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Hormonal regulation during initial berry development in grapevine

par

María Francisca Godoy Santin

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Dr. Virginie LAUVERGEAT, Université Bordeaux1

Rapporteur
Rapporteuse
Examinatrice
Examineur
Co-Directeur de thèse
Co-Directrice de thèse

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Glossary

2-4D, Dichlorophenoxy-Acetic Acid

4-CPA, 4-Chlorophenoxy-Acetic Acid

ABA, Absciscic Acid

ASB1, Anthranilate Synthase Subunit 1

BRs, Brassinosteroids

CKs, Cytokinins

CS, Castasterone

DAE, Days After Emasculation

DAF, Days After Flowering

DAP: Days After Pollination

DPA, Days Post Anthesis

DPP, Days Post Pollination

ENP, Emasculated Not Pollinated

GA₃, Gibberellin A₃

GAs, Gibberellins

IAA, Indole-3-Acetic Acid

PAC: Paclobutrazol

PCR: Polymerase Chain Reaction

tZ: *trans*-Zeatin.

RESUMEN GENERAL

Vitis vinifera es una de las especies más cultivadas del mundo, La mayor parte de la investigación se ha centrado en la maduración del fruto, y se conoce poco de los estados iniciales del desarrollo de la baya, el cual comprende las primeras dos semanas después de la floración. Durante esta fase ocurren procesos clave: polinización, fertilización y cuaja, los cuales darán lugar a un fruto semillado. La cuaja se define como un rápido crecimiento del ovario producto de la polinización y fertilización. Debido a que la cuaja ha sido descrita como una de las etapas más sensibles a distintos tipos de estrés durante el desarrollo completo del fruto, esta investigación se enfocó en identificar los principales factores que la determinan.

En este trabajo se han realizado análisis de expresión global y perfil hormonal para dilucidar los principales factores que afectan a la cuaja. El análisis de RNA-seq fue realizado en cuatro puntos entre polinización y cuaja, revelando patrones dinámicos transientes durante el desarrollo del fruto. Interesantemente, la expresión de un importante número de genes se encontraba reprimida después de la fertilización. El perfil hormonal indicó que las giberelinas eran las hormonas activas con niveles más altos durante antesis, mientras que auxina, *trans*-zeatina y ABA mostraron niveles más altos durante la cuaja. Estos resultados podrían indicar un nuevo modelo del desarrollo inicial del fruto, diferente a los previamente descritos en otras especies de estudio como tomate y *Arabidopsis*.

Para poder confirmar la función de algunas hormonas seleccionadas presentes durante el desarrollo inicial del fruto, se inhibió la síntesis de giberelinas mediante el compuesto Paclobutrazol, y por otro lado, la inhibición de las respuestas inducidas por auxina mediante el

tratamiento con IAA-Trp. Estos estudios demostraron que tanto la división celular como el desarrollo del mesocarpo se vieron fuertemente afectados, confirmando que ambas hormonas son críticas para el establecimiento de la cuaja en vid.

En conjunto, los datos de transcriptoma y perfil hormonal proveen por primera vez patrones dinámicos de expresión génica que pueden ser asociados a biosíntesis de hormonas, y el efecto de éstas en el desarrollo del mesocarpo durante los estadíos iniciales del fruto de vid. Además se demuestra que la presencia, así como el crosstalk entre auxinas y giberelinas es crucial para el establecimiento de la cuaja en vid.

Chapter I

Bibliographic synthesis of events involved in early development of the grapevine berry: morphological, molecular and hormonal aspects.

Review submitted to publication in October 1st, 2013 under the title: “Early steps of fruit development in grapevine: defining reproductive, morphological and physiological landmarks”

Authors: Francisca Godoy, Nathalie Kühn and Patricio Arce-Johnson

Synthèse bibliographique des évènements clés impliqués lors du développement précoce du fruit chez la vigne: aspects morphologiques, moléculaires et hormonaux.

RÉSUMÉ

La pollinisation, la fécondation et le développement embryonnaire sont des processus clés connus pour réguler la croissance des fruits. Ces processus sont sous contrôle d'un programme développemental qui est mis en place lors du passage d'un ovaire « en sommeil » à un ovaire « en développement ». Les signaux générés par ces processus sont nécessaires pour obtenir un fruit pleinement développé, et toute modification survenant au cours de cette période peut conduire à l'inhibition de la formation du fruit, à son abscission, au développement anormal de l'embryon, à la parthénocarpie, et d'autres anomalies. L'un des signaux générés par la pollinisation et la fécondation est la modification substantielle du contenu en hormones végétales, au niveau soit de la paroi de l'ovaire ou soit de l'embryon. Cependant, les mécanismes permettant le contrôle de la croissance du fruit via la régulation hormonale restent peu connus chez la vigne. Bien que la compréhension de ces mécanismes soit essentielle pour permettre d'améliorer la production ainsi que la qualité organoleptique des raisins et des vins, les étapes précoces du développement des baies représentent toujours la pièce manquante du puzzle du développement du fruit. Bien que les changements régulant la phase de reproduction, la morphologie du fruit ainsi que les principales hormones qui agissent au cours de ces phases aient été identifiés, les termes utilisés ne sont pas toujours les mêmes et les mécanismes sous-jacents sont souvent mal compris.

Cette revue décrit les principaux aspects du développement précoce des baies, en donnant la priorité aux événements de reproduction, morphologiques et physiologiques les plus pertinents, et en tenant compte de l'état actuel des connaissances en ce qui concerne l'expression des gènes au cours de ce stade. L'objectif de cette synthèse bibliographique est de contribuer à une meilleure compréhension de la formation initiale des baies, en particulier en redéfinissant un consensus terminologique des mécanismes identifiés chez la vigne.

ABSTRACT

Pollination, fertilization and embryo development are key processes known to regulate fruit growth through the control of developmental programs that will set in motion the change from a dormant to a developing ovary. Signals generated by these processes are required to obtain a fully developed seeded fruit, and alterations occurring at this period may lead to fruit formation inhibition, fruit abscission, abnormal embryo development, parthenocarpy, and other abnormalities. One of the signals generated by pollination and fertilization is the substantial change in the content of several plant hormones, either from the ovary or in later stages of the embryo. However, until now the mechanisms underlying growth control by these hormones in grapevine remain unclear. Although the understanding of fruit formation in this species is essential for improving yield and quality of grapes and wines, the early steps of berry development are still the missing piece of the fruit developmental puzzle. While there is relevant information available describing reproductive and morphological changes, and also the main hormones acting during this phase have been identified, there is no consensus terminology and some concepts are not clearly defined and are often misunderstood. This review covers the main aspects of early berry development, giving emphasis in the most relevant reproductive, morphological and physiological events, and taking into consideration the current knowledge regarding gene expression during this stage. This review aims to contribute to a better understanding of initial fruit formation in grapevine, proposing consensus terminology and a comprehensive understanding of this relevant topic.

INTRODUCTION

Grapevine berries are non-climacteric fleshy fruits that undergo a double-sigmoidal growth pattern, in which three phases can be distinguished [1]. Phase I is characterized by active growth of the fleshy tissue; phase II is a slow growth period; and phase III, when the ripening process occurs, is characterized by an important size increase due to water accumulation, according to Coombe and Hale, 1973.

Much effort has been done in order to understand the processes that occur during phase II and III, which are related to important agronomic traits such as color and sugar content. In contrast, phase I, when berry formation occurs, remains poorly characterized. During phase I sigmoidal growth takes place [1] and three periods can be distinguished: an initial period of accelerated growth, a second period of linear growth and a final period of decelerated growth. The initial accelerated phase I period, which starts at pollination, comprises the first 2 to 3 weeks of berry development, and flower-to-fruit transition (also known as fruit set) takes place. During this period berries increase their size several times and nearly final cell number per berry is established, since about 75% of the total DNA of the berry has already accumulated at this point [2]. Additionally, the number of berries per bunch is defined, since berry abscission occurs mainly at this stage [3].

Given the large amount of processes associated to rapid growth promotion, this period should be highly regulated. This idea is supported by the ample and drastic changes in the concentration of several hormones, such as auxin, gibberellins and cytokinins [4, 5, 6, 7]. On the other hand, the substantial variations in the levels of senescence associated hormones, such

as abscisic acid (ABA) and ethylene around fruit set [8, 5, 7] suggesting that abscission has to be fine-tuned in order to establish final berry number.

Our understanding of this period at the molecular level is scarce; however, as omics research is starting, it could shed light in the regulation of processes related to berry formation. Hence, prior to a more exhaustive characterization, it is important to define landmarks corresponding to reproductive, morphological and physiological events, in order to have a consensus terminology and a clear picture of this period. So, the aim of this review is to establish a detailed chronology, from post-pollination to fruit set in grapevine.

Reproductive landmarks

When we think about the beginning of berry development the key concept is receptivity, which is part of a more complex, named anthesis. Anthesis is a vague word despite its importance as the zero point of grapevine reproductive development. It implies that female organs are receptive to pollination and male organs are ready to deliver mature pollen. It has been reported that around anthesis, a drop of sugar solution covers the stigma, but no other morphological features associated with this receptivity state have been described in detail in grapevine [9].

Variations in flower morphology can be used to recognize the moment of flower receptivity. The elongation of flower style and thickening of the stigma, which acquires an open mouth-form, allows us to visually identify when anthesis is occurring and they are indicative of female receptivity (Figure 1). On the other hand, stamens, which emulate a spring that pushes up the fused petals or flower cap exposing the pistil, acquire an expanded aspect at anthesis

(Figure 1a). These changes are easily visible when flowers have been emasculated, a procedure in which the flower caps are manually removed. These morphological features plus the drop upon the stigma are important cues indicating that fruit development is at zero point or, more precisely, at zero days post anthesis (0 DPA). However, anthesis concept is difficult to apply in the vineyard, since flowers are in different developmental states within a bunch and it is not always possible to observe the reproductive structures which are covered by the flower cap. Occasionally, little bunches or arms of a bunch are fully synchronized (Figure 1b), but this is not the general rule. Furthermore, as anthesis is dependent on temperature, bunches from the same plant can be at different receptivity states due to differential sunlight exposure. For this reason, it is much more appropriate to use other conventions in order to determine the beginning of berry development. One possibility is to estimate the number of open flowers (without flower cap) in a given bunch and define zero point as a percentage of flowering or percentage of cap-fall. This time point is named 0 days after flowering (0 DAF). Another useful nomenclature is based on the establishment of an artificial reference. For example, it is possible to remove flower caps and stamens and hand pollinate pistils, thus defining zero point as zero days post pollination (0 DPP). Finally, zero point has also been set as zero days post emasculation (0 DAE). All these methods are valid, but care must be taken in order to establish which one is more appropriate to adopt depending on the experiment and cultivar.

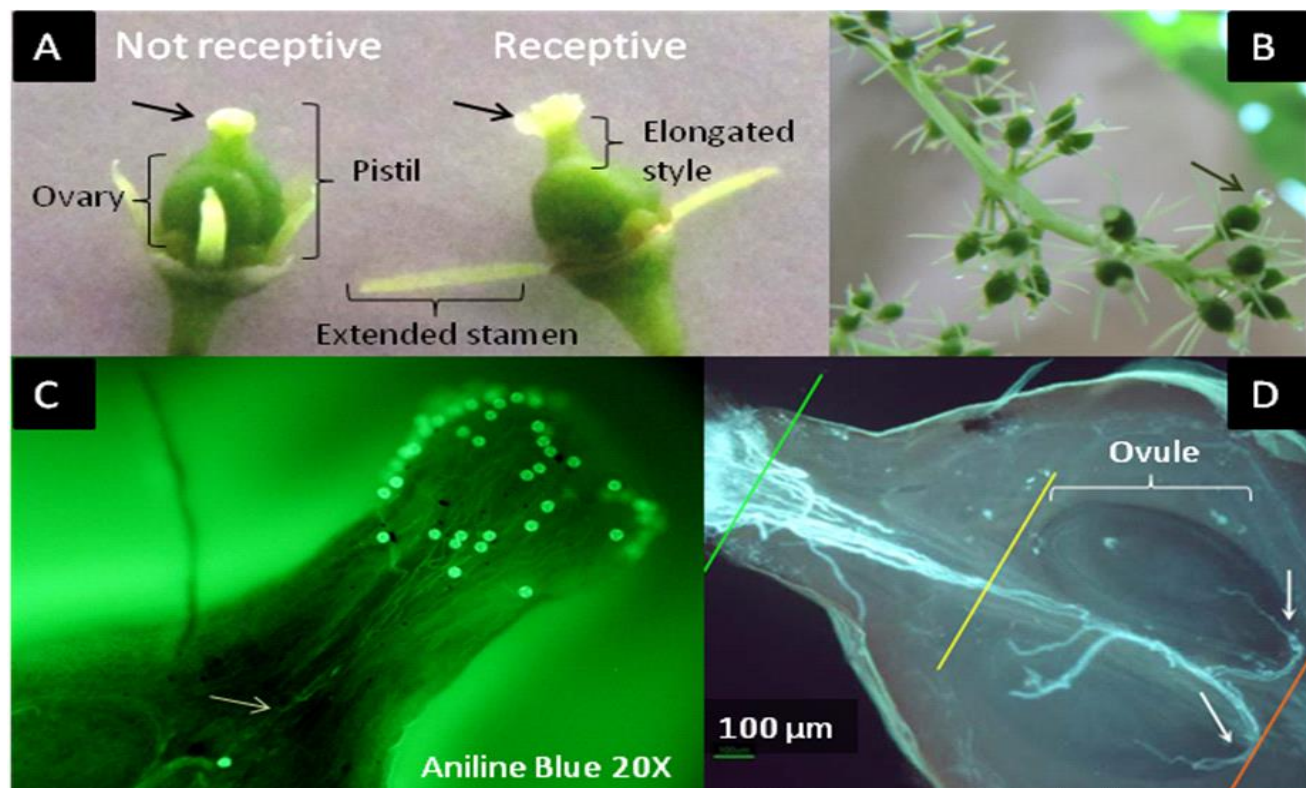


Figure 1: Reproductive traits and events occurring shortly after pollination at anthesis.

(A) Receptive versus non receptive flower. Both flowers are emasculated (removed anthers and flower cap). Arrows show differences observed in the stigma between both flowers, where the receptive one present a more expanded and moisture stigma. Also the filaments are different: in non receptive flowers they are short, whereas in receptive flowers they are fully expanded. (B) Fully synchronized arm of an emasculated bunch. Note that the stamens are fully expanded and there is a drop upon each pistil (pointed by an arrow). (C) Callose present in pollen grains revealed by aniline blue staining and UV microscopy. Pollen germination upon stigma and growth through the style is observed. Arrow indicates the growing pollinic tube. (D) The same technique allows visualizing the penetration of pollen tubes into the ovules, in their way to the megagametophyte, so it is possible to establish when fertilization occurs. Colored lines separate the flower in segments: stigma, style and end of the ovary. Arrows indicate pollinic tubes reaching the ovules. Images in (D) were kindly provided by Dr. Mardi Longbottom (University of Adelaide, Australia).

A clear definition of zero point allows to establish a timeline for fruit development, and relevant reproductive events can be set accordingly. Therefore, the first event of such timeline is pollen germination, which occurs soon after pollination at anthesis (Figure 1c). Later pollen tubes grow through the style until they reach at least one of the four ovules of the flower pistil (Figure 1d). Based on pollen tube growth tracing (Figure 1d), it has been established that fertilization of the ovule takes place between 2 to 3 DPP (Dr. Mardi Longbottom, personal communication). The former is in agreement with the expression of the grape embryonic marker *Leafy Cotyledon 1* (*VvL1L*, [10]), which has been detected in Red Globe cultivar as early as 2 DPP (Figure 2). Once fertilization occurs, first zygotic divisions take place only around 2 to 3 weeks after flowering, as summarized previously by Pratt, 1971 [9]. Hence, the beginning of embryo development is quite displaced in relation to the rapid fruit growth period, considering that the exponential growth is recorded within the first 2 to 3 weeks of berry development. This is important to point out, since the role of embryo in triggering fruit set still is matter of considerable discussion. Fertilization *per se* could be a signal influencing fruit growth, so it would be interesting to evaluate the early effect of fertilization, soon after pollen tubes reach the ovules.

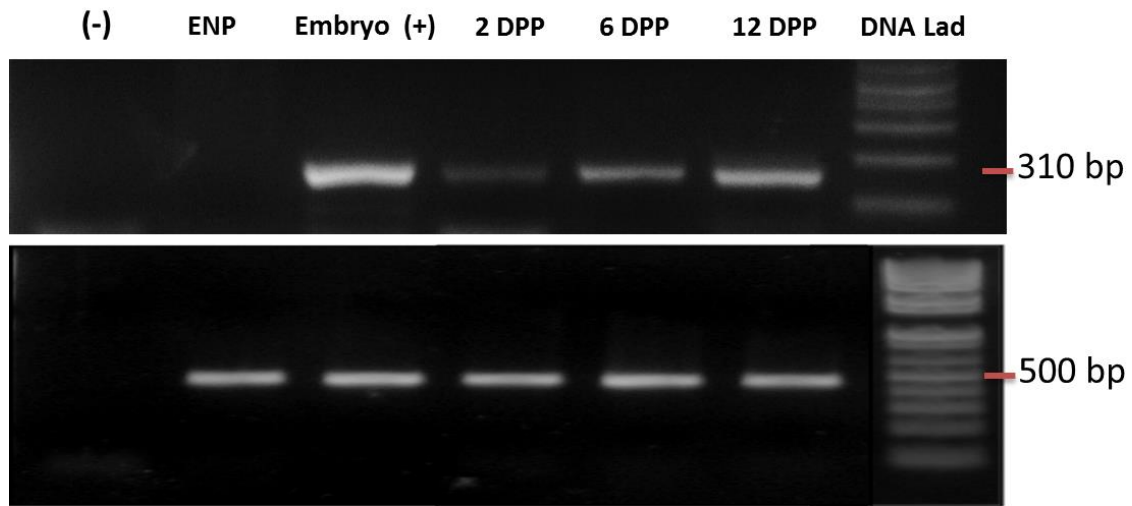


Figure 2: Expression of a fertilization marker during initial development.

Agarose gel showing the expression of the grape embryonic marker *Leafy Cotyledon 1* (*VvL1L*) [10] in Red Globe cultivar at 2, 6 and 12 DPP by RT-PCR. Embryo is the positive control for *VvL1L* expression (310 bp amplicon); ENP, emasculated not pollinated, is an unpollinated flower sample and corresponds to the negative control. Lower part: GAPDH constitutive expression (500 bp amplicon).

Morphological landmarks

Flower-to-berry conversion due to abrupt changes at the morphological level is another key concept of the accelerated growth period of phase I. This is related to the activation of different developmental programs, such as senescence of flower structures and promotion of cell division and cell enlargement in the flower ovary. Therefore, it is important to define when fruit set occurs, since is the moment when berries increase their size several times and acquire their final fruit shape. In agreement with the idea of conversion, fruit set has been defined as “the changeover from the static condition of the ovary to the rapidly growing condition of the young fruit” [11]. A useful way to quantitatively define fruit set is to measure berry volume or weight, and consider it as the point at which a substantial change in the slope of the volume/weight versus time graph occurs. This method allowed us to define fruit set at 17 DAF in the Autumn Royal seedless cultivar (Figure 3). In a similar way, it is also possible to plot the thickness increase of the internal mesocarp, which is the tissue from the flesh will originate and achieves the greatest size change (Figure 4a). It is worth to mention that fruit set does not necessary coincide with the cell multiplication peak occurring the first days after pollination, which has been estimated based on total DNA content measurements in Shiraz berries [2]. Surprisingly, at 5 DAF 25% of the total DNA has already accumulated, indicating that this is a period of intense cell division. From 5 DAF to 35 DAF cell multiplication declines and cell enlargement accounts for the following increase in berry size. Beside the DNA measurement approach, it is also possible to directly measure cell multiplication by cell counting of internal mesocarp (Figure 4b). However, cell division is not representative of fruit set. As shown by Ojeda *et al.*, 1999 [2], between flowering and 5 DAF a transition from a low dividing tissue to an active dividing tissue takes place. Nevertheless, at 5 DAF the fruitlet is

small and still looks like a flower. Therefore, cell division and cell enlargement are required to achieve fruit set around the second week of development. It is also important to consider variations in growth between cultivars, thus fruit set for each cultivar should be established. For instance, we have determined that the seedless Autumn Royal cultivar fruit set occurs at 17 DAF while in the seeded Red Globe cultivar occurs at 12 DPP (Figure 3).

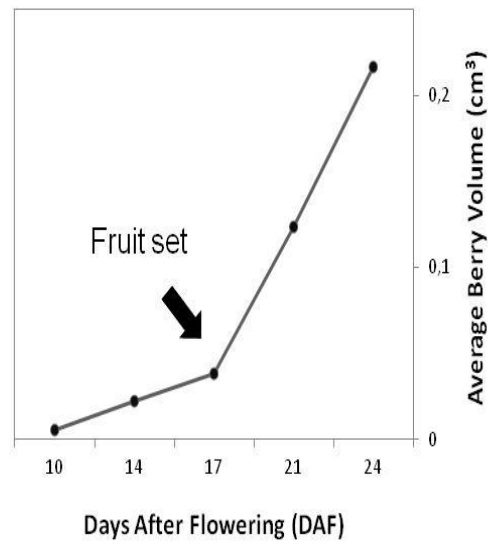


Figure 3: Definition of fruitset by changes in berry volume during initial development.

Berry volume was recorded between 10 and 24 DAF in Autumn Royal cultivar. An arrow indicates the moment when the slope changes, setting the fruit set time of this cultivar at 17 DAF.

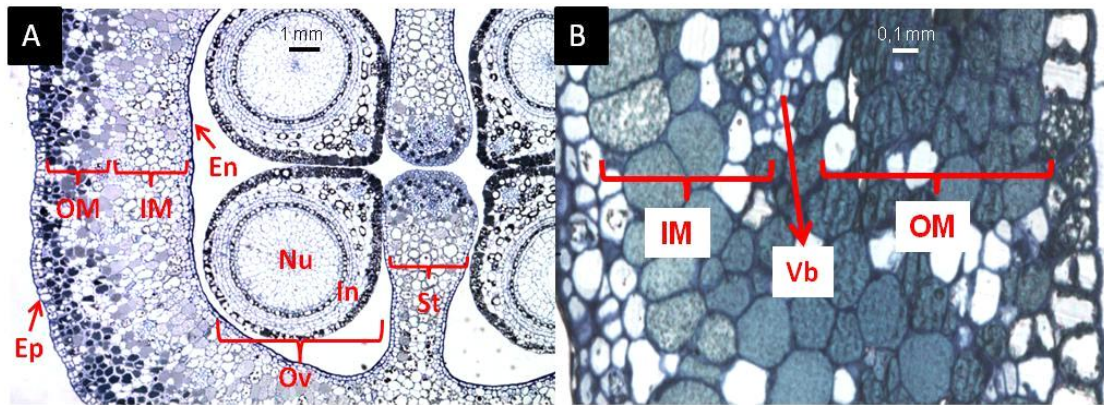


Figure 4: Grapevine immature berry seen by light microscopy.

(A) Female structures at 0 DPA: Pericarp, which is composed by an epidermis named epicarp (Ep), an outer mesocarp (OM), an internal mesocarp (IM) and an inner epidermis called endocarp (En), surrounds four ovules (Ov), each one able to originate a seed (Pratt, 1971). Berry skin is originated from the epicarp and some cells of the outer mesocarp, while flesh is originated from the internal mesocarp plus the endocarp, according to [9]. Internal mesocarp size can be measured throughout development since this is the tissue that attains the greatest size changes. (B) Vascular bundles (Vb) are regularly positioned between internal an outer mesocarp. Cell counting of the internal mesocarp at different time points allows to estimate when the peak in cell multiplication occurs. In, integuments; Nu, nucella; St, Septum.

Hormonal regulation during early berry development

One of the most important physiological events occurring between pollination and fruit set is related to growth regulation achieved by different hormones. This regulation is not only associated with growth promotion but also with senescence inhibition in the fruitlet, as several hormones change their content and regulate initial berry development, controlling respiration and photosynthesis, among other physiological parameters [12, 13]. In grapevine, fruit initiation is achieved mainly by the hormones auxin and gibberellin. The role of these growth promoters was investigated by Weaver and McCune [14] in the sixties, who applied either the synthetic auxin 4-chlorophenoxy-acetic acid (4-CPA), or the bioactive gibberellin GA₃, to emasculated flowers of Tokay cultivar. Both treatments promoted berry growth with slight differences in berry size compared to unemasculated control [14]. More recently, it has been shown that GA₃ or IAA treatments are able to induce setting of ovaries grown *in vitro* [15]. These results show that pollination or fertilization could be replaced by the addition of these growth promoters and also suggest that the growth-triggering program could be controlled by auxins and gibberellins separately. Around fruit set time, the importance of some hormones has been demonstrated. In the case of gibberellins and cytokinins, it has been shown that they produce berry size increase when applied to the flower bunches during the first two weeks after flowering [16, 17, 18]. Remarkably, the levels of these hormones change significantly fast along the growth period. Auxin content is high at pollination and fruit set and then declines to low levels at the end of phase I [4] while gibberellins and cytokinins concentrations are high around fruit set [6, 7 respectively]. However, a recent work showed that bioactive gibberellins GA₁ and GA₄ were present at high levels at anthesis, and decreased afterwards [19]. The biological function of other hormones that change their levels at this

stage is not completely understood. For instance, a role of brassinosteroids in parthenocarpic fruit growth promotion has been reported in cucumber [20], and as they are present at high levels prior and at fruit set in developing grapevine fruits [21], they could be controlling berry growth. Likewise, ABA levels are high around fruit set [5, 7], and possibly regulate berry abscission. Ethylene could also be involved in berry abscission, since its levels are high at fruit set [8].

To our knowledge, there is a lack of studies about grapevine physiology at this initial stage of fruit development, specifically regarding water relations, photosynthesis and respiration, among others. Coombe [22] has summarized the findings on this topic showing that water needed for cell expansion during the first weeks of development derives from both xylem and phloem transport into the berry. Beside these studies, there is practically no research concerning berry physiology during initial development. In summary, there is information about the content of several hormones in the early stages of berry development, whose abrupt changes suggest that they could be regulating several physiological processes, thus allowing growth. All landmarks described above are summarized in Figure 5.

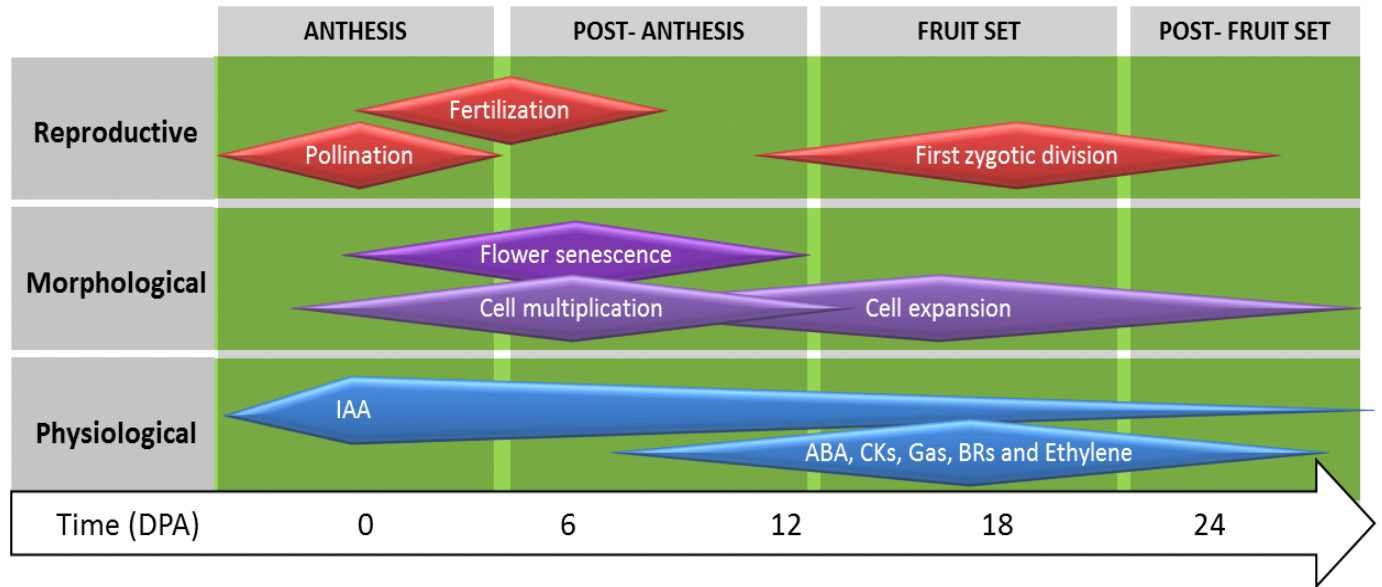


Figure 5: Main features defining early berry development in grapevine.

The scheme represents developmental changes of a complete bunch (*i. e.*, a population of berries) so the reproductive, morphological and physiological landmarks depicted occur within a period of time. The middle point of an anthesis period is fixed as zero. Anthesis, post-anthesis, fruit set and post-fruit periods are shown. Diamonds represent events and/ or hormone content variations. Cell multiplication and enlargement occur mainly in the internal mesocarp. Changes in other physiological events are not shown. The scheme is referential and timing depends on the cultivar. ABA, abscisic acid; CKs, cytokinins; BRs, brassinosteroids (castasterone); DPA, days post anthesis; GAs, gibberellins; IAA, indole-3-acetic acid. This summary derives from data from different publications [4, 5, 6, 19, 21, 25, 27].

Genetic landmarks: the beginning?

Initial berry development in grapevine has been poorly described at the gene expression level. In 2006 Fernández *et al.*, [23] described a natural grapevine mutant, called “Fleshless Berry” (*flb*), in which the berries did not develop the internal mesocarp tissue, so the berries practically did not present pulp. Global gene expression analysis using microarrays and SSH approach between wild type and *flb* mutants during the first stages of pericarp development were conducted and the expression of selected transcription factors that may be involved in flesh morphogenesis, such as *VvBURP1*, *VvHB13*, *VvSP2* and others was evaluated. Differences in the expression pattern of these genes between the wild type and the *flb* mutant were detected, thus some of these transcription factors may be involved in mesocarp development [24]. This work has provided an insight into which some genes may be involved in initial berry development. Recently, it was shown that pollination/fertilization stimulus is involved in the regulation of *VvHB13* transcript abundance, since it was differentially expressed in berries of pollination/non pollination treatments of emasculated grapevine flowers [25]. So, pollination/fertilization landmarks depicted in Figure 5 are linked to the expression of this gene, which could have an important role in flesh morphogenesis. As the homeobox family has been related to tissue morphogenesis among other processes [26], it would be interesting to evaluate the importance of the homeobox transcription factors during this developmental stage in grapevine.

The expression of hormone related genes has also been investigated. Transcript levels of a gene coding for a protein of the first step of auxin biosynthesis, anthranilate synthase subunit 1, ASB1, was found to be induced at 13 DAE (which corresponds to 6 DPP) when compared

to emasculated non pollinated flowers, thus correlating with higher auxin levels after pollination [25]. In this work also genes related to gibberellin and cytokinin biosynthesis presented differential expression between pollinated/fertilized and non pollinated flowers. Thus, pollination and fertilization generated changes in hormone biosynthetic gene expression that may account for the subsequent variation in hormone levels.

Recently, it has been shown how quickly pollination exerts its effect on gene expression related to hormone biosynthesis. Only 4 hours after pollination/non-pollination treatments were necessary to detect differences in the transcripts abundance of genes coding for ABA and gibberellin biosynthetic enzymes [27].

In the future, it would be interesting to assess how pollination and fertilization separately affect the generation of signals needed to achieve fruitset. Also, it is still unknown how berry tissues contribute to hormone synthesis. For instance, is it all being synthesized in the ovary wall? This and many other questions remain to be answered.

Figure 6 shows changes in the expression pattern of putative *VvCDK* and *VvCYC* transcripts from 0 to 12 DPP in the Red Globe cultivar. These genes encode putative cell cycle related proteins and variations in their transcript abundance are in accordance to the landmarks previously defined, such as the cell multiplication peak (Figure 5). In fact, high levels of *VvCDK* and *VvCYC* transcripts observed at 6 DPP correlate with the peak in DNA accumulation occurring at 5 DAF, as previously reported in Shiraz cultivar [2].

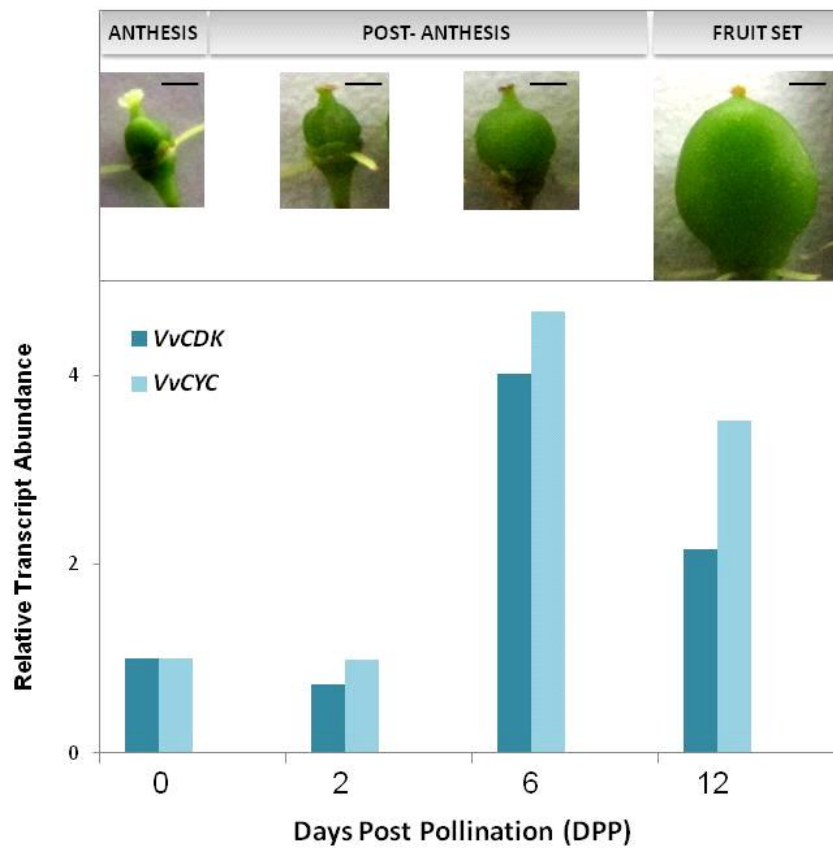


Figure 6: Transcript abundance changes of putative cell cycle related genes during initial grapevine berry development.

Red Globe flowers were emasculated, manually pollinated and bunches covered with paper bags in order to avoid contact with other pollen sources. (A) Representative pictures of each time point illustrate flower-to-berry size and morphology changes. (B) Relative abundance of *VvCDK* and *VvCYC* transcripts, coding for putative cell cycle proteins, at different time points after pollination. Bars = 20 mm. Transcript abundance is indicated relative to *VvUBI1*.

CONCLUSIONS

As grapevine is one of the most cultivated species in the world because of its fruit, it is crucial to understand the morphological and physiological aspects of berry development. In particular, initial development is a critical period since important features such as berry size and number are defined. Hence, improving our understanding of the events occurring at this period is needed in order to correctly interpret new findings. In line with that idea, as grapevine genome sequence is available since 2007 and omics technologies are starting to be massively used, complete understanding of the processes occurring during initial berry development is mandatory to interpret large scale sequencing information. To our knowledge pollination/fertilization signals, cell division and cell enlargement changes and growth regulation mediated by hormones, are the main events occurring during this stage, defining time periods with characteristic transcriptomic and metabolomic profiles. This review pretends to be a reference for future investigation focused on this exciting period of grapevine berry development.

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Chapter II

Problem Statement: Hypothesis and Objectives

As grapevine berry is very important, both economically as well as a study model, the Berry development has obtained considerable attention during the past few years. However, information about the first two weeks of development is very scarce. In tomato, this stage of development has been more investigated, due to the importance of fruitset in yield. Pollination, fertilization and fruitset are the most sensible stages of tomato fruit development, and stresses like cold and drought can cause production losses as high as 70%. This also happens in other species, and highlights the importance to obtain further information and understand the occurring processes in grapevine.

During the early steps of fruit development processes decisive for a seeded fruit to develop take place. In grapevine it is known that pollination triggers changes in gene expression as early as four hours after pollination in hormone biosynthetic genes. Also, hormones as auxin, gibberellins, abscisic acid and ethylene change their levels after pollination and fertilization. Application of auxin or gibberellin, or both, in non-pollinated flowers induced its development into a fully formed berry. In other model species (*Arabidopsis* and tomato) auxin is the first hormone to change its levels after pollination, and by hormone crosstalk gibberellins and other hormones accumulate. These signals give rise to fruitset, also known as “the point of no return”, as it marks the moment where the flower will finally grow and become a fruit or not.

Although hormones have been measure at this stage of development in grapevine, each study has been performed on different cultivars and treatments. No information is available on how the main hormones behave in during the first two weeks of development.

Taking into consideration that:

- Hormones are crucial for fruitset to take place in grapevine
- Hormone biosynthetic gene expression is affected by pollination treatments.
- It is unknown if hormone-related genes are affected by pollination.
- A general hormone profile during the first two weeks of grapevine berry development is not available.

I propose the following hypothesis:

Grapevine fruitset achievement is regulated by changes in pollination-induced global gene expression that determine variations in gibberellin and indole-acetic acid levels.

The general objective of this work is:

To determine early changes in hormone levels and gene expression in response to them before and during fruitset, and to evaluate by means of chemical inhibitors the effect of hormones involved in this process.

And the specific objectives of this thesis are:

- 1.- To characterize at the morphological level fruit stages previous to fruitset and to analyze global gene expression in them.**
- 2.- To establish the main hormones present during early stages of berry development, and to determine the gene expression profile of hormone-biosynthetic genes of the studied hormones.**
- 3.- To evaluate the effect of hormone inhibitors on fruitset establishment.**

Chapter III

Transcriptomic and hormonal regulation in early berry development: from pollination to fruitset

**Publication submitted in October under the title “Transcriptomic and hormonal regulation in
early berry development: from pollination to fruitset”.**

Authors: Francisca Godoy, Nathalie Kühn, Mindy Muñoz, Germán Marchandon, Laurent Deluc,
Virginie Lauvergeat, Serge Delrot and Patricio Arce-Johnson.

Signaux transcriptomiques et hormonaux au cours du développement précoce de la baie: de la pollinisation à la nouaison

RÉSUMÉ

La vigne, *Vitis vinifera*, est l'une des espèces les plus cultivées dans le monde. Alors que les processus impliqués dans la maturation des baies de raisin ont été particulièrement étudiés, il existe très peu de données sur les premiers stades de formation du fruit. Or, pendant les deux premières semaines après la floraison, des événements majeurs ont lieu: pollinisation, fertilisation et nouaison, permettant de donner lieu à un fruit contenant des graines.

Dans ce travail, nous avons réalisé des analyses transcriptomiques et hormonales afin d'identifier les principaux facteurs affectant la nouaison. L'expression des gènes a été suivie avec la technologie RNAseq, à quatre dates entre la pollinisation et la nouaison. Les résultats ont révélé des modèles dynamiques transitoires d'expression pendant le développement. De façon intéressante, un nombre important de gènes est réprimé après la fécondation. Le profil hormonal a montré les gibbérellines comme les hormones majoritaires à l'anthèse, tandis que l'auxine, la *trans*-zéatine et l'ABA sont présents à des quantités supérieures à la nouaison.

Ces résultats permettent de proposer un nouveau modèle du développement précoce de la baie, différent de celui décrit chez la tomate et d'autres espèces modèles.

Finalement, l'utilisation d'inhibiteurs chimiques de la synthèse de gibbérellines et des réponses à l'auxine a montré que la division cellulaire ainsi que le développement du mésocarpe sont fortement affectés, ce qui démontre que ces deux hormones sont essentielles pour l'étape de nouaison chez la vigne.

L'ensemble des données du transcriptome et le profil hormonal fournissent pour la première fois des informations détaillées sur la nouaison et les stades précoces de développement de la baie chez la vigne.

ABSTRACT:

Grapevine, *Vitis vinifera*, is one of the most cultivated species in the world. Most research work has been centered on berry maturation, and little is known about early berry development, which comprises the first two weeks after flowering. During this stage key processes occur: pollination, fertilization and fruitset, which will give rise to a seeded fruit.

In this work we have performed global transcriptomic analyses and hormone profiling in order to elucidate the main factors affecting fruitset. RNA-seq analysis was performed at four time points between pollination and fruitset revealing transient dynamic patterns through development. Interestingly, an important number of genes were repressed after fertilization. Over-represented functional categories included photosynthesis, cell wall, cell cycle, hormones and transcription factors. Hormone profiling showed IAA and gibberellins as the main hormones present at anthesis, whereas *trans*-zeatin and ABA presented higher levels at fruitset. Also IAA presented higher levels at fruitset. These results may indicate a new model of early berry development, different from the one described in tomato and other model species.

In order to confirm the role of selected hormones in berry development, chemical inhibition of gibberellin biosynthesis and auxin responses studies showed that cell division as well as mesocarp development were highly affected, demonstrating that both hormones are critical for fruitset achievement in grapevine.

Altogether, transcriptome data set and hormone profiling provide for the first time a gene expression dynamic patterns that can be associated to hormone biosynthesis, and their effect on mesocarp growth during early berry development in grapevine. Photosynthesis, cell wall,

cell cycle, transcription factors and hormones are the main over-represented categories. Also, auxin and gibberellin, as well as the crosstalk that takes place between them, is crucial for fruitset establishment in grapevine.

1. INTRODUCTION

Grapevine is one of the most cultivated species in the world, reaching a planted surface of 7.6 million ha (Food and Agricultural Organization of the United Nations <http://apps.fao.org>). Grapevine berries are mainly used for wine making and fresh consumption. Investigations have been carried out in order to improve table grape berries (sugar content, caliber, among others), using molecular genetics and cross-breeding. Breeders need to perform initial agricultural management to obtain high yield in the field, such as hormone treatment, pruning and specific fruit harvesting time.

The grapevine fruit development has been thoroughly described: during the first phase, or phase I, the berry accumulates organic acids, and cellular division occurs. At the end of this phase the number of cells in the berry is defined. In the second phase, also known as lag phase, cell division stops, and the embryo matures completely. During the third phase sugars, anthocyanins and other secondary compounds accumulate (Coombe 1992, Deluc et al., 2007). Most of the investigations have been centered during the past years in phases II and III, mainly because during these stages all the compounds essential for grape berry organoleptic quality (sugars, organic acids and aromas) are synthesized. However, initial berry development is poorly understood despite the crucial processes that take place within it.

During the early stages of fruit development key processes must occur in order to obtain a fruit: pollination, fertilization and fruitset. At anthesis, while the flower stigma is receptive, pollination takes place. Fruitset has been described as a rapid ovary growth after pollination and fertilization take place (Coombe, 1960, Gillaspie et al., 1993). This stage marks the

decision to either abort or continue with the fruit development, and for this reason it has been studied in other species such as tomato and strawberry (Kang et al., 2013, Sun et al., Wang et al., 2009). Grapevine flowers are usually self-pollinated. Pollen tubes grow through the stigma, reach the ovules and fertilize it in approximately two to three days (depending on temperature). Fruitset takes place ten to fourteen days after pollination, depending on the cultivar. An interesting work by Fernandez et al., (2006) described a natural mutant, called Fleshless berry (*flb*), which presented its first phenotype as wrinkles in the ovary wall at anthesis. Later on, the fleshless berry mutant produced berries with an 80% of reduction in the flesh volume at ripening stage. This is an example that severe phenotypes can be observed when developmental anomalies occur as early as anthesis (Fernandez et al., 2007). Also, it has been described that the set phase is the most sensitive stage to changes due to internal and external factors during berry and seed development in crop species such as tomato (Ruan et al., 2012). In grapevine similar responses have been described during this stage (Keller 2010), and for this reasons initial berry development becomes an interesting topic of investigation.

Hormones are important players during this early development period, and their role has been specially studied in tomato (Ozga and Reinecke 2003, de Jong et al., 2009). In this specie it has been described that pollination initially triggers an increase in auxin levels in the ovary, which is in concordance to the high cellular division levels taking place after pollination and fertilization. Gibberellins start accumulating after pollination and fertilization. A crosstalk between auxins and gibberellins has been described during initial berry development, where auxins induce the expression of GA 20-oxidases and GA 3-oxidases in tomato, both gene

families related to gibberellin biosynthesis (Serrani et al., 2008). Also, transgenic tomato lines silenced for Indole Acetic Acid 9 (IAA9), a gene that encodes an Aux/IAA protein, presented parthenocarpic fruits. In pollination-dependent fruitset a high number of transcription factors were differentially expressed. Additionally, when expression of genes involved in hormone responses was analyzed in pollination-dependent fruitset, auxins and ethylene were the most predominant categories (Wang et al., 2009). All the fruitset regulators described so far act as repressors, that is, when this genes are downregulated, fruitset occurs in absence of pollination and fertilization. This indicates that the genetic program which triggers the ovary growth is tightly controlled (Goetz et al., 2006, Lora et al., 2011, Wang et al., 2005). Also, several global gene expression assays have been performed in tomato and other species in order to determine key genes related to pollination, fertilization and parthenocarpy (Wang 2009, Jiang et al., 2013, Kang et al., 2013).

However, little is known about the hormone contents or global gene expression during this stage in grapevine. Weaver and McCune (1962) applied 4-chlorophenoxy-acetic acid (4-CPA) or GA₃ to emasculated grapevine flowers, resulting in berry growth comparable to pollination-induced berries. Also, gibberellin or auxin treatments to *in-vitro* grown ovaries promoted their setting (Shiozaki et al., 1995). Both works demonstrate that these growth promoters can replace the pollination signal and trigger fruitset in grapevine, either together or separately. As pollination is the first process that afterwards triggers fruitset, it is believed that IAA or GA treatments replace the pollination signaling. Also, Casanova et al. (2006) demonstrated that the application of GA₃ at early stages of development produce a 50-90% increase of fresh

berry weight. Hence, hormones at this stage not only trigger fruitset, but also influence the subsequent berry development. Previous reports have described high auxin levels at anthesis that decrease afterwards, and low levels of gibberellins at anthesis, that increase significantly (Böttcher et al., 2010, Pérez et al., 2000, Zhang et al., 2003). However, recent studies indicate different auxin and gibberellin accumulation patterns during early berry development (Symons et al., 2006, Giacomelli et al., 2013). ABA and ethylene presented high levels at fruitset and may be related to berry abscission taking place at this stage (Inaba et al., 1976, Hilt and Bessis, 2003; Zhang et al., 2003). Still, scarce information is available regarding the molecular mechanisms during this stage. Dauelsberg et al. (2011) evaluated the expression of hormone related genes such as Anthranilate subunit B 1 (ASB1), GA-20ox, and isopentenyl transferase (IPT) for auxin, gibberellin and cytokinin biosynthesis, respectively, in *Vitis vinifera* cv. Red Globe fruits. It was mainly showed that all genes presented differential expression in pollinated flowers compared to unpollinated controls. This suggests that pollination and fertilization triggered expression changes in hormone biosynthetic gene expression that activate, at least in part, fruitset. Still, more information is needed to identify all components related to this developmental program initiation.

Today, a useful approach to study global gene expression in non-model species is RNA-seq. This technique is highly accurate; it detects rare transcripts and splicing variants, and also can help to improve gene annotation. In the specific case of initial stage of grapevine fruit development, this tool is very useful since we have scarce to none information of it and RNA-seq provides a complete picture of transcriptomic dynamics throughout this process. In this

work, a global gene transcription analysis using RNAseq technology was performed in order to characterize the initial stages of grapevine berry development. Additionally, detailed hormone profiles were obtained during at this stage of berry development. Both approaches can provide an integrated view of the regulatory mechanisms controlling flower to fruit transition in grapevine.

The aim of this work is to describe the particularities of fruitset achievement in grapevine, a model species in which the fruitset developmental program may differ from what has been previously described in tomato and *Arabidopsis*. The purpose is to understand the contribution of transcription factors, structural genes and hormones during initial berry development, from pollination to fruitset, where the embryo is at the torpedo stage. Our study showed that genes related to both hormone biosynthesis and response, biotic and abiotic stress, and transcription factors from a wide variety of families were differentially expressed throughout early berry development, presenting dynamic patterns. Given the crucial role of growth regulators during early berry development, we also performed a hormone profile, finding that gibberellin, rather than auxin, is the first hormone that may trigger the developmental program that will end in fruitset achievement. Chemical inhibition of gibberellin biosynthesis and auxin responses in pollinated flowers confirmed the requirement of at least one of these hormones to trigger the fruitset developmental program. To our knowledge, this is the first study that deepens into the effect of pollination and fertilization on gene transcription and hormone levels performed on grapevine. Results of this work are crucial to understand the mechanism of initial berry development, a process poorly described in grapevine so far.

2. MATERIALS AND METHODS

2.1 Flower emasculation, sampling and hormone inhibitor treatments of ovaries and fruits

Twelve *Vitis vinifera* var. Red Globe plants were selected from an experimental field in Curacaví Valley, Chile. Ten bunches with approximately 200 flowers each were used for each time-point. Flowers were carefully emasculated using tweezers at seven to ten days (green flower cap) before flower opening. Receptive emasculated flowers were hand-pollinated with pollen from the same variety and subsequently covered with a paper bag to avoid pollination by opened flowers nearby (Figure 1). Samples were collected at 0 (anthesis), 2 (post-pollination), 6 (post-fertilization) and 12 (fruitset) days after pollination (DAP), immediately frozen in liquid nitrogen and stored at -80°C.

In the case of hormone inhibitor treatments flowers were emasculated as described before. At anthesis flowers were pollinated, and one day after treated with Paclobutrazol or IAA-Trp (kindly provided by Dr Staswick, University of Nebraska, US) at a 20 μ M concentration. A mixture of lanoline: baseline (1:1) was used to apply the treatments. Four flower bunches from different plants were used per treatment.

2.2 Sample fixation and microscopy observation

Samples of 2, 6, 10 and 12 DAP were fixed in 5% glacial acetic acid, 3.7% formaldehyde and 50% ethanol for microscopy analysis. Afterwards, fixed samples were vacuum treated and

passed through an increasing ethanol series for complete tissue dehydration, then paraffin-embedded, cut into 6–8 μm sections (Johansen 1940) and stained with toluidine blue.

Images were obtained using a Nikon microscope Eclipse 80i, NIS Element software. Cell number per transverse section and mesocarp thickness were quantified with the open source software ImageJ® (Abràmoff et al, 2004). These parameters were measured in eight biological and two technical replicates per time point.

2.3 RNA extraction, cDNA synthesis and PCR analysis

RNA extraction was performed using the method described by Poupin et al., 2007. Briefly, total RNA was extracted from 200 mg of frozen tissue using the CTAB-Spermidine method. DNase treatments were achieved using Ambion® TURBO DNA-free™ DNase, following manufacturer's instructions. For cDNA synthesis, 1.5 μg of total RNA was reverse transcribed using SuperScript™ II reverse transcriptase (Invitrogen), according to the manufacturer's instructions: 1,5 μg of previously DNase-treated RNA were mixed with 50ng of random hexamers and 1 μl of dNTP mix (10 mM) in a final volume of 12 μl . Samples were incubated at 65°C for 5 min, and then transferred immediately to ice, and 4 μl of 5X First-strand buffer and 2 μl of 0.1 DTT (Invitrogen) were added. Samples were incubated 2 min at 25°C, then 1 μl of SuperScript II reverse transcriptase was added, and samples were incubated for another 10 min at 25°C, 50 min at 42°C and finally 15 min at 70°C.

PCR reactions were made in a final volume of 20 μl and Taq DNA polymerase from Invitrogen was used. Buffers and primer concentrations (200 pmoles each) were as

recommended by the supplier. After a denaturation step at 94°C for 3 min, 35 cycles of the following steps were performed: 30 seconds at 94°C (denaturation), 30 seconds at 55-57°C (hybridization) and 60 seconds per 1000 nucleotides at 72°C (extension). Then, a final elongation step (72°C) for 10 min was performed and samples were cooled down to 4°C. Samples were analyzed by agarose gel electrophoresis. Primer information is in Supplemental Table 1.



Figure 1: Emasculation and hand-pollination technique on *Vitis vinifera* cv. Red Globe flowers

(A) Flowers of *Vitis vinifera* cv. Red Globe were emasculated. Left: open flower with its anthers (non-emasculated). Right: flower after anther removal. (B) Approximately five to seven days after emasculation flowers were receptive to pollination (drop on the stigma, red arrow) and covered with a paper bag to avoid pollination from nearby flowers. (C) Receptive flowers were hand-pollinated and (D) samples at different time points were collected.

2.4 RNAseq analysis

Library construction was performed by MacroGen Inc. (Seoul, Korea) and paired-end sequenced using the Illumina HiSeq2000 platform. Reads were mapped to the grapevine reference genome (ftp://ftp.jgi-psf.org/pub/compugen/phytozome/v9.0/Vvinifera_annotation/) with TopHat 2.0.4 (Trapnell et al., 2009).

Differential gene expression between time points after pollination (0, 2, 6 and 12 DAP) was assessed using Cufflinks/Cuffdiff 2.0.2 (FDR 0.05) (Trapnell et al., 2010), obtaining significant FPKM values. A list of 2822 genes was obtained, from which a subset of 543 genes were in the sequential time-points. Genes that presented differential expression in at least one time-point (i.e. between T0-T2) were selected and included in the sublist. This list was used for subsequent analysis.

Gene Ontology (GO) categories were assigned by Blast2GO (Conesa et al., 2005) to the complete list (2822 genes). MIPS categories were assigned to the 543 sub-list of sequential time-points (<http://www.helmholtz-muenchen.de/en/ibis>).

For cluster creation the program Cluster 3.0 was used (Eisen y cols., 1998) with Pearson correlation (Cluster 3.0, <http://bonsai.ims.u-tokyo.ac.jp/mdehoon/software/cluster>). To obtain the expression profiles the program MeV 4.8.1 (MultiExperiment Viewer) (Saeed et al., 2003) was utilized (with the k-means method), and the program Treeview 1.1.6r2 for its visualization.

