49% (52.05%)	42.55% (48.51%)	96.04% (96.04%)		69.96% (73.25%)
MdARF7	24.35% (26.09%)	47.27% (54.3%)	42.86% (52.1%)	40.76% (47.9%)	68.85% (72.13%)	69.96% (73.25%)	

Table S5.6: Identity and similarity percentages of the aminoacidic sequences of the PB1 domain. The similarity percentage is reported in brackets.

	PavARF7	AtARF7	SlARF7	CaARF7	PpeARF7	PduARF7	MdARF7
PavARF7		90.43% (94.68%)	91.49% (94.68%)	93.62% (95.74%)	100% (100%)	100% (100%)	93.62% (95.74%)
AtARF7	90.43% (94.68%)		89.36% (94.68%)	91.49% (95.74%)	90.43% (94.68%)	90.43% (94.68%)	87.23% (93.62%)
SlARF7	91.49% (94.68%)	89.36% (94.68%)		96.81% (98.94%)	91.49% (94.68%)	91.49% (94.68%)	87.23% (92.55%)
CaARF7	93.62% (95.74%)	91.49% (95.74%)	96.81% (98.94%)		93.62% (95.74%)	93.62% (95.74%)	89.36% (93.62%)
PpeARF7	100% (100%)	90.43% (94.68%)	91.49% (94.68%)	93.62% (95.74%)		100% (100%)	93.62% (95.74%)
PduARF7	100% (100%)	90.43% (94.68%)	91.49% (94.68%)	93.62% (95.74%)	100% (100%)		93.62% (95.74%)
MdARF7	93.62% (95.74%)	87.23% (93.62%)	87.23% (92.55%)	89.36% (93.62%)	93.62% (95.74%)	93.62% (95.74%)	

Table S5.7: Identity percentages between the cDNA sequences. PavAUX/IAA9* is used to indicate Pav_sc0002327.1_g560.1.mk while PavAUX/IAA9 for Pav_sc0002393.1_g030.1.mk.

	*PavAUX/IAA9**	*AtAUX/IAA9*	*SlAUX/IAA9*	*StAUX/IAA9*	*CaAUX/IAA9*	*PpeAUX/IAA8*	*PduAUX/IAA8*	*MdAUX/IAA8-like*	*MdAUX/IAA8-like*	*PavAUX/IAA9*	*PpeAUX/IAA9*	*PduAUX/IAA9*	*MdAUX/IAA9*
*PavAUX/IAA9**		35.44%	46.02%	44.12%	31.72%	39.51%	51.28%	63.41%	63.12%	43.86%	29.39%	30.77%	41.52%
AtAUX/IAA9	35.44%		40.96%	41.70%	32.21%	23.26%	25.83%	34.88%	41.13%	43.14%	31.31%	29.53%	36.99%
SlAUX/IAA9	46.02%	40.96%		83.63%	51.54%	27.50%	31.36%	46.87%	50.93%	48.51%	29.56%	31.18%	41.35%
StAUX/IAA9	44.12%	41.70%	83.63%		54.42%	27.19%	31.09%	46.40%	50.22%	48.54%	28.73%	30.91%	41.05%
CaAUX/IAA9	31.72%	32.21%	51.54%	54.42%		26.24%	22.30%	35.33%	37.84%	38.87%	21.30%	22.77%	31.81%
PpeAUX/IAA8	39.51%	23.26%	27.50%	27.19%	26.24%		82.60%	33.80%	37.65%	27.68%	35.23%	37.86%	24.32%
PduAUX/IAA8	51.28%	25.83%	31.36%	31.09%	22.30%	82.60%		41.85%	44.42%	31.41%	38.11%	41.23%	28.96%
MdAUX/IAA8-like	63.41%	34.88%	46.87%	46.40%	35.33%	33.80%	41.85%		65.77%	46.54%	29.20%	30.81%	45.51%
MdAUX/IAA8-like	63.12%	41.13%	50.93%	50.22%	37.84%	37.65%	44.42%	65.77%		31.73%	31.73%	33.56%	43.50%
PavAUX/IAA9	43.86%	43.14%	48.51%	48.54%	38.87%	27.68%	31.41%	46.54%	31.73%		51.28%	56.05%	62.94%
PpeAUX/IAA9	29.39%	31.31%	29.56%	28.73%	21.30%	35.23%	38.11%	29.20%	31.73%	51.28%		87.15%	40.46%
PduAUX/IAA9	30.77%	29.53%	31.18%	30.91%	22.77%	37.86%	41.23%	30.81%	33.56%	56.05%	87.15%		42.98%
MdAUX/IAA9	41.52%	36.99%	41.35%	41.05%	31.81%	24.32%	28.96%	45.51%	43.50%	62.94%	40.46%	42.98%	

Table S5.8: Identity and similarity percentages of the aminoacidic sequences. PavAUX/IAA9* is used to indicate Pav_sc0002327.1_g560.1.mk while PavAUX/IAA9 for Pav_sc0002393.1_g030.1.mk. The similarity percentage is reported in brackets.

	PavAUX/IAA9*	AtAUX/IAA9	SlAUX/IAA9	StAUX/IAA9	CaAUX/IAA9	PpeAUX/IAA8	PduAUX/IAA8	MdAUX/IAA8-like	MdAUX/IAA8-like	PavAUX/IAA9	PpeAUX/IAA9	PduAUX/IAA9	MdAUX/IAA9
PavAUX/IAA9*		46.38% (58.21%)	61.15% (67.42%)	60.9% (67.92%)	61.4% (68.42%)	81.73% (82.2%)	82.2% (82.67%)	78.54% (83.33%)	80.05% (84.85%)	57.75% (65.96%)	56.81% (65.49%)	56.81% (65.26%)	52.58% (59.86%)
AtAUX/IAA9	46.38% (58.21%)		54.79% (64.38%)	53.97% (64.38%)	54.25% (63.56%)	49.75% (63.18%)	50% (63.68%)	52.23% (64.04%)	52.23% (64.57%)	61.78% (71.2%)	60.47% (70.42%)	60.47% (70.42%)	57.56% (66.84%)
SlAUX/IAA9	61.15% (67.42%)	54.79% (64.38%)		97.42% (97.99%)	93.12% (95.42%)	63% (69%)	63.25% (69.25%)	69.4% (75.96%)	69.67% (75.96%)	63.01% (69.64%)	62.24% (69.39%)	62.24% (68.88%)	57.4% (62.76%)
StAUX/IAA9	60.9% (67.92%)	53.97% (64.38%)	97.42% (97.99%)		93.41% (94.84%)	62.75% (69.5%)	63% (69.75%)	68.58% (76.23%)	69.4% (76.23%)	62.24% (69.39%)	61.48% (69.13%)	61.48% (68.62%)	56.89% (62.24%)
CaAUX/IAA9	61.4% (68.42%)	54.25% (63.56%)	93.12% (95.42%)	93.41% (94.84%)		63% (69.75%)	63.25% (70%)	69.4% (76.23%)	70.49% (77.32%)	61.73% (68.37%)	60.97% (68.11%)	60.97% (67.6%)	57.4% (62.5%)
PpeAUX/IAA8	81.73% (82.2%)	49.75% (63.18%)	63% (69%)	62.75% (69.5%)	63% (69.75%)		99.5% (99.5%)	80.1% (84.13%)	81.61% (85.64%)	65.16% (75.19%)	64.16% (74.69%)	64.41% (74.44%)	59.65% (68.42%)
PduAUX/IAA8	82.2% (82.67%)	50% (63.68%)	63.25% (69.25%)	63% (69.75%)	63.25% (70%)	99.5% (99.5%)		80.35% (84.63%)	81.86% (86.15%)	65.41% (75.69%)	64.41% (75.19%)	64.66% (74.94%)	59.9% (68.67%)
MdAUX/IAA8-like	78.54% (83.33%)	52.23% (64.04%)	69.4% (75.96%)	68.58% (76.23%)	69.4% (76.23%)	80.1% (84.13%)	80.35% (84.63%)		91.46% (92.84%)	64.47% (71.83%)	63.45% (71.32%)	63.45% (71.07%)	59.39% (65.74%)
MdAUX/IAA8-like	80.05% (84.85%)	52.23% (64.57%)	69.67% (75.96%)	69.4% (76.23%)	70.49% (77.32%)	81.61% (85.64%)	81.86% (86.15%)	91.46% (92.84%)		63.45% (71.32%)	63.45% (71.32%)	63.45% (71.07%)	59.14% (65.99%)
PavAUX/IAA9	57.75% (65.96%)	61.78% (71.2%)	63.01% (69.64%)	62.24% (69.39%)	61.73% (68.37%)	65.16% (75.19%)	65.41% (75.69%)	64.47% (71.83%)	63.45% (71.32%)		98.15% (99.21%)	97.62% (98.68%)	88.1% (89.68%)
PpeAUX/IAA9	56.81% (65.49%)	60.47% (70.42%)	62.24% (69.39%)	61.48% (69.13%)	60.97% (68.11%)	64.16% (74.69%)	64.41% (75.19%)	63.45% (71.32%)	63.45% (71.32%)	98.15% (99.21%)		98.41% (99.47%)	87.3% (89.42%)
PduAUX/IAA9	56.81% (65.26%)	60.47% (70.42%)	62.24% (68.88%)	61.48% (68.62%)	60.97% (67.6%)	64.41% (74.44%)	64.66% (74.94%)	63.45% (71.07%)	63.45% (71.07%)	97.62% (98.68%)	98.41% (99.47%)		86.51% (88.89%)
MdAUX/IAA9	52.58% (59.86%)	57.56% (66.84%)	57.4% (62.76%)	56.89% (62.24%)	57.4% (62.5%)	59.65% (68.42%)	59.9% (68.67%)	59.39% (65.74%)	59.14% (65.99%)	88.1% (89.68%)	87.3% (89.42%)	86.51% (88.89%)	

Table S5.9: Identity and similarity percentages of the "TELTLGLPG" motif in the EAR domain (Domain I). PavAUX/IAA9* is used to indicate Pav_sc0002327.1_g560.1.mk while PavAUX/IAA9 for Pav_sc0002393.1_g030.1.mk. The similarity percentage is reported in brackets.

	PavAUX/IAA9*	AtAUX/IAA9	SlAUX/IAA9	StAUX/IAA9	CaAUX/IAA9	PpeAUX/IAA8	PduAUX/IAA8	MdAUX/IAA8-like	MdAUX/IAA8-like	PavAUX/IAA9	PpeAUX/IAA9	PduAUX/IAA9	MdAUX/IAA9
PavAUX/IAA9*		77.78% (88.89%)	88.89% (100%)	88.89% (100%)	88.89% (100%)	100% (100%)	100% (100%)	88.89% (100%)	88.89% (100%)	88.89% (100%)	88.89% (100%)	88.89% (100%)	88.89% (100%)
AtAUX/IAA9	77.78% (88.89%)		88.89% (88.89%)	88.89% (88.89%)	88.89% (88.89%)	77.78% (88.89%)	77.78% (88.89%)	88.89% (88.89%)	88.89% (88.89%)	88.89% (88.89%)	88.89% (88.89%)	88.89% (88.89%)	88.89% (88.89%)
SlAUX/IAA9	88.89% (100%)	88.89% (88.89%)		100% (100%)	100% (100%)	88.89% (100%)	88.89% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)
StAUX/IAA9	88.89% (100%)	88.89% (88.89%)	100% (100%)		100% (100%)	88.89% (100%)	88.89% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)
CaAUX/IAA9	88.89% (100%)	88.89% (88.89%)	100% (100%)	100% (100%)		88.89% (100%)	88.89% (100%)	100% (100%)	88.89% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)
PpeAUX/IAA8	100% (100%)	77.78% (88.89%)	88.89% (100%)	88.89% (100%)	88.89% (100%)		100% (100%)	88.89% (100%)	88.89% (100%)	88.89% (100%)	88.89% (100%)	88.89% (100%)	88.89% (100%)
PduAUX/IAA8	100% (100%)	77.78% (88.89%)	88.89% (100%)	88.89% (100%)	88.89% (100%)	100% (100%)		88.89% (100%)	88.89% (100%)	88.89% (100%)	88.89% (100%)	88.89% (100%)	88.89% (100%)
MdAUX/IAA8-like	88.89% (100%)	88.89% (88.89%)	100% (100%)	100% (100%)	100% (100%)	88.89% (100%)	88.89% (100%)		100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)
MdAUX/IAA8-like	88.89% (100%)	88.89% (88.89%)	100% (100%)	100% (100%)	100% (100%)	88.89% (100%)	88.89% (100%)	100% (100%)		100% (100%)	100% (100%)	100% (100%)	100% (100%)
PavAUX/IAA9	88.89% (100%)	88.89% (88.89%)	100% (100%)	100% (100%)	100% (100%)	88.89% (100%)	88.89% (100%)	100% (100%)	100% (100%)		100% (100%)	100% (100%)	100% (100%)
PpeAUX/IAA9	88.89% (100%)	88.89% (88.89%)	100% (100%)	100% (100%)	100% (100%)	88.89% (100%)	88.89% (100%)	100% (100%)	100% (100%)	100% (100%)		100% (100%)	100% (100%)
PduAUX/IAA9	88.89% (100%)	88.89% (88.89%)	100% (100%)	100% (100%)	100% (100%)	88.89% (100%)	88.89% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)		100% (100%)
MdAUX/IAA9	88.89% (100%)	88.89% (88.89%)	100% (100%)	100% (100%)	100% (100%)	88.89% (100%)	88.89% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	

Table S5.10: Identity and similarity percentages of the "GWPPV" motif in the dregon domain (Domain II). PavAUX/IAA9* is used to indicate Pav_sc0002327.1_g560.1.mk while PavAUX/IAA9 for Pav_sc0002393.1_g030.1.mk. The similarity percentage is reported in brackets.

	PavAUX/IAA9*	AtAUX/IAA9	SlAUX/IAA9	StAUX/IAA9	CaAUX/IAA9	PpeAUX/IAA8	PduAUX/IAA8	MdAUX/IAA8-like	MdAUX/IAA8-like	PavAUX/IAA9	PpeAUX/IAA9	PduAUX/IAA9	MdAUX/IAA9
PavAUX/IAA9*		80% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)
AtAUX/IAA9	80% (100%)		80% (100%)	80% (100%)	80% (100%)	80% (100%)	80% (100%)	80% (100%)	80% (100%)	80% (100%)	80% (100%)	80% (100%)	80% (100%)
SlAUX/IAA9	100% (100%)	80% (100%)		100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)
StAUX/IAA9	100% (100%)	80% (100%)	100% (100%)		100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)
CaAUX/IAA9	100% (100%)	80% (100%)	100% (100%)	100% (100%)		100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)
PpeAUX/IAA8	100% (100%)	80% (100%)	100% (100%)	100% (100%)	100% (100%)		100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)
PduAUX/IAA8	100% (100%)	80% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)		100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)
MdAUX/IAA8-like	100% (100%)	80% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)		100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)
MdAUX/IAA8-like	100% (100%)	80% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)		100% (100%)	100% (100%)	100% (100%)	100% (100%)
PavAUX/IAA9	100% (100%)	80% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)		100% (100%)	100% (100%)	100% (100%)
PpeAUX/IAA9	100% (100%)	80% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)		100% (100%)	100% (100%)
PduAUX/IAA9	100% (100%)	80% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)		100% (100%)
MdAUX/IAA9	100% (100%)	80% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	100% (100%)	

Table S5.11: Identity and similarity percentages of the PB1 domain (Domain III and IV). PavAUX/IAA9* is used to indicate Pav_sc0002327.1_g560.1.mk while PavAUX/IAA9 for Pav_sc0002393.1_g030.1.mk. The similarity percentage is reported in brackets.

	PavAUX/IAA9*	AtAUX/IAA9	SlAUX/IAA9	StAUX/IAA9	CaAUX/IAA9	PpeAUX/IAA8	PduAUX/IAA8	MdAUX/IAA8-like	MdAUX/IAA8-like	PavAUX/IAA9	PpeAUX/IAA9	PduAUX/IAA9	MdAUX/IAA9
PavAUX/IAA9*		74.76% (86.41%)	88.35% (94.17%)	88.35% (94.17%)	91.26% (96.12%)	100% (100%)	100% (100%)	98.04% (99.02%)	97.06% (98.04%)	87.38% (94.17%)	87.38% (94.17%)	87.38% (94.17%)	87.38% (94.17%)
AtAUX/IAA9	74.76% (86.41%)		81.55% (90.29%)	81.55% (90.29%)	81.55% (90.29%)	74.76% (86.41%)	74.76% (86.41%)	74.76% (85.44%)	74.76% (86.41%)	79.61% (90.29%)	79.61% (90.29%)	79.61% (90.29%)	78.64% (90.29%)
SlAUX/IAA9	88.35% (94.17%)	81.55% (90.29%)		97.09% (97.09%)	97.09% (98.06%)	88.35% (94.17%)	88.35% (94.17%)	87.38% (93.2%)	88.35% (94.17%)	90.29% (97.09%)	90.29% (97.09%)	90.29% (97.09%)	90.29% (97.09%)
StAUX/IAA9	88.35% (94.17%)	81.55% (90.29%)	97.09% (97.09%)		96.12% (97.09%)	88.35% (94.17%)	88.35% (94.17%)	87.38% (93.2%)	91.26% (96.12%)	90.29% (97.09%)	90.29% (97.09%)	90.29% (97.09%)	90.29% (97.09%)
CaAUX/IAA9	91.26% (96.12%)	81.55% (90.29%)	97.09% (98.06%)	96.12% (97.09%)		91.26% (96.12%)	91.26% (96.12%)	90.29% (95.15%)	97.06% (98.04%)	91.26% (97.09%)	91.26% (97.09%)	91.26% (97.09%)	91.26% (97.09%)
PpeAUX/IAA8	100% (100%)	74.76% (86.41%)	88.35% (94.17%)	88.35% (94.17%)	91.26% (96.12%)		100% (100%)	98.04% (99.02%)	97.06% (98.04%)	87.38% (94.17%)	87.38% (94.17%)	87.38% (94.17%)	87.38% (94.17%)
PduAUX/IAA8	100% (100%)	74.76% (86.41%)	88.35% (94.17%)	88.35% (94.17%)	91.26% (96.12%)	100% (100%)		98.04% (99.02%)	97.06% (98.04%)	87.38% (94.17%)	87.38% (94.17%)	87.38% (94.17%)	87.38% (94.17%)
MdAUX/IAA8-like	98.04% (99.02%)	74.76% (85.44%)	87.38% (93.2%)	87.38% (93.2%)	90.29% (95.15%)	98.04% (99.02%)	98.04% (99.02%)		97.06% (97.06%)	86.41% (93.2%)	86.41% (93.2%)	86.41% (93.2%)	86.41% (93.2%)
MdAUX/IAA8-like	97.06% (98.04%)	74.76% (86.41%)	88.35% (94.17%)	88.35% (94.17%)	91.26% (96.12%)	97.06% (98.04%)	97.06% (98.04%)	97.06% (97.06%)		87.38% (94.17%)	87.38% (94.17%)	87.38% (94.17%)	87.38% (94.17%)
PavAUX/IAA9	87.38% (94.17%)	79.61% (90.29%)	90.29% (97.09%)	90.29% (97.09%)	91.26% (97.09%)	87.38% (94.17%)	87.38% (94.17%)	86.41% (93.2%)	87.38% (94.17%)		100% (100%)	100% (100%)	98.06% (100%)
PpeAUX/IAA9	87.38% (94.17%)	79.61% (90.29%)	90.29% (97.09%)	90.29% (97.09%)	91.26% (97.09%)	87.38% (94.17%)	87.38% (94.17%)	86.41% (93.2%)	87.38% (94.17%)	100% (100%)		100% (100%)	98.06% (100%)
PduAUX/IAA9	87.38% (94.17%)	79.61% (90.29%)	90.29% (97.09%)	90.29% (97.09%)	91.26% (97.09%)	87.38% (94.17%)	87.38% (94.17%)	86.41% (93.2%)	87.38% (94.17%)	100% (100%)	100% (100%)		98.06% (100%)
MdAUX/IAA9	87.38% (94.17%)	78.64% (90.29%)	90.29% (97.09%)	90.29% (97.09%)	91.26% (97.09%)	87.38% (94.17%)	87.38% (94.17%)	86.41% (93.2%)	87.38% (94.17%)	98.06% (100%)	98.06% (100%)	98.06% (100%)	

Table S5.12: Identity percentages between the cDNA sequences.

