Genes and SSR Markers for Exogenous and Endogenous Control of the Time of Flowering in *Vaccinium corymbosum*

**Abstract**

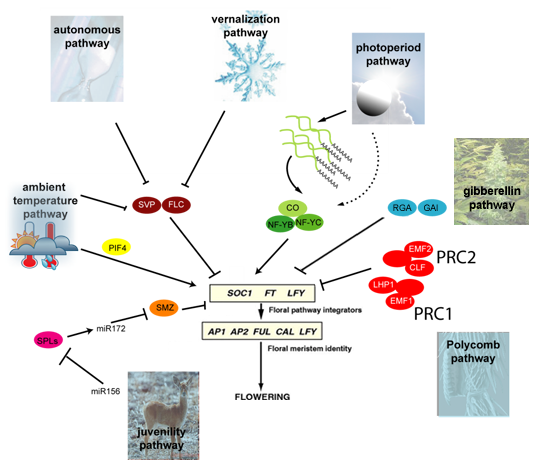
I undertook a genome-wide investigation to identify genes related to the time of flowering in *Vaccinium corymbosum*, the Northern highbush blueberry. For the investigated genes, different alleles result in an alteration in the number of leaves or number of days required until flowering, thereby corroborating their control over the flowering process. I examined the seven pathways controlling flowering (age, ambient temperature, autonomous, gibberellin, light signaling, polycomb, and vernalization) and found a total of 72 orthologs in *Vaccinium corymbosum*. I generated three simple sequence repeats (SSRs) for 69 of the 72 orthologs. Through the screening of particular alleles with SSR markers, future blueberry varieties can be selected for adaptation to environmental stresses.

**Introduction**

Flowering is the shift from a vegetative growth stage to a reproductive growth in plants. Vegetative growth is characterized by the production of stems and leaves, while reproductive growth encompasses flower bud initiation, floral fertilization, fruit and seed production, and offspring seed germination (Higgins *et al.*, 2010). The transition to reproductive growth halts leaf development and initiates floral growth in a group of undifferentiated cells in the shoot, called the apical meristem (Fornara *et al.*, 2010). Flowering enables sexual reproduction through pollination, which results in seed development. Therefore, the switch to flowering is carefully controlled to ensure optimal conditions for successful pollination and offspring growth. In essence, the time of flowering is the result of regulatory networks coordinating endogenous cues and external stimuli in order to promote genes that ultimately initiate flowering (Jung *et al.*, 2012).

Previous research has identified core pathways, primary genes, and specific mechanisms that control flowering in the model dicot *Arabidopsis thaliana*. Through loss-of-function mutations and transgenic organisms, over 180 *Arabidopsis* genes in seven major pathways control the time of flowering (Fornara *et al.*, 2010). The photoperiod pathway responds to changes in light throughout the year (Figure 1). The vernalization pathway is a reaction to several months of cold winter. The ambient temperature pathway correlates with daily changes in temperature. The other four pathways – age, autonomous, gibberellin, and polycomb – reflect endogenous fluctuations in the plant (Fornara *et al.*, 2010). The seven pathways act on a group of regulatory genes, the floral pathway integrators (*SOC1*, *FT* and *LFY*), which merge the upstream signals. The three floral pathway integrators initiate five floral meristem identity genes, which in turn trigger flowering. The floral meristem identity genes include *APETALA1* (*AP1*), *APETALA2* (*AP2*), *FRUITFUL* (*FUL*), and *CAULIFLOWER* (*CAL*; Henderson and Dean, 2004).

**Figure 1.** The seven pathways and important genes controlling flowering (from Henderson and Dean, 2004, and from Turck and Adrian).



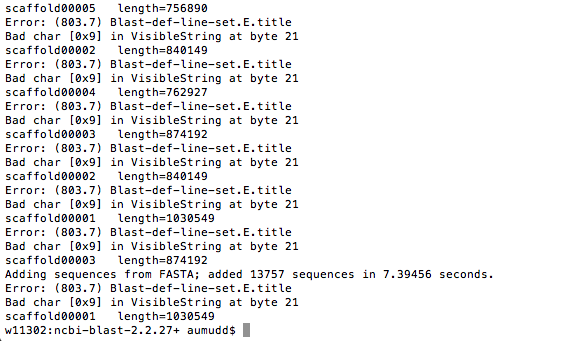
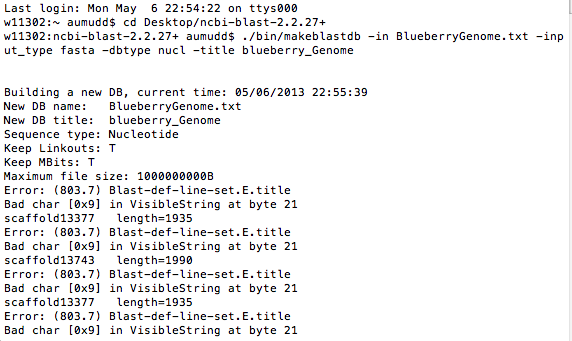
For my research, I studied primary genes involved in the seven pathways controlling flowering. I identified genes in *Arabidopsis thaliana*, and using *Arabidopsis* amino acid sequences, I discovered 72 *Vaccinium* orthologs related to the seven pathways controlling flowering. I determined simple sequence repeats (SSRs) for as many blueberry orthologs as possible. The seven pathways have a significant effect on the timing of flowering and the plant’s ability to flower, as demonstrated by loss-of-function mutations or altered expression of particular genes.

