Novel insights on female gametophyte development in the apomictic model species *Boechera spp.* and *Hypericum spp*.

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Summary

With a world population expected to exceed the 9 billion people by 2050, it is calculated that to feed the world would require an increase of crops productions of about 70% (FAO.org). This scenario introduces food security issues that have to be solved by optimizing many aspects of the productive processes and by improving the outcome of breeding programs.

Heterosis is a phenomenon that is used since long time in many breeding programs, *e.g.* hybrid maize production. However, it presents the disadvantage of being very difficult to fix due to its dependence from specific allelic combinations and its susceptibility to allele segregation.

Apomixis is an asexual mode of reproduction through seed, that could be used as a tool for the fixation of heterotic vigor. This would produce significant improvements in breeding programs, and would make the constitution of new varieties a much faster and dynamic process.

Unfortunately, the main crops are not apomictic, therefore the creation of an apotechnology requires big efforts from the scientific community in order to dissect this reproductive mode, identifying its molecular bases and finally engineering it into crops.

This project aims to move toward a better understanding of apomixis by studying it in two different apomictic model organisms, the diplosporic *Boechera spp.* and the aposporic *Hypericum spp.*

The mechanisms of the sexual female gametophyte development are very complex and still largely unexplored. Even more complicated is the identification of the key players behind the apomictic developmental pathway.

During this study this problem was approached from multiple angles. The evaluation of several reproductive traits in apomictic and sexual lines, the comparative study of ploidy dynamics and finally the deep morphological characterization of ovule development accompanied by a multi-stage ovule transcriptomic study.

The comparative morphological characterization of ovule and female gametophyte development, was achieved on sexual and apomictic lines of both model organisms by performing an unprecedented number of observations and by organizing the resulting data into a detailed phenotyping panel of development that provides an overview of the sexual and apomictic mode of reproduction and facilitates the comparison between them.

Furthermore, a visual atlas was assembled in order to provide an easily understandable source of information to be used for future research.

In both model organisms the apomicts resulted to have developmental problems that led to higher abortion rates in comparison to the sexual lines. The morphological characterization of *Hypericum*, allowed to identify a point in development in which the aposporic initial cells (AIs) started to differentiate immediately after the shrinking of the growing gametophytic domain. This suggested that AIs are rescuer of the ovule development and reboot the gametophytic development providing a new start at the stage of functional megaspore. This represent a change in paradigm from previous literature, that defined the aposporic initials as a factor of perturbation for the growing sexual female gametophyte.

The transcriptomic analysis was conducted on ovules from sexual and apomictic lines of *Hypericum perforatum* at the 4 stages of development that were considered crucial for the aposporic process.

The combination of developmental phenotyping and transcriptomic analysis allowed to associate the stage specific differential expression of several genes with precise developmental events, developing in this way a model of aposporous development in *Hypericum*.

Introduction

Food security problematics

Agriculture is the technological innovation that 12000 years ago changed forever our lifestyle and led us to the modern era. The list of technological advances in agriculture is endless but probably the Green Revolution in the 1960s is the period that granted the highest increase in crops production.

For many years after the Green Revolution mankind has been used to very reassuring statistics showing exponential growth of crops productions. This led to the common misconception that food resources were practically unlimited. In reality exponential growth in grain production are feasible only for limited periods otherwise only linear production increases occur over decades (Grassini et al., 2013).

FAO statistics show that food security improved a lot in the last forty years with the number of undernourished people that went down from 1015 million in 1991 to 805 million in 2014 (http://www.fao.org/hunger/en/). 805 million is still a dramatic reality. World population is growing at an exponential rhythm and this put us in front of our next challenge; food and energy resources management.

By 2050, world population is expected to reach 9 billion individuals. Such a demographic growth could only be sustainable by increasing the actual food production by about 50%. A recent study showed how the optimistic statistics following the Green Revolution were in reality overestimations and the exponential curves describing the cereals production growth have never rendered a good description of reality (Grassini et al., 2013).

For the first time since the 1960s the declining of grain prices has stopped. Grain yields are still growing but a linear increase of cultivated areas is necessary to guarantee this continuous linear growth. In simple words, productions per unit of cultivated surface are not growing anymore at a significant rate. Continuing to increase the cultivated area is simply not environmentally sustainable, considering that agriculture productions and indirect emissions associated with the change of land use are already responsible for about 25% of the greenhouse gas emissions (Grassini et al., 2013).

The study from Grassini et al. (2013) shows that the best models for describing the increase in crop production since 1965 are linear and not exponential as often described.

The challenge of today is to overcome this plateau and rise again the production levels.

Breeders are trying to make use of new genetic variation hoping that this will give room for new yield improvement; for this reason, Genebanks all over the world are more and more a useful source of new genetic variability with inherent great benefits. Nevertheless, traditional breeding in the short term may not be enough to solve the problem, especially considering how time consuming is the process of constitution of new crop varieties. For this reason, it is necessary to rethink the breeding process and make it more dynamic, fast and powerful.

A promising strategy that could guarantee an increase in yield in a reasonable short time is the use of heterotic vigor also known as heterosis (Hochholdinger and Hoecker, 2007). Heterotic vigor was already characterized by Charles Darwin in 1876 (Chen, 2010) and it is described as the phenotypic superiority of the hybrid progeny in comparison to its parents in parameters such as: vigor, size, resistance to biotic and abiotic stresses and increase in yield parameters (Hochholdinger and Hoecker, 2007; Kaeppler, 2012; Lippman and Zamir, 2007). Heterotic vigor has been widely used for agricultural purposes and today it is considered the foundation of the modern maize breeding programs (Crow, 1998).

As explained by Crow (1998), maize breeding is a good example of hybrid vigor use in crops and it comprises three main steps:

1. Development of inbred lines
2. Evaluation of inbred lines by GCA (general combining ability) or SCA (specific combining ability)
3. Production of hybrid seed

This method led to a five times increase of maize production from the 1920s but it requires the production of fresh hybrid seed every year obliging the farmers to buy new seed material every time they want to start another cycle of cultivation (Crow, 1998). Despite of its advantages, heterotic vigor largely depends on particular allelic combinations (Schnable and Springer, 2013) making it difficult to be fixed due to the alleles segregation associated with sexual reproduction.

Another method by which a certain fixation of heterosis is possible, makes use of polyploidy and more specifically allopolyploidy (hybridization followed by polyploidisation).

Triticale or cotton (*Gossipium hyrsutum*) are known examples of how hybridization combined with polyploidization can lead to superior phenotypes of industrial or agricultural interest (Chen, 2010).

Fixing heterotic vigor in the offspring of crops could be the base of a new technology capable to revolutionize breeding as we know it and the process from which this technology could be derived is apomixis.

Apomixis

Apomixis can be defined as the asexual reproduction via seed (Schranz et al., 2006). This process avoids meiosis and fertilization of the egg cell and has as a result the formation of an embryo of asexual origin (Bicknell and Koltunow, 2004). This would lead to offspring genetically identical to the mother plant guaranteeing an absolute crop uniformity, the possibility to fix permanently heterotic vigor (Van Dijk and Van Damme, 2000) and the possibility of creating in a very short time new varieties based on a single desirable plant (Frisvold et al., 2005). Such kind of achievement if engineered in crop plants, would represent a big leap in breeding technology and would have huge social and economic implications (Grimanelli et al., 2001). A simple graphical representation of this process can be found in the following figure (Figure 1).

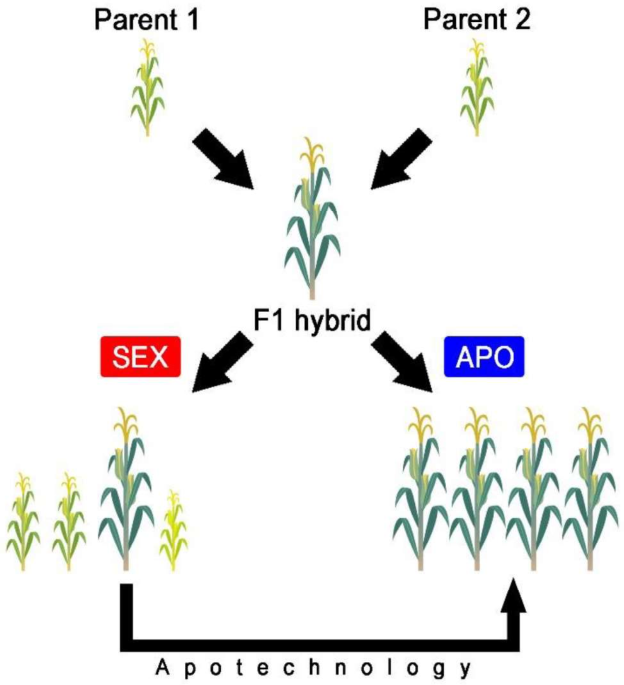

Figure 1. Representation of the potential benefits that an apomictic technology would bring in agriculture and crop breeding programs (modified from Grimanelli et al., 2001).

Estimated benefits of apomixis can be summarized in few points (Frisvold et al.,2005):

- Rapid development of new hybrid varieties
- Increased biodiversity by fixing immediately new genetic combinations
- Economic hybrid seed production
- Easier propagation of hybrid seed
- Increased reproduction efficiency
- General reduction of prices

The introduction of apomixis only in rice is expected to give direct benefits for an amount of over 8 billion dollars in a period of 30 years (Frisvold et al., 2005). Considering indirect benefits and introduction of the apomictic trait in other species than rice, gives an idea of the scale of the advantages that the “apotechnology” could give worldwide.

On the road to this technology, a big obstacle has to be overcome. Apomixis is known to be present on more than 400 species distributed on over 40 plant families but it is absent in the most economically interesting crop species (Spillane et al., 2004). The challenge is obviously to transfer this trait into species or even families where it is naturally absent.

In order to understand how apomixis works, it is first of all necessary to have a good understanding of the sexual developmental pathway that occurs in the majority of flowering plants. For this reason in the following section a general description of the plant life cycle and of the processes that lead to the formation of the sexual female gametophyte is given.

Plant life cycle and female gametophyte.

Flowering plants (angiosperms) are a highly complex clade comprising more than 250000 species characterized by a spectacular reproductive diversity built in over 400 million years of evolution (Parkinson et al., 1999).

The transition from green algae to land plants is estimated to have occurred during the end of the Devonian period (420 – 350 mya) and can be considered one of the most exciting period in plants evolution. This is the time when plants evolved from simple organism made of few cells into complex organisms showing very innovative structures such as stomata, sporangia, gametangia, seeds and vascular systems that finally lead to the transition into the tree habit (Kenrick and Crane, 1997). This incredible transition required great changes in plant life cycle.

It is generally accepted that Embryophytes differentiated from Charophycean algae about 400 million years ago (Niklas et al., 2010) and this implied the passage from a haplobiontic haploid to a diplobiontic life cycle, during which the plant oscillates between two different multicellular generations: the diploid sporophyte and the haploid gametophyte (Niklas et al., 2010).

There are still many unanswered question about this transition period but it seems likely that, coming from the haplobiontic haploid model of the Charophyceae, plants introduced a diploid multicellular generation that became what we nowadays call sporophyte (Niklas et al., 2010).

While on ancient plants haploid phase was dominant over the diploid one, in modern plants the diploid sporophyte became dominant and the haploid gametophytes (male and female) are hidden in the sporophytic reproductive tissues of the flower (Bowman et al., 2007).

A simplified scheme of the plants life cycle with its alternation between gametophytic and sporophytic phase is provided in Figure 2.

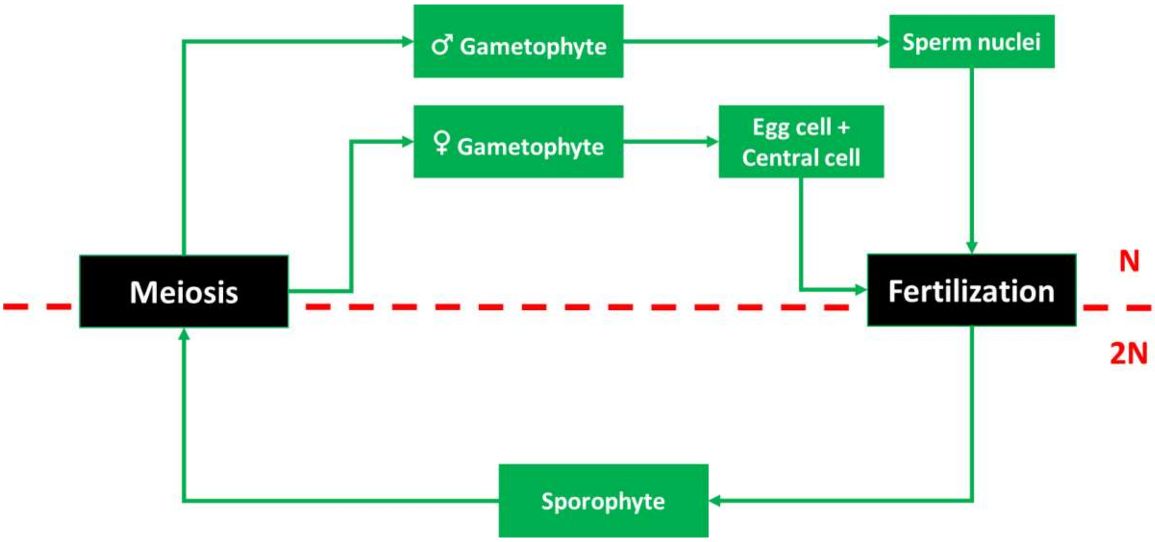

Figure 2. Simplified scheme of the plants life cycle.

There is plenty of literature focusing on the formation and interactions between the two phases of the plant life cycle but this study will focus mainly on gametophytes development with a particular attention to the female gametophyte development.

Female gametophyte is the final result of hundreds millions years of evolution. Several embryological studies show that many of the most ancient lineages of angiosperms (Amborellaceae, Nymphaeales Illiciales, Trimeniaceae and Austrobaileyaceae) belonging to the ANITA grade evolved a gametophytic model of development including three different developmental modules leading to a four-celled female gametophyte carrying the gametes ready for the double fertilization (Friedman and Williams, 2003).

During the first developmental module a somatic cell is programmed to follow a reproductive cell fate and after meiotic division and a tetrad formation, only one of the four nuclei survives and it is positioned in a cytoplasmic domain in the center of the ovule (pole). The second module consists of a sequence of two free-nuclear mitotic divisions leading to a tetra-nucleated gametophyte (Friedman and Williams, 2003). In the third module three of the four nuclei are partitioned in three uninucleate cells (that will form the so called egg apparatus) close to the micropylar pole while the fourth nucleus is confined in the central region of the gametophyte originating the central cell (in this developmental scheme the chalazal pole of the gametophyte remains empty).

The majority of extant angiosperms follow a slightly different ontology model called Polygonum type that differs from the ancestral one for the final number of nuclei (eight), for the presence of nuclei in the chalazal pole and for the formation of a triploid endosperm (Friedman and Williams, 2003). It is hypothesized that the 8-nucleated Polygonum type gametophyte (typical also of *Hypericum perforatum* and *Boechera spp.*), was originated by a duplication of the second developmental module rising in this way the number of mitotical divisions from two to three and allowing the transition from a 4-nucleate to an 8-nucleate female gametophyte (Friedman and Williams, 2003). The development of the Polygonum type is extensively described in literature (Brukhin et al., 2005; Drews et al., 1998; Drews and Koltunow, 2011a; Yadegari and Drews, 2004; Yang et al., 2010). A schematic representation of this process is given in Figure 3.

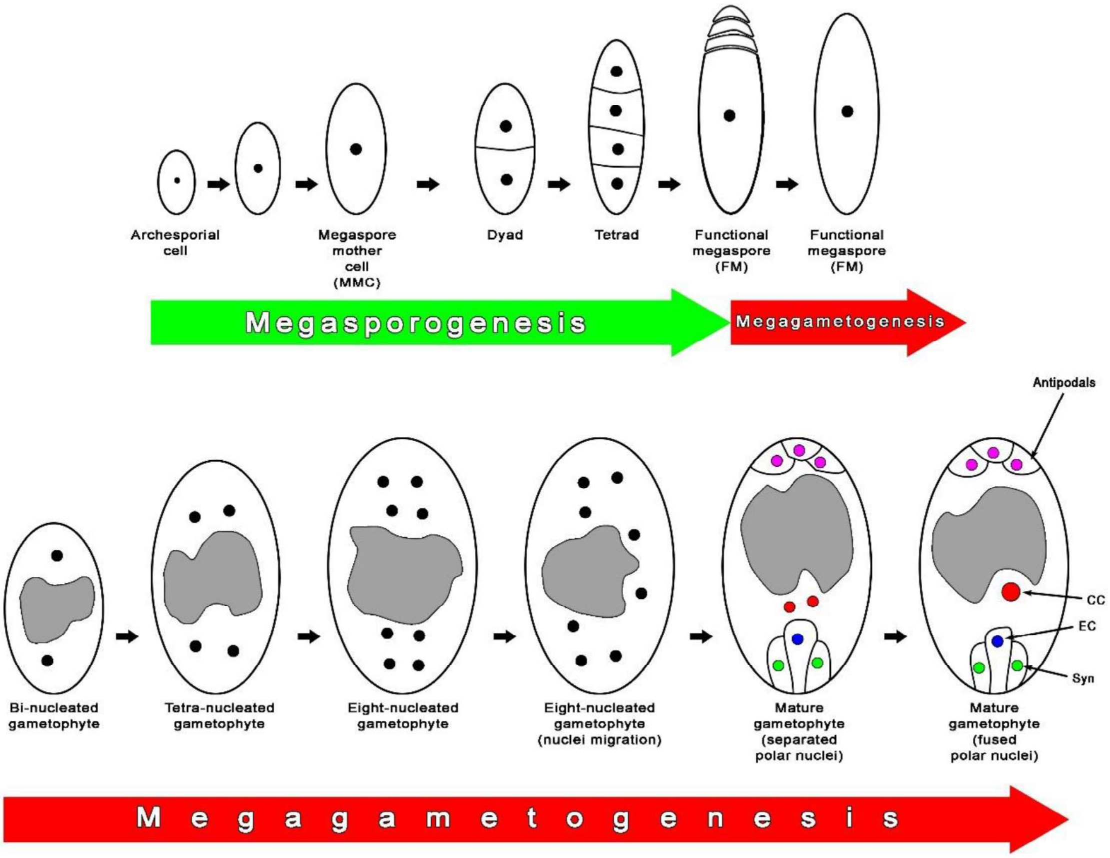

Figure 3. Representation of the Polygonum type female gametophyte development. CC = central cell; EC = egg cell; Syn = synergids. (Drews and Koltunow, 2011b) modified.

The first step of this process is the formation of ovule primordia as finger like projections coming out from the placental tissue of the pistil (Figure 26 B). One subepidermal sporophytic cell of the primordium differentiate into an “archesporial initial” that will increase in size becoming the megaspore mother cell (MMC). MMC increases in size occupying a big part of the distal portion of the ovule and finally undergoes meiosis giving origin to a tetrad of megaspores. Three of them will degenerate leaving only one survivor meiotic product; the functional megaspore (FM) (Drews and Koltunow, 2011a). The process that starts with the MMC and through meiosis leads to the formation of the functional megaspore, is called megasporogenesis.

It is important to note that in Arabidopsis and many other species (including *Boechera spp.* and *Hypericum spp.*), the archesporial cell differentiates directly into the MMC so it is possible to argue that there is no functional difference between an archesporial cell and a megaspore mother cell (Drews and Koltunow, 2011a).

The functional megaspore represents the beginning of the haploid generation in the diplobiontic life cycle of an angiosperm and from it starts the second part of the female gametophyte development called megagametogenesis (Drews and Koltunow, 2011a; Grimanelli et al., 2001).

Megagametogenesis starts with a first free-nuclear mitotic division of the functional megaspore with consequent formation of a binucleate female gametophyte. The two nuclei of the female gametophyte migrate toward the poles (micropylar and chalazal) of the ovule and are typically separated by a small vacuole. These 2 nuclei simultaneously undergo other two free nuclear mitotic divisions and this leads to the formation of an 8-nucleate haploid gametophyte comprising 4 cells at the micropylar pole and other 4 at the chalazal one (Drews and Koltunow, 2011a).

One nucleus per pole, with the help of a dedicated cytoskeleton, migrates to the central region of the ovule forming the pair of polar nuclei. Polar nuclei fuse together giving origin to the central cell (CC); one of the two gametes (the diploid one) arising from the megagametogenesis. The three nuclei at the chalazal pole constitute the antipodals (Ad). Their developmental fate is one of the most variable traits among angiosperms. In many species including for instance Arabidopsis thaliana they degenerate at late stages of embryo sac development. In other species such as grasses they strongly proliferate giving rise to a mass of cells with putative nutritive functions (Friedman et al., 2003).

In summary, the essential processes of gametophyte development are: formation of the megaspore mother cell, meiotic reduction, selection of the functional megaspore and apoptotic abortion of the three remaining tetrads, three haploid mitotic divisions leading to eight nuclei, spatial rearrangements of the nuclei, polar nuclei fusion and cellularization, formation of the two gametes, the homodiploid central cell and the haploid egg cell ready for double fertilisation.

It is important to remark that the female gametophyte is completely embedded into the maternal sporophyte and the described process is highly integrated with the development of the surrounding sporophytic tissues of the ovule (Pagnussat et al., 2009; Figueiredo and Köhler, 2016).

At the MMC stage the ovule starts to show primordia of outer and inner integuments and by the time of the FM formation, the ovule highly increased its size and starts to bend the funiculum, a tissue that connect the ovule with the placental tissue, assuming the anatropous position with the micropyle facing the funiculum. At female gametophytic maturity, the ovule has reached its maximum size and is completely embedded in the inner and outer integuments like in the case of species with bitegmic ovules such as *Arabidopsis thaliana*.

It is important to remark that ovule development inside the pistil is not perfectly synchronized but an acropetal developmental gradient is observed in most cases with older and bigger ovules in the basal portion of the pistil and earlier developmental stages in the stigmatic region; this is an important aspect to be considered in this study.

Fertilization and embryogenesis

The formation of the mature female gametophyte is followed by pollination. Male gametes are the result of a developmental process called microsporogenesis. This process starts with the division of a diploid sporophytic cell in the anther originating one tapetal initial and a pollen mother cell (PMC) (McCormick, 2004). The pollen mother cells undergoes meiosis resulting in the formation of tetrads that are soon released as single haploid microspores due to the action of the enzyme callase. Every uninucleate microspore undergoes an asymmetric mitotic division that leads to the formation of a binucleate pollen grain with the small generative cell completely enclosed into the bigger vegetative cell. In most of the plant species this is the stage at which the pollen grain is released from the anther and can pollinate the pistil by reaching the stigma and growing a pollen tube inside the pistil.

During the growth of the pollen tube the generative cell undergoes mitosis and by the time the tubule reaches the micropyle of an ovule, two sperm nuclei are already formed, (McCormick, 2004).

Next step after pollination is double fertilization of the ovule. The pollen tube, most probably guided by specific micropylar secretions, penetrate into the embryo sac (gametophyte) provoking the degeneration of one of the two synergids and releasing the two sperm nuclei. One of them fertilizes the egg cell creating a diploid zygote that starts to proliferate through repeated mitotic divisions with formation of the diploid embryo that represents the beginning of a new sporophytic generation (Hafidh et al., 2016).

At the same time the second sperm nuclei fertilizes the homodiploid central cell which giving origin to the endosperm, a syncytial triploid tissue essential for the further development of the embryo. Depending on the species, the endosperm will eventually cellularize and differentiates into an outer cell layer, the enzymatically active aleurone, and a more central vacuolar storage endosperm (Berger, 1999).

The alternative developmental pathway of apomixis

The above described processes characterize the majority of species that adopted a Polygonum type female gametophyte developmental pathway. However, sexuality is not the only way of reproduction that evolved in plants.

Several species of Angiosperms and Gymnosperms show an asexual way of reproduction via seed described as apomixis.

Apomixis can be shortly defined as the formation of a seed from the maternal tissues of the ovule, avoiding the processes of meiosis and fertilization and leading to the development of an embryo (Bicknell and Koltunow, 2004)

Apomixis can occur through different developmental processes but all of them should have three main developmental traits in common (Koltunow and Grossniklaus, 2003):

1. Absence of meiosis
2. Formation of an embryo without fertilization of the egg cell (parthenogenesis)
3. Formation of a functional endosperm with or without fertilization of the central cell (pseudogamous and autonomous endosperm, respectively)

There are two main types of apomixis: the sporophytic and the gametophytic apomixis (Drews and Koltunow, 2011a). Sporophytic apomixis is typical of many species of the genus *Citrus* and consists in the proliferation of a somatic cell of the nucellus (maternal sporophytic tissue) that through mitosis and completely skipping the gametophytic phase, gives origin to a diploid embryo genetically identical to the maternal sporophyte (Bicknell and Koltunow, 2004). Gametophytic apomixis on the other hand is characterized by the formation of an unreduced female gametophyte that can be originated via diplospory or via apospory (Bicknell and Koltunow, 2004).

In diplospory the developmental process seems morphologically identical to the sexual one until the stage of MMC. In sexual reproduction this cell undergoes meiosis with formation of a tetrad of haploid cells one of which survives and becomes the haploid functional megaspore (FM). In diplospory MMC fails to undergo normal meiosis and rather undergoes a modified meiosis called apomeiosis in which there is only one instead of two meiotic divisions. A diplosporic development is characterized by the formations of dyads instead of tetrads and by an unreduced diploid functional megaspore that through 3 mitotic divisions leads to the formation of an 8-nucleate 7-celled female gametophyte with a diploid egg cell and a tetraploid central cell. At this stage the egg cell starts to divide without being fertilized with consequent formation of an embryo (parthenogenesis). The central cell on the other side may or may not need fertilization. In the first case there will be the formation of a pentaploid (if pollinated with a haploid sperm cell) or a hexaploid (if pollinated with a diploid unreduced sperm cell) pseudogamous endosperm; otherwise, in the absence of central cell fertilization a tetraploid autonomous endosperm is formed.

Apospory is another type of gametophytic apomixis. Here a sexual gametophyte normally develops but at some point one or multiple somatic cells start to proliferate initiating the development of one or more diploid somatic gametophytes. This dividing cells are referred to as aposporous initials (AI) and, as described in several aposporous species, they can differentiate at different developmental stages.

The formation of an aposporous gametophyte even in later developmental stages, implies that the sexual and the aposporous gametophytes can coexist, nevertheless this is most of the times a transitory condition that may end with the death of the sexual gametophyte and its replacement by the aposporous one. Aposporous initials are thought to behave as a functional megaspore.

It is currently unclear if the differentiation of the AI is triggered by some developmental defect of the sexual female gametophyte or if the AI forms an aposporous gametophyte that crushes the sexual one taking its place. This is one of the biological question that this study tried to answer.

Hypericum perforatum a brief description

Hypericum perforatum has been chosen as a model species for the study of apospory during this PhD project.

This species belongs to the family Hypericaceae that includes 9 genera: *Cratoxylum, Eliea, Harungana, Lianthus, Santomasia, Tornea, Triadenum, Vismia* and *Hypericum* (Crockett and Robson, 2011). The last one includes about 80% of the diversity of the family and has been studied from a morphological and biochemical point of view in order to get a clear classification of the nearly 500 species belonging to it (Crockett and Robson, 2011; Nürk et al., 2013a).

The genus *Hypericum* is mainly composed by perennial herbs (in rare cases is also found in the form of trees or shrubs) and it is distributed all around the world (with the exception of Antartica) showing a high capacity of adaptation to all kind of conditions with the exception of extremely cold, hot or dry environments (Nürk et al., 2013b).

The inflorescence is a double helicoid cyme (bostryx). The flowers are hermaphrodites with a calyx composed of 5 fused sepals, a corolla composed of 5 yellow petals (the yellow color of the petals is very peculiar of the genus *Hypericum* within Hypericaceae) (Crockett and Robson, 2011), the ovary is superior and is most of the times 3-merous (3 carpels) with few exceptions where it has been observed to be 2or 4-merous (Rizzo, own observation).

Above the ovary, the pistil has one independent style for every carpel so normally 3 independent styles ending with magenta stigmas are easily visible in the open flower.

The stamens are more than 10 and organized in fascicles with anthers that are typically dehiscent at the stage of open flower. In summary the floral formula is K(5) C5 A∞ G(3).

The fruit is a dehiscent capsule containing cylindrical seeds (Crockett and Robson, 2011) and at maturity more than 100 seeds can be contained in one capsule.

One very important trait of *Hypericum perforatum* is the presence of two kind of glands: pale (or translucent) glands and dark (or red) glands. These structures are present in many organs (Soelberg et al., 2007).

Leaves are often characterized by the presence of several pale glands all over the lamina and they give the visual effect of a perforated leaf from which comes the name "*perforatum*" (Ciccarelli et al., 2001).

Dark glands may be present in different organs (Figure 4) all over the plants: e.g. leaf lamina or most frequently leaf rim, in the petals, in the sepals in the anthers or other tissues depending on the analyzed line.

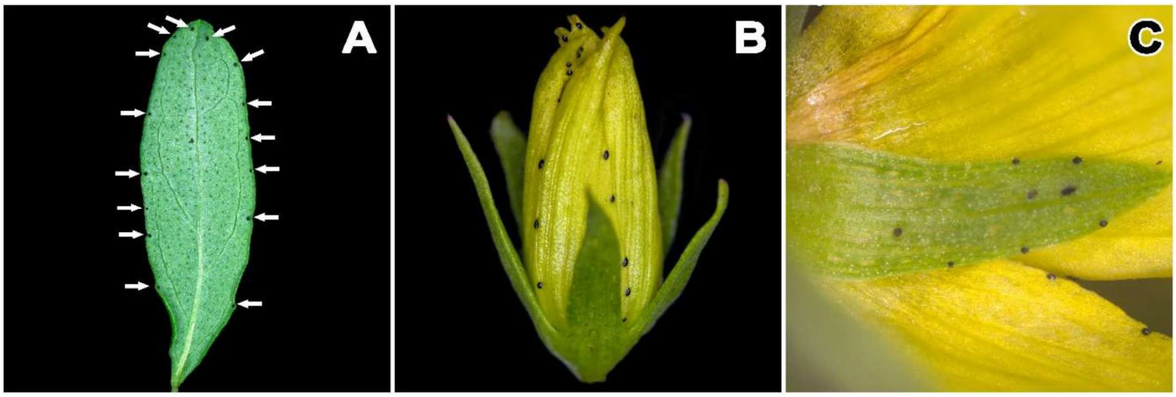

Figure 4. Dark glands in *Hypericum perforatum*. A: dark glands preferentially located in the leaf rim (highlighted by white arrows); B: dark glands on the petals of a flower bud; C: dark glands on the sepal of an open flower.

The importance of these glands is connected to the accumulation of special secondary metabolites. The dark glands accumulate hypericin, whereas hyperforin is found in the pale glands (Piovan et al., 2004; Soelberg et al., 2007). These compounds are the reason for the pharmaceutical interest in the species and are in the focus of several metabolomic studies. Hyperforin has been used for the treatment of mild forms of depression (Stevinson and Ernst, 1999). Although recent studies have challenged the efficacy of the extract, the species remains in the focus of pharmaceutical research due to possible application of hypericin as labelling drug useful in cancer research and therapy (Garg et al., 2010). Moreover, promising recent observations suggest that extracts of *Hypericum perforatum* might be beneficial for the treatment of Alzheimer disease (Hofrichter et al., 2013). Many aspects of these applications require further analysis. Nevertheless, products derived from *Hypericum perforatum* are among the top ten of the best-selling plant dietary supplements in the US, and Germany alone moves a business of over 70 million Euros (Crockett and Robson, 2011). The genus *Hypericum* presents cases of apomixis and more precisely apospory.

Matzk et al. described apomixis in 16 species of the family Hypericaceae but only one (*H. scabrum*) is an obligate apomictic (Matzk et al., 2001; Pank et al., 2003) while in *H. perforatum* apomixis is facultative ranging from very high levels close to 100% until predominant sexuality with apomixis levels under 5% (with a lot of intermediate cases).

The basic chromosome number is n=2x=16 for the diploids but in most cases tetraploid and hexaploid lines are detected.

The origin of apomixis in *Hypericum* is a debated topic but recent studies showed molecular evidence that apomixis evolved at least 4 times and independently in Hypericaceae with one event in the clade *Triadenum*, 1 event in the clade *Ascyreia* and 2 events in the core *Hypericum* clade (Nürk et al., 2013a).

The Genus *Boechera*, a brief description

The genus *Boechera* has been used during this work as a model for the study of diplospory. This genus belongs to the family of Brassicaceae and includes over 80 species (Dobeš et al., 2004). It originated in northern America and Greenland and includes sexual and apomictic (aposporic and diplosporic) lineages naturally distributed over a broad variety of environments (from lowlands to high mountains) and adapted to very variable conditions ranging from dry deserts to very humid habitats (Dobeš et al., 2004).

The species that has been adopted in this study as a reference for the comparison with all other *Boechera* species is the diploid sexual *Boechera stricta*. This species is characterized by a basal rosette of leaves 5 to 8 cm long topped by a stem about 80 cm tall and carrying the inflorescences at its extremity. Inflorescence is a non-bracted raceme. Flowers are bisexual with: 4 sepals, 4 free (normally white) petals, 6 anthers (lower numbers are sometimes observed) and a dimerous gynoecium that after pollination develops into a 2-valved silique (up to 8 cm long) carrying a number of small seeds (1-2 mm long) that can range from under 60 to over 100 organized in two rows. Other species like *Boechera divaricarpa* or *Boechera gunnisoniana* show relevant differences with *B. stricta* like the presence of a branched stem and a higher number of inflorescences per plant.

Boechera stricta has a very high level of autogamy as most of the other species of this genus used during this study (e.g. *B. divaricarpa* and *B. gunnisoniana*).

The use of *Boechera* as a model genus has several advantages like the close relationship with the model plant *Arabidopsis thaliana* (Song et al., 2006; Schranz et al., 2006, 2007) that makes many traits easily comparable between the two species. Furthermore, apomixis is a trait most of the times associated with polyploidy meaning that in other genera the comparison between sexual and apomictic individuals implies a comparison between diploids and polyploids with consequent higher complexity of the information deriving from such comparison. In the case of the genus *Boechera*, there are some exceptions to the association between apomixis and polyploidy in fact there are species like *Boechera divaricarpa* that are apomictic even if diploid and this opens the possibility to less problematic comparison between diploid sexual and diploid apomictic individuals.

The base chromosome number of the genus is X=7 with an estimated genome size of 260 Mb for the diploid *B. stricta*. (Mitchell-Olds, 2001; Gebauer-jung et al., 2006)

The big interest for the genus *Boechera* led to a big number of scientific studies that tried to give an answer to some important questions about the molecular basis of apomixes. Its evolutionary history, the association between apomixis and polyploidy, the existence of low recombination apomictic loci, the role of B chromosomes in apomictic plants, the adaptive implications of apomixis, the developmental peculiarities of apomictic plants and several other questions, some of which have been object of interest during this study.

Aims of this study

This study was conceived with the intention to provide meaningful progress in the understanding of apomixis, by performing a deep comparative morphological and molecular analysis of the sexual and asexual developmental processes. Progress in this field is essential in order to move further steps toward the establishment of the apotechnology that modern agriculture needs in order to face the increasing food security challenges.

Two different model organisms were chosen for the study of diplospory and apospory, *Boechera spp.* and *Hypericum spp.*, respectively.

The **first aim** of this study was the identification of the most relevant morphological differences between the sexual and apomictic female gametophyte development. In order to achieve this, an in-depth histological characterization of the female gametophytic development was performed by analyzing ovules from a number of sexual and apomictic lines at defined developmental stages. The informations derived from that characterization, were intended to understand whether in the aposporous *Hypericum spp.* the differentiation of aposporic initial cells is a cause or a consequence of the failure of sexual female gametophyte development.

A **second aim** was to understand whether the apomictic pathway represents an advantage or a disadvantage for these two model organisms. In order to answer this question, fitness-connected traits like germination rates, seedset and flowering time, were evaluated.

A **third aim** of this study was to better understand the ploidy dynamics of apomictic lines in comparison with the sexual ones. Apomixis is many times associated with polyploidy (Lovell et al., 2013; Matzk et al., 2003; Bicknell et al., 2000; Schranz et al., 2005). In order to understand if these two model apomictic organisms have more relaxed constraints on the control of ploidy levels, several ploidy measurements on specific tissues were carried out in a number of sexual and apomictic lines across multiple generations.

Finally, the **fourth aim** of this study was to produce novel knowledge regarding the molecular basis of apomixis through deep transcriptomic analysis of ovules at multiple developmental stages in apomictic and sexual lines that would allow selecting genes putatively connected with the apomictic pathway. This selection was performed linking transcriptome data analysis with the information derived from the morphological characterization. In this way, it is possible to connect specific developmental anomalies detected in apomicts with specific expression patterns detected in certain stages of ovule development.

Materials and methods

Plant material

The *Boechera spp.* lines used in this study, were provided by Dr. Amal Johnston, a former member of Gene Regulation group at IPK-Gatersleben.

The *Hypericum* plant material was provided by the Gene Regulation group and the Apomixis group at IPK-Gatersleben and by Prof. Marcus Koch from the Center for Organismal Studies in Heidelberg. A list of the lines used for this study, is given in Table 24 (supplemental data).

Seeds germination and growth conditions (*Hypericum spp.*)

Mature dry seeds of *Hypericum spp.* were vernalized in sterile water for 10 days in darkness, at a temperature of 4 °C and directly put to germinate in soil without any sterilization. Germination was induced by sowing 50 seeds in a 12x10 cm pot at a depth of 1 cm in a growth chamber with long day conditions (16 hours of light) with light intensity of 250 µmol (sec^{-1} m^2) at a temperature of 21°C during day hours and 18 °C during darkness. Humidity levels were kept as high as possible by using germination capsules with translucent caps.

After 4 weeks in the growth chamber the seedlings were transferred in 6x6 cm pots containing soil (3 parts of peat, 1 part of Klasmann substrate1, 1.5 parts of sand) and moved to greenhouse conditions with illumination from 6 am to 10 pm (300-400 µmol (sec^{-1} m^2)), 21 °C during the day and 17 °C during the night with average humidity of 70%.

After 3 weeks in the greenhouse plants were placed in bigger pots (16 x 15 cm) containing the above mentioned soil mix.

After 12 weeks at greenhouse conditions flowering was induced by switching to absolutely standardized conditions by the use of a phytotron with 16 hours of light (400-450 µmol (sec^{-1} m^{-2})) and temperatures of 23 °C during the day and 18°C during the night with constant humidity of 70%. These standardized conditions were necessary in order to minimize variations in the transcriptomics profiles that could be associated to environmental differences.

A minimum of 30 plants per line were grown at the same time in pots at field conditions with the purpose of producing seed (field guarantee adequate pollination levels) and detecting eventual phenotypic differences between plants grown in greenhouse and field conditions.

Germination rates of *Hypericum* were calculated per line and analyzed for statistical differences through a multifactorial ANOVA on data transformed through the equation: $arcsin\sqrt{y}$ and following conversion to degrees. Comparisons of means was performed through a Tukey test. The aforementioned procedure was made by using the statistical software InfoStat vr 2015, InfoStat Group (www.infostat.com.ar).

Flowering time after germination was evaluated for each line in two generations. Statistical analysis was performed with a Kruskal-Wallis test using the statistical software InfoStat vr 2015, InfoStat Group (www.infostat.com.ar).

Cuttings (*Hypericum spp.*)

After obtaining adult plants, cuttings were performed on these plants in order to continue to work on genetically identical material avoiding in this way the disadvantage of free pollination and segregation normally present at significant percentages even in many apomictic lines.

Vegetative propagation was obtained using portion of stems of about 1 cm explanted from adult plants.

Explants have been immerged in water and immediately treated with Rhizopon® powder (to induce root formation). The treated cuttings were grown in 6x6 cm pots containing the afore mentioned soil mix in long days (16h light) conditions at a constant temperature of 20 °C and at a constant humidity of 70%.

This protocol was successful in more than 90% of the cases independently from the propagated line.

Seed germination and growth conditions (*Boechera spp.*)

Mature dry seeds of several *Boechera* lines were sterilized by treatment with 70% ethanol for 2 minutes, 5% Sodium hypochlorite for 10 minutes and 6 washes with sterile distilled water (2 times 2 minutes, 1 time 5 minutes and 3 times 10 minutes).

The sterilized seeds were vernalized in water (from the last wash) at 4 °C for a period of 3 weeks in darkness.

After vernalization, 50 seeds were plated on petri dishes containing MS medium and kept for 4 weeks in a growth chamber with long day conditions (16 hours of light) with a temperature of 23 °C during the day and 18 °C during the night at an average humidity of 70%.

After 4 weeks in the growth chamber, the majority of the viable seeds had already germinated and the resulting seedlings were transferred in 6x6 cm pots containing soil (3 parts of peat, 1 part of Klasmann substrate 2, 1,5 parts of sand) and placed in a greenhouse at long day conditions (artificial light from 6am to 10pm) with a temperature of 18 °C during the day and 16 °C during the night at an average humidity of 70%. The artificial light of this greenhouse had an intensity between 250 and 300 µmol (sec^{-1} m^{-2}).

After the first 4-5 weeks in these conditions, plants were transferred to bigger pots (12x10 cm) and remained there until the end of their cycle.

It is important to mention that right before the transfer of seedlings into the pots, a screening of germinated seeds was carried out in order to collect data about the germination rate of every line. The progeny of three plants per line have been followed for three generations screening when possible 900 seeds over three generations for every analyzed line.

Germination rates of *Boechera* were calculated per line and analyzed for statistical differences through a multifactorial ANOVA on data transformed through the equation: $arcsin\sqrt{y}$ and following conversion to degrees. Comparisons of means was performed through a Tukey test. The aforementioned procedure was made by using the statistical software InfoStat vr 2015, InfoStat Group (www.infostat.com.ar).

Flowering time after germination was evaluated for each line in each analyzed generation. Statistical analysis was performed with a Kruskal-Wallis test using the statistical software InfoStat vr 2015, InfoStat Group (www.infostat.com.ar).

Seed set analysis (*Boechera spp.*)

In order to determine the levels of sterility of every line, 5 siliques per plant for 5 plants per line were screened for seed set. The analysis was conducted by separating the two halves of a semi dry silique using a small scalpel under a Stemi2000 Zeiss Stereomicroscope. Seeds in the silique were counted and visually classified in three possible categories (Figure 5):

1. Fertile (normally developed seeds still green and turgid).
2. Infertile (very small and white).
3. Aborted (small to medium size, brown color, they have a shrunk appearance).

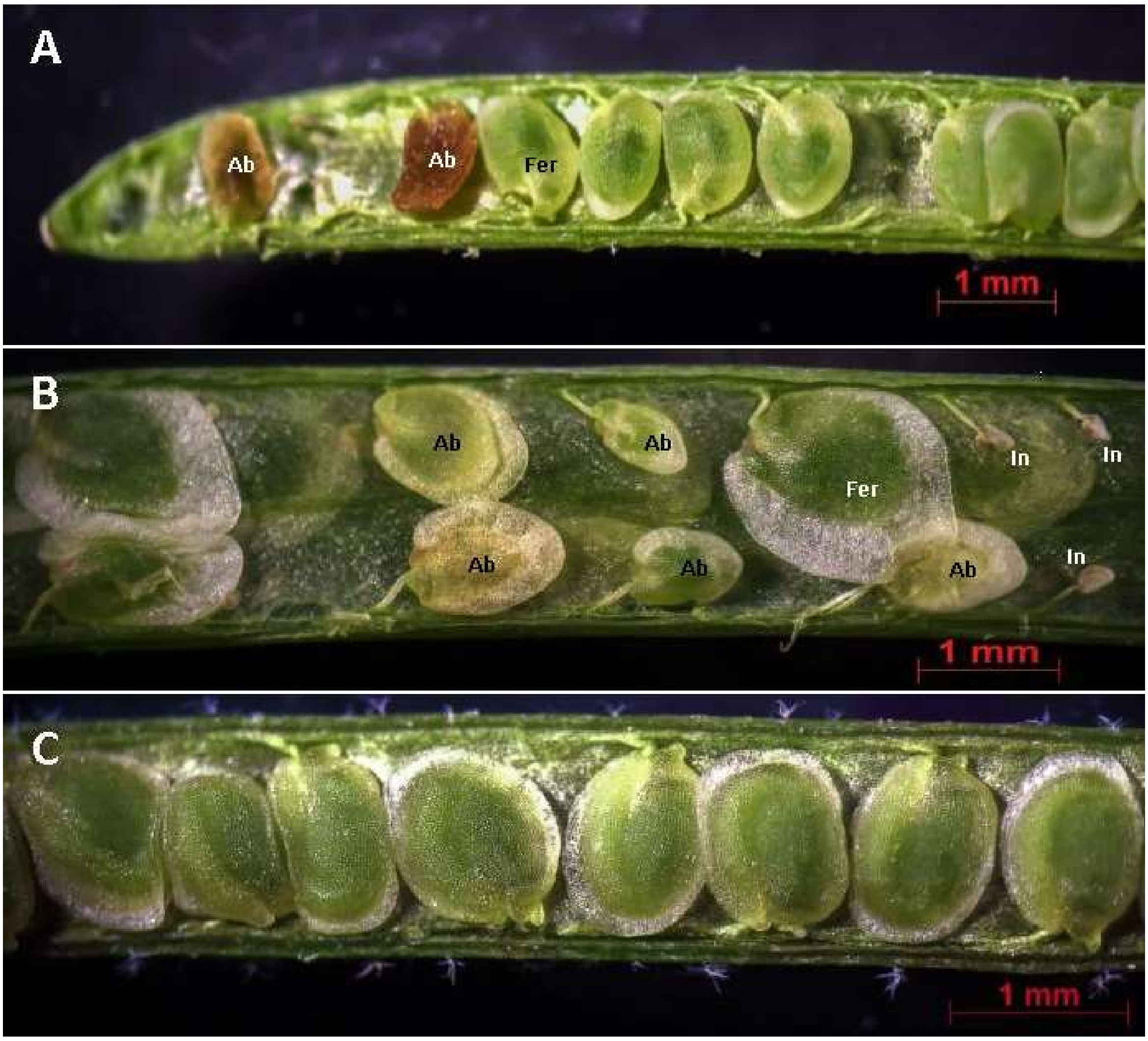

Figure 5 Examples of criteria for seed set evaluation in Boechera spp. A: silique showing aborted seeds (Ab). B: Silique showing Fertile (Fer) Aborted (Ab) and Infertile (In) seeds. C: Silique with 100% fertile seeds

Trends of seed set levels in association with reproductive way and ploidy levels were determined by calculating the percentages of sterility (Infertile + Aborted) and its complementary (Fertility).

Seed set analysis in *Hypericum* lines

The analysis of seed set in *Hypericum* was performed on 16 lines across two generations. Plants used for this analysis were grown under field condition due to the entomophily of this genus that requires the presence of active pollinators. The seed classification adopted for this analysis was performed following the same method described for *Boechera spp.*

Statistical data analysis of seed set for both *Boechera* and *Hypericum* was performed through a multifactorial ANOVA on data transformed through the equation: $arcsin\sqrt{y}$ and following conversion to degrees. Comparisons of means were performed through a Tukey test. The aforementioned procedure was made by using the statistical software InfoStat vr 2015, InfoStat Group (www.infostat.com.ar).

Number of siliques or capsules per plant

Number of siliques or capsules per plant were counted in each line of both *Hypericum* and *Boechera* across the generations used for this study. Statistical data analysis was performed through a multifactorial ANOVA. Comparisons of means were performed through a Tukey test. The aforementioned procedure was made by using the statistical software InfoStat vr 2015, InfoStat Group (www.infostat.com.ar).

Potential fitness calculation

In order to calculate the fitness potential of every analyzed line in *Hypericum* and *Boechera*, average values of: germination rates ($\bar{x}_{gr}$), average number of fertile seeds per capsule / silique ($\bar{x}_{fspslq}$) and average number of capsules / siliques per plant ($\bar{x}_{slqpp}$) were multiplied with each other.

The following is the resulting equation used for the evaluation of fitness potential in *Hypericum* lines. For *Boechera spp.* same logic was applied.

$$Potential\ fitness = \bar{x}_{gr} * \bar{x}_{fspslq} * \bar{x}_{slqpp}$$

Equation 1. Potential fitness calculation for *Hypericum spp.* and *Boechera spp.*

The potential fitness was also corrected by taking in account the flowering time (*FT*)-of each line. This resulted in the following equation that calculates the Flowering time-corrected potential fitness $PF_{(FT)}$ where *PF* is the potential fitness value from the previous equation and *WD* is the number of days of the warm season.

$$PF_{(FT)} = PF * \frac{WD}{FT}$$

Equation 2. $PF_{(FT)}$ = Potential fitness (flowering time corrected); *PF* = Potential fitness value (*Figure 11*); *WD* = warm season days (given standard value of 180 days); *FT* = flowering time (days after germination).

Ploidy analysis

Measurements of ploidy have been performed on young leaves and mature dry seeds.

Partec CyFlow Space flow cytometer equipped with UV led light and green laser have been used for the majority of ploidy measurements on *H. perforatum* and Boechera.

More specifically the UV LED lamp (375 nm wavelength) coupled with an appropriate filter has been used in order to detect the fluorescence of DAPI dyed material while the green laser light (wavelength 532 nm) coupled with appropriate filter has been used in order to detect Propidium Iodide (PI) fluorescence.

In some other cases, when higher accuracy was needed (for example genome size measurements), the BD FACS Aria IIu flow sorter was used. In this last case the used dye was always PI and the excitation light was provided by a blue laser (wave length 488 nm) coupled with a 610/620 filter.

Leaves samples were always processed by chopping them repeatedly for about 30-40 seconds with a razor blade in 300 µl of MA VI buffer containing DAPI (Table 12 supplemental data). After the chopping, other 700 µl of buffer were added and after a brief filtration using 30µm Partec CellTrics filters, samples were finally loaded in the Partec CyFlow Space. Seeds were chopped for 60-80 seconds and were subjected to the same procedure with the difference that Propidium Iodide (and not DAPI) was used as dye (Table 13 supplemental data).

Ploidy analysis of seeds (Flow Cytometric Seed Screen = FCSS) was carried out in order to detect the different ploidy levels of embryo and endosperm and from this derive the reproductive mode (sexual or apomictic) that lead to the formation of the analyzed seed (Matzk et al; 2000).

When accurate genome size calculation was necessary, a sample of *Raphanus sativus* leaf was used as reference therefore mixed with the analyzed *Boechera* or *Hypericum* tissue.

Hypericum spp. female gametophyte morphological analysis

In order to achieve a detailed morphological characterization of the female gametophyte development in *Hypericum*, all the flower buds from a minimum of three inflorescences per line coming from different plants were dissected.

Dissections were always performed under a Zeiss Stemi 2000-C stereo microscope.

The length of every flower bud was measured using the Axio Vision SE64 v4. Software from Zeiss coupled with a Cc5 Zeiss Digital Camera.

After size measurements, pistils were manually isolated from the flowers using 0,4mm hypodermic needles and kept overnight at 4°C in Farmer's fixative (3:1 Ethanol:Glacial Acetic Acid).

The following day, fixative was pipetted off and immediately replaced with 90% ethanol. After 1 hour, 90% ethanol was replaced with 70% ethanol. Samples were kept at 4°C in 70% ethanol for a minimum time of 1 hour up to several days (samples is quite stable at this stage). When ready for the next step, ethanol was replaced with clearing solution (Table 14 supplemental data). Samples were kept at 4 °C in clearing solution until they completely sunk. This required a minimum clearing time of 12 hours (overnight); nonetheless, bigger pistils required longer clearing time; as a consequence, pistils coming from open flowers had to be kept in clearing solution for a time of 7 to 9 days. When the clearing was complete the tissues lost all the chlorophyll and looked semitransparent.

Cleared pistils were dissected on microscope slides in a drop of fresh clearing solution and ovules were isolated with hypodermic needles (0,3mm of diameter).

Pistil tissues were carefully removed from the slides in order to keep only the free ovules. The samples were covered with a coverslip and observed at a Zeiss Axioplan 2 microscope using a DIC II filter. Every slide contained ovules from one pistil.

All the ovules visible on every slide were morphologically characterized taking in consideration: ovule size, inner and outer integument development, funiculus bending (start of anatropous development) and above all female gametophyte developmental stages.

All the developmental stages starting from archesporial cell until seven nucleated mature female gametophyte were recorded on a phenotyping table. The parameters included in this table were the following ones:

- Flower bud size
- Pre-archesporial cell
- Archesporial cell
- Megaspore mother cell + small integuments
- Megaspore mother cell + medium integuments
- Megaspore mother cell + big integuments
- Multiple megaspore mother cell
- Aborted
- Aposporous initial + small integuments
- Aposporous initial + medium integuments

- Aposporous initial + big integuments
- Dyads
- Tetrads
- Functional megaspore
- Multiple functional megaspore
- Binucleated gametophyte
- Tetranucleated gametophyte
- 8 nucleated gametophyte
- Mature gametophyte
- Embryo
- Other

Relative frequencies of the above mentioned stages were calculated.

Differences in gametophytic developmental speed and ovules synchronization between sexual and apomictic lines were underlined by using heat maps of the relative frequencies on every phenotyping table.

Finally, these phenotyping tables were used to determine the frequency and timing of aposporous initial formation, a critical developmental point for this study.

Boechera female gametophyte morphological analysis

All the flower buds from a minimum of 3 inflorescences per line from different plants were dissected and pistils were fixed, dehydrated and cleared following the same procedure used for *Hypericum spp*. In the case of *Boechera*, pistils are quite small if compared with *Hypericum* so the maximum clearing time was limited to 48 hours.

Slides preparation and DIC microscopy observations were carried out following the same procedure described for *Hypericum*.

Morphological characterization of female gametophyte development was performed using the same methodology of *Hypericum* however, in this case the phenotyping table was customized in order to fit the diplosporic reproductive mode of apomictic *Boechera* lines (e. g. aposporic initital stages typical of *Hypericum* but absent in the *Boechera* lines, were removed from the table).

Also in this case like in *Hypericum*, main developmental differences were highlighted using heat maps representations (see results).

Ovules dissection (*Hypericum perforatum*)

Ovule developmental stages were characterized and associated with flower bud size through a deep characterization work performed on 2 sexual diploid lines (HyPR_1 and HyPR_3) and 2 apomictic tetraploid lines (HyPR_5 and HyPR_9).

Flower buds were harvested and measured one by one with an electronic caliper under a stereomicroscope and several classes of size have been collected for every processed line.

Pistils were removed from every flower bud and preconditioned in 70% ethanol at 4°C.

The size classes are reported in Table 1.

For every line, 10 classes of flower bud size have been collected (40 samples in total). Every sample was constituted by a number of ovules in the order of thousands that would guarantee to obtain enough RNA to be used for cDNA libraries preparation and Illumina high throughput sequencing without any amplification steps.

Table 1. Flower bud size classes chosen for ovule RNAseq

Line	**Stage Code**	**Flower Bud Size (mm)**
HyPR_1	25	2.5-3.49
HyPR_1	35	3.5-4.49
HyPR_1	45	4.5-5.49
HyPR_1	55	5.5-6.49
HyPR_1	65	6.5-7.49
HyPR_1	75	7.5-8.49
HyPR_1	85	8.5-9.49
HyPR_1	95	9.5-10.49
HyPR_1	105	10.5-11.49
HyPR_1	OF	Open flower
HyPR_3	25	2.5-3.49
HyPR_3	35	3.5-4.49
HyPR_3	45	4.5-5.49
HyPR_3	55	5.5-6.49
HyPR_3	65	6.5-7.49
HyPR_3	75	7.5-8.49

HyPR_3	85	8.5-9.49
HyPR_3	95	9.5-10.49
HyPR_3	105	10.5-11.49
HyPR_3	OF	Open flower
HyPR_5	25	2.5-3.49
HyPR_5	35	3.5-4.49
HyPR_5	45	4.5-5.49
HyPR_5	55	5.5-6.49
HyPR_5	65	6.5-7.49
HyPR_5	75	7.5-8.49
HyPR_5	85	8.5-9.49
HyPR_5	95	9.5-10.49
HyPR_5	105	10.5-11.49
HyPR_5	OF	Open flower
HyPR_9	25	2.5-3.49
HyPR_9	35	3.5-4.49
HyPR_9	45	4.5-5.49
HyPR_9	55	5.5-6.49
HyPR_9	65	6.5-7.49
HyPR_9	75	7.5-8.49
HyPR_9	85	8.5-9.49
HyPR_9	95	9.5-10.49
HyPR_9	105	10.5-11.49
HyPR_9	OF	Open flower

Four out of 10 samples per line were selected to be analyzed via RNA deep sequencing (25, 45, 55 and 65). This resulted in the production of 16 samples in total (4 stages per line over 4 lines) using an Illumina® HiSeq 2500 high throughput system with a depth of sequencing of about $20*10^6$ read pairs per library.

The chosen classes span the part of development going from the formation of the archeosporial cell until the differentiation of the aposporous initial.

Having in mind the different size of the ovules at different developmental stages, the number of ovules per sample was increasing with the decreasing of their average size (Table 2).

Table 2. Estimated number of dissected ovules per samples considering an average number of dissected ovules per pistils equal to 100. Classes highlighted in orange are the ones chosen for RNAseq.

Flower Bud Size	**Number of Plants**	**Number of pistils**	**Number of ovules**
Class 25	30	120	12000
Class 35	30	100	10000
Class 45	30	90	9000
Class 55	30	80	8000
Class 65	30	70	7000
Class 75	30	60	6000
Class 85	30	40	4000
Class 95	30	30	3000
Class 105	20	30	3000
Open Flower	20	30	3000

DNA extraction

In order to use several routine molecular techniques, DNA was extracted from several plants using different protocol for *Boechera* and *Hypericum*.

In the case of *Boechera* a fast DNA extraction was performed using the following "fast extraction protocol".

1. Freeze in liquid nitrogen a young leaf.
2. Grind the frozen tissues with a Retsch® MM400 mill for 120 seconds at 30 oscillations per second.
3. Immediately pipette in the tube 400 µl extraction buffer.
4. Vortex 30 seconds.
5. Centrifuge at 13000 rpm for 2 minutes.
6. Transfer 300 µl of supernatant in a new Eppendorf tube.
7. Add 300 µl of Isopropanol and incubate for 2 minutes at room temperature.
8. Centrifuge at 13000 rpm for 5 minutes.
9. Remove the supernatant.
10. Wash with 200 µl 70% ethanol.
11. Centrifuge at 13000 rpm for 3 minutes.
12. Remove the supernatant and let the pellet dry for 5-10 minutes.

13. Dissolve the pellet in 100 µl TE buffer (Table 15).

One microliter of the resulting DNA solution normally guarantee a good concentration for a 25 µl PCR reaction nevertheless it is advisable to quantify and check the DNA quality via Nanodrop using a working concentration of 20 to 50 ng/µl of DNA.

The previous protocol was not suitable for DNA extraction from *Hypericum* leaves, for this reason DNA from *Hypericum* leaves was extracted with the Invisorb® Spin Plant Minikit following the indication of the producer.

RNA extraction

Transcriptome analyses via RNA deep sequencing and consequent validation via qRT-PCR were core experiments in the frame of this study therefore different tissue samples were prepared following different procedures and RNA has been extracted from vegetative and reproductive tissues of *Hypericum* using different extraction protocols depending on the amount of tissue and content of problematic compounds.

Hypericum leaves were frozen in liquid nitrogen and grinded using a Retsch® MM400 mill for 120 seconds at 30 oscillations per second.

After this first homogenization step, RNA was extracted using the TRIzol® reagent and following the instructions of the producer.

The TRIzol protocol was not suitable for reproductive tissues due to the presence of many dark compounds in the flower. In order to remove the "red compounds" from the reproductive tissues, harvested flowers or flower parts (especially pistils) were vacuum infiltrated with 70% ethanol/ 0.1% TWEEN for 2 to 5 minutes on ice and kept shaking overnight at 4 °C before proceeding with the RNA extraction. This preconditioning allowed to remove most of the red compounds (ethanol solution should be pink after preconditioning) from the collected tissues.

Prior to RNA extraction, the samples were washed twice with fresh 70% ethanol solution.

Afterwards the Invitrap® Spin Plant RNA mini Kit was used following the instructions of the producer including an extra DNAse digestion step.

Independently from the used RNA extraction protocol, all the RNA samples were analyzed with an Agilent 2100 Bioanalyzer and only the samples with very high quality (RIN>9.0) have been used for further application like RNAseq or cDNA synthesis.

cDNA libraries preparation and sequencing

cDNA libraries have been prepared from a starting amount of total RNA comprised between 400 and 1000 ng.

Every library was obtained by following a modified TruSeq RNA v2 protocol from Illumina.

PolyA+ RNA was isolated through affinity chromatography on oligo-(dT) magnetic beads and broken rising the temperature at 94°C for 8 minutes and using divalent lead ions.

First strand cDNA was synthetized using random hexamer primers and the Superscript II reverse transcriptase from Invitrogen. After that the second strand was synthetized at a temperature of 60°C for 60 minutes and the resulting cDNA was purified by: PEG precipitation on beads surface (using magnetic AMPure XP beads), 2 washes with ethanol >99% and final elution in 10 mM Tris-HCl (pH adjusted at 8,5).

cDNA fragments were blunted at 30°C for 30 minutes, purified on AMPure XP beads, A-tailed at 37 °C for 30 minutes and finally ligated to Y-shaped adapters containing P5 and P7 sequences for hybridization on an Illumina flow cell plus specific adapters (necessary to distinguish the different libraries in the flow cell during the run).

The libraries were again purified using AMPure XP beads and DNA fragments containing the adapters were amplified by PCR using a cocktail of primers that anneal with the ends of P5 and P7 (PCR program: 98°C, 30 seconds; 15 cycles (98°C, 10sec; 60°C, 30 sec; 72°C, 30 sec) 72°C, 5 minutes; Hold at 4°C).

Every library was purified using the QiaQuick® PCR purification kit from Qiagen and following the indications of the producer. The resulting samples were ran on a 2% agarose gel containing SYBR® Gold Nucleic Acid Gel Stain (Life Technologies) and the regions of gel containing fragments of 300 to 400 bps were cut and purified with the MinElute PCR purification Kit from Qiagen using the indications of the producer.

After purification, the size of the extracted fragments was validated using a Bioanalyzer 2100 from Agilent. The concentration of each library was confirmed via comparison with qPCR reactions performed on cDNA libraries of known concentration following the indications of the Illumina Sequencing Library qPCR Quantification Guide.

All the indexed libraries were normalized to a 10 nM concentration, loaded into the DCT (Diluted Cluster Template) plate and mixed in equal amounts on the PDP plate.

Libraries were finally loaded into 2 different lanes of the used flow cell.

An Illumina HiSeq-2500 was used for the sequencing of all the samples.

Considering that each lane of the flow cell should guarantee approximately 180 million reads, samples have been loaded with a density of 5 per lane in order to get approx. 35 million paired end reads of 101 bps.

All the loading steps, run monitoring steps, read 2 reagents preparation and loading have been carried on following the TruSeq v3 Run provided by Illumina.

RNAseq data processing

The sequencing run generated a total of 400 million read pairs that were exported in fastq file format and underwent the following preliminary steps:

Quality check

Quality check was performed on all the data set using the free software FastQC following the standard workflow that includes the screening of: per base sequence content, per base GC content, per sequence GC content, sequence duplication levels and Kmer content.

Adapter trimming

In order to cut out the adapter sequences from every read the complete data set was processed with the software "CutAdapt".

A new trimmed dataset was generated and used for the quality trimming step.

Quality trimming

The quality trimming was performed using the CLC workbench (CLC_quality_trim).

In order to keep only very high quality reads, the trimmed reads shorter than 90 bps were discarded (CLC is set on 50 bps by default). Finally, only read pairs (not single reads) with both reads longer than 90 bps were kept in the database and used for the assembly.

Transcriptome assembly

All the trimmed read pairs of the data set were assembled in a unique transcriptome using the "CLC assembler".

Mapping

All the contigs obtained from the assembling process were blasted using the Blastx algorithm vs the assembled genomes of: *Arabidopsis thaliana*, *Ricinus communis*, *Manihot esculenta*, *Populus trichocarpa* and *Linuum usitatissimum*. In order to increase the significance of the BlastX matches, only hits with a length equal or superior to the 30% of the subject were retained in the results.

Calculation of expression levels

Considering that the aim of this experiment was to compare two sexual lines with two apomictic lines of *Hypericum*, two libraries from the sexual lines at a defined developmental stage were always compared with their apomictic counterpart (2 sex vs 2 apo).

Expression levels of every mapped gene were calculated based on the reads number. All the libraries were normalized and corrected for multiple testing following the Benjamini-Hochberg procedure; furthermore, the complete data set was processed using the statistical R package DeSeq2. The algorithm used in this package proved to be stricter in terms of differential expression detection if compared with another method where comparison between libraries was based on normalized reads number. This difference between the two methods is detectable by looking at the corresponding MA plots that in the case of DeSeq2 processed data show a cloud of dots much closer to the zero giving in this way a lower number of events that can be considered differentially expressed in a significant way (Figure 6).

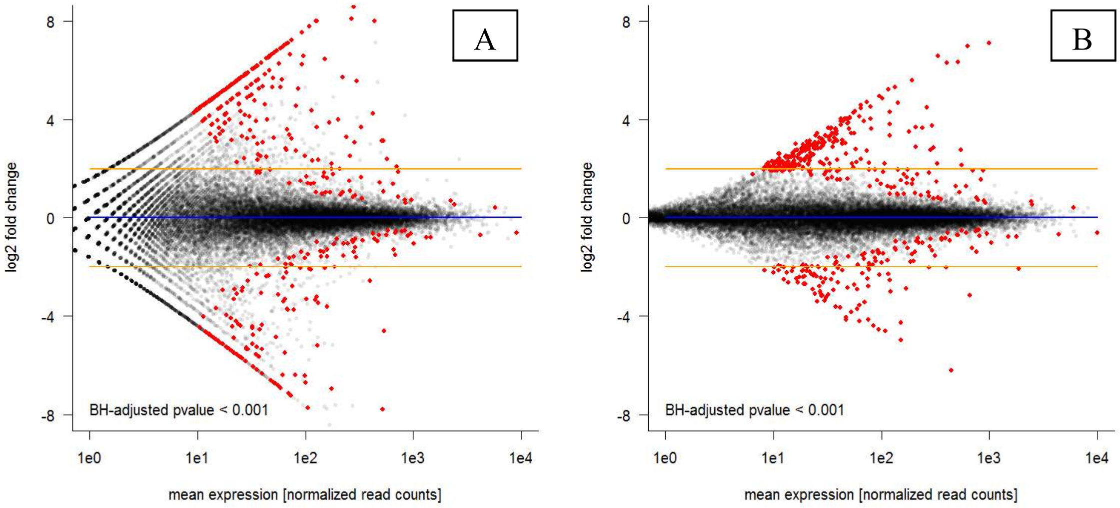

Figure 6. MA plot examples. Raw data vs DeSeq2 processed data

Results

Germination rates (*Boechera spp.*)

Germination rate is one of the key factors that contribute to fecundity and fitness of a plant, therefore collecting data about this parameter clarified more aspects of the real fitness of apomictic lines in comparison to the sexual ones.

With the aim to understand if there is a different trend of germination between apomictic and sexual lines and between diploids and higher ploidy levels, several *Boechera* lines were tested for germination rates.

After performing the factorial ANOVA, it was determined that the generation had no significant influence on the germination rates (P = 0.853748). There were highly significant differences between the lines (P<0.00000001) and no interaction between variables was significant (P = 0.958647). The germination rates for the analyzed lines are given in Figure 7.

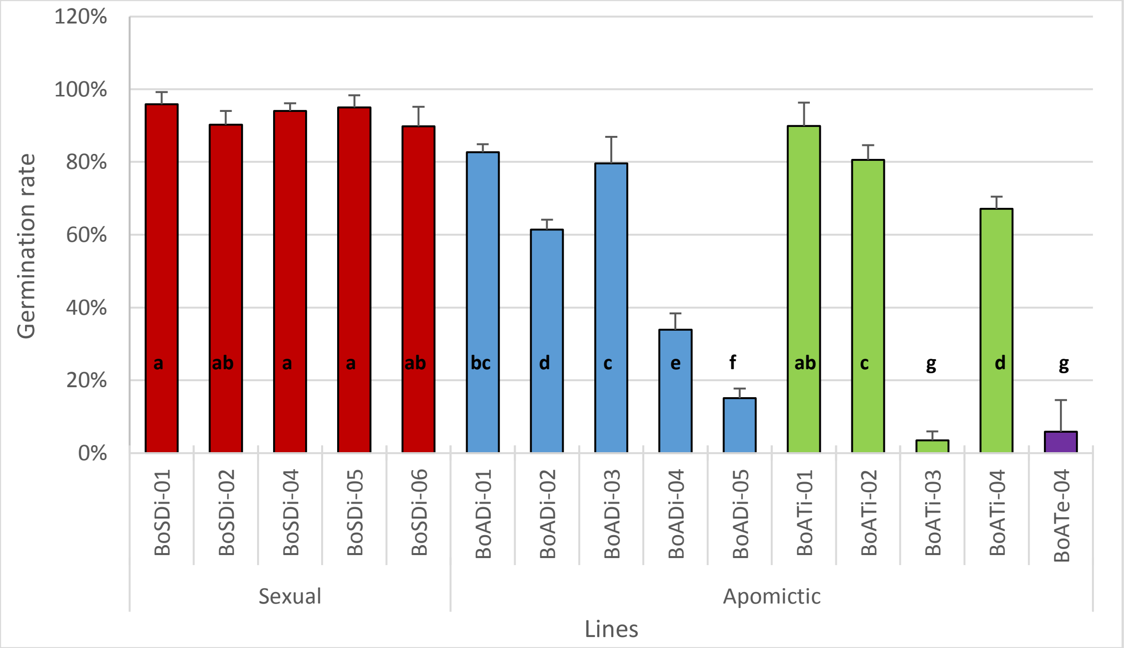

Figure 7. Germinability of seeds from 15 *Boechera spp.* lines over three generations. Red = sexual diploid lines; Blue = apomictic diploid lines; Green = apomictic triploid lines; Violet = apomictic tetraploid line. Different letters = significant differences between the lines according to Tukey test. $R^2 = 0.977$; $P < 0.05$ on transformed data (Arcsin(√y)).

From the results of these experiments emerged a clear trend. Sexual diploid lines produced seeds with a significantly higher rate of germination if compared with the majority of apomictic lines. Sexual lines also show uniform levels of germinability while the apomictic ones are characterized by a broader variety of germination rates that in some cases can drop down dramatically (Figure 7).

It is important to underline that also a tetraploid line was analyzed (BoATe-04). This line spontaneously emerged from the progeny of a diploid apomictic line (BoADi-01) and showed a very poor seed set (see next section) together with an extremely low germination rate, suggesting that *Boechera spp*. may not tolerate polyploidization events.

Seed set analysis (*Boechera spp.*)

Fertility is an important parameter to evaluate the seed set of the silique therefore, for assessing the potential fitness of a line. The *Boechera* lines reported in the previous section were also analyzed for fertility levels of their siliques over a period of three generations (Figure 8).

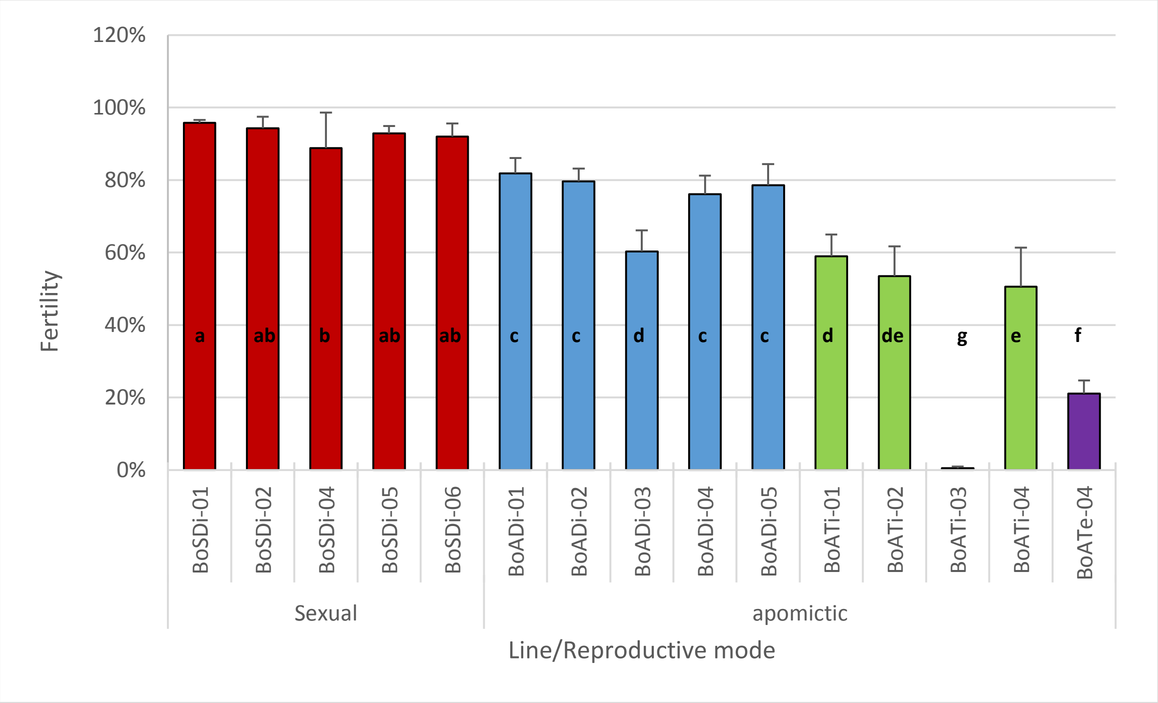

Figure 8. Fertility levels (%) of 15 lines of *Boechera* over three generations; Red = sexual diploid lines; Blue = apomictic diploid lines; Green = apomictic triploid lines; Violet = apomictic tetraploid line. Different letters indicate significant differences between the lines according to Tukey test. R^2 = 0,963; $P < 0.05$ on transformed data (Arcsin(√y)).

As for the germination rate, the factor "generation" did not have significant influence on the fertility levels (P = 0.512674). On the other hand, the lines showed highly significant differences (P<0.0000001), while there were no significant interactions between line and generation (P = 0.520404).

Through a Tukey test, it was possible to determine that sexual lines had significantly higher percentage of fertility than apomictic lines (Figure 8). With the exception of BoADi-03 and BoATi-02, that do not show statistically significant differences, the data show a trend of fertility levels that was uniformly high in the sexual diploid lines, where seed set was most of the time close to 100% fertility, while apomictic diploids reached at best 80% of fertility and were generally, but not always, characterized by better seed set than the apomictic triploids or tetraploids.

Number of siliques per plant (*Boechera spp.*)

The reproductive phenotyping included also the count of siliques per plant in 15 *Boechera* lines across 3 generations.

It was common in many lines of *Boechera* to have siliques, which did not undergo normal development, but stopped growing immediately after pollination and reached a final size that was several times smaller than a fully developed silique. These kinds of siliques were considered aborted.

The results collected during this observation considered only fully developed siliques and are summarized in the following graph (Figure 9).

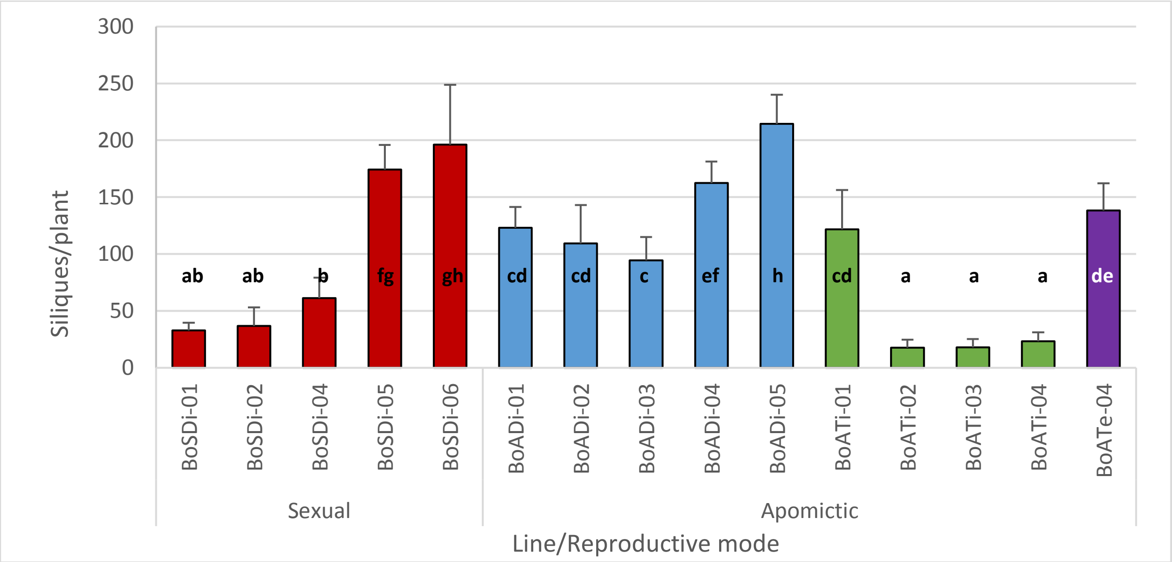

Figure 9. Average number of siliques per plant in 15 lines of *Boechera spp.* over three generations; Red = sexual diploid lines; Blue = apomictic diploid lines; Green = apomictic triploid lines; Violet = apomictic tetraploid line. Different letters indicate significant differences between the lines according to Tukey test. $R^2 = 0.88$; $P < 0.05$ untransformed data.

The factor “generation” in this statistical analysis did not have a significant influence over the number of siliques per plant ($P = 0.0719$). Highly significant statistical differences were detected between the lines (P<0.0000001), whereas there were no significant interactions between line and generation (P = 0.5183).

Unlike the cases of "germination rates" and "fertility levels", the sexual and the apomictic lines did not show a clear tendency regarding their reproduction, suggesting that the number of siliques per plant is line dependent but not strictly connected with the reproductive mode. There was no clear separation between diploid and triploid apomicts even if the last ones showed significantly lower number of siliques in 3 out of 4 lines when compared with diploid apomictic lines.

Remarkably, in the lines BoATi-02, BoATi-03, BoATi-04 and BoATe-04, plants that never flowered and never produced any siliques were detected (Figure 10). These plants were dwarf and did not show any vegetative growth for a period of up to 12 months before undergoing natural death.

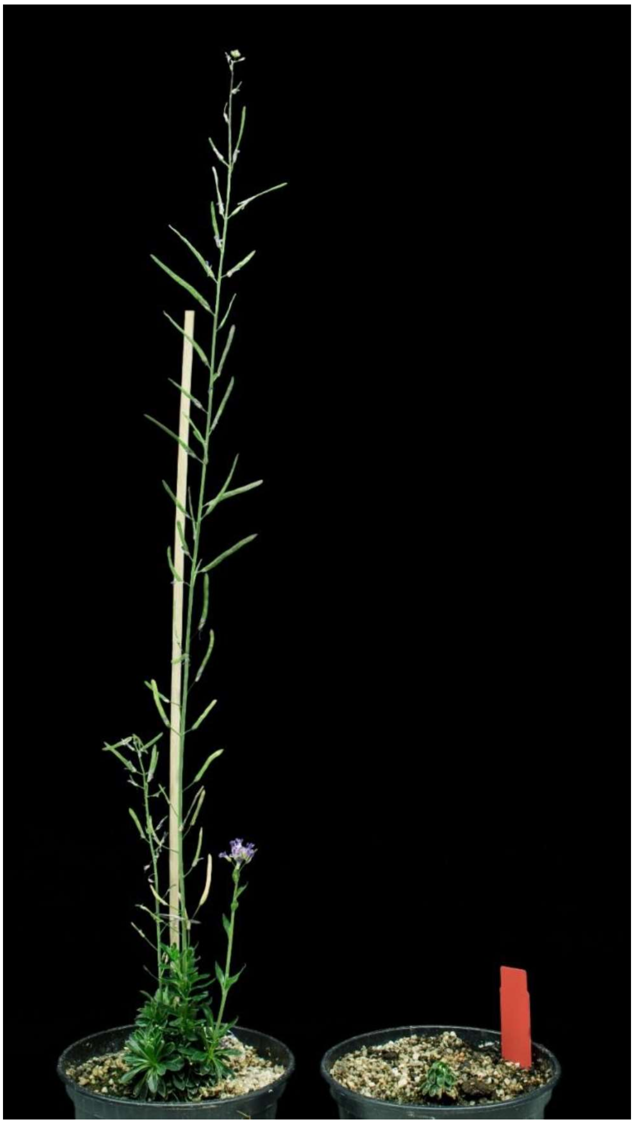

Figure 10. Line BoATi-04 showing normal vegetative and reproductive development (plant on the left) and dwarf phenotype with no differentiation of any reproductive organs.

In this study, this phenotype was never detected in any diploid line independently from their reproductive mode, therefore, supporting the hypothesis that ploidy levels higher than 2C may not be well tolerated by many *Boechera* lines.

Potential fitness in *Boechera*

The results presented so far, indicate that for every analyzed trait, there were highly significant differences between lines, but still did not answer a fundamental question about the level of fitness of these 15 lines of *Boechera spp.*

An accurate evaluation of fitness would require the observation of these lines in their habitat, in different environments and over many generations. Nevertheless, the data regarding germination rate, seed set (fertility level), number of fertile seeds per siliques and number of siliques per plant, can be combined in order to obtain an evaluation of the potential fitness. With the aim to perform such evaluation, the average values of the aforementioned traits for every line were multiplied between each other. The result of this calculation is summarized in the following graph (Figure 11).

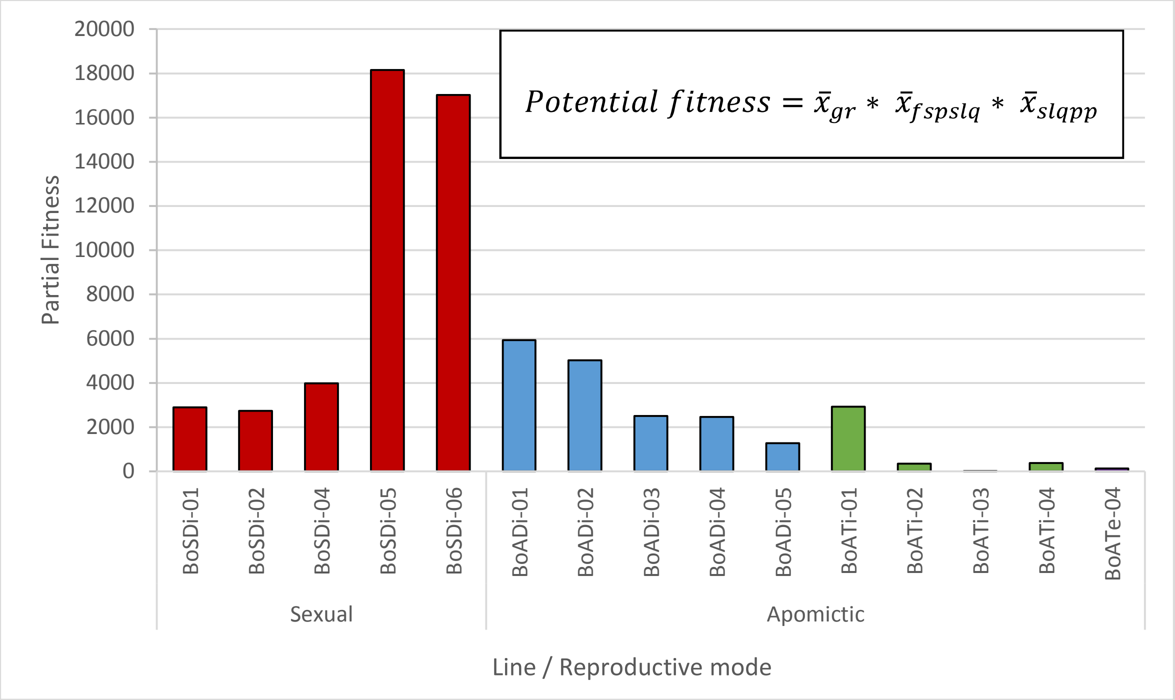

Figure 11. Potential fitness in 15 *Boechera spp.* lines; Red = sexual diploid lines; Blue = apomictic diploid lines; Green = apomictic triploid lines; Violet = apomictic tetraploid line. $\bar{x}_{gr}$ = average germination rate; $\bar{x}_{fspslq}$ = average fertile seeds number per silique; $\bar{x}_{slqpp}$ = average siliques number per plant.

The values represented in Figure 11 clearly show a superior fitness of lines BoSDi-05 and BoSDi-06 that are characterized by values of partial fitness nearly 3 times higher than the third better line (BoADi-01). Nevertheless, excluding BoSDi-05 and 06, there was not a clear separation between sexual and apomictic diploid lines, with BoADi-01 and BoADi-02 showing fitness levels even higher than many sexual diploids like: BoSDi-01, 02, 04. This similarity between sexual and apomictic diploids could be due the fact that, although BoADi lines produced less fertile seeds per silique, they were at the same time able to produce a relatively higher amount of siliques, compensating in this way the gap of fitness with the sexual diploids.

BoATi and BoATe lines showed very low fitness values, which goes in accordance with the hypothesis that *Boechera spp.* may not tolerate very well higher ploidy levels.

Flowering time in *Boechera* and possible influence on fitness

A more complex estimation of fitness could be performed taking also into account the flowering time. An extremely short flowering time could allow some lines to have two generations during the warm season, especially in environments characterized by shorter winters, and this would mean a much higher production of seeds and consequently higher fitness levels.

The results of flowering time measurements are represented in Figure 12.

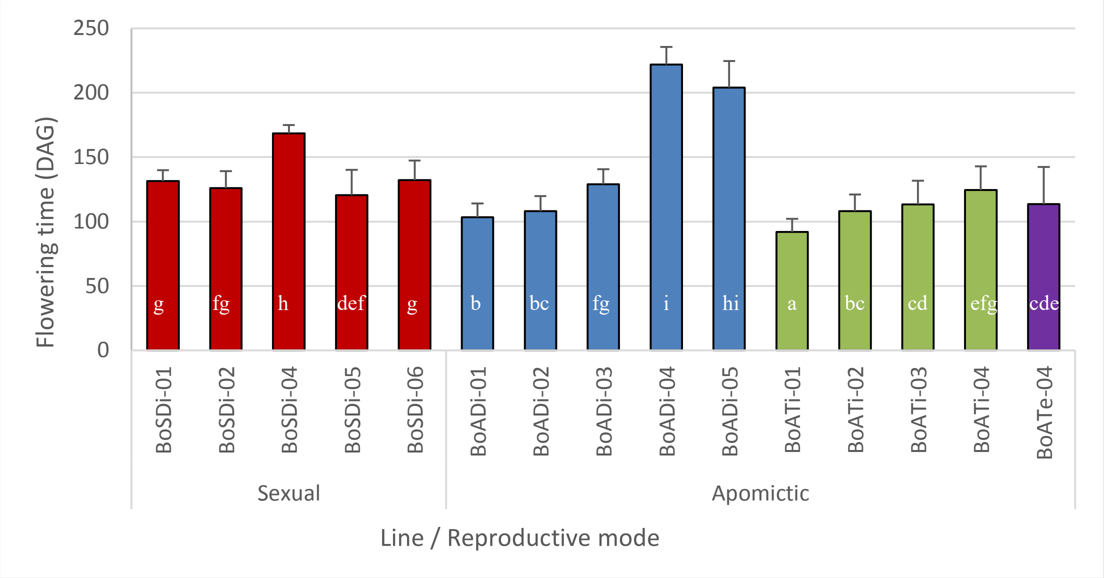

Figure 12. Flowering time of 15 Boechera spp. lines. Red = sexual diploid lines; Blue = apomictic diploid lines; Green = apomictic triploid lines; Violet = apomictic tetraploid line. DAG = days after germination. Different letters indicate significant differences

The statistical analysis showed no significant effect of the generation, therefore, the test was repeated taking into account only the line as a factor of analysis. These results do not show a clear tendency between sexual and apomictic lines, neither between different ploidy levels. Nevertheless, the lines BoADi-01, BoADi-02, BoATi-01 and BoATi-02 were characterized by flowering times short enough to theoretically complete two generations in a warm season of six months. The aforementioned lines are all apomictic.

The data collected were used to generate a potential fitness estimation corrected for flowering time (Figure 13). In order to get such estimation, and considering that there is no published equation for this kind of corrections, Equation 2 was applied to the data.

$$PF_{(FT)} = PF * \frac{WD}{FT}$$

Equation 2. $PF_{(FT)}$ = Potential fitness (flowering time corrected); PF = Potential fitness value (*Figure 11*); WD = warm season days (given standard value of 180 days); FT = flowering time (days after germination).

The partial fitness data corrected for flowering time are reported in the following graph (Figure 13).

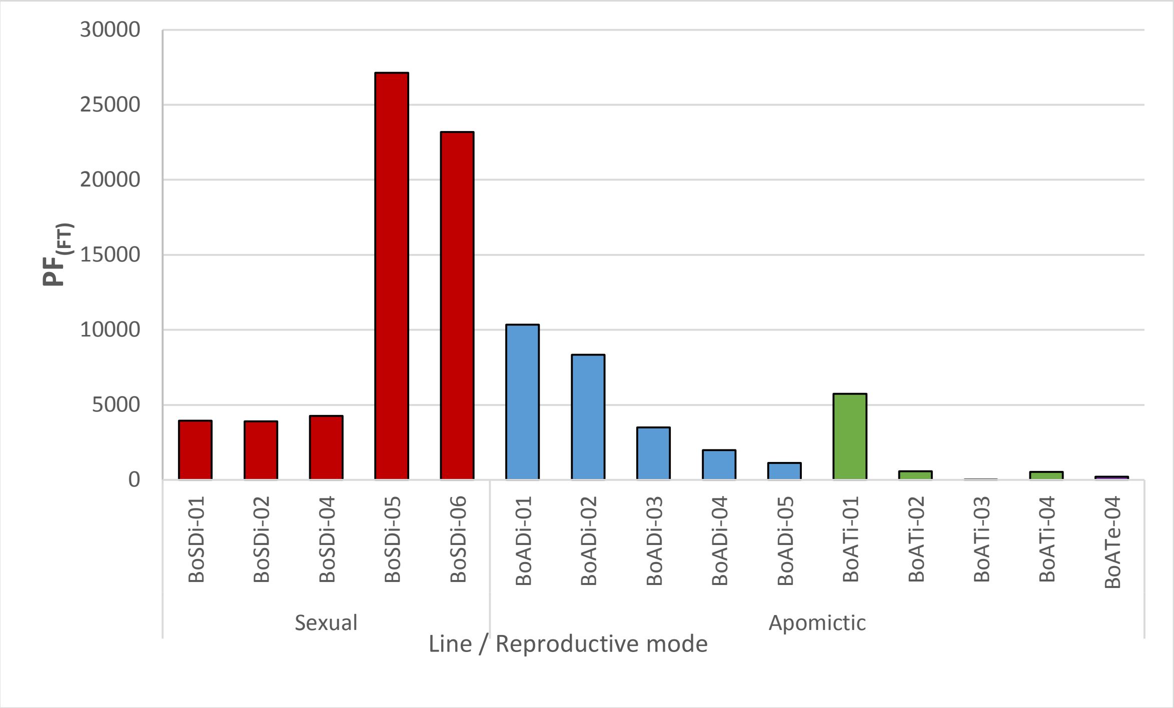

Figure 13. Estimation of potential fitness in 15 *Boechera spp.* lines corrected for flowering time (**$PF_{(FT)}$**); Red = sexual diploid lines; Blue = apomictic diploid lines; Green = apomictic triploid lines; Violet = apomictic tetraploid line.