	PavRGL2	*AtRGL1*	*AtRGL2*	*SlDELLA*	*StDELLA*	*CaDELLA*	*PpeRGL2*	*PduRGL2*	*MdRGL2*	*MdRGL2*
PavRGL2		41.16%	40.70%	40.70%	41.46%	57.35%	55.70%	60.87%	72.48%	73.51%
AtRGL1	41.16%		49.29%	41.17%	45.32%	41.40%	41.37%	44.71%	43.19%	42.95%
AtRGL2	40.70%	49.29%		41.40%	49%	40.92%	42.63%	45.99%	43.47%	43.85%
SlDELLA	40.70%	41.17%	41.40%		67.33%	70.50%	38.57%	42.13%	57.83%	58.70%
StDELLA	41.46%	45.32%	49%	67.33%		53.17%	43.74%	47.45%	42.93%	43.40%
CaDELLA	57.35%	41.40%	40.92%	70.50%	53.17%		38.93%	42.48%	56.87%	57.59%
PpeRGL2	55.70%	41.37%	42.63%	38.57%	43.74%	38.93%		89.10%	51.83%	52.61%
PduRGL2	60.87%	44.71%	45.99%	42.13%	47.45%	42.48%	89.10%		56.81%	57.54%
MdRGL2	72.48%	43.19%	43.47%	57.83%	42.93%	56.87%	51.83%	56.81%		91.01%
MdRGL2	73.51%	42.95%	43.85%	58.70%	43.40%	57.59%	52.61%	57.54%	91.01%	

Table S5.13: Identity and similarity percentages of the aminoacidic sequences. The similarity percentage is reported in brackets.

	PavRGL2	AtRGL1	AtRGL2	SlDELLA	StDELLA	CaDELLA	PpeRGL2	PduRGL2	MdRGL2	MdRGL2
PavRGL2		55.96% (64.77%)	55.8% (64.37%)	55.8% (64.37%)	61.48% (69.02%)	62.69% (70.98%)	87.52% (88.2%)	87.42% (88.09%)	75.63% (79.66%)	77.42% (79.77%)
AtRGL1	55.96% (64.77%)		59.89% (70.14%)	56.08% (65.71%)	56.01% (66.33%)	54.06% (64.01%)	58.15% (68.07%)	57.86% (67.89%)	59.35% (68.1%)	60.41% (68.94%)
AtRGL2	55.8% (64.37%)	59.89% (70.14%)		56.38% (66.5%)	56.46% (66.56%)	55.03% (67.05%)	58.31% (67.77%)	58.14% (67.61%)	58.54% (68.53%)	59.7% (68.47%)
SlDELLA	55.8% (64.37%)	56.08% (65.71%)	56.38% (66.5%)		91.05% (93.58%)	75.73% (80.78%)	65.53% (74.47%)	65.21% (74.11%)	64.42% (74.63%)	67.11% (75.66%)
StDELLA	61.48% (69.02%)	56.01% (66.33%)	56.46% (66.56%)	91.05% (93.58%)		77.04% (82.08%)	65.04% (74.31%)	65.05% (74.27%)	64.42% (75.45%)	66.78% (76.15%)
CaDELLA	62.69% (70.98%)	54.06% (64.01%)	55.03% (67.05%)	75.73% (80.78%)	77.04% (82.08%)		64.94% (74.15%)	64.63% (74.12%)	63.03% (73.94%)	64.61% (74.35%)
PpeRGL2	87.52% (88.2%)	58.15% (68.07%)	58.31% (67.77%)	65.53% (74.47%)	65.04% (74.31%)	64.94% (74.15%)		98.66% (98.99%)	82.44% (87.12%)	85.12% (87.96%)
PduRGL2	87.42% (88.09%)	57.86% (67.89%)	58.14% (67.61%)	65.21% (74.11%)	65.05% (74.27%)	64.63% (74.12%)	98.66% (98.99%)		81.86% (86.69%)	84.53% (87.69%)
MdRGL2	75.63% (79.66%)	59.35% (68.1%)	58.54% (68.53%)	64.42% (74.63%)	64.42% (75.45%)	63.03% (73.94%)	82.44% (87.12%)	81.86% (86.69%)		89.91% (94.36%)
MdRGL2	77.42% (79.77%)	60.41% (68.94%)	59.7% (68.47%)	67.11% (75.66%)	66.78% (76.15%)	64.61% (74.35%)	85.12% (87.96%)	84.53% (87.69%)	89.91% (94.36%)	

Table S5.14: Identity and similarity percentages of the aminoacidic sequences of the DELLA domain. The similarity percentage is reported in brackets.

	PavRGL2	AtRGL1	AtRGL2	SlDELLA	StDELLA	CaDELLA	PpeRGL2	PduRGL2	MdRGL2	MdRGL2
PavRGL2		52% (56%)	42.86% (51.02%)	48% (58%)	48% (58%)	52% (58%)	69.39% (69.39%)	69.39% (69.39%)	65.31% (69.39%)	67.35% (69.39%)
AtRGL1	52% (56%)		68% (78%)	72% (82%)	72% (82%)	72% (82%)	78% (84%)	78% (84%)	76% (84%)	80% (84%)
AtRGL2	42.86% (51.02%)	68% (78%)		64% (74%)	64% (74%)	64% (74%)	69.39% (79.59%)	69.39% (79.59%)	65.31% (79.59%)	67.35% (79.59%)
SlDELLA	48% (58%)	72% (82%)	64% (74%)		100% (100%)	94% (100%)	74% (86%)	74% (86%)	72% (86%)	76% (86%)
StDELLA	48% (58%)	72% (82%)	64% (74%)	100% (100%)		94% (100%)	74% (86%)	74% (86%)	72% (86%)	76% (86%)
CaDELLA	52% (58%)	72% (82%)	64% (74%)	94% (100%)	94% (100%)		78% (86%)	78% (86%)	72% (86%)	76% (86%)
PpeRGL2	69.39% (69.39%)	78% (84%)	69.39% (79.59%)	74% (86%)	74% (86%)	78% (86%)		100% (100%)	91.84% (95.92%)	93.88% (95.92%)
PduRGL2	69.39% (69.39%)	78% (84%)	69.39% (79.59%)	74% (86%)	74% (86%)	78% (86%)	100% (100%)		91.84% (95.92%)	93.88% (95.92%)
MdRGL2	65.31% (69.39%)	76% (84%)	65.31% (79.59%)	72% (86%)	72% (86%)	72% (86%)	91.84% (95.92%)	91.84% (95.92%)		95.92% (100%)
MdRGL2	67.35% (69.39%)	80% (84%)	67.35% (79.59%)	76% (86%)	76% (86%)	76% (86%)	93.88% (95.92%)	93.88% (95.92%)	95.92% (100%)	

Table S5.15: Identity and similarity percentages of the aminoacidic sequences of the GRAS domain. The similarity percentage is reported in brackets.

	PavRGL2	AtRGL1	AtRGL2	SlDELLA	StDELLA	CaDELLA	PpeRGL2	PduRGL2	MdRGL2	MdRGL2
PavRGL2		72.78% (82.48%)	74.47% (84.04%)	81.56% (87.27%)	81.56% (87.27%)	80.53% (87.37%)	98.38% (98.92%)	98.92% (99.19%)	91.62% (94.32%)	94.05% (95.95%)
AtRGL1	72.78% (82.48%)		69.15% (80.05%)	67.36% (76.68%)	67.36% (76.94%)	66.14% (76.64%)	72.78% (82.75%)	72.78% (82.75%)	72.97% (81.62%)	74.12% (82.48%)
AtRGL2	74.47% (84.04%)	69.15% (80.05%)		69.74% (80.26%)	69.74% (80.51%)	68.83% (82.08%)	74.73% (84.57%)	74.47% (84.31%)	73.33% (83.47%)	74.47% (83.24%)
SlDELLA	81.56% (87.27%)	67.36% (76.68%)	69.74% (80.26%)		99.48% (99.48%)	89.09% (92.47%)	80.78% (86.75%)	81.04% (87.01%)	79.74% (87.01%)	82.08% (87.79%)
StDELLA	81.56% (87.27%)	67.36% (76.94%)	69.74% (80.51%)	99.48% (99.48%)		89.35% (92.47%)	80.78% (86.75%)	81.04% (87.01%)	79.74% (87.01%)	82.08% (87.79%)
CaDELLA	80.53% (87.37%)	66.14% (76.64%)	68.83% (82.08%)	89.09% (92.47%)	89.35% (92.47%)		80.26% (87.37%)	80.53% (87.63%)	79.47% (87.37%)	81.58% (88.42%)
PpeRGL2	98.38% (98.92%)	72.78% (82.75%)	74.73% (84.57%)	80.78% (86.75%)	80.78% (86.75%)	80.26% (87.37%)		99.46% (99.73%)	91.35% (94.32%)	94.05% (95.95%)
PduRGL2	98.92% (99.19%)	72.78% (82.75%)	74.47% (84.31%)	81.04% (87.01%)	81.04% (87.01%)	80.53% (87.63%)	99.46% (99.73%)		91.62% (94.59%)	94.05% (96.22%)
MdRGL2	91.62% (94.32%)	72.97% (81.62%)	73.33% (83.47%)	79.74% (87.01%)	79.74% (87.01%)	79.47% (87.37%)	91.35% (94.32%)	91.62% (94.59%)		93.51% (96.22%)
MdRGL2	94.05% (95.95%)	74.12% (82.48%)	74.47% (83.24%)	82.08% (87.79%)	82.08% (87.79%)	81.58% (88.42%)	94.05% (95.95%)	94.05% (96.22%)	93.51% (96.22%)	

Annex

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Review

Fruit Development in Sweet Cherry

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Abstract: Fruits are an important source of vitamins, minerals and nutrients in the human diet. They also contain several compounds of nutraceutical importance that have significant antioxidant and anti-inflammatory roles, which can protect the consumer from diseases, such as cancer, and cardiovascular disease as well as having roles in reducing the build-up of LDL-cholesterol in blood plasma and generally reduce the risks of disease and age-related decline in health. Cherries contain high concentrations of bioactive compounds and minerals, including calcium, phosphorous, potassium and magnesium, and it is, therefore, unsurprising that cherry consumption has a positive impact on health. This review highlights the development of sweet cherry fruit, the health benefits of cherry consumption, and the options for increasing consumer acceptance and consumption.

Keywords: tree fruit; fruit ripening; rootstock; *Prunus avium*

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Citation: Vignati, E.; Lipska, M.; Dunwell, J.M.; Caccamo, M.; Simkin, A.J. Fruit Development in Sweet Cherry. *Plants* **2022**, *11*, 1531. https://doi.org/10.3390/plants11121531

Academic Editor: Bruno Mezzetti

Received: 21 April 2022
Accepted: 4 June 2022
Published: 7 June 2022

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1. Introduction

Cherry (*Prunus avium*) is believed to be native to Europe and southern Asia [1] and to a small isolated region in the western Himalayas. Commonly called sweet cherry, it is a deciduous tree, 15–32 m in height and with a trunk up to 1.5 m in circumference. It belongs to the Rosaceae family, which includes many plants, such as rose, apple (*Malus x domestica*), peach (*Prunus persica*) and strawberry (*Fragaria vesca* and *F. ananassa)* that are very important for the human economy. The sweet cherry genome is diploid (2n = 16), simple, compact and about 350 Mb in size. The genome structure is predicted to be similar to that of the peach, although the sequences have diverged [2–4] See (http://www.rosaceae.org accessed on 1 June 2022) [5].

Young cherry trees show strong apical dominance with a straight trunk and symmetrical conical crown that becomes rounded to irregular for old trees. All parts of the plant, except for the ripe fruit, are slightly toxic, due to the presence of cyanogenic glycosides. The species has also become naturalized in North America and Australia since it is largely cultivated in these regions.

Cherry production has seen remarkable growth in the last few years. Worldwide, cherry production has increased by 37% since 2000 (Figure 1). This fact shows that growers are committing more resources to cherry production, and growing consumer interest is one of the drivers behind these increases.

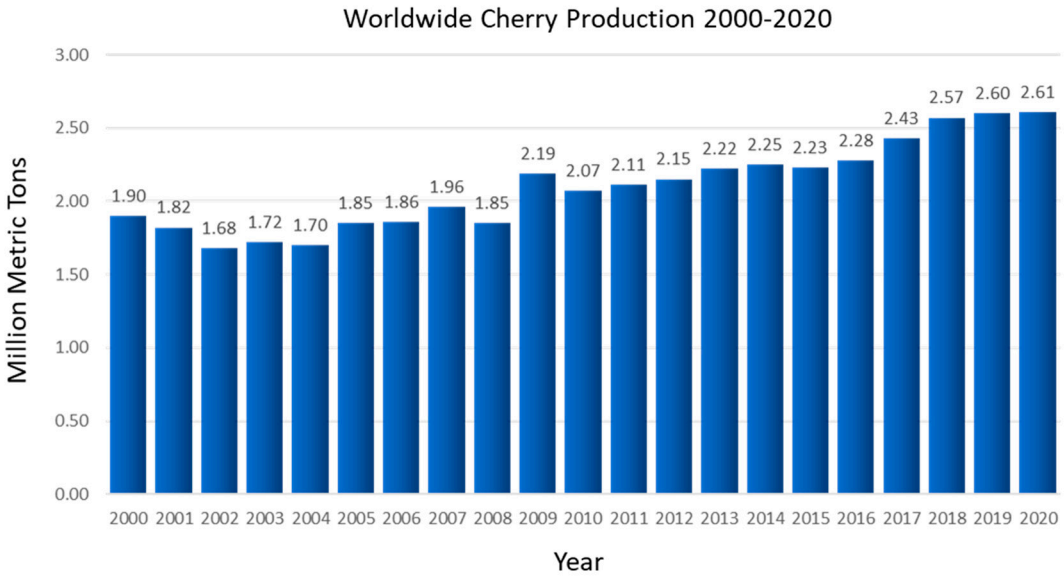

Figure 1. Graphical representation of worldwide cherry production between 2000 and 2020 (Statista.org).

2. Cherry from Flower to Fruit

2.1. Cherry Flower

2.1.1. Cherry Flower Pollination

The sweet cherry flower is hermaphroditic; possessing both female and male reproductive organs. Each flower is approximately 2.5 cm in diameter, with five petals surrounded by five green sepals, a single upright pistil with an ovary, two ovules, and 30 stamens. The stamens are the male reproductive organs consisting of anthers, where the pollen develops; it sits on top of the stalk-like filaments, which allows water and nutrients to reach the anthers from the mother plant and facilitate pollen dispersal [6,7]. The pistil or gynoecium is the female reproductive organ, and it occupies the centre of the flower.

The flowers open for between three and five days and the stigma is receptive to pollination at this time. The anthers begin to open shortly after the flower and continue into the second day [8]. In sweet cherry, it takes two to three days for the pollen tube to grow from the stigma to the base of the style, whilst fertilization occurs six to eight days after pollination [9,10]. Stösser and Anvari [11] determined that effective pollination takes between 4 and 5 days; however, under some conditions, effective pollination can last up to 13 days [12]. There are a number of varieties of sweet cherry that exhibit self-fertility, the first and most notable being 'Stella', which was first identified in Canada [13], and is highly sought-after and considered a cultivar of great importance [14–16]. However, most sweet cherry cultivars exhibit self-incompatibility (SI), a characteristic that involves inhibition of pollen tube growth, and is genetically controlled by multiple allelic *S*-loci [17–20]. SI sweet cherry varieties still produce a small number of fruit through self-pollination; however, different varieties are considered to have different levels of self-sterility, with important commercial varieties, such as 'Kordia' and 'Regina' being highly incompatible and setting virtually no fruit in the absence of cross-pollination [21].

The nectar of sweet cherry is rich in sugars (from 28% to 55% sugar), the most abundant of which are fructose, glucose and sucrose, which are highly attractive to pollinating insects, including bees [22]. It is well known that insect-mediated pollination in sweet cherry is important for the production of a viable crop and besides the environmental conditions, pollinating insects are the most important factor governing yield [23]. Work by Holzschuch et al. [24] showed that bagged flowers produced only 3% of the number of fruits produced by unbagged flowers and that the rates of pollination and fruit set were related to wild bee visitation. Wild pollinators, including solitary bees, have been described as being instrumental in achieving adequate sweet cherry yields [25]. These authors also

showed that pollination by wild bees surpassed pollination by honeybees. However, even with this knowledge, less than 17% of growers provide trap nests for solitary bees in their orchards and rely on commercial domesticated honeybees (*Apis mellifera*) to carry out this function at a cost up to 1000 Euro per hectare—a considerable investment for commercial cherry producers. A recent review has outlined grower knowledge of the role of insects on sweet cherry crops [23].

Air temperature is also known to influence flowering and fruit sets and has no influence on the level of SI; however, the air temperature may influence pollen tube growth [26]. The optimal temperature for flowering has been reported to be around 20 °C, with temperatures as low as 15 °C slowing the disappearance of the embryo sac, as compared to 25 °C [27]. Temperatures exceeding 30 °C are considered too high for successful flowering [26,28,29]. Furthermore, it has been reported that a sudden fall in temperature at the end of the flowering period can result in a total loss of the crop [21].

2.1.2. The ABCDE and the Floral Quartet Models

Flower organs are arranged in whorls, with sepals that are located in the most external whorl and carpels in the inner whorl, in the form of petals and stamens. Floral homeotic mutants, i.e., mutants with an altered floral organ identity, such as in *Arabidopsis thaliana* and *Antirrhinum majus* (snapdragon), have been studied and used to propose the ABC model of flower formation [30,31]. ABC genes encode three different classes of MADS-domain transcription factors involved in the flower organ identity determination. These factors interact to give the organ identity to sepal, petals, stamens and carpel. Further studies showed the existence of two other classes: the D class, which is responsible for the ovule identity, and the E-class, which has been proposed as another class of redundant floral organ identity genes [32]. This enhanced ABCDE model postulates that sepals are specified by A + E, petals by A + B + E, stamens by B + C + E, carpels by C + E and ovules by C + D + E (Figure 2) [32–35].

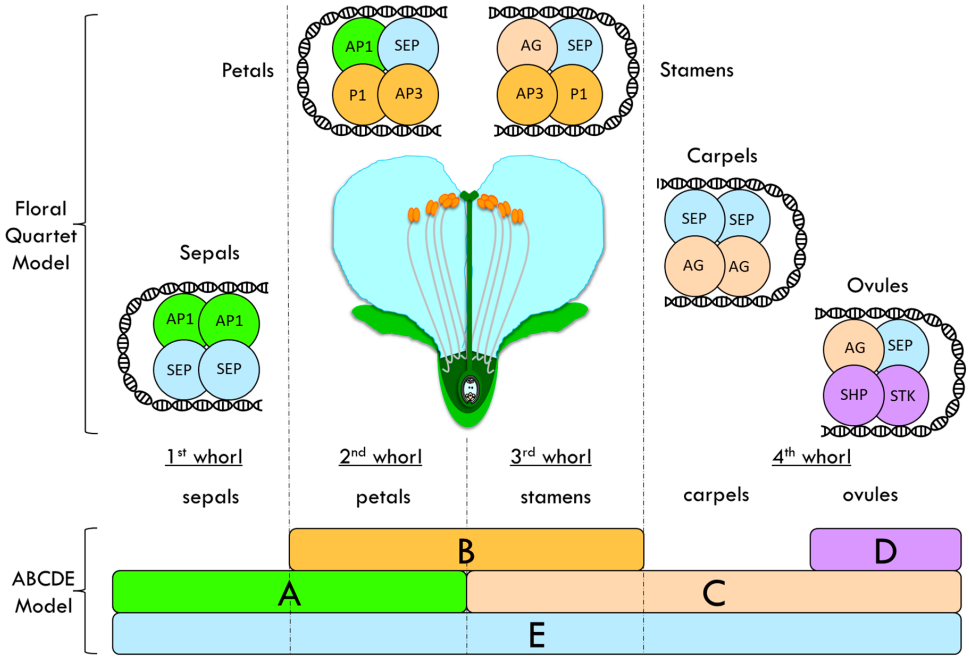

Figure 2. Floral quartet model (FQM) integrated into the ABCDE model proposed to explain the flower whorls' identity determination in *Arabidopsis thaliana*. This enhanced ABCDE model postulates that sepals are specified by A + E, petals by A + B + E, stamens by B + C + E, carpels by C + E and ovules by C + D + E. Class-A protein: APETALA1 (AP1); Class-B proteins: PISTILLATA (PI) and APETALA3 (AP3); Class-C protein: AGAMOUS (AG); Class-D proteins: SEEDSTICK (STK) and SHATTERPROOF (SHP); Class-E protein: SEPALLATA (SEP).

In addition, the floral quartet model (FQM, Figure 2) has been suggested to integrate the ABCDE model [32]. According to the FQM, the factors form tetrameric complexes to carry out their functions, binding the DNA to activate or repress the expression of their target genes [32]. In particular, two MIKC-type MADS-box transcription factors belonging to the same class form a dimer, which can interact with another dimer of the same class or of a different class, to promote the development of a specific floral organ [35]. The MIKC-type MADS-box transcription factors are composed of specific domains:

1. MADS (M) domain: a DNA-binding domain, but it is also involved in dimerization and in nuclear localization. It is the most conserved domain among the MADS-box transcription factors [36].
2. Intervening (I) domain: takes part in the selective formation of DNA-binding dimers. It shows only limited conservation [37].
3. Keratin-like (K) domain: an essential element for dimerization and multimeric complex formation. This domain has a particular structural organization (amphipathic helices) in which the hydrophobic and charged residues are conserved and regularly spaced [38,39].
4. C-terminal (C) domain: is somewhat variable. In some cases, it takes part in the transcriptional activation of the target genes or in the formation of multimeric complexes [37].