2.5 Quantitative comparison of gene expression

Fifteen genes related to hormone biosynthesis and response were selected for validation using Real Time RT-PCR with gene specific primers designed with Primer3plus (Rozen y Skaletsky 2000) (Table S1). Real time RT-PCR was performed as described by Poupin et al. (2007) using the Stratagen Mx3000P instrument. Relative gene expression calculations were conducted following the MxPro QPCR Software manufacturer's instructions: an accurate ratio between the expression of the gene of interest (GOI) and the housekeeping gene (UBI) was generated according to Eq. (1):

$$2^{-(\Delta Ct_{GOI-UBI})} \quad (1)$$

UBIQUITIN1 (TC53702, TGI database, VvGi5) and ACTIN (NCBI database XM_002282480.2) genes were used for normalization (Downey et al., 2003), obtaining similar results for both housekeeping genes. Gene expression levels were calibrated to the expression of the 0 DAP sample. All experiments were performed using three biological and three technical replicates.

2.6 Hormone measurements

Absciscic acid (ABA) was purchased from Sigma-Aldrich (Oakville, ON, Canada). Indole-3-acetic acid (IAA), IAA-aspartate (IAA-Asp), IAA-alanine (IAA-Ala), IAA-glutamic (IAA-Glu) GA₁, GA₃, GA₈ and *trans*-zeatin (tZ) were purchased from Olchemim Ltd., (Olomouc, Czech Republic). Auxin precursors Indol-3-pyruvic acid (IPyA) and Indol-3-acetamide (IAM) were purchased from Sigma. oxIAA, and oxIAA-Glu were kindly provided by Dr. Hisashi Miyagawa (Division of Applied Life Sciences, Graduate School of Agriculture, Kyoto

University, Japan). The internal standards used for each compound were: for ABA: d4-ABA, NRC-PBI, Saskatchewan, Canada; for tZ: d₅-tZ, Olchemim. Dr Miyagawa provided us with the next internal standards: for oxIAA: d₂-Ox-IAA; for oxIAA-Glu: d₂-oxIAA-Glu; for oxIAA-Asp: d₂-oxIAA. The following internal standards were purchased from Olchemim: for GA₁, GA₃ and GA₈ d₂-GA₁, d₂-GA₃ and d₂-GA₈, respectively; for IAA d₅-IAA; for IPyA d₅-IAA, for IAM d₅-IAA; for IAA-Glu d₆-IAA-Glu; for IAA-Asp d₆-IAA-Asp; for IAA-Trp d₆-IAA-Trp. Extraction method is described in Gouthu et al., 2013. Briefly, fifty milligrams of lyophilized tissue were extracted in 3 ml of extraction solvent (Methanol: Formic acid: Water, 15:1:4), and 100 µL of internal standard solution containing 20 ng of each standard was added. Hormone analysis were performed on a hybrid triple quadrupole/linear ion trap 4000 QTRAP LC-MS/MS instrument equipped with a Turbo V source (Applied Biosystems, USA), and analytical method used was LC–tandem mass spectrometry in multiple reaction monitoring mode (LC-MRM). This experiment was performed in collaboration with Laurent Deluc (Oregon State University, USA).

3. RESULTS:

3.1 Morphological changes during early berry development: mesocarp cell division and cell expansion.

Vitis vinifera cv. Red Globe flowers were emasculated and hand-pollinated when flowers were receptive to pollination by visual inspection. During anthesis, the stigma releases a sticky solution that retains and rehydrates the received pollen (Meneghetti et al., 2006). When flowers are emasculated, this solution takes the form of a drop at the end of the stigma, announcing anthesis. The selected time-points reflected the main processes taking place during early stages of development: 0 DAP corresponds to anthesis, 2 DAP to a post-pollination time, 6 DAP to a post-fertilization stage and finally, 12 DAP corresponds to fruitset. An important growth of the ovary wall is observed between 6 and 12 DAP (Figure 2 A) when representative samples of each time point were compared.

To examine in more detail the effect of pollination and fertilization in ovary development, individual flowers at different time points were analyzed by light microscopy. A representative cross-section of Red Globe flowers is presented in Figure 2B. As early as 2 DAP it is possible to differentiate the outer mesocarp (OM) from the inner mesocarp (IM), as the later presented lighter coloration with toluidine blue. These two structures are separated by the vascular bundles (VB). The outer mesocarp will give rise to the skin of the berry, and the inner mesocarp will originate the pulp. In this cultivar commonly four ovules (Ov) are observed in each flower, immersed in the loculus (LOC).

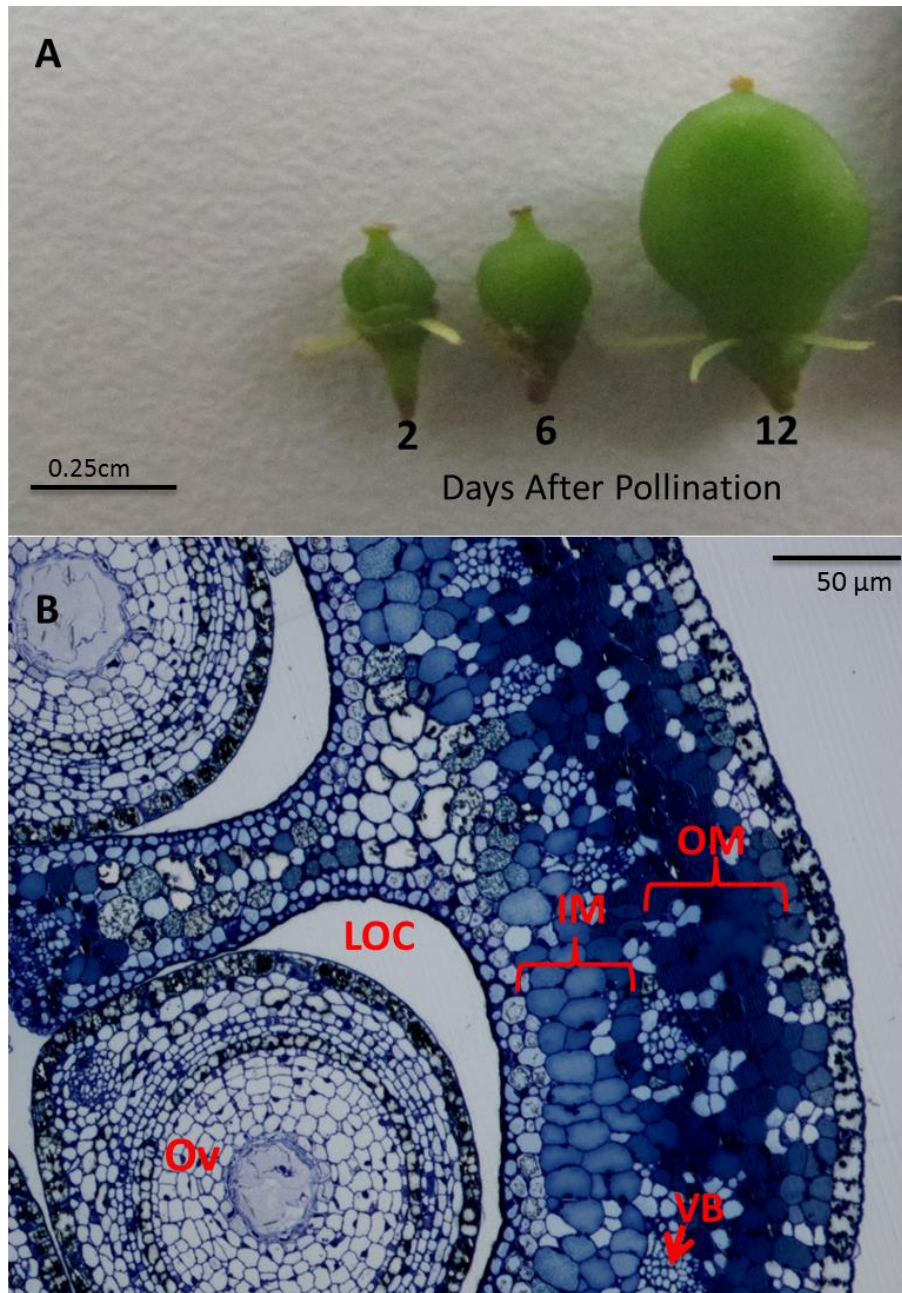
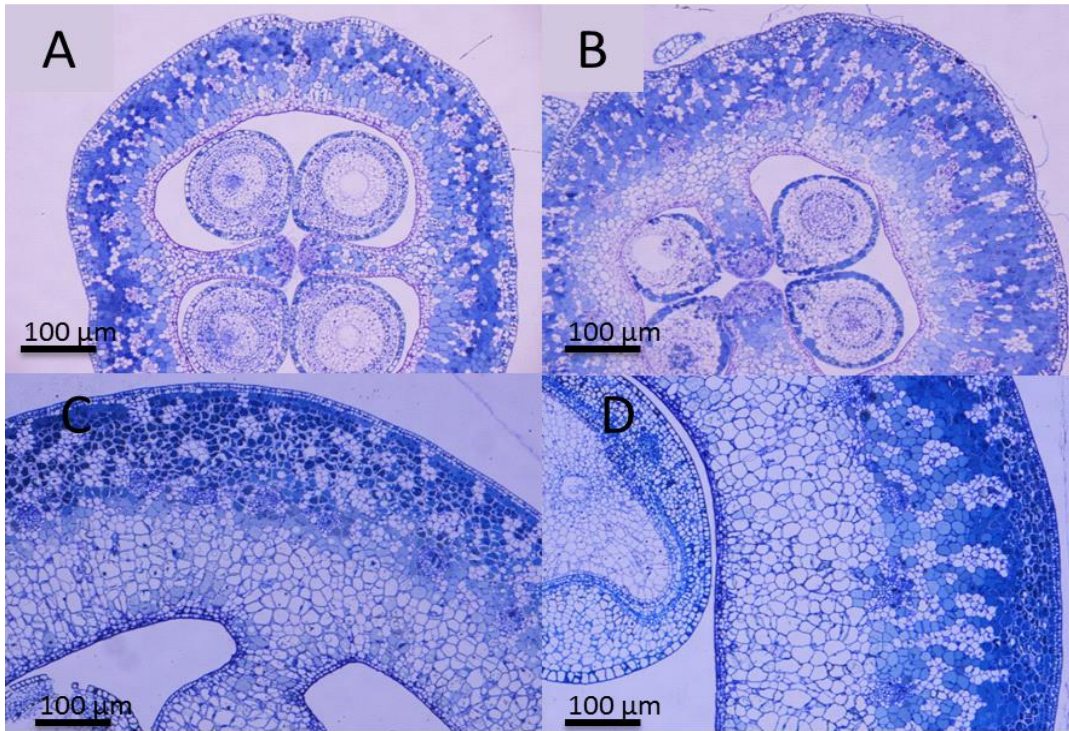


Figure 2: Effect of pollination/fertilization on fruit and mesocarp development in grapevine.

(A) Early berry morphology in grapevine cv. Red Globe. Representative samples at 2, 6 and 12 DAP, corresponding to post-pollination, post-fertilization and fruitset, respectively, are shown. A fast growth of the fruit is visible, specially between 6 and 12 DAP. (B) A representative cross-section from grapevine carpel/berry at 2 DAP. Light microscopy of outer and inner mesocarp cells, stained with Toluidin Blue. Ov: ovules, LOC, Loculus, OM: Outer mesocarp, IM: Inner mesocarp, VB: Vascular Bundles.

Given that flower size between 0 and 2 DAP did not change significantly (data not shown), an extra time point closer to fruitset was selected for further analyses. Cell number per transverse section and mesocarp thickness were measured at 2, 6, 10 and 12 DAP (Figure 3 A). Cell division was detected as early as 6 DAP, and increased steadily. On the other hand, mesocarp length significantly increased from 6 DAP onwards. Cell division cannot account for the mesocarp enlargement observed between 6 and 12 DAP, therefore also cell expansion is taking place during this stage. Inner mesocarp cells exhibited a pronounced expansion in comparison with the outer cell layer (Figure 3). Therefore, for fruitset to occur, cell division and cell expansion must take place.



E

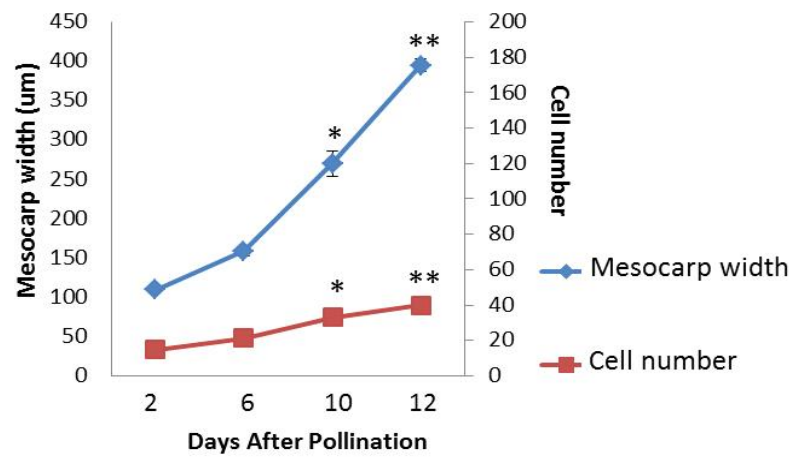


Figure 3: Changes in mesocarp morphology triggered by pollination/fertilization in grapevine

Mesocarp development during early berry development. (A) Mesocarp at 2 DAP. (B) Mesocarp at 6 DAP. (C) Mesocarp at 10 DAP. (D) Mesocarp at 12 DAP. (E) Mesocarp width measurement and mesocarp cell counting at different 2, 6, 10 and 12 DAP. One-way ANOVA analysis was performed and asterisks indicate statistically-significant differences between time-points. Bars indicate standard error. Scale bars: 100 μm .

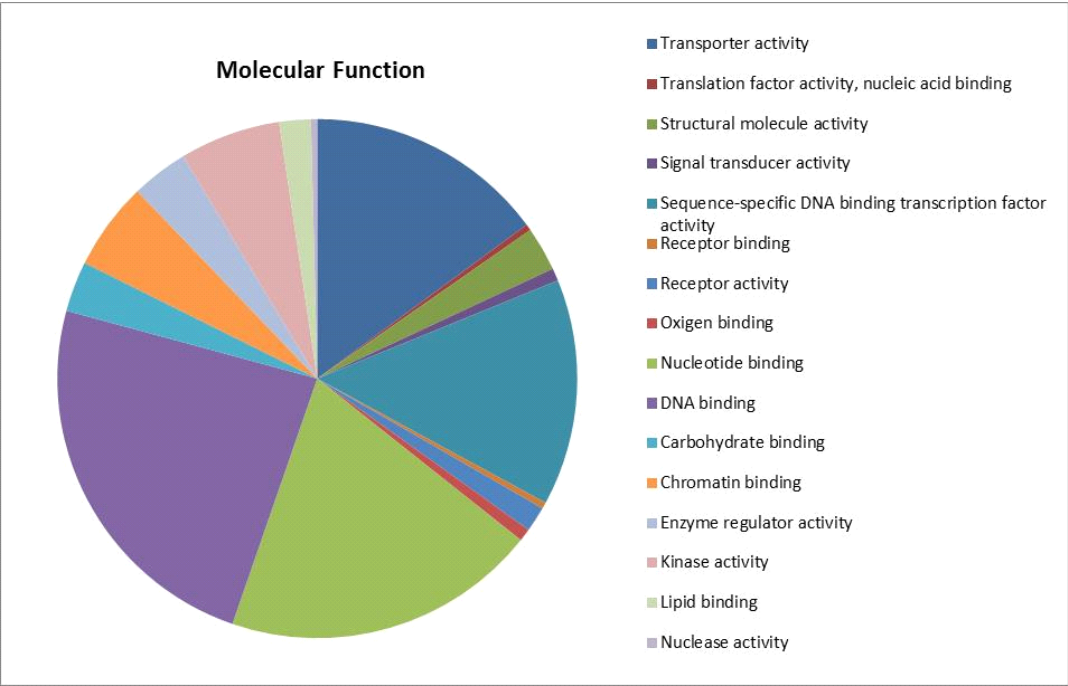
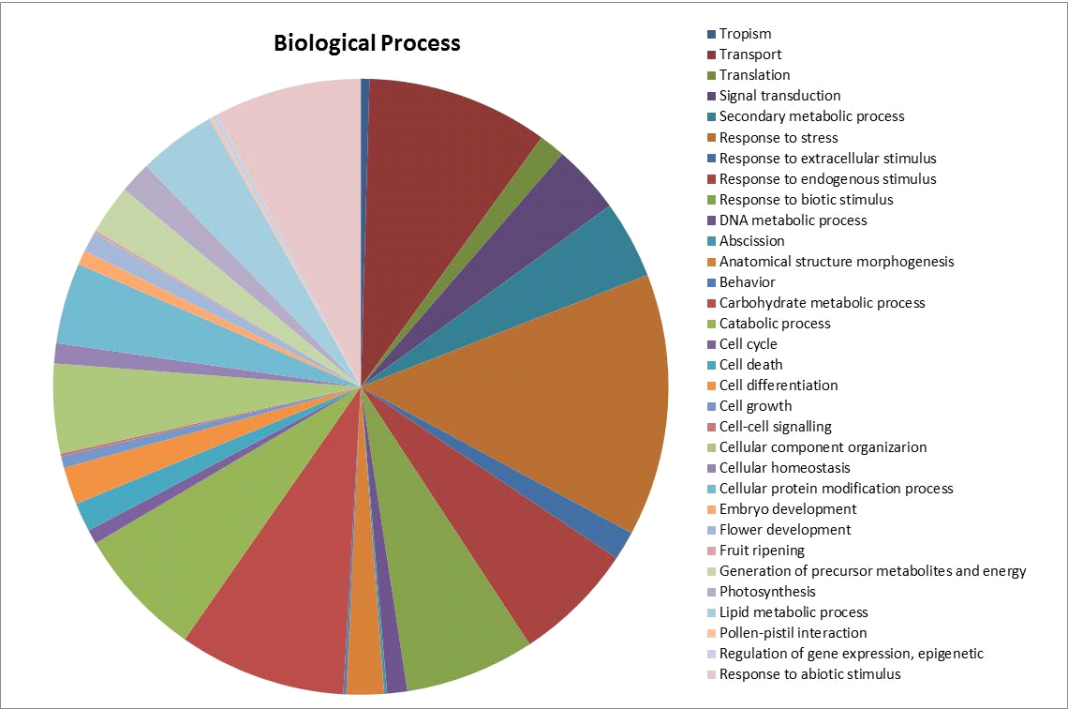
3.2 Global gene expression from pollination to fruitset: a dynamic process.

In order to understand the processes taking place in early fruit development, global gene expression analysis was assessed using RNA-seq technology at 0 (anthesis), 2 (post-pollination), 6 (post-fertilization) and 12 (fruitset) DAP. It is important to remark that, because the flowers were previously emasculated, sepals and stamens were not included, so the expression profiles obtained included inner and outer mesocarp, vascular bundles and embryo. Approximately 200 million reads were obtained for each time point. Reads that misaligned or had multiple matches were discarded, and the remaining sequences were aligned to the grapevine genome (sequence obtained from CRIBI Grape Genome (<http://genomes.cribi.unipd.it/grape/>)). From RNA-seq analysis a list of 2822 genes with differential expression (FDR 0.05) was obtained (Supplemental Table 2). In order to highlight the transcriptional changes related to pollination and fertilization necessities to achieve fruitset, only sequential time points were selected for further analysis, generating a sub-list of 543 genes (obtained with a FDR of 0.01). Sequential time points, that is, from 0 to 2 DAP, then 2 to 6 DAP, and from 6 to 12 DAP, were selected to have a better understanding of the progressive changes occurring naturally through berry development. The number of differentially expressed genes for T0-T2 was 88 (71 induced and 17 repressed), for T2-T6 269 (171 induced and 98 repressed) and finally for T6-T12 339 (69 induced and 270 repressed). As some of these genes are present at more than one time-point, the total number is 696. In this case, 153 genes were differentially expressed in more than one time-point.

Analysis of the major biological process present among the 543 differentially expressed genes (induced and repressed) using Blast2GO showed that the categories with more representation were “response to stress”, “transport”, “carbohydrate metabolic process”, “response to abiotic stimulus”, “response to biotic stimulus”, “catabolic process” and “response to endogenous stimulus” (Figure 4 A).

The main molecular functional categories found in the differentially expressed genes during initial berry development were “DNA binding”, “nucleotide binding”, “transporter activity” and “sequence-specific DNA binding transcription” (Figure 4 B).

Finally, cellular component categories were assigned by Blast2GO, and the main categories found were “plasma membrane”, “plastid”, “extracellular region” and “cell wall” (Figure 4 C).



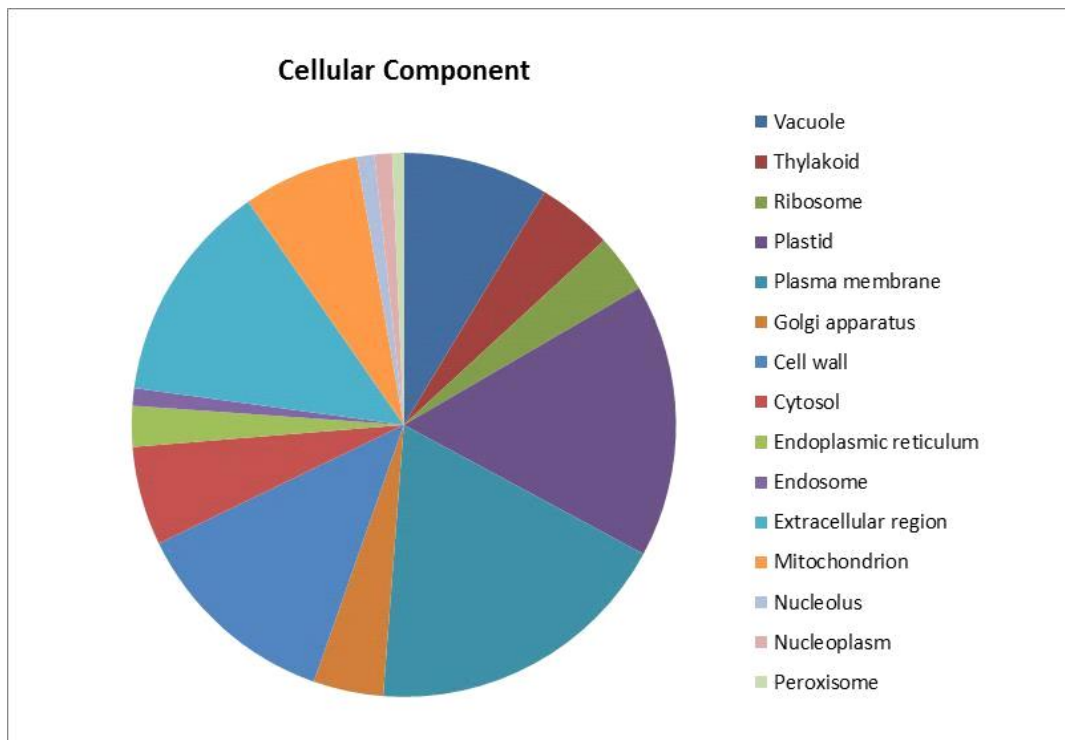


Figure 4: Gene Ontology distribution of differentially expressed genes found during sequential time-points of initial berry development.

GO annotations for differentially expressed genes during initial berry development in grapevine were assigned using Blast2GO. (A): Biological Process. (B) Molecular Function. (C) Cellular Component.

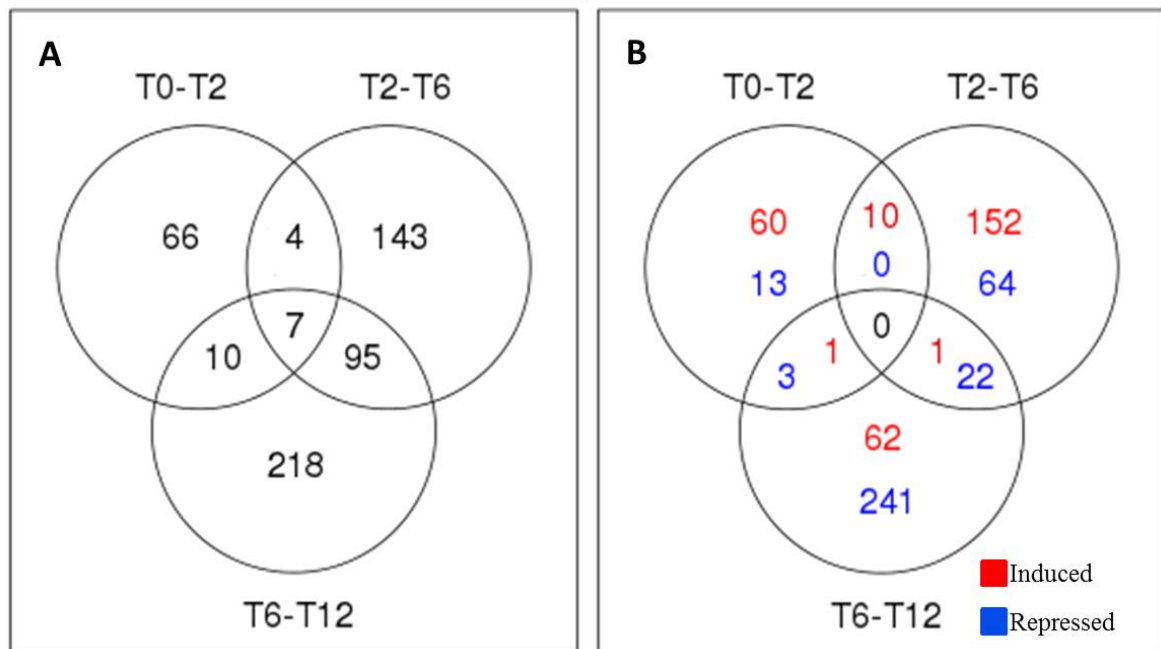


Figure 5: Venn diagrams of differentially expressed transcripts during early berry development in grapevine

Venn diagram showing the number of commonly and uniquely expressed genes during early stages of berry development at sequential time-points. (A) Total number of differentially expressed genes from pollination to fruitset. (B) Venn diagram showing the induced genes (red) and repressed genes (blue). Some genes are induced at one stage and repressed at another, giving a different pattern at the diagram.

A Venn diagram of this list (Figure 5) shows that 266 genes are repressed between 6 and 12 DAP. No common genes were found between these three sequential lists, but 4 were common between T0-T2 and T6-T12; also, 23 genes were common between T2-T6 and T6-T12. Finally, 10 genes were found to be induced in T0-T2 and T2-T6. The number of induced genes is higher than the repressed ones at early times of development (T0-T2) but this relation is reversed when comparing T6-T12, finding most genes repressed (266 repressed genes against 64 induced ones). This suggests that the early fruit development is a highly dynamic process.

To functionally categorize the differentially expressed genes, MIPS (Munich Information Center for Protein Sequences) terms were assigned (Figure 6).

It is possible to observe that the number of genes induced between anthesis and post-pollination (T0-T2, in blue) is higher than the number of repressed genes at the same period (depicted in green), and they are mainly in the categories “transcription”, “subcellular localization”, “storage protein”, “protein with binding function or cofactor requirement” and “metabolism”. This suggests a high regulation in genetic and metabolic activity at the initial stages of berry development. Between post-pollination and post-fertilization times (T2-T6) the induced genes (in orange) are predominantly in the categories “subcellular localization”, “storage protein”, “protein with binding function or cofactor requirement” and “metabolism”. The repressed genes during this period (in brown) are fewer in number but presented the same distribution. Finally, post-fertilization versus fruitset showed an interesting change: the number of induced genes (in yellow) is significantly lower than the number of repressed genes (in light blue). In both groups the genes are mainly in the same MIPS categories:

“transcription”, “subcellular localization”, “storage protein”, “protein with binding function or cofactor requirement”, “metabolism” and “energy”.

In summary, in the early stages of berry development (T0-T2) genes related to transcription factors, subcellular localization, protein storage and metabolism were induced. Similar groups of genes were found to be induced during the T2-T6 stages, and also genes related to energy and transport. The greatest gene repression was observed at T6-T12 stages, in which genes related to transcription factors, subcellular localization, protein storage, proteins with binding function, metabolism and energy were the most present.

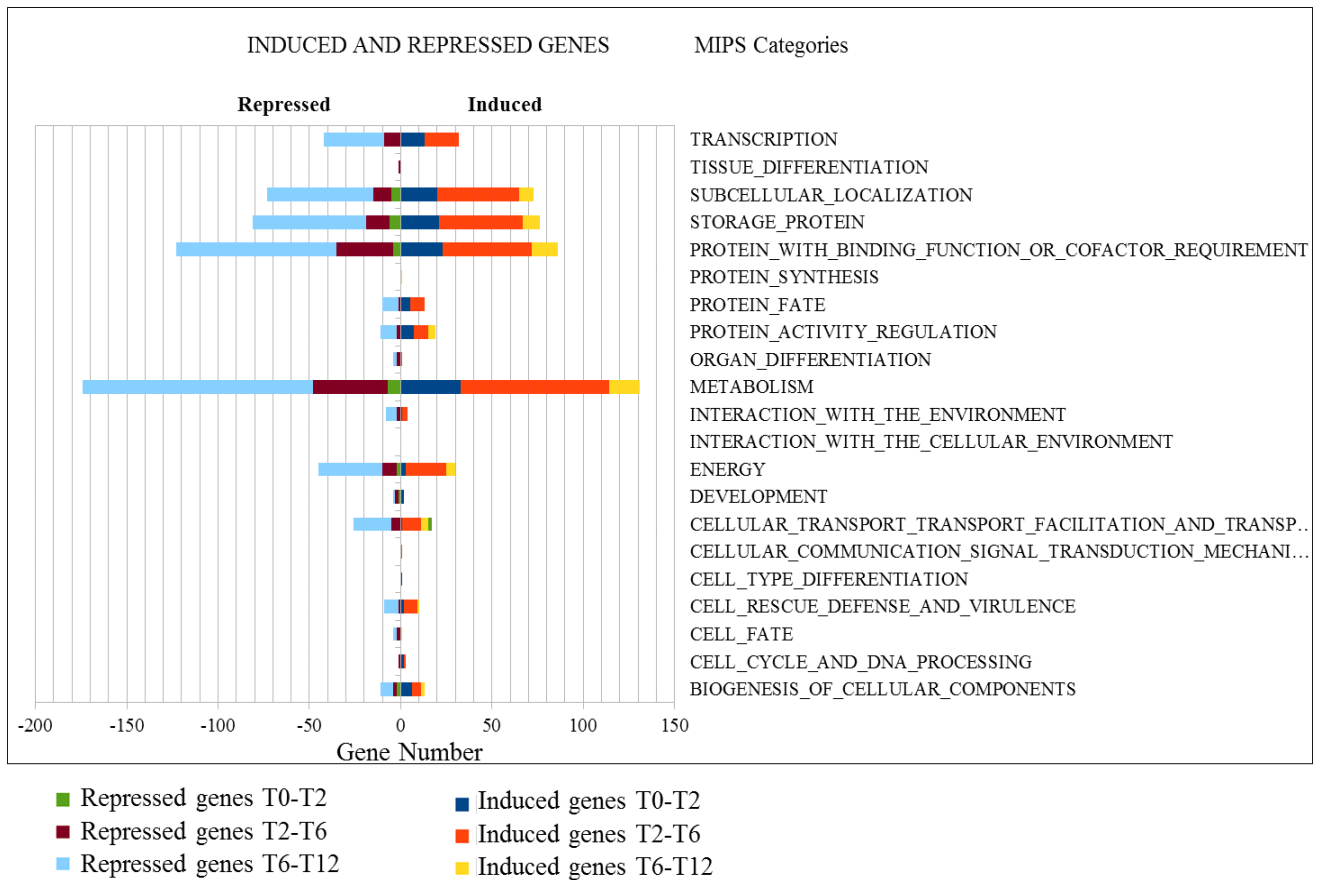


Figure 6: MIPS categories distribution for differentially expressed genes during early berry development

MIPS categories for induced and repressed genes during early stages of berry development. It is possible to observe an important number of induced genes at T2-T6 DAP, but this is inversed afterwards when most genes are repressed between T6-T12 DAP.

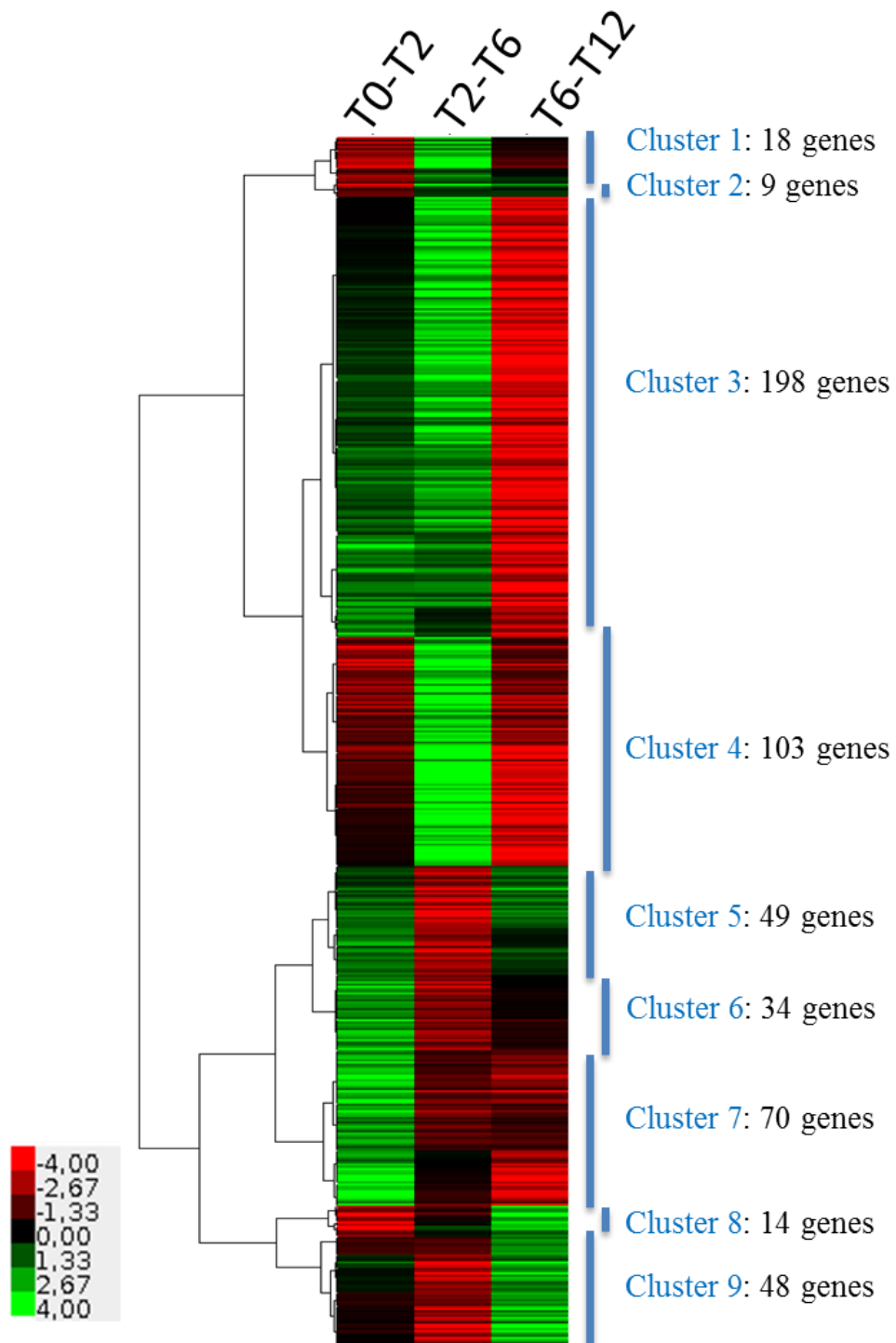


Figure 7: Cluster of differentially expressed genes through early berry development

Overview of the hierarchical cluster display of differentially expressed genes for sequential time-points during early berry development was obtained using Cluster 3.0 (Pearson correlation) and TreeView 1.1.6r2. Nine distinct expression patterns are distinguished. It is evident the transient changes occurring during these stages of development.

When hierarchical cluster analysis was performed on the sub-list of sequential time-points transient induction or repression of expression was observed between them for most of the genes (Figure 7). Nine distinct profiles were observed. Group 1 and 2 comprised 18 and 9 genes, respectively, with diverse functions. Group 3 presented 198 genes, where 3 members of GA2-ox are present, as well as 16 transcription factors from different families (MYBs, NAC, WRKY, Homeobox and others). Group 4 comprised 103 genes, including genes related to photosynthesis and transcription and WRKY transcription factors. Group 5 presented 49 genes, and among them auxin biosynthetic related genes, gibberellin response genes and MYB and NAC transcription factors can be found. Group 6 and 8 comprised 34 and 14 genes, respectively, with diverse functions. Group 7 presented 70 genes, with functions related to ethylene response and transcription. Finally, group 9 presented 48 members, including auxin-response genes.

When hierarchical cluster analysis was performed comparing anthesis (T0) against the other time-points a different pattern emerged (Supplemental Figure 1). An important number of genes was repressed and induced between T0 and T2, whereas most genes did not present significant changes in gene expression between T0-T6. Finally, between T0 and T12, the opposite pattern to what was observed between T0-T2 occurred, that is, genes that were repressed at initial stages of berry development were induced, and genes that were induced were found to be repressed. This also demonstrates a transient expression pattern during early stages of berry development. Also, it suggest a dynamic where genes induced or repressed by pollination reach their regular levels at post-fertilization time (non-significant levels), and present the opposite pattern from the one observed at post-pollination.

In order to identify the key players during early berry development, a study of the over-represented functional categories was performed. The results are shown in Figure 8. The most over-represented categories among the selected ones were cell wall, photosynthesis and hormone-related genes (Figure 8 A). Also, the induced and repressed genes within each over-represented category were separated, indicating that photosynthesis and cell-cycle related genes were mostly induced, whereas in the rest of the categories the number of induced and repressed genes is similar (Figure 8 B). Also when the same analysis was performed for the main hormones, we observed that the percentage of genes related to abscisic acid, auxin, cytokinin gibberellin and ethylene were over-represented in this study compared to the percentage of genes found in the grapevine genome. The brassinosteroid category was not over-represented (Figure 9).

As one of the over-represented categories was hormones, we decided to perform a more detailed analysis on the expression patterns for auxin and gibberellin, the two hormones with the largest number of differentially expressed genes (from the total list of 2822 genes). We considered only the hormone-related genes present in the sequential time-points. In the case of auxin-related genes (Figure 10 A) three expression patterns can be distinguished: no significant expression during anthesis, afterwards induction and finally, between post-fertilization and fruitset strong repression of gene expression. In this group auxin biosynthetic genes can be found. The second cluster presents the opposite expression pattern at T2-T6 and T6-T12, and finally the third cluster presented genes with strong induced expression at anthesis, and no significant expression at fruitset. The same analysis was performed for gibberellin related genes (Figure 10 B) where half of the genes are strongly repressed at fruitset

(comprising genes related to gibberellin biosynthesis), and the other half induced at this stage (including genes related to gibberellin catabolism).

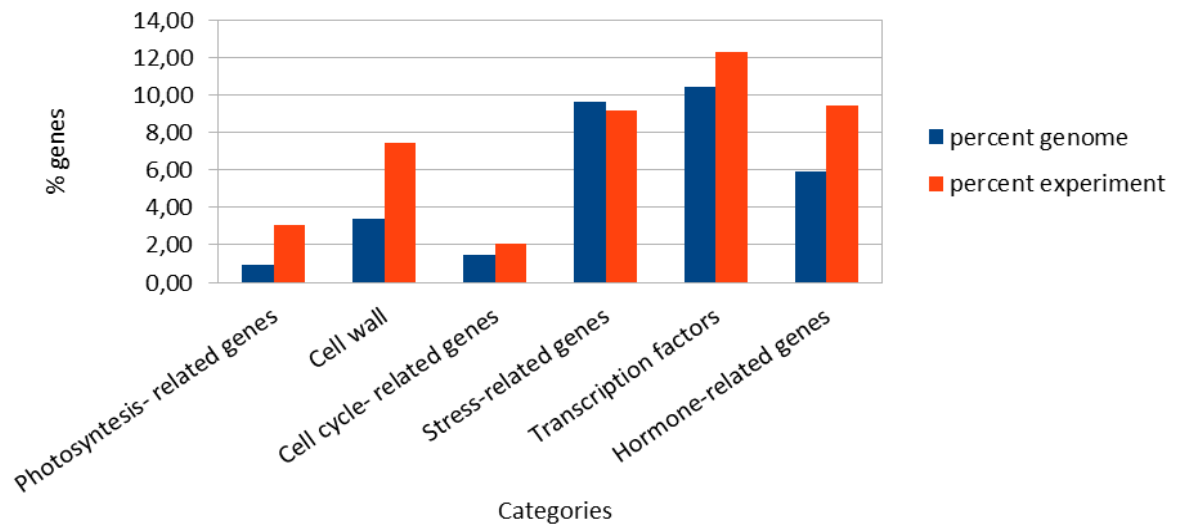
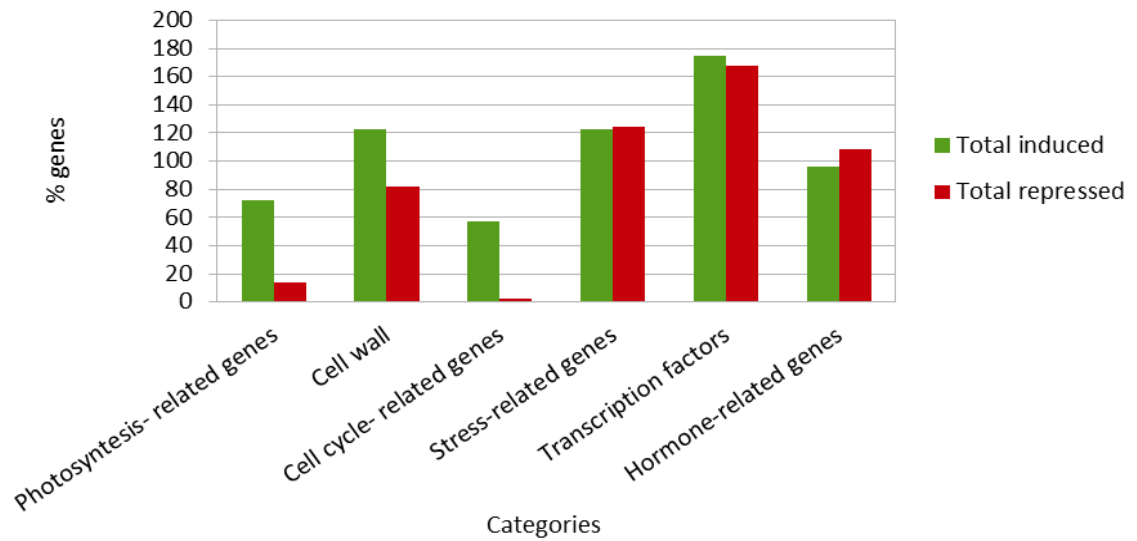
A Over-representation of selected functional categories**B** Induced and repressed genes within functional categories

Figure 8: Over-representation of selected categories during early stages of berry development.

Over-representation of five functional categories during initial berry development in grapevine. (A) Shows the percentage of genes for each category found in the genome (blue bars) and in the current experiment (orange bars). (B) Presents the percentage of genes induced and repressed for the previously shown functional categories.

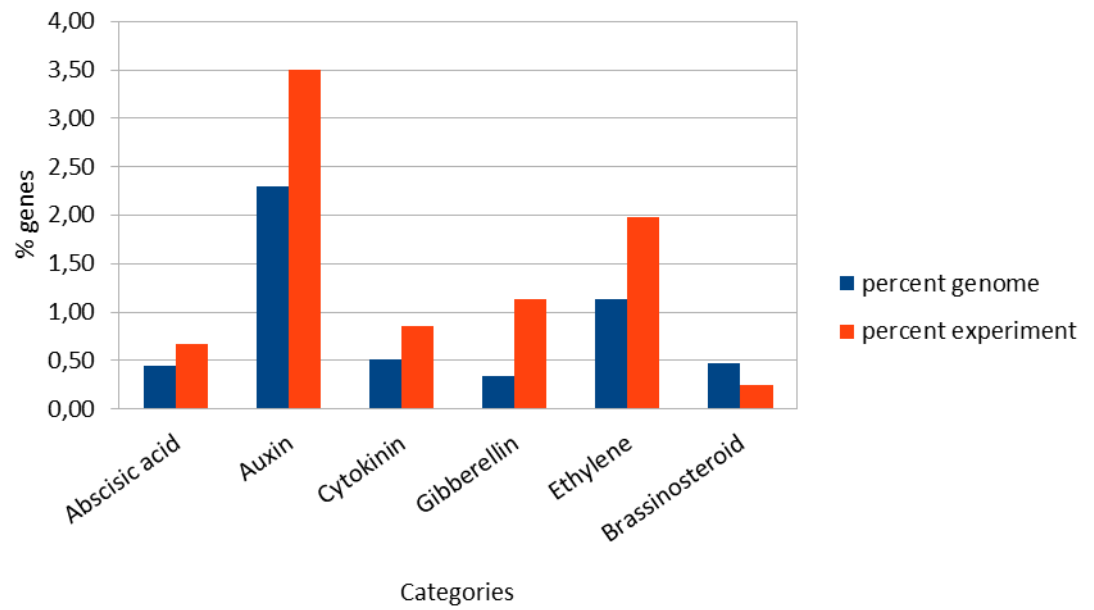
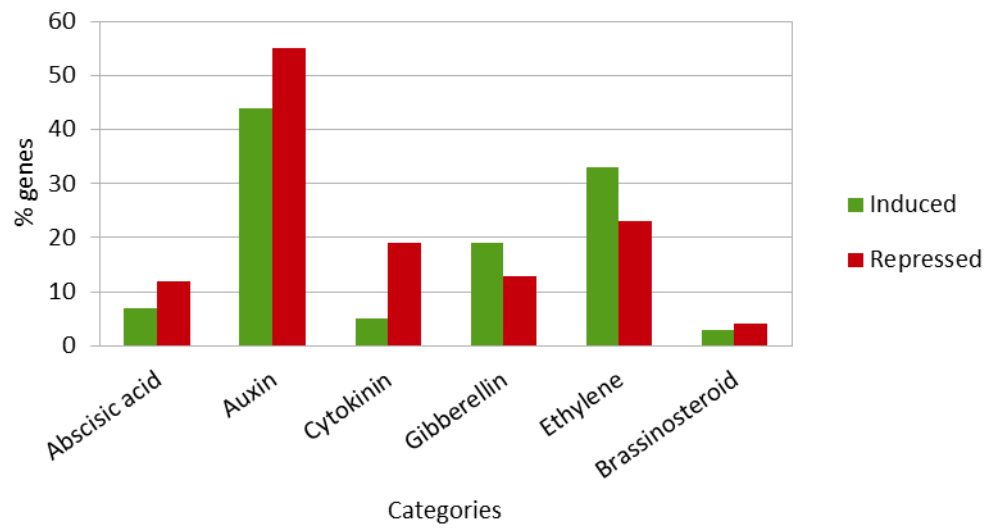
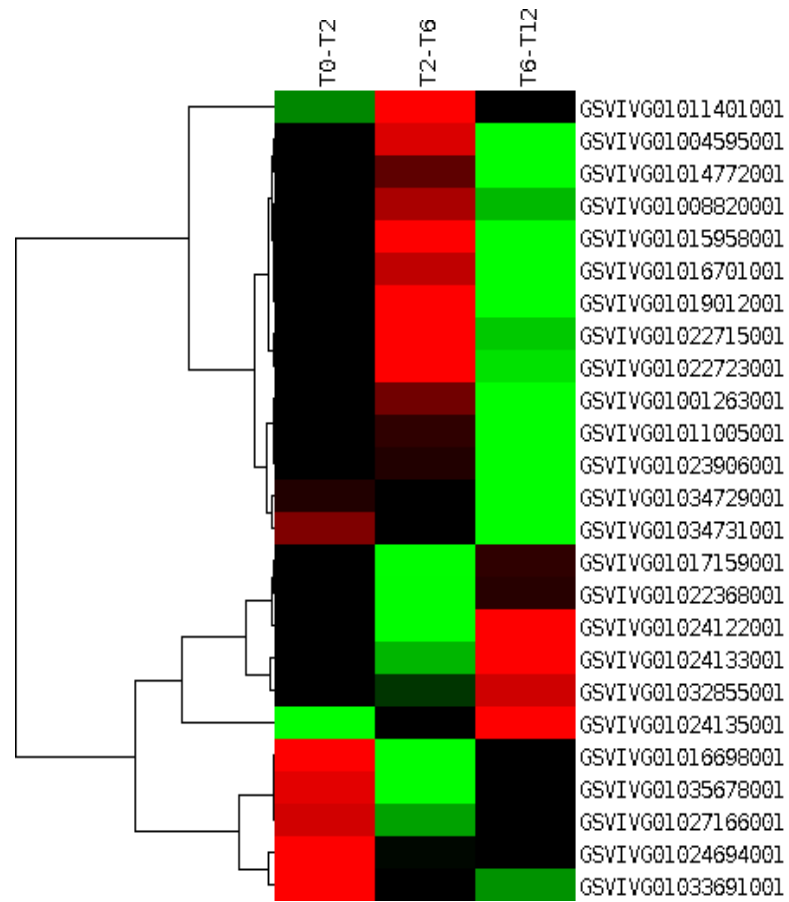
A Over-representation of hormone-related categories**B** Percentage of induced and repressed genes within hormone categories

Figure 9: Over-representation of hormone-specific categories during early berry development in grapevine.

(A) Percentage of genes for the phytohormones abscisic acid, auxin, cytokinin, gibberellin, ethylene and brassinosteroids found in the genome (blue bars) and in the current experiment (orange bars). (B) Percentage of induced and repressed genes for each category during early berry development.

A



B

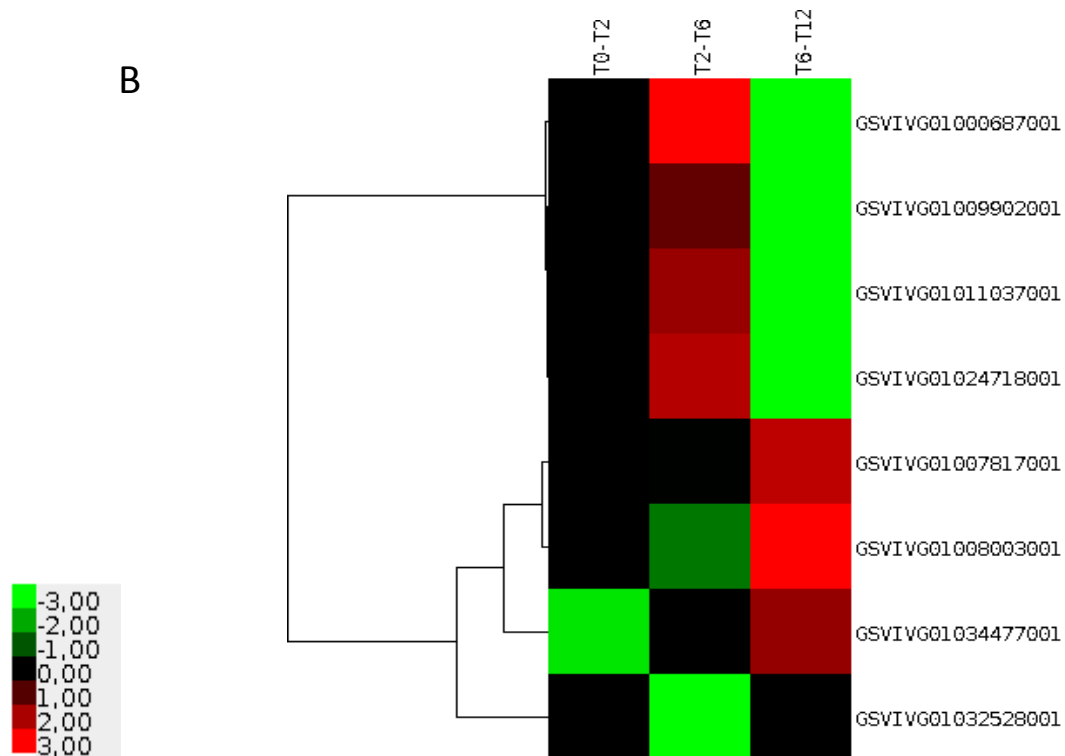


Figure 10: Hierarchical cluster of auxin and gibberellin-related genes during early berry development

Overview of the cluster display of hormone-related differentially expressed genes for sequential time-points during early berry development was obtained using Cluster 3.0 (Pearson correlation) and TreeView 1.1.6r2. (A) Cluster of auxin-related genes with differential expression in at least one sequential time-point. (B) Cluster of gibberellin related genes with differential expression in at least one time-point.

3.3 Hormone-related gene expression during early berry development: the importance of auxins and gibberellins.

In this study, 73 genes related to auxin, gibberellin, cytokinins (CKs) and abscisic acid (ABA) biosynthesis and response were found to be differentially expressed through initial berry development. The number of genes related to CKs and ABA biosynthesis and response were 9 and 4, respectively. On the other hand, 44 and 21 genes were related to auxin and gibberellin biosynthesis and response, respectively. This suggests that these two phytohormones are the main regulators during initial berry development.

Interestingly, more genes related to auxin response (40) than to auxin biosynthesis (3) were found differentially expressed (Figure 11 A-D). A member from the YUCCA family (here named VvYUC10) validated by Real-Time qPCR presented lower expression levels at anthesis, then its expression increased, reaching the highest point at post-fertilization time. At fruitset, however, it abruptly decreases its expression again (Figure 11 A). On the other hand, genes from the SAUR and ARF families (both described as auxin-responsive family genes) presented a pattern where the transcripts are low at anthesis and reach their highest level at fruitset (Figure 11 B-D).

There are 3 main gene families related to gibberellin biosynthesis: GA20 oxidases, GA3 oxidases and GA2 oxidases. In this study members from the GA20 and the GA2 oxidase family have been found to be differentially expressed through initial berry development, and were validated by means of qPCR (Figure 11 E-F). The two GA20 oxidase (here designated VvGA20ox1 and VvGA20ox2) members presented high transcript levels at anthesis, and

decreased through development. On the other hand, GA2ox presented a very interesting expression pattern: it was transiently (and only) expressed at 6 DAP (Figure 11 F).