**Methods**

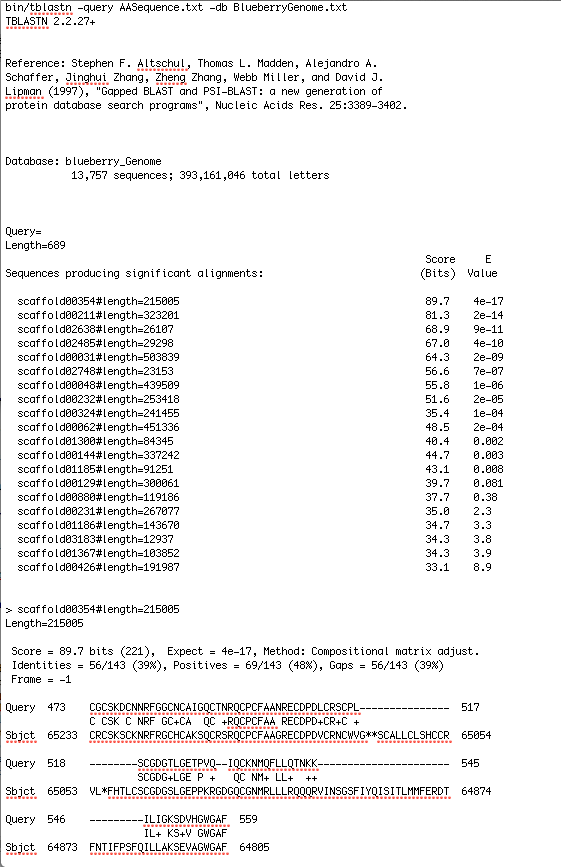
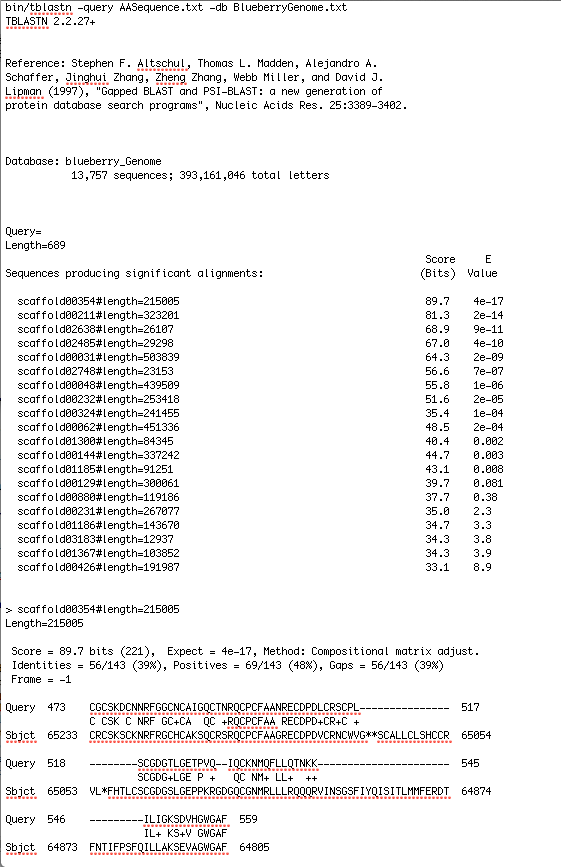
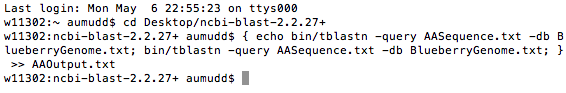
The first half of my project focused on determining the genes involved in the time of flowering. My primary resource was a genomic analysis of soybean by Jung *et al.* (2012) which listed 183 *Arabidopsis* genes that previous studies found are directly involved in the flowering regulatory pathways as well as 24 additional uncharacterized paralogs that may have regulatory functions. The total 207 genes fell into two categories: 1) 99 flowering pathway integrators/meristem identity genes and 2) 108 condition pathway genes responding to endogenous and exogenous changes. Dr. Jeannie Rowland of the USDA Genetic Improvement for Fruits and Vegetables Laboratory advised me to focus on the condition pathway genes (personal communication). Therefore, I concentrated on the 108 genes from the seven pathways that control flowering.