According to the FQM, MADS-box transcription factors form dimers, which bind the DNA where the CArG-boxes are present. The two dimers that are present in the tetramer recognize and bind the two different CArG-boxes—which can be far away in the DNA sequence—by looping the DNA and making them spatially close [32,35,40].

3. Cherry Fruit Development

3.1. Cherry Fruit

The sweet cherry fruit is a drupe—an indehiscent fruit of 1–2 cm in diameter (in some cultivars the diameter can be larger) that has an attractive appearance due to its color (bright red to dark purple depending on the cultivar) and desirable, intense flavor. Three parts can be identified in a drupe: the outer exocarp or skin; the mesocarp, which is the fleshy part of the fruit; and a single central stone, which is the lignified endocarp that surrounds the seed. Drupe development in cherry fruit is consistent with the reported stages of growth in other drupes, as described below.

Cherry varieties can be divided into early, mid and late ripening types (Table 1) based on the ripening of the reference variety at the European level, Burlat, a widespread cultivated cherry across Europe.

Table 1. Some of the most commonly commercially cultivated varieties of sweet cherry. Early, mid and late ripening types based on the ripening of the reference variety, Burlat, a widespread cultivated cherry across Europe. Comparisons to the variety Bing are based on interviews with growers in Stanislaus County, California and on published data. NR—not reported.

Ripen	Days Post-Burlat *	Days Post Bing **	Variety	Reported Qualities and Region of Origin
Burlat	0	NR	Burlat	The most widespread and cultivated cherry among existing varieties. It has good flavor, high resistance to cracking compared to most varieties, and exceeds in its time.
Early	0–11	NR	Merchant	Self-sterile, mature 7 days post-Burlat. Producing good yields of large, dark red fruit in early summer. Self-sterile, mature 9 days after Burlat.
		NR	Carmen	Developed and cultivated in Hungary. Fruit have large size and good flavor. Spreading in Germany due to its high yields.

Table 1. *Cont.*

Ripen	Days Post-Burlat *	Days Post Bing **	Variety	Reported Qualities and Region of Origin
Mid	12–19	NR	Grace Star	Recent Italian variety. Self-fertile with maturation occurring 12 days post-Burlat. Large fruit, firm texture, excellent flavor qualities, and highly valued by consumers.
		−5	Cristalina^{Tm}	Self-sterile cherry of Canadian origin. Mature 12 days post-Burlat. High productivity, under conditions of moderate load. Fruit have good firmness and very good flavor and is moderately sensitive to cracking.
		0	Stella	One of the first self-fertile varieties (Canadian origin). Ripens 19 days post-Burlat. Large fruit, blood-red hue, good resistance to cracking, sensitive to cold. Highly sought-after. Considered a cultivar of great importance.
		Bing	Bing	Most traditional and representative cherry of America. Ripening occurs 19 days post-Burlat. Fruit are dark red, large, firm, and highly valued for their excellent flavor and is the preeminent fresh-market cherry.
		0	Rainer	Bicolor cherry from the United States. The variety is self-sterile and ripens 19 days post-Burlat. Variety is appreciated by the industry owing to the large size and good flavor of the fruit.
Late	20–27	NR	Kordia	Originating in the Czech Republic with good resistance to cracking. Very popular in Germany. Ripens 24 days post-Burlat. Known for large, firm fruit and good flavor. Highly incompatible and setting virtually no fruit in the absence of cross-pollination.
		3	Sonata^{Tm}	Self-fertile Canadian variety with good productivity. Ripens 22 days post-Burlat. Fruit have a good taste and are large and firm in size. Unfortunately, it is highly susceptible to cracking.
		5–7	Lapins	Highly productive self-fertile from the United States. Currently, most planted cherry in the world. Good flavor with cracking resistance. Variety is appreciated by farmers. Ripens 24 days post-Burlat (see Skeena^{Tm}).
		7–10	Benton^{Tm}	Another self-fertile cherry tree that ripens mid-season and has been reputed to surpass Bing cherries.
		10–14	Skeena^{Tm}	Characterized as an improved Lapins. Similar characteristics, but lower productivity, which helps to produce cherries of greater caliber and quality. In the United States, replacing Lapins. Mature 25 days post-Burlat.
		11–13	Sweetheart^{Tm}	Late maturation with large fruit. Prolific fruiters with a dark red, medium to large cherries. Pruning is required to keep trees productive.
Extra Late	More than 28	NR	Regina	Self-sterile variety of German origin. Low productivity with maturation occurring 31 days post-Burlat. Large sized fruit, good taste and cultivated due to its high resistance to cracking. Highly incompatible and setting virtually no fruit in the absence of cross-pollination.
		NR	Ambrunes	Spanish Cherry is traditionally grown in Cáceres. Firm fruit with very good flavor. High resistance to cracking. Ripens 31 days post-Burlat.

* https://en.excelentesprecios.com/cherry-tree-varieties, (3 June 2022); ** https://m.blog.naver.com/PostView.naver?isHttpsRedirect=true&blogId=2jw67&logNo=90164242596 1 June 2022. Tm = trademark.

During early fruit development, there is constant communication between the developing fruit and the developing seed. These signals can be hormones, such as auxin and gibberellins, produced in the endosperm or in the seed coat and are involved in the developmental synchronization of all these different structures [41–44]. The disruption of this communication is one of the triggers of fruit drop—the loss of a significant proportion of their fruit before ripening. This loss, which is often referred to as 'June Drop' or 'Cherry Run Off', varies from year to year and, in some seasons, can result in a total loss of the crop.

3.2. Physiological Changes during Cherry Fruit Development

The developmental growth rate of the drupe can be described by a double sigmoid curve, where three well-marked stages can be identified (Figure 3). In the first phase (stage I), the ovary either aborts or starts all the subsequent morphological changes that will lead to the formation of the fruit [45–51]. The traditional definition of phase I, beginning at anthesis, also includes the acceleration of the growth of the ovary approximately two weeks before anthesis [52].

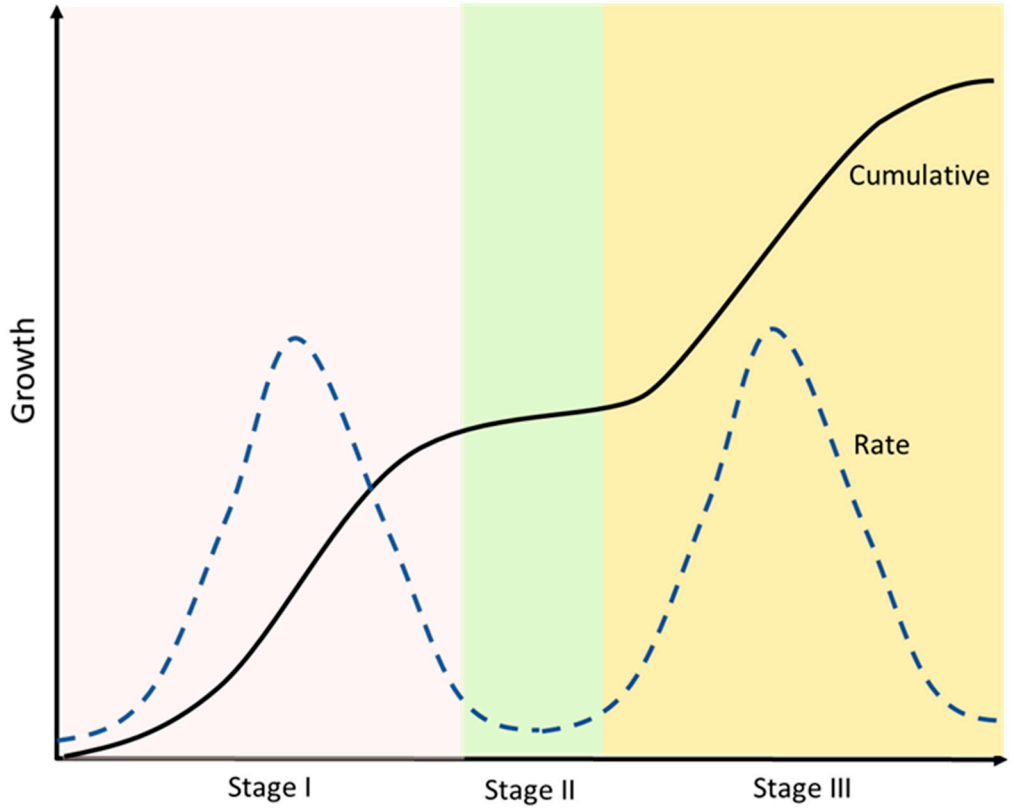

Figure 3. A double sigmoid growth curve representation. Cumulative and rate of growth are defined. After an initial exponential phase (Stage I) a second plateau phase occurs (Stage II), which is followed then by a second exponential phase (Stage III) until the complete ripening of the fruit. Developmental phases are allocated with respect to peaks and troughs in growth rate.

The outer epidermis of the developing cherry fruit consists of a single row of cells that are covered externally by a cuticle, which is interrupted only where the stomata are present (see Section 4). During the pre-flowering period, the cells of the epidermis are already well-differentiated, with an elongated shape and no hairs, and increase their size slowly, mainly in the radial direction. The mitotic activity is low since the increase in the number of cells is very limited, while it is high during the first half of stage I (Figure 4). The second half of stage I is characterized by an increase in cell size, both radially and tangentially. Moreover, during the second half of stage I, the cuticle reaches its full thickness. No cell division is observed during stage II, which is characterized by slight tangential elongation

of cells and additional cell wall thickening. Lastly, during the final phase (stage III), cells start to enlarge by as much as 100-fold, contributing to the final fruit size. After these three phases, a green immature fruit is formed, which has the dimensions of the mature fruit and starts the maturation process (see Section 3.3) [45–51]. A more than two-fold tangential enlargement of the cells occurs, with a decrease in the radial diameter and cuticle thickness, in order to generate a large increase in the fruit surface area [53].

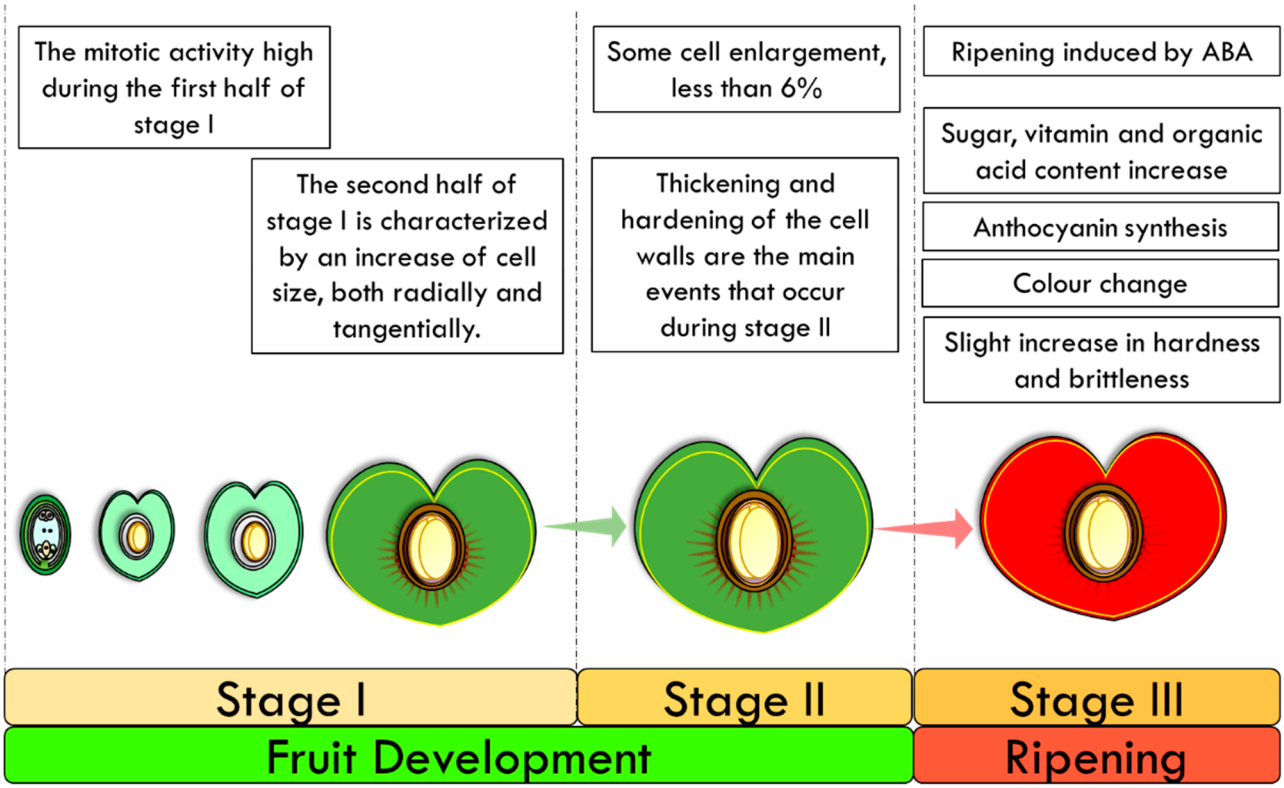

Figure 4. Fruit Ripening in the cultivated cherry. After an initial exponential phase (Stage I) a plateau phase occurs (Stage II), which is followed then by a second exponential phase (Stage III) until the complete ripening of the fruit.

During the pre-bloom period, the fleshy mesocarp is composed of isodiametric parenchymatous cells, which elongate according to a gradient tangentially to slightly radial from the epidermis to the stony endocarp, respectively. The increase in tissue thickness, more than double, is due mostly to cell division. The first half of stage I is characterized by cell mitotic divisions, accomplishing an increase of about 20–30% in the number of cells from the epidermis to the stone, and no further divisions are observed after completion of this stage [53]. The cells increase in diameter more than four-fold, mostly during the second half of stage I. Moreover, differentiation of a hypodermal layer, five or six cells thick, occurs just under the epidermis, by considerable thickening of the cells. These cells become slightly greater in size than those of the epidermis and become tangentially elongated. On the other side, adjacent to the stone, a layer of small isodiametric cells, three or four cells wide, differentiates, during the second half of stage I. During stage II, some cell enlargement, less than 6%, occurs and intercellular spaces remain prominent. The cells just under the epidermis continue slowly to elongate tangentially, while limited cell division can be found in the thin layer of small cells adjacent to the stone, otherwise, there is none. Stage III is also called "the final swell" and during this period, four parts of the fleshy mesocarp can be recognized (from the epidermis to the stony endocarp):

1. The hypodermal layer of collenchyma;
2. The peripheral layer of thin-walled parenchyma, extending to a line just inside the ring of vascular bundles;

3. The layer of radially elongated cells, extending from this line nearly to the stone;
4. The thin layer of small cells adjacent to the stone.

The transition from one layer to the other is not precise, since there is a gradual transition from a tissue in which one cell type predominates to one in which another one is dominant. A gradient of cell elongation can be identified, from tangential in the hypodermal cells to radial in the ones close to the stone. The rapid cell enlargement brings a decrease in the thickness of the cell walls and the disappearance of the intercellular spaces that are now difficult to identify [53].

The ventral and the dorsal capillary bundles do not enter the stony endocarp, while the two bundles that supply the two ovules (in peach called "funicular bundles") are at either side of the ventral suture and adjacent to the ovarian cavity. Pit bundles traversing the stony endocarp, of the type found in peach, are not present in cherry. During the pre-bloom period, the differentiation of a ring of vascular bundles, which extends through the fleshy mesocarp parallel to the central axis, occurs. However, the walls of xylem elements do not become sufficiently thickened to become conspicuous until about the full-bloom period. The number of bundles is fixed, so that as the fruit develops, the vasculature system extends progressively throughout the flesh, mostly by a transverse divergence of small bundles from the main ones. At maturity, a skeleton network of conductive tissue is present [53].

The innermost ovary wall comprises a single layer of cells, called the inner epidermis, and three or four layers of pericarp cells. These cells, which are going to become part of the stony endocarp, are smaller than the cells that are going to become the fleshy mesocarp, and this size difference persists to maturity. During the pre-bloom period, the inner epidermal cells elongate tangentially and divide transversally just before full bloom, to form with adjacent pericarp cells with a similar orientation—a "hoop" shape that surrounds the ovary cavity. The presence of this hoop is also reported in other species [54,55]. The group of cells that differentiate into the stony endocarp do not give rise to the fleshy mesocarp and vice versa. Stage I is characterized by a large increase in both the number and size of the inner layer cells (tangential elongation) and the outer layer cells (central radial elongation). No cell divisions are observed in the inner layer during the second half of stage I, while there is a greater increase in the mitotic divisions and cell size in the outer layer. Cell walls become progressively thicker but do not harden significantly until the end of this stage, which is when the pit cannot be sectioned without special treatment [53]. The thickening and hardening of the cell walls are the main events that occur during stage II, and no cell divisions are observed after the mid-point of this stage. Hardening does not occur uniformly in the stony endocarp, but it begins near the apical end at the hilum, and continues downwards toward the chalaza before finally including the whole endocarp. Although lignification occurs, cells are living and nuclei are abundant, even though the cellular lumen is frequently scarcely larger than the nucellus. At the end of stage II, the stony endocarp is made of 26–27 layers of very thick-walled lignified cells. This number of layers is the same as that present in the fleshy mesocarp, although the thickness is much less due to the very different destinies of the two tissues. During stage III, there is a slight increase in hardness and brittleness that is associated with a loss of moisture. It is possible to find occasional living cells with active nuclei [53].

3.3. Final Ripening Stages of Mature Cherry

Fruit ripening is a highly variable process with numerous differences when different plant species are compared; however ripening is often characterized by the accumulation of pigments, such as carotenoid sand anthocyanins (Figure 5) [56]. Despite these differences, fruit ripening has been classified into two distinct groups, climacteric and non-climacteric, which differ in their patterns of ethylene production and respiration at the onset of the ripening process [57,58]. Climacteric fruit, such as tomato, display a rise in respiration and a burst of ethylene modulating the differentiation of chloroplast to chromoplast and the accumulation of carotenoids [59,60]. In contrast, cherry fruit are non-climacteric and ripening is promoted by abscisic acid (ABA) [61]. No burst of ethylene and respiration

has been observed in sweet cherry during fruit development and ripening. Moreover, the exogenous ethylene treatment has no significant effects on the fruit's respiration rate or on its softening [62,63]. Ethylene concentrations remain low [64,65], although ethylene may affect the accumulation of anthocyanins [66]. However, it should be noted that the ethylene concentration in some sweet cherry cultivars has been shown to increase sharply before harvest [67], suggesting that it may play some role in fruit ripening during the maturation phase of development [68]. In sweet cherry, ABA levels increase before maturation and decrease near harvest [64,69]. Furthermore, in grapes, another non-climacteric fruit, the onset of ripening is ABA related; ABA modulates the changes in color and the accumulation of sugars and has a role in fruit softening in the later stages of ripening [70–72].