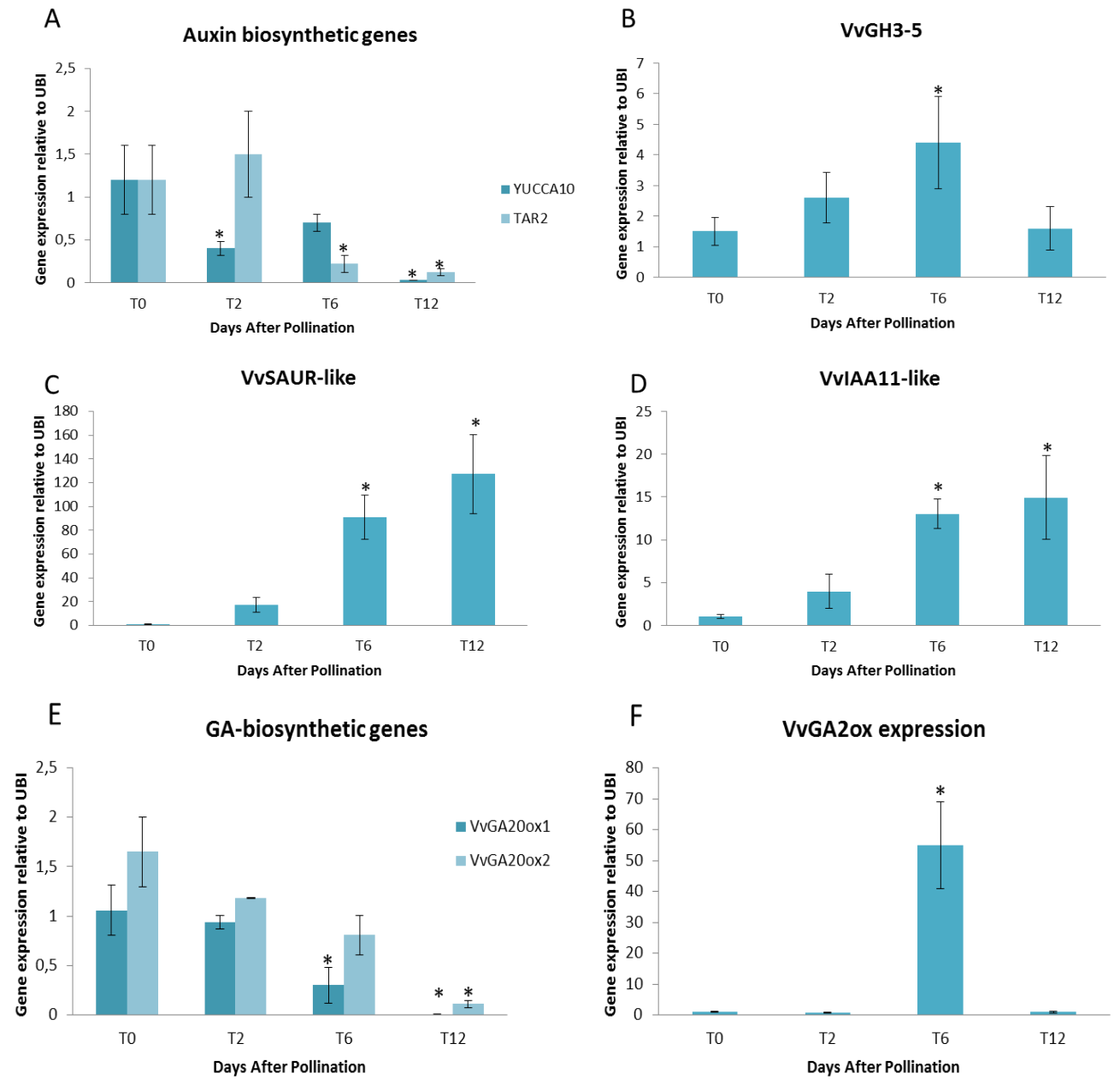


Figure 11: Expression of hormone related genes during early steps of berry development

Auxin and gibberellin -related gene expression during the first twelve DAP in grapevine berry development, measured by quantitative RT-PCR. A-D: Expression of auxin related genes. E-F: Expression of gibberellin biosynthetic genes. Gene expression is normalized to VvUBIQUITIN (ANOVA, $p \leq 0.05$). Bars represent Standar error.

3.4 Main hormones involved during initial berry development.

Given the importance of phytohormones in the changes produced during early berry development, and our findings on gene expression induction of hormone-biosynthesis and metabolism related genes (Dauelsberg et al., 2011) we decided to determine the levels of the main hormones during the first two weeks of berry development.

Free Indole-acetic acid (IAA) was measured at 0, 2 and 12 DAP (Figure 12). It was present at constant levels during anthesis and after pollination and fertilization (corresponding to 2 and 12 DAP). No significant difference in IAA levels were found between anthesis and fruitset (T0-T12), but were found to be significantly higher between post-pollination and fruitset (T2-T12) (Figure 12 A). To determine whether changes in free auxin content were related to auxin precursor levels, Indole-3-pyruvic acid (IPA) and Indole-3-acetamide (IAM) were measured. IPA levels were relatively constant through development (Figure 12 B), but IAM levels changed significantly, decreasing drastically after post-fertilization time (6 DAP) (Figure 12 C).

An important system to regulate free auxin levels is to control the conjugated and oxidated forms of this hormone (reviewed in Rosquete et al., 2012). For this reason, we also measured them, in order to have a broader picture of auxin homeostasis during early berry development (Figure 10). Auxin conjugated to aspartate or glutamate (IAA-Asp or IAA-Glu) were present at high levels at anthesis and decreased through development (Figure 12 D and E, respectively) reaching the lowest levels at fruitset. A similar accumulation pattern was observed for Ox-IAA-Glu, the oxidated form of IAA-Glu (Figure 12 F). However, when the

total amount of oxidated auxin (Ox-IAA) was measured, no significant differences were detected.

Gibberellins also play a crucial role in initial berry development. Bioactive gibberellins GA₃ and GA₁ were measured, as well as GA₈, an inactive gibberellin (Figure 13 A-C). Both bioactive hormones were present at high levels at anthesis, but their levels decreased drastically at post-fertilization and fruitset. On the other hand, GA₈, the inactive gibberellin, was relatively high through development but presented low levels at fruitset.

Absciscic acid is very important for embryo development and seed storage protein accumulation (Cutler et al., 2010). ABA presented a similar accumulation pattern than that of *trans*-Zeatin (tZ), where low levels were found at the initial period, and the highest levels of ABA were reached at fruitset (Figure 13 D).

Cytokinins (CKs) are also important growth regulators, and also promote early fruit development in Arabidopsis and tomato (Marsch-Martínez et al., 2012, Matsuo et al., 2012). Trans-zeatin (tZ) was the only bioactive cytokinin measured during this stage of development. This growth regulator was present at low levels from anthesis to post-fertilization time, but increased drastically afterwards (Figure 13 E).

Figure 14 summarizes the levels of IAA, GA₃, GA₁, *trans*-zeatin and ABA found during early berry development in grapevine.

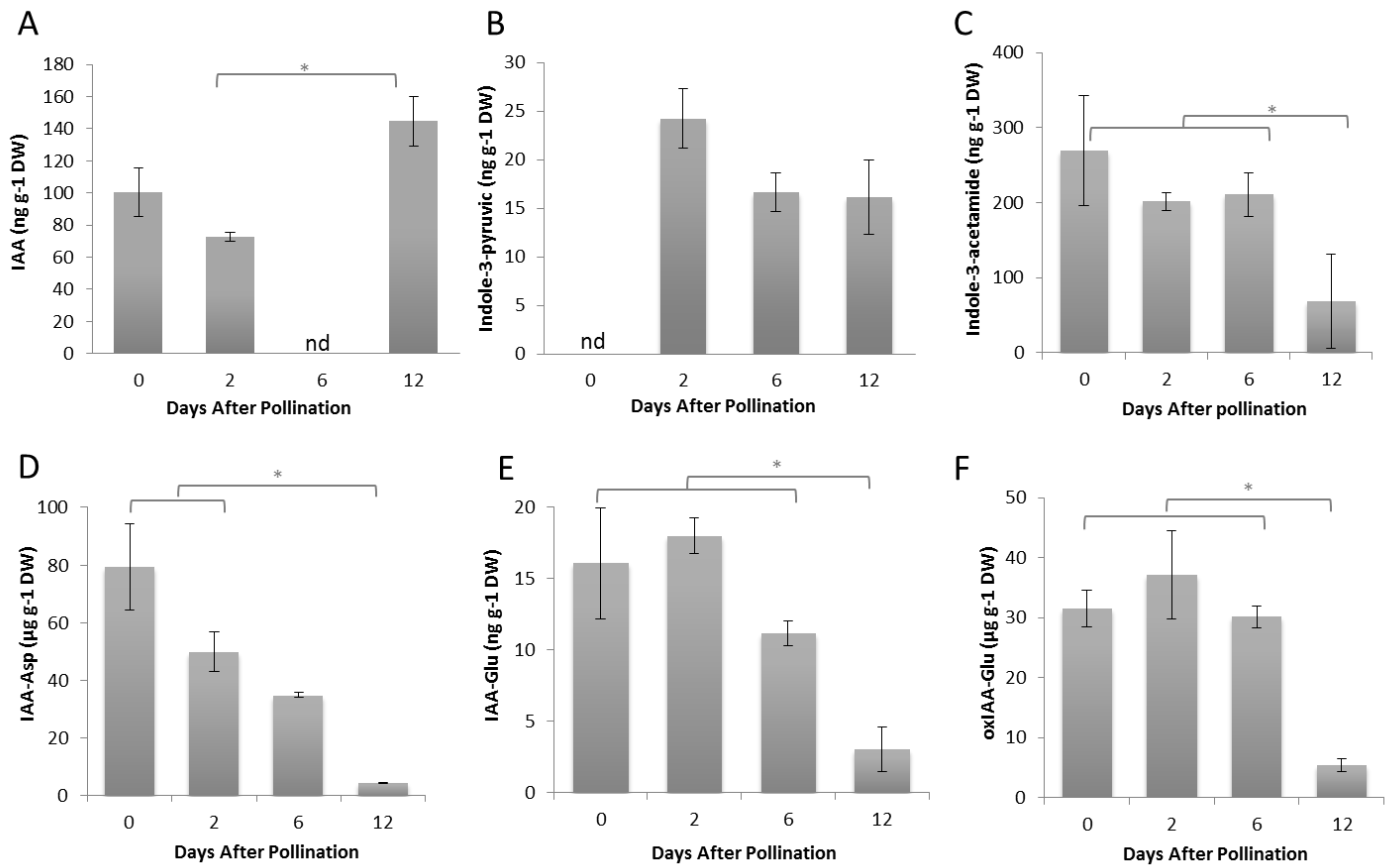


Figure 12: Auxin and auxin-related compounds during early grapevine berry development. (A-C) Indole-3-acetic acid and precursor levels during early stages of grapevine berry development. Precursor levels are higher during anthesis than fruitset, whereas free auxin levels presented the inversed pattern. (D-F) Conjugated and Conjugated-oxidated auxin levels during initial berry development in grapevine. IAA-Asp, IAA-Glu and Ox-IAA-Glu presented higher levels during anthesis, and decreased thereafter. *: significant difference. (ANOVA, $p \leq 0.05$). Bars represent Standar error.

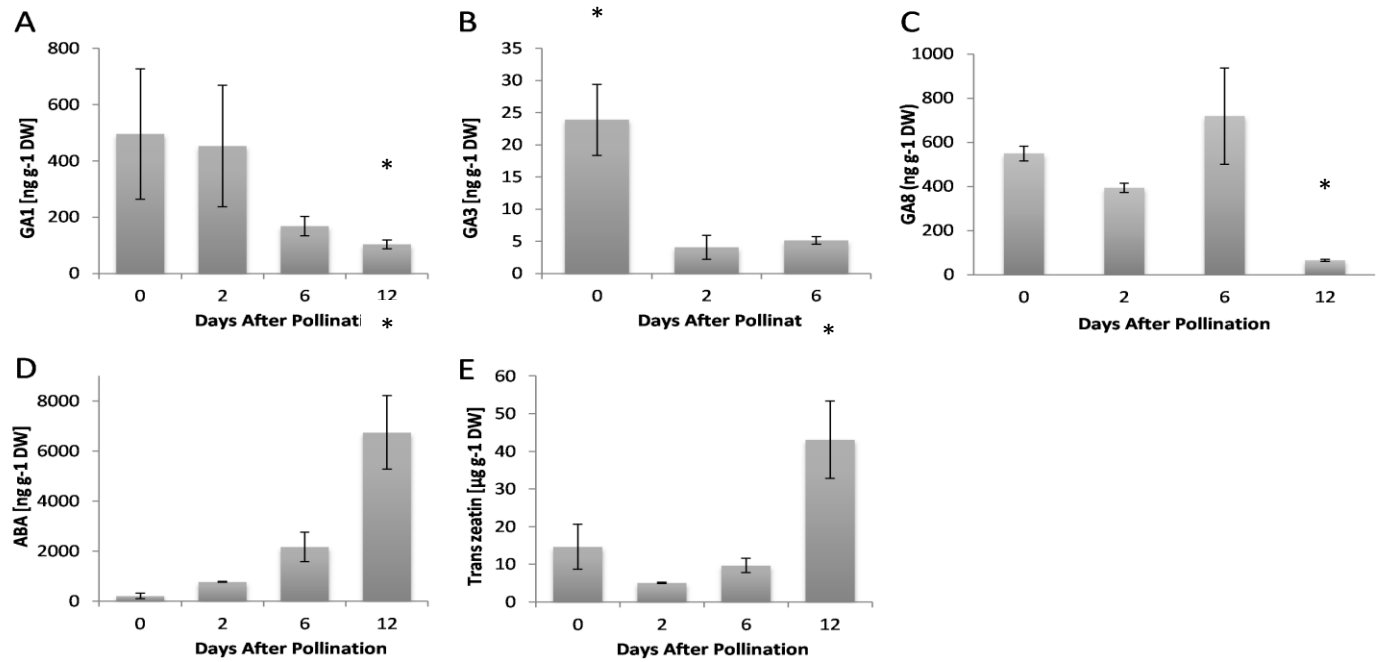


Figure 13: Gibberellins, abscisic acid and *trans*-Zeatin levels at initial stages of berry development

(A-C): Active (GA₃ and GA₁) and inactive (GA₈) gibberellin levels during berry initial development. Bioactive gibberellins presented the same pattern of accumulation (high at anthesis and low at fruitset), while GA₈ was somehow constant from anthesis to post-fertilization, and decreased at fruitset. (D-E): Absciscic acid and *trans*-Zeatin levels during early stages of berry development, respectively. Both hormones present the same accumulation pattern. *: significant difference. (ANOVA, $p \leq 0.05$). Bars represent Standard error.

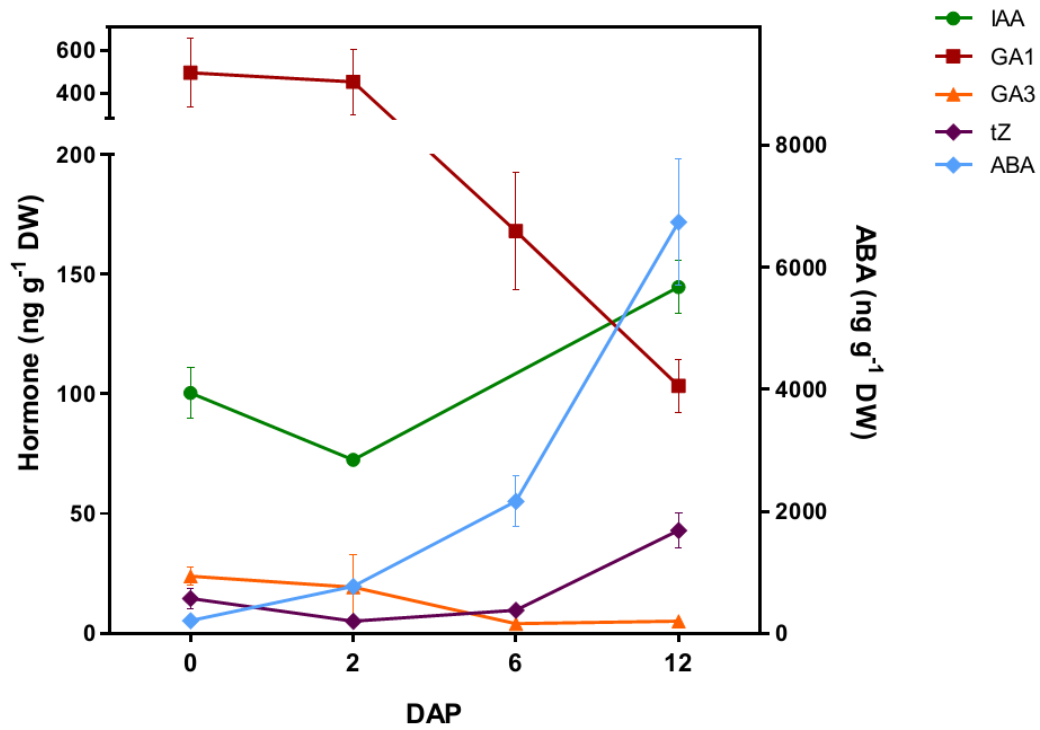


Figure 14: Levels of the bioactive hormones measured from anthesis to fruitset in grapevine.

Levels from IAA (green), GA₁ (red), GA₃ (orange), *trans*-zeatin (dark purple) and ABA (light blue) were measured at 0, 2, 6 and 12 DAP. Bars represent standard error.

3.5 Effect of hormone inhibitors in fruitset achievement.

Because auxins and gibberellins have been described in *Arabidopsis* and tomato as crucial during the early stages of fruit development, and a higher number of genes related to auxin and gibberellin than to CKs or ABA were found to be differentially expressed, a new set of experiments were performed focusing on these two phytohormones, in order to address if they have a pivotal role in process in grapevine as well. For this, we applied to one-day hand pollinated flowers paclobutrazol (PAC), an inhibitor of GA biosynthesis (Hedden and Graebe, 1985) or IAA-Trp, a conjugated form of auxin recently described as an inhibitor of auxin growth responses (Staswick., 2009), and the effects were observed twelve days after treatment (corresponding to fruitset). After inhibitor application it was possible to observe that the fruit did not develop significantly (Figure 15 A), maintaining the size of an unpollinated flower, either in the case of gibberellin or auxin biosynthesis/signaling inhibition.

To further characterize auxins and gibberellins role during early berry development cytological analyses were carried out in order to measure the effect of the treatments on mesocarp development (Figure 15 B). Samples from emasculated flowers were pollinated and treated with the inhibitors. Pollinated (12 DAP) and non-pollinated (ENP) were used as controls. We observed that the mesocarp from pollinated flowers greatly developed at 12 DAP when compared to ENP. Mesocarp of flowers treated with PAC or IAA-Trp were significantly thinner than that of 12 DAP, therefore inhibition of mesocarp development is taking place. This inhibition was not complete, as both treatments produced flowers with a more developed

mesocarp than that of ENP. Therefore, even though treatments have a significant effect on mesocarp development, other factors are involved. When comparing mesocarp development between treatments, it was found that PAC treated flowers presented significantly thinner mesocarps than IAA-Trp treated flowers (Figure 15 C). Hence, each hormone had a distinct effect on mesocarp development at early stages of development. Similar results were obtained when cell division was quantified. Cell division was significantly higher at 12 DAP when compared to ENP, and both PAC and IAA-Trp treatments presented higher cell division than that found in ENP. However, cell number in both treatments was similar, thus possibly the observed difference in mesocarp thickness is due to less cell expansion (Figure 15 D).

Finally, expression of genes related to hormone biosynthesis was evaluated in hormone inhibitor treatments. VvGA20ox (Gibberellin biosynthesis) (Figure 15 E) and VvYUC10 (auxin biosynthesis) (Figure 15 F) were selected because they encode for step-limiting enzymes in the biosynthesis process. Both genes presented a similar expression pattern. When compared to 12 DAP (corresponding to fruitset) either under PAC or IAA-Trp treatment both genes presented high expression levels. This difference was also significant between treatments.

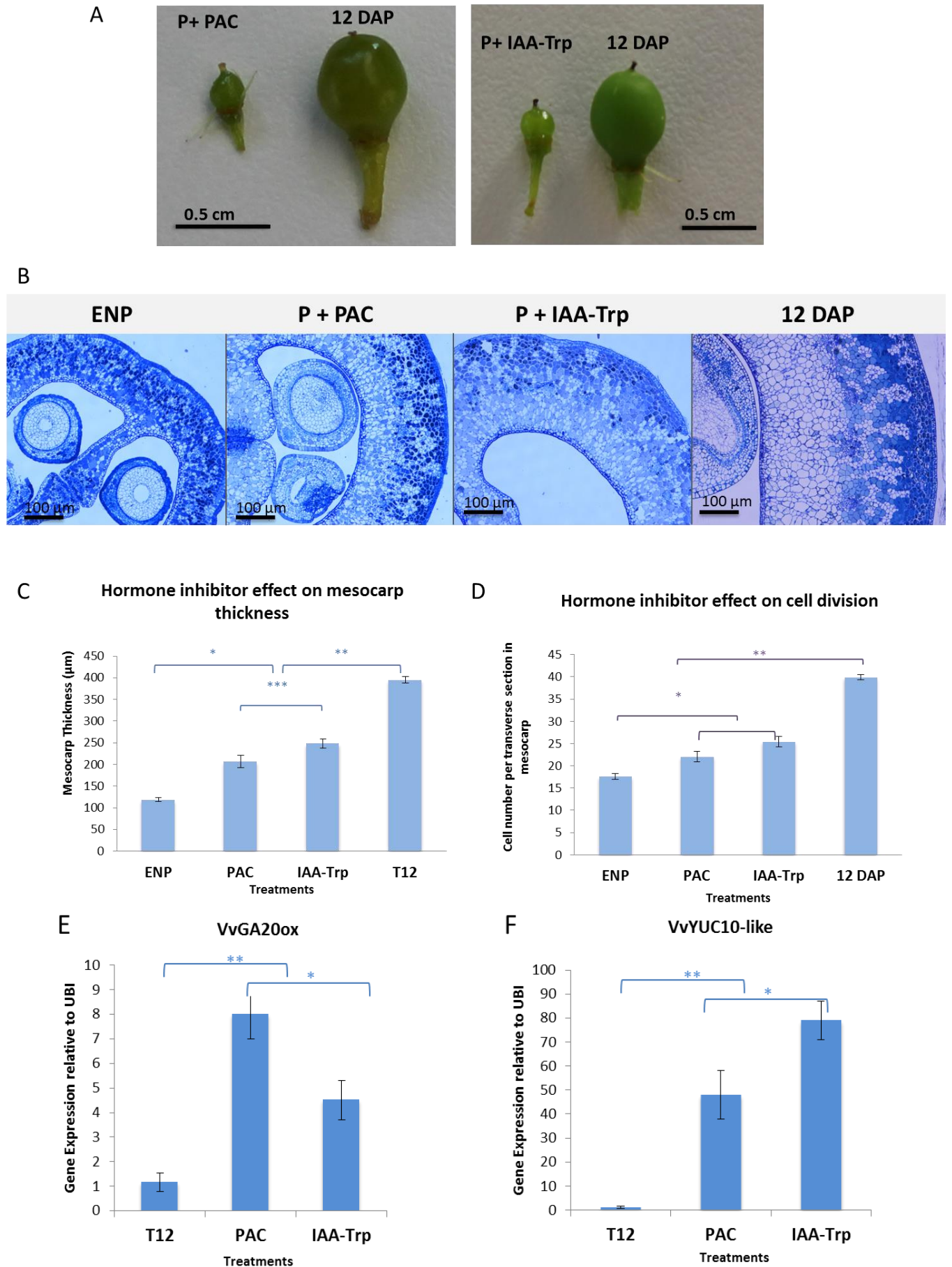


Figure 15: Inhibition of gibberellin biosynthesis (with Paclobutrazol) and auxin induced responses (with IAA-Trp) and its effect on fruitset.

(A) Effect of PAC (left) and IAA-Trp (right) treatments on fruitset achievement. (B) Effect of treatments on mesocarp development. Representative cross-sections of mesocarp in emasculated non pollinated flowers (ENP, negative control), pollinated + PAC, pollinated + IAA-Trp, and pollinated (12 DAP). All samples were obtained 12 days after pollination or anthesis (in the ENP treatment). (C) Treatment effect on mesocarp width. (D) Treatment effect on mesocarp cell division. (E-F) Expression of gibberellin and auxin biosynthetic genes, respectively. *: significant difference. (ANOVA, $p \leq 0.05$). Bars represent Standard error.

4. DISCUSSION

4.1 Mesocarp development due to cell division and expansion triggered by pollination

Pollination and fertilization in grapevine flowers trigger a complex developmental program that will set in motion the change from a dormant ovary to a developing one. In grapevine pollination and fertilization take longer than in other studied species, such as sweet pepper, tomato or *Arabidopsis* (Tiwari et al., 2012, Iwahori 1966, Faure et al., 2002, Staudt., 1982, Mardi Longbottom, personal communication). Initial fruit development in *Vitis vinifera* cv. Red Globe is given mainly by mesocarp growth (Figure 3). After pollination no significant changes in mesocarp width and cell number were observed, and mesocarp cell number and thickness increased significantly between 10 and 12 DAP, that is, after fertilization. In non-pollinated flowers the mesocarp does not develop (ENP, Figure 15). Thus, pollination and fertilization play a crucial role promoting mesocarp development, and significant changes in the mesocarp structure are observed after fertilization. Cell number and mesocarp width increment significantly after 10 DAP, but the mesocarp growth reached at 12 DAP cannot be accounted only for a cell division process. Therefore, cell expansion also occurs during these early stages of development. From the cytological analyses it is clear that cell expansion occurs predominantly in the inner mesocarp. This is consistent with the fact that this structure will give rise to the berry pulp, which presents cells as big as 300-400 μm (Fernández et al., 2006). Ojeda et al. (1999) measured the DNA content of Shiraz berries through development, and found that most of the mitotic activity was found between the first 15 days after anthesis, and mainly in the first 5 days. This also agrees with our results, although with a different

temporality likely because of differences in the cultivar. Similar findings have been recently published for *Capsium annuum* (sweet pepper) (Tiwari et al., 2012) where, after pollination, cell division contributed significantly to fruit growth during the first days, and afterwards cell expansion was more significant.

4.2 Early berry development presents a dynamic gene expression profile

RNAseq technology has many advantages over the Affymetrix technology, especially for non-model species such as grapevine. Current affymetrix chips contain between 50 to 80% of the grapevine genes, whereas sequencing technology detects all transcripts present in a sample. Also, it is very useful for annotation improvement. As not many genes related to early berry development in grapevine are known, this technique was selected to further characterize the global gene expression.

Our comparative study of global gene expression during the first days of fruit development showed that 2822 genes presented differential expression. A sub-list of 543 genes comprises those with differential expression between sequential time-points. We have focused the analyses on this list in order to characterize more accurately the berry, following their natural developmental cycle. It is interesting to observe that there are dynamic expression patterns. There is a significant group of genes that present low expression levels between anthesis and post-anthesis stage, then are highly induced between post-anthesis and post-fertilization stage, and finally the expression levels diminish again at fruitset. There is also a cluster of genes which expression is high at the initial and final stages, but between post-pollination and post-fertilization its expression is highly repressed. Therefore, many of the transcriptional

inductions/repressions observed may be transient. This is in accordance with previous studies performed in tomato where Wang et al. (2009) found that an important number of genes undergo transient up- or down- regulation from bud (-2 DAP) to post-anthesis stage (4 DAP). Also, Schmid et al. (2005) performed a gene expression map of Arabidopsis development, including silique and seed. At early stages (seeds including siliques) 800 genes were induced, and 1500 genes repressed. Global gene expression in Arabidopsis silique/seed development consists of mostly repressed genes, and as the seed develops, the pattern is inverted. It is clear that the initial berry development is a very dynamic process in grapevine, as described previously for other species.

Over-represented categories during early berry development corresponded to photosynthesis, hormones, cell cycle, cell wall and transcription factors (Figure 8 A). When genes induced and repressed within these categories were separated, the categories with more induced vs repressed genes were photosynthesis and cell cycle, indicating that these processes are highly induced during early berry development (Figure 8 B). This is in accordance with the mesocarp development taking place at this stage where energy is needed and cell division is crucial for fruitset establishment.

Most of the hormone biosynthesis and response genes found to be differentially expressed were auxin-related (43), followed by gibberellin-related genes (26). In both cases, more genes related to hormone response and signaling than hormone biosynthesis were found. Interestingly, the three auxin-biosynthetic genes found in this study are from the two gene families needed in the same biosynthetic pathway to synthesize IAA from L-Trp (Mashigushi et al., 2011).

4.3 New insights into hormone regulation during initial grape berry development

As auxin has been described as one of the main fruitset regulators in many species, we measured free IAA levels, as well as some of its precursors. Free IAA levels were found to be higher at anthesis (T0) and fruitset (12 DAP), whereas at least one of its precursors (IAM) presented the opposite accumulation pattern: elevated levels at anthesis and lower levels at fruitset. Interestingly, all genes related to auxin biosynthesis found in this study to be differentially expressed through initial berry development are from the Indole-3-Pyruvic acid (IPyA) pathway, which is supposed to be the main IAA contributor: two YUCCA members and one Tryptophan aminotransferase-related (TAR) protein. It has been suggested that TAA1/TAR and YUCCA gene families function together to synthesize IAA from L-Trp (Mashigushi et al., 2011, Stepanova et al., 2011, Won et al., 2011). Also, Mashiguchi et al. (2011) have described that YUCCA proteins catalyze the rate-limiting step of IPyA dependent auxin biosynthesis. To our knowledge, this is the first time IAM and IPyA levels are reported in grapevine, and as it is possible to find all IPyA pathway main players, this strongly suggests that this pathway is operational in grapevine, at least during this stage in early berry development. Therefore, auxin biosynthetic pathway in grapevine could be similar to the pathways reported for other species (Zhao 2012).

A member of the YUCCA family in Arabidopsis, AtYUCCA4, has been reported to show alternative splicing through development (Kriechbaumer et al., 2012). In this study we have found the putative ortholog of this gene repressed at fruitset. Future work will elucidate if alternative splicing occurs during early berry development in this gene, regulating auxin

levels, and also if other genes present alternative splicing that is important for fruitset to take place.

It has been described previously in *Arabidopsis* that auxin homeostasis is regulated mainly by conjugation and oxidation (reviewed in Rosquete et al., 2012). Auxin works at its optimum at a restricted concentration. For this reason, it has many mechanisms for its homeostasis such as biosynthesis, transport, conjugation, oxidation and degradation (reviewed in Ludwig-Müller 2011). To further understand auxin homeostasis during early berry development, we also measured conjugated auxin and oxidated-conjugated auxin levels. These compounds are strongly diminished at fruitset. Recently it was reported that the grapevine genome presents nine Gretchen Hagen (GH3) genes with similar protein sequence to IAA-amido synthetases, responsables for IAA conjugation (Böttcher et al., 2011). In this study we were able to detect the expression of a GH3 member (Grape Genome Browser ID: GSVIVT01000422001) which was found to be repressed between anthesis and fruitset, in correlation with conjugated auxin levels. This GH3 corresponds to GH3-5 according to previous work from Böttcher et al., 2011, and they found that this gene is mainly expressed during the first two weeks of berry development, presenting the same pattern of expression observed in Red Globe cultivar. Interestingly, this GH3 is the only member of the family that presents a specific expression pattern (first two weeks after flowering, and almost no expression afterwards). It is possible that this GH3 protein has not only a tissue-specific function but a temporal-specific as well.

Auxin regulates cell division and cell expansion (Wang et al., 2013). IAA presence at anthesis and fruitset suggests that it controls cell cycle-related genes (during anthesis) and cell division and cell expansion at fruitset. Another possible function of IAA during the early stages of

berry development is to regulate other hormone levels (such as gibberellin) by crosstalk (as we observed in Figure 15) and also to respond rapidly to stress, as this stage is very delicate.

The other main hormones, apart from auxin, that is deeply involved in fruitset regulation are gibberellins. In this study, Gibberellins GA₁ and GA₃ were found to be present at high levels at anthesis, and decrease rapidly after fertilization. This correlates with the expression pattern of three GA20-oxidase members found in our transcriptomic analysis. Likewise, a member from the GA2-oxidase gene family is expressed uniquely at 6 DAP, the time point where gibberellins levels diminishes. In opposition to studies showing that in tomato gibberellins accumulate after pollination (Mariotti et al., 2011) we have found that during anthesis the predominant hormone is gibberellin in grapevine. A recent publication has confirmed our findings of higher GA₁ levels at anthesis than fruitset in this specie. This group also described all protein members of the VvGA20ox and VvGA3ox as functional (Giacomelli et al., 2013). Also, gibberellin can control spatial cell division in maize leaf (Nelissen et al., 2012). Discussion has arisen as to whether auxin or gibberellin is the first signal after pollination that will trigger carpel development. GA₃ induced the carpel development in tomato flowers, but did not induce the expression of auxin-related genes that are normally induced by pollination (de Jong et al., 2009, Vriezen et al., 2008). Unpollinated tomato flowers treated with inhibitors of auxin and GA biosynthesis resulted in a reduced fruit development. Therefore, auxin-mediated fruit development is achieved at least in part by the gibberellin pathway (Serrani et al., 2008). Crosstalk between auxin and gibberellin has recently coming to light: AtGA20-ox2 is induced by auxin, as proved by Frigerio et al. (2006) in *Arabidopsis*, and Nitsch et al.

(2009) demonstrated that 2,4-D application to tomato ovaries induced the expression of several SlGA20-ox and SlGA3-ox genes, and repressed SlGA2-ox genes.

In this case, the presence of gibberellin at anthesis suggests that it may be regulating cell division, together with auxin. Its decrease at fruitset may indicate that at this stage auxin and cytokinin are the hormones responsible for cell expansion. As it has been described that a local GA maximum regulates cell division in maize leaf (Nelissen et al., 2012), it may be needed to determine the bioactive gibberellin localization in the future, to have a better understanding of the grapevine fruit growth regulation by this hormone.

Serrani et al. (2008) applied Paclobutrazol to pollinated tomato ovaries, totally inhibiting fruitset. When GA₃ was co-applied fruitset took place, but the fruit developed to a lesser extent. Also, PAC application induced the expression of gibberellin biosynthetic genes. In this work treatments with PAC and IAA-Trp confirmed that auxin and gibberellin are crucial for fruitset to occur in grapevine. Fruitset inhibition mediated by PAC observed in our experiments is in accordance to its effect on tomato fruit development (Figure 15). It is interesting that, even though mesocarp width was significantly less than at 12 DAP, it is significantly developed to some extent in both treatments than in the ENP flowers. This effect is also evident when counting the number of cells per transverse section. This indicates that, apart from auxin and gibberellin, pollination is inducing other signals that trigger partially mesocarp development. Expression of two hormone biosynthetic genes (VvGA20ox and VvYUC10-like) presented compensatory patterns, that is, their expression was induced when auxin or gibberellin was decreased, supporting a crosstalk between auxin and gibberellin biosynthetic genes. The induction of VvGA20ox expression is also in accordance to the work

on tomato (Serrani et al., 2008). It is interesting that gene expression for both genes is impaired with PAC treatment as well as with IAA-Trp. This indicates that a crosstalk between these two hormones affects hormone-biosynthetic genes, and that this regulation goes from auxin to gibberellin, and from gibberellin to auxin. This crosstalk seems crucial for fruitset to take place, and more investigation will be needed in order to elucidate this process. Transcription factors are possible players in crosstalk, as many of them present differential gene expression under hormone treatments.

Trans-Zeatin and ABA presented a similar accumulation pattern: almost undetectable levels at anthesis, and high levels at fruitset. Given that their levels were highly induced after 6 DAP, it is possible to hypothesize that fertilization was the signal that triggered that induction. Although most studies have centered on auxin and gibberellin, it is known that cytokinin also plays an important role during early fruit formation. Treatment of unpollinated Arabidopsis pistils with Benzyladenine (BA) resulted in parthenocarpic development (Vivian-Smith and Koltunow, 1999). Cytokinin oxidase/dehydrogenase (CKX) genes codify for proteins responsible for Cytokinin breakdown, and mutations in some of these genes produce higher seed yield (Ashikari et al., 2005, Bartrina et al., 2011). One member of this family was found to be differentially expressed during early berry development in grapevine, presenting high transcript levels at 2 and 6 DAP, and decreasing to almost undetectable levels at fruitset. This is in agreement with high levels of tZ found at this later stage. Bioactive levels of CKs not only depend on synthesis and degradation (by CKXs), but also on glycosilation, phosphorylation and deribosilation of the CK nucleoside (reviewed in Sakakibara 2006). It would be interesting to analyze in more detail how cytokinin homeostasis is controlled during initial fruit development in grapevine.

Also abscisic acid seems to play a role in this process, albeit it has not been described in detail yet. In tomato, it has been described that ABA decreases its levels after pollination, as well as ABA biosynthetic genes (*SINCE*D). Also, ABA levels in unpollinated flowers remained high. As ABA has been described before as a negative regulator of cell cycle via CDKA1 expression inhibition (Smalle et al., 2003), it was suggested by these authors that ABA restrains carpel development until pollination takes place (Nitsch et al., 2009). Recently Nitsch et al. (2011) described for the first time an ABA-deficient *notabilis/flacca* (*ntb/flc*) double mutant in tomato. This mutant presents smaller fruit size and all tissues are affected (placenta, locule and pericarp). Although the number of cell layers in the pericarp is similar to the wild type, cell size is significantly smaller. Also, transgenic tomato plants overexpressing ABA 8'-hydroxylase showed the same phenotype (Nitsch et al., 2009), confirming that ABA promotes cell expansion in tomato. In grapevine, ABA might promote cell expansion after pollination and fertilization take place. Nitsch et al. (2009) demonstrated GA₃ treatment in tomato flowers at anthesis inhibited *SINCE*D expression, an ABA biosynthetic gene. As in grapevine we have observed high levels of GA₃ during anthesis, VvNCED may be repressed at this stage, and might explain ABA absence. At fruitset, however, ABA is present at high levels. Possibly in grapevine ABA is involved in other functions, such as regulation of flower abscission, which takes place around 12-18 DAP in this specie, and embryo development.

4.4 Fruitset establishment in grapevine.

In this work, we have found that auxin and gibberellin behave differently than expected from the classic tomato model: gibberellins are present at high levels at anthesis and diminish after fertilization, and free auxin levels are present at anthesis, decreases afterwards, and finally reaches its highest level at fruitset. It has been suggested that in *Arabidopsis* and tomato auxin is the first signal for induction of carpel development (Serrani et al., 2008, Dorcey et al., 2009, Fuentes et al., 2012), but it seems that in grapevine this role is complemented with gibberellins, given that they are also the earliest hormones to change after pollination and GA₁ is present at higher levels than free IAA. As it can be seen in Figure 3, mesocarp develops slowly from 0 to 6 DAP, and afterwards there is a significant increment in both, cell division and mesocarp thickness. In the Woodland Strawberry *Fragaria vesca*, *Arabidopsis* and tomato early fruit development is much faster than in grapevine (Boavida et al., 2011, Kang et al., 2013, Xiao et al., 2009). This is also evident by the lower number of cell cycle-related genes found in this study in comparison to transcriptomic studies carried out in tomato (Lemaire-Chamley et al., 2005). This different developmental pattern may reflect a distinctive regulatory mechanism. It is known that auxin and gibberellin have distinct effects on fruit development. For instance, auxin treatments produce tomato fruit with more pericarp cells, while gibberellin treatments produce fruits with fewer pericarp cells but greater in size (Serrani et al., 2007). To achieve fruits similar to the originated by natural pollination, both auxin and gibberellin must be applied (Serrani et al., 2007). It has been demonstrated that auxin regulates GA-biosynthetic genes (GA20ox), but it has also been recently proven in *Arabidopsis* that GA can control PIN-FORMED (PIN) proteins as well, therefore regulating auxin levels (Willige et al., 2011). An auxin-gibberellin crosstalk is possible both ways. To our knowledge, this is the first

time free auxin, auxin-related metabolites, GA₁, GA₃, ABA and *trans*-zeatin are evaluated during early stages of grapevine fruit development using a highly accurate method. There have been other hormone measurements (Zhang et al., 2003, Böttcher et al., 2010) where different hormone dynamics were described, where auxin presents at high concentrations at anthesis, and cytokinin together with gibberellins being predominant at fruitset. However, those works used different techniques and timepoints, usually separated by weeks. Our study highlights changes occurring within a twelve-day period, which may be overlooked in bigger timeframes. Also, our results are in accordance with previous reports (Giacomelli et al., 2013, Symons et al., 2006). It is possible that differences in hormone levels at anthesis and fruitset between our study and previous reports may be due to the technique or cultivar used. Finally, and according to what has been described for tomato and Arabidopsis, *trans*-Zeatin and ABA are present at fruitset, possibly regulating processes related to organ formation and cell expansion (Nitsch et al., 2011, Marsch-Martínez et al., 2012). Based on the temporal appearances of each hormone, the differentially expressed genes found in our study and literature, we propose a simplified model for fruitset establishment in grapevine (Figure 16). During anthesis (0 DAP) it is possible to find high levels of free IAA, conjugated auxins, the gibberellins GA₁ and GA₃. Also, transcripts related to gibberellin biosynthesis present high expression at this stage. The mesocarp has not developed yet. At fruitset (12 DAP) conjugated forms of auxin diminish drastically their levels, as well as gibberellins, and IAA, ABA and *trans*-Zeatin present high accumulation levels. Transcripts related to auxin response also present high expression at fruitset. In summary, the main bioactive phytohormones present at anthesis are gibberellins (specially GA₁), and IAA, and at fruitset IAA, ABA and *trans*-zeatin reach their highest

levels, suggesting that gibberellins and IAA are the first factors needed for induction of mesocarp development, and ABA and *trans*-zeatin participate in posterior processes.

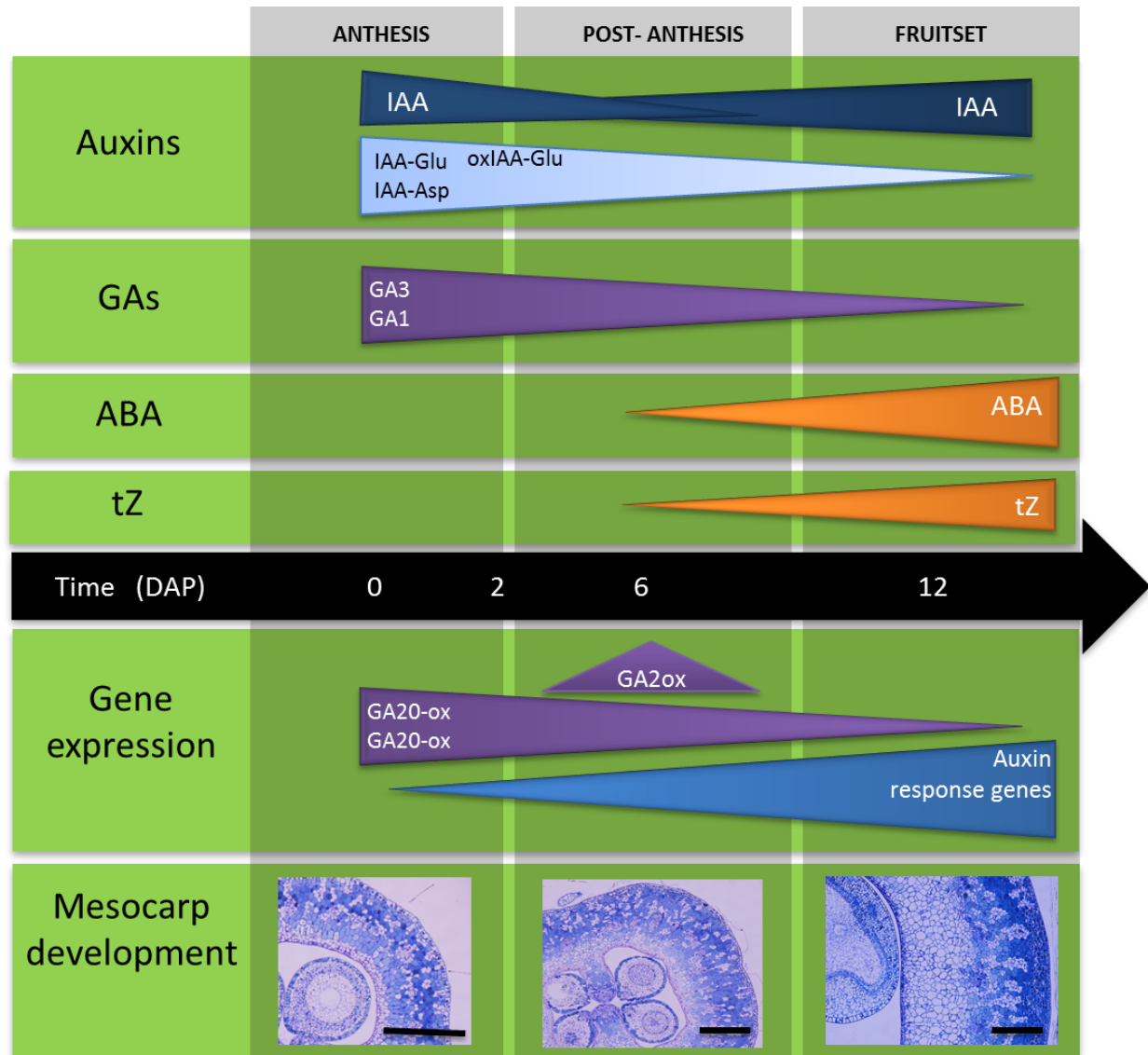


Figure 16: Fruitset establishment model in early grapevine berry development.

After pollination and fertilization take place GA_1 and GA_3 levels decrease, due in part to less transcription of *VvGA20ox* members. IAA presents high levels at anthesis and decreases at post-fertilization time. Afterwards, at fruitset, IAA, tZ and ABA levels increase. DAP: Days After Pollination. Scale Bar: 100 μ m.

5. CONCLUSIONS:

In this work we have performed a global transcriptomic analysis and hormone profiling of early stages of grapevine berry development to better understand fruitset establishment in this species. Global gene expression showed dynamic transient patterns, and a strong gene repression between post-fertilization and fruitset, which agrees to studies in tomato and *Arabidopsis*. The biological processes mostly present are “response to stress”, “transport”, “response to abiotic stimulus” and “response to biotic stimulus”. Genes related to hormone biosynthesis and response are differentially expressed throughout early berry development. To complement this analysis hormone measurements were performed. It was found that, contrary to tomato, during pollination the predominant hormone is GA₁ and GA₃. Free IAA is also present during anthesis, and decreased its levels after fertilization. Afterwards auxin, *trans*-zeatin and ABA increased at fruitset. Also, auxin conjugation may play a crucial role in auxin homeostasis at this stage of early development. Chemical treatments confirmed a crosstalk between auxin and gibberellin, and also that both hormones are crucial for fruitset to occur in grapevine. Taken together, these results revealed a new model for early fleshy fruit development, although more experiments are needed to determine the sequential order in which each hormone affects fruitset achievement. To our knowledge, this is the first study that evaluates global gene expression and hormone functions in order to understand fruitset establishment in grapevine.

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7. SUPPLEMENTAL MATERIAL

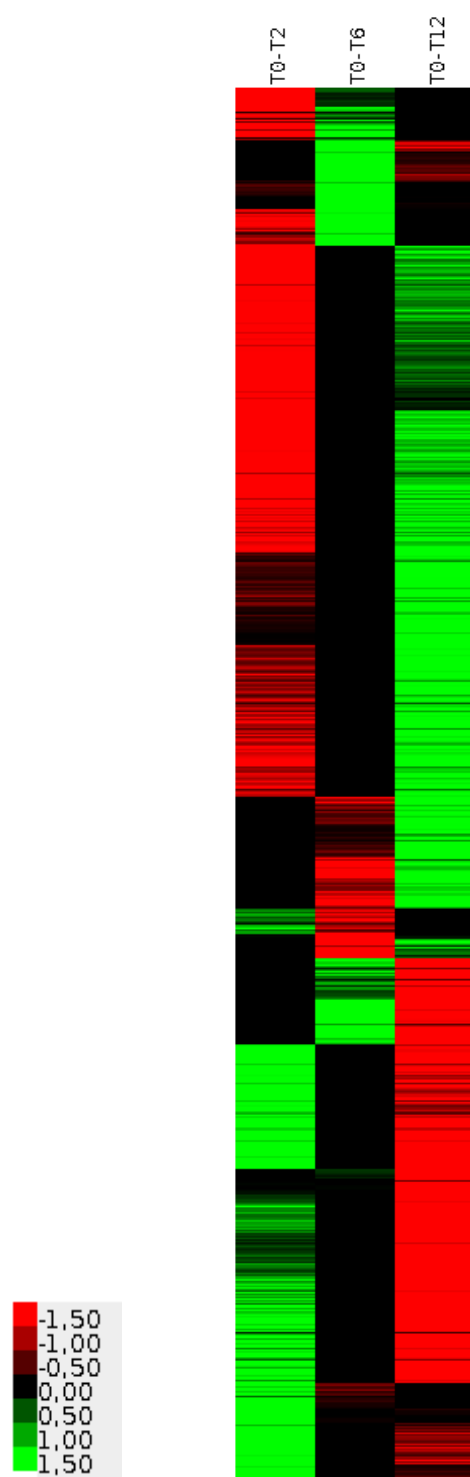


Figure S1: Cluster of differentially expressed genes through early berry development

Overview of the hierarchical cluster display of differentially expressed genes during early berry development was obtained using Cluster 3.0 (Pearson correlation) and TreeView 1.1.6r2. Time-points were compared to T0 (anthesis). Transient expression patterns are observed.