Comparing the fitness values before and after the correction for flowering time, it was clear that there were no major changes; nevertheless, the relative difference between BoSDi-05 and BoSDi-06 and all the others appear to be smaller, and some apomictic lines like BoATi-01 improved their fitness ranking after correction (to compare the fitness values before and after correction, see supplemental data Table 16).

These estimations are theoretical and not based on the flowering time in their natural habitat. However, this analysis suggests, that the differences in flowering time between the aforementioned lines are not big enough to provoke major changes of potential fitness.

Ploidy dynamics in *Boechera spp.*

Leaves flow cytometry

The ploidy of 15 *Boechera spp.* lines was measured on leaves across 3 generations in order to understand which percentage of plants had the expected ploidy and to detect eventual ploidy anomalies such as polyploidization events. At the same time, a similar analysis was performed on seeds of 13 out of the 15 aforementioned lines (BoADi-05 and BoATi-03 did not provide the minimum amount of seeds to perform this kind of analysis).

The results of ploidy measurements of leaves are represented in Figure 16 where it is evident that all analyzed sexual lines had a very stable ploidy. The three generations that were evaluated showed only diploid adult plants in diploid sexual lines *i.e.* no polyploidization events were detected. On the other hand, the apomictic lines did not show this kind of stability, in fact, tetraploid adult plants were detected in progeny of diploid apomictic lines (BoADi-01 and BoADi-02) and hexaploids in the progeny of triploid apomicts (BoATi-03). Furthermore, a tetraploid line (BoATe-04) derived by the diploid apomictic BoADi-01 was screened for three generations, and diploids were also detected among its progeny, demonstrating that apomictic lines are not only able to undergo polyploidization but can also revert to their original ploidy level.

The polyploidized plants were phenotyped for reproductive traits like seed set and flowering time. What emerged from this observation is that in some cases they showed longer flowering time and highly sterile seed set (data not shown). One extreme case is the triploid line BoATi-04, the hexaploid plants originated from this line do not flower at all and always show a dwarf phenotype (Figure 14) that persists until senescence at about 13 to 15 months after germination.

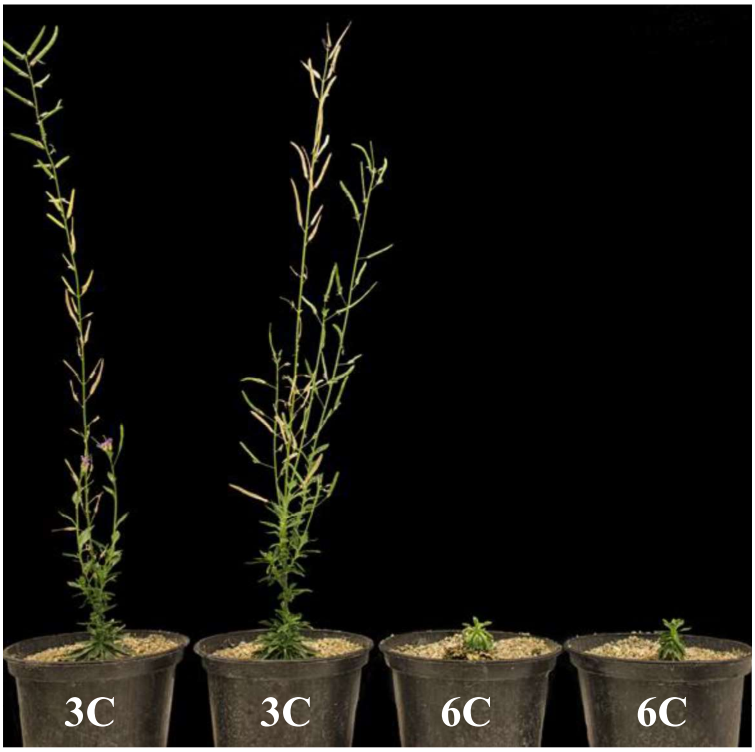

Figure 14. Plants from line BoATi-04. 2 triploids (on the left); 2 hexaploids (on the right). 250 days after germination.

The only exception to the phenotype “6C-no-flowering” was the plant BoATi-04.2.5 (left in Figure 15), that flowered after 7 months and produced some siliques carrying only sterile seeds.

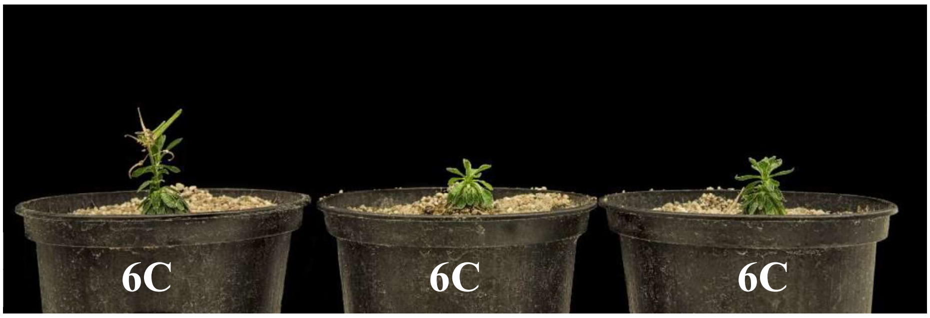

Figure 15. Plant BoATi-04.04.2.5 (on the left) in comparison with other two hexaploids individual of the same line 250 days after germination.

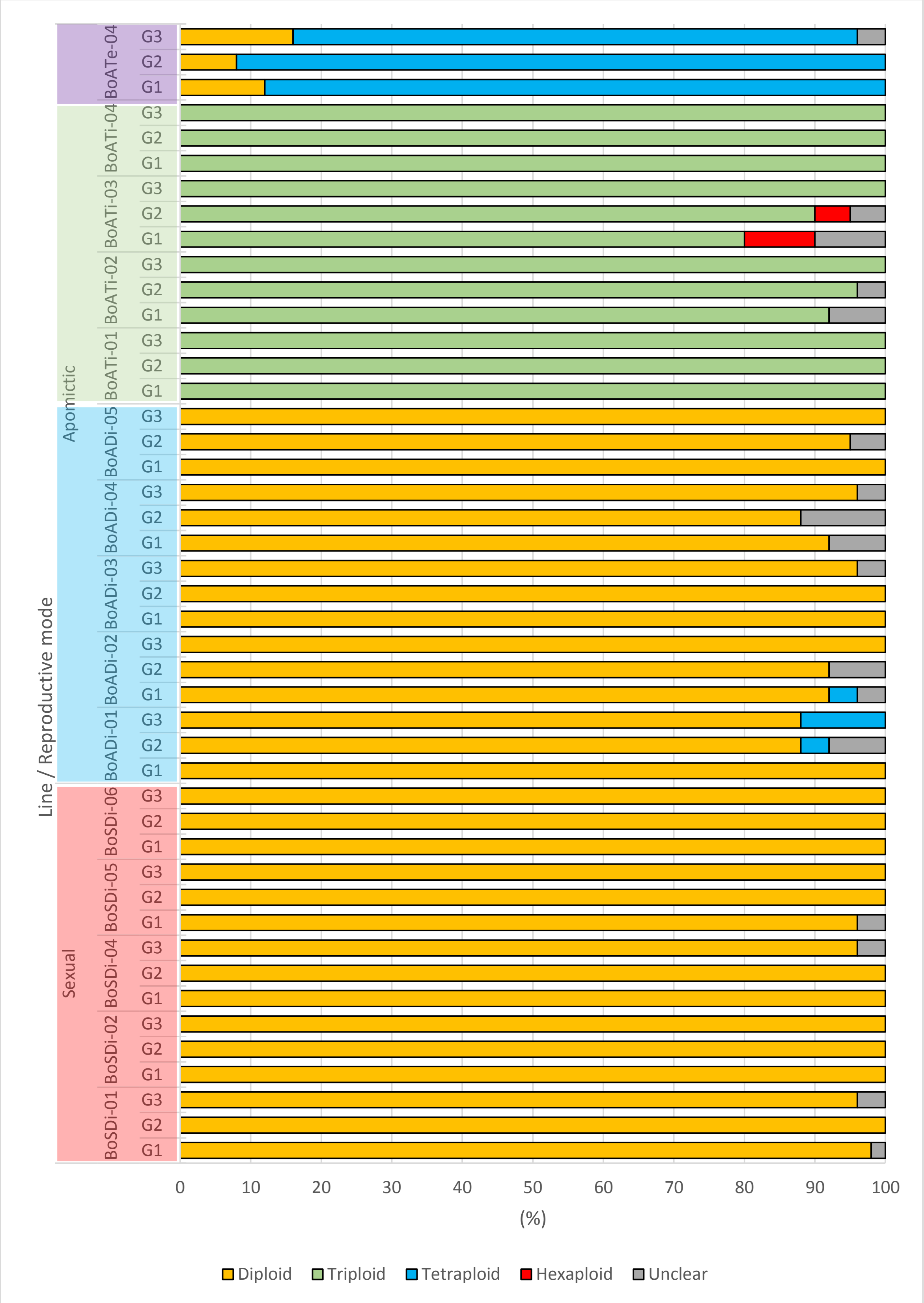

Figure 16. Leaf ploidy level of 15 lines *Boechera spp.* measured across three generations (G1, G2, G3). Red area = diploid sexual lines; Blue area = diploid apomictic lines; Green area = triploid apomictic lines; Violet area = tetraploid apomictic line.

Flow cytometric seed screen (FCSS)

The ploidy dynamics of *Boechera spp.* were studied also through Flow Cytometric Seed Screen (FCSS) in order to confirm the evidences observed through the ploidy measurements of leaves and to obtain information about the reproductive mode of every line across three generations. The results of these observations are summarized in Figure 18.

Seeds of the analyzed apomictic lines showed variations in the embryo and endosperm ploidy levels, with the exception of line BoADi-03, in which no polyploidization event was detected in any of the three observed generations.

Polyploidization barrier in *Boechera spp.*

From the comparison of leaves and seed ploidy data, emerged that the percentage of polyploidized adult plants was at best equal but most of the times lower than the percentage of polyploidized seeds as shown in Table 3.

Table 3. Percentage of polyploidization in leaves (adult plants) and embryos (FCSS data) in 6 *Boechera spp.* lines.

Line	**BoADi-01**			**BoADi-02**			**BoADi-04**			**BoATi-02**			**BoATi-04**			**BoATe-04**		
Generation	**G1**	**G2**	**G3**	**G1**	**G2**	**G3**	**G1**	**G2**	**G3**	**G1**	**G2**	**G3**	**G1**	**G2**	**G3**	**G1**	**G2**	**G3**
% Polyploidized (Leaves)	0	4	12	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
% Polyploidized (Embryo)	0	4	12	8	12	4	4	0	4	4	20	4	4	8	4	3.3	3.3	0

This suggests that, there was a partial barrier for the development of polyploidized seeds (confirmed by the low germination levels of BoATe-04), that in some lines were not able to germinate. BoADi-01 and 02 were the only lines where this barrier was at least partially overcome and BoATe-04 was the only adult tetraploid progeny derived from the diploid BoADi-01, which was possible to propagate and study as a new line. Interestingly, the BoATe-04 is the line where a reversion of ploidy was observed, with the formation of diploid and octoploid seeds from the same tetraploid mother plant. From that offspring, diploid seeds gave origin to diploid adults, very similar to the rest of the tetraploid population (high sterility levels and low germination rates), while octoploid seeds never developed into adult plants.

All studied apomictic lines except one, showed a 1:3 ploidy ratio between embryo and endosperm, confirming that fertilization of the central cell is still necessary for the endosperm formation in apomicts, and that in most of the observed apomictic lines the pollen that fertilize the central cell is unreduced. Line BoADi-03 is the only apomict that showed not only 1:3 ploidy ratios, but 1:2.5 as well indicating that in this case the central cell was sometimes fertilized by reduced pollen. To better understand the interpretation of the FCSS data, a list of ploidy histograms representing the main types of observed seeds is given in Figure 17. The FCSS data showed the reproductive mode of every analyzed line.

Both sexual and apomictic lines were very stable in terms of their mode of reproduction and no switch from apomixis to sexuality or vice versa was observed in any generation. In rare cases ambiguous peaks (red arrows in Figure 17) could be detected. Eventually, they can be interpreted as events of embryo endoreduplication or autonomous endosperm formation and require further investigations. Together the experiment confirms the instability of the ploidy level in apomicts as already deduced from the measurements of the ploidy levels in leaves. Furthermore, no switch in the mode of reproduction could be detected in any of the analyzed lines demonstrating the high stability of their reproductive mode.

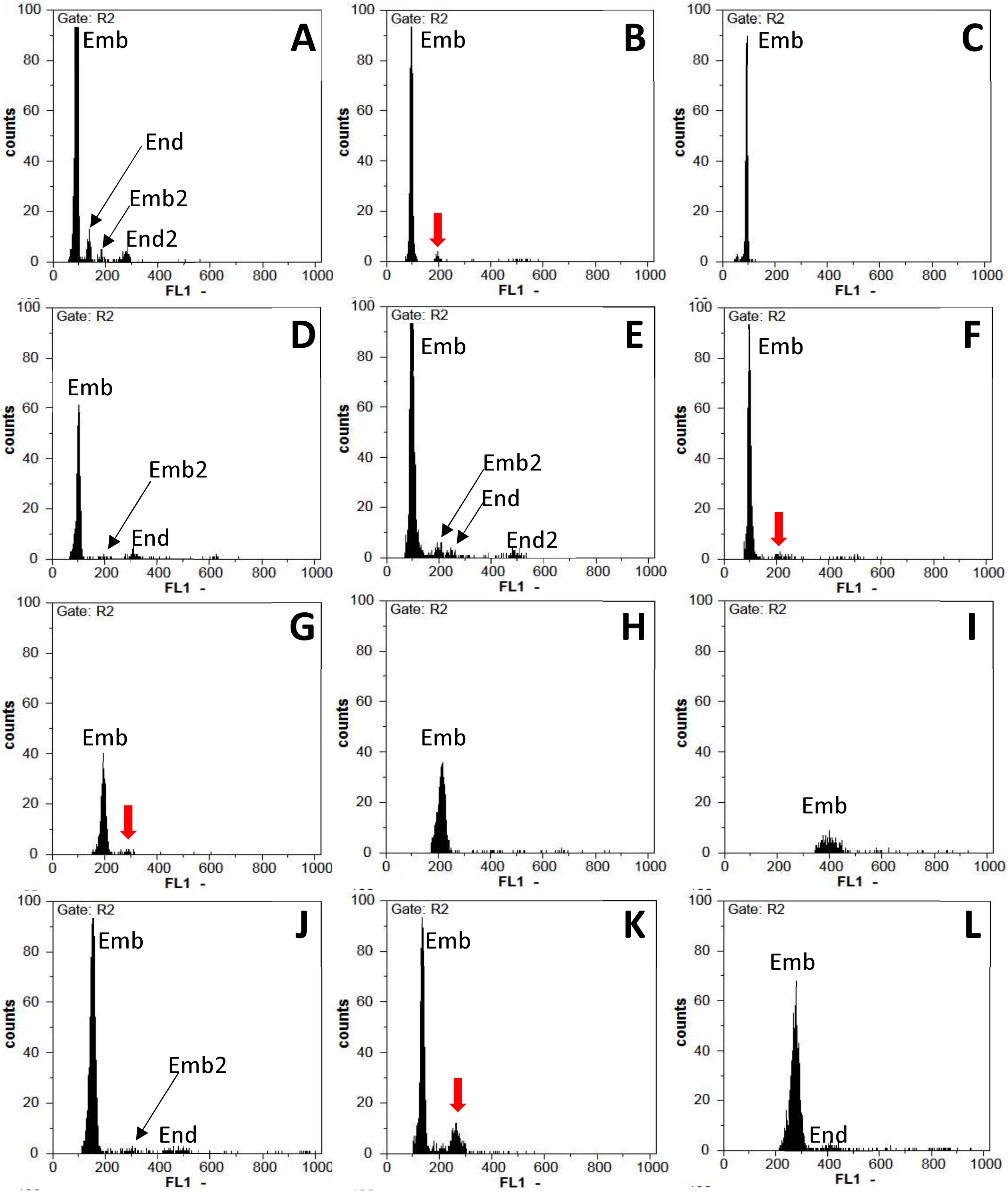

Figure 17. FCSS (Flow cytometric seed screen) Histograms types in 15 *Boechera spp*. lines. **A**: Seed from diploid sexual line (2C embryo, 3C endosperm, 4C embryo endoreduplication, 6C endosperm endoreduplication); **B**: Seed from diploid sexual line (2C embryo, endosperm unclear or absent); **C**: Seed from diploid sexual line (2C embryo, endosperm not detected); **D**: Seed from diploid apomictic line (2C embryo, 4C embryo reduplication, 6C endosperm fertilized by unreduced pollen); **E**: Seed from diploid apomictic line (2C embryo, 4C embryo endoreduplication, 5C endosperm fertilized by reduced pollen, 10C endosperm endoreduplication); **F**: seed from diploid apomictic line (2C embryo, endosperm unclear or not detected); **G** seed from the tetraploid BoATe-04 (2C embryo, 4C embryo endoreduplication or autonomous endosperm); **H** seed from BoATe-04 (2C embryo, endosperm not detected); **I** seed from BoATe-04 (8C embryo, endosperm not detected); **J** seed from triploid apomictic line (3C embryo, 6C embryo endoreduplication, 9C endosperm fertilized by unreduced pollen); **K** seed from triploid apomictic line (3C embryo, 6C embryo endoreduplication or autonomous endosperm), **L** seed from triploid apomictic line (6C embryo, 9C endosperm fertilized by unreduced pollen). **Emb** = embryo; **Emb2** = embryo endoreduplication; **End** = endosperm; **End2** = endosperm endoreduplication; **Red arrow** = ambiguous peak (embryo endoreduplication or autonomous endosperm).

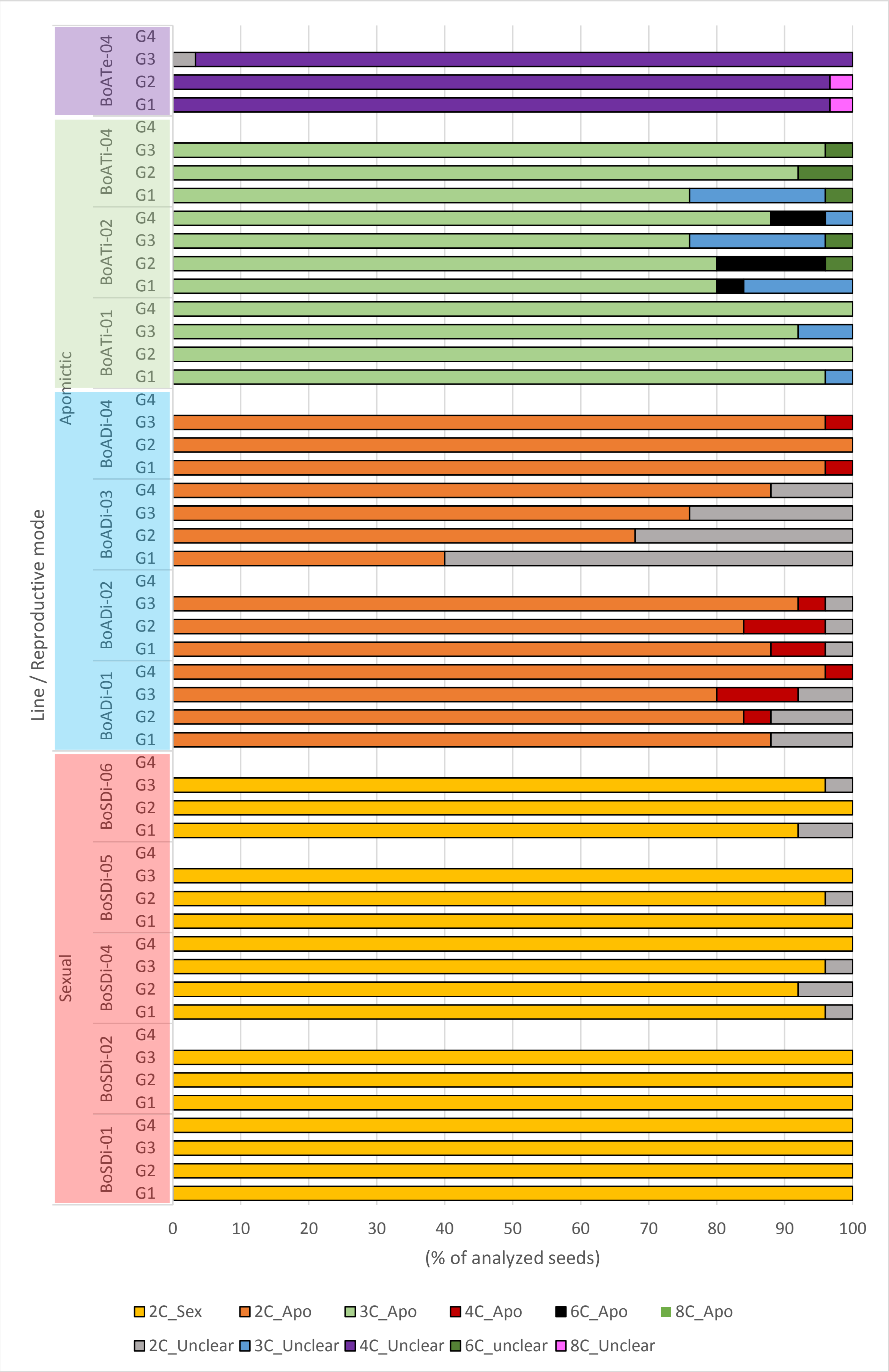

Figure 18. Results of flow cytometric seed screen (FCSS) in 15 lines of *Boechera spp.* during a period of three or four generations (G1, G2, G3, G4). Red area = diploid sexual lines; Blue area = diploid apomictic lines; Green area = triploid apomictic lines; Violet area = tetraploid apomictic line.

Ovule and female gametophyte development in *Boechera spp.*

The in depth histological analysis of 25531 ovules across several lines, characterized by different reproductive modes and different ploidy levels, generated a data set that constitutes a highly detailed visual atlas of *Boechera spp.* female gametophytic development.

A general summary of the data collected during this characterization is reported in Table 4.

Table 4- Ovule and female gametophyte development of: 3 diploid sexual lines, 3 diploid apomictic lines, 3 triploid apomictic lines and 1 tetraploid line of *Boechera spp.* Classes: 1=0.5-1mm; 2=1.01-1.5mm; 3=1.51-2mm; 4=2.01-2.5mm; 5=2.51-3mm; 6=3.01-3.5mm; 7=3.51-4mm; 8=4.01-4.5mm; 9=4.51-5mm; 10=5.01-5.5mm; 11=5.51-6mm; 12=6.01-6.5mm; 13=6.51-7mm; 14=7,01-7,5mm. **OvP**=ovule primordia; **AC**=archesporial cell; **MMC/SI**= megaspore mother cell/small integuments primordia; **MI**=medium integuments primordia; **BI**=big integuments primordia; **FM**=functional megaspore; **2NG**=binucleated gametophyte; **4NG**=tetranucleated gametophyte; **Mature**=mature gametophyte.

Ploidy	**Reproduction**	**Class**	**Mean FB size (mm)**	**OvP**	**AC**	**MMC/SI**	**MMC/MI**	**MMC/BI**	**Multi MMC**	**Dyads**	**Tetrads**	**FM**	**Multi FM**	**2NG**	**4NG**	**Mature**	**Aborted**	**Other**	**Number of observed ovules**
Diploid	Sexual	1	0.94	96.3%	3.7%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	751
Diploid	Sexual	2	1.27	78.0%	18.7%	1.0%	0.7%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	1.2%	3462
Diploid	Sexual	3	1.80	14.3%	26.3%	28.3%	20.3%	4.7%	0.1%	0.3%	0.4%	2.7%	0.0%	0.0%	0.0%	0.0%	0.3%	2.0%	2877
Diploid	Sexual	4	2.34	0.0%	0.3%	12.3%	71.7%	12.3%	0.4%	1.7%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	1.7%	1498
Diploid	Sexual	5	2.75	0.0%	0.0%	4.3%	24.3%	23.7%	0.1%	0.6%	0.7%	22.7%	0.3%	10.7%	7.0%	3.7%	0.3%	2.7%	1997
Diploid	Sexual	6	3.21	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	8.7%	0.0%	19.7%	39.3%	32.0%	0.0%	0.7%	498
Diploid	Sexual	7	3.80	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	16.5%	5.0%	1.5%	41.0%	11.0%	0.0%	25.0%	163
Diploid	Sexual	8	4.39	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	9.0%	5.0%	5.0%	47.0%	34.5%	0.0%	0.0%	355
Diploid	Sexual	9	4.70	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	23.3%	76.0%	0.0%	1.0%	511
Diploid	Sexual	10	5.13	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	5.3%	94.0%	0.0%	0.7%	283
Diploid	Sexual	12	6.12	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	14.0%	86.0%	0.0%	0.0%	74
Diploid	Apomictic	1	0.93	13.7%	70.7%	16.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	257
Diploid	Apomictic	2	1.26	8.3%	58.7%	23.0%	7.0%	0.0%	0.3%	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	2.8%	1804
Diploid	Apomictic	3	1.75	9.2%	18.4%	27.2%	27.7%	5.2%	1.6%	2.4%	0.0%	2.7%	0.0%	0.0%	0.7%	0.0%	0.7%	5.1%	1292
Diploid	Apomictic	4	2.26	0.0%	1.3%	8.2%	37.8%	23.2%	1.8%	3.5%	0.0%	11.2%	0.3%	2.0%	0.7%	0.0%	1.2%	9.0%	917
Diploid	Apomictic	5	2.79	0.0%	0.0%	1.3%	11.2%	13.3%	0.2%	0.9%	0.0%	34.2%	0.7%	16.0%	3.1%	0.1%	7.2%	11.4%	1261
Diploid	Apomictic	6	3.08	0.0%	0.0%	0.0%	6.0%	8.0%	0.0%	0.0%	0.0%	29.5%	0.0%	23.5%	23.5%	0.0%	6.5%	3.5%	127
Diploid	Apomictic	7	3.96	0.0%	0.0%	0.0%	0.0%	1.0%	0.0%	0.0%	0.0%	55.0%	0.0%	23.0%	11.0%	0.0%	9.0%	2.0%	124
Diploid	Apomictic	8	4.31	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	13.7%	0.0%	26.3%	32.0%	9.0%	14.0%	5.7%	493
Diploid	Apomictic	9	4.54	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	17.0%	0.0%	40.0%	19.0%	10.0%	9.0%	5.0%	86
Diploid	Apomictic	10	5.27	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	16.5%	0.2%	41.5%	17.5%	9.5%	10.5%	4.0%	415
Diploid	Apomictic	11	5.57	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	60.0%	0.0%	40.0%	25
Triploid	Apomictic	1	0.94	0.0%	5.5%	89.5%	5.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	88
Triploid	Apomictic	2	1.25	0.5%	2.5%	36.0%	31.0%	8.5%	1.0%	4.0%	0.0%	10.5%	0.0%	0.0%	0.0%	0.0%	0.0%	0.5%	1182
Triploid	Apomictic	3	1.76	0.0%	0.0%	0.0%	2.5%	5.5%	0.0%	1.0%	0.0%	39.0%	1.0%	46.5%	3.0%	0.0%	0.5%	1.0%	751
Triploid	Apomictic	4	2.25	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	5.5%	0.3%	36.5%	28.0%	19.5%	9.0%	1.5%	1071
Triploid	Apomictic	5	2.60	0.0%	0.0%	0.0%	1.5%	2.0%	0.0%	0.2%	0.0%	4.5%	0.0%	9.0%	22.5%	41.5%	17.5%	0.5%	707
Triploid	Apomictic	6	3.22	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	6.5%	54.0%	27.0%	12.0%	348
Triploid	Apomictic	7	3.70	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	61.0%	33.0%	7.0%	103
Triploid	Apomictic	8	4.40	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	7.0%	38.0%	40.0%	15.0%	127
Triploid	Apomictic	9	4.75	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	36.0%	53.0%	12.0%	104
Triploid	Apomictic	10	5.12	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	71.0%	27.0%	2.0%	115
Tetraploid	Apomictic	1	0.86	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0
Tetraploid	Apomictic	2	1.26	17.0%	1.0%	19.0%	0.0%	0.0%	15.0%	1.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	4.0%	7.0%	230
Tetraploid	Apomictic	3	1.67	0.0%	0.0%	41.0%	0.0%	0.0%	24.0%	4.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	11.0%	4.0%	185
Tetraploid	Apomictic	4	2.29	0.0%	0.0%	46.0%	28.0%	1.0%	12.0%	8.0%	1.0%	0.0%	0.0%	0.0%	0.0%	0.0%	7.0%	1.0%	512
Tetraploid	Apomictic	5	2.71	0.0%	0.0%	30.0%	36.0%	24.0%	5.0%	2.0%	0.0%	4.0%	0.0%	1.0%	0.0%	0.0%	0.0%	0.0%	247
Tetraploid	Apomictic	6	3.22	0.0%	0.0%	0.0%	25.0%	0.0%	0.0%	1.0%	0.0%	10.0%	0.0%	10.0%	0.0%	0.0%	30.0%	0.0%	115
Tetraploid	Apomictic	7	3.82	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	15.0%	20.0%	5.0%	15.0%	0.0%	60
Tetraploid	Apomictic	8	4.25	0.0%	0.0%	0.0%	4.0%	20.0%	0.0%	0.0%	0.0%	12.0%	0.0%	16.0%	0.0%	30.0%	20.0%	0.0%	62
Tetraploid	Apomictic	10	5.23	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	2.0%	5.0%	17.0%	69.0%	3.0%	254
																		Total	**25531**

The heat map helps to visualize the ovule development as a red color gradient that crosses the sections of the table diagonally, showing that bigger flower buds contain ovules at more advanced developmental stages.

In this way, faster development implies increased percentage of ovules reaching the gametophyte maturity at an earlier class number *e.g.* the triploid apomicts started to reach the stage of mature female gametophyte in flower buds of the class 4, in contrast with diploid sexual lines and diploid apomicts that reached the same stage at class 5 and class 8 respectively.

Looking more in detail at the earliest stages (up to FM), it appeared that the sexual diploid lines had a slower development pace in comparison to the diploid apomicts that were surpassed in developmental speed by the triploid apomicts.

These observations are reported in Figure 19 that have been derived from Table 4.

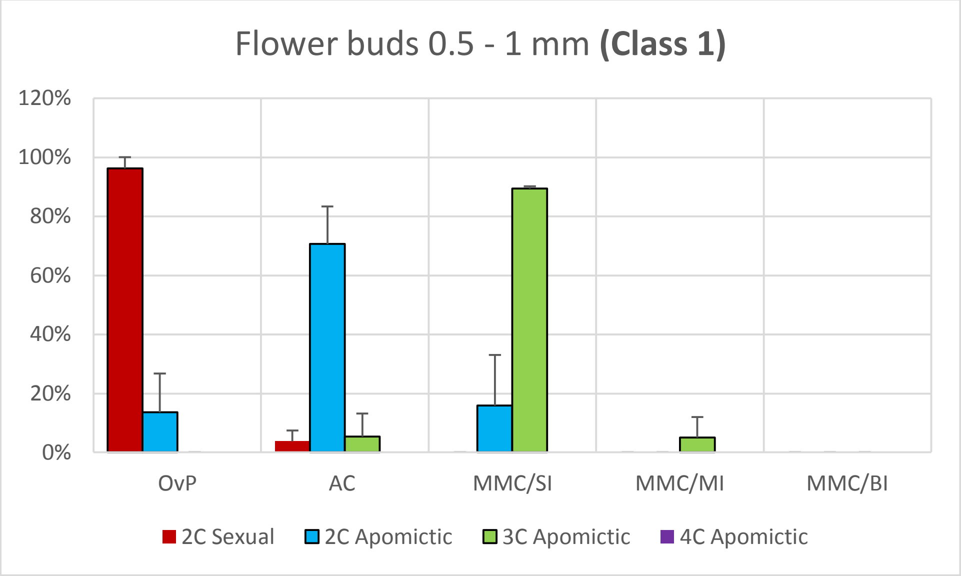

Figure 19. Frequencies of development stages in several *Boechera spp.* at flower bud size 0.5-1mm. **OvP**=ovule primordia; **AC**=archesporial cell; **MMC/SI**= megaspore mother cell/small integuments primordia; **MI**=medium integuments primordia; **BI**=big integuments primordia.

In flower buds of class 1, the diploid sexual lines did not develop yet Archesporial cells (AC) but only ovules primordia without any visible enlarged nuclei while at the same time diploid apomicts differentiated ACs and in few cases even MMCs (Figure 19). The triploid apomicts are visible in green on the right part of the graph, characterized by a majority of ovules carrying already MMCs and integuments primordia of medium size (an explanation for the meaning of: small, medium and big integuments primordia is available in supplemental data Figure 71). The tetraploid line carried only one flower bud belonging to class 1 (0.5-1mm), but not even the ovules primordia were formed, therefore, this line is not represented in Figure 19.

The developmental situation is very similar in flower buds belonging to the class 2 (Figure 20).

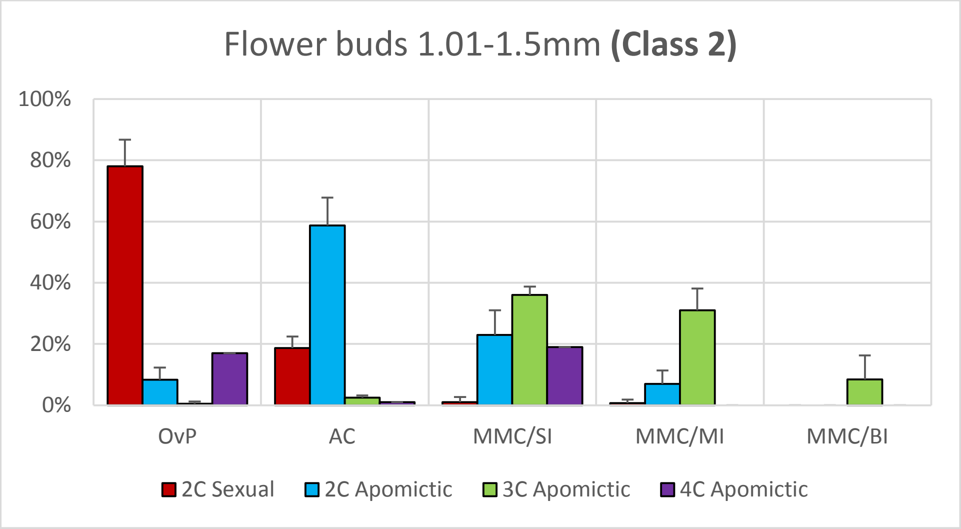

Figure 20. Frequencies of development stages in several *Boechera spp.* at flower bud size 1.01-1.5mm. **OvP**=ovule primordia; **AC**=archesporial cell; **MMC/SI**= megaspore mother cell/small integuments primordia; **MI**=medium integuments primordia; **BI**=big integuments primordia.

In this class, the sexual diploids are mainly stuck at the OvP stages with only 20% of the ovules carrying ACs. On the other hand, the triploid apomicts reached already the stage of megaspore mother cell accompanied in some cases by big integuments primordia.

The difference in developmental speed between the triploids and the rest of the lines is higher in class 3 (Figure 21) where diploids (sexual and apomictic) together with tetraploids were entering megagametogenesis by differentiating MMCs while the triploid apomicts had already successfully formed FMs that in some case already underwent a first mitotic division with formation of bi-nucleated gametophytes (2NG).

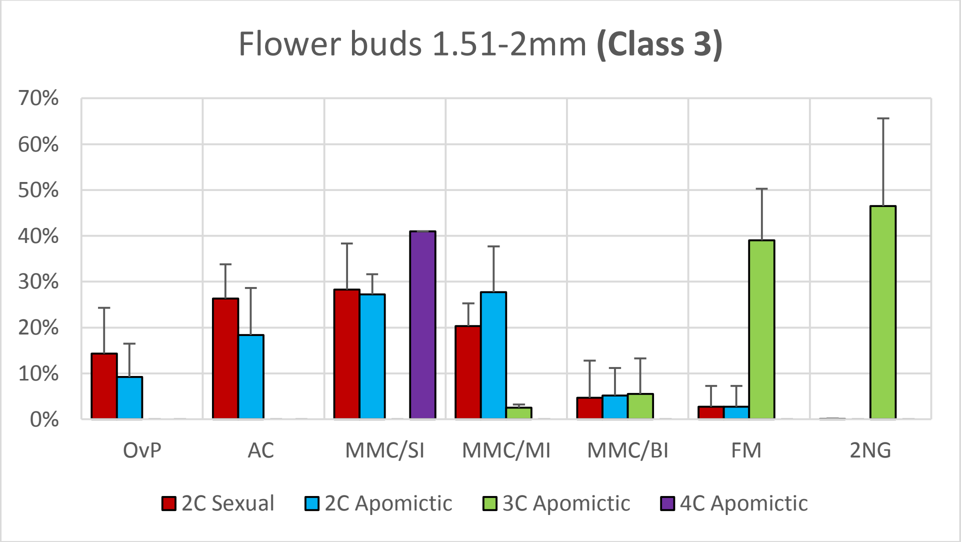

Figure 21. Frequencies of development stages in *Boechera spp.* at flower bud size 1.51-2mm. **OvP**=ovule primordia; **AC**=archesporial cell; **MMC/SI**= megaspore mother cell/small integuments primordia; **MI**=medium integuments primordia; **BI**=big integuments primordia; **FM**=functional megaspore; **2NG**=binucleated gametophyte.

In the triploid apomictic lines, nearly 20% of the ovules carried mature gametophytes when the flower bud was only 2 to 2.5 mm long (class 4) as shown in Figure 22, in opposition to 2C Sex and 2C Apo which were slower in development.

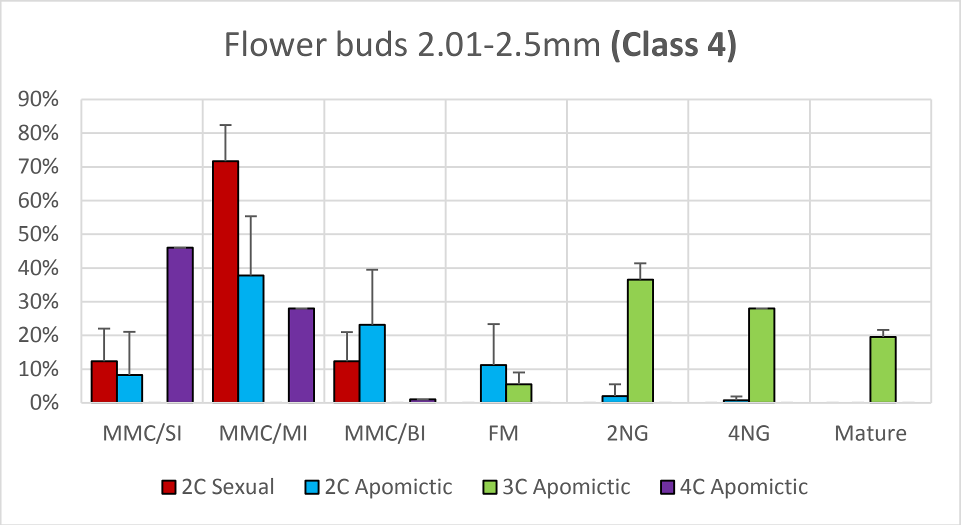

Figure 22. Frequencies of development stages in *Boechera spp.* at flower bud size 2.01-2.5mm. **MMC/SI**= megaspore mother cell/small integuments primordia; **MI**=medium integuments primordia; **BI**=big integuments primordia; **FM**=functional megaspore; **2NG**=binucleated gametophyte; **4NG**=tetranucleated gametophyte; **Mature**=mature gametophyte.

The developmental gap between the 3C apomicts and the other lines was not evident anymore with further development of the flower buds (class 8) suggesting that 2C Sex, 2C Apo and 4C Apo catched up with the 3C Apo lines that have already completed the gametophytic development (Figure 23).

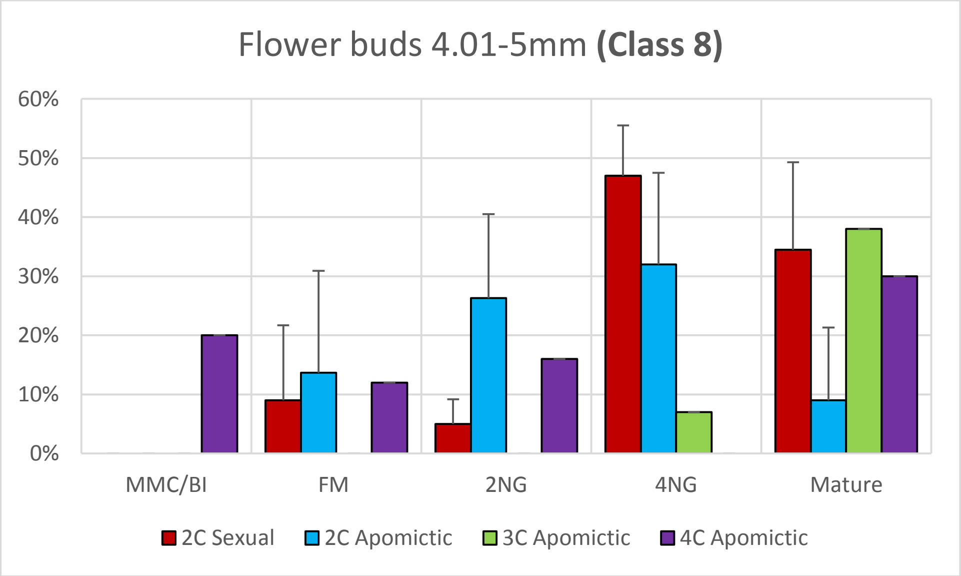

Figure 23. Frequencies of development stages in *Boechera spp.* at flower bud size 4.01-5mm. **MMC/BI**= megaspore mother cell/big integuments primordia; **FM**=functional megaspore; **2NG**=binucleated gametophyte; **4NG**=tetranucleated gametophyte; **Mature**=mature gametophyte.

The window of development going from the functional megaspore (FM) to the maturity of the female gametophyte was characterized by desynchronization of the ovules within the same pistils. This was expected considering that the development along the pistils is known to be acropetal. Nevertheless, the tetraploid apomictic lines represent an extreme example of developmental desynchronization, carrying MMCs and mature gametophytes within the same pistil at the same time (Figure 23).

Multiple megaspore mother cells (multi-MMCs)

Another aspect of development that was analyzed was the frequency of multiple MMCs. The apomictic lines showed a slightly higher percentage of multi-MMCs, that was not always significantly different from the sexual lines; however, the 2C-Sex lines showed frequencies of multi-MMCs significantly lower than 2C-Apo lines (Figure 24), suggesting that the reproductive mode might play a key role in this kind of developmental anomaly. On the other side, the 3C-Apo lines were not significantly different neither from the 2C-Sex lines nor from the 2C-Apo, indicating that the interaction between ploidy and reproductive mode might be important. Unfortunately, this kind of interaction cannot be tested due to the lack of 3C-Sex and 4C-Sex lines.

Finally, the 4C-Apo line, derived by the BoADi-01 2C-Apo line, showed peaks of multi-MMCs up to 20 times higher than its mother line. However, due to the high variance of this trait in this line, no statistical difference with any 2C-Apo line was found.

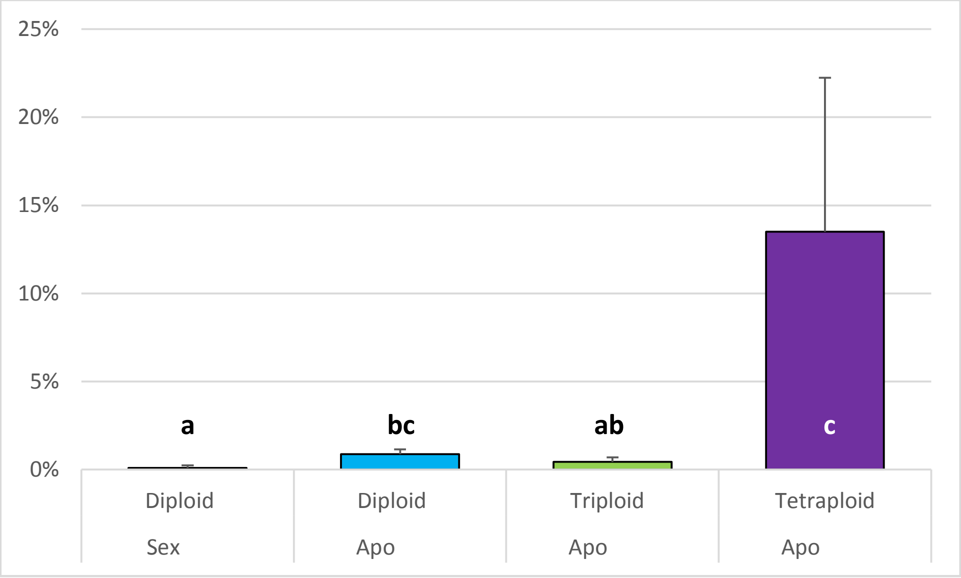

Figure 24. Average percentage of multi-MMCs from class 2 to class 5 (flower bud size) in 9 different *Boechera* lines divided in 4 classes. Means with a common letter are not significantly different (p<=0.05) according to Kruskal-Wallis test.

Abortion rates in apomicts are higher than in sexual lines

Abortion rates are a good example of how reproductive mode could affect developmental processes.

The sexual lines presented significantly lower levels of abortion in comparison to all the apomictic lines independently from their ploidy levels (Figure 25).

Although there was a tendency to increase abortion rates with increasing ploidy in apomictic lines, significant differences were not found between all apomictic lines, meaning that higher abortion rates are independent from the ploidy level in apomictic lines.

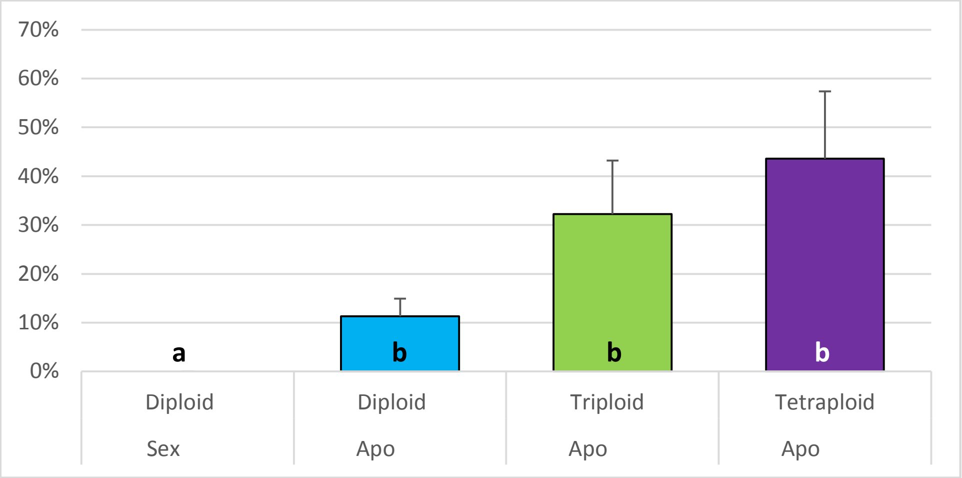

Figure 25. Average percentage of aborted ovules from class 6 to 10 (flower bud size) in 9 different *Boechera* lines divided in 4 classes. Means with a common letter are not significantly different (p<=0.05) according to Kruskal-Wallis test.

Visual atlas of ovule and female gametophyte development in *Boechera spp.*

The in depth histological analysis of 25531 ovules, allowed to assemble a visual atlas that was organized in visual panels (Figure 26, Figure 27, Figure 28, Figure 29) given in this section. Through this atlas, the results reported in the previous sections, are also understandable from a histological point of view.

Figure 26 describes the development of ovules from flower buds belonging to classes from 1 to 4.

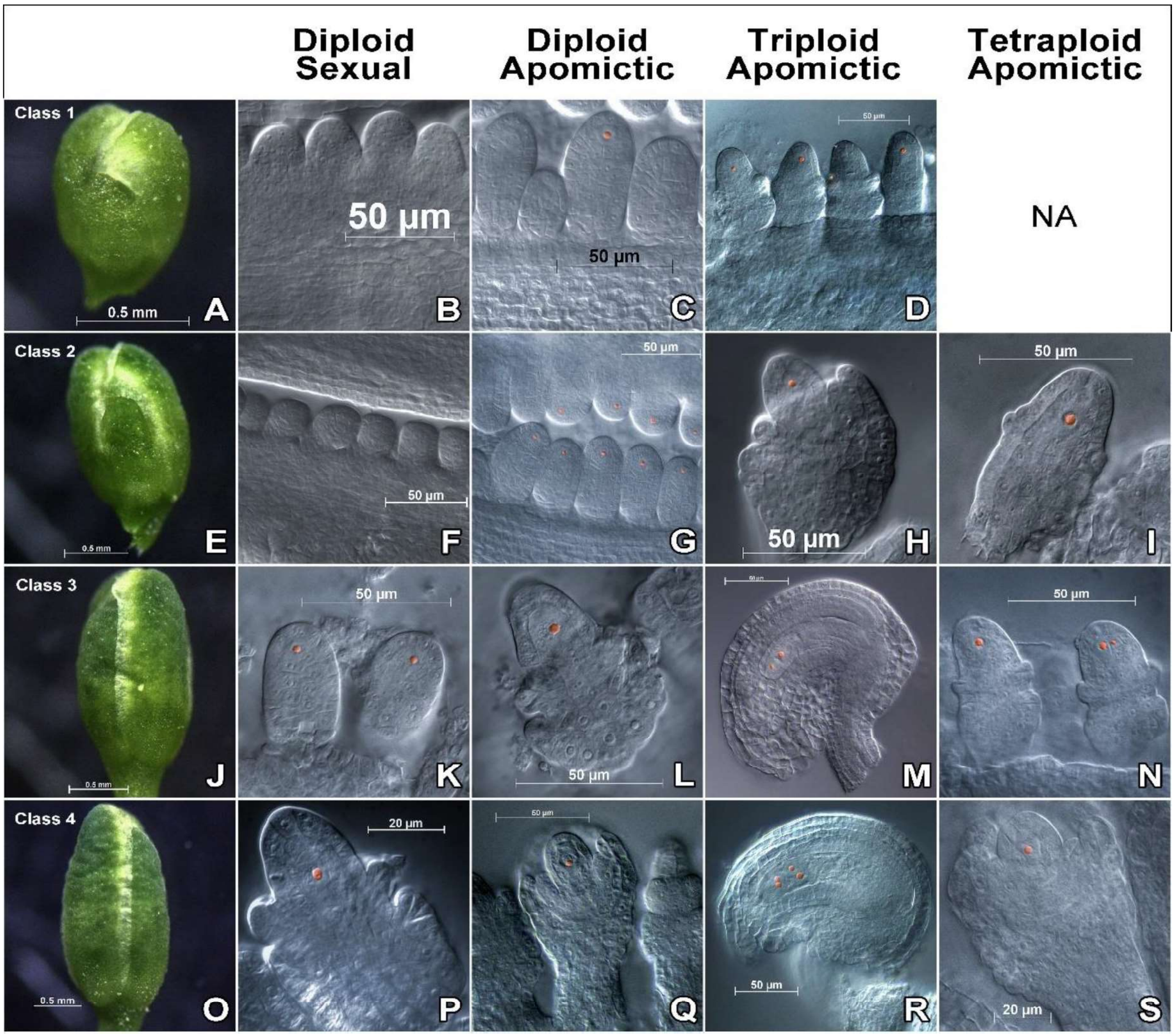

Figure 26. Ovule and female gametophyte development in several *Boechera spp.* lines. **A**: Class 1 flower bud (length 0.5-1mm) of a sexual diploid *Boechera* line; **B**: Ovules primordia (OvP) from a Class 1 flower bud of a diploid sexual line (Archesporial cells not yet visible); **C**: Ovules primordia form a Class 1 flower bud of a diploid apomictic line, one of the four ovules has differentiated an archesporial cell (nucleus highlighted in orange); **D**: Four ovules at megaspore mother cell (MMC) stage with small integument primordia (MMC nucleus highlighted in orange) from a Class1 flower bud of a triploid apomictic line; **E**: Class 2 flower bud (length 1.01-1.5mm) of a sexual diploid Boechera line; **F**: Ovules primordia from a Class 2 flower bud of a diploid apomictic line; **G**: Ovules at AC stage from a Class 2 flower bud of a diploid apomictic line (AC nuclei highlighted in orange); **H**: Ovule at MMC stage with medium size integuments primordia from a Class 2 flower bud of a triploid apomictic line (MMC nucleus highlighted in orange); **I**: Ovule at MMC stage with small integuments primordia from a Class 2 flower bud of a tetraploid apomictic line (MMC nucleus highlighted in orange); **J**: Class 3 flower bud (length 1.51-2mm) of a sexual diploid *Boechera* line; **K**: Ovules at the AC stage with no visible integuments primordia from a Class 3 flower bud of a diploid sexual line (AC nucleus highlighted in orange); **L**: Ovule at the MMC stage with small integuments primordia from a Class 3 flower bud of a diploid apomictic line (MMC nucleus highlighted in orange); **M**: Ovule at the stage of bi-nucleated gametophyte (2NG) from a Class 3 flower bud of a triploid apomictic line (the 2 nuclei of the gametophyte are highlighted in orange); **N**: Ovules at the MMC stage (the ovule on the right has differentiated a double MMC) with small integuments primordia from a Class 3 flower bud of a tetraploid apomictic line (MMC nuclei highlighted in orange); **O**: Class 4 flower bud (length 2.01-2.5mm) of a sexual diploid *Boechera* line; **P**: Ovule at the MMC stage with small/medium integuments primordia from a Class 4 flower bud of a diploid sexual line (MMC nucleus highlighted in orange); **Q**: Ovule at the MMC stage with big integuments primordia from a Class 4 flower bud of a diploid apomictic line (MMC highlighted in orange); **R**: Ovule at the stage of tetra-nucleated gametophyte (4NG) from a Class 4 flower bud of a triploid apomictic line (nuclei in the gametophyte are highlighted in orange); **S**: Ovule at the MMC stage with medium size integuments primordia from a Class 4 flower bud of a tetraploid apomictic line (MMC highlighted in orange).

The previous picture shows that, in the early stages of development, the apomictic lines developed faster than the sexual. In fact, the row of images corresponding to class 1 show a diploid sexual ovule containing only OvP (Figure 26 B), that did not present any archesporial cells. At the same time, the diploid apomictic had bigger OvP with the first AC already visible (Figure 26 C) and the triploid apomictic reached the stage of MMC with integuments primordia that were already visible (Figure 26 D).

In flower buds of class 2, the diploid lines did not advance significantly. However, the diploid apomictic lines had clearly differentiated AC in most of the ovules (Figure 26 G), while the sexuals were stuck at the OvP stage (Figure 26 F); at the same time the triploid continued to develop reaching MMC stage with medium size integuments primordia (Figure 26 H).

In class 3, the developmental differences between lines became more evident when compared to sexual lines, which at that stage, just differentiated archesporial cells (Figure 26 K). At the same time, the apomictic diploid lines had much bigger ovules at MMC stage (Figure 26 L) and the triploid reached already the bi-nucleate gametophyte stage (Figure 26 M).

The sexual diploid lines entered the MMC stage only in class 4 (Figure 26 P), while the triploid lines showed already tetra-nucleated gametophytes (Figure 26 R).

The only available tetraploid line, originated from a diploid parent (BoADi-01), did not show any relevant visual differences with the diploid apomictic lines except for a much higher differentiation of multiple MMC (Figure 26 N).

Unlike the early stages, that showed clear developmental differences between lines with different ploidy and reproduction, later stages appeared to be much closer in terms of development. This suggest that the developmental paces were changing, allowing the slower lines to reduce their developmental gap with the fastest ones. The dynamic changes in developmental speed were visible when the flower buds reached class 7; at this time point, the female gametophyte was mature in the majority of the ovules of the triploid apomictic lines while, all the others were mainly at the bi-nucleated or tetra-nucleated stage as shown in Figure 27. Furthermore, the diploid apomictic lines, that had previously a faster development, slowed down in comparison with their sexual counterparts, which as visible in Figure 27 B, were mainly at the 4NG stage while diploid apomicts still carried ovules at the FM stage (Figure 27 C).

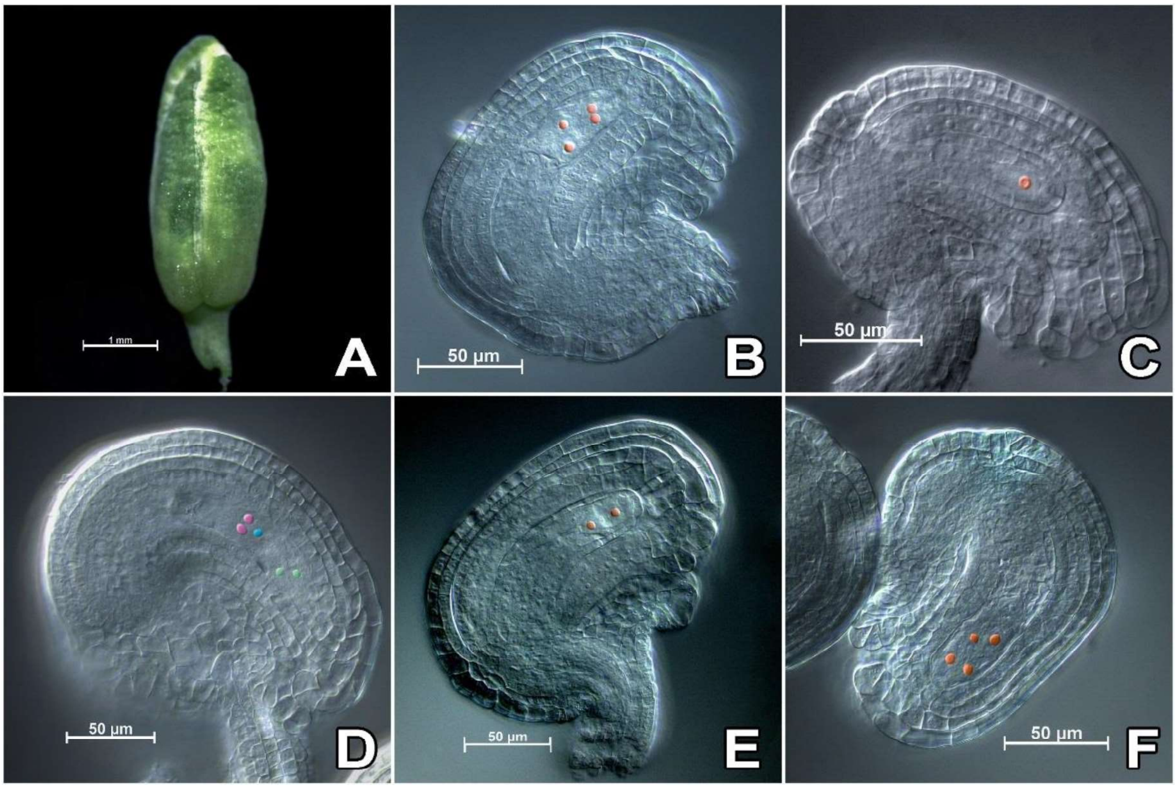

Figure 27. Female gametophyte development of ovules from flower buds at **class 7** from different *Boechera spp.* lines. **A**: class 7 flower bud (3.51-4mm) from a diploid sexual line; **B**: Ovule at the stage of tetra-nucleated female gametophyte (4NG) with well-developed integuments from a class 7 flower bud of a sexual diploid line (nuclei of the gametophyte highlighted in orange); **C**: Ovule at the stage of functional megaspore (FM) with well-developed integuments from a class 7 flower bud of a diploid apomictic line (FM highlighted in orange); **D**: Ovule carrying a mature female gametophyte from a class7 flower bud of an apomictic triploid line (synergids highlighted in green, polar nuclei highlighted in pink, egg cell highlighted in blue) ; **E**: Ovule at the bi-nucleated gametophyte stage (2NG) with well-developed integuments from a class 7 flower bud of a tetraploid apomictic line (nuclei of the gametophyte highlighted in orange); **F**: Ovule at the tetra-nucleated gametophyte stage (2NG) with well-developed integuments from a class 7 flower bud of a tetraploid apomictic line (nuclei of the gametophyte highlighted in orange).

Further histological analysis of ovules and female gametophyte development in class 8 flower buds, showed that the sexual diploid lines were mainly at 4NG stage (Figure 28 B) or at mature gametophyte stage (Figure 28 C), while the diploid apomicts were mainly at 2NG (Figure 28 D) and 4NG (Figure 28 E). This means, that the sexual diploid (slower in the early stages) went further in development if compared with their apomictic counterpart. Triploid apomictic lines, that already reached the maturity of gametophyte in class 7, were at the same stage also in class 8 as shown in Figure 28 F (one of the rare pictures of mature female gametophyte with 2 out of 3 antipodals that are still visible).

Figure 28 G, H and I (respectively: FM, 2NG and mature gametophyte stage) displays ovules coming from the same pistil of the tetraploid apomictic line. This line is slightly faster than its diploid apomictic mother; however, it was also characterized by a higher desynchronization of development, showing ovules of the same pistil that extended through 4 or 5 different developmental stages (*i.e.* from MMC/BI to mature female gametophyte).

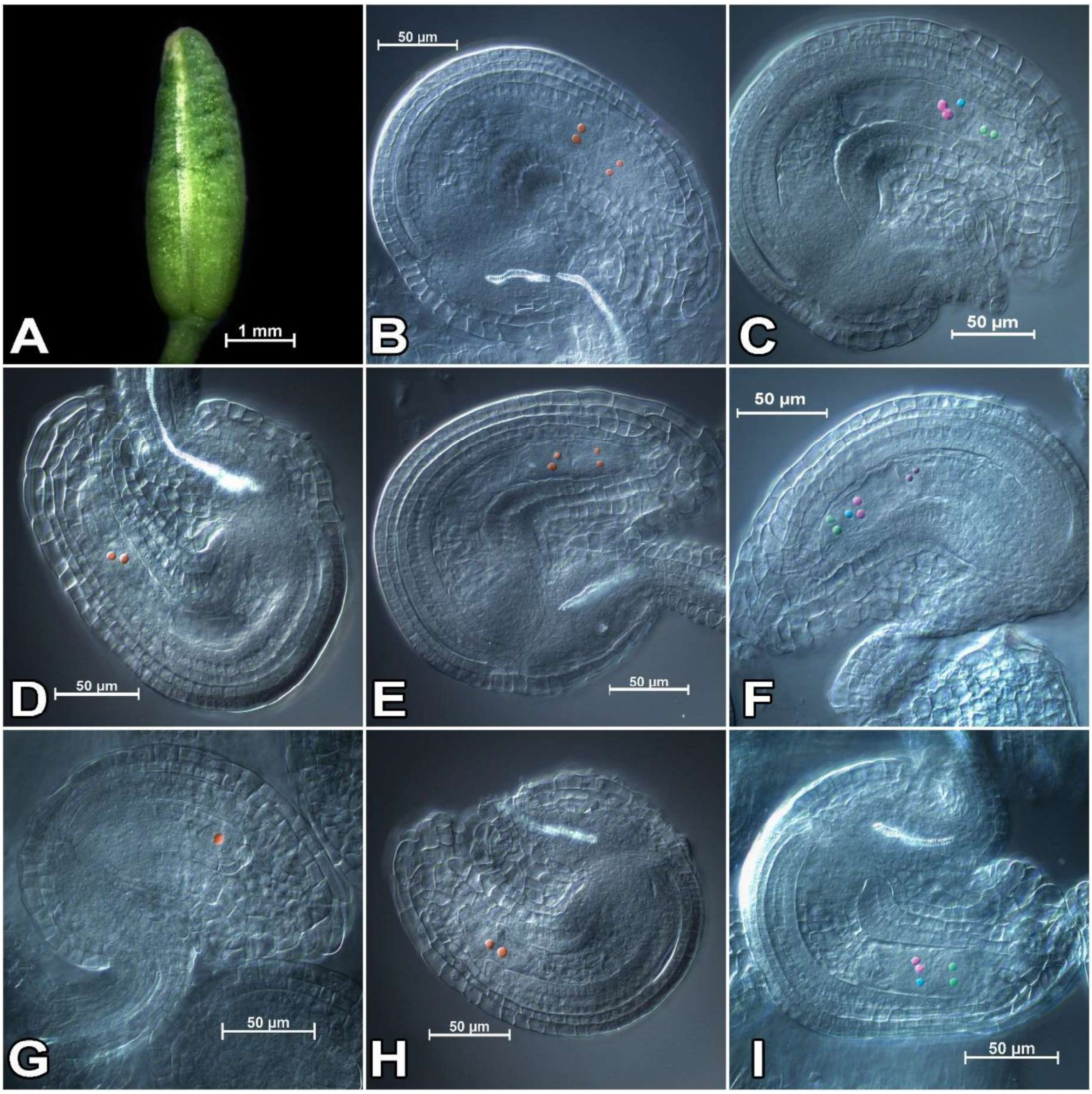

Figure 28. Female gametophyte development of ovules from flower buds at **class 8** from different *Boechera spp.* lines. **A**: class 8 flower bud (4.01-4.5mm) from a diploid sexual line; **B**: Ovule at the stage of tetra-nucleated female gametophyte (4NG) with well-developed integuments from a class 8 flower bud of a sexual diploid line (nuclei of the gametophyte highlighted in orange); **C**: Ovule carrying a mature female gametophyte with well-developed integument from a class 8 flower bud of a sexual diploid line (synergids in green, egg cell in blue, polar nuclei in pink); **D**: Ovule at the 2NG stage with well-developed integuments from a class 8 flower bud of a diploid apomictic line (nuclei of the gametophyte highlighted in orange); **E**: Ovule at 4NG stage with well-developed integuments from a class 8 flower bud of a diploid apomictic line (nuclei of the gametophyte highlighted in orange); **F**: Ovule carrying a mature female gametophyte from a class 8 flower bud of a triploid apomictic line (synergids in green, egg cell in blue, polar nuclei in pink, antipodals in violet); **G**: Ovule at the stage of functional megaspore (FM) with well-developed integuments from a class 8 flower bud of a tetraploid apomictic line (FM nucleus highlighted in orange); **H**: Ovule at the 2NG stage with well-developed integuments from a class 8 flower bud of a tetraploid apomictic line (nuclei of the gametophyte highlighted in orange); **I**: Ovule carrying a mature female gametophyte with well-developed integument from a class 8 flower bud of a tetraploid apomictic line (synergids in green, egg cell in blue, polar nuclei in pink).

Class 9 and 10 flower buds are the two latest stages that are reported in this study. They include mainly mature gametophyte stages or, in the case of apomictic lines, several aborted ovules. In any case, in these classes, mainly one or two developmental stages were detected. Therefore, it was not possible to see big visual differences between sexual and apomictic lines, with the exception of a much higher percentage of aborted ovules. A visual overview of developmental stages at class 10 is reported in Figure 29.

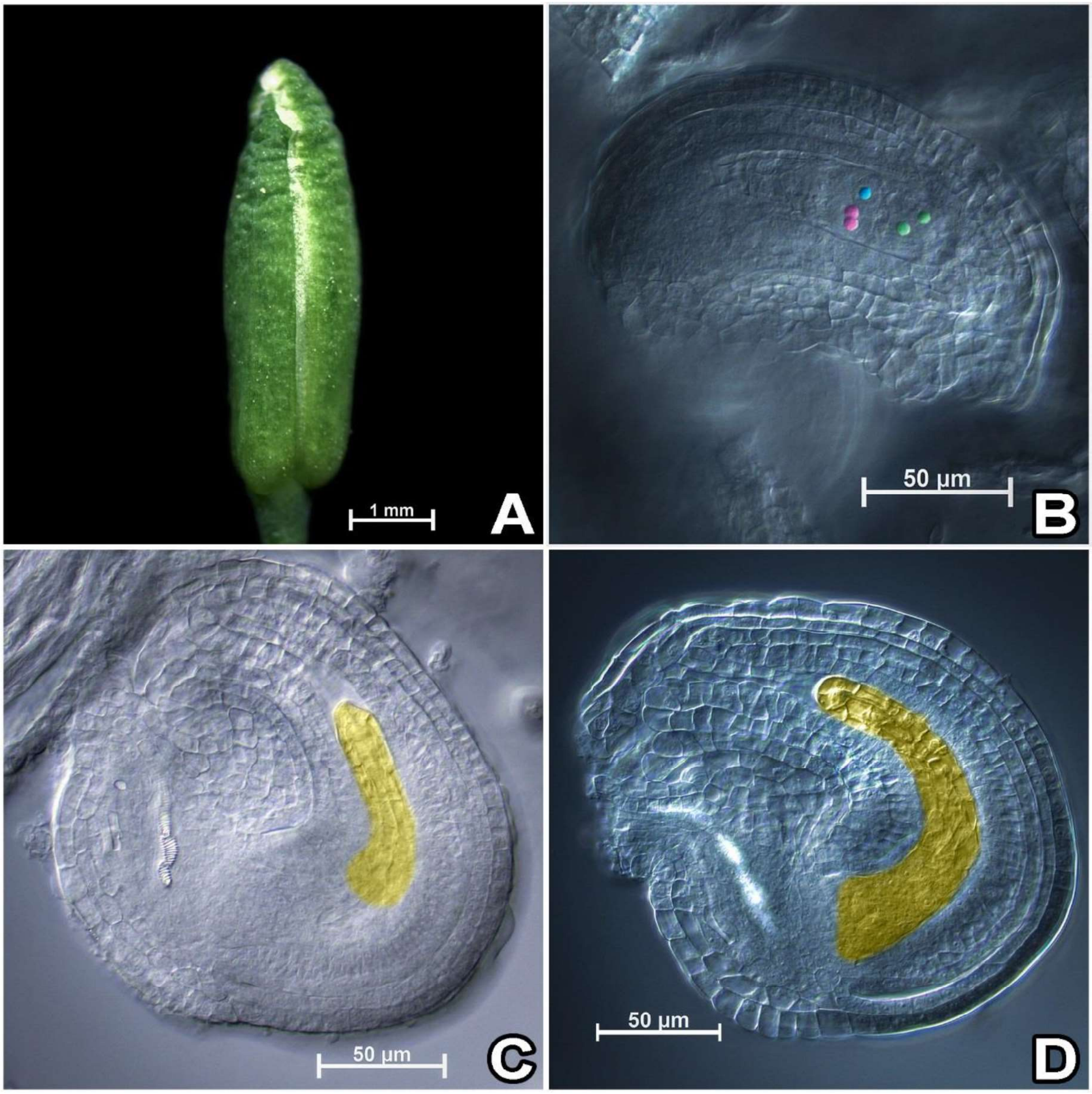

Figure 29. Female gametophyte development of ovules from flower buds at **class 10** from different *Boechera spp.* lines. **A**: Class 10 flower bud (5.01-5.5mm) from a diploid apomictic line; **B**: Ovule carrying a mature female gametophyte from a Class 10 flower bud of a diploid apomictic line (synergids in green, egg cell in blue, polar nuclei in pink); **C** and **D**: Ovules carrying an aborted gametophyte from a Class 10 flower bud of a diploid apomictic line (gametophytic region highlighted in yellow).

Figure 29 (A, B and C) corresponds to ovules belonging to the same pistil of a class 10 flower bud in a diploid apomictic line. The ovule of Figure 29 B is smaller than C and D. This is because it was located in the distal part of the pistil, where ovules are not as developed as in the basal area. This acropetal gradient of development is not easily detectable at the early stages, but becomes evident with the increase of flower bud size, especially after class 8.

Ovules C and D of Figure 29 were formed in the basal region of the pistil, and unlike ovule B, they do not carry any gametophyte, and their gametophytic domain (highlighted in yellow) appeared to be shrunk and smaller than the corresponding domain showed in Figure 29 B. The colored tissues in Figure 29 C and D did not contain enlarged visible nuclei, meaning that the developing female gametophyte was aborted. This is consistent with the abortion frequencies reported in Table 4, which show higher abortion rates in the analyzed apomictic lines.

Germination rates in *Hypericum*

Germinability of seeds is an important trait that contributes to the general fitness of an individual. For this reason, the germination rates of different lines of *Hypericum perforatum* were tested by sowing 300 seeds per line over two generations, in order to determine if there were significant differences of germinability between lines.

The results deriving from these observations are reported in the following graph (Figure 30).

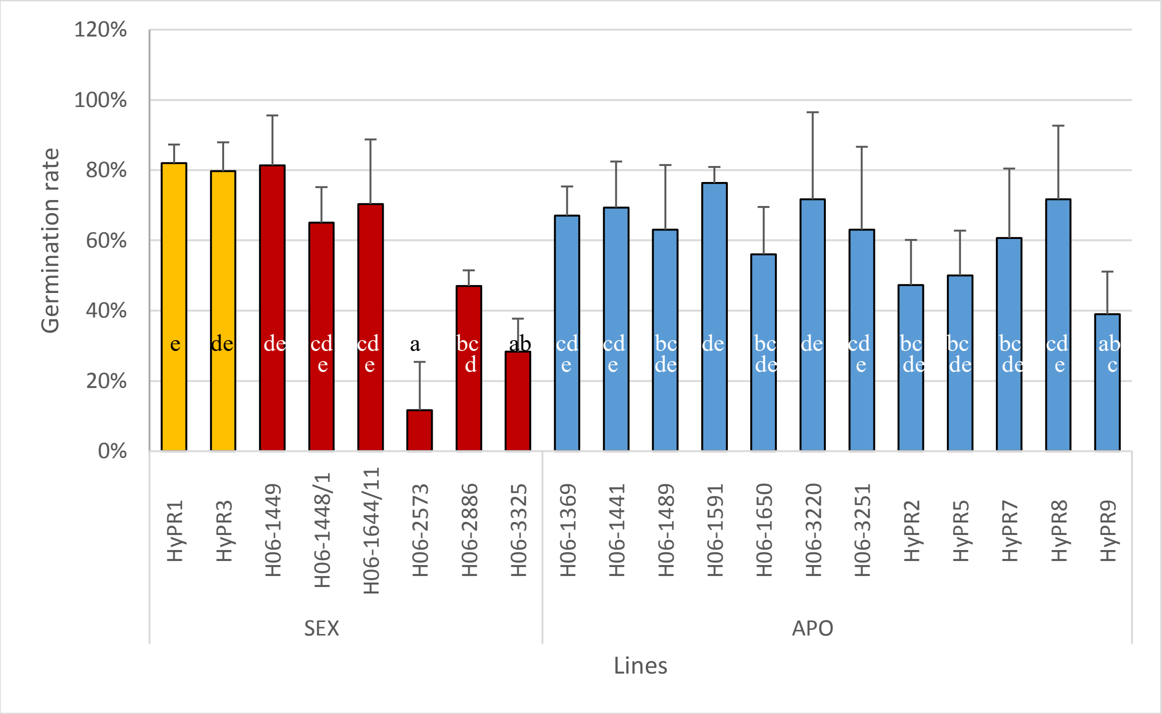

Figure 30. Germinability of seeds from 20 *Hypericum* lines. Yellow = diploid sexual lines; Red = hexaploid sexual lines; Blue = tetraploid apomictic lines. Different letters = significant differences between the lines according to Tukey test. $R^2 = 0.977$; factorial ANOVA $P < 0.05$ on transformed data (Arcsin($\sqrt{y}$)).

Hypericum lines rarely reached germination rates that are close to 100%. The statistical analysis showed that the germinability of each line is stable through both analyzed generations, and that the differences obtained, were due to the effect of the line ($P<0.0001$)

and neither to the type of reproduction nor to the interaction between the analyzed factors (generation, reproduction and line).

Seed set analysis in *Hypericum*

The seed set data analysis showed that the apomictic lines had levels of fertility with the tendency to be higher than sexual lines (Figure 31).

Line H06-3220 presented the highest value and was statistically different from all sexual lines (Figure 31). The factorial ANOVA performed on these data, showed that the type of reproduction had a significant effect on the fertility (P<0.0001) as did the factor line (P<0.0001).

No statistical effect was documented for the generation nor in the interaction between the factors.

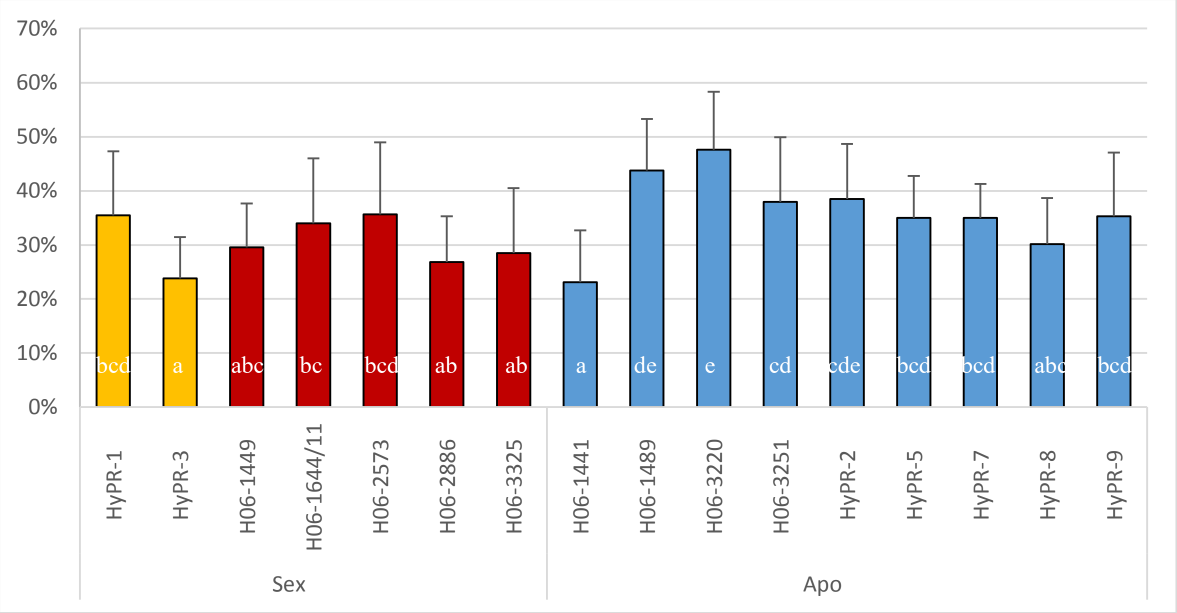

Figure 31. Levels of fertility (%) of 16 *Hypericum* lines over two generations. Yellow = sexual diploid lines; Red = sexual hexaploid lines; Blue = apomictic tetraploid lines. Different letters indicate significant differences between the lines according to Tukey test. $R^2 = 0{,}963$; multifactorial ANOVA $P < 0.05$ on transformed data (Arcsin($\sqrt{y}$)).

Even if the differences in fertility are not visually striking like in the case of *Boechera*, there was ca. 6% of difference between the mean of percentage of fertile ovules per capsule of all sexual lines vs all apomictic lines.

In the case of *Hypericum,* were rarely detected capsules with more than 50% of fertile seeds. This was due to a morphological limitation of the mature capsule in *Hypericum* lines. Although a pistil could differentiate between 150 and 350 ovules (223.5 in average), only 50 to 100 fertile seeds (76.9 in average) could fit into the mature capsule.

An average capsule of *Hypericum* was typically filled with fully grown seeds (Figure 32 C and D), except in the case of very high sterility levels, where the capsule was semi-empty, and hundreds of white infertile small ovules were still attached to the placental tissue (Figure 32 A and B).

At maturity, the fertile seeds turned black (Figure 32 E), while the infertile ovules dried out and were more difficult to detect, therefore this was not considered the most appropriate stage for a proper evaluation of seed set.

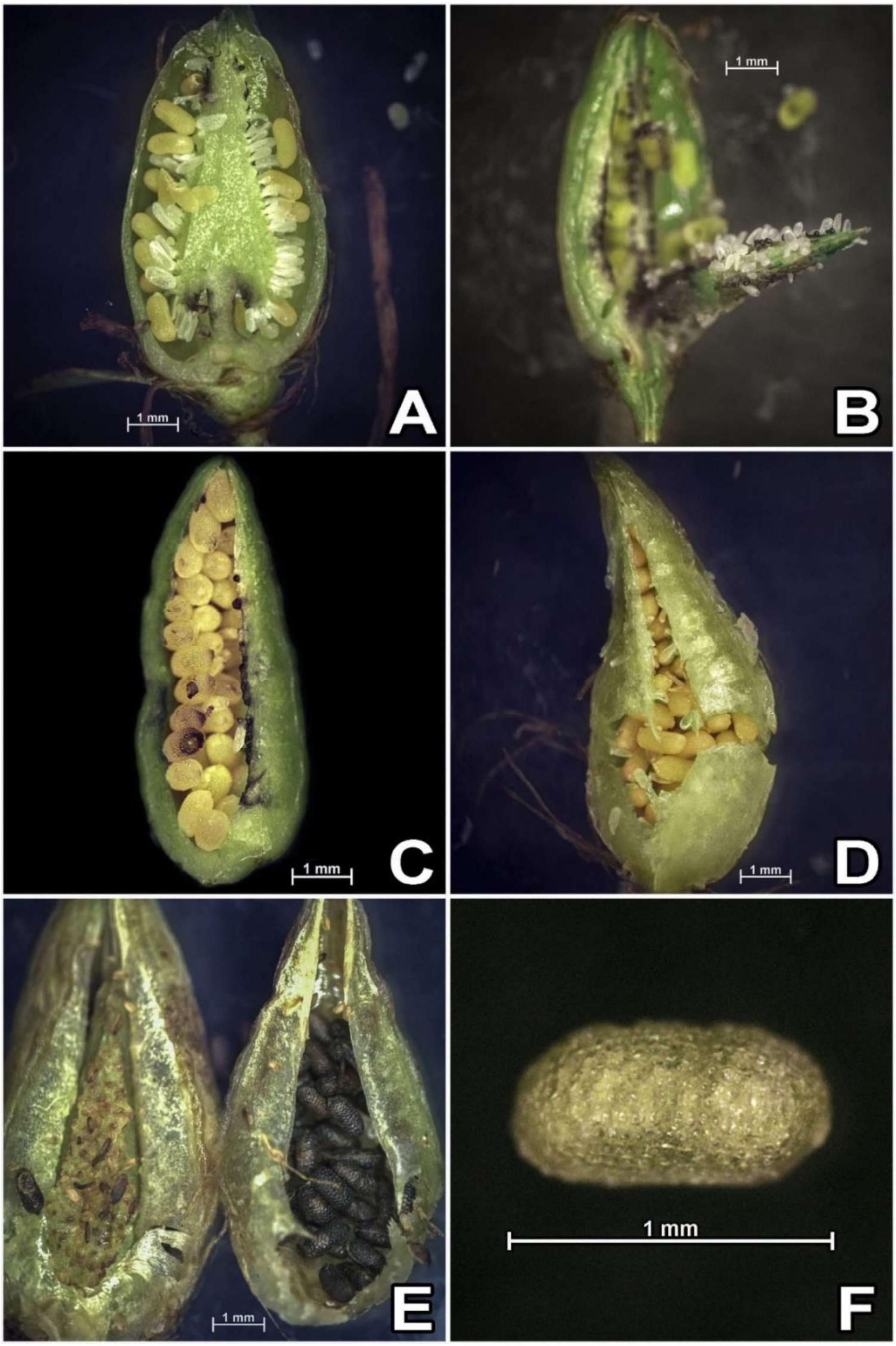

Figure 32. Dissected capsules of *Hypericum perforatum.* **A**: Longitudinal section of a capsule from sexual line HyPR1 (small infertile ovules attached to the placental tissue); **B**: Capsule from line HyPR-1 with excised placental tissue; **C**: Dissected carpel of a capsule from sexual line HyPR-1 filled with fertile seeds; **D**: Dissected carpel of a capsule from apomictic line HyPR-7 filled with fertile seeds; **E**: Dissected capsule from sexual line HyPR-1 at seeds maturity (seeds turned black); **F**: Detail of a single seed from sexual line HyPR-1 right before turning black at maturity.

Number of capsules per plant in *Hypericum*

The number of capsules per plant was measured on 16 lines over two generations. This trait, like in the case of seed set, can be measured exclusively in the field between September and October, about one month after the flowering season, due to the entomophily of *Hypericum*. The plants grown in greenhouse or phytotron conditions, produced several hundreds of flowers (up to 1000 per plant), but it is extremely rare to find a capsule containing seeds in these growth conditions because of the lack of pollinators.

Through this analysis, high variability in the number of capsules per plant even between plants of the same line was detected. The results reported in Figure 33 (especially the amplitude of standard deviations), confirm that this trait is not as stable as the other ones reported in this study. The analysis of variance showed significant differences between lines ($P = 0.0005$), reproduction modes ($P<0.0001$) but also between the two analyzed generations ($P = 0.0001$).

The difference between generations is probably due not only to the highly variable nature of the trait, but also to the fact that these data were obtained from plants grown in the field during two different years. The data from the IPK weather station (supplemental data Figure 72 and Figure 73) showed that, the year of the second generation was warmer with an accumulation of at least 100 Growing-degrees-day higher than the previous year (calculated for the 30th of June, right before the beginning of the flowering time in July).

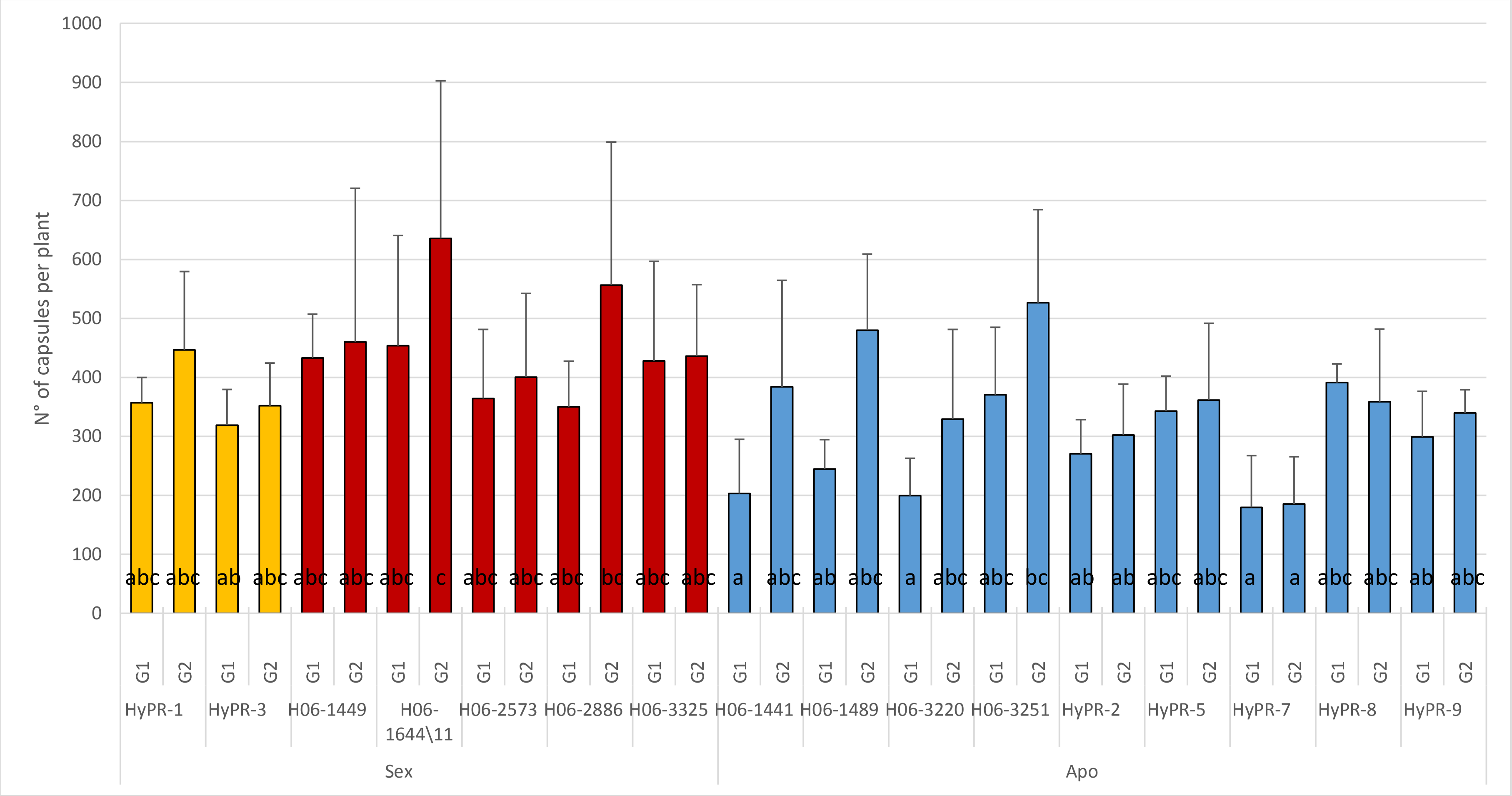

Figure 33 Number of capsules per plant measured on 16 *Hypericum* lines over two generations (G1, G2). Yellow = sexual diploid lines; Red = sexual hexaploid lines; Blue = apomictic tetraploid lines. Different letters indicate significant differences between the lines according to Tukey test. $R^2 = 0,44$; $P<0.05$ (multifactorial ANOVA).

Estimation of potential fitness in *Hypericum*

An estimation of potential fitness was performed for 16 *Hypericum* lines using data measured over 2 generations.

In order to calculate the potential fitness in *Hypericum*, the same procedure adopted in *Boechera* was used, following the Equation 1:

$$\boxed{Potential\ fitness = \bar{x}_{gr} * \bar{x}_{fspcpl} * \bar{x}_{cplpp}}$$

Where $\bar{x}_{gr}$ is the average germination rate, $\bar{x}_{fspcpl}$ is the average number of fertile seeds per capsule and $\bar{x}_{cplpp}$ is the average number of capsules per plant.

This formula was applied twice and independently for the two analyzed generations because the trait "number of capsules per plant" was significantly different between generations. The results of this evaluation are given in Figure 34.