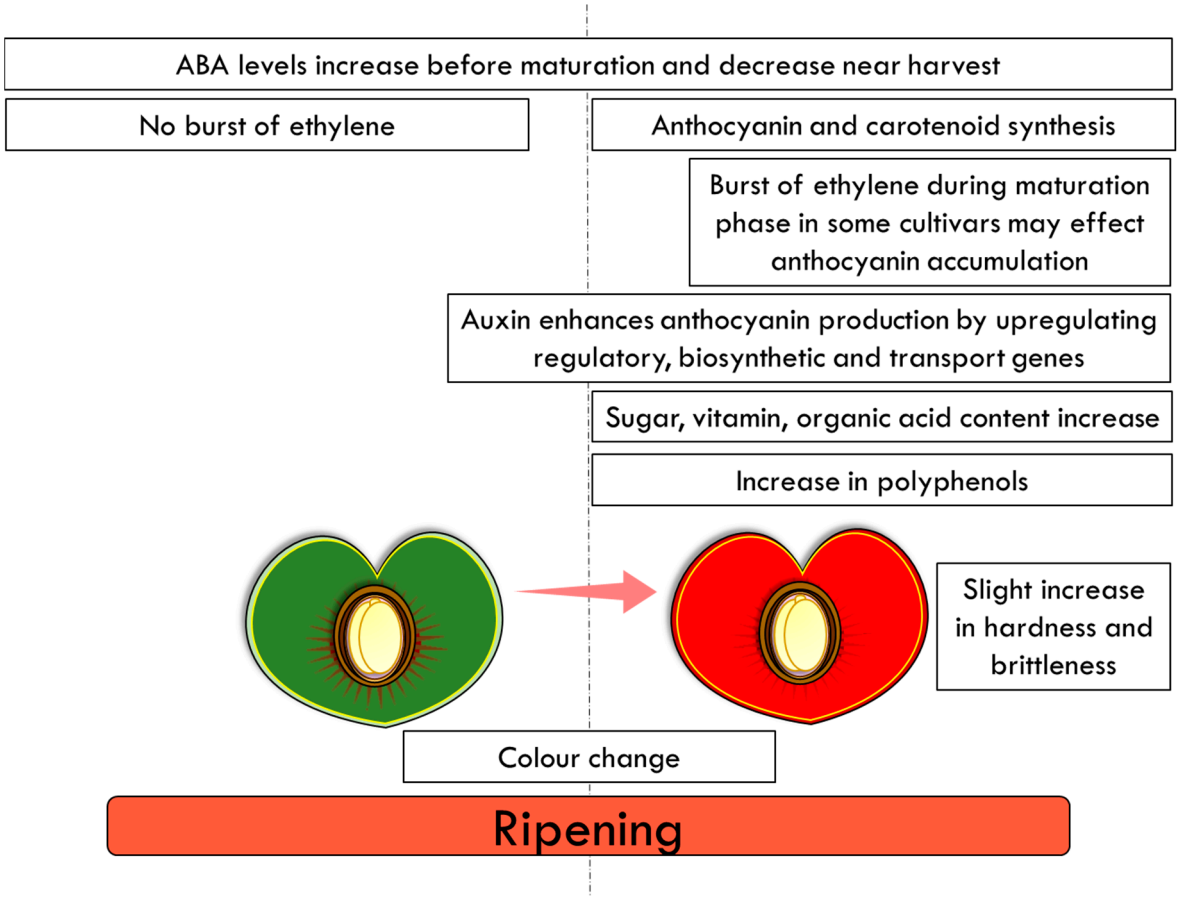

Figure 5. Final stages of fruit ripening in the cultivated cherry.

Cherry ripening is associated with changes in color, sugar, vitamin and organic acid content (Figure 5). In sweet cherries, ABA has been associated with the regulation of anthocyanin synthesis and the organoleptic properties (ratio of total soluble sugars to total acidity) [64,66,73]. The color of the fruit is attributed to the accumulation of these water-soluble health-promoting anthocyanins (a class of flavonoids), which are responsible for the blue, purple and red colors [74,75]. In addition to ABA, cytokinins, jasmonic acid (JA), gibberellins (GAs), and auxins, all play roles in the ripening of non-climacteric fruit. Auxin (1-naphthaleneacetic acid (NAA)) treatment has been shown to enhance anthocyanin production in sweet cherry by upregulating key anthocyanin regulatory, biosynthetic and transport genes [76]. This study demonstrated that treatment with NAA alters ethylene production, induces ripening, and enhances anthocyanin production, probably through ABA metabolism [76].

Size, color, firmness, sweetness and flavor intensity are considered the most critical attributes that drive consumer acceptance and, ultimately, the value of the crop to the producers [77–80]. However, consumers from different countries and regions place different

values on their requirements for a good cherry. For example, consumers in Norway prefer dark, large cherries [81,82]. Similar results were found in the UK [83] and in American markets [84]. These consumer requirements may differ from those of the growers and supermarkets. Growers want cherries that are resistant to cracking and can be left on the trees longer to ripen, are easy to harvest (long peduncles) and firm enough to resist damage during picking, processing, and transporting. Supermarkets want cherries with long shelf lives, even weeks once in store.

4. The Physiological Role of Cherry Fruit Stomata

Although stomata are routinely found on the surface of cherry fruit [85], they are not uniformly distributed over the surface of the epicarp (Figure 6). They are found in high numbers near the apex and few are near the stem end.

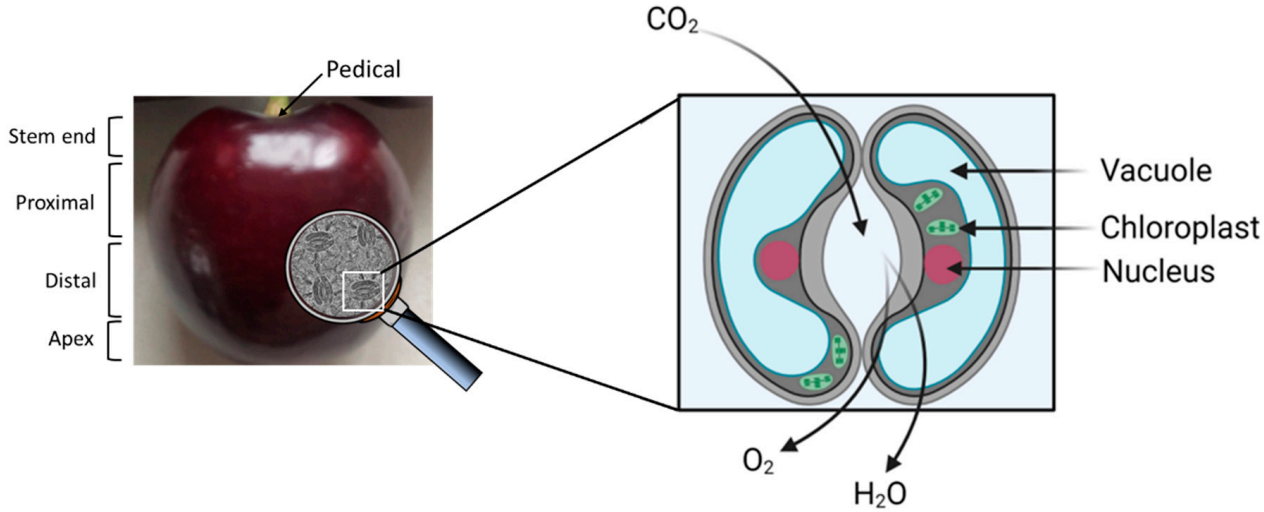

Figure 6. Schematic representation of stomatal pores on the surface of cherry fruit. They are found in high numbers near the apex and few near the stem end. When the stomata open, Ribulose–1,5-bisphosphate carboxylase (Rubisco) assimilates atmospheric CO_2 that diffuses into the cells through the stomatal pores. Simultaneously, water and oxygen are lost (Figure created using Biorender.com 1 June 2022).

The full differentiation of stomata can already be found during the pre-bloom period and the guard cells increase in size as the fruit develops, but at a lower rate than the epidermal cells. In the ripe fruit, the cells of the epidermis have a bright red color due to the presence of the chromoplasts, which are absent in the guard cells and in the cells that are immediately adjacent, resulting in a yellowish, straw-color [53]. Studies that have evaluated photosynthesis in non-foliar tissue, including fruit, have assumed that the photosynthetic pathway is similar to that observed in the mesophyll. However, non-foliar tissue photosynthesis has two potential major sources of CO_2. Firstly, Ribulose–1,5-bisphosphate carboxylase (Rubisco) assimilates atmospheric CO_2 that diffuses into the cells through the stomatal pores and, secondly, CO_2, released by mitochondrial respiration, is re-fixed (recycling photosynthesis) [86,87].

The fruit of cucumber (Cucumis sativus) was shown to contribute 9.4% of its own carbon requirements, and as much as 88% of the respiratory CO_2 in fruit was re-fixed [88].

Tomato fruits also have no stomata on their surface [89,90]; however, work carried out by Tanaka et al. [91], Hetherington et al. [92] and Obiadalla-Ali et al. [93] in green developing tomato fruit showed that fruit contributed between 10% and 15% of the total fixed carbon of the fruit. Similar to the tomato, cherry fruit are green at the early stages of development and contain the necessary pigments to carry out photosynthesis (for a review of photosynthetic pigments and fruit photosynthesis, see [86,89,94,95].

These data suggest that the stomata on the surface of cherry fruit carry out a real physiological role, contributing carbon either directly by assimilating carbon from the atmosphere or through recycling photosynthesis, recapturing the CO_2 liberated by mitochondrial respiration. A better understanding of this process could lead to better quality and a more nutritious product.

5. Genetic Control of Fruit Development

Fruit development is tightly controlled and regulated in order to produce, in the end, the complex structure that bares the developing seed. There are several models used to explain this complicated process, however, the most commonly used is the silique of *A. thaliana*, which is a dry fruit made from several distinct tissues, including the valves (seedpod walls), replum (middle ridge), septum, and valve margins [96], and tomato (*Solanum lycopersicum*), which has become the primary model to study fleshy fruit development and ripening because of the availability of advanced molecular and genetic toolkits, mutant collections and ease of handling [59,97].

The features of an organ are determined at a very early stage of development. During the very first phases of development, many aspects of floral organs, such as ovary identity and size, and at least partially final fruit size and ripening, are determined. Therefore, it is not surprising that some transcription factors involved in flower organ determination are also involved in fruit development.

The C-clade MADS-box transcription factor iAGAMOUS (AG), is involved in stamen, carpel and ovule identity determination [98]. AG is also expressed both in the stamens and in the carpels of peach. The PpeAG sequence present in GenBank (accession AAU29513) was used for the sequence alignment. PpeAG is also expressed at high levels in the mesocarp and the endocarp during fruit development [99]. In tomato, the downregulation of TOMATO AGAMOUS 1 (TAG1) by RNAi not only causes flower defects, such as stamen with petaloid tissue, but also leads to a loss of flower and fruit determinacy, producing flower-in-flower and fruit-in-fruit phenotypes [100,101]. The important role of AG in both flower and fruit development is reported in other species, such as strawberry (Fragaria × ananassa), cocoa (*Theobroma cacao* L.) and grape (*Vitis vinifera* L.), which produce different types of fruit [102–104].

Another gene involved in the post-fertilization differentiation of fruit tissues is FRUITFULL (FUL). This gene encodes a MADS-box transcription factor that negatively regulates the valve-margin identity genes in *A. thaliana* [105], and its expression is first observed in the carpel primordia during early flower development and later only in the valves' regions. Targets of AtFUL are the SHATTERPROOF1 (SHP1) and SHATTERPROOF2 (SHP2) genes. The AtSHP genes also encode the MADS-box transcription factors, which are necessary for the differentiation of the dehiscence zone, at the valve margin close to the replum, and for the lignification of the neighboring cells. AtSHP1 and AtSHP2 are involved at the beginning of the genetic pathway that regulates the formation of the dehiscence zone [106]. These genes are also important in tomato fruit development. Indeed, a reduction in SlFUL1 and SlFUL2, which are the homologs of AtFUL, greatly affects late fruit development, impacting the ethylene-independent ripening process [107–109]. Moreover, knock-down of the tomato SHP orthologue, TOMATO AGAMOUS-LIKE1 (TAGL1), affects both the flower and fruit development, causing a loss of the style trichomes and a thinner fruit pericarp, respectively [110], while its ectopic expression leads to the development of lycopene-rich fleshy sepals, supporting the typical function of the C-type genes [100,111]. Finally, the combination of these mutant phenotypes and the gene expression patterns during fruit development seems to support the model of a negative regulation of TAGL1 by SlFUL1 and SlFUL2, also in tomato, thus, confirming the conservation of their roles and their regulatory interactions. This model is further supported by the results found in peach (*Prunus persica*). Whilst very little is known about the genetic regulation that occurs during the differentiation of the cherry fruit in all its components, many studies have been carried out in peach, which is emerging as a plant model for tree species, thanks to its small genome

size of 300 Mb, which is slightly smaller than that of cherry (350 Mb), and about twice that of *A. thaliana* (135 Mb), and with a moderately short juvenile phase of 2–3 years.

Peach, like cherry, belongs to the same clade of Rosids as Arabidopsis and they share anatomical and physiological similarities regarding their flowers and fruits. In the peach genome, one putative PpeFUL ortholog gene and two copies of the PpeSHP genes have been identified. Once aligned to the closest matching homologous protein sequences, both PpeFUL and PpeSHP showed the MADS domain are conserved, along with the conserved regions in the I and K domains, while the C-terminal domain was observed to be more divergent in both cases [112]. In addition, PpeSHP has been shown to maintain its typical function as a C-type MADS-box transcription, since once overexpressed in tomato, it promotes the formation of carpel-like fleshy and reddish sepals [113]. PpeFUL is expressed mostly in the mesocarp and in the exocarp, while its expression is very low in the endocarp. In contrast, PpeSHP gene expression is high in the endocarp but almost zero in the mesocarp and in the exocarp [114]. Furthermore, peach cultivars with the split-pit phenotype, which is associated with a higher degree of lignification, show higher expression of PpSHP. Interestingly, the split-pit is a structure similar to the dehiscence zone of the dry fruits, where the important role of FUL and SHP in regulating lignin deposition, cell expansion and cell separation processes have been demonstrated [106,112,115,116]. Thus, all these results suggest that this regulatory pathway, where FUL is responsible for the inhibition of SHP, which in turn, is upstream in the lignification pathway and seems to be conserved in dry and fleshy fruits, at least in the core eudicots.

Lastly, SHP1 and SHP2 are found to be associated with a D-class transcription factor, SEEDSTICK (STK). In Arabidopsis, STK is not only involved in the differentiation within the endocarp of the layer that will lignify upon maturation but is also a master regulatory gene of ovule development, since ectopic expression of STK is sufficient to induce the formation of ectopic ovules [117]. On the other hand, one of the most evident phenotypes observed in the stk single mutant is the failure of the seed release from the mature fruit, due to a lack of lignification [118]. In peach, one putative copy of the STK gene was found and comparative analysis showed that it belongs to the D lineage along with the other D-type MADS-box transcription factors genes and that the typical D-lineage sequences at the C-terminus and the extension between the stop codon and the AG motif II are conserved [99]. PpeSTK expression is very high in the endocarp at the beginning of the fruit development, and it decreases progressively during the following weeks, while it remains low both in the exocarp and in the mesocarp [114]. Therefore, it seems that there is a spatial regulation of gene expression during peach fruit development, and it could resemble the expression pattern observed in Arabidopsis. In conclusion, STK seems to be involved in the specification of the endocarp, since another example is reported in the fruit of oil palm where the natural stk mutant is almost stoneless [119].

6. The Accumulation of Bioactive Compounds during Ripening

Sweet cherry fruits are nutrient-dense, high in fibre and accumulate a number of bioactive compounds, including, carotenoids, polyphenols, anthocyanins, vitamin C and potassium, during ripening [120,121]. (For a review, see Ansari and Emami, [122]; Aloum et al. [123]; Moshiri et al. [124], Milani et al. [125], Faienza et al. [126], Chockchaisawasdee et al. [127] and Pashirzad et al. [128]). In cherry fruit, polyphenols are concentrated in the skin and anthocyanins, cyanidin 3-glucoside, cyanidin 3-rutinoside, cyanidin 3-sophoroside, pelargonidin 3-glucoside, pelargonidin 3-rutinoside, 3-glucoside, and peonidin 3-rutinoside, have also been identified [129–131]. Cyanidin 3-O-glucoside has been shown to possess strong antioxidant activity [132] and to have a positive effect on liver ischemia-reperfusion injury (preventing cell death following the restoration of blood flow) [133]. Human trials have suggested that anthocyanins slow glucose production from more complex carbohydrates, promoting healthy glucose regulation and decreasing the likelihood of type-2 diabetes [134].

Given the high concentrations of bioactive compounds (carotenoids, polyphenols anthocyanins, etc.) in cherries, it is not surprising that their consumption has a positive impact on health. These data indicate that the regular consumption of fruits promotes health and reduces the risks of disease and age-related decline in health [135–140].

Published trials on animal and human subjects have suggested that cherry fruit consumption may reduce the risk of several chronic inflammatory diseases (i.e., arthritis, diabetes), and improve sleep and cognitive function. In the last few years, cherries have also generated great interest because of their health benefits, the subject of several reviews [120,121,141–144]. These data suggest that increased cherry consumption may improve the health and quality of life of consumers. Identifying a means of generating a seedless, stoneless cherry has the potential to make the fruit even more attractive to the consumer. Previous data has shown that seedless cultivars of fruit, such as sweet orange (*C. sinensis*), grape (*V. vinifera*), and watermelon (*Citrullus lanatus*) have significantly increased consumer consumption [145].

7. Cherry Tree Cultivation, Environment and Tree Management

7.1. Climate Impacts on Cherry Tree Cultivation and Yield

It is important to note that climate plays an important part in cherry tree cultivation and final crop yield. With global increases in temperature of 2 °C, an increase in atmospheric [CO_2] from 420 ppm to 550 ppm by 2050 (the former already elevated compared to pre-industrial values (278 ppm) and 700 ppm by 2100 [146–150], and an increase in rainfall in some areas and a reduction in rainfall in others, it is important to understand how these environmental conditions will affect cherry tree cultivation. To determine the role of atmospheric changes on cherry tree development, sweet clonal cherry (*Prunus avium* L.) plants were propagated for 19 months under glass at ambient (1994–358 ppm; 1995–360 ppm) or elevated [CO_2] (*e*[CO_2]) (700 ppm—expected by 2100). Initially, in (*e*[CO_2]), photosynthesis increased and a concomitant increase in dry matter (leaf—55% and stem −61%) was observed after two months of growth, suggesting that increasing [CO_2] could be beneficial for cherry tree cultivation. However, after 10 months, photosynthetic rates decreased, and only small increases in dry mass were still evident, which suggests sweet cherry acclimates to *e*[CO_2] due to long-term exposure [151]. Due to the young nature of the plants studied, no information is available to determine the impacts of *e*[CO_2] on fruit yield or quality, however, these results suggest that cherry trees may not benefit significantly from increased atmospheric [CO_2].

In addition, future climates may also encounter increased rainfall, which can result in rain-induced cracking, a major cause of crop loss in sweet cherry production in many regions of the world [152]. Cracking is thought to be induced by water uptake on the surface of the fruit, and via the root system (heavy rain during the harvest period), resulting in swelling of the epidermis, localised bursting of the cells releasing malic acid, and a weakening of the epidermal and hypodermal cells until finally, cracking occurs (for a review, see Carreia et al. [152]). This may become more of a problem in regions where increased rainfall is observed due to climate change. Currently, pre-harvest foliar treatment with calcium, in combination with gibberellic acid, is used to mitigate cracking due to an increased water uptake [153,154].

In other regions, a reduction in rainfall is expected. Water availability influences growth [155,156], yield and fruit quality characteristics of sweet cherry [157]. Water is an important requirement in cherry fruit production and irrigation is essential in areas where rainfall is limited (areas likely to increase in future years). A reduction in rainfall in some areas will increase the reliance on irrigation and the use of groundwater for crop production, which may also be limiting. Cherry production may not be seen as a priority in areas of low rainfall, where water is required to irrigate crops of greater importance as the population increases, and the need for higher calorific crops, such as wheat and maize, are prioritized. Changes in rainfall may also change soil moisture and soil temperature. Under

these circumstances, a change in rootstock might be required to successfully propagate cherries (see Section 7.4).

Recent changes in climate have also resulted in a requirement to protect crops against extreme environments, heavy rain and hail, and have resulted in the introduction of new protected growing environments, such as polytunnels (see Section 7.5) [158].

7.2. The Use of Hormone and Biostimulant in Cherry Cultivation

Many temperate woody plants, including cherry, possess a dormancy cycle to prevent premature bud bursts during short periods of warmer weather, which are then subsequently followed by colder weather, thus causing shoot damage (see below) [159]. Following a period of exposure to low temperatures, dormancy is broken, and bud growth is initiated, following a return to favorable growing conditions [160–163]. Some varieties, such as Bing (Table 1), require up to 700 h at temperatures below 7 °C to break dormancy. In the absence of sufficient chill hours, seen more often due to rising global temperatures, with an expected mean global temperature increase of 2 °C by 2050 [164], cherry yields can be considerably reduced [163]. There are currently several agents on the market that synchronize fruit ripening following application in the absence of required chill hours. One of these reagents, hydrogen cyanamide, has been associated with an increase in flower numbers per shoot [165–168]. ERGER® is a biostimulant used to promote uniform bud break and has been shown to break dormancy in axillary and terminal buds in a number of woody species, including apples [169].

At a later stage of development, cherry trees are often treated with plant hormones such as gibberellic acid to stimulate fruit growth and increase fruit firmness [170,171]. A recent publication by Basile et al. [172] evaluated the use of biostimulants (tropical-plant extract) on two sweet cherry varieties, Kordia and Regina (Table 1). In both cultivars, foliar application of this extract induced significant increases in fruit yield. In Kordia, treatment was also shown to improve fruit quality (enhanced fruit calcium concentration by 26.2%, soluble solids content by 11.8%, increased flesh firmness, and skin color by 6.7%, and 12.0%, respectively) [172]. These authors have suggested that biostimulants could be a sustainable and effective alternative to the exogenous application of synthetic hormones and nutrients currently used in cherry cultivation.