Primer Name	Sequence	T _m (°C)	Grapevine ID	Size product (bp)
qSAUR-F	CAGTCCTCAAGAAGTGGCCC	58	GSVIVG01016698001	249
qSAUR-R	GCAAGTGCTCGAACAGAACC	57		
qVvGA2-oxF	TCCAAGTTGGAAGCTGAAGC	55	GSVIVG01000687001	104
qVvGA2-oxR	ATCGCCGCTTGATCCAATTC	55		
qVvGH3.5-F	TGCTGATGCCTGTGATGAAC	55	GSVIVT01000422001	146
qVvGH3.5-R	TTTGACACAGCCCACAAAGC	56		
qVvYUC10F	CAGGGGAAAATGGAATGTTGGG	56	GSVIVT01011005001	94
qVvYUC10R	ACAAACGCATCGCTCGTTTC	56		
qIAA11-F	TTCTATTGGCTGCCGTTGT	57	GSVIVG01027166001	226
qIAA11-R	AGCACGACCAACTGCTACTC	57		
qTAR2F	GGGGGACATAACAACCATTG	54	GSVIVG01007679001	74
qTAR2R	GGCTCCAAAAACCAGCATAG	54		
qGA20ox53001F	TGGGTGGCCTTCAAGTGTTT	57.5	GSVIVG01018453001	91
qGA20ox53001R	ATGAAGGTGTCGCCGATGTT	57		
qLAX3-F	GAAAGGGAAGAAGGCGATTC	54	GSVIVG01008917001	113
qLAX3-R	TGGGCAACCTGATTAGAAGC	55		
qGA20ox72001F	TTGTGAAGCCATGAGCAGAC	55	GSVIVG01027572001	143
qGA20ox72001R	GTTTTTGGCATGGTGGGTAG	54		
qVvUBI99-F	TCTGAGGCTTCGTGGTGTA	56	TC53702 (TGI database)	99
qVvUBI99-R	AGGCGTGCATAACATTTGCG	56		
qVvActin-F	TCCTTGCCTTGCGTCATCTAT	55	XM_002282480.2	80
qVvActin-R	CACCAATCACTCTCCTGCTACAA	56		

Supplemental Table 1: Primers used for gene amplification

Grapevine ID	S1	S2	val_1	val_2	log2 (fold_change)	Functional Annotation
GSVIVG01014558001	T2	T12	24,9461	0,00509595	-12,2572	Vetispiradiene synthase
GSVIVG01014558001	T0	T12	21,6472	0,00509595	-12,0525	Vetispiradiene synthase
GSVIVG01014557001	T2	T12	17,5262	0,00455225	-11,9106	(-)-germacrene D synthase
GSVIVG01014557001	T0	T12	16,9322	0,00455225	-11,8609	(-)-germacrene D synthase
GSVIVG01036342001	T2	T12	485,962	0,153794	-11,6256	valencene synthase-like
GSVIVG01036352001	T0	T12	246,276	0,0862979	-11,4787	valencene synthase-like
GSVIVG01036352001	T2	T12	246,048	0,0862979	-11,4773	valencene synthase-like
GSVIVG01017588001	T0	T12	301,295	0,115228	-11,3525	CYP82A2
GSVIVG01036315001	T0	T12	162,946	0,0623352	-11,3521	(-)-germacrene D synthase
GSVIVG01003153001	T0	T12	789,229	0,397976	-10,9535	Cinnamyl alcohol dehydrogenase
GSVIVG01036315001	T2	T12	117,368	0,0623352	-10,8787	(-)-germacrene D synthase
GSVIVG01036342001	T0	T12	246,855	0,153794	-10,6484	valencene synthase-like
GSVIVG01008191001	T0	T12	293,058	0,185302	-10,6271	Strictosidine synthase
GSVIVG01017582001	T0	T12	399,339	0,265595	-10,5542	CYP82M1v3
GSVIVG01024756001	T0	T12	16,3692	0,0111805	-10,5158	CYP71E
GSVIVG01019901001	T0	T12	2,67967	0,00249647	-10,068	Subtilisin P69F protein
GSVIVG01028186001	T0	T12	489,111	0,462113	-10,0477	Boron transporter-like protein 1
GSVIVG01017588001	T2	T12	116,537	0,115228	-9,98208	CYP82A2
GSVIVG01025660001	T0	T6	10,1009	0,0102964	-9,93812	fasciclin arabinogalactan-protein (FLA11)
GSVIVG01038174001	T0	T12	28,532	0,0337991	-9,72138	Stearoyl-acyl-[acyl-carrier-protein] desaturase
GSVIVG01011584001	T0	T12	212,365	0,266091	-9,64041	Chalcone reductase
GSVIVG01003153001	T2	T12	309,954	0,397976	-9,60516	Cinnamyl alcohol dehydrogenase
GSVIVG01031038001	T0	T12	50,4734	0,0753193	-9,38829	CYP735A1
GSVIVG01015567001	T0	T12	149,357	0,229965	-9,34314	Axial regulator YABBY5
GSVIVG01015567001	T2	T12	141,694	0,229965	-9,26715	Axial regulator YABBY5
GSVIVG01028966001	T0	T6	2,36083	0,00393843	-9,22746	HcrVf3 protein
GSVIVG01015408001	T0	T12	2,75951	0,00487783	-9,14396	Sec7 domain-containing protein
GSVIVG01011584001	T2	T12	149,813	0,266091	-9,13703	Chalcone reductase
GSVIVG01027067001	T0	T12	4,57251	0,00826432	-9,1187	NADPH HC toxin reductase
GSVIVG01036344001	T0	T12	97,4407	0,177005	-9,10459	valencene synthase-like
GSVIVG01028186001	T2	T12	250,149	0,462113	-9,08033	Boron transporter-like protein 1
GSVIVG01037073001	T0	T12	278,127	0,51425	-9,07906	Isoflavone reductase protein 2
GSVIVG01028152001	T0	T12	68,0092	0,125932	-9,07694	Glycerol-3-phosphate acyltransferase 3 (AtGPAT3)
GSVIVG01019695001	T0	T12	115,979	0,218694	-9,05073	Naringenin,2-oxoglutarate 3-dioxygenase
GSVIVG01027572001	T0	T12	4,57956	0,00872165	-9,03639	Gibberellin 20-oxidase
GSVIVG01027067001	T2	T12	4,19168	0,00826432	-8,98642	NADPH HC toxin reductase
GSVIVG01036344001	T2	T12	86,8725	0,177005	-8,93897	valencene synthase-like
GSVIVG01017582001	T2	T12	126,078	0,265595	-8,89087	CYP82M1v3
GSVIVG01024031001	T0	T12	2,76156	0,00609177	-8,82441	D-galactoside/L-rhamnose binding SUEL lectin
GSVIVG01021359001	T0	T12	25,0119	0,0554617	-8,81691	Xyloglucan endotransglycosylase/hydrolase precursor
GSVIVG01036343001	T0	T12	73,765	0,168606	-8,77313	Germacrene-D synthase
GSVIVG01034049001	T0	T12	3,31461	0,0077892	-8,73315	TTL1 (tetrairicopeptide-repeat thioredoxin-like 1)
GSVIVG01019901001	T2	T12	1,04315	0,00249647	-8,70684	Subtilisin P69F protein
GSVIVG01037073001	T2	T12	212,708	0,51425	-8,69218	Isoflavone reductase protein 2
GSVIVG01038764001	T2	T12	1,57905	0,00383936	-8,68398	Leucine-rich repeat protein kinase
GSVIVG01036343001	T2	T12	67,9829	0,168606	-8,65537	Germacrene-D synthase
GSVIVG01008191001	T2	T12	67,8616	0,185302	-8,51657	Strictosidine synthase
GSVIVG01035076001	T2	T12	333,498	0,930914	-8,48481	Pathogenesis protein 10 [Vitis vinifera]
GSVIVG01030106001	T0	T12	61,501	0,183594	-8,38795	AarF domain containing kinase
GSVIVG01027579001	T0	T12	4,63585	0,0143483	-8,33581	MADS-box protein AGL20
GSVIVG01027448001	T0	T12	2166,48	6,72098	-8,33246	Catechol O-methyltransferase
GSVIVG01032452001	T0	T12	1053,26	3,38949	-8,27957	Myb domain protein 24
GSVIVG01024756001	T2	T12	3,4267	0,0111805	-8,25969	CYP71E
GSVIVG01035692001	T2	T12	2,78202	0,00962374	-8,17532	RD22 [Vitis vinifera]
GSVIVG01018904001	T6	T12	141,982	0,524825	-8,07966	S-adenosyl-L-methionine:salicylic acid carboxyl
GSVIVG01035695001	T2	T12	166,719	0,650642	-8,00134	RD22
GSVIVG01013162001	T0	T12	8,26572	0,032564	-7,98772	Microspore-specific promoter 2
GSVIVG01008829001	T0	T6	13,2262	0,0522891	-7,98268	Metal transporter Nramp1
GSVIVG01030865001	T6	T12	12,6199	0,0512343	-7,94438	PMI2 (plastid movement impaired 2)
GSVIVG01033362001	T0	T2	0,650961	0,00268532	-7,92134	Polygalacturonase PG1
GSVIVG01015958001	T6	T12	12,8735	0,0546899	-7,87891	N-acetyltransferase hookless1 HLS1
GSVIVG01030106001	T2	T12	42,9745	0,183594	-7,87082	AarF domain containing kinase
GSVIVG01028055001	T6	T12	159,384	0,684267	-7,86373	Erg-1
GSVIVG01019695001	T2	T12	50,1642	0,218694	-7,8416	Naringenin,2-oxoglutarate 3-dioxygenase
GSVIVG01027449001	T2	T12	1149,46	5,1558	-7,80054	Caffeate 3-O-methyltransferase 1
GSVIVG01014531001	T2	T6	2,37536	0,0108774	-7,77066	S-locus protein kinase
GSVIVG01000402001	T0	T12	1179,71	5,60398	-7,71776	#####
GSVIVG01027456001	T0	T12	630,835	3,00312	-7,71466	Myb CCA1 (circadian clock associated 1)
GSVIVG01014557001	T6	T12	0,947966	0,00455225	-7,70211	(-)-germacrene D synthase

GSVIVG01014558001	T6	T12	1,04745	0,00509595	-7,68331	Vetispiradiene synthase
GSVIVG01035076001	T0	T12	189,31	0,930914	-7,66789	Pathogenesis protein 10 [Vitis vinifera]
GSVIVG01021359001	T0	T6	25,0119	0,124589	-7,6493	Xyloglucan endotransglycosylase/hydrolase precursor
GSVIVG01035272001	T0	T12	255,953	1,28768	-7,63496	Acyl-CoA synthetases (Acyl-activating enzyme 11)
GSVIVG01024031001	T2	T12	1,20068	0,00609177	-7,62278	D-galactoside/L-rhamnose binding SUEL lectin
GSVIVG01008890001	T6	T12	9,11764	0,046424	-7,61765	Nodulin MtN21 family
GSVIVG01007896001	T6	T12	2,72389	0,0140099	-7,60308	UDP-glucosyltransferase HRA25
GSVIVG01035013001	T6	T12	143,012	0,742126	-7,59025	Beta-1,3-glucanase
GSVIVG01031975001	T0	T12	2007,22	10,7469	-7,54514	Myb RAD (Transcription factor RAD)
GSVIVG01027448001	T2	T12	1248,42	6,72098	-7,53722	Catechol O-methyltransferase
GSVIVG01035695001	T0	T12	120,526	0,650642	-7,53327	RD22
GSVIVG01025660001	T2	T6	1,90719	0,0102964	-7,53316	fasciclin arabinogalactan-protein (FLA11)
GSVIVG01011699001	T0	T12	7,40824	0,0406688	-7,50907	Pectinesterase family
GSVIVG01028055001	T2	T12	122,907	0,684267	-7,48879	Erg-1
GSVIVG01019901001	T6	T12	0,445841	0,00249647	-7,4805	Subtilisin P69F protein
GSVIVG01000403001	T0	T12	827,297	4,64624	-7,4762	isoprene synthase
GSVIVG01007042001	T6	T12	2,48496	0,0140737	-7,46407	cellulose synthase-like protein e6-like
GSVIVG01019886001	T0	T6	32,6766	0,188235	-7,43957	Senescence-inducible chloroplast stay-green protein 2
GSVIVG01014591001	T0	T12	13,264	0,0769818	-7,42879	Constans-like 11
GSVIVG01019017001	T2	T12	31,0381	0,183266	-7,40396	Anthocyanidin 3-O-glucosyltransferase
GSVIVG01009849001	T0	T12	16,1416	0,0962374	-7,38997	Cytochrome P450, family 83, subfamily B, polypeptide 1
GSVIVG01010047001	T6	T12	55,8832	0,339267	-7,36385	Pathogen-related
GSVIVG01030133001	T0	T12	4,04821	0,0250269	-7,33766	Exostosin
GSVIVG01038174001	T2	T12	5,31462	0,0337991	-7,29684	Stearoyl-acyl-[acyl-carrier-protein] desaturase
GSVIVG01011445001	T6	T12	137,618	0,878677	-7,29112	NAC domain containing protein 100
GSVIVG01035272001	T0	T6	255,953	1,66786	-7,26174	Acyl-CoA synthetases (Acyl-activating enzyme 11)
GSVIVG01037011001	T6	T12	14,069	0,0936163	-7,23155	Pathogenesis related protein 1 precursor [Vitis vinifera]
GSVIVG01031982001	T0	T12	50,9001	0,347986	-7,19249	Radialis-like protein 6
GSVIVG01030133001	T2	T12	3,65025	0,0250269	-7,18837	Exostosin
GSVIVG01004118001	T2	T12	61,6115	0,430172	-7,16214	Disease resistance protein
GSVIVG01008191001	T0	T6	293,058	2,06571	-7,14841	Strictosidine synthase
GSVIVG01038069001	T0	T12	24,8435	0,175144	-7,14818	3-ketoacyl-CoA synthase
GSVIVG01034563001	T0	T12	28,5552	0,202044	-7,14294	Ethylene-responsive transcription factor related to
GSVIVG01028236001	T6	T12	12,5196	0,0886275	-7,14222	CYP709B2
GSVIVG01038125001	T6	T12	63,6436	0,452072	-7,13732	Chitinase class IV
GSVIVG01031466001	T2	T12	1,47949	0,0105723	-7,12867	BHLH transcriptional regulator bHLH029
GSVIVG01035061001	T6	T12	13,2942	0,0953794	-7,12291	pathogenesis-related protein 10
GSVIVG01032452001	T2	T12	468,54	3,38949	-7,11096	Myb domain protein 24
GSVIVG01031975001	T2	T12	1485,16	10,7469	-7,11055	Myb RAD (Transcription factor RAD)
GSVIVG01027572001	T2	T12	1,20332	0,00872165	-7,1082	Gibberellin 20-oxidase
GSVIVG01026806001	T0	T12	349,589	2,56031	-7,0932	Eceriferum 1 (CER1 protein) Sterol desaturase
GSVIVG01009875001	T0	T12	71,1518	0,523935	-7,08537	Auxin-induced SAUR
GSVIVG01005971001	T0	T12	461,771	3,47954	-7,05214	Esterase/lipase/thioesterase
GSVIVG01031038001	T0	T6	50,4734	0,380694	-7,05075	CYP735A1
GSVIVG01036331001	T0	T12	23,2757	0,177655	-7,0336	(-)-germacrene D synthase
GSVIVG01028152001	T2	T12	16,0114	0,125932	-6,99031	Glycerol-3-phosphate acyltransferase 3 (AtGPAT3)
GSVIVG01020928001	T0	T12	341,399	2,70092	-6,98186	Sucrose-phosphate synthase
GSVIVG01036331001	T2	T12	22,2868	0,177655	-6,97097	(-)-germacrene D synthase
GSVIVG01019886001	T0	T12	32,6766	0,260693	-6,96976	Senescence-inducible chloroplast stay-green protein 2
GSVIVG01033978001	T6	T12	21,2599	0,169802	-6,96814	Alpha-1,4-glycosyltransferase
GSVIVG01028055001	T0	T12	84,331	0,684267	-6,94536	Erg-1
GSVIVG01036352001	T6	T12	10,1389	0,0862979	-6,87635	valencene synthase-like
GSVIVG01009902001	T0	T12	122,29	1,06162	-6,84789	Gibberellin-regulated protein 1 (GASA1)
GSVIVG01027579001	T2	T12	1,64497	0,0143483	-6,84104	MADS-box protein AGL20
GSVIVG01006638001	T0	T12	1,96676	0,0173065	-6,82836	(E,E)-alpha-farnesene synthase
GSVIVG01030261001	T0	T12	2,73621	0,0241654	-6,82309	Protein phosphatase 1D
GSVIVG01013162001	T2	T12	3,67984	0,032564	-6,82022	Microspore-specific promoter 2
GSVIVG01000403001	T2	T12	519,623	4,64624	-6,80526	isoprene synthase
GSVIVG01011638001	T6	T12	24,4903	0,219342	-6,80288	S-adenosyl-L-methionine:salicylic acid carboxyl
GSVIVG01020785001	T2	T12	11,4991	0,103842	-6,79098	PMR5 (powdery mildew resistant 5)
GSVIVG01025864001	T0	T12	3,72207	0,0339287	-6,77746	Copper-binding family protein
GSVIVG01036328001	T0	T12	6,34516	0,0595275	-6,73596	Germacrene-D synthase
GSVIVG01032676001	T0	T6	11,4164	0,110076	-6,69647	MATE efflux family protein
GSVIVG01026810001	T0	T12	43,787	0,423828	-6,69088	Eceriferum 1 (CER1 protein) Sterol desaturase
GSVIVG01037742001	T0	T12	244,759	2,39608	-6,67454	Aspartyl protease
GSVIVG01006399001	T0	T12	8,6168	0,0843776	-6,67415	(E,E)-alpha-farnesene synthase
GSVIVG01024031001	T6	T12	0,611699	0,00609177	-6,64982	D-galactoside/L-rhamnose binding SUEL lectin
GSVIVG01013934001	T6	T12	1,79943	0,0181023	-6,63522	Ethylene-responsive transcription factor 5
GSVIVG01015743001	T2	T12	145,97	1,46912	-6,63458	Cis-zeatin O-beta-D-glucosyltransferase
GSVIVG01000402001	T2	T12	544,073	5,60398	-6,6012	#####
GSVIVG01026244001	T2	T12	1,2072	0,0125423	-6,58871	Serine carboxypeptidase II

GSVIVG01014325001	T0	T12	0,962496	0,0100461	-6,58208	(-)-germacrene D synthase
GSVIVG01024713001	T6	T12	875,428	9,31856	-6,55374	Asparagine synthetase
GSVIVG01010993001	T0	T6	31,7909	0,339926	-6,54725	Nodulin MtN3 family
GSVIVG01015743001	T0	T12	137,135	1,46912	-6,5445	Cis-zeatin O-beta-D-glucosyltransferase
GSVIVG01030865001	T2	T12	4,77983	0,0512343	-6,54371	PMI2 (plastid movement impaired 2)
GSVIVG01020785001	T0	T12	9,68082	0,103842	-6,54266	PMR5 (powdery mildew resistant 5)
GSVIVG01031982001	T0	T6	50,9001	0,547201	-6,53945	Radialis-like protein 6
GSVIVG01028186001	T0	T6	489,111	5,33565	-6,51835	Boron transporter-like protein 1
GSVIVG01027579001	T6	T12	1,31023	0,0143483	-6,5128	MADS-box protein AGL20
GSVIVG01021155001	T2	T12	42,6894	0,483765	-6,46343	glutamate receptor -like
GSVIVG01007896001	T2	T12	1,2288	0,0140099	-6,45465	UDP-glucosyltransferase HRA25
GSVIVG01019952001	T6	T12	282,461	3,23468	-6,44828	NAC domain-containing protein 29
GSVIVG01001082001	T2	T12	28,6522	0,328376	-6,44715	SOUL heme-binding
GSVIVG01019627001	T0	T12	3,49332	0,0401714	-6,44228	Aluminum activated malate transporter 1
GSVIVG01018142001	T2	T12	230,91	2,65545	-6,44223	Proteinase inhibitor 1 PPI3B2
GSVIVG01024756001	T0	T6	16,3692	0,188369	-6,44128	CYP71E
GSVIVG01024270001	T0	T12	650,461	7,61769	-6,41597	CYP89A5
GSVIVG01007896001	T0	T12	1,18538	0,0140099	-6,40276	UDP-glucosyltransferase HRA25
GSVIVG01037742001	T2	T12	195,589	2,39608	-6,35101	Aspartyl protease
GSVIVG01023922001	T6	T12	191,662	2,34958	-6,35002	Endochitinase 1, basic
GSVIVG01038069001	T0	T6	24,8435	0,306886	-6,33902	3-ketoacyl-CoA synthase
GSVIVG01027456001	T2	T12	240,197	3,00312	-6,32161	Myb CCA1 (circadian clock associated 1)
GSVIVG01019849001	T6	T12	191,195	2,39189	-6,32075	Osmotin
GSVIVG01017593001	T0	T6	27,041	0,339793	-6,31435	CYP82M1v4
GSVIVG01035061001	T2	T12	7,55285	0,0953794	-6,3072	pathogenesis-related protein 10
GSVIVG01001082001	T0	T12	25,8772	0,328376	-6,30019	SOUL heme-binding
GSVIVG01012363001	T0	T12	75,2185	0,957204	-6,29612	Myrcene synthase, chloroplastic
GSVIVG01036171001	T0	T12	0,73225	0,00934127	-6,29257	Male sterility 2 (MS2) Acyl-CoA reductase
GSVIVG01011582001	T2	T12	1,95262	0,0249228	-6,2918	Galacturonic acid reductase
GSVIVG01031975001	T0	T6	2007,22	25,7122	-6,28661	Myb RAD (Transcription factor RAD)
GSVIVG01018669001	T0	T12	16,7753	0,215456	-6,2828	SRG1 (senescence-related gene 1) oxidoreductase
GSVIVG01009875001	T2	T12	40,6676	0,523935	-6,27835	Auxin-induced SAUR
GSVIVG01019627001	T0	T6	3,49332	0,0451205	-6,27467	Aluminum activated malate transporter 1
GSVIVG01017588001	T0	T6	301,295	3,89332	-6,27403	CYP82A2
GSVIVG01026244001	T6	T12	0,963589	0,0125423	-6,26354	Serine carboxypeptidase II
GSVIVG01015682001	T0	T12	41,8592	0,554667	-6,23778	Zinc finger (C3HC4-type ring finger)
GSVIVG01030865001	T0	T12	3,84619	0,0512343	-6,23018	PMI2 (plastid movement impaired 2)
GSVIVG01011699001	T6	T12	2,9929	0,0406688	-6,20148	Pectinesterase family
GSVIVG01003280001	T0	T6	1,49218	0,0203177	-6,19854	Xyloglucan:xyloglucosyl transferase
GSVIVG01011873001	T0	T12	95,8254	1,31846	-6,18349	BEE1 (BR Enhanced expression 1)
GSVIVG01005971001	T2	T12	252,681	3,47954	-6,18228	Esterase/lipase/thioesterase
GSVIVG01036311001	T2	T6	3,32055	0,0463412	-6,16298	Sesquiterpene synthase
GSVIVG01017582001	T0	T6	399,339	5,57665	-6,16207	CYP82M1v3
GSVIVG01031738001	T0	T12	108,972	1,53076	-6,15356	ABA 8'-hydroxylase CYP707A1
GSVIVG01003153001	T6	T12	28,0298	0,397976	-6,13814	Cinnamyl alcohol dehydrogenase
GSVIVG01037719001	T0	T12	47,4297	0,682722	-6,11835	Light induced protein like
GSVIVG01009319001	T6	T12	7,06997	0,102801	-6,10378	Serine carboxypeptidase S10
GSVIVG01026244001	T0	T12	0,85833	0,0125423	-6,09665	Serine carboxypeptidase II
GSVIVG01036311001	T0	T6	3,12295	0,0463412	-6,07447	Sesquiterpene synthase
GSVIVG01014591001	T2	T12	5,18412	0,0769818	-6,07344	Constans-like 11
GSVIVG01015125001	T6	T12	25,3503	0,378026	-6,06738	Ankyrin repeat family protein
GSVIVG01008553001	T6	T12	73,8658	1,10407	-6,064	WRKY DNA-binding protein 75
GSVIVG01034731001	T2	T12	16,9538	0,253414	-6,06397	Gamma-aminobutyric acid transporter
GSVIVG01033904001	T0	T12	61,8652	0,924963	-6,06359	Pro-X carboxypeptidase Lysosomal
GSVIVG01037758001	T0	T12	635,476	9,73122	-6,02907	Pirin
GSVIVG01010098001	T0	T12	116,624	1,79778	-6,01951	UDP-glucuronosyl and UDP-glucosyl transferase
GSVIVG01029269001	T0	T12	4,22134	0,0651387	-6,01804	Allyl alcohol dehydrogenase
GSVIVG01024193001	T0	T12	276,349	4,29842	-6,00654	ferulate 5-hydroxylase
GSVIVG01025223001	T0	T12	9,22501	0,143538	-6,00605	Kiwellin Ripening-related protein grip22
GSVIVG01012363001	T0	T6	75,2185	1,17613	-5,99897	Myrcene synthase, chloroplastic
GSVIVG01025051001	T6	T12	6,30024	0,0986955	-5,99628	Exocyst subunit EXO70 H7
GSVIVG01007043001	T0	T12	344,795	5,40581	-5,99508	Cellulose synthase CSLE1
GSVIVG01001263001	T6	T12	1,65311	0,0262351	-5,97754	Auxin-responsive SAUR11
GSVIVG01037077001	T0	T12	145,723	2,32077	-5,97248	Isoflavone reductase
GSVIVG01018044001	T2	T12	2494,65	40,0299	-5,96162	ELIP1 (early light-inducible protein)
GSVIVG01035122001	T0	T12	26,0558	0,420137	-5,9546	MATE efflux family protein
GSVIVG01019886001	T2	T6	11,5916	0,188235	-5,9444	Senescence-inducible chloroplast stay-green protein 2
GSVIVG01008267001	T0	T12	999,902	16,3291	-5,93627	Aspartyl protease
GSVIVG01002752001	T0	T2	86,0812	1,43033	-5,91128	NADH dehydrogenase subunit 3
GSVIVG01021359001	T2	T12	3,3098	0,0554617	-5,89911	Xyloglucan endotransglycosylase/hydrolase precursor
GSVIVG01028851001	T6	T12	16,1924	0,271773	-5,89677	Metal ion binding

GSVIVG01024186001	T0	T12	72,0673	1,21111	-5,89494	ferulate 5-hydroxylase
GSVIVG01035306001	T0	T12	2,39337	0,0402598	-5,89356	Leucine-rich repeat family protein
GSVIVG01029838001	T0	T12	138,716	2,34704	-5,88515	Translation initiation factor IF-2B subunit delta
GSVIVG01032983001	T2	T12	58,4236	0,991579	-5,88068	Ethylene-responsive transcription factor ERF113
GSVIVG01019012001	T6	T12	542,401	9,22129	-5,87825	Homeobox protein 5
GSVIVG01026962001	T0	T6	2,37623	0,0409009	-5,8604	ACC synthase
GSVIVG01015420001	T0	T12	21,3209	0,368746	-5,85349	Copper-binding family protein
GSVIVG01036315001	T6	T12	3,60077	0,0623352	-5,85211	(-)-germacrene D synthase
GSVIVG01031975001	T2	T6	1485,16	25,7122	-5,85202	Myb RAD (Transcription factor RAD)
GSVIVG01008889001	T0	T12	4,62537	0,0801344	-5,851	Nodulin MtN21 family
GSVIVG01009723001	T0	T12	3,96223	0,0687279	-5,84927	Radialis-like protein 6
GSVIVG01025276001	T0	T12	12,5335	0,217616	-5,84786	Aldehyde dehydrogenase 3B1
GSVIVG01032676001	T0	T12	11,4164	0,198844	-5,84333	MATE efflux family protein
GSVIVG01022916001	T0	T12	273,39	4,79333	-5,83378	Cupin
GSVIVG01010807001	T2	T12	23,3653	0,409688	-5,8337	Strictosidine synthase
GSVIVG01035076001	T6	T12	52,6591	0,930914	-5,82189	Pathogenesis protein 10 [Vitis vinifera]
GSVIVG01011380001	T0	T12	69,5478	1,23752	-5,81248	Basic helix-loop-helix (bHLH) family
GSVIVG01034563001	T2	T12	11,2419	0,202044	-5,79807	Ethylene-responsive transcription factor related to
GSVIVG01011066001	T2	T12	2,35767	0,0425521	-5,79199	GATL4 (Galacturonosyltransferase-like 4)
GSVIVG01014532001	T2	T6	1,49947	0,0271429	-5,78774	S-locus protein kinase
GSVIVG01001210001	T6	T12	0,746368	0,0136729	-5,7705	Chlorophyllase 1
GSVIVG01037121001	T0	T12	66,2509	1,22188	-5,76077	Avr9 elicitor response
GSVIVG01024563001	T2	T12	10,4787	0,193326	-5,76028	Lipid transfer protein 3
GSVIVG01038125001	T0	T12	24,4832	0,452072	-5,7591	Chitinase class IV
GSVIVG01008655001	T2	T12	18,5414	0,343245	-5,75537	LEAFY protein (Floricaula/leafy protein)
GSVIVG01024838001	T6	T12	4,36815	0,0812754	-5,74806	copper transporter
GSVIVG01034896001	T0	T12	12,305	0,229561	-5,74422	Nodulin
GSVIVG01018044001	T0	T12	2144,49	40,0299	-5,74341	ELIP1 (early light-inducible protein)
GSVIVG01018982001	T2	T12	2,06955	0,0389853	-5,73024	Proline extensin-like receptor kinase 1 (PERK1)
GSVIVG01010807001	T2	T6	23,3653	0,440786	-5,72814	Strictosidine synthase
GSVIVG01032550001	T0	T12	2,57053	0,0484954	-5,72808	Proton-dependent oligopeptide transport (POT) family
GSVIVG01025002001	T2	T12	0,567327	0,0108391	-5,70986	Nitric-oxide reductase, cytochrome b-containing subunit I
GSVIVG01019840001	T0	T12	10,3465	0,198227	-5,70585	Thaumatococcus
GSVIVG01031954001	T2	T12	1,31141	0,0251869	-5,7023	Proline extensin-like receptor kinase 1 (PERK1)
GSVIVG01034896001	T2	T12	11,9149	0,229561	-5,69774	Nodulin
GSVIVG01037667001	T2	T12	2,61623	0,0504064	-5,69774	Myb domain protein 101
GSVIVG01022520001	T0	T12	79,1056	1,52414	-5,69771	Translation initiation factor eIF-2 beta subunit
GSVIVG01036342001	T2	T6	485,962	9,37985	-5,69513	valencene synthase-like
GSVIVG01011733001	T0	T12	6,43771	0,124373	-5,69381	Major latex-like protein 34
GSVIVG01036599001	T2	T12	18,247	0,355181	-5,68296	Steroid sulfotransferase
GSVIVG01007968001	T0	T12	29,2223	0,573179	-5,67194	Exonuclease
GSVIVG01031738001	T2	T12	77,8731	1,53076	-5,66881	ABA 8'-hydroxylase CYP707A1
GSVIVG01008829001	T0	T12	13,2262	0,260479	-5,66609	Metal transporter Nramp1
GSVIVG01021490001	T0	T12	4,5931	0,0907725	-5,66107	Beta-amylin synthase
GSVIVG01026595001	T0	T6	7,4072	0,146777	-5,65723	MTN21
GSVIVG01008829001	T2	T6	2,63619	0,0522891	-5,6558	Metal transporter Nramp1
GSVIVG01037667001	T0	T12	2,50278	0,0504064	-5,63378	Myb domain protein 101
GSVIVG01008072001	T2	T12	426,513	8,63234	-5,62669	probable peptide nitrate transporter at5g62680-like
GSVIVG01006876001	T2	T12	147,25	2,98628	-5,62378	Aspartic proteinase nepenthesin-1 precursor
GSVIVG01020928001	T0	T6	341,399	6,92825	-5,62282	Sucrose-phosphate synthase
GSVIVG01024267001	T0	T12	201,382	4,09189	-5,62102	CYP89A2
GSVIVG01028851001	T0	T12	13,294	0,271773	-5,61223	Metal ion binding
GSVIVG01008597001	T0	T6	9,35969	0,191423	-5,61163	Nodulin MtN3 family
GSVIVG01007777001	T0	T12	3,05072	0,0625998	-5,60685	Nodulin MtN3
GSVIVG01030668001	T0	T6	14,465	0,298143	-5,60042	Potassium channel SKOR
GSVIVG01034731001	T0	T12	12,2947	0,253414	-5,6004	Gamma-aminobutyric acid transporter
GSVIVG01010312001	T0	T6	4,41302	0,0914365	-5,59285	Vinoreline synthase
GSVIVG01009849001	T6	T12	4,63074	0,0962374	-5,5885	Cytochrome P450, family 83, subfamily B, polypeptide 1
GSVIVG01007614001	T6	T12	5,34904	0,111792	-5,5804	CYP71A26
GSVIVG01034985001	T2	T12	2,14295	0,0449275	-5,57586	Pectinesterase family
GSVIVG01026879001	T0	T12	3,91818	0,0831925	-5,55759	Cofilin
GSVIVG01028186001	T2	T6	250,149	5,33565	-5,55098	Boron transporter-like protein 1
GSVIVG01013272001	T0	T12	179,134	3,87447	-5,5309	1,4-alpha-D-glucan maltohydrolase
GSVIVG01031885001	T6	T12	1,09487	0,0236826	-5,53079	AOS (allene oxide synthase)
GSVIVG01025060001	T2	T12	1,74506	0,0377647	-5,53009	Leucine-rich repeat protein kinase
GSVIVG01033359001	T0	T12	5,24385	0,114626	-5,51562	Polygalacturonase PG1
GSVIVG01018142001	T0	T12	121,197	2,65545	-5,51225	Proteinase inhibitor 1 PPI3B2
GSVIVG01011005001	T0	T12	18,6193	0,408409	-5,51064	flavin-containing monooxygenase
GSVIVG01037073001	T0	T6	278,127	6,135	-5,50254	Isoflavone reductase protein 2
GSVIVG01036315001	T0	T6	162,946	3,60077	-5,49994	(-)-germacrene D synthase
GSVIVG01033904001	T2	T12	41,6652	0,924963	-5,49331	Pro-X carboxypeptidase Lysosomal

GSVIVG01027761001	T0	T12	4,08234	0,0908964	-5,48903	1-aminocyclopropane-1-carboxylate oxidase homolog 1
GSVIVG01036599001	T0	T12	15,9386	0,355181	-5,48782	Steroid sulfotransferase
GSVIVG01036330001	T0	T6	5,04614	0,112473	-5,48753	(+)-delta-cadinene synthase isozyme XC1
GSVIVG01017118001	T0	T12	64,8834	1,4549	-5,47886	Sulfate transporter 3.4
GSVIVG01019886001	T2	T12	11,5916	0,260693	-5,47459	Senescence-inducible chloroplast stay-green protein 2
GSVIVG01011424001	T6	T12	2,57349	0,0579466	-5,47286	Beta-1,3-galactosyltransferase
GSVIVG01011637001	T6	T12	41,8432	0,943013	-5,47157	S-adenosyl-L-methionine:carboxyl methyltransferase
GSVIVG01032263001	T2	T12	1,01328	0,0228826	-5,46863	Receptor-like protein kinase PRK1
GSVIVG01016362001	T6	T12	6,13271	0,13858	-5,46774	Anthocyanin 5-aromatic acyltransferase
GSVIVG01020177001	T0	T12	27,3289	0,618925	-5,46452	N-hydroxythioamide S-beta-glucosyltransferase
GSVIVG01004265001	T2	T12	129,658	2,94224	-5,46165	Aspartic proteinase nepenthesin-1 precursor
GSVIVG01007043001	T2	T12	238,112	5,40581	-5,46099	Cellulose synthase CSLE1
GSVIVG01019916001	T6	T12	2,65611	0,0603698	-5,45934	Carboxyl-terminal peptidase
GSVIVG01009381001	T0	T12	20,5134	0,468053	-5,45375	Tetrapeptide repeat (TPR)-containing
GSVIVG01016352001	T2	T12	1,00845	0,0231397	-5,44562	APETALA2 (AP2) floral homeotic protein
GSVIVG01026962001	T0	T12	2,37623	0,054622	-5,44305	ACC synthase
GSVIVG01008595001	T0	T12	285,485	6,56435	-5,44262	Nodulin MtN3 family
GSVIVG01036322001	T2	T6	0,645571	0,0148809	-5,43904	(-)-germacrene D synthase
GSVIVG01037758001	T2	T12	421,868	9,73122	-5,43803	Pirin
GSVIVG01037719001	T2	T12	29,391	0,682722	-5,42793	Light induced protein like
GSVIVG01004595001	T6	T12	24,4472	0,568096	-5,42739	Expansin beta 1 precursor
GSVIVG01018878001	T6	T12	84,886	1,97702	-5,42412	Dehydrin 1b
GSVIVG01020511001	T0	T12	2,38104	0,0557363	-5,41683	WAG1
GSVIVG01008597001	T2	T6	8,14032	0,191423	-5,41025	Nodulin MtN3 family
GSVIVG01008072001	T0	T12	365,873	8,63234	-5,40545	probable peptide nitrate transporter at5g62680-like
GSVIVG01030227001	T6	T12	24,9197	0,59074	-5,39862	Alanine--glyoxylate aminotransferase 2 3, mitochondrial
GSVIVG01032000001	T0	T12	0,779111	0,018489	-5,39709	Disease resistance protein (NBS-LRR class)
GSVIVG01035812001	T0	T12	2,8747	0,0683171	-5,39502	Ammonium transporter 2
GSVIVG01036862001	T0	T12	21,1592	0,502968	-5,39468	9-cis-epoxycarotenoid dioxygenase
GSVIVG01010047001	T2	T12	14,1354	0,339267	-5,38075	Pathogen-related
GSVIVG01009902001	T2	T12	44,1042	1,06162	-5,37657	Gibberellin-regulated protein 1 (GASA1)
GSVIVG01038599001	T0	T12	41,4088	1,00406	-5,36602	Oligopeptide transporter 6
GSVIVG01006642001	T0	T6	5,2504	0,127331	-5,36577	(E,E)-alpha-farnesene synthase
GSVIVG01018217001	T0	T12	1,81934	0,0442192	-5,3626	Carotenoid cleavage dioxygenase 7, chloroplast (AtCCD7)
GSVIVG01031170001	T0	T12	5,41954	0,13195	-5,3601	Nodulin MtN3 family
GSVIVG01011584001	T0	T6	212,365	5,206	-5,35023	Chalcone reductase
GSVIVG01021155001	T0	T12	19,6746	0,483765	-5,34588	glutamate receptor -like
GSVIVG01014073001	T0	T12	29,8839	0,455577	-5,32487	Purine permease 11 PUP11
GSVIVG01038174001	T0	T6	28,532	0,713708	-5,32111	Stearoyl-acyl-[acyl-carrier-protein] desaturase
GSVIVG01010959001	T0	T6	14,3975	0,361761	-5,31463	Nuclear transcription factor Y subunit B-5
GSVIVG01024270001	T0	T6	650,461	16,4191	-5,30801	CYP89A5
GSVIVG01032999001	T0	T12	5,10113	0,128906	-5,30643	Sex determination protein tasselseed-2
GSVIVG01005286001	T0	T12	6,75808	0,171743	-5,29829	33 kDa secretory protein
GSVIVG01038172001	T0	T6	7,07389	0,179782	-5,29818	Stearoyl-acyl-carrier protein desaturase
GSVIVG01024563001	T6	T12	7,59568	0,193326	-5,29607	Lipid transfer protein 3
GSVIVG01036339001	T0	T2	4,80284	0,122271	-5,29573	(+)-delta-cadinene synthase
GSVIVG01022916001	T2	T12	188,269	4,79333	-5,29562	Cupin
GSVIVG01030613001	T0	T12	4,61055	0,118259	-5,28492	Legumin
GSVIVG01001842001	T0	T12	5,35424	0,13748	-5,28338	Glyceraldehyde-3-phosphate dehydrogenase
GSVIVG01024578001	T6	T12	11,087	0,286907	-5,27214	WNK5 (Arabidopsis WNK kinase 5)
GSVIVG01029838001	T2	T12	90,6018	2,34704	-5,27063	Translation initiation factor IF-2B subunit delta
GSVIVG01019910001	T6	T12	16,3268	0,424448	-5,26552	cytochrome p450
GSVIVG01020511001	T2	T12	2,14219	0,0557363	-5,26432	WAG1
GSVIVG01036339001	T0	T6	4,80284	0,125421	-5,25904	(+)-delta-cadinene synthase
GSVIVG01034943001	T6	T12	14,5304	0,379991	-5,25696	Myb domain protein 108
GSVIVG01009849001	T2	T12	3,67985	0,0962374	-5,25691	Cytochrome P450, family 83, subfamily B, polypeptide 1
GSVIVG01035695001	T6	T12	24,8612	0,650642	-5,25589	RD22
GSVIVG01003731001	T2	T12	2,00587	0,0525748	-5,25371	Glycerophosphodiester phosphodiesterase
GSVIVG01037077001	T2	T12	87,6726	2,32077	-5,23945	Isoflavone reductase
GSVIVG01033020001	T0	T6	60,4906	1,60367	-5,23726	UPF0497 family
GSVIVG01011873001	T6	T12	49,6777	1,31846	-5,23568	BEE1 (BR Enhanced expression 1)
GSVIVG01007418001	T0	T12	3,40866	0,0910784	-5,22595	flavonoid 3-monooxygenase
GSVIVG01011222001	T0	T12	0,936896	0,0252864	-5,21146	Lipase GDSL
GSVIVG01017484001	T6	T12	11,3843	0,309642	-5,2003	Photosystem I P700 chlorophyll a apoprotein A1
GSVIVG01020928001	T2	T12	99,185	2,70092	-5,1986	Sucrose-phosphate synthase
GSVIVG01000187001	T0	T12	1,25221	0,0344389	-5,18429	CYP81E1 Isoflavone 2'-hydroxylase
GSVIVG01017147001	T6	T12	7,64923	0,210582	-5,18286	Kelch repeat-containing F-box family protein
GSVIVG01008649001	T2	T12	6,5522	0,18299	-5,16214	Ethylene-responsive transcription factor ERF114
GSVIVG01028044001	T2	T12	2,8498	0,0796556	-5,16094	Polygalacturonase PGA4
GSVIVG01024592001	T0	T12	7,55884	0,211507	-5,15939	Lateral organ boundaries Domain 15
GSVIVG01010807001	T0	T12	14,5774	0,409688	-5,15306	Strictosidine synthase

GSVIVG01006485001	T0	T12	36,2788	1,0213	-5,15065	NAC domain-containing protein 25
GSVIVG01019715001	T0	T12	2,48759	0,0705616	-5,13972	Nodulin MtN21 family
GSVIVG01024592001	T2	T12	7,43046	0,211507	-5,13468	Lateral organ boundaries Domain 15
GSVIVG01000687001	T6	T12	39,9277	1,14186	-5,12793	Gibberellin 2-beta-dioxygenase 1
GSVIVG01027652001	T6	T12	163,408	4,69302	-5,12182	Pectinesterase family
GSVIVG01026810001	T0	T6	43,787	1,26107	-5,11779	Eceriferum 1 (CER1 protein) Sterol desaturase
GSVIVG01037073001	T2	T6	212,708	6,135	-5,11566	Isoflavone reductase protein 2
GSVIVG01015682001	T2	T12	19,1714	0,554667	-5,11119	Zinc finger (C3HC4-type ring finger)
GSVIVG01033248001	T0	T12	8,52454	0,24738	-5,10682	Glycosyl transferaseHGA1
GSVIVG01036879001	T6	T12	15,7432	0,459122	-5,0997	protein
GSVIVG01024193001	T2	T12	146,944	4,29842	-5,09532	ferulate 5-hydroxylase
GSVIVG01026806001	T0	T6	349,589	10,2288	-5,09495	Eceriferum 1 (CER1 protein) Sterol desaturase
GSVIVG01031614001	T6	T12	5,66898	0,16593	-5,09444	UDP-glucose:flavonoid 7-O-glucosyltransferase
GSVIVG01026627001	T6	T12	5,12237	0,150264	-5,09124	Monooxygenase
GSVIVG01017588001	T6	T12	3,89332	0,115228	-5,07843	CYP82A2
GSVIVG01015345001	T2	T12	1,88601	0,0558614	-5,07734	Xyloglucan endo-transglycosylase, C-terminal
GSVIVG01009902001	T6	T12	35,7367	1,06162	-5,07306	Gibberellin-regulated protein 1 (GASA1)
GSVIVG01022520001	T2	T12	51,1262	1,52414	-5,06799	Translation initiation factor eIF-2 beta subunit
GSVIVG01010525001	T6	T12	60,1534	1,79746	-5,06462	WRKY DNA-binding protein 75
GSVIVG01010015001	T0	T12	83,6003	2,50163	-5,06257	Nodulin MtN3 family
GSVIVG01001422001	T6	T12	7,36332	0,220587	-5,06094	Alliin lyase precursor
GSVIVG01037496001	T0	T6	4,55212	0,137119	-5,05304	Amino acid permease
GSVIVG01019696001	T0	T12	29,1797	0,879196	-5,05264	flavanone 3-beta-hydroxylase
GSVIVG01003973001	T0	T12	3,07895	0,0927943	-5,05226	PQ-loop repeat / transmembrane
GSVIVG01020785001	T6	T12	3,44263	0,103842	-5,05105	PMR5 (powdery mildew resistant 5)
GSVIVG01010807001	T0	T6	14,5774	0,440786	-5,04751	Strictosidine synthase
GSVIVG01017147001	T0	T12	6,94351	0,210582	-5,04321	Kelch repeat-containing F-box family protein
GSVIVG01011873001	T2	T12	43,3231	1,31846	-5,03821	BEE1 (BR Enhanced expression 1)
GSVIVG01008191001	T2	T6	67,8616	2,06571	-5,03789	Strictosidine synthase
GSVIVG01013455001	T6	T12	10,084	0,307387	-5,03586	PLATZ transcription factor
GSVIVG01024852001	T6	T12	32,9591	1,00603	-5,03393	Glutathione S-transferase 25 GSTU7
GSVIVG01038039001	T0	T6	841,617	25,699	-5,03338	Glutathione S-transferase 25 GSTU25
GSVIVG01036315001	T2	T6	117,368	3,60077	-5,0266	(-)-germacrene D synthase
GSVIVG01015567001	T6	T12	7,49577	0,229965	-5,02659	Axial regulator YABBY5
GSVIVG01036340001	T0	T6	5,36502	0,164762	-5,02513	(+)-delta-cadinene synthase
GSVIVG01034731001	T6	T12	8,23496	0,253414	-5,02219	Gamma-aminobutyric acid transporter
GSVIVG01038599001	T2	T12	32,6085	1,00406	-5,02133	Oligopeptide transporter 6
GSVIVG01006642001	T0	T12	5,2504	0,161949	-5,01881	(E,E)-alpha-farnesene synthase
GSVIVG01016362001	T0	T12	4,4736	0,13858	-5,01265	Anthocyanin 5-aromatic acyltransferase
GSVIVG01015369001	T0	T12	21,1734	0,657441	-5,00925	Rho guanyl-nucleotide exchange factor ROPGEF8
GSVIVG01019601001	T2	T12	33,6587	1,05269	-4,99882	Nodulin MtN3 family protein
GSVIVG01016196001	T0	T12	6,45999	0,202211	-4,9976	Nodulin-like protein
GSVIVG01029662001	T6	T12	66,5741	2,08442	-4,99725	F-type H ⁺ -transporting ATPase subunit c
GSVIVG01028171001	T6	T12	6,69991	0,21015	-4,99465	Myb domain protein 78
GSVIVG01011583001	T0	T12	26,6883	0,83738	-4,99418	Deoxymugineic acid synthase
GSVIVG01031843001	T2	T12	3,5945	0,113195	-4,9889	Leucine-rich repeat family protein / extensin
GSVIVG01008234001	T6	T12	39,1483	1,24579	-4,97382	TCP family transcription factor BRC2/TCP12 (branched2)
GSVIVG01017158001	T0	T12	1269,12	40,6874	-4,9631	IAA19
GSVIVG01008806001	T0	T12	223,359	7,18031	-4,95918	PISTILLATA (PI) floral homeotic protein
GSVIVG01025798001	T6	T12	17,6133	0,568665	-4,95294	Nodulin MtN21
GSVIVG01027081001	T0	T12	1,23444	0,0399804	-4,94842	Lipase class 3
GSVIVG01024894001	T2	T12	12,9496	0,421047	-4,94278	Tropinone reductase
GSVIVG01011005001	T2	T12	12,5575	0,408409	-4,94239	flavin-containing monooxygenase
GSVIVG01000403001	T0	T6	827,297	26,9146	-4,94194	isoprene synthase
GSVIVG01037005001	T6	T12	222,886	7,25431	-4,94132	Pathogenesis-related protein 1 precursor (PRP 1)
GSVIVG01011005001	T6	T12	12,4846	0,408409	-4,934	flavin-containing monooxygenase
GSVIVG01008595001	T2	T12	200,657	6,56435	-4,93393	Nodulin MtN3 family
GSVIVG01035033001	T6	T12	27,6664	0,905152	-4,93383	Glycosyl hydrolase family 3 beta xylosidase BXL1
GSVIVG01036330001	T2	T6	3,432	0,112473	-4,9314	(+)-delta-cadinene synthase isozyme XC1
GSVIVG01034672001	T2	T12	1,1374	0,0375534	-4,92065	Glycosyl transferase family 47 protein
GSVIVG01030023001	T2	T12	3,15171	0,104144	-4,91948	Polygalacturonase PGA3
GSVIVG01019005001	T0	T12	2,39823	0,0794604	-4,91559	Cupin family protein
GSVIVG01016196001	T2	T12	6,09076	0,202211	-4,91269	Nodulin-like protein
GSVIVG01001710001	T0	T12	9,88775	0,32839	-4,91216	CYP714A1
GSVIVG01021490001	T0	T6	4,5931	0,152934	-4,90849	Beta-amyrin synthase
GSVIVG01035882001	T0	T12	0,802294	0,026718	-4,90825	Sucrose-phosphate synthase
GSVIVG01035061001	T0	T12	2,86221	0,0953794	-4,90731	pathogenesis-related protein 10
GSVIVG01036015001	T0	T12	12,862	0,429202	-4,90532	Aspartic proteinase nepenthesin-2 precursor
GSVIVG01017588001	T2	T6	116,537	3,89332	-4,90364	CYP82A2
GSVIVG01035078001	T0	T12	21,1992	0,708463	-4,90318	Copper-binding family protein
GSVIVG01019715001	T2	T12	2,10005	0,0705616	-4,8954	Nodulin MtN21 family

GSVIVG01029174001	T2	T12	2,38312	0,0800726	-4,8954	Xyloglucan endotransglucosylase-hydrolase XTH3
GSVIVG01032550001	T2	T12	1,44013	0,0484954	-4,89221	Proton-dependent oligopeptide transport (POT) family
GSVIVG01030652001	T2	T12	7,46439	0,252475	-4,88581	Shoot gravitropism 7
GSVIVG01015141001	T6	T12	2,83046	0,0959389	-4,88278	Ankyrin repeat
GSVIVG01034672001	T0	T12	1,10586	0,0375534	-4,88008	Glycosyl transferase family 47 protein
GSVIVG01027470001	T2	T12	4,02907	0,13781	-4,86969	No apical meristem cup-shaped cotyledon2
GSVIVG01035710001	T2	T12	3,36531	0,115107	-4,86969	Arsenite transport protein (ArsB)
GSVIVG01030618001	T6	T12	63,0365	2,16271	-4,86528	photosystem i subunit viii
GSVIVG01010307001	T0	T12	3,01725	0,103714	-4,86256	Cyp71A1
GSVIVG01038653001	T6	T12	44,9234	1,54528	-4,86153	caffeic acid o-methyltransferase
GSVIVG01031651001	T6	T12	2,6744	0,0921358	-4,85931	Aldo/keto reductase AKR
GSVIVG01026525001	T0	T12	20,2222	0,696951	-4,85874	PGSIP1 (Plant glycogenin-like starch initiation protein 1)
GSVIVG01029488001	T0	T6	2,45731	0,0847276	-4,8581	Beta-amyrin synthase
GSVIVG01011584001	T2	T6	149,813	5,206	-4,84685	Chalcone reductase
GSVIVG01032550001	T6	T12	1,39552	0,0484954	-4,84681	Proton-dependent oligopeptide transport (POT) family
GSVIVG01019695001	T6	T12	6,26499	0,218694	-4,84033	Naringenin,2-oxoglutarate 3-dioxygenase
GSVIVG01027584001	T2	T12	5,84669	0,204176	-4,83974	Subtilisin serine endopeptidase (XSP1)
GSVIVG01002752001	T6	T12	121,048	4,22973	-4,83887	NADH dehydrogenase subunit 3
GSVIVG01035882001	T2	T12	0,760072	0,026718	-4,83025	Sucrose-phosphate synthase
GSVIVG01007745001	T6	T12	13,0197	0,459538	-4,82437	Carbonic anhydrase chloroplast
GSVIVG01025864001	T0	T6	3,72207	0,131475	-4,82324	Copper-binding family protein
GSVIVG01037758001	T0	T6	635,476	22,4949	-4,82017	Pirin
GSVIVG01034563001	T6	T12	5,69062	0,202044	-4,81584	Ethylene-responsive transcription factor related to
GSVIVG01003153001	T0	T6	789,229	28,0298	-4,81541	Cinnamyl alcohol dehydrogenase
GSVIVG01028557001	T0	T12	394,568	14,0962	-4,8069	3-ketoacyl-CoA thiolase PED1
GSVIVG01035272001	T2	T12	36,0438	1,28768	-4,8069	Acyl-CoA synthetases (Acyl-activating enzyme 11)
GSVIVG01030135001	T0	T12	23,4655	0,845048	-4,79536	Heavy-metal-associated domain-containing protein
GSVIVG01027716001	T6	T12	5,40153	0,194795	-4,79334	cellulose synthase-like protein g2-like
GSVIVG01034943001	T0	T12	10,466	0,379991	-4,7836	Myb domain protein 108
GSVIVG01027448001	T2	T6	1248,42	45,3623	-4,78247	Catechol O-methyltransferase
GSVIVG01031038001	T0	T2	50,4734	1,83446	-4,78209	CYP735A1
GSVIVG01011635001	T6	T12	14,2482	0,519487	-4,77754	NSL1 (necrotic spotted lesions 1)
GSVIVG01031355001	T0	T12	6,72035	0,245801	-4,77298	SNARE YKT6 1
GSVIVG01034125001	T6	T12	97,7304	3,58348	-4,76937	Proteinase inhibitor
GSVIVG01022354001	T6	T12	67,3264	2,47518	-4,76557	NAC domain containing protein 2
GSVIVG01024267001	T0	T6	201,382	7,41826	-4,76271	CYP89A2
GSVIVG01035122001	T2	T12	11,3823	0,420137	-4,75979	MATE efflux family protein
GSVIVG01035035001	T0	T6	22,4416	0,829942	-4,75702	Aldo-keto reductase
GSVIVG01010993001	T2	T6	9,17888	0,339926	-4,75502	Nodulin MtN3 family
GSVIVG01018903001	T0	T12	2090,67	77,7412	-4,74915	S-adenosyl-L-methionine:salicylic acid carboxyl
GSVIVG01011616001	T6	T12	9,70813	0,361947	-4,74535	Avr9/Cf-9 rapidly elicited protein
GSVIVG01025223001	T0	T6	9,22501	0,344873	-4,74141	Kiwelmin Ripening-related protein grip22
GSVIVG01031948001	T0	T12	25,058	0,940268	-4,73606	Specific tissue protein 2
GSVIVG01038068001	T0	T12	8,41156	0,3159	-4,73483	3-ketoacyl-CoA synthase
GSVIVG01037077001	T0	T6	145,723	5,47405	-4,73448	Isoflavone reductase
GSVIVG01021359001	T2	T6	3,3098	0,124589	-4,73149	Xyloglucan endotransglycosylase/hydrolase precursor
GSVIVG01036344001	T0	T6	97,4407	3,68085	-4,72641	valencene synthase-like
GSVIVG01033356001	T0	T12	10,2854	0,388696	-4,72582	Basic helix-loop-helix (bHLH) family
GSVIVG01009563001	T6	T12	20,1851	0,763459	-4,7246	Calmodulin-binding protein AR781
GSVIVG01036342001	T0	T6	246,855	9,37985	-4,71795	valencene synthase-like
GSVIVG01028354001	T6	T12	4,60961	0,175635	-4,71399	NAC domain-containing protein 74
GSVIVG01024563001	T0	T12	5,06755	0,193326	-4,71218	Lipid transfer protein 3
GSVIVG01017147001	T2	T12	5,49947	0,210582	-4,70684	Kelch repeat-containing F-box family protein
GSVIVG01005067001	T2	T12	4,2457	0,16374	-4,69652	Methyl jasmonate esterase
GSVIVG01024578001	T0	T12	7,43268	0,286907	-4,69523	WNK5 (Arabidopsis WNK kinase 5)
GSVIVG01032452001	T6	T12	87,8052	3,38949	-4,69516	Myb domain protein 24
GSVIVG01027472001	T2	T12	23,8163	0,919584	-4,69482	NAC transcription factor-like 9 NTL9
GSVIVG01015203001	T6	T12	132,029	5,10723	-4,69217	Beta-galactosidase
GSVIVG01028152001	T6	T12	3,22868	0,125932	-4,68023	Glycerol-3-phosphate acyltransferase 3 (AtGPAT3)
GSVIVG01007418001	T2	T12	2,32665	0,0910784	-4,675	flavonoid 3-monooxygenase
GSVIVG01037719001	T6	T12	17,4148	0,682722	-4,67287	Light induced protein like
GSVIVG01010015001	T2	T12	63,6084	2,50163	-4,66828	Nodulin MtN3 family
GSVIVG01027910001	T0	T12	25,7837	1,01584	-4,66571	CCT motif constans-like
GSVIVG01031020001	T0	T12	45,7284	1,82015	-4,65096	BEE1 (BR Enhanced expression 1)
GSVIVG01011380001	T2	T12	31,07	1,23752	-4,65	Basic helix-loop-helix (bHLH) family
GSVIVG01024592001	T6	T12	5,28185	0,211507	-4,64227	Lateral organ boundaries Domain 15
GSVIVG01024186001	T2	T12	29,9204	1,21111	-4,62672	ferulate 5-hydroxylase
GSVIVG01000402001	T0	T6	1179,71	47,8471	-4,62386	#####
GSVIVG01009560001	T0	T12	18,1124	0,736359	-4,62043	Serine carboxypeptidase
GSVIVG01016197001	T0	T12	1,01357	0,0414615	-4,61154	Nodulin-like protein
GSVIVG01031038001	T2	T12	1,83446	0,0753193	-4,60619	CYP735A1