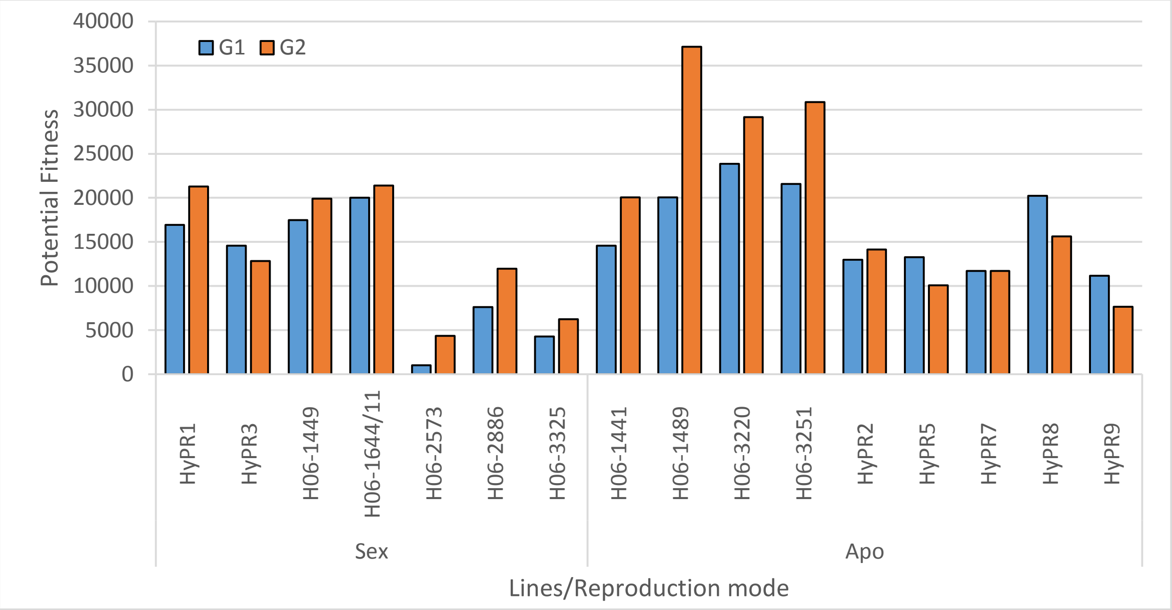

Figure 34. Estimation of potential fitness in 16 *Hypericum*. lines; $\bar{x}_{gr}$ = average germination rate; $\bar{x}_{fspcpl}$ = average number of fertile seeds per capsule; $\bar{x}_{cplpp}$ = average number of capsules per plant. G1 = generation 1; G2 = generation 2

From a fitness point of view, the analyzed lines were highly heterogeneous. T-test analysis between apomictic and sexual reproduction mode, performed separately for each generation, did not detect any statistically significant differences.

Flowering time in *Hypericum* lines

The flowering time from the emergence of seedlings was measured on 16 *Hypericum* lines on 10 plants per line over two generations (320 screened plants in total). The results of these measurements are reported in Figure 35.

Number of capsules per plants showed significant differences between the two analyzed generations, confirming that the detected differences were not only related to line or reproductive mode, but to environmental growth conditions as well. According to the Kruskal-Wallis there were also significant differences between reproductive modes and between lines ($P \leq 0.05$).

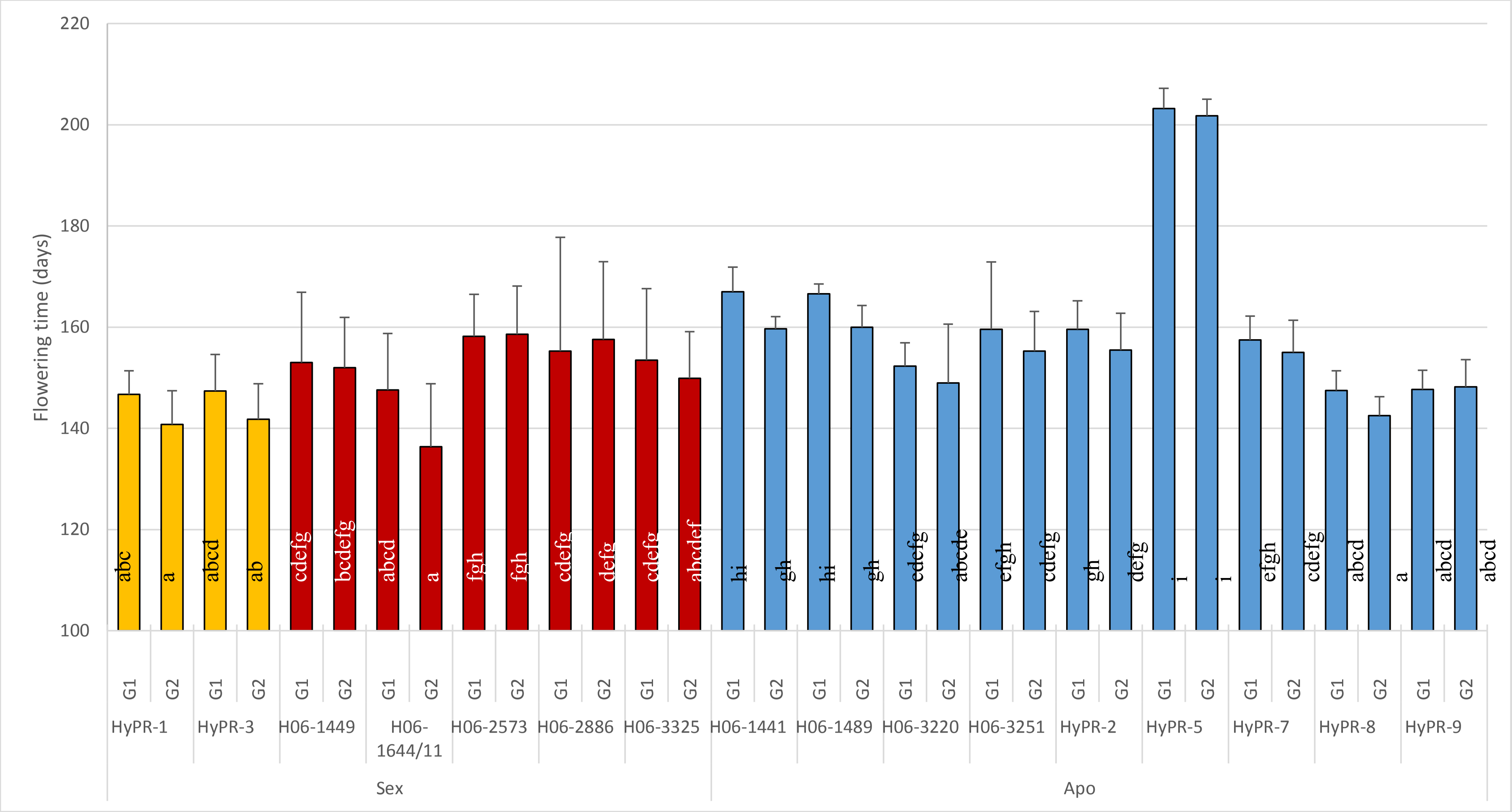

Figure 35. Flowering time measured on 16 *Hypericum* lines over two generations (G1, G2). Yellow = sexual diploid lines; Red = sexual hexaploid lines; Blue = apomictic tetraploid lines. Different letters indicate significant differences between the lines according to Kruskal-Wallis test ($P \leq 0.05$).

Flowering time is another essential trait for assessing the potential fitness. A fast flowering line may have a higher number of generations during one year. In order to incorporate this trait in the estimation of potential fitness, the formula reported in the material and methods was used considering a warm season period (*WD*) of 200 days (from march 15th to September 30th, when plants were able to grow or flower in the field). The outcome of this calculation corresponds to values of partial fitness corrected for their flowering time ($PF_{(FT)}$) (Figure 36).

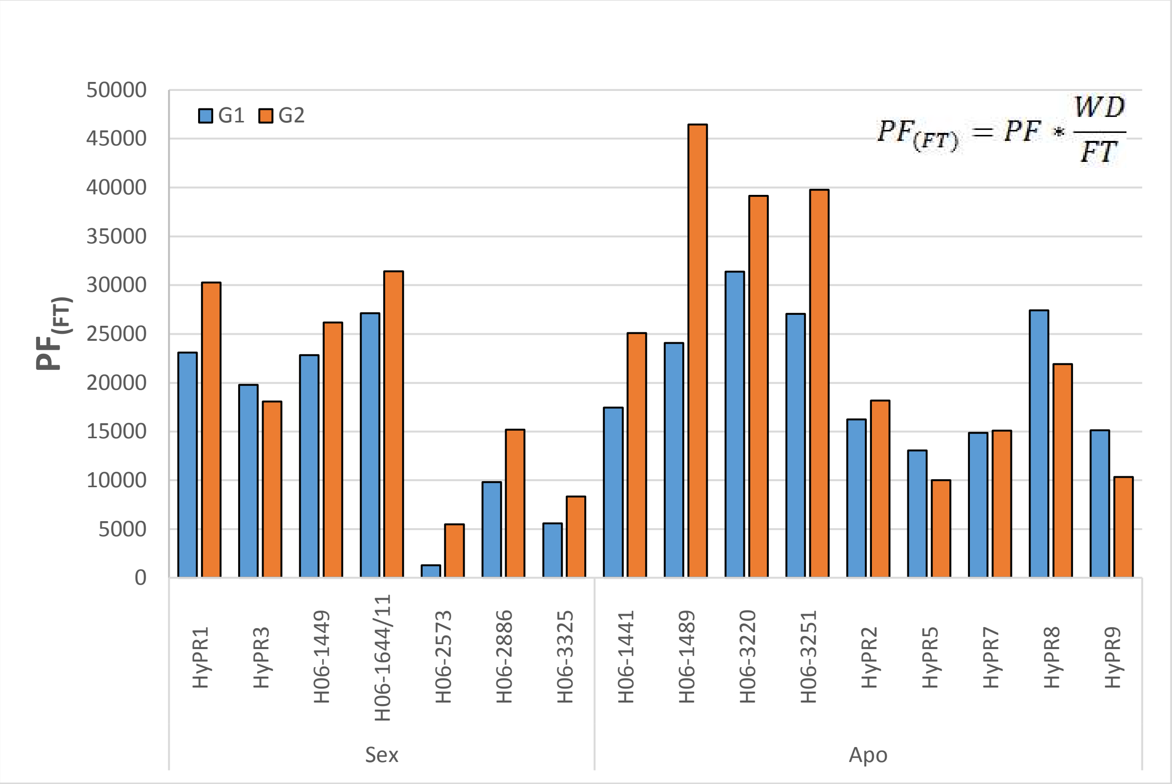

Figure 36. Partial estimation of fitness in 16 *Hypericum.* Lines corrected for flowering time using equation 1 (reported in the graph area) where: $PF_{(FT)}$=Partial fitness (flowering time corrected); PF = Partial fitness non corrected; WD = warm season days (in this case 200 days); FT = flowering time from emergence (days). G1 = generation 1; G2 = generation 2

The values reported in this graph are also available in Table 18 (supplemental data), where it is shown a mild effect of the flowering time correction over the potential fitness ranking. According to the T-test, sexual and apomictic lines had no statistical difference in any of the generations evaluated in this study (G1: $P = 0.2425$; G2: $P = 0.3627$).

Ploidy dynamics in *Hypericum* lines

In order to understand the reproduction dynamics and to detect eventual polyploidization events, the ploidy level of leaves and seeds of 15 *Hypericum* lines were measured over two generations.

Leaves flow cytometry

Ploidy analysis of leaf material (Figure 37) showed that in several lines there were individuals that deviated from the expected ploidy of the line. This probably was the result of cross pollination between lines of different ploidy, that were grown in the same field in the presence of free pollinators. As a confirmation of the abovementioned phenomenon, sexual lines (diploid and hexaploid) showed higher percentages of individuals that deviated from the expected ploidy level in comparison with apomictic lines (Figure 38).

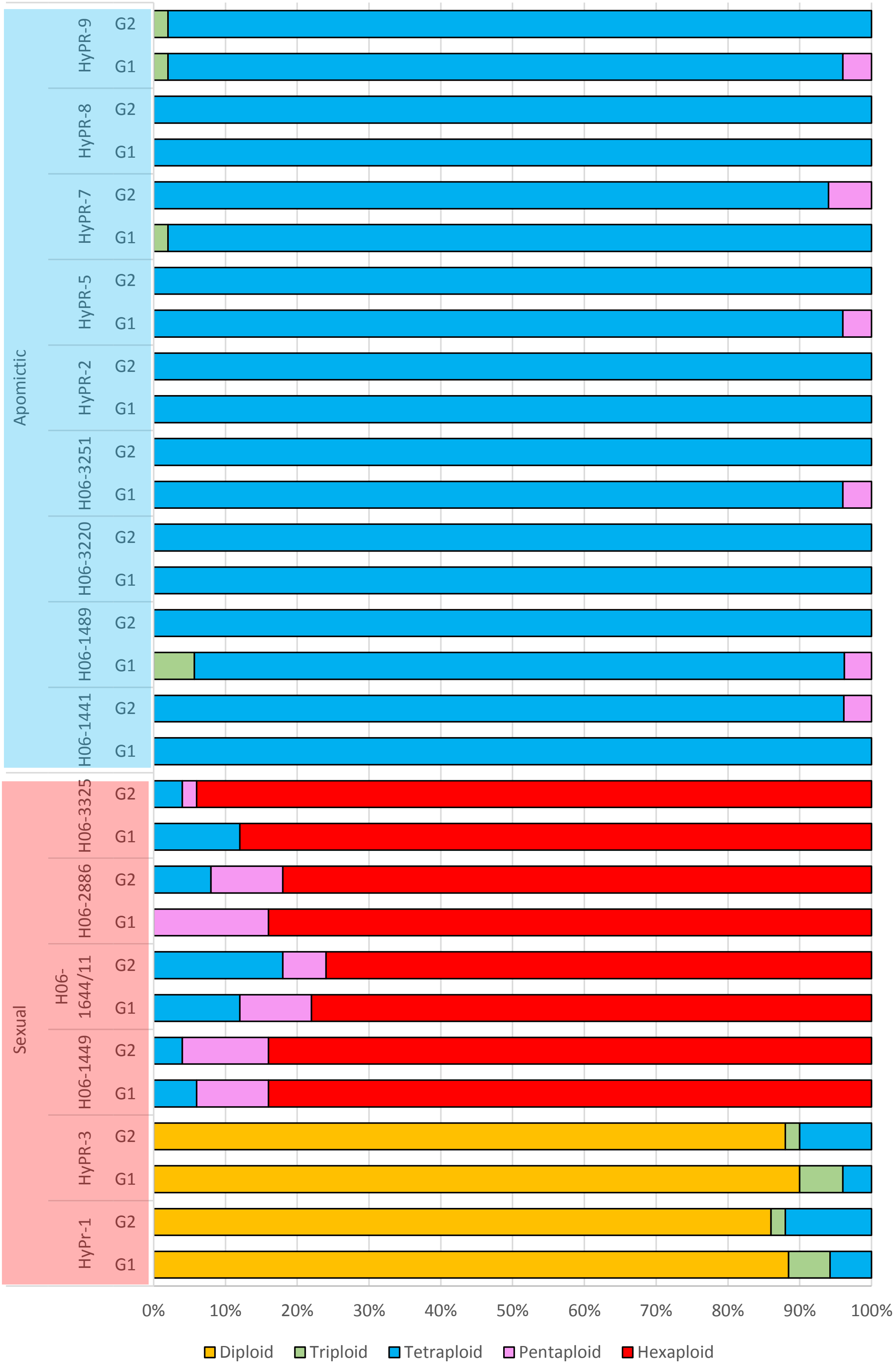

Figure 37. Leaves ploidy levels of 15 lines of *Hypericum* measured across two generations (G1, G2). Red area includes all the sexual lines; Blue area includes all the apomictic lines.

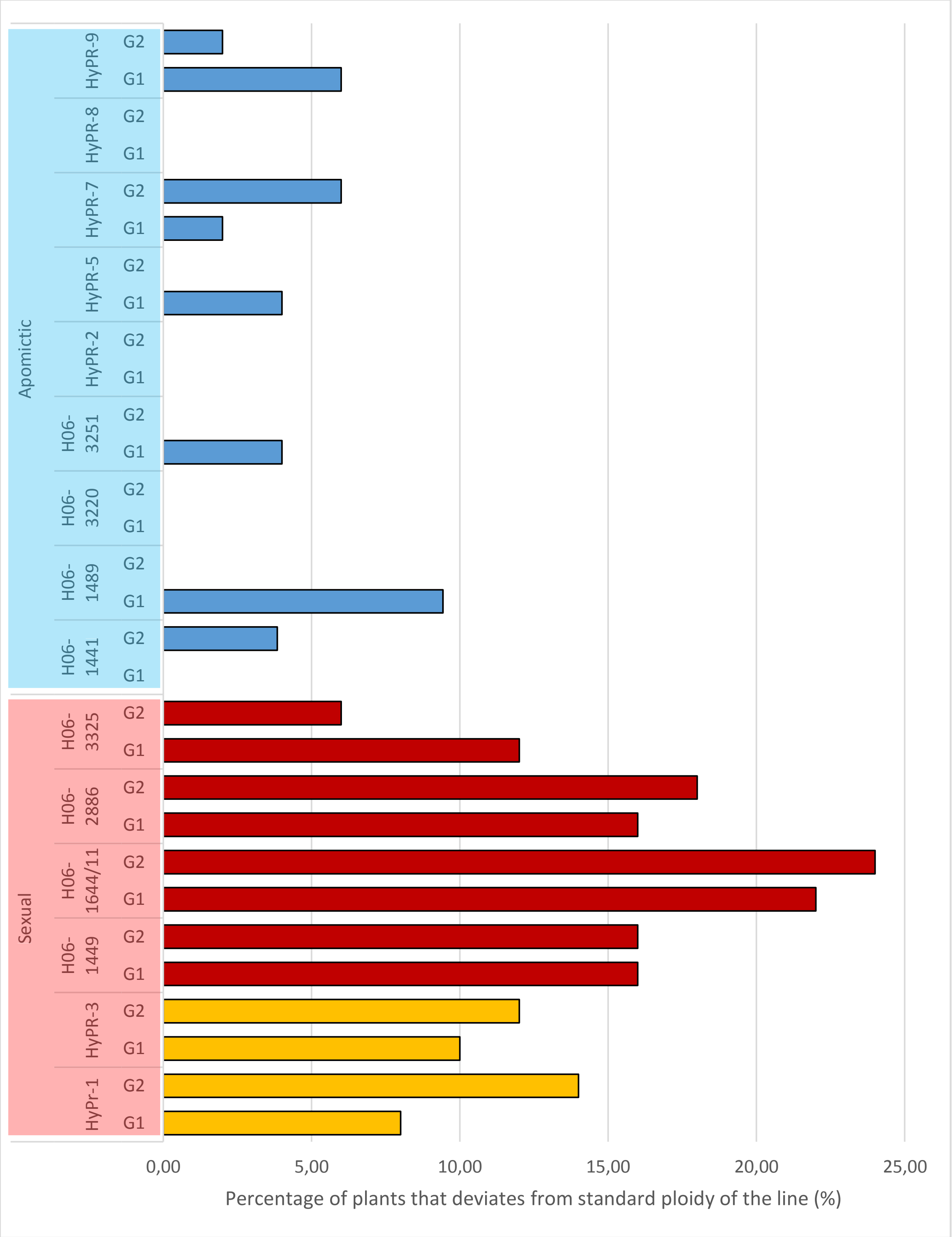

Figure 38. Percentage of individuals with deviations from the original ploidy level of the corresponding *Hypericum* line. These percentages are derived from the same dataset summarized in *Figure 37* by adding together the categories: triploid and tetraploid detected in the diploid sexual lines, tetraploid and pentaploid detected in the hexaploid sexual lines and triploid and pentaploid detected in the tetraploid apomictic lines. Yellow = sexual diploid line; Red = sexual hexaploid line; Blue = apomictic tetraploid line. Red area includes all the sexual lines; Blue area includes all the apomictic lines.

Flow cytometric seed screen (FCSS)

The individuals of the first generation that deviated from the standard ploidy of their corresponding line were eliminated from the field before flowering, so only diploids (from diploid sexual lines), tetraploids (from tetraploid apomictic lines) or hexaploids (from hexaploid sexual lines) were allowed to produce new seeds. These seeds were used to generate G2 plants, but they were also analyzed for embryo and endosperm ploidy, in order to determine the reproductive mode of the line and, when present, its cross with other lines of different ploidy.

The FCSS showed that many seeds in several lines carried embryos deviating from the expected level of ploidy. Like in the case of *Boechera*, also for *Hypericum,* the percentage of deviation from expected ploidy detected in seeds and in leaves were compared (Figure 39). As a result, it was detected that percentages of deviation in seeds were always higher than the corresponding percentages in leaves. This suggested that there could be a partial reproductive barrier against these ploidy deviations.

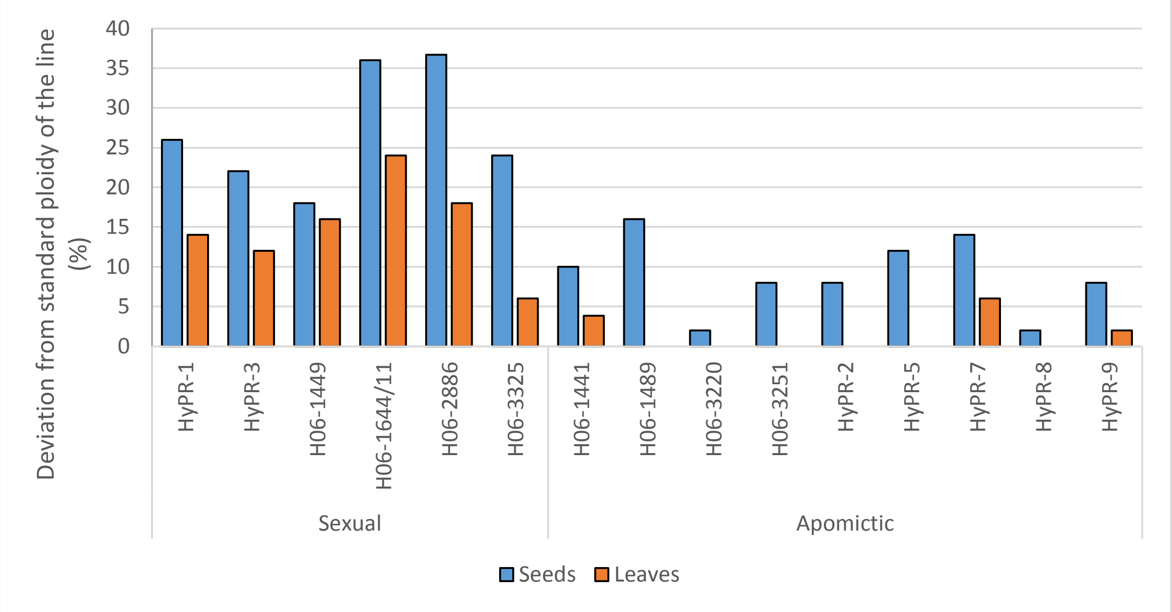

Figure 39. Percentage of seeds carrying embryos whose ploidy deviates from the standard ploidy of the corresponding *Hypericum* line. These percentages are calculated by adding together: triploid and tetraploid detected in the diploid sexual lines, tetraploid and pentaploid detected in the hexaploid sexual lines and triploid and pentaploid detected in the tetraploid apomictic lines.

The ploidy analysis on seeds (flow cytometric seeds screen: FCSS), identified 10 different types of seed, 9 of which are reported in Figure 40. The tenth class includes all the seeds that gave unclear results. The FCSS showed normally two peaks: a bigger one associated with the embryo, which constitutes the bigger portion of the seed, and the smaller one that is associated with the endosperm. The relative positions of the two peaks on the axis x, are used to determine the reproductive mode. An embryo/endosperm ratio of 1:1.5 (Figure 40 A and B) is associated with sexual reproduction, while 2:2.5 (Figure 40 C) indicates apomictic reproduction accompanied by formation of non-autonomous endosperm.

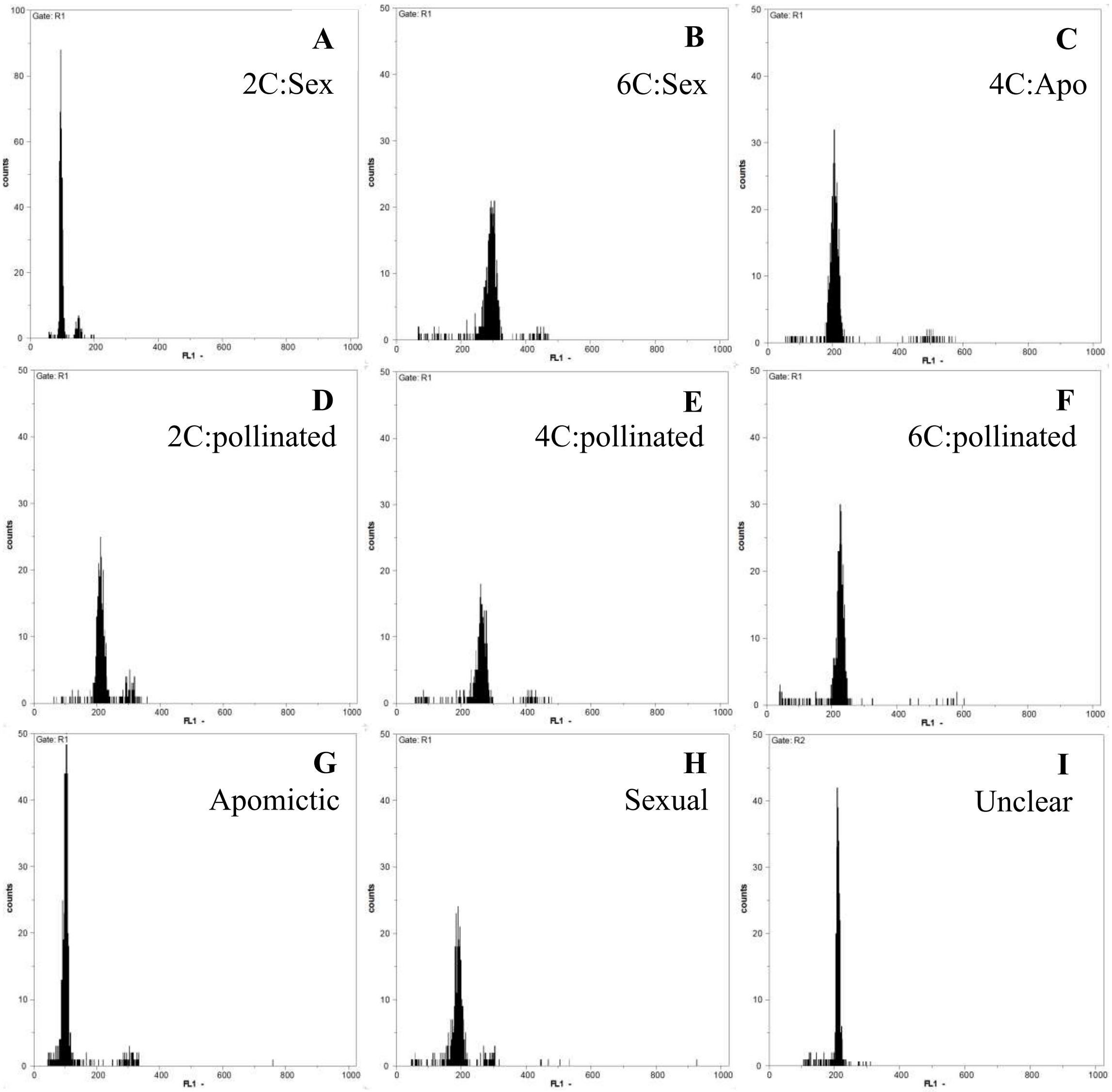

Figure 40. FCSS (flow cytometric seed screen) histograms from 15 different *Hypericum* lines. **A**: seed from a diploid sexual line (2C embryo, 3C endosperm); **B**: seed from an hexaploid sexual line (6C embryo, 9C endosperm); **C**: seed from a tetraploid apomictic line (4C embryo, 10C endosperm); **D**: seed from an hexaploid sexual line carrying a 4C embryo and a 6C endosperm as a result of pollination from a diploid line (2C:pollinated); **E**: seed from an hexaploid sexual line carrying a 5C embryo and an 8C endosperm as a result of pollination from a tetraploid line (4C:pollinated); **F**: seed from a diploid line carrying a tetraploid embryo (very weak endosperm signal) as a result of pollination from an hexaploid line (6C:pollinated); **G**: seed from a diploid sexual line carrying a 2C embryo and a 6C endosperm as a result of apomictic reproductive mode (apomictic seed from sexual line); **H**: seed from a tetraploid apomictic line carrying a 4C embryo and a 6C endosperm as a result of sexual reproductive mode (sexual seed from apomictic line); **I**: seed from a tetraploid apomictic line with no endosperm detected as a result of probable endosperm failure (no endosperm).

The frequencies of the ten types of seeds in all the analyzed *Hypericum* lines are reported in Figure 41, where it is visible another trend associated with the mode of reproduction. The green category “no endosperm” is more represented in the apomictic lines, where this trait in average is found in 19.77% of the analyzed seeds in comparison with the sexual lines, where the average is only 5.8%. A representation of this trait alone is available in supplemental data (Figure 74).

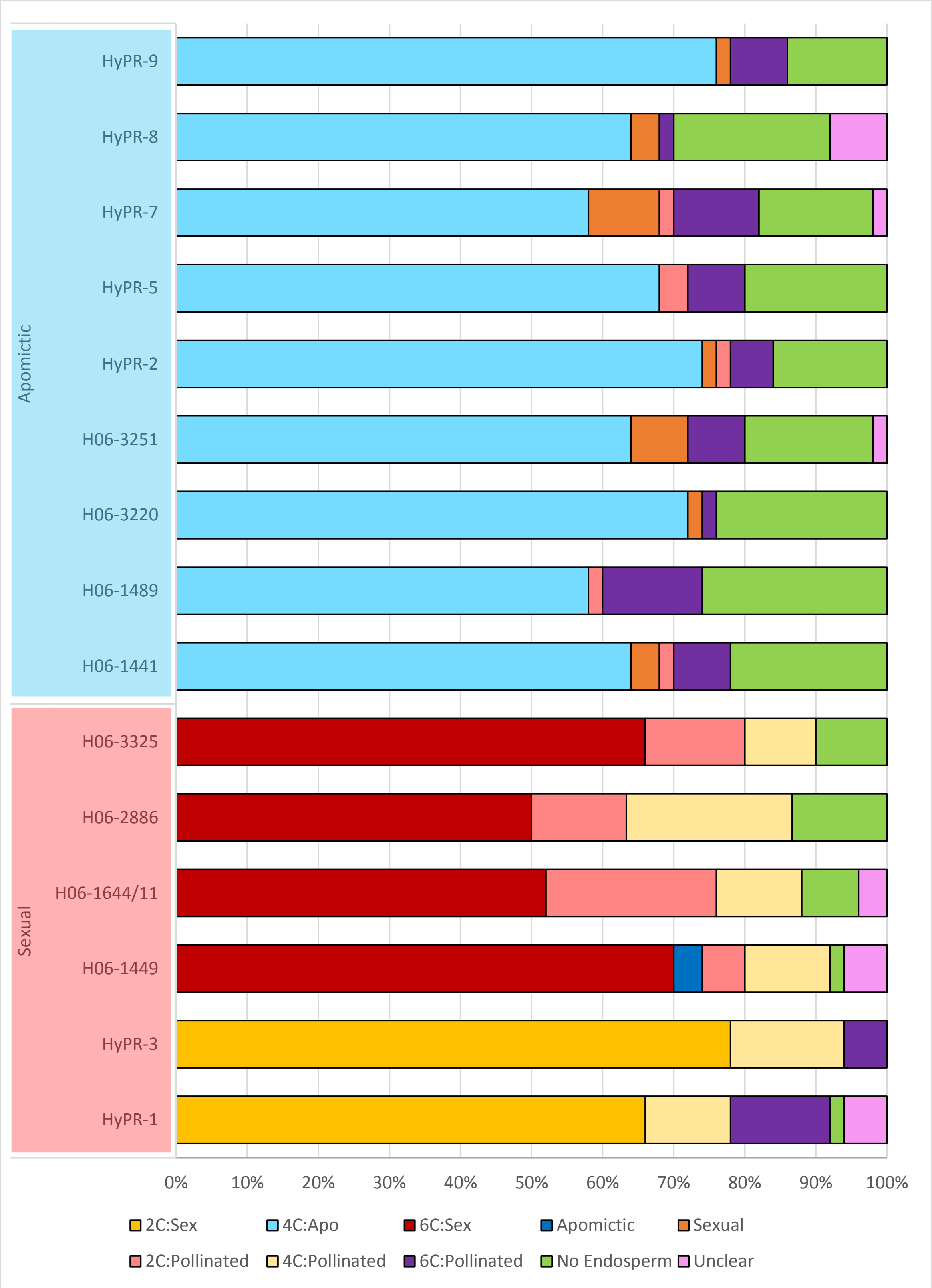

Figure 41. FCSS results in 15 *Hypericum* lines.

Ovule and female gametophyte development in *Hypericum*

The ovule and female gametophyte development was characterized in 9 different *Hypericum* lines: 2 sexual diploid, 3 tetraploid apomictic and 4 hexaploid sexual. The observation and classification of 38316 ovules led to a detailed characterization of ovule and female gametophyte development that is summarized in Table 5, where relative frequencies of every developmental stage from ovule primordium (OvP) to mature embryo-sac, are reported.

Like in the case of *Boechera spp.*, the heat map representation helps to visualize and evaluate the developmental speed in *Hypericum* and to detect, when present, any deviation from the standard development of sexual lines.

The megasporogenesis process in apomictic lines proceeded at a higher speed during the early stages of ovule development (Table 5 and Figure 42). The class 2 flower buds of diploid sexual lines mainly carried ovules at MMC (megaspore mother cell) stage, but apomicts (and at a minor level, hexaploid sexual lines) at this stage showed a 15% of ovules already at the dyad stage.

Table 5. Ovule and female gametophyte development of: 2 diploid sexual lines, 4 hexaploid sexual lines and 3 tetraploid apomictic lines of *Hypericum*. The parameter "Class" refers to the flower bud length: 1 = 2.00-2.49 mm, 2 = 2.5-2.99 mm, 3 = 3.0-3.49 mm, 4 = 3.5-3.99 mm, 5 = 4.0 – 4.49 mm, 6 = 4.5-4.99 mm, 7= 5.0-5.49 mm, 8 = 5.5-5.99 mm, 9 = 6.0-6.49mm, 10 = 6.5-6.99 mm, 11 = 7.0-7.49 mm, 12 = 7.5-7.99 mm; 13 = 8.0-8.49 mm, 14 = 8.5-8.99 mm, 15 = 9.0-9.49 mm, 16 = 9.5-9.99, 17 = 10.00-12.00 mm, 18 = open flower; **OvP** = ovule primordium; **AC** = archesporial cell; **MMC** = megaspore mother cell; **SI** = small integuments primordia; **MI** = medium integuments primordia; **BI** = big integuments primordia; **Multi MMC** = multiple megaspore mother cell in the same ovule; **AI** = aposporous initial; **FM** = functional megaspore; **2NG** = bi-nucleated gametophyte; **4NG** = tetra-nucleated gametophyte; **8NG** = mature gametophyte; **E** = embryo. Values at each stage are shown as % of the total number of observed ovules within the stage. Percentages are formatted with a color gradient where 0% is colored in white and 100% is colored in dark red.

Ploidy	**Reproduction**	**Class**	**OvP**	**AC**	**MMC/SI**	**MMC/MI**	**MMC/BI**	**Multi MMC**	**Aborted**	**AI**	**Dyads**	**Tetrads**	**FM**	**2NG**	**4NG**	**8NG**	**E**	**Other**	**Number of observed ovules**
Tetraploid	Apomictic	1	43%	13%	40%	5%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	116
Tetraploid	Apomictic	2	0%	5%	41%	31%	1%	10%	0%	0%	15%	0%	0%	0%	0%	0%	0%	0%	626
Tetraploid	Apomictic	3	0%	1%	40%	29%	0%	9%	1%	0%	21%	1%	0%	0%	0%	0%	0%	0%	1833
Tetraploid	Apomictic	4	0%	0%	10%	43%	1%	9%	3%	0%	31%	2%	0%	0%	0%	0%	0%	1%	906
Tetraploid	Apomictic	5	0%	0%	0%	27%	14%	5%	37%	3%	9%	1%	4%	0%	0%	0%	0%	1%	1174
Tetraploid	Apomictic	6	0%	0%	0%	1%	13%	1%	67%	5%	2%	0%	4%	0%	0%	0%	0%	8%	752
Tetraploid	Apomictic	7	0%	0%	0%	0%	6%	1%	83%	8%	0%	0%	2%	0%	0%	0%	0%	1%	1327
Tetraploid	Apomictic	8	0%	0%	0%	0%	2%	1%	82%	10%	0%	0%	6%	1%	0%	0%	0%	0%	1377
Tetraploid	Apomictic	9	0%	0%	0%	0%	1%	0%	64%	19%	0%	0%	10%	7%	0%	0%	0%	0%	1094
Tetraploid	Apomictic	10	0%	0%	0%	0%	0%	0%	45%	28%	0%	0%	15%	11%	3%	0%	0%	0%	949
Tetraploid	Apomictic	11	0%	0%	0%	0%	0%	0%	41%	10%	0%	0%	25%	20%	5%	1%	0%	0%	1007
Tetraploid	Apomictic	12	0%	0%	0%	0%	0%	0%	51%	0%	0%	0%	16%	22%	6%	6%	0%	0%	875
Tetraploid	Apomictic	13	0%	0%	0%	0%	0%	0%	50%	1%	0%	0%	5%	12%	13%	19%	0%	0%	462
Tetraploid	Apomictic	14	0%	0%	0%	0%	0%	0%	45%	2%	0%	0%	8%	13%	15%	18%	0%	0%	1262
Tetraploid	Apomictic	15	0%	0%	0%	0%	0%	0%	47%	6%	0%	0%	7%	12%	5%	24%	0%	0%	852
Tetraploid	Apomictic	16	0%	0%	0%	0%	0%	0%	46%	0%	0%	0%	3%	8%	12%	33%	0%	0%	439
Tetraploid	Apomictic	17	0%	0%	0%	0%	0%	0%	51%	1%	0%	0%	3%	7%	5%	34%	0%	0%	1517
Tetraploid	Apomictic	18	0%	0%	0%	0%	0%	0%	54%	0%	0%	0%	2%	5%	6%	33%	2%	0%	1131
Diploid	Sexual	2	0%	14%	56%	31%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	264
Diploid	Sexual	3	0%	5%	40%	50%	2%	1%	3%	0%	0%	1%	0%	0%	0%	0%	0%	0%	790
Diploid	Sexual	4	0%	0%	16%	66%	13%	1%	3%	0%	2%	0%	0%	0%	0%	0%	0%	1%	719
Diploid	Sexual	5	0%	0%	1%	22%	62%	1%	9%	0%	1%	0%	4%	1%	0%	0%	0%	1%	867
Diploid	Sexual	6	0%	0%	0%	9%	54%	0%	8%	0%	2%	1%	25%	4%	1%	0%	0%	1%	557
Diploid	Sexual	7	0%	0%	0%	2%	19%	1%	3%	0%	0%	2%	66%	9%	0%	0%	0%	1%	511
Diploid	Sexual	8	0%	0%	0%	0%	2%	0%	3%	0%	1%	0%	39%	52%	5%	0%	0%	1%	1008
Diploid	Sexual	9	0%	0%	0%	0%	0%	0%	3%	0%	1%	0%	22%	53%	23%	1%	0%	0%	577
Diploid	Sexual	10	0%	0%	0%	0%	0%	0%	3%	0%	0%	0%	31%	26%	23%	12%	0%	6%	695
Diploid	Sexual	11	0%	0%	0%	0%	0%	0%	3%	0%	0%	0%	5%	23%	40%	22%	0%	8%	690
Diploid	Sexual	12	0%	0%	0%	0%	0%	0%	6%	0%	0%	0%	0%	19%	35%	38%	0%	4%	601
Diploid	Sexual	13	0%	0%	0%	0%	0%	0%	7%	0%	0%	0%	1%	8%	38%	45%	0%	4%	823
Diploid	Sexual	14	0%	0%	0%	0%	0%	0%	1%	0%	0%	0%	0%	6%	36%	52%	0%	6%	400
Diploid	Sexual	15	0%	0%	0%	0%	0%	0%	11%	0%	0%	0%	0%	0%	21%	61%	0%	8%	385
Diploid	Sexual	16	0%	0%	0%	0%	0%	0%	9%	0%	0%	0%	0%	1%	22%	64%	0%	6%	401
Diploid	Sexual	17	0%	0%	0%	0%	0%	0%	13%	0%	0%	0%	0%	0%	12%	62%	0%	14%	451
Diploid	Sexual	18	0%	0%	0%	0%	0%	0%	11%	0%	0%	0%	0%	0%	5%	74%	0%	11%	625
Hexaploid	Sexual	1	0%	20%	62%	0%	0%	6%	0%	0%	13%	0%	0%	1%	0%	0%	0%	0%	166
Hexaploid	Sexual	2	0%	8%	74%	11%	1%	3%	0%	0%	3%	1%	0%	0%	0%	0%	0%	0%	837
Hexaploid	Sexual	3	0%	0%	63%	26%	3%	2%	0%	0%	6%	0%	0%	0%	0%	0%	0%	0%	587
Hexaploid	Sexual	4	0%	0%	23%	60%	4%	4%	0%	0%	7%	2%	0%	0%	0%	0%	0%	2%	596
Hexaploid	Sexual	5	0%	0%	5%	64%	12%	3%	2%	0%	12%	2%	1%	0%	0%	0%	0%	0%	663
Hexaploid	Sexual	6	0%	0%	3%	66%	20%	1%	6%	0%	3%	0%	1%	0%	0%	0%	0%	1%	553
Hexaploid	Sexual	7	0%	0%	0%	48%	41%	0%	9%	0%	1%	0%	2%	0%	0%	0%	0%	2%	375
Hexaploid	Sexual	8	0%	0%	3%	37%	33%	1%	6%	0%	13%	1%	5%	0%	0%	0%	0%	3%	792
Hexaploid	Sexual	9	0%	0%	3%	19%	41%	1%	13%	0%	7%	2%	12%	0%	0%	0%	0%	2%	455
Hexaploid	Sexual	10	0%	0%	0%	5%	37%	2%	16%	0%	3%	1%	30%	1%	1%	0%	0%	6%	755
Hexaploid	Sexual	11	0%	0%	0%	0%	34%	0%	15%	0%	2%	1%	38%	8%	1%	0%	0%	3%	506
Hexaploid	Sexual	12	0%	0%	0%	1%	2%	0%	12%	0%	0%	0%	33%	28%	13%	0%	0%	12%	401
Hexaploid	Sexual	13	0%	0%	0%	0%	2%	0%	13%	0%	0%	0%	14%	35%	31%	0%	0%	5%	522
Hexaploid	Sexual	14	0%	0%	0%	0%	0%	0%	15%	0%	0%	0%	22%	38%	19%	2%	0%	4%	619
Hexaploid	Sexual	15	0%	0%	0%	0%	0%	0%	18%	0%	0%	0%	3%	23%	36%	16%	0%	6%	355
Hexaploid	Sexual	16	0%	0%	0%	0%	0%	0%	16%	0%	0%	0%	0%	13%	43%	23%	0%	5%	588
Hexaploid	Sexual	17	0%	0%	0%	0%	0%	0%	18%	0%	0%	0%	0%	2%	26%	45%	0%	11%	797
Hexaploid	Sexual	18	0%	0%	0%	0%	0%	0%	20%	0%	0%	0%	0%	0%	10%	60%	0%	10%	686
																			38316

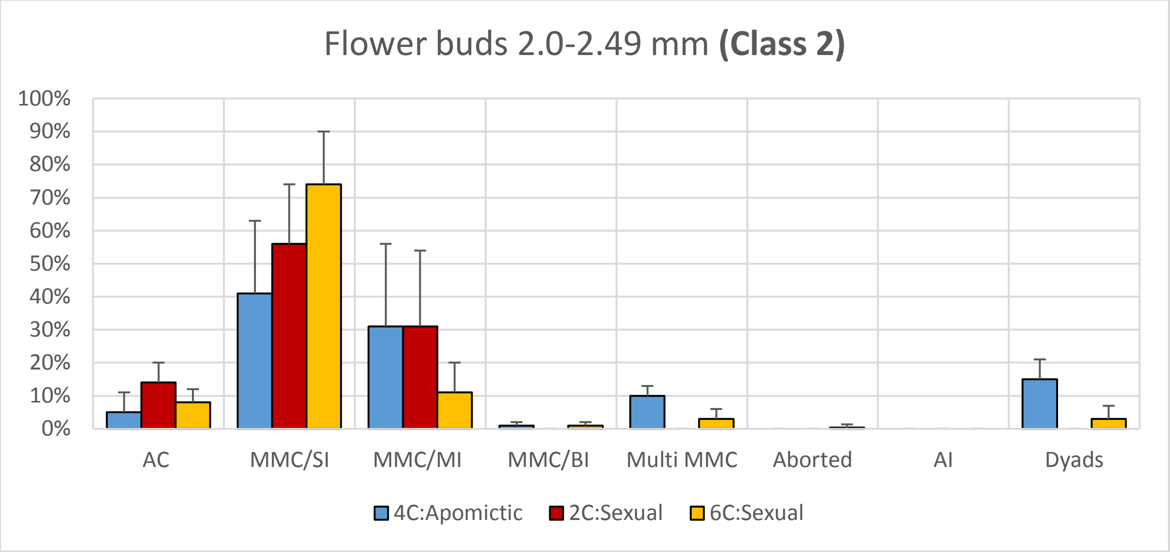

Figure 42. Frequencies of development stages in several *Hypericum* lines at flower bud size 2.0-2.49 mm (class 2). **AC** = archesporial cell; **MMC** = megaspore mother cell; **SI** = small integuments primordia; **MI** = medium integuments primordia; **BI** = big integuments primordia; **Multi MMC** = multiple megaspore mother cell in the same ovule; **AI** = aposporous initial.

The same kind of developmental trend is even stronger in flower buds belonging to the class 4 as shown in Figure 43, where the percentage of detected dyads is even higher than 30%. The former is an unusually high frequency for such a transient stage, not only for *Hypericum*, *i.e.* dyads were very difficult to detect even in other species like *Boechera spp.* In the apomictic tetraploid *Hypericum,* this anomalous accumulation of dyads could suggest a malfunction of some meiotic process, especially during meiosis II.

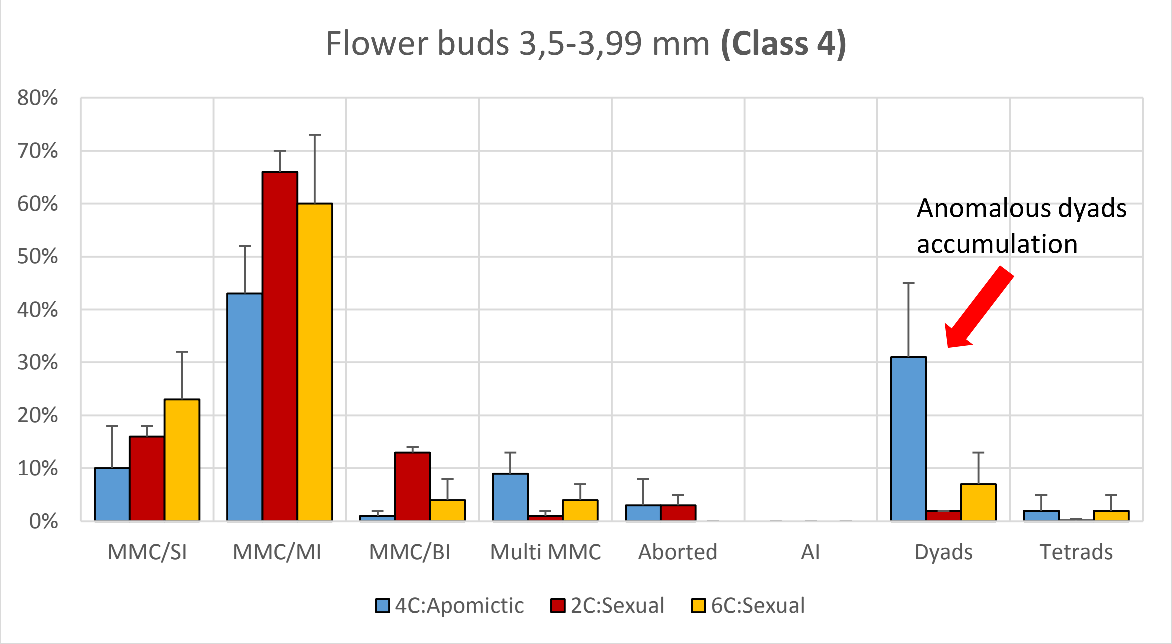

Figure 43. Frequencies of development stages in several *Hypericum* lines at flower bud size 3.5-3.99 mm (class 4). **MMC** = megaspore mother cell; **SI** = small integuments primordia; **MI** = medium integuments primordia; **BI** = big integuments primordia; **Multi MMC** = multiple megaspore mother cell in the same ovule; **AI** = aposporous initial.

Class 5 flower buds were characterized by a marked difference between apomicts and the rest of the analyzed lines, consisting of an abnormal increase in the frequency of aborted ovules (Figure 44).

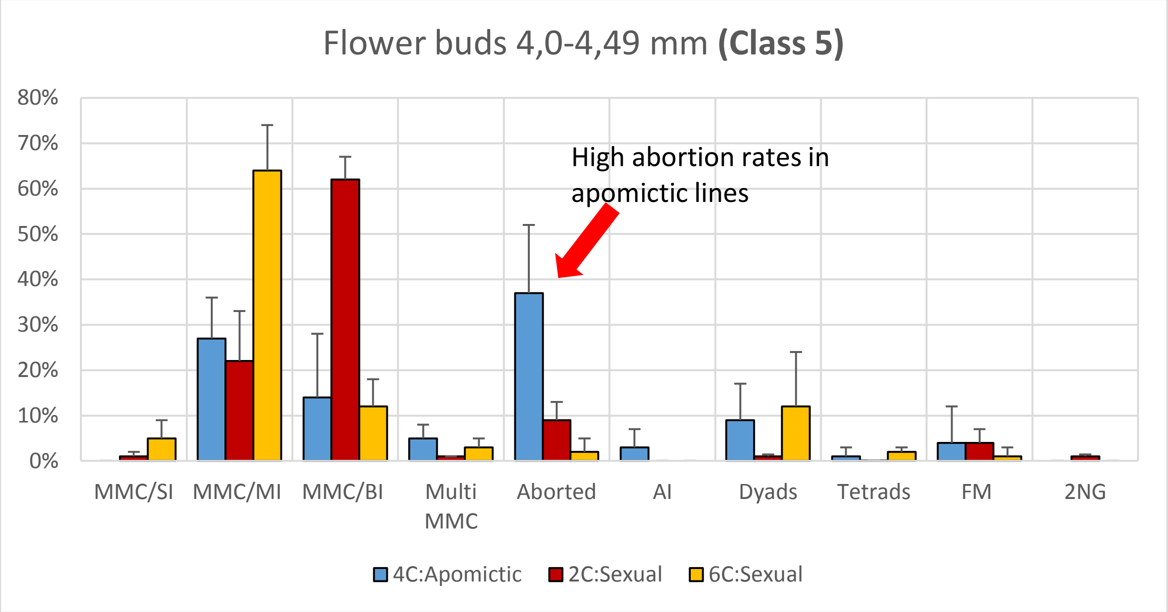

Figure 44. Frequencies of development stages in several *Hypericum* lines at flower bud size 4.0-4.49 mm (class 5). **MMC** = megaspore mother cell; **SI** = small integuments primordia; **MI** = medium integuments primordia; **BI** = big integuments primordia; **Multi MMC** = multiple megaspore mother cell in the same ovule; **AI** = aposporous initial; **FM** = functional megaspore; **2NG** = bi-nucleated gametophyte.

In class 5 flower buds, the sexual diploid lines started a transition to post-meiotic stages, showing already ca. 5% of ovules at the functional megaspore (FM) stage, without any peak in abortion rates neither any anomalous increase of dyads or tetrads frequencies. This suggested, that the meiotic processes continued without any apparent problems. Tetraploid apomicts and hexaploid sexuals on the other hand, showed ca. 10% of ovules at the dyad stage.

Furthermore, class 5 was characterized by the differentiation of enlarged cells localized at the margins of the gametophytic domains that were considered aposporous initials (AIs). These cells could take over the developmental process of the gametophyte immediately after the failure of the sexual developmental pathway. This observation challenges previous literature on aposporic development in *Hypericum* (Galla et al., 2011) according to which, AIs were competing with the sexual gametophyte, eventually displacing it and originating a new aposporous gametophyte with several morphological anomalies. The frequency of AIs is even higher in flower buds belonging to the following classes.

In class 7 the advantage of sexual diploid lines over the rest of the lines was evident. Sexual diploids reached the stage of FM or even bi-nucleated gametophyte (2NG), while the apomictic lines presented in average ca. 80% of aborted ovules and the hexaploid sexual lines showed a very slow advance in development and remained at the MMC stage (Figure 45).

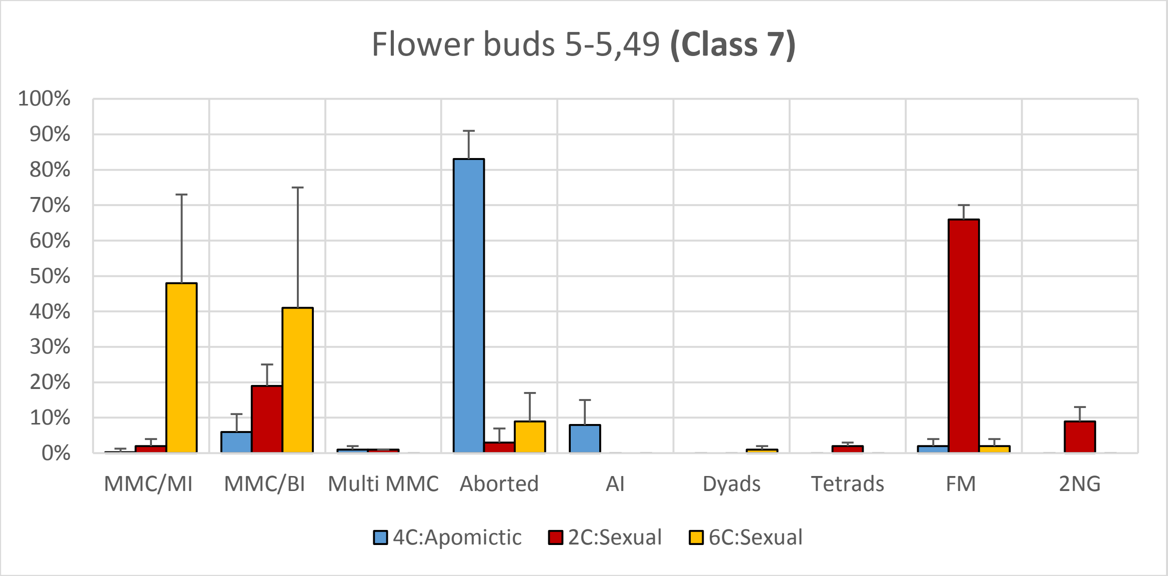

Figure 45. Frequencies of development stages in several *Hypericum* lines at flower bud size 5.0-5.49 mm (class 7). **MMC/MI** = megaspore mother cell / medium integuments primordia; **BI** = big integuments primordia; **Multi MMC** = multiple megaspore mother cell in the same ovule; **AI** = aposporous initial; **FM** = functional megaspore; **2NG** = bi-nucleated gametophyte.

The analysis of the following flower bud classes showed that the high abortion rates of apomicts at class 7 gradually stabilized on values between 40 and 50%. This was visible in flower buds of class 10 (Figure 46), where aborted ovules in apomicts were 45%.

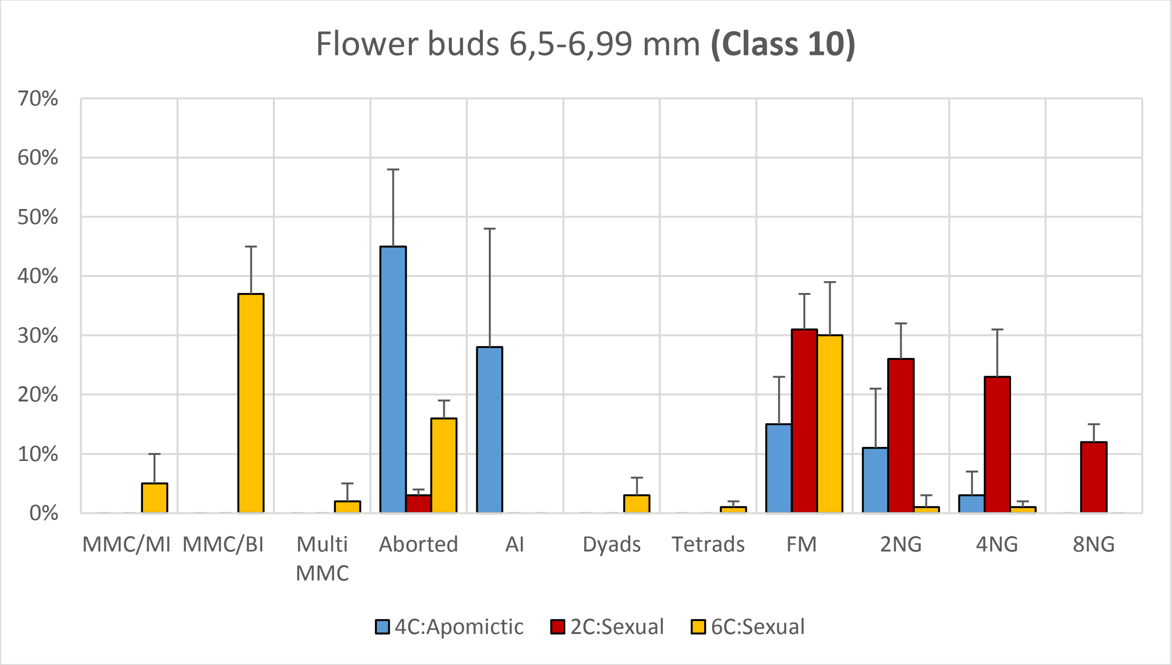

Figure 46. Frequencies of development stages in several *Hypericum* lines at flower bud size 6.5-6.99 mm (class 10). **MMC** = megaspore mother cell; **MI** = medium integuments primordia; **BI** = big integuments primordia; **Multi MMC** = multiple megaspore mother cell in the same ovule; **AI** = aposporous initial; **FM** = functional megaspore; **2NG** = bi-nucleated gametophyte; **4NG** = tetra-nucleated gametophyte; **8NG** = mature gametophyte.

At the developmental stage of class 10, the lines that were closer to complete the gametophytic development were the diploid sexuals, with 12% of the ovules carrying a mature embryo sac. The ovules of hexaploid sexual lines were still distributed between pre and post-meiotic stages, *i.e.* MMC and FM. The tetraploid apomictic lines reduced their previous gap with the sexual diploid lines, and despite their high abortion rate, entered in the post meiotic stages with 15% of ovules at FM stage and 11% at 2NG stage.

When flower buds reached the size of class 14, all the lines overcame the pre-meiotic stages and tetraploid apomicts reached the same developmental point of the sexual diploid lines with the exception of the aborted ovules. The most represented stages of both groups of lines were the tetra-nucleated and the mature gametophyte (Figure 47). Hexaploid sexual lines on the other hand were mainly at the 2NG stage.

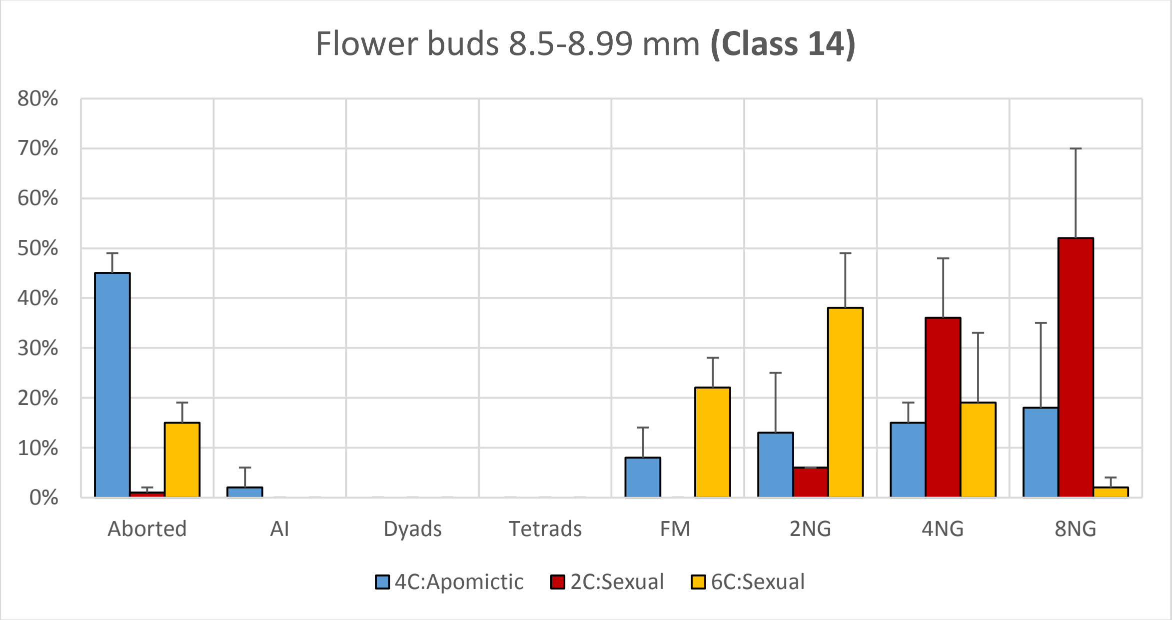

Figure 47. Frequencies of development stages in several *Hypericum* lines at flower bud size 8.5-8.99 mm (class 14). **AI** = aposporous initial; **FM** = functional megaspore; **2NG** = bi-nucleated gametophyte; **4NG** = tetra-nucleated gametophyte; **8NG** = mature gametophyte.

The last time point at which the ovules characterization was performed was the class 18, which corresponds to the stage of open flower (Figure 48). At this time point, all the lines had mature gametophytes in the majority of their ovules. The mature gametophyte (8NG) frequency in the apomict was lower (33%) if compared with the sexual lines, due to the high percentage of aborted ovules. However, if this percentage were recalculated excluding those aborted ovules, then, the average of ovules at 8NG stage in apomicts would be 70.2%, very close to the 74% of the sexual diploid.

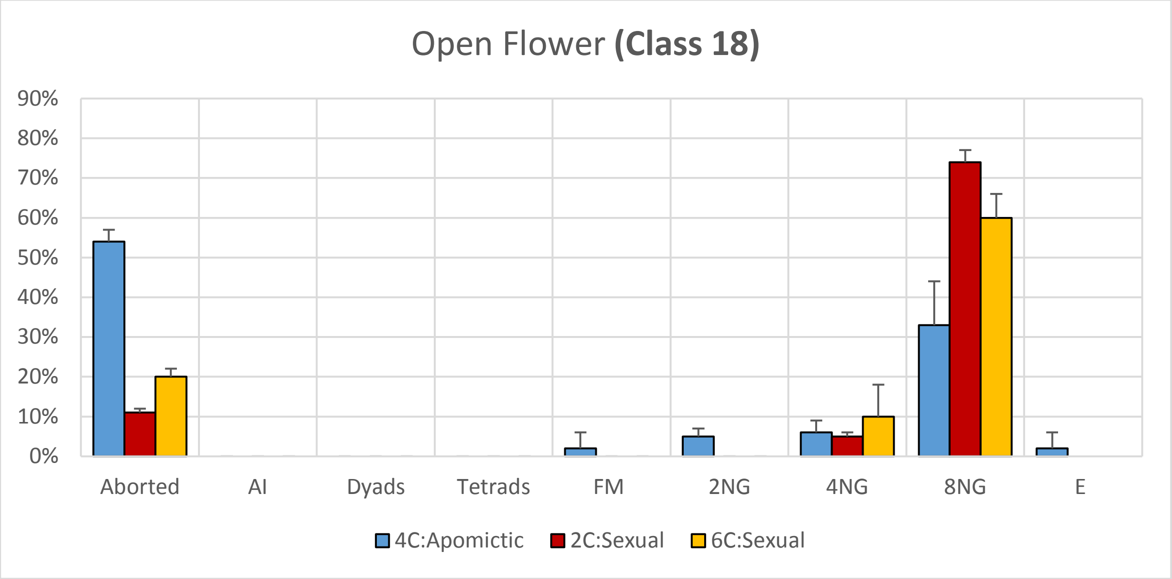

Figure 48. Frequencies of gametophyte developmental stages in several *Hypericum* lines at the open flower stage (class 18). **AI** = aposporous initial; **FM** = functional megaspore; **2NG** = bi-nucleated gametophyte; **4NG** = tetra-nucleated gametophyte; **8NG** = mature gametophyte; **E** = embryo

The visualization tools described above report the ovule development in a stage-wise manner. Two developmental anomalies, the abortion rate (Figure 49) as well as the formation of multiple MMCs (Figure 50), were represented throughout all stages and deserve a special consideration.

According to Kruskal-Wallis ($P \leq 0.05$), apomictic lines showed significantly higher percentages of abortion in comparison with their sexual counterparts in 13 of the 14 stages represented in Figure 49.

The frequency of ovule abortion reached its maximum in flower buds of class 7. Remarkably, the high abortion rate did not lead into a developmental dead end, but rather resulted in a developmental rebooting. This is also consistent with the observation that the abortion rate tended to diminish in the following stages of ovule development. Furthermore, apomictic lines exhibited a significantly higher percentage of multiple MMCs in comparison to sexual lines with flower buds of the classes 2, 3 and 4.

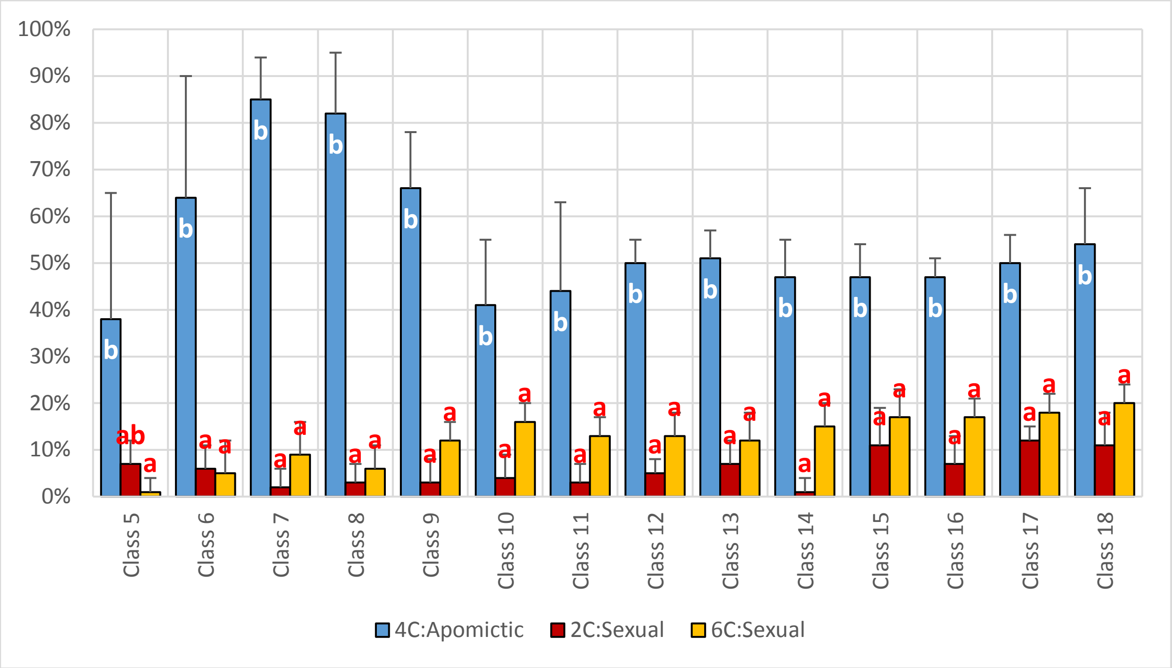

Figure 49. Average frequencies of aborted ovules in several *Hypericum* lines spanning the flower bud development from class 5 to class 18. Different letters = significant differences between the lines according to Kruskal-Wallis test, P<0.05. Analysis of variance was performed by class.

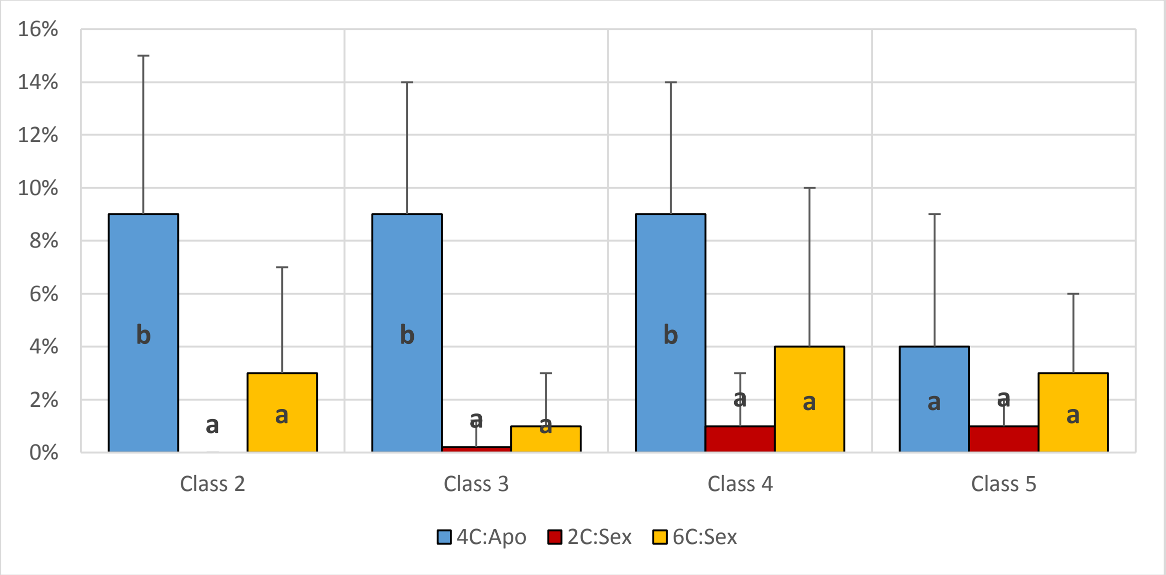

Figure 50. Average percentage of multi-MMCs from flower buds of class 2 to class 5 in 9 different *Hypericum* lines grouped in 3 clusters: 4C:Apo, 2C:Sex and 6C:Sex. Means with a common letter are not significantly different (P<0.05) according to Kruskal-Wallis test. Analysis of variance was performed by class.

Visual atlas of ovule and female gametophyte development in *Hypericum*

The results reported in this section are based on the morphological characterization of 38316 ovules through DIC microscopy. Therefore, they are supported by a large set of pictures that constitute a detailed visual atlas of ovule and female gametophyte development in several *Hypericum* lines, characterized by different reproductive modes and ploidy levels.

The visual information given in this section describes the ovule and female gametophyte development of *Hypericum* at 6 different time points and it is organized in as many visual panels.

The first visual panel includes ovules dissected from class 2 flower buds (Figure 51). This panel shows that the diploid sexual had a faster development of integuments and a slightly faster growth in ovule size. The hexaploid sexual and especially the tetraploid, although smaller, already reached the dyad stage.

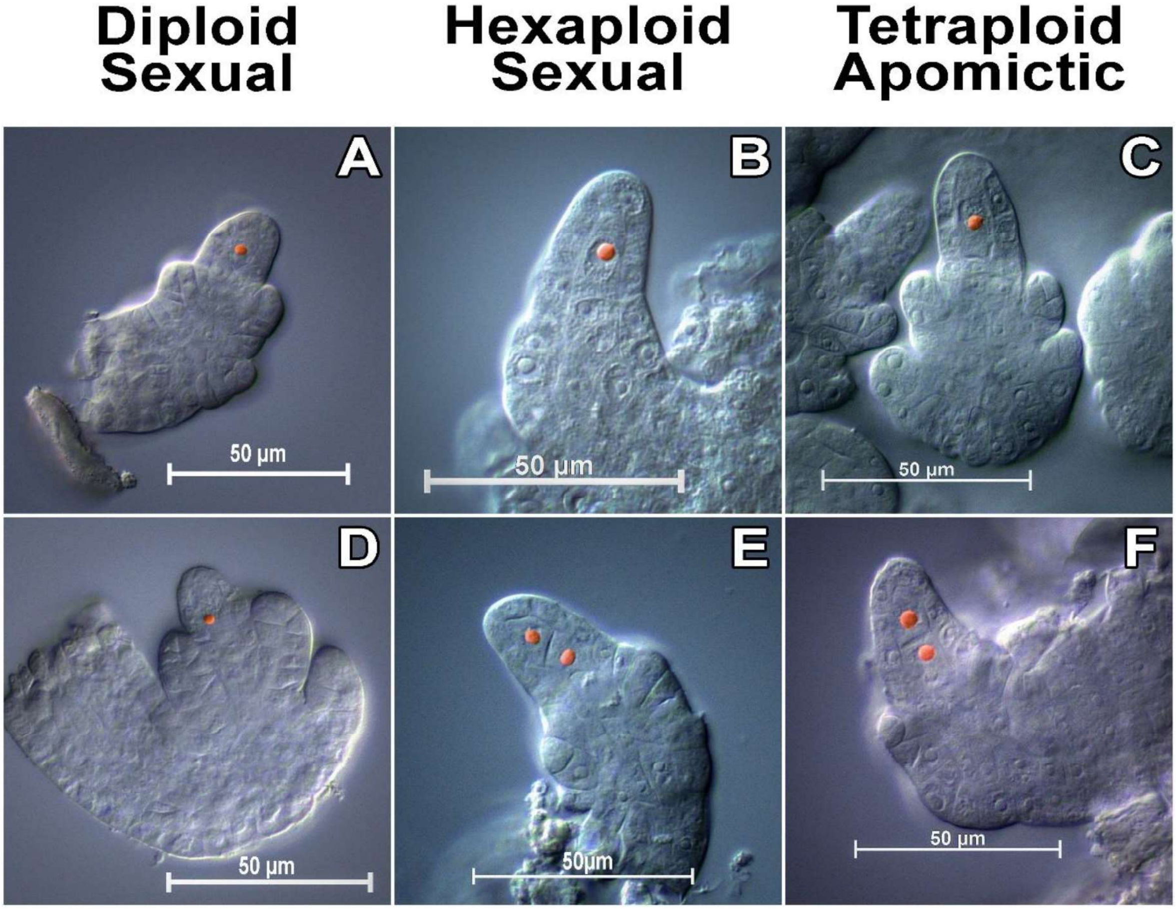

Figure 51. Ovule and female gametophyte development in **class 2 (2.0-2.49 mm)** flower buds of *Hypericum* diploid sexual (A,D), hexaploid sexual (B,E) and tetraploid apomictic (C,F). **A,B,C**: ovules with small integuments primordia carrying a megaspore mother cell (highlighted in orange); **D**: ovule with medium size integument primordia carrying an MMC (highlighted in orange); **E** and **F**; ovules with small integuments primordia carrying dyads (dyads nuclei are highlighted in orange).

The second visual panel (Figure 52) shows ovules from class 5 flower buds. In this class it was possible to detect relevant percentages of aborted ovules in the apomictic tetraploid lines (Figure 52 C). At the same time point, the other lines (2C:Sex and 6C:Sex) reached bigger ovule sizes, but they were still carrying a MMC (Figure 52 A and B) like in flower buds of class 2, suggesting a long persistence of the MMC.

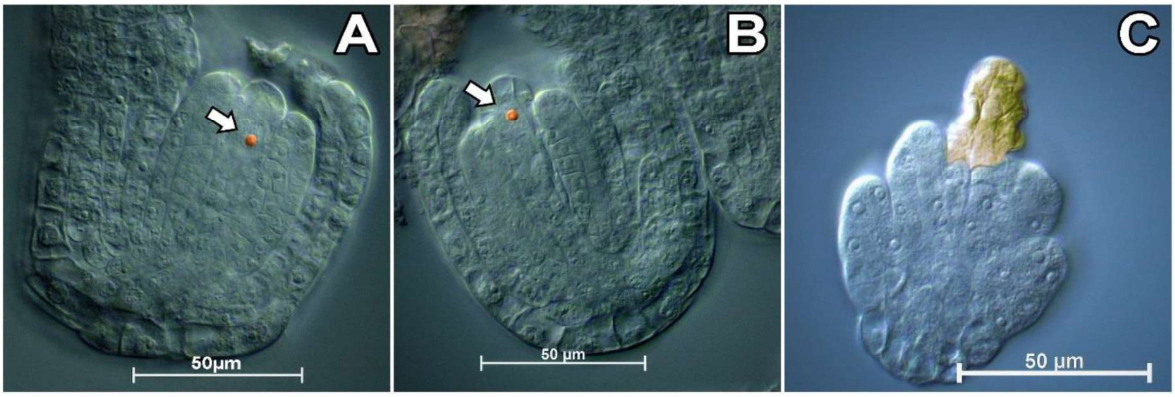

Figure 52. Ovule and female gametophyte development in **class 5 (4.0-4.49 mm)** flower buds of *Hypericum perforatum*. **A**: ovule from a diploid sexual line with big integuments primordia carrying a megaspore mother cell (highlighted in orange); **B**: ovule from an hexaploid sexual line with medium size integuments primordia carrying a megaspore mother cell (highlighted in orange); **C**: aborted ovule from a tetraploid apomictic with small integuments primordia and a shrinking distal part (highlighted in yellow).

The third panel (Figure 53) shows developing ovules from flower buds of the class 7. The diploid and hexaploid lines proceeded at different speed of development but with no apparent developmental malfunction (Figure 53 A and B), while the apomictic lines have to deal with very high percentages of aborted ovules, that reach their maximum in flower buds of this class. The aborted ovules are characterized by a shrunk gametophytic domain (Figure 53 C).

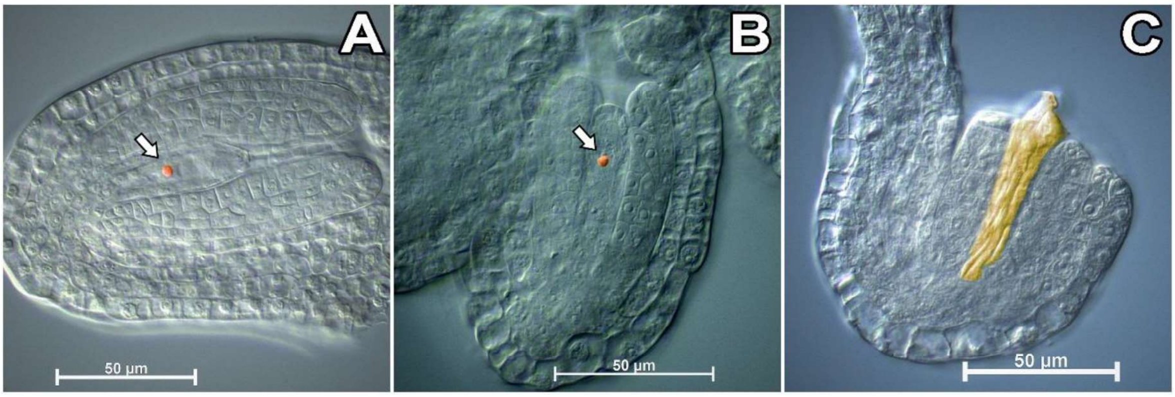

Figure 53. Ovule and female gametophyte development in **class 7 (5.0-5.49 mm)** flower buds of *Hypericum perforatum* lines. **A**: ovule from a diploid sexual line at the functional megaspore (FM) stage (nucleus of the functional megaspore, highlighted in orange); **B**: ovule from a hexaploid sexual line at MMC stage with big integuments primordia (MMC, highlighted in orange); **C**: ovule from a tetraploid apomictic line characterized by a shrinking tissue (highlighted in yellow) located in the portion of ovule that normally hosts the developing female gametophyte.

The fourth visual panel (Figure 54) shows developing ovules from class 9 flower buds. In this class, the sexual diploid lines reached the post-meiotic stages carrying ovules that spanning from functional megaspore (Figure 54 A) to bi- or tetra-nucleated gametophyte

(Figure 54 D and G). The hexaploid sexual lines were found in a transition phase between pre and post-meiotic stages. These lines showed at the same time ovules still carrying MMCs (Figure 54 B), others already at the FM stage (Figure 54 H) and ca. 15% of aborted ovules (Figure 54 E), suggesting that hexaploids were affected by developmental anomalies like in the case of tetraploids, but with a milder effect on abortion rates.

The tetraploid apomictic lines continued to show ovule abortion. This was evidenced by the shrinking of the gametophytic domain (Figure 54 C). This phenotype was the most represented in tetraploids with an average frequency of 64%. Nevertheless, at this point of development, ca. 20% of the ovules of apomictic lines showed enlarged cells differentiating in the periphery of the gametophytic domain (Figure 54 F) and ca. 15% of ovules at the FM (Figure 54 I) or 2NG stage.

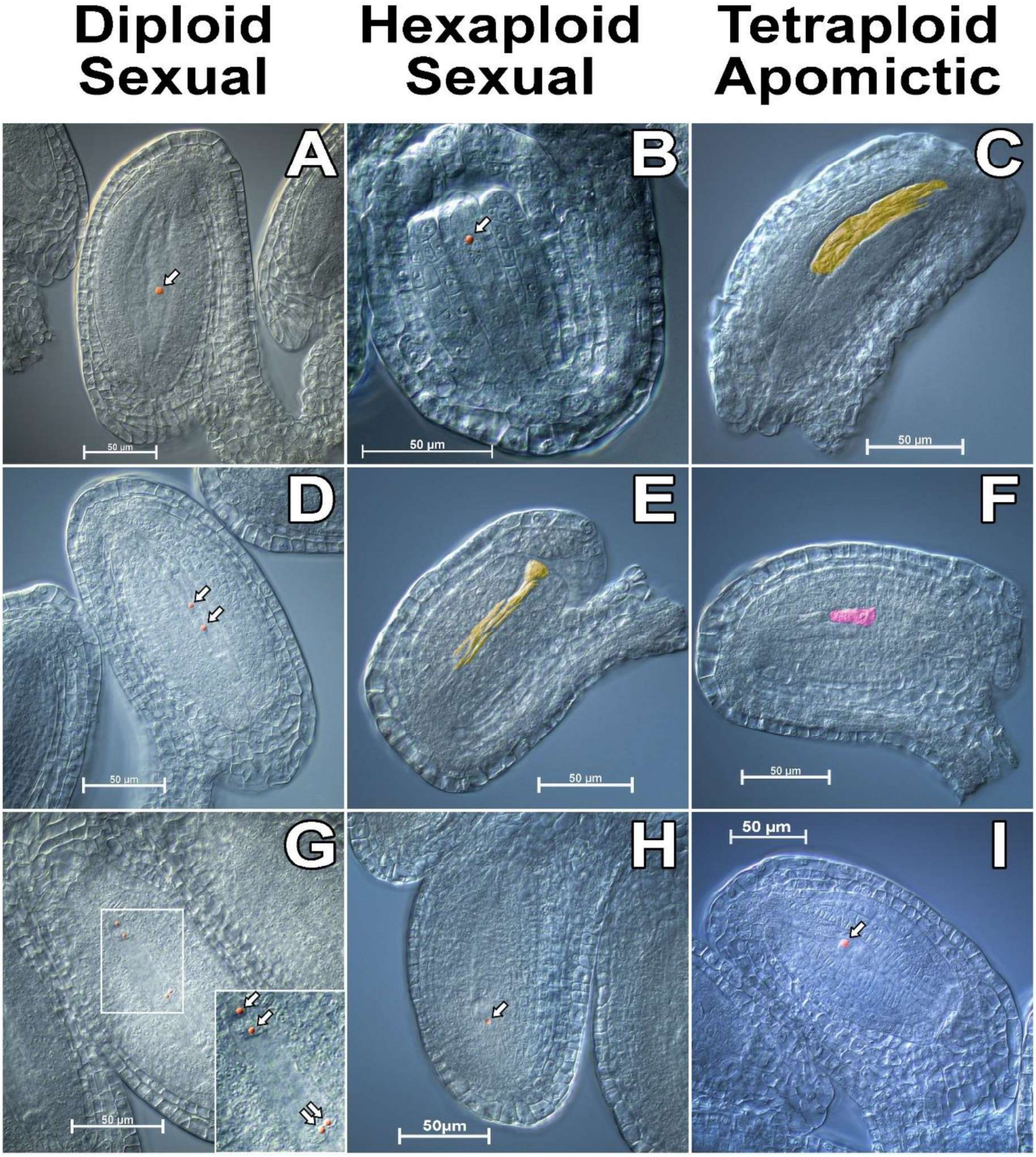

Figure 54. Ovule and female gametophyte development in **class 9 (6.0 – 6.49 m)** flower buds of *Hypericum perforatum* lines grouped in 3 categories: diploid sexual (A,D,G), hexaploid sexual (B,E,H), tetraploid apomictic (C,F,I). **A**: ovule carrying a functional megaspore (nucleus of the functional megaspore highlighted in orange); **B**: ovule at the MMC stage with big integuments primordia (nucleus of the MMC highlighted in orange); **C**: aborted ovule showing a shrank tissue in the gametophytic space (highlighted in yellow); **D**: ovule carrying a bi-nucleated gametophyte (2NG) (nuclei of the bi-nucleated gametophyte highlighted in orange); **E**: aborted ovule showing a shrank tissue in the gametophytic space (highlighted in yellow); **F**: ovule carrying an aposporous initial (AI) in the peripheral part of the gametophytic space in direct contact with the nucellar tissue (AI highlighted in pink); **G**: ovule carrying a tetra-nucleated gametophyte (4NG) with the four nuclei highlighted in orange; **H** and **I**: ovules carrying a functional megaspore (nuclei of the FMs highlighted in orange).

This phenotype suggests that the observed enlarged cells were the aposporous initials, which assumed the role of a functional megaspore and rescued the gametophytic development of the ovules in which the sexual gametophyte failed.

This interpretation was supported by the observation of several ovules in which a peripheral enlarged cell (aposporous initial) developed in the gametophytic domain, right next to a shrunk tissue that seemed to have been displaced to the opposite side of the ovule (Figure 55).

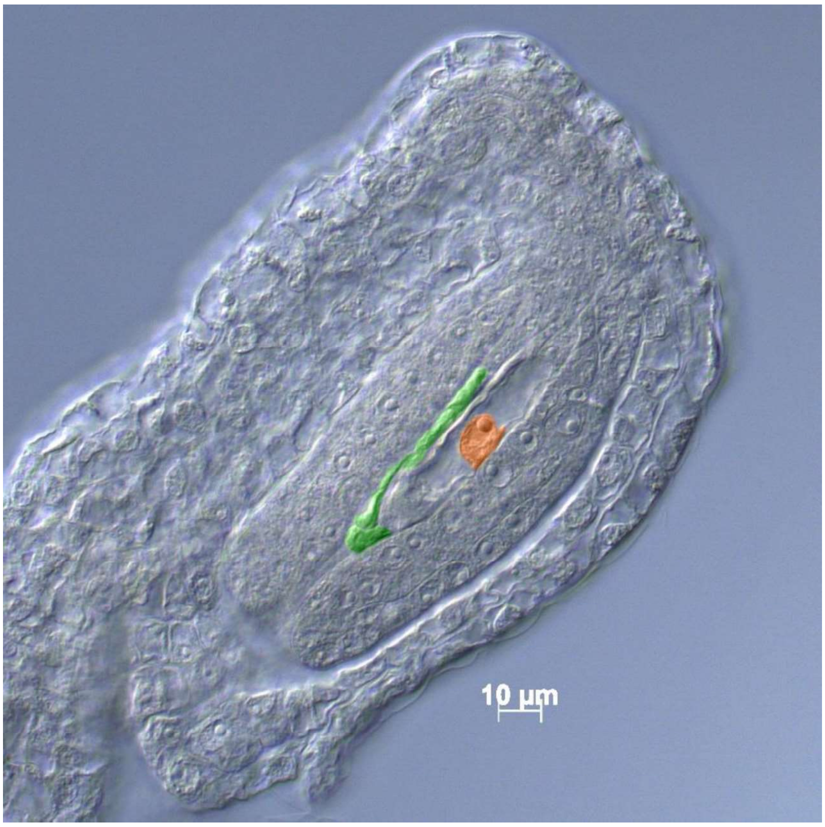

Figure 55. Aposporic initial (AI) (highlighted in orange) emerging from the nucellus and developing in the gametophytic domain of the ovule while displacing a shrunk gametophytic tissue (highlighted in green).

The fifth visual panel (Figure 56) represents the gametophyte development observed in flower buds of the class 14. In this class the majority of ovules of the sexual diploids reached the stage of mature female gametophyte (Figure 56 A). Sexual hexaploids and the tetraploid apomicts were at the 2NG and 4NG stage respectively (Figure 56 B and C). This panel shows how the three different categories are characterized by slightly different developmental speed with the sexual-2C being the faster and the sexual-6C being the slower.

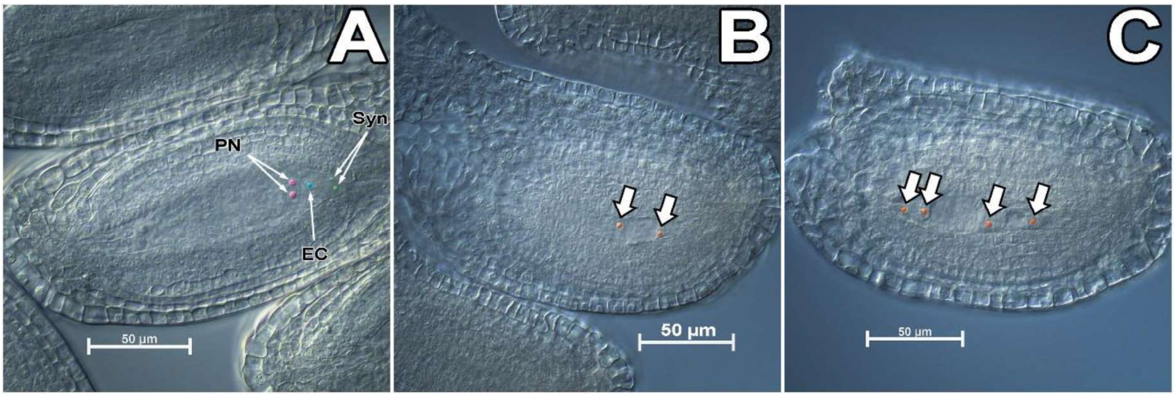

Figure 56. Ovule and female gametophyte development in **class 14 (8.5 – 8.99 mm)** flower buds of *Hypericum perforatum*. **A**: ovule from a diploid sexual line at the mature gametophyte stage (PN=polar nuclei, EC=egg cell, Syn=synergids); **B**: ovule from a hexaploid sexual line at the 2NG stage (nuclei of the bi-nucleated gametophyte highlighted in orange and marked with a white arrow); **C**: ovule from a tetraploid apomictic line at the 4NG stage (nuclei of the tetra-nucleated gametophyte highlighted in orange and marked with a white arrow).