7.3. Thinning and the Environment

Many trees produce a large quantity of flowers, and as observed in apples and pears, the trees thin themselves, so as to not overburden the plant and reduce the chance that branches will break under the weight. This process, referred to as 'June Drop', begins in late June until mid-July, with the expectation that just one in twenty flowers produce fruit. However, cherry trees often do not drop flowers, and thus require additional resources and mechanical and hormonal thinning to protect the yield and quality. In the past, the requirement for thinning during cherry production was rare; however, due to the introduction of dwarfing rootstock (see Section 7.4), thinning has become necessary to avoid excessive flowering [173]. Thinning can be carried out via large-scale pruning, mechanical hand removal of flowers or chemical thinning. These different methods have recently been reviewed by Rutkowski and Lysiak [173]. Thinning, however, comes with inherent risks. Firstly, thinning increases the size of the remaining fruit, which also increases cracking susceptibility [174], and importantly, this can reduce the harvest if a late frost occurs after thinning. For example, the process, 'June drop' can be triggered by unfavorable environmental conditions. A late-spring frost may damage bud tissue, and lead to cherry trees losing a fraction of their fruit before ripening [175], which, if this occurs after thinning, can result in a significant loss of yield. This loss can vary from year to year. In 2020, in the UK, late frosts resulted in a 90% loss of fruit before harvest.

7.4. Cherry Rootstock

Traditional cherry trees can be challenging when grown on their own rootstock due to their large size. Cherry trees also take up a large amount of space and fruit is often high up in the branches, making harvest challenging. The introduction of dwarfing rootstocks, that produce more manageable trees, makes the cultivation and harvest of cherry fruit easier due to the short stature of the plants (Table 2). However, cherry trees grown on dwarf rootstocks produce excessive numbers of small fruits with a low sugar content [176]. To overcome this, flower thinning (see Section 7.3) is undertaken to prevent over-yielding and to increase the quality of the fruit [176]. For a review, see Ruthowski and Lysiak [173] and Kurlus et al. [177]. Different rootstocks also provide advantages in different regions, (i.e., adapted for soil moisture content, soil types and soil temperatures), allowing the selection of rootstocks for the growing conditions.

Table 2. Some of the most commonly used Cherry rootstocks for commercially cultivated sweet cherry.

Rootstock	Reported Qualities of Dwafing Rootstocks
Mazzard F12.1	Original traditional *Prunus avium* cherry seedling rootstock used for centuries. Very compatible with most current cherry varieties. Produces a tree more than 20 ft in height. It is cold hardy, but not as hardy as Gisela rootstocks. Natural resistance to bacterial canker.
Mahaleb	A traditional seedling cherry rootstock. It produces a large slow-growing tree about 16 ft–20 ft tall. Suitable for a wide range of soils and suitable for drought conditions, but unsuitable for wet soils. Not compatible with all cherry varieties. Perfect for traditional orchards, although fruit may be difficult to harvest due to the height of the tree.
Gisela 5 (G5)	Originated from Justus Liebig University in Giessen, Germany in the 1960s. It produces a tree about 3 m/10 ft tall after 5 years. Has established itself as the rootstock of choice, producing a tree with manageable proportions. Trees cannot support themselves, requiring a permanent means of support (equivalent to the apple M26 rootstock). G6 can cause trees to flower early (by a few days), and have branches lower to the ground, increasing the likelihood of exposure to late frosts.
Gisela 6 (G6)	Produces a slightly larger tree than Gisela 5. An advantage over Gisela 5 is that it is much less fussy about soil conditions. Usually free-standing and does not need support (roughly equivalent to the apple MM106 rootstock). Suitable for a wide range of soil types, but good drainage is essential.
Gisela 12 (G12)	Produces a tree slightly more vigorous than Gisela 6. Gisela 12 is highly productive, self-supporting, and tolerant of most soils. Adapted to a range of soils.
Weigi 1	This sister rootstock is of Weigi 2. Semi-dwarf class, about 10% more vigorous than Gisela 5 (and Weigi 2). The rootstock of choice for poor soils and less vigorous varieties. Better productivity and larger fruit size than Gisela 5. Able to cope with high summer temperatures and a level of drought tolerance.
Weigi ® 2	New semi-dwarf rootstock. This cherry tree is very similar in size to the Gisela 5. An advantage for UK growers is yield and fruit size are slightly improved compared to Gisela 5. More tolerant of drought and the higher summer temperatures found in southern Europe.
Krymsk 5	Widely used in commercial cherry orchards in the Pacific North West of the USA. Similar or slightly more vigorous than Gisela 6. Trees require no support. Not as productive as the Gisela, but fruit quality is good and trees are easier to manage. Developed specifically for cold-hardiness, but performs well in hot climates and heavy soils.
Krymsk 6	Developed from *Prunus cerasus* (the sour cherry). It is a semi-dwarf rootstock, suitable for hot and cold climates.
Colt	Developed at East Malling Research Station in Kent in 1977. Cross between the sweet cherry *Prunus avium* and the less vigorous *Prunus pseudocerasus*. First dwarfing rootstock for sweet cherries. Considered the best rootstock for growing trees in large gardens and community orchards. The tree has a height of 12–15 ft and tolerates poorer soils better than Gisela 5 and needs less looking after (comparable to the apple MM111 rootstock and the PyroDwarf pear rootstock). Colt is resistant to phytophthora root rot, bacterial canker and stem-pitting, but is more susceptive to crown gall.

https://www.orangepippintrees.co.uk/articles/fruit-tree-gardening/rootstocks-for-cherry-trees 1 June 2022. https://www.goodfruit.com/a-lot-of-choices-for-cherry-rootstocks/, 1 June 2022.

In addition to these rootstocks (Table 2), new rootstocks are currently being commercialised, including Gisela 13 and 17, which have been described as vigorous, precocious, and productive; Weigel 3, described as semi-vigorous and adaptive to hot, dry conditions; and Krymsk 7, described as being the most vigorous of the Krymsk rootstocks to date. These new rootstocks currently require widespread evaluation. The requirement for newer rootstocks adapted to hotter, dryer conditions, such as Weigel 3, may be essential for protecting cherry cultivation from environmental change.

7.5. Protected Growth Environments

The introduction of dwarfing rootstocks and the use of biostimulants to initiate bud break, has also allowed for changes in methods of cultivation. In recent years, some cherry tree cultivators have started growing trees under cover in polytunnels, which provide protection from periodic weather extremes that can negatively impact yields, including late frosts [158]. Growth in polytunnels also protects the trees from excess rainfall (and rain-induced cracking), hail and from birds. Under extreme late season conditions, cultivators now use gas-powered heaters to prevent damaging frosts by propelling warm air 70 m along the polytunnel. Growth in a polytunnel also allows for unrestricted mechanical or hormonal "thinning" and fruit can be harvested irrespective of the weather. One drawback to this method of cultivation is the reduction or absence of wild pollinators, including solitary bees [25] inside the tunnel, thereby increasing reliance on domesticated honeybees (see Section 2.1.1).

8. Conclusions

Cherry is a nutritious and health-promoting fruit and worldwide production has increased by almost 40% in the last 20 years. These increases have been driven in part by a warming climate in parts of Europe, making the cultivation more advantageous, and by the introduction of dwarfing rootstocks and new methods of cultivation. However, cherry fruit contains a large stone and seed, the presence of which makes it a potential choking hazard for small children and inconvenient to eat 'on the move'. Removal of the stone, through breeding or genetic manipulation, could be transformative for the cherry industry and facilitate rapid market expansion. The absence of the seeds/stone would also reduce processing costs, increase profits, and for the consumer, increases the potential of the fruit as a snacking product, therefore increasing consumer acceptance and consumption. An interesting model for stoneless fruit has been identified in *P. domestica* (Plum). This cultivar, known as 'stoneless', has been known in France for several hundred years and has been crossed with commercial varieties to transmit the stoneless trait. However, these results were not commercially viable [178], although segregation analysis suggested that the stoneless trait is linked to a single dominant gene [178]. Furthermore, RNA expression comparisons have shown that more than 2000 genes are differentially expressed when comparing 'stoneless' to normal stoned fruit, providing the first step to understanding the mechanism for the production of parthenocarpic fruit. Finally, parthenocarpic fruit has been identified in multiple species. Can this information provide a route to the development of a seedless cherry? Parthenocarpy has been reported in 96 Angiosperm taxa [179,180], and interestingly, almost half of all parthenocarpic species are trees. In particular, *Prunus persica* (L.) Batsch and *Prunus cerasifera* are the two woody plants with a drupe-type fruit in which parthenocarpy had been reported [179–181].

Over the last few decades, agricultural research has adopted technologies, such as genetic engineering and, more recently, 'genome editing' to improve traits in key crops [182–186]. There have been recent advances in the tools available to carry out this work, including vectors for multiple gene insertions [187–191] and tissue-specific promoters [192–197]. The generation of parthenocarpic fruit via genetic manipulation brings its own challenges. CRISPR-Cas9 genome editing has previously been used to generate parthenocarpic tomato plants, demonstrating the potential for this technology to manipulate seed development. However, fruit trees are the most reluctant species for

in vitro tissue culture. In cherry, regeneration and transformation protocols have been created, using leaves, shoots and cotyledons as explants [198–203], suggesting that genome editing is a viable option for the generation of a stoneless, seedless fruit in cherry.

Author Contributions: All authors contributed to the writing of this manuscript. All authors have read and agreed to the published version of the manuscript.

Funding: E.V. was supported by the 'Understanding Fruit Development in the Cultivated Cherry' project funded by Berry Gardens Growers Ltd. (Maidstone, UK), awarded to A.J.S.; E.V. and A.J.S. drafted and wrote the manuscript with input from M.C., J.M.D. and M.Z., who also edited the final version. A.J.S. is supported by the Growing Kent and Medway Program, UK; grant number 107139.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: Not applicable.

Acknowledgments: We would like to thank Nicholas H Doddrell for help with biorender and the creation of Figure 6 (BioRender.com 21 April 2022).

Conflicts of Interest: The authors declare no conflict of interest.

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Planta (2022) 256:90
https://doi.org/10.1007/s00425-022-04005-y

REVIEW

Options for the generation of seedless cherry, the ultimate snacking product

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Received: 21 June 2022 / Accepted: 21 September 2022 / Published online: 28 September 2022
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Abstract

Main conclusion **This manuscript identifies cherry orthologues of genes implicated in the development of pericarpic fruit and pinpoints potential options and restrictions in the use of these targets for commercial exploitation of parthenocarpic cherry fruit.**

Abstract Cherry fruit contain a large stone and seed, making processing of the fruit laborious and consumption by the consumer challenging, inconvenient to eat 'on the move' and potentially dangerous for children. Availability of fruit lacking the stone and seed would be potentially transformative for the cherry industry, since such fruit would be easier to process and would increase consumer demand because of the potential reduction in costs. This review will explore the background of seedless fruit, in the context of the ambition to produce the first seedless cherry, carry out an in-depth analysis of the current literature around parthenocarpy in fruit, and discuss the available technology and potential for producing seedless cherry fruit as an 'ultimate snacking product' for the twenty-first century.

Keywords Parthenocarpy · Fruit · Cherry · Seed · June drop

Introduction

Cherry (*Prunus avium*) trees are believed to be native to Europe, south Asia and to an isolated region of the western Himalaya (Faust and Surányi 1997). Commonly known as sweet cherry, it is a deciduous tree belonging to the Rosaceae family (https://sweetbiomics.com/) (Ganopoulou et al. 2022), which also includes apple (*Malus x domestica*), peach (*Prunus persica*), and strawberry (*Fragaria vesca* and *F. ananassa*). Young cherry trees show strong apical dominance with a straight trunk which grows to between 15 and 32 m in height. The species has become naturalized in North America and Australia, since it is largely cultivated in these regions due to its commercial importance.

The sweet cherry fruit is a drupe, 1–2 cm in diameter with an attractive appearance, due to its colour (bright red to dark purple) and pleasant intense flavour. The fruit are also nutrient dense, high in fibre and contain a large range of bioactive compounds including polyphenols, anthocyanins, carotenoids, and vitamins (Kelley et al. 2018; McCune et al. 2011; Vignati et al. 2022). Cherries also contain high levels of minerals including magnesium (10 mg/100 g), potassium (200 mg/100 g), phosphorous (20 mg/100 g), and calcium (14 mg/100 g) (Ferretti et al. 2010). Cherries are also a good source of tryptophan and serotonin (Cubero et al. 2010; Garrido et al. 2012). These data suggest that increasing cherry consumption could be beneficial to human health and quality of life of consumers (Alba et al. 2019; Bell et al. 2014; Coelho Rabello Lima et al. 2015; Ferretti et al. 2010; Kelley et al. 2018; McCune et al. 2011;). Some of the most critical attributes desired by consumers include colour, firmness, sweetness,

Communicated by Gerhard Leubner.

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and flavour intensity (Cliff et al. 1996; Guyer et al. 1993; Kappel et al. 1996; Zheng et al. 2016); however, consumers from different regions set different requirements for what is considered a good cherry. For example, in Norwegian, American, and UK markets, consumers prefer larger dark cherries (Crisosto et al. 2003; Lyngstad and Sekse 1995; Sekse and Lyngstad 1996; Wermund and Fearne 2000). Growers and supermarkets often have a different set of criteria for evaluating cherry quality. Specifically, growers want cherries that are firm enough to resist damage during picking, processing, and transporting and easy to harvest (long peduncles), while supermarkets insist on a long shelf life.

Worldwide, cherry production has increased by almost 40% over the last 20 years as the fruit becomes more popular with consumers (Fig. 1). However, cherry fruit contains a large stone and seed, the presence of which makes it a potential choking hazard for small children and inconvenient to eat 'on the move'. Identifying a means of generating a seedless, stoneless cherry has the potential of making the fruit even more attractive to the consumer. Previous data have shown that seedless cultivars of fruit such as sweet orange (*Citrus sinensis*), grape (*Vitis vinifera*), and watermelon (*Citrullus lanatus*) have significantly increased consumer consumption (Pollack 2001). In the case of cherry, the absence of the seeds/stone would likewise increase its potential as a snacking product and would also reduce processing costs, thus improving profit margins. An interesting model for stoneless fruit has been identified in *P. domestica* (Plum).

Stoneless plum, a retrospective

The role of fruit is to protect the embryo and seed during development and facilitate their dispersal within the environment. Normally, after fertilization of the ovules, fruits develop from the ovary, a process that is coordinated by signals from the developing embryo (Gillaspy et al. 1993). This process of seed, stone, and fruit development is controlled and synchronized by phytohormones (Gillaspy et al. 1993). Previous work, however, has demonstrated that fruit set can be uncoupled from fertilization, resulting in the formation of seedless crops (Gorguet et al. 2005; Hu et al. 2018; Varoquaux et al. 2000). A fruit is considered seedless if it is devoid of seeds, has a significant reduction in seed number, or contains a small number of aborted seeds (Varoquaux et al. 2000). Seedless fruits can be obtained by two different routes, first, parthenocarpy, where the fruit develops without fertilization (Joldersma and Liu 2018; Picarella and Mazzucato 2019) and second, stenospermocarpy, where the seeds abort following fertilization, resulting in traces of aborted seed within the fruit (Varoquaux et al. 2000). Seedlessness has been reported in many species, including grape, citrus, tomato, pear, and banana (Ding et al. 2013; Kim et al. 1992; Klap et al. 2017; Royo et al. 2018; Simmonds 1953; Talon et al. 1990; Wang et al. 2021).

An interesting model for stoneless fruit is seen in a naturally occurring plum (*P. domestica*) cultivar called "Stoneless" (or "Pitless"), a name given on the basis that it has an underdeveloped stone that makes the fruit partially stoneless. The "Stoneless" ancestor is the variety "Sans-Noyau", which

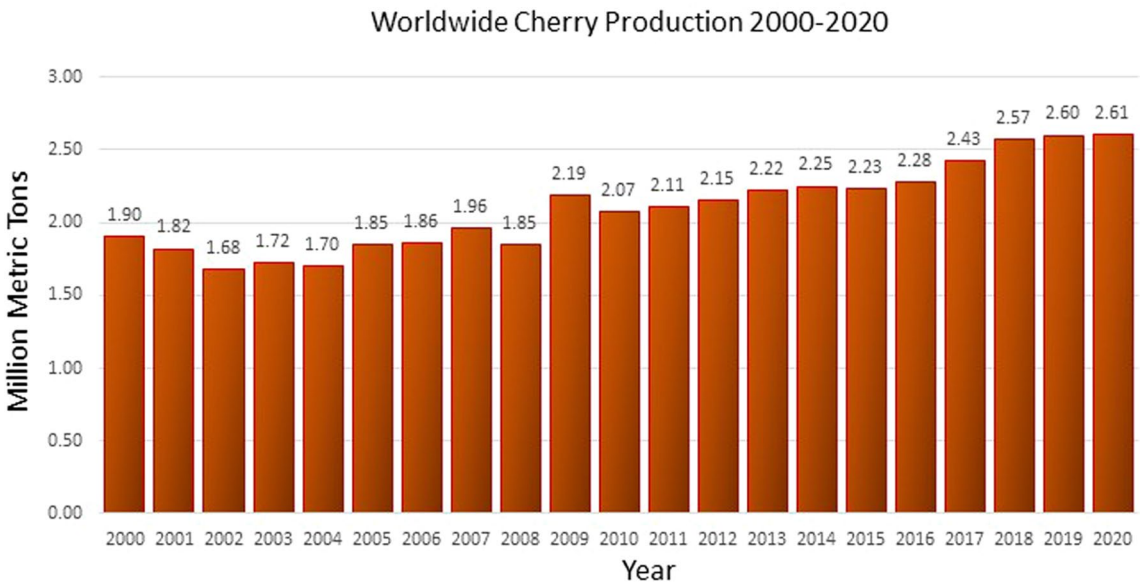

Fig. 1 Graphical representation of worldwide cherry production between 2000 and 2020 (Statista.org). Cherry production has increased by 37% between 2000 and 2020 with the lowest production in 2002

is also stoneless (its name in French means "without pit"). "Sans-Noyau" has been known in France for several hundred years and in the 1890s was transported to the U.S., where it was crossed with varieties of commercial interest to transmit the stoneless trait. However, the results were not commercially successful (Callahan et al. 2015). Compared to a stoned plum, the expression pattern of lignin biosynthetic genes is similar (Galimba et al. 2020). However, the number of cells in the endocarp has been shown to be reduced compared to the stoned control used in the study (Callahan et al. 2009, 2015). An RNA expression comparison between "Stoneless" and normal stoned cultivars showed that more than 2000 genes are differentially expressed during fruit development, although the authors did not report the identity of these genes and confirmed the necessity of further analysis to find the gene mutation responsible of the stoneless phenotype (Galimba et al. 2020). Segregation analysis suggested that the "Stoneless" trait is dominant and linked to a single gene (Callahan et al. 2015).

Physiological changes during cherry seed development

In the cherry ovary, there are two ovules that arise from the opposite placentae of the single carpel, while in some cultivars, one of the two fertilized arrests its growth before full bloom and collapses; in other cultivars, both ovules develop, but one of the two embryos aborts.

During fertilization, one of the two sperm cells fuses with the egg cell to form the diploid zygote, 2n, and the other one fuses with the central cell, which is 2n, to form the triploid tissue called the endosperm, the function of which is to accumulate nutrients that will be used by the embryo during the seed development. At the time of fertilization, there is a rapid elongation of the megasporocyte, which is enclosed by the megaspore membrane, while after fertilization occurs, both the embryo and the endosperm develop very slowly for a considerable time. In the first stages of the endosperm development after mitosis, there is no cell wall formation, leading to the formation of a non-cellularized syncytium. Cellularization starts at the micropylar pole of the megagametophyte and proceeds progressively to the chalazal end and from the periphery inwards to the centre. The delayed development period of the endosperm is followed by a period of very rapid enlargement (Tukey 1933).

The first zygotic division is transverse and asymmetric, leading to the formation of two cells, a smaller one above a larger cell, the suspensor cell, which forms the suspensor, the function of which is to connect the embryo to the mother plant, allowing the exchanges of nutrients and signal molecules. The suspensor is small, and it persists through to maturity of the embryo. The development of the embryo is even slower than that of the endosperm at the beginning, and then, this phase is followed by a sudden rapid development. At maturity, the embryo is made by two well-formed developed cotyledons, surrounded by a thin layer of endosperm and a fine line of nucellar tissue, and everything is enclosed by the seed coat, a completely maternal tissue, since it is derived from the ovule integuments. As noted above, two embryos can be formed in some cultivars, but one of the two suddenly arrests in development with the nucellar tissue that collapses and the integuments that shrivel. The aborted embryo can either disintegrate 5 days after arrest or can remain intact for up to 42 days.

There is a wide variation in the stage of the fruit and embryo development at which abortion can occur. Seed abortion is usually associated with fruit drop (see section June drop), but it could also be a feature of mature fruits in certain varieties. For example, early ripening varieties produce only about 15% of viable seeds, while the seeds of the late-ripening varieties are nearly 100% viable (Fig. 2).