GSVIVG01020617001	T6	T12	1,92882	0,0792094	-4,60591	MLO1
GSVIVG01030023001	T6	T12	2,53104	0,104144	-4,60308	Polygalacturonase PGA3
GSVIVG01024270001	T2	T12	185,092	7,61769	-4,60275	CYP89A5
GSVIVG01036352001	T0	T6	246,276	10,1389	-4,60231	valencene synthase-like
GSVIVG01034049001	T0	T6	3,31461	0,136482	-4,60206	TTL1 (tetrairicopeptide-repeat thioredoxin-like 1)
GSVIVG01036352001	T2	T6	246,048	10,1389	-4,60097	valencene synthase-like
GSVIVG01009645001	T0	T12	12,3889	0,510788	-4,60017	1-acyl-sn-glycerol-3-phosphate acyltransferase 4
GSVIVG01020177001	T0	T6	27,3289	1,12756	-4,59915	N-hydroxythioamide S-beta-glucosyltransferase
GSVIVG01034896001	T0	T6	12,305	0,508319	-4,59736	Nodulin
GSVIVG01038662001	T0	T12	211,922	8,77532	-4,59394	Copper-binding family protein
GSVIVG01010098001	T2	T12	43,3191	1,79778	-4,59071	UDP-glucuronosyl and UDP-glucosyl transferase
GSVIVG01024709001	T6	T12	14,2677	0,592537	-4,5897	MAPKKK14
GSVIVG01007968001	T2	T12	13,7788	0,573179	-4,58733	Exonuclease
GSVIVG01019017001	T6	T12	4,40377	0,183266	-4,58673	Anthocyanidin 3-O-glucosyltransferase
GSVIVG01035103001	T2	T12	5,1622	0,214941	-4,58598	Polygalacturonase GH28
GSVIVG01019413001	T6	T12	14,9139	0,622332	-4,58283	Heavy-metal-associated domain-containing protein
GSVIVG01014558001	T2	T6	24,9461	1,04745	-4,57386	Vetispiradiene synthase
GSVIVG01036320001	T0	T6	16,199	0,680429	-4,57332	Germacrene-D synthase
GSVIVG01014933001	T0	T12	2,03206	0,0860923	-4,56092	Receptor protein kinase
GSVIVG01036344001	T2	T6	86,8725	3,68085	-4,56079	valencene synthase-like
GSVIVG01030652001	T0	T12	5,95381	0,252475	-4,5596	Shoot gravitropism 7
GSVIVG01027456001	T0	T6	630,835	26,7837	-4,55784	Myb CCA1 (circadian clock associated 1)
GSVIVG01006538001	T0	T6	152,409	6,48733	-4,55418	Phosphoenolpyruvate carboxykinase
GSVIVG01034896001	T2	T6	11,9149	0,508319	-4,55088	Nodulin
GSVIVG01022814001	T6	T12	31,7798	1,35769	-4,54888	Alternative oxidase 1a, (AOX1A)
GSVIVG01020229001	T6	T12	6,0869	0,260581	-4,5459	Armadillo/beta-catenin repeat
GSVIVG01036343001	T6	T12	3,92517	0,168606	-4,54102	Germacrene-D synthase
GSVIVG01032676001	T2	T6	2,55681	0,110076	-4,53778	MATE efflux family protein
GSVIVG01018142001	T6	T12	61,4994	2,65545	-4,53354	Proteinase inhibitor 1 PPI3B2
GSVIVG01013268001	T6	T12	0,812712	0,0351076	-4,53289	Pleckstrin (PH) domain-containing protein
GSVIVG01018019001	T6	T12	22,6019	0,976762	-4,53229	Homocysteine S-methyltransferase 3
GSVIVG01001292001	T6	T12	115,645	4,99867	-4,53202	Nitrate transporter
GSVIVG01001052001	T2	T12	2,84718	0,123818	-4,52324	H(+)-ATPase 8 AHA8
GSVIVG01030258001	T6	T12	14,1817	0,619178	-4,51753	WRKY DNA-binding protein 33
GSVIVG01031948001	T0	T6	25,058	1,09451	-4,51691	Specific tissue protein 2
GSVIVG01010307001	T2	T12	2,37029	0,103714	-4,51438	Cyp71A1
GSVIVG01030135001	T2	T12	19,2953	0,845048	-4,51307	Heavy-metal-associated domain-containing protein
GSVIVG01022824001	T2	T12	42,7136	1,87463	-4,51002	DNA (cytosine-5)-methyltransferase (ATHIM)
GSVIVG01018044001	T2	T6	2494,65	109,574	-4,50886	ELIP1 (early light-inducible protein)
GSVIVG01033651001	T0	T12	99,9466	4,39163	-4,50833	S-adenosylmethionine synthetase
GSVIVG01033243001	T6	T12	6,40994	0,281795	-4,50759	Cis-zeatin O-beta-D-glucosyltransferase
GSVIVG01013272001	T2	T12	88,1222	3,87447	-4,50743	1,4-alpha-D-glucan maltohydrolase
GSVIVG01017118001	T0	T6	64,8834	2,86865	-4,4994	Sulfate transporter 3.4
GSVIVG01017582001	T2	T6	126,078	5,57665	-4,49878	CYP82M1v3
GSVIVG01017239001	T0	T12	43,066	1,90562	-4,49822	6-4 photolase
GSVIVG01035078001	T2	T12	15,9953	0,708463	-4,49681	Copper-binding family protein
GSVIVG01022100001	T0	T12	288,941	12,8123	-4,49518	Caffeoyl-CoA O-methyltransferase 1
GSVIVG01026806001	T2	T12	57,6905	2,56031	-4,49394	Eceriferum 1 (CER1 protein) Sterol desaturase
GSVIVG01013268001	T0	T12	0,78921	0,0351076	-4,49055	Pleckstrin (PH) domain-containing protein
GSVIVG01027022001	T0	T2	12,945	0,576393	-4,4892	Acidic endochitinase (CHIB1)
GSVIVG01012613001	T6	T12	10,3317	0,460528	-4,48764	NADH dehydrogenase subunit 7
GSVIVG01033870001	T0	T6	8,85211	0,394668	-4,48731	Transposon protein, Mutator sub-class
GSVIVG01000720001	T0	T12	21,5959	0,967357	-4,48056	Auxin-induced protein 22D
GSVIVG01035710001	T0	T12	2,56609	0,115107	-4,47852	Arsenite transport protein (ArsB)
GSVIVG01028851001	T2	T12	6,0546	0,271773	-4,47756	Metal ion binding
GSVIVG01031020001	T6	T12	40,4904	1,82015	-4,47545	BEE1 (BR Enhanced expression 1)
GSVIVG01016302001	T2	T12	10,192	0,458618	-4,47401	MLO1
GSVIVG01016197001	T2	T12	0,914947	0,0414615	-4,46384	Nodulin-like protein
GSVIVG01028033001	T6	T12	1264,73	57,3301	-4,46339	Late embryogenesis abundant protein 5
GSVIVG01006876001	T0	T12	65,8546	2,98628	-4,46286	Aspartic proteinase nepenthesin-1 precursor
GSVIVG01026810001	T2	T12	9,32295	0,423828	-4,45923	Eceriferum 1 (CER1 protein) Sterol desaturase
GSVIVG01030227001	T2	T12	12,9884	0,59074	-4,45856	Alanine--glyoxylate aminotransferase 2 3, mitochondrial
GSVIVG01017737001	T6	T12	74,9004	3,40781	-4,45806	SRG1 (senescence-related gene 1)
GSVIVG01036320001	T2	T6	14,952	0,680429	-4,45775	Germacrene-D synthase
GSVIVG01038111001	T0	T12	13,7103	0,625674	-4,45371	Chitinase class IV
GSVIVG01018144001	T0	T12	314,176	14,348	-4,45265	Cellulose synthase CSLG2
GSVIVG01026525001	T0	T6	20,2222	0,926147	-4,44856	PGSIP1 (Plant glycogenin-like starch initiation protein 1)
GSVIVG01011635001	T2	T12	11,3394	0,519487	-4,44812	NSL1 (necrotic spotted lesions 1)
GSVIVG01012879001	T2	T12	44,8697	2,05573	-4,44802	Protein phosphatase 2C DBP
GSVIVG01038199001	T0	T12	123,643	5,66753	-4,44732	BT3 (BTB and TAZ domain protein 3)
GSVIVG01035518001	T0	T12	12,9401	0,593689	-4,446	Kelch repeat-containing F-box protein

GSVIVG01035272001	T2	T6	36,0438	1,66786	-4,43368	Acyl-CoA synthetases (Acyl-activating enzyme 11)
GSVIVG01030137001	T2	T12	18,6413	0,864318	-4,43079	Heavy-metal-associated domain-containing protein
GSVIVG01007898001	T6	T12	4,58792	0,213242	-4,42728	UDP-glucuronosyl and UDP-glucosyl transferase
GSVIVG01006399001	T0	T6	8,6168	0,401205	-4,42474	(E,E)-alpha-farnesene synthase
GSVIVG01019769001	T2	T12	13,3498	0,623317	-4,4207	Cu2+-exporting ATPase HMA5 (heavy metal ATPase 5)
GSVIVG01029709001	T6	T12	29,5113	1,3799	-4,41864	NAC domain containing protein 104
GSVIVG01035231001	T0	T12	14,7035	0,691068	-4,41119	CIR1/RVE2 (circadian 1)
GSVIVG01021412001	T0	T12	20,0667	0,949942	-4,40082	Glycosyl hydrolase family 17 protein
GSVIVG01009359001	T6	T12	46,71	2,2157	-4,3979	Salt tolerance zinc finger
GSVIVG01028152001	T0	T6	68,0092	3,22868	-4,39672	Glycerol-3-phosphate acyltransferase 3 (AtGPAT3)
GSVIVG01027454001	T6	T12	107,499	5,10611	-4,39596	Naringenin,2-oxoglutarate 3-dioxygenase
GSVIVG01007190001	T6	T12	11,0334	0,525255	-4,39271	Chitinase precursor
GSVIVG01017582001	T6	T12	5,57665	0,265595	-4,3921	CYP82M1v3
GSVIVG01028265001	T2	T12	8,63275	0,411305	-4,39154	pectinesterase pectinesterase inhibitor 28-like
GSVIVG01031982001	T2	T12	7,29063	0,347986	-4,38894	Radialis-like protein 6
GSVIVG01036344001	T6	T12	3,68085	0,177005	-4,37818	valencene synthase-like
GSVIVG01018028001	T0	T12	161,919	7,79707	-4,3762	Sulfate transporter 3.1 (AST12) (AtST1)
GSVIVG01032117001	T0	T12	3,41748	0,164795	-4,37419	low quality protein: polygalacturonase-like
GSVIVG01036015001	T2	T12	8,88429	0,429202	-4,37153	Aspartic proteinase nepenthesin-2 precursor
GSVIVG01014558001	T0	T6	21,6472	1,04745	-4,36923	Vetispiradiene synthase
GSVIVG01006876001	T6	T12	61,5681	2,98628	-4,36576	Aspartic proteinase nepenthesin-1 precursor
GSVIVG01008021001	T2	T12	14,1515	0,688	-4,3624	Phytochrome kinase substrate 1
GSVIVG01030137001	T0	T12	17,7633	0,864318	-4,36119	Heavy-metal-associated domain-containing protein
GSVIVG01006166001	T0	T6	215,472	10,4889	-4,36056	Phosphoenolpyruvate carboxykinase
GSVIVG01022812001	T6	T12	5,51235	0,268559	-4,35936	Alternative oxidase 1D
GSVIVG01007679001	T0	T12	210,188	10,2755	-4,3544	Alliinase
GSVIVG01012363001	T2	T12	19,562	0,957204	-4,35308	Myrcene synthase, chloroplastic
GSVIVG01005206001	T0	T12	75,8563	3,72474	-4,34806	Ubiquitin-conjugating enzyme E2 O
GSVIVG01016302001	T0	T12	9,33969	0,458618	-4,34801	MLO1
GSVIVG01002752001	T0	T12	86,0812	4,22973	-4,34706	NADH dehydrogenase subunit 3
GSVIVG01012879001	T0	T12	41,6758	2,05573	-4,34149	Protein phosphatase 2C DBP
GSVIVG01008806001	T0	T6	223,359	11,0537	-4,33676	PISTILLATA (PI) floral homeotic protein
GSVIVG01002031001	T6	T12	34,6436	1,71715	-4,3345	Stem-specific protein TSJT1
GSVIVG01009875001	T0	T6	71,1518	3,5309	-4,33279	Auxin-induced SAUR
GSVIVG01008553001	T2	T12	22,1238	1,10407	-4,3247	WRKY DNA-binding protein 75
GSVIVG01007071001	T2	T12	23,5405	1,17821	-4,32048	MATE efflux family protein ripening responsive
GSVIVG01006763001	T2	T12	18,375	0,920155	-4,31972	Cellulose synthase CSLE1
GSVIVG01015567001	T0	T6	149,357	7,49577	-4,31655	Axial regulator YABBY5
GSVIVG01004265001	T6	T12	58,3864	2,94224	-4,31065	Aspartic proteinase nepenthesin-1 precursor
GSVIVG01033248001	T6	T12	4,90071	0,24738	-4,30819	Glycosyl transferaseHGA1
GSVIVG01024267001	T2	T12	80,372	4,09189	-4,29585	CYP89A2
GSVIVG01011641001	T6	T12	26,295	1,34126	-4,29312	Jasmonate O-methyltransferase
GSVIVG01019664001	T0	T12	94,7169	4,83421	-4,29227	Cellulase CEL2
GSVIVG01017593001	T2	T6	6,65706	0,339793	-4,29216	CYP82M1v4
GSVIVG01017696001	T0	T12	1,52947	0,0780811	-4,29192	P-glycoprotein 11
GSVIVG01024578001	T2	T12	5,61762	0,286907	-4,2913	WNK5 (Arabidopsis WNK kinase 5)
GSVIVG01018044001	T0	T6	2144,49	109,574	-4,29065	ELIP1 (early light-inducible protein)
GSVIVG01011584001	T6	T12	5,206	0,266091	-4,29018	Chalcone reductase
GSVIVG01030995001	T6	T12	3,16414	0,16207	-4,28712	Receptor-like kinase ARK1AS
GSVIVG01030106001	T6	T12	3,58123	0,183594	-4,28586	AarF domain containing kinase
GSVIVG01000046001	T0	T12	4,73788	0,243625	-4,28151	Glycosyl transferase family 8 protein
GSVIVG01021420001	T2	T12	1,32078	0,0683575	-4,27215	Cation/hydrogen exchanger (CHX15)
GSVIVG01038653001	T2	T12	29,8391	1,54528	-4,27127	caffeic acid o-methyltransferase
GSVIVG01000167001	T6	T12	1,45609	0,0754088	-4,27122	Transducin family protein / WD-40 repeat
GSVIVG01000403001	T2	T6	519,623	26,9146	-4,271	isoprene synthase
GSVIVG01017158001	T2	T12	784,465	40,6874	-4,26905	IAA19
GSVIVG01014073001	T2	T12	14,3241	0,745577	-4,26394	Purine permease 11 PUP11
GSVIVG01018421001	T0	T6	0,676944	0,0352545	-4,26316	Eceriferum 1 (CER1 protein) Sterol desaturase
GSVIVG01032983001	T0	T12	18,9265	0,991579	-4,25454	Ethylene-responsive transcription factor ERF113
GSVIVG01015408001	T0	T6	2,75951	0,14464	-4,25388	Sec7 domain-containing protein
GSVIVG01008003001	T0	T6	250,971	13,1788	-4,25123	GASA like
GSVIVG01014104001	T0	T6	2,83008	0,14872	-4,25017	PMR5 (powdery mildew resistant 5)
GSVIVG01017151001	T6	T12	40,4894	2,1278	-4,25011	Kelch repeat-containing F-box family protein
GSVIVG01038653001	T0	T12	29,294	1,54528	-4,24466	caffeic acid o-methyltransferase
GSVIVG01019697001	T0	T6	3,91787	0,207024	-4,2422	Soluble inorganic pyrophosphatase
GSVIVG01028766001	T0	T12	5,11313	0,270442	-4,24082	Disease resistance
GSVIVG01015567001	T2	T6	141,694	7,49577	-4,24056	Axial regulator YABBY5
GSVIVG01027451001	T0	T6	44,9886	2,3837	-4,23828	Quercetin 3-O-methyltransferase 1
GSVIVG01030090001	T0	T12	541,988	28,7712	-4,23556	Jasmonate O-methyltransferase
GSVIVG01038230001	T0	T6	242,507	12,8743	-4,23546	Amine oxidase
GSVIVG01036343001	T0	T6	73,765	3,92517	-4,23211	Germacrene-D synthase

GSVIVG01008649001	T0	T12	3,43602	0,18299	-4,2309	Ethylene-responsive transcription factor ERF114
GSVIVG01038111001	T2	T12	11,7411	0,625674	-4,23001	Chitinase class IV
GSVIVG01038125001	T2	T12	8,48129	0,452072	-4,22966	Chitinase class IV
GSVIVG01024057001	T6	T12	289,076	15,4108	-4,22943	Co-chaperone-curved DNA binding protein A
GSVIVG01037758001	T2	T6	421,868	22,4949	-4,22912	Pirin
GSVIVG01013149001	T0	T12	250,391	13,377	-4,22636	PLATZ transcription factor
GSVIVG01007435001	T6	T12	5,67049	0,303646	-4,22301	Stem-specific protein TSJT1
GSVIVG01011583001	T6	T12	15,5088	0,83738	-4,21106	Deoxymugineic acid synthase
GSVIVG01019695001	T0	T6	115,979	6,26499	-4,2104	Naringenin,2-oxoglutarate 3-dioxygenase
GSVIVG01014557001	T2	T6	17,5262	0,947966	-4,20853	(-)-germacrene D synthase
GSVIVG01035295001	T0	T12	10,5079	0,568417	-4,20838	IAA6
GSVIVG01008461001	T6	T12	66,8288	3,62117	-4,20594	3-hydroxyisobutyrate dehydrogenase
GSVIVG01019909001	T6	T12	26,201	1,42256	-4,20306	Geraniol 10-hydroxylase
GSVIVG01017696001	T2	T12	1,43271	0,0780811	-4,19763	P-glycoprotein 11
GSVIVG01019601001	T0	T12	19,2373	1,05269	-4,19175	Nodulin MtN3 family protein
GSVIVG01007898001	T0	T12	3,89413	0,213242	-4,19074	UDP-glucuronosyl and UDP-glucosyl transferase
GSVIVG01008069001	T6	T12	35,6344	1,95745	-4,18622	Isopiperitenol dehydrogenase
GSVIVG01009381001	T2	T12	8,51717	0,468053	-4,18563	Tetratricopeptide repeat (TPR)-containing
GSVIVG01024756001	T2	T6	3,4267	0,188369	-4,18519	CYP71E
GSVIVG01032091001	T0	T12	14,5673	0,802604	-4,1819	ferric reductase defective 3
GSVIVG01008129001	T2	T12	1,09786	0,0605811	-4,17968	Phytochelatin synthetase
GSVIVG01019183001	T0	T12	5,35006	0,295969	-4,17604	CYP706A12
GSVIVG01038230001	T0	T12	242,507	13,4262	-4,17491	Amine oxidase
GSVIVG01006763001	T0	T12	16,6099	0,920155	-4,17403	Cellulose synthase CSLE1
GSVIVG01008655001	T0	T12	6,16673	0,343245	-4,1672	LEAFY protein (Floricula/leafy protein)
GSVIVG01022916001	T6	T12	85,9649	4,79333	-4,16465	Cupin
GSVIVG01006458001	T0	T12	99,169	5,54321	-4,1611	Mannitol dehydrogenase
GSVIVG01007898001	T2	T12	3,81195	0,213242	-4,15997	UDP-glucuronosyl and UDP-glucosyl transferase
GSVIVG01014557001	T0	T6	16,9322	0,947966	-4,15879	(-)-germacrene D synthase
GSVIVG01034729001	T0	T12	7,12519	0,399103	-4,1581	Amino acid transporter family
GSVIVG01011583001	T2	T12	14,9404	0,83738	-4,15719	Deoxymugineic acid synthase
GSVIVG01015682001	T6	T12	9,88135	0,554667	-4,15501	Zinc finger (C3HC4-type ring finger)
GSVIVG01030090001	T0	T6	541,988	30,4758	-4,15252	Jasmonate O-methyltransferase
GSVIVG01009295001	T6	T12	11,1807	0,630766	-4,14777	Photosystem I P700 chlorophyll a apoprotein A2
GSVIVG01027451001	T2	T6	42,1654	2,3837	-4,14478	Quercetin 3-O-methyltransferase 1
GSVIVG01023631001	T0	T12	22,9232	1,29678	-4,1438	Hydroxycinnamoyl-CoA shikimate/quinate
GSVIVG01014403001	T6	T12	99,0009	5,60067	-4,14377	NAC domain containing protein 19
GSVIVG01033538001	T6	T12	11,7939	0,667891	-4,14228	Beta 1-3 glucanase
GSVIVG01027022001	T0	T12	12,945	0,735526	-4,13747	Acidic endochitinase (CHIB1)
GSVIVG01031738001	T6	T12	26,8425	1,53076	-4,1322	ABA 8'-hydroxylase CYP707A1
GSVIVG01008668001	T0	T12	97,0574	5,53986	-4,13092	MtN19
GSVIVG01022824001	T0	T12	32,564	1,87463	-4,1186	DNA (cytosine-5)-methyltransferase (ATHIM)
GSVIVG01034729001	T2	T12	6,91919	0,399103	-4,11577	Amino acid transporter family
GSVIVG01036343001	T2	T6	67,9829	3,92517	-4,11434	Germacrene-D synthase
GSVIVG01021305001	T2	T12	2,80848	0,162405	-4,11212	Lipase GDSL
GSVIVG01033610001	T0	T12	145,21	8,40048	-4,11153	ARR3 typeA
GSVIVG01018904001	T0	T12	9,04853	0,524825	-4,10778	S-adenosyl-L-methionine:salicylic acid carboxyl
GSVIVG01009560001	T2	T12	12,6893	0,736359	-4,10706	Serine carboxypeptidase
GSVIVG01008267001	T2	T12	281,246	16,3291	-4,10632	Aspartyl protease
GSVIVG01013757001	T6	T12	3,07844	0,179001	-4,10416	Protein disulfide isomerase
GSVIVG01030106001	T0	T6	61,501	3,58123	-4,10208	AarF domain containing kinase
GSVIVG01015369001	T2	T12	11,2897	0,657441	-4,10201	Rho guanyl-nucleotide exchange factor ROPGEF8
GSVIVG01014405001	T0	T12	113,78	6,64641	-4,09753	NAC domain containing protein 2
GSVIVG01016487001	T6	T12	56,5464	3,30442	-4,09697	Tropinone reductase
GSVIVG01012001001	T0	T12	1,65966	0,0970639	-4,09581	EXS family protein / ERD1/XPR1/SYG1
GSVIVG01033020001	T2	T6	27,4196	1,60367	-4,09576	UPF0497 family
GSVIVG01036604001	T0	T12	60,2383	3,53323	-4,09162	AC112
GSVIVG01016838001	T2	T12	8,12203	0,476494	-4,09131	Pyruvoyl-dependent arginine decarboxylase
GSVIVG01001082001	T2	T6	28,6522	1,68528	-4,08759	SOUL heme-binding
GSVIVG01027811001	T6	T12	20,7883	1,22396	-4,08614	Myb domain protein 14
GSVIVG01005596001	T0	T6	421,247	24,8969	-4,08063	Phosphoenolpyruvate carboxykinase
GSVIVG01013055001	T0	T12	22,9909	1,361	-4,07832	Xyloglucan endotransglucosylase/hydrolase 30
GSVIVG01027067001	T0	T6	4,57251	0,272905	-4,06652	NADPH HC toxin reductase
GSVIVG01035122001	T0	T6	26,0558	1,55726	-4,06452	MATE efflux family protein
GSVIVG01005971001	T6	T12	57,9701	3,47954	-4,05834	Esterase/lipase/thioesterase
GSVIVG01012363001	T2	T6	19,562	1,17613	-4,05593	Myrcene synthase, chloroplastic
GSVIVG01028557001	T0	T6	394,568	23,7759	-4,0527	3-ketoacyl-CoA thiolase PED1
GSVIVG01008917001	T0	T12	58,8294	3,54957	-4,05082	Auxin transporter protein 4
GSVIVG01010743001	T2	T12	2,57354	0,155508	-4,04869	Calcium-dependent protein kinase 24 CPK24
GSVIVG01027472001	T2	T6	23,8163	1,44603	-4,04178	NAC transcription factor-like 9 NTL9
GSVIVG01017737001	T0	T12	56,0618	3,40781	-4,0401	SRG1 (senescence-related gene 1)

GSVIVG01025485001	T0	T12	5,47494	0,332999	-4,03925	Hcr2-p4.1
GSVIVG01033248001	T2	T12	4,05643	0,24738	-4,03541	Glycosyl transferaseHGA1
GSVIVG01017687001	T2	T12	4,50681	0,275	-4,0346	Pectinesterase; Pectinesterase inhibitor
GSVIVG01036015001	T6	T12	7,02616	0,429202	-4,03301	Aspartic proteinase nepenthesin-2 precursor
GSVIVG01017239001	T0	T6	43,066	2,6347	-4,03084	6-4 photolyase
GSVIVG01010098001	T0	T6	116,624	7,1384	-4,03013	UDP-glucuronosyl and UDP-glucosyl transferase
GSVIVG01009645001	T0	T6	12,3889	0,761185	-4,02465	1-acyl-sn-glycerol-3-phosphate acyltransferase 4
GSVIVG01038037001	T0	T12	9,93144	0,613983	-4,01573	Glutathione S-transferase 8 GSTU19
GSVIVG01006662001	T6	T12	5,66204	0,351931	-4,00796	Photosystem II PsbC
GSVIVG01037077001	T2	T6	87,6726	5,47405	-4,00144	Isoflavone reductase
GSVIVG01011872001	T6	T12	115,417	7,21282	-4,00014	(myb domain protein 62
GSVIVG01027910001	T2	T12	16,2516	1,01584	-3,99983	CCT motif constans-like
GSVIVG01033999001	T6	T12	31,0617	1,94201	-3,99952	Anthranilate N-benzoyltransferase
GSVIVG01014025001	T6	T12	10,0417	0,628332	-3,99833	Hexose transporter [Vitis vinifera]
GSVIVG01032983001	T6	T12	15,845	0,991579	-3,99815	Ethylene-responsive transcription factor ERF113
GSVIVG01012005001	T0	T12	16,0844	1,00738	-3,99698	Phospholipid-transporting ATPase
GSVIVG01019511001	T6	T12	22,6278	1,41898	-3,99517	WRKY DNA-binding protein 53
GSVIVG01029662001	T0	T12	33,1915	2,08442	-3,9931	F-type H+-transporting ATPase subunit c
GSVIVG01034495001	T0	T6	227,027	14,3865	-3,98007	Permease nonimprinted in Prader-Willi/Angelman
GSVIVG01001052001	T6	T12	1,94938	0,123818	-3,97672	H(+)-ATPase 8 AHA8
GSVIVG01009273001	T0	T12	7,61585	0,483906	-3,97621	Homeobox protein knotted-1 like 1 (KNAT1)
GSVIVG01008553001	T0	T12	17,3381	1,10407	-3,97304	WRKY DNA-binding protein 75
GSVIVG01013493001	T0	T12	10,5506	0,672119	-3,97247	Peptide transporter PTR2-B
GSVIVG01007071001	T0	T12	18,4846	1,17821	-3,97166	MATE efflux family protein ripening responsive
GSVIVG01027744001	T0	T12	5,78462	0,368716	-3,97164	1-aminocyclopropane-1-carboxylate oxidase homolog 1
GSVIVG01009295001	T0	T12	9,89263	0,630766	-3,97118	Photosystem I P700 chlorophyll a apoprotein A2
GSVIVG01009166001	T2	T12	17,2487	1,10206	-3,96822	Basic helix-loop-helix (bHLH) family
GSVIVG01033131001	T0	T12	0,965952	0,0617421	-3,96762	Glutamate receptor protein
GSVIVG01026453001	T0	T6	75,2668	4,81153	-3,96745	GA 20-oxidase 2
GSVIVG01020827001	T6	T12	10,6681	0,682233	-3,9669	Myb family
GSVIVG01028265001	T6	T12	6,42478	0,411305	-3,96537	pectinesterase pectinesterase inhibitor 28-like
GSVIVG01030017001	T2	T12	7,04875	0,453703	-3,95755	Exopolysaccharuronase
GSVIVG01024852001	T2	T12	15,5898	1,00603	-3,95386	Glutathione S-transferase 25 GSTU7
GSVIVG01014286001	T6	T12	40,2335	2,61226	-3,94503	Tyrosine aminotransferase
GSVIVG01016701001	T6	T12	77,6773	5,05219	-3,94251	Dormancy/auxin associated protein
GSVIVG01001082001	T0	T6	25,8772	1,68528	-3,94062	SOUL heme-binding
GSVIVG01007992001	T0	T12	56,9463	3,71748	-3,9372	Cycling DOF factor 2
GSVIVG01013838001	T0	T12	4,34281	0,283847	-3,93545	Pectinesterase PPME1
GSVIVG01018453001	T2	T12	17,1213	1,12078	-3,93322	Gibberellin 3-beta-dioxygenase.
GSVIVG01032613001	T0	T12	153,205	10,0439	-3,93107	Beta-ketoacyl-CoA synthase
GSVIVG01018669001	T0	T6	16,7753	1,10152	-3,92877	SRG1 (senescence-related gene 1) oxidoreductase
GSVIVG01031534001	T0	T12	15,3356	1,00762	-3,92786	WD40
GSVIVG01010611001	T6	T12	8,58882	0,568057	-3,91835	Dehydration-responsive protein
GSVIVG01008072001	T6	T12	130,188	8,63234	-3,9147	probable peptide nitrate transporter at5g62680-like
GSVIVG01006485001	T2	T12	15,2547	1,0213	-3,90077	NAC domain-containing protein 25
GSVIVG01014591001	T0	T6	13,264	0,889363	-3,8986	Constans-like 11
GSVIVG01034495001	T0	T12	227,027	15,2805	-3,8931	Permease nonimprinted in Prader-Willi/Angelman
GSVIVG01013974001	T6	T12	13,4009	0,902691	-3,89195	Disease resistance protein
GSVIVG01015418001	T2	T12	42,3032	2,85345	-3,88999	MEE55 (maternal effect embryo arrest 55)
GSVIVG01033651001	T0	T6	99,9466	6,7482	-3,88858	S-adenosylmethionine synthetase
GSVIVG01037121001	T2	T12	18,067	1,22188	-3,88619	Avr9 elicitor response
GSVIVG01036069001	T0	T12	2,85082	0,19379	-3,87881	Secoisolaricresinol dehydrogenase
GSVIVG01024834001	T0	T12	10,6762	0,727259	-3,87578	Phosphatidic acid phosphatase / PAP2
GSVIVG01025675001	T0	T12	109,282	7,44454	-3,87573	Zinc finger (C3HC4-type ring finger)
GSVIVG01004265001	T0	T12	43,1561	2,94224	-3,87458	Aspartic proteinase nepenthesin-1 precursor
GSVIVG01028940001	T0	T12	21,0471	1,43541	-3,87408	4-coumarate-CoA ligase
GSVIVG01000144001	T6	T12	16,3996	1,11988	-3,87224	Peroxidase 73
GSVIVG01035829001	T2	T12	77,2725	5,28293	-3,87054	BZIP protein HY5 (HY5)
GSVIVG01017239001	T2	T12	27,83	1,90562	-3,86831	6-4 photolyase
GSVIVG01036069001	T0	T6	2,85082	0,195899	-3,8632	Secoisolaricresinol dehydrogenase
GSVIVG01036389001	T0	T12	29,8788	2,05498	-3,86193	Ethylene-responsive transcription factor ERF021
GSVIVG01036331001	T0	T6	23,2757	1,60299	-3,85999	(-)-germacrene D synthase
GSVIVG01021412001	T2	T12	13,7731	0,949942	-3,85787	Glycosyl hydrolase family 17 protein
GSVIVG01032545001	T6	T12	8,67852	0,600599	-3,85297	Metalloendopeptinase 1 precursor
GSVIVG01033610001	T0	T6	145,21	10,0618	-3,85118	ARR3 typeA
GSVIVG01017159001	T0	T6	228,308	15,9225	-3,84184	IAA17
GSVIVG01007967001	T0	T6	15,1245	1,0561	-3,84007	Exonuclease
GSVIVG01020928001	T2	T6	99,185	6,92825	-3,83956	Sucrose-phosphate synthase
GSVIVG01028557001	T2	T12	201,706	14,0962	-3,83888	3-ketoacyl-CoA thiolase PED1
GSVIVG01031170001	T0	T2	5,41954	0,378963	-3,83804	Nodulin MtN3 family
GSVIVG01019769001	T0	T12	8,87151	0,623317	-3,83114	Cu2+-exporting ATPase HMA5 (heavy metal ATPase 5)

GSVIVG01024186001	T0	T6	72,0673	5,0686	-3,82969	ferulate 5-hydroxylase
GSVIVG01038662001	T0	T6	211,922	15,0434	-3,81633	Copper-binding family protein
GSVIVG01036483001	T2	T12	32,2084	2,28964	-3,81424	Proline oxidase
GSVIVG0103631001	T2	T6	22,2868	1,60299	-3,79735	(-)-germacrene D synthase
GSVIVG01037121001	T0	T6	66,2509	4,7663	-3,797	Avr9 elicitor response
GSVIVG01001710001	T0	T6	9,88775	0,7144	-3,79084	CYP714A1
GSVIVG01022368001	T0	T6	64,0776	4,6392	-3,78787	Amidase
GSVIVG01030261001	T0	T6	2,73621	0,198141	-3,78758	Protein phosphatase 1D
GSVIVG01027806001	T0	T12	292,16	21,2159	-3,78355	Cryptochrome 2
GSVIVG01030227001	T0	T12	8,12343	0,59074	-3,78149	Alanine--glyoxylate aminotransferase 2 3, mitochondrial
GSVIVG01037005001	T0	T12	99,752	7,25431	-3,78144	Pathogenesis-related protein 1 precursor (PRP 1)
GSVIVG01022403001	T0	T2	62,6235	4,55788	-3,78027	Ribulose 1,5-bisphosphate carboxylase large subunit
GSVIVG01008806001	T2	T12	98,5755	7,18031	-3,77911	PISTILLATA (PI) floral homeotic protein
GSVIVG01032117001	T0	T6	3,41748	0,249041	-3,77848	low quality protein: polygalacturonase-like
GSVIVG01032117001	T0	T2	3,41748	0,249349	-3,7767	low quality protein: polygalacturonase-like
GSVIVG01018028001	T2	T12	106,679	7,79707	-3,7742	Sulfate transporter 3.1 (AST12) (AtST1)
GSVIVG01021155001	T6	T12	6,61353	0,483765	-3,77304	glutamate receptor -like
GSVIVG01013162001	T0	T6	8,26572	0,607159	-3,76699	Microspore-specific promoter 2
GSVIVG01036361001	T0	T6	12,7806	0,939834	-3,76541	(-)-germacrene D synthase
GSVIVG01000550001	T6	T12	15,2439	1,12192	-3,76419	Quinolate synthase
GSVIVG01032858001	T6	T12	132,677	9,80304	-3,75855	Nematode-resistance protein
GSVIVG01006210001	T6	T12	14,9395	1,10755	-3,75369	ATP synthase CF1 beta subunit
GSVIVG01028371001	T0	T12	155,685	11,5524	-3,75236	Alcohol oxidase
GSVIVG01029013001	T2	T12	2,19652	0,163466	-3,74815	R protein L6
GSVIVG01032435001	T2	T12	7,09491	0,528224	-3,74756	Cysteine-rich receptor-like protein kinase 42
GSVIVG01033785001	T2	T6	945,041	70,4689	-3,74532	Phytosulfokines PSK1
GSVIVG01027499001	T2	T12	34,9917	2,62008	-3,73933	Hydrolase, alpha/beta fold
GSVIVG01013737001	T6	T12	18,4555	1,38283	-3,73836	Mov34 STAM-binding protein
GSVIVG01033785001	T0	T6	937,809	70,4689	-3,73423	Phytosulfokines PSK1
GSVIVG01000720001	T2	T12	12,863	0,967357	-3,73303	Auxin-induced protein 22D
GSVIVG01011165001	T0	T12	58,3321	4,38842	-3,73252	Leucoanthocyanidin dioxygenase
GSVIVG01007071001	T2	T6	23,5405	1,77294	-3,73092	MATE efflux family protein ripening responsive
GSVIVG01016820001	T0	T12	18,8184	1,41759	-3,73062	Hydroxyproline-rich glycoprotein
GSVIVG01009260001	T0	T12	60,3738	4,5514	-3,72954	Amino acid permease 6
GSVIVG01027886001	T6	T12	2,21324	0,167447	-3,72438	Cyclopropane fatty acid synthase
GSVIVG01027499001	T0	T12	34,5905	2,62008	-3,7227	Hydrolase, alpha/beta fold
GSVIVG01022368001	T0	T12	64,0776	4,86196	-3,72021	Amidase
GSVIVG01021495001	T0	T12	0,296104	0,022545	-3,71522	Beta-amyrin synthase
GSVIVG01009260001	T2	T12	59,6837	4,5514	-3,71296	Amino acid permease 6
GSVIVG01020678001	T6	T12	265,445	20,3281	-3,70686	trichome birefringence-like 39
GSVIVG01007968001	T0	T6	29,2223	2,23842	-3,70652	Exonuclease
GSVIVG01014073001	T0	T6	29,8839	2,28955	-3,70623	Purine permease 11 PUP11
GSVIVG01008995001	T0	T12	55,5192	4,25919	-3,70434	glucan -beta-glucosidase
GSVIVG01007562001	T0	T12	19,5348	1,5073	-3,69601	Nitrate-responsive NOI protein
GSVIVG01012139001	T0	T12	27,0229	2,10267	-3,68389	Polygalacturonase QRT3
GSVIVG01005041001	T0	T12	13,4925	1,05118	-3,68208	Cytokinin oxidase
GSVIVG01033904001	T0	T6	61,8652	4,82034	-3,68192	Pro-X carboxypeptidase Lysosomal
GSVIVG01007789001	T6	T12	54,2777	4,23443	-3,68012	Trehalose 6-phosphate synthase
GSVIVG01005410001	T0	T6	348,296	27,2139	-3,6779	Copper amine oxidase
GSVIVG01017151001	T0	T12	27,1866	2,1278	-3,67546	Kelch repeat-containing F-box family protein
GSVIVG01034729001	T6	T12	5,09826	0,399103	-3,67517	Amino acid transporter family
GSVIVG01027499001	T2	T6	34,9917	2,74403	-3,67265	Hydrolase, alpha/beta fold
GSVIVG01011165001	T2	T12	55,9293	4,38842	-3,67183	Leucoanthocyanidin dioxygenase
GSVIVG01008021001	T0	T12	8,74241	0,688	-3,66755	Phytochrome kinase substrate 1
GSVIVG01014350001	T6	T12	18,6567	1,47178	-3,66406	Whitefly-induced gp91-phox
GSVIVG01019052001	T2	T12	38,9649	3,07862	-3,66182	DCL2 (DICER 2)
GSVIVG01023557001	T0	T2	36,9473	2,92598	-3,65847	CC-NBS-LRR class
GSVIVG01027499001	T0	T6	34,5905	2,74403	-3,65601	Hydrolase, alpha/beta fold
GSVIVG01027477001	T2	T12	45,8069	3,63674	-3,65485	nac transcription factor-like 9
GSVIVG01027876001	T0	T12	40,4891	3,22329	-3,65093	Peptide transporter protein 3
GSVIVG01009381001	T0	T6	20,5134	1,63503	-3,64918	Tetratricopeptide repeat (TPR)-containing
GSVIVG01035829001	T2	T6	77,2725	6,17071	-3,64645	BZIP protein HY5 (HY5)
GSVIVG01017159001	T2	T6	199,324	15,9225	-3,64598	IAA17
GSVIVG01033785001	T2	T12	945,041	75,7888	-3,64032	Phytosulfokines PSK1
GSVIVG01007679001	T2	T12	128,101	10,2755	-3,64	Alliinase
GSVIVG01033433001	T0	T12	4,73001	0,37985	-3,63834	Male sterility 2
GSVIVG01005410001	T0	T12	348,296	28,1207	-3,63061	Copper amine oxidase
GSVIVG01037853001	T2	T12	19,9004	1,60804	-3,62942	Lateral organ boundaries protein 38
GSVIVG01033785001	T0	T12	937,809	75,7888	-3,62924	Phytosulfokines PSK1
GSVIVG01011348001	T2	T12	4,93265	0,398969	-3,62801	Pectate lyase
GSVIVG01024193001	T0	T6	276,349	22,4952	-3,6188	ferulate 5-hydroxylase

GSVIVG01007038001	T6	T12	1,59653	0,130042	-3,61789	Cellulose synthase CSLE1
GSVIVG01038718001	T0	T12	9,55453	0,779433	-3,61569	Ser/Thr receptor-like kinase1
GSVIVG01004905001	T0	T12	11,0092	0,898964	-3,61431	Cyclobutane pyrimidine dimer photolyase
GSVIVG01013974001	T2	T12	11,0225	0,902691	-3,61008	Disease resistance protein
GSVIVG01008668001	T2	T12	67,5202	5,53986	-3,6074	MtN19
GSVIVG01036862001	T0	T6	21,1592	1,73794	-3,60584	9-cis-epoxycarotenoid dioxygenase
GSVIVG01023906001	T6	T12	47,8767	3,93691	-3,60419	LYS/HIS transporter 7
GSVIVG01028321001	T0	T12	23,6408	1,94535	-3,60318	Inorganic phosphate transporter 1-4
GSVIVG01011635001	T0	T12	6,29291	0,519487	-3,59857	NSL1 (necrotic spotted lesions 1)
GSVIVG01011037001	T6	T12	112,828	9,3431	-3,59407	Gibberellin receptor GID1L2
GSVIVG01032871001	T0	T12	389,579	32,2893	-3,59279	CYP72A1
GSVIVG01014960001	T0	T6	93,7162	7,77428	-3,59152	Glutathione S-transferase 25 GSTU25
GSVIVG01008917001	T2	T12	42,6636	3,54957	-3,58729	Auxin transporter protein 4
GSVIVG01027584001	T0	T12	2,45199	0,204176	-3,58607	Subtilisin serine endopeptidase (XSP1)
GSVIVG01030106001	T2	T6	42,9745	3,58123	-3,58495	AarF domain containing kinase
GSVIVG01032452001	T0	T6	1053,26	87,8052	-3,58441	Myb domain protein 24
GSVIVG01004076001	T2	T12	9,78474	0,816721	-3,58262	MATE efflux family protein
GSVIVG01003672001	T0	T12	5,64964	0,47335	-3,57718	Equilibrative nucleoside transporter ENT3
GSVIVG01037073001	T6	T12	6,135	0,51425	-3,57652	Isoflavone reductase protein 2
GSVIVG01024887001	T2	T12	11,3973	0,956849	-3,57425	Tropinone reductase
GSVIVG01018398001	T0	T12	82,7519	6,9533	-3,57302	Ent-kaurenoic acid oxidase
GSVIVG01008995001	T2	T12	50,611	4,25919	-3,5708	glucan -beta-glucosidase
GSVIVG01019592001	T0	T12	119,215	10,0365	-3,57023	Zinc finger (C3HC4-type ring finger)
GSVIVG01033243001	T0	T12	3,34403	0,281795	-3,56887	Cis-zeatin O-beta-D-glucosyltransferase
GSVIVG01036604001	T2	T12	41,8892	3,53323	-3,56752	AC1112
GSVIVG01019664001	T2	T12	57,2628	4,83421	-3,56625	Cellulase CEL2
GSVIVG01033366001	T6	T12	14,1596	1,1956	-3,56598	CYP93A1 2-hydroxyisoflavanone synthase
GSVIVG01011716001	T6	T12	100,946	8,52529	-3,5657	major latex
GSVIVG01010015001	T0	T6	83,6003	7,06378	-3,56499	Nodulin MtN3 family
GSVIVG01012879001	T2	T6	44,8697	3,80042	-3,56151	Protein phosphatase 2C DBP
GSVIVG01011718001	T6	T12	24,5365	2,07863	-3,56123	Major Latex Protein Family
GSVIVG01025798001	T2	T12	6,70613	0,568665	-3,55983	Nodulin MtN21
GSVIVG01018398001	T0	T6	82,7519	7,03718	-3,55572	Ent-kaurenoic acid oxidase
GSVIVG01032466001	T0	T12	62,7694	5,34466	-3,55389	Carbonic anhydrase, chloroplast precursor
GSVIVG01033356001	T2	T12	4,56477	0,388696	-3,55383	Basic helix-loop-helix (bHLH) family
GSVIVG01021211001	T2	T12	18,6523	1,59023	-3,55205	Pollen Ole e 1 allergen and extensin
GSVIVG01013055001	T6	T12	15,9317	1,361	-3,54916	Xyloglucan endotransglucosylase/hydrolase 30
GSVIVG01014405001	T0	T6	113,78	9,74478	-3,54548	NAC domain containing protein 2
GSVIVG01032523001	T0	T6	5,72627	0,490715	-3,54464	Cellulose synthase CSLC04
GSVIVG01031241001	T2	T12	53,0611	4,56585	-3,5387	KNAT2 (knotted1-like homeobox gene 6)
GSVIVG01025266001	T0	T12	109,645	9,44881	-3,53656	MATE efflux family protein
GSVIVG01027451001	T0	T12	44,9886	3,89301	-3,5306	Quercetin 3-O-methyltransferase 1
GSVIVG01028186001	T6	T12	5,33565	0,462113	-3,52935	Boron transporter-like protein 1
GSVIVG01016302001	T6	T12	5,29392	0,458618	-3,52897	MLO1
GSVIVG01013149001	T6	T12	154,411	13,377	-3,52895	PLATZ transcription factor
GSVIVG01033108001	T6	T12	6,32622	0,549775	-3,52443	Chloride channel protein B
GSVIVG01025313001	T0	T12	10,8125	0,941692	-3,5213	Basic helix-loop-helix (bHLH) family
GSVIVG01021595001	T0	T12	29,5304	2,5724	-3,52101	Glutathione S-conjugate ABC transporter (MRP2)
GSVIVG01005206001	T2	T12	42,7528	3,72474	-3,52081	Ubiquitin-conjugating enzyme E2 O
GSVIVG01037742001	T0	T6	244,759	21,3881	-3,51649	Aspartyl protease
GSVIVG01016476001	T2	T6	14,0781	1,23039	-3,51626	Regulator of chromosome condensation (RCC1)
GSVIVG01007779001	T2	T12	25,8622	2,26186	-3,51526	Nodulin MtN3
GSVIVG01033433001	T0	T6	4,73001	0,413749	-3,51501	Male sterility 2
GSVIVG01013601001	T0	T2	184,419	16,1331	-3,51489	Reverse transcriptase
GSVIVG01024834001	T2	T12	8,28929	0,727259	-3,51071	Phosphatidic acid phosphatase / PAP2
GSVIVG01000402001	T2	T6	544,073	47,8471	-3,5073	#####
GSVIVG01010448001	T2	T6	129,499	11,3947	-3,50651	Signal peptidase complex subunit 1
GSVIVG01019403001	T6	T12	9,30113	0,818614	-3,50615	Beta-carotene hydroxylase
GSVIVG01008560001	T0	T12	77,3212	6,83355	-3,50016	MADS-box protein AGL20
GSVIVG01015332001	T6	T12	56,1754	4,96683	-3,49954	MSS1 (sugar transport protein 13)
GSVIVG01024270001	T2	T6	185,092	16,4191	-3,49479	CYP89A5
GSVIVG01017796001	T6	T12	82,4014	7,32109	-3,49254	UPF0497 family
GSVIVG01025446001	T0	T12	94,4418	8,41191	-3,48892	Accelerated cell death 1 ACD1
GSVIVG01033062001	T0	T12	44,3012	3,96316	-3,48262	Alcohol dehydrogenase
GSVIVG01025918001	T0	T12	17,0439	1,52733	-3,48017	R protein L6
GSVIVG01018453001	T0	T12	12,4308	1,12078	-3,47135	Gibberellin 3-beta-dioxygenase.
GSVIVG01017159001	T0	T12	228,308	20,5919	-3,47083	IAA17
GSVIVG01008150001	T0	T12	324,169	29,2427	-3,4706	L-asparaginase
GSVIVG01017118001	T0	T2	64,8834	5,85822	-3,46931	Sulfate transporter 3.4
GSVIVG01024624001	T6	T12	40,1243	3,62444	-3,46865	WRKY DNA-binding protein 33
GSVIVG01003153001	T2	T6	309,954	28,0298	-3,46702	Cinnamyl alcohol dehydrogenase

GSVIVG01038039001	T0	T12	841,617	76,2935	-3,46353	Glutathione S-transferase 25 GSTU25
GSVIVG01023135001	T0	T6	200,269	18,1613	-3,463	Pectinesterase family
GSVIVG01022100001	T0	T6	288,941	26,2362	-3,46115	Caffeoyl-CoA O-methyltransferase 1
GSVIVG0100950001	T6	T12	13,1793	1,19698	-3,4608	Protein kinase
GSVIVG01034295001	T0	T12	22,7887	2,07621	-3,45629	Isopentenyltransferase
GSVIVG01012879001	T0	T6	41,6758	3,80042	-3,45498	Protein phosphatase 2C DBP
GSVIVG01025276001	T0	T6	12,5335	1,14658	-3,45037	Aldehyde dehydrogenase 3B1
GSVIVG01027922001	T6	T12	8,20665	0,751278	-3,44938	3-isopropylmalate dehydratase large subunit 2
GSVIVG01031241001	T0	T12	49,7908	4,56585	-3,44692	KNAT2 (knotted1-like homeobox gene 6)
GSVIVG01031486001	T2	T12	13,1874	1,21131	-3,44451	Xyloglucan endotransglucosylase/hydrolase 32
GSVIVG01010896001	T0	T12	22,9662	2,11238	-3,44257	Cd2+-exporting ATPase HMA2 (Heavy metal ATPase 2)
GSVIVG01008064001	T0	T6	92,2768	8,50119	-3,44023	Nitrate transporter 1:2
GSVIVG01025652001	T2	T6	109,799	10,1158	-3,44018	Mlo3
GSVIVG01006485001	T0	T6	36,2788	3,34392	-3,43951	NAC domain-containing protein 25
GSVIVG01026248001	T2	T12	100,835	9,30453	-3,43792	Zinc finger (C3HC4-type ring finger)
GSVIVG01030508001	T6	T12	35,8781	3,31129	-3,43764	1-aminocyclopropane-1-carboxylate oxidase 1
GSVIVG01024267001	T2	T6	80,372	7,41826	-3,43754	CYP89A2
GSVIVG01027451001	T2	T12	42,1654	3,89301	-3,4371	Quercetin 3-O-methyltransferase 1
GSVIVG01008984001	T2	T12	9,7359	0,899352	-3,43636	Low affinity sulphate transporter
GSVIVG01024338001	T0	T12	99,5734	9,19854	-3,43628	PLATZ transcription factor
GSVIVG01015743001	T2	T6	145,97	13,4944	-3,43523	Cis-zeatin O-beta-D-glucosyltransferase
GSVIVG01028371001	T0	T6	155,685	14,4564	-3,42886	Alcohol oxidase
GSVIVG01015952001	T6	T12	32,1877	2,99286	-3,42691	WRKY DNA-binding protein 40
GSVIVG01008910001	T0	T6	89,8287	8,38308	-3,42162	Flavonol synthase
GSVIVG01009754001	T0	T12	10,5174	0,982569	-3,42008	S-adenosyl-L-methionine:salicylic acid carboxyl
GSVIVG01001089001	T6	T12	17,1766	1,61451	-3,41128	Ethylene-responsive transcription factor ERF114
GSVIVG01015418001	T2	T6	42,3032	4,00181	-3,40204	MEE55 (maternal effect embryo arrest 55)
GSVIVG01017239001	T2	T6	27,83	2,6347	-3,40093	6-4 photolyase
GSVIVG01007039001	T0	T12	18,45	1,74784	-3,39998	Cellulose synthase CSLE1
GSVIVG01018944001	T0	T12	95,7156	9,12674	-3,39058	Myb family
GSVIVG01022368001	T2	T6	48,6503	4,6392	-3,3905	Amidase
GSVIVG01017737001	T2	T12	35,6732	3,40781	-3,38792	SRG1 (senescence-related gene 1)
GSVIVG01008655001	T2	T6	18,5414	1,77157	-3,38765	LEAFY protein (Floricula/leafy protein)
GSVIVG01026707001	T6	T12	39,1909	3,74916	-3,38588	Phosphatidylglycerol specific phospholipase C
GSVIVG01020067001	T0	T12	12,4182	1,18814	-3,38568	Pectate lyase
GSVIVG01018144001	T2	T12	149,858	14,348	-3,38468	Cellulose synthase CSLG2
GSVIVG01007071001	T0	T6	18,4846	1,77294	-3,3821	MATE efflux family protein ripening responsive
GSVIVG01005878001	T0	T12	175,464	16,8317	-3,38193	Trehalose-6-phosphate phosphatase
GSVIVG01011947001	T6	T12	44,3222	4,25363	-3,38126	AP2 domain-containing protein RAP2.8
GSVIVG01007679001	T0	T6	210,188	20,1917	-3,37985	Alliinase
GSVIVG01020067001	T2	T12	12,3662	1,18814	-3,37963	Pectate lyase
GSVIVG01020688001	T6	T12	48,9008	4,73677	-3,36788	Basic helix-loop-helix (bHLH) family
GSVIVG01027476001	T2	T12	131,994	12,8938	-3,35573	No apical meristem cup-shaped cotyledon2
GSVIVG01023905001	T0	T12	19,9786	1,95524	-3,35303	LYS/HIS transporter 7 LHT7
GSVIVG01034748001	T0	T12	3,67373	0,359554	-3,35296	ABC transporter G member 22
GSVIVG01015743001	T0	T6	137,135	13,4944	-3,34516	Cis-zeatin O-beta-D-glucosyltransferase
GSVIVG01013737001	T0	T12	14,0197	1,38283	-3,34177	Mov34 STAM-binding protein
GSVIVG01022153001	T0	T12	39,6906	3,93283	-3,33516	Nodulation protein
GSVIVG01025614001	T0	T12	16,5142	1,63741	-3,33422	Inositol-1,4,5-trisphosphate 5-phosphatase CVP2, type I
GSVIVG01035071001	T2	T6	880,635	87,3809	-3,33315	Major allergen Pru ar 1
GSVIVG01015420001	T0	T6	21,3209	2,1169	-3,33224	Copper-binding family protein
GSVIVG01008984001	T0	T12	9,00179	0,899352	-3,32325	Low affinity sulphate transporter
GSVIVG01022368001	T2	T12	48,6503	4,86196	-3,32284	Amidase
GSVIVG01005878001	T2	T12	168,273	16,8317	-3,32156	Trehalose-6-phosphate phosphatase
GSVIVG01019696001	T0	T6	29,1797	2,91888	-3,32148	flavanone 3-beta-hydroxylase
GSVIVG01035885001	T6	T12	98,685	9,88029	-3,32021	WRKY DNA-binding protein 18
GSVIVG01031534001	T2	T12	10,0425	1,00762	-3,31709	WD40
GSVIVG01008985001	T0	T12	11,1579	1,12576	-3,3091	Sulfate transporter 1.3
GSVIVG01006538001	T0	T12	152,409	15,4468	-3,30257	Phosphoenolpyruvate carboxykinase
GSVIVG01018028001	T6	T12	76,4283	7,79707	-3,2931	Sulfate transporter 3.1 (AST12) (AtST1)
GSVIVG01023631001	T6	T12	12,6991	1,29678	-3,29171	Hydroxycinnamoyl-CoA shikimate/quinate
GSVIVG01019601001	T2	T6	33,6587	3,45257	-3,28524	Nodulin MtN3 family protein
GSVIVG01022823001	T2	T12	12,0061	1,2338	-3,28259	Leucine Rich Repeat receptor-like kinase
GSVIVG01017159001	T2	T12	199,324	20,5919	-3,27496	IAA17
GSVIVG01000689001	T6	T12	16,886	1,74993	-3,27046	GA 20-oxidase 2
GSVIVG01029038001	T0	T12	18,4348	1,91325	-3,26834	Leucine-rich repeat protein kinase
GSVIVG01016476001	T2	T12	14,0781	1,46155	-3,26788	Regulator of chromosome condensation (RCC1)
GSVIVG01013935001	T6	T12	53,7091	5,58105	-3,26656	Ethylene-responsive transcription factor ERF105
GSVIVG01023631001	T2	T12	12,4528	1,29678	-3,26346	Hydroxycinnamoyl-CoA shikimate/quinate
GSVIVG01025675001	T2	T12	71,2684	7,44454	-3,25901	Zinc finger (C3HC4-type ring finger)
GSVIVG01007039001	T2	T12	16,6481	1,74784	-3,25172	Cellulose synthase CSLE1