The sixth and last panel (Figure 57) includes pictures of ovules from open flowers (class 18). At this stage, all the analyzed lines reached the maturity of the female gametophyte, suggesting that independently from the different developmental speed, differences between lines tended to disappear as close as the flower buds were to the stage of open flower. Nevertheless, the apomicts can only partially overcome these differences, since even at open flower stage, about half of their ovules are aborted.

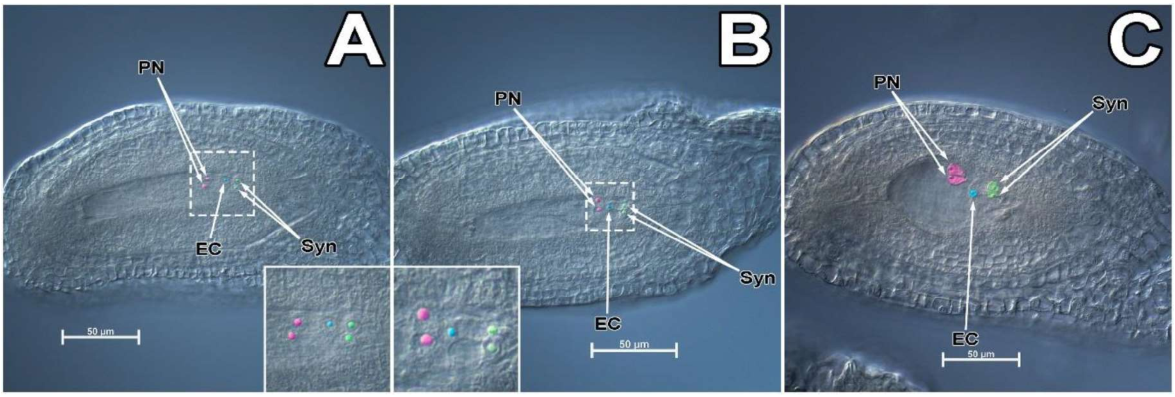

Figure 57. Ovule and female gametophyte development in **class 18 (open flower)** in several *Hypericum* lines. **A:** ovule from a diploid sexual line carrying a mature gametophyte; **B:** ovule from a hexaploid sexual line carrying a mature gametophyte; **C**: ovule from a tetraploid apomictic line carrying a mature gametophyte. **PN**=polar nuclei, **EC**=egg cell, **Syn**=synergids.

In summary, the analysis of ovule and female gametophyte development in different *Hypericum* lines, showed that apomicts had to face developmental anomalies, that started with the accumulation of dyads during the megagametogenesis, and included high abortion rates that were overcome with the differentiation of aposporic initials cells functioning as rescuer of the gametophytic development.

Multi-stage transcriptomic analysis of ovules from *Hypericum perforatum*

The last step of the *Hypericum* research reported in this study was the transcriptomic analysis of manually dissected ovules at multiple stages of development.

Like in the case of morphological characterization, the transcriptomic analysis aimed to point out differences between the sexual and the apomictic developmental pathways, by comparing the transcriptome of two sexual diploid lines (HyPR-1 and HyPR-3) with two apomictic tetraploid lines (HyPR-5 and HyPR-9). For each of these four lines, the transcriptomic analysis was performed on 4 samples (16 in total). Each sample was constituted of dissected ovules from flower buds of two adjacent classes, chosen to target the most crucial parts of development according to the morphological analysis. More detailed information on the developmental stages chosen for dissection are available in the materials and methods section.

The samples belonging to the earliest developmental stages were analyzed with the aim of detecting differences in gene expression, directly or indirectly connected with anomalies of the meiotic processes. The other three samples spanned the flower buds classes from 6 to 11 characterized by the highest percentages of aposporic initial differentiation.

As reported in the methods section, each of these samples harbored thousands of ovules that provided enough material to avoid all the biases involved with RNA amplification.

The Illumina RNAseq of the 16 sequenced samples (4 stages in four lines) generated a data set of 129303902 reads that led to the assembly of 94463 contigs. In order to keep only the highest quality data, contigs with no BLASTX hit against *Arabidopsis thaliana* genome were filtered out reducing their number from 94463 to 38520, and the number of reads from 129303092 to 123936148. This means that while the 59.22% of the contigs were filtered out during this step, only 4.15% of the reads were excluded. In this way, the amount of information that was left out was minimum and the quality of the data set was highly improved.

The data processing went through other 4 filtering steps that aimed to generate a very high quality set of data, where only the most reliable information was kept and which consisted of 28275 contigs. A scheme of all the performed filtering steps is reported in Table 6.

Table 6. Data filtering of the *Hypericum perforatum* ovules RNAseq data set.

Filtering process	N° of contigs before	N° of contigs after	Percentage of excluded contigs	N° of reads before	N° of reads after	Percentage of excluded reads
Exclude contigs without any BLASTX hit	94463	38520	59.22%	129303092	123936148	4.15%
Exclude contigs with Arabidopsis cp and mt hits	38520	38265	0.66%	123936148	122158821	1.43%
Exclude contigs matching Hypericum rRNA covering ≥ 20% of contig length	38265	38260	0.01%	122158821	110959032	9.17%
Remove contigs with length ≤ 30% of required CDS length	38260	28770	24.80%	110959032	107787021	2.86%
Remove contigs with BLASTN against cp (Ricinus) + mt (Hevea) covering ≥ 30% of contig length	28770	28725	0.16%	107787021	107698326	0.08%
Total filtering process	94463	28725	69.59%	129303092	107698326	16.71%

These results constitute the first assembled transcriptome of ovules of *Hypericum perforatum*, which limit the amount of literature available for comparison. Nevertheless, a *de-novo* assembly of whole plants of *Hypericum perforatum* was previously released (He et al., 2012), and a comparison regarding the contigs size between this previously published transcriptome and the data set obtained during this PhD project was performed. The outcome of such comparison is summarized in Figure 58. More details on the two compared data set are given in the following table (Table 7).

Table 7. Comparison between He et al. and the data set produced in this study.

Contigs	Total	Assembly length (bps)	Average length (bps)	N50 length	N° contigs > 1000 bp	Unique BLASTX hits (E-value ≤ 10^{-10}) At
All	94463	62097048	657.38	932	15108	33231
Used	28275	35757515	1244.82	1704	13358	25620
He et al.	59184	24986432	422.18	532	5136	NA

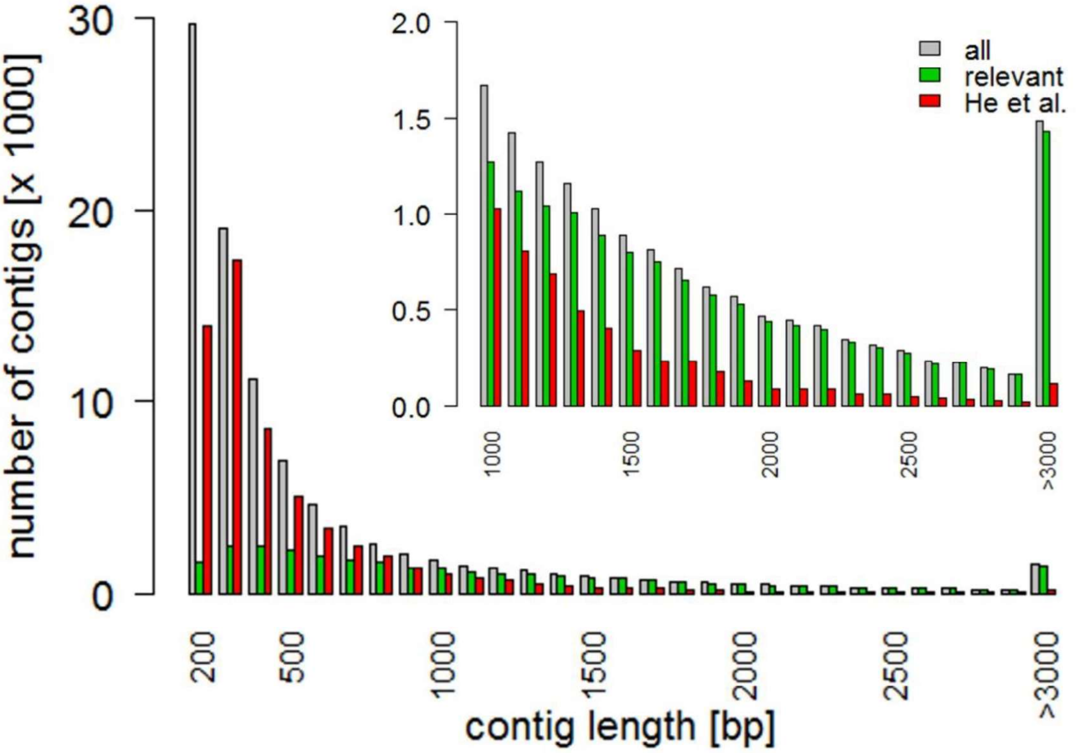

Figure 58. Distribution of contigs length obtained from the comparison with He et al. 2012. The smaller chart is a magnification of the bigger one for all the contigs longer than 1000 bases. Grey = dataset including all the assembled contigs before any filtering step; green = data sets constituted by all the contigs that were kept after the filtering process; red = data set from He et al. 2012.

The high quality of the transcriptome data set produced in this study is characterized by a longer average contigs length (1244.82 vs 422.18 bps) and higher N50 value (1704 vs 532 bps), in comparison with previously published work (He et al., 2012), as explained in Figure 58.

After the filtering process, the contigs kept in the data set were analyzed for the three classes of GO (gene ontology) terms: molecular function (divided in 15 categories), cellular component (divided in 16 categories) and biological process (divided in 14 categories). The Figure 59, Figure 60 and Figure 61 are the final outcome of this first GO-term analysis and constitute the first gene ontology profile of developing ovules of *Hypericum perforatum*.

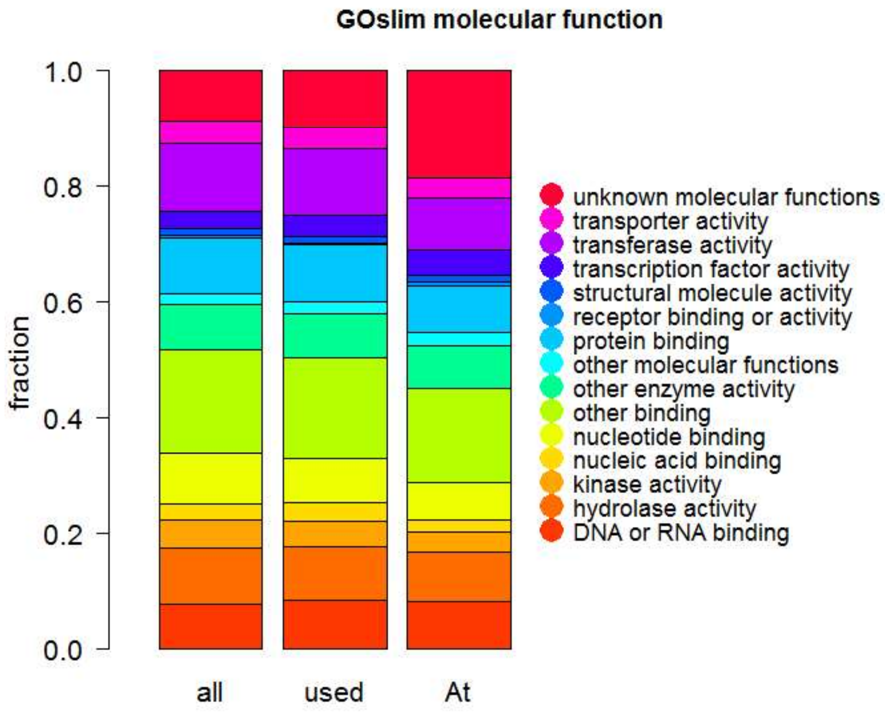

Figure 59. Gene ontology of molecular function for the data set including all the assembled contigs (all), only the contigs kept after the filtering process (used) and the contigs that gave a unique BLAST hit with *Arabidopsis thaliana* (At).

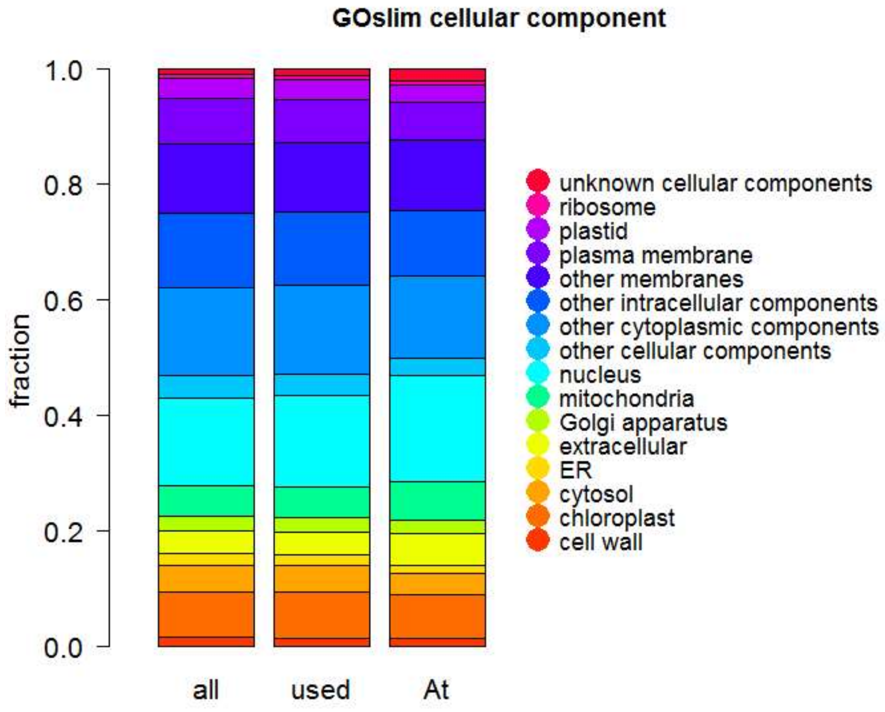

Figure 60. Gene ontology of cellular component for the data set including all the assembled contigs (all), only the contigs kept after the filtering process (used) and the contigs that gave a unique BLAST hit with *Arabidopsis thaliana* (At).

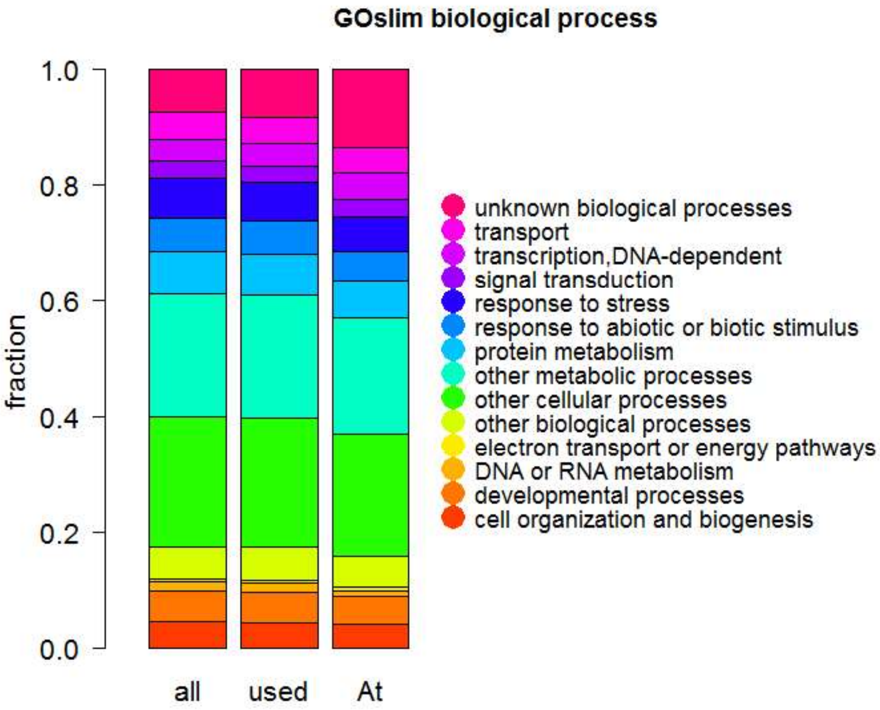

Figure 61. Gene ontology of biological process for the data set including all the assembled contigs (all), only the contigs kept after the filtering process (used) and the contigs that gave a unique BLAST hit with *Arabidopsis thaliana* (At).

Through Figure 59, Figure 60 and Figure 61 is visible that the composition of the data set does not significantly change after the filtering procedure (all *vs* used), confirming that the quality of the data set has been increased without losing relevant information or altering the original composition of the transcriptome assembly.

The next step was the analysis of differential expression that was performed by setting the p-adjusted value at different levels of strictness. Differential expression was calculated in a reproduction specific way, by considering all the 8 sequenced samples, from sexual lines against the 8 samples from apomicts and also in a reproduction + stage specific way, by comparing sexual vs apomicts within each of the four considered stages. The outcome of the reproduction specific comparison is summarized in Table 8.

Table 8. Number of differentially expressed contigs calculated with different false discovery rate adjusted p-values (padj) and with different limitations of log fold change (lfc). Green: less strict calculation; Red: strictest calculation; Yellow: chosen calculation.

	padj-10^{-1}	padj-10^{-2}	padj-10^{-3}	padj-10^{-4}	padj-10^{-5}	padj-10^{-6}
lfc0diff	7848	4199	2843	2120	1722	1438
lfc1diff	3721	2673	2050	1673	1427	1233
lfc2diff	1237	1237	1237	1203	1098	974
lfc3diff	587	587	587	587	587	587
lfc0up	3863	2198	1551	1167	955	801
lfc1up	1950	1468	1143	946	816	700
lfc2up	755	755	755	736	676	599
lfc3up	376	376	376	376	376	376
lfc0down	3985	2001	1292	953	767	637
lfc1down	1771	1205	907	727	611	533
lfc2down	482	482	482	467	422	375
lfc3down	211	211	211	211	211	211

The most relaxed calculation settings (p adjusted value ≤ 0.1 and no fold change limitations) produced 7848 differentially expressed contigs (in green in Table 8), while the strictest calculation (padj≤1e-6 and log fold change > 3) detected 587 differentially expressed contigs (in red in Table 8).

The results reported in this section refer to a third calculation performed with the following conditions: p-adjusted value ≤ 1e-3 with lfc ≥ 1 that detected 2050 differentially expressed contigs (highlighted in yellow in Table 8). The choice of these settings was considered the best balance between accuracy and number of detected entities. The term p-adj ≤ 1e-3 means, that statistically, only 2 out of 2050 differentially expressed contigs are expected to be false positives. Lower p-values would not produce a relevant improvement of reliability, but only a drastic reduction of differentially expressed entities.

It is important to remark that 2050 is the total number of differentially expressed entities resulting from a reproduction specific data analysis (all 4 sexual stages compared with all 4 apomictic stages). Nevertheless, the stage wise data analysis generated a different set of results, which is largely overlapping with the reproduction wise results. The two sets of results comprehend a total of 2121 entities. A graphical representation of the described set of results is given in the Venn diagram provided in the supplemental data (Figure 75).

K-means clustering

The K-means clustering of the 2121 differentially expressed entities was organized in 19 clusters given in Figure 62.

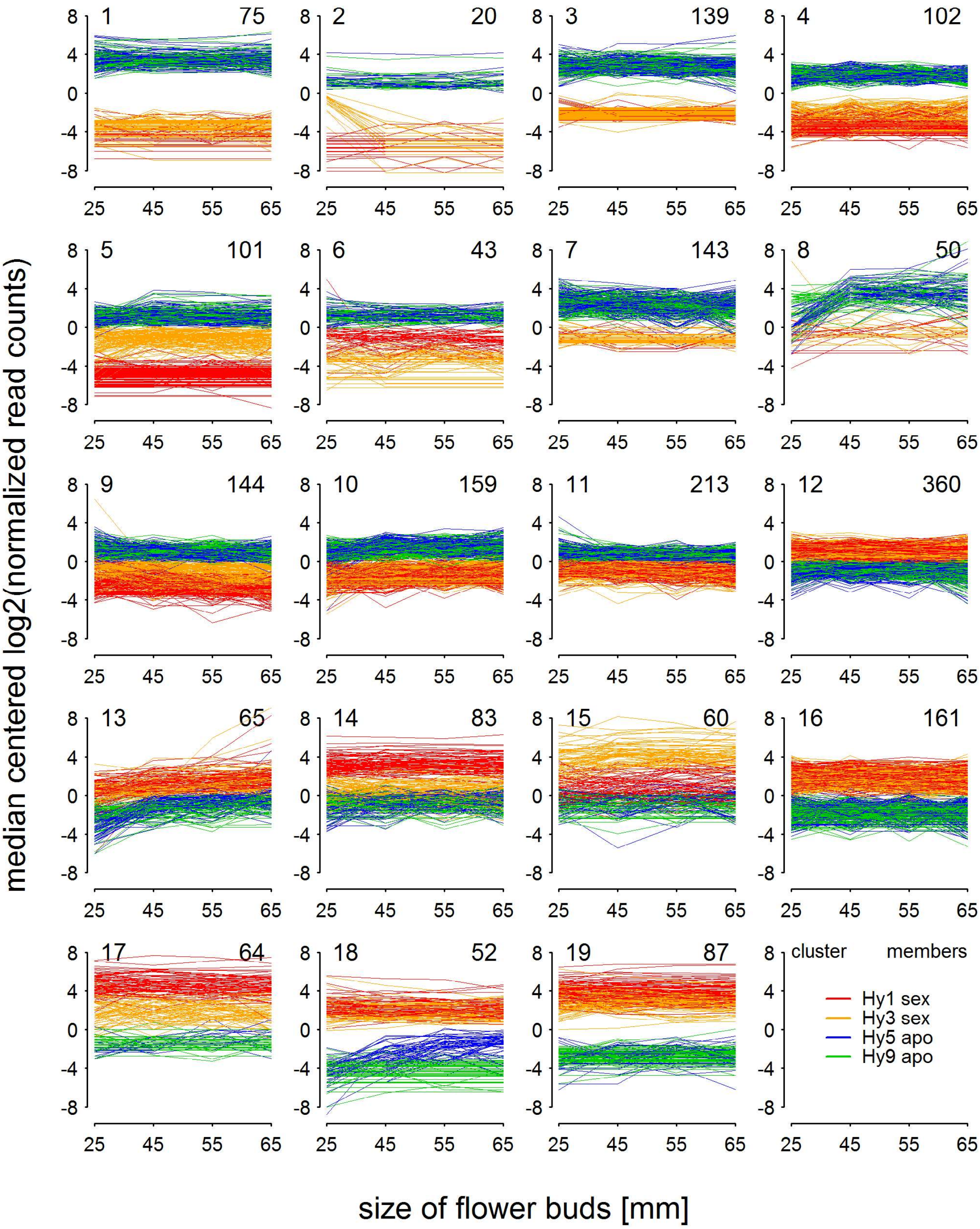

Figure 62. K-means clustering of 2121 differentially expressed contigs resulting from the reproduction wise comparison of the two sexual diploid lines HyPR-1 and HyPR3 with the two tetraploid apomicts HyPR5 and HyPR9. Flower bud sizes: 25 = 2.5-3.5 mm; 45 = 4.5-5.5 mm; 55 = 5.5-6.5 mm; 65 = 6.5-7.5 mm. Cluster n°: upper left of every chart; Entities number: upper right side of every chart.

Most of the clusters showed a steady differential expression. Clusters 1 to 11 presented entities upregulated in apomicts vs sexuals. Clusters 12 to 19 showed the opposite behavior. Cluster 8 is the only cluster where the sexual and apomictic lines seemed to have similar expression profile in the first analyzed stage (fb25), while afterwards the two expression profiles diverged.

For every cluster, GOslim terms were assigned in order to detect the enrichment in some ontology categories. The results of this analysis are reported in Figure 63, Figure 64 and Figure 65. Every figure refers to a different GOslim terms class: cellular component (Figure 63), molecular function (Figure 64) and biological process (Figure 65).

GO-terms for cellular component (Figure 63) showed significant enrichment of entities related to extracellular localization, mitochondria localization and nucleus localized entities (cluster 15, 16 and 19 respectively).

In addition, clusters 1, 3, 7 and 17, presented a significant enrichment of unknown cellular components.

GOslim for molecular function (Figure 64) showed a trend regarding the entities connected with nucleic acid binding functions, which were significantly enriched in clusters 1, 3,6 and 7. This is the strongest trend of enrichment in the whole dataset, and it was detected only in contigs including entities that are overexpressed in the apomictic lines.

The GO-terms for biological process analysis (Figure 65) showed enrichment of the category “DNA and RNA metabolism” in the clusters 1, 3 and 7, while clusters 4 and 15 were enriched in entities known to be connected with stress response processes. Cluster 4 also showed enrichment in GOslim terms of the category signal transduction.

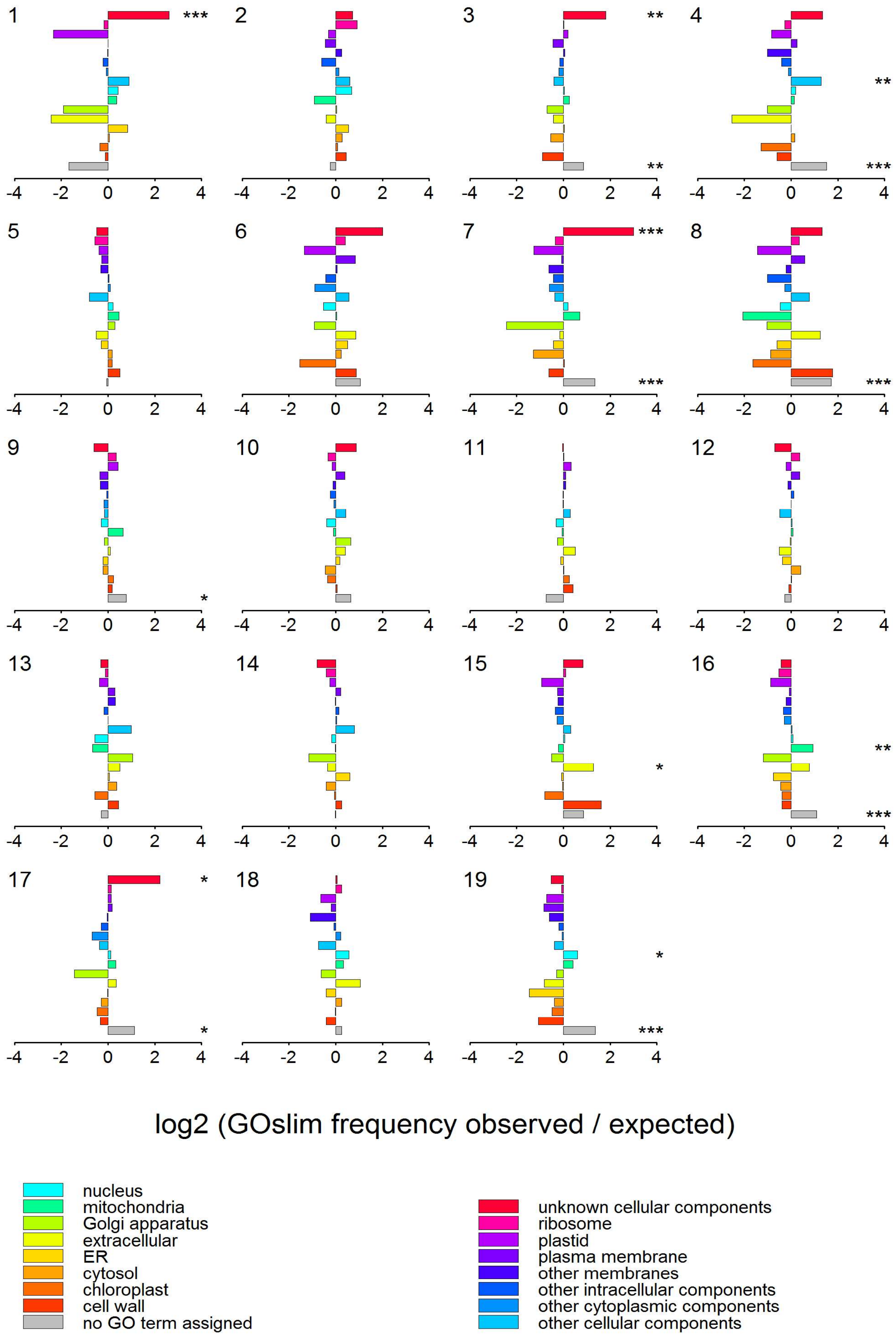

Figure 63. GOslim terms for **cellular component** in a cluster wise comparison of apomicts vs sexual lines.

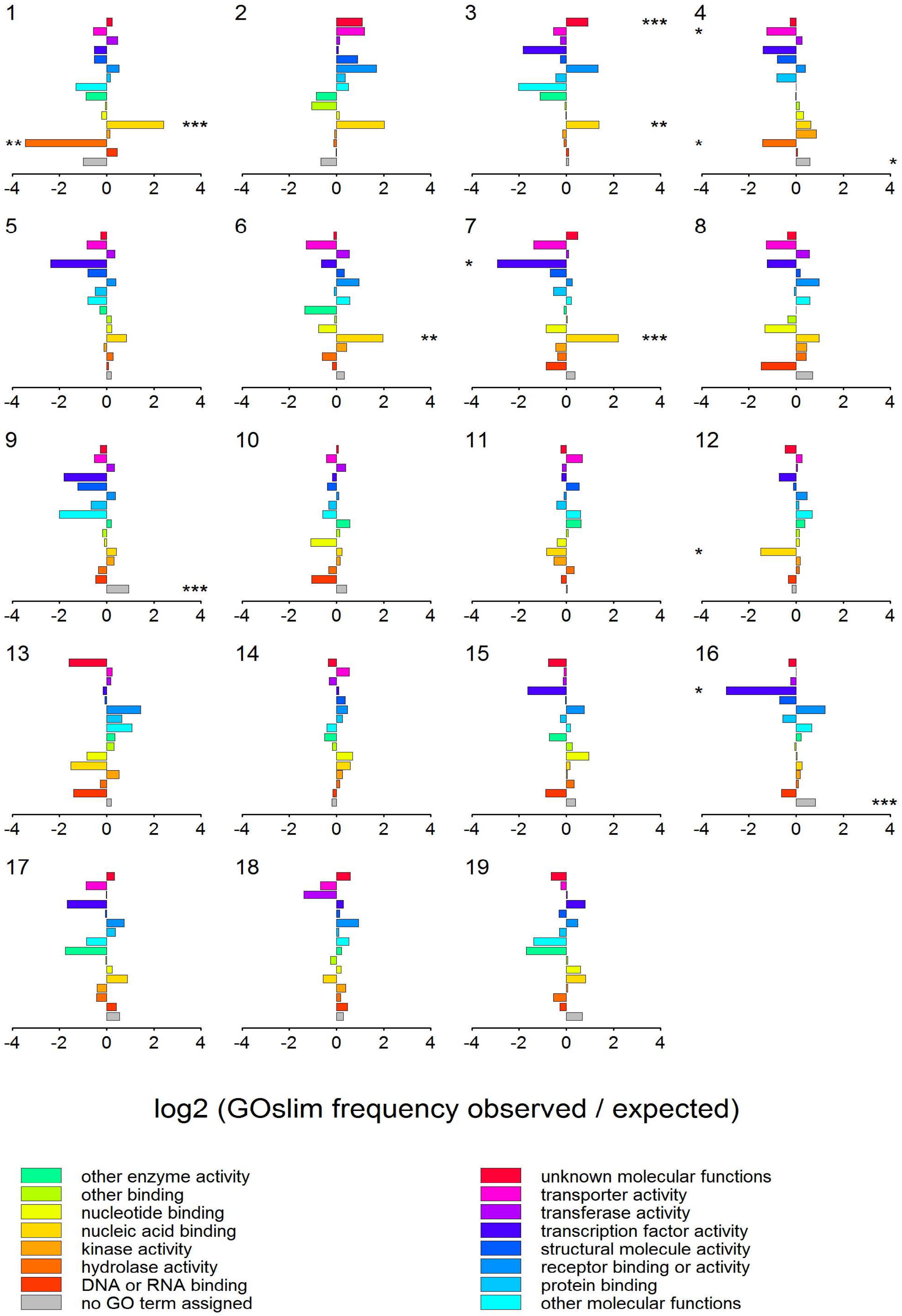

Figure 64. GOslim terms for **molecular function** in a cluster wise comparison of apomicts vs sexual lines.

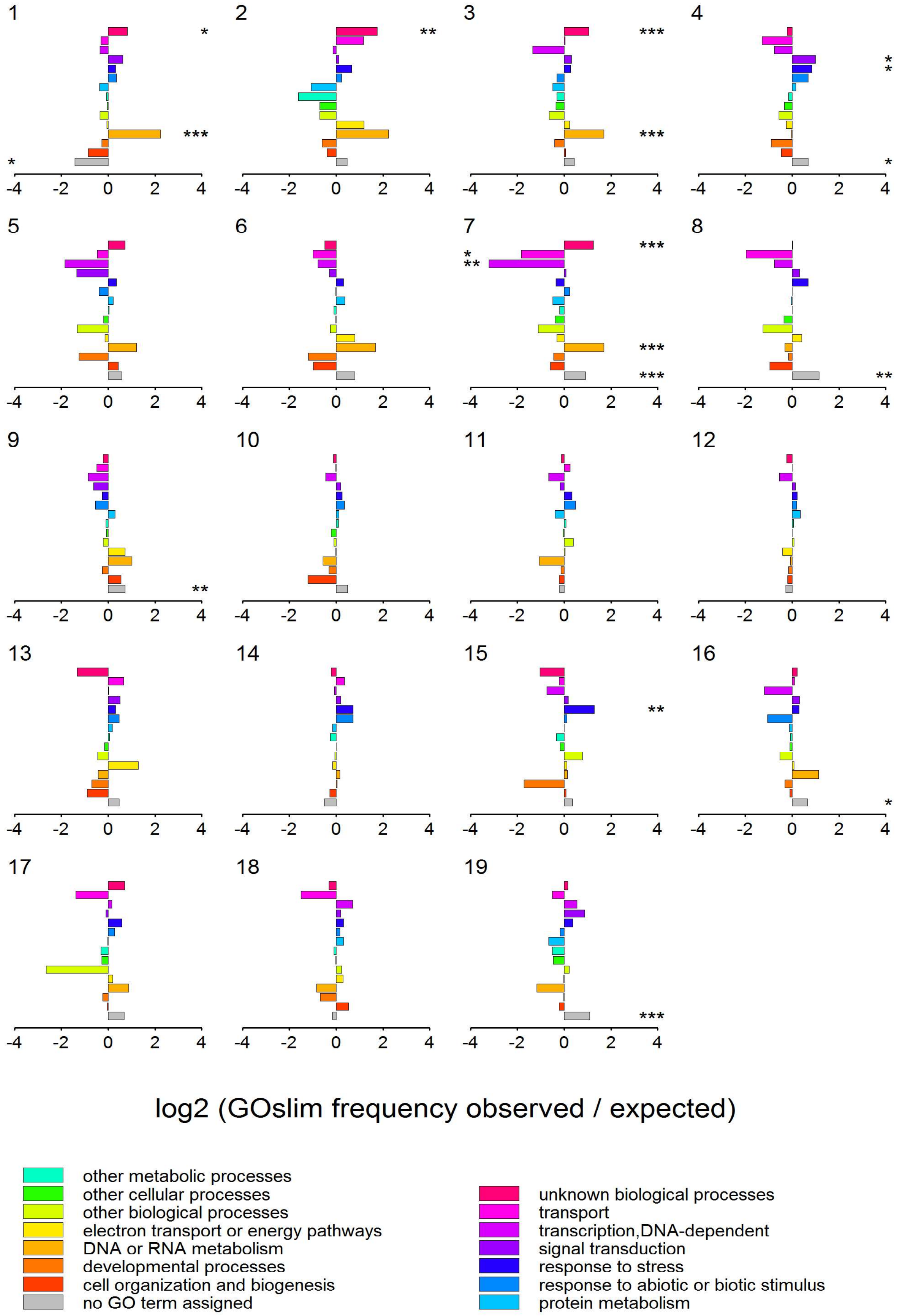

Figure 65. GOslim terms for **biological process** in a cluster wise comparison of apomicts vs sexual lines.

Stage-wise comparison

As mentioned before, the differentially expressed entities were also analyzed in a stage-wise comparison between sexual and apomictic lines. Stage specific expression patterns for every differentially expressed contig are given in Table 23. The results of stage specific calculation for differential expression are given in the supplemental data (Table 19, Table 20, Table 21 and Table 22). The number of differentially expressed contigs between apomictic and sexual lines in every flower bud size was: **378** for flower buds of length between 2.5 and 3.5 mm, **395** for flower buds of length between 4.5 and 5.5 mm, **375** for flower buds of length between 5.5 and 6.5 mm and again **375** for flower buds of length between 6.5 and 7.5 mm.

The majority of the entities, differentially expressed in every considered stage, appeared also as differentially expressed in the other three stages. This is represented in Figure 66, which shows how **228** entities resulted to be differentially expressed in all four analyzed stages. 212 out of these 228 contigs are steadily up or downregulated in apomictic lines, while only 16 showed more unstable expression patterns. This confirms what was shown in Figure 62, where all clusters (except number 8) had steady patterns of expression with the majority of entities either up or down regulated at all stages.

Stage specific differential expression was also detected with **69** contigs differential only in fb25, **38** only in fb 45, **23** in fb55 and **59** in fb65.

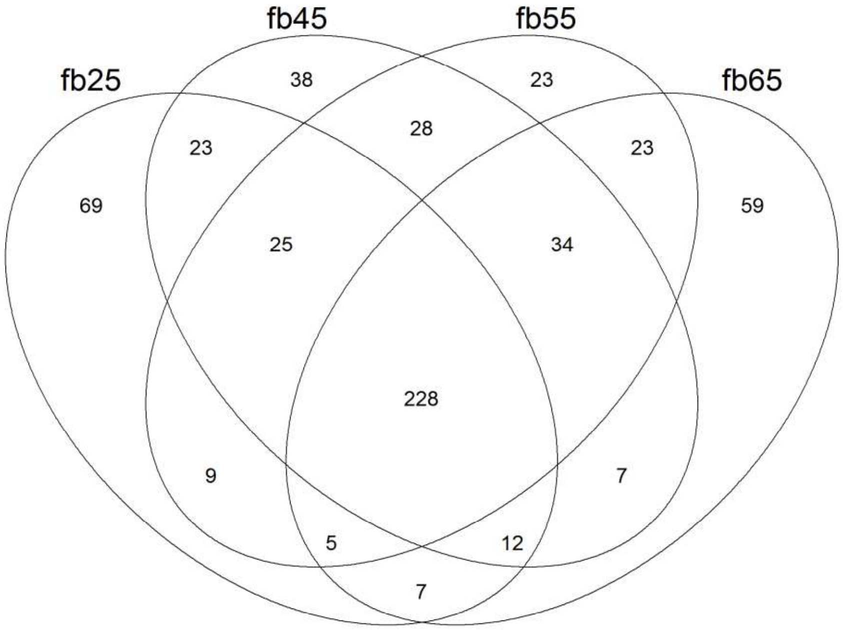

Figure 66. Venn diagram of stage-wise differential expression. Fb25 = flower buds 2.5 – 3.5mm; fb45 = flower buds 4.5 – 5.5 mm; fb55 = flower buds 5.5 – 6.5 mm; fb65 = flower buds 6.5 – 7.5 mm.

Differential expression exclusively detected in ovules from fb25 flower buds

The group of 69 entities that were differentially expressed exclusively in ovules from fb25 flower buds included contig_804, which matched with the *Arabidopsis* gene *AtPS1* known to have an essential function during the second meiotic division (Erfurth et al., 2008). This contig was significantly upregulated exclusively in ovules from apomictic lines collected from fb25 flower buds. Nevertheless, there were other 14 entities in the data set of 2121 differentially expressed contigs, which showed significant differences between sexual and apomictic lines and that matched with *Arabidopsis* meiotic genes. This is the case of the strongly downregulated contig_3615 matching with the meiotic gene *AtTTN7* (Ma, 2006; Schubert et al., 2013).

Another gene matching with contigs that were upregulated specifically at the fb25 stage in apomicts is *CHR11* (hosted in contig_78097), a chromatin remodeling factor known for regulating different transcriptional programs during plant development, especially during female gametogenesis (Huanca-Mamani et al., 2005). A similar fb25 specific up regulation was detected for contig_43283 which matched with the *Arabidopsis* gene *PUMILIO 12* of the PUF protein family, known to target specific cis-acting mRNAs, therefore having the translational control of many RNAs transcribed all over the genome (Francischini and Quaggio, 2009).

The contig_45032 is another example of stage specific up regulation. Its sequence highly matches with the *Arabidopsis thaliana* gene *USPL1* (*Ubiquitin Specific Protease-Like 1*) which encodes for a peptidase that can bind with SUMO, playing in this way, an important role in protein modification mechanisms (Schulz et al., 2012), seed development and drought stress response (Harshavardhan et al., 2014).

Fb25 specific downregulation was also detected in many entities, *e.g.* the case of contig_9875, matching with another chromatin modifier (like *Chromatin11*), known in *Arabidopsis* as *BRUSHY1* (*BRU1*), which keeps the transcriptional silencing of many heterochromatic genes many of which are top regulators of important developmental programs, such as stem cell maintenance and embryogenesis in plants (Ohno et al., 2011).

GOslim terms enrichment in stage wise comparison between sexual and apomictic lines

The GOslim terms enrichments were calculated also for stage wise comparison as shown in Figure 67 (cellular component), Figure 68 (molecular function) and Figure 69 (biological process).

GOterms for cellular components rarely showed significant enrichments, with the exception of extracellular localization at the fb65 stage and mitochondria in the overall comparison (Figure 67). The categories “no GOterms assigned”, “unknown cellular components” and “other cellular components” showed significant enrichments but they are not informative.

The analysis of GOslim terms regarding molecular functions (Figure 68), showed an enrichment in the nucleic acid binding category, suggesting a significant difference in the expression pattern of genes involved in regulatory mechanisms. This enrichment was limited to the up regulated entities at all the analyzed stages. This suggests a potentiated regulatory machinery and confirms what was shown in the gene enrichment analysis of the K-means clusters, where the same kind of trend was detected (Figure 64, Clusters 1, 3, 6 and 7). The GOterms relative to molecular function also showed a significant enrichment in up regulated transferase activity for the overall comparison.

Finally, the GOterms of the class “biological process” (Figure 69), detected a trend of enrichment in up regulated entities of the category “DNA or RNA metabolism” at all stages, in agreement with what was found in the K-means clustering.

The category “nucleic acid binding” from the GOslim class molecular function contained a group of contigs that was partially overlapping with the ones in category “RNA or DNA metabolism” from the GOslim class biological process. This overlapping is represented in Table 9 on the lower row.

Table 9. Significantly higher expressed entities in apomictic lines belonging to the two GOslim categories: “nucleic acid binding” and “DNA or RNA metabolism”. (F) = molecular function, (P) = biological process.

	fb25	fb45	fb55	fb65	All
All UP members	244	266	247	238	1143
(F) nucleic acid binding	35	37	33	33	112
(P) DNA or RNA metabolism	17	16	16	14	64
Both categories	13	13	12	11	39

In the previous table, all the entities of the last row are matching with the *Arabidopsis* gene AT4G29090 known to encode for a RNA directed DNA polymerase (reverse transcription) and to extensively overlap with the transposable element AT4TE67780 (as visible in the arabidopsis.org and ftp.arabidopsis.org websites). This evidence suggests an activation of these transposable elements in ovules from apomictic lines for all analyzed stages.

Response to stress is another category of biological process GOslim terms, that is significantly enriched in the list of differentially expressed at every stage. Nonetheless, in this case there was no steady up- or down regulation. The up regulated entities of this category were enriched only at fb45, while in fb65 stage there was enrichment in down regulated entities connected with response to stress. The category “response to abiotic or biotic stimulus” was enriched in the list of all differentially expressed entities only in stage fb25, and the category “signal transduction” was enriched in the overall differentially expressed and in the up regulated entities only in stage fb55 (Figure 69).

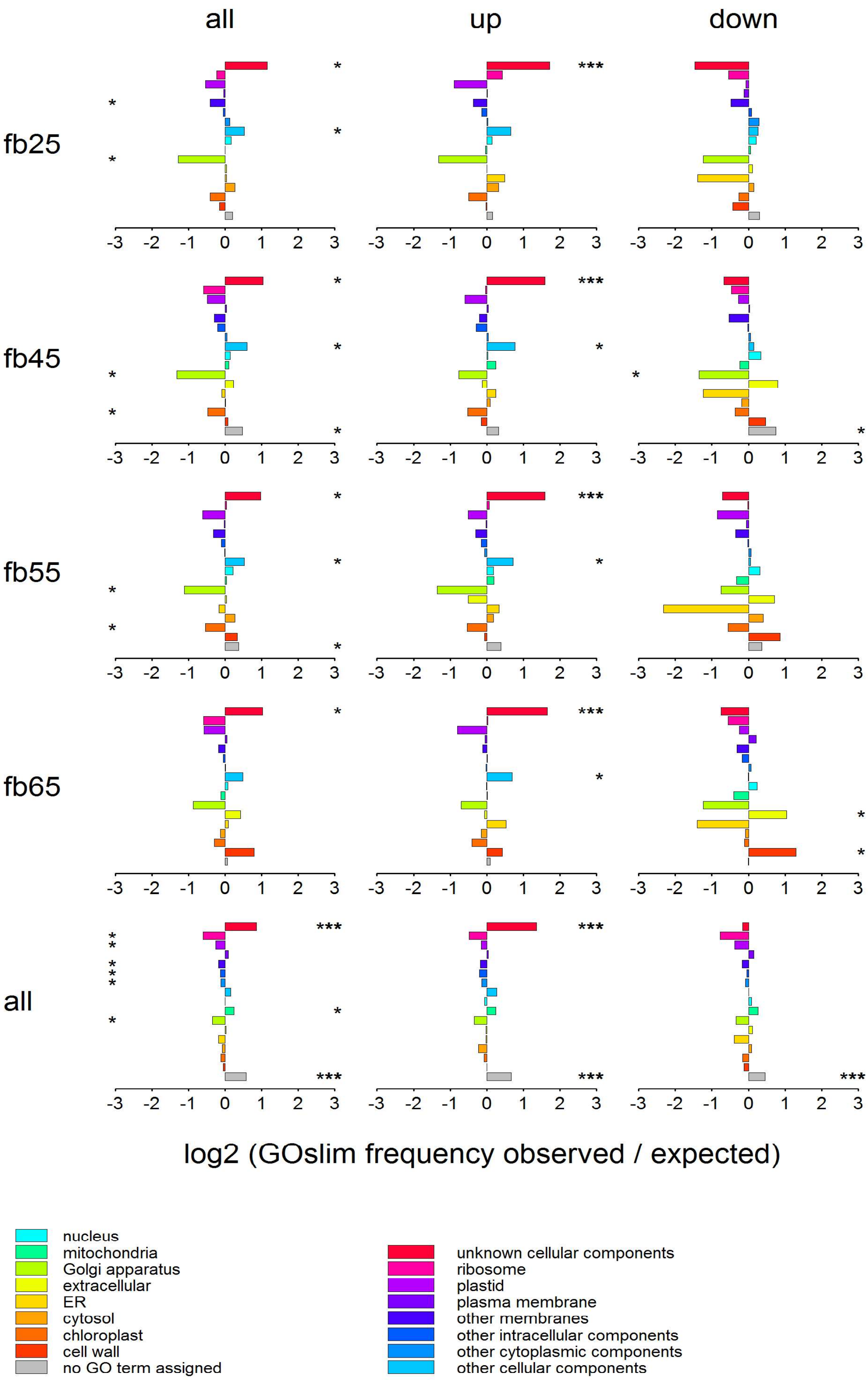

Figure 67. GOslim terms for **cellular component** enrichment in a stage wise comparison of sexual vs apomictic ovules transcriptome. Fb25 = flower buds 2.5 – 3.5 mm; fb45 = flower buds 4.5 -5.5 mm; fb55 = flower buds 5.5 – 6.5 mm; fb65 = flower buds 6.5 – 7.5 mm; all (y axes) = all stages; all (header) = all differentially expressed entities; up = only upregulated (in apomicts) entities, down = only downregulated entities.

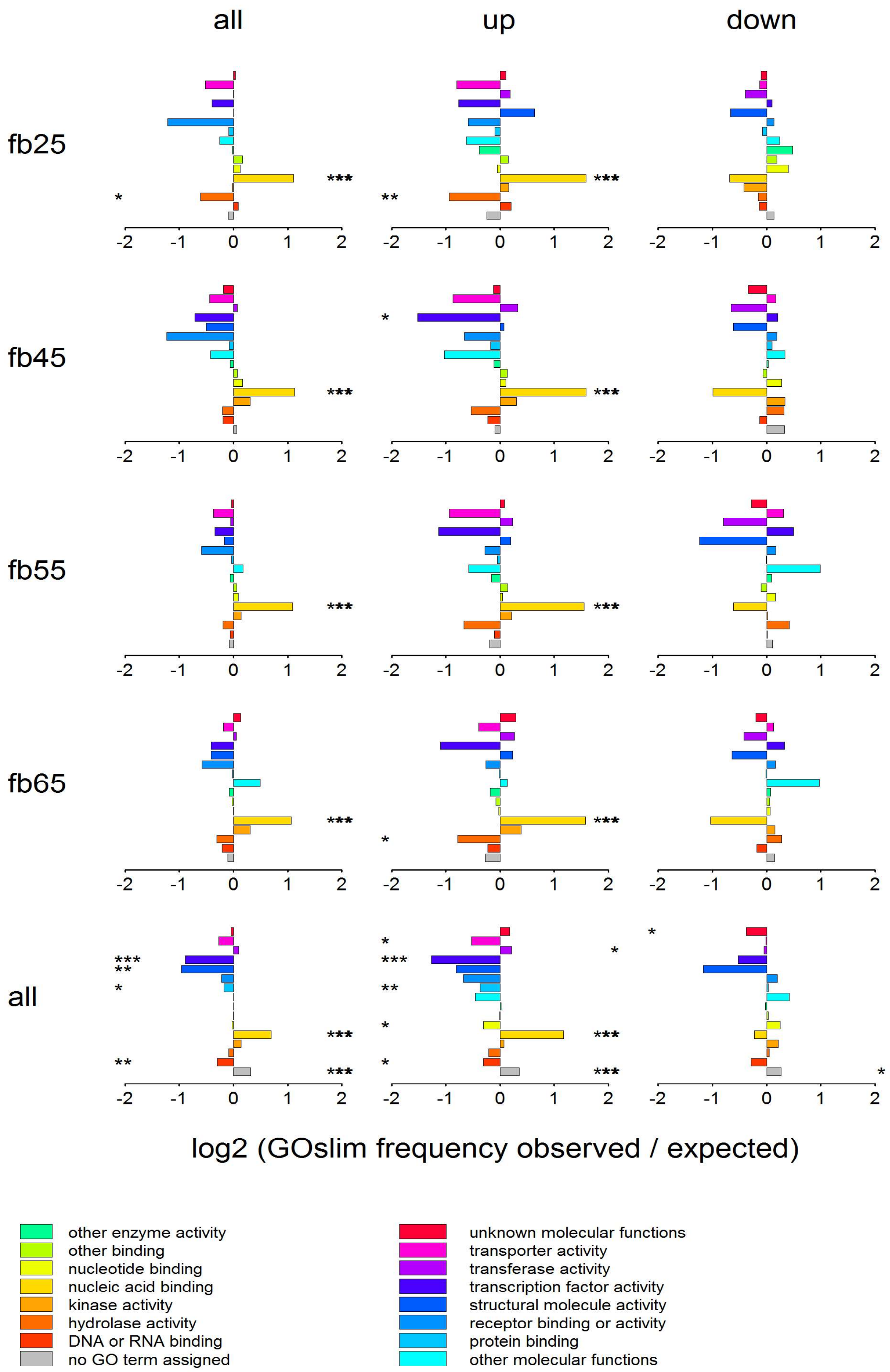

Figure 68. GOslim terms for **molecular function** enrichment in a stage wise comparison of sexual vs apomictic ovules transcriptome. Fb25 = flower buds 2.5 – 3.5 mm; fb45 = flower buds 4.5 -5.5 mm; fb55 = flower buds 5.5 – 6.5 mm; fb65 = flower buds 6.5 – 7.5 mm; all (y axes) = all stages; all (header) = all differentially expressed entities; up = only upregulated (in apomicts) entities, down = only downregulated entities.

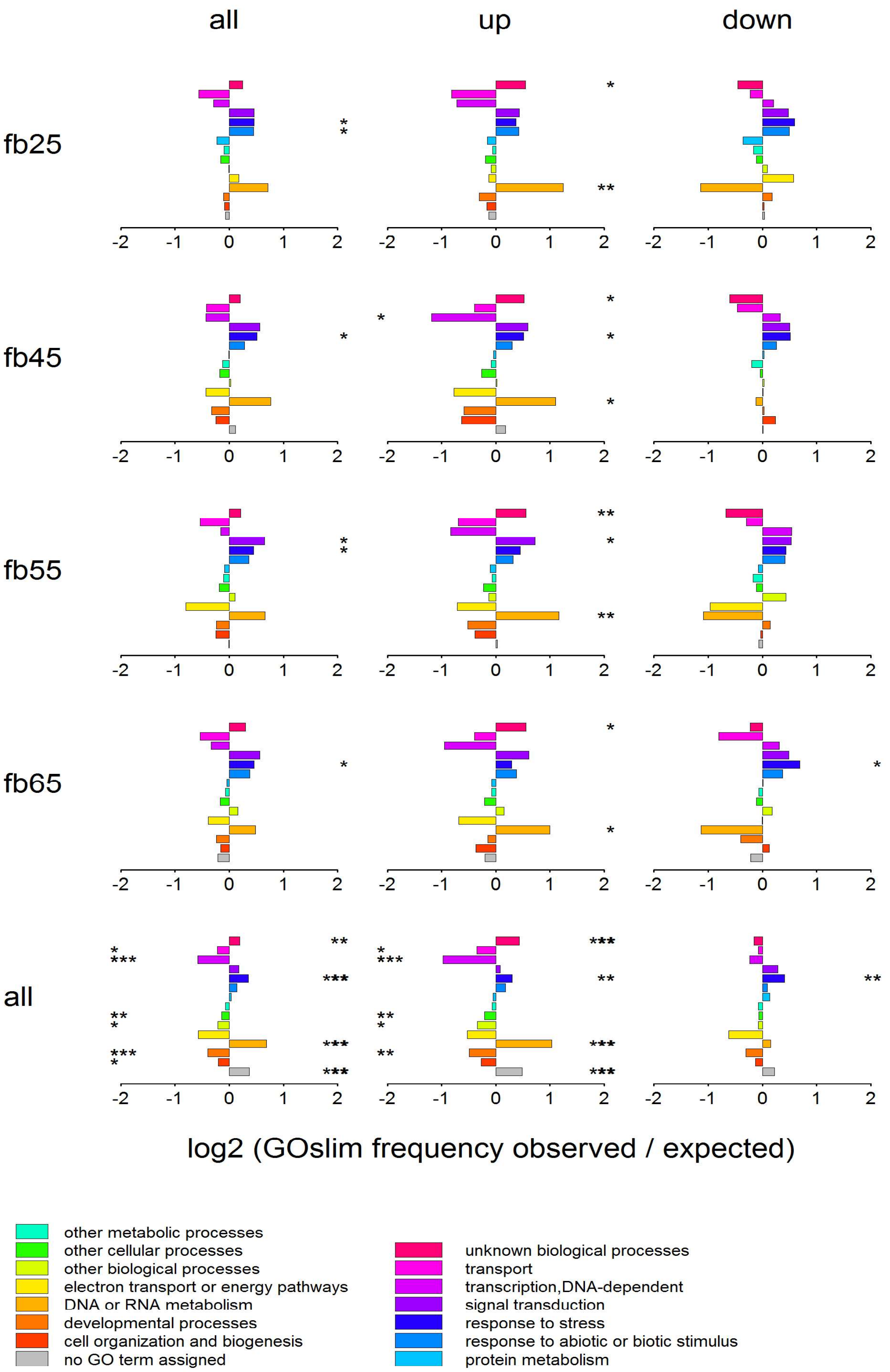

Figure 69. GOslim terms for **biological process** enrichment in a stage wise comparison of sexual vs apomictic ovules transcriptome. Fb25 = flower buds 2.5 – 3.5 mm; fb45 = flower buds 4.5 -5.5 mm; fb55 = flower buds 5.5 – 6.5 mm; fb65 = flower buds 6.5 – 7.5 mm; all (y axes) = all stages; all (header) = all differentially expressed entities; up = only upregulated (in apomicts) entities, down = only downregulated entities.

Expression patterns diverging at stage fb45

As mentioned before, in the nineteen clusters obtained during the K-means clustering, only cluster 8 did not show a steady up or down regulation in apomictic lines. Its expression patterns were very similar in sexual and apomictic ovules at stage fb25 and diverged afterwards, starting at the same time point when apomictic lines started to differentiate relevant percentages of aposporic initial cells. From the 50 entities belonging to cluster 8, six were non differential at stage fb25 and up regulated at stage fb45 as reported in Table 10.

Table 10. Contigs from cluster 8 that show no differential expression in flower buds fb25 but that are significantly upregulated at least in flower buds fb45.

contigID	cluster	saccAt	evalue At	diff_**fb25**_apo/sex	diff_**fb45**_apo/sex	diff_**fb55**_apo/sex	diff_**fb65**_apo/sex	diff_apo/sex
contig_81354	8	AT1G06620.1	3.0E-148	NA	UP	NA	NA	UP
contig_44293	8	AT1G49570.1	1.0E-27	NA	UP	UP	NA	UP
contig_41204	8	AT2G22590.1	1.0E-20	NA	UP	UP	UP	UP
contig_32516	8	AT3G14067.1	9.0E-115	NA	UP	UP	UP	UP
contig_93823	8	AT5G54160.1	1.0E-128	NA	UP	UP	NA	UP
contig_64775	8	NA	NA	NA	UP	UP	NA	UP

Following the expression profiles detected in cluster 8, further data mining was performed and the data set of 2121 differentially expressed contigs, was searched for entities non differentially expressed at fb25 but up regulated in fb45. As a result, 76 entities (including the 6 of Table 10) were identified. In this bigger group, six entities were associated with signal transduction and 13 were contigs associated with stress response. Two contigs of this group were matching with *Arabidopsis* genes involved in developmental processes.

Contig_26601 (Table 11) matched with the *Arabidopsis* gene AT5G02190 known as *PCS1* (*Promotion of Cell Survival 1*), which encodes an aspartic protease and is considered an anti-apoptotic gene, that is able to prevent cell death and to influence the cell fate during embryonic development and other reproductive processes (Ge et al., 2005).

Contig_11340 (Table 11) matched with AT3G23050 known as *IAA7* (*indol-3-acetic acid 7*) or *AXR2* (*auxin resistant 2*), that encodes for an AUX/IAA protein, that like other proteins of the same family can modulate the response of auxin signaling, influencing in this way a wide variety of developmental processes (Nagpal et al., 2000; Mai et al., 2011; Sato et al., 2015).

Table 11 Two contigs extracted from the list of 76 entitites non differentially expressed (NA) in fb25 and up regulated in fb45.

contigID	cluster	saccAt	evalue At	diff_**fb25**_apo/sex	diff_**fb45**_apo/sex	diff_**fb55**_apo/sex	diff_**fb65**_apo/sex	diff_apo/sex
contig_26601	10	AT5G02190.1	1.0E-34	NA	UP	NA	UP	UP
contig_11340	11	AT3G23050.1	3.0E-104	NA	UP	UP	UP	UP

Data mining was not limited to up regulated entities at fb45 but was extended as well to the contigs that resulted to be non-differentially expressed at stage fb25 and down regulated at fb45. This search identified a group of 31 entities including contigs matching with *Arabidopsis* genes involved in response to stress, regulation of cell cycle, ubiquitination and histone modification. Contig_14043 belongs to the latter category. It is not differentially expressed at fb25 stage but it is significantly down regulated in fb45, fb55 and fb65 in apomictic lines. It matches with the *Arabidopsis* gene AT1G70060 known as *SNL4*, a repressor of transcription that encodes for a histone deacetylase and that is characterized by a cell-to-cell mobile mRNA (Bowen et al., 2010; Thieme et al., 2015).

It is important to remark that GOterms enrichment and peculiar expression patterns were not the only guide that led to the identification of interesting candidates, putatively connected with the occurrence of the aposporous developmental pathway. Even entities differentially expressed in a steady way could potentially play a regulatory role connected with the apomictic development. In the light of this consideration, a general screening of the list of 228 entities differentially expressed at all stages (see Venn diagram of Figure 66) was performed, in order to highlight contigs matching with genes that are known to play important regulatory roles in several developmental processes. As a result of such screening, it was detected that even this group of 228 contigs included several entities, matching with genes involved in signaling mechanisms (22 entities) and developmental processes (20 entities).

Some of these entities matched with high rank regulatory genes, *e.g.* contig_9868 that has a strong BLAST hit with *Arabidopsis thaliana IBM1*, a gene encoding for a jmjC domain-containing protein that regulates genome-wide methylation levels, by preventing the deposition of ectopic non-CG methylation, and guarantying in this way a normal functioning of several developmental process that keep the genome integrity (Miura et al., 2009; Saze et al., 2008). This entity resulted to be down regulated in apomictic lines for all the analyzed stages.

Contig_13097 resulted up regulated in apomictic lines at all analyzed stages and it matched with the *Arabidopsis CDT1*, a gene that encodes for a protein with an essential role in gametophytes development and regulation of cell cycle. An overexpression of such gene is known to induce a re-replication of DNA due to the activation of all cell cycle checkpoints with consequent accumulation of ssDNA (Domenichini et al., 2012). This extreme promotion of DNA re-replication can, in some cases, lead to tumorigenesis and may be counteracted by the simultaneous activation of apoptotic processes in adjacent cells (Truong and Wu, 2011). Generally the proper expression of this gene is essential in order to keep the integrity of the genome (Domenichini et al., 2012). The initiation of apoptotic processes associated with the overexpression of *CDT1* fits very well with the characterized cell death, that affected the gametophytic domain of the ovule in the apomictic lines, and is supported by the significant up regulation of the contig_15774 and contig_26136. These entities had strong BLAST hits respectively with the *Arabidopsis* genes *SOG1* and *MYB30*, known in literature for their capacity to induce hypersensitive cell death response (Raffaele et al., 2008) and apoptosis in response to heavy cell damage (Yoshiyama et al., 2009).

Discussion

Potential fitness in *Boechera spp.*

The evaluation of fitness is a very challenging task due to the many parameters that contribute to it. In this study we evaluated several reproductive traits that were combined to provide a general evaluation of the potential fitness of the analyzed lines.

The sexual lines showed to be significantly better than the apomictic ones regarding germinability and number of fertile seeds per silique. On the other hand, the traits: number of siliques per plant and flowering time, did not show clear differences between apomictic and sexual lines.

The potential fitness calculated in this study could be considered as a comprehensive evaluation of the aforementioned traits, aimed to understand if there is or not a clear separation in terms of reproductive potential between apomictic and sexual lines.

The two lines with the highest values of potential fitness were both sexual diploids (BoSDi-05 and 06), in agreement with the observations performed during the morphological analysis and the ploidy measurements, which suggested that *Boechera spp.* may not tolerate higher levels of ploidy.

On the other hand, BoSDi-05 and 06 showed values of potential fitness two to three times higher than the third best line, therefore, they could be considered as outliers. Excluding these lines from the potential fitness evaluation, would leave a group of 15 lines (5 sexual and 10 apomicts) in which there is not a clear separation in potential fitness between the two reproductive modes.

This result led to the conclusion that, despite the clear superiority of sexual lines in terms of germinability and especially fertility rates, the apomicts are not clearly inferior, in fact many sexual lines were surpassed in potential fitness by their apomictic counterparts. This can be considered as a proof of concept, which theoretically apomictic lines can compete at the same level of their sexual counterparts even in their natural environment.

Ploidy dynamics in *Boechera spp.*

The simultaneous study of leaves and seeds ploidy in *Boechera spp.* suggested that sexual reproduction guarantees a higher stability to the development machinery of the studied lines. All individuals of all analyzed sexual lines were diploid, produced seeds containing a diploid embryo and a triploid endosperm. In sexual lines no polyploidization event was detected even after three to four generations. In contrast, the analyzed apomicts were less stable and exhibited polyploidization events over several generations. The diploid apomictic line BoADi-01 represented an extreme case. Within only two generations, the ploidy level changed from a diploid to tetraploid sporophyte, even producing seeds with octoploid embryos. Although no adult octoploid plants could be found, these observations demonstrated the ability of apomictic individuals to switch back and forth between different ploidies. Most likely, apomicts lack some unknown constraints required for genome stability in sexual lines.

The data also suggested that seeds carrying polyploidized embryos suffer from developmental problems such as higher sterility levels and lower germination rates. BoATe-04 is a tetraploid line that was able to show many of these interesting characteristics (8C embryos and the reversing to a diploid state). In the light of this successful experiment, continuous work has been done to produce not only more tetraploid lines derived from diploids, but also to obtain hexaploid lines from triploids.

Another important topic connected with ploidy concerns the endosperm development. In several apomictic lines, 20 to 25% of the analyzed seeds showed only one main ploidy peak that corresponded to the embryo, but there were no other visible peaks in the flow cytometry histogram. In this cases, it was not possible to exclude that the endosperm was simply not detected, even if still present. Nevertheless, a percentage of 20-25% of seeds showing only one ploidy peak would be consistent with a comparable percentage of seeds that underwent late abortion (data not shown) or that were not able to germinate (Figure 7). Therefore, it is possible to argue that the absence of the endosperm peak may be connected, at least in some cases, with the total or partial failure of endosperm in many apomictic lines.

Another problem of interpretation is represented by the FCSS histograms where only two peaks with 1:2 ploidy ratio were visible. It is not possible to exclude that these seeds presented an autonomous endosperm, but considering that the vast majority of the samples of the same line showed 1:3 peak ratios (meaning apomixis with non-autonomous endosperm), the 1:2 ratio appears to be most likely related to endosperm failure. This means that the second peak may be derived from the endoreduplication of the first one. Finally, the FCSS data were essential to confirm the reproductive mode of every analyzed line. This indicated that sexual and apomictic lines were very stable in terms of reproductive mode. It was never detected any switch from sexuality to apomixis or vice versa. This was expected considering that apomixis seems to be many times associated with intra or interspecific hybridization events, and once it is established within a new hybrid, it can be a quite stable trait (Hörandl, 2006; Hörandl et al., 2007).

In order to detect some cases of switching from sexuality to apomixis, it would be interesting to perform crosses between different lines.

The results reported in this study support the thesis of Hegarty et al., (2006), who showed how genome duplications may be a suitable strategy for newly generated interspecific hybrids, to limit the effects on altered gene expression ("transcriptomic shock"), as a consequence of the hybridization event.

Female gametophyte development in *Boechera spp.*

The morphological analysis performed on *Boechera spp.* generated novel information on the ovule and female gametophyte development characterized by high level of detail.

The two main aspects that emerged from this observation were:

- The faster developmental speed of triploid apomicts in comparison with the other lines.
- The highest abortion rates of apomictic lines.

The difference in developmental speed emerged especially at the earliest stages. Pistils from flower buds of the class 1 contained finger-like ovules primordia in the diploid sexual lines. Diploid and triploid apomicts were mainly at the archesporial cell and MMC, respectively. Apomictic lines were able to differentiate MMCs already in class 1, while sexual lines reached this stage only in class 3.

In order to get a more detailed idea of how fast the megagametogenesis was, Table 4 provided the frequencies of three different classes of MMC: SI, MI, BI; namely: small, medium and big integuments primordia (Figure 71).

This connection between the differentiation of MMCs and the size of integuments primordia, made possible to understand how persistent was the MMC. Per example, diploid sexual lines and diploid apomicts showed MMCs accompanied by small, medium and big integuments, indicating a relevant persistence of this stage. The triploid apomicts on the other hand, showed MMCs accompanied by small and medium, but not big integuments. This was a consequence that, by the time the integuments primordia grew, the gametophyte was already at the stage of functional megaspore or later stages.

The morphological results derived from BoATe-01, the only analyzed tetraploid line (originated from BoADi-01), supported the hypothesis that *Boechera* does not tolerate well polyploidization events. This is evident from the results of Table 4, where this line does not show clear patterns of development due to the extreme persistence of MMCs (visible up to class 8) and the high desynchronization of its gametophytic development. These developmental anomalies were accompanied by the highest levels of abortion.

The fast development of apomicts came at the cost of higher abortion rates in comparison with sexual lines. This might be due to various reasons. Firstly, it could be interspecific hybridization. It is known that in *Boechera*, apomictic lines are more heterozygous than the sexual lines (Lovell et al., 2013) and especially the triploid apomicts are characterized by the highest levels of heterozygosity, while the sexual diploids are basically inbred (diploid apomict have intermediate levels of heterozygosity). The results collected during this study fit with these evidences. The higher abortion rates, that have been detected in triploid apomicts, could be connected with their higher levels of heterozygosity. It is known that heterozygosity, derived from hybridization events, may lead to higher abortion rates as mentioned by Pennington et al. (2008), who clearly described this phenomenon in maize. This could also be considered as the consequence of the encounter between two different genomes, reported in several studies to perturb the normal seed development. Such events, can alter the transcriptome and several epigenetic regulations necessary to get a fertile viable seed, therefore leading to seed abortion (Gehring et al., 2004, Grossniklaus et al., 2001).

Previous work (Berger, 2003) on seed development stressed the importance of imprinting for postzygotic endosperm development as a crucial step for viable seed formation. The data reported here suggest that in apomicts early prezygotic abortion events also contribute to endosperm failure.

Taken together, this detailed morphological atlas of ovule and gametophyte development in *Boechera* provides valuable information for current and future decisions concerning molecular analyses of gene expression programs relevant for the apomictic pathway.

Potential fitness in *Hypericum spp.*

Unlike *Boechera*, that showed striking differences between reproductive modes in nearly all the analyzed traits, *Hypericum* lines did not always show clear trends that could easily distinguish sexual from apomicts. This is the case of germinability. Unlike *Boechera*, where the lowest germination rates where always detected in apomictic lines, and where the sexual lines were always close to 100% of germinability, in *Hypericum* the best lines had germination rates of about 80% (Figure 30).

The seed set on the other hand, is a trait that in *Hypericum* showed significant differences between sexual and apomictic lines, but also in this case the detected differences are less extreme in comparison to that of *Boechera spp.*

The analysis of the seed set in *Hypericum* showed that all the lines are characterized by a relatively low percentage of fertile seeds (above 50% only in the most fertile capsules). This is not necessarily due to a constitutional malfunction of the seed developmental process, rather to a morphological limitation of *Hypericum*, where the fully grown capsule is not big enough to let all ovules develop into seeds. As a result, even the most fertile lines fill the available space within the capsule with fertile seeds, but half of the ovules/seeds anyway abort before reaching maturity.

When all these traits were analyzed together, they showed no significant difference of potential fitness between sexual and apomicts. This is a crucial point that suggests how an apomict line, even if affected by developmental anomalies, is able to compensate with higher number of capsules per plant, reaching a potential fitness comparable (and in some cases superior) to its sexual counterparts.

During this work, it was also hypothesized that flowering time could play a relevant role in the determination of potential fitness, nonetheless, after correcting for flowering time, no major changes in the fitness ranking were observed.

Ploidy dynamics of *Hypericum spp.*

The ploidy analyses of leaves and seeds performed on 15 *Hypericum* lines revealed that several plants and seeds show deviation from the characteristic ploidy of the line. These deviations are explainable most of the times with events of cross pollination between lines, evidenced by different ploidy levels. An example of this phenomenon is the detection of seeds carrying a tetraploid embryo in sexual hexaploid lines, resulting from the fertilization of the triploid egg cell, by a haploid sperm nucleus (from a diploid sexual).

Following the same logic, it was possible to explain the tetraploid plants originated from batch of seeds of diploid sexuals, or the triploid and pentaploid plants derived from tetraploid apomictic lines.

The FCSS results also demonstrated that apomictic lines still maintain a residual percentage of sexuality (3.5% of all seeds derived from apomicts), whereas sexual lines exhibit an average of 0.6% of apomictic seeds. Despite of this low frequency, this is a proof of concept that rare apomictic events can occur in sexual lines of *Hypericum*. This is different from

Boechera where no sexual line has ever shown the formation of seeds via asexual reproduction.

Another interesting aspect of the deviation from the expected ploidy of the line is that in all 15 analyzed lines seeds showed always higher percentages of deviation in comparison with leaves of the same line. This means that the crosses between lines of different ploidy levels are not as viable as seeds derived by self-pollination or at least by crosses between lines of the same ploidy.

Rarely, the hexaploid sexual lines originated seeds carrying a 4C embryo and an 8C endosperm, indicating apomixis accompanied by autonomous endosperm. This kind of observation even if rare, suggests that crosses between diploid sexuals and hexaploid sexuals can lead to tetraploid apomicts.

Finally, the FCSS has detected a trend regarding the “no-endosperm” seed type. Several seeds during the analyses of all 15 lines did not show any detectable trace of endosperm. The overall average of no-endosperm seeds was 5.8% for the sexual lines and 19.7% for the apomictic ones, indicating that endosperm failure could be another developmental anomaly associated with asexual reproduction in the genus *Hypericum* (see also supplemental data Figure 74).

Ovule and female gametophyte development in *Hypericum spp.*

At the beginning of this work, several biological questions were formulated regarding:

- General morphology of the female gametophyte development in *Hypericum*
- Main developmental anomalies in *Hypericum* apomicts (intended as deviations from the sexual developmental pathway) and possible causes of these anomalies.
- Differentiation of the aposporic initial cells (AIs) and their role in the frame of the gametophytic development.
- Identification of the most suitable stages for a multi-stage transcriptomic comparison of the female gametophyte development in sexual and apomictic lines.

Previous literature could provide useful information regarding this topic (Galla et al., 2011). However, the amount of information was limited. In order to fill up this gap of knowledge, a deep histological analysis of ovules and female gametophyte development in several

Hypericum lines was necessary. The observation and classification of 38316 ovules provided novel insights about this topic.

General description of ovule and female gametophyte development in *Hypericum spp.*

The previous work of Galla et al., (2011) provided valuable, yet basic information that helped during the preliminary stages of this analysis. However, the reported pictures and number of intervals in which the development was subdivided in that study were not sufficient for the purposes of this project.

In the frame of this work, a step forward was moved. As a result, a detailed visual atlas of *Hypericum* ovule and female gametophyte development, from the stage of archesporial cell to the formation of a female mature gametophyte across 18 classes of flower-bud growth, was produced.

The development observed in diploid sexual lines was considered as the standard for comparison with the other types of lines (6C-sexuals and 4C-apomicts).

Ovules emerged as finger-like primordia from the placental tissue of the pistil. In class 2 flower buds, the ovules were about 70 µm long and showed already very well defined integument primordia, carrying already a MMC (Figure 51). The MMCs may persist until the flower buds reach class 5 (Figure 52).

The first MMCs differentiated in ovules with small integuments primordia and were still visible in many ovules that already grew big integuments. At this point in development, the ovules of the diploid sexual lines were already anatropous and it was possible to observe the first post-meiotic stages (about 5% of the ovules carried a functional megaspore).

In class 7, ovules were about 150 µm long, with even bigger integuments primordia (Figure 53) and the development fully entered the post-meiotic stages.

In class 9, the ovules were 200 to 300 µm long with fully developed integuments (Figure 54). Class 14 to 18 were characterized by ovules many times longer than 300 µm and they carried increasing percentages of mature female gametophytes.

The gametophyte development clearly followed a *Polygonum* type (Yadegari and Drews, 2004) model with a functional megaspore that underwent 3 mitotic divisions and led to a 8-nucleated gametophyte.

Most of the ovules carrying a mature gametophyte showed separated polar nuclei. The polar nuclei together with the egg cell apparatus were positioned very close to the micropylar pole and, in contrast with previous literature (Galla et al., 2011), this micropylar position seemed to be highly conserved between sexual and apomictic lines and across different ploidy levels.

Apomictic lines of *Hypericum* presented anomalies in female gametophytic development

In very early stages of development, while the sexual diploids were mainly at the MMC stage, the analyzed apomictic lines already differentiated dyads (Figure 51). This suggested a faster development in very young flower buds, and a deregulation of the normal meiotic processes that occurred later in the diploid sexual lines.

The hypothesis that meiotic machinery (especially meiosis II) could be malfunctioning in apomicts is not only suggested by the early dyads differentiation, but also by their anomalous accumulation in ovules from class 2 to class 4 flower buds. Dyads (and tetrads) are very transient stages, and are normally difficult to detect even in other species like *Arabidopsis thaliana* and *Boechera spp.* Nonetheless, in the case of tetraploid apomictic lines of *Hypericum,* the percentage of ovules carrying dyads peaked to an astonishing 31% in flower buds of the class 4.

The analysis of ovules from flower buds of classes 2 to 5 showed a significantly higher frequency of multiple MMC (2 most of the times). This over proliferation constitutes the same phenotype observed in mutants of the *argonaute 9* in *Arabidopsis thaliana* (Olmedo-Monfil et al., 2010). The presence of more than one MMC suggests that the signaling responsible for limiting the role of MMC to a single cell is partially defective in apomictic lines. This evidence may direct the attention of future research towards the study of small RNAs and transposable elements, which are known to affect the cell fate during megagametogenesis.

The most striking difference observed between the sexual and the apomictic *Hypericum* is the high abortion rate of the latter starting at class 5 (Figure 49). In this case, the abortion does not consist in a total arrest of development of the whole ovule, rather a selective shrinking of the region that normally hosts the developing female gametophyte (gametophytic domain/space), while the rest of the ovule continues to grow. The high specificity of the tissue affected by this shrinking point towards apoptotic events, that finally lead to ca. 50% of aborted ovules in the later stages of gametophytic development.

Female gametophyte development is a highly complex process that needs the perfect timing of many developmental steps and the orchestration of the gene expression of several genes (Figueiredo and Köhler, 2016; Pagnussat et al., 2005, 2009; Yadegari and Drews, 2004). It is possible that a defective meiotic machinery activates the programmed cell death of the tissues that will host the sexual female gametophyte. This hypothesis fits with the fact that until the early differentiation of dyads in the apomictic lines, there was practically no abortion detected. However, many ovules from flower buds of class 5 begun to abort. This abortion could reach percentages close to 100% in ovules from flower buds of class 7 in some apomictic lines.

This looked like a dead end of development, but the differentiation of AIs suggests that this is rather a developmental reboot (at least in half of the cases), which marked the death of the female sexual gametophyte and the beginning of the development of a newly formed gametophyte of aposporous origin.

Aposporic initial differentiation and its role in the frame of female gametophyte development

The number of AIs started to peak after class 5 (Figure 45). This timing suggests a rescuing function of the AIs, that are probably recruited to carry on a gametophytic development by assuming the role of a functional megaspore, and from there, undergoing mitotic divisions that lead to the formation of a functioning female gametophyte of aposporous origin. This rescue of development was not always successful, ca. 50% of the ovules were able to differentiate a perfectly formed gametophyte. Considering the abortion levels in class 7, AIs were able to avoid a low or no seed set at all. This is the most relevant advantage that the plant gets from the differentiation of AIs.

Critical stages for transcriptomic analysis

From the morphological characterization of ovule and female gametophyte development in different *Hypericum* lines some crucial facts emerged.

a. At very early stages (**class 2**), deviations from the normal meiotic processes were detected in the apomictic lines.
b. High abortion rates starting in class 5 and reaching their maximum in **class 7**.
c. Differentiation of AIs starting in class 5 and reaching the highest peak in **class10**.
d. AIs continue to be visible until flower buds reach **class 11**, afterwards they become much rarer.

In the light of these evidences, ovules from class 2 and 3 were dissected in order to investigate the meiotic anomalies at the transcriptomic level.

Ovules from class 6 to class 11 were dissected in order to investigate the detected apoptotic events, and search for candidates putatively involved in AIs differentiation.

Transcriptome analysis in ovules of *Hypericum perforatum*

The results derived from the RNAseq experiments that are reported in this study constitute the first de novo assembled transcriptome of ovules at multiple stages of development in *Hypericum perforatum*. This data set has been compared with other transcriptomics studies in *Hypericum perforatum* (He et al., 2012), demonstrating a very high quality level especially in terms of contigs length and BLAST hits with annotated genes from other species.

Four different time points during gametophytic development, allowed to determine the expression pattern of several contigs/genes for a frame that spanned from pre-meiotic stages (as megaspore mother cell), until multinucleate gametophyte.

In the case of the apomictic lines, the analysed development frame included the differentiation of AI cells that were observed right after the increase of abortion rates in apomicts.

The comparative morphological analysis of the sexual and apomictic development led to the identification of three main events, crucial for the occurrence of apospory:

- The accumulation of dyads that could be associated with a defective meiosis II
- The subsequent shrinking of the gametophytic domain of many ovules in apomicts, most likely due to localized apoptotic events
- The differentiation of AIs, which were able to rescue the gametophyte development by assuming the role of a functional megaspore.

This was translated in an experimental design where the fb25 flower buds were mainly used to detect the deregulation of genes involved in meiotic processes (especially meiosis II) and the other 3 stages (fb45, 55, 65) were used to detect the differential expression of regulatory genes, putatively involved in apospory.

The hypothesis of a defective meiosis was supported by the analysis of the transcriptomic data set, in which 15 differentially expressed entities matching with meiotic *Arabidopsis* genes were detected. One of these entities resulted overexpressed exclusively at the fb25 and it matched with the *Arabidopsis PS1* (*Parallel Spindle 1*), a gene that when misexpressed can lead to problems in the spindle formation during meiosis II (Cigliano et al., 2011; Erfurth et al., 2008), in accordance with the hypothesis derived from the previously performed morphological characterization.

The other 14 entities, matching with *Arabidopsis* meiotic genes, showed differential expression also in other stages than fb25. Their expression levels significantly different between sexual and apomictic lines, suggest that the meiotic problems may be connected also with the defective expression of other genes. A good example that supports this hypothesis is the strong down regulation at all stages of contig_3615 matching with the meiotic *Arabidopsis* gene *SMC3=TTN7*, essential for homolog pairing and synapsis recombination during meiosis (Ma, 2006; Schubert et al., 2013).

Other entities differentially expressed only at fb25 were detected. These entities did not give hits with any meiotic genes. Yet, they matched with important regulatory genes such as *CHR11*, which is known to regulate different transcriptional programs during plant development and to be essential for the female gametogenesis (Huanca-Mamani et al., 2005). Other regulatory genes that resulted differentially expressed only at fb25 were *PUM12* and *BRU1*. The former resulted to be up regulated in fb25 of apomictic lines. It is known to be highly conserved even between plants and animals, and due to its RNA-binding capacity, can control the expression of several mRNAs all over the genome (Francischini and Quaggio, 2009). *BRU1* is a chromatin remodeling gene, that was strongly down regulated at fb25 in apomicts. *BRU1* is known for keeping the DNA and H3K9 methylation, preventing in this way the expression of several heterochromatin genes, some of which are top regulators of development (Ohno et al., 2011). The defective expression of this gene in *bru1* mutants lead to the release of these transcriptional constraints affecting important mechanisms like stem cell maintenance and embryogenesis.

The exact role of the deregulation of *CHR11*, *PUM12* and *BRU1* in the frame of the apomictic developmental pathway of *Hypericum* has still to be clarified. However, it is possible to hypothesize, that due to the strong regulatory power of these entities, their deregulation in apomicts can indirectly affect meiosis, and start a reprogramming process that could lead to the failure of megagametogenesis and/or the abortion events that preceded the AIs differentiation.

As mentioned before, the morphological results of this study suggest a divergence of the sexual pathway, which starts with the accumulation of dyads and continues with the differentiation of aposporic initials. For this reason, it was hypothesized that also the expression patterns of some entities could eventually diverge starting at fb45 stage. A first confirmation of this divergence at the transcriptomic level came from the observation of the cluster 8 in the K-means clustering, which showed a visual trend of up regulation in apomicts starting exactly at fb45. Following this observation, entities with similar divergence patterns were extracted from the whole data set. This selection generated a list of 107 contigs, including 9 entities connected with signal transduction, 18 entities connected with response to stress, 10 entities putatively localized in mitochondria and 21 entities matching *Arabidopsis* genes involved in nucleic acid binding processes. This list of 107 contigs hosted genes that all together have a high regulatory potential. At the current stage of this research it is difficult to dissect every function of such genes; nevertheless, it is possible to point the attention to some of them, such as *AUX/IAA7* coding for a protein that is involved in auxin response (Nagpal et al., 2000; Sato et al., 2015). Any variation of the auxin signaling can have very strong effects on female gametophyte development (Pagnussat et al., 2009). Therefore, an up regulation of *IAA7* starting at fb45 may have a role in shaping the development of the aposporous female gametophyte.

The detection of 10 contigs matching with *Arabidopsis* genes known for their mitochondria-localized expression is another evidence that goes in the direction of auxin signaling deregulation. Mitochondria are key players in signaling and metabolic homeostasis of the plant cell, and in the past it was shown that there is a crosstalk between mitochondria and nuclear transcription machinery, and that mitochondrial perturbations can negatively affect auxin signaling (Kerchev et al., 2014).

The response to stress is another ontology category that includes many processes directly or indirectly connected with signaling or response to a stress-associated signaling able to totally change the cell fate of a sporophytic cell and to shape the female gametophyte development in apomicts.

The group of entities with a divergent expression pattern starting at fb45, included also regulatory genes like *PCS1*, that when overexpressed can prevent the programmed cell death and can determine the cell fate in different reproductive tissues (Ge et al., 2005). Due to its regulatory power and to its expression pattern, *PCS1* can be considered an interesting candidate, putatively connected with AI differentiation. Further investigation on this gene is necessary in order to elucidate its function.

SNL4 is another regulatory gene, which had a divergent expression pattern starting at fb 45. In this case, a strong down regulation was detected in apomicts at fb45, 55 and 65. SNL proteins are histone deacetylases known in *Arabidopsis* to be part of the SIN3 co-repressor complex (Mazur and van den Burg, 2012). Due to their histone modification ability, these proteins can determine chromatin changes that prevent the expression of several genes at a genome-wide scale. The strong down regulation of *SNL4* would suggest the release of large expression constraints that are normally maintained during the sexual developmental pathway.

The genes that in this study were considered interesting candidates, most of the times were selected on the base of their expression pattern. Nonetheless, many entities steadily up or down regulated at all stages were considered interesting candidates due to their BLAST hit with important regulatory genes. This is the case of *IBM1*, which is able to prevent the non-GC methylation at a genome-wide scale. A defect of this mechanism, releases this methylation constraint with consequent hypermethylation of thousands of genes all over the genome.

SOG1 and *MYB30* are two other up regulated candidates, which might have a connection with the high abortion rates detected in apomictic lines. They are involved in DNA damage response (Yoshiyama et al., 2009) and hypersensitive response (Raffaele et al., 2008), respectively. They have a common characteristic, their capacity of inducing apoptosis in tissues where they are highly expressed. Therefore, they could be responsible for the cell death events detected in the gametophytic domain of many apomictic lines. *In-situ* hybridization might unravel their spatial pattern of expression, and would be very valuable for the continuation of this research.

The screening of the transcriptomic data set produced during this study, was performed not only by looking at temporal expression patterns, but also by using GO annotation and looking for enrichment of gene ontology categories in the K-means clusters and in the stage wise comparison. The strongest trend that emerged from this kind of screening was the highly significant enrichment of “nucleic acid binding” and “DNA or RNA metabolism”. This enrichment was detected at all analyzed stages and was always associated with up regulated entities in apomicts. A plausible explanation for this is the potentiation of several regulatory genes, that probably affect the development and could be responsible for the events that lead to the formation of a female gametophyte of aposporous origin. Although, the analysis of these two enriched gene ontologies revealed another interesting trend, further investigation is necessary to validate this hypothesis. Furthermore, these categories had 39 entities in common (Table 9), all of these matching with the same *Arabidopsis* transposable element.

The activation of transposons is typically observed after hybridization events eventually accompanied by polyploidization (Comai, 2000). Their presence in this data set could be a consequence of evolutionary events that led to the formation of apomicts in *Hypericum*.

It is known that apomixis arose in many families in concomitance with events of hybridization and polyploidization (Hörandl, 2006; Nürk et al., 2013b). An explanation for this combination (hybridization + polyploidization + apomixis) was given by Hörandl (2006), with the theory that hybrids have to face several problems such as the introgression of their parents and several meiotic defects. In such situation, polyploidization may stabilize the newly formed hybrid by creating a partial reproductive barrier with the diploid parent and preventing their introgression.

Apomixis on the other hand, would mild the negative effects of a malfunctioning meiosis by providing an alternative to the sexual pathway, highly dependent from this process. This theory concurs with the observations made in this study, not only regarding the observed accumulation of dyads in *Hypericum* apomictic lines, but also regarding the concept that the AIs are a rescuer rather than a destroyer of the female gametophyte development, in contrast with previous literature (Galla et al., 2011).

In the light of these considerations, it is plausible to hypothesize, that the activation of transposable elements detected during the transcriptomic analysis could be a symptom of hybridization that occurred in the evolutionary history of *Hypericum* and that led to the establishment of allopolyploid apomicts (Nürk et al., 2013b).

Hybridization meant as the encounter between two different genomes is known to provoke a transcriptomic shock (Buggs et al., 2011), in which the normal expression of many genes is disrupted and many times it is further modified by whole genome duplication (Buggs et al., 2011). In this situation many genes may lose their tissue specificity, transposons can be activated and consequently the genome integrity can be compromised.

This data set supports the idea of a compromised genome integrity in apomicts, not only due to the up regulation of entities probably hosting transposons sequences, but also because of several entities matching with genes involved with chromatin remodeling resulted significantly deregulated in apomicts. Chromatin remodeling machinery is one of the main players in the maintenance of genome integrity (Papamichos-Chronakis and Peterson, 2013). Contigs matching with *CHR11* and *BRU1* are only two of the 35 differentially expressed entities associated with this process.

Proposed model for aposporous developmental pathway in *Hypericum perforatum*

Understanding the role of every detected differential expression is a challenging task. Nevertheless, in this study, the morphological analysis provided a guide that was used to hypothesize the role of several genes in the frame of this developmental program.