During the pre-bloom phase, both the early ripening and the late-ripening varieties develop similarly in all parts, with the only difference being that the early ripening varieties develop slightly in advance and at a slightly greater rate than the late-ripening cherries (Stage I). In early ripening varieties, stage II lasts about half the time compared to late-ripening varieties (about 7 days versus about 14 days when comparing the Early Purple Guigne and the Downer cultivars). The rapid embryo and endosperm development starts at about the same time in both types, and while in the early ripening varieties, this also coincides with the beginning of stage III; in the late-ripening ones, this precedes stage III by 6 days (Tukey 1933).

At the beginning of stage III, there is a big difference in embryo and cellular endosperm lengths between the early and the late-ripening varieties (0.52 mm vs 3.0 mm and 2.4 mm vs 4.8 mm, respectively). In early-ripening varieties, embryo and endosperm development is halted at varying stages, so a viable seed is produced only rarely, while in the late-ripening varieties, they are regular and uniform, allowing the formation of a viable seed. Indeed, the seeds formed by early-ripening varieties are shrivelled, because both the nucellus and the integuments collapse, while the seed of the late-ripening varieties are plump and well filled. Seed abortion occurs at an earlier date in the early ripening varieties, producing smaller aborted embryos, compared with those ripening a few days later. Moreover, seed abortion seems to be not necessarily associated with poor pollination, sterility, incompatibilities, or even nutrition (Tukey 1933, 1934).

The role of hormones in seed development

Gibberellin is sufficient to initiate fruit set

Hormones play an essential role during all the developmental processes and it has long been known that the

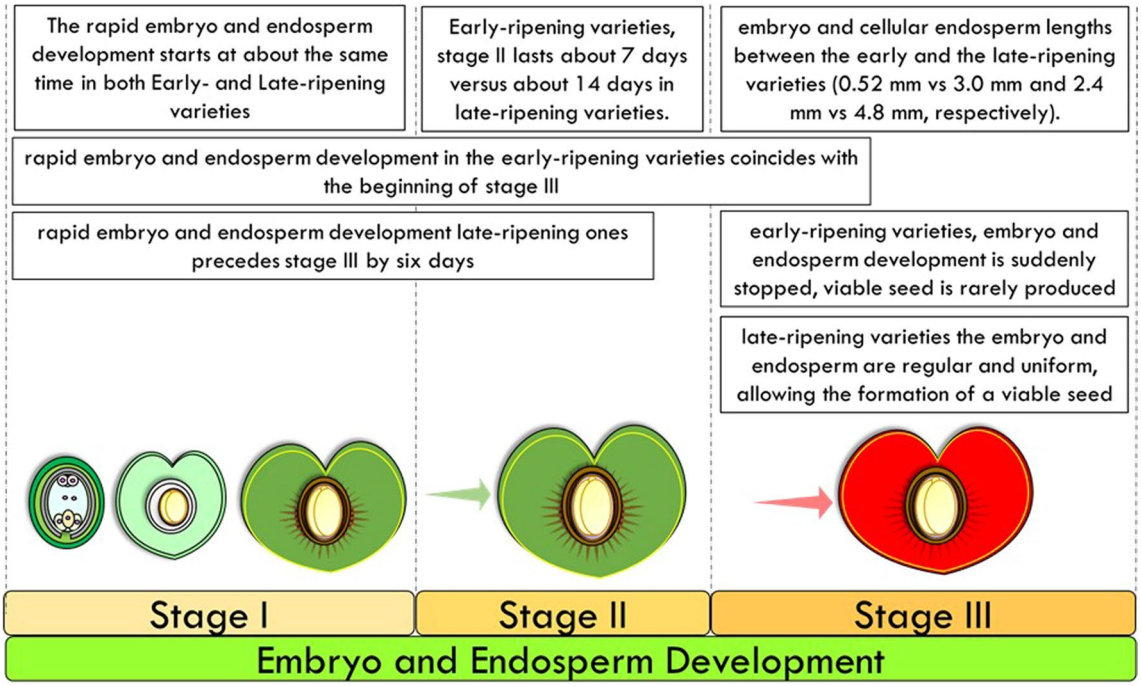

Fig. 2 Graphical representation of embryo and endosperm development in the cultivated cherry during the three stages of fruit development

application of phytohormones to emasculated flowers induces the formation of parthenocarpic fruit (Sjut and Bangerth 1982). Crane et al. (1960) showed that gibberellin (GA) treatment of different plants belonging to the *Prunus* genus is sufficient to start fruit set in some of them. Indeed, while *P. domestica* (plum) and *P. avium* (sweet cherry) did not produce any parthenocarpic fruit, *P. dulcis* (almond), *P. armeniaca* (apricot), and *P. persica* (peach) developed parthenocarpic fruits with a success rate of 11.8%, 15.4% (500 ppm GA treatment), and 73.4%, respectively (50 ppm GA treatment applied twice). Although the highest fruit set was recorded in peach with the lowest concentration of GA, the highest concentration (500 ppm) led to a higher level of stone development and degree of sclerification, which is absent in the fruits treated with 50 ppm solution. The parthenocarpic peaches reached maturation about 10 days before the seeded fruit (Crane et al. 1960). It is likely that the failure to induce parthenocarpy in cherry was due to an incorrect concentration or type of GA, because Wen et al. (2019) showed that treating emasculated *P. pseudocerasus* (Chinese cherry) pistils with 300 mg/L GA_3 solution was enough to initiate the development of parthenocarpic fruit. At 7 days after treatment (DAT), there is an upregulation of *the Gibberellin 2-beta-dioxygenase gene (PaGA2ox),* which encodes a GA biosynthetic enzyme. Moreover, a list of differentially expressed genes has been reported, and this could be used to identify those involved in the fruit set process in cherry (Wen et al. 2019). Furthermore, Galimba et al. showed that the application of GA_3 to Honeycrisp apple flowers triggers the development of parthenocarpic apple fruit (Galimba et al. 2019).

As regards mode of action, gibberellins seem to be involved in the activation of the cell cycle in the ovary-wall cells. In fact, Mesejo et al. (2016) compared the GA levels and the gene expression in two different species of Citrus, Satsuma (*Citrus unshiu)* and the hybid clementine (*Citrus x clementina)*, which are obligate and facultative parthenocarpic, respectively. In Satsuma, the expression levels of *CYCA1.1*, which encodes for a cyclin expressed during the G2 phase and controls the G2/M phases of the cell cycle (Fabian et al. 2000), are higher than in clementine. Interestingly, in Satsuma, there is a peak of *GA20 oxidase 2 (GA20ox2)* expression just before the peak of *CYCA1.1* expression, while in clementine, this is delayed. Another GA biosynthesis-related gene, *GA3 oxidase 2*, has a higher expression level in Satsuma than clementine, during fruit development. Treatments with GA_3 caused an increase of GA_{20} and GA_1, which is the most important GA precursor in Satsuma ovaries. More importantly, a 132% increase of *CYCA1.1* expression has been observed 6 h after treatment, and this effect was lost after 2 days. The treatment with paclobutrazol (PBZ), an inhibitor of GA biosynthesis, caused a decrease of *CYCA1.1* expression after 6 h and this effect was maintained up to 2 days after, proving once again that GAs influence the transcription rate of *CYCA1.1*. GA_3 enhances cell division, increasing the number of cell layers in the pericarp (effect lost

at 15 DAT), while the opposite and expected effect has been observed after PBZ treatment. These effects on cell division and parthenocarpic fruit set upon GA_3 application have also been observed in clementine (Mesejo et al. 2016).

GAs have also been shown to promote the transcriptional activation of many other genes that are involved in fruit development. For example, transcriptome analysis of the "Dangshansuli" pear treated with GA_{4+7}, which induces parthenocarpic fruits, showed that 31 cyclin and 2 CDK genes were up-regulated at 3 DAT, while in the pollinated control, this occurred at 9 DAT. Also, genes encoding expansins, enzymes involved in the modification of the cell wall, have been shown be up-regulated in both the GA_{4+7}-treated and pollinated ovaries. Briefly, 103 cell wall-related DEGs have been identified between unpollinated and GA_{4+7}-treated ovaries and 72 DEGs between unpollinated and pollinated ones at 3 DAT. Moreover, the number of differentially expressed transcription factor genes with similar expression patterns between GA_{4+7} and pollinated ovaries increases with time (32 at 3DAT, 139 at 9 DAT and 329 at 14 DAT). These transcription factors belong mostly to the bHLH, MYB, NAC, and WRKY families. The treatment with GA also influences the other hormonal pathways, since the treated ovaries showed a small but significant increase of IAA at 3 and 14 DAT, and a significant drop of ABA. Indeed, *PbARF5, PbARF6, PbARF18, PbARF19-like*, and *Pb9-cis-epoxycarotenoid dioxygenase* (NCED), which encode key enzymes in the steps for the synthesis of ABA (Schwartz et al. 1997, 2003; Simkin 2021), have been found to be down-regulated both in the GA_{4+7}-treated and pollinated ovaries. Therefore, the model proposed by Liu and collaborators suggests that GA_{4+7} mimics the effect that pollination has in changing the hormones levels, causing a downstream change of expression of gene involved in different aspects of the transition from ovary to fruit (Liu et al. 2018) (Fig. 3).

Auxins can act as an alternative signal replacing pollination and fertilization

Auxins not only plays a central role in embryogenesis, but also during the development of the other two seed structures, the endosperm and the seed coat. This class of compounds seems to be the driving force behind the development of all the seed components, and to be involved in their growth synchronization. The main type of auxin in higher plants is indole-3-acetic acid (IAA) the biosynthesis of which starts from tryptophan through a process that comprises two steps and is well conserved among higher plants (Mano and Nemoto 2012; Zhao 2014).

It has been proposed that auxin(s) can act as an alternative signal replacing pollination and fertilization to initiate the fruit growth (Serrani et al. 2008). Indeed, exogenous application of auxin to unfertilized ovules or ectopic production in the central cell is enough to activate mitosis in this cell and starts endosperm development (Figueiredo et al. 2015). Interestingly, the "Dangshansuli" pear emasculated pistils treated with the synthetic auxin 2,4-D have been shown to produce parthenocarpic fruits, which are significantly smaller than the seeded fruits. Furthermore, ovaries treated simultaneously with 2,4-D and Paclobutrazol (PBZ) show a significant reduction of cortex thickness, cells' division, and cell expansion. PBZ is a triazole plant growth regulator that inhibits cell elongation and internode extension by inhibiting gibberellin biosynthesis (Davis et al. 1991). Moreover, in the ovaries treated with 2,4-D, two pear cyclin-dependent genes, *Pbcyclin-dependent kinase B2-2* and, *Pbcyclin-dependent kinase B2-2-like,* and one expansin gene, *Pbexpansine-A10*,

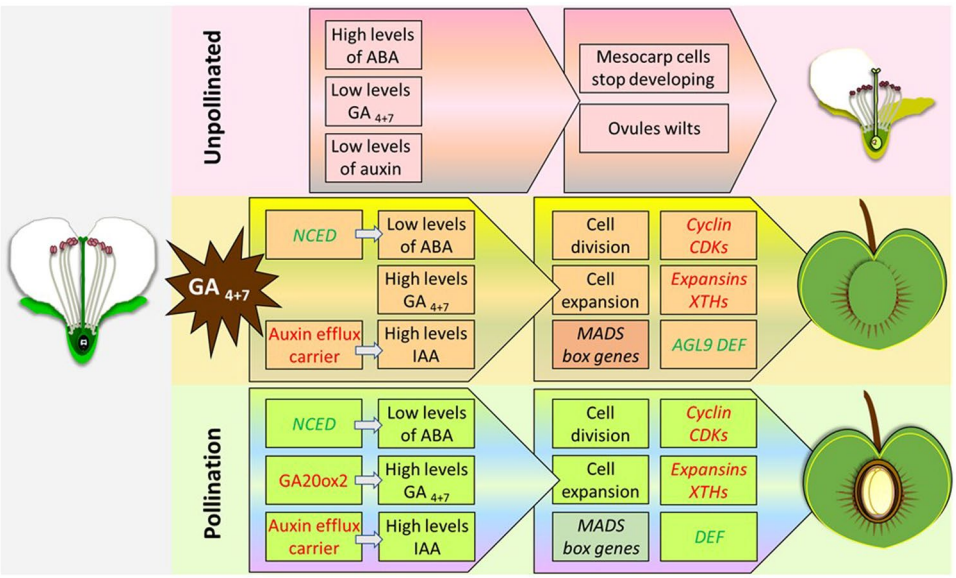

Fig. 3 Proposed model of the crosstalk between auxin and GA signalling pathways during fruit development. In this model, three different scenarios are represented: unpollinated, GA_{4+7}-treated, and following pollination. Red font represents genes up-regulated and green font genes down-regulated

were up-regulated. On the contrary, they demonstrated down-regulation when co-application with PZB occurred.

Auxin acts upstream of gibberellin

Auxin seems to act upstream of GA in the induction of fruit set, since auxin can trigger GA biosynthesis but not vice versa (Dorcey et al. 2009). 2,4-D mostly induces the production of bioactive GA_4 (fourfold increase) but not GA_3, in the treated ovaries and a decrease when PBZ was also applied. The final evidence consists of the upregulation of *PbGA20ox2-like* and *PbGA3ox-1*, involved in the production of GA_4, and the down-regulation of *PbGA2ox1-like* and *PbGA2ox2-like*, which converts the GA_4 precursors into an inactive form (Cong et al. 2019). Furthermore, in tomato, auxin-induced parthenocarpic fruit development is mediated partially by GA, since co-application of auxin and PBZ causes a significant reduction in parthenocarpy (Serrani et al. 2008). Moreover, bioactive GAs levels are high in the auxin-induced and entire parthenocarpic fruits because of the increased expression of GA biosynthetic genes and the repression of GA catabolism genes (Mignolli et al. 2014; Serrani et al. 2008). However, while IAA application promotes the formation of a parthenocarpic fruit by increasing the pericarp cell layers and enlarging the placenta, GA-treated fruits have fewer cell layers, but cells are larger. Parthenocarpic fruits induced by simultaneous application of IAA and GA display a final size and cellular structure that are similar to the seeded fruit. Through different types of experiments, such as Yeast two Hybrid (Y2H), Y3H, and co-immunoprecipitation, it has been shown that SlARF7, which is an activator of ARF, interacts both with SlIAA and SlDELLA, through different regions (Hu et al. 2018) (Fig. 4).

In addition, ARF7 can form homodimers and heterodimers, but while the homodimerization is not affected by the interactions with SlDELLA or SlIAA9, the heterodimerization is slightly affected. A luciferase assay demonstrated that while *GA20ox1, GA3ox1*, and *GH3.2*, which encode an auxin-amino acid conjugating enzyme that converts auxin to an inactive form, are repressed by SlARF7–SLIAA9 complex, they are induced by the SlDELLA-SlARF7 complex. Interestingly, SlDELLA seems to antagonize the SlARF7–SLIAA9 repressive effect on the target genes, such as *Expansin5 (EXP5)* and *ACC oxidase4 (ACO4),* which is an ethylene biosynthetic gene. As mentioned above, simultaneous application of auxin and GAs produces the formation of a fruit with a structure similar to the seeded fruit, and this has been observed also in the *e pro* and *SlARF7i pro* double mutants, where both the pathways are affected. This can be explained by the fact that in tomato, the crosstalk between GAs and IAA, during the fruit set, occurs through DELLA, ARFs, and IAA9 (Hu et al. 2018). These data and those highlighted by Sharif et al. (Sharif et al. 2022) demonstrate that synergistic and antagonistic crosstalk between hormones is essential for determining the fate of fruit set.

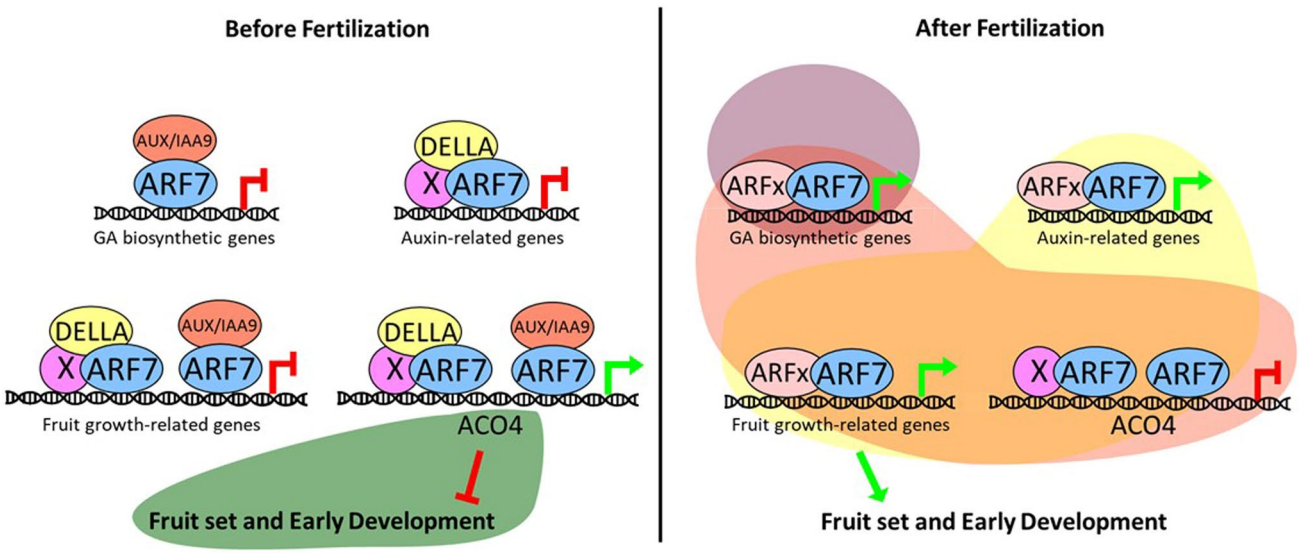

Fig. 4 Proposed model of the crosstalk between auxin and GA signalling pathways during tomato fruit development. Before fertilization, SlARF7 (Auxin Response Factor 7) interacts with SlDELLA and SlAUX/IAA9, repressing the transcription of GA biosynthetic genes and the auxin-related genes. They also activate the transcription of ACO4, enhancing ethylene (green area) levels in the ovary which stays frozen. After fertilization, auxin signal (purple circle) comes from the fertilized ovule, promoting the degradation of SlAUX/IAA9. Gibberellins (yellow area) are synthetised and promote the degradation of SlDELLA and a further accumulation of auxin (pink area). SlARF7 can interact with other SlARF proteins and promote fruit set

Genetic control of seed development

Seed development is a very elaborate process where three different components develop, each fundamental for reproductive success. Although seed development still has many unknown elements that have to be understood, some important discoveries have been made, especially in *Arabidopsis thaliana*, and one aspect that is clear is that not only is there synchronization of growth of the embryo, endosperm, and seed coat, but also it seems that there is a crosstalk between them, a transfer of signals and information that regulates and coordinates this elaborate process. The *TRYPTOPHAN AMINOTRANSFERASE OF ARABIDOPSIS (TAA/TAR)* gene family encodes enzymes that conduct auxin biosynthesis during the first step, while the *YUCCA (YUC)* family works during the second step. There are also alternative biosynthetic pathways, but the *TAA/TAR-YUCCA* one is the major pathway (Mashiguchi et al. 2011). Mutations in either of the two steps of auxin biosynthesis led to aberrant embryo phenotypes: the *yuc1 yuc4 yuc10* quadruple mutant and the *taa1 tar1 tar2* triple mutant have similar phenotypes, with abnormal division of the hypophysis, rootless seedlings, very short or no hypocotyl and the majority of them has only one cotyledon (Cheng et al. 2007; Stepanova et al. 2008). Notably, mutants in auxin biosynthesis show aberrant embryo phenotypes of the same type as those present in mutants in which the transport of auxin is affected. More precisely, loss of PIN functionality leads to severe effects on embryo development, i.e., the level of aberration increases with the higher loss of PINs. According to their phosphorylation state, PIN proteins change their intracellular localization. If they are phosphorylated, they are targeted to the apical part of the plasma membrane, while if dephosphorylated, they are targeted to the basal part of the plasma membrane. The phosphorylation and dephosphorylation is effected by PID and PROTEIN PHOSPHATASE 2A (PP2A), respectively, which are serine–threonine protein kinases; *pid and pp2a* mutants exhibit similar phenotypes to the one reported for the pin mutants, where the auxin distribution is altered (Bennett et al. 1995; Benjamins et al. 2001; Friml et al. 2004; Michniewicz et al. 2007). In addition, the correct perception of auxin, together with AUX/IAA degradation, is fundamental as well during embryogenesis, since mutants display the same phenotypes as those observed when either biosynthesis or transport are impaired. Mutation of the F-box protein, TIR1, which is involved, upon auxin binding, in the degradation of AUX/IAA proteins, is not enough to affect embryo development, since redundancy has been observed with the closely related AUXIN SIGNALLING F-BOX PROTEIN 1 (AFB1), AFB2, and AFB3 (Dharmasiri et al. 2005a, b; Kepinski and Leyser 2005; Tan et al. 2007). Indeed, the quadruple mutant shows defects in embryogenesis, because it often fails to produce the hypocotyl and the root, and has only one cotyledon (Parry et al. 2009). AUXIN RESPONSE FACTOR (ARF) proteins are fundamental players in auxin signalling, and for this reason, there is a quite high degree of redundancy, so it is unlikely that a mutation in only one of these genes leads to a strong phenotype. The only factor that does not follow this is *MONOPTEROS/ARF5 (MP/ARF5)* whose mutant is rootless, because it exhibits an aberrant division pattern in the hypophysis (Berleth and Jurgens 1993; Hardtke and Berleth 1998; Weijers et al. 2006). Moreover, most of the defects observed and reported in mutants where auxin biosynthesis, transport, or signalling is affected can be explained by the alteration in the activity of MP/ARF5. Indeed, some of the targets of MP are essential transcription factors involved in embryogenesis; these include the *WUSCHEL RELATED HOMEOBOX 9 (WOX9)* transcription factor gene, which is differentially expressed during the early embryo development. Mutations in *MP*, *WOX2*, *WOX8*, and *WOX9* have synergistic effects, meaning that both regulatory pathways converge in controlling the same embryo patterning processes (Haecker et al. 2004); *mp*, *pin1*, and *pid* mutants all fail to demonstrate separate cotyledons and to establish the bilateral symmetry of the cotyledons. Two NAC transcription factor genes, *CUP SHAPED COTYLEDON1 (CUC1)* and *CUC2*, are responsible for the formation of the boundaries between different developing areas and work redundantly to regulate the initial formation of the SAM and the separation of the cotyledons, together with *SHOOT MERISTEMLESS (STM)*. While *CUC1* and *CUC2* are restricted to the cotyledon margins, *STM* is localized only in the SAM (Aida et al. 1997, 1999). *MP*, *PIN1*, and *PID* have been observed to be required for the activation of *CUC2* in the boundaries and the repression of *CUC1* in the cotyledons (Aida et al. 2002; Furutani et al. 2004). Mutation of *CUC1* partially restores the correct cotyledon development in the double mutant *pin1pid*, meaning that probably the defects observed are partially caused by an ectopic expression of *CUC1* in the cotyledons (Furutani et al. 2004). However, it is still unclear if MP directly regulates the expression of CUC genes or just promotes *PIN1* expression and this has a downstream effect on *CUC1* and *CUC2*.