GSVIVG01012922001	T6	T12	39,0243	4,11624	-3,24497	Alpha-amylase/subtilisin inhibitor
GSVIVG01022321001	T0	T12	22,2975	2,35891	-3,24069	Amino acid permease 2
GSVIVG01025652001	T2	T12	109,799	11,6909	-3,23141	Mlo3
GSVIVG01029838001	T0	T6	138,716	14,7791	-3,2305	Translation initiation factor IF-2B subunit delta
GSVIVG01016762001	T6	T12	36,6056	3,90429	-3,22893	Growth-regulating factor 5
GSVIVG01008763001	T6	T12	21,1226	2,25316	-3,22877	Peroxidase 64
GSVIVG01005041001	T6	T12	9,84997	1,05118	-3,22811	Cytokinin oxidase
GSVIVG01019729001	T0	T12	71,4063	7,62523	-3,2272	Aquaporin NIP5;1
GSVIVG01005878001	T6	T12	157,565	16,8317	-3,2267	Trehalose-6-phosphate phosphatase
GSVIVG01015223001	T0	T12	17,0526	1,82208	-3,22634	MYB divaricata
GSVIVG01023135001	T0	T12	200,269	21,4112	-3,2255	Pectinesterase family
GSVIVG01027449001	T6	T12	48,1987	5,1558	-3,22473	Caffeate 3-O-methyltransferase 1
GSVIVG01021595001	T2	T12	24,0072	2,5724	-3,22228	Glutathione S-conjugate ABC transporter (MRP2)
GSVIVG01004076001	T0	T12	7,62072	0,816721	-3,22201	MATE efflux family protein
GSVIVG01016999001	T0	T12	9,2007	0,987548	-3,21982	ABC transporter g family pleiotropic drug resistance 7
GSVIVG01022520001	T6	T12	14,1672	1,52414	-3,21648	Translation initiation factor eIF-2 beta subunit
GSVIVG01031020001	T2	T12	16,9022	1,82015	-3,21508	BEE1 (BR Enhanced expression 1)
GSVIVG01017931001	T0	T12	110,426	11,9598	-3,20682	Cyclin-T1-4
GSVIVG01008064001	T0	T12	92,2768	10,0222	-3,20277	Nitrate transporter 1:2
GSVIVG01015223001	T6	T12	16,7271	1,82208	-3,19853	MYB divaricata
GSVIVG01026248001	T0	T12	85,2834	9,30453	-3,19626	Zinc finger (C3HC4-type ring finger)
GSVIVG01007987001	T0	T12	155,391	16,9709	-3,19477	Alpha-expansin 3
GSVIVG01037742001	T2	T6	195,589	21,3881	-3,19295	Aspartyl protease
GSVIVG01015991001	T6	T12	360,873	39,6966	-3,1844	Co-chaperone-curved DNA binding protein A
GSVIVG01021530001	T6	T12	92,9195	10,2274	-3,18354	Inositol transporter 2
GSVIVG01034295001	T0	T6	22,7887	2,51315	-3,18075	Isopentenyltransferase
GSVIVG01014405001	T2	T12	60,1945	6,64641	-3,17898	NAC domain containing protein 2
GSVIVG01022823001	T0	T12	11,1485	1,2338	-3,17567	Leucine Rich Repeat receptor-like kinase
GSVIVG01014960001	T0	T12	93,7162	10,3777	-3,17481	Glutathione S-transferase 25 GSTU25
GSVIVG01019733001	T2	T12	25,6961	2,85126	-3,17188	Potassium channel tetramerisation domain-containing
GSVIVG01010015001	T2	T6	63,6084	7,06378	-3,1707	Nodulin MtN3 family
GSVIVG01032681001	T0	T6	106,778	11,8664	-3,16967	Expansin [Vitis labrusca x Vitis vinifera] EXPA8
GSVIVG01027456001	T2	T6	240,197	26,7837	-3,16479	Myb CCA1 (circadian clock associated 1)
GSVIVG01017959001	T0	T12	58,571	6,53883	-3,16308	Copper amine oxidase
GSVIVG01031528001	T0	T12	22,3527	2,50039	-3,16023	ABC transporter G member 7
GSVIVG01027456001	T6	T12	26,7837	3,00312	-3,15682	Myb CCA1 (circadian clock associated 1)
GSVIVG01008806001	T2	T6	98,5755	11,0537	-3,15669	PISTILLATA (PI) floral homeotic protein
GSVIVG01035314001	T6	T12	15,786	1,78454	-3,14502	receptor-like protein kinase hsl1-like
GSVIVG01007987001	T2	T12	149,904	16,9709	-3,14291	Alpha-expansin 3
GSVIVG01027454001	T0	T12	44,5357	5,10611	-3,12467	Naringenin,2-oxoglutarate 3-dioxygenase
GSVIVG01008461001	T0	T12	31,4106	3,62117	-3,11673	3-hydroxyisobutyrate dehydrogenase
GSVIVG01029244001	T0	T6	92,0136	10,6098	-3,11645	AHA2 (Arabidopsis H(+)-ATPase 2)
GSVIVG01014092001	T0	T12	31,6135	3,65508	-3,11256	Alpha,alpha-trehalose-phosphate synthase
GSVIVG01033904001	T2	T6	41,6652	4,82034	-3,11164	Pro-X carboxypeptidase Lysosomal
GSVIVG01019729001	T2	T12	65,4825	7,62523	-3,10226	Aquaporin NIP5;1
GSVIVG01019442001	T2	T12	32,3412	3,77651	-3,09825	AAA-type ATPase
GSVIVG01012005001	T2	T12	8,61672	1,00738	-3,09654	Phospholipid-transporting ATPase
GSVIVG01000402001	T6	T12	47,8471	5,60398	-3,09391	#####
GSVIVG01019459001	T0	T6	29,4375	3,46578	-3,0864	Cation/hydrogen exchanger (CHX18)
GSVIVG01028557001	T2	T6	201,706	23,7759	-3,08468	3-ketoacyl-CoA thiolase PED1
GSVIVG01013149001	T2	T12	113,377	13,377	-3,08331	PLATZ transcription factor
GSVIVG01008820001	T6	T12	35,5326	4,19287	-3,08313	Amino acid permease 3
GSVIVG01019592001	T0	T6	119,215	14,0946	-3,08035	Zinc finger (C3HC4-type ring finger)
GSVIVG01016999001	T6	T12	8,32494	0,987548	-3,07552	ABC transporter g family pleiotropic drug resistance 7
GSVIVG01024718001	T6	T12	15,0042	1,78292	-3,07306	Gibberellin 2-beta-dioxygenase 7
GSVIVG01028321001	T0	T6	23,6408	2,81658	-3,06926	Inorganic phosphate transporter 1-4
GSVIVG01034295001	T2	T12	17,3948	2,07621	-3,06663	Isopentenyltransferase
GSVIVG01029244001	T0	T12	92,0136	10,9857	-3,06622	AHA2 (Arabidopsis H(+)-ATPase 2)
GSVIVG01003181001	T6	T12	50,4497	6,05172	-3,05943	Sugar transporter 1
GSVIVG01032466001	T0	T6	62,7694	7,59626	-3,0467	Carbonic anhydrase, chloroplast precursor
GSVIVG01008480001	T0	T12	45,6841	5,53789	-3,04428	Potassium transporter 2
GSVIVG01027407001	T0	T12	54,1967	6,5744	-3,04327	Homeobox-leucine zipper protein HB-7
GSVIVG01025446001	T0	T6	94,4418	11,5285	-3,03422	Accelerated cell death 1 ACD1
GSVIVG01025968001	T0	T12	15,0139	1,83484	-3,03257	R protein L6
GSVIVG01027876001	T2	T12	26,3143	3,22329	-3,02924	Peptide transporter protein 3
GSVIVG01006458001	T0	T6	99,169	12,1549	-3,02835	Mannitol dehydrogenase
GSVIVG01032613001	T0	T6	153,205	18,789	-3,0275	Beta-ketoacyl-CoA synthase
GSVIVG01003673001	T0	T6	53,4145	6,56106	-3,02523	Octicosaepptide/Phox/Bem1p (PB1) domain-containing
GSVIVG01021530001	T0	T12	83,0696	10,2274	-3,02188	Inositol transporter 2
GSVIVG01003954001	T2	T6	68,8149	8,47257	-3,02185	Metal transporter Nramp6
GSVIVG01030090001	T2	T12	233,613	28,7712	-3,02142	Jasmonate O-methyltransferase

GSVIVG01036525001	T2	T12	21,5529	2,65587	-3,02063	Lipase GDSL 7
GSVIVG01026525001	T0	T2	20,2222	2,49907	-3,01648	PGSIP1 (Plant glycogenin-like starch initiation protein 1)
GSVIVG01037005001	T0	T2	99,752	12,3818	-3,01013	Pathogenesis-related protein 1 precursor (PRP 1)
GSVIVG01017151001	T2	T12	17,1355	2,1278	-3,00956	Kelch repeat-containing F-box family protein
GSVIVG01019695001	T2	T6	50,1642	6,26499	-3,00127	Naringenin,2-oxoglutarate 3-dioxygenase
GSVIVG01014350001	T0	T12	11,7551	1,47178	-2,99766	Whitefly-induced gp91-phox
GSVIVG01023146001	T2	T12	18,7297	2,35526	-2,99137	Proton-dependent oligopeptide transport (POT) family
GSVIVG01002066001	T0	T6	69,0646	8,69186	-2,99021	Heat shock transcription factor B2A
GSVIVG01008139001	T0	T12	36,1556	4,55248	-2,9895	SEPALLATA1
GSVIVG01015418001	T0	T12	22,6592	2,85345	-2,98932	MEE55 (maternal effect embryo arrest 55)
GSVIVG01020084001	T0	T12	186,37	23,5713	-2,98307	Proton-dependent oligopeptide transport (POT) family
GSVIVG01016999001	T2	T12	7,79603	0,987548	-2,98082	ABC transporter g family pleiotropic drug resistance 7
GSVIVG01022403001	T6	T12	135,244	17,1445	-2,97975	Ribulose 1,5-bisphosphate carboxylase large subunit
GSVIVG01002106001	T0	T12	18,2519	2,31401	-2,97957	Cinnamyl alcohol dehydrogenase
GSVIVG01025923001	T0	T6	93,4802	11,8529	-2,97942	12-oxophytodienoate reductase 2
GSVIVG01030508001	T2	T12	26,066	3,31129	-2,97671	1-aminocyclopropane-1-carboxylate oxidase 1
GSVIVG01014772001	T6	T12	39,7369	5,06011	-2,97324	Amino acid permease 7
GSVIVG01008139001	T2	T12	35,6181	4,55248	-2,96789	SEPALLATA1
GSVIVG01008595001	T0	T6	285,485	36,5038	-2,96729	Nodulin MtN3 family
GSVIVG01013493001	T2	T12	5,23368	0,672119	-2,96104	Peptide transporter PTR2-B
GSVIVG01007982001	T6	T12	65,3191	8,43305	-2,95338	NAC domain containing protein 100
GSVIVG01025740001	T6	T12	27,1618	3,50723	-2,95318	F-box family protein
GSVIVG01034944001	T6	T12	137,504	17,8925	-2,94204	Beta-fructofuranosidase
GSVIVG01027876001	T6	T12	24,7295	3,22329	-2,93963	Peptide transporter protein 3
GSVIVG01030090001	T2	T6	233,613	30,4758	-2,93838	Jasmonate O-methyltransferase
GSVIVG01021897001	T2	T6	24,8003	3,24112	-2,93579	Beta-ketoacyl-CoA synthase
GSVIVG01031432001	T6	T12	75,42	9,86295	-2,93486	Aspartic proteinase nepenthesin-2 precursor
GSVIVG01001112001	T2	T12	25,3916	3,35358	-2,92058	Indole-3-acetic acid amido synthetase
GSVIVG01007992001	T0	T6	56,9463	7,54691	-2,91564	Cycling DOF factor 2
GSVIVG01016762001	T2	T12	29,4502	3,90429	-2,91515	Growth-regulating factor 5
GSVIVG01022153001	T2	T12	29,6298	3,93283	-2,91341	Nodulation protein
GSVIVG01019732001	T0	T12	23,2167	3,11083	-2,89979	Hydroxyproline-rich glycoprotein
GSVIVG01019769001	T2	T6	13,3498	1,79205	-2,89713	Cu2+-exporting ATPase HMA5 (heavy metal ATPase 5)
GSVIVG01035689001	T2	T12	52,5809	7,06149	-2,89649	RNA recognition motif (RRM)-containing protein
GSVIVG01033076001	T6	T12	106,058	14,2496	-2,89586	Nodulin
GSVIVG01024259001	T2	T12	93,2471	12,5571	-2,89255	10-deacetylbaecatin III 10-O-acetyltransferase
GSVIVG01023585001	T0	T12	55,8787	7,59686	-2,87882	Basic helix-loop-helix (bHLH) family
GSVIVG01008995001	T6	T12	31,2993	4,25919	-2,87748	glucan -beta-glucosidase
GSVIVG01027477001	T2	T6	45,8069	6,23361	-2,87742	nac transcription factor-like 9
GSVIVG01025652001	T0	T6	74,0705	10,1158	-2,87229	Mlo3
GSVIVG01031432001	T0	T12	71,8661	9,86295	-2,86522	Aspartic proteinase nepenthesin-2 precursor
GSVIVG01013272001	T0	T6	179,134	24,6617	-2,8607	1,4-alpha-D-glucan maltohydrolase
GSVIVG01008820001	T0	T12	30,4409	4,19287	-2,86	Amino acid permease 3
GSVIVG01026462001	T0	T12	38,0652	5,25576	-2,8565	Protein kinase
GSVIVG01006166001	T0	T12	215,472	29,8203	-2,85313	Phosphoenolpyruvate carboxykinase
GSVIVG01019729001	T6	T12	55,0333	7,62523	-2,85145	Aquaporin NIP5;1
GSVIVG01010850001	T0	T12	36,8126	5,106	-2,84993	Lectin
GSVIVG01038611001	T0	T12	105,457	14,6553	-2,84715	Metal-nicotinamine transporter YSL3
GSVIVG01010044001	T6	T12	57,6605	8,01833	-2,84621	Pathogenesis-related
GSVIVG01008738001	T0	T12	152,829	21,2695	-2,84506	Thioredoxin-like protein CDSP32
GSVIVG01025446001	T2	T12	60,1762	8,41191	-2,83869	Accelerated cell death 1 ACD1
GSVIVG01035689001	T0	T12	50,5134	7,06149	-2,83862	RNA recognition motif (RRM)-containing protein
GSVIVG01025923001	T0	T12	93,4802	13,0732	-2,83805	12-oxophytodienoate reductase 2
GSVIVG01008003001	T2	T6	94,087	13,1788	-2,83578	GASA like
GSVIVG01007043001	T6	T12	38,5482	5,40581	-2,83408	Cellulose synthase CSLE1
GSVIVG01020215001	T6	T12	92,1704	12,9651	-2,82967	probable -trehalose-phosphate synthase
GSVIVG01028879001	T2	T12	112,687	15,8967	-2,82552	AnthoMATE1, anthocyanin permease AM1
GSVIVG01019017001	T2	T6	31,0381	4,40377	-2,81723	Anthocyanidin 3-O-glucosyltransferase
GSVIVG01016733001	T0	T12	189,338	26,8733	-2,81672	Ferredoxin 4Fe-4S, iron-sulfur binding
GSVIVG01031715001	T0	T12	66,8373	9,49808	-2,81495	Caffeoyl-CoA O-methyltransferase
GSVIVG01023817001	T0	T6	170,199	24,3393	-2,80586	Basic leucine-zipper 11 GBF6
GSVIVG01022100001	T0	T2	288,941	41,3431	-2,80506	Caffeoyl-CoA O-methyltransferase 1
GSVIVG01021113001	T0	T12	27,7044	3,96811	-2,80359	Homeobox-1
GSVIVG01028844001	T6	T12	58,9282	8,50744	-2,79216	Heavy-metal-associated domain-containing protein
GSVIVG01028677001	T0	T6	51,5364	7,44916	-2,79044	SEC14 cytosolic factor
GSVIVG01008495001	T0	T12	58,7581	8,5542	-2,78008	Cyclin-dependent kinase G-2
GSVIVG01008064001	T2	T6	58,2194	8,50119	-2,77576	Nitrate transporter 1:2
GSVIVG01006458001	T2	T12	37,4557	5,54321	-2,75639	Mannitol dehydrogenase
GSVIVG01027448001	T6	T12	45,3623	6,72098	-2,75475	Catechol O-methyltransferase
GSVIVG01023817001	T2	T6	163,805	24,3393	-2,75062	Basic leucine-zipper 11 GBF6
GSVIVG01020828001	T0	T12	115,833	17,2379	-2,74839	Phytoene synthase, chloroplast precursor

GSVIVG01024259001	T0	T12	84,2917	12,5571	-2,74688	10-deacetylbaecatin III 10-O-acetyltransferase
GSVIVG01021530001	T2	T12	68,651	10,2274	-2,74684	Inositol transporter 2
GSVIVG01035695001	T2	T6	166,719	24,8612	-2,74545	RD22
GSVIVG01031528001	T0	T6	22,3527	3,33984	-2,7426	ABC transporter G member 7
GSVIVG01035279001	T6	T12	68,1437	10,1826	-2,74248	Cold induced protein
GSVIVG01019361001	T0	T12	106,862	15,9847	-2,74098	Na ⁺ /H ⁺ antiporter, isoform 6
GSVIVG01032681001	T0	T12	106,778	15,9745	-2,74078	Expansin [Vitis labrusca x Vitis vinifera] EXPA8
GSVIVG01033804001	T0	T12	22,1718	3,32956	-2,73532	ABC transporter G member 22
GSVIVG01038198001	T0	T12	59,7591	9,00129	-2,73095	BT3 (BTB and TAZ domain protein 3)
GSVIVG01018119001	T0	T12	14,9246	2,24993	-2,72974	Zinc knuckle
GSVIVG01003194001	T0	T6	36,3984	5,48896	-2,72927	WD-repeat protein
GSVIVG01028677001	T0	T12	51,5364	7,81155	-2,72191	SEC14 cytosolic factor
GSVIVG01024193001	T2	T6	146,944	22,4952	-2,70758	ferulate 5-hydroxylase
GSVIVG01022838001	T0	T12	45,7557	7,01273	-2,7059	T-complex protein 11
GSVIVG01031707001	T0	T12	84,4742	12,9627	-2,70414	IMP dehydrogenase
GSVIVG01010844001	T0	T6	72,6494	11,1735	-2,70087	Sterol-4-alpha-carboxylate 3-dehydrogenase,
GSVIVG01032914001	T0	T12	41,4803	6,39219	-2,69805	LNG1 (LONGIFOLIA1)
GSVIVG01019052001	T2	T6	38,9649	6,0072	-2,69741	DCL2 (DICER 2)
GSVIVG01024338001	T2	T12	59,3698	9,19854	-2,69025	PLATZ transcription factor
GSVIVG01038039001	T2	T6	165,444	25,699	-2,68656	Glutathione S-transferase 25 GSTU25
GSVIVG01025266001	T0	T6	109,645	17,0825	-2,68225	MATE efflux family protein
GSVIVG01016441001	T0	T2	32,808	5,13272	-2,67625	Photosystem II PsbA
GSVIVG01007679001	T2	T6	128,101	20,1917	-2,66545	Alliinase
GSVIVG01025652001	T0	T12	74,0705	11,6909	-2,66352	Mlo3
GSVIVG01035076001	T2	T6	333,498	52,6591	-2,66292	Pathogenesis protein 10 [Vitis vinifera]
GSVIVG01005836001	T0	T12	93,3675	14,7795	-2,65932	3'(2') 5'-bisphosphate nucleotidase
GSVIVG01008738001	T0	T6	152,829	24,2278	-2,65718	Thioredoxin-like protein CDSP32
GSVIVG01024338001	T6	T12	57,9989	9,19854	-2,65655	PLATZ transcription factor
GSVIVG01031814001	T0	T6	57,5236	9,14716	-2,65276	Nodulin 1A, Senescence-associated
GSVIVG01033332001	T0	T12	91,3324	14,7318	-2,6322	Carboxyl-terminal processing protease
GSVIVG01014405001	T2	T6	60,1945	9,74478	-2,62693	NAC domain containing protein 2
GSVIVG01012714001	T0	T12	168,372	27,2715	-2,62619	Lactoylglutathione lyase
GSVIVG01030058001	T0	T12	19,9249	3,24245	-2,61942	Histidine kinase (AHK2)
GSVIVG01016869001	T0	T12	68,652	11,3081	-2,60194	Cell wall apoplastic invertase
GSVIVG01008461001	T2	T12	21,9002	3,62117	-2,59642	3-hydroxyisobutyrate dehydrogenase
GSVIVG01010024001	T2	T6	13,0836	78,7625	2,58975	Alcohol dehydrogenase 1
GSVIVG01033769001	T6	T12	26,408	159,068	2,5906	Peroxisomal type 2
GSVIVG01027166001	T0	T12	7,55594	46,0596	2,60782	Auxin response factor 18
GSVIVG01003748001	T6	T12	12,8482	78,4933	2,61101	Anthranilate N-benzoyltransferase protein 1
GSVIVG01016739001	T2	T6	9,73717	59,7803	2,6181	flavonoid 3-monooxygenase
GSVIVG01026510001	T0	T12	18,1949	112,594	2,62952	Alcohol dehydrogenase 6
GSVIVG01023260001	T0	T12	16,6098	102,96	2,63197	Lactoylglutathione lyase
GSVIVG01034166001	T0	T2	17,2382	107,484	2,64044	Myb domain protein 91
GSVIVG01032682001	T2	T12	29,7563	185,567	2,64067	Non-specific lipid-transfer protein
GSVIVG01008728001	T0	T12	8,07126	50,5016	2,64546	Protein kinase
GSVIVG01002361001	T2	T6	20,5424	128,902	2,64959	catalase
GSVIVG01018058001	T0	T6	3,73868	23,4609	2,64966	Calcium-transporting ATPase 13 ACA13
GSVIVG01019833001	T2	T6	16,3272	102,485	2,65006	UDP-glucose 4-epimerase
GSVIVG01020258001	T0	T12	16,5772	104,125	2,65104	Amino acid permease
GSVIVG01016698001	T2	T12	17,884	112,816	2,65724	Auxin-induced protein
GSVIVG01012635001	T2	T12	12,7852	81,0498	2,66433	Xyloglucan endotransglucosylase/hydrolase 8
GSVIVG01000226001	T0	T12	22,2383	141,508	2,66976	Cyclin D
GSVIVG01010949001	T0	T12	5,2487	33,4185	2,67062	HAK5 (High affinity K ⁺ transporter 5)
GSVIVG01012052001	T0	T12	25,6252	163,286	2,67177	Ribosomal protein L36a/L44 (RPL36aB) 60S
GSVIVG01023906001	T0	T6	7,45761	47,8767	2,68254	LYS/HIS transporter 7
GSVIVG01032029001	T2	T6	3,63134	23,3394	2,68419	Lipoxygenase LOX1
GSVIVG01019636001	T0	T12	13,09	84,3325	2,68763	Plastocyanin domain-containing protein
GSVIVG01007849001	T0	T12	6,55752	42,2728	2,6885	Replication protein A 70 kDa DNA-binding subunit
GSVIVG01009097001	T0	T6	9,11442	58,908	2,69224	Basic helix-loop-helix (bHLH) family
GSVIVG01033871001	T2	T12	4,56498	29,5233	2,69317	Kinesin family member 11
GSVIVG01011034001	T0	T6	27,467	178,209	2,6978	Histone H2AXb HTA3
GSVIVG01026582001	T0	T6	46,3424	300,918	2,69896	Histone H3
GSVIVG01009097001	T0	T12	9,11442	59,2555	2,70073	Basic helix-loop-helix (bHLH) family
GSVIVG01003139001	T0	T6	27,1105	177,303	2,70929	Histone H2A variant 1 HTA11
GSVIVG01032682001	T0	T12	28,3735	185,567	2,70933	Non-specific lipid-transfer protein
GSVIVG01015027001	T0	T12	14,2974	93,5149	2,70944	Peroxisomal bcp
GSVIVG01009178001	T0	T6	2,13511	14,0181	2,71491	Kinesin family member 4/7/21/27
GSVIVG01033871001	T0	T6	3,4537	22,7223	2,71789	Kinesin family member 11
GSVIVG01018857001	T2	T12	7,77318	51,1537	2,71826	CYP90D1 ROT3 (ROTUNDIFOLIA 3) steroid hydroxylase
GSVIVG01019114001	T0	T6	33,7318	222,018	2,71849	Photosystem I subunit XI (PSAL)
GSVIVG01012841001	T0	T12	5,70202	37,5688	2,71999	Vacuolar pyrophosphatase

GSVIVG01029920001	T0	T12	15,9758	105,298	2,72051	MATE efflux family protein
GSVIVG01029368001	T0	T6	9,94954	65,7207	2,72365	Kinase interacting protein
GSVIVG01033935001	T6	T12	11,8873	78,6856	2,72668	Aspartyl protease
GSVIVG01015370001	T2	T12	3,29889	21,856	2,72798	Myb-related protein 3R-1 (Plant c-MYB-like protein 1)
GSVIVG01035663001	T2	T12	3,75857	24,9716	2,73203	Myb-related protein 3R-1 (Plant c-MYB-like protein 1)
GSVIVG01009972001	T0	T12	19,1154	127,16	2,73384	Mannitol dehydrogenase
GSVIVG01015564001	T0	T12	8,58746	57,4249	2,74137	Thylakoid luminal 16.5 kDa protein, chloroplast precursor
GSVIVG01025781001	T0	T12	6,99555	46,8078	2,74224	Cyclin B-type
GSVIVG01036543001	T0	T12	12,6028	84,4426	2,74423	Pollen Ole e 1 allergen and extensin
GSVIVG01028041001	T0	T6	5,07411	34,0848	2,7479	Pectinesterase family
GSVIVG01013734001	T2	T12	25,4228	171,194	2,75144	Quinone oxidoreductase, chloroplast precursor
GSVIVG01003545001	T0	T12	9,87902	66,6735	2,75467	Ribosomal protein L25
GSVIVG01032527001	T0	T12	23,6178	159,77	2,75804	Heavy-metal-associated domain-containing protein
GSVIVG01016712001	T0	T12	14,4783	98,0166	2,75913	S-2-hydroxy-acid oxidase, peroxisomal
GSVIVG01036141001	T0	T12	18,6312	126,378	2,76194	esterase lipase thioesterase family protein
GSVIVG01034674001	T2	T6	15,1613	102,974	2,76382	Bark storage protein A precursor
GSVIVG01034510001	T0	T12	98,3986	668,855	2,76498	Histone H3
GSVIVG01010330001	T0	T12	9,37517	63,7982	2,7666	Ankyrin repeat
GSVIVG01011417001	T0	T12	8,26918	56,3544	2,76871	Myb domain protein 94
GSVIVG01000121001	T0	T12	88,7259	604,801	2,76903	Ribosomal protein L26 (RPL26A) 60S
GSVIVG01009442001	T2	T12	13,7111	93,4664	2,76911	LRX1 (leucine-rich repeat/extensin 1)
GSVIVG01014842001	T0	T12	89,9524	613,787	2,7705	Photosystem I reaction center subunit V (PSAG)
GSVIVG01036262001	T0	T2	12,421	84,7611	2,77062	AN3 (ANGUSITFOLIA3)
GSVIVG01037043001	T0	T12	5,8821	40,2432	2,77434	Pyruvate kinase isozyme A, chloroplast precursor
GSVIVG01016739001	T0	T6	8,72631	59,7803	2,77623	flavonoid 3-monooxygenase
GSVIVG01013218001	T0	T12	9,66487	66,2337	2,77674	Dynammin-like protein 2b
GSVIVG01025162001	T6	T12	2,55675	17,5541	2,77943	MLO1
GSVIVG01030881001	T0	T12	17,1774	118,039	2,78069	Beta-mannosidase
GSVIVG01011511001	T2	T12	7,78135	53,5615	2,7831	Biotin carboxyl carrier protein of acetyl-CoA carboxylase
GSVIVG01020728001	T0	T12	5,48721	37,8263	2,78525	Serine/threonine-protein kinase NAK
GSVIVG01011840001	T0	T6	12,7339	87,8106	2,78572	Zinc finger (C3HC4-type ring finger)
GSVIVG01031547001	T2	T12	11,0141	76,0255	2,78713	Ubiquitin-conjugating enzyme E2 C
GSVIVG01017644001	T0	T2	7,04032	48,6708	2,78934	Polygalacturonase GH28
GSVIVG01020616001	T6	T12	23,5181	162,753	2,79085	fasciclin arabinogalactan-protein (FLA13)
GSVIVG01008925001	T2	T12	8,23523	57,1102	2,79387	Zinc finger (C2H2 type) family
GSVIVG01028071001	T2	T12	3,18606	22,183	2,79961	Cellulose synthase CSLD5
GSVIVG01018512001	T2	T12	4,47493	31,2141	2,80226	Microtubule associated protein (MAP65/ASE1) pleiade
GSVIVG01021193001	T0	T12	11,029	76,9539	2,80269	Ribosomal protein L34
GSVIVG01032654001	T2	T12	16,168	113,026	2,80544	CENP-E like kinetochore protein
GSVIVG01036141001	T6	T12	18,0358	126,378	2,80881	esterase lipase thioesterase family protein
GSVIVG01017717001	T0	T12	12,1577	85,3748	2,81194	Pectinacetylase
GSVIVG01026444001	T2	T12	14,915	104,87	2,81377	3-hydroxy-3-methylglutaryl-coenzyme A reductase 3
GSVIVG01009624001	T2	T6	9,64475	67,8657	2,81487	Photosystem II PsbO protein
GSVIVG01034704001	T6	T12	19,1773	135,083	2,81638	CYP77A2
GSVIVG01034361001	T0	T12	35,1391	248,421	2,82164	High mobility group B 6
GSVIVG01021149001	T0	T12	17,6686	125,028	2,82299	Lipase GDSL
GSVIVG01009099001	T0	T6	13,9109	98,44	2,82303	Gibberellin 20 oxidase 2
GSVIVG01007348001	T6	T12	27,3844	194,034	2,82488	Extensin
GSVIVG01032906001	T2	T6	17,2835	122,645	2,82702	Hydroxyproline-rich glycoprotein
GSVIVG01032906001	T0	T6	17,2782	122,645	2,82746	Hydroxyproline-rich glycoprotein
GSVIVG01017868001	T0	T12	8,00449	57,0531	2,83343	Glutamine synthetase
GSVIVG01016518001	T0	T12	5,88113	41,9192	2,83345	Cell division cycle 20-like protein 1
GSVIVG01029789001	T0	T12	45,0861	321,939	2,83603	LHCB6 (light harvesting complex PSII)
GSVIVG01013446001	T0	T12	5,71997	40,8451	2,83608	Spindle checkpoint protein Bub1b
GSVIVG01010028001	T2	T12	3,80518	27,1816	2,8366	Stearyl acyl carrier protein desaturase
GSVIVG01035991001	T2	T12	172,832	1235,19	2,83728	Cytochrome b5 domain-containing protein
GSVIVG01013190001	T0	T12	10,18	72,7628	2,83746	LOL1 (LSD ONE like 1)
GSVIVG01017014001	T0	T12	8,88421	63,5111	2,83769	Integral membrane family protein UPF0497
GSVIVG01035471001	T0	T12	2,79307	19,9702	2,83792	ferredoxin-related
GSVIVG01015564001	T2	T12	7,99541	57,4249	2,84443	Thylakoid luminal 16.5 kDa protein, chloroplast precursor
GSVIVG01018916001	T0	T12	5,14277	36,9848	2,84632	S-adenosyl-L-methionine:salicylic acid carboxyl
GSVIVG01013401001	T0	T6	9,16207	66,0693	2,85023	Glucan endo-1,3-beta-glucosidase 7 precursor
GSVIVG01032047001	T0	T6	23,3251	168,79	2,85527	Histone H3
GSVIVG01032411001	T0	T6	4,25838	30,8247	2,85571	Chitinase, class III
GSVIVG01016434001	T0	T12	4,41245	32,0303	2,85979	MEE60 (maternal effect embryo arrest 60)
GSVIVG01015086001	T0	T12	5,02228	36,5989	2,86538	GCN5 N-acetyltransferase (GNAT)
GSVIVG01022645001	T0	T12	3,8567	28,1521	2,8678	Myb family
GSVIVG01009925001	T0	T12	6,34313	46,3802	2,87024	Ferredoxin:nadp+ Oxidoreductase PETH
GSVIVG01009178001	T2	T12	2,76582	20,2563	2,87259	Kinesin family member 4/7/21/27
GSVIVG01001298001	T0	T12	130,746	962,017	2,8793	Protease inhibitor/seed storage/lipid transfer protein (LTP)
GSVIVG01034510001	T0	T6	98,3986	724,112	2,8795	Histone H3

GSVIVG01034510001	T2	T12	90,8767	668,855	2,87971	Histone H3
GSVIVG01008217001	T0	T12	1,86852	13,792	2,88386	Partner of Nob1
GSVIVG01020686001	T0	T12	4,36023	32,1978	2,88449	Methyltransferase type 11
GSVIVG01010027001	T0	T12	6,82926	50,4612	2,88537	Alcohol dehydrogenase 3
GSVIVG01020666001	T0	T12	4,70441	34,7634	2,88548	TCP family transcription factor 4
GSVIVG01012635001	T0	T12	10,9645	81,0498	2,88597	Xyloglucan endotransglucosylase/hydrolase 8
GSVIVG01012841001	T2	T12	5,07892	37,5688	2,88694	Vacuolar pyrophosphatase
GSVIVG01009913001	T2	T12	43,1803	319,462	2,8872	Tubulin beta-1 chain
GSVIVG01031017001	T2	T12	16,8465	124,787	2,88895	Mannose-6-phosphate isomerase
GSVIVG01032528001	T0	T2	5,07412	37,6024	2,88959	GASA like
GSVIVG01014841001	T0	T6	2,34531	17,4076	2,89187	WD-40 repeat
GSVIVG01015754001	T0	T6	31,2867	233,604	2,90044	Phosphate-induced protein 1
GSVIVG01031316001	T0	T12	2,78144	20,8033	2,90291	Protein-serine/threonine kinase haspin-related
GSVIVG01025827001	T0	T12	10,1255	75,7448	2,90316	ZIFL2 (zinc induced facilitator-like 2)
GSVIVG01015059001	T0	T12	7,21538	53,98	2,90328	Strictosidine synthase (YLS2)
GSVIVG01008551001	T0	T12	66,3405	497,107	2,90559	Protein transport protein SEC61 gamma subunit
GSVIVG01032405001	T6	T12	61,8568	464,035	2,90723	Ribosomal protein L27A (RPL27aC) 60S
GSVIVG01038125001	T2	T6	8,48129	63,6436	2,90766	Chitinase class IV
GSVIVG01034166001	T0	T12	17,2382	129,474	2,90898	Myb domain protein 91
GSVIVG01027038001	T0	T6	2,94799	22,1794	2,91142	Alpha-L-fucosidase
GSVIVG01014068001	T2	T12	22,8102	171,641	2,91164	Glucan endo-1,3-beta-glucosidase 4 precursor
GSVIVG01003762001	T6	T12	43,3894	326,538	2,91184	Pathogenesis-related protein 1 precursor (PRP 1)
GSVIVG01032528001	T6	T12	11,992	90,2992	2,91265	GASA like
GSVIVG01038620001	T2	T6	2,03854	15,3949	2,91685	Subtilisin protease
GSVIVG01013218001	T2	T12	8,75461	66,2337	2,91945	Dynamin-like protein 2b
GSVIVG01014585001	T0	T12	3,34585	25,3744	2,92293	Kinesin family member C1
GSVIVG01018556001	T0	T12	49,6553	376,785	2,92372	Phosphate-induced protein 1
GSVIVG01000829001	T2	T6	7,75351	58,8472	2,92405	Annexin ANN4
GSVIVG01011034001	T2	T12	62,3673	473,552	2,92466	Histone H2AXb HTA3
GSVIVG01026478001	T0	T12	33,6151	255,283	2,92491	Photosystem I reaction center subunit N (PSAN)
GSVIVG01030386001	T0	T12	10,8867	82,6777	2,92493	NADPH-protochlorophyllide oxidoreductase
GSVIVG01014291001	T0	T6	6,30872	48,0118	2,92797	Ethylene responsive element binding factor 4
GSVIVG01008333001	T0	T12	1,55631	11,8473	2,92836	Kinesin motor HIK (HINKEL)
GSVIVG01016100001	T0	T12	4,44912	33,893	2,92939	Aspartyl protease
GSVIVG01031006001	T0	T12	24,707	188,299	2,93003	Hexose transporter, Plastid
GSVIVG01030386001	T2	T12	10,8375	82,6777	2,93146	NADPH-protochlorophyllide oxidoreductase
GSVIVG01009895001	T2	T6	3,57741	27,3031	2,93208	Cyclin-dependent protein kinase regulator CYCB2_4
GSVIVG01002138001	T0	T12	82,4377	630,024	2,93403	Polyadenylate-binding protein 2
GSVIVG01032268001	T0	T12	3,0297	23,1702	2,93502	Potyviral helper component protease-interacting protein 2
GSVIVG01037973001	T2	T6	6,80375	52,136	2,93788	VPS2.2 SNF7
GSVIVG01001603001	T2	T6	2,97881	22,8263	2,93789	Laccase
GSVIVG01032029001	T0	T12	5,08414	39,0333	2,94063	Lipoxygenase LOX1
GSVIVG01037540001	T0	T6	1,25623	9,66267	2,94332	Kinesin motor protein
GSVIVG01017071001	T0	T6	47,4348	365,445	2,94564	Photosystem I reaction center subunit VI PSAH
GSVIVG01025012001	T2	T12	5,02734	38,7947	2,94799	Alcohol dehydrogenase 3
GSVIVG01016801001	T2	T12	1,47504	11,401	2,95033	Calmodulin-binding region IQD6
GSVIVG01009624001	T0	T6	8,77634	67,8657	2,95099	Photosystem II PsbO protein
GSVIVG01010028001	T0	T6	1,55328	12,0214	2,95221	Stearyl acyl carrier protein desaturase
GSVIVG01018182001	T0	T12	23,7673	184,15	2,95383	protein transport protein sec61 subunit beta-like
GSVIVG01037766001	T2	T12	2,16258	16,7688	2,95495	Kinesin motor protein
GSVIVG01014841001	T2	T6	2,24256	17,4076	2,9565	WD-40 repeat
GSVIVG01009155001	T0	T6	37,087	287,944	2,9568	Aspartic proteinase nepenthesin-1 precursor
GSVIVG01035465001	T0	T12	5,13004	39,9089	2,95967	Trihelix DNA-binding protein (GT2)
GSVIVG01022645001	T2	T12	3,59994	28,1521	2,9672	Myb family
GSVIVG01006484001	T2	T12	7,08636	55,4599	2,96833	Alpha-galactosidase
GSVIVG01009751001	T2	T12	10,6047	83,183	2,97158	Jasmonate O-methyltransferase
GSVIVG01011015001	T0	T6	2,52618	19,8707	2,97562	Rac GTPase activating protein
GSVIVG01006002001	T0	T12	15,1717	119,376	2,97606	Carboxyl-terminal peptidase
GSVIVG01035382001	T2	T12	4,53129	35,6628	2,97643	Calmodulin-binding region IQD6
GSVIVG01013401001	T2	T12	35,3087	278,346	2,97878	Glucan endo-1,3-beta-glucosidase 7 precursor
GSVIVG01028071001	T0	T12	2,81227	22,183	2,97965	Cellulose synthase CSLD5
GSVIVG01015304001	T0	T12	21,1516	166,974	2,98078	ERD7 (EARLY-responsive TO dehydration 7)
GSVIVG01031017001	T0	T12	15,7722	124,787	2,98402	Mannose-6-phosphate isomerase
GSVIVG01033912001	T2	T12	9,51339	75,2717	2,98408	Secoisolariciresinol dehydrogenase
GSVIVG01007336001	T0	T12	2,79558	22,1487	2,986	Kinesin family member C1
GSVIVG01025206001	T0	T2	9,11298	72,2315	2,98663	Lysine decarboxylase
GSVIVG01032138001	T2	T12	3,76407	29,854	2,98756	DNA topoisomerase, ATP-hydrolyzing
GSVIVG01020578001	T0	T12	20,2848	161,103	2,98951	Squamosa promoter-binding protein 4 (SPL4)
GSVIVG01020595001	T0	T12	8,51284	67,6328	2,99001	Reticulon family protein
GSVIVG01015332001	T0	T6	7,06482	56,1754	2,99121	MSS1 (sugar transport protein 13)
GSVIVG01007643001	T0	T12	2,47176	19,6734	2,99264	AAA-type ATPase

GSVIVG01000546001	T2	T12	4,8922	38,9648	2,99362	Lipase GDSL
GSVIVG01009079001	T0	T12	7,96704	63,4685	2,99393	L-ascorbate peroxidase, chloroplast
GSVIVG01034510001	T2	T6	90,8767	724,112	2,99423	Histone H3
GSVIVG01004595001	T2	T6	3,06054	24,4472	2,99781	Expansin beta 1 precursor
GSVIVG01012210001	T0	T12	12,6982	101,431	2,99781	Acclimation of photosynthesis to environment
GSVIVG01003169001	T0	T12	8,50114	67,9771	2,99932	Receptor kinase
GSVIVG01028205001	T0	T12	34,8764	279,317	3,00158	S-adenosylmethionine synthetase 1 (SAM1)
GSVIVG01033852001	T0	T12	19,0136	152,707	3,00566	Carbonic anhydrase precursor
GSVIVG01009079001	T2	T12	7,89787	63,4685	3,0065	L-ascorbate peroxidase, chloroplast
GSVIVG01035369001	T0	T6	13,1986	106,085	3,00676	Calcineurin B protein 10
GSVIVG01032821001	T2	T12	20,8853	168,055	3,00838	Early flowering 4
GSVIVG01033526001	T0	T12	9,8799	79,6018	3,01023	Rhodanese domain-containing protein
GSVIVG01023936001	T0	T6	5,63929	45,4409	3,01041	Chitin elicitor-binding CEBIP LysM domain-containing
GSVIVG01015308001	T0	T6	8,97212	72,304	3,01055	ABI1 (ABA insensitive 1)
GSVIVG01032138001	T0	T6	2,69114	21,691	3,01081	DNA topoisomerase, ATP-hydrolyzing
GSVIVG01014246001	T2	T12	4,7392	38,2164	3,01147	BZIP transcription factor
GSVIVG01020411001	T0	T12	4,26125	34,3629	3,0115	Iojap protein
GSVIVG01013658001	T2	T12	25,5289	206,315	3,01464	Oxidoreductase N-terminal domain-containing
GSVIVG01036591001	T0	T6	4,62707	37,4124	3,01535	CXE carboxylesterase
GSVIVG01031700001	T2	T12	5,38722	43,7321	3,02108	LRX2 (leucine-rich repeat/extensin 2)
GSVIVG01000223001	T0	T6	4,06721	33,0216	3,0213	Microtubule end binding protein 1 (EB1)
GSVIVG01000048001	T0	T12	3,67504	29,9271	3,02562	Tangled
GSVIVG01000126001	T0	T12	6,38393	52,1739	3,03081	BT4 (BTB and TAZ Domain protein 4)
GSVIVG01018182001	T6	T12	22,5208	184,15	3,03155	protein transport protein sec61 subunit beta-like
GSVIVG01016698001	T6	T12	13,7899	112,816	3,03229	Auxin-induced protein
GSVIVG01033598001	T0	T12	0,971289	7,96001	3,0348	Condensin subunit 1
GSVIVG01006002001	T2	T12	14,5575	119,376	3,03568	Carboxyl-terminal peptidase
GSVIVG01027175001	T0	T12	14,8935	122,155	3,03596	Kinesin light chain
GSVIVG01025683001	T0	T12	65,2828	535,749	3,03678	Ribosomal protein L12 (RPL12C) 60S
GSVIVG01030258001	T2	T6	1,72682	14,1817	3,03785	WRKY DNA-binding protein 33
GSVIVG01015332001	T2	T6	6,82144	56,1754	3,04179	MSS1 (sugar transport protein 13)
GSVIVG01025777001	T0	T12	56,9776	470,542	3,04585	Tubulin beta-1 chain
GSVIVG01034173001	T0	T12	1,66369	13,7535	3,04734	Kinesin family member 22
GSVIVG01037540001	T0	T12	1,25623	10,4	3,04941	Kinesin motor protein
GSVIVG01000468001	T2	T12	2,36977	19,6471	3,0515	Quercetin 3-O-glucoside-6"-O-malonyltransferase
GSVIVG01030467001	T2	T6	1,56295	12,9663	3,05242	Cellulose synthase CSLB04
GSVIVG01025318001	T0	T12	57,7599	479,525	3,05346	Histone H3
GSVIVG01008401001	T0	T12	17,3525	144,073	3,05359	Myb domain protein 6
GSVIVG01015359001	T0	T12	39,8035	330,683	3,05448	Rac-like GTP-binding protein ARAC7 (GTPase protein)
GSVIVG01020725001	T0	T12	6,99421	58,2593	3,05825	Triacylglycerol lipase
GSVIVG01016487001	T0	T6	6,76828	56,5464	3,06258	Tropinone reductase
GSVIVG01023978001	T2	T12	2,96723	24,8117	3,06384	Cyclin B2;4
GSVIVG01027648001	T0	T12	16,7963	140,575	3,06513	Abnormal floral organs
GSVIVG01020725001	T0	T6	6,99421	58,6994	3,06911	Triacylglycerol lipase
GSVIVG01009895001	T0	T6	3,25305	27,3031	3,0692	Cyclin-dependent protein kinase regulator CYCB2_4
GSVIVG01038619001	T0	T12	16,014	134,429	3,06943	Homeobox-leucine zipper protein HB-12
GSVIVG01011716001	T2	T6	12,0177	100,946	3,07035	major latex
GSVIVG01020725001	T2	T12	6,91237	58,2593	3,07523	Triacylglycerol lipase
GSVIVG01030002001	T2	T12	5,04384	42,5746	3,0774	Vesicle-associated membrane protein
GSVIVG01024455001	T6	T12	46,6499	394,179	3,0789	Seed specific protein Bn15D1B
GSVIVG01026582001	T2	T12	32,9607	279,057	3,08174	Histone H3
GSVIVG01013734001	T0	T12	20,2077	171,194	3,08265	Quinone oxidoreductase, chloroplast precursor
GSVIVG01008048001	T6	T12	5,83416	49,5168	3,08532	Cupin, RmlC-type
GSVIVG01020725001	T2	T6	6,91237	58,6994	3,08609	Triacylglycerol lipase
GSVIVG01009299001	T0	T6	2,40826	20,4566	3,08651	Growth-regulating factor 1
GSVIVG01036262001	T0	T6	12,421	105,562	3,08723	AN3 (ANGUSITFOLIA3)
GSVIVG01013328001	T0	T6	1,16923	9,93891	3,08752	Beta-D-xylosidase
GSVIVG01035972001	T0	T6	10,2865	87,4549	3,08779	Plastocyanin domain-containing protein
GSVIVG01006462001	T2	T12	2,47198	21,0614	3,09087	Mannitol dehydrogenase
GSVIVG01010283001	T0	T12	2,91426	24,8338	3,0911	Indeterminate(ID)-domain 5
GSVIVG01010448001	T0	T2	15,1923	129,499	3,09153	Signal peptidase complex subunit 1
GSVIVG01014068001	T0	T6	12,3477	105,276	3,09187	Glucan endo-1,3-beta-glucosidase 4 precursor
GSVIVG01033871001	T0	T12	3,4537	29,5233	3,09564	Kinesin family member 11
GSVIVG01016053001	T0	T12	9,43443	80,8305	3,09889	Anthrilate N-benzoyltransferase
GSVIVG01014291001	T0	T2	6,30872	54,1096	3,10046	Ethylene responsive element binding factor 4
GSVIVG01007740001	T0	T2	5,06558	43,4628	3,10098	ATMYB66/WER/WER1 (WEREWOLF 1)
GSVIVG01030002001	T0	T12	4,94923	42,5746	3,10472	Vesicle-associated membrane protein
GSVIVG01035991001	T6	T12	143,488	1235,19	3,10573	Cytochrome b5 domain-containing protein
GSVIVG01009497001	T2	T12	4,9737	42,847	3,1068	Dem protein
GSVIVG01016765001	T0	T2	6,34018	54,6841	3,10852	ATMYB66/WER/WER1 (WEREWOLF 1)
GSVIVG01020830001	T2	T12	2,97141	25,6516	3,10983	Electron transfer flavoprotein alpha-subunit precursor