The majority of the entities of this transcriptome data set showed a steady up or down regulation. This could be due to constitutive differences between lines, but also to a transcriptomic shock, that arose after allopolyploidization events and disrupted the normal expression patterns of many genes. A steady up or downregulation of some genes could provide the necessary background for the functioning of the aposporic machinery. A smaller group of entities, that showed more stage specific differential expression, could provide the trigger that works in the frame of this given transcriptomic background. It cannot be excluded that some of these entities, even if characterized, by a steady up or down regulation, can also play a regulatory role at specific stages. Further investigation is necessary in order to solve these uncertainties.

A model of the aposporous developmental pathway in *Hypericum,* combining morphological and molecular data is proposed in Figure 70.

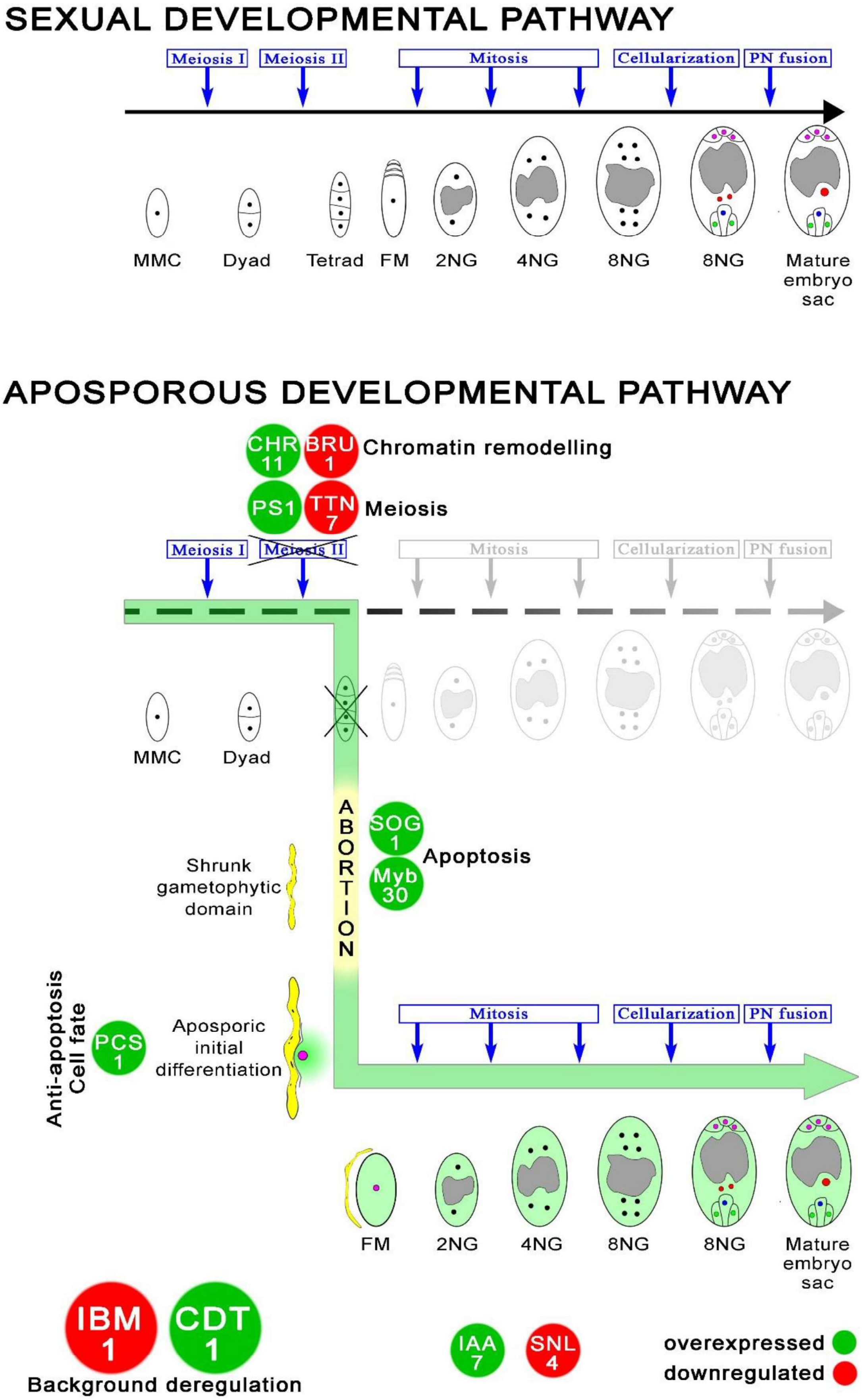

Figure 70. Model of the aposporous developmental pathway in *Hypericum perforatum* derived from the morphological and transcriptomic comparative analysis of sexual and apomictic lines.

Conclusive remarks

This project constitutes a step forward in the knowledge and understanding of the female gametophyte developmental processes in the two model species *Boechera spp.* and *Hypericum spp.*

The reproductive processes analyzed during this study, suggested that *Boechera* apomicts have generally lower performance in terms of germination and seed set. This performance seems to be in some cases affected from the ploidy levels, *e.g.* fertility rates of *Boechera spp,* significantly decreasing with the increase of ploidy.

In the case of the aposporous *Hypericum spp.*, the differences between sexual and apomictic lines were not as pronounced as in the diplosporic model *Boechera*.

For both model organisms, the morphological characterization performed in this study, generated an unprecedented amount of observations that led to extensively document the apomictic reproductive pathway and its deviations from the sexual pathway.

Both model organisms demonstrated that apomicts have to deal with malfunction of the ovule development. This resulted in significantly higher abortion rates of the apomictic lines in both genera. Furthermore, the study of aposporic initials in *Hypericum* suggested that they are not the cause of the failure of sexual gametophyte rather they rescue the ovule development by providing a new unreduced gametophyte of aposporous origin after the abortion of the gametophytic domain. This constitutes a shift in the paradigm described in previous literature.

Finally, a transcriptomic analysis at multiple stages of ovule development identified over 2000 differentially expressed entities between apomictic and sexual *Hypericum perforatum* lines. These molecular results were connected with the morphological evidences studied in the first phase of the project. As a result, an integrated model including candidate genes putatively involved in developmental events and in background deregulation was proposed. Furthermore, this transcriptome dataset supports the hypothesis of a compromised genome integrity as a result of events of allopolyploidization known to be associated with the evolution of apomixis in many other clades.

This study is a novel piece of knowledge and at the same time is the basis for further and deeper research in order to continue unraveling the molecular basis of apomixis.

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Supplemental data

Table 12. DAPI buffer Ma VI for flow cytometry measurements (100 ml).

Reagents	**Quantity**
$MgCl_2$ x $6H_2O$	0.107 g
NaCl	0.5 g
Tris	1.211 g
Triton x-100	0.10 ml (=0,0939 g)
DAPI stock solution	1 ml
Sodium Citrate x $2H_2O$	0.9 g
H_2O	Up to 100 ml
pH	7

Table 13. Propidium iodide buffer for flow cytometry measurements (100 ml).

Reagents	**Quantity**
$MgCl_2$ x $6H_2O$	0.107 g
NaCl	0,5 g
Tris	1.211 g
Triton x-100	0.10 ml (=0,0939 g)
Propidium Iodide	5 ml
RNAse A (1 mg/ml stock solution)	5 ml
Sodium Citrate x $2H_2O$	0.9 g
H_2O	Up to 100 ml
pH	7

Table 14. Clearing solution for ovules Nomarski microscopy observation (50 ml)

Reagents	**Quantity**
Chloral Hydrate	40 g
Water	10 ml
Glycerol	10 ml
Formalin	5 ml

Table 15. Extraction Buffer (50 ml)

Reagents	**Quantity**
1M Tris-HCl (pH 7,5)	10 ml
5M NaCl	2.5 ml
0,5M EDTA	2.5 ml
SDS 10%	2.5 ml
H_2O	32.5 ml

Table 16. Comparison of partial fitness values (PF) before and after correction for flowering time ($PF_{(FT)}$) in 15 *Boechera spp.* lines.

Ranking before correction	**Line**	**PF**	**Ranking after correction**	**Line**	**$PF_{(FT)}$**
1	BoSDi-05	18149,2883	1	BoSDi-05	27133,48749
2	BoSDi-06	17021,76531	2	BoSDi-06	23179,88921
3	BoADi-01	5942,1792	3	BoADi-01	10340,21903
4	BoADi-02	5019,412151	4	BoADi-02	8351,767306
5	BoSDi-04	3987,26568	5	BoATi-01	5736,722194
6	BoATi-01	2928,277973	6	BoSDi-04	4260,404977
7	BoSDi-01	2889,632379	7	BoSDi-01	3955,390328
8	BoSDi-02	2741,10088	8	BoSDi-02	3914,615665
9	BoADi-03	2506,101831	9	BoADi-03	3497,428513
10	BoADi-04	2455,093196	10	BoADi-04	1992,770451
11	BoADi-05	1278,340326	11	BoADi-05	1128,389852
12	BoATi-04	370,3421973	12	BoATi-02	568,7602843
13	BoATi-02	341,192975	13	BoATi-04	535,2625303
14	BoATe-04	132,8194133	14	BoATe-04	210,4532958
15	BoATi-03	0,129259667	15	BoATi-03	0,205246471

Table 17. Phenotyping table of ovule and female gametophyte development in several *Boechera spp.* lines (**lines kept separated**).

Ploidy	Reproduction	Ranking	Line	FB size	BeforeAC	AC	MMC/SI	MMC/MI	MMC/BI	Multi MMC	Dyads	Tetrads	FM	Multi FM	2NG	4NG	8NG	Aborted	Other
Diploid	Sexual	1	BoSDi-01	0.91	99%	1%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Diploid	Sexual	2	BoSDi-01	1.27	82%	17%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Diploid	Sexual	3	BoSDi-01	1.83	24%	22%	32%	21%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	1%
Diploid	Sexual	4	BoSDi-01	2.35	0%	0%	23%	66%	5%	1%	1%	0%	0%	0%	0%	0%	0%	0%	3%
Diploid	Sexual	5	BoSDi-01	2.75	0%	0%	5%	32%	12%	0%	0%	0%	25%	0%	13%	7%	5%	0%	1%
Diploid	Sexual	6	BoSDi-01	3.09	0%	0%	0%	0%	0%	0%	0%	0%	18%	0%	29%	36%	16%	0%	2%
Diploid	Sexual	8	BoSDi-01	4.32	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	2%	53%	45%	0%	0%
Diploid	Sexual	9	BoSDi-01	4.7	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	9%	88%	0%	3%
Diploid	Sexual	10	BoSDi-01	5.06	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	1%	99%	0%	0%
Diploid	Sexual	1	BoSDi-04	0.98	98%	2%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Diploid	Sexual	2	BoSDi-04	1.29	84%	16%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Diploid	Sexual	3	BoSDi-04	1.78	15%	22%	36%	25%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	1%
Diploid	Sexual	4	BoSDi-04	2.39	0%	0%	4%	84%	10%	0%	3%	0%	0%	0%	0%	0%	0%	0%	0%
Diploid	Sexual	5	BoSDi-04	2.74	0%	0%	4%	17%	23%	0%	0%	1%	20%	1%	12%	13%	6%	0%	6%
Diploid	Sexual	6	BoSDi-04	3.27	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	14%	36%	49%	0%	0%
Diploid	Sexual	7	BoSDi-04	3.71	0%	0%	0%	0%	0%	0%	0%	0%	33%	10%	3%	46%	8%	0%	0%
Diploid	Sexual	8	BoSDi-04	4.46	0%	0%	0%	0%	0%	0%	0%	0%	18%	10%	8%	41%	24%	0%	0%
Diploid	Sexual	9	BoSDi-04	4.66	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	8%	93%	0%	0%
Diploid	Sexual	10	BoSDi-04	5.14	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	98%	0%	2%
Diploid	Sexual	1	BoSDi-05	0.94	92%	8%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Diploid	Sexual	2	BoSDi-05	1.25	68%	23%	3%	2%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	3%
Diploid	Sexual	3	BoSDi-05	1.78	4%	35%	17%	15%	14%	0%	0%	1%	8%	0%	0%	0%	0%	1%	4%
Diploid	Sexual	4	BoSDi-05	2.28	0%	1%	10%	65%	22%	0%	1%	0%	0%	0%	0%	0%	0%	0%	2%
Diploid	Sexual	5	BoSDi-05	2.77	0%	0%	4%	24%	36%	0%	1%	1%	23%	0%	7%	1%	0%	1%	1%
Diploid	Sexual	6	BoSDi-05	3.26	0%	0%	0%	0%	0%	0%	0%	0%	8%	0%	16%	46%	31%	0%	0%
Diploid	Sexual	7	BoSDi-05	3.89	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	36%	14%	0%	50%
Diploid	Sexual	9	BoSDi-05	4.75	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	53%	47%	0%	0%
Diploid	Sexual	10	BoSDi-05	5.18	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	15%	85%	0%	0%
Diploid	Sexual	12	BoSDi-05	6.12	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	14%	86%	0%	0%
Diploid	Apomictic	1	BoADi-01	0.87	26%	61%	14%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Diploid	Apomictic	2	BoADi-01	1.22	9%	60%	23%	5%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	3%
Diploid	Apomictic	3	BoADi-01	1.69	12%	17%	27%	27%	3%	2%	3%	0%	0%	0%	0%	0%	0%	1%	9%
Diploid	Apomictic	4	BoADi-01	2.2	0%	4%	23%	58%	7%	1%	3%	0%	0%	0%	0%	0%	0%	0%	6%
Diploid	Apomictic	5	BoADi-01	2.8	0%	0%	3%	9%	22%	0%	0%	0%	46%	0%	5%	0%	0%	9%	6%
Diploid	Apomictic	6	BoADi-01	3.04	0%	0%	0%	12%	16%	0%	0%	0%	59%	0%	9%	0%	0%	4%	0%
Diploid	Apomictic	8	BoADi-01	4.2	0%	0%	0%	0%	0%	0%	0%	0%	33%	0%	33%	17%	0%	9%	7%
Diploid	Apomictic	10	BoADi-01	5.31	0%	0%	0%	0%	0%	0%	0%	0%	16%	0%	45%	17%	10%	9%	2%
Diploid	Apomictic	1	BoADi-03	0.93	15%	85%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Diploid	Apomictic	2	BoADi-03	1.27	12%	67%	15%	4%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	2%
Diploid	Apomictic	3	BoADi-03	1.723	15%	29%	32%	18%	1%	2%	2%	0%	0%	0%	0%	0%	0%	0%	1%
Diploid	Apomictic	4	BoADi-03	2.295	0%	0%	2%	29%	40%	2%	6%	0%	10%	0%	0%	0%	0%	4%	10%
Diploid	Apomictic	5	BoADi-03	2.77	0%	0%	1%	23%	18%	0%	3%	0%	37%	0%	0%	0%	0%	8%	10%
Diploid	Apomictic	7	BoADi-03	3.96	0%	0%	0%	0%	1%	0%	0%	0%	55%	0%	23%	11%	0%	9%	2%
Diploid	Apomictic	8	BoADi-03	4.38	0%	0%	0%	0%	0%	0%	0%	0%	8%	0%	36%	31%	4%	19%	3%
Diploid	Apomictic	9	BoADi-03	4.54	0%	0%	0%	0%	0%	0%	0%	0%	17%	0%	40%	19%	10%	9%	5%
Diploid	Apomictic	10	BoADi-03	5.22	0%	0%	0%	0%	0%	0%	0%	0%	17%	0%	38%	18%	9%	12%	6%
Diploid	Apomictic	1	BoADi-04	0.99	0%	66%	34%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Diploid	Apomictic	2	BoADi-04	1.29	4%	49%	31%	12%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	3%
Diploid	Apomictic	3	BoADi-04	1.83	1%	9%	23%	38%	12%	1%	2%	0%	8%	0%	0%	2%	0%	1%	5%
Diploid	Apomictic	4	BoADi-04	2.29	0%	0%	0%	27%	23%	3%	2%	0%	24%	1%	6%	2%	0%	0%	11%
Diploid	Apomictic	5	BoADi-04	2.81	0%	0%	0%	2%	0%	0%	0%	0%	20%	2%	43%	9%	0%	5%	18%
Diploid	Apomictic	6	BoADi-04	3.12	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	38%	47%	0%	9%	7%
Diploid	Apomictic	8	BoADi-04	4.36	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	10%	48%	23%	14%	7%
Diploid	Apomictic	11	BoADi-04	5.57	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	60%	0%	40%
Triploid	Apomictic	1	BoATi-01	0.99	0%	11%	89%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Triploid	Apomictic	2	BoATi-01	1.24	1%	3%	34%	26%	3%	1%	5%	0%	15%	0%	0%	0%	0%	0%	0%
Triploid	Apomictic	3	BoATi-01	1.78	0%	0%	0%	3%	0%	0%	1%	0%	31%	1%	60%	4%	0%	0%	0%
Triploid	Apomictic	4	BoATi-01	2.25	0%	0%	0%	0%	0%	0%	0%	0%	8%	0%	33%	28%	21%	8%	2%
Triploid	Apomictic	5	BoATi-01	2.71	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	14%	20%	45%	21%	0%
Triploid	Apomictic	6	BoATi-01	3.21	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	9%	58%	21%	12%
Triploid	Apomictic	7	BoATi-01	3.7	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	61%	33%	7%
Triploid	Apomictic	8	BoATi-01	4.4	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	7%	38%	40%	15%
Triploid	Apomictic	9	BoATi-01	4.75	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	36%	53%	12%
Triploid	Apomictic	10	BoATi-01	5.12	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	71%	27%	2%
Triploid	Apomictic	1	BoATi-02	0.89	0%	0%	90%	10%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Triploid	Apomictic	2	BoATi-02	1.25	0%	2%	38%	36%	14%	1%	3%	0%	6%	0%	0%	0%	0%	0%	1%
Triploid	Apomictic	3	BoATi-02	1.73	0%	0%	0%	2%	11%	0%	1%	0%	47%	1%	33%	2%	0%	1%	2%
Triploid	Apomictic	4	BoATi-02	2.25	0%	0%	0%	0%	0%	0%	0%	0%	3%	0%	40%	28%	18%	10%	1%
Triploid	Apomictic	5	BoATi-02	2.49	0%	0%	0%	3%	4%	0%	0%	0%	9%	0%	4%	25%	38%	14%	1%
Triploid	Apomictic	6	BoATi-02	3.22	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	4%	50%	33%	12%
Tetraploid	Apomictic	1	BoATe-04	0.860	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
Tetraploid	Apomictic	2	BoATe-04	1.260	17%	1%	19%	0%	0%	15%	1%	0%	0%	0%	0%	0%	0%	4%	7%
Tetraploid	Apomictic	3	BoATe-04	1.670	0%	0%	41%	0%	0%	24%	4%	0%	0%	0%	0%	0%	0%	11%	4%
Tetraploid	Apomictic	4	BoATe-04	2.290	0%	0%	46%	28%	1%	12%	8%	1%	0%	0%	0%	0%	0%	7%	1%
Tetraploid	Apomictic	5	BoATe-04	2.710	0%	0%	30%	36%	24%	5%	2%	0%	4%	0%	1%	0%	0%	0%	0%
Tetraploid	Apomictic	6	BoATe-04	3.220	0%	0%	0%	25%	0%	0%	1%	0%	10%	0%	10%	0%	0%	30%	0%
Tetraploid	Apomictic	7	BoATe-04	3.820	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	15%	20%	5%	15%	0%
Tetraploid	Apomictic	8	BoATe-04	4.250	0%	0%	0%	4%	20%	0%	0%	0%	12%	0%	16%	0%	30%	20%	0%
Tetraploid	Apomictic	10	BoATe-04	5.230	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	2%	5%	17%	69%	3%

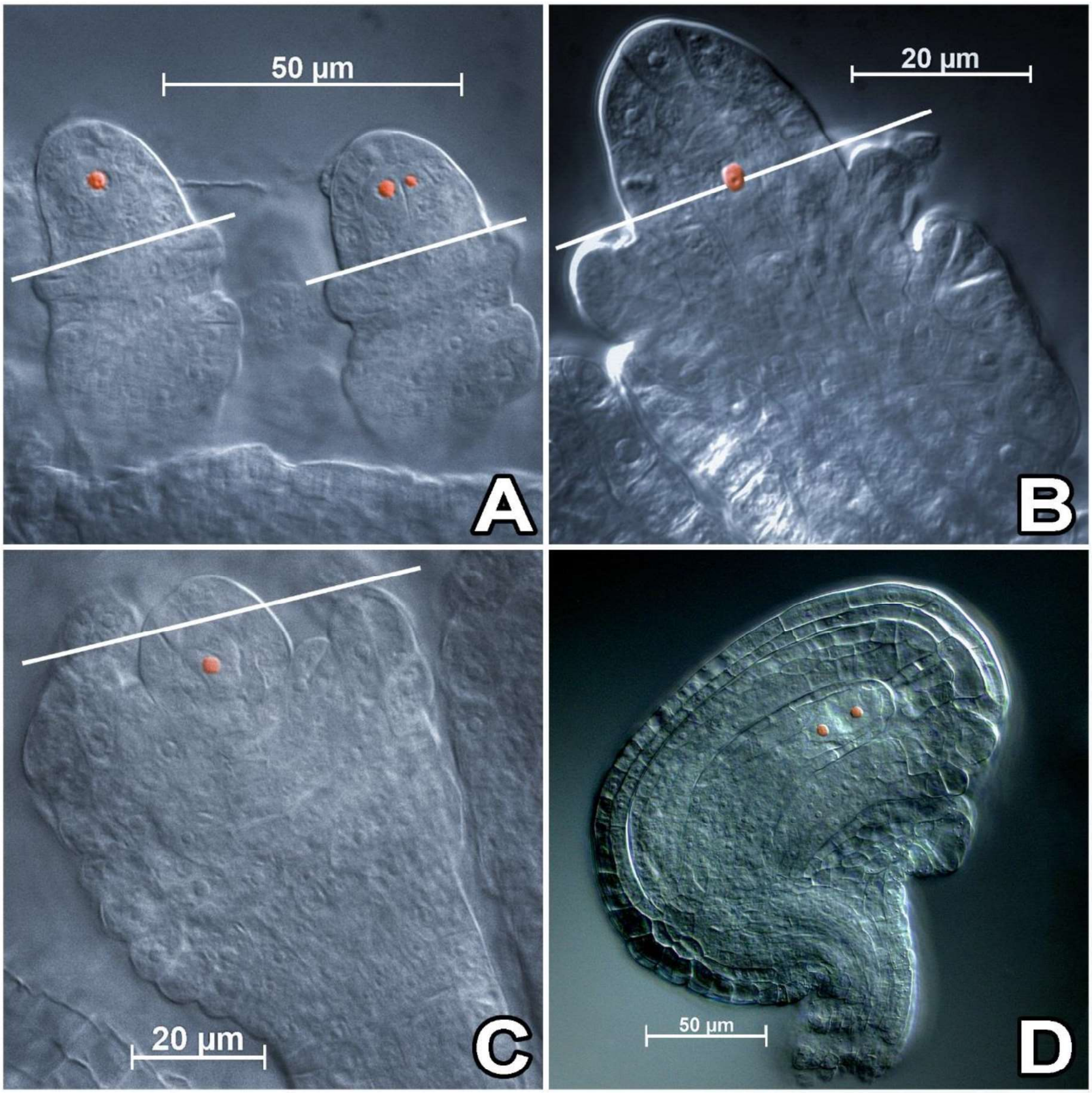

Figure 71. Explanatory figure for integument primordia size classification. The white segments drawn on the ovules represent an indicator of the integument size, they are drawn at the extremity of the integuments primordia in order to see if these primordia reach a: lover, higher or same level of the MMC (highlighted in orange). **A**: Ovules at MMC stage with small integuments primordia (indicator lays underneath the MMC); **B**: Ovule at MMC stage with medium size integuments primordia (indicator intersects the MMC); **C**: Ovule at MMC stage with big integuments primordia (indicator is higher than the position of the MMC); **D**: Ovule carrying a bi-nucleated female gametophyte surrounded by well-developed integuments (the two nuclei of the gametophyte are highlighted in orange).

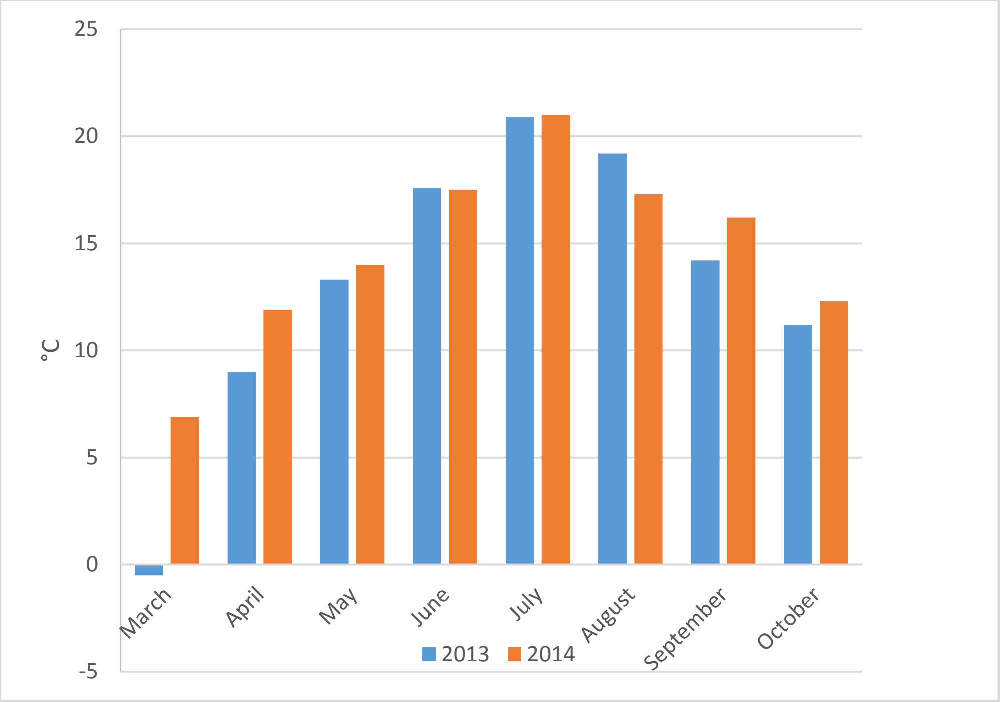

Figure 72. Average month temperature 5 cm above the ground from IPK weather station.

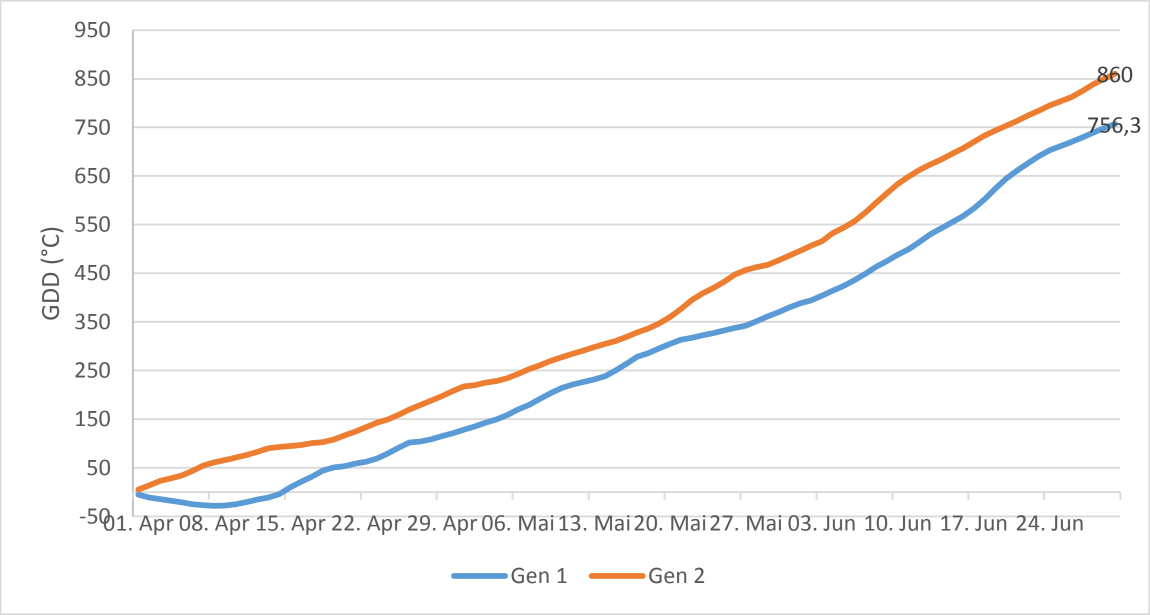

Figure 73. Accumulated values of Growing degree days derived from average temperature at 5cm above the ground from data of the IPK weather station. T_{base} for *Hypericum* set at 5°C.

Table 18. Comparison of partial fitness values (PF) before and after correction for flowering time (PF$_{(FT)}$) in 16 Hypericum lines.

Generation 1				Generation 2			
Line	**PF**	**Line**	**PF$_{(FT)}$**	**Line**	**PF**	**Line**	**PF$_{(FT)}$**
H06-3220	23893.94	H06-3220	31377.47	H06-1489	37155.89	H06-1489	46444.86
H06-3251	21602.91	HyPR8	27429.31	H06-3251	30886.14	H06-3251	39776.10
HyPR8	20229.12	H06-1644/11	27116.03	H06-3220	29176.28	H06-3220	39162.79
H06-1489	20052.77	H06-3251	27071.32	H06-1644/11	21432.06	H06-1644/11	31425.30
H06-1644/11	20011.63	H06-1489	24072.96	HyPR1	21317.69	HyPR1	30280.81
H06-1449	17482.81	HyPR1	23093.98	H06-1441	20030.98	H06-1449	26188.47
HyPR1	16939.44	H06-1449	22853.34	H06-1449	19903.23	H06-1441	25085.76
HyPR3	14587.87	HyPR3	19793.58	HyPR8	15622.15	HyPR8	21925.83
H06-1441	14585.49	H06-1441	17467.65	HyPR2	14138.61	HyPR2	18184.71
HyPR5	13261.53	HyPR2	16255.48	HyPR3	12819.20	HyPR3	18080.68
HyPR2	12971.87	HyPR9	15144.95	H06-2886	11977.07	H06-2886	15199.32
HyPR7	11705.84	HyPR7	14864.56	HyPR7	11716.19	HyPR7	15117.66
HyPR9	11184.54	HyPR5	13052.68	HyPR5	10086.51	HyPR9	10331.16
H06-2886	7621.29	H06-2886	9814.92	HyPR9	7655.39	HyPR5	9996.54
H06-3325	4281.88	H06-3325	5579.00	H06-3325	6240.15	H06-3325	8325.75
H06-2573	1028.85	H06-2573	1300.69	H06-2573	4343.78	H06-2573	5477.65

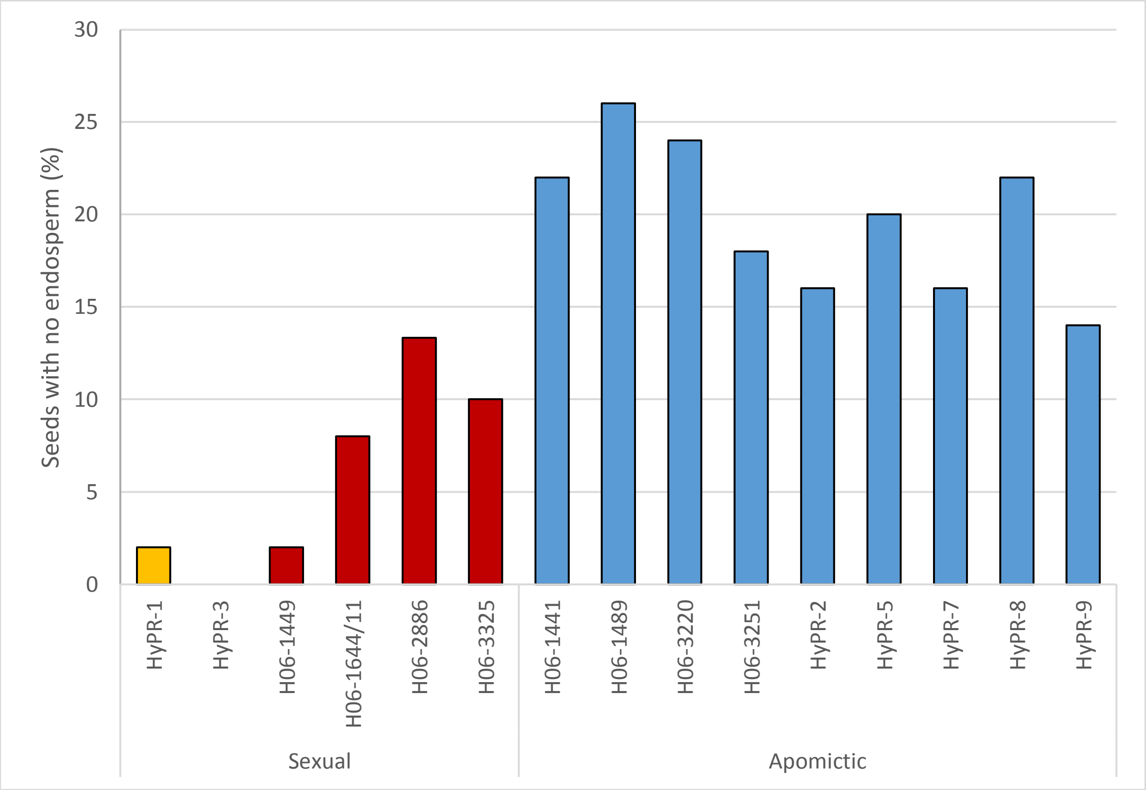

Figure 74. Percentage of seeds with no detectable endosperm in 15 *Hypericum* lines. Results derived from the FCSS data set.

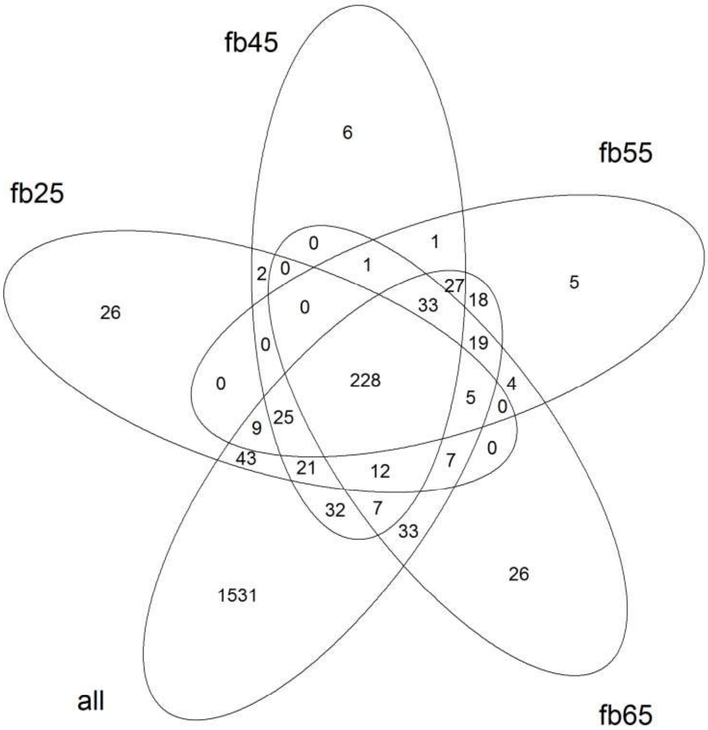

Figure 75. Venn diagram of differential expression calculated in a reproduction wise way (all ellipsis) and in a stage wise way. All = all apo stages vs all sex stages; fb25 = flower buds 2.5mm – 3.5mm; fb45 = flower buds 4.5 – 5.5 mm; fb55 = flower buds 5.5 mm – 6.5mm; fb65 = flower buds 6.5 – 7.5mm.

Table 19. Number of differentially expressed contigs calculated with different false discovery rate adjusted p-values (padj) and with different limitations of log fold change (lfc) in ovules from two sexual diploid lines (HyPR-1 and HyPR-3) versus two tetraploid apomictic lines (HyPR-5 and HyPR-9) dissected from flower buds of length between 2.5 and 3.5 mm (fb25).

	padj-1	padj-2	padj-3	padj-4	padj-5	padj-6
lfc0diff	1470	724	417	291	237	185
lfc1diff	1035	603	378	276	229	180
lfc2diff	265	265	265	227	199	166
lfc3diff	107	107	107	107	107	107
lfc0up	823	428	267	188	159	132
lfc1up	582	362	244	179	154	127
lfc2up	185	185	185	158	141	122
lfc3up	78	78	78	78	78	78
lfc0down	647	296	150	103	78	53
lfc1down	453	241	134	97	75	53
lfc2down	80	80	80	69	58	44
lfc3down	29	29	29	29	29	29

Table 20 Number of differentially expressed contigs calculated with different false discovery rate adjusted p-values (padj) and with different limitations of log fold change (lfc) in ovules from two sexual diploid lines (HyPR-1 and HyPR-3) versus two tetraploid apomictic lines (HyPR-5 and HyPR-9) dissected from flower buds of length between 4.5 and 5.5 mm (fb45).

	padj-1	padj-2	padj-3	padj-4	padj-5	padj-6
lfc0diff	1420	682	438	307	236	187
lfc1diff	1011	581	395	288	228	184
lfc2diff	286	286	286	244	201	166
lfc3diff	103	103	103	103	103	103
lfc0up	782	406	283	205	159	129
lfc1up	583	363	266	195	155	128
lfc2up	204	204	204	175	143	121
lfc3up	77	77	77	77	77	77
lfc0down	638	276	155	102	77	58
lfc1down	428	218	129	93	73	56
lfc2down	82	82	82	69	58	45
lfc3down	26	26	26	26	26	26

Table 21 Number of differentially expressed contigs calculated with different false discovery rate adjusted p-values (padj) and with different limitations of log fold change (lfc) in ovules from two sexual diploid lines (HyPR-1 and HyPR-3) versus two tetraploid apomictic lines (HyPR-5 and HyPR-9) dissected from flower buds of length between 5.5 and 6.5 mm (fb55).

	padj-1	padj-2	padj-3	padj-4	padj-5	padj-6
lfc0diff	1434	678	418	310	220	182
lfc1diff	1046	587	375	291	214	180
lfc2diff	279	279	279	245	190	167
lfc3diff	107	107	107	107	107	107
lfc0up	770	405	263	205	150	129
lfc1up	607	367	247	198	148	128
lfc2up	203	203	203	179	139	123
lfc3up	80	80	80	80	80	80
lfc0down	664	273	155	105	70	53
lfc1down	439	220	128	93	66	52
lfc2down	76	76	76	66	51	44
lfc3down	27	27	27	27	27	27

Table 22 Number of differentially expressed contigs calculated with different false discovery rate adjusted p-values (padj) and with different limitations of log fold change (lfc) in ovules from two sexual diploid lines (HyPR-1 and HyPR-3) versus two tetraploid apomictic lines (HyPR-5 and HyPR-9) dissected from flower buds of length between 6.5 and 7.5 mm (fb65).

	padj-1	padj-2	padj-3	padj-4	padj-5	padj-6
lfc0diff	1610	707	422	295	227	184
lfc1diff	1128	586	375	275	219	179
lfc2diff	255	255	255	225	192	160
lfc3diff	96	96	96	96	96	96
lfc0up	909	429	262	195	153	123
lfc1up	649	360	238	182	147	120
lfc2up	171	171	171	156	134	112
lfc3up	71	71	71	71	71	71
lfc0down	701	278	160	100	74	61
lfc1down	479	226	137	93	72	59
lfc2down	84	84	84	69	58	48
lfc3down	25	25	25	25	25	25

Table 23. Significantly differentially expressed RNAseq contigs identified via R-package, DESeq2. lfc (25 to 65) = log2 fold change of normalized reads number in apo vs sex comparison at the stage fb25 to fb 65 respectively; lfcall = log2 fold change of normalized reads number in apo vs sex comparison considering all the stages simultaneously. Padj = P-adjusted value after correction for multiple testing from Benjamini-Hochberg. Empty cells corresponds to absolute lfc < 1 and padj > 10^{-3}.

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
79	AT1G53850.1	9e-49	-1.23	-1.30	-1.65	-1.21	-1.78	4.9e-02	3.1e-02	2.2e-03	5.5e-02	3.2e-13
124	AT3G14470.1	4e-61	-1.30				-1.25	5.8e-02	6.4e-01	8.6e-01	3.0e-01	3.4e-04
139	AT5G42920.1	1e-130					-1.08	2.4e-01	1.5e-01	1.1e-01	1.9e-01	5.1e-08
151	AT5G18590.1	0				-1.02		5.0e-01	2.9e-05	3.7e-04	6.8e-05	1.0e-03
167	AT3G13410.1	9e-38			-1.00			3.3e-03	1.0e-04	2.3e-06	2.8e-04	7.3e-10
168	AT3G13410.1	8e-58	3.74	3.66	3.72	4.21	4.08	1.6e-47	2.4e-45	7.7e-51	3.4e-61	8.6e-128
171	AT5G15170.1	0		-1.33		-1.08	-1.20	2.7e-01	6.4e-03	2.5e-01	5.0e-02	2.3e-10
233	AT4G20440.1	4e-44	-1.11				-1.36	1.5e-01	3.4e-01	3.9e-01	4.7e-01	3.6e-05
237	AT1G79830.1	6e-17					1.96	NA	NA	NA	NA	1.9e-04
264	AT3G47930.1	5e-50			-1.01		-1.10	3.0e-01	5.7e-01	1.3e-01	1.6e-01	9.2e-07
283	AT5G24400.1	2e-12	-1.67	-1.32	-1.24	-1.47	-1.90	2.0e-03	2.7e-02	4.8e-02	1.1e-02	8.0e-15
343	AT1G22970.1	2e-83	-3.06	-2.47	-2.23	-2.26	-3.18	1.8e-12	2.8e-08	7.0e-07	7.7e-07	4.2e-42
435	AT4G02620.1	2e-13	1.56	1.57	1.75	1.26	3.81	1.1e-02	9.9e-03	2.6e-03	6.2e-02	4.7e-17
468	AT3G27950.1	6e-121	1.64	1.16			1.09	4.5e-04	3.4e-02	4.9e-01	6.9e-01	5.6e-02
471	AT1G01820.1	2e-44		-1.24		-1.06	-1.22	1.2e-01	2.2e-02	4.0e-01	7.3e-02	1.2e-08
502	AT3G19420.1	2e-62	1.00	1.18	1.06		2.75	1.8e-01	7.3e-02	1.4e-01	1.9e-01	2.0e-08
533	AT4G36760.1	1e-118	1.16	1.18	1.29	1.28	3.58	1.0e-01	9.2e-02	4.9e-02	5.2e-02	1.4e-20
581	AT3G17910.1	2e-73		-1.06			-2.55	1.7e-01	1.2e-01	3.3e-01	3.5e-01	1.7e-07
607	AT5G15080.1	1e-37	-2.40	-2.07	-1.90	-1.34	-5.04	5.1e-06	1.7e-04	8.5e-04	4.5e-02	7.2e-28
620	AT5G37930.1	2e-49	-1.45	-1.53	-1.32	-1.54	-2.76	2.9e-02	1.7e-02	6.2e-02	1.7e-02	4.4e-14
657	AT1G05570.1	0	-1.38	-1.12		-1.02	-1.41	2.2e-02	1.0e-01	2.3e-01	1.6e-01	2.5e-06
683	AT3G52870.1	6e-93		-1.06	-1.56	-1.98	-1.80	6.6e-01	1.6e-01	7.6e-03	2.0e-04	2.7e-06
717	AT2G20580.1	0	-1.47	-1.66	-1.82	-1.47	-2.35	1.9e-02	4.6e-03	1.2e-03	1.9e-02	1.5e-16
722	AT1G09640.1	5e-74					1.10	2.6e-01	4.5e-01	6.4e-01	3.2e-01	2.2e-04
736	AT3G44110.1	3e-48		-1.01	-1.11	-1.22	-1.68	2.5e-01	2.3e-01	1.6e-01	9.0e-02	1.7e-07
749	AT1G68560.1	5e-74		-1.38	-1.77	-1.94	-2.65	6.1e-01	4.3e-02	3.2e-03	8.0e-04	2.8e-10
804	AT1G34355.1	9e-21	1.18					5.0e-05	6.2e-02	8.0e-02	2.5e-02	1.1e-07
815			-1.17				-1.01	7.4e-02	5.6e-01	3.3e-01	7.1e-01	1.9e-04
820	AT2G27230.1	2e-73	-2.48	-2.32	-1.52	-2.02	-2.70	6.1e-07	3.4e-06	9.5e-03	1.6e-04	1.4e-15
914	AT1G49570.1	5e-37					1.86	9.7e-01	4.7e-01	5.5e-01	7.2e-01	5.9e-04
915	AT1G49570.1	5e-41					3.27	8.5e-01	2.0e-01	2.4e-01	3.7e-01	4.6e-11
938	AT3G14470.1	1e-39	2.65	2.09	1.80	1.66	3.72	3.4e-07	1.7e-04	2.5e-03	7.2e-03	5.7e-20
980	AT5G21940.1	2e-15				1.09	2.70	2.4e-01	NA	NA	6.0e-02	1.0e-07
991							-1.75	4.0e-01	2.4e-01	2.5e-01	5.3e-01	8.4e-05
1000	AT1G25350.1	1e-70	-1.03	-1.01	-1.07		-1.05	7.7e-03	7.8e-03	3.1e-03	1.3e-01	1.2e-15
1010	AT1G48900.1	6e-60	1.03	1.05	1.10	1.16	3.10	1.7e-01	1.5e-01	1.2e-01	8.3e-02	3.4e-12
1081	AT1G65980.1	1e-49	-1.35	-1.43	-1.56	-1.46	-1.72	6.4e-03	2.6e-03	6.2e-04	2.1e-03	2.8e-15
1186	AT3G09480.1	4e-25	-1.42	-1.24	-1.42	-1.25	-1.53	7.8e-04	5.3e-03	7.1e-04	4.8e-03	3.6e-18
1228	AT1G15210.1	0		1.02				5.0e-04	5.4e-07	1.6e-05	2.7e-04	2.0e-17
1234	AT1G20693.1	2e-34	1.07					4.8e-06	2.6e-01	1.2e-01	2.2e-02	2.7e-03
1244	AT4G34880.1	3e-45			-1.09	-1.20	-1.20	4.1e-01	2.1e-01	7.2e-02	3.7e-02	6.0e-08
1273				-1.20	-1.08	-1.06	-1.41	4.7e-01	7.2e-02	1.3e-01	1.4e-01	4.8e-08
1276			1.75	1.36	1.13	1.28	3.12	2.9e-03	4.3e-02	1.4e-01	6.2e-02	2.7e-15
1297			-1.68	-2.30	-2.48	-2.83	-3.11	2.0e-03	2.1e-06	1.6e-07	1.2e-09	3.5e-30
1317	AT5G20950.1	0	-1.31	-1.78	-1.83	-1.79	-1.84	1.2e-03	6.6e-07	1.7e-07	3.6e-07	2.7e-13
1330	AT5G55160.1	3e-15	-1.13	-1.21	-1.05	-1.36	-1.24	4.2e-06	4.2e-07	1.6e-05	1.4e-08	7.7e-39
1355	AT3G06850.1	2e-30	1.46	1.42	1.31		2.26	2.7e-02	3.4e-02	6.4e-02	3.1e-01	1.2e-09
1399	AT5G42890.1	1e-24		1.28		1.28	1.07	1.2e-01	1.2e-07	1.1e-04	1.7e-07	1.8e-14
1422	AT1G47670.1	0				1.21		9.6e-01	8.0e-01	8.1e-01	1.0e-06	8.3e-02
1468	AT1G03280.1	7e-36	-1.37	-1.18		-1.22	-1.41	5.2e-03	2.1e-02	7.8e-02	2.3e-02	2.2e-12

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
1480	AT1G48630.1	1e-78			-1.20			3.4e-03	2.4e-06	2.5e-09	2.9e-04	4.3e-07
1514	AT1G05490.1	1e-114	-2.05	-2.03	-1.86	-1.61	-2.28	2.5e-06	3.1e-06	3.0e-05	6.4e-04	5.2e-29
1522	AT1G55930.1	1e-51	1.66	2.31	2.46	1.53	3.41	7.0e-03	1.6e-05	3.0e-06	1.7e-02	4.4e-18
1525	AT2G33150.1	1e-127				1.05		9.5e-01	1.1e-02	1.3e-03	1.3e-04	3.8e-02
1538	AT1G14790.1	2e-130					-2.58	4.5e-01	3.2e-01	5.7e-01	6.5e-01	6.0e-07
1605			-2.62	-2.91	-2.88	-2.94	-5.18	2.9e-07	4.5e-09	6.3e-09	3.1e-09	6.4e-37
1615	AT4G39030.1	3e-19		-1.12			-1.78	5.2e-01	1.5e-01	5.4e-01	4.2e-01	9.4e-07
1645	AT1G13790.1	7e-50	-1.34				-1.09	3.8e-03	3.1e-01	2.0e-01	7.7e-02	2.9e-07
1664	AT1G75200.1	2e-48	-1.92	-1.64	-1.87	-1.79	-2.93	8.6e-04	7.3e-03	1.2e-03	2.6e-03	2.6e-21
1665	AT1G70730.3	3e-50	-1.07	-1.31		-1.01	-1.08	6.0e-04	6.5e-07	2.3e-03	3.6e-04	1.1e-08
1669	AT5G38690.1	6e-133	-3.37	-3.01	-3.08	-2.87	-3.52	3.5e-22	3.4e-19	7.6e-20	1.3e-15	4.8e-80
1670	AT5G38690.1	3e-137			1.12	1.23	1.07	1.2e-05	2.0e-04	3.7e-07	7.7e-08	1.9e-15
1736	AT2G23530.1	1e-88	-3.79	-4.39	-4.45	-3.97	-6.17	9.7e-18	1.2e-24	2.4e-25	1.9e-19	2.2e-65
1778	AT2G01050.1	2e-41	-1.71	-1.76	-1.56	-1.59	-4.70	3.5e-03	2.4e-03	1.1e-02	9.0e-03	2.8e-26
1786	AT3G11910.1	9e-33	1.30	1.38	1.45	1.47	1.66	9.8e-03	5.6e-03	2.9e-03	4.1e-03	7.3e-13
1795	AT5G06600.1	4e-15	-1.09		-1.01		-2.13	1.4e-01	3.9e-01	2.0e-01	4.0e-01	7.3e-06
1814			-1.12				1.82	8.4e-03	9.5e-01	8.9e-01	8.5e-01	7.9e-04
1853	AT1G04820.1	2e-100	2.15	2.13	2.21	2.39	3.00	2.1e-05	2.6e-05	1.0e-05	1.1e-06	2.4e-30
1860	AT3G47340.1	0		-1.33	-1.44	-2.23	-2.10	2.8e-01	3.9e-02	2.1e-02	1.7e-05	7.2e-10
1874	AT1G30230.2	2e-11	1.71	1.54	1.38	1.46	1.70	1.0e-06	2.2e-05	2.4e-04	1.0e-04	1.3e-17
1984	AT5G17680.1	1e-158					-2.03	4.0e-01	5.0e-01	6.0e-01	7.0e-01	1.1e-04
2022					-1.07	-1.16	-2.41	3.1e-01	4.6e-01	1.5e-01	9.1e-02	6.7e-08
2090	AT5G28740.1	0	-1.32	-1.28	-1.46	-1.42	-1.65	8.7e-03	1.1e-02	2.5e-03	4.9e-03	3.0e-16
2116	AT1G21410.1	2e-48	1.72	1.54	1.45	1.27	2.19	2.5e-03	9.6e-03	1.9e-02	5.6e-02	3.2e-17
2134	AT4G14605.1	5e-81			1.26		1.04	2.1e-01	4.2e-01	1.7e-02	5.1e-01	1.4e-06
2156	AT2G17840.1	2e-110	-2.31	-2.71	-2.72	-3.00	-3.35	2.1e-07	5.9e-11	4.1e-11	2.1e-12	1.6e-41
2197	AT5G02040.1	2e-32		1.18			2.88	4.4e-01	NA	NA	2.2e-01	6.6e-09
2237	AT3G48200.1	2e-47				1.59		4.4e-01	3.0e-01	4.1e-02	2.3e-06	8.7e-02
2251	AT3G48470.1	1e-35	-1.05	-1.14			-1.12	3.2e-02	8.7e-03	9.2e-02	6.7e-02	3.8e-09
2252	AT3G48470.1	6e-96	1.47	1.76	1.24	1.83	2.14	1.2e-02	1.2e-03	5.1e-02	6.9e-04	4.4e-18
2261	AT1G73840.1	7e-28	-3.77	-3.82	-3.59	-3.71	-5.94	5.9e-17	1.8e-17	1.6e-15	3.6e-16	1.9e-58
2273	AT3G21570.1	9e-13			-1.22		-1.91	6.3e-01	4.0e-01	8.8e-02	2.2e-01	1.4e-05
2300	AT1G73840.1	1e-12					1.91	5.1e-01	5.9e-01	7.7e-01	5.4e-01	2.5e-04
2313	AT1G63880.1	1e-12	2.21	2.23	2.20	2.17	3.56	4.0e-05	2.5e-05	3.2e-05	5.8e-05	4.9e-39
2315	AT3G27570.1	6e-16		1.25	1.45	1.59	2.72	4.7e-01	7.3e-02	2.4e-02	9.4e-03	3.3e-10
2380	AT4G28250.2	8e-83		1.27	1.00	1.43	1.35	1.2e-01	1.2e-02	7.8e-02	2.6e-03	1.3e-05
2457	AT5G58380.1	5e-128				-1.00	-3.64	2.1e-01	3.3e-01	2.4e-01	1.1e-01	5.6e-14
2481	AT2G38620.2	1e-30	3.42	2.88	2.77	3.23	5.14	8.7e-13	4.9e-09	2.4e-08	2.9e-11	1.2e-43
2490	AT4G30890.1	2e-17	1.37	1.95	1.74	1.91	2.23	1.6e-02	8.2e-05	7.3e-04	1.6e-04	3.4e-20
2504							-4.03	1.8e-01	1.8e-01	1.4e-01	2.0e-01	3.1e-17
2524	AT1G15520.1	2e-114					-1.07	2.2e-01	5.9e-01	8.8e-01	2.8e-01	3.8e-05
2552	AT3G62300.1	1e-22	-6.28	-6.22	-5.82	-5.56	-7.27	1.0e-69	3.8e-73	2.6e-64	1.2e-55	8.8e-171
2625	AT5G17680.1	1e-137	2.15	1.82	1.66	1.68	3.52	1.2e-04	2.0e-03	7.0e-03	6.3e-03	2.1e-21
2648	AT5G15550.1	1e-112					-2.77	3.8e-01	4.6e-01	4.9e-01	5.3e-01	5.3e-08
2657	AT5G25754.1	5e-29	3.83	3.43	3.35	3.22	5.43	1.3e-17	7.9e-14	4.0e-13	6.9e-12	8.7e-45
2667	AT3G19320.1	7e-35	-1.84				-1.56	1.4e-03	4.2e-01	6.9e-01	6.0e-01	2.6e-04
2718	AT5G52980.1	9e-26	1.29				1.38	7.1e-02	5.2e-01	7.2e-01	6.0e-01	1.6e-04
2752	AT5G34850.1	0	-1.22	-1.21	-1.06		-1.15	3.7e-07	5.1e-07	2.5e-05	9.7e-04	4.6e-13
2759	AT3G62300.1	1e-21	-2.62	-2.46	-2.52	-2.07	-4.98	5.9e-07	3.7e-06	2.0e-06	2.5e-04	4.2e-33
2897	AT5G32440.3	1e-68			-1.18	-1.09	-1.16	1.5e-02	3.6e-02	1.6e-03	6.2e-03	1.1e-16
2898	AT5G32440.1	5e-11		1.08			2.49	3.6e-01	1.2e-01	5.2e-01	4.3e-01	2.8e-09
2900	AT1G14590.1	1e-52		-1.08			-1.06	6.9e-01	1.1e-01	2.1e-01	3.2e-01	2.9e-04
3019	AT5G58240.2	5e-45	2.68	2.61	2.71	2.50	3.92	3.3e-08	8.7e-08	1.8e-08	4.0e-07	1.2e-65
3046	AT5G16850.1	1e-77	-1.41	-1.20	-1.11		-1.32	1.5e-03	9.9e-03	2.2e-02	2.2e-01	1.4e-09

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
3059	AT5G59950.1	3e-23	3.14	3.05	3.03	2.77	5.33	1.3e-10	4.0e-10	5.4e-10	3.8e-08	7.7e-40
3081	AT4G23160.1	3e-102		-1.22	-1.03		-2.25	7.8e-01	5.6e-02	1.5e-01	5.1e-01	4.1e-06
3103	AT2G29570.1	7e-22			-1.20		-1.37	4.1e-01	2.3e-01	8.4e-02	3.3e-01	2.4e-06
3163	AT1G13570.1	2e-35	-1.69	-1.54	-1.53	-1.55	-4.84	3.5e-03	1.1e-02	1.2e-02	1.1e-02	1.5e-28
3165	AT3G22960.1	0	1.19					5.4e-06	6.1e-02	5.2e-01	4.4e-01	2.9e-04
3169	AT3G55370.2	1e-30	1.31					2.1e-06	2.7e-03	1.2e-02	9.6e-01	6.0e-05
3220	AT2G43810.1	3e-53					2.15	2.9e-01	5.0e-01	7.1e-01	5.1e-01	1.8e-05
3245	AT5G23210.1	2e-51					2.09	9.7e-01	5.5e-01	5.5e-01	5.2e-01	8.7e-05
3248	AT1G67430.1	2e-37	1.20				1.96	8.5e-02	5.2e-01	5.1e-01	5.7e-01	9.2e-06
3263	AT5G28770.1	2e-40		-1.35		-1.27	-1.34	6.2e-01	3.2e-02	2.2e-01	5.3e-02	7.3e-05
3291	AT1G52310.1	5e-28	-1.11				-1.05	6.2e-02	1.2e-01	6.5e-01	2.2e-01	3.9e-06
3331	AT1G70580.1	6e-25		1.09			1.62	3.9e-01	1.6e-01	5.0e-01	6.2e-01	3.9e-04
3335	AT2G43770.1	3e-32					-1.85	6.1e-01	8.2e-01	7.2e-01	6.3e-01	6.4e-04
3343	AT1G21980.1	6e-38	-1.18	-1.56	-1.27	-1.14	-3.62	8.5e-02	8.2e-03	5.5e-02	9.8e-02	7.9e-15
3353	AT1G57610.1	1e-70				1.16		9.7e-01	2.3e-02	9.4e-02	5.0e-04	8.2e-02
3362	AT5G22070.1	1e-58	1.43	2.26	2.38	2.85	1.83	3.2e-02	3.7e-05	1.1e-05	3.4e-08	6.8e-04
3403	AT3G60210.1	3e-29	5.83	5.21	5.09	5.01	7.13	2.1e-57	5.4e-45	3.2e-43	8.4e-41	3.6e-84
3405	AT5G17920.1	6e-92	1.11					2.5e-04	2.8e-02	1.7e-01	1.7e-01	2.1e-09
3409	AT3G20430.1	4e-11	-2.44	-1.92	-2.05	-2.42	-3.54	2.8e-06	5.6e-04	2.0e-04	4.2e-06	1.1e-24
3457	AT4G09740.1	1e-34	-1.39	-1.45	-1.45	-1.35	-1.86	2.2e-02	1.5e-02	1.7e-02	3.2e-02	1.1e-08
3514	AT1G71750.1	1e-28	-1.25	-1.18	-1.26	-1.23	-3.78	5.4e-02	7.7e-02	5.2e-02	5.7e-02	4.2e-16
3518	AT4G38470.1	0	-1.31	-1.10		-1.08	-1.41	2.9e-02	9.6e-02	4.6e-01	1.1e-01	2.6e-08
3543	AT3G03360.1	7e-17	3.29	4.02	4.15	4.20	5.90	1.7e-13	1.7e-19	7.1e-21	3.6e-21	2.4e-83
3615	AT2G27170.1	2e-84	-3.07	-2.90	-2.94	-2.23	-3.59	1.4e-12	8.1e-12	6.4e-12	1.0e-06	2.2e-50
3620	AT3G22880.1	4e-109		1.60	1.74	1.78	3.25	2.8e-01	9.7e-03	3.4e-03	2.6e-03	2.7e-14
3632	AT5G51970.1	5e-11	-1.64			-1.31	-3.16	3.8e-03	2.1e-01	4.5e-01	3.8e-02	3.0e-11
3638	AT1G03080.1	0				-1.19		4.6e-04	2.9e-03	1.1e-05	8.3e-11	2.1e-17
3685	AT2G22240.1	0				1.07	1.23	6.0e-01	2.9e-01	2.8e-01	1.5e-01	4.9e-05
3725	AT3G50830.1	3e-43	-1.29	-1.47	-1.51	-1.70	-1.50	3.6e-09	6.9e-11	1.5e-11	4.2e-14	4.4e-17
3772	AT3G44280.1	3e-13					-2.84	5.7e-01	5.7e-01	2.1e-01	1.3e-01	1.7e-08
3833	AT2G44760.1	3e-42	-1.05	-1.13	-1.27	-1.20	-3.91	1.4e-01	9.5e-02	4.4e-02	6.1e-02	4.3e-17
3850							2.36	5.0e-01	5.1e-01	3.7e-01	2.2e-01	4.1e-07
3932	AT1G67970.1	2e-40	-2.43	-1.88	-1.98	-2.10	-4.06	5.3e-06	1.3e-03	5.3e-04	1.8e-04	3.2e-29
3940	AT1G75560.1	5e-51			-1.26	-1.01	-1.27	1.2e-01	1.5e-01	2.0e-02	9.9e-02	2.4e-09
3991	AT2G25950.1	5e-26	-2.19	-2.15	-1.87	-1.93	-4.13	7.8e-05	1.1e-04	1.4e-03	8.7e-04	1.0e-28
4026	AT3G19300.1	0		-1.06		-1.10	-1.14	4.3e-01	5.8e-02	1.4e-01	4.5e-02	7.5e-08
4152	AT5G25560.1	1e-155	-1.34	-1.06		-1.26	-1.03	1.9e-05	1.6e-03	1.8e-01	8.6e-05	9.9e-04
4176	AT1G49570.1	2e-47	-4.35	-3.17	-3.53	-3.48	-3.53	7.7e-23	2.8e-12	2.3e-15	9.0e-15	4.5e-15
4189			1.24				1.70	8.9e-02	3.0e-01	3.6e-01	4.8e-01	1.7e-06
4226	AT4G29410.1	1e-73	2.56	1.77	1.42	1.50	1.99	1.5e-15	1.6e-07	6.6e-05	3.2e-05	3.0e-25
4276	AT5G35750.1	3e-95	-1.51	-1.37	-1.40	-1.02	-3.61	1.2e-02	3.0e-02	2.6e-02	1.8e-01	9.2e-15
4300	AT5G04730.1	9e-39		-1.09			-2.31	1.1e-01	6.3e-02	5.9e-01	8.9e-01	1.1e-05
4320	AT4G39210.1	1e-135	1.13	1.19	1.38	1.21	1.63	9.2e-02	6.2e-02	1.9e-02	5.4e-02	2.7e-11
4340	AT1G30470.1	0	-1.06	-1.15	-1.00	-1.24	-1.15	1.7e-07	2.5e-09	4.1e-07	2.6e-10	1.1e-49
4372	AT5G55630.1	3e-43			1.03	1.17	1.02	1.0e-01	5.8e-01	3.5e-02	1.6e-02	3.7e-08
4413	AT3G57330.1	9e-124			-1.61	-1.51	-1.29	1.8e-01	8.6e-02	9.4e-06	3.8e-05	5.0e-05
4435	AT4G12560.1	3e-20		-1.20	-1.04	-1.06	-1.31	2.9e-01	3.9e-02	1.0e-01	9.2e-02	1.1e-09
4460	AT1G01030.1	1e-48	-1.48	-1.88	-1.93	-2.10	-4.39	2.1e-02	1.1e-03	7.2e-04	1.6e-04	9.4e-24
4534	AT1G12240.1	8e-63		-1.37	-1.37	-1.39	-2.62	2.5e-01	4.1e-02	4.2e-02	3.8e-02	2.9e-10
4562	AT2G31510.1	1e-72	-1.18	-1.07	-1.07	-1.01	-1.22	5.6e-03	1.3e-02	1.2e-02	2.4e-02	2.9e-16
4563	AT2G31510.1	2e-94	1.44	1.44	1.52	1.67	1.89	5.1e-03	4.7e-03	2.1e-03	5.3e-04	3.0e-21
4620	AT1G29950.1	3e-27		-1.06	-1.24		-1.09	2.2e-01	5.7e-03	7.7e-04	1.4e-02	9.8e-14
4647	AT2G18040.1	8e-14	4.40	3.88	3.82	3.82	6.14	1.6e-24	6.6e-19	2.2e-18	4.4e-18	5.7e-57
4686	AT3G17090.1	4e-72		-1.20	-1.28		-1.86	4.7e-01	1.1e-01	7.1e-02	5.7e-01	7.5e-07

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
4708	AT1G56460.1	6e-11	3.15	3.02	3.09	2.92	5.25	4.7e-11	3.4e-10	1.0e-10	2.1e-09	8.6e-39
4760			1.33	1.50	1.36	1.38	2.10	4.7e-02	1.7e-02	4.0e-02	3.4e-02	1.7e-12
4785	AT5G66330.1	7e-18	-1.44	-1.42	-1.59	-1.42	-2.03	2.6e-02	2.7e-02	7.7e-03	2.5e-02	5.6e-08
4799	AT2G24280.1	4e-23				-1.24	-2.43	2.8e-01	3.2e-01	3.5e-01	5.9e-02	1.4e-07
4868	AT5G52740.1	3e-18	3.08	2.42	2.25	1.39	3.32	8.5e-11	1.4e-06	1.1e-05	2.8e-02	4.4e-21
4907	AT1G24430.1	6e-22			1.02		1.99	NA	NA	NA	NA	1.8e-04
4915	AT3G50950.2	5e-21					-1.59	2.9e-01	5.9e-01	6.4e-01	5.4e-01	4.2e-04
4958	AT2G07727.1	0	1.55	1.91				4.3e-04	3.0e-06	5.7e-01	5.6e-01	3.7e-01
5005	AT5G28740.1	0	-1.86	-2.05	-1.51	-1.36	-1.98	4.6e-06	1.0e-07	2.9e-04	2.8e-03	8.7e-29
5018	AT3G56150.1	3e-98	5.10	3.80	3.86	3.94	4.74	1.5e-49	2.9e-31	3.7e-32	6.5e-30	4.1e-83
5029	AT2G05840.1	5e-85			-1.14		-1.02	4.9e-04	6.6e-06	9.5e-08	1.4e-04	1.2e-17
5048	AT4G34100.1	2e-52					-1.82	8.5e-01	9.1e-01	9.0e-01	8.1e-01	6.3e-04
5101	AT5G40770.1	3e-112	4.14	3.50	3.86	3.69	4.17	5.9e-47	9.4e-34	2.0e-38	3.2e-36	1.1e-128
5145	AT5G05780.1	9e-28	-4.27	-4.14	-3.95	-3.62	-6.06	1.7e-22	3.2e-21	1.6e-19	3.6e-16	7.9e-69
5186	AT5G51030.1	1e-164	-1.09					1.5e-04	2.4e-02	9.9e-03	2.6e-03	8.0e-19
5187	AT5G51030.1	2e-35	1.64	1.97	2.14	1.96	3.75	8.3e-03	5.6e-04	1.1e-04	6.7e-04	1.1e-18
5226	AT5G35080.1	8e-16	1.19	1.21	1.13	1.21	3.50	7.2e-02	6.5e-02	1.0e-01	6.1e-02	8.4e-14
5244	AT2G27600.1	7e-112	3.56	3.53	3.53	3.63	5.42	1.1e-15	2.0e-15	3.0e-15	4.7e-16	8.8e-54
5278	AT1G49820.1	0	1.03					1.0e-04	1.8e-01	6.1e-01	2.5e-01	1.4e-05
5302	AT2G18750.1	2e-85					1.85	8.2e-01	5.2e-01	4.5e-01	4.4e-01	1.5e-04
5304	AT4G15080.1	2e-32					1.62	7.6e-01	4.4e-01	4.5e-01	4.8e-01	5.2e-04
5308	AT4G39860.1	5e-13					-3.49	3.3e-01	2.7e-01	2.5e-01	1.8e-01	7.7e-13
5326							2.09	NA	NA	NA	NA	8.1e-05
5335	AT4G29960.1	2e-31	1.51	1.26	1.39	1.42	3.23	1.7e-02	7.4e-02	3.7e-02	3.0e-02	1.7e-18
5374	AT3G06340.1	4e-13	-3.38	-3.38	-3.01	-2.53	-5.31	1.4e-12	1.5e-12	6.3e-10	7.7e-07	4.4e-38
5384	AT4G29090.1	1e-46	-1.22	-1.02	-1.08	-1.10	-3.58	5.4e-02	1.6e-01	1.2e-01	1.0e-01	1.5e-14
5389					1.14	1.31	1.10	2.7e-04	2.6e-04	1.4e-05	8.7e-07	1.2e-10
5464	AT5G26680.1	1e-78	1.59	1.44	1.15	1.26	2.05	9.5e-03	2.6e-02	1.2e-01	6.9e-02	8.4e-12
5494	AT5G48230.2	3e-69					1.75	5.8e-01	7.2e-01	7.7e-01	5.4e-01	9.4e-04
5521	AT3G47570.1	2e-82					-2.45	1.4e-01	2.8e-01	5.1e-01	7.3e-01	1.9e-06
5522	AT3G47570.1	7e-52					-1.79	3.9e-01	5.1e-01	6.8e-01	7.8e-01	8.7e-04
5539	AT3G48610.1	0		1.52	1.07	1.09	1.18	8.5e-02	4.4e-06	4.8e-03	5.5e-03	9.0e-10
5546	AT5G58300.1	9e-131					-2.58	7.0e-01	4.6e-01	3.3e-01	2.6e-01	5.2e-07
5575	AT5G55520.1	2e-24					1.75	9.1e-01	4.8e-01	4.2e-01	2.3e-01	4.1e-06
5579	AT3G22425.1	2e-69	-1.87	-1.66	-1.87	-1.77	-3.77	1.3e-03	6.6e-03	1.4e-03	3.0e-03	1.5e-19
5582	AT4G26100.1	9e-110	2.16	2.50	1.91	2.01	3.78	9.4e-05	1.7e-06	8.3e-04	4.1e-04	5.9e-23
5599	AT1G06220.2	0	-1.45	-1.37	-1.52	-1.40	-1.56	1.2e-05	3.9e-05	3.1e-06	5.7e-05	4.5e-19
5631			2.32	2.30	1.85	1.51	3.65	1.9e-05	2.1e-05	1.6e-03	2.0e-02	3.6e-20
5731	AT1G06850.1	1e-61	-1.15	-1.06			-2.93	8.8e-02	1.4e-01	2.2e-01	1.9e-01	1.7e-10
5754	AT5G15950.1	2e-32	1.17					2.9e-05	9.9e-01	8.9e-01	7.7e-01	5.0e-02
5767	AT2G23530.1	1e-89	1.08	1.45	1.37	1.41	1.42	7.3e-03	5.5e-05	1.8e-04	1.4e-04	7.3e-13
5799	AT5G56750.1	1e-134	1.15		1.56	1.00	2.83	1.1e-01	3.0e-01	1.0e-02	1.9e-01	9.8e-11
5843	AT2G41520.1	1e-53	-1.55	-1.80	-1.72	-1.50	-1.91	1.8e-04	2.9e-06	1.1e-05	3.3e-04	6.2e-34
5952	AT1G58025.1	4e-12	3.96	3.62	3.76	3.78	5.82	6.6e-20	9.5e-17	5.4e-18	6.9e-18	4.6e-54
5953	AT1G58025.1	2e-12	-1.13				-1.02	4.1e-03	5.3e-02	1.1e-01	5.2e-02	6.4e-12
5962	AT2G42740.1	1e-57					2.46	2.6e-01	5.7e-01	6.9e-01	5.9e-01	1.4e-06
5970	AT3G13080.1	0	-1.29	-1.37	-1.24	-1.46	-1.40	8.3e-06	8.8e-07	1.5e-05	9.8e-08	6.4e-12
6003				1.77	2.49	2.48	1.48	1.3e-01	2.6e-07	3.9e-14	1.8e-13	1.5e-04
6005	AT3G26600.1	3e-32			1.34		1.82	7.8e-01	7.8e-01	3.4e-02	3.2e-01	1.5e-04
6011	AT4G30190.1	0	-1.12					4.8e-04	9.2e-01	9.9e-01	8.5e-01	3.6e-01
6018	AT4G01560.1	8e-52					1.05	4.6e-01	2.0e-01	2.7e-01	5.0e-01	1.6e-04
6080	AT2G32170.1	1e-39					-2.65	7.1e-01	2.1e-01	2.6e-01	4.1e-01	2.1e-07
6142	AT5G52540.1	3e-18		1.12	1.43	1.24	1.64	3.2e-01	1.2e-01	1.9e-02	6.1e-02	2.2e-10
6173	AT5G54770.1	8e-152	1.24	1.57	1.45	1.36	1.48	3.9e-03	7.4e-05	3.6e-04	1.2e-03	1.7e-07

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
6231	AT2G29380.1	8e-65					2.01	NA	NA	NA	NA	1.8e-04
6269	AT3G48530.1	1e-132				-1.16	-1.29	3.8e-01	7.8e-01	4.8e-01	1.2e-01	6.2e-04
6299	AT4G21770.1	1e-36	-1.52				-1.38	1.7e-02	3.5e-01	5.7e-01	6.2e-01	2.4e-04
6300	AT1G80440.1	1e-37	1.58	1.86	2.29	1.95	3.82	1.3e-02	1.5e-03	2.6e-05	7.8e-04	4.6e-30
6322	AT1G73620.1	5e-70	1.09			1.12	1.00	1.3e-03	2.7e-02	7.7e-02	1.1e-03	6.1e-05
6392	AT1G58030.1	2e-117	-2.25	-2.39	-2.31	-2.35	-5.06	4.2e-05	9.0e-06	2.2e-05	1.4e-05	2.1e-33
6476	AT1G09200.1	3e-80	1.18					1.7e-04	3.7e-03	7.3e-02	3.7e-02	1.2e-11
6482	AT1G67560.1	2e-106	-1.08	-1.12	-1.01		-1.12	2.6e-02	1.3e-02	3.3e-02	2.8e-01	3.0e-10
6505	AT4G00560.1	3e-42				1.14	2.81	4.5e-01	NA	NA	5.7e-02	1.9e-08
6517	AT1G22450.1	2e-50	1.40	1.20	1.07	1.14	2.61	3.4e-02	9.8e-02	1.8e-01	1.2e-01	3.1e-11
6584	AT3G52155.1	9e-64	-1.58	-1.39	-1.34	-1.36	-1.74	1.2e-03	5.9e-03	1.0e-02	1.1e-02	2.6e-15
6589	AT2G34730.1	2e-74		-1.17			-1.04	4.1e-02	4.2e-03	5.0e-02	1.9e-01	3.2e-11
6596			-1.31	-1.36		-1.05	-1.38	7.2e-03	4.1e-03	1.4e-01	5.8e-02	7.4e-12
6632	AT2G33040.1	2e-22	4.26	4.02	4.01	4.06	6.16	1.7e-24	8.0e-22	7.8e-22	5.6e-22	3.0e-59
6645	AT4G01040.1	9e-88					-2.41	2.1e-01	3.3e-01	3.0e-01	3.9e-01	6.0e-07
6647	AT1G63900.1	2e-71	1.58	1.36	1.70	1.76	3.68	1.1e-02	4.2e-02	4.5e-03	2.9e-03	1.8e-18
6656	AT1G48930.1	0	1.15					2.2e-05	9.9e-03	2.5e-02	1.2e-03	3.8e-09
6663	AT2G23260.1	2e-98	2.70	3.01	2.74	1.59	4.52	1.6e-07	1.3e-09	6.9e-08	1.1e-02	8.3e-25
6689	AT2G07734.1	1e-150	1.72	2.22		1.10	1.14	1.1e-03	4.2e-06	9.3e-01	9.3e-02	1.8e-02
6709	AT4G31700.1	5e-41	1.58	1.52	1.45	1.51	1.65	1.8e-06	7.6e-06	2.4e-05	1.6e-05	1.4e-21
6726	AT1G74670.1	1e-38	-4.68	-4.99	-4.63	-4.42	-6.26	6.9e-32	9.8e-37	3.3e-32	1.1e-27	6.4e-103
6754	AT5G15610.1	6e-77		-1.06	-1.05		-1.01	2.8e-01	2.1e-02	2.3e-02	1.8e-01	4.7e-08
6883	AT5G45900.1	2e-55	-1.31	-1.30		-1.13	-1.45	3.2e-02	3.0e-02	3.7e-01	9.5e-02	3.7e-08
6884	AT3G03520.1	0	-1.86	-1.73	-1.93	-1.91	-2.05	5.5e-07	2.1e-06	3.9e-08	7.9e-08	3.8e-22
6898	AT3G22630.1	3e-46	-1.53				-2.75	7.9e-03	4.8e-01	4.5e-01	1.9e-01	3.4e-09
6901	AT5G64440.1	3e-139	-1.57		-1.38	-1.03	-2.16	1.3e-02	2.4e-01	4.2e-02	2.1e-01	1.0e-06
6955	AT4G38470.1	8e-36	-1.04				-1.04	1.2e-01	4.6e-01	5.3e-01	2.7e-01	8.4e-06
6992	AT5G40740.1	2e-16	1.19			1.07	3.32	6.0e-02	1.8e-01	1.9e-01	1.1e-01	4.6e-12
7001	AT2G02820.2	4e-44	-1.17	-1.54	-1.54		-1.71	6.7e-02	5.6e-03	5.7e-03	2.1e-01	6.0e-11
7007				1.09			1.95	9.1e-01	NA	NA	5.3e-01	1.4e-04
7056	AT5G23740.1	7e-26		1.64	1.65	1.38	3.71	2.5e-01	5.5e-03	5.0e-03	3.0e-02	3.4e-16
7077	AT1G04240.1	1e-45		-1.00			-1.39	5.6e-01	2.4e-01	4.0e-01	2.4e-01	1.4e-04
7093	AT2G02980.1	5e-118	1.46	1.42			2.26	2.7e-02	3.3e-02	3.6e-01	2.8e-01	1.2e-10
7138	AT1G04910.1	2e-114				-1.06	-1.33	4.6e-01	4.2e-01	2.7e-01	1.6e-01	2.9e-06
7216	AT3G51240.1	0	-1.70	-1.11	-1.26		-1.30	2.4e-05	1.0e-02	2.6e-03	1.3e-01	2.4e-04
7263	AT5G06460.1	3e-69					-1.49	6.7e-01	2.8e-01	5.7e-01	2.4e-01	1.7e-04
7284	AT4G39010.1	6e-30	-1.74	-2.27	-2.43	-2.68	-3.55	3.2e-03	2.2e-05	3.2e-06	1.4e-07	3.7e-22
7298	AT3G22400.1	0	-2.23	-1.59	-1.41		-2.18	4.3e-05	1.1e-02	3.6e-02	3.6e-01	5.5e-06
7348	AT4G02620.1	2e-42					1.47	3.4e-01	8.8e-01	3.3e-01	5.1e-01	6.3e-04
7350	AT3G52115.1	6e-40	1.23			1.18	1.45	5.0e-02	2.0e-01	2.0e-01	7.0e-02	1.2e-09
7378	AT4G27190.1	6e-48		-1.21	-1.44	-1.59	-1.97	5.2e-01	1.0e-01	3.2e-02	1.2e-02	2.3e-07
7388			-1.32	-1.53	-1.29	-1.24	-3.37	4.8e-02	1.3e-02	5.5e-02	6.6e-02	2.6e-14
7395			2.16	1.73	1.90	1.91	2.58	8.2e-06	7.2e-04	1.3e-04	2.7e-04	5.9e-25
7415	AT5G25170.1	4e-76	1.51	1.54	1.18	1.36	1.60	3.1e-04	2.8e-04	9.5e-03	4.0e-03	1.3e-16
7424	AT5G22450.1	8e-21					-2.79	2.7e-01	5.5e-01	5.7e-01	2.8e-01	3.9e-08
7436	AT5G22450.1	4e-12					-2.27	7.6e-01	NA	NA	3.3e-01	1.3e-05
7445	AT5G06910.1	4e-35	3.58	3.26	3.12	2.96	5.43	1.3e-14	4.5e-12	5.0e-11	9.8e-10	1.0e-41
7452	AT4G32620.1	4e-97	-2.70	-2.62	-2.46	-3.02	-4.47	1.2e-07	2.6e-07	2.1e-06	1.2e-09	8.3e-40
7475	AT4G24800.1	5e-62					-2.19	5.3e-01	4.6e-01	4.7e-01	5.8e-01	3.2e-05
7515	AT5G65020.1	7e-12	-1.11	-1.12	-1.16	-1.44	-2.38	1.6e-01	1.5e-01	1.3e-01	2.8e-02	1.9e-09
7607	AT4G23640.1	1e-65	-1.15	-1.40	-1.28	-1.45	-4.05	1.0e-01	2.3e-02	5.0e-02	1.6e-02	2.5e-19
7614	AT3G58760.1	3e-22			-1.04		-1.23	5.7e-01	3.8e-01	2.0e-01	5.0e-01	6.9e-05
7615	AT5G20290.1	1e-48				1.09		1.0e-01	3.7e-03	5.9e-03	6.0e-04	1.4e-05
7654	AT5G33370.1	2e-160			1.02	1.35	1.01	6.0e-01	1.8e-02	5.3e-03	4.3e-05	1.3e-07

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
7702	AT3G57330.1	4e-170			-1.33	-1.42	-1.25	2.3e-01	3.1e-01	3.9e-03	1.5e-03	2.0e-04
7714	AT1G74390.1	2e-137	-3.11	-3.10	-2.64	-2.42	-4.99	2.2e-10	2.3e-10	1.9e-07	3.7e-06	1.5e-34
7721	AT2G47620.1	1e-15	2.07	1.80	1.93	1.67	4.22	2.2e-04	2.2e-03	7.9e-04	6.3e-03	8.7e-22
7724	AT3G20770.1	6e-70	1.76	1.79	1.70	1.90	3.54	3.4e-03	2.5e-03	5.3e-03	1.2e-03	3.7e-19
7740	AT1G11870.2	2e-25					-1.24	4.3e-01	4.3e-01	7.9e-01	5.2e-01	7.0e-04
7752	AT3G62300.1	1e-26	-1.60	-1.32	-1.11		-4.26	4.2e-03	3.2e-02	1.1e-01	2.7e-01	1.0e-19
7755	AT5G40810.1	8e-61	-1.77	-1.72	-1.95	-2.03	-5.13	2.6e-03	3.8e-03	5.8e-04	2.8e-04	3.7e-32
7795	AT1G16330.1	2e-39	-1.06	-1.36	-1.20	-1.12	-1.27	1.5e-03	2.4e-06	1.1e-04	1.4e-03	8.4e-15
7796	AT3G55440.1	5e-155	2.81	2.75	2.13	2.30	2.72	2.8e-21	5.0e-20	2.6e-12	4.6e-14	1.8e-71
7809	AT3G13300.1	7e-98	3.66	4.71	4.86	4.70	5.89	1.9e-19	1.4e-34	1.2e-35	4.5e-33	8.0e-58
7857	AT1G16330.1	5e-90	1.57	1.87	1.98	2.11	2.27	1.1e-03	3.1e-05	8.1e-06	1.8e-06	8.3e-28
7907	AT3G55005.1	1e-28	-1.12	-1.21	-1.51	-1.35	-3.70	1.2e-01	7.3e-02	1.2e-02	3.2e-02	1.5e-15
7916	AT5G65110.1	0				1.11		4.8e-01	9.5e-05	2.1e-05	3.4e-11	3.9e-08
7921	AT4G14605.1	3e-70	-3.84	-3.61	-3.55	-3.41	-5.31	2.4e-19	4.4e-17	1.1e-16	7.4e-15	6.2e-52
7922	AT4G14605.1	4e-47	-1.08	-1.22			-1.43	1.8e-01	9.5e-02	7.5e-01	4.9e-01	1.9e-05
8010	AT2G42680.1	1e-32					-2.01	4.3e-01	4.0e-01	5.2e-01	4.4e-01	1.7e-04
8032	AT3G55360.1	1e-19				1.33		4.2e-01	2.2e-01	1.5e-01	2.7e-04	1.0e-08
8076	AT2G04842.1	2e-43		-1.24			-1.37	8.5e-01	9.0e-02	4.4e-01	3.6e-01	7.9e-05
8099	AT1G17280.1	7e-78		-1.30		-1.03	-1.17	1.1e-01	2.7e-03	1.3e-01	4.3e-02	1.9e-11
8156	AT1G24360.1	4e-143	-1.03	-1.31	-1.18	-1.19	-1.21	5.5e-07	1.1e-11	1.8e-09	1.0e-09	3.3e-29
8161	AT3G17611.2	1e-56	-2.42	-3.15	-3.01	-2.84	-4.24	1.3e-06	1.0e-11	8.3e-11	1.9e-09	9.7e-35
8173	AT5G52820.1	0			1.02	1.42		4.7e-04	5.2e-07	8.3e-15	1.4e-27	7.7e-15
8263	AT5G10910.1	1e-124	-1.45				-1.10	5.8e-07	5.0e-03	1.4e-02	2.9e-02	1.1e-10
8285	AT5G19440.1	3e-35	1.54	3.02	3.06	3.38	4.05	1.3e-02	1.2e-09	5.2e-10	4.3e-12	3.1e-22
8290	AT2G30470.1	1e-116	-1.47	-1.27	-1.23	-1.24	-1.70	8.3e-03	3.4e-02	4.3e-02	4.3e-02	1.3e-12
8330	AT4G23800.1	7e-39					-3.05	6.3e-01	4.3e-01	4.7e-01	5.2e-01	1.3e-09
8369	AT1G60060.1	8e-139		-1.52	-1.15	-1.46	-1.26	9.1e-01	2.2e-03	4.6e-02	5.1e-03	1.5e-04
8424	AT5G48240.1	4e-80			-1.04	-1.19	-1.05	1.8e-01	9.3e-02	1.6e-02	3.8e-03	5.4e-12
8433	AT1G06950.1	7e-71	-1.85	-1.90	-1.65	-1.46	-3.75	1.5e-03	9.5e-04	7.2e-03	2.6e-02	2.8e-20
8435				-1.09			-1.83	2.7e-01	1.5e-01	6.8e-01	4.9e-01	3.2e-05
8446	AT4G01460.1	1e-19		1.21	1.44	1.38	2.23	7.3e-01	9.6e-02	2.8e-02	3.8e-02	1.5e-06
8475	AT1G19390.1	1e-143	-1.05	-2.15	-1.84	-1.58	-4.55	1.8e-01	6.1e-05	1.2e-03	9.4e-03	1.7e-23
8499							-2.52	1.6e-01	4.0e-01	4.6e-01	5.0e-01	2.9e-08
8500				1.02		1.27	1.11	5.0e-01	1.2e-01	4.3e-01	3.4e-02	7.8e-06
8529							-2.52	4.6e-01	3.8e-01	5.5e-01	3.8e-01	7.6e-07
8534	AT1G07615.1	2e-59	1.45	2.04	1.44	1.69	2.44	2.2e-02	1.9e-04	2.4e-02	5.4e-03	7.1e-13
8625	AT5G23140.1	8e-27					1.10	4.7e-01	4.3e-01	4.2e-01	3.0e-01	2.3e-05
8633	AT3G58530.1	2e-76	1.00				2.58	1.7e-01	4.6e-01	2.8e-01	3.2e-01	5.0e-09
8634	AT3G58530.1	1e-76	-1.07			-1.02	-1.46	1.7e-01	3.8e-01	2.6e-01	2.0e-01	2.2e-07
8655	AT3G19420.1	8e-66	-1.90	-2.35	-1.64	-1.90	-3.03	9.2e-04	8.9e-06	6.4e-03	9.1e-04	4.4e-19
8670	AT5G04560.1	3e-21		1.07	1.43	1.02	1.39	1.9e-01	8.9e-02	7.4e-03	1.2e-01	9.8e-07
8685	AT2G33150.1	0					-1.06	2.6e-01	5.0e-01	4.3e-01	5.5e-01	1.9e-04
8733	AT3G55120.1	3e-89		-1.23			-1.74	6.1e-01	8.1e-02	2.4e-01	6.1e-01	3.3e-04
8734	AT3G55120.1	1e-89	3.87	3.74	4.00	3.95	4.04	1.2e-29	2.9e-31	6.0e-35	3.4e-30	9.8e-41
8820	AT4G35770.1	8e-19	4.39	3.40	3.07	3.12	5.42	1.0e-22	2.4e-13	8.8e-11	5.4e-11	2.7e-38
8833	AT4G36970.1	7e-17	-1.16				-1.13	6.7e-02	3.6e-01	1.5e-01	3.1e-01	7.2e-06
8838	AT1G04760.1	8e-34				1.03	1.50	3.9e-01	4.6e-01	9.1e-01	1.9e-01	9.9e-04
8842	AT5G22030.2	7e-55		-1.19	-1.08	-1.06	-1.23	5.6e-02	7.8e-03	2.5e-02	3.6e-02	1.1e-11
8894	AT1G17130.1	2e-15		1.36	1.21	1.34	1.21	3.4e-01	3.4e-03	1.4e-02	4.9e-03	1.9e-05
8899	AT2G01050.1	8e-13	-1.33	-1.20	-1.26	-1.20	-1.65	2.7e-02	5.9e-02	4.4e-02	5.9e-02	3.5e-11
8911	AT1G13320.1	2e-53		-1.36		-1.43	-1.73	2.7e-01	4.4e-02	6.1e-01	3.1e-02	9.7e-07
8942	AT1G04810.1	4e-62	-1.27	-1.19	-1.49	-1.15	-1.48	5.0e-03	8.1e-03	3.7e-04	1.6e-02	5.4e-19
8947	AT3G26400.1	8e-31	-1.68	-1.48	-1.21	-1.14	-3.93	3.0e-03	1.4e-02	7.3e-02	9.8e-02	1.6e-16
8991	AT5G13710.1	3e-133					-1.87	5.7e-01	5.4e-01	4.3e-01	2.8e-01	9.5e-05