YUC10 and *TAR1* have been demonstrated to be imprinted in the endosperm and paternally expressed. This epigenetic regulatory mechanism is conserved among distantly related species, such as *Oryza sativa*, *Capsella. rubella*, and *A. lyrata* (Du et al. 2014; Hatorangan et al. 2016; Klosinska et al. 2016; Luo et al. 2011). Another example is strawberry, where the homologues of *YUC10* and *TAR1* are specifically expressed in the endosperm, although their imprinting has not yet been determined (Kang et al. 2013). An interesting hypothesis is that there is a sort of auxin transport from the endosperm to the embryo, and since *YUC10* and *YUC11* are specifically expressed in the endosperm, this could explain the defects observed in the embryos of those mutants

(Figueiredo et al. 2015; Figueiredo and Köhler 2018; Robert et al. 2013). To support this hypothesis, it is known that the auxin importer gene *LAX1* is specifically expressed in the tip of the cotyledons, but to date, the import of auxin from the endosperm has not yet been demonstrated (Robert et al. 2015). In Arabidopsis, in particular, it has been demonstrated that if auxin biosynthesis or signalling is altered, there is a dramatic effect on the endosperm proliferation rate. Another example of the crucial role of auxin in endosperm development can be found in the woody plant *Jatropha curca*, and in particular, *JcARF9* has been proven to activate cell cycle regulators in the endosperm, such as *JcCKA1*, *JcCYCD2*, and *JcCYCD5* (Sun et al. 2017). Endosperm development is also highly sensitive to auxin in both raspberry and blackberry seeds (Jennings et al. 1967; Jennings 1971). However, although this crucial role of auxin during endosperm development has been observed, very little is known about its dynamics and transport during the process.

Seed coat development has been proven to be triggered only after fertilization of the central cell and not of the egg cell, meaning that the endosperm is involved in sending signals to the ovule integuments to initiate their conversion to seed coat (Roszak and Köhler 2011; Weijers et al. 2003). However, no cytoplasmic connections have been found between the endosperm and the seed coat, and thus, the communication between these two structures has to rely on small molecules such as peptides and hormones that can cross the plasma membrane (Figueiredo and Köhler 2016; Ingram 2010). Further experimental evidence that auxin produced in the endosperm affects seed coat development has been found in plants where auxin biosynthesis is down-regulated in the endosperm, resuting in seed coat development being significantly altered. Both the transport of auxin from the endosperm to the embryo, and the transport from the triploid tissue to the seed coat remain to be investigated. MADS-box transcription factor *AGAMOUS-LIKE62 (AGL62)* mutant has been shown to lack the ability to export auxin to the seed coat, and as a consequence, to form it, although the reason why is still unclear. It also appears that epigenetics has a role in the initiation of the seed coat development, blocking it in the unfertilized ovule, and that auxin plays a role in the regulation of this epigenetic mechanism (Figueiredo and Köhler 2016; Roszak and Köhler 2011). Epigenetics is also involved in endosperm development, since a large group of the polycomb repressive complex (PcG) proteins have been identified in the endosperm (Pien and Grossniklaus 2007).

Furthermore, auxin is not the only hormone that has a role during seed development. Gibberellins (GAs) are tetracyclic diterpenoids and they are required for the correct development of the seed, since the GA-deficient mutants display an altered seed development and a significant level of abortions. In tomato, the GA-deficient mutant *ga-1* displays altered development, not only of the seed, but also of the flower and the fruit (Groot et al. 1987), while in pea, the *lh* mutant, which has a significant reduction in the synthesis of GA, has an clear decrease in the seed weight and reduction in seed number in each pod (Swain et al. 1993, 1997). Another example comes from a study involving the constitutive overexpression of the pea *GA2 oxidase2 (GA2ox2)* gene, which encodes for an enzyme that irreversibly converts active GAs and their precursors into the inactive forms. In Arabidopsis, this causes seed abortion at different stages of the developmental process, since only 3% of the viable seeds carry the *GA2ox2* transgene. Thus, the effect of the over expression of *GA2ox2* reduces the seed number, due to seed abortion, and the fruit size. However, it has not been possible to measure the GA levels in the aborted seeds because of their small size, so although it is likely that the abortion of the seeds was caused by a low level of active GAs, it has not been demonstrated in this study (Singh et al. 2002). The target of the GA signalling pathway is the *Gibberellic Acid Stimulated Arabidopsis (GASA)* gene family whose expression is activated and stimulated in response to GAs (Herzog et al. 1995). *GASA4*, for example, is activated in the shoot apex, in the developing flowers and embryos, and its overexpression leads to a significant increase in seed size and seed weight, while the gasa4 mutant has smaller seeds (Roxrud et al. 2007). Gibberellins act downstream of auxin, since exogenous application of the latter to unfertilized ovules is enough to activate the transcription of the GA biosynthetic genes (Dorcey et al. 2009). Finally, a predominant role of cytokinins has been observed during the early endosperm development, influencing the final dimension of the seed (Day et al. 2008). Arabidopsis histidine kinases (AHKs) are used by the plant cells as cytokinin receptors, and they target the Arabidopsis histidine phosphotransfer proteins (AHPs), which are involved in cytokinin signal transduction. Both *ahk2ahk3ahk4* and *ahp2ahp3ahp5* triple mutants produce seeds that are twice the size of those in the wild type (Hutchison et al. 2006; Müller and Sheen 2007; Riefler et al. 2006).

As mentioned above, MADS-box transcription factor genes are also involved in ovule seed development, and among these *SEEDSTICK* (*STK*), *SHATTERPROOF 1* (*SHP1*) and *SHP2* are included. Indeed, the *stk shp1 shp2* triple mutant has a visible funiculus, but the integuments are converted to carpel-like structures, showing that these three genes together are indispensable for ovule identity determination (Brambilla et al. 2007; Pinyopich et al. 2003). Moreover, STK has been shown to work in association with the MADS-box transcription factor ARABIDOPSIS B_{sister} (ABS) in the development of the endothelium, which is the innermost layer of the seed coat, directly in contact with the endosperm. The *stk abs* double mutant, which lacks the endothelium presence in the seed coat, shows a great reduction of seed production due to abortions during both ovule and seed development (Mizzotti et al. 2012). Moreover, STK

is responsible for the correct formation of the cell wall in the seed coat, since it directly regulates factors that take part in the biosynthesis of the cellulose–pectin matrix of the cell wall (Ezquer et al. 2016). In addition, the *stk* mutant not only shows cells in the seed coat with an altered morphology, but also an altered accumulation of proanthocyanidins. RNA-seq and in-situ hybridization and ChIP data have shown that STK binds the promoter of *BANYULS/ANTHOCYANIDIN REDUCTASE (BAN/ANR),* which is involved in the proanthocyanidins biosynthetic pathway. Therefore, STK is also involved in the control of secondary metabolism in the seed coat (Mizzotti et al. 2014). Finally, STK seems to be essential for correct seed development, and its mutation can lead to the production of a stenospermocarpic fruit.

Seedless fruit has been identified in multiple species: can this information provide a route to the development of a seedless cherry?

Parthenocarpy and stenospermocarpy in fruiting plants

In some horticultural crops, fruit set and development can occur without the fertilization of the ovules in a process known as parthenocarpy (from Greek "virgin fruit") (Picarella and Mazzucato 2019; Sharif et al. 2022). Natural parthenocarpy can be obligated in sterile species, such as banana and pineapple, or facultative as in some tomato mutants.

Parthenocarpy has been reported in 96 Angiosperm taxa (Gustafson 1942; Picarella and Mazzucato 2019). The group that presents the highest number of parthenocarpic fruits is the Rosidae (49.8%), where the Rosaceae contribute with six species (the second bigger contribution after the Anacardiaceae and the Rutaceae with eight species). Interestingly, about a half of the parthenocarpic species are trees and between the monospermic fruit-type species, the ones that develop a drupe-type fruit make up the majority. In particular, *Prunus persica* (L.) Batsch and *Prunus cerasifera* Ehrh are the two examples of woody plants with a drupe-type fruit that belong to the Rosaceae, in which parthenocarpy had been reported (Gustafson 1939, 1942; Picarella and Mazzucato 2019). Parthenocarpy is an important agricultural trait that can mitigate poor fruit setting caused by unfavorable pollination conditions (Gou et al. 2022). Similarly, seedless fruit can be formed by a preocess termed stenospermocarpy, which is the formation of fruit with spontaneous or induced abortion of fertilized seeds (watermelon and grapes). However, this process, unlike parthenocarpy, requires pollination.

Genetic insights of seedlessness

The MADS-box transcription factors involved in the identity determination of the floral whorls, according to the ABCDE model (Theißen 2001), have been observed to be involved in the formation of a seedless fruit. Indeed, the apple mutant Rae Ime has been reported to be parthenocarpic if not pollinated, while if it is pollinated, it produces seeds with smaller embryos. Its flowers have no petals and stamens, while an apple wild-type flower has five petals and between 9 and 20 stamens, Rae Ime also posesses two whorls of five sepals and an increased number, up to 15, styles and carpels, while the wild-type flower typically has five (Pratt 1988; Yao et al. 2001).

There are other apple mutants, Spencer Seedless and Wallington Bloomless for example, which produce flowers with a similar phenotype of Rae Ime, and are parthenocarpic. This phenotype is similar to that observed in the Arabidopsis mutants *pi* and *ap3*. *PISTILLATA (PI)* and *APETALA3* (*AP3*) belong to the B-class and are involved in the identity determination of the petals, and stamens, with the A-class and C-class MADS-box transcription factors, respectively (Goto and Meyerowitz 1994; Jack et al. 1992; Theißen and Saedler 2001). It has been observed that the apple gene *MdPI*, which encodes a protein with 64% identity to that encoded by *AtPI* and which has a similar expression pattern compared to Arabidopsis, in Rae Ime has a 9332 bp LRT-retrotransposon insertion that affects the function of this gene. The mutation of *MdPI* has also been found in Spencer Seedless and Wallington Bloomless (Table 1) (Yao et al. 2001). Furthermore, co-suppression of *MdPI* in transgenic apple was also shown to result in parthenocarpy [see Tanaka and Wade (2022) for review].

SEPALLATA (*SEP*) genes encode for E-class MADS-box transcription factors, which are necessary for the function of all the other classes. Indeed, the *sep1sep2sep3* triple mutant displays an indeterminate flower growth where all the whorls are composed of sepals (Ditta et al. 2004; Pelaz et al. 2000; Theißen 2001).

Tomato MADS-box 29 (*TM29*) is a single copy gene and has been shown to be the *SEPALLATA* homolog in tomato, since the encoded protein shares a 68%, 63%, and 58% amino acid sequence identity with AtSEP1, AtSEP2, and AtSEP3, respectively, and also, the expression pattern is conserved. In addition, *TM29* has been found in the vegetative and inflorescence meristems, so it seems to have an additional function compared to SEP1. Down-regulation of *TM29* through RNAi in tomato leads the production of a mutant with some flower defects, such as green and sterile anthers, and a pistil that develops a parthenocarpic fruit without pollination and fertilization (Table 1). The transgenic fruit is bigger than the wild type, although they remains green for a longer time before starting the maturation process. Moreover, ectopic shoot formation has been observed in the transgenic fruit, which becomes swollen and misshapen. The shoot produces in turn a new fruit from which a new ectopic shoot arises, and this cycle can be repeated three or four times

Table 1 Summary of the genes involved in parthenocarpic fruit development and potential targets to induce parthenocarpy in cherry

Target	Pathway	Plant	Phenotype	Reference
Auxin Response Factor 7 (ARF7)	Auxin	Arabidopsis	Parthenocarpy, seedless/pseudoembryos, size, and shape similar to WT	Goetz et al. (2007)
		Tomato	Down-regulation of ARF7 resulted in the formation of parthenocarpic fruit and altered shape. SlARF7 RNAi lines also display a down-regulation of SlARF5 and SlARF8B, suggesting that ARF7 cannot promote parthenocarpy unless ARF5 levels are also reduced	de Jong et al. (2009, 2011); Hu et al. (2018)
Auxin Response Factor 8 (ARF8)	Auxin	Eggplant	Natural parthenocarpic mutant showed that ARF8, is down-regulated in buds compared to wild-type plants. Transgenic RNAi lines of ARF8 exhibited parthenocarpy in unfertilized flowers. ARF8 negatively regulates fruit initiation	Du et al. (2016)
		Arabidopsis	Mutations in ARF8 uncouple fruit initiation from fertilization, resulting in the formation of seedless, parthenocarpic fruit/pseudoembryos, size, and shape similar to wt	Goetz et al. (2007)
		Tomato	Expression of an aberrant ARF8 mutant transcript from Arabidopsis in tomato results in parthenocarpy	Goetz et al. (2007)
Indole-3-Acetic Acid Inducible 9 (IAA/9)	Auxin	Tomato	down-regulation of IAA9 resulted in parthenocarpic fruit and auxin-related alterations in the leaf morphology	Zhang et al. (2007)
			Parthenocarpy, seedless, early fruit growth, normal size, and shape	Wang et al. (2005)
AUCSIA	Auxin	Tomato	Aucsia gene silencing causes parthenocarpic fruit development in tomato. Aucsia silenced tomato plants are characterized by facultative (seedless fruits when flowers are emasculated) and rarely, obligate parthenocarpy (i.e., seedless fruit from pollinated flowers). The facultative parthenocarpic fruits were similar in shape to wild-type fruit	Molesini et al. (2009, 2020)
PIN4	Auxin-transport	Tomato	The mutation of the auxin efflux carrier encoding gene PIN4 in tomato has been reported to trigger the development of parthenocarpic fruit	Mounet et al. (2012)
DELLA	GA	Arabidopsis	Parthenocarpy observed in DELLA mutants is directly attributed to the constitutive activation of GA signalling	Fuentes et al. (2012)
DELLA Pistillata (PI)	GA MADS-Box	Arabidopsis	DELLA mutants have impaired fertilization (seed set)	Dorcey et al. (2009)
		Tomato	Silencing of DELLA induces facultative parthenocarpy, seedless fruit with reduced size, altered morphology	Martí et al. (2007); Livne et al. (2015); Carrera et al. (2012)
		Apple	Abolishing the normal expression of the Pistillata gene in apple confers parthenocarpic fruit development	Yao et al. (2001)

Table 1 (continued)

Target	Pathway	Plant	Phenotype	Reference
Sepallata (SEP)	MADS-Box	Tomato	Antisense and co-suppression of Sepallata in the transgenic ovary developed into parthenocarpic fruit without pollination. The transgenic fruit are bigger than the wild type, although it remains green for a longer before starting the maturation process	Ampomah-Dwamena et al. (2002)
SEEDSTICK (STK)	MADS-Box	Arabidopsis	Controls structural and mechanical properties of the Arabidopsis seed coat	Ezquer et al. (2016)
AGAMOUS like-6 (AGL6)	MADS-Box	Tomato	Seedless fruits are of normal weight and shape. Down-regulation in natural mutant causes parthenocarpy and low seed	Klap et al. (2017); Takisawa et al. (2018)
AGAMOUS like-11 (AGL11)	MADS-Box	Tomato	Gene silencing of AGL11 in tomato produces seedless fruits. Seedlessness is proportional to transcript accumulation levels	Ocarez and Mejía (2016)
		Tomato	Gene silencing of both AGL11 and a second MADS-Box gene, MBP3, produces all flesh seedless fruit exhibit enhanced firmness and improved post-harvest storage	Huang et al. (2021)
		Grape	Seed abortion caused by a single amino acid substitution in VviAGL11 is the major cause of seedlessness	Royo et al. (2018)
		Grape	Dominant mutation in VviAGL11, homologue of STK, are seedless Seeded fruit is bigger than seedless fruit due to higher expression of VviAGL11	Mejía et al. (2011)

(Ampomah-Dwamena et al. 2002). This severe phenotype can be explained by the fact the *SEPALLATA* genes are very basal factors (E-class) that work in the determination of all the whorls.

The opposite scenario can be observed in tomato and grapevine mutants of *TOMATO AGAMOUS-LIKE 11 (AGL11/TAG11)* and *Vitis vinifera AGAMOUS-LIKE 11 (VviAGL11)* respectively (Table 1). TAGL11 is the STK homolog in tomato, it shares 81% similarity at the nucleotide level with the Arabidopsis gene, and it controls fruit and seed development, being expressed in the inner integuments of the ovule. *TAG11* has been silenced using an antisense construct and the lines produced do not exhibit any significant difference in fruit number, date of maturity, final ripening colour, and fruit size. Most of these lines are seedless, and some have few seeds, smaller seeds, or ovule traces. The number of seeds is positively correlated with the expression level of *TAG11* in these lines (Ocarez and Mejía 2016). Further work by Huang et al (2021) used crispr/cas9 to silence *AGL11* and a second MADS-Box gene, *MBP3* in the same lines. This work resulted in the production of all-flesh, seedless transgenic lines with enhanced firmness and improved post-harvest storage; however, average fruit size was severely reduced. Similar results have been reported in pepper, with parthenocarpic fruit reported to be 30% smaller than seeded fruit (Heuvelink and Körner 2001). These data suggest that multi-target approaches may be necessary to achieve seedless cherry and maintain fruit size. *VviAGL11* is the homolog of *STK* in grapevine and it starts to be highly expressed when the seed begins to develop, immediately after berry set (Mejía et al. 2011). Comparing different seeded and seedless genotypes of grapevine has shown that the seeded ones have bigger fruit and a higher expression of *VviAGL11* than the seedless ones. Seedless Ruby is a stenospermocarpic mutant that has a dominant mutation in *VviAGL11*, since the heterozygous plants are seedless. The dominant phenotype is due to a single missense mutation (Arg197 to Leu197), which does not allow the formation of the correct transcriptional complex that is involved in activating all the genes necessary for the normal seed coat

development and lignification, which, as mentioned in the previous paragraphs, is crucial for the correct endosperm and embryo development (Ocarez and Mejía 2016; Royo et al. 2018) (Fig. 5).

Two members of the Auxin Response Factor (ARF) family, *ARF7* and *ARF8*, have recently been implicated in fruit initiation (Table 1). The transcript levels of both genes are highly expressed in non-pollinated flowers and are down-regulated after pollination. Down-regulation of *ARF7* in tomato resulted in the formation of parthenocarpic fruit and a significant reduction in the accumulation of GAs compared to seeding fruit (de Jong et al. 2009, 2011). Hu et al. (2018) reported that *SlARF7* RNAi lines also display a down-regulation of SlARF5 and SlARF8B. These results clearly demonstrate that ARF7 acts to modulate both auxin and gibberellin during fruit set and mediates crosstalk between auxin and gibberellin signalling during tomato fruit development; however, the co-down-regulation of *SlARF5* suggests that *SlARF7* cannot promote parthenocarpy unless *SlARF5* levels are also reduced.