GSVIVG01010325001	T2	T12	7,10047	61,3417	3,11088	Mitotic spindle checkpoint protein (MAD2)
GSVIVG01018021001	T0	T12	5,44087	47,0078	3,11099	TSO1 (chinese for 'ugly')
GSVIVG01012709001	T0	T12	2,89516	25,0322	3,11207	Monocopper oxidase SKS4 (SKU5 Similar 4)
GSVIVG01024997001	T0	T6	23,3042	201,561	3,11256	Osmotin
GSVIVG01032405001	T2	T12	53,6358	464,035	3,11297	Ribosomal protein L27A (RPL27aC) 60S
GSVIVG01025019001	T0	T12	62,384	539,885	3,1134	Histone H2A.4 HTA12
GSVIVG01010948001	T0	T12	1,62944	14,1235	3,11565	Protein kinase WEE1
GSVIVG01016690001	T2	T12	4,66697	40,4782	3,11659	Lipase GDSL 1
GSVIVG01034666001	T0	T12	6,14303	53,3204	3,11767	Phytol kinase 2, chloroplast precursor
GSVIVG01024607001	T2	T6	12,7021	110,277	3,11799	Nodulin
GSVIVG01027038001	T2	T12	8,54294	74,2217	3,11904	Alpha-L-fucosidase
GSVIVG01033671001	T2	T12	7,41475	64,5681	3,12235	Pectate lyase
GSVIVG01034674001	T0	T6	11,7642	102,974	3,12981	Bark storage protein A precursor
GSVIVG01034173001	T2	T12	1,56991	13,7535	3,13104	Kinesin family member 22
GSVIVG01036671001	T0	T6	35,2837	309,587	3,13327	Pepsin A
GSVIVG01009517001	T0	T6	2,89385	25,4698	3,13772	BK11 (BR1 kinase inhibitor 1)
GSVIVG01001126001	T0	T2	2,34323	20,6498	3,13956	Protein binding protein
GSVIVG01009751001	T0	T12	9,40619	83,183	3,14461	Jasmonate O-methyltransferase
GSVIVG01000012001	T0	T12	7,96827	70,4764	3,1448	Basic helix-loop-helix (bHLH) family
GSVIVG01036062001	T0	T6	7,09165	62,7769	3,14604	CCR4-NOT transcription complex subunit 7/8
GSVIVG01034614001	T0	T12	2,11268	18,7609	3,15058	Glutaredoxin family protein
GSVIVG01009497001	T0	T6	3,41008	30,3077	3,15181	Dem protein
GSVIVG01027166001	T0	T2	7,55594	67,4064	3,1572	Auxin response factor 18
GSVIVG01032782001	T2	T12	1,54713	13,8122	3,15828	Cyclin 1b (CYC1b)
GSVIVG01003762001	T2	T12	36,5257	326,538	3,16027	Pathogenesis-related protein 1 precursor (PRP 1)
GSVIVG01033852001	T2	T12	17,0431	152,707	3,16351	Carbonic anhydrase precursor
GSVIVG01028911001	T0	T12	1,27938	11,4708	3,16445	Kinesin motor
GSVIVG01034267001	T0	T12	1,62062	14,5491	3,16632	LRX2 (leucine-rich repeat/extensin 2)
GSVIVG01018466001	T0	T12	14,3184	128,55	3,16638	Subtilase
GSVIVG01021831001	T0	T12	4,67536	42,0066	3,16747	NIMA protein kinase
GSVIVG01025734001	T0	T6	15,0447	135,304	3,16887	Heavy-metal-associated domain-containing protein
GSVIVG01027396001	T0	T12	4,1211	37,0737	3,1693	GTPase RABA3
GSVIVG01034626001	T2	T12	3,50811	31,6269	3,17239	VPS60.1 SNF7
GSVIVG01024081001	T6	T12	9,50093	85,6798	3,17281	Proline-rich protein 4
GSVIVG01017315001	T0	T12	9,23706	83,4007	3,17455	ERF/AP2 transcription factor sub B-6 SHINE
GSVIVG01028041001	T2	T12	10,724	96,909	3,17579	Pectinesterase family
GSVIVG01021405001	T0	T12	124,633	1132,67	3,18397	LHCII type I CAB-1
GSVIVG01009003001	T0	T12	7,17531	65,2135	3,18406	Glycosyl hydrolase family 3 protein
GSVIVG01024916001	T2	T12	1,77764	16,1774	3,18595	ARR1 typeB
GSVIVG01035718001	T2	T12	2,01352	18,3505	3,18803	Cyclin A2
GSVIVG01021727001	T0	T12	8,91374	81,2916	3,189	SEC14 cytosolic factor
GSVIVG01024916001	T0	T12	1,77314	16,1774	3,1896	ARR1 typeB
GSVIVG01035382001	T0	T6	2,42732	22,1467	3,18965	Calmodulin-binding region IQD6
GSVIVG01035716001	T0	T12	5,18833	47,3465	3,18991	ferredoxin
GSVIVG01026582001	T2	T6	32,9607	300,918	3,19055	Histone H3
GSVIVG01028485001	T0	T12	1,56859	14,3358	3,19208	Lipase GDSL
GSVIVG01018512001	T0	T12	3,41283	31,2141	3,19316	Microtubule associated protein (MAP65/ASE1) pleiade
GSVIVG01020616001	T2	T6	2,56474	23,5181	3,19688	fasciclin arabinogalactan-protein (FLA13)
GSVIVG01037973001	T0	T6	5,68447	52,136	3,19718	VPS2.2 SNF7
GSVIVG01032545001	T0	T6	0,944868	8,67852	3,19926	Metalloendoproteinase 1 precursor
GSVIVG01013175001	T0	T12	8,75266	80,5693	3,20244	Glycine cleavage system H protein, mitochondrial
GSVIVG01007646001	T2	T12	1,86642	17,2398	3,2074	Protein kinase ATN1
GSVIVG01024754001	T0	T6	5,24817	48,5947	3,21091	CYP71E
GSVIVG01015283001	T0	T12	3,1604	29,3191	3,21366	MAP kinase kinase 6
GSVIVG01015370001	T0	T12	2,35329	21,856	3,21528	Myb-related protein 3R-1 (Plant c-MYB-like protein 1)
GSVIVG01013420001	T2	T12	1,63661	15,2359	3,2187	Cysteine endopeptidase, papain-type (XCP1)
GSVIVG01018744001	T0	T6	1,54765	14,4287	3,22079	Tetrapeptide repeat domain male sterility MS5
GSVIVG01032821001	T0	T12	18,0083	168,055	3,2222	Early flowering 4
GSVIVG01038652001	T2	T6	1,63373	15,2471	3,22229	Flavanone 3-hydroxylase
GSVIVG01027973001	T2	T12	7,5056	70,1227	3,22384	Rapid ALkalinization Factor RALFL11
GSVIVG01030475001	T0	T6	1,20709	11,2834	3,2246	Chromosome associate protein subunit H
GSVIVG01038629001	T0	T2	12,1936	114,05	3,22547	Growth-regulating factor 7
GSVIVG01000547001	T2	T12	5,00029	46,9697	3,23165	Alpha-L-fucosidase 2 precursor
GSVIVG01033769001	T0	T12	16,9276	159,068	3,2322	Peroxisome protein 2
GSVIVG01036739001	T2	T12	1,18182	11,1357	3,23612	Cyclin-dependent protein kinase CYCB3
GSVIVG01010646001	T6	T12	333,789	3153,7	3,24004	sorbitol dehydrogenase
GSVIVG01000050001	T0	T12	0,756355	7,15071	3,24095	Kinesin motor protein
GSVIVG01020577001	T0	T12	1,12165	10,6046	3,241	Serine/threonine-protein kinase bub1,checkpoint-associated
GSVIVG01019511001	T2	T6	2,39301	22,6278	3,2412	WRKY DNA-binding protein 53
GSVIVG01021753001	T2	T12	1,22354	11,587	3,24337	CHUP1 (chloroplast unusual positioning 1)
GSVIVG0100007001	T0	T12	8,76245	83,0389	3,24438	Lipase GDSL

GSVIVG01009178001	T0	T12	2,13511	20,2563	3,24598	Kinesin family member 4/7/21/27
GSVIVG01020584001	T0	T12	2,52948	24,0548	3,24941	Ethylene-responsive transcription factor 9
GSVIVG01026068001	T2	T12	2,07782	19,7835	3,25115	Proton-dependent oligopeptide transport (POT) family
GSVIVG01038652001	T0	T6	1,59824	15,2471	3,25397	Flavanone 3-hydroxylase
GSVIVG01015002001	T0	T12	2,77909	26,5607	3,25661	DNA repair protein RAD51
GSVIVG01036445001	T0	T12	24,4538	233,84	3,25739	Allene oxide cyclase
GSVIVG01016765001	T0	T12	6,34018	60,6668	3,25831	ATMYB66/WER/WER1 (WEREWOLF 1)
GSVIVG01031547001	T0	T12	7,93439	76,0255	3,26029	Ubiquitin-conjugating enzyme E2 C
GSVIVG01006231001	T0	T2	9,7246	93,2346	3,26115	DIR1 (defective IN induced resistance 1)
GSVIVG01034574001	T0	T6	4,59816	44,1598	3,2636	Peroxidase 12
GSVIVG01015030001	T0	T12	415,573	3993,74	3,26457	Invertase/pectin methylesterase inhibitor
GSVIVG01033673001	T0	T12	13,1418	126,711	3,2693	Carbonic anhydrase precursor
GSVIVG01025781001	T2	T12	4,85248	46,8078	3,26995	Cyclin B-type
GSVIVG01015203001	T2	T6	13,6606	132,029	3,27276	Beta-galactosidase
GSVIVG01016295001	T0	T12	32,5369	314,974	3,27508	LHCA1
GSVIVG01000048001	T2	T12	3,09035	29,9271	3,27561	Tangled
GSVIVG01024825001	T0	T6	5,78998	56,0834	3,27594	Tubulin beta-3 chain
GSVIVG01009299001	T0	T12	2,40826	23,3402	3,27675	Growth-regulating factor 1
GSVIVG01027551001	T2	T12	6,6717	64,7715	3,27923	CYP76C2
GSVIVG01026654001	T2	T6	21,8757	213,085	3,28402	catalase
GSVIVG01024879001	T6	T12	6,75265	65,8091	3,28476	Tropinone reductase
GSVIVG01009925001	T2	T12	4,75595	46,3802	3,28571	Ferredoxin:nadp+ Oxidoreductase PETH
GSVIVG01009972001	T6	T12	12,984	127,16	3,29183	Mannitol dehydrogenase
GSVIVG01028716001	T0	T12	8,7063	85,3347	3,293	Myb Triptychon
GSVIVG01010448001	T6	T12	11,3947	111,837	3,29496	Signal peptidase complex subunit 1
GSVIVG01018247001	T0	T12	5,37641	52,8017	3,29587	Arabidopsis thaliana homeobox protein 2
GSVIVG01000499001	T0	T12	1,33162	13,0959	3,29787	CYP72A1
GSVIVG01033540001	T0	T6	7,27524	71,6308	3,29951	Beta-1,3-glucanase
GSVIVG01035476001	T0	T12	12,4766	122,852	3,29962	ER (ERECTA)
GSVIVG01028236001	T2	T6	1,27131	12,5196	3,2998	CYP709B2
GSVIVG01022750001	T0	T12	4,38007	43,2542	3,30382	Anthraniloyal-CoA: methanol anthraniloyal transferase
GSVIVG01013769001	T2	T12	3,89851	38,5219	3,30468	Naphthoate synthase
GSVIVG01018916001	T2	T12	3,74215	36,9848	3,30499	S-adenosyl-L-methionine:salicylic acid carboxyl
GSVIVG01007789001	T0	T6	5,48771	54,2777	3,30608	Trehalose 6-phosphate synthase
GSVIVG01009305001	T0	T6	1,53866	15,3117	3,31489	Kinesin ZCF125
GSVIVG01003320001	T0	T12	9,18263	91,4313	3,31571	Cystatin
GSVIVG01001299001	T0	T6	15,9783	159,234	3,31696	Protease inhibitor/seed storage/lipid transfer protein (LTP)
GSVIVG01007348001	T0	T12	19,4527	194,034	3,31826	Extensin
GSVIVG01033912001	T6	T12	7,54441	75,2717	3,31863	Secoisolaricresinol dehydrogenase
GSVIVG01030933001	T2	T12	1,77225	17,7644	3,32533	UDP-glucosyl transferase 73C7
GSVIVG01028911001	T2	T12	1,14329	11,4708	3,3267	Kinesin motor
GSVIVG01035716001	T2	T12	4,70674	47,3465	3,33046	ferredoxin
GSVIVG01027549001	T6	T12	1,55092	15,6069	3,33099	Geraniol 10-hydroxylase
GSVIVG01008414001	T2	T12	2,83574	28,5485	3,33162	Peptidyl-prolyl cis-trans isomerase FKBP-type
GSVIVG01024060001	T0	T6	27,7888	280,665	3,33628	Phospholipase C.
GSVIVG01017779001	T0	T12	3,72932	37,6692	3,3364	Receptor protein kinase
GSVIVG01008914001	T0	T12	0,605739	6,12907	3,3389	Flavonol synthase
GSVIVG01010942001	T0	T12	64,5087	652,971	3,33945	Glutathione S-transferase 13 GSTF13
GSVIVG01007817001	T6	T12	22,0342	223,376	3,34166	LTCOR11
GSVIVG01008423001	T0	T2	54,2946	550,868	3,34283	Thaumatococcus
GSVIVG01018058001	T0	T12	3,73868	37,9563	3,34374	Calcium-transporting ATPase 13 ACA13
GSVIVG01009563001	T2	T6	1,98801	20,1851	3,3439	Calmodulin-binding protein AR781
GSVIVG01013658001	T0	T12	20,3159	206,315	3,34416	Oxidoreductase N-terminal domain-containing
GSVIVG01032858001	T2	T6	13,0373	132,677	3,3472	Nematode-resistance protein
GSVIVG01009624001	T2	T12	9,64475	98,3977	3,35081	Photosystem II PsbO protein
GSVIVG01031576001	T0	T12	2,03315	20,774	3,35299	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01024890001	T0	T12	3,85951	39,4763	3,3545	Tropinone reductase
GSVIVG01016180001	T0	T12	1,87256	19,1741	3,35607	RAB GTPase RAB_ALPHA
GSVIVG01010003001	T0	T12	2,76567	28,3563	3,35797	Blue (type 1) copper domain
GSVIVG01025610001	T2	T12	1,28036	13,1466	3,36006	Kinesin motor protein
GSVIVG01011969001	T0	T12	3,96511	40,7162	3,36017	Cytochrome B561
GSVIVG01018865001	T0	T6	2,90035	29,909	3,36628	Peroxidase 72
GSVIVG01007554001	T0	T12	9,23728	95,3637	3,3679	Lipase GDSL
GSVIVG01033090001	T0	T12	10,9709	113,308	3,36849	Ribonucleotide reductase R2
GSVIVG01017173001	T2	T12	0,825946	8,54293	3,37061	Gibberellin 3beta-hydroxylase3
GSVIVG01030475001	T0	T12	1,20709	12,5229	3,37496	Chromosome associate protein subunit H
GSVIVG01023937001	T0	T12	5,15047	53,4745	3,37608	Chitin elicitor-binding CEBIP LysM domain-containing
GSVIVG01010644001	T0	T12	33,8606	351,7	3,37667	L-idonate dehydrogenase
GSVIVG01022185001	T0	T2	12,0287	124,957	3,37687	Hyperosmotically inducible periplasmic protein
GSVIVG01017915001	T0	T12	1,46616	15,2376	3,37752	STE11 protein kinase homolog NPK1
GSVIVG01032901001	T6	T12	29,9621	311,67	3,37881	Spiral 1 like 2

GSVIVG0103559001	T2	T12	4,84182	50,5688	3,38463	Syntaxin-related protein KNOLLE
GSVIVG01028481001	T2	T12	26,3305	275,125	3,38528	Photosystem I reaction center subunit IV B (PSAE B)
GSVIVG01037973001	T2	T12	6,80375	71,1225	3,3859	VPS2.2 SNF7
GSVIVG01020033001	T0	T12	44,8137	468,679	3,38659	Homeobox-leucine zipper protein HB13
GSVIVG01015276001	T2	T12	13,6295	142,677	3,38794	Leucine-rich repeat family protein / extensin
GSVIVG01030675001	T0	T2	2,37111	24,8459	3,38937	Aspartyl protease
GSVIVG01013769001	T0	T12	3,67438	38,5219	3,39011	Naphthoate synthase
GSVIVG01021727001	T2	T12	7,75132	81,2916	3,39059	SEC14 cytosolic factor
GSVIVG01007243001	T2	T12	3,91822	41,116	3,39143	Calcium-binding EF hand family
GSVIVG01035033001	T0	T6	2,63552	27,6664	3,39197	Glycosyl hydrolase family 3 beta xylosidase BXL1
GSVIVG01010646001	T2	T12	299,353	3153,7	3,39712	sorbitol dehydrogenase
GSVIVG01016487001	T2	T6	5,36624	56,5464	3,39745	Tropinone reductase
GSVIVG01032682001	T6	T12	17,5763	185,567	3,40024	Non-specific lipid-transfer protein
GSVIVG01014681001	T2	T12	9,9482	105,149	3,40186	1,4-alpha-D-glucan maltohydrolase
GSVIVG01011760001	T0	T12	1,49237	15,7895	3,40328	Molecular chaperone DnaJ
GSVIVG01036077001	T0	T6	29,9833	317,745	3,40564	Photosystem I subunit O (PSAO)
GSVIVG01010913001	T0	T12	27,637	293,105	3,40675	Phospholipase A2 alpha
GSVIVG01035449001	T0	T12	34,8678	370,185	3,40828	PSBX (photosystem II subunit X)
GSVIVG01009924001	T2	T6	1,5996	17,0059	3,41025	Molecular chaperone DnaJ
GSVIVG01035323001	T0	T12	6,16549	65,6614	3,41276	Serine/threonine-protein kinase Aurora-1
GSVIVG01033047001	T0	T12	13,5873	144,721	3,41294	Pollen proteins Ole e I
GSVIVG01032855001	T6	T12	3,70791	39,4985	3,41312	AUX1 auxin influx carrier protein
GSVIVG01027551001	T0	T2	0,625323	6,6717	3,41538	CYP76C2
GSVIVG01004595001	T0	T6	2,2829	24,4472	3,42073	Expansin beta 1 precursor
GSVIVG01034944001	T2	T6	12,8016	137,504	3,42507	Beta-fructofuranosidase
GSVIVG01032029001	T2	T12	3,63134	39,0333	3,42613	Lipoxygenase LOX1
GSVIVG01020678001	T2	T6	24,6947	265,445	3,42614	trichome birefringence-like 39
GSVIVG01031290001	T0	T12	7,42448	79,9624	3,42896	Lipase GDSL
GSVIVG01033358001	T2	T12	4,25325	45,8831	3,43133	UVI4 (polychrome, UV-B-insensitive 4)
GSVIVG01034174001	T0	T12	1386,1	14970,7	3,43304	Metallothionein
GSVIVG01030001001	T0	T12	2,20837	23,8714	3,43423	Wound-induced
GSVIVG01037881001	T0	T12	33,4031	361,834	3,43727	SWIB complex BAF60b domain-containing protein
GSVIVG01009417001	T2	T6	0,541326	5,86557	3,4377	S-domain receptor kinase
GSVIVG01007789001	T2	T6	5,00907	54,2777	3,43774	Trehalose 6-phosphate synthase
GSVIVG01005100001	T0	T12	11,875	128,72	3,43825	Ankyrin repeat protein
GSVIVG01036739001	T0	T12	1,02677	11,1357	3,43902	Cyclin-dependent protein kinase CYCB3
GSVIVG01001292001	T0	T6	10,6238	115,645	3,44433	Nitrate transporter
GSVIVG01011705001	T2	T12	1,42057	15,4852	3,44634	CRR3 (chlororespiratory reduction 3)
GSVIVG01024852001	T0	T2	1,4298	15,5898	3,44672	Glutathione S-transferase 25 GSTU7
GSVIVG01008552001	T0	T12	1,68033	18,3221	3,44677	RGP1 (reversibly glycosylated polypeptide 1)
GSVIVG01000461001	T2	T6	1,82606	19,9233	3,44765	Hydroxycinnamoyl-CoA quinate
GSVIVG01038086001	T0	T12	6,44878	70,396	3,4484	Myosin heavy chain-like protein
GSVIVG01035323001	T2	T12	6,01342	65,6614	3,44879	Serine/threonine-protein kinase Aurora-1
GSVIVG01000461001	T0	T6	1,8231	19,9233	3,44999	Hydroxycinnamoyl-CoA quinate
GSVIVG01003762001	T0	T2	3,34196	36,5257	3,45014	Pathogenesis-related protein 1 precursor (PRP 1)
GSVIVG01022306001	T6	T12	19,4351	212,817	3,45287	Zinc finger (C3HC4-type ring finger)
GSVIVG01029368001	T0	T12	9,94954	109,046	3,45416	Kinase interacting protein
GSVIVG01019913001	T0	T6	4,33161	47,5037	3,45507	Growth-regulating factor 5
GSVIVG01021406001	T2	T12	6,75901	74,1275	3,45513	LHCII type I CAB-1
GSVIVG01021354001	T2	T12	3,03578	33,2987	3,45533	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01019403001	T0	T6	0,845832	9,30113	3,45896	Beta-carotene hydroxylase
GSVIVG01003201001	T2	T12	2,26849	24,9512	3,4593	LHCB3 (light-harvesting chlorophyll binding protein 3)
GSVIVG01029843001	T2	T12	10,949	120,485	3,45999	Cyclin-dependent kinase B1;2
GSVIVG01019377001	T0	T12	31,7933	349,911	3,46019	LHCA3 (Photosystem I light harvesting complex gene 3)
GSVIVG01013722001	T0	T6	1,21525	13,3792	3,46066	Polygalacturonase BURP
GSVIVG01005132001	T0	T6	15,31	168,568	3,46078	ATFP3 (Arabidopsis thaliana farnesylated protein 3)
GSVIVG01013841001	T0	T12	1,19683	13,1889	3,46204	Metacaspase 1
GSVIVG01037277001	T0	T12	4,26945	47,2068	3,46687	Phosphatidylglycerol specific phospholipase C
GSVIVG01015266001	T2	T6	4,03039	44,6346	3,46917	Myo-inositol oxygenase
GSVIVG01032138001	T0	T12	2,69114	29,854	3,47164	DNA topoisomerase, ATP-hydrolyzing
GSVIVG01028204001	T0	T6	2,48628	27,5891	3,47204	LHCII type I CAB-1
GSVIVG01009646001	T2	T12	6,11196	68,2443	3,481	Thaumatococcus SCUTL2
GSVIVG01019504001	T2	T12	6,56278	73,3097	3,48163	High mobility group HMG1/2
GSVIVG01020033001	T2	T12	41,9343	468,679	3,4824	Homeobox-leucine zipper protein HB13
GSVIVG01009624001	T0	T12	8,77634	98,3977	3,48693	Photosystem II PsbO protein
GSVIVG01034125001	T2	T6	8,71104	97,7304	3,48789	Proteinase inhibitor
GSVIVG01038642001	T0	T6	0,779608	8,76493	3,49092	Subtilase
GSVIVG01033671001	T0	T12	5,73721	64,5681	3,4924	Pectate lyase
GSVIVG01011705001	T0	T12	1,37473	15,4852	3,49367	CRR3 (chlororespiratory reduction 3)
GSVIVG01015111001	T0	T12	11,6649	131,438	3,49414	Replication protein A 70 kDa DNA-binding subunit
GSVIVG01035115001	T0	T12	0,546425	6,15838	3,49446	Epoxide hydrolase

GSVIVG01025610001	T0	T12	1,16436	13,1466	3,49708	Kinesin motor protein
GSVIVG01029167001	T2	T6	15,168	171,274	3,4972	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01014454001	T0	T6	5,36219	60,5723	3,49776	Myb domain protein 102
GSVIVG01018744001	T2	T12	2,4797	28,1084	3,50276	Tetratricopeptide repeat domain male sterility MS5
GSVIVG01000828001	T2	T12	2,46492	27,975	3,50453	Annexin ANN3
GSVIVG01036557001	T0	T12	5,06594	57,598	3,50712	Alpha-1,4-glucan-protein synthase 1
GSVIVG01026614001	T6	T12	0,65513	7,46562	3,51041	Nodulin MtN21 family
GSVIVG01033197001	T2	T12	1,85809	21,184	3,51108	Ulp1 protease , C-terminal catalytic domain containing
GSVIVG01024152001	T0	T12	0,41835	4,77272	3,51203	Auxin responsive SAUR protein
GSVIVG01024077001	T6	T12	8,30841	94,7891	3,51208	unnamed protein product
GSVIVG01031226001	T0	T6	1,42604	16,272	3,51231	Universal stress protein (USP) family protein
GSVIVG01035314001	T2	T6	1,38167	15,786	3,51416	receptor-like protein kinase hsl1-like
GSVIVG01029167001	T2	T12	15,168	173,378	3,51482	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01006462001	T0	T6	1,57356	18,0035	3,51618	Mannitol dehydrogenase
GSVIVG01009895001	T2	T12	3,57741	41,0348	3,51986	Cyclin-dependent protein kinase regulator CYCB2_4
GSVIVG01000223001	T2	T12	5,683	65,3495	3,52345	Microtubule end binding protein 1 (EB1)
GSVIVG01016504001	T2	T12	4,42504	51,0244	3,52742	Thaumatococcus
GSVIVG01010611001	T0	T6	0,743676	8,58882	3,52971	Dehydration-responsive protein
GSVIVG01019913001	T0	T12	4,33161	50,1082	3,53207	Growth-regulating factor 5
GSVIVG01030219001	T0	T6	0,998885	11,5694	3,53385	Cationic peroxidase
GSVIVG01024879001	T0	T12	5,67729	65,8091	3,53501	Tropinone reductase
GSVIVG01030327001	T0	T12	0,898841	10,4269	3,5361	Nudix hydrolase 15, mitochondrial precursor (AtNUDT15)
GSVIVG01012253001	T0	T12	2,26932	26,3753	3,53886	Universal stress protein (USP) family protein
GSVIVG01037277001	T2	T12	4,05979	47,2068	3,53952	Phosphatidylglycerol specific phospholipase C
GSVIVG01009442001	T2	T6	13,7111	159,57	3,54078	LRX1 (leucine-rich repeat/extensin 1)
GSVIVG01035406001	T2	T12	5,29909	61,9021	3,54617	CGA1 (cytokinin-responsive GATA factor 1)
GSVIVG01026341001	T0	T6	19,5873	229,475	3,55035	Lipase GDLS
GSVIVG01037177001	T0	T12	3,01063	35,289	3,55108	Isopentenyltransferase 1
GSVIVG01018675001	T0	T12	2,11571	24,8108	3,55175	GDP-mannose transporter (GONST1)
GSVIVG01000144001	T2	T6	1,39285	16,3996	3,55754	Peroxidase 73
GSVIVG01021753001	T0	T6	0,583064	6,8662	3,55779	CHUP1 (chloroplast unusual positioning 1)
GSVIVG01015203001	T0	T6	11,2036	132,029	3,55882	Beta-galactosidase
GSVIVG01003201001	T0	T12	2,11669	24,9512	3,55923	LHCB3 (light-harvesting chlorophyll binding protein 3)
GSVIVG01025051001	T2	T6	0,53315	6,30024	3,56279	Exocyst subunit EXO70 H7
GSVIVG01027534001	T0	T12	20,7186	244,906	3,56323	fasciclin arabinogalactan-protein (FLA8)
GSVIVG01008823001	T0	T6	1,74766	20,6688	3,56396	Cyclin A1
GSVIVG01000451001	T0	T12	1,26095	14,914	3,56409	Cyclin D6
GSVIVG01009305001	T2	T12	2,53257	29,9683	3,56477	Kinesin ZCF125
GSVIVG01024221001	T0	T6	1,60718	19,0478	3,56702	Beta-D-galactosidase
GSVIVG01001270001	T0	T12	29,1101	345,291	3,56822	Multi-copper oxidase (SKU5)
GSVIVG01031761001	T2	T12	2,18704	25,9464	3,56848	Transcriptional factor B3
GSVIVG01011015001	T0	T12	2,52618	29,9929	3,56959	Rac GTPase activating protein
GSVIVG01014319001	T0	T12	0,662396	7,86627	3,56991	
GSVIVG01024997001	T0	T2	23,3042	276,941	3,57092	Osmotin
GSVIVG01024152001	T2	T12	0,401387	4,77272	3,57175	Auxin responsive SAUR protein
GSVIVG01014203001	T0	T12	28,5765	339,861	3,57204	Ribulose biphosphate carboxylase, large chain
GSVIVG01037766001	T0	T12	1,40757	16,7688	3,5745	Kinesin motor protein
GSVIVG01007123001	T2	T12	9,70223	115,705	3,57599	Polyphenol oxidase II, chloroplast precursor
GSVIVG01011476001	T0	T12	54,1794	646,564	3,57698	Plastocyanin domain-containing protein
GSVIVG01009065001	T0	T2	2,94845	35,3282	3,58279	Phosphate-induced protein 1
GSVIVG01032661001	T0	T6	1,30772	15,6786	3,58367	WRKY DNA-binding protein 70
GSVIVG01008823001	T2	T12	3,3965	40,7508	3,58471	Cyclin A1
GSVIVG01031123001	T0	T12	32,5993	391,834	3,58733	Histone H2A.4 HTA12
GSVIVG01007740001	T0	T12	5,06558	60,9954	3,5899	ATMYB66/WER/WER1 (WEREWOLF 1)
GSVIVG01022723001	T2	T6	0,642335	7,73448	3,5899	Nitrilase 4B
GSVIVG01010027001	T2	T12	4,19059	50,4612	3,58995	Alcohol dehydrogenase 3
GSVIVG01032654001	T0	T12	9,38536	113,026	3,59009	CENP-E like kinetochore protein
GSVIVG01023354001	T0	T2	1,87077	22,5681	3,59258	dopamine beta-
GSVIVG01001327001	T2	T12	2,65387	32,0305	3,59328	Pectinesterase family
GSVIVG01009099001	T0	T12	13,9109	168,984	3,60259	Gibberellin 20 oxidase 2
GSVIVG01030370001	T2	T12	1,10676	13,4534	3,60355	Ankyrin repeat protein
GSVIVG01006712001	T0	T6	1,01552	12,3707	3,60663	fiber protein
GSVIVG01001126001	T0	T6	2,34323	28,5481	3,60682	Protein binding protein
GSVIVG01024718001	T0	T6	1,22833	15,0042	3,6106	Gibberellin 2-beta-dioxygenase 7
GSVIVG01008305001	T0	T12	1,66137	20,3116	3,61186	Basic helix-loop-helix (bHLH) family
GSVIVG01010003001	T0	T6	2,76567	33,829	3,61256	Blue (type 1) copper domain
GSVIVG01001053001	T2	T12	6,25952	76,6207	3,61361	Ribosomal protein L39 (RPL39C) 60S
GSVIVG01028109001	T0	T6	0,828542	10,1691	3,61748	Universal stress protein (USP) family protein
GSVIVG01009319001	T0	T6	0,575601	7,06997	3,61856	Serine carboxypeptidase S10
GSVIVG01007123001	T0	T12	9,40654	115,705	3,62065	Polyphenol oxidase II, chloroplast precursor
GSVIVG01032193001	T2	T12	0,588054	7,23442	3,62086	RNA polymerase sigma subunit SigD

GSVIVG01036560001	T2	T12	2,48757	30,6498	3,62307	MAP3K-like protein kinase, putative, expressed
GSVIVG01035315001	T2	T6	2,44273	30,1183	3,62407	receptor-like protein kinase hsl1-like
GSVIVG01026614001	T2	T12	0,605284	7,46562	3,62458	Nodulin MtN21 family
GSVIVG01034477001	T6	T12	17,1236	211,532	3,62682	GASA like
GSVIVG01035640001	T0	T12	3,9863	49,2513	3,62704	Aquaporin TIP4;1
GSVIVG01031576001	T2	T6	0,667693	8,26906	3,63047	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01028698001	T0	T6	0,651491	8,07323	3,63133	Protein phosphatase 2C
GSVIVG01009066001	T0	T12	0,625809	7,75873	3,63203	Phosphate-induced protein 1
GSVIVG01015517001	T2	T12	4,65445	57,7518	3,63318	Sodium hypersensitive 1
GSVIVG01035466001	T2	T12	0,732733	9,12082	3,6378	CYP72A58
GSVIVG01023353001	T0	T2	1,00695	12,5461	3,63917	probable lrr receptor-like serine threonine-protein kinase
GSVIVG01015559001	T0	T12	3,32418	41,4796	3,64133	Plastocyanin domain-containing protein
GSVIVG01016978001	T0	T12	0,826614	10,3219	3,64235	Taurine dioxygenase
GSVIVG01016504001	T0	T12	4,08542	51,0244	3,64263	Thaumatococcus
GSVIVG01030616001	T2	T12	10,3694	129,63	3,64399	Peroxidase ATP11A (gb X98802).
GSVIVG01037973001	T0	T12	5,68447	71,1225	3,64521	VPS2.2 SNF7
GSVIVG01035718001	T0	T12	1,46318	18,3505	3,64864	Cyclin A2
GSVIVG01009497001	T0	T12	3,41008	42,847	3,65132	Dem protein
GSVIVG01011382001	T2	T12	45,9305	577,283	3,65176	Tubulin alpha
GSVIVG01009895001	T0	T12	3,25305	41,0348	3,65698	Cyclin-dependent protein kinase regulator CYCB2_4
GSVIVG01028230001	T0	T12	3,37926	42,6803	3,65879	Pectinacetylesterase
GSVIVG01019114001	T2	T12	59,3616	750,13	3,65954	Photosystem I subunit XI (PSAL)
GSVIVG01034574001	T0	T12	4,59816	58,2498	3,66312	Peroxidase 12
GSVIVG01030549001	T0	T6	1,67533	21,2508	3,665	Caffeic acid O-methyltransferase
GSVIVG01016576001	T6	T12	7,38733	94,1698	3,67214	Histone H4
GSVIVG01035991001	T0	T12	96,6346	1235,19	3,67604	Cytochrome b5 domain-containing protein
GSVIVG01030552001	T0	T6	1,37019	17,5221	3,67672	Photosystem II psbZ
GSVIVG01037072001	T0	T12	1,67754	21,4694	3,67787	Serine carboxypeptidase SCPL17
GSVIVG01011715001	T0	T12	13,8351	177,157	3,67862	Phosphoethanolamine N-methyltransferase 1
GSVIVG01035894001	T0	T12	22,5243	289,029	3,68166	Armado/beta-catenin repeat
GSVIVG01022354001	T2	T6	5,23993	67,3264	3,68355	NAC domain containing protein 2
GSVIVG01013440001	T2	T12	9,46166	121,734	3,68549	Cyclin-dependent kinase B2;1
GSVIVG01000190001	T2	T6	0,30854	3,98401	3,6907	Ribulose biphosphate carboxylase/oxygenase large subunit
GSVIVG01015045001	T0	T6	1,50019	19,4314	3,69518	LHCA6 (Photosystem I light harvesting complex gene 6)
GSVIVG01013467001	T0	T6	1,89096	24,5098	3,69617	Calmodulin CML37
GSVIVG01003762001	T0	T6	3,34196	43,3894	3,69858	Pathogenesis-related protein 1 precursor (PRP 1)
GSVIVG01025204001	T6	T12	0,213416	2,77576	3,70114	Glycosyl transferase family 2 protein
GSVIVG01035678001	T0	T2	1,56701	20,3916	3,70188	Dimethylaniline monooxygenase, N-oxide-forming
GSVIVG01019017001	T0	T2	2,38482	31,0381	3,70209	Anthocyanidin 3-O-glucosyltransferase
GSVIVG01026228001	T2	T12	1,10381	14,374	3,7029	DNAJ heat shock N-terminal domain-containing protein
GSVIVG01032901001	T0	T12	23,8783	311,67	3,70625	Spiral 1 like 2
GSVIVG01017894001	T2	T6	2,16613	28,3691	3,71113	7S globulin precursor, basic
GSVIVG01005100001	T0	T6	11,875	156,069	3,71619	Ankyrin repeat protein
GSVIVG01008048001	T2	T12	3,74045	49,5168	3,72663	Cupin, RmlC-type
GSVIVG01031943001	T6	T12	2,24114	29,7392	3,73006	Organ-specific protein S2
GSVIVG01016690001	T0	T12	3,04765	40,4782	3,73138	Lipase GDSL 1
GSVIVG01027454001	T2	T6	8,0858	107,499	3,73279	Naringenin,2-oxoglutarate 3-dioxygenase
GSVIVG01027536001	T0	T6	0,779906	10,4095	3,73845	Aurora kinase 3
GSVIVG01028109001	T0	T12	0,828542	11,0704	3,73999	Universal stress protein (USP) family protein
GSVIVG01006462001	T0	T12	1,57356	21,0614	3,7425	Mannitol dehydrogenase
GSVIVG01022118001	T0	T12	63,0121	845,627	3,74632	Rapid ALkalinization Factor RALFL34
GSVIVG01030095001	T0	T6	0,51969	6,97432	3,74633	Nudix hydrolase 2
GSVIVG01032855001	T2	T12	2,94308	39,4985	3,7464	AUX1 auxin influx carrier protein
GSVIVG01031614001	T2	T6	0,421843	5,66898	3,74831	UDP-glucose:flavonoid 7-O-glucosyltransferase
GSVIVG01032028001	T0	T12	0,0294375	0,395911	3,74945	Lipoxygenase
GSVIVG01017848001	T0	T6	0,563936	7,5874	3,75	Endonuclease
GSVIVG01024825001	T2	T12	10,793	145,49	3,75276	Tubulin beta-3 chain
GSVIVG01021354001	T0	T12	2,46816	33,2987	3,75396	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01010939001	T0	T12	13,0826	177,228	3,75989	Glutathione S-transferase 11 GSTF7
GSVIVG01017173001	T0	T12	0,630433	8,54293	3,76032	Gibberellin 3beta-hydroxylase3
GSVIVG01020678001	T0	T6	19,5762	265,445	3,76124	trichome birefringence-like 39
GSVIVG01022502001	T0	T12	0,89986	12,225	3,76399	NAD(P)H-quinone oxidoreductase subunit 6, chloroplastic
GSVIVG01032720001	T0	T2	0,815468	11,086	3,76497	Basic helix-loop-helix (bHLH) family
GSVIVG01033502001	T0	T12	74,8336	1017,71	3,76549	Omega-6 fatty acid desaturase, endoplasmic reticulum
GSVIVG01011098001	T2	T6	1,542	20,9764	3,76589	Circadian clock coupling factor ZGT
GSVIVG01011414001	T6	T12	3,27995	44,6312	3,76631	Mini zinc finger 2 MIF2
GSVIVG01038017001	T2	T6	2,39989	32,6568	3,76635	Ribosomal protein S19
GSVIVG01032858001	T0	T6	9,73523	132,677	3,76856	Nematode-resistance protein
GSVIVG01014265001	T0	T12	0,437215	5,96496	3,7701	Anthocyanidin 3-O-glucosyltransferase
GSVIVG01014681001	T0	T12	7,65622	105,149	3,77966	1,4-alpha-D-glucan maltohydrolase
GSVIVG01008423001	T0	T12	54,2946	750,975	3,78988	Thaumatococcus

GSVIVG01015979001	T0	T12	15,2073	210,885	3,79362	Plastocyanin domain-containing protein
GSVIVG01028204001	T2	T12	7,68187	106,715	3,79617	LHCII type I CAB-1
GSVIVG01014068001	T0	T12	12,3477	171,641	3,79708	Glucan endo-1,3-beta-glucosidase 4 precursor
GSVIVG01017836001	T0	T6	0,255196	3,54763	3,79718	Sugar transporter ERD6-like 16
GSVIVG01013905001	T2	T6	1,21221	16,8536	3,79734	Ethylene-responsive transcription factor ERF105
GSVIVG01035115001	T2	T12	0,442849	6,15838	3,79766	Epoxide hydrolase
GSVIVG01028236001	T0	T6	0,898546	12,5196	3,80045	CYP709B2
GSVIVG01029967001	T0	T12	0,766266	10,6776	3,80059	Anthranilate phosphoribosyltransferase
GSVIVG01024221001	T0	T12	1,60718	22,4344	3,80311	Beta-D-galactosidase
GSVIVG01021584001	T0	T12	41,6448	581,676	3,80401	Photosystem I subunit X (PSAK)
GSVIVG01029998001	T0	T12	2,08037	29,1074	3,80648	Wound-induced
GSVIVG01019955001	T0	T12	0,941993	13,1845	3,80699	Oxygen evolving enhancer 3 (PsbQ)
GSVIVG01011637001	T2	T6	2,9696	41,8432	3,81665	S-adenosyl-L-methionine:carboxyl methyltransferase
GSVIVG01011978001	T0	T12	1,58498	22,3455	3,81745	Nudix hydrolase 1
GSVIVG01020894001	T2	T6	0,414573	5,89189	3,82903	Ankyrin repeat protein
GSVIVG01009646001	T0	T6	1,10034	15,6441	3,8296	Thaumatococcus SCUTL2
GSVIVG01032906001	T2	T12	17,2835	245,783	3,82992	Hydroxyproline-rich glycoprotein
GSVIVG01024060001	T2	T6	19,7356	280,665	3,82998	Phospholipase C.
GSVIVG01000468001	T0	T12	1,38131	19,6471	3,83021	Quercetin 3-O-glucoside-6"-O-malonyltransferase
GSVIVG01032906001	T0	T12	17,2782	245,783	3,83036	Hydroxyproline-rich glycoprotein
GSVIVG01036077001	T2	T12	60,2187	857,171	3,8313	Photosystem I subunit O (PSAO)
GSVIVG01022715001	T2	T6	1,32715	18,9079	3,83259	Nitrilase 4 (NIT4)
GSVIVG01033197001	T0	T12	1,48605	21,184	3,83342	Ulp1 protease , C-terminal catalytic domain containing
GSVIVG01030616001	T0	T12	9,08726	129,63	3,83441	Peroxidase ATP11A (gbIX98802).
GSVIVG01020830001	T0	T6	0,845067	12,0656	3,83569	Electron transfer flavoprotein alpha-subunit precursor
GSVIVG01008287001	T0	T12	0,19094	2,73308	3,83933	Kinesin motor protein-related
GSVIVG01010612001	T2	T12	0,0928995	1,33575	3,84584	S-N-methylcoclaurine 3'-hydroxylase
GSVIVG01035972001	T2	T12	16,8206	243,852	3,85771	Plastocyanin domain-containing protein
GSVIVG01023354001	T0	T6	1,87077	27,1686	3,86023	dopamine beta-
GSVIVG01038620001	T0	T6	1,05851	15,3949	3,86235	Subtilisin protease
GSVIVG01025792001	T0	T6	0,656241	9,54469	3,8624	Thylakoid lumenal 20 kDa protein
GSVIVG01015266001	T0	T6	3,06532	44,6346	3,86405	Myo-inositol oxygenase
GSVIVG01024057001	T0	T6	19,8416	289,076	3,86485	Co-chaperone-curved DNA binding protein A
GSVIVG01033935001	T0	T12	5,39959	78,6856	3,86518	Aspartyl protease
GSVIVG01021195001	T2	T12	0,440631	6,42816	3,86676	Cysteine protease RCR3
GSVIVG01009779001	T0	T12	1,46943	21,4802	3,86968	BEL1-like homeodomain 10
GSVIVG01022306001	T0	T12	14,518	212,817	3,8737	Zinc finger (C3HC4-type ring finger)
GSVIVG01035382001	T0	T12	2,42732	35,6628	3,87698	Calmodulin-binding region IQD6
GSVIVG01019504001	T0	T12	4,98414	73,3097	3,87859	High mobility group HMG1/2
GSVIVG01001327001	T0	T12	2,17572	32,0305	3,87988	Pectinesterase family
GSVIVG01001413001	T2	T12	1,43692	21,1623	3,88045	Alliin lyase precursor
GSVIVG01030517001	T0	T12	1,09998	16,2646	3,88618	Lipase family
GSVIVG01007815001	T0	T6	2,83883	42,0167	3,88759	N-hydroxythioamide S-beta-glucosyltransferase
GSVIVG01033358001	T0	T12	3,09811	45,8831	3,8885	UVI4 (polychrome, UV-B-insensitive 4)
GSVIVG01036612001	T0	T12	2,2495	33,3385	3,88952	flavonol sulfotransferase
GSVIVG01012615001	T0	T12	0,552987	8,25565	3,90007	Tetratricopeptide repeat (TPR)-containing SET domain
GSVIVG01026444001	T0	T12	7,0215	104,87	3,90068	3-hydroxy-3-methylglutaryl-coenzyme A reductase 3
GSVIVG01035123001	T0	T12	2,29623	34,2958	3,90069	Senescence-associated protein
GSVIVG01015517001	T0	T12	3,85778	57,7518	3,90403	Sodium hypersensitive 1
GSVIVG01029170001	T2	T6	0,341664	5,1217	3,90597	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01033252001	T0	T12	0,25233	3,78901	3,90844	Kinesin motor protein
GSVIVG01031860001	T2	T12	0,259452	3,899	3,90957	CYP82C4
GSVIVG01033540001	T2	T6	4,76258	71,6308	3,91076	Beta-1,3-glucanase
GSVIVG01005132001	T0	T12	15,31	231,37	3,91765	ATFP3 (Arabidopsis thaliana farnesylated protein 3
GSVIVG01029967001	T2	T12	0,705082	10,6776	3,92065	Anthranilate phosphoribosyltransferase
GSVIVG01007243001	T0	T6	1,01437	15,3702	3,92148	Calcium-binding EF hand family
GSVIVG01000829001	T0	T12	16,1855	245,269	3,92159	Annexin ANN4
GSVIVG01004517001	T0	T6	0,410581	6,23493	3,92464	Calmodulin-binding
GSVIVG01030452001	T2	T6	0,324231	4,93414	3,9277	MAPKKK15
GSVIVG01018478001	T6	T12	0,625994	9,54354	3,9303	Embryo-specific 3
GSVIVG01022541001	T0	T12	1,51692	23,2786	3,93979	Alpha-L-arabinosidase
GSVIVG01037975001	T0	T12	3,38113	51,9618	3,94187	CYP71D7
GSVIVG01000469001	T0	T12	3,77443	58,0477	3,94291	Anthocyanin 5-aromatic acyltransferase
GSVIVG01016691001	T0	T12	11,4912	177,588	3,94993	Lipase GDSL 1
GSVIVG01022715001	T0	T6	1,22081	18,9079	3,95308	Nitrilase 4 (NIT4)
GSVIVG01011616001	T0	T6	0,622994	9,70813	3,9619	Avr9/Cf-9 rapidly elicited protein
GSVIVG01022723001	T0	T6	0,496283	7,73448	3,96207	Nitrilase 4B
GSVIVG01020095001	T0	T12	0,535653	8,35017	3,96243	Wall-associated kinase 4
GSVIVG01015045001	T2	T6	1,24132	19,4314	3,96844	LHCA6 (Photosystem I light harvesting complex gene 6)
GSVIVG01018904001	T0	T6	9,04853	141,982	3,97188	S-adenosyl-L-methionine:salicylic acid carboxyl
GSVIVG01033177001	T0	T12	7,07738	111,097	3,97247	Sarcosine oxidase

GSVIVG01011872001	T2	T6	7,32292	115,417	3,97829	(myb domain protein 62
GSVIVG01003823001	T0	T6	0,162884	2,56781	3,97862	Strictosidine synthase
GSVIVG01008925001	T0	T12	3,6223	57,1102	3,97877	Zinc finger (C2H2 type) family
GSVIVG01025204001	T0	T12	0,175887	2,77576	3,98016	Glycosyl transferase family 2 protein
GSVIVG01013328001	T0	T12	1,16923	18,4532	3,98024	Beta-D-xylosidase
GSVIVG01002809001	T0	T12	55,207	872,589	3,98238	Photosystem II oxygen-evolving enhancer protein PSBQ
GSVIVG01026054001	T0	T12	0,477035	7,53995	3,98239	UDP-glucose: anthocyanidin 5,3-O-glucosyltransferase
GSVIVG01015522001	T2	T6	0,243392	3,85478	3,98529	Nitrate transporter
GSVIVG01010024001	T0	T12	13,9847	222,069	3,98909	Alcohol dehydrogenase 1
GSVIVG01034072001	T0	T12	4,01037	63,7344	3,99027	Glyoxal oxidase
GSVIVG01013347001	T0	T6	0,308686	4,91414	3,99273	Xylan 1,4-beta-xylosidase
GSVIVG01011382001	T0	T12	36,1436	577,283	3,99746	Tubulin alpha
GSVIVG01008733001	T0	T12	46,0662	736,437	3,99878	Plastocyanin, chloroplast precursor
GSVIVG01011511001	T0	T12	3,33981	53,5615	4,00336	Biotin carboxyl carrier protein of acetyl-CoA carboxylase
GSVIVG01012922001	T0	T6	2,43064	39,0243	4,00497	Alpha-amylase/subtilisin inhibitor
GSVIVG01000223001	T0	T12	4,06721	65,3495	4,00606	Microtubule end binding protein 1 (EB1)
GSVIVG01029843001	T0	T12	7,49435	120,485	4,00691	Cyclin-dependent kinase B1;2
GSVIVG01012613001	T2	T6	0,640961	10,3317	4,0107	NADH dehydrogenase subunit 7
GSVIVG01023353001	T0	T6	1,00695	16,2488	4,01226	probable lrr receptor-like serine threonine-protein kinase
GSVIVG01013440001	T0	T12	7,54072	121,734	4,01289	Cyclin-dependent kinase B2;1
GSVIVG01001055001	T2	T12	4,18717	68,1022	4,02365	Ribosomal protein L39 (RPL39C) 60S
GSVIVG01028091001	T0	T12	5,65481	92,221	4,02755	Myb domain protein 12
GSVIVG01024057001	T2	T6	17,6825	289,076	4,03105	Co-chaperone-curved DNA binding protein A
GSVIVG01032545001	T2	T6	0,530658	8,67852	4,0316	Metalloendoprotease 1 precursor
GSVIVG01011401001	T0	T6	1,2027	19,6874	4,03293	Amino acid permease
GSVIVG01007122001	T0	T12	31,818	524,906	4,04415	Polyphenol oxidase [Vitis vinifera]
GSVIVG01000401001	T2	T12	0,477094	7,87669	4,04525	Isoprene synthase
GSVIVG01030371001	T0	T12	0,444138	7,33325	4,04537	Ankyrin repeat
GSVIVG01023002001	T2	T12	44,7604	740,397	4,048	Plastocyanin domain-containing protein
GSVIVG01006303001	T2	T6	0,204788	3,3923	4,05006	Sinapyl alcohol dehydrogenase
GSVIVG01014682001	T0	T12	0,704662	11,6906	4,05228	Pectate lyase 2
GSVIVG01011585001	T2	T12	1,0349	17,2078	4,05549	NADPH-dependent codeinone reductase
GSVIVG01016489001	T0	T12	2,27334	37,8089	4,05584	Laccase
GSVIVG01000546001	T0	T12	2,3391	38,9648	4,05814	Lipase GDSL
GSVIVG01030208001	T2	T6	0,324341	5,40379	4,05839	Xanthine/uracil permease
GSVIVG01026614001	T0	T12	0,44799	7,46562	4,05872	Nodulin MtN21 family
GSVIVG01015194001	T2	T12	3,84844	64,1418	4,05892	FAD linked oxidase, N-terminal
GSVIVG01022967001	T0	T12	1,04922	17,5055	4,06041	F-box family protein
GSVIVG01016801001	T0	T12	0,681989	11,401	4,06327	Calmodulin-binding region IQD6
GSVIVG01013601001	T2	T6	16,1331	270,101	4,0654	Reverse transcriptase
GSVIVG01017836001	T0	T12	0,255196	4,28263	4,06882	Sugar transporter ERD6-like 16
GSVIVG01036277001	T2	T12	30,3716	511,027	4,0726	Photosystem II reaction centre W (PsbW)
GSVIVG01033445001	T0	T12	0,669494	11,2993	4,07702	Disease resistance-responsive
GSVIVG01020584001	T0	T2	2,52948	42,8887	4,08368	Ethylene-responsive transcription factor 9
GSVIVG01017071001	T0	T12	47,4348	804,941	4,08487	Photosystem I reaction center subunit VI PSAH
GSVIVG01010024001	T2	T12	13,0836	222,069	4,08517	Alcohol dehydrogenase 1
GSVIVG01035614001	T0	T12	1,5735	26,8167	4,09109	GATA transcription factor 11
GSVIVG01033445001	T2	T12	0,662824	11,2993	4,09147	Disease resistance-responsive
GSVIVG01014403001	T2	T6	5,80485	99,0009	4,09211	NAC domain containing protein 19
GSVIVG01016711001	T2	T12	0,409599	6,99795	4,09465	Zinc finger (CCCH-type) family protein
GSVIVG01018059001	T0	T12	0,14406	2,46393	4,09622	Calcium-transporting ATPase 12 ACA12
GSVIVG01000545001	T0	T6	0,277527	4,74744	4,09645	Acetylcholinesterase
GSVIVG01030573001	T0	T12	2,1289	36,4963	4,09957	Glutamate formiminotransferase
GSVIVG01000575001	T2	T12	1,58906	27,2999	4,10265	CYP86A2
GSVIVG01016261001	T2	T12	0,189592	3,25946	4,10366	BTB/POZ; NPH3
GSVIVG01011034001	T0	T12	27,467	473,552	4,10775	Histone H2AXb HTA3
GSVIVG01023936001	T0	T12	5,63929	97,4169	4,11059	Chitin elicitor-binding CEBIP LysM domain-containing
GSVIVG01014999001	T0	T6	5,42887	93,9055	4,11249	Pectinesterase PME3
GSVIVG01003139001	T0	T12	27,1105	469,516	4,11425	Histone H2A variant 1 HTA11
GSVIVG01003823001	T2	T6	0,148223	2,56781	4,11469	Strictosidine synthase
GSVIVG01000545001	T0	T12	0,277527	4,82026	4,11841	Acetylcholinesterase
GSVIVG01011855001	T0	T6	0,88275	15,3392	4,11907	Sterol-C5(6)-desaturase
GSVIVG01022309001	T2	T12	0,162105	2,82039	4,12089	Tonoplast monosaccharide transporter2
GSVIVG01015125001	T2	T6	1,45519	25,3503	4,12273	Ankyrin repeat family protein
GSVIVG01014388001	T0	T12	39,1502	682,274	4,12326	NADPH:protochlorophyllide oxidoreductase
GSVIVG01022491001	T2	T6	0,540969	9,43335	4,12415	CXE carboxylesterase
GSVIVG01009319001	T2	T6	0,405239	7,06997	4,12486	Serine carboxypeptidase S10
GSVIVG01029165001	T0	T2	0,47592	8,30452	4,12511	Xyloglucan endotransglycosylase 6
GSVIVG01019913001	T0	T2	4,33161	75,6118	4,12564	Growth-regulating factor 5
GSVIVG01010028001	T0	T12	1,55328	27,1816	4,12924	Stearyl acyl carrier protein desaturase
GSVIVG01024997001	T0	T12	23,3042	409,857	4,13646	Osmotin