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
9067	AT2G43970.1	6e-64					3.46	2.3e-01	2.1e-01	2.6e-01	2.4e-01	6.6e-18
9181	AT3G14810.1	3e-89		1.29	1.53		1.28	6.8e-01	1.2e-02	1.3e-03	1.7e-01	2.4e-04
9191	AT1G71980.1	2e-39		1.07	1.51	1.48	3.32	2.3e-01	1.5e-01	1.2e-02	1.4e-02	3.2e-12
9207	AT5G03420.1	1e-17	-1.87	-1.08	-1.08	-2.02	-1.86	1.8e-04	8.1e-02	8.6e-02	5.4e-05	1.3e-13
9220	AT2G12550.1	6e-105	-1.29	-1.64	-1.57	-1.61	-4.13	5.6e-02	6.0e-03	9.6e-03	7.3e-03	3.2e-22
9260	AT1G13570.1	4e-19					-1.30	3.7e-01	4.4e-01	5.6e-01	3.8e-01	8.5e-05
9279			-1.43	-1.49	-1.21	-1.02	-3.98	1.8e-02	1.2e-02	6.9e-02	1.6e-01	6.4e-18
9318	AT1G15440.1	5e-85	1.16				1.22	9.8e-02	5.6e-01	5.7e-01	2.4e-01	8.3e-06
9325	AT2G21340.1	1e-117		-1.12		-1.33	-1.24	4.9e-01	7.0e-02	2.2e-01	2.0e-02	4.6e-07
9358	AT3G13620.1	0				-2.13	-2.31	3.4e-01	7.5e-01	3.4e-01	4.8e-05	6.8e-06
9396	AT4G28630.1	7e-22	-3.42	-3.20	-2.45	-1.55	-4.36	1.7e-12	6.7e-11	3.0e-06	1.4e-02	1.9e-23
9456	AT1G21700.1	3e-69	3.58	3.33	3.67	3.61	3.92	2.2e-33	5.2e-29	1.1e-32	1.9e-28	6.8e-103
9463	AT2G20300.1	6e-41	-1.87	-2.10	-2.11	-2.05	-5.02	1.4e-03	1.6e-04	1.4e-04	2.8e-04	2.1e-35
9467	AT5G08160.1	2e-50	1.20	1.05	1.10		3.05	5.3e-02	NA	NA	5.2e-01	4.7e-10
9505	AT1G43760.1	1e-52		1.10	1.34		1.38	3.4e-01	1.2e-01	3.4e-02	4.8e-01	4.5e-07
9508	AT1G43760.1	3e-34	4.11	3.93	4.22	3.33	5.22	3.3e-22	2.3e-21	2.9e-24	2.4e-14	3.2e-55
9509	AT1G43760.1	2e-20	1.22	1.44	1.72	1.32	3.07	9.1e-02	2.7e-02	4.3e-03	5.3e-02	5.3e-14
9537	AT5G45290.1	2e-22	1.19	1.52	1.47	1.25	3.30	1.1e-01	1.5e-02	2.2e-02	7.2e-02	5.1e-19
9554	AT5G01260.2	7e-41	-1.01	-1.10	-1.33	-1.62	-1.41	3.7e-02	1.1e-02	6.8e-04	1.1e-05	8.4e-07
9556	AT2G29970.1	1e-14	-1.18	-1.35			-1.45	7.5e-02	2.5e-02	2.8e-01	2.6e-01	2.0e-08
9582	AT1G72820.1	1e-51	-1.13		-1.01	-1.12	-3.35	9.0e-02	2.0e-01	1.6e-01	9.1e-02	9.4e-13
9592	AT5G32440.1	1e-34					2.47	4.7e-01	5.1e-01	5.4e-01	4.5e-01	2.1e-07
9657	AT3G09180.1	2e-30	1.56	1.67	1.50	1.89	3.01	1.5e-02	6.3e-03	2.2e-02	1.2e-03	1.9e-15
9658	AT3G09470.1	3e-81	1.40	1.08	1.12		1.27	3.5e-04	1.7e-02	1.2e-02	1.5e-01	3.6e-11
9660	AT5G16840.1	5e-80	1.91	2.04	2.01	2.20	4.21	1.1e-03	3.0e-04	4.3e-04	7.1e-05	1.6e-28
9672	AT5G55190.1	2e-16	2.12	1.42	1.27	1.47	1.74	5.1e-10	1.7e-04	1.2e-03	9.7e-05	2.5e-25
9746	AT2G27035.1	2e-18			1.11		1.72	3.1e-01	5.2e-01	1.3e-01	7.3e-01	3.5e-04
9749	AT3G55120.1	8e-70	4.93	5.59	5.59	4.62	7.04	1.1e-33	1.7e-44	2.3e-44	1.9e-29	7.0e-85
9752	AT3G09700.1	6e-19	-2.51	-2.79	-2.62	-2.16	-3.23	1.4e-08	1.3e-10	2.1e-09	3.6e-06	8.3e-41
9759	AT1G24020.1	3e-26	3.79	4.30	5.06	5.27	6.40	1.4e-18	2.4e-24	7.6e-34	2.5e-36	2.1e-62
9803	AT3G01160.1	5e-35	-1.28	-1.11	-1.44	-1.39	-1.43	4.0e-04	3.2e-03	3.2e-05	1.4e-04	1.7e-20
9812	AT5G12320.1	9e-24					-1.03	2.9e-01	4.8e-01	7.2e-01	5.3e-01	4.5e-04
9815	AT4G29090.1	2e-69					1.86	6.8e-01	5.6e-01	5.4e-01	7.4e-01	3.5e-04
9845	AT1G24020.1	7e-60				1.55	1.12	3.9e-02	2.7e-02	9.8e-03	2.0e-06	6.9e-04
9865			-1.02			-1.07	-1.12	4.5e-02	4.8e-02	1.2e-01	2.5e-02	3.7e-12
9866			1.14	1.19	1.03	1.19	2.83	1.2e-01	9.6e-02	2.0e-01	8.9e-02	8.7e-15
9868	AT3G07610.1	7e-144	-1.39	-1.52	-1.55	-1.38	-1.53	6.0e-10	4.4e-12	1.0e-12	9.8e-10	4.5e-65
9875	AT3G18730.1	2e-62	-1.93	-1.60	-1.28		-3.79	4.2e-04	6.9e-03	5.5e-02	2.8e-01	1.0e-15
9881			-1.24	-1.52	-1.13	-1.17	-1.62	3.4e-02	3.8e-03	6.5e-02	5.8e-02	1.1e-12
9900	AT5G02800.1	1e-83			1.44	1.09	1.35	1.6e-01	1.1e-01	4.6e-03	5.8e-02	3.1e-10
9911	AT5G60620.1	6e-51					1.94	2.4e-01	4.0e-01	3.3e-01	3.7e-01	1.8e-05
9922	AT4G29090.1	2e-63					1.93	3.1e-01	4.2e-01	4.1e-01	4.0e-01	1.8e-06
9933	AT4G36190.1	2e-37		-1.41		-1.13	-1.61	7.9e-01	3.5e-02	5.9e-01	1.4e-01	4.5e-05
9936	AT2G02800.1	0		1.25	1.28	1.72	1.50	3.3e-01	2.1e-02	1.5e-02	3.5e-04	1.8e-12
9955	AT4G05320.2	4e-63				-1.05	-2.35	8.4e-01	3.0e-01	1.9e-01	1.1e-01	2.5e-06
9962	AT4G12020.1	2e-16	-1.06	-1.23		-1.15	-1.18	2.0e-03	1.0e-04	1.0e-02	5.4e-04	3.7e-22
9984	AT5G55300.1	2e-11		-1.29	-1.22	-1.06	-2.76	2.7e-01	5.0e-02	8.0e-02	1.5e-01	6.7e-10
10022	AT1G73240.1	2e-12	1.22				1.14	3.4e-02	2.9e-01	3.5e-01	3.5e-01	1.5e-06
10023			1.27	1.18			1.16	3.0e-03	7.0e-03	9.7e-02	7.1e-02	2.0e-09
10047	AT5G35080.1	4e-21	-1.13	-1.43	-1.32	-1.46	-2.32	1.5e-01	3.1e-02	5.9e-02	2.8e-02	6.6e-11
10096	AT4G20380.2	1e-42					1.23	2.1e-01	2.5e-01	2.4e-01	4.2e-01	2.3e-07
10108	AT1G63450.1	1e-51				1.35	1.31	2.1e-01	5.7e-01	2.3e-01	3.5e-02	6.9e-06
10111	AT4G29090.1	8e-68	5.00	4.47	4.21	4.11	5.26	5.4e-44	1.2e-33	3.2e-31	2.2e-29	4.7e-104
10112	AT4G29090.1	2e-69					2.22	4.6e-01	7.3e-01	9.1e-01	8.8e-01	2.1e-05

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
10126	AT3G13110.1	6e-147					-1.53	7.1e-01	4.7e-01	4.4e-01	4.3e-01	6.8e-04
10137	AT3G58660.1	1e-42	1.34	1.40			2.13	5.5e-02	3.8e-02	2.7e-01	2.9e-01	4.7e-09
10189							1.75	4.3e-01	7.5e-01	5.9e-01	6.4e-01	7.1e-04
10220	AT1G02640.1	0		-1.07	-1.68	-1.61	-1.39	3.6e-01	1.2e-02	2.9e-06	1.2e-05	1.9e-12
10244	AT3G14770.1	6e-86				-1.23		4.1e-01	1.0e-02	3.7e-02	4.6e-04	9.8e-09
10251	AT2G35800.1	1e-90	1.51	1.95	1.79	1.25	1.95	3.0e-03	2.3e-05	9.5e-05	2.0e-02	5.7e-16
10282	AT1G50380.1	1e-38	-1.08		-1.14		-1.05	9.6e-02	3.5e-01	6.7e-02	9.6e-01	3.6e-04
10285	AT5G38840.1	1e-24		-1.44	-1.17	-1.28	-1.31	5.1e-02	3.4e-05	1.5e-03	4.2e-04	3.3e-16
10286	AT5G38840.1	7e-47	1.21	1.76	1.76	1.69	2.56	9.9e-02	3.0e-03	2.9e-03	5.3e-03	3.4e-07
10302	AT1G64160.1	4e-24	3.14	1.96	1.73	2.04	3.02	1.2e-10	4.0e-04	3.4e-03	2.5e-04	8.9e-12
10306	AT2G23200.1	7e-18	1.09				2.55	9.9e-02	2.9e-01	6.6e-01	2.0e-01	1.0e-07
10327	AT5G17680.1	2e-47	-2.38	-2.70	-2.71	-2.45	-4.74	7.0e-06	1.2e-07	9.7e-08	3.0e-06	1.2e-32
10331	AT5G05400.1	4e-45		-1.10	-1.22	-1.23	-4.25	6.9e-01	8.7e-02	4.2e-02	3.8e-02	5.6e-19
10332				-1.73	-1.49		-3.23	2.5e-01	2.4e-03	1.5e-02	2.8e-01	8.1e-12
10366	AT5G03260.1	1e-17	-1.55	-1.25	-1.11		-3.47	7.6e-03	5.5e-02	1.2e-01	2.0e-01	2.7e-13
10379	AT5G43960.1	3e-130				1.44		7.5e-02	2.1e-02	1.5e-02	1.9e-05	7.2e-03
10386			1.26	1.27	1.16	1.05	1.30	7.3e-04	5.6e-04	2.4e-03	9.2e-03	2.0e-17
10420	AT4G39090.1	2e-26	1.55	1.65	1.36	1.35	1.54	7.0e-07	7.4e-08	2.0e-05	1.5e-05	2.3e-13
10457	AT1G13340.1	2e-48		1.11			1.01	6.7e-01	9.9e-02	6.6e-01	2.3e-01	1.5e-04
10462	AT3G63130.1	2e-126	-1.96	-1.52	-1.59	-1.51	-2.28	2.0e-04	8.5e-03	4.8e-03	9.9e-03	1.5e-18
10512			-1.66	-1.58	-1.62	-1.54	-3.43	7.0e-03	1.2e-02	9.1e-03	1.5e-02	3.7e-19
10514	AT3G17860.1	3e-32		-1.30	-1.29	-1.17	-1.73	8.6e-01	6.6e-02	7.2e-02	1.2e-01	2.8e-05
10538	AT2G02390.3	2e-11	2.92	2.82	3.16	3.52	5.28	3.0e-09	1.0e-08	4.3e-11	9.3e-14	5.7e-38
10558	AT2G21830.1	5e-16	-1.04	-1.29			-1.22	9.9e-02	1.3e-02	1.4e-01	3.4e-01	2.9e-05
10568	AT2G05920.1	3e-148		1.95	1.14			9.0e-01	3.8e-09	2.6e-03	1.9e-01	4.0e-02
10593	AT1G74600.1	1e-77	-1.28				-1.47	5.3e-02	2.9e-01	2.6e-01	2.4e-01	7.5e-09
10619	AT3G09350.1	2e-148	-1.00				-2.19	2.0e-01	3.2e-01	3.9e-01	2.4e-01	1.1e-06
10620	AT3G09350.1	2e-81		1.11	1.09	1.23	2.37	3.5e-01	1.2e-01	1.3e-01	6.2e-02	1.9e-06
10622	AT4G39120.1	2e-69					1.54	2.9e-01	4.0e-01	2.9e-01	3.0e-01	2.6e-07
10623	AT5G43330.1	2e-91	-2.76	-2.87	-2.79	-2.93	-3.45	7.2e-12	5.6e-13	2.6e-12	2.5e-13	7.9e-69
10632	AT1G63050.1	1e-56	2.34	2.19	2.25	2.39	4.61	1.4e-05	6.2e-05	3.2e-05	8.2e-06	1.5e-27
10641	AT1G19870.1	6e-58			-1.12		-1.05	2.1e-04	1.1e-03	6.7e-06	1.8e-04	5.4e-20
10651	AT1G43760.1	2e-46	3.06	2.95	3.08	2.77	5.07	2.3e-10	1.1e-09	1.3e-10	2.1e-08	1.2e-37
10676	AT1G31860.1	3e-18	1.63	1.06		1.03	3.16	4.1e-03	1.4e-01	2.4e-01	1.5e-01	7.2e-11
10680	AT4G00630.1	1e-78	-1.04	-1.33	-1.20	-1.11	-4.02	1.4e-01	2.9e-02	6.3e-02	9.8e-02	5.1e-18
10689	AT4G14605.1	1e-11	-1.46	-1.10		-1.26	-2.65	1.9e-02	1.5e-01	5.6e-01	5.8e-02	1.0e-09
10716	AT1G03230.1	3e-69		-1.03	-1.70	-1.93	-1.64	6.5e-01	2.0e-01	3.8e-03	5.4e-04	9.2e-05
10718	AT2G33470.1	2e-109	1.56				1.17	3.8e-04	2.0e-01	3.4e-01	9.0e-02	5.2e-09
10729	AT5G20930.1	0	-4.06	-4.53	-4.05	-4.16	-5.45	1.4e-23	1.9e-30	4.5e-26	1.7e-25	7.9e-84
10759							-2.92	3.7e-01	1.6e-01	2.6e-01	4.1e-01	3.3e-09
10783			2.59	2.82	2.94	2.34	4.50	3.6e-07	1.1e-08	1.6e-09	9.3e-06	3.5e-31
10841	AT5G04590.1	0					1.22	3.6e-01	4.8e-01	7.5e-01	6.0e-01	4.2e-04
10869	AT4G27220.1	2e-55					-2.76	1.3e-01	5.7e-01	6.5e-01	6.3e-01	6.6e-08
10870	AT4G27190.1	3e-23					-3.60	6.7e-01	2.5e-01	1.1e-01	1.6e-01	2.5e-13
10901	AT5G24690.1	4e-115		1.03	1.13		2.02	2.8e-01	2.2e-01	1.4e-01	4.4e-01	1.8e-08
10931	AT2G38020.1	7e-57	-1.33	-1.15			-2.26	5.0e-02	1.3e-01	3.6e-01	2.8e-01	2.7e-08
10942	AT2G37710.1	2e-66					-2.23	8.3e-01	3.8e-01	4.5e-01	4.6e-01	2.3e-05
10953	AT1G73990.1	1e-25		-1.01			-1.59	5.5e-01	2.2e-01	7.3e-01	3.1e-01	2.0e-04
10960	AT2G37860.2	3e-15	-1.52	-1.92	-1.77	-1.83	-2.03	5.1e-04	5.0e-07	4.6e-06	2.9e-06	1.7e-22
10994	AT5G61040.1	4e-66	-1.79	-1.66	-1.54	-1.36	-3.10	2.6e-03	7.1e-03	1.7e-02	4.7e-02	1.1e-15
11012	AT4G17250.1	6e-14		1.18		1.53	1.83	4.8e-01	1.1e-01	3.8e-01	1.8e-02	1.5e-07
11013	AT5G47580.1	9e-48	-1.75	-1.31	-1.12		-2.30	3.3e-03	6.1e-02	1.6e-01	3.4e-01	1.8e-09
11047	AT5G12200.1	0	1.98	1.95	1.71	1.21	1.70	1.4e-06	1.2e-06	2.9e-05	9.4e-03	4.8e-07
11050	AT2G21170.1	3e-79	-1.50	-1.55	-1.51	-1.20	-3.89	1.5e-02	1.1e-02	1.5e-02	8.5e-02	6.9e-21

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
11058	AT5G07840.1	5e-21			-1.27	-1.06	-1.69	6.7e-01	3.4e-01	7.6e-02	1.8e-01	1.0e-05
11081	AT4G24830.1	2e-65					1.63	9.1e-01	5.7e-01	2.5e-01	3.1e-01	2.1e-05
11137	AT3G14470.1	2e-65					-2.79	2.9e-01	5.4e-01	4.9e-01	4.9e-01	4.0e-08
11138	AT3G14470.1	5e-101					-1.82	6.4e-01	5.0e-01	5.3e-01	4.6e-01	3.9e-04
11166	AT2G42840.1	1e-21	1.04	1.32	1.35	1.87	1.49	3.8e-02	2.9e-03	2.1e-03	2.4e-06	1.2e-08
11172				-1.14		-1.10	-1.85	2.8e-01	1.4e-01	4.7e-01	1.6e-01	2.4e-07
11180	AT4G30890.1	3e-20	-1.23	-1.73	-1.72	-1.46	-1.80	9.3e-03	2.2e-05	2.4e-05	8.2e-04	9.5e-25
11185	AT1G74790.1	0			-1.05	-1.07	-1.10	5.9e-02	3.0e-02	1.6e-02	1.2e-02	6.3e-06
11197			-1.16		-1.07	-1.38	-1.69	1.1e-01	2.5e-01	1.7e-01	3.2e-02	1.1e-09
11294	AT5G04750.1	2e-20	1.11				1.74	1.6e-01	6.1e-01	3.9e-01	3.5e-01	4.6e-06
11295			1.09	1.14	1.23	1.16	2.76	1.6e-01	1.3e-01	8.4e-02	1.1e-01	8.4e-16
11340	AT3G23050.1	3e-104		2.20	2.01	1.94	1.99	2.9e-01	9.8e-07	1.3e-05	5.6e-05	2.8e-11
11354	AT1G59900.1	8e-55				1.01	1.91	7.3e-01	3.3e-01	4.8e-01	1.9e-01	6.0e-06
11389			-3.81	-4.21	-3.55	-3.52	-5.71	1.4e-17	9.5e-22	8.3e-16	6.2e-15	1.3e-64
11391			-1.22	-1.15	-1.02	-1.04	-4.31	4.9e-02	7.4e-02	1.5e-01	1.3e-01	3.4e-20
11393			-3.74	-3.55	-3.42	-3.02	-5.64	1.1e-15	4.4e-14	4.1e-13	4.3e-10	6.7e-57
11396	AT1G11800.1	1e-30	1.05				1.29	1.9e-01	3.5e-01	7.8e-01	2.5e-01	4.9e-06
11419	AT3G59480.1	4e-143	-1.20				-1.06	1.4e-03	3.4e-02	1.9e-02	3.7e-02	6.1e-10
11431	AT5G25350.1	0		-1.19	-1.46	-1.93	-1.43	9.1e-01	1.6e-02	1.0e-03	1.7e-06	3.7e-05
11432	AT4G38670.1	1e-16					2.43	1.6e-01	NA	NA	3.1e-01	3.0e-06
11471	AT1G56580.1	2e-18					-1.84	6.3e-01	3.8e-01	5.8e-01	4.9e-01	2.7e-04
11481	AT1G52600.1	4e-31	-1.70	-1.77	-1.45	-2.10	-2.25	1.8e-03	6.5e-04	1.0e-02	3.7e-05	2.7e-16
11491			-2.25	-2.51	-2.34	-1.72	-4.41	3.4e-05	1.8e-06	1.4e-05	4.5e-03	2.2e-24
11498	AT1G77130.1	8e-142	-1.06				-1.02	4.5e-02	1.1e-01	3.4e-01	1.1e-01	5.0e-08
11529	AT4G29040.1	0					-1.37	3.7e-01	3.9e-01	5.7e-01	5.2e-01	3.6e-04
11531	AT1G30570.1	0		-1.19	-1.06	-1.24	-1.18	1.8e-01	7.7e-03	2.6e-02	8.5e-03	1.7e-07
11546	AT4G27720.1	3e-34					1.94	5.9e-01	5.8e-01	5.7e-01	6.1e-01	4.2e-05
11554	AT1G32340.1	0	-1.16	-1.17	-1.22	-1.02	-1.60	9.6e-02	9.1e-02	6.9e-02	1.7e-01	1.1e-09
11599	AT5G39710.1	2e-29	-1.11	-1.74	-1.23	-1.19	-2.40	1.6e-01	3.9e-03	9.1e-02	1.1e-01	5.8e-11
11601	AT5G51200.1	3e-50	-1.52	-1.44	-1.35	-1.35	-1.91	8.3e-03	1.4e-02	2.8e-02	2.8e-02	1.3e-13
11622	AT2G25220.1	6e-126				-1.66	-1.20	5.8e-01	8.7e-01	2.5e-01	2.8e-03	1.2e-04
11673	AT5G57290.1	9e-18	-1.02		-1.07	-1.31	-1.48	1.9e-01	2.0e-01	1.5e-01	4.3e-02	3.3e-06
11712	AT4G02930.1	2e-58					2.65	2.6e-01	5.0e-01	2.8e-01	3.3e-01	2.2e-08
11726	AT4G17420.1	1e-55	1.01	1.54	1.78	1.73	3.34	2.2e-01	1.4e-02	2.4e-03	3.5e-03	7.9e-16
11737	AT2G15430.1	7e-35	-1.31	-1.19	-1.64	-1.18	-1.69	2.2e-02	4.8e-02	1.6e-03	5.1e-02	1.2e-12
11779	AT5G23740.1	6e-12	1.12	1.50	1.70	1.29	3.48	1.4e-01	1.6e-02	3.8e-03	5.1e-02	4.2e-15
11793	AT5G45230.1	1e-55	1.96	1.98	1.88	1.79	3.87	6.6e-04	5.2e-04	1.2e-03	2.8e-03	8.0e-22
11808	AT5G23960.1	2e-101	-1.34	-1.87	-1.46	-1.01	-3.28	4.5e-02	1.0e-03	2.2e-02	2.0e-01	2.1e-13
11850	AT5G06860.1	4e-54			-1.13	-1.52	-1.65	3.2e-01	3.5e-01	1.3e-01	1.5e-02	1.4e-06
11861	AT4G17615.1	6e-52	-2.08	-2.02	-1.69	-1.66	-3.89	2.2e-04	3.6e-04	5.7e-03	7.3e-03	1.8e-25
11882	AT1G73880.1	2e-52					-2.11	9.5e-01	5.5e-01	3.3e-01	2.7e-01	7.3e-05
11904	AT5G12080.1	0					1.14	2.8e-01	2.2e-01	4.7e-01	1.8e-01	1.3e-06
11925	AT1G07030.1	2e-144					-2.94	3.4e-01	5.7e-01	5.1e-01	4.9e-01	6.8e-09
11945	AT3G14470.1	2e-38		-1.17	-1.06		-2.92	3.1e-01	7.6e-02	1.3e-01	3.3e-01	8.2e-10
12010	AT5G45200.1	7e-70					-2.96	1.6e-01	2.8e-01	2.7e-01	4.0e-01	1.3e-09
12026	AT2G30660.1	8e-79	-1.06	-1.01	-1.14	-1.09	-1.74	2.0e-01	2.3e-01	1.4e-01	1.7e-01	1.5e-07
12048	AT5G65560.1	9e-69	-1.12				-1.43	1.6e-01	4.3e-01	5.7e-01	4.3e-01	2.0e-04
12067	AT3G16730.1	6e-83	-1.48	-1.94	-1.69	-1.52	-3.47	2.4e-02	7.0e-04	5.4e-03	1.8e-02	5.6e-19
12071	AT1G04950.1	2e-14	-1.17	-1.15	-1.09		-2.73	9.2e-02	1.0e-01	1.4e-01	4.5e-01	1.2e-10
12089	AT2G38430.1	4e-47					1.68	7.1e-01	5.3e-01	5.4e-01	2.0e-01	4.6e-04
12090	AT3G54310.1	6e-50					-2.26	3.2e-01	5.2e-01	4.2e-01	3.0e-01	5.3e-06
12135	AT1G15570.1	2e-79	4.48	4.33	4.01	4.12	6.28	4.0e-27	2.2e-25	6.4e-22	1.7e-22	3.8e-65
12138	AT3G26040.1	4e-57	1.76	1.82	1.48	1.41	2.01	6.1e-04	2.8e-04	6.6e-03	1.2e-02	2.4e-14
12146	AT1G18340.1	1e-24	2.40	2.16	1.89	1.59	4.22	7.0e-06	8.4e-05	1.2e-03	1.1e-02	1.3e-21

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
12195	AT3G16000.1	7e-53	1.43	1.30	1.05	1.01	1.56	9.5e-03	2.6e-02	1.1e-01	1.5e-01	1.9e-11
12213	AT1G60690.1	2e-107		1.10	1.25	1.23	1.66	7.4e-01	1.6e-01	8.2e-02	8.5e-02	1.4e-06
12214	AT1G60710.1	3e-106	-1.04	-1.01		-1.06	-1.52	2.0e-01	2.2e-01	3.5e-01	1.7e-01	4.4e-07
12242	AT3G07530.1	6e-65	-1.13	-1.33			-1.31	7.3e-02	1.7e-02	3.6e-01	2.4e-01	1.1e-08
12249	AT4G26680.1	3e-144		1.22		1.26	1.13	6.8e-01	3.0e-02	4.9e-01	2.3e-02	1.2e-06
12256	AT5G42080.1	3e-66	-1.36	-1.14	-1.14	-1.20	-4.34	2.4e-02	9.0e-02	8.8e-02	6.1e-02	2.5e-21
12269	AT1G80600.1	9e-144	3.69	3.11	3.19	2.98	4.93	5.5e-16	3.3e-11	6.6e-12	2.9e-10	4.4e-48
12270	AT1G80600.1	0	-1.06					7.9e-08	1.3e-04	3.9e-06	2.2e-04	8.4e-19
12354	AT3G27460.1	2e-28					2.40	4.4e-01	NA	NA	4.2e-01	4.1e-06
12365	AT4G23810.1	1e-38					-1.83	4.6e-01	3.3e-01	5.1e-01	4.1e-01	9.9e-05
12438			-5.00	-4.26	-4.97	-4.85	-5.93	5.6e-41	2.6e-33	1.1e-42	1.0e-38	2.1e-119
12444	AT3G22750.1	1e-79	-1.48	-1.69	-1.35	-1.11	-3.07	2.1e-02	5.4e-03	4.9e-02	1.4e-01	6.2e-14
12463	AT3G11710.1	9e-76		1.40	1.42	1.33	1.65	4.3e-01	3.5e-02	3.3e-02	5.2e-02	1.0e-04
12472	AT2G40060.1	2e-32	-1.16				-1.02	1.9e-02	3.1e-01	7.6e-02	2.3e-01	4.8e-06
12479	AT1G06950.1	2e-87		-1.07			-2.07	2.7e-01	1.7e-01	4.5e-01	2.7e-01	1.2e-06
12494	AT4G14620.1	1e-24	1.08	1.59	1.08	1.07	2.82	1.6e-01	8.7e-03	1.6e-01	1.6e-01	2.1e-10
12498	AT3G19000.1	5e-151	-1.51	-1.26	-1.27	-1.21	-1.31	1.1e-03	6.0e-03	4.1e-03	7.1e-03	3.6e-04
12502	AT5G34850.1	3e-101					-2.29	7.4e-01	2.4e-01	1.7e-01	2.8e-01	2.6e-06
12514	AT2G01050.1	4e-51	1.05	1.02				1.6e-04	1.7e-04	8.3e-04	9.8e-03	5.8e-13
12526	AT1G13570.1	5e-27	-2.34	-2.29	-2.17	-2.33	-4.59	1.5e-05	2.6e-05	8.9e-05	1.9e-05	1.8e-31
12527	AT1G13570.1	8e-26	-1.71	-1.37	-1.23	-1.16	-3.45	2.9e-03	3.3e-02	7.4e-02	9.8e-02	1.3e-14
12532	AT2G19730.1	6e-51					-2.15	5.6e-01	4.8e-01	5.9e-01	6.3e-01	4.6e-05
12553	AT5G19840.1	2e-42	-1.15			-1.10	-1.94	1.3e-01	5.3e-01	2.7e-01	1.6e-01	8.1e-07
12554	AT5G19840.1	1e-75					-2.41	3.6e-01	2.5e-01	2.0e-01	3.8e-01	3.4e-07
12587			-1.42	-1.25		-1.04	-1.86	3.3e-02	8.3e-02	5.9e-01	2.0e-01	5.2e-07
12614	AT1G17840.1	2e-76					-2.34	5.6e-01	2.2e-01	1.7e-01	2.9e-01	1.1e-06
12624	AT3G01790.1	8e-85	-1.20		-1.06		-1.46	8.1e-02	2.0e-01	1.5e-01	2.7e-01	5.7e-08
12647	AT1G22940.1	4e-140	-1.14	-1.05	-1.06		-1.39	8.0e-02	1.2e-01	1.2e-01	2.3e-01	7.4e-10
12660	AT1G54310.2	2e-74	2.53	2.11	1.72	1.62	3.61	1.6e-06	1.5e-04	4.4e-03	9.7e-03	1.2e-21
12666	AT4G14605.1	2e-112	-1.77	-1.59	-1.30	-1.25	-4.06	1.9e-03	7.7e-03	5.1e-02	6.2e-02	8.1e-19
12680	AT4G34020.1	5e-161	-1.74	-1.71	-1.82	-2.25	-2.22	6.8e-05	8.2e-05	1.7e-05	5.4e-08	5.3e-31
12705	AT5G05780.1	7e-71	-1.21					6.0e-04	1.6e-02	9.4e-02	1.5e-01	1.5e-12
12706	AT1G59600.1	8e-36	-1.73	-1.89	-2.10	-1.65	-3.86	3.9e-03	1.1e-03	1.7e-04	7.9e-03	7.1e-21
12711					1.13		2.08	3.9e-01	5.6e-01	1.1e-01	4.2e-01	4.3e-06
12719	AT1G07530.1	4e-62	-1.43	-1.30	-1.40	-1.36	-3.93	2.2e-02	4.7e-02	2.8e-02	3.3e-02	7.9e-20
12766	AT2G35680.1	4e-77	-2.90	-2.84	-3.12	-2.59	-4.10	5.5e-10	1.4e-09	1.2e-11	4.9e-08	2.4e-50
12864	AT5G12480.1	5e-34	-3.00	-3.12	-3.06	-3.19	-4.82	1.6e-10	2.4e-11	5.0e-11	1.1e-11	1.9e-45
12881	AT1G65320.1	1e-178			-1.04	-1.18		4.9e-01	1.3e-01	7.0e-03	8.5e-04	4.3e-05
12911	AT4G11610.1	0		2.46	1.40	1.28	1.98	8.0e-01	3.1e-06	3.6e-02	6.9e-02	5.3e-06
12916	AT3G21420.1	1e-176				-1.01	-1.01	4.5e-01	2.2e-01	1.5e-01	8.6e-02	6.9e-07
12921	AT1G12290.1	2e-27		-1.11			-1.23	4.7e-01	1.5e-01	5.1e-01	5.1e-01	1.4e-04
12932	AT3G28720.1	1e-26				1.58	1.17	4.3e-01	4.8e-01	4.2e-01	7.4e-03	3.4e-04
12972	AT1G20410.1	3e-39	1.96	1.79	1.29	1.41	3.42	5.9e-04	2.5e-03	6.7e-02	3.3e-02	1.3e-15
13037	AT3G53690.1	2e-74	1.46	1.81	1.42	1.60	2.56	2.5e-02	2.1e-03	3.2e-02	1.0e-02	7.5e-18
13038	AT3G53690.1	1e-42	2.92	2.82	2.61	2.94	4.55	2.1e-09	6.6e-09	1.2e-07	1.5e-09	8.3e-40
13043	AT5G13510.1	7e-15	2.22	1.50	1.27	1.27	3.77	3.5e-05	1.6e-02	6.4e-02	6.0e-02	7.9e-16
13052	AT3G11710.1	8e-107		1.51	1.55	1.04	1.67	2.5e-01	1.1e-02	8.4e-03	1.6e-01	1.9e-08
13054	AT5G15210.1	4e-30				1.38		9.2e-01	9.4e-01	9.5e-01	7.4e-04	9.2e-01
13073	AT5G40550.1	2e-22					2.13	NA	NA	NA	NA	6.0e-05
13097	AT2G31270.1	4e-21	2.88	2.73	2.79	3.01	3.48	1.6e-13	4.3e-12	7.1e-13	4.4e-14	3.9e-80
13168	AT3G56900.1	6e-93		1.02			2.44	2.3e-01	1.6e-01	1.9e-01	1.8e-01	1.2e-06
13174	AT3G12110.1	4e-115					-1.92	4.9e-01	6.5e-01	5.8e-01	5.0e-01	6.9e-05
13198	AT2G21050.1	3e-152				1.54		4.8e-01	4.0e-01	1.0e-01	4.7e-04	7.8e-02
13213	AT4G37980.1	3e-17	-1.48	-1.21			-1.04	1.6e-03	1.3e-02	5.1e-01	5.4e-01	5.2e-06

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
13286	AT5G66230.1	4e-23	-3.89	-3.70	-3.72	-3.38	-6.16	2.9e-17	1.3e-15	8.3e-16	8.5e-13	2.1e-56
13314			1.10	1.19	1.26		1.72	1.6e-01	1.1e-01	7.4e-02	5.8e-01	1.4e-07
13329	AT1G75170.1	3e-120			-1.07	-1.15	-1.42	2.8e-01	2.0e-01	1.5e-01	9.9e-02	7.6e-07
13334	AT1G11580.1	9e-176		-1.12	-1.93	-2.67	-1.92	8.0e-01	1.4e-01	7.0e-04	2.1e-07	3.4e-04
13418	AT2G27230.1	7e-71	4.48	4.03	4.05	3.91	6.18	4.4e-27	1.0e-21	5.4e-22	4.9e-20	5.6e-59
13520	AT2G01050.1	2e-47	1.38	1.95	1.81	1.87	3.00	4.1e-02	5.9e-04	2.1e-03	1.2e-03	7.9e-10
13532	AT5G12470.1	8e-137	1.36	1.46	1.48	1.74	2.24	3.9e-02	2.2e-02	2.0e-02	3.0e-03	1.4e-13
13540							-1.86	7.1e-01	NA	NA	7.3e-01	6.4e-04
13554	AT3G05030.1	0	-1.44	-1.28	-1.03	-1.30	-1.29	1.0e-05	3.1e-05	1.8e-03	3.0e-05	2.4e-09
13590	AT5G36930.1	3e-55	2.33	2.08	2.32	1.96	4.31	1.6e-05	1.8e-04	1.6e-05	6.4e-04	1.2e-24
13606	AT4G02180.1	6e-24					-2.66	5.9e-01	4.1e-01	5.3e-01	6.8e-01	2.2e-07
13611	AT5G34850.1	4e-75	-1.86	-1.52	-1.38	-1.34	-3.75	1.0e-03	1.4e-02	3.5e-02	4.3e-02	1.2e-17
13613	AT5G45130.1	3e-20	2.97	3.20	3.57	2.94	5.05	5.0e-10	6.4e-12	6.0e-15	7.1e-10	1.8e-42
13638	AT4G30840.1	7e-11	1.61	1.56	1.68	1.77	2.52	7.2e-03	1.1e-02	4.4e-03	2.7e-03	3.3e-15
13656	AT5G55600.1	4e-16	-1.05				-1.66	2.0e-01	2.5e-01	5.6e-01	6.5e-01	6.6e-05
13657	AT5G55600.1	2e-16	1.39	1.68	1.97	1.28	3.55	3.6e-02	5.3e-03	5.0e-04	6.3e-02	2.2e-16
13699	AT2G22840.1	7e-35	-2.61	-2.51	-2.28	-1.81	-4.56	7.2e-07	2.2e-06	2.9e-05	2.5e-03	5.4e-33
13705	AT2G33430.1	8e-49				-1.10	-1.00	5.4e-03	1.1e-02	1.6e-03	3.1e-04	7.5e-09
13721	AT2G18280.1	5e-22		-1.33	-1.23		-3.48	4.1e-01	2.6e-02	5.2e-02	1.5e-01	3.2e-13
13733	AT3G27570.1	2e-68					-1.44	3.9e-01	6.8e-01	6.2e-01	3.8e-01	9.0e-04
13739	AT3G57280.1	8e-22					1.84	6.7e-01	6.6e-01	7.0e-01	5.6e-01	7.3e-04
13790	AT4G17720.1	3e-13			-1.11		-2.82	5.1e-01	1.8e-01	9.3e-02	1.7e-01	8.4e-09
13832	AT5G19440.1	4e-154	1.06	1.35	1.33	1.13	1.86	1.9e-01	4.5e-02	5.3e-02	1.3e-01	2.5e-08
13861	AT2G24280.1	1e-59	-1.31	-1.28	-1.29	-1.61	-4.10	4.4e-02	5.2e-02	4.9e-02	5.8e-03	5.6e-20
13887	AT5G02130.1	4e-35	-1.04	-1.14			-3.38	1.3e-01	7.6e-02	1.9e-01	2.5e-01	1.8e-12
13906	AT1G51560.1	4e-70	1.00		1.11		1.42	2.1e-01	3.2e-01	1.2e-01	2.0e-01	5.9e-08
13953	AT4G17616.1	1e-63	1.25	1.47	1.35		2.50	6.3e-02	1.7e-02	3.6e-02	8.8e-01	1.7e-07
14043	AT1G70060.1	0	-1.81	-2.28	-2.17	-2.94	-3.48	1.7e-03	1.5e-05	4.6e-05	3.4e-09	2.8e-26
14056	AT4G29090.1	1e-76	6.92	6.33	6.28	6.30	8.68	3.1e-76	2.0e-62	6.7e-62	1.5e-61	1.2e-141
14080			-1.82	-1.45	-2.35	-3.37	-2.37	9.2e-08	1.4e-04	4.8e-12	3.0e-23	3.8e-16
14082	AT1G72340.1	1e-74	-2.02	-1.86	-1.85	-1.90	-4.10	3.8e-04	1.5e-03	1.7e-03	1.1e-03	6.4e-25
14109	AT4G27190.1	2e-39					-2.05	9.9e-01	2.7e-01	2.8e-01	4.8e-01	1.3e-04
14117	AT1G56290.1	4e-50	-1.45		-1.14	-1.39	-1.57	8.9e-03	2.3e-01	6.9e-02	1.5e-02	3.7e-12
14134	AT4G36440.1	6e-26					-1.87	8.7e-01	NA	NA	6.1e-01	4.7e-04
14145	AT3G18420.1	1e-95			1.01		1.98	9.6e-01	2.8e-01	1.2e-01	4.7e-01	1.5e-04
14159	AT5G63020.1	3e-140					1.73	5.8e-01	5.1e-01	6.8e-01	3.1e-01	5.6e-04
14208				-1.10	-1.15	-1.01	-2.51	4.8e-01	1.2e-01	9.9e-02	1.8e-01	6.4e-08
14258	AT1G75220.1	3e-38					-2.28	5.4e-01	4.0e-01	7.5e-01	4.9e-01	1.5e-05
14282	AT3G54470.1	5e-24	1.06		1.11	1.16	1.21	2.1e-02	4.4e-02	1.5e-02	1.2e-02	3.5e-11
14309					-1.33		-1.49	4.7e-01	2.9e-01	5.2e-02	3.3e-01	1.3e-05
14310			2.96	3.07	2.84	2.55	5.00	3.4e-09	5.9e-10	1.5e-08	9.7e-07	9.8e-41
14326	AT3G01590.2	2e-151				-1.43		1.0e+00	4.5e-01	6.3e-02	4.5e-07	1.4e-02
14341	AT5G38300.1	4e-20					1.56	4.6e-01	2.9e-01	3.3e-01	6.0e-01	3.2e-04
14354	AT5G58560.1	5e-77	-2.30	-1.42	-1.85	-1.89	-2.42	2.1e-06	1.3e-02	3.0e-04	3.0e-04	7.3e-19
14363	AT3G09850.1	9e-35	-1.46				-1.41	1.7e-02	3.1e-01	3.3e-01	3.0e-01	6.9e-07
14381	AT3G57560.1	3e-19	1.30	1.64	1.65	1.90	1.94	2.2e-02	1.7e-03	1.5e-03	1.4e-04	1.7e-11
14403	AT5G45200.1	7e-44					-2.39	4.9e-01	6.0e-01	4.5e-01	6.5e-01	4.8e-06
14416	AT2G01850.1	8e-33					2.11	5.5e-01	NA	NA	3.5e-01	3.5e-05
14458	AT2G30480.2	2e-11	-1.43	-1.13	-1.18		-2.84	2.3e-02	1.3e-01	9.8e-02	2.5e-01	4.4e-11
14464	AT3G63530.1	5e-50	-1.71	-1.84	-1.49	-1.34	-2.02	7.4e-04	2.2e-04	4.8e-03	1.9e-02	2.5e-16
14525			-3.46	-3.25	-3.26	-3.16	-5.52	1.0e-13	4.4e-12	4.0e-12	2.9e-11	7.2e-44
14533			-1.50	-1.66	-1.67	-1.18	-3.72	1.5e-02	5.3e-03	4.9e-03	9.6e-02	4.2e-16
14540	AT3G05740.1	0	-1.25	-1.45	-1.46	-1.23	-2.69	8.6e-02	2.8e-02	2.6e-02	8.6e-02	1.9e-12
14573	AT3G18480.1	1e-77	1.42	1.87	1.50	1.24	2.04	1.7e-02	3.2e-04	7.7e-03	5.4e-02	5.3e-14

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
14575	AT2G01940.1	2e-156		-1.34	-1.82	-1.29	-1.15	6.3e-01	9.1e-03	8.7e-05	1.7e-02	4.2e-03
14587	AT5G47500.1	3e-96	3.80	3.02	2.56	1.90	2.97	5.5e-25	3.5e-13	3.9e-09	2.3e-04	7.4e-11
14634							1.86	NA	NA	NA	NA	6.2e-04
14647	AT5G66230.1	4e-23	1.15					8.4e-06	1.2e-03	1.8e-01	3.0e-02	3.2e-13
14651	AT3G57290.1	8e-31		-1.04			-2.97	2.7e-01	9.3e-02	4.0e-01	5.1e-01	2.5e-09
14652	AT4G31080.1	7e-30	-1.45	-1.58	-1.55	-1.12	-3.71	2.0e-02	8.7e-03	1.1e-02	1.2e-01	7.9e-16
14747	AT3G61600.1	3e-39	-1.10			-1.22	-1.24	3.5e-02	1.3e-01	7.3e-02	1.6e-02	3.4e-13
14762	AT3G22170.1	4e-70	-2.79	-2.80	-2.86	-2.68	-5.29	4.1e-08	3.7e-08	1.4e-08	1.9e-07	1.2e-38
14808	AT1G72010.1	4e-38			-1.15	-1.73	-1.41	7.0e-01	8.0e-01	1.1e-01	2.7e-03	2.3e-04
14810	AT5G62710.1	1e-51	-2.47	-2.47	-2.35	-2.02	-4.41	3.5e-06	3.1e-06	1.3e-05	4.1e-04	7.1e-32
14813	AT3G42170.1	5e-23					-2.33	1.9e-01	6.0e-01	8.4e-01	7.2e-01	8.7e-06
14851			1.21	1.10	1.06		1.33	3.0e-02	6.7e-02	8.3e-02	2.4e-01	8.9e-11
14959	AT1G27970.1	2e-12	2.53	2.84	2.78	2.94	2.06	1.8e-06	3.7e-08	7.8e-08	9.3e-09	1.0e-04
14965	AT2G43360.1	7e-119					-1.15	2.6e-01	3.9e-01	2.2e-01	4.5e-01	3.9e-05
15002	AT1G19430.1	4e-85	-1.58	-1.73	-1.48	-1.79	-3.96	1.0e-02	3.6e-03	2.1e-02	2.1e-03	1.3e-18
15037	AT3G61760.1	0					-1.95	7.1e-01	5.2e-01	6.5e-01	7.0e-01	3.2e-04
15067	AT1G61190.1	3e-38	-1.68	-1.56	-1.49	-1.43	-2.14	3.4e-03	7.3e-03	1.2e-02	2.0e-02	1.0e-15
15068			-4.02	-4.15	-4.06	-3.92	-6.12	9.9e-22	3.0e-23	2.4e-22	2.2e-20	1.1e-58
15106	AT5G20480.1	4e-29	-1.02	-1.12			-2.29	1.9e-01	1.2e-01	5.7e-01	2.8e-01	3.7e-07
15154			1.95	2.21	1.90	2.00	2.24	5.9e-09	3.2e-11	1.1e-08	2.1e-09	9.7e-60
15169	AT3G12200.1	2e-24					1.93	3.9e-01	5.1e-01	6.8e-01	5.9e-01	7.5e-05
15197	AT5G54160.1	2e-154		1.36	1.27		1.04	4.9e-01	8.3e-06	6.1e-05	4.2e-02	3.5e-06
15198	AT5G27350.1	1e-139	-1.01	-1.34	-1.09	-1.09	-1.34	9.3e-02	5.4e-03	3.2e-02	3.8e-02	1.7e-09
15199	AT5G19330.1	6e-103	-1.60	-1.66	-1.70	-1.32	-3.38	9.7e-03	7.0e-03	4.9e-03	5.2e-02	1.9e-16
15206	AT2G01410.1	4e-36					-3.09	2.9e-01	4.3e-01	1.8e-01	2.4e-01	4.0e-10
15227	AT5G03040.1	6e-85					-1.04	6.5e-02	1.2e-01	9.0e-02	1.1e-01	1.0e-11
15231	AT3G49400.1	3e-40	-1.86	-1.99	-1.78	-1.72	-3.99	1.5e-03	4.5e-04	2.9e-03	4.3e-03	6.4e-22
15288	AT4G23520.1	7e-18	-1.24				-1.96	5.4e-02	5.6e-01	6.3e-01	4.4e-01	1.2e-04
15305	AT4G34190.1	5e-34	1.24	1.27			1.10	1.5e-03	2.3e-03	4.9e-02	5.4e-01	8.1e-06
15329	AT1G48280.1	5e-20	1.18		1.09		1.88	9.3e-02	5.4e-01	1.4e-01	6.4e-01	1.2e-04
15368	AT5G07620.1	1e-56	1.63	1.52	1.50	1.84	3.91	7.3e-03	1.5e-02	1.7e-02	1.4e-03	5.3e-18
15376			1.96	1.64	1.72	1.82	3.56	7.1e-04	8.1e-03	4.7e-03	2.2e-03	5.3e-20
15385	AT4G15450.1	1e-11	-1.34	-1.26		-1.07	-2.47	4.9e-02	7.7e-02	2.4e-01	1.7e-01	3.4e-10
15393	AT4G27190.1	4e-30					-3.17	3.8e-01	4.9e-01	4.8e-01	3.1e-01	2.6e-10
15394	AT4G27190.1	7e-25	-1.01				-3.34	1.1e-01	2.4e-01	3.4e-01	4.0e-01	1.0e-11
15396	AT1G13570.1	2e-31				-1.11	-1.04	1.5e-01	8.2e-01	1.8e-01	5.4e-02	6.7e-05
15420	AT2G02850.1	9e-36			-1.35	-1.49	-1.09	9.1e-01	1.5e-01	1.3e-02	6.0e-03	7.7e-04
15421	AT2G02850.1	1e-41					-1.92	2.3e-01	5.9e-01	2.9e-01	4.0e-01	1.5e-04
15434	AT4G27220.1	4e-79		-1.12	-1.19		-3.48	4.0e-01	7.8e-02	5.2e-02	2.2e-01	6.1e-13
15435	AT4G27220.1	4e-75	-4.01	-4.05	-3.77	-3.41	-5.98	6.0e-20	1.9e-20	1.3e-17	5.4e-14	2.2e-53
15436	AT4G10780.1	1e-55	-2.14	-2.15	-1.58	-2.15	-4.22	1.1e-04	1.0e-04	1.2e-02	1.0e-04	1.2e-21
15454	AT5G59440.2	1e-19					-2.25	3.6e-01	NA	NA	1.9e-01	9.8e-06
15480	AT1G77670.1	3e-39	-1.31				-1.18	4.6e-02	2.7e-01	4.2e-01	9.6e-01	8.0e-04
15501	AT4G21105.1	1e-19	-1.01	-1.07	-1.27	-1.15	-1.24	1.0e-02	5.0e-03	3.2e-04	2.1e-03	1.7e-18
15540	AT2G33290.1	1e-45	-1.80	-1.55		-1.08	-2.57	2.4e-03	1.4e-02	4.0e-01	1.6e-01	6.4e-10
15554	AT3G14360.1	3e-173	1.10				1.82	1.1e-01	NA	NA	7.0e-01	2.0e-04
15568			-4.63	-4.61	-4.56	-4.40	-6.97	2.0e-27	2.2e-27	8.1e-27	1.7e-24	1.2e-79
15582	AT3G52155.1	4e-72		1.22	1.35	1.17	3.44	2.1e-01	7.3e-02	3.7e-02	8.8e-02	1.3e-20
15583	AT3G14470.1	3e-26	-1.05				-3.13	9.7e-02	1.8e-01	4.2e-01	3.6e-01	1.9e-10
15611	AT3G61170.1	2e-128			1.11		1.14	3.4e-01	2.4e-01	9.4e-02	4.5e-01	5.9e-06
15616	AT2G25140.1	7e-143		1.39	2.00	1.47	1.78	2.2e-01	1.4e-02	5.7e-05	1.0e-02	6.7e-11
15624	AT1G52600.1	4e-49		1.25			1.35	4.5e-01	5.5e-02	2.8e-01	2.0e-01	3.4e-08
15626	AT5G13640.1	4e-132	-1.77	-1.15	-1.35	-1.85	-1.75	4.1e-05	2.0e-02	3.1e-03	2.6e-05	9.1e-18
15630	AT1G80530.1	4e-15	1.49	1.36	1.26		1.84	1.6e-02	3.4e-02	6.4e-02	2.5e-01	2.1e-11

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
15637	AT1G78700.1	2e-12		-1.19		-1.05	-1.26	3.3e-01	8.3e-02	4.1e-01	1.7e-01	4.1e-04
15644	AT4G24000.1	4e-156	-1.16					6.5e-05	2.4e-01	2.3e-01	7.4e-01	4.6e-03
15702	AT5G18580.1	1e-116			1.03	1.02		3.2e-03	2.0e-05	1.1e-05	2.1e-05	3.3e-25
15720				-1.15	-1.44	-1.29	-2.75	3.3e-01	1.2e-01	2.5e-02	5.6e-02	4.7e-11
15742	AT3G57000.1	8e-20			1.23		1.13	1.8e-01	3.0e-01	3.3e-02	2.5e-01	2.3e-04
15743	AT3G57000.1	2e-20					-2.81	2.0e-01	4.3e-01	5.6e-01	6.9e-01	3.6e-08
15755			1.97	1.79	1.57	1.51	3.75	5.6e-04	2.6e-03	1.3e-02	1.9e-02	2.0e-21
15774	AT1G25580.1	2e-129	6.91	6.59	6.56	6.21	8.50	9.0e-92	1.8e-82	1.4e-82	2.3e-72	3.4e-137
15815			-1.72	-1.77	-1.70	-1.42	-4.57	3.3e-03	2.2e-03	3.8e-03	2.6e-02	9.6e-25
15837	AT1G22970.1	4e-67	1.02			1.04	1.65	2.3e-01	2.5e-01	2.6e-01	2.0e-01	1.2e-06
15866	AT3G07040.1	4e-91		-1.45			-1.64	3.4e-01	2.5e-02	2.6e-01	2.5e-01	3.4e-07
15873	AT3G14470.1	7e-115	-1.14				-2.50	6.4e-02	NA	NA	6.0e-01	5.9e-07
15909	AT3G56160.1	3e-27	-1.10				-1.75	1.1e-01	4.9e-01	6.2e-01	8.6e-01	2.6e-04
15937						1.24	2.29	5.4e-01	3.9e-01	2.6e-01	6.5e-02	4.1e-08
15942	AT2G14050.1	8e-22					-1.10	4.9e-01	4.6e-01	7.5e-01	5.3e-01	7.5e-04
15943	AT2G02220.1	1e-139			-1.11	-1.45	-1.31	5.1e-01	9.3e-01	1.3e-01	2.2e-02	3.3e-04
16021			-3.30	-2.05	-1.79	-1.08	-3.45	4.0e-11	2.8e-04	2.8e-03	1.8e-01	3.2e-13
16097	AT2G41670.1	2e-73	-1.73	-1.65	-1.72	-1.56	-4.18	3.3e-03	6.4e-03	3.7e-03	1.1e-02	6.4e-21
16098	AT2G41670.1	1e-63					1.96	6.7e-01	6.2e-01	5.5e-01	7.2e-01	5.5e-05
16138	AT2G01050.1	4e-45	6.02	6.29	6.38	6.30	7.69	6.6e-72	2.3e-76	2.5e-78	6.5e-73	4.4e-192
16152	AT4G34020.1	7e-59	1.23				2.29	5.6e-02	3.1e-01	5.4e-01	5.4e-01	1.3e-06
16174	AT2G27950.1	3e-21		-1.03			-1.03	4.7e-02	1.7e-02	5.2e-02	9.7e-02	7.7e-09
16192	AT5G16960.1	1e-41	-1.40	-1.06	-1.81	-2.42	-2.37	2.5e-02	1.6e-01	1.1e-03	1.7e-06	7.6e-13
16210			1.89	1.62	1.63	1.96	4.01	1.1e-03	8.2e-03	7.9e-03	5.5e-04	2.9e-19
16227	AT2G47000.1	0	-1.02		-1.07		-1.01	1.3e-03	6.4e-03	5.0e-04	2.4e-02	1.1e-17
16280	AT3G14470.1	2e-85					-2.05	6.4e-01	8.2e-01	6.7e-01	4.6e-01	1.3e-04
16306	AT1G19880.1	3e-83	-1.12	-1.37	-1.36	-1.40	-1.64	6.0e-02	9.3e-03	1.1e-02	9.8e-03	3.8e-15
16310	AT4G38120.1	2e-43	-1.00	-1.34	-1.18	-1.19	-3.73	1.8e-01	2.8e-02	7.4e-02	6.4e-02	1.8e-15
16326	AT2G37630.1	3e-23				1.34	1.19	5.3e-01	1.5e-01	3.9e-01	2.3e-02	7.2e-06
16359	AT2G47640.1	5e-14	-1.03	-1.24	-1.19		-1.44	1.5e-01	4.7e-02	6.2e-02	2.0e-01	3.4e-08
16361	AT4G23160.1	3e-86		1.02	1.03		2.12	4.1e-01	1.8e-01	1.8e-01	5.8e-01	1.2e-06
16375	AT5G37140.1	4e-146		1.10	1.30	1.27	1.44	3.6e-01	9.1e-02	2.7e-02	3.1e-02	1.9e-07
16387	AT4G37870.1	0			-1.72	-1.39	-1.36	2.0e-01	2.8e-01	3.9e-04	5.9e-03	1.6e-03
16390			1.55			1.24	3.19	9.1e-03	2.3e-01	2.1e-01	6.2e-02	6.0e-14
16405	AT3G53990.1	7e-73			-1.23	-1.34		8.7e-01	8.7e-01	3.0e-03	7.3e-04	2.7e-03
16409	AT5G43330.1	2e-101					2.10	3.7e-01	4.5e-01	5.9e-01	3.0e-01	7.8e-06
16456	AT1G18840.1	5e-25					1.91	5.7e-01	4.1e-01	4.3e-01	4.4e-01	1.5e-04
16484	AT3G61600.1	2e-122	-1.22	-1.46	-1.48	-1.47	-5.09	6.9e-02	1.5e-02	1.3e-02	1.5e-02	1.2e-29
16509	AT1G13570.1	3e-11				-1.31	-1.71	4.9e-01	4.5e-01	2.5e-01	6.0e-02	7.8e-07
16549	AT3G20890.1	2e-75	1.91	2.02	1.74	1.63	3.66	1.0e-03	3.4e-04	3.9e-03	8.6e-03	8.2e-19
16617			-1.07				-2.05	1.0e-01	1.5e-01	7.4e-01	7.7e-01	7.1e-05
16630	AT1G29660.1	2e-72					2.18	4.6e-01	7.0e-01	5.0e-01	5.7e-01	2.0e-06
16665							-1.81	3.8e-01	6.6e-01	6.1e-01	6.5e-01	6.2e-04
16680	AT1G29670.1	1e-29				1.68	1.20	1.9e-01	2.0e-01	1.5e-01	8.2e-04	8.4e-04
16698	AT1G28520.1	2e-78	-2.13	-1.84	-2.08	-1.96	-2.14	4.7e-11	2.0e-09	1.1e-12	2.4e-11	8.3e-28
16699	AT1G28520.1	1e-79	2.78	3.17	2.96	3.16	4.04	1.1e-09	8.5e-13	1.9e-11	4.7e-13	4.9e-44
16700	AT1G28520.1	2e-36	2.78	2.69	2.82	2.70	5.06	4.0e-08	1.1e-07	1.7e-08	1.1e-07	4.1e-35
16709	AT2G25870.1	2e-125	-1.47	-1.56	-1.69	-1.58	-2.19	1.4e-02	5.8e-03	2.1e-03	8.3e-03	4.0e-14
16725	AT1G33265.1	2e-28	1.96	1.08		1.03	2.16	6.8e-04	1.8e-01	4.7e-01	2.1e-01	5.0e-08
16751	AT3G21360.1	1e-132					-2.29	2.7e-01	NA	NA	4.8e-01	6.7e-06
16783	AT5G15050.1	4e-33					1.81	7.9e-01	5.4e-01	5.8e-01	3.9e-01	3.5e-04
16785	AT5G13640.1	9e-82	3.68	4.03	4.02	4.10	5.86	5.9e-18	1.8e-21	9.9e-22	5.5e-22	1.7e-60
16786	AT5G20480.1	3e-47					-1.67	3.7e-01	3.4e-01	7.0e-01	7.3e-01	4.5e-04
16791	AT2G40550.1	2e-35		-1.25	-1.17		-2.17	7.5e-01	6.1e-02	9.4e-02	3.8e-01	4.5e-06

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
16860	AT1G07790.1	2e-50	-1.09	-1.12	-1.23	-1.02	-1.58	1.4e-01	1.3e-01	7.1e-02	1.8e-01	3.4e-08
16866	AT3G14470.1	4e-48					2.36	3.6e-01	3.1e-01	4.1e-01	6.3e-01	1.7e-08
16876	AT4G37440.1	1e-21	1.35		1.01	1.01	1.24	9.0e-03	2.0e-01	6.9e-02	7.4e-02	2.2e-09
16898				-2.14	-2.14	-1.47	-2.69	8.9e-01	1.0e-04	1.0e-04	2.3e-02	3.8e-08
16925	AT4G01320.1	0				-1.31	-1.14	3.0e-01	3.0e-01	4.8e-01	1.8e-02	7.8e-07
16927	AT4G35320.1	4e-30					-1.21	5.8e-01	2.2e-01	3.4e-01	3.3e-01	1.7e-05
16940	AT4G14605.1	2e-95	-2.40	-2.47	-2.18	-2.03	-4.68	7.0e-06	3.2e-06	7.8e-05	3.4e-04	4.6e-28
16954	AT4G17830.1	1e-64	-1.32	-1.39	-1.16	-1.22	-4.50	3.2e-02	2.1e-02	8.6e-02	6.0e-02	1.1e-22
16957	AT5G51040.1	2e-63	-1.56	-1.64	-1.71	-1.49	-1.82	1.1e-04	1.6e-05	6.5e-06	2.1e-04	3.2e-30
16975	AT4G05020.1	0		1.12		1.19	1.59	2.6e-01	1.4e-01	4.6e-01	9.8e-02	3.9e-09
16981				1.03	1.15	1.21	2.33	7.7e-01	1.6e-01	9.0e-02	6.3e-02	1.9e-06
17002	AT1G20160.1	2e-107	1.44			1.00	1.23	2.0e-03	1.1e-01	4.1e-01	8.0e-02	2.9e-08
17015							1.83	7.2e-01	2.6e-01	2.1e-01	4.5e-01	1.1e-04
17043	AT4G29090.1	5e-61	6.68	7.11	7.10	7.16	5.88	4.3e-81	2.7e-83	3.2e-85	2.4e-84	2.0e-40
17076	AT5G65120.1	7e-19	2.03	1.75	1.73	1.24	3.44	3.5e-04	3.2e-03	4.0e-03	8.3e-02	3.3e-16
17138	AT5G39840.1	0	-1.18			-1.02	-3.83	5.7e-02	1.5e-01	2.3e-01	1.3e-01	5.8e-16
17145	AT3G21820.1	6e-38	-1.47	-1.03	-1.34	-1.01	-1.76	1.7e-02	1.9e-01	3.9e-02	2.1e-01	2.4e-07
17166	AT3G11240.1	3e-27	-1.03				-1.77	1.7e-01	6.9e-01	6.2e-01	3.6e-01	1.1e-04
17182	AT1G65290.1	2e-13	-1.47	-1.26	-1.82	-1.90	-2.79	2.5e-02	7.8e-02	2.1e-03	1.0e-03	9.4e-15
17184	AT3G61360.1	9e-115	-1.46	-1.49	-1.69	-1.80	-2.07	8.8e-03	5.8e-03	1.2e-03	5.8e-04	4.4e-17
17190	AT3G02470.1	3e-18					2.07	6.4e-01	3.5e-01	5.5e-01	3.0e-01	6.3e-05
17238	AT2G31140.1	3e-32	-1.33	-1.24	-1.49	-1.07	-1.62	1.3e-02	2.4e-02	3.4e-03	8.1e-02	2.5e-15
17252	AT4G27190.1	4e-75					-2.97	5.5e-01	5.2e-01	3.6e-01	4.3e-01	4.5e-09
17359	AT4G31300.1	2e-59					-2.12	8.6e-01	6.4e-01	5.5e-01	5.2e-01	5.9e-05
17451	AT2G46225.1	1e-61					1.02	2.3e-01	8.0e-01	3.9e-01	1.7e-01	3.2e-05
17469	AT5G36930.1	4e-39	-1.43	-1.41	-1.69	-1.65	-3.71	2.7e-02	3.1e-02	4.4e-03	6.7e-03	2.9e-17
17484	AT2G45510.1	4e-175	-1.29					5.1e-04	9.0e-01	4.3e-01	1.9e-01	7.2e-03
17543	AT4G25600.1	4e-19	-1.04				-2.08	1.7e-01	4.9e-01	4.2e-01	2.6e-01	3.7e-06
17598	AT1G49050.1	2e-38	-1.80	-1.68	-2.38	-2.88	-3.74	2.2e-03	5.9e-03	8.1e-06	1.2e-08	9.8e-20
17605	AT4G04190.1	2e-26					-1.10	3.9e-01	3.5e-01	3.8e-01	8.0e-01	4.2e-04
17623							-1.10	5.0e-01	6.0e-01	5.6e-01	6.4e-01	8.6e-04
17624	AT1G14130.1	7e-25		1.16	1.10		1.60	5.7e-01	1.3e-01	1.6e-01	8.6e-01	3.4e-05
17664			-1.06	-1.78	-1.82	-1.79	-3.30	2.0e-01	2.9e-03	2.2e-03	2.8e-03	1.7e-16
17669	AT5G35400.1	1e-60					-2.31	3.1e-01	5.3e-01	3.9e-01	3.1e-01	2.6e-06
17693	AT1G79610.1	2e-122	-1.14		-1.04		-1.12	4.4e-02	1.4e-01	5.7e-02	1.2e-01	7.2e-05
17703	AT5G52200.1	3e-21			-1.06	-1.09	-2.02	2.7e-01	3.8e-01	1.9e-01	1.6e-01	8.2e-07
17724	AT2G24270.2	3e-61	1.35		1.01		1.26	6.1e-03	1.1e-01	8.8e-02	1.7e-01	3.9e-05
17826	AT2G02040.1	0	5.21	4.86	4.88	5.10	7.07	1.9e-41	1.0e-35	3.4e-36	4.3e-39	1.4e-84
17834					1.32	1.21	1.32	3.2e-01	1.6e-01	2.2e-02	4.5e-02	1.8e-07
17889	AT1G07030.1	2e-23					-2.03	NA	NA	NA	NA	1.5e-04
17926	AT5G54160.1	3e-57		1.51	1.37	1.17	2.41	8.7e-01	1.4e-02	3.7e-02	9.2e-02	7.1e-07
17979	AT1G47530.1	0	-1.06	-1.36	-1.37	-1.08	-1.36	3.0e-02	6.9e-04	8.3e-04	2.5e-02	1.3e-06
17989	AT1G51590.1	8e-41					-1.11	6.7e-01	2.6e-01	4.8e-01	3.5e-01	3.8e-05
18016	AT4G30480.1	2e-14	-1.57	-1.48		-1.19	-2.65	1.1e-02	2.0e-02	3.9e-01	9.8e-02	8.9e-10
18017	AT5G66060.1	3e-59	1.19	1.21	1.23	1.46	2.42	1.1e-01	1.0e-01	9.3e-02	2.7e-02	3.2e-14
18027	AT4G16480.1	7e-83					-2.43	3.8e-01	6.3e-01	4.2e-01	1.6e-01	1.8e-06
18055	AT3G12587.1	1e-15	1.47	1.34	1.32	1.36	1.58	3.5e-04	2.4e-03	3.5e-03	3.1e-03	1.2e-15
18074	AT4G15417.1	1e-75	-1.20			-1.11	-3.45	5.6e-02	2.0e-01	2.5e-01	8.8e-02	2.6e-13
18080				1.13		1.58	3.11	2.6e-01	1.0e-01	2.3e-01	5.7e-03	1.6e-10
18081			-3.80	-3.43	-3.43	-3.56	-4.69	4.8e-20	3.3e-16	1.1e-16	1.7e-17	1.5e-65
18087	AT2G31400.1	1e-38	-1.03				-1.26	2.2e-01	4.2e-01	5.9e-01	6.7e-01	4.4e-04
18092	AT1G12680.1	1e-62	-1.53	-1.75	-1.16	-2.29	-2.42	1.0e-02	1.9e-03	9.3e-02	9.4e-06	3.4e-15
18094	AT1G22100.1	1e-112	-1.40				-1.62	3.9e-02	4.4e-01	6.6e-01	5.3e-01	1.2e-04
18116	AT4G39150.1	0				1.18		3.3e-08	1.2e-06	2.7e-08	4.1e-13	6.5e-15

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
18148					-1.17	-1.14	-2.79	3.8e-01	2.4e-01	8.1e-02	8.3e-02	5.6e-09
18176	AT4G00340.1	2e-90	-1.19	-1.15	-1.22	-1.32	-1.43	8.7e-02	8.3e-02	5.4e-02	2.9e-02	7.3e-04
18201	AT4G18700.1	7e-17	1.82	2.37	2.14	2.25	2.70	1.1e-04	7.9e-08	2.2e-06	6.1e-07	2.3e-38
18208	AT5G36930.1	1e-23	3.19	3.02	3.07	2.56	5.38	8.4e-11	1.0e-09	4.9e-10	8.4e-07	8.3e-40
18243	AT2G19350.1	4e-25	-1.41		-1.09	-1.08	-1.46	3.0e-02	5.9e-01	1.4e-01	1.4e-01	6.6e-05
18261	AT5G63100.1	1e-110	-1.05		-1.24		-1.12	1.2e-01	6.2e-01	3.6e-02	5.4e-01	1.5e-06
18288			1.86	2.26	1.75	2.04	3.97	1.5e-03	3.2e-05	3.4e-03	3.2e-04	7.1e-22
18340	AT1G80460.1	2e-74		-1.33	-1.01	-1.49	-1.52	2.6e-01	2.3e-02	1.4e-01	6.3e-03	1.0e-07
18417	AT4G39630.1	2e-24	-2.18	-1.71	-1.70	-1.46	-4.26	6.4e-05	4.3e-03	4.4e-03	2.3e-02	2.6e-21
18436	AT1G56290.1	8e-38					-1.29	3.7e-01	4.0e-01	3.4e-01	4.1e-01	2.8e-05
18438	AT4G38620.1	4e-75		1.47	1.21	1.15	1.68	1.0e+00	2.6e-02	1.0e-01	1.3e-01	6.9e-05
18440	AT5G66820.1	1e-20				1.18	1.35	3.3e-01	4.0e-01	4.4e-01	1.0e-01	4.2e-05
18444	AT3G46200.1	7e-115			1.17	1.18	1.50	2.4e-01	3.8e-01	1.0e-01	9.7e-02	3.8e-07
18445	AT3G46200.1	8e-102	-1.51	-1.38	-1.58	-1.48	-3.55	1.7e-02	3.5e-02	1.0e-02	1.9e-02	2.3e-15
18470			-1.18				-1.16	4.6e-02	2.6e-01	1.6e-01	4.8e-01	3.6e-07
18471				-1.01		-1.14	-1.43	9.3e-01	2.3e-01	5.4e-01	1.3e-01	6.6e-04
18489	AT3G10700.1	9e-40	1.24	1.13	1.27	1.12	3.49	5.6e-02	9.8e-02	4.9e-02	9.6e-02	1.3e-13
18518	AT3G49810.1	7e-66					-1.12	7.5e-01	4.1e-01	5.6e-01	4.6e-01	8.7e-04
18522	AT2G14050.1	2e-69		1.37	1.66	1.08	3.29	3.1e-01	2.8e-02	3.8e-03	1.3e-01	6.9e-12
18527	AT4G34000.1	8e-26	-2.06	-1.96	-2.22	-2.16	-4.86	2.6e-04	6.1e-04	4.8e-05	9.5e-05	7.7e-30
18533	AT2G40890.1	0		1.42	1.06	1.31	1.40	1.0e+00	2.7e-02	1.8e-01	5.2e-02	3.5e-05
18542				1.25	1.10		1.09	5.5e-02	5.8e-04	3.4e-03	1.5e-02	1.1e-08
18562	AT1G16040.1	8e-20	1.28	1.14		1.01	2.68	5.2e-02	1.1e-01	4.5e-01	1.8e-01	2.7e-09
18626	AT5G60900.1	6e-26	1.02		1.35	1.28	1.63	2.1e-01	4.7e-01	4.3e-02	6.1e-02	4.2e-08
18639	AT3G03380.1	0	1.12				1.09	8.1e-02	4.9e-01	2.4e-01	2.6e-01	4.8e-05
18721	AT1G65950.1	4e-45	-1.10	-1.93		-1.20	-1.77	1.6e-01	6.0e-04	4.8e-01	9.9e-02	3.6e-05
18741	AT4G32560.1	2e-40		-1.28		-1.04	-3.02	3.9e-01	3.5e-02	3.7e-01	1.2e-01	5.2e-10
18781	AT1G20640.1	0	1.38			1.29	1.24	2.2e-03	1.5e-01	9.6e-02	4.3e-03	6.5e-10
18851	AT2G23790.1	2e-41			1.08		2.93	2.1e-01	NA	NA	3.7e-01	2.9e-09
18856	AT3G01160.1	5e-57	-1.67	-1.70	-1.43	-1.24	-2.62	6.9e-03	5.3e-03	3.2e-02	8.6e-02	1.2e-15
18917	AT1G63440.1	0		1.43	1.94	1.93	1.75	8.3e-01	2.7e-02	5.5e-04	6.5e-04	3.4e-04
18945	AT1G49630.1	1e-27					-1.22	4.6e-01	3.0e-01	5.4e-01	2.4e-01	8.4e-05
18999	AT4G27190.1	1e-53				-1.05	-2.74	4.4e-01	1.8e-01	2.8e-01	1.2e-01	9.4e-09
19032			1.14	1.56	1.43	1.40	3.22	1.3e-01	1.1e-02	2.7e-02	3.3e-02	1.3e-14
19047	AT5G67460.1	7e-40	-1.49	-1.44	-1.37	-1.17	-2.13	2.1e-02	2.7e-02	4.2e-02	1.1e-01	1.0e-11
19111							2.81	4.7e-01	4.2e-01	4.0e-01	3.4e-01	3.2e-14
19146			-1.29	-1.92			-1.80	5.7e-02	5.0e-04	2.4e-01	4.9e-01	5.2e-08
19165	AT3G07480.1	2e-34					-1.12	3.9e-01	6.1e-01	5.0e-01	6.5e-01	4.6e-04
19174	AT3G19490.1	3e-64					-1.38	5.6e-01	3.2e-01	7.1e-01	3.3e-01	2.3e-04
19176	AT5G08540.1	4e-67					-2.02	6.4e-01	7.1e-01	7.4e-01	7.3e-01	1.4e-04
19183	AT5G08160.1	3e-25	-1.22	-1.08	-1.05		-1.56	8.2e-02	1.6e-01	1.8e-01	2.7e-01	4.1e-08
19184	AT5G08160.1	8e-14					-1.97	5.4e-01	NA	NA	7.4e-01	2.6e-04
19187	AT5G09310.1	4e-15			-1.02	-1.09	-1.48	4.0e-01	2.8e-01	2.1e-01	1.5e-01	7.4e-07
19258	AT1G80530.1	4e-62	4.29	3.85	3.80	3.43	5.95	1.1e-22	4.1e-18	7.6e-18	5.5e-14	2.1e-54
19319	AT1G13030.1	3e-19	1.03	1.02			3.46	1.5e-01	1.5e-01	1.9e-01	2.6e-01	4.2e-18
19321	AT3G14310.1	1e-154	1.46					5.8e-05	4.3e-01	9.7e-01	9.8e-01	3.7e-01
19329	AT5G05680.1	3e-123		1.22	1.07	1.20	1.47	3.0e-01	6.5e-02	1.4e-01	7.2e-02	2.6e-07
19385	AT2G25570.1	6e-33	2.67	2.74	2.77	2.25	4.90	2.2e-07	6.7e-08	4.8e-08	3.6e-05	6.5e-32
19416	AT1G45000.1	2e-12	1.36	1.07		1.12	2.12	4.8e-02	1.9e-01	2.6e-01	1.5e-01	1.6e-08
19428	AT3G56190.1	1e-12	2.86	3.08	3.34	3.20	5.30	5.9e-09	1.6e-10	1.7e-12	2.6e-11	2.7e-41
19473	AT5G08100.2	3e-76	-1.01		-1.34	-1.32	-1.36	8.2e-02	1.1e-01	3.5e-03	4.5e-03	1.5e-08
19480			2.66	2.15	2.28	2.31	4.52	2.9e-07	9.5e-05	2.3e-05	1.9e-05	2.5e-27
19507	AT1G69630.1	1e-23	-1.02	-1.41	-1.16	-1.34	-3.78	1.7e-01	2.1e-02	8.7e-02	3.0e-02	3.0e-16
19533	AT2G33030.1	6e-48					2.04	5.8e-01	NA	NA	2.8e-01	6.0e-05

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
19550	AT4G33490.1	1e-38		-1.04			-2.58	7.1e-01	NA	NA	1.4e-01	3.9e-07
19582					1.25		2.35	2.4e-01	5.7e-01	6.0e-02	3.4e-01	2.0e-07
19669	AT5G51560.1	3e-53	-1.15				-1.09	9.3e-02	8.4e-01	2.4e-01	3.9e-01	2.8e-04
19688	AT4G34880.1	3e-22					-1.30	4.9e-01	8.5e-01	4.2e-01	4.2e-01	9.4e-04
19697	AT5G50380.1	2e-97	-1.38	-1.08	-1.09		-1.23	3.5e-05	1.8e-03	1.6e-03	8.4e-03	1.6e-21
19746	AT5G63440.1	6e-66					-2.40	4.4e-01	3.1e-01	3.8e-01	4.4e-01	2.1e-06
19758	AT1G01690.1	1e-36					1.60	5.4e-01	2.5e-01	5.0e-01	2.4e-01	3.0e-05
19767	AT2G25490.1	4e-64	1.90	1.79	1.46	1.93	2.35	5.5e-04	1.7e-03	2.1e-02	6.1e-04	3.7e-09
19792	AT2G01050.1	3e-14					-2.18	3.9e-01	4.3e-01	6.3e-01	6.1e-01	3.3e-05
19845	AT5G43060.1	2e-39	-1.14	-1.56		-1.38	-1.43	2.7e-02	3.1e-04	1.4e-01	6.3e-03	1.4e-08
19863	AT5G61230.1	3e-40	-1.14			-1.02	-1.37	1.2e-01	2.8e-01	5.8e-01	2.0e-01	4.3e-06
19922	AT1G43760.1	5e-37	1.04	1.66	1.46	1.54	2.89	2.1e-01	7.0e-03	2.7e-02	1.7e-02	4.8e-16
19925	AT2G01210.1	8e-79	1.78	1.52	1.41	1.80	3.54	2.5e-03	1.6e-02	3.4e-02	2.4e-03	2.9e-18
19928	AT1G03510.1	3e-154	-2.22	-2.00	-1.89	-1.33	-3.97	4.6e-05	3.9e-04	1.2e-03	5.1e-02	1.4e-19
19952	AT1G51160.1	7e-38	-1.56	-1.42	-1.72	-1.24	-1.88	2.6e-03	7.6e-03	5.7e-04	2.9e-02	9.7e-19
19953	AT1G51160.1	1e-14	1.63		1.48	1.13	1.84	4.6e-03	2.4e-01	1.5e-02	1.1e-01	3.5e-10
19954	AT1G48635.1	2e-32					-1.70	2.8e-01	3.1e-01	6.9e-01	7.6e-01	2.4e-04
19955	AT1G48635.1	3e-32	1.81	1.94	2.19	1.66	4.19	2.2e-03	6.8e-04	6.1e-05	6.7e-03	1.9e-21
19957	AT3G16490.1	3e-58	-1.25		-1.47			2.4e-02	3.0e-01	9.3e-04	2.2e-01	9.9e-02
19958	AT1G15520.1	0		-1.12	-1.20	-1.36	-1.50	3.2e-01	9.4e-02	5.6e-02	2.4e-02	3.5e-08
19960	AT4G34260.1	0			1.18	1.05	1.05	2.0e-02	3.0e-02	2.6e-04	3.8e-03	2.3e-07
19981	AT1G79380.1	5e-63	-1.67	-1.48	-1.30	-1.24	-1.55	1.2e-06	6.1e-06	1.1e-04	5.1e-04	1.0e-29
20012	AT3G56550.1	8e-49					-1.42	5.9e-01	2.7e-01	8.1e-01	3.6e-01	7.5e-04
20025							-1.80	6.1e-01	3.4e-01	6.7e-01	5.5e-01	7.0e-04
20027	AT4G00355.3	1e-42	-1.46		-1.04		-1.33	1.3e-02	3.6e-01	1.4e-01	3.2e-01	6.1e-07
20030	AT1G68080.1	1e-67					1.75	7.0e-01	4.7e-01	6.8e-01	4.3e-01	3.8e-04
20032	AT1G68080.1	3e-69		-1.42	-1.22	-1.16	-2.56	6.3e-01	2.6e-02	8.1e-02	9.9e-02	1.2e-08
20082	AT2G46160.1	2e-46		-1.19	-1.08	-1.04	-1.30	1.4e-01	2.6e-02	5.1e-02	6.9e-02	6.0e-13
20131	AT3G27520.1	6e-20	3.32	3.35	2.87	3.22	4.81	2.3e-13	2.4e-13	8.1e-10	5.0e-12	5.0e-44
20163	AT1G48910.1	7e-111	1.11				1.15	1.2e-01	2.8e-01	4.6e-01	2.5e-01	8.1e-04
20187	AT2G23450.2	3e-94	-1.50	-2.01	-1.93	-1.60	-4.40	1.8e-02	3.2e-04	6.7e-04	9.3e-03	1.6e-24
20189	AT2G01050.1	1e-29		-1.01	-1.16	-1.07	-1.34	4.7e-01	1.6e-01	7.9e-02	1.2e-01	7.4e-08
20217	AT5G60900.1	2e-13	-1.09	-1.44	-1.26	-1.05	-1.84	1.5e-01	2.6e-02	7.1e-02	1.8e-01	9.2e-09
20219	AT4G23160.1	1e-103					-1.39	3.1e-01	5.1e-01	4.2e-01	7.0e-01	1.2e-04
20227	AT4G33360.1	3e-42	-1.44	-1.18	-1.12		-1.33	2.9e-03	2.5e-02	3.7e-02	2.7e-01	6.6e-11
20240	AT2G40510.1	2e-13		-1.00	-1.01	-1.02	-1.37	2.9e-01	2.0e-01	2.0e-01	1.8e-01	8.6e-07
20280	AT1G73100.1	3e-20					-1.88	4.3e-01	NA	NA	7.2e-01	1.3e-04
20332							1.76	3.2e-01	NA	NA	7.5e-01	2.2e-04
20361	AT3G27950.1	5e-29		1.78	1.59	1.24	1.27	7.0e-01	5.0e-04	3.9e-03	5.5e-02	4.0e-03
20380	AT3G18860.1	1e-21	-2.72	-2.70	-2.73	-2.31	-4.95	1.0e-07	1.3e-07	7.6e-08	1.7e-05	9.2e-33
20388	AT1G56260.1	3e-11		-1.10			-1.77	6.3e-01	1.6e-01	4.5e-01	2.4e-01	2.3e-05
20389	AT1G56260.1	4e-14	1.13				2.47	NA	NA	NA	NA	1.7e-06
20392	AT3G54560.1	2e-15			-1.00	-1.07	-1.34	4.7e-01	4.4e-01	2.2e-01	1.5e-01	2.0e-06
20409	AT5G21930.1	1e-124	1.71	1.66	1.73	1.48	3.94	3.9e-03	5.6e-03	3.4e-03	1.9e-02	1.4e-18
20438	AT3G24255.1	7e-19	1.33	1.45	1.54		1.80	3.1e-02	1.4e-02	6.5e-03	3.2e-01	3.1e-12
20455	AT1G24180.1	3e-158	-1.27					2.4e-04	1.3e-02	6.8e-02	4.0e-01	1.6e-10
20459	AT1G22260.1	2e-85	-1.89	-1.97	-1.72	-1.75	-2.81	1.0e-03	4.5e-04	3.7e-03	3.3e-03	3.9e-16
20460	AT1G22275.1	9e-71					1.84	3.9e-01	8.1e-01	5.9e-01	7.4e-01	1.8e-04
20474	AT1G22400.1	4e-47	1.19	1.57	1.98	2.46	1.90	2.2e-02	6.8e-04	7.0e-06	8.5e-08	3.1e-09
20477	AT5G04750.1	3e-18	-1.60	-1.57	-1.69	-2.21	-2.89	1.0e-02	1.2e-02	5.2e-03	5.7e-05	7.4e-19
20517	AT5G63020.1	8e-102					1.67	3.3e-01	4.6e-01	3.6e-01	3.9e-01	6.6e-06
20541	AT4G33680.1	1e-34	1.16		1.08	1.03	1.27	3.9e-02	1.6e-01	6.7e-02	9.4e-02	5.0e-07
20567							-2.11	7.0e-01	5.9e-01	6.5e-01	7.2e-01	7.1e-05
20580				-1.08	-1.34	-1.33	-1.33	7.3e-02	1.6e-02	1.0e-03	1.3e-03	1.1e-09

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
20582	AT5G06870.1	1e-30					-1.91	6.6e-02	NA	NA	5.9e-01	4.1e-04
20590			1.85	1.67	1.84	1.83	2.52	6.2e-04	2.6e-03	6.0e-04	6.3e-04	2.8e-22
20591				-1.13		-1.41	-1.38	2.3e-01	5.8e-02	1.8e-01	8.3e-03	1.3e-09
20618	AT3G19290.1	1e-35	-2.06	-2.10	-2.33	-2.66	-5.03	2.8e-04	1.8e-04	1.8e-05	3.8e-07	8.4e-32
20633	AT1G77140.1	6e-136					-2.08	4.3e-01	3.5e-01	2.8e-01	6.0e-01	1.1e-05
20693							-2.20	5.3e-01	4.5e-01	5.1e-01	4.0e-01	2.1e-05
20697	AT2G38680.1	5e-78	1.95	1.88	2.15	1.65	4.13	6.6e-04	1.1e-03	9.7e-05	7.0e-03	7.1e-21
20699	AT2G38680.1	2e-75	-2.20	-2.17	-1.92	-2.07	-3.74	5.9e-05	7.4e-05	7.7e-04	2.3e-04	4.9e-27
20751	AT5G20410.1	3e-74	-1.33				-1.22	2.6e-02	5.8e-01	2.0e-01	3.5e-01	4.3e-07
20787	AT4G21215.2	7e-17		1.28	1.43			9.6e-02	1.6e-04	1.1e-05	8.7e-01	3.2e-04
20803			2.19	2.08	1.78	2.18	4.10	7.5e-05	2.0e-04	2.9e-03	7.9e-05	1.9e-23
20859	AT2G13680.1	0		-1.18		-1.23	-1.05	3.1e-01	5.3e-03	2.2e-01	8.2e-03	7.8e-05
20879	AT2G47330.1	1e-99	-1.13	-1.58	-1.01	-1.35	-2.38	1.5e-01	1.3e-02	2.4e-01	4.7e-02	3.8e-10
20913	AT2G45470.1	6e-21				1.51	1.90	1.0e+00	NA	NA	2.5e-03	3.9e-04
20928	AT1G10510.1	7e-30					1.92	4.8e-01	6.6e-01	3.0e-01	3.9e-01	1.6e-04
20936	AT5G10910.1	4e-13					2.20	4.2e-01	5.0e-01	6.3e-01	6.6e-01	1.5e-06
20948	AT3G14470.1	5e-23			1.23	1.04	2.73	2.5e-01	5.1e-01	5.6e-02	1.4e-01	3.3e-09
21007				1.24	1.80	1.13	1.78	4.3e-01	8.7e-02	2.4e-03	1.4e-01	2.4e-05
21034	AT3G66654.1	3e-52	1.04	1.37	1.26	1.66	1.54	3.1e-02	1.3e-03	3.6e-03	4.0e-05	1.2e-20
21036	AT4G29090.1	2e-58	1.69	1.45	1.42		3.50	3.3e-03	1.9e-02	2.4e-02	3.0e-01	1.0e-13
21108	AT3G18480.1	3e-18					1.46	7.6e-01	4.2e-01	3.4e-01	5.5e-01	3.8e-04
21116	AT1G78955.1	4e-14	1.68	2.59	2.29	1.68	4.07	6.2e-03	6.5e-07	2.3e-05	6.0e-03	3.5e-20
21120	AT2G16430.1	1e-89	-1.09	-1.70	-1.36	-1.18	-2.91	1.6e-01	4.5e-03	4.4e-02	1.1e-01	3.6e-12
21142	AT3G10040.1	1e-110			-1.08	-1.07	-1.13	5.5e-01	4.2e-01	1.1e-01	1.2e-01	2.6e-05
21162	AT2G29650.1	0		1.12	1.18	1.04	1.31	5.9e-01	1.1e-01	7.8e-02	1.5e-01	6.7e-07
21235			-1.76				-1.82	3.6e-03	3.5e-01	4.9e-01	6.5e-01	5.0e-05
21272	AT1G03560.1	2e-78	-3.14	-3.00	-2.88	-2.99	-5.34	1.0e-10	9.8e-10	5.3e-09	1.3e-09	7.5e-40
21274	AT1G73590.1	3e-165				1.44		8.4e-01	7.6e-01	3.9e-01	3.5e-05	4.6e-01
21276				-1.01	-1.33	-1.38	-1.83	2.7e-01	2.4e-01	5.7e-02	4.0e-02	2.4e-05
21284	AT1G43760.1	1e-44	3.97	4.95	4.56	4.29	6.13	2.0e-20	2.2e-32	1.2e-28	7.2e-24	4.0e-61
21298				1.07	1.00		2.78	4.1e-01	NA	NA	4.1e-01	1.7e-08
21315	AT1G52260.1	7e-63	1.14				1.24	1.3e-01	4.4e-01	4.6e-01	4.4e-01	9.8e-04
21346	AT3G17130.1	1e-20		1.20	1.39	1.58	1.99	7.7e-01	1.1e-01	4.2e-02	1.2e-02	4.8e-08
21404	AT1G79610.1	1e-38	1.38	1.48	1.42	1.19	3.56	3.0e-02	1.6e-02	2.4e-02	8.1e-02	1.6e-14
21450	AT1G29840.1	1e-39					1.76	7.2e-01	6.9e-01	7.2e-01	6.1e-01	7.2e-04
21536	AT5G48520.1	6e-92					-2.25	1.2e-01	3.8e-01	8.0e-01	8.5e-01	2.0e-05
21540	AT5G57260.1	6e-120					1.88	3.5e-01	6.9e-01	7.5e-01	7.3e-01	3.4e-04
21559	AT2G17695.1	1e-85	-1.90	-1.38	-1.18	-1.58	-1.74	1.6e-06	1.1e-03	8.7e-03	1.9e-04	6.2e-24
21606	AT2G30720.1	4e-55					1.82	6.8e-01	6.3e-01	7.3e-01	6.7e-01	2.2e-04
21635				-1.28	-1.05	-1.10	-1.48	2.0e-01	3.6e-02	1.3e-01	1.1e-01	5.9e-10
21640	AT3G52040.1	9e-15	2.30	2.30	2.19	2.25	4.56	2.2e-05	1.9e-05	6.6e-05	3.9e-05	7.1e-27
21651	AT5G07900.1	5e-21	1.03				1.03	1.7e-01	6.9e-01	3.5e-01	6.4e-01	1.3e-04
21663	AT1G60550.1	1e-63	2.04	1.09		1.11	2.48	1.8e-04	1.4e-01	8.6e-01	1.2e-01	1.0e-06
21712							-2.97	3.0e-01	3.2e-01	2.3e-01	3.0e-01	7.4e-10
21714	AT3G52470.1	3e-53	-1.37	-1.14	-1.25	-1.53	-1.76	2.8e-02	9.6e-02	4.6e-02	6.7e-03	8.4e-08
21727	AT4G09640.1	2e-69					-2.10	4.5e-01	5.1e-01	6.3e-01	7.3e-01	7.3e-05
21764	AT1G27180.1	7e-26	1.86	2.04	2.13	1.60	4.36	1.4e-03	2.5e-04	1.1e-04	1.0e-02	3.4e-23
21790	AT5G54590.1	9e-116					-2.71	4.3e-01	2.4e-01	2.0e-01	3.1e-01	1.2e-08
21792	AT4G21380.1	0		-1.12	-1.30	-1.38	-1.63	2.8e-01	1.4e-01	5.3e-02	3.3e-02	1.8e-04
21804	AT4G03610.2	5e-28		-1.22		-1.40	-1.59	7.6e-01	9.8e-02	4.3e-01	3.5e-02	1.2e-04
21875							-1.70	2.9e-01	2.7e-01	4.3e-01	5.2e-01	1.6e-05
21906	AT2G39710.1	0	-1.86		-1.26	-1.18	-3.24	8.8e-04	2.8e-01	6.4e-02	8.5e-02	7.4e-12
21920			-2.87	-2.94	-3.04	-3.07	-5.57	1.3e-08	4.5e-09	8.9e-10	7.1e-10	1.6e-43
21959	AT2G21160.1	1e-28	1.03	1.17			1.48	2.1e-01	1.2e-01	5.2e-01	3.6e-01	3.5e-06