Similar results have been found with *AUXIN RESPONSE FACTOR8 (ARF8)* in tomato, eggplant, and Arabidopsis. In Arabidopsis, *ARF8* mutants display parthenocarpic siliques and the expression of the Arabidopsis mutant allele in tomato results in the production of seedless fruits (Goetz et al. 2006, 2007; Du et al. 2016). The introduction of the mutant *ARF8* allele into Arabidopsis did not result in the suppression of the endogenous *ARF8* transcript; however, the aberrant transcripts compromised the function of endogenous *ARF8* (Goetz et al. 2007). It has been proposed that in both Arabidopsis and tomato, ARF proteins can bind Aux/IAA proteins to form a protein complex that inhibits or activates auxin responsive genes (Hardtke et al. 2004; Tatematsu et al. 2004; Ulmasov et al. 1999). The accumulation of the mutant transcript is thought to destabilize the formation and/or function of the ARF-IAA complex, permitting fruit set in the absence of pollination (Goetz et al. 2006; Swain and Koltunow 2006). Furthermore, the down-regulation of *Indole-3-acetic acid inducible 9* (*IAA9)* (Table 1), the second member of this complex, using an antisense approach in tomato, resulted in parthenocarpic fruit development and auxin-related alterations in leaf morphology (Wang et al. 2005). Kim et al (2020) reported that the silencing of *AUX/IAA9* in tomato mimics an increase in auxin levels in the unpollinated ovaries and promotes the expression of auxin and gibberellins biosynthetic genes, which are activated during the fruit set. Auxin and GA crosstalk has been better investigated by Hu et al. (2018). Indeed, the tomato *entire* (SlIAA9 loss of function), *SlARF7* RNAi, and *procera* (SlDELLA loss of function) mutants show strong parthenocarpy.

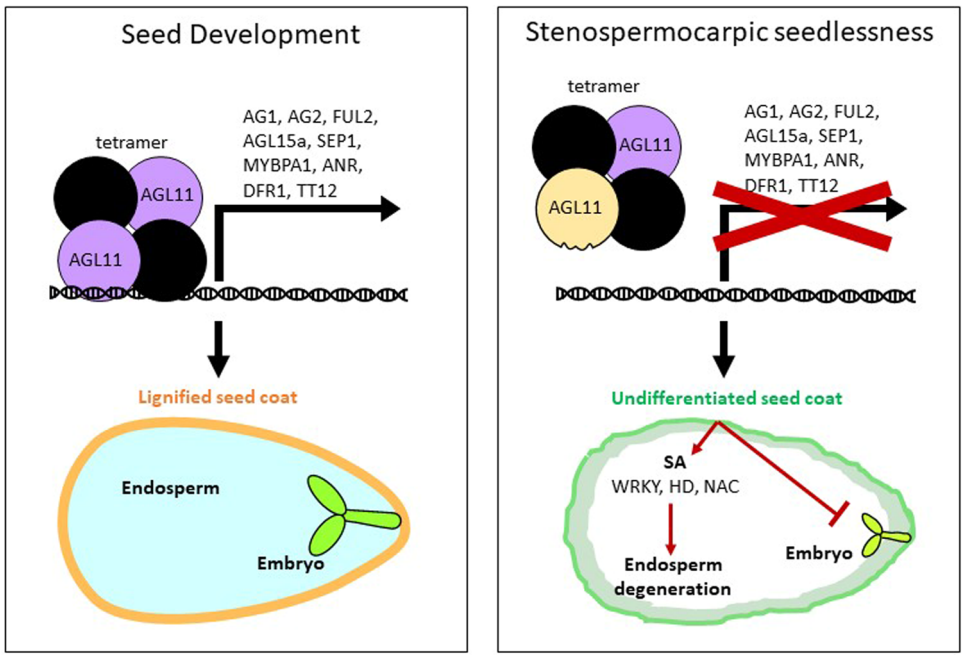

Fig. 5 Model of seedlessness proposed by Royo et al. (Royo et al. 2018) to explain the seedless phenotype in grape. The panel on the left shows the initiation of seed morphogenesis that occurs under normal development. The wild-type VviAGL11 (AGAMOUS-LIKE11) protein complex (shown in purple) either directly or indirectly initiates the expression of genes involved in seed coat sclerification, permitting embryo development. The panel on the right shows a heterozygous individual with a dominant phenotype due to a single missense mutation in the VviAGL11 protein (Arg197 to Leu197; shown in yellow). This mutation prevents the assembly of the multi-protein complex halting seed coat differentiation, leading to degeneration of the embryo and endosperm

June drop

Fruit trees produce a large quantity of flowers, more than are necessary to produce a healthy crop of fruit. In the case of pears and apples, the trees thin themselves, dropping small fruit so as to not overburden the plant, and thereby reducing the chance that branches will break under excessive weight. This process, often referred to as 'June drop' or 'cherry run-off', begins in late June and continues until mid-July. If just one in 20 flowers produces a fruit, the tree is carrying a healthy crop. These remaining fruits develop normally, becoming bigger at the expense of the fruitlets lost earlier. However, cherries, and other stone fruit, often do not need thinning and do not drop excess flowers requiring extra manual resources to protect crop yield. However, in some years, sweet cherry trees lose a significant proportion of their fruit before ripening. This loss varies from year to year and, in some seasons, can result in a total loss of the crop. In the UK in 2000, for example, cherry trees lost as much as 90% of the fruit set before harvest.

At the start of fruit drop in cherry, when fruits with aborted seeds are abscising, there is significantly more ethylene in the pedicels than in the flesh of the fruits. In both sweet and tart cherry, ethylene was shown to be elevated (fivefold) in fruit flesh and pedicles of abscising fruit compared to adhering fruits (Blanpied 1972). Furthermore, since the application of endogenous ethylene promote the abscission of sweet and tart cherries (Edgerton and Hatch 1969), the combined data suggest that ethylene may play a role in early fruit drop. Furthermore, polar auxin transport inhibitors increased fruit abscission by 30%, demonstrating that maintaining auxin (indole-3-acetic acid, IAA) transport and concentrations in the abscission zone plays a role in fruit retention (Blanusa et al. 2005; Guinn and Brummett 1987). It has been reported that IAA delays abscission by lowering the cells sensitivity to ethylene (Sexton et al. 1985), and yet also stimulates ethylene production, while ethylene is a potent inhibitor of auxin transport (An et al. 2020). This interplay between these two hormones demonstrates the extreme complexity between the regulation of fruit set and fruit abscission (for review see (An et al. 2020; Taylor and Whitelaw 2001). As previously noted, during fruit development, communication between the seed/embryo and the fruit, necessary for the developmental synchronization during fruit formation, involves phytohormones (auxin and gibberellins) produced either in the developing embryo, endosperm, or in the seed coat (Figueiredo and Köhler 2016; Gillaspy et al. 1993; Ingram 2010; Varoquaux et al. 2000).

The complex inter-hormonal signalling mechanism that identifies an aborting seed to the tree and results in fruit abscission is poorly understood; however, it is probable that either a signal travels from the aborting seed to the tree to induce fruit abscission or there is a loss of signal from the seed coat, embryo, or endosperm, that would normally be present during successful seed development.

Options for the generation of seedless cherry and intellectual property rights in the domain of seedless fruit

Seed, stone, and fruit development is a tightly controlled process involving key phytohormones, such as gibberellins, auxins, and environmental cues. The absence of the seeds/stone would be advantageous for producers, reducing processing costs and increasing profits and for the consumer. The presence of the stone and seed makes it both inconvenient to eat 'on the move' and potentially dangerous for children. Removal of this stone through genetic means could be potentially transformative for the cherry industry and facilitate rapid market expansion in the UK and beyond. Furthermore, parthenocarpic fruits are firmer and fleshier than pollinated fruits due to the absence of the seeds (Gou et al. 2022; Varoquaux et al. 2000).

Exogenous application of plant hormones has been shown to result in the development of parthenocarpic fruit; however, large-scale introduction of such treatments would prove costly to implement; thus, genetic engineering and genome editing strategies aimed at altering hormone biosynthesis or signalling to obtain parthenocarpic fruits seems a preferable approach. This review highlights some of the potential gene targets for the generation of seedless fruit. We have identified, in the genome databases, orthologues of many of these genes in cherry (Table 2). Manipulation of the listed genes have been shown to induce, directly or indirectly, the development of seedless fruit in the listed species. The table highlights the action required in cherry to potentially obtain a seedless cherry. Previous results in tomato have shown that the down-regulation of *ARF7* promotes parthenocarpy; however, this induction requires the co-down-regulation of *ARF5* in these plants (Hu et al. 2018). Orthologues of both *ARF7* and *ARF5* have been identified in the Cherry (Table 2). To obtain parthenocarpic cherry fruit, it may be necessary to knock-down both *ARF7* and *ARF5* simultaneously.

As previously noted, down-regulation of *DELLA* in tomato causes parthenocarpy (Carrera et al. 2012; Martí et al. 2007; Livne et al. 2015). A single copy of *DELLA* has been identified in tomato. Here, we have identified a single copy of *DELLA* in sweet cherry making it an ideal target for generating seedless fruit. In tomato, we should note that the fruit is smaller than wild type. However, in tomato, a mutation in *DELLA* (*procera*) includes elongated internode length, thinner leaves, and reduced lobing of the main leaflets, which could influence fruit development and fruit size. One option in sweet cherry would be to use a targeted approach, down-regulating *DELLA* at early fruit development and in the fruit leaving wild-type levels in the

Table 2 A list of cherry homologs of the genes involved the development and parthenocarpic fruit in tested species

Gene	Species	Ref	Putative cherry orthologue	Action
ARF8	Arabidopsis, Tomato, Eggplant	Goetz et al. (2007; Du et al. (2016)	*Pav_sc0001314.1_g050.1.mk*	Knock-out
ARF7	Tomato	de Jong et al. (2009)	*Pav_sc0000129.1_g1480.1.mk*	Knock-out
ARF5	Tomato	Hu et al. (2018)	*Pav_sc0002080.1_g180.1.mk*	Knock-out
ARF5-putative	Tomato	Hu et al. (2018)	*Pav_sc0011314.1_g020.1.br* *Pav_sc0003104.1_g030.1.br* *Pav_sc0002826.1_g100.1.br* *Pav_sc0001759.1_g010.1.br*	Knock-out
AUX/IAA9	Tomato, Eggplant	Zhang et al. (2007); Chen et al. (2017)	*Pav_sc0002393.1_g030.1.mk* *Pav_sc0002327.1_g560.1.mk*	Knock-out
AUCSIA	Tomato	Molesini et al. (2020)	*Pav_sc0000175.1_g020.1.mk*	Knock-out
PIN4	Tomato	Mounet et al. (2012)	*Pav_sc0000103.1_g670.1.mk*	Knock-out
DELLA	Arabidopsis. Tomato	Martí et al. (Fuentes et al. (2012; Livne et al. (2015); 2007;	*Pav_sc0000464.1_g350.1.mk*	Knock-out
GA20ox	Arabidopsis, Tomato, Citrus	García-Hurtado et al. (2012); Mesejo et al. (2016)	*Pav_sc0000072.1_g640.1.mk*	Up-regulation
SEPETALLA (TM29)	Tomato	Ampomah-Dwamena et al. (2002)	*Pav_sc0000176.1_g060.1.mk* *Pav_sc0000091.1_g150.1.mk* *Pav_sc0000661.1_g410.1.mk* *Pav_sc0001080.1_g900.1.mk*	Knock-out
PISTILLATA	Apple, Grape	Yao et al. (2001); Fernandez et al. (2013)	*Pav_sc0000195.1_g010.1.mk*	Knock-out
HYDRA	Tomato	Rojas-Gracia et al. (2017)	*Pav_sc0000124.1_g160.1.mk* *Pav_sc0002264.1_g290.1.mk*	Knock-out
AGL6	Tomato	Klap et al. (2017); Takisawa et al. (2018)	*Pav_sc0000072.1_g670.1.mk*	Knock-out
AGL11	Grape, Tomato	Ocarez and Mejía (2016); Royo et al. (2018)	*Pav_sc0002136.1_g280.1.mk*	Knock-out

Cherry genes were identifed in the Genome Database Rosaceae: https://www.rosaceae.org/species/prunus_avium/genome_v1.0.a1 and AUCSIA and HYDRA were identified by blast of tomato sequences against the cherry genome on EnsemblPlants. Manipulation of the listed genes has been shown to induce, directly or indirectly, the development of parthenocarpic fruit in the listed species

vegetative tissues. The identified orthologue of DELLA gene in the cherry database, *Pav_sc0000464.1_g350.1.mk* (Table 2), is highly expressed in the unpollinated ovaries at anthesis and decreases only after pollination.

Another option, the down-regulation of the *SEPETALLA* gene in tomato resulted in parthenocarpic fruit that is bigger than the wild type (Ampomah-Dwamena et al. 2002), suggesting that this may be a more viable target in sweet cherry; however, in this instance, four copies of the *PISTILLATA* gene have been identified in sweet cherry genome; therefore, identifying the correct target may be more complex.

Over the last few decades, agricultural research has adopted technologies such as genetic engineering and more recently 'genome editing' to improve traits in key crops (Aglawe et al. 2018; Georges and Ray 2017; Simkin 2019; Wilson et al. 2019). There have been recent advances in the tools available to carry out this work, including vectors for multiple gene insertion (Engler et al. 2008, 2009, 2014; Exposito-Rodriguez et al. 2017; Marillonnet and Werner 2015) and tissue-specific promoters (Alotaibi et al. 2018, 2019; Kuntz et al. 1998; Mukherjee et al. 2015; Simkin et al. 2006, 2007).

It has previously been demonstrated that the CRISPR-Cas9 genome editing system can be used to breed parthenocarpic tomato plants (Huang et al. 2021). To use site-directed mutagenesis to obtain knock-out mutants of the cherry orthologues, two factors need to be taken into account. First, fruit trees are included in the group of the most reluctant species for in vitro tissue culture. In vitro cherry regeneration and transformation are remarkably challenging, because it has a low success rate and is time-consuming (Vergara et al. 2021). There are, however, a few regeneration and transformation protocols developed for commercially important cherry varieties; these involve the use of leaves, shoots, cotyledons, and epicotyls as initial explants (Bhagwat and Lane 2004; Blando et al. 2007; Canli and Tian 2008; Feeney et al. 2007; Matt and Jehle 2005; Zong et al. 2019; Vergara et al. 2021). Second, the interest is in confirming the phenotype at the flower and fruit level, and sweet cherry has a long juvenile phase (from 4 to 10 years), since it is a woody plant. This obstacle could be overcome

by overexpressing a florigen gene such as *FLOWERING LOCUS-T* (*FT*). In fact, in plum (*P. domestica*), the overexpression of the poplar ortholog of *FT1* has significantly reduced the juvenile phase, allowing to fruits set just 1 year after seed germination (Srinivasan et al. 2012).

The development of a commercially viable stoneless and seedless cherry must take into account current intellectual property rights (Table 3) that may affect where and how a new variety can be marketed and whether licensing agreements are required before a products can be commercialised. *PIN4*, for example, a copy of which has been identifed in sweet cherry (Table 2), known to be involved in the development of parthenocarpic tomato fruit (Mounet et al. 2012), is the subject of an active patent until at least 2036 (Van Dun et al. 2021). Other potatial targets, including the manipulation of the Auxin Response Factor (Bouzayen et al. 2013), and DELLA (Ariizumi et al. 2021), are also covered by patent applications (Table 3). One of the most promising targets, down-regulation of *AGL6* (Table 1) has been shown to result in seedless tomato fruit, and importantly, these fruits were described as being of nornal weight and shape (Klap et al. 2017; Takisawa et al. 2018), which is not always the case; however, use of *AGL6* is the subject of a patent application (Barg et al. 2021).

When granted, patents may potentially restrict the use of specific technologies for the development of parthenocarpic cherry, restrict gene targets to induce parthenocpary using genome editing, or restrict access to the market in specific countries or regions. It should be stressed that patent applications often contain speculative or unsubstantiated claims and there is no certainty that the applications in this summary will be approved and thereby achieve the status of a granted patent.

Conclusions

Seedless/stoneless cherry fruit would be highly advantageous to the cherry industry. First, it is well known that sweet cherry pollination is mediated by insects, which is important for the production of a viable crop (Eeraerts et al. 2020). Wild pollinators, including solitary bees, are essential to ensure sweet cherry yields (Eeraerts et al. 2019); however, growers rely on commercial domesticated honeybees (*Apis mellifera*) for pollination at a cost up to 1000 euro per hectare, a considerable investment for commercial cherry producers. The absence of the need for pollination also beings the potential for higher fruit yields and the absence of the seed/stone an increase in flesh content. With no need for pollination, the significant costs of providing commercial domesticated honeybees to carry out this function would no longer be required, thus

Table 3 Summary of the relevant patent (legal status denoted as active) and patent applications (denoted as pending) for targets identified in Tables 1 and 2 pertaining to the development of seedless and stoneless fruit

Patent number	Gene	Title	Applicants	Pub	Earliest priority	Legal status	Ref
US 10941411 B2	PIN4	Modified gene resulting in parthenocarpic fruit set	Rijk Zwaan Zaadteelt en Zaadhandel Bv	Mar 9, 2021	Jan 30, 2015	Active until 2036	Van Dun et al. (2021)
WO 2013 034722 A1	ARF	New parthenocarpic plants with modified expression of auxin response factors and the microRNAs inducing said modified expression	Institut National Polytechnique de Toulouse	Mar 14, 2013	Sep 7, 2011	Pending	Bouzayen et al. (2013)
US 2021 0037779 A1	AGL6	Parthenocarpic plants and methods of producing same	The State of Israel Ministry of Agriculture	Feb 11, 2021	Jan 21, 2016	Pending	Barg et al. (2021)
WO 2020 252167 A1	STK	Methods of producing plants with altered fruit development and plants derived therefrom	Pairwise Plants Services Inc	Dec 17, 2020	Jun 11, 2019	Pending	Crawford and Poorten (2020)
WO 2021 040011 A1	DELLA	Fruit-bearing plant exhibiting high temperature resistance, high yield, and parthenocarpy	Univ Tsukuba, Ibaraki, Japan	Mar 4, 2021	Aug 30, 2018	Pending	Ariizumi et al. (2021)

The earliest priority date is the date at which the patent application claims priority over any other applications filed after that date

not only reducing production costs but also the reliance on the presence of wild bee populations and solitary bees, which also play a considerable role in fruit set. Furthermore, reliance on honeybees also comes with the drawback that they remain inactive under unfavorable weather conditions, such as at temperatures below 12 °C or heavy rainfall, which can provide additional drawbacks to cherry production. Second, one of the possible causes of 'June drop' is poor or inadequate pollination, possibly due to a reduction in insect activity. Fruit set without pollination has the potential to mitigate June drop and increase and protect yields. Finally, there is also the suggestion that June drop occurs due to signals received by the plant from the aborted seed. In the absence of the seed, that signal is removed, and fruit previously dropped may develop to full maturity, thereby increasing cherry yield for growers and potentially reducing cost to the consumer. The absence of the seed has been reported to increase fruit quality (seed can have a hard texture and/or unpleasant flavour). Furthermore, seeds can release compounds that result in fruit spoilage, and therefore, the absence of the seed can increase shelf life. In such instances, a seedless fruit may still be advantageous to growers even if the stone remains; removal of the need for pollination increasing yields and the inhibition of June drop reducing yield loss. Seedless fruit has also been reported to reduce yield fluctuations in pepper (Heuvelink and Körner 2001).

In conclusion, there are a large number of factors involved in fruit set and the pathways are not linear, but there are regulation checkpoints at different levels, redundancy and crosstalk, which together make this process extremely complicated. There is still a lot that has to be learnt and constantly new proteins, pathways, and hormones are being found to have a function in this already complex scenario; these variables include the role of jasmonic acid and its derivatives (Schubert et al. 2019), SPOROCYELESS/NOZZLE (Rojas-Gracia et al. 2017), and also microRNAs (Wang et al. 2018). It should be noted that we have addressed the removal of the seed from cherry fruit in this review; however, the seed is contained within a lignified stone, which remains in the absence of the seed. The removal of the stone would be the next step in the breeding of a truly seedless/stoneless fruit fit for industrial exploitation.

Author contribution statement EV and AJS: wrote the first draft of the manuscript; ML, MC, and JMD: contributed to the revised version of the manuscript.

Acknowledgements E.V. was supported by 'Understanding Fruit Development in the Cultivated Cherry' project funded by Berry Gardens Growers Ltd awarded (https://www.berrygardens.co.uk/) to A.J.S. A.J.S. is supported by the Growing Kent and Medway Programme, UK; Ref 107139.

Data availability Data sharing is not applicable to this article as no datasets were generated or analysed during the current study.

Declarations

Conflict of interest The authors report no conflicts of interest in this work and have nothing to disclose.

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