GSVIVG01036277001	T0	T12	28,9806	511,027	4,14024	Photosystem II reaction centre W (PsbW)
GSVIVG01032774001	T0	T12	0,598863	10,5759	4,14241	BUB family protein kinase
GSVIVG01011002001	T0	T12	2,15784	38,3078	4,14998	Kinase interacting family protein
GSVIVG01025512001	T0	T12	0,408734	7,25624	4,14999	Kinesin family member C3
GSVIVG01007190001	T2	T6	0,619994	11,0334	4,15348	Chitinase precursor
GSVIVG01032528001	T0	T12	5,07412	90,2992	4,15348	GASA like
GSVIVG01030467001	T0	T6	0,727025	12,9663	4,15662	Cellulose synthase CSLB04
GSVIVG01037975001	T0	T6	3,38113	60,4716	4,16068	CYP71D7
GSVIVG01001292001	T2	T6	6,46159	115,645	4,16167	Nitrate transporter
GSVIVG01034125001	T0	T2	0,484992	8,71104	4,16681	Proteinase inhibitor
GSVIVG01006300001	T6	T12	1,70403	30,6298	4,16791	Major Facilitator Superfamily
GSVIVG01009950001	T2	T6	0,732403	13,1793	4,1695	Protein kinase
GSVIVG01037005001	T2	T6	12,3818	222,886	4,17002	Pathogenesis-related protein 1 precursor (PRP 1)
GSVIVG01024879001	T2	T12	3,65417	65,8091	4,17067	Tropinone reductase
GSVIVG01029165001	T0	T6	0,47592	8,59093	4,17402	Xyloglucan endotransglycosylase 6
GSVIVG01027914001	T0	T12	4,78427	86,5138	4,17656	Import receptor subunit TOM22 homolog 2, Mitochondrial
GSVIVG01030552001	T2	T12	4,27466	77,3576	4,17766	Photosystem II psbZ
GSVIVG01018744001	T0	T12	1,54765	28,1084	4,18285	Tetratricopeptide repeat domain male sterility MS5
GSVIVG01014403001	T0	T6	5,44933	99,0009	4,18329	NAC domain containing protein 19
GSVIVG01033392001	T0	T6	0,986752	17,9301	4,18355	Aldose 1-epimerase
GSVIVG01018577001	T0	T12	2,21705	40,3222	4,18486	Myb domain protein 85
GSVIVG01036560001	T0	T6	0,955617	17,3967	4,18624	MAP3K-like protein kinase, putative, expressed
GSVIVG01029166001	T0	T6	0,525417	9,56788	4,18666	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01019570001	T0	T2	0,156746	2,86532	4,1922	Cellulose synthase CSLG3
GSVIVG01014246001	T0	T12	2,08504	38,2164	4,19604	BZIP transcription factor
GSVIVG01029998001	T2	T12	1,5853	29,1074	4,19856	Wound-induced
GSVIVG01019909001	T0	T6	1,42562	26,201	4,19996	Geraniol 10-hydroxylase
GSVIVG01033393001	T2	T12	0,812894	14,9685	4,20272	Galactose mutarotase
GSVIVG01008059001	T0	T12	0,411252	7,58198	4,20448	Isochorismate synthase 1, chloroplast precursor
GSVIVG01032055001	T2	T6	0,371986	6,86153	4,20521	Basic helix-loop-helix (bHLH) family
GSVIVG01015276001	T0	T12	7,73326	142,677	4,20553	Leucine-rich repeat family protein / extensin
GSVIVG01025051001	T0	T6	0,34112	6,30024	4,20706	Exocyst subunit EXO70 H7
GSVIVG01027652001	T2	T6	8,83149	163,408	4,20968	Pectinesterase family
GSVIVG01002955001	T0	T12	0,808761	14,9904	4,21218	Calmodulin-binding
GSVIVG01030573001	T2	T12	1,96497	36,4963	4,21517	Glutamate formiminotransferase
GSVIVG01027406001	T0	T12	0,392969	7,30551	4,2165	Ubiquitin thiolesterase
GSVIVG01002264001	T0	T12	0,539785	10,0577	4,21978	Integral membrane family protein
GSVIVG01025389001	T0	T2	0,452867	8,44402	4,22077	Pentatricopeptide (PPR) repeat-containing protein
GSVIVG01000401001	T2	T6	0,477094	8,89707	4,22099	Isoprene synthase
GSVIVG01027944001	T0	T6	0,387998	7,2501	4,22388	AWPM-19
GSVIVG01032044001	T2	T6	0,413388	7,73051	4,22499	Polygalacturonase inhibiting protein 1 PGIP1
GSVIVG01033393001	T0	T12	0,797646	14,9685	4,23004	Galactose mutarotase
GSVIVG01015124001	T0	T12	0,120389	2,26769	4,23545	Phenylalanine ammonia-lyase
GSVIVG01024892001	T0	T12	1,28702	24,3925	4,24433	Tropinone reductase
GSVIVG01006231001	T0	T6	9,7246	184,485	4,24572	DIR1 (defective IN induced resistance 1)
GSVIVG01028041001	T0	T12	5,07411	96,909	4,2554	Pectinesterase family
GSVIVG01011445001	T2	T6	7,20373	137,618	4,25578	NAC domain containing protein 100
GSVIVG01010525001	T0	T6	3,1396	60,1534	4,25999	WRKY DNA-binding protein 75
GSVIVG01009052001	T0	T12	0,40536	7,80069	4,26633	Cis-zeatin O-beta-D-glucosyltransferase
GSVIVG01014386001	T0	T6	11,3757	218,959	4,26663	Stem-specific protein TSJT1
GSVIVG01014205001	T2	T6	0,545301	10,5412	4,27284	Curculin (mannose-binding) lectin
GSVIVG01009065001	T0	T6	2,94845	57,1008	4,27548	Phosphate-induced protein 1
GSVIVG01004517001	T0	T12	0,410581	7,95187	4,27556	Calmodulin-binding
GSVIVG01025792001	T2	T12	1,34378	26,049	4,27687	Thylakoid lumenal 20 kDa protein
GSVIVG01028171001	T2	T6	0,345169	6,69991	4,27877	Myb domain protein 78
GSVIVG01009305001	T0	T12	1,53866	29,9683	4,28369	Kinesin ZCF125
GSVIVG01011098001	T0	T12	0,581012	11,3174	4,28384	Circadian clock coupling factor ZGT
GSVIVG01035640001	T6	T12	2,52823	49,2513	4,28396	Aquaporin TIP4;1
GSVIVG01027173001	T0	T12	0,301187	5,90021	4,29204	Lateral organ boundaries protein 1
GSVIVG01027973001	T0	T12	3,54968	70,1227	4,30412	Rapid ALKalinization Factor RALFL11
GSVIVG01028044001	T0	T2	0,144164	2,8498	4,30508	Polygalacturonase PGA4
GSVIVG01029166001	T0	T2	0,525417	10,4096	4,30831	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01021753001	T0	T12	0,583064	11,587	4,31271	CHUP1 (chloroplast unusual positioning 1)
GSVIVG01019418001	T0	T12	0,158181	3,15056	4,31596	DNA topoisomerase VIA
GSVIVG01023557001	T2	T6	2,92598	58,8344	4,32967	CC-NBS-LRR class
GSVIVG01010611001	T2	T6	0,426527	8,58882	4,33175	Dehydration-responsive protein
GSVIVG01010525001	T2	T6	2,98591	60,1534	4,3324	WRKY DNA-binding protein 75
GSVIVG01016577001	T0	T12	30,3082	611,3	4,3341	Histone H4
GSVIVG01032055001	T0	T6	0,337827	6,86153	4,34417	Basic helix-loop-helix (bHLH) family
GSVIVG01011156001	T2	T12	0,417921	8,49067	4,34457	Rhodanese domain-containing protein
GSVIVG01000547001	T0	T6	0,997721	20,324	4,34841	Alpha-L-fucosidase 2 precursor

GSVIVG01035314001	T0	T6	0,774305	15,786	4,3496	receptor-like protein kinase hsl1-like
GSVIVG01031943001	T2	T12	1,45866	29,7392	4,34965	Organ-specific protein S2
GSVIVG01032044001	T2	T12	0,413388	8,43382	4,35062	Polygalacturonase inhibiting protein 1 PGIP1
GSVIVG01033935001	T2	T12	3,85012	78,6856	4,35312	Aspartyl protease
GSVIVG01011401001	T0	T12	1,2027	24,609	4,35484	Amino acid permease
GSVIVG01033691001	T0	T6	0,141474	2,92841	4,37151	Expansin EXPA9
GSVIVG01007745001	T2	T6	0,628475	13,0197	4,37269	Carbonic anhydrase chloroplast
GSVIVG01030023001	T0	T2	0,15118	3,15171	4,38179	Polygalacturonase PGA3
GSVIVG01018577001	T0	T6	2,21705	46,2931	4,38409	Myb domain protein 85
GSVIVG01033978001	T2	T6	1,01598	21,2599	4,38719	Alpha-1,4-glycosyltransferase
GSVIVG01010727001	T2	T12	0,133325	2,79491	4,38978	Ankyrin repeat protein family
GSVIVG01009066001	T0	T2	0,625809	13,1219	4,39011	Phosphate-induced protein 1
GSVIVG01009065001	T0	T12	2,94845	62,2639	4,40037	Phosphate-induced protein 1
GSVIVG01007817001	T2	T12	10,5095	223,376	4,40971	LTCOR11
GSVIVG01013757001	T2	T6	0,144742	3,07844	4,41064	Protein disulfide isomerase
GSVIVG01024838001	T0	T6	0,205065	4,36815	4,41287	copper transporter
GSVIVG01035559001	T0	T12	2,36575	50,5688	4,41788	Syntaxin-related protein KNOLLE
GSVIVG01031228001	T0	T12	0,36639	7,83358	4,41822	Universal stress protein (USP) family protein
GSVIVG01001126001	T0	T12	2,34323	50,5975	4,43249	Protein binding protein
GSVIVG01019910001	T0	T6	0,753679	16,3268	4,43715	cytochrome p450
GSVIVG01019570001	T0	T6	0,156746	3,40521	4,44125	Cellulose synthase CSLG3
GSVIVG01006662001	T2	T6	0,260578	5,66204	4,44153	Photosystem II PsbC
GSVIVG01032405001	T0	T12	21,3484	464,035	4,44204	Ribosomal protein L27A (RPL27aC) 60S
GSVIVG01014386001	T2	T6	10,0538	218,959	4,44484	Stem-specific protein TSJT1
GSVIVG01004798001	T0	T6	0,523581	11,4179	4,44674	Ethylene responsive element binding factor 1
GSVIVG01011868001	T0	T6	0,414186	9,04887	4,44939	Zinc finger protein 6
GSVIVG01031761001	T0	T12	1,18711	25,9464	4,45001	Transcriptional factor B3
GSVIVG01035013001	T2	T6	6,527	143,012	4,45357	Beta-1,3-glucanase
GSVIVG01023110001	T2	T6	0,223908	4,91951	4,45753	Glutathione S-transferase Z1 GSTZ1
GSVIVG01025005001	T0	T12	31,5037	692,652	4,45854	Histone H4
GSVIVG01021406001	T0	T12	3,36488	74,1275	4,46138	LHCII type I CAB-1
GSVIVG01036262001	T0	T12	12,421	274,195	4,46434	AN3 (ANGUSITFOLIA3)
GSVIVG01035463001	T0	T2	0,198263	4,37721	4,46453	Myb domain protein 32
GSVIVG01010612001	T0	T12	0,0603546	1,33575	4,46804	S-N-methylcoclaureine 3'-hydroxylase
GSVIVG01019114001	T0	T12	33,7318	750,13	4,47496	Photosystem I subunit XI (PSAL)
GSVIVG01021314001	T2	T12	1,46178	32,5417	4,47649	Subtilase
GSVIVG01032743001	T2	T12	5,50822	122,871	4,47941	Proteinase inhibitor (LUTI)
GSVIVG01028108001	T0	T12	5,22086	116,499	4,47989	Ribosomal protein L29e
GSVIVG01011445001	T0	T6	6,15376	137,618	4,48305	NAC domain containing protein 100
GSVIVG01014286001	T2	T6	1,7987	40,2335	4,48337	Tyrosine aminotransferase
GSVIVG01030327001	T2	T12	0,463413	10,4269	4,49187	Nudix hydrolase 15, mitochondrial precursor (AtNUDT15)
GSVIVG01038619001	T0	T6	16,014	361,654	4,4972	Homeobox-leucine zipper protein HB-12
GSVIVG01008048001	T0	T12	2,19058	49,5168	4,49853	Cupin, RmlC-type
GSVIVG01028481001	T0	T12	12,0868	275,125	4,50859	Photosystem I reaction center subunit IV B (PSAE B)
GSVIVG01024133001	T6	T12	0,649072	14,8174	4,51277	Auxin-responsive
GSVIVG01029170001	T2	T12	0,341664	7,85533	4,52302	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01024852001	T0	T6	1,4298	32,9591	4,52679	Glutathione S-transferase 25 GSTU7
GSVIVG01025389001	T0	T6	0,452867	10,4573	4,52929	Pentatricopeptide (PPR) repeat-containing protein
GSVIVG01034126001	T0	T6	0,265219	6,14097	4,53321	Lectin receptor kinase 7
GSVIVG01036167001	T6	T12	0,919407	21,3748	4,53906	Subtilisin-like proteinase AIR3
GSVIVG01029662001	T2	T6	2,86118	66,5741	4,54028	F-type H ⁺ -transporting ATPase subunit c
GSVIVG01008823001	T0	T12	1,74766	40,7508	4,54333	Cyclin A1
GSVIVG01030933001	T0	T12	0,759843	17,7644	4,54714	UDP-glucosyl transferase 73C7
GSVIVG01013722001	T2	T12	2,60713	61,2081	4,55319	Polygalacturonase BURP
GSVIVG01033392001	T2	T6	0,761394	17,9301	4,5576	Aldose 1-epimerase
GSVIVG01027551001	T0	T6	0,625323	14,7348	4,55848	CYP76C2
GSVIVG01032193001	T0	T12	0,306522	7,23442	4,56081	RNA polymerase sigma subunit SigD
GSVIVG01013856001	T2	T6	0,796284	18,8135	4,56234	Ribulose 1,5-bisphosphate carboxylase [Vitis aestivalis]
GSVIVG01027549001	T2	T12	0,660251	15,6069	4,56303	Geraniol 10-hydroxylase
GSVIVG01035972001	T0	T12	10,2865	243,852	4,56718	Plastocyanin domain-containing protein
GSVIVG01011947001	T2	T6	1,86061	44,3222	4,57418	AP2 domain-containing protein RAP2.8
GSVIVG01015124001	T0	T6	0,120389	2,86821	4,57438	Phenylalanine ammonia-lyase
GSVIVG01001603001	T0	T12	4,41289	106,246	4,58955	Laccase
GSVIVG01036871001	T0	T12	3,57454	86,074	4,58975	SWIB complex BAF60b domain-containing protein
GSVIVG01023002001	T0	T12	30,7347	740,397	4,59036	Plastocyanin domain-containing protein
GSVIVG01014243001	T0	T6	0,0912915	2,19937	4,59047	Sodium/calcium exchanger family protein
GSVIVG01013347001	T0	T12	0,308686	7,44733	4,59251	Xylan 1,4-beta-xylosidase
GSVIVG01021195001	T0	T12	0,265327	6,42816	4,59856	Cysteine protease RCR3
GSVIVG01023688001	T2	T12	0,463007	11,2598	4,60401	Serine carboxypeptidase II
GSVIVG01026987001	T0	T12	0,303809	7,4025	4,60678	Anthocyanidine rhamnosyl-transferase
GSVIVG01036879001	T0	T6	0,643812	15,7432	4,61194	protein

GSVIVG01009066001	T0	T6	0,625809	15,3277	4,61428	Phosphate-induced protein 1
GSVIVG01027536001	T0	T12	0,779906	19,2793	4,62761	Aurora kinase 3
GSVIVG01025204001	T2	T12	0,11217	2,77576	4,62913	Glycosyl transferase family 2 protein
GSVIVG01028354001	T0	T6	0,186161	4,60961	4,63003	NAC domain-containing protein 74
GSVIVG01036167001	T2	T12	0,862405	21,3748	4,6314	Subtilisin-like proteinase AIR3
GSVIVG01009519001	T0	T12	0,335269	8,36472	4,64092	Transcriptional factor B3
GSVIVG01036905001	T2	T12	0,136075	3,39546	4,64113	10-deacetylbaecatin III 10-O-acetyltransferase
GSVIVG01034477001	T0	T12	8,42097	211,532	4,65075	GASA like
GSVIVG01024825001	T0	T12	5,78998	145,49	4,65122	Tubulin beta-3 chain
GSVIVG01027038001	T0	T12	2,94799	74,2217	4,65404	Alpha-L-fucosidase
GSVIVG01009155001	T0	T12	37,087	934,463	4,65515	Aspartic proteinase nepenthesin-1 precursor
GSVIVG01029709001	T0	T6	1,168	29,5113	4,65916	NAC domain containing protein 104
GSVIVG01024077001	T0	T6	0,328531	8,30841	4,66047	unnamed protein product
GSVIVG01014999001	T0	T12	5,42887	137,596	4,66365	Pectinesterase PME3
GSVIVG01015952001	T2	T6	1,26115	32,1877	4,67371	WRKY DNA-binding protein 40
GSVIVG01007585001	T2	T12	0,102864	2,6255	4,67379	Cysteine proteinase
GSVIVG01037851001	T0	T6	0,255924	6,54258	4,67607	Salt tolerance zinc finger
GSVIVG01014318001	T0	T12	0,974171	25,0537	4,68471	Dynamin family protein
GSVIVG01030371001	T2	T12	0,284979	7,33325	4,68553	Ankyrin repeat
GSVIVG01027173001	T2	T12	0,228609	5,90021	4,68981	Lateral organ boundaries protein 1
GSVIVG01015194001	T0	T12	2,48205	64,1418	4,69166	FAD linked oxidase, N-terminal
GSVIVG01033392001	T0	T12	0,986752	25,5203	4,69282	Aldose 1-epimerase
GSVIVG01035467001	T0	T12	0,371399	9,66696	4,70202	ATMYB66/WER/WER1 (WEREWOLF 1)
GSVIVG01013914001	T0	T12	0,208762	5,44233	4,7043	Ethylene responsive element binding factor 5
GSVIVG01033957001	T0	T12	0,082848	2,16731	4,70929	Phospholipase C
GSVIVG01032855001	T0	T12	1,50143	39,4985	4,71739	AUX1 auxin influx carrier protein
GSVIVG01033064001	T0	T2	0,118057	3,14615	4,73604	Squamosa promoter-binding protein 13 (SPL13)
GSVIVG01015045001	T0	T12	1,50019	40,1771	4,74316	LHCA6 (Photosystem I light harvesting complex gene 6)
GSVIVG01012253001	T2	T12	0,977032	26,3753	4,75464	Universal stress protein (USP) family protein
GSVIVG01024607001	T0	T6	4,0716	110,277	4,75939	Nodulin
GSVIVG01011929001	T0	T12	0,214705	5,85611	4,76951	Basic/Leu zipper protein HBP-1b
GSVIVG01021600001	T0	T12	0,904099	24,7299	4,77363	Ankyrin
GSVIVG01015952001	T0	T6	1,17567	32,1877	4,77495	WRKY DNA-binding protein 40
GSVIVG01020584001	T0	T6	2,52948	69,2625	4,77516	Ethylene-responsive transcription factor 9
GSVIVG01029996001	T0	T12	0,541964	14,8546	4,77657	Wound-induced
GSVIVG01002270001	T2	T12	0,227156	6,23852	4,77945	Carrier protein, Mitochondrial
GSVIVG01030222001	T0	T12	0,238694	6,56692	4,78199	Basic helix-loop-helix (bHLH) family
GSVIVG01021569001	T0	T12	0,318911	8,81134	4,78814	Tyrosine decarboxylase
GSVIVG01006231001	T0	T12	9,7246	269,83	4,79427	DIR1 (defective IN induced resistance 1)
GSVIVG01015124001	T2	T12	0,0810488	2,26769	4,80629	Phenylalanine ammonia-lyase
GSVIVG01002448001	T2	T6	0,344579	9,64932	4,80752	F-type H+-transporting ATPase alpha chain
GSVIVG01015479001	T0	T12	0,0941124	2,63784	4,80883	Potassium channel AKT1
GSVIVG01029173001	T0	T6	0,18334	5,14454	4,81045	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01020616001	T0	T6	0,830545	23,5181	4,82357	fasciclin arabinogalactan-protein (FLA13)
GSVIVG01011855001	T2	T12	2,25362	63,8716	4,82486	Sterol-C5(6)-desaturase
GSVIVG01008303001	T0	T6	0,27235	7,77873	4,836	(myb domain protein 62
GSVIVG01030258001	T0	T6	0,496145	14,1817	4,83713	WRKY DNA-binding protein 33
GSVIVG01036077001	T0	T12	29,9833	857,171	4,83735	Photosystem I subunit O (PSAO)
GSVIVG01019849001	T2	T6	6,67267	191,195	4,84063	Osmotin
GSVIVG01006303001	T0	T12	0,071517	2,04929	4,84069	Sinapyl alcohol dehydrogenase
GSVIVG01029173001	T0	T2	0,18334	5,2946	4,85193	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01038619001	T0	T2	16,014	464,766	4,85909	Homeobox-leucine zipper protein HB-12
GSVIVG01035033001	T2	T6	0,952294	27,6664	4,86058	Glycosyl hydrolase family 3 beta xylosidase BXL1
GSVIVG01035406001	T0	T12	2,12999	61,9021	4,86107	CGA1 (cytokinin-responsive GATA factor 1)
GSVIVG01014243001	T0	T12	0,0912915	2,65824	4,86385	Sodium/calcium exchanger family protein
GSVIVG01017796001	T0	T6	2,79627	82,4014	4,88109	UPF0497 family
GSVIVG01017955001	T0	T6	0,0765058	2,26686	4,88898	S-receptor kinase
GSVIVG01022403001	T2	T6	4,55788	135,244	4,89106	Ribulose 1,5-bisphosphate carboxylase large subunit
GSVIVG01029109001	T0	T12	0,159636	4,74187	4,8926	1-deoxy-D-xylulose-5-phosphate synthase
GSVIVG01003959001	T2	T12	0,2278	6,81154	4,90214	Anthocyanidine rhamnosyl-transferase
GSVIVG01024133001	T0	T12	0,491646	14,8174	4,91352	Auxin-responsive
GSVIVG01013226001	T0	T6	0,210411	6,36992	4,92	Calcium-binding EF-hand
GSVIVG01028171001	T0	T6	0,221254	6,69991	4,92037	Myb domain protein 78
GSVIVG01001128001	T0	T12	0,16395	4,97082	4,92216	Glyceraldehyde-3-phosphate dehydrogenase
GSVIVG01020830001	T0	T12	0,845067	25,6516	4,92384	Electron transfer flavoprotein alpha-subunit precursor
GSVIVG01014205001	T0	T12	0,0895591	2,7194	4,9243	Curculin (mannose-binding) lectin
GSVIVG01013401001	T0	T12	9,16207	278,346	4,92506	Glucan endo-1,3-beta-glucosidase 7 precursor
GSVIVG01033337001	T2	T12	0,159643	4,86788	4,93037	Arabinogalactan protein 23 AGP23
GSVIVG01021569001	T6	T12	0,287103	8,81134	4,93972	Tyrosine decarboxylase
GSVIVG01024694001	T0	T2	0,708407	21,8335	4,94582	N-acetyltransferase hookless1 HLS1
GSVIVG01033691001	T0	T2	0,141474	4,37	4,94903	Expansin EXPA9

GSVIVG01028328001	T2	T6	0,0884241	2,73706	4,95204	Myb domain protein 14
GSVIVG01019568001	T0	T6	0,333397	10,3545	4,95688	Cellulose synthase CSLG3
GSVIVG01031576001	T2	T12	0,667693	20,774	4,95945	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01035013001	T0	T6	4,59649	143,012	4,95946	Beta-1,3-glucanase
GSVIVG01016328001	T0	T12	1,63085	50,9923	4,96658	Lateral organ boundaries protein 1
GSVIVG01032044001	T0	T6	0,245912	7,73051	4,97435	Polygalacturonase inhibiting protein 1 PGIP1
GSVIVG01009519001	T2	T12	0,265543	8,36472	4,9773	Transcriptional factor B3
GSVIVG01036671001	T0	T12	35,2837	1112,13	4,97818	Pepsin A
GSVIVG01016978001	T2	T12	0,327351	10,3219	4,97872	Taurine dioxygenase
GSVIVG01000829001	T2	T12	7,75351	245,269	4,98337	Annexin ANN4
GSVIVG01014286001	T0	T6	1,25695	40,2335	5,0004	Tyrosine aminotransferase
GSVIVG01030222001	T0	T6	0,238694	7,64607	5,00149	Basic helix-loop-helix (bHLH) family
GSVIVG01015958001	T0	T6	0,401811	12,8735	5,00174	N-acetyltransferase hookless1 HLS1
GSVIVG01036560001	T0	T12	0,955617	30,6498	5,0033	MAP3K-like protein kinase, putative, expressed
GSVIVG01037117001	T0	T12	0,236459	7,58969	5,00438	GDA2
GSVIVG01015045001	T2	T12	1,24132	40,1771	5,01642	LHCA6 (Photosystem I light harvesting complex gene 6)
GSVIVG01012389001	T2	T12	0,35975	11,6662	5,0192	Cinnamyl alcohol dehydrogenase
GSVIVG01007585001	T0	T6	0,384625	12,5277	5,02552	Cysteine proteinase
GSVIVG01000469001	T6	T12	1,77816	58,0477	5,02878	Anthocyanin 5-aromatic acyltransferase
GSVIVG01010649001	T0	T12	0,459511	15,026	5,03122	Mandelonitrile lyase-like protein
GSVIVG01024122001	T0	T12	0,833464	27,6869	5,05394	Auxin-induced SAUR
GSVIVG01011637001	T0	T6	1,25698	41,8432	5,05696	S-adenosyl-L-methionine:carboxyl methyltransferase
GSVIVG01035315001	T0	T6	0,903853	30,1183	5,05841	receptor-like protein kinase hsl1-like
GSVIVG01032263001	T0	T2	0,0303702	1,01328	5,06023	Receptor-like protein kinase PRK1
GSVIVG01024135001	T0	T12	0,521606	17,4495	5,06408	Auxin-responsive SAUR31
GSVIVG01033392001	T2	T12	0,761394	25,5203	5,06686	Aldose 1-epimerase
GSVIVG01035207001	T0	T6	0,132021	4,46192	5,07883	Steroid sulfotransferase
GSVIVG01004701001	T2	T6	0,35787	12,1227	5,08213	Ankyrin
GSVIVG01032055001	T2	T12	0,371986	12,6251	5,0849	Basic helix-loop-helix (bHLH) family
GSVIVG01015140001	T0	T6	0,035228	1,20205	5,09264	Phenylalanine ammonia-lyase
GSVIVG01014147001	T0	T6	0,0323697	1,10781	5,09692	RKF1 (receptor-like kinase in flowers 1)
GSVIVG01032044001	T0	T12	0,245912	8,43382	5,09997	Polygalacturonase inhibiting protein 1 PGIP1
GSVIVG01013916001	T0	T2	0,0939818	3,22558	5,10103	Ethylene-responsive transcription factor ERF105
GSVIVG01019012001	T2	T6	15,7807	542,401	5,10313	Homeobox protein 5
GSVIVG01012389001	T0	T12	0,334351	11,6662	5,12483	Cinnamyl alcohol dehydrogenase
GSVIVG01013918001	T0	T6	0,178531	6,25923	5,13174	Ethylene-responsive transcription factor ERF105
GSVIVG01001053001	T6	T12	2,18181	76,6207	5,13414	Ribosomal protein L39 (RPL39C) 60S
GSVIVG01015124001	T2	T6	0,0810488	2,86821	5,14522	Phenylalanine ammonia-lyase
GSVIVG01011840001	T0	T12	12,7339	452,483	5,15111	Zinc finger (C3HC4-type ring finger)
GSVIVG01029170001	T0	T6	0,143793	5,1217	5,15456	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01001603001	T2	T12	2,97881	106,246	5,15653	Laccase
GSVIVG01035207001	T0	T2	0,132021	4,71585	5,15868	Steroid sulfotransferase
GSVIVG01024204001	T2	T12	0,176031	6,29643	5,16063	Salt tolerance homolog2
GSVIVG01032743001	T6	T12	3,43332	122,871	5,1614	Proteinase inhibitor (LUTI)
GSVIVG01011098001	T0	T6	0,581012	20,9764	5,17406	Circadian clock coupling factor ZGT
GSVIVG01000230001	T0	T2	7,1814	259,459	5,1751	Proteinase inhibitor se60
GSVIVG01011872001	T0	T6	3,18655	115,417	5,17871	(myb domain protein 62
GSVIVG01029173001	T0	T12	0,18334	6,67316	5,18578	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01013914001	T0	T2	0,208762	7,63345	5,19241	Ethylene responsive element binding factor 5
GSVIVG01032720001	T0	T6	0,815468	30,0036	5,20136	Basic helix-loop-helix (bHLH) family
GSVIVG01010047001	T0	T6	1,51657	55,8832	5,20353	Pathogen-related
GSVIVG01017836001	T2	T6	0,0962489	3,54763	5,20394	Sugar transporter ERD6-like 16
GSVIVG01012138001	T0	T12	0,0425489	1,57088	5,20631	Polygalacturonase QRT3
GSVIVG01030549001	T0	T12	1,67533	61,8984	5,20738	Caffeic acid O-methyltransferase
GSVIVG01028315001	T2	T6	0,273927	10,1219	5,20755	Transcription factor TSRF1
GSVIVG01016576001	T0	T12	2,54181	94,1698	5,21134	Histone H4
GSVIVG01002270001	T0	T12	0,168341	6,23852	5,21175	Carrier protein, Mitochondrial
GSVIVG01036879001	T2	T6	0,423735	15,7432	5,21542	protein
GSVIVG01031897001	T2	T12	0,109911	4,08937	5,21748	DC1 domain-containing protein
GSVIVG01001205001	T6	T12	0,134001	4,98902	5,21844	Chlorophyllase
GSVIVG01032055001	T0	T12	0,337827	12,6251	5,22387	Basic helix-loop-helix (bHLH) family
GSVIVG01011868001	T0	T2	0,414186	15,6821	5,2427	Zinc finger protein 6
GSVIVG01015958001	T2	T6	0,338779	12,8735	5,24792	N-acetyltransferase hookless1 HLS1
GSVIVG01033337001	T0	T12	0,127656	4,86788	5,25296	Arabinogalactan protein 23 AGP23
GSVIVG01015037001	T0	T12	0,152955	5,858	5,25923	DREB sub A-5 of ERF/AP2 transcription factor
GSVIVG01006754001	T0	T6	0,0768554	2,97927	5,27667	Ankyrin repeat protein
GSVIVG01021314001	T0	T6	0,216952	8,42069	5,27849	Subtilase
GSVIVG01013914001	T0	T6	0,208762	8,13395	5,28403	Ethylene responsive element binding factor 5
GSVIVG01011638001	T0	T6	0,628009	24,4903	5,28528	S-adenosyl-L-methionine:salicylic acid carboxyl
GSVIVG01027641001	T2	T12	0,182584	7,13293	5,28787	Protease inhibitor/seed storage/lipid transfer protein (LTP)
GSVIVG01011401001	T2	T6	0,497741	19,6874	5,30574	Amino acid permease

GSVIVG01025792001	T0	T12	0,656241	26,049	5,31086	Thylakoid lumenal 20 kDa protein
GSVIVG01018878001	T2	T6	2,13242	84,886	5,31497	Dehydrin 1b
GSVIVG01028328001	T0	T12	0,0394032	1,58339	5,32856	Myb domain protein 14
GSVIVG01029529001	T0	T2	0,0205932	0,829114	5,33133	Receptor-like protein kinase PRK1
GSVIVG01013934001	T2	T6	0,0445993	1,79943	5,33437	Ethylene-responsive transcription factor 5
GSVIVG01007243001	T0	T12	1,01437	41,116	5,34105	Calcium-binding EF hand family
GSVIVG01028315001	T0	T6	0,249337	10,1219	5,34324	Transcription factor TSRF1
GSVIVG01033978001	T0	T6	0,518134	21,2599	5,35867	Alpha-1,4-glycosyltransferase
GSVIVG01010933001	T0	T6	0,0871632	3,61152	5,37274	High-affinity K ⁺ transporter 1 (HKT1)
GSVIVG01013913001	T0	T6	0,0851344	3,56896	5,38962	Ethylene-responsive transcription factor ERF105
GSVIVG01025389001	T0	T12	0,452867	19,0203	5,39231	Pentatricopeptide (PPR) repeat-containing protein
GSVIVG01024694001	T0	T6	0,708407	29,828	5,39595	N-acetyltransferase hookless1 HLS1
GSVIVG01035614001	T2	T12	0,633811	26,8167	5,40294	GATA transcription factor 11
GSVIVG01006754001	T2	T6	0,0695677	2,97927	5,4204	Ankyrin repeat protein
GSVIVG01028204001	T0	T12	2,48628	106,715	5,42363	LHCII type I CAB-1
GSVIVG01015125001	T0	T6	0,578571	25,3503	5,45337	Ankyrin repeat family protein
GSVIVG01011638001	T2	T6	0,557834	24,4903	5,45623	S-adenosyl-L-methionine:salicylic acid carboxyl
GSVIVG01012125001	T0	T6	0,0519085	2,28432	5,45965	PLATZ transcription factor
GSVIVG01019614001	T0	T12	0,705317	31,177	5,46607	MYB Domain protein 6
GSVIVG01030222001	T2	T12	0,148541	6,56692	5,46628	Basic helix-loop-helix (bHLH) family
GSVIVG01030618001	T2	T6	1,42089	63,0365	5,47132	photosystem i subunit viii
GSVIVG01017836001	T2	T12	0,0962489	4,28263	5,47558	Sugar transporter ERD6-like 16
GSVIVG01020519001	T2	T12	0,0614759	2,7403	5,47817	Ankyrin repeat
GSVIVG01023189001	T0	T12	0,0476677	2,14673	5,49298	Disease resistance protein RPS2
GSVIVG01004701001	T2	T12	0,35787	16,1337	5,4945	Ankyrin
GSVIVG01024610001	T2	T12	0,0344666	1,55884	5,49913	Taxadien-5-alpha-ol-O-acetyltransferase
GSVIVG01034477001	T2	T12	4,6742	211,532	5,50001	GASA like
GSVIVG01015266001	T2	T12	4,03039	183,365	5,50766	Myo-inositol oxygenase
GSVIVG01007817001	T0	T12	4,90298	223,376	5,50967	LTCOR11
GSVIVG01030545001	T0	T12	0,422512	19,2826	5,51216	Caffeic acid O-methyltransferase
GSVIVG01015141001	T0	T6	0,0618974	2,83046	5,51501	Ankyrin repeat
GSVIVG01022491001	T0	T6	0,205728	9,43335	5,51896	CXE carboxylesterase
GSVIVG01001055001	T6	T12	1,47258	68,1022	5,53128	Ribosomal protein L39 (RPL39C) 60S
GSVIVG01033064001	T0	T12	0,118057	5,51703	5,54634	Squamosa promoter-binding protein 13 (SPL13)
GSVIVG01001299001	T2	T12	82,6099	3862,01	5,54689	Protease inhibitor/seed storage/lipid transfer protein (LTP)
GSVIVG01000547001	T0	T12	0,997721	46,9697	5,55695	Alpha-L-fucosidase 2 precursor
GSVIVG01027652001	T0	T6	3,44997	163,408	5,56575	Pectinesterase family
GSVIVG01006303001	T0	T6	0,071517	3,3923	5,56783	Sinapyl alcohol dehydrogenase
GSVIVG01036228001	T0	T6	0,318745	15,1404	5,56986	ERF12
GSVIVG01011259001	T0	T6	0,0369771	1,77745	5,58703	flavonol 3-sulfotransferase
GSVIVG01000687001	T2	T6	0,826568	39,9277	5,59411	Gibberellin 2-beta-dioxygenase 1
GSVIVG01026341001	T0	T12	19,5873	962,76	5,61919	Lipase GDSL
GSVIVG01001055001	T0	T12	1,3846	68,1022	5,62017	Ribosomal protein L39 (RPL39C) 60S
GSVIVG01011401001	T2	T12	0,497741	24,609	5,62764	Amino acid permease
GSVIVG01002031001	T0	T6	0,698368	34,6436	5,63246	Stem-specific protein TSJT1
GSVIVG01013722001	T0	T12	1,21525	61,2081	5,65439	Polygalacturonase BURP
GSVIVG01024607001	T2	T12	12,7021	640,198	5,65538	Nodulin
GSVIVG01032720001	T0	T12	0,815468	41,2756	5,66152	Basic helix-loop-helix (bHLH) family
GSVIVG01033744001	T0	T12	0,406758	20,6467	5,6656	Late meristem identity1 HB51/LMI1
GSVIVG01029801001	T0	T12	0,0511736	2,62188	5,67906	Alpha-L-arabinosidase
GSVIVG01009474001	T2	T12	0,0863707	4,42592	5,67929	Subtilase family protein
GSVIVG01030222001	T2	T6	0,148541	7,64607	5,68578	Basic helix-loop-helix (bHLH) family
GSVIVG01020681001	T0	T12	0,0681885	3,52652	5,69257	1-aminocyclopropane-1-carboxylate oxidase
GSVIVG01016112001	T2	T12	0,690349	35,7143	5,69303	Acid phosphatase
GSVIVG01015527001	T0	T6	0,0620094	3,21162	5,69467	Allyl alcohol dehydrogenase
GSVIVG01023922001	T2	T6	3,63088	191,662	5,7221	Endochitinase 1, basic
GSVIVG01023306001	T2	T12	0,024601	1,30432	5,72844	Disease resistance protein
GSVIVG01035463001	T0	T6	0,198263	10,5437	5,73282	Myb domain protein 32
GSVIVG01033744001	T0	T6	0,406758	21,7149	5,73837	Late meristem identity1 HB51/LMI1
GSVIVG01007435001	T0	T6	0,106054	5,67049	5,74061	Stem-specific protein TSJT1
GSVIVG01010649001	T6	T12	0,279991	15,026	5,74594	Mandelonitrile lyase-like protein
GSVIVG01032718001	T6	T12	0,0842411	4,53577	5,75068	Hypoxia-responsive
GSVIVG01019952001	T2	T6	5,22861	282,461	5,75548	NAC domain-containing protein 29
GSVIVG01036905001	T0	T12	0,0624747	3,39546	5,76419	10-deacetylbaicatin III 10-O-acetyltransferase
GSVIVG01029170001	T0	T12	0,143793	7,85533	5,77161	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01018878001	T0	T6	1,54349	84,886	5,78126	Dehydrin 1b
GSVIVG01015037001	T0	T6	0,152955	8,4405	5,78615	DREB sub A-5 of ERF/AP2 transcription factor
GSVIVG01003548001	T0	T12	0,116375	6,42547	5,78694	Lateral organ boundaries domain gene 36
GSVIVG01033064001	T0	T6	0,118057	6,55029	5,79401	Squamosa promoter-binding protein 13 (SPL13)
GSVIVG01015704001	T0	T12	0,227619	12,6658	5,79817	Transferase family
GSVIVG01019570001	T0	T12	0,156746	8,76026	5,80448	Cellulose synthase CSLG3

GSVIVG01030552001	T0	T12	1,37019	77,3576	5,81909	Photosystem II psbZ
GSVIVG01011868001	T0	T12	0,414186	23,5872	5,83158	Zinc finger protein 6
GSVIVG01029951001	T0	T12	0,351717	20,2109	5,84458	Cupin, RmlC-type
GSVIVG01015527001	T2	T6	0,0552524	3,21162	5,86112	Allyl alcohol dehydrogenase
GSVIVG01013226001	T0	T12	0,210411	12,2423	5,86252	Calcium-binding EF-hand
GSVIVG01019916001	T2	T6	0,0453289	2,65611	5,87274	Carboxyl-terminal peptidase
GSVIVG01031885001	T2	T6	0,0186713	1,09487	5,87379	AOS (allene oxide synthase)
GSVIVG01019849001	T0	T6	3,20508	191,195	5,89854	Osmotin
GSVIVG01015266001	T0	T12	3,06532	183,365	5,90253	Myo-inositol oxygenase
GSVIVG01013934001	T0	T6	0,0300321	1,79943	5,90489	Ethylene-responsive transcription factor 5
GSVIVG01016112001	T2	T6	0,690349	41,5279	5,91061	Acid phosphatase
GSVIVG01011259001	T0	T2	0,0369771	2,23557	5,91787	flavonol 3-sulfotransferase
GSVIVG01016698001	T0	T6	0,227142	13,7899	5,92388	Auxin-induced protein
GSVIVG01009474001	T0	T12	0,0726999	4,42592	5,92788	Subtilase family protein
GSVIVG01025514001	T2	T12	0,0303377	1,85475	5,93397	S-adenosyl-L-methionine:salicylic acid carboxyl
GSVIVG01000687001	T0	T6	0,652255	39,9277	5,93581	Gibberellin 2-beta-dioxygenase 1
GSVIVG01024694001	T0	T12	0,708407	43,3654	5,93582	N-acetyltransferase hookless1 HLS1
GSVIVG01015139001	T2	T6	0,05055	3,12841	5,95157	Ankyrin repeat
GSVIVG01009646001	T0	T12	1,10034	68,2443	5,95469	Thaumatococcus SCUTL2
GSVIVG01020616001	T2	T12	2,56474	162,753	5,98773	fasciclin arabinogalactan-protein (FLA13)
GSVIVG01017796001	T2	T6	1,29476	82,4014	5,99191	UPF0497 family
GSVIVG01026803001	T6	T12	0,772337	49,168	5,99235	Isoflavone methyltransferase/Orcinol O-methyltransferase 2
GSVIVG01012708001	T0	T12	0,0868686	5,58521	6,00663	Monocopper oxidase SKS4 (SKU5 Similar 4)
GSVIVG01016345001	T0	T12	0,601268	38,8951	6,01544	RNA recognition motif (RRM)-containing protein
GSVIVG01001210001	T0	T6	0,0113418	0,746368	6,04017	Chlorophyllase 1
GSVIVG01029165001	T0	T12	0,47592	31,3493	6,04157	Xyloglucan endotransglycosylase 6
GSVIVG01001053001	T0	T12	1,15094	76,6207	6,05685	Ribosomal protein L39 (RPL39C) 60S
GSVIVG01036388001	T0	T6	0,260681	17,5619	6,07402	Ethylene-responsive transcription factor ERF021
GSVIVG01019450001	T2	T12	0,0903408	6,12664	6,08358	Pinorensin forming dirigent protein
GSVIVG01018478001	T2	T12	0,137804	9,54354	6,11384	Embryo-specific 3
GSVIVG01028328001	T0	T6	0,0394032	2,73706	6,11817	Myb domain protein 14
GSVIVG01020877001	T0	T12	0,0739589	5,21584	6,14003	Ankyrin repeat protein
GSVIVG01006754001	T0	T12	0,0768554	5,45321	6,14881	Ankyrin repeat protein
GSVIVG01012777001	T0	T12	0,0356157	2,53322	6,15231	Myb domain protein 4
GSVIVG01029167001	T0	T6	2,40269	171,274	6,15551	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01008890001	T2	T6	0,126359	9,11764	6,17306	Nodulin MtN21 family
GSVIVG01029167001	T0	T12	2,40269	173,378	6,17313	Xyloglucan endotransglucosylase/hydrolase 23
GSVIVG01036228001	T0	T2	0,318745	23,0576	6,1767	ERF12
GSVIVG01011855001	T0	T12	0,88275	63,8716	6,17703	Sterol-C5(6)-desaturase
GSVIVG01010932001	T0	T12	0,252468	18,4137	6,18853	High-affinity K+ transporter 1 (HKT1)
GSVIVG01036388001	T0	T12	0,260681	19,0973	6,19494	Ethylene-responsive transcription factor ERF021
GSVIVG01016112001	T0	T12	0,484233	35,7143	6,20466	Acid phosphatase
GSVIVG01013905001	T0	T6	0,227508	16,8536	6,21099	Ethylene-responsive transcription factor ERF105
GSVIVG01017183001	T0	T12	0,0378138	2,82632	6,22387	2-oxoglutarate-dependent dioxygenase
GSVIVG01021195001	T6	T12	0,0834426	6,42816	6,26748	Cysteine protease RCR3
GSVIVG01023306001	T6	T12	0,0168231	1,30432	6,27671	Disease resistance protein
GSVIVG01006754001	T2	T12	0,0695677	5,45321	6,29254	Ankyrin repeat protein
GSVIVG01021736001	T2	T12	0,0515881	4,04944	6,29454	Reticuline oxidase
GSVIVG01016698001	T0	T2	0,227142	17,884	6,29893	Auxin-induced protein
GSVIVG01029709001	T2	T6	0,370036	29,5113	6,31746	NAC domain containing protein 104
GSVIVG01003959001	T0	T6	0,0185558	1,49246	6,32967	Anthocyanidine rhamnosyl-transferase
GSVIVG01036167001	T0	T12	0,263038	21,3748	6,34449	Subtilisin-like proteinase AIR3
GSVIVG01021600001	T6	T12	0,303939	24,7299	6,34633	Ankyrin
GSVIVG01019012001	T0	T6	6,66511	542,401	6,34659	Homeobox protein 5
GSVIVG01023688001	T0	T6	0,0571396	4,6922	6,35963	Serine carboxypeptidase II
GSVIVG01002031001	T2	T6	0,421692	34,6436	6,36026	Stem-specific protein TSJT1
GSVIVG01010650001	T2	T12	0,0246907	2,04012	6,36854	Glucose-methanol-choline (GMC) oxidoreductase family
GSVIVG01010932001	T2	T12	0,221387	18,4137	6,37806	High-affinity K+ transporter 1 (HKT1)
GSVIVG01008479001	T0	T12	0,105093	8,80518	6,38861	Homeobox protein knotted-1 like 1 (KNAT1)
GSVIVG01010646001	T0	T12	37,3594	3153,7	6,39943	sorbitol dehydrogenase
GSVIVG01008234001	T2	T6	0,463614	39,1483	6,39988	TCP family transcription factor BRC2/TCP12 (branched2)
GSVIVG01009807001	T0	T12	0,0865297	7,30945	6,40042	Papain cysteine proteinase isoform I
GSVIVG01002752001	T2	T6	1,43033	121,048	6,4031	NADH dehydrogenase subunit 3
GSVIVG01009807001	T6	T12	0,0853636	7,30945	6,42	Papain cysteine proteinase isoform I
GSVIVG01016112001	T0	T6	0,484233	41,5279	6,42224	Acid phosphatase
GSVIVG01009809001	T0	T12	0,0551377	4,92711	6,48156	Papain cysteine proteinase isoform II
GSVIVG01032743001	T0	T12	1,36429	122,871	6,49285	Proteinase inhibitor (LUTI)
GSVIVG01000469001	T2	T12	0,625591	58,0477	6,53588	Anthocyanin 5-aromatic acyltransferase
GSVIVG01011532001	T2	T12	0,0108942	1,04466	6,58332	Carboxyl-terminal proteinase
GSVIVG01007981001	T0	T12	0,0164582	1,58727	6,5916	MYB transcription factor MIXTA-like 2
GSVIVG01027772001	T0	T6	0,398176	38,4145	6,5921	Ethylene response factor ERF1

GSVIVG01003762001	T0	T12	3,34196	326,538	6,61041	Pathogenesis-related protein 1 precursor (PRP 1)
GSVIVG01015139001	T0	T6	0,0319116	3,12841	6,6152	Ankyrin repeat
GSVIVG01010631001	T0	T12	0,0595975	5,91537	6,63307	DREB sub A-1 of ERF/AP2 transcription factor (CBF4)
GSVIVG01010940001	T0	T12	0,113639	11,6104	6,67481	Glutathione S-transferase 13 GSTF13
GSVIVG01018913001	T2	T6	0,144352	14,7527	6,67525	SAM dependent carboxyl methyltransferase Methyltransf_7
GSVIVG01033744001	T0	T2	0,406758	41,839	6,68453	Late meristem identity1 HB51/LMI1
GSVIVG01011585001	T0	T12	0,167201	17,2078	6,68533	NADPH-dependent codeinone reductase
GSVIVG01027551001	T0	T12	0,625323	64,7715	6,69461	CYP76C2
GSVIVG01027549001	T0	T12	0,150051	15,6069	6,70059	Geraniol 10-hydroxylase
GSVIVG01019511001	T0	T6	0,217418	22,6278	6,70148	WRKY DNA-binding protein 53
GSVIVG01017242001	T0	T12	0,0167159	1,76326	6,72088	Tesmin/TSO1-like CXC domain-containing
GSVIVG01013735001	T0	T6	0,0286213	3,14688	6,78069	ATMYB66/WER/WER1 (WEREWOLF 1)
GSVIVG01035207001	T0	T12	0,132021	15,1118	6,83876	Steroid sulfotransferase
GSVIVG01024077001	T2	T12	0,820652	94,7891	6,85181	unnamed protein product
GSVIVG01014205001	T0	T6	0,0895591	10,5412	6,87898	Curculin (mannose-binding) lectin
GSVIVG01023922001	T0	T6	1,62646	191,662	6,88069	Endochitinase 1, basic
GSVIVG01008890001	T0	T6	0,0770183	9,11764	6,88732	Nodulin MtN21 family
GSVIVG01035466001	T0	T12	0,0760383	9,12082	6,90629	CYP72A58
GSVIVG01024713001	T2	T6	7,23114	875,428	6,91962	Asparagine synthetase
GSVIVG01007585001	T2	T6	0,102864	12,5277	6,92824	Cysteine proteinase
GSVIVG01024122001	T6	T12	0,225711	27,6869	6,93858	Auxin-induced SAUR
GSVIVG01036924001	T0	T12	0,0335261	4,14271	6,94915	Glycosyl transferase family 1 protein
GSVIVG01019916001	T0	T6	0,0214617	2,65611	6,95141	Carboxyl-terminal peptidase
GSVIVG01000230001	T0	T6	7,1814	936,963	7,02758	Proteinase inhibitor se60
GSVIVG01018904001	T2	T6	1,08747	141,982	7,02859	S-adenosyl-L-methionine:salicylic acid carboxyl
GSVIVG01008406001	T2	T12	0,0193146	2,54589	7,04234	Laccase
GSVIVG01036924001	T2	T12	0,0309793	4,14271	7,06313	Glycosyl transferase family 1 protein
GSVIVG01035463001	T0	T12	0,198263	26,5303	7,06408	Myb domain protein 32
GSVIVG01021736001	T6	T12	0,0302382	4,04944	7,06521	Reticuline oxidase
GSVIVG01007435001	T2	T6	0,0419988	5,67049	7,07698	Stem-specific protein TSJT1
GSVIVG01009807001	T2	T12	0,0538483	7,30945	7,08472	Papain cysteine proteinase isoform I
GSVIVG01036228001	T0	T12	0,318745	43,4723	7,09155	ERF12
GSVIVG01014147001	T2	T6	0,00801179	1,10781	7,11137	RKF1 (receptor-like kinase in flowers 1)
GSVIVG01027412001	T0	T12	0,0162701	2,27524	7,12765	Basic helix-loop-helix (bHLH) family
GSVIVG01011330001	T0	T12	0,0151388	2,12921	7,13592	Basic helix-loop-helix (bHLH) family
GSVIVG01005915001	T0	T6	0,00776997	1,11101	7,15975	EXPANSIN-like B1
GSVIVG01021314001	T0	T12	0,216952	32,5417	7,22877	Subtilase
GSVIVG01024607001	T0	T12	4,0716	640,198	7,29678	Nodulin
GSVIVG01011947001	T0	T6	0,280777	44,3222	7,30246	AP2 domain-containing protein RAP2.8
GSVIVG01028313001	T0	T6	0,00931839	1,47626	7,30765	Ethylene-responsive transcription factor ERF098
GSVIVG01006300001	T0	T12	0,190677	30,6298	7,32766	Major Facilitator Superfamily
GSVIVG01024135001	T6	T12	0,105942	17,4495	7,36377	Auxin-responsive SAUR31
GSVIVG01010933001	T0	T12	0,0871632	14,7109	7,39895	High-affinity K+ transporter 1 (HKT1)
GSVIVG01012343001	T2	T6	0,00320424	0,568613	7,47132	Laccase
GSVIVG01011259001	T0	T12	0,0369771	6,64942	7,49045	flavonol 3-sulfotransferase
GSVIVG01019575001	T2	T12	0,0162495	2,9762	7,51693	Cellulose synthase CSLG3
GSVIVG01019952001	T0	T6	1,54036	282,461	7,51864	NAC domain-containing protein 29
GSVIVG01021569001	T2	T12	0,0477867	8,81134	7,52661	Tyrosine decarboxylase
GSVIVG01010621001	T0	T6	0,00999026	1,84242	7,52687	MATE efflux family protein
GSVIVG01027641001	T0	T12	0,038421	7,13293	7,53646	Protease inhibitor/seed storage/lipid transfer protein (LTP)
GSVIVG01015946001	T2	T12	0,00963747	1,83362	7,57183	Carnitine/acylcarnitine translocase
GSVIVG01020616001	T0	T12	0,830545	162,753	7,61441	fasciclin arabinogalactan-protein (FLA13)
GSVIVG01021134001	T0	T6	0,145805	28,6713	7,61943	Isoflavone methyltransferase/ Orcinol O-methyltransferase
GSVIVG01023688001	T0	T12	0,0571396	11,2598	7,62248	Serine carboxypeptidase II
GSVIVG01012309001	T2	T12	0,133404	26,8753	7,65433	Copper transporter 2
GSVIVG01034125001	T0	T6	0,484992	97,7304	7,6547	Proteinase inhibitor
GSVIVG01009810001	T0	T12	0,03712	7,72671	7,70151	Papain cysteine proteinase isoform I
GSVIVG01001614001	T0	T6	0,00527916	1,13657	7,75017	Diphenol oxidase
GSVIVG01015527001	T0	T12	0,0620094	13,409	7,7565	Allyl alcohol dehydrogenase
GSVIVG01028801001	T2	T6	0,0158689	3,51597	7,79158	Receptor serine/threonine kinase PR5K
GSVIVG01013735001	T0	T12	0,0286213	6,63624	7,85713	ATMYB66/WER/WER1 (WEREWOLF 1)
GSVIVG01008234001	T0	T6	0,16621	39,1483	7,87979	TCP family transcription factor BRC2/TCP12 (branched2)
GSVIVG01001299001	T0	T12	15,9783	3862,01	7,91709	Protease inhibitor/seed storage/lipid transfer protein (LTP)
GSVIVG01015527001	T2	T12	0,0552524	13,409	7,92295	Allyl alcohol dehydrogenase
GSVIVG01038764001	T0	T2	0,00636957	1,57905	7,95365	Leucine-rich repeat protein kinase
GSVIVG01001207001	T0	T12	0,00183636	0,487034	8,05103	Chlorophyllase 1
GSVIVG01016293001	T2	T6	0,0155527	4,17977	8,07011	Protein kinase
GSVIVG01012309001	T0	T12	0,0962476	26,8753	8,12532	Copper transporter 2
GSVIVG01004701001	T0	T6	0,0430323	12,1227	8,13807	Ankyrin
GSVIVG01010648001	T2	T12	0,0091878	2,65007	8,1721	Mandelonitrile lyase-like protein
GSVIVG01024077001	T0	T12	0,328531	94,7891	8,17255	unnamed protein product

GSVIVG01000230001	T0	T12	7,1814	2119,25	8,20507	Proteinase inhibitor se60
GSVIVG01018913001	T0	T6	0,0486015	14,7527	8,24576	SAM dependent carboxyl methyltransferase Methyltransf_7
GSVIVG01037349001	T0	T6	0,00447519	1,36342	8,25106	Pectinesterase family
GSVIVG01001205001	T0	T12	0,0149943	4,98902	8,37819	Chlorophyllase
GSVIVG01024135001	T2	T12	0,0516409	17,4495	8,40046	Auxin-responsive SAUR31
GSVIVG01021308001	T0	T12	0,0154554	5,49642	8,47424	Lipase GDSL
GSVIVG01003959001	T0	T12	0,0185558	6,81154	8,51997	Anthocyanidine rhamnosyl-transferase
GSVIVG01004701001	T0	T12	0,0430323	16,1337	8,55044	Ankyrin
GSVIVG01009809001	T2	T12	0,0109177	4,92711	8,81793	Papain cysteine proteinase isoform II
GSVIVG01016698001	T0	T12	0,227142	112,816	8,95617	Auxin-induced protein
GSVIVG01025060001	T0	T2	0,00348069	1,74506	8,96969	Leucine-rich repeat protein kinase
GSVIVG01009810001	T2	T12	0,0147001	7,72671	9,03789	Papain cysteine proteinase isoform I

Supplemental Table 2: Genes with differential expression across early berry development (FDR 0.05). Grapevines ID with no hit or hit with unknown proteins have been deleted from the list.