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
21991	AT1G77120.1	8e-171	-1.33			-1.24	-1.24	1.6e-02	2.3e-01	4.1e-01	2.4e-02	2.6e-06
22005	AT5G51960.1	2e-38	-1.45	-1.24		-1.37	-1.51	9.9e-03	3.6e-02	4.1e-01	1.9e-02	5.8e-11
22024	AT5G10260.1	1e-72			-1.01		-1.04	3.7e-01	7.2e-01	2.0e-01	6.6e-01	2.3e-04
22041	AT1G17650.1	3e-78	-1.46	-1.21	-1.38	-1.51	-2.66	2.7e-02	1.0e-01	4.3e-02	1.9e-02	5.1e-12
22089	AT1G65610.1	0				-1.49	-1.65	4.1e-01	7.1e-01	4.1e-01	2.3e-02	5.0e-04
22091	AT5G53970.1	5e-129	-2.28	-1.89	-1.77	-1.83	-2.61	7.0e-06	3.8e-04	1.1e-03	7.4e-04	2.7e-20
22102	AT2G39660.1	1e-74		1.07	1.21		1.91	4.1e-01	1.8e-01	9.9e-02	3.6e-01	3.4e-07
22109	AT2G27020.1	5e-42			-1.02		-1.03	7.1e-01	3.1e-01	1.4e-01	3.4e-01	4.6e-05
22116			-1.82	-1.61	-1.69	-2.10	-4.01	1.8e-03	9.0e-03	5.3e-03	1.5e-04	3.3e-19
22117			1.56				1.24	1.9e-03	1.3e-01	2.0e-01	6.1e-01	7.3e-08
22128			2.12	2.17	1.67	1.52	3.08	1.4e-04	8.1e-05	5.9e-03	1.8e-02	8.4e-23
22157	AT5G16760.1	2e-29	1.52	1.94	1.77	1.59	2.58	1.4e-02	4.8e-04	2.0e-03	8.4e-03	5.5e-21
22158	AT5G16760.1	3e-34					-1.88	7.5e-01	6.0e-01	3.7e-01	5.0e-01	2.9e-04
22179	AT1G18480.1	9e-120	-1.07				-1.33	1.7e-01	3.6e-01	3.2e-01	3.7e-01	2.0e-05
22234	AT2G34930.1	2e-46	-1.03	-1.15			-1.44	2.0e-01	1.2e-01	6.9e-01	3.0e-01	1.1e-05
22240	AT5G18880.1	9e-12					2.35	3.9e-01	2.8e-01	3.4e-01	5.2e-01	2.3e-07
22254	AT5G20290.1	7e-34					1.28	2.7e-01	5.1e-01	6.9e-01	4.6e-01	8.9e-05
22282			1.03	1.67	1.67	1.74	2.03	1.7e-01	2.9e-03	2.9e-03	1.8e-03	4.5e-13
22342	AT5G23330.1	1e-54		-1.08		-1.10	-1.07	9.9e-01	1.1e-01	2.5e-01	1.2e-01	7.2e-04
22382	AT4G25220.1	1e-58	-1.83	-2.01	-1.45	-1.33	-2.94	1.8e-03	3.8e-04	2.8e-02	5.4e-02	4.8e-17
22391	AT1G61770.1	6e-74					-1.08	4.1e-01	3.4e-01	4.3e-01	2.1e-01	1.5e-05
22421	AT4G25440.1	8e-100	1.03					1.2e-05	1.2e-03	9.8e-05	1.1e-03	8.6e-23
22450	AT2G33040.1	2e-21	1.48	1.47	1.27		2.04	1.9e-02	2.2e-02	6.7e-02	2.5e-01	5.4e-10
22462			-1.40	-1.36	-1.07		-3.15	2.8e-02	3.6e-02	1.7e-01	2.8e-01	1.5e-16
22463	AT1G13570.1	6e-24	-1.66	-1.51	-1.49	-1.30	-4.72	4.1e-03	1.2e-02	1.5e-02	4.6e-02	1.0e-25
22479	AT1G13570.1	1e-45	3.87	3.65	3.80	3.64	5.83	5.2e-19	7.1e-17	2.0e-18	1.7e-16	2.1e-51
22481	AT1G33970.1	3e-57			-1.24	-1.10	-1.24	2.5e-01	1.1e-01	1.4e-02	4.4e-02	3.4e-09
22485	AT5G23300.1	2e-54	-1.53	-1.18	-1.12	-1.04	-1.65	7.1e-03	7.3e-02	1.0e-01	1.5e-01	7.0e-09
22486	AT5G23300.1	5e-56	1.40	1.11	1.23		3.22	2.6e-02	1.3e-01	7.2e-02	2.1e-01	1.1e-15
22517	AT5G21990.1	4e-91					-2.31	3.8e-01	4.4e-01	4.8e-01	3.5e-01	4.1e-06
22565	AT3G04760.1	2e-55				-1.05	-1.13	3.2e-01	5.5e-01	6.6e-01	1.6e-01	1.2e-04
22595	AT4G14240.1	1e-173	-1.74	-1.87	-1.25	-1.54	-1.92	7.9e-05	1.3e-05	1.1e-02	7.9e-04	5.7e-24
22659			1.04	1.16		1.23	3.28	1.4e-01	8.0e-02	2.6e-01	4.7e-02	7.3e-12
22677	AT4G12010.1	3e-47	1.90	2.02	2.06	1.80	4.39	1.1e-03	3.4e-04	2.4e-04	2.3e-03	9.5e-25
22712	AT3G60500.1	2e-99					-1.38	6.9e-01	4.1e-01	5.2e-01	3.5e-01	2.7e-04
22715	AT3G57710.1	3e-65					-1.97	6.7e-01	5.1e-01	5.0e-01	2.3e-01	2.3e-04
22733	AT4G33565.1	2e-39		1.23				4.4e-01	9.3e-04	1.2e-01	5.2e-02	2.7e-07
22777	AT1G61310.1	1e-24	1.89	1.40	1.69	1.16	3.15	1.2e-03	3.7e-02	5.8e-03	1.2e-01	1.2e-17
22806	AT5G45900.1	8e-116				-1.07	-1.26	2.2e-01	2.8e-01	6.2e-01	1.6e-01	3.7e-06
22820	AT1G12910.1	1e-56	2.03	1.41	1.33	1.40	3.36	3.1e-04	3.1e-02	5.3e-02	3.3e-02	2.3e-15
22829	AT4G23160.1	1e-92	-1.05	-1.34	-1.31	-1.18	-2.70	1.9e-01	4.5e-02	5.3e-02	1.0e-01	2.1e-10
22834	AT2G05170.1	4e-22	-3.51	-3.08	-3.11	-2.99	-5.34	4.3e-14	1.0e-10	5.5e-11	5.2e-10	9.9e-40
22835	AT2G05170.1	4e-22	1.84	1.37	1.00	1.42	1.50	1.7e-09	2.3e-05	4.4e-03	9.3e-06	2.0e-24
22845	AT5G53970.1	2e-174	1.24		1.07		1.72	9.3e-02	2.9e-01	1.9e-01	3.6e-01	3.0e-05
22851							-2.24	2.3e-01	5.4e-01	4.7e-01	4.5e-01	1.0e-05
22897	AT1G08880.1	4e-21	-1.96	-2.54	-2.19	-2.32	-2.72	1.2e-05	7.1e-10	2.2e-07	4.3e-08	2.3e-31
22946	AT1G21280.1	8e-19		1.05			2.98	3.5e-01	NA	NA	3.5e-01	1.3e-09
22951	AT3G63470.1	2e-56	-1.62	-1.92	-2.14	-2.41	-4.76	8.6e-03	8.3e-04	1.1e-04	6.1e-06	3.0e-28
22990	AT3G53440.1	4e-27					1.21	2.1e-01	3.6e-01	3.2e-01	5.2e-01	3.7e-05
23030							-1.79	3.4e-01	NA	NA	7.6e-01	2.1e-04
23054	AT2G17695.1	4e-24	1.33	1.41		1.70	3.44	4.0e-02	2.5e-02	2.2e-01	3.2e-03	3.1e-13
23055	AT2G17695.1	4e-23	2.70	2.06	2.16	2.52	4.57	1.7e-07	2.1e-04	8.7e-05	1.7e-06	2.1e-26
23164	AT3G49660.1	4e-57			-1.10	-1.22	-1.63	7.9e-01	5.7e-01	1.7e-01	9.3e-02	7.1e-05
23228	AT1G01725.1	4e-14	1.53	1.81	1.81	1.86	4.07	1.5e-02	2.0e-03	2.0e-03	1.3e-03	4.5e-20

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
23239	AT5G16250.1	3e-21	2.48	2.65	2.49	2.38	4.81	2.4e-06	2.7e-07	2.0e-06	8.9e-06	1.1e-30
23259	AT1G13570.1	3e-20	-1.95	-1.59	-1.69	-1.68	-3.68	6.4e-04	1.1e-02	5.4e-03	5.8e-03	8.6e-20
23260	AT1G13570.1	2e-23	-1.24	-1.17	-1.07	-1.11	-4.11	4.8e-02	7.3e-02	1.2e-01	9.3e-02	1.5e-18
23313	AT2G43280.1	2e-28					-1.01	3.1e-01	3.4e-01	5.1e-01	4.4e-01	2.2e-05
23315	AT5G36800.1	3e-33	3.72	3.16	3.23	3.34	5.64	9.7e-16	2.9e-11	7.8e-12	1.7e-12	1.5e-45
23400	AT2G46240.1	2e-38					-1.87	6.9e-01	7.2e-01	7.7e-01	6.0e-01	5.6e-04
23432	AT3G11220.1	7e-20					2.32	NA	NA	NA	NA	7.0e-06
23500					-1.02		-2.26	6.3e-01	3.1e-01	1.6e-01	3.7e-01	2.3e-06
23522	AT1G71950.1	6e-17	-1.44	-1.32	-1.71	-1.84	-2.67	3.0e-02	5.8e-02	4.7e-03	1.8e-03	2.3e-11
23524	AT4G25360.1	3e-35	1.12				1.68	1.5e-01	3.5e-01	5.7e-01	3.7e-01	3.5e-06
23535	AT3G48460.1	4e-60					-2.23	8.1e-01	6.9e-01	4.5e-01	2.0e-01	2.5e-05
23571	AT3G46550.1	3e-15	1.18			1.17	3.10	6.4e-02	2.8e-01	2.6e-01	6.2e-02	1.9e-10
23579	AT5G35570.1	5e-17		1.10			2.62	3.5e-01	1.2e-01	2.3e-01	2.2e-01	7.0e-09
23627	AT1G09390.1	2e-45					-1.82	4.4e-01	7.4e-01	7.0e-01	5.0e-01	7.3e-04
23743	AT1G11050.1	9e-104		-1.12			-1.11	2.2e-01	9.9e-02	5.9e-01	5.2e-01	1.7e-05
23768			2.92	2.57	2.61	2.44	4.60	4.1e-09	4.4e-07	2.9e-07	2.9e-06	2.1e-32
23788	AT5G20680.1	2e-22					-1.06	4.3e-01	3.7e-01	6.6e-01	4.0e-01	8.0e-05
23799	AT3G57560.1	7e-45	-1.60	-1.37	-1.54	-1.60	-2.12	4.2e-03	2.5e-02	7.2e-03	5.7e-03	7.3e-17
23800	AT3G57560.1	4e-34				1.17	2.79	3.6e-01	3.5e-01	2.8e-01	7.8e-02	3.3e-12
23813	AT1G07520.1	1e-57	-1.44	-1.41	-1.33	-1.15	-3.98	1.8e-02	2.4e-02	3.8e-02	9.7e-02	6.5e-19
23875			-1.01				-1.38	2.3e-01	4.1e-01	5.6e-01	6.4e-01	3.6e-04
23881	AT2G20390.1	3e-59	1.13			1.11	1.05	4.6e-02	6.8e-01	3.6e-01	5.1e-02	3.8e-07
23980	AT3G27020.1	9e-168					-2.56	7.2e-01	1.6e-01	1.7e-01	1.6e-01	2.7e-07
23990	AT4G23520.1	4e-18					-2.72	1.5e-01	5.7e-01	6.6e-01	4.6e-01	1.0e-07
23998	AT3G19420.1	1e-42	-1.16	-1.22		-1.32	-1.43	5.9e-02	3.7e-02	2.3e-01	2.3e-02	4.1e-09
24068							2.34	4.1e-01	2.5e-01	3.0e-01	5.4e-01	2.9e-06
24071	AT3G01410.1	2e-69	3.24	2.39	2.37	2.29	2.93	1.9e-19	9.2e-12	8.3e-12	2.7e-10	3.8e-65
24082			2.57	2.21	2.46	2.11	4.72	9.9e-07	5.2e-05	3.6e-06	1.6e-04	5.8e-29
24142	AT4G38090.1	2e-41		-1.25			-1.77	8.1e-01	7.1e-02	4.5e-01	3.9e-01	1.8e-04
24206	AT1G43630.1	1e-17					-2.04	NA	NA	NA	NA	1.4e-04
24263	AT5G11800.1	1e-39		-1.07			-1.61	7.0e-01	1.8e-01	5.0e-01	3.0e-01	5.6e-05
24269	AT5G42620.1	2e-79	-1.40	-1.07			-1.24	2.5e-02	1.3e-01	5.6e-01	6.5e-01	1.7e-04
24329			-1.53	-1.03	-1.17		-1.41	5.9e-03	1.4e-01	6.7e-02	2.5e-01	2.7e-06
24360	AT1G17200.1	2e-55					2.03	8.1e-01	6.9e-01	7.3e-01	4.8e-01	1.5e-04
24418	AT4G35580.1	2e-59	3.26	2.74	2.86	2.37	5.00	2.0e-11	5.4e-08	8.4e-09	7.5e-06	3.8e-33
24419				-1.40			-1.19	2.4e-01	1.6e-02	1.9e-01	5.7e-01	5.8e-04
24420	AT5G49300.1	7e-21					-1.95	3.7e-01	4.6e-01	6.1e-01	4.4e-01	7.9e-05
24421			3.28	2.34	2.72	2.37	4.80	1.8e-11	1.0e-05	8.0e-08	8.2e-06	2.2e-29
24458	AT3G26310.1	4e-116	2.70	1.98	2.11	1.62	4.00	1.8e-07	5.0e-04	1.4e-04	9.5e-03	1.6e-21
24507	AT4G27220.1	4e-61				1.22	1.07	2.9e-01	1.5e-01	1.2e-01	2.2e-02	1.7e-04
24552	AT4G27220.1	1e-14		1.06	1.27		2.54	2.7e-01	1.5e-01	5.3e-02	2.6e-01	4.4e-08
24582	AT2G04845.1	7e-41	1.21	1.32	1.19	1.57	2.37	1.0e-01	5.9e-02	1.1e-01	1.3e-02	1.9e-11
24585	AT3G25805.1	1e-13					2.16	NA	NA	NA	NA	4.7e-05
24586	AT4G31790.1	3e-53	-2.65	-2.64	-2.35	-2.05	-4.57	2.2e-07	2.6e-07	1.0e-05	2.3e-04	6.1e-27
24587	AT4G31790.1	2e-53		1.21	1.10		2.18	2.9e-01	7.1e-02	1.2e-01	3.5e-01	2.2e-05
24653	AT4G14370.1	1e-36	-2.04	-1.36	-1.13	-1.17	-3.28	2.1e-04	3.9e-02	1.4e-01	9.9e-02	2.8e-15
24683	AT3G56740.1	2e-16					2.31	5.8e-01	5.8e-01	5.2e-01	3.3e-01	6.2e-07
24732	AT2G37790.1	4e-135					-1.08	2.2e-01	1.7e-01	3.5e-01	2.8e-01	4.4e-06
24762	AT1G76270.1	0	-1.01	-1.01			-1.02	1.7e-02	1.2e-02	5.7e-02	5.0e-02	2.9e-10
24763	AT1G76270.1	2e-172					2.21	6.5e-01	4.4e-01	3.4e-01	4.8e-01	5.0e-06
24828			1.08		1.23	1.19	1.74	1.8e-01	4.8e-01	9.3e-02	1.1e-01	5.1e-07
24842	AT5G51130.1	6e-45	1.25				1.20	2.0e-02	1.7e-01	1.8e-01	1.9e-01	5.9e-10
24843			-1.70	-1.35	-1.11		-3.08	3.2e-03	3.7e-02	1.3e-01	4.2e-01	9.1e-12
24926	AT1G65650.1	3e-96	-1.43	-1.95	-1.27	-1.54	-2.45	3.0e-02	5.7e-04	7.0e-02	1.5e-02	5.3e-14

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
24929	AT1G26690.1	4e-27		-1.07	-1.05		-2.35	3.5e-01	1.6e-01	1.7e-01	2.2e-01	7.4e-08
24947	AT1G77140.1	1e-100	-1.10	-1.12			-1.82	1.4e-01	1.3e-01	7.3e-01	4.7e-01	1.8e-04
24999	AT1G18680.1	3e-25		1.39	1.19	1.42	2.17	3.2e-01	2.8e-02	8.9e-02	2.3e-02	3.5e-05
25016	AT5G60930.1	1e-13	2.06	2.39	2.28	2.54	3.18	3.2e-05	4.4e-07	1.8e-06	8.7e-08	2.0e-39
25032	AT4G20070.1	4e-15	1.97	2.48	1.92	1.85	3.47	5.3e-04	2.0e-06	7.1e-04	1.5e-03	3.9e-24
25034			1.38		1.27	1.34	1.83	3.5e-02	3.8e-01	6.2e-02	4.7e-02	5.9e-10
25103	AT3G02040.1	3e-34	1.49	1.57	1.09	1.26	3.65	1.4e-02	8.1e-03	1.4e-01	5.6e-02	4.1e-15
25107	AT4G37360.1	1e-93	1.59				1.81	1.1e-02	7.2e-01	7.1e-01	2.8e-01	1.6e-05
25154	AT1G35220.1	2e-61	1.42	1.27	1.27	1.38	3.61	2.2e-02	5.6e-02	5.6e-02	2.8e-02	5.6e-15
25291	AT4G29090.1	1e-40	1.26	1.25	1.41	1.35	3.23	6.7e-02	7.3e-02	3.0e-02	4.0e-02	2.9e-14
25303	AT4G34050.1	2e-81	1.04	1.66	1.33	1.14	1.39	5.6e-02	1.9e-04	8.2e-03	6.6e-02	3.0e-04
25331			1.18	1.24	1.31	1.34	3.38	8.8e-02	6.5e-02	4.7e-02	3.4e-02	1.6e-13
25361	AT1G17350.1	7e-32					1.07	2.5e-01	7.8e-01	5.7e-01	5.2e-01	3.2e-04
25371				-1.11			-2.30	NA	NA	NA	NA	1.1e-05
25380	AT2G34730.1	1e-33			1.15		1.77	7.9e-01	3.5e-01	1.2e-01	2.9e-01	4.6e-05
25397	AT1G34300.1	1e-109	-1.81	-1.49	-1.82	-2.02	-2.61	1.6e-03	1.6e-02	1.2e-03	2.2e-04	4.2e-18
25399	AT4G35040.1	4e-13					-2.51	7.8e-01	NA	NA	3.2e-01	1.2e-06
25417	AT4G01970.1	9e-167	1.94	1.58	1.01	1.41	1.67	1.6e-06	6.0e-04	8.5e-02	6.6e-03	2.2e-05
25428	AT3G21820.1	3e-88	2.12	1.67	2.05	1.43	3.39	1.7e-04	6.9e-03	2.9e-04	3.3e-02	3.8e-20
25437	AT3G21820.1	2e-46	-1.21				-1.40	9.7e-02	7.4e-01	3.3e-01	2.7e-01	4.2e-05
25441	AT2G37195.1	5e-25					1.93	NA	NA	NA	NA	3.6e-04
25450	AT5G15680.1	1e-12					-1.18	3.8e-01	4.7e-01	5.2e-01	3.8e-01	1.9e-04
25464	AT2G30360.1	3e-15			1.06		1.50	4.5e-01	5.1e-01	1.9e-01	4.5e-01	7.8e-04
25482	AT4G30470.1	7e-133			1.27	1.63	1.16	9.1e-01	1.5e-01	5.4e-03	1.7e-04	1.4e-03
25485	AT1G09290.1	8e-13					2.91	1.6e-01	NA	NA	1.5e-01	3.3e-09
25516	AT3G25440.1	2e-67		1.01			1.07	4.5e-01	2.2e-01	6.2e-01	8.2e-01	6.1e-04
25541	AT2G25870.1	5e-75	1.07				2.92	8.7e-02	NA	NA	4.2e-01	3.7e-09
25620							1.61	4.9e-01	3.6e-01	3.5e-01	6.5e-01	4.1e-05
25625	AT4G11610.1	0		2.50	1.74	1.53	1.85	8.9e-01	1.1e-06	3.0e-03	1.6e-02	7.8e-05
25629	AT5G66180.1	4e-34					2.60	NA	NA	NA	NA	3.0e-07
25647	AT5G17370.1	8e-23			1.04		2.86	5.5e-01	NA	NA	4.0e-01	1.1e-08
25652	AT2G43400.1	4e-51	-1.70	-1.18	-1.09	-1.36	-1.88	2.4e-03	8.3e-02	1.3e-01	3.0e-02	5.9e-14
25658	AT2G43400.1	9e-52				1.24	1.12	1.9e-02	2.4e-02	3.7e-02	8.8e-04	5.9e-13
25660	AT4G22260.1	8e-54				-1.21	-1.44	6.0e-01	4.8e-01	4.9e-01	9.8e-02	1.3e-04
25713			1.17		1.03	1.56	1.30	2.2e-02	1.5e-01	3.8e-02	2.2e-04	2.2e-08
25715	AT5G51630.1	4e-24	4.03	4.02	3.86	3.45	5.78	8.1e-21	6.9e-21	1.5e-19	8.8e-15	1.5e-54
25737	AT3G48120.1	3e-23			-1.10		-1.16	4.4e-01	2.8e-01	9.1e-02	3.3e-01	9.8e-07
25798	AT2G36840.1	0				-1.57		4.6e-01	9.8e-01	1.6e-01	1.7e-06	3.5e-03
25824	AT4G23160.1	5e-86					1.28	5.9e-01	3.1e-01	6.9e-01	4.7e-01	1.7e-04
25852	AT2G21170.1	3e-78					1.39	5.9e-01	4.6e-01	6.3e-01	5.2e-01	7.3e-04
25872			1.07		1.00		1.26	1.8e-01	6.5e-01	2.4e-01	7.3e-01	2.2e-04
25880	AT1G11660.1	6e-36	-1.37	-1.39			-2.77	3.4e-02	3.1e-02	2.4e-01	2.1e-01	1.7e-10
25887	AT2G23460.1	0				-1.25	-1.06	2.7e-01	8.9e-01	4.4e-01	3.9e-02	5.6e-04
25910	AT4G20520.1	8e-27					2.80	5.7e-01	NA	NA	4.8e-01	2.4e-08
25965	AT3G46180.1	2e-85					-1.90	6.5e-01	NA	NA	4.8e-01	1.3e-04
25972					1.02	1.12	2.49	8.4e-01	NA	NA	6.3e-02	9.0e-07
25980	AT5G51550.1	3e-15	1.03	1.18	1.24	1.34	2.29	2.2e-01	1.2e-01	8.8e-02	5.1e-02	5.0e-11
26016	AT4G13250.1	1e-51	-1.30				-2.16	3.2e-02	4.3e-01	6.1e-01	4.7e-01	1.4e-05
26030	AT5G59770.1	9e-36	-1.48	-1.31	-1.89	-1.73	-2.01	4.7e-03	1.4e-02	3.1e-05	3.0e-04	6.3e-18
26038	AT5G59770.1	6e-25	1.64	1.51	1.34	1.53	1.77	4.9e-04	1.1e-03	5.6e-03	6.8e-04	2.0e-14
26061	AT5G42960.1	8e-72					-1.01	3.5e-01	3.6e-01	2.5e-01	5.2e-01	1.2e-04
26082			-1.10	-1.66			-2.99	1.1e-01	2.6e-03	1.8e-01	6.4e-01	1.3e-09
26083	AT5G54090.1	1e-19					-1.87	9.7e-01	NA	NA	6.3e-01	5.2e-04
26098	AT1G55930.1	4e-13		1.18	1.40		2.37	2.7e-01	9.9e-02	3.1e-02	5.0e-01	4.6e-07

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
26136	AT3G28910.1	1e-84	3.05	2.75	2.76	3.19	3.24	1.8e-22	1.7e-18	1.0e-18	1.2e-24	8.1e-91
26164	AT1G79910.2	1e-33					1.89	3.8e-01	7.2e-01	5.6e-01	5.4e-01	5.7e-05
26185	AT4G09740.1	2e-17	1.25	1.11			2.00	5.1e-02	1.1e-01	7.5e-01	7.5e-01	1.0e-04
26204	AT3G52050.2	2e-57					1.15	4.0e-01	7.8e-01	7.6e-01	3.5e-01	8.0e-04
26259	AT1G05870.1	1e-33	-1.64		-1.43	-1.26	-1.57	2.2e-03	1.8e-01	8.1e-03	3.0e-02	2.7e-08
26306	AT2G01050.1	4e-51					2.73	7.9e-01	NA	NA	2.4e-01	7.1e-08
26369	AT1G12220.1	2e-27					2.27	3.9e-01	NA	NA	5.4e-01	1.8e-06
26373	AT3G51550.1	0					1.42	8.0e-01	3.5e-01	5.5e-01	2.8e-01	7.5e-04
26392	AT5G63180.1	8e-163			1.25	2.23	1.16	9.1e-01	8.5e-02	8.0e-03	5.4e-08	4.7e-04
26445			1.09	1.61	1.32	1.32	2.96	1.6e-01	8.3e-03	5.4e-02	5.1e-02	3.7e-12
26446	AT1G53490.1	6e-66					1.74	8.2e-01	7.6e-01	5.5e-01	6.1e-01	2.6e-04
26458	AT3G47080.1	4e-84					-1.94	7.5e-01	6.5e-01	6.3e-01	5.3e-01	3.3e-04
26522							-2.02	NA	NA	NA	NA	1.7e-04
26555	AT3G14470.1	4e-93					-2.61	5.5e-01	4.3e-01	6.2e-01	4.0e-01	3.8e-07
26557	AT3G54300.1	1e-45	-2.17	-1.40	-1.57	-1.38	-2.04	5.3e-06	9.9e-03	2.3e-03	1.2e-02	7.4e-18
26563	AT2G36070.1	4e-16	1.23				1.18	3.2e-02	5.5e-01	1.8e-01	1.5e-01	7.0e-07
26577	AT2G45180.1	1e-32	-1.81					1.1e-06	8.8e-01	2.4e-01	5.0e-01	6.3e-01
26582	AT2G41520.1	2e-13	-1.81	-2.24	-2.00	-1.42	-4.00	2.1e-03	3.9e-05	4.0e-04	3.3e-02	3.4e-20
26585	AT5G40610.1	3e-73					2.24	4.8e-01	NA	NA	8.5e-01	1.8e-05
26601	AT5G02190.1	1e-34	1.14	2.11	1.26	2.36	2.48	1.3e-01	1.0e-04	6.5e-02	5.7e-06	3.7e-11
26604	AT3G54300.1	2e-143		1.22	1.28	1.45	1.56	1.5e-01	3.5e-02	2.4e-02	6.9e-03	8.8e-15
26605	AT3G54300.1	9e-143	-1.63	-1.57	-1.72	-1.87	-3.36	8.7e-03	1.3e-02	4.8e-03	1.4e-03	3.9e-19
26617	AT4G14605.1	3e-25	-1.25	-1.73	-1.40	-1.06	-2.24	8.0e-02	3.7e-03	3.4e-02	1.8e-01	6.3e-12
26627			-1.59	-1.42	-1.17		-3.00	6.4e-03	2.3e-02	9.4e-02	5.6e-01	4.5e-10
26646	AT5G12080.1	1e-95	-1.33	-1.79	-1.32		-2.66	5.0e-02	2.2e-03	5.2e-02	6.1e-01	1.6e-08
26698	AT5G11980.1	2e-17			-1.05		-2.30	5.8e-01	2.6e-01	1.4e-01	3.6e-01	9.6e-07
26705	AT5G53850.2	2e-122	-1.54	-1.42	-1.31	-1.46	-1.56	9.4e-06	2.5e-05	1.6e-04	6.2e-05	1.7e-28
26741	AT5G42905.1	1e-18	-1.90	-1.84	-1.74	-1.59	-5.02	8.1e-04	1.3e-03	3.0e-03	9.0e-03	1.9e-30
26771	AT2G21550.1	2e-24	1.48		1.54	1.38	3.05	1.7e-02	5.6e-01	1.2e-02	3.1e-02	1.0e-11
26779					1.47	1.03	1.56	5.1e-01	3.3e-01	2.3e-02	2.0e-01	3.2e-06
26782	AT2G21170.1	2e-47	-1.83	-1.63	-1.35	-1.50	-2.62	1.9e-03	8.2e-03	5.0e-02	2.1e-02	1.1e-16
26816	AT4G19880.1	2e-53			1.21	1.06	1.37	9.8e-01	4.0e-01	1.0e-01	1.8e-01	3.8e-04
26890	AT1G22400.1	5e-128	-1.13				-2.13	5.7e-02	3.5e-01	7.1e-01	8.0e-01	4.1e-05
26894	AT5G09300.1	5e-72	-1.38	-1.35	-1.32	-1.24	-3.66	2.9e-02	3.4e-02	4.2e-02	6.1e-02	2.4e-15
26898	AT3G01435.1	1e-38				1.03	1.07	2.8e-02	3.0e-02	7.8e-02	1.9e-02	2.3e-15
26910	AT3G13226.1	2e-26		1.16	1.02	1.05	2.71	5.6e-01	8.5e-02	1.7e-01	1.4e-01	2.6e-09
26915	AT3G18670.1	3e-18	1.12	1.41	1.42	1.36	3.57	1.2e-01	2.5e-02	2.4e-02	3.1e-02	6.4e-15
26917	AT1G75130.1	2e-67				1.22	2.47	7.5e-01	NA	NA	3.9e-02	1.2e-06
26921			-1.40	-1.62	-1.49	-1.46	-3.71	3.0e-02	7.2e-03	1.8e-02	2.0e-02	3.8e-16
26945	AT1G48900.1	6e-77	1.89	1.79	1.79	2.38	3.04	1.3e-03	2.7e-03	2.8e-03	1.1e-05	1.3e-12
26947			2.08	2.22	2.40	1.92	4.31	2.4e-04	5.5e-05	8.4e-06	9.4e-04	5.0e-30
27028	AT2G22400.1	7e-27	1.03	1.11			1.33	2.0e-01	1.4e-01	5.4e-01	5.1e-01	2.0e-05
27066	AT2G38430.1	3e-15	1.20	1.19	1.09	1.08	3.22	6.7e-02	7.4e-02	1.2e-01	1.2e-01	1.5e-11
27079							2.11	NA	NA	NA	NA	7.6e-05
27104	AT4G23160.1	1e-108					1.82	7.5e-01	5.2e-01	5.1e-01	7.3e-01	5.6e-04
27195				-1.05			-2.99	5.2e-01	1.1e-01	2.4e-01	1.4e-01	1.4e-09
27228	AT5G67360.1	9e-26		-1.08			-1.83	6.9e-01	1.6e-01	3.1e-01	3.9e-01	5.5e-05
27232			-2.06	-1.85	-1.23		-2.21	2.0e-04	1.3e-03	8.7e-02	3.2e-01	2.0e-09
27260	AT1G11840.2	3e-11	1.35	2.04	2.34	1.46	3.89	4.6e-02	2.5e-04	1.3e-05	2.4e-02	1.8e-17
27264	AT1G70750.1	7e-91	1.09	1.11	1.39		2.17	1.7e-01	1.6e-01	4.1e-02	3.2e-01	4.8e-08
27284							-1.84	4.3e-01	6.1e-01	6.1e-01	6.1e-01	6.7e-04
27318	AT5G14220.1	5e-79				1.15	1.05	2.8e-01	3.3e-01	8.3e-01	8.8e-02	6.4e-05
27322	AT5G15400.1	7e-18					1.71	3.6e-01	3.3e-01	5.7e-01	4.8e-01	3.3e-05
27356							-1.82	NA	NA	NA	NA	8.2e-04

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
27417	AT1G65590.1	1e-20			1.02		1.71	8.8e-01	2.3e-01	1.9e-01	5.2e-01	7.0e-04
27427	AT5G25770.1	9e-86			1.36		1.50	6.8e-01	4.3e-01	4.9e-02	4.4e-01	1.2e-05
27518	AT1G01140.2	3e-16					-1.06	4.5e-01	4.2e-01	3.4e-01	7.7e-01	9.7e-04
27521	AT2G31580.1	2e-105				1.02	1.48	3.9e-01	4.6e-01	3.7e-01	2.2e-01	1.9e-05
27534	AT1G43760.1	3e-44	4.15	4.09	4.28	3.86	6.18	1.4e-22	5.7e-22	2.7e-24	1.8e-19	7.5e-63
27535	AT4G29090.1	5e-37	1.01	1.19	1.17		3.25	1.5e-01	6.2e-02	7.1e-02	3.1e-01	1.6e-11
27580			7.26	6.99	7.24	7.58	9.22	1.0e-104	8.5e-96	3.2e-104	9.9e-113	7.6e-169
27604	AT3G47370.2	5e-12	3.73	3.15	2.95	3.18	5.23	7.8e-16	3.3e-11	8.3e-10	3.4e-11	3.1e-45
27638	AT1G71190.1	2e-14	1.13	1.02	1.36	1.52	3.33	1.1e-01	1.8e-01	3.3e-02	1.0e-02	2.4e-12
27639	AT1G71190.1	1e-30				-1.30	-1.07	7.5e-01	6.2e-01	1.8e-01	2.7e-02	4.0e-05
27697	AT5G24600.1	1e-36		-1.02			-2.21	8.2e-01	8.8e-02	4.0e-01	5.2e-01	2.9e-05
27701	AT1G25380.1	3e-13	1.46	1.02			1.62	2.7e-02	2.3e-01	7.3e-01	5.3e-01	2.3e-05
27756	AT2G45320.1	2e-25		-1.06		-1.38	-1.37	9.2e-01	1.9e-01	4.2e-01	4.2e-02	8.4e-04
27772	AT3G14470.1	8e-37	1.93	2.06	2.48	2.35	3.67	6.6e-04	1.8e-04	2.0e-06	9.7e-06	2.8e-30
27776			-1.52			-1.35	-1.43	9.1e-03	3.9e-01	4.8e-01	3.0e-02	4.0e-07
27834	AT4G33870.1	4e-13	-1.43	-1.14		-1.19	-1.37	1.8e-02	7.9e-02	5.5e-01	7.3e-02	6.5e-06
27849	AT3G61600.1	2e-36					-1.24	6.3e-01	4.5e-01	6.4e-01	3.9e-01	5.2e-04
27874	AT5G17680.1	1e-100	-1.36	-2.16	-2.32	-2.21	-4.05	4.6e-02	9.2e-05	1.9e-05	5.8e-05	2.6e-20
27879	AT4G27720.1	1e-46				-1.18	-1.29	4.3e-01	6.8e-01	5.3e-01	1.1e-01	5.5e-05
27890	AT1G14590.1	3e-71					1.12	7.1e-01	5.9e-01	4.6e-01	2.9e-01	3.1e-04
27924	AT3G45300.1	8e-149	2.30	2.86	2.28	2.48	3.73	6.6e-06	4.2e-09	7.0e-06	1.0e-06	2.1e-39
27927				-1.41		-1.37	-1.57	3.6e-01	2.5e-02	5.0e-01	3.3e-02	1.3e-07
27930	AT5G63640.1	4e-12	-1.83		-1.40	-1.36	-2.00	1.6e-03	3.6e-01	3.3e-02	4.1e-02	7.6e-11
28017							2.40	2.6e-01	NA	NA	6.6e-01	3.8e-06
28028	AT5G47890.1	2e-11	-1.22	-1.23			-2.33	7.7e-02	7.3e-02	6.1e-01	4.0e-01	1.7e-07
28029	AT4G14605.1	1e-13	1.67	1.45	1.03	1.27	3.10	5.1e-03	2.3e-02	2.1e-01	6.2e-02	2.1e-12
28060			1.21	1.18	1.25		1.98	1.0e-01	1.2e-01	8.4e-02	6.3e-01	1.8e-08
28081	AT1G26460.1	1e-36	-1.19				-1.64	1.1e-01	3.2e-01	8.5e-01	2.6e-01	1.3e-04
28098	AT4G39230.1	1e-117	1.26				2.05	4.1e-02	4.0e-01	8.9e-01	3.2e-01	7.3e-05
28113	AT3G25680.1	7e-22					1.82	4.3e-01	4.6e-01	4.2e-01	2.9e-01	1.5e-06
28114	AT1G14590.1	2e-71	-1.23	-1.60	-1.54	-2.00	-3.71	8.3e-02	9.0e-03	1.4e-02	3.1e-04	7.6e-16
28137	AT4G33170.1	5e-24	1.86	1.35	1.52	1.20	2.41	1.4e-03	4.6e-02	1.7e-02	9.8e-02	3.5e-15
28141	AT1G68310.2	3e-60	1.53		1.03	1.43	2.68	1.5e-02	2.8e-01	2.1e-01	2.5e-02	2.9e-10
28192	AT2G32810.1	1e-96			-1.09	-1.45	-1.24	6.3e-01	9.6e-02	4.7e-02	2.4e-03	7.6e-05
28195	AT4G24210.1	2e-38	1.11		1.07	1.04	1.21	5.7e-02	4.1e-01	7.3e-02	1.1e-01	2.7e-07
28205	AT1G56080.1	7e-34	1.21	1.24	1.19	1.41	3.08	8.7e-02	7.4e-02	9.4e-02	2.7e-02	1.4e-13
28210	AT5G10610.1	3e-50		-1.24	-1.54	-1.30	-2.59	5.4e-01	7.1e-02	1.1e-02	4.8e-02	8.6e-08
28253	AT4G17420.1	3e-37					2.54	3.4e-01	5.0e-01	4.6e-01	5.5e-01	8.9e-10
28270	AT3G53970.2	1e-12	-1.55	-1.74	-1.56	-1.61	-3.65	1.4e-02	3.7e-03	1.4e-02	9.4e-03	7.8e-20
28278	AT3G53970.2	2e-20	2.38	2.25	2.80	2.40	3.66	2.2e-06	8.3e-06	5.7e-09	1.8e-06	5.0e-38
28338	AT3G01990.1	7e-161			-1.32	-1.14	-1.31	6.8e-01	3.5e-01	3.3e-02	9.5e-02	4.1e-05
28409	AT2G33590.1	1e-30				1.06	1.91	5.7e-01	2.3e-01	4.8e-01	1.5e-01	3.5e-05
28452	AT5G24090.1	7e-126					-2.41	5.5e-01	4.0e-01	3.2e-01	3.3e-01	1.9e-06
28461	AT5G62620.1	6e-113	1.07	1.09	1.00		3.54	1.3e-01	1.2e-01	1.8e-01	2.7e-01	7.3e-24
28518	AT5G23340.1	2e-22	2.82	2.45	2.69	2.82	4.95	2.8e-08	3.0e-06	1.5e-07	2.5e-08	3.2e-34
28550	AT5G06530.2	0	-1.13	-1.36			-1.72	1.5e-01	4.7e-02	4.4e-01	7.2e-01	1.3e-04
28623	AT2G02250.1	3e-16			-1.10		-2.03	5.4e-01	2.8e-01	1.4e-01	2.2e-01	3.0e-05
28635				-1.22	-1.38	-1.38	-4.07	2.0e-01	6.2e-02	2.4e-02	2.2e-02	2.0e-18
28655				-1.31	-1.58	-1.51	-2.48	6.0e-01	6.2e-02	1.2e-02	1.9e-02	3.7e-10
28728	AT1G38131.1	1e-22			1.09		2.19	7.1e-01	2.2e-01	1.2e-01	3.7e-01	1.1e-05
28730							-1.90	4.6e-01	4.5e-01	8.4e-01	7.1e-01	4.6e-04
28770	AT4G27300.1	0	-1.00	-1.51	-1.49	-1.18	-1.88	2.4e-01	1.9e-02	2.4e-02	1.1e-01	1.4e-04
28776	AT4G24140.1	7e-35	2.19	1.93	1.74	1.87	2.02	2.4e-16	8.7e-13	1.6e-10	5.0e-12	2.1e-35
28784	AT2G37400.1	5e-64	-1.02	-1.07	-1.09	-1.18	-2.21	2.2e-01	1.8e-01	1.7e-01	1.1e-01	3.1e-08

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
28807	AT2G44190.1	1e-35		1.48	1.11	1.11	1.75	4.4e-01	2.4e-02	1.6e-01	1.6e-01	4.0e-06
28842							-2.06	5.1e-01	3.5e-01	4.0e-01	6.5e-01	1.7e-05
28849	AT2G17420.1	2e-31		-1.16	-1.23		-1.36	2.5e-01	7.8e-02	5.3e-02	2.8e-01	4.7e-06
28904	AT4G29130.1	8e-71			-1.21		-1.19	4.1e-01	2.2e-01	3.8e-02	1.8e-01	1.6e-08
28907			1.41	1.72	1.55	1.63	2.98	3.6e-02	4.7e-03	1.5e-02	9.1e-03	1.8e-22
28940	AT3G02100.1	6e-60				-1.22	-1.72	6.0e-01	5.2e-01	5.3e-01	8.1e-02	1.2e-04
28951	AT5G19440.1	5e-67	-1.93	-1.34	-1.17	-1.03	-1.36	6.4e-05	8.7e-03	3.3e-02	7.6e-02	3.9e-04
28973	AT4G02330.1	1e-67		1.48			1.14	4.1e-01	1.2e-02	7.9e-01	6.2e-01	6.2e-04
28990	AT5G57290.1	1e-16	2.01	1.70	1.83	1.55	2.51	1.5e-04	2.6e-03	8.5e-04	9.3e-03	2.5e-19
29023	AT4G16850.1	3e-46					-1.17	6.6e-01	6.4e-01	3.0e-01	4.2e-01	6.3e-04
29028				1.07			2.86	2.2e-01	1.2e-01	3.4e-01	2.4e-01	9.6e-10
29097	AT3G17880.1	6e-55	-2.30	-2.16	-2.10	-1.92	-4.27	2.4e-05	1.0e-04	1.8e-04	9.4e-04	3.5e-29
29099	AT1G48120.1	3e-37	1.19	1.27	1.22	1.12	3.02	9.6e-02	6.3e-02	8.5e-02	1.2e-01	1.7e-14
29332	AT1G74700.1	6e-54	1.03	1.24			2.02	2.1e-01	7.8e-02	3.0e-01	7.2e-01	5.5e-07
29363	AT2G47640.1	1e-32			-1.19	-1.33	-1.22	8.0e-02	4.0e-02	6.4e-03	2.7e-03	2.6e-09
29370	AT4G23160.1	3e-56					1.62	6.3e-01	8.3e-01	6.8e-01	3.7e-01	6.9e-04
29372			-1.21			-1.77	-2.16	1.1e-01	2.5e-01	5.0e-01	3.0e-03	2.8e-08
29392	AT3G27520.1	3e-21	1.63	1.85	2.10	2.15	3.32	8.6e-03	1.4e-03	1.6e-04	1.1e-04	1.9e-30
29427	AT2G31140.1	3e-32					1.98	3.9e-01	6.8e-01	6.9e-01	6.4e-01	6.6e-05
29461	AT3G55470.1	3e-37		1.02	1.53	1.56	1.65	3.5e-01	1.5e-01	4.8e-03	4.1e-03	4.2e-08
29477	AT3G14470.1	1e-67	1.44	1.14	1.50		1.86	2.5e-02	1.3e-01	1.9e-02	5.4e-01	1.6e-08
29482							2.20	NA	NA	NA	NA	3.2e-05
29514			1.06				1.31	1.4e-01	3.3e-01	2.1e-01	2.7e-01	4.0e-05
29534	AT1G18440.1	3e-31	1.35	1.09	1.37		3.43	2.8e-02	1.2e-01	2.6e-02	2.4e-01	4.8e-13
29548	AT4G27585.1	7e-17					-1.71	2.2e-01	4.4e-01	8.0e-01	4.3e-01	1.6e-04
29588	AT1G54540.1	2e-73			1.03		1.02	4.5e-01	5.3e-01	1.7e-01	7.7e-01	6.8e-04
29624	AT2G38710.1	3e-19					1.83	6.4e-01	6.8e-01	6.2e-01	4.8e-01	5.1e-04
29640	AT1G13570.1	2e-31					-2.16	6.0e-01	5.9e-01	6.4e-01	4.3e-01	4.7e-05
29645	AT3G46550.1	4e-36	-1.03	-1.08		-1.05	-2.42	1.8e-01	1.5e-01	3.5e-01	1.6e-01	5.2e-08
29646	AT3G46550.1	2e-31			1.22	1.09	2.05	7.5e-01	3.2e-01	7.9e-02	1.4e-01	6.6e-06
29647	AT3G18620.1	1e-31		1.03	1.01		1.96	6.4e-01	NA	NA	5.4e-01	3.2e-05
29658	AT4G02980.1	2e-16	1.46	1.40	1.15	1.03	3.47	1.6e-02	2.3e-02	1.0e-01	1.6e-01	1.7e-13
29688	AT2G31900.1	0	-1.02	-1.21	-1.13		-2.10	2.1e-01	9.3e-02	1.4e-01	3.2e-01	7.8e-06
29734	AT3G49590.2	5e-36				-1.21	-1.11	5.5e-01	4.1e-01	1.8e-01	3.8e-02	1.1e-05
29761	AT3G11370.1	4e-14	2.40	2.45	2.58	2.73	4.67	5.8e-06	3.0e-06	5.7e-07	9.7e-08	1.1e-31
29762							-1.84	NA	NA	NA	NA	6.6e-04
29763	AT2G37025.1	1e-21	-1.19	-1.58	-1.72	-1.80	-1.90	2.9e-02	4.3e-04	7.4e-05	5.2e-05	4.5e-17
29813	AT2G30720.1	2e-41	-1.21	-1.26	-1.31	-1.30	-3.40	7.4e-02	5.9e-02	4.5e-02	4.3e-02	3.6e-13
29834	AT5G54310.1	2e-35					-1.65	2.2e-01	5.8e-01	6.6e-01	4.7e-01	2.1e-04
29911	AT5G42920.1	3e-25		-1.05		-1.05	-1.31	3.1e-01	1.5e-01	2.9e-01	1.5e-01	1.5e-07
30093	AT5G44530.1	4e-54	-2.02	-1.91	-2.33	-2.65	-4.48	3.8e-04	9.7e-04	1.6e-05	3.9e-07	3.9e-25
30121	AT5G03570.1	7e-73					-2.04	NA	NA	NA	NA	1.4e-04
30134	AT1G02010.1	6e-86					-1.80	9.1e-01	5.7e-01	6.6e-01	2.2e-01	9.0e-04
30137	AT1G21280.1	2e-11		1.10	1.09		1.77	4.9e-01	1.7e-01	1.7e-01	4.7e-01	1.3e-07
30138	AT4G39520.1	2e-28					2.37	3.6e-01	5.1e-01	6.9e-01	4.4e-01	3.7e-07
30143					1.04		2.41	7.3e-01	NA	NA	4.9e-01	3.7e-06
30165	AT1G31160.1	1e-63			1.12		1.54	4.4e-01	6.4e-01	1.6e-01	3.5e-01	4.3e-06
30174	AT5G17165.1	3e-27			-1.49	-1.59	-1.28	3.8e-01	6.9e-01	3.4e-03	8.0e-04	2.8e-03
30195	AT3G21670.1	0	-1.18	-1.14	-1.71	-1.71	-2.38	1.1e-01	1.4e-01	4.4e-03	5.0e-03	5.3e-12
30224	AT3G06560.1	3e-62	-1.27	-1.06	-1.06		-2.62	5.0e-02	1.5e-01	1.5e-01	4.8e-01	1.5e-08
30262	AT4G03100.1	3e-21	3.03	2.81	2.77	2.18	4.61	6.5e-10	1.6e-08	2.7e-08	5.5e-05	1.6e-31
30328							-3.06	4.3e-01	3.9e-01	3.7e-01	4.3e-01	1.2e-09
30332	AT4G38380.1	5e-142			1.40		1.23	9.0e-01	2.5e-01	3.0e-02	2.9e-01	1.4e-04
30333	AT2G17900.1	2e-27					1.82	5.9e-01	6.0e-01	5.8e-01	5.2e-01	1.5e-04

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
30334	AT2G17900.1	5e-43					-1.28	7.3e-01	3.5e-01	7.0e-01	3.5e-01	4.7e-04
30440				-1.18	-1.07	-1.30	-2.89	2.5e-01	8.5e-02	1.5e-01	4.3e-02	4.2e-10
30459	AT2G36750.1	1e-44	-1.39	-1.31			-1.63	3.8e-02	5.8e-02	2.7e-01	8.5e-01	4.2e-06
30461	AT1G13570.1	8e-28	2.76	2.49	2.31	2.37	4.58	5.9e-08	1.7e-06	1.5e-05	8.2e-06	8.7e-29
30478	AT3G53990.2	3e-39	1.33	1.65	1.52	1.78	2.17	5.0e-02	6.4e-03	1.6e-02	2.3e-03	4.4e-05
30504	AT3G14130.1	2e-146		1.26			1.21	2.5e-01	3.5e-02	2.6e-01	3.9e-01	3.9e-06
30526	AT1G09280.1	5e-63	2.03	2.09	2.08	1.34	4.07	3.3e-04	1.6e-04	1.9e-04	5.0e-02	1.1e-20
30544	AT5G25610.1	4e-65		1.49	1.45	1.75	1.35	8.4e-01	1.5e-03	2.4e-03	1.8e-04	2.9e-05
30645	AT3G48250.1	1e-35			-1.04		-1.31	2.0e-01	2.6e-01	1.7e-01	4.5e-01	2.5e-05
30672	AT4G10150.1	2e-28	1.34				1.18	5.1e-02	8.2e-01	5.1e-01	6.8e-01	5.5e-04
30694				1.11			1.93	2.1e-01	9.8e-02	7.3e-01	8.3e-01	9.4e-05
30777	AT1G53050.1	0		-1.18	-1.07	-1.04	-1.80	7.2e-01	1.1e-01	1.9e-01	1.9e-01	8.1e-05
30796							-2.16	4.3e-01	NA	NA	7.2e-01	4.8e-05
30915	AT5G13430.1	7e-26					3.11	1.5e-01	1.3e-01	3.6e-01	3.1e-01	1.9e-10
30919						-1.33	-1.05	1.3e-01	4.0e-01	7.4e-02	1.1e-03	1.5e-04
30953	AT2G33560.1	7e-13		-1.40	-1.27		-3.00	2.9e-01	1.7e-02	4.1e-02	6.0e-01	1.3e-09
30969	AT3G03300.1	3e-87		-1.24		-1.26	-1.37	9.4e-01	7.9e-02	3.2e-01	6.5e-02	1.0e-04
30970	AT5G45170.1	7e-17			1.01		1.21	4.6e-01	3.2e-01	2.2e-01	7.3e-01	1.5e-04
30987	AT2G01050.1	5e-46					2.23	4.9e-01	6.5e-01	4.8e-01	5.9e-01	1.2e-06
31027				-1.09		-1.26	-2.59	3.7e-01	1.3e-01	2.7e-01	5.3e-02	2.3e-08
31035	AT4G25600.1	5e-28					2.43	NA	NA	NA	NA	2.8e-06
31080	AT5G23960.1	2e-132	1.61	1.10			2.48	6.2e-03	1.3e-01	6.2e-01	2.5e-01	5.1e-07
31120	AT2G05590.2	1e-106					-1.93	5.8e-01	2.2e-01	5.1e-01	7.3e-01	1.4e-04
31155	AT3G54250.1	1e-13					1.71	5.5e-01	7.5e-01	2.5e-01	2.5e-01	6.9e-05
31161	AT3G44710.1	5e-23	1.19	1.14			2.63	7.6e-02	9.6e-02	4.2e-01	3.3e-01	4.8e-08
31170					1.13		2.33	2.5e-01	2.5e-01	1.3e-01	2.3e-01	1.7e-09
31176			1.45	1.27	1.57	1.06	1.47	5.7e-06	1.4e-04	6.7e-07	4.8e-03	2.4e-21
31239			2.16	1.73	2.15	1.89	3.34	9.6e-05	3.7e-03	9.1e-05	1.1e-03	3.3e-26
31256	AT1G13810.1	9e-69					-3.27	3.3e-01	1.7e-01	3.8e-01	4.5e-01	4.1e-11
31261	AT3G23410.1	5e-46			-1.54	-1.62	-2.54	8.1e-01	3.0e-01	8.7e-03	5.1e-03	5.9e-07
31266	AT4G26190.1	5e-25					-1.83	2.2e-01	2.3e-01	7.5e-01	7.3e-01	1.8e-04
31277	AT4G24220.1	5e-90		2.79	2.43	1.78	2.10	2.5e-01	1.4e-11	7.5e-09	1.0e-04	1.4e-11
31312	AT5G50150.1	1e-125	1.25					2.9e-07	1.3e-04	2.6e-02	2.1e-01	2.4e-12
31358	AT4G13110.1	1e-12	1.09	1.14	1.63	1.06	3.33	1.3e-01	1.0e-01	4.7e-03	1.4e-01	2.8e-12
31407				1.13	1.07		3.16	2.1e-01	NA	NA	1.6e-01	5.5e-11
31470			1.19	1.09	1.20		2.72	8.9e-02	1.5e-01	8.5e-02	2.0e-01	9.6e-10
31500	AT4G36250.1	0		1.20	1.58	1.83	1.53	5.6e-02	1.1e-03	3.0e-06	2.2e-08	1.2e-14
31544	AT4G29090.1	8e-71	1.04	1.12	1.16		3.05	1.5e-01	9.7e-02	7.9e-02	4.2e-01	4.3e-11
31560	AT5G59930.1	4e-12	-1.20				-1.34	8.3e-02	3.0e-01	5.3e-01	2.6e-01	5.3e-06
31564	AT2G33793.1	4e-59					1.30	2.4e-01	2.3e-01	2.5e-01	3.2e-01	3.6e-06
31575	AT3G59500.1	6e-113			1.29		1.33	2.4e-01	4.8e-01	6.7e-02	8.9e-01	8.4e-04
31616	AT3G61870.1	7e-28					-2.22	3.8e-01	5.4e-01	4.2e-01	5.5e-01	9.8e-06
31625	AT2G42610.1	8e-77					-2.44	3.4e-01	4.4e-01	8.3e-01	5.9e-01	2.8e-06
31632							-1.33	3.4e-01	2.8e-01	5.5e-01	3.8e-01	5.4e-05
31657	AT5G11720.1	3e-158		1.31	1.03	1.05	1.58	7.2e-01	6.0e-02	2.2e-01	2.0e-01	4.8e-04
31693	AT5G01950.1	0	-1.16	-1.09			-2.39	8.4e-02	1.2e-01	4.3e-01	5.6e-01	1.0e-06
31697	AT2G25140.1	0	1.50	2.20	2.27	2.08	2.59	5.9e-03	4.9e-06	2.1e-06	3.5e-05	7.9e-24
31703	AT3G14000.1	1e-164					-1.09	2.7e-01	2.2e-01	6.2e-01	2.9e-01	2.0e-04
31766	AT4G16860.1	8e-26			1.14		2.77	8.0e-01	1.3e-01	5.6e-02	2.6e-01	4.7e-08
31795	AT1G65340.1	6e-72	2.05	2.25	2.07	2.04	2.84	4.1e-05	3.9e-06	2.8e-05	4.9e-05	7.4e-37
31811	AT4G36440.1	3e-34	1.52	1.43	1.69	1.09	3.61	1.3e-02	2.4e-02	3.9e-03	1.4e-01	5.5e-15
31832	AT5G24530.1	2e-72	-2.00	-1.61	-1.66	-2.08	-1.98	1.1e-06	5.1e-05	1.8e-05	1.6e-08	2.8e-11
31834							-3.23	4.2e-01	2.5e-01	2.4e-01	2.4e-01	5.5e-11
31849	AT2G30050.1	1e-97		-1.22	-1.06	-1.50	-3.23	2.2e-01	7.1e-02	1.5e-01	1.2e-02	1.0e-12

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
31874	AT5G14930.2	2e-16	1.85	1.86	1.61	1.81	4.06	1.5e-03	1.3e-03	9.4e-03	2.1e-03	5.6e-20
31877			-1.91	-1.59	-1.64	-1.13	-3.50	8.8e-04	1.0e-02	7.4e-03	1.3e-01	7.5e-17
31879	AT5G45530.1	2e-62		1.35	1.29	1.85	2.40	3.8e-01	4.7e-02	7.0e-02	1.7e-03	6.1e-09
31921			-1.33	-1.34	-1.65	-1.85	-3.81	4.6e-02	4.4e-02	5.8e-03	1.1e-03	9.8e-17
31926	AT4G02920.1	3e-20	-1.65	-1.72	-1.49	-1.74	-2.94	7.8e-03	4.6e-03	2.2e-02	4.0e-03	1.8e-17
31928	AT4G02920.2	7e-34	1.51	1.03	1.01		2.59	1.6e-02	2.0e-01	2.3e-01	2.4e-01	1.3e-11
31937	AT5G11680.1	2e-69					1.73	3.2e-01	2.5e-01	4.3e-01	2.5e-01	3.4e-07
31952			-2.05	-2.22	-2.11	-2.26	-4.52	2.7e-04	5.1e-05	1.5e-04	3.5e-05	5.6e-26
31959	AT4G23160.1	3e-44	1.27	1.16	1.14	1.56	2.21	7.6e-02	1.3e-01	1.4e-01	1.5e-02	3.3e-10
32004				1.45	1.29	1.69	2.04	7.1e-01	2.7e-02	6.7e-02	5.8e-03	1.2e-08
32015	AT1G09280.1	7e-29	1.46		1.14	1.11	2.90	1.8e-02	2.4e-01	1.2e-01	1.3e-01	7.4e-12
32035	AT5G14790.1	9e-26	-1.14	-1.03			-1.31	1.2e-01	1.8e-01	5.4e-01	2.6e-01	2.3e-05
32039	AT3G55580.1	1e-48		-1.61	-1.26		-1.84	8.5e-01	1.0e-02	8.0e-02	2.4e-01	1.2e-05
32044	AT4G39670.1	1e-44					2.69	1.6e-01	2.4e-01	5.1e-01	4.9e-01	2.3e-10
32049	AT2G31110.2	2e-15					-2.17	5.4e-01	NA	NA	7.2e-01	4.4e-05
32056	AT1G43760.1	7e-48	2.29	2.44	2.86	2.22	4.65	2.3e-05	3.4e-06	1.4e-08	4.9e-05	7.3e-28
32115	AT1G48120.1	4e-80	1.48	1.14	1.10	1.31	3.29	1.5e-02	1.1e-01	1.4e-01	4.2e-02	7.0e-13
32134	AT1G79080.1	6e-34	-1.29				-1.81	7.1e-02	3.0e-01	3.0e-01	5.7e-01	3.5e-07
32147	AT4G32300.1	2e-28		1.47	1.37	1.07	3.18	6.9e-01	1.1e-02	2.3e-02	1.1e-01	9.2e-11
32165	AT5G42905.1	8e-35					-2.13	9.1e-01	4.8e-01	3.9e-01	5.4e-01	6.1e-05
32313					1.07		2.16	4.3e-01	2.2e-01	1.6e-01	4.0e-01	1.4e-07
32387	AT2G42570.1	3e-172		-1.62	-2.11	-1.97	-1.91	9.5e-01	6.9e-03	7.9e-05	3.6e-04	4.3e-05
32516	AT3G14067.1	9e-115		3.68	2.84	1.89	2.17	9.0e-01	1.0e-15	2.1e-09	3.9e-04	2.8e-05
32577			-2.13	-1.68	-1.78	-1.88	-4.47	1.2e-04	5.6e-03	2.5e-03	1.1e-03	1.5e-24
32586							1.84	4.9e-01	8.2e-01	5.3e-01	4.3e-01	2.6e-04
32587	AT2G19220.1	4e-17					2.02	6.7e-01	6.2e-01	6.2e-01	5.3e-01	2.8e-06
32628	AT4G23160.1	4e-108					3.33	8.0e-01	4.1e-01	4.9e-01	4.9e-01	6.2e-13
32633	AT3G01090.1	3e-12					1.68	8.9e-01	4.5e-01	2.9e-01	4.4e-01	3.1e-04
32646	AT2G14050.1	2e-95	1.21	1.51	1.74	1.28	3.71	8.3e-02	1.4e-02	2.6e-03	5.3e-02	1.0e-15
32679	AT1G49750.1	2e-17					1.95	2.6e-01	2.2e-01	3.2e-01	3.9e-01	4.6e-05
32681	AT4G23520.1	4e-23			-1.07	-1.26	-2.70	2.1e-01	2.7e-01	1.5e-01	5.5e-02	1.5e-09
32848							1.88	NA	NA	NA	NA	5.3e-04
32853	AT5G47700.1	3e-13	-1.58		-1.60	-1.08	-1.91	8.3e-03	2.5e-01	7.4e-03	1.5e-01	3.4e-09
32865	AT4G36850.1	6e-59			-1.18	-1.33	-3.10	3.3e-01	2.4e-01	7.2e-02	2.8e-02	9.2e-11
32873	AT5G42905.1	2e-41	-1.07	-1.28	-1.12		-3.43	1.3e-01	4.0e-02	1.0e-01	1.7e-01	2.2e-13
33011							-1.82	3.9e-01	4.5e-01	7.7e-01	5.4e-01	3.4e-04
33036	AT4G11720.1	0	1.83	1.31	1.45	1.27	3.04	1.9e-03	6.0e-02	2.7e-02	6.7e-02	1.1e-12
33079	AT1G60460.1	1e-58			1.01	1.05	1.12	3.8e-01	4.3e-01	1.3e-01	1.1e-01	1.5e-06
33146	AT2G22460.1	3e-13	1.74	1.27	1.00		3.26	1.6e-03	4.7e-02	1.9e-01	3.6e-01	1.9e-11
33257	AT2G15630.1	5e-48	-1.37				-2.56	1.5e-02	4.6e-01	2.1e-01	7.2e-01	4.5e-07
33287	AT3G28700.1	7e-33					2.29	1.9e-01	NA	NA	2.5e-01	3.0e-06
33296	AT1G11320.1	1e-23				-1.08	-1.27	5.1e-01	5.9e-01	7.8e-01	1.7e-01	3.8e-04
33320						1.08	1.35	4.3e-01	5.1e-01	2.3e-01	1.6e-01	1.2e-06
33374	AT4G23160.1	3e-144	2.90	3.43	3.67	3.31	5.18	1.7e-09	3.1e-13	3.4e-15	4.3e-12	8.7e-52
33446	AT3G26200.1	2e-50		1.47	1.56	1.47	2.87	5.0e-01	2.1e-02	1.2e-02	2.1e-02	1.1e-10
33448	AT4G23160.1	3e-161	3.60	2.80	3.05	2.69	5.08	9.7e-15	1.0e-08	1.7e-10	7.0e-08	1.6e-34
33495	AT5G42905.1	8e-38	-1.05	-1.54	-1.26	-1.33	-3.46	1.7e-01	1.0e-02	5.9e-02	3.6e-02	1.7e-13
33548	AT3G14470.1	2e-75	-1.85	-1.22	-1.35	-1.40	-3.75	1.1e-03	8.0e-02	4.1e-02	2.8e-02	6.1e-16
33553	AT4G17720.1	7e-17					1.77	6.1e-01	2.3e-01	6.0e-01	5.8e-01	4.1e-05
33600	AT2G21070.1	6e-27	-2.00	-2.40	-2.09	-1.79	-4.47	4.6e-04	7.5e-06	2.0e-04	2.6e-03	2.4e-26
33614							1.19	3.3e-01	4.8e-01	6.1e-01	4.3e-01	7.0e-04
33683	AT5G51280.1	0	1.34	1.37		1.20	2.66	4.8e-02	3.8e-02	3.1e-01	9.4e-02	1.7e-10
33719	AT5G53130.1	1e-124		1.00	1.35	1.29	1.39	5.7e-01	1.8e-01	2.7e-02	3.9e-02	1.8e-07
33765			1.83	2.14	1.96	2.02	4.14	2.0e-03	1.1e-04	6.5e-04	3.9e-04	3.9e-24

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
33813	AT4G28390.1	9e-66	1.05		1.12		2.82	1.4e-01	NA	NA	2.4e-01	2.3e-09
33828	AT1G07520.1	1e-57					1.73	6.4e-01	6.8e-01	7.7e-01	5.9e-01	4.7e-04
33831	AT1G47420.1	6e-12	2.39	1.93	2.22	2.19	4.48	8.6e-06	7.4e-04	4.7e-05	7.2e-05	1.9e-25
33848	AT4G11280.1	2e-169	2.95	1.01			2.35	4.6e-09	2.2e-01	2.4e-01	7.1e-01	6.9e-06
33951				1.26		1.03	2.10	3.8e-01	7.6e-02	3.5e-01	1.9e-01	7.4e-07
33952				-1.10		-1.11	-1.72	4.2e-01	1.6e-01	4.0e-01	1.5e-01	4.7e-06
33988	AT2G45460.1	7e-26	-1.17	-1.05	-1.35	-1.09	-1.93	1.2e-01	2.0e-01	4.8e-02	1.6e-01	4.4e-09
34007	AT2G47600.1	1e-118	-2.25	-2.30	-2.29	-2.46	-3.93	2.9e-05	1.5e-05	1.6e-05	2.5e-06	1.0e-28
34017	AT1G56260.1	2e-31					2.73	1.3e-01	NA	NA	2.8e-01	5.5e-08
34030	AT1G13890.1	5e-14					-2.42	4.7e-01	3.8e-01	5.4e-01	4.3e-01	3.3e-06
34036					1.18		1.91	3.3e-01	6.3e-01	8.6e-02	6.1e-01	3.3e-05
34040	AT2G46060.1	7e-83	1.66	2.02	2.28	2.09	4.21	6.8e-03	3.3e-04	2.5e-05	1.8e-04	1.0e-21
34116			-1.28	-1.07			-1.42	6.4e-02	1.7e-01	4.4e-01	6.2e-01	3.0e-06
34155	AT4G23160.1	6e-161	4.59	3.25	3.25	2.66	4.83	2.4e-26	6.2e-13	7.1e-13	3.5e-08	9.5e-32
34159	AT1G17100.1	5e-92			-1.05	-1.70	-1.46	2.1e-01	3.8e-01	1.3e-01	1.6e-03	3.8e-06
34167	AT5G17680.1	7e-98	1.81	1.79	1.33		3.40	1.5e-03	1.7e-03	4.5e-02	4.5e-01	5.0e-13
34214	AT3G07490.1	1e-37					1.77	3.8e-01	NA	NA	6.3e-01	1.9e-04
34218	AT1G08490.1	3e-15		1.04			1.45	7.0e-01	2.0e-01	4.4e-01	7.4e-01	1.8e-04
34269	AT3G49400.1	5e-15		-1.02			-1.27	6.3e-01	2.3e-01	5.4e-01	4.3e-01	1.1e-04
34272	AT1G24440.1	6e-43				-1.08	-1.35	8.3e-01	5.6e-01	4.2e-01	1.7e-01	5.7e-04
34282	AT2G05160.1	2e-166	1.68		1.43		1.61	2.9e-03	2.4e-01	2.2e-02	6.1e-01	4.6e-07
34284	AT2G38740.1	1e-29					1.39	6.1e-01	2.7e-01	3.7e-01	6.4e-01	3.1e-05
34362			2.51	2.14	2.14	1.83	3.42	1.3e-06	8.1e-05	8.2e-05	1.4e-03	4.7e-23
34370	AT1G01710.1	0		-1.03			-1.04	5.6e-01	1.8e-01	6.7e-01	4.8e-01	2.7e-04
34379	AT2G45620.1	1e-11		-1.32	-1.07		-3.00	3.4e-01	3.0e-02	1.2e-01	2.7e-01	2.9e-10
34387	AT2G19660.1	2e-14		1.14	1.14	1.25	1.40	5.3e-01	8.0e-02	7.9e-02	4.3e-02	2.3e-08
34409	AT5G40190.1	1e-29					-2.08	7.8e-01	6.3e-01	3.6e-01	2.3e-01	7.0e-05
34414	AT3G27050.1	2e-34	-1.74	-1.58	-1.66	-1.56	-2.01	2.0e-04	6.7e-04	3.2e-04	1.0e-03	7.4e-25
34415	AT3G27050.1	1e-34	1.82	2.34	2.28	2.35	4.42	2.1e-03	1.5e-05	2.7e-05	1.5e-05	1.8e-33
34509	AT4G23160.1	2e-125	2.11	2.13	1.77	1.50	3.66	1.7e-04	1.1e-04	3.0e-03	2.1e-02	5.7e-19
34534	AT3G14470.1	2e-112	-3.58	-3.66	-3.65	-3.41	-5.68	2.3e-15	3.6e-16	4.2e-16	5.6e-14	3.8e-53
34545	AT3G05570.1	2e-33					1.04	6.0e-01	4.5e-01	6.1e-01	4.3e-01	1.6e-04
34565	AT2G36670.1	5e-55		-1.15			-1.16	5.4e-01	9.2e-02	5.3e-01	3.5e-01	9.2e-05
34590	AT5G05790.1	9e-76	2.23					3.0e-08	3.3e-01	1.0e+00	1.2e-01	7.0e-01
34603	AT1G53240.1	0	1.19				1.62	1.1e-01	5.6e-01	2.4e-01	6.7e-01	4.0e-04
34613	AT1G19360.1	2e-29	-1.64	-1.31	-1.33	-1.58	-3.84	5.4e-03	4.9e-02	4.6e-02	8.8e-03	2.6e-17
34621				1.14	1.44	1.02	2.23	4.3e-01	1.3e-01	2.9e-02	2.1e-01	3.9e-08
34639	AT1G43260.1	1e-35	-1.02	-1.22	-1.02		-3.26	1.5e-01	5.5e-02	1.6e-01	2.3e-01	1.1e-11
34693	AT3G47120.1	3e-16	1.42	1.47	1.59	1.37	3.66	2.6e-02	1.9e-02	8.8e-03	3.4e-02	1.4e-15
34694	AT4G16835.1	2e-119			-1.13		-2.88	3.2e-01	3.0e-01	8.6e-02	1.8e-01	2.1e-09
34700							2.08	2.7e-01	3.0e-01	5.7e-01	5.3e-01	2.8e-05
34747	AT1G10610.1	5e-19		1.37	1.16		1.21	1.2e-01	5.9e-03	3.7e-02	7.8e-01	4.4e-05
34751	AT4G32770.1	5e-27	1.61	1.63	1.57		3.71	7.2e-03	5.9e-03	9.5e-03	2.0e-01	9.6e-16
34760	AT4G23160.1	2e-148	-1.35	-1.11	-1.06		-3.18	2.6e-02	1.1e-01	1.4e-01	3.6e-01	5.6e-12
34802	AT2G03710.1	6e-29	-2.52	-2.63	-2.71	-2.49	-4.97	1.8e-06	4.2e-07	1.5e-07	2.4e-06	4.6e-37
34907	AT2G18030.2	3e-31		-1.27			-2.45	7.0e-01	NA	NA	5.4e-01	2.4e-06
34977	AT4G00560.1	2e-79	-1.97	-2.21	-1.73	-1.85	-3.39	5.7e-04	5.0e-05	3.9e-03	1.6e-03	4.9e-24
35059	AT4G36930.1	8e-19	-2.55	-2.43	-2.17	-1.90	-4.66	1.2e-06	5.1e-06	8.1e-05	1.1e-03	2.1e-27
35120	AT1G51340.2	0	-1.34		-1.33	-1.42	-2.35	5.4e-02	3.5e-01	5.7e-02	3.3e-02	7.2e-10
35156							-1.87	NA	NA	NA	NA	5.7e-04
35204	AT1G69850.1	3e-155	-1.01				-1.51	2.2e-01	4.4e-01	6.1e-01	7.9e-01	4.8e-04
35238	AT5G48440.1	8e-75					-1.44	8.6e-01	4.3e-01	3.3e-01	4.9e-01	9.6e-04
35249	AT3G53970.2	1e-35					2.13	2.9e-01	5.1e-01	5.4e-01	4.2e-01	1.0e-06
35276	AT4G02920.1	1e-35	-1.95	-2.00	-1.75	-1.55	-2.76	4.5e-04	2.2e-04	2.4e-03	1.2e-02	4.2e-19

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
35353	AT5G66200.1	6e-70	1.22	1.20			1.55	9.7e-02	1.0e-01	5.8e-01	5.1e-01	2.2e-06
35373	AT1G51550.1	3e-19		-1.33			-1.59	7.7e-01	4.6e-02	5.3e-01	7.7e-01	3.8e-04
35466	AT5G60590.2	1e-29	-1.06	-1.35			-2.99	1.2e-01	NA	NA	3.8e-01	1.1e-09
35473	AT1G32410.1	4e-13	1.37	1.41	1.49	1.30	2.46	4.6e-02	3.5e-02	2.2e-02	6.2e-02	1.6e-12
35665			-1.06				-3.52	8.4e-02	1.6e-01	4.2e-01	4.2e-01	5.9e-13
35668	AT1G60640.1	5e-15					-1.91	NA	NA	NA	NA	4.3e-04
35698	AT5G17680.1	2e-86	-3.17	-3.40	-3.30	-2.98	-5.38	1.3e-11	1.8e-13	1.0e-12	4.3e-10	2.0e-41
35701	AT3G57000.1	9e-13	-1.55	-1.40	-1.04		-3.71	7.1e-03	2.1e-02	1.6e-01	2.4e-01	2.7e-15
35702	AT3G07640.1	5e-13		1.33	1.32	1.48	1.83	2.2e-01	4.0e-02	4.6e-02	1.7e-02	8.0e-04
35705	AT2G45470.1	6e-72				-1.97	-1.26	9.7e-01	6.2e-01	4.3e-01	6.0e-04	3.2e-02
35729	AT3G18020.1	1e-139			1.39	1.27	1.48	4.2e-01	2.4e-01	2.5e-02	5.3e-02	3.8e-08
35738	AT2G46070.1	2e-16	-2.38	-2.64	-2.45	-2.63	-4.45	5.7e-06	1.9e-07	2.1e-06	2.4e-07	1.5e-29
35796	AT4G37200.1	7e-46					1.89	2.9e-01	NA	NA	2.9e-01	2.4e-04
35819							-1.80	6.8e-01	NA	NA	4.0e-01	6.7e-04
35831					-1.12		-2.84	2.1e-01	NA	NA	5.9e-01	1.1e-08
35864	AT3G15290.1	6e-11					-2.22	7.9e-01	2.0e-01	2.6e-01	3.1e-01	1.0e-05
35869	AT3G13050.1	1e-38					-1.43	3.0e-01	2.5e-01	6.0e-01	4.1e-01	2.3e-05
35876	AT5G64150.1	6e-68	-1.19	-1.22			-1.31	6.9e-02	5.6e-02	3.5e-01	6.5e-01	7.6e-07
35895	AT2G46520.1	3e-47		1.05			1.87	2.6e-01	1.7e-01	4.0e-01	7.8e-01	3.3e-05
35958	AT5G03870.1	3e-33	-1.34	-1.19	-1.30	-1.12	-2.43	5.3e-02	1.2e-01	6.5e-02	1.4e-01	6.2e-13
35980	AT3G18670.1	9e-57	2.54	3.62	3.54	2.99	4.97	4.4e-07	6.1e-15	2.7e-14	6.8e-10	2.3e-38
36035	AT3G19400.2	9e-13		1.07	1.05		2.36	9.7e-01	NA	NA	3.1e-01	5.1e-06
36063	AT3G11220.1	2e-26					1.91	NA	NA	NA	NA	4.2e-04
36087			-1.13		-1.10	-1.16	-2.84	1.1e-01	3.0e-01	1.3e-01	8.6e-02	1.8e-09
36115	AT3G16000.1	3e-36	-2.31	-2.42	-1.76	-1.53	-3.79	2.2e-05	6.2e-06	3.5e-03	1.8e-02	3.8e-22
36166	AT1G48900.1	1e-56	1.64	1.19	1.29	1.57	2.34	7.8e-03	1.1e-01	6.7e-02	1.3e-02	1.3e-06
36192	AT5G46290.1	0				1.20		6.0e-01	7.6e-02	8.4e-03	5.4e-04	1.3e-09
36218	AT5G51040.1	6e-18	2.45	2.03	2.05	2.16	4.45	4.2e-06	2.9e-04	2.7e-04	9.7e-05	6.2e-25
36219	AT5G51040.1	5e-18	1.83	1.53	1.76	1.62	3.92	1.7e-03	1.5e-02	2.9e-03	7.8e-03	2.7e-18
36277	AT3G60310.1	1e-25	-1.00				-1.65	2.3e-01	6.6e-01	3.3e-01	3.8e-01	7.3e-05
36375	AT1G43760.1	2e-39	1.65	2.51	2.01	2.33	3.81	7.5e-03	1.7e-06	3.6e-04	1.6e-05	1.4e-24
36384	AT4G15475.1	8e-56					1.79	4.9e-01	NA	NA	8.2e-01	6.2e-04
36393	AT3G13050.1	2e-96	-1.04	-1.22			-1.03	3.1e-02	4.6e-03	6.6e-01	6.6e-02	3.3e-07
36412	AT2G18890.1	2e-75	1.11		1.01	1.24	1.86	1.6e-01	3.5e-01	2.4e-01	8.5e-02	2.1e-09
36466	AT5G15730.2	7e-122	1.88	1.99	1.90	1.95	3.83	1.4e-03	4.6e-04	1.1e-03	8.0e-04	3.0e-27
36512	AT5G01600.1	6e-53			1.19	1.36	1.75	2.6e-01	2.4e-01	1.0e-01	4.2e-02	1.1e-08
36523	AT3G15358.1	8e-37	1.43	2.05	1.95	1.98	3.94	3.1e-02	2.5e-04	6.8e-04	5.0e-04	1.4e-19
36541			-2.23	-2.01	-2.01	-2.06	-2.45	3.3e-08	8.3e-07	5.9e-07	2.6e-07	1.2e-34
36578	AT3G26300.1	2e-58	1.22		1.06		1.63	9.4e-02	8.3e-01	1.9e-01	7.0e-01	3.3e-04
36592			-1.41	-1.38	-1.26	-1.09	-2.91	3.0e-02	3.7e-02	7.2e-02	1.5e-01	1.5e-11
36631			1.68	1.99	1.73	1.37	3.79	5.6e-03	4.1e-04	3.8e-03	3.9e-02	9.3e-19
36711	AT1G34380.2	1e-58	-1.56	-1.65	-1.44	-1.16	-3.44	1.1e-02	6.2e-03	2.8e-02	1.1e-01	2.7e-16
36752	AT5G58510.1	2e-42	1.30	1.54	1.44	1.19	3.57	4.9e-02	1.1e-02	2.2e-02	8.2e-02	1.2e-14
36755	AT4G33920.1	1e-55					3.07	3.7e-01	6.1e-01	5.7e-01	7.9e-01	6.2e-11
36791			-1.81	-1.60	-1.24	-1.08	-3.34	1.7e-03	8.4e-03	7.9e-02	1.5e-01	5.1e-14
36803	AT4G31080.1	2e-12					-2.88	3.0e-01	1.1e-01	5.4e-01	4.8e-01	9.9e-09
36824	AT4G23160.1	1e-128		1.17	1.10		3.26	3.4e-01	6.2e-02	9.4e-02	2.3e-01	1.3e-11
36840	AT3G27340.1	3e-18	-1.04				-1.80	1.5e-01	NA	NA	8.0e-01	2.5e-04
36860	AT3G24150.1	2e-15					-1.81	9.8e-01	3.6e-01	2.6e-01	6.4e-01	9.6e-04
36893	AT5G25930.1	3e-154				-1.29	-1.35	5.6e-01	8.6e-01	5.0e-01	6.6e-02	3.8e-04
36920	AT4G35730.1	1e-33	2.01	2.15	2.27	2.27	4.32	4.6e-04	1.0e-04	2.9e-05	3.4e-05	3.0e-29
36952	AT5G41040.1	2e-66	2.55	2.81	3.02	2.19	4.71	8.8e-07	2.4e-08	9.2e-10	5.8e-05	1.8e-33
36953			-1.02			-1.09	-2.91	1.4e-01	3.5e-01	3.2e-01	9.1e-02	2.5e-09
37039	AT3G25440.1	1e-45					-2.55	1.7e-01	NA	NA	3.7e-01	1.5e-07

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
37048	AT4G07990.1	2e-23	1.54	1.95	1.93	1.51	4.05	1.4e-02	5.3e-04	6.8e-04	1.7e-02	1.0e-19
37190	AT4G23160.1	1e-32		-1.06			-1.48	5.1e-01	2.0e-01	5.9e-01	3.0e-01	1.9e-05
37198	AT1G43760.1	2e-12					-2.04	4.4e-01	NA	NA	7.5e-01	1.4e-04
37221	AT5G14180.1	2e-135	2.00				2.26	9.4e-05	6.1e-01	4.8e-01	7.4e-01	1.6e-05
37256	AT1G53035.1	2e-20					2.26	3.6e-01	4.4e-01	3.3e-01	1.9e-01	1.8e-06
37268	AT2G01050.1	6e-27					2.40	NA	NA	NA	NA	3.5e-06
37311	AT4G31115.1	4e-64				1.28	1.92	2.8e-01	4.2e-01	5.4e-01	5.7e-02	1.6e-05
37399	AT2G22590.1	3e-61		1.73	2.47	2.69	2.77	6.5e-01	2.9e-03	1.5e-06	8.5e-08	8.3e-11
37505	AT5G11680.1	5e-47	-1.33	-1.61	-1.20	-1.48	-3.63	4.1e-02	7.2e-03	8.8e-02	1.6e-02	3.9e-15
37538	AT4G23160.1	9e-103		-1.39			-1.58	6.1e-01	4.0e-02	2.6e-01	5.4e-01	3.9e-05
37584	AT4G20520.1	2e-24				1.13	2.49	4.5e-01	NA	NA	6.6e-02	5.7e-07
37596	AT3G22550.1	4e-27	1.14				1.85	9.1e-02	3.4e-01	5.0e-01	9.0e-01	1.6e-04
37634	AT5G14280.1	1e-11					-1.99	NA	NA	NA	NA	2.2e-04
37650			1.01				1.41	2.4e-01	3.3e-01	2.8e-01	6.2e-01	3.0e-04
37763	AT3G14470.1	3e-57	2.53	2.48	2.63	2.35	4.78	1.3e-06	2.1e-06	3.5e-07	1.2e-05	2.3e-30
37905	AT1G04910.1	7e-52	1.60	1.56	1.86	2.06	2.05	8.0e-05	1.6e-04	1.5e-06	7.0e-08	1.1e-30
37976	AT1G34380.2	3e-61			1.11		1.62	3.1e-01	5.3e-01	1.6e-01	6.1e-01	5.0e-05
38048	AT2G01050.1	3e-39			1.19	1.39	1.89	2.6e-01	3.0e-01	1.1e-01	4.0e-02	1.0e-07
38162	AT3G18830.1	0	1.26	1.26		1.29	1.96	8.1e-02	8.0e-02	6.6e-01	6.6e-02	4.2e-07
38259	AT4G29090.1	7e-55					1.77	5.7e-01	6.0e-01	5.2e-01	6.9e-01	9.3e-04
38289	AT4G29090.1	5e-56		-1.33	-1.27	-1.03	-2.88	6.4e-01	3.1e-02	4.7e-02	1.4e-01	3.2e-09
38315	AT1G44350.1	9e-138					-1.93	9.1e-01	NA	NA	2.3e-01	3.5e-04
38349	AT3G22450.1	1e-21	1.00				2.54	1.7e-01	5.6e-01	3.1e-01	1.6e-01	5.7e-08
38367	AT1G15670.1	1e-23	2.79	2.39	2.84	2.91	4.96	3.2e-08	5.4e-06	1.4e-08	6.0e-09	5.6e-33
38375	AT5G45530.1	2e-66		1.35	1.71	2.01	2.41	6.3e-01	4.7e-02	4.7e-03	4.4e-04	1.4e-07
38521			-1.65	-1.89	-1.41	-1.28	-2.51	6.8e-03	9.0e-04	3.3e-02	6.5e-02	3.0e-15
38611	AT1G60610.1	1e-55	1.46	1.93	1.82	1.24	2.85	2.6e-02	8.0e-04	2.1e-03	8.7e-02	1.1e-17
38647	AT5G41040.1	6e-36	-1.01	-1.36	-1.29	-1.64	-2.54	2.3e-01	4.6e-02	6.9e-02	8.0e-03	7.3e-12
38648	AT2G40116.1	0	-1.19	-1.09			-1.57	1.1e-01	1.6e-01	4.0e-01	2.4e-01	1.6e-07
38686	AT4G26570.1	3e-17					-1.89	5.7e-01	6.7e-01	5.5e-01	4.6e-01	3.2e-04
38706	AT1G70630.1	0	1.48		1.11	1.25	2.10	2.4e-02	5.3e-01	1.6e-01	7.9e-02	4.3e-08
38788				-1.12	-1.02		-1.46	4.0e-01	1.5e-01	2.3e-01	7.7e-01	3.1e-05
38811	AT2G16600.1	1e-37	-1.76	-1.28	-1.38	-1.42	-3.76	2.4e-03	6.1e-02	3.5e-02	2.7e-02	2.5e-19
38846							-1.86	NA	NA	NA	NA	6.6e-04
38850	AT4G10130.1	1e-39	1.35	1.50	1.53	1.12	3.55	3.6e-02	1.4e-02	1.2e-02	1.1e-01	6.0e-15
38867	AT1G79750.1	1e-160		1.76	1.83	1.40	2.40	3.5e-01	3.2e-03	1.8e-03	3.8e-02	1.5e-11
39028	AT1G22380.1	1e-24		1.23	1.73	1.60	1.66	2.5e-01	6.4e-02	2.0e-03	7.9e-03	1.7e-05
39079							-2.35	6.0e-01	6.7e-01	5.8e-01	4.5e-01	7.1e-06
39105			-1.40		-1.15	-1.32	-2.96	2.7e-02	2.8e-01	1.1e-01	4.2e-02	4.6e-11
39242			-1.07		-1.15		-2.98	1.1e-01	NA	NA	4.7e-01	1.2e-09
39397	AT4G23160.1	7e-41					2.35	NA	NA	NA	NA	6.6e-06
39400	AT4G23160.1	9e-99	3.47	3.61	3.85	3.80	4.63	5.5e-19	1.4e-20	5.0e-23	4.3e-22	9.6e-92
39464	AT2G30330.1	3e-29	-1.71	-1.39	-1.16	-1.23	-2.39	5.2e-03	4.0e-02	1.3e-01	9.0e-02	1.8e-10
39546	AT2G44970.1	1e-51	1.62	1.21		1.08	1.64	3.0e-03	5.6e-02	1.7e-01	1.1e-01	8.9e-14
39550			1.27	1.96	1.32	1.00	2.48	7.3e-02	5.6e-04	5.8e-02	2.3e-01	3.6e-08
39571	AT1G22275.1	2e-11	1.98	1.46	1.95	1.68	3.58	5.2e-04	2.6e-02	6.9e-04	6.1e-03	8.9e-19
39608	AT4G23160.1	1e-37			1.10	1.08	1.55	8.7e-01	6.1e-01	1.6e-01	1.7e-01	2.5e-04
39645	AT1G33500.1	8e-14		-1.16	-1.02		-2.74	7.3e-01	NA	NA	1.8e-01	5.1e-08
39653	AT5G17680.1	1e-43	1.65	2.21	2.28	1.84	4.40	7.3e-03	5.1e-05	2.6e-05	1.7e-03	8.7e-24
39671	AT3G57830.1	8e-60		1.16	1.97	2.07	2.76	3.5e-01	1.3e-01	5.8e-04	2.6e-04	2.7e-10
39713	AT5G22030.2	2e-23					1.83	6.1e-01	NA	NA	5.1e-01	4.2e-04
39751	AT4G15450.1	1e-27	1.64	1.55	1.53	1.56	3.86	6.4e-03	1.1e-02	1.4e-02	1.1e-02	1.3e-17
39768	AT3G55820.1	7e-38					-2.12	NA	NA	NA	NA	6.8e-05
39769	AT3G55820.1	3e-25	1.17	1.08			2.72	9.4e-02	1.4e-01	3.0e-01	3.1e-01	1.6e-11

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
39798	AT2G45600.1	2e-20		-1.22			-2.38	3.9e-01	6.5e-02	5.0e-01	3.0e-01	2.1e-07
39856	AT2G43760.1	1e-11	-1.00				-1.58	2.1e-01	2.7e-01	6.1e-01	8.0e-01	4.6e-04
40031	AT3G20350.1	5e-17	1.34				2.21	3.2e-02	5.1e-01	5.0e-01	3.4e-01	5.0e-06
40036	AT5G54930.1	2e-16	1.68	1.93	2.00	1.28	2.55	5.7e-03	6.9e-04	3.6e-04	6.4e-02	7.2e-07
40042	AT5G04780.1	1e-42					1.80	NA	NA	NA	NA	9.4e-04
40167	AT5G51380.1	1e-40					2.03	NA	NA	NA	NA	1.2e-04
40177	AT4G23160.1	4e-75	1.35			1.29	3.00	3.4e-02	2.4e-01	2.4e-01	4.7e-02	7.3e-12
40206	AT4G29090.1	4e-25					-2.01	2.1e-01	7.2e-01	5.6e-01	5.3e-01	9.3e-05
40213			2.64	1.94	1.79	1.53	4.10	4.4e-07	6.9e-04	2.5e-03	1.7e-02	1.4e-19
40290			-1.85	-1.63	-1.41	-1.32	-4.14	1.0e-03	6.5e-03	2.9e-02	4.5e-02	8.6e-20
40328	AT2G43760.1	3e-11			1.01		1.33	6.5e-01	4.1e-01	2.4e-01	3.9e-01	8.0e-05
40357	AT1G74640.1	7e-166			1.05		1.00	1.7e-01	3.0e-02	1.2e-02	5.1e-02	7.2e-07
40501	AT3G52870.1	6e-17		-1.02	-1.34	-1.04	-1.70	5.2e-01	2.2e-01	5.2e-02	2.0e-01	7.7e-04
40505	AT2G45600.1	2e-18	1.11	1.99	1.69	1.48	2.20	1.3e-01	2.6e-04	3.6e-03	1.8e-02	1.2e-12
40583							2.52	NA	NA	NA	NA	8.7e-07
40613							2.17	NA	NA	NA	NA	4.5e-05
40641				1.03			2.92	2.3e-01	1.5e-01	4.2e-01	3.2e-01	5.3e-16
40642			-1.02	-1.13	-1.19		-3.39	1.4e-01	8.3e-02	6.2e-02	3.3e-01	1.8e-12
40644	AT1G68760.1	1e-18					-1.66	5.5e-01	4.9e-01	6.8e-01	2.2e-01	2.0e-04
40684	AT1G13570.1	5e-19	-1.25	-1.35	-1.04		-2.78	7.1e-02	4.0e-02	1.9e-01	2.2e-01	8.5e-11
40708	AT1G69550.1	2e-108	-1.79	-1.19	-1.51	-1.54	-1.87	8.7e-04	5.3e-02	5.1e-03	5.1e-03	1.4e-10
40875	AT4G29090.1	5e-56		1.46	1.42	1.13	2.29	9.6e-01	1.5e-02	2.1e-02	1.0e-01	8.4e-06
40889	AT1G73860.1	0					-3.28	1.7e-01	2.3e-01	2.4e-01	2.7e-01	1.1e-11
40938	AT3G54310.1	2e-24	1.22			1.13	2.96	4.9e-02	NA	NA	7.6e-02	1.7e-09
40944	AT4G33910.1	1e-28				1.06	2.48	4.4e-01	4.4e-01	5.0e-01	1.1e-01	7.4e-08
41054	AT5G12470.1	2e-12		1.27	1.03		1.79	9.4e-01	6.9e-02	2.1e-01	2.4e-01	1.6e-05
41062	AT1G20640.1	0				-1.02	-1.81	4.7e-01	4.1e-01	2.8e-01	2.1e-01	8.3e-06
41080	AT4G23160.1	1e-98	1.43		1.01		1.58	2.9e-02	3.6e-01	2.2e-01	3.3e-01	5.6e-07
41108	AT2G33560.1	4e-38					1.66	8.1e-01	4.7e-01	7.2e-01	6.2e-01	9.6e-04
41112	AT3G55530.1	6e-34	1.49	1.44	1.38	1.44	3.51	1.7e-02	2.5e-02	3.5e-02	2.4e-02	1.7e-15
41126	AT4G12010.1	5e-135	-1.51	-1.27	-1.37	-1.34	-4.65	1.0e-02	5.0e-02	2.8e-02	3.3e-02	6.3e-25
41128						1.39	2.62	2.7e-01	4.8e-01	3.3e-01	2.2e-02	1.2e-08
41153	AT5G15500.2	3e-14					1.68	7.6e-01	6.2e-01	8.3e-01	5.8e-01	8.1e-04
41159	AT4G23160.1	4e-116	2.38	2.82	2.87	2.27	4.54	7.6e-06	1.8e-08	9.8e-09	2.3e-05	9.0e-32
41204	AT2G22590.1	1e-20		2.09	2.25	2.55	2.86	9.3e-01	1.6e-04	3.5e-05	1.0e-06	1.8e-08
41276	AT1G58290.1	4e-35					-2.21	4.2e-01	4.0e-01	4.9e-01	3.3e-01	6.3e-06
41393	AT1G51540.1	1e-14	1.12	1.09			2.88	8.7e-02	NA	NA	4.5e-01	3.8e-09
41493	AT5G36930.1	4e-53					-1.81	6.9e-01	7.3e-01	7.4e-01	7.1e-01	8.4e-04
41497	AT1G61550.1	7e-85	-1.11				-3.05	9.9e-02	2.2e-01	2.6e-01	1.7e-01	5.1e-11
41519	AT4G23160.1	3e-39	1.41	1.02	1.39	1.02	2.83	2.7e-02	2.1e-01	3.5e-02	2.0e-01	6.5e-12
41548							-1.81	NA	NA	NA	NA	9.6e-04
41664	AT1G43760.1	3e-18					-2.51	2.9e-01	NA	NA	6.9e-01	1.1e-06
41702	AT1G12210.1	8e-19					-2.30	3.4e-01	6.8e-01	7.2e-01	7.5e-01	1.1e-05
41739	AT1G12990.1	8e-62		-1.37	-1.45	-1.35	-3.51	4.9e-01	2.6e-02	1.5e-02	2.8e-02	1.8e-13
41789	AT5G47530.1	1e-171		1.16		1.16	2.02	9.4e-01	9.5e-02	2.6e-01	9.4e-02	2.7e-05
41833	AT4G37400.1	6e-76	1.10	1.05	1.75	1.52	1.91	1.4e-01	1.8e-01	2.4e-03	1.4e-02	7.3e-10
41844	AT5G02120.1	1e-33		1.09	1.13		1.01	2.2e-01	4.1e-02	3.2e-02	3.4e-01	5.7e-04
41866	AT2G36570.1	5e-34	1.15		1.11	1.23	2.02	1.3e-01	4.0e-01	1.6e-01	8.6e-02	1.7e-07
41913	AT3G07120.1	6e-37				-1.39	-1.43	4.9e-01	3.7e-01	2.2e-01	2.6e-02	7.2e-06
41944			1.63	1.76	1.55	1.59	3.99	7.1e-03	2.5e-03	1.2e-02	9.4e-03	4.6e-19
41988	AT5G21070.1	9e-16	1.74	1.14	1.43	1.24	3.49	2.5e-03	1.1e-01	2.4e-02	6.3e-02	9.3e-14
42107	AT5G14280.1	4e-11					-2.30	1.9e-01	NA	NA	7.2e-01	9.5e-06
42141	AT1G50170.1	1e-12		1.11	1.02		1.29	7.1e-01	1.3e-01	1.9e-01	3.5e-01	6.2e-06
42350	AT5G49800.1	1e-63					-1.11	5.2e-01	4.6e-01	2.5e-01	3.7e-01	3.4e-05

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
42416							-2.20	4.3e-01	NA	NA	9.3e-01	2.7e-05
42429	AT1G07430.1	6e-138		1.27	1.07	1.39	2.55	6.9e-01	5.9e-02	1.6e-01	2.7e-02	1.8e-08
42477	AT1G23780.1	1e-14	1.42	1.41	1.46	1.42	3.62	2.6e-02	2.7e-02	2.1e-02	2.6e-02	6.6e-16
42653	AT1G55700.1	1e-12					-2.25	3.8e-01	NA	NA	6.8e-01	2.0e-05
42718	AT4G39300.1	1e-15	1.79	1.28		1.05	3.40	1.2e-03	4.7e-02	3.0e-01	1.4e-01	1.5e-12
42725	AT5G40160.1	2e-95					1.05	1.9e-01	2.4e-01	5.8e-01	5.1e-01	4.0e-06
42759	AT5G41980.1	1e-41					1.74	5.3e-01	4.0e-01	6.0e-01	7.3e-01	4.5e-04
42821	AT3G55180.1	6e-37	-1.02				-2.03	1.7e-01	3.0e-01	6.9e-01	4.6e-01	9.3e-06
42846	AT3G02160.1	3e-11					1.69	3.1e-01	7.2e-01	8.7e-01	5.7e-01	9.1e-04
42854	AT3G57710.1	3e-18			1.06	1.45	3.05	2.4e-01	5.1e-01	1.2e-01	1.0e-02	6.4e-10
42867				1.28	1.18	1.40	2.82	2.5e-01	5.5e-02	9.7e-02	2.7e-02	2.6e-10
42933	AT4G29090.1	1e-13	-1.21	-1.00			-3.06	4.8e-02	1.5e-01	2.8e-01	4.2e-01	2.9e-10
42966	AT3G03150.1	2e-14	2.16	1.59	1.29	1.75	2.07	2.9e-06	1.8e-03	2.0e-02	2.5e-04	4.1e-14
43019	AT5G56580.1	1e-27					-2.20	3.3e-01	NA	NA	5.3e-01	2.6e-05
43060	AT4G22280.1	9e-14	1.47	1.34	1.06		2.64	2.3e-02	4.6e-02	1.9e-01	2.6e-01	1.6e-10
43225							-1.61	7.3e-01	3.9e-01	7.5e-01	5.2e-01	6.7e-04
43235	AT3G59550.1	6e-12					1.66	7.1e-01	6.7e-01	6.9e-01	7.0e-01	9.7e-04
43248	AT5G49665.1	2e-19					-2.41	5.2e-01	NA	NA	5.7e-01	3.8e-06
43269	AT4G28700.1	0		1.21			1.39	4.1e-01	1.0e-01	4.7e-01	4.1e-01	5.6e-04
43278	AT5G36930.1	1e-68	4.32	4.05	4.08	4.29	6.26	3.1e-25	4.7e-22	1.5e-22	1.0e-24	1.2e-61
43283	AT5G56510.1	5e-68	2.08	1.32			1.93	2.4e-04	5.8e-02	8.0e-01	3.9e-01	3.1e-06
43302			1.69	1.76	2.23	1.25	3.64	5.6e-03	3.3e-03	4.2e-05	7.8e-02	3.1e-18
43384	AT1G15125.1	3e-12			1.05	1.00	1.80	5.0e-01	7.6e-01	1.8e-01	1.9e-01	7.1e-05
43400	AT1G10070.1	2e-178		-1.64	-1.69	-1.38	-2.27	6.2e-01	8.5e-03	5.9e-03	4.2e-02	1.2e-08
43425	AT5G40250.1	1e-19	2.00	2.32	2.30	1.15	3.82	4.7e-04	1.5e-05	2.3e-05	1.3e-01	8.4e-18
43494	AT2G02040.1	8e-130	2.00	2.22	2.20	1.73	4.43	4.7e-04	4.8e-05	5.7e-05	4.3e-03	1.7e-24
43501	AT4G00760.1	3e-11		1.02			2.21	NA	NA	NA	NA	2.4e-05
43580	AT3G61170.1	2e-72	-1.14	-1.05			-2.93	7.7e-02	NA	NA	3.6e-01	2.4e-09
43585	AT5G50720.1	8e-37		1.16	1.06		1.49	2.6e-01	1.2e-01	2.0e-01	6.4e-01	1.1e-05
43589	AT5G59980.1	2e-72	1.81	2.06	2.09	1.75	3.98	2.2e-03	2.3e-04	1.7e-04	3.6e-03	3.1e-21
43614							1.61	4.8e-01	2.4e-01	2.7e-01	7.5e-01	7.1e-05
43765	AT3G07070.1	3e-106			1.28		1.60	4.3e-01	3.7e-01	7.4e-02	5.1e-01	6.0e-06
43786	AT4G23160.1	2e-149					-1.85	9.1e-01	2.8e-01	5.9e-01	8.6e-01	5.0e-04
43843	AT1G60600.1	4e-46	1.34				1.81	3.0e-02	NA	NA	8.3e-01	5.2e-04
43906	AT4G23160.1	9e-117					-2.54	7.7e-02	2.5e-01	6.4e-01	8.3e-01	9.7e-07
43910	AT1G48460.1	3e-18					-2.16	5.9e-01	NA	NA	4.9e-01	4.8e-05
43961	AT2G01050.1	1e-33	1.94	1.93	1.95	1.93	4.27	7.4e-04	7.1e-04	6.7e-04	8.2e-04	1.1e-22
44183	AT5G25190.1	1e-65		-1.46	-1.18	-1.01	-1.61	7.3e-01	2.7e-02	1.2e-01	2.2e-01	8.2e-04
44187	AT3G55140.1	9e-62					1.76	7.8e-01	6.9e-01	4.9e-01	6.4e-01	1.8e-04
44210	AT5G17680.1	5e-43	2.02	2.26	2.22	1.29	3.95	3.8e-04	3.0e-05	5.0e-05	6.4e-02	3.5e-20
44211							2.15	NA	NA	NA	NA	5.4e-05
44212							2.62	4.2e-01	NA	NA	5.5e-01	2.8e-07
44293	AT1G49570.1	1e-27		2.89	2.74	1.50	2.22	3.2e-01	1.1e-11	1.7e-10	3.5e-03	6.3e-07
44311	AT5G22540.1	1e-132					1.59	3.6e-01	2.5e-01	5.9e-01	6.3e-01	1.6e-04
44595	AT1G53460.1	1e-12	1.63	1.13	1.16	1.00	2.14	8.7e-03	1.5e-01	1.3e-01	2.3e-01	1.1e-09
44609							1.98	NA	NA	NA	NA	2.3e-04
44685	AT5G36930.1	2e-33	1.14	1.27	1.39	1.16	3.28	1.2e-01	6.4e-02	3.2e-02	1.1e-01	2.3e-19
44790	AT5G36930.1	1e-83		-1.28	-1.06	-1.07	-3.35	4.4e-01	3.4e-02	1.2e-01	1.1e-01	3.4e-12
44821	AT1G52140.1	7e-31	1.90				1.82	4.9e-04	4.0e-01	9.7e-01	7.3e-01	7.3e-04
44941	AT2G33280.1	3e-38	1.28	1.01	1.11		2.67	4.5e-02	1.8e-01	1.2e-01	5.6e-01	1.2e-08
45032	AT1G49320.1	4e-69	1.97					3.4e-04	8.7e-01	8.8e-01	1.0e+00	2.6e-01
45057	AT5G42905.1	2e-47	2.06	2.57	2.22	2.30	4.40	2.8e-04	1.0e-06	5.4e-05	2.6e-05	8.3e-31
45076				-1.14			-1.34	3.1e-01	1.2e-01	5.1e-01	3.3e-01	4.6e-06
45108	AT4G34050.1	8e-16		1.91	1.21	1.41	1.73	4.9e-01	7.7e-04	9.4e-02	3.5e-02	8.9e-05

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
45166	AT3G44670.1	7e-28	1.83	1.73	1.37	1.49	3.24	1.9e-03	4.1e-03	4.5e-02	2.1e-02	1.7e-16
45188	AT2G20740.1	5e-74	-1.27		-1.54	-1.90	-2.52	7.5e-02	2.5e-01	1.6e-02	1.1e-03	2.9e-10
45222	AT3G42170.1	7e-22					-1.90	9.5e-01	NA	NA	5.6e-01	4.6e-04
45226	AT5G02070.1	0	1.24	1.19	1.39	1.42	3.49	6.6e-02	8.8e-02	2.9e-02	2.3e-02	1.5e-14
45254	AT4G17050.1	7e-45			1.16	1.20	2.90	2.8e-01	NA	NA	4.7e-02	5.4e-09
45296	AT1G21150.1	7e-15				1.03	2.11	7.7e-01	4.3e-01	5.2e-01	1.5e-01	1.1e-06
45458	AT4G29090.1	1e-59	4.75	4.65	4.97	4.82	6.65	2.0e-31	6.8e-31	5.6e-35	1.4e-31	6.4e-103
45470	AT1G02010.1	0					-1.88	7.7e-01	3.3e-01	3.4e-01	4.4e-01	1.3e-04
45545	AT3G06990.1	2e-12	1.94	1.90	2.01	1.50	2.36	5.6e-05	7.5e-05	2.7e-05	5.5e-03	3.9e-25
45569	AT1G51850.1	3e-180		1.78	2.97	3.74	3.39	6.7e-01	2.8e-03	4.1e-09	1.8e-14	6.2e-12
45578	AT3G11660.1	1e-47			-1.00	-1.32	-1.56	6.1e-01	8.6e-01	2.4e-01	5.3e-02	9.5e-04
45628	AT4G13440.1	5e-28	3.54	3.34	3.35	2.99	5.30	1.5e-14	6.4e-13	5.4e-13	4.2e-10	8.2e-48
45630	AT5G26040.1	6e-25		1.16	1.67		2.93	2.3e-01	9.2e-02	3.5e-03	4.3e-01	7.3e-10
45755	AT2G01050.1	1e-42		1.09			2.80	4.9e-01	8.0e-02	1.7e-01	4.2e-01	1.6e-08
45826	AT1G43760.1	7e-12					-2.26	8.9e-01	3.7e-01	4.9e-01	6.1e-01	1.8e-05
45834			2.01				1.86	9.0e-05	6.7e-01	9.4e-01	7.2e-01	6.4e-04
45853	AT1G18140.1	0			1.20	1.66	1.35	4.3e-01	5.8e-01	5.8e-02	2.8e-03	6.0e-07
45899	AT2G45550.1	3e-44	1.56	1.88	1.77	1.46	3.83	1.3e-02	1.1e-03	2.7e-03	2.3e-02	1.7e-18
45987	AT3G50340.1	3e-30	1.61	1.72	1.75	1.89	3.95	9.0e-03	3.8e-03	3.2e-03	1.0e-03	9.3e-19
45996			1.46	1.44	1.30		3.30	1.5e-02	1.7e-02	4.4e-02	4.8e-01	6.5e-12
46016				1.19	1.10	1.01	3.18	1.9e-01	6.5e-02	1.1e-01	1.5e-01	3.8e-11
46038	AT1G21370.1	9e-19		1.58	1.06	1.08	3.16	2.6e-01	6.0e-03	1.4e-01	1.2e-01	6.2e-11
46061	AT1G56520.1	6e-12	-1.13	-1.14	-1.40	-1.62	-3.54	1.2e-01	1.1e-01	2.7e-02	5.7e-03	4.8e-15
46098	AT5G37210.1	8e-24				1.04	2.31	8.7e-01	4.2e-01	1.8e-01	1.0e-01	4.7e-06
46253	AT1G64890.1	4e-117					2.00	8.7e-01	NA	NA	6.6e-01	1.9e-04
46334	AT5G04520.1	6e-36	-1.86	-1.72	-1.70	-1.50	-4.03	1.3e-03	4.0e-03	4.4e-03	1.8e-02	1.9e-19
46344	AT5G45160.1	4e-64			1.05	1.22	2.50	8.0e-01	5.5e-01	1.3e-01	4.7e-02	1.0e-07
46410						-1.01	-2.65	2.6e-01	7.7e-01	4.2e-01	8.6e-02	2.0e-07
46411			2.29	2.16	2.14	2.42	3.05	1.0e-05	2.9e-05	2.6e-05	7.1e-07	3.4e-17
46467	AT4G23160.1	6e-175	1.80	3.92	4.02	3.16	4.20	6.0e-04	6.2e-19	3.6e-20	5.4e-12	5.8e-28
46500							1.72	6.2e-01	8.7e-01	6.3e-01	4.9e-01	7.6e-04
46651	AT1G56570.1	3e-23					1.97	7.7e-01	NA	NA	2.3e-01	1.2e-04
46680	AT1G43760.1	2e-23	1.05	1.69	1.71		3.35	1.7e-01	3.2e-03	2.9e-03	3.1e-01	2.4e-12
46756	AT3G18670.1	2e-81			1.04	1.19	1.86	9.1e-01	4.8e-01	1.5e-01	6.3e-02	4.9e-04
46875	AT1G76340.1	2e-73					-1.88	NA	NA	NA	NA	5.2e-04
46883	AT2G01050.1	8e-46	3.66	3.61	3.30	3.27	4.94	2.4e-16	4.6e-16	5.0e-14	4.3e-13	5.6e-63
47000	AT2G01050.1	1e-46	1.08				2.78	7.8e-02	NA	NA	4.9e-01	3.0e-08
47016	AT5G17300.1	1e-22	2.15	1.52	2.47	1.49	3.67	1.2e-04	1.8e-02	3.5e-06	2.2e-02	2.5e-19
47043	AT3G15500.1	3e-65		-1.07			-1.66	3.0e-01	1.9e-01	6.3e-01	5.5e-01	3.9e-05
47046	AT2G43750.1	2e-13					1.81	1.7e-01	5.8e-01	8.3e-01	8.0e-01	2.2e-04
47051	AT5G20080.1	2e-87	1.38	1.34	1.27	1.42	1.57	1.4e-03	1.6e-03	3.8e-03	7.6e-04	2.3e-23
47098			1.57	1.56	1.29	1.55	3.49	1.0e-02	1.1e-02	6.5e-02	1.3e-02	4.8e-16
47120	AT3G18620.1	5e-106			-1.06		-1.23	4.8e-01	4.8e-01	1.8e-01	3.7e-01	4.8e-05
47126	AT3G18620.1	3e-66					2.30	2.8e-01	NA	NA	5.6e-01	5.1e-06
47139				1.01	1.03	1.03	2.15	2.7e-01	2.2e-01	2.1e-01	2.0e-01	1.9e-07
47159	AT3G08970.1	2e-172	2.54	2.88	2.91	2.76	4.65	7.6e-07	5.3e-09	2.7e-09	3.5e-08	6.9e-37
47209			-1.71	-1.95	-1.84	-1.76	-4.28	4.3e-03	6.1e-04	1.6e-03	2.9e-03	2.2e-22
47303					1.04		2.42	1.7e-01	7.2e-01	1.4e-01	3.1e-01	3.4e-07
47310	AT5G33406.1	8e-35	3.00	2.96	2.99	2.46	5.06	1.1e-09	1.5e-09	8.6e-10	2.2e-06	5.2e-35
47401	AT5G63160.1	5e-101			-1.28	-1.44	-1.33	4.2e-01	8.1e-01	5.7e-02	2.1e-02	7.0e-04
47462	AT5G56860.1	2e-21			1.38		1.75	8.2e-01	2.6e-01	3.7e-02	6.3e-01	9.8e-05
47585	AT3G24255.1	6e-18	1.63		1.04		2.83	2.8e-03	NA	NA	6.1e-01	1.6e-08
47622	AT1G78600.1	3e-11	1.48	1.34	1.47	1.85	3.78	1.8e-02	4.3e-02	2.0e-02	1.1e-03	1.6e-16
47632				-1.14			-1.43	2.5e-01	1.4e-01	5.5e-01	8.0e-01	3.0e-04

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
47802			1.00		1.02	1.02	2.46	2.0e-01	4.5e-01	1.9e-01	1.7e-01	3.1e-08
47883	AT1G74180.1	3e-20		1.05			1.75	6.0e-01	1.9e-01	4.4e-01	4.5e-01	2.9e-05
48009	AT1G05680.1	4e-110					-1.81	5.1e-01	NA	NA	5.7e-01	5.8e-04
48020	AT5G49140.1	1e-40		1.58	1.69	1.24	2.68	9.6e-01	5.6e-03	2.5e-03	5.1e-02	1.6e-07
48064	AT5G14280.1	1e-14	-1.34		-1.06		-2.70	2.0e-02	NA	NA	2.1e-01	1.0e-07
48075	AT5G38260.1	6e-21	2.56	2.17	1.72	1.62	3.66	1.1e-06	8.3e-05	4.3e-03	1.0e-02	5.7e-20
48107	AT3G31430.1	1e-13	1.26				3.28	2.8e-02	2.5e-01	4.3e-01	2.8e-01	2.1e-11
48261				1.19			2.77	6.7e-01	NA	NA	1.3e-01	3.2e-08
48306				1.12	1.20	1.02	1.62	4.3e-01	1.5e-01	1.0e-01	2.2e-01	2.6e-05
48434	AT5G42905.1	7e-47	1.56	2.00	1.86	1.58	4.05	1.2e-02	3.6e-04	1.3e-03	1.1e-02	1.1e-19
48449	AT2G23540.1	7e-123		-1.50	-1.34	-1.42	-2.75	2.8e-01	1.9e-02	5.1e-02	3.0e-02	1.0e-10
48456	AT5G05340.1	1e-130	1.09	1.48		1.13	2.37	1.7e-01	2.1e-02	2.7e-01	1.4e-01	5.4e-09
48471	AT4G02550.2	2e-14	1.88	1.47	1.64	1.43	3.83	1.0e-03	2.1e-02	6.6e-03	2.7e-02	3.1e-17
48472	AT2G30020.1	9e-63				-1.10	-1.83	6.5e-01	5.3e-01	3.6e-01	1.4e-01	3.6e-05
48494	AT4G23160.1	7e-135					-1.70	6.1e-01	4.2e-01	7.1e-01	4.2e-01	6.8e-04
48803	AT3G25810.1	4e-137		1.66	1.17		2.33	2.8e-01	3.2e-03	8.6e-02	5.2e-01	6.8e-06
48812	AT2G20770.1	1e-15					1.84	3.3e-01	6.3e-01	8.3e-01	3.7e-01	1.6e-04
48821	AT1G04635.1	7e-56		-1.07	-1.33	-1.41	-3.04	2.3e-01	1.6e-01	4.2e-02	2.4e-02	1.1e-11
48888	AT3G18670.1	8e-26					2.31	9.5e-02	NA	NA	6.3e-01	1.0e-05
48923			1.18		1.28		2.90	9.0e-02	2.1e-01	5.2e-02	2.2e-01	6.9e-11
48963	AT4G32320.1	4e-17	1.39	1.35	1.18		3.26	2.0e-02	2.7e-02	7.4e-02	5.5e-01	1.7e-11
48983	AT3G58610.1	2e-16				-1.03	-2.36	4.8e-01	NA	NA	1.5e-01	7.6e-07
49040	AT3G13300.1	3e-43	1.09				1.97	NA	NA	NA	NA	2.6e-04
49047	AT3G28740.1	1e-66					1.83	NA	NA	NA	NA	8.1e-04
49146	AT3G51550.1	4e-72			1.20	1.20	3.05	2.1e-01	1.8e-01	7.2e-02	6.6e-02	6.7e-11
49196				-1.22	-1.07		-2.95	4.9e-01	4.6e-02	1.1e-01	2.8e-01	2.1e-09
49197							-2.57	3.7e-01	7.0e-01	3.1e-01	4.9e-01	6.0e-07
49198						1.56	2.90	4.5e-01	NA	NA	4.8e-03	5.3e-09
49229	AT5G59920.1	1e-22		1.23	1.35	1.75	2.16	8.7e-01	8.4e-02	4.6e-02	2.9e-03	2.5e-05
49261	AT4G38180.1	5e-47			-1.01		-2.02	2.0e-01	5.6e-01	1.6e-01	4.8e-01	8.0e-05
49368	AT1G57650.1	1e-11		1.19	1.08		2.75	2.6e-01	NA	NA	4.8e-01	1.3e-08
49465	AT1G68190.1	5e-70		-1.07	-1.19	-1.38	-1.73	9.5e-01	1.8e-01	1.1e-01	3.8e-02	8.4e-04
49653	AT5G54130.2	3e-14	1.45	1.34	1.14		3.01	1.3e-02	2.7e-02	9.3e-02	7.6e-01	8.1e-10
49698	AT4G38840.1	3e-11					1.86	NA	NA	NA	NA	6.0e-04
49888	AT5G51070.1	4e-18					2.00	NA	NA	NA	NA	2.0e-04
49927	AT3G14470.1	5e-25					-1.94	NA	NA	NA	NA	3.5e-04
49950			1.32	1.88	1.96	1.43	3.55	5.7e-02	1.1e-03	6.1e-04	2.8e-02	1.3e-16
49980	AT3G22220.1	5e-62	1.67	1.71	1.98	1.46	4.11	5.6e-03	4.1e-03	4.4e-04	2.3e-02	3.7e-20
49991	AT2G20340.1	2e-62					2.06	3.7e-01	4.0e-01	5.1e-01	7.3e-01	3.7e-06
50133	AT2G17760.1	4e-116	1.08	1.11			1.56	1.8e-01	1.6e-01	4.2e-01	5.5e-01	5.0e-05
50150	AT2G17760.1	2e-151				-1.25	-1.99	6.9e-01	5.5e-01	2.6e-01	6.4e-02	1.6e-05
50185	AT2G01050.1	8e-45	-1.26	-1.40	-1.19	-1.17	-3.22	6.3e-02	2.9e-02	9.4e-02	9.6e-02	1.6e-13
50231	AT4G29090.1	2e-25	1.98	1.63	1.45		3.17	4.4e-04	7.6e-03	2.6e-02	4.1e-01	1.7e-12
50422	AT3G48990.1	7e-73				1.00	2.46	4.3e-01	NA	NA	8.2e-02	2.1e-06
50447	AT3G13960.1	3e-18		-1.06	-1.03	-1.15	-2.45	8.7e-01	1.3e-01	1.5e-01	7.7e-02	3.8e-07
50502	AT2G01050.1	2e-42		-1.15	-1.17	-1.04	-3.69	7.7e-01	5.6e-02	5.2e-02	1.0e-01	4.5e-14
50513	AT2G14540.1	4e-16	1.48	1.68	1.79	1.36	3.42	2.2e-02	5.5e-03	2.5e-03	4.2e-02	8.1e-17
50929	AT1G09970.1	4e-38	1.28	1.55	1.44	1.44	3.58	5.8e-02	1.1e-02	2.3e-02	2.2e-02	8.7e-15
51057	AT4G29090.1	6e-69	-1.24	-1.27	-1.10	-1.19	-4.34	5.1e-02	4.1e-02	1.1e-01	6.4e-02	3.4e-21
51106	AT2G31710.1	5e-20	1.16				2.06	9.4e-02	5.1e-01	6.3e-01	3.9e-01	9.8e-06
51161	AT2G01050.1	7e-47	-1.41	-1.96	-2.06	-2.08	-4.32	3.3e-02	5.7e-04	2.3e-04	1.9e-04	2.3e-23
51249	AT3G06240.1	7e-15					-1.93	7.0e-01	6.5e-01	7.2e-01	5.2e-01	3.6e-04
51556	AT3G27020.1	1e-78					-2.09	9.2e-01	3.6e-01	5.0e-01	3.9e-01	9.4e-05
51634				-1.02			-2.95	3.5e-01	1.1e-01	4.3e-01	3.7e-01	3.2e-09

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
51764	AT3G31430.1	1e-11	2.76	2.65	2.30	2.59	4.30	4.9e-08	1.9e-07	1.3e-05	3.9e-07	2.1e-34
51839	AT1G68200.1	1e-66			1.47	1.46	2.57	2.4e-01	2.8e-01	2.3e-02	2.3e-02	3.5e-10
51880	AT1G54580.1	5e-20	1.88			1.05	2.67	2.8e-04	6.4e-01	6.3e-01	1.2e-01	1.7e-07
51887	AT1G58170.1	1e-15					-1.95	NA	NA	NA	NA	2.9e-04
51928	AT3G09270.1	1e-76		-1.12			-2.05	5.2e-01	1.3e-01	3.0e-01	4.6e-01	3.6e-06
51974	AT2G31290.1	6e-38					2.08	6.0e-01	5.3e-01	6.9e-01	5.4e-01	8.9e-06
52035	AT5G44640.1	0					-2.00	1.7e-01	NA	NA	7.3e-01	1.5e-04
52064	AT5G04520.1	9e-38	1.04	1.39	1.20	1.46	2.27	2.1e-01	4.1e-02	1.1e-01	2.8e-02	2.1e-11
52169	AT3G49660.1	6e-15					2.13	NA	NA	NA	NA	6.3e-05
52170	AT3G49660.1	6e-27	1.31				2.91	2.4e-02	NA	NA	1.8e-01	4.6e-09
52442	AT5G14740.1	4e-121		1.86	1.39			1.0e+00	2.9e-04	1.5e-02	5.4e-01	1.3e-01
52514	AT3G09510.1	6e-23					2.18	NA	NA	NA	NA	4.1e-05
52520				1.12	1.04	1.00	2.42	7.6e-01	NA	NA	1.6e-01	1.1e-06
52713	AT1G53920.1	1e-40					-1.65	4.8e-01	7.7e-01	6.4e-01	3.7e-01	6.0e-04
52938	AT5G42905.1	4e-20			1.15		1.21	4.1e-01	5.4e-01	1.3e-01	7.8e-01	3.0e-04
53009	AT5G07900.1	4e-19	1.31			1.24	1.48	5.2e-02	6.5e-01	5.1e-01	7.6e-02	6.4e-06
53025	AT1G68300.1	5e-23					1.91	NA	NA	NA	NA	4.2e-04
53030	AT2G31290.1	8e-39	-1.20			-1.32	-3.00	6.5e-02	NA	NA	2.9e-02	8.3e-10
53107	AT2G30480.1	3e-14			1.24		2.08	2.1e-01	3.1e-01	6.5e-02	6.5e-01	1.7e-05
53173	AT1G70590.1	3e-36		1.27			2.74	4.5e-01	3.8e-02	1.9e-01	3.6e-01	8.5e-09
53206	AT4G23160.1	6e-113	1.44	1.14	1.51	1.15	3.06	2.5e-02	1.3e-01	1.7e-02	1.1e-01	1.2e-13
53273	AT4G35550.1	4e-18				-1.06	-2.53	2.8e-01	3.6e-01	2.3e-01	1.4e-01	2.9e-08
53399				-1.04		-1.05	-3.33	1.9e-01	1.2e-01	3.1e-01	1.1e-01	6.3e-12
53456	AT4G37360.1	8e-60	1.00				1.68	1.7e-01	6.9e-01	7.1e-01	6.3e-01	8.7e-04
53544	AT2G01410.1	4e-23					-1.92	9.3e-01	NA	NA	4.1e-01	3.8e-04
53567	AT1G65780.1	2e-17					1.63	6.6e-01	6.5e-01	2.8e-01	6.5e-01	7.5e-04
53618	AT2G01050.1	4e-44	3.37	3.42	3.48	3.62	5.80	7.2e-13	2.4e-13	7.2e-14	8.0e-15	1.4e-49
53687	AT3G55810.1	2e-11					-2.02	NA	NA	NA	NA	1.7e-04
53726	AT3G47110.1	9e-82					1.55	3.6e-01	6.0e-01	6.0e-01	4.2e-01	5.7e-05
53845	AT4G15630.1	6e-57		1.44	1.59	1.40	1.96	9.9e-01	2.3e-02	8.3e-03	2.7e-02	2.6e-04
53993	AT5G08335.1	3e-33		-1.08			-2.94	2.2e-01	NA	NA	2.4e-01	2.0e-09
54102			1.05				2.44	1.3e-01	4.4e-01	3.3e-01	3.9e-01	4.4e-07
54226	AT3G05070.1	3e-37	1.73	1.12	1.30	1.40	3.42	2.9e-03	1.3e-01	5.2e-02	2.8e-02	8.4e-14
54358	AT5G35100.1	2e-24					1.86	NA	NA	NA	NA	6.0e-04
54526	AT3G51680.1	2e-43					1.65	2.5e-01	3.4e-01	7.3e-01	5.9e-01	2.1e-04
54539	AT3G28140.1	3e-26	-1.20			-1.13	-1.45	7.6e-02	2.4e-01	2.1e-01	1.1e-01	4.0e-08
54747	AT3G01410.1	2e-21		-1.42	-1.50	-1.47	-3.98	2.2e-01	2.2e-02	1.3e-02	1.5e-02	9.8e-18
54785			1.89	2.31	1.94	1.81	4.25	1.2e-03	1.8e-05	7.0e-04	2.3e-03	3.4e-22
54938	AT4G23160.1	9e-49	1.37	1.87	1.51	1.05	3.25	4.1e-02	1.1e-03	1.8e-02	1.8e-01	7.4e-14
55042							1.98	8.4e-01	NA	NA	9.8e-02	2.1e-04
55059	AT4G11650.1	5e-38					2.31	NA	NA	NA	NA	1.0e-05
55221	AT3G11660.1	8e-31					-1.82	7.6e-01	8.2e-01	5.4e-01	5.6e-01	8.9e-04
55267				1.00	1.04		2.61	4.3e-01	1.8e-01	1.5e-01	2.9e-01	3.8e-09
55338							-1.45	6.1e-01	3.7e-01	6.0e-01	3.7e-01	8.5e-04
55487							1.66	8.8e-01	3.4e-01	3.1e-01	4.8e-01	5.1e-04
55518	AT2G01050.1	8e-44	2.96	3.11	3.12	3.13	5.28	1.1e-09	6.2e-11	5.4e-11	6.2e-11	2.0e-39
55583	AT5G66200.1	4e-14		1.19	1.50		3.11	3.0e-01	7.6e-02	1.1e-02	2.1e-01	5.6e-11
55588	AT3G19300.1	2e-36					2.44	5.8e-01	NA	NA	2.5e-01	1.7e-06
55793	AT3G25900.1	0					1.49	5.6e-01	5.6e-01	7.3e-01	3.9e-01	8.5e-04
55974	AT5G18470.1	5e-17					-1.88	NA	NA	NA	NA	5.3e-04
56002	AT3G45070.1	6e-83					2.09	5.4e-01	6.9e-01	5.9e-01	4.7e-01	2.5e-06
56059	AT1G80660.1	8e-131		1.29			1.80	5.3e-01	NA	NA	9.8e-01	3.9e-04
56328	AT4G36850.1	1e-10					-1.86	7.4e-01	4.9e-01	5.4e-01	4.9e-01	4.8e-04
56355							1.86	NA	NA	NA	NA	6.4e-04

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
56453							-2.39	7.6e-01	NA	NA	6.1e-01	5.0e-06
56481	AT4G24120.1	1e-138					2.45	4.6e-01	2.6e-01	2.1e-01	2.4e-01	3.7e-09
56605	AT1G69510.1	4e-35	1.49	1.39			2.35	1.7e-02	2.8e-02	6.5e-01	4.7e-01	1.0e-06
56855	AT5G40770.1	3e-137			1.02		1.76	7.9e-01	8.7e-01	1.5e-01	2.9e-01	3.6e-04
57037	AT2G39705.1	2e-16		1.03	1.18	1.17	2.88	3.7e-01	1.5e-01	7.4e-02	7.6e-02	1.7e-09
57102	AT3G61170.1	3e-100					1.76	5.1e-01	7.8e-01	8.4e-01	5.7e-01	1.7e-04
57242	AT3G59710.1	6e-29		-1.09			-1.93	8.0e-01	7.0e-02	2.7e-01	8.9e-01	3.0e-04
57335	AT4G29090.1	7e-32					-1.98	3.4e-01	3.7e-01	5.0e-01	3.8e-01	1.6e-04
57353	AT2G38080.1	0					-2.20	8.6e-01	NA	NA	6.0e-01	3.0e-05
57358	AT4G29090.1	7e-49	3.92	3.60	3.56	3.17	5.79	4.4e-18	4.0e-15	7.5e-15	2.0e-11	1.3e-48
57417							1.91	7.3e-01	2.4e-01	6.3e-01	5.1e-01	7.8e-05
57479	AT5G06440.2	2e-33					1.87	NA	NA	NA	NA	5.7e-04
57628	AT5G07010.1	1e-91	1.70	1.80	1.82	1.89	2.65	3.8e-03	1.5e-03	1.2e-03	6.8e-04	1.0e-16
57640	AT1G07400.1	7e-12					-2.57	5.5e-01	NA	NA	4.0e-01	5.8e-07
57681	AT4G29090.1	1e-65	2.51	3.29	3.47	3.60	4.97	4.4e-07	1.8e-12	4.7e-14	6.2e-15	1.9e-39
57743	AT5G38650.1	5e-13	1.27	1.22	1.37	1.28	3.37	5.6e-02	7.5e-02	3.3e-02	5.0e-02	1.9e-13
57844						1.05	2.49	5.2e-01	NA	NA	6.6e-02	1.4e-06
57923	AT2G01050.1	1e-41	3.41	3.44	3.63	3.05	5.07	1.1e-13	4.3e-14	8.3e-16	5.2e-11	5.3e-67
57927	AT2G01050.1	2e-41	3.56	3.66	3.65	3.30	5.72	3.4e-15	3.6e-16	4.7e-16	8.6e-13	2.0e-48
57940	AT4G29090.1	2e-80	1.08	1.40	1.27		3.19	1.2e-01	1.8e-02	4.3e-02	5.6e-01	5.4e-11
58005	AT1G12550.1	2e-82	2.17	2.05	2.27	1.70	4.34	9.2e-05	2.6e-04	3.0e-05	5.5e-03	1.7e-24
58056	AT5G47950.1	1e-14					2.46	7.4e-01	NA	NA	7.7e-01	2.1e-06
58075							-3.22	4.5e-01	2.4e-01	2.4e-01	3.3e-01	8.0e-11
58086	AT4G20520.1	2e-23	1.68	2.02	1.98	1.61	4.09	5.7e-03	2.9e-04	5.0e-04	9.0e-03	3.1e-20
58211	AT5G42905.1	7e-29					2.61	4.4e-01	NA	NA	2.8e-01	1.7e-07
58355	AT3G54130.1	2e-40		1.36		1.22	3.10	2.5e-01	NA	NA	5.2e-02	1.8e-10
58383	AT3G08947.1	2e-160	1.93	1.61	1.52	1.47	3.87	6.4e-04	8.4e-03	1.6e-02	2.1e-02	1.2e-17
58515							-2.24	NA	NA	NA	NA	2.1e-05
58535	AT2G45560.1	9e-28	1.01				2.14	1.7e-01	2.2e-01	3.5e-01	6.3e-01	5.3e-06
58734	AT4G30190.1	1e-85					1.73	7.9e-01	NA	NA	7.6e-01	5.6e-04
58879							-2.23	7.7e-01	4.5e-01	5.8e-01	6.9e-01	2.3e-05
58970	AT2G23740.2	0	1.26	1.42	1.08		2.11	8.2e-02	3.3e-02	1.8e-01	5.1e-01	2.5e-08
58975	AT1G55850.1	0					1.77	2.5e-01	7.5e-01	4.2e-01	4.1e-01	3.9e-05
59055	AT2G25737.1	0			-1.32		-1.72	5.2e-01	3.4e-01	5.6e-02	3.7e-01	4.1e-04
59064	AT5G05960.1	3e-47	1.26				2.29	4.1e-02	4.6e-01	3.3e-01	6.0e-01	4.2e-06
59381	AT4G29090.1	4e-45					2.60	6.5e-01	4.1e-01	3.8e-01	3.6e-01	2.8e-08
59547	AT3G26770.1	2e-31					1.88	NA	NA	NA	NA	5.1e-04
59659	AT4G29090.1	2e-66	4.56	4.59	4.49	4.47	6.40	4.4e-31	1.5e-31	2.5e-31	2.0e-29	1.5e-73
59709							1.76	4.3e-01	NA	NA	7.5e-01	9.7e-04
59720	AT5G28020.1	2e-15					1.64	4.9e-01	7.2e-01	5.7e-01	3.8e-01	4.5e-04
59805	AT5G15500.2	4e-14	-1.75	-1.34	-1.31		-3.31	2.3e-03	4.1e-02	5.2e-02	2.3e-01	6.4e-13
59828	AT1G12910.1	9e-16					-1.90	NA	NA	NA	NA	4.7e-04
59838	AT4G29090.1	1e-32					-3.38	1.7e-01	2.4e-01	1.9e-01	4.6e-01	5.7e-12
59928	AT2G22360.1	6e-80	1.17		1.28		3.00	7.0e-02	NA	NA	5.1e-01	1.0e-09
60052	AT4G29090.1	3e-57	3.00	2.94	3.32	3.05	5.49	1.2e-09	2.8e-09	5.0e-12	5.6e-10	1.7e-42
60079					1.26		2.95	2.4e-01	NA	NA	1.8e-01	7.3e-10
60266			1.23	1.60	1.71	1.23	3.81	7.2e-02	6.9e-03	3.3e-03	6.9e-02	1.5e-16
60272	AT1G43760.1	1e-36	3.00	2.94	3.48	2.95	4.89	2.1e-10	5.2e-10	3.3e-14	8.3e-10	1.7e-41
60399	AT5G49800.1	8e-35				-1.00	-2.82	4.3e-01	NA	NA	1.1e-01	1.7e-08
60429			1.56	1.35	1.35	1.49	3.66	9.7e-03	3.7e-02	3.9e-02	1.6e-02	1.5e-15
60726	AT5G19260.1	1e-25					-1.82	6.9e-01	NA	NA	9.2e-01	8.2e-04
60989	AT2G01050.1	9e-46					2.39	4.6e-01	NA	NA	3.7e-01	3.0e-06
61127	AT1G47480.1	7e-25					-2.18	8.2e-01	NA	NA	1.8e-01	9.8e-06
61152	AT4G23690.1	2e-23				1.03	2.10	8.1e-01	NA	NA	8.2e-02	5.9e-05

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
61263	AT4G35160.1	2e-72	1.11	1.42	1.38	1.70	3.08	1.5e-01	3.0e-02	3.9e-02	4.6e-03	2.5e-13
61425	AT5G51040.1	9e-41	3.00	2.97	2.95	3.15	5.22	7.6e-10	9.0e-10	1.1e-09	6.2e-11	3.1e-38
61483	AT1G79070.1	1e-15	1.02				1.86	1.4e-01	NA	NA	7.8e-01	1.9e-04
61756			1.59	2.25	2.53	2.09	4.29	1.1e-02	3.2e-05	1.6e-06	1.8e-04	2.6e-22
61789	AT1G24140.1	1e-102			1.25		2.32	7.7e-01	NA	NA	3.8e-01	2.2e-06
61961			1.47	1.48	1.59	1.40	3.74	1.9e-02	1.7e-02	8.5e-03	2.8e-02	2.7e-16
61992	AT5G58280.1	3e-19		-1.10	-1.28		-1.94	7.5e-01	1.5e-01	6.5e-02	3.1e-01	8.9e-06
62096	AT4G29090.1	6e-34					-1.83	NA	NA	NA	NA	8.1e-04
62203	AT5G05880.1	2e-29		1.06		1.02	1.91	1.0e+00	NA	NA	1.1e-01	4.3e-04
62298	AT5G20540.1	2e-11	1.14				2.79	7.8e-02	NA	NA	1.6e-01	1.1e-08
62431							2.71	7.4e-01	NA	NA	2.1e-01	6.1e-08
62595	AT4G29090.1	5e-22					1.97	NA	NA	NA	NA	2.6e-04
62596	AT4G29090.1	9e-23					2.21	NA	NA	NA	NA	3.0e-05
62814	AT4G31805.1	3e-16		1.03	1.02	1.03	2.08	6.9e-01	1.9e-01	2.0e-01	1.8e-01	2.2e-06
62846	AT4G29090.1	1e-49	1.32	1.52	1.31	1.80	3.70	4.8e-02	1.4e-02	5.2e-02	1.6e-03	1.0e-15
63017	AT1G47740.1	1e-11	1.11	1.29	1.07		2.89	1.0e-01	NA	NA	5.6e-01	3.1e-09
63159	AT2G01050.1	6e-28					1.89	NA	NA	NA	NA	5.0e-04
63182	AT2G01050.1	4e-44					2.54	2.0e-01	3.6e-01	4.2e-01	2.5e-01	1.4e-09
63470	AT1G07790.1	3e-13					-2.63	5.2e-01	NA	NA	2.0e-01	1.4e-07
63596	AT1G43760.1	2e-12					-1.90	NA	NA	NA	NA	4.5e-04
63686	AT4G39230.1	5e-58	1.02	1.93	1.85	1.25	2.45	2.3e-01	6.7e-04	1.4e-03	7.8e-02	7.6e-13
63700							-2.02	4.9e-01	NA	NA	7.8e-01	1.7e-04
63870	AT5G42930.1	0	-1.26	-1.16	-1.33	-1.16	-1.98	8.0e-02	1.3e-01	5.8e-02	1.3e-01	7.5e-07
64151	AT5G47550.1	2e-24		-2.03	-3.60	-3.64	-1.21	9.6e-01	4.5e-05	6.1e-17	4.4e-18	3.0e-02
64154	AT4G03460.1	1e-13					2.42	2.1e-01	NA	NA	4.3e-01	2.4e-06
64308	AT4G29090.1	1e-39					2.38	6.0e-01	NA	NA	4.7e-01	2.1e-06
64675							1.92	2.6e-01	5.2e-01	4.5e-01	6.0e-01	1.6e-04
64694	AT3G48080.1	8e-19	-1.03				-2.01	7.1e-02	NA	NA	9.7e-01	1.8e-04
64775				2.22	2.02	1.47	2.22	9.9e-01	4.9e-05	3.4e-04	2.4e-02	2.1e-05
64860	AT5G38280.1	1e-108		1.15			2.88	4.6e-01	NA	NA	2.4e-01	6.3e-09
64892							2.23	NA	NA	NA	NA	2.0e-05
64916	AT3G01090.1	0					-2.45	6.8e-01	4.8e-01	5.2e-01	4.5e-01	2.5e-06
64920	AT3G25760.1	6e-19			1.14	1.41	1.82	1.0e+00	NA	NA	1.0e-02	8.7e-04
65280	AT4G20520.1	6e-12	3.20	2.97	3.14	2.65	5.27	4.0e-11	1.2e-09	8.6e-11	1.8e-07	1.9e-38
65297	AT2G45660.1	7e-16	1.10				1.79	1.3e-01	2.9e-01	8.2e-01	5.5e-01	1.1e-04
65348							-2.43	6.8e-01	2.5e-01	3.2e-01	6.1e-01	2.7e-06
65442							-2.34	3.7e-01	NA	NA	5.5e-01	7.7e-06
65525	AT3G09830.1	7e-124		1.01			1.54	3.7e-01	2.3e-01	7.8e-01	5.4e-01	4.6e-04
65853	AT5G04590.1	1e-30			1.00	1.20	1.48	5.6e-01	4.9e-01	2.4e-01	9.8e-02	2.6e-06
66327	AT1G73230.1	2e-28					1.97	7.5e-01	7.8e-01	5.8e-01	1.5e-01	6.5e-05
66441	AT2G01050.1	2e-44		1.06			2.66	6.3e-01	NA	NA	4.0e-01	1.8e-07
66563	AT4G23160.1	4e-83					2.27	2.3e-01	4.6e-01	5.9e-01	3.0e-01	8.7e-07
66791	AT2G38060.1	4e-15	3.01	2.82	3.12	2.61	5.09	1.1e-09	1.4e-08	1.5e-10	3.6e-07	3.9e-39
66970	AT4G23160.1	6e-30					1.86	3.0e-01	2.5e-01	4.0e-01	6.9e-01	2.7e-07
67291	AT2G01050.1	2e-35	1.18	1.14	1.45		3.09	7.4e-02	NA	NA	5.3e-01	2.3e-10
67322	AT2G01050.1	6e-45	3.15	3.18	3.41	2.80	4.91	2.3e-11	6.4e-12	1.2e-13	7.2e-09	7.2e-43
67420	AT5G13840.1	3e-48					2.04	NA	NA	NA	NA	1.4e-04
67776	AT4G23160.1	2e-18					1.91	NA	NA	NA	NA	4.1e-04
67816	AT2G01050.1	2e-20		1.02	1.05		3.07	2.0e-01	NA	NA	3.5e-01	3.0e-10
68017	AT4G01930.1	2e-18	-1.09	-1.06			-1.48	1.7e-01	2.0e-01	5.8e-01	7.0e-01	1.7e-04
68084	AT3G50340.1	2e-50					2.52	5.3e-01	NA	NA	3.3e-01	1.0e-06
68089	AT3G50340.1	1e-41					1.88	NA	NA	NA	NA	5.3e-04
68237	AT3G01600.1	8e-12		1.06	1.18	1.25	2.25	1.0e+00	9.9e-02	5.0e-02	2.9e-02	2.0e-05
68270	AT1G74960.2	0					2.28	8.2e-01	3.3e-01	4.7e-01	3.4e-01	3.4e-07

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
68374	AT1G43760.1	9e-38	4.73	4.50	4.73	4.71	6.51	3.3e-33	1.9e-30	1.3e-33	1.6e-33	1.9e-79
68392	AT5G64570.1	0		-1.17	-1.48	-1.73	-2.92	5.8e-01	1.0e-01	1.7e-02	2.8e-03	7.3e-10
68402							2.49	3.2e-01	NA	NA	1.7e-01	8.2e-07
68476	AT3G55470.1	3e-14		1.07	1.77	1.49	2.41	4.0e-01	1.9e-01	3.1e-03	2.2e-02	1.4e-10
68636	AT2G01050.1	1e-48					2.74	5.0e-01	NA	NA	1.6e-01	5.9e-08
68640	AT1G43760.1	4e-14		1.01			2.99	3.9e-01	NA	NA	3.9e-01	1.3e-09
68690	AT3G11945.1	2e-66			1.31	1.16	1.53	5.6e-01	2.8e-01	5.9e-02	1.2e-01	1.4e-04
68854				1.08	1.43	1.31	2.74	2.8e-01	1.5e-01	2.7e-02	4.8e-02	4.2e-10
69112							2.73	5.8e-01	NA	NA	2.5e-01	6.1e-08
69289	AT5G54160.1	5e-116		1.92	1.88	1.66	3.77	2.6e-01	6.1e-04	9.7e-04	5.7e-03	2.2e-16
69397							2.57	2.7e-01	NA	NA	6.7e-01	3.4e-07
69959	AT1G67180.1	2e-15					2.13	6.5e-01	NA	NA	3.3e-01	1.9e-05
70359	AT5G15120.1	7e-69			-1.38		-2.06	8.4e-01	4.0e-01	2.4e-02	3.6e-01	5.3e-05
70997	AT5G12200.1	2e-19					2.04	8.5e-01	NA	NA	8.5e-01	1.5e-04
71043	AT5G01130.1	5e-16	3.23	2.51	2.12	2.24	4.73	8.4e-11	1.7e-06	1.3e-04	4.5e-05	1.5e-27
71234	AT2G01050.1	2e-43					-3.17	1.8e-01	5.4e-01	4.1e-01	3.7e-01	2.1e-10
71360						1.01	2.32	3.7e-01	NA	NA	1.3e-01	2.8e-06
71492	AT3G62230.1	3e-14					1.78	9.0e-01	NA	NA	3.5e-01	5.1e-04
71549	AT1G43760.1	2e-21					1.85	NA	NA	NA	NA	6.8e-04
71553	AT5G42905.1	3e-35	1.20	1.01			2.99	5.7e-02	1.6e-01	4.1e-01	2.6e-01	2.5e-10
71800							2.27	NA	NA	NA	NA	1.5e-05
72035			1.08	1.51	1.69	1.30	3.56	1.5e-01	1.4e-02	3.7e-03	5.0e-02	2.8e-15
72036	AT4G02180.1	5e-23	1.78	2.43	2.51	1.67	4.27	2.8e-03	4.8e-06	2.0e-06	6.5e-03	6.4e-22
72159	AT3G17450.1	9e-53					-1.97	7.4e-01	6.0e-01	8.3e-01	6.5e-01	2.2e-04
72456	AT1G21280.1	8e-24	3.24	2.93	2.81	2.08	4.96	4.5e-11	4.4e-09	2.5e-08	2.0e-04	1.2e-31
72641	AT3G31430.1	4e-12	1.49	1.37	1.13		3.33	1.2e-02	2.7e-02	1.1e-01	2.6e-01	2.7e-12
72780	AT1G59720.1	2e-32	1.46	1.24	1.40		3.03	2.1e-02	7.5e-02	3.1e-02	3.2e-01	9.7e-14
73037	AT2G01050.1	2e-46	1.45	1.53	1.79		3.46	2.1e-02	1.2e-02	1.9e-03	3.1e-01	5.6e-14
73292	AT1G15170.1	2e-116				1.47	2.05	5.6e-01	6.8e-01	5.3e-01	1.3e-02	5.6e-05
73490	AT5G13840.1	2e-34		1.07	1.13		3.19	2.1e-01	1.2e-01	8.6e-02	1.8e-01	3.5e-11
73651	AT4G15760.1	1e-76			-1.34		-2.50	6.9e-01	4.0e-01	1.7e-02	5.1e-01	8.5e-07
73680	AT4G29090.1	1e-36					1.75	8.3e-01	5.1e-01	5.9e-01	7.5e-01	6.4e-04
73702	AT2G22330.1	1e-91	1.06				1.97	1.1e-01	6.9e-01	8.3e-01	4.6e-01	4.6e-05
73825	AT4G29090.1	3e-11	1.56		1.24	1.33	2.92	1.1e-02	2.6e-01	7.5e-02	4.1e-02	1.8e-10
73891	AT4G26780.1	6e-45		1.22			3.01	1.7e-01	NA	NA	2.7e-01	8.2e-10
73918	AT3G58030.1	8e-12		1.19			3.00	1.6e-01	NA	NA	2.7e-01	8.7e-10
73945				1.12	1.02		2.89	1.9e-01	NA	NA	5.4e-01	5.4e-09
74041			2.27	2.23	2.20	1.98	4.47	3.0e-05	4.3e-05	6.1e-05	5.4e-04	2.2e-25
74134	AT4G27670.1	1e-44		-1.41	-1.17		-2.26	7.5e-01	7.2e-03	4.6e-02	9.3e-01	1.7e-05
74230	AT1G43760.1	1e-35					-2.92	4.2e-01	3.6e-01	5.4e-01	5.2e-01	9.0e-09
74391	AT2G01050.1	1e-33					2.41	NA	NA	NA	NA	3.5e-06
74595	AT2G18180.1	0				-1.75	-1.60	8.9e-01	7.0e-01	4.6e-01	3.5e-03	6.0e-04
74607			1.26	1.29	1.03	1.16	3.42	5.0e-02	4.0e-02	1.7e-01	7.9e-02	4.5e-13
74783	AT5G58050.1	1e-51					1.84	3.1e-01	NA	NA	9.0e-01	5.2e-04
75045							2.06	NA	NA	NA	NA	1.2e-04
75072	AT1G43760.1	1e-40	2.10	2.72	2.62	2.46	4.77	1.8e-04	1.2e-07	4.5e-07	3.4e-06	1.4e-29
75107	AT1G11680.1	2e-82				1.89	2.35	7.5e-01	2.8e-01	3.0e-01	5.9e-04	2.8e-06
75130	AT4G23990.1	0			-1.11	-1.50	-2.31	9.2e-01	5.8e-01	8.6e-02	5.9e-03	1.0e-05
75308	AT2G01050.1	7e-49	2.65	2.76	2.63	2.55	5.01	3.1e-07	5.6e-08	3.5e-07	1.0e-06	6.3e-34
75324							2.08	NA	NA	NA	NA	1.0e-04
75566			2.97	2.33	2.51	2.54	4.37	1.7e-09	8.0e-06	9.4e-07	8.2e-07	2.3e-34
75628	AT1G43760.1	4e-38	2.10	1.84	1.82	1.39	4.01	1.7e-04	1.5e-03	1.9e-03	3.6e-02	3.7e-19
75801							2.23	NA	NA	NA	NA	2.4e-05
75983	AT2G01050.1	3e-43	3.86	4.12	4.29	4.15	6.41	2.6e-18	4.4e-21	5.5e-23	3.4e-21	4.4e-64

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
76012	AT3G07040.1	4e-100		1.51	1.40	1.46	3.51	4.7e-01	1.0e-02	2.3e-02	1.5e-02	1.8e-13
76224	AT3G25780.1	6e-93					1.78	2.3e-01	4.9e-01	4.5e-01	7.7e-01	1.2e-04
76544	AT4G33270.1	2e-24					1.76	3.8e-01	NA	NA	6.5e-01	1.8e-04
76703	AT4G23160.1	3e-92	1.72	1.72	2.01	1.59	3.92	4.3e-03	4.1e-03	3.6e-04	1.1e-02	2.3e-19
76790	AT4G29090.1	2e-37	1.56	1.95	1.88	1.70	4.28	1.2e-02	5.3e-04	1.1e-03	4.8e-03	2.9e-22
76918			1.57	1.39	1.85	1.74	4.00	1.0e-02	3.4e-02	1.2e-03	3.0e-03	6.9e-19
76987	AT2G01050.1	2e-50	2.64	2.66	2.84	2.74	5.02	2.9e-07	1.8e-07	1.4e-08	6.9e-08	2.6e-34
77089	AT4G37370.1	4e-176	2.08					1.2e-04	2.8e-01	9.8e-01	9.1e-01	1.2e-01
77239	AT1G43760.1	2e-39	2.19	3.02	3.78	4.63	4.70	3.2e-05	1.9e-10	1.1e-16	1.7e-25	2.2e-25
77419	AT3G58030.1	9e-21	1.54	2.08	2.26	1.73	3.99	1.6e-02	2.0e-04	3.2e-05	4.2e-03	7.7e-22
77454					1.26		2.81	3.4e-01	NA	NA	3.3e-01	1.9e-08
77484	AT1G43760.1	2e-29					-2.51	4.6e-01	3.5e-01	4.3e-01	8.1e-01	1.3e-06
77814	AT4G29090.1	1e-69		1.02	1.19		2.02	8.0e-01	1.6e-01	6.7e-02	3.9e-01	7.7e-05
78097	AT3G06400.1	2e-11	2.10	1.56	1.54	1.44	3.91	1.5e-04	1.2e-02	1.4e-02	2.5e-02	6.4e-18
78224							2.00	NA	NA	NA	NA	2.0e-04
78501	AT3G61220.1	4e-110	2.42	1.82	2.27	1.90	4.12	5.8e-06	1.9e-03	2.7e-05	1.1e-03	3.1e-22
78752			1.58	1.66	1.59	1.06	3.73	8.8e-03	4.8e-03	8.7e-03	1.5e-01	5.4e-16
78920	AT1G66910.1	1e-19					2.15	NA	NA	NA	NA	5.3e-05
79016	AT5G58050.1	3e-61	1.38	1.14			2.57	2.4e-02	9.8e-02	3.8e-01	6.1e-01	4.8e-08
79189			1.09		1.52	1.11	1.90	1.8e-01	3.1e-01	1.9e-02	1.5e-01	2.7e-05
79558	AT2G01050.1	7e-45	4.32	4.46	4.54	4.18	6.44	1.1e-25	2.5e-27	1.3e-28	1.6e-23	7.3e-70
79691					1.10		3.00	1.9e-01	NA	NA	3.5e-01	9.8e-10
80200	AT5G41761.1	2e-22				1.19	1.91	6.2e-01	3.6e-01	3.8e-01	8.8e-02	1.0e-05
80259	AT4G23160.1	1e-166	3.12	3.77	3.76	3.19	5.79	9.4e-11	4.8e-16	6.3e-16	3.6e-11	2.1e-47
80273	AT4G23160.1	1e-155	2.68	2.48	2.50	2.50	4.15	1.4e-07	1.2e-06	8.8e-07	1.3e-06	3.7e-36
80287	AT2G01050.1	5e-18					2.03	NA	NA	NA	NA	1.6e-04
80573	AT1G25580.1	1e-14					-2.07	7.5e-01	NA	NA	4.4e-01	1.1e-04
80613	AT5G42905.1	5e-31					2.53	NA	NA	NA	NA	8.0e-07
80842	AT4G23160.1	7e-54					2.26	NA	NA	NA	NA	1.7e-05
80851	AT4G39230.1	4e-40		1.64	1.71		1.89	6.2e-01	8.2e-03	4.8e-03	7.3e-01	5.5e-05
81120							2.36	2.9e-01	NA	NA	4.6e-01	6.2e-06
81232	AT1G62820.1	5e-33					-2.70	3.6e-01	5.8e-01	4.5e-01	2.0e-01	1.1e-07
81262	AT3G31430.1	1e-20					1.86	9.3e-01	NA	NA	5.0e-01	4.4e-04
81354	AT1G06620.1	3e-148		1.78	1.38		2.91	6.6e-01	6.9e-04	2.1e-02	5.4e-01	8.2e-09
81523	AT1G69490.1	6e-31					2.27	4.3e-01	2.9e-01	2.4e-01	4.1e-01	1.5e-06
81527	AT5G59050.1	2e-23			1.31	1.28	2.67	6.5e-01	NA	NA	3.3e-02	9.4e-08
81574	AT1G21280.1	2e-40	1.24	1.77	1.54	1.64	3.31	8.8e-02	3.0e-03	1.6e-02	8.1e-03	7.8e-19
81708	AT4G29090.1	7e-18					-2.42	NA	NA	NA	NA	2.8e-06
81881	AT1G21280.1	1e-29	1.23	1.46	1.04	1.30	3.53	6.4e-02	1.5e-02	1.7e-01	3.9e-02	5.6e-14
81903	AT5G54160.1	5e-65	1.96	1.85	1.47	1.17	3.54	5.5e-04	1.3e-03	2.3e-02	1.1e-01	1.2e-15
82142	AT5G54160.1	2e-49		1.13	1.68	1.65	2.02	8.7e-01	1.4e-01	6.4e-03	7.9e-03	5.6e-05
82210	AT1G17710.1	8e-49					1.83	7.6e-01	NA	NA	5.4e-01	5.3e-04
82458	AT1G40390.1	8e-13					2.04	NA	NA	NA	NA	1.5e-04
82495	AT2G02910.1	4e-14	1.36	1.36	1.21	1.28	3.60	3.1e-02	3.0e-02	7.4e-02	4.7e-02	8.0e-15
82587	AT5G20080.1	4e-11		1.35	1.37	1.15	1.80	2.8e-01	3.7e-02	3.7e-02	1.1e-01	1.9e-10
82591							2.03	7.5e-01	1.9e-01	3.3e-01	3.9e-01	1.7e-05
82646	AT5G64220.1	6e-16	1.87	1.62	1.59	1.49	3.93	1.1e-03	7.5e-03	9.9e-03	1.9e-02	2.7e-18
82976	AT1G53885.1	4e-22					1.80	NA	NA	NA	NA	9.1e-04
83123	AT1G52820.1	2e-54	1.29				2.48	1.6e-02	NA	NA	5.5e-01	1.6e-06
83199			2.06	1.76	2.19	2.11	3.79	2.6e-04	3.1e-03	6.1e-05	1.6e-04	3.9e-22
83231	AT4G29090.1	1e-34					-2.14	4.3e-01	7.6e-01	8.3e-01	5.3e-01	5.4e-05
83376	AT1G70850.1	6e-50					1.93	5.4e-01	NA	NA	5.1e-01	1.2e-04
83874	AT4G29090.1	2e-26					2.02	2.9e-01	NA	NA	9.1e-01	5.8e-05
84083	AT5G17680.1	1e-151	2.02	2.47	2.67	2.47	4.59	3.8e-04	2.2e-06	1.9e-07	2.7e-06	4.1e-27

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
84094	AT4G20520.1	5e-16					2.48	NA	NA	NA	NA	1.5e-06
84783	AT4G31940.1	2e-64					2.20	NA	NA	NA	NA	3.2e-05
85246	AT1G43760.1	4e-14	1.14			1.05	2.88	7.2e-02	NA	NA	1.0e-01	7.3e-09
85440	AT5G59310.1	5e-12			-2.42	-3.45		1.0e+00	8.9e-01	6.9e-06	3.7e-12	2.9e-01
85520	AT1G65680.1	4e-95				-1.48		1.0e+00	9.9e-01	7.9e-01	5.5e-04	5.4e-01
85577							1.77	NA	NA	NA	NA	9.3e-04
85928							1.81	NA	NA	NA	NA	8.9e-04
85953					2.53	4.64	1.75	9.4e-01	7.8e-01	1.5e-06	5.3e-23	1.0e-03
85962	AT1G75130.1	4e-55					1.97	9.3e-01	NA	NA	1.8e-01	2.0e-04
86053	AT5G67090.1	3e-120	2.38				1.90	1.3e-06	3.1e-01	6.3e-01	9.8e-01	4.7e-04
86122	AT1G43760.1	5e-42	1.17	1.37	1.58	1.23	2.85	1.2e-01	4.1e-02	1.2e-02	8.4e-02	8.1e-13
86187	AT5G67090.1	1e-100					1.72	6.7e-01	3.9e-01	3.5e-01	5.7e-01	8.4e-04
86305	AT2G01050.1	2e-48	1.01	1.03			2.47	1.7e-01	1.6e-01	3.5e-01	5.5e-01	1.6e-08
86374	AT4G23160.1	6e-106	1.85	2.03	1.87	1.33	4.06	1.5e-03	2.8e-04	1.2e-03	4.8e-02	3.6e-20
86406							2.28	NA	NA	NA	NA	1.4e-05
86491							2.33	9.5e-01	NA	NA	1.5e-01	9.2e-06
86538	AT4G13420.1	0					3.00	2.6e-01	NA	NA	3.1e-01	1.1e-09
86602	AT2G01050.1	4e-44	4.03	4.26	4.43	3.96	6.24	2.3e-21	4.3e-24	2.2e-26	1.1e-20	8.7e-64
86638	AT5G48050.1	2e-11	3.79	2.54	2.40	2.92	4.79	4.4e-16	5.9e-07	3.6e-06	3.1e-09	3.4e-28
87068	AT2G37970.1	5e-14	1.10	1.13			3.03	9.7e-02	NA	NA	1.6e-01	6.0e-10
87105	AT4G27750.1	6e-33	2.98	3.43	3.54	3.23	5.42	4.3e-10	8.2e-14	7.5e-15	5.4e-12	9.7e-42
87231	AT3G24255.1	3e-17					-2.50	NA	NA	NA	NA	1.0e-06
87248	AT5G65900.1	3e-23	1.62	3.05	3.26	3.26	4.83	9.0e-03	9.6e-10	3.7e-11	4.5e-11	8.5e-28
87399	AT1G75950.1	9e-27	5.97	5.31	5.30	4.98	7.25	3.9e-59	6.5e-46	4.2e-46	1.2e-39	6.4e-87
87411	AT2G39360.1	0		1.20	1.23	1.13	2.28	9.5e-01	7.0e-02	6.3e-02	9.7e-02	5.9e-06
87526	AT1G30800.1	3e-32	1.21	1.77	1.86	1.41	3.79	8.9e-02	2.4e-03	1.1e-03	2.8e-02	1.7e-16
87694	AT5G11730.1	7e-47		1.10		1.75	2.37	3.4e-01	1.5e-01	3.3e-01	3.3e-03	1.0e-07
87722	AT2G26670.1	7e-12					2.80	2.7e-01	NA	NA	1.5e-01	2.2e-08
87943	AT1G05894.1	1e-31					2.64	7.3e-01	NA	NA	1.5e-01	1.7e-07
88107	AT5G21105.1	1e-133					1.84	NA	NA	NA	NA	7.5e-04
88289							2.00	3.0e-01	NA	NA	8.4e-01	1.5e-04
88604	AT3G09510.1	1e-48	-1.58				1.21	3.0e-04	9.4e-01	9.6e-01	8.6e-01	3.7e-02
88850							1.81	7.7e-01	NA	NA	3.1e-01	6.9e-04
88851	AT1G79740.1	6e-13	1.25	1.14	1.32	1.27	3.37	5.7e-02	1.0e-01	4.2e-02	5.0e-02	9.1e-13
88880							2.66	4.7e-01	NA	NA	2.4e-01	4.6e-08
89347	AT2G01050.1	2e-50	2.46	2.90	3.05	3.07	5.06	2.2e-06	4.0e-09	3.4e-10	3.8e-10	1.6e-34
89465	AT5G05390.1	7e-57					2.08	NA	NA	NA	NA	8.6e-05
89636	AT1G43760.1	4e-17	1.21	1.20			3.10	5.3e-02	NA	NA	3.4e-01	2.0e-10
89690	AT4G29090.1	8e-69	3.66	3.92	3.80	3.18	5.81	9.7e-16	2.6e-18	4.2e-17	1.2e-11	1.2e-51
89773	AT1G43760.1	6e-41	2.02	2.18	2.54	2.39	4.55	4.1e-04	7.5e-05	1.4e-06	8.8e-06	1.7e-28
89775	AT3G04880.1	3e-13					2.66	2.9e-01	NA	NA	5.7e-01	1.6e-07
89822							1.97	2.8e-01	5.5e-01	3.2e-01	8.1e-01	3.0e-05
89886	AT4G29090.1	3e-11					2.33	1.2e-01	NA	NA	9.3e-01	8.2e-06
90237	AT3G18670.1	9e-54		1.32	1.83	1.20	3.15	4.3e-01	4.3e-02	1.2e-03	7.5e-02	4.0e-11
90238	AT5G04730.1	4e-50	-1.02		-1.00		-2.55	1.6e-01	3.8e-01	1.8e-01	2.5e-01	6.7e-08
90309	AT3G31430.1	2e-13					2.13	NA	NA	NA	NA	6.0e-05
90371	AT3G09510.1	6e-13					2.47	1.4e-01	NA	NA	6.2e-01	1.3e-06
90561							2.42	NA	NA	NA	NA	3.0e-06
91151	AT1G43760.1	3e-29					1.82	4.1e-01	NA	NA	7.7e-01	5.1e-04
91168						1.98		9.9e-01	9.7e-01	6.6e-01	1.1e-05	2.5e-01
91323	AT5G45290.1	3e-11		1.02			2.93	2.3e-01	NA	NA	2.9e-01	2.6e-09
91398	AT5G51490.1	2e-57			1.01		2.11	1.0e+00	1.9e-01	9.4e-02	1.1e-01	7.2e-05
91511	AT2G01050.1	1e-29					2.32	NA	NA	NA	NA	8.8e-06
91808	AT1G43760.1	2e-42				1.95		1.0e+00	9.1e-01	5.3e-01	2.5e-05	9.3e-02

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
92449	AT2G01050.1	6e-46					2.33	3.7e-01	2.8e-01	2.3e-01	4.4e-01	1.8e-06
92453	AT5G42905.1	8e-54	1.05	1.20	1.09		3.15	1.2e-01	5.3e-02	1.0e-01	4.6e-01	9.0e-11
92492	AT4G23160.1	1e-123	1.97	2.28	2.14	2.23	4.46	6.1e-04	2.4e-05	1.1e-04	4.9e-05	2.5e-25
92668			1.20	1.09			3.22	5.9e-02	1.1e-01	2.0e-01	2.0e-01	2.0e-11
92698			1.91	2.16	2.19	1.49	4.12	9.6e-04	8.2e-05	6.1e-05	2.1e-02	1.4e-20
92723	AT5G46330.1	0	1.93	2.60	1.76	1.87	4.22	8.6e-04	5.7e-07	3.4e-03	1.3e-03	3.3e-21
92802	AT1G43760.1	4e-36	3.23	2.79	3.06	2.46	5.12	2.8e-11	2.1e-08	3.4e-10	2.3e-06	2.7e-35
92811	AT4G23160.1	4e-66					2.36	5.9e-01	NA	NA	2.9e-01	4.5e-06
92864			1.53				2.27	3.2e-03	6.6e-01	5.7e-01	6.9e-01	1.5e-05
93079	AT1G47890.1	5e-157	1.35	2.32	2.09	1.96	4.19	4.9e-02	1.5e-05	1.7e-04	6.1e-04	7.5e-21
93199	AT4G29090.1	1e-38	2.87	3.08	3.28	2.68	5.15	5.3e-09	1.5e-10	4.5e-12	9.7e-08	1.4e-36
93203	AT1G43760.1	3e-27				1.08	2.84	3.3e-01	NA	NA	7.5e-02	1.3e-08
93207	AT5G63050.1	2e-29	1.41	1.35	1.59		3.37	2.4e-02	3.4e-02	7.0e-03	3.7e-01	1.4e-12
93208	AT4G23160.1	1e-127	3.17	3.34	3.11	3.07	5.39	3.1e-11	1.2e-12	6.0e-11	2.0e-10	2.0e-41
93209	AT4G29090.1	1e-43	2.11	2.05	2.06	1.79	4.30	1.6e-04	2.5e-04	2.3e-04	2.6e-03	5.3e-23
93212	AT2G01050.1	1e-45	1.54	1.36	1.20	1.45	3.55	1.1e-02	3.4e-02	8.7e-02	1.9e-02	2.3e-14
93219			1.84	2.25	2.04	1.79	4.19	1.8e-03	3.3e-05	2.8e-04	2.6e-03	1.4e-21
93231	AT4G29090.1	7e-23					2.14	NA	NA	NA	NA	5.8e-05
93234	AT1G43760.1	3e-15					1.97	NA	NA	NA	NA	2.7e-04
93235	AT1G51980.1	3e-14	1.82	2.00	1.94	2.00	4.26	2.0e-03	4.0e-04	7.1e-04	4.2e-04	2.1e-22
93236	AT2G01050.1	8e-43					2.23	NA	NA	NA	NA	2.5e-05
93241	AT2G01050.1	9e-11	1.44		1.27	1.11	3.37	1.5e-02	3.3e-01	4.6e-02	9.9e-02	1.6e-12
93242	AT5G03240.1	9e-14	2.07	2.31	2.11	2.15	4.46	2.5e-04	1.8e-05	1.4e-04	1.0e-04	3.3e-25
93246	AT2G17920.1	2e-12	2.05	2.06	2.15	1.63	4.43	2.7e-04	2.2e-04	1.0e-04	8.6e-03	3.6e-24
93259	AT1G43760.1	4e-24					2.74	3.5e-01	NA	NA	4.6e-01	5.2e-08
93266	AT1G43760.1	3e-36					1.96	NA	NA	NA	NA	2.7e-04
93268	AT1G21280.1	2e-31	1.58	1.41	1.24	1.28	3.53	8.3e-03	2.6e-02	6.9e-02	5.2e-02	3.2e-14
93293	AT1G43760.1	5e-13				1.40	2.69	6.1e-01	NA	NA	1.1e-02	1.2e-07
93317			1.10				2.91	8.0e-02	NA	NA	1.8e-01	4.6e-09
93318	AT4G29090.1	3e-12					2.53	2.1e-01	NA	NA	3.1e-01	8.5e-07
93321	AT2G01050.1	2e-37	1.68	1.88	2.03	1.94	4.19	5.9e-03	1.1e-03	3.2e-04	7.0e-04	1.2e-21
93324	AT1G21280.1	2e-15	1.39	1.37	1.66	1.05	3.72	2.7e-02	3.0e-02	4.1e-03	1.5e-01	1.1e-15
93330	AT4G29090.1	2e-17					2.07	NA	NA	NA	NA	1.1e-04
93332	AT1G43760.1	7e-41	1.55	1.12	1.28	1.35	3.48	9.3e-03	1.2e-01	5.3e-02	3.4e-02	1.0e-13
93342	AT1G43760.1	9e-18					2.10	NA	NA	NA	NA	8.3e-05
93365	AT2G01050.1	6e-46	2.05	2.05	2.08	2.03	4.30	2.9e-04	2.5e-04	1.9e-04	3.3e-04	3.2e-23
93372	AT3G31430.1	1e-15		1.77	1.80	1.77	3.66	2.5e-01	2.3e-03	2.0e-03	2.4e-03	3.2e-15
93408					1.32		2.73	2.7e-01	NA	NA	7.1e-01	6.6e-08
93416	AT4G29090.1	2e-21	1.27	1.20	1.34		3.18	4.5e-02	6.5e-02	3.0e-02	4.8e-01	4.5e-11
93419				1.18			2.95	2.4e-01	NA	NA	3.8e-01	2.3e-09
93423	AT2G01050.1	1e-15					2.07	NA	NA	NA	NA	1.1e-04
93425	AT1G43760.1	2e-16	1.41	1.42		1.02	3.29	2.1e-02	1.9e-02	2.3e-01	1.6e-01	5.0e-12
93456							2.45	8.4e-01	NA	NA	5.9e-01	2.2e-06
93462	AT2G01050.1	6e-39					2.37	NA	NA	NA	NA	4.9e-06
93470	AT1G21280.1	8e-30					2.81	1.8e-01	NA	NA	2.1e-01	1.9e-08
93479	AT3G62230.1	1e-26			1.24	1.01	2.76	7.8e-01	NA	NA	1.2e-01	4.7e-08
93486	AT5G42905.1	6e-41					2.25	NA	NA	NA	NA	2.0e-05
93514							1.81	NA	NA	NA	NA	8.6e-04
93520	AT2G01050.1	7e-43		1.04	1.06		2.89	5.0e-01	NA	NA	3.4e-01	5.1e-09
93530	AT1G40390.1	3e-14			1.07		2.66	6.0e-01	NA	NA	3.6e-01	1.6e-07
93549	AT3G06140.1	6e-33					2.28	NA	NA	NA	NA	1.5e-05
93558							2.24	NA	NA	NA	NA	2.0e-05
93568	AT1G43760.1	2e-16					1.85	NA	NA	NA	NA	6.8e-04
93607	AT2G13450.1	3e-14					2.65	1.5e-01	NA	NA	2.8e-01	1.7e-07

contig #	AGI	E-val	lfc 25	lfc 45	lfc 55	lfc 65	lfc all	padj 25	padj 45	padj 55	padj 65	padj all
93608	AT1G43760.1	2e-22					2.09	NA	NA	NA	NA	9.0e-05
93627	AT5G42905.1	2e-41					2.86	4.6e-01	NA	NA	2.6e-01	9.4e-09
93628	AT2G01050.1	4e-13					2.42	NA	NA	NA	NA	2.8e-06
93656	AT4G23160.1	7e-131					2.77	2.1e-01	NA	NA	3.4e-01	2.9e-08
93657	AT5G42905.1	3e-44					2.00	NA	NA	NA	NA	1.9e-04
93665	AT4G29090.1	1e-30		1.19	1.03		2.84	5.3e-01	NA	NA	2.5e-01	1.2e-08
93756	AT1G43760.1	5e-14		1.55	1.33	1.34	3.43	2.9e-01	8.7e-03	3.8e-02	3.3e-02	4.0e-13
93766							2.07	NA	NA	NA	NA	1.1e-04
93776	AT5G42905.1	3e-49					1.92	NA	NA	NA	NA	3.8e-04
93781	AT3G10710.1	3e-56				1.04	2.95	4.3e-01	NA	NA	9.2e-02	2.5e-09
93812							2.13	NA	NA	NA	NA	6.0e-05
93823	AT5G54160.1	1e-128		1.93	2.22	1.77	3.30	7.8e-01	5.6e-04	3.4e-05	2.4e-03	2.2e-11
93840	AT4G13320.1	1e-11					1.83	NA	NA	NA	NA	7.5e-04
93863	AT5G42905.1	5e-24					2.04	NA	NA	NA	NA	1.4e-04
93875	AT3G14310.1	3e-34		1.62	2.03	1.69	2.46	1.0e+00	5.9e-03	1.7e-04	3.2e-03	2.2e-06
93994							1.93	NA	NA	NA	NA	3.5e-04
94044	AT4G33200.3	1e-70					1.97	NA	NA	NA	NA	2.5e-04
94073	AT1G21280.1	3e-29					1.85	NA	NA	NA	NA	6.6e-04
94076							2.07	NA	NA	NA	NA	1.1e-04

Table 24. Plant material used for this study.

Line	Other ID	Species	Source	Origin	Ploidy	Reproduction
BoSDi-01	SAD12	*Boechera stricta*	Dr. Johnston	Colorado	2x	Sexual
BoSDi-02	ES850,ES111	*Boechera lasiocarpa*	Dr. Johnston	Idaho	2x	Sexual
BoSDi-04	L105	*Boechera polyantha*	Dr. Johnston	Montana	2x	Sexual
BoSDi-05	ES744, ES81	*Boechera perennans*	Dr. Johnston	New Mexico	2x	Sexual
BoSDi-06		NA	Dr. Johnston	NA	2x	Sexual
BoADi-01	ES9.6	*Boechera divaricarpa*	Dr. Johnston	Montana	2x	Apomictic
BoADi-02	ES517	*Boechera divaricarpa*	Dr. Johnston	Montana	2x	Apomictic
BoADi-03	ES649	*Boechera stricta ?*	Dr. Johnston	Colorado	2x	Apomictic
BoADi-04	BAJP3	NA	Dr. Johnston	Montana	2x	Apomictic
BoADi-05	67.5	*B. retrofracta/divaricarpa*	Dr. Johnston	Montana	2x	Apomictic
BoATi-01		*B. gunnisoniana*	Dr. Johnston	Colorado	3x	Apomictic
BoATi-02	ES598, ES34	*B. divaricarpa ?*	Dr. Johnston	Washington	3x	Apomictic
BoATi-03	ES704	*B. divaricarpa ?*	Dr. Johnston	Idaho	3x	Apomictic
BoATi-04		NA	Dr. Johnston	NA	3x	Apomictic
BoATe-04		*Boechera divaricarpa*	New line	BoADi-01	4x	Apomictic
HyPR1	NMN104	*Hypericum perforatum*	Heidelberg	Heidelberg Bot.Gard.	2x	Sexual
HyPR3	704579	*Hypericum perforatum*	Heidelberg	Italy	2x	Sexual
H06-1449		*Hypericum perforatum*	Apomixis-IPK	Wisconsin	6x	Sexual
H06-1644/11		*Hypericum perforatum*	Apomixis-IPK	Ontario	6x	Sexual
H06-2573		*Hypericum perforatum*	Apomixis-IPK	Spain	6x	Sexual
H06-2886		*Hypericum perforatum*	Apomixis-IPK	Italy	6x	Sexual
H06-3325		*Hypericum perforatum*	Apomixis-IPK	Germany	6x	Sexual
H06-1369		*Hypericum perforatum*	Apomixis-IPK	Illinois	4x	Apomictic
H06-1441		*Hypericum perforatum*	Apomixis-IPK	Wisconsin	4x	Apomictic
H06-1489		*Hypericum perforatum*	Apomixis-IPK	Wisconsin	4x	Apomictic
H06-1591		*Hypericum perforatum*	Apomixis-IPK	Wisconsin	4x	Apomictic
H06-1650		*Hypericum perforatum*	Apomixis-IPK	Ontario	4x	Apomictic
H06-3220		*Hypericum perforatum*	Apomixis-IPK	England	4x	Apomictic
H06-3251		*Hypericum perforatum*	Apomixis-IPK	Czech Rep.	4x	Apomictic
HyPR2	H06-1883	*Hypericum maculatum*	Apo/Gene Reg. IPK	Michigan	4x	Apomictic
HyPR5		*Hypericum perforatum*	Apo/Gene Reg. IPK	NA	4x	Apomictic
HyPR7	H06-1378	*Hypericum maculatum*	Apo/Gene Reg. IPK	Michigan	4x	Apomictic
HyPR8	H06-1359	*Hypericum perforatum*	Apo/Gene Reg. IPK	Illinois	4x	Apomictic
HyPR9	H06-2719	*Hypericum perforatum*	Apo/Gene Reg. IPK	Spain	4x	Apomictic

Curriculum Vitae

Personal Information

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Education

IPK-GATERSLEBEN June 2011 - to date Molecular Genetics Department	PhD student in the Gene Regulation Group. Supervisor: Dr. Helmut Bäumlein. Topic: “Molecular and Morphological Dissection of Apomixis in Plants”.
UNIVERSITY OF PALERMO Faculty of Agricultural Sciences, Palermo, Italy 09/1998 – 07/2006	B.Sc and M.Sc. in Agricultural Sciences with emphasis in Biotechnology. Thesis work on “Study on androgenesis in Prunus avium (L.) (hon)”. Supervisor: Prof. M. Germaná,
SCIENTIFIC HIGH SCHOOL **BENEDETTO CROCE SCHOOL** Palermo, Italy 09/1993 – 07/1998	High School degree (hon.)

Professional experience

IPK-GATERSLEBEN April 2007 – September 2010	Research Assistant in the Group "Plant Reproductive Biology". Dr. Jochen Kumlehn. Work involving wheat transformation, isolation of Wheat egg cells, and analysis of wheat egg cell transcriptomes.
"Terre del Sud", Martea's Company Palermo, Italy February 2004 - January 2007	Participation in the research project "Phenotypic evaluation of several legumes ecotypes from southern Italy" within the framework of the research network
UNIVERSITY OF PALERMO Faculty of Agricultural Sciences, Palermo, Italy February 2000 - July 2006	Research assistant in the Laboratory of Biotechnology and Micropropagation

Workshops during PhD study

Microdissection and Expression Analysis. March 2013. Graduate school of the IPK, Gatersleben and Martin Luther University, Halle (Germany).

Histological and ultrastructural analysis of plant tissue using Light, Scanning and Transmission Electron Microscopy. 13-17th April 2015. Graduate school of the IPK, Gatersleben and Martin Luther University, Halle (Germany).

International

Workshop on Molecular Evolution. July 24th - August 5th 2011. Fort Collins, Colorado (USA). (http://evomics.org/workshops/workshop-on-molecular-evolution/2011-evolution-fort-collins/)

Participation in scientific conferences during the PhD study

Poster presentation

Paride Rizzo, Olga Kirioukhova, Helmut Bäumlein, Jörg Fuchs, Amal Johnston. 2-4 October, 2013. Connecting ploidy with female gametophyte development of the two apomicts *Boechera spp*. and *Hypericum perforatum*. European Frontiers of Plant Reproduction Research, Oslo, Norway.

Bui Thi Mai Huong, Francesca Tedeschi, Paride Rizzo, Andreas Czihal, Twan Rutten, Markus Kuhlmann, Lothar Altschmied, Claude Becker, Helmut Bäumlein. September,

2013. ET Factors: Novel epigenetic regulators of plant reproduction are involved in DNA-methylation control. Institute's Day, IPK-Gatersleben, Germany.

Francesca Tedeschi, Paride Rizzo, Twan Rutten, Helmut Bäumlein. September, 2013. The Arabidopsis RKD transcription factor family plays an essential role in the control of female gametophyte development. Institute's Day, IPK-Gatersleben, Germany.

Bui Thi Mai Huong, Twan Rutten, Paride Rizzo, Francesca Tedeschi, Andreas Czihal, Markus Kuhlmann, Helmut Bäumlein. October 2014. ET Factors: Novel epigenetic regulators reproduction involved in DNA-demethylation. Institute's Day, IPK-Gatersleben, Germany.

Paride Rizzo, Olga Kirioukhova, Jörg Fuchs, Twan Rutten, Helmut Bäumlein, Amal Johnston. October, 2014. Connecting ploidy with female gametophyte development of two apomicts *Boechera spp* and *Hypericum perforatum.* Institute's Day, IPK-Gatersleben, Germany.

Francesca Tedeschi, Paride Rizzo, Lothar Altschmied, Helmut Bäumlein. October 2014. RKD transcription factors control cell fate and differentiation during female gametophyte development in Arabidopsis. Institute's Day, IPK-Gatersleben, Germany.

*Underlined author was presenting the work

Participation in scientific conferences before PhD study

Participation as a listener in the 21st International Conference on Sexual Plant Reproduction. 2nd-6th August 2010. Bristol, United Kingdom.

Participation as a listener in the 3rd International Conference on Apomixis. June 27th - July 2nd 2007. Wernigerode, Germany.

Participation as a listener in the International conference: "Gametic Cells and Molecular Breeding for Crop Improvement" – Workshop of the working group: Technology advancement in gametic embryogenesis of recalcitrant genotypes, November 2004. Palermo, Italy.

I, the undersigned, declare that the information provided above is, to the best of my knowledge, accurate and complete.

Paride Rizzo

Gatersleben, July 1st 2016

Declaration (Eklärung)

I, Paride Rizzo, declare that the submitted scientific work has been completed by me and, that I have not used any other than permitted reference sources or materials or engaged any plagiarism. All the references and the other sources used in the presented work have been appropriately acknowledged in the work. I further declare that the work has not been previously submitted for the purpose of academic examination, either in its original or similar form, anywhere else.

Ich, Paride Rizzo, erkläre hiermit, dass die eingereichte wissenschaftliche Arbeit von mir verfasst wurde und ich keine anderen als die erlaubten Quellen oder Hilfsmittel verwendet habe oder irgendein Plagiat begangen habe. Alle Quellen und Literaturangaben wurden als solche in der Arbeit korrekt kenntlich gemacht. Desweiteren erkläre ich, dass die vorliegende Arbeit vorher noch nie zur Begutachtung eingereicht wurde, weder in ihrer jetzigen Form noch in einer ähnlichen. Ich bewerbe mich damit zum ersten Mal um einen Doktorgrad.

Paride Rizzo
Gatersleben, July 1st 2016

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