Having identified 108 genes of interest, I progressed into the second half of my project, finding SSRs for each gene. To begin, I copied a text file with the scaffolds of the blueberry genome onto a computer and used Unix syntax (Figure 2) in Mac terminal to create a local database of the blueberry genome that could be queried with BLAST. I found amino acid sequences for all *Arabidopsis* genes at The Arabidopsis Information Resource (TAIR) using a nomenclature search (Huala *et al.*, 2001). I used the Unix syntax (Figure 3) in Mac terminal to run the amino acid sequences via local tBLASTn against the blueberry scaffolds and to find the closest match (Altschul *et al.*, 1997). A tBLASTn compares the amino acid sequence of a protein with a translated nucleotide sequence to find the best matches. Since most amino acids are translated from several codons, the use of a tBLASTn eliminated the impact of point mutations if the two sequences had identical amino acids but different codons. Furthermore, running a tBLASTn correlated similar amino acids, given that the two amino acids are comparable in polarity and have the same effect on the shape of the two proteins. I only examined the *Vaccinium* gene with the smallest E value for each tBLASTn query, as long as the gene was within the E value cutoff of 1e-04. I assumed that the *Vaccinium* gene with the smallest E value was the ortholog of the inputted *Arabidopsis* gene. I determined appropriate SSRs by importing the scaffold of the best match *Vaccinium* gene into the SSR Tool at the Genome Database for *Vaccinium* (*Genome Database for Vaccinium, 2011*), specifying a motif frequency of at least five for dinucleotides and four for trinucleotides. For each gene, I selected three di/trinucleotide SSRs near the gene location on the scaffold, with the optimal SSR having more than ten repeats and being within 10,000 bases of the start of the query sequence. All SSRs had forward and reverse primers without repeats in their sequences, and the total PCR products were between 100 and 700 base pairs in length.

**Figure 2.** Unix syntax and an abbreviation of the resulting output that created a local database of the blueberry genome. /bin/makeblastdb runs the executable file makeblastdb, which creates a local database from the input file (-in) BlueberryGenome.txt. The input file is a nucleotide sequence (-dbtype nucl) in FASTA format (-input\_type fasta), and the resulting database will be titled Blueberry\_Genome (-title).



**Figure 3.** Unix syntax and an abbreviation of the resulting output from a tBLASTn of an *Arabidopsis* amino acid sequence against the blueberry scaffolds. The syntax echo bin/tblastn -query AASequence.txt -db BlueberryGenome.txt simply copies “bin/tblastn -query AASequence.txt -db BlueberryGenome.txt” and places it at the top of the tBLASTn results on the AAOutput.txt file. That way, the tBLASTn results can be quickly identified by nomenclature search of the AAOutput.txt file. bin/tblastn runs the executable file tblastn, which compares the input amino acid query AASequence.txt (-query) with the translated nucleotide database BlueberryGenome.txt (-db) for the best matches. The results are then exported to AAOutput.txt, and >> means that the results will be written at the bottom of the file, whereas > means that the results will overwrite the entire file.



**Results**

From the original 108 *Arabidopsis* genes, I found a total of 72 orthologs in *Vaccinium corymbosum*. Of the 72 orthologs, I identified three SSRs for 69 genes, one SSR for one gene, and zero SSRs for two genes (Table 1). For the two *Vaccinium* orthologs that had zero SSRs identified, the results did not include forward and reverse primers. Nonetheless, I successfully identified SSRs for 69 genes related to the time of flowering in *Vaccinium corymbosum*.

|  |  |  |
| --- | --- | --- |
| ***Arabidopsis* Locus** | **Best Match *Vaccinium* Scaffold** | **Number of SSRs** |
| AT4G02560 | Scaffold 00002 | 3 |
| AT4G26000 | Scaffold 00021 | 3 |
| AT4G00650 | Scaffold 00039 | 3 |
| AT1G22770 | Scaffold 00100 | 3 |
| AT3G05120 | Scaffold 00101 | 3 |
| AT2G33835 | Scaffold 00102 | 3 |
| AT4G16280 | Scaffold 00104 | 3 |
| AT3G15270 | Scaffold 00105 | 3 |
| AT1G68050 | Scaffold 00110 | 3 |
| AT5G02810 | Scaffold 00125 | 3 |
| AT1G27370 | Scaffold 00127 | 3 |
| AT3G12810 | Scaffold 00147 | 3 |
| AT5G13480 | Scaffold 00166 | 3 |
| AT5G03840 | Scaffold 00181 | 3 |
| AT3G10390 | Scaffold 00232 | 3 |
| AT3G33520 | Scaffold 00246 | 3 |
| AT5G11530 | Scaffold 00253 | 3 |
| AT2G40080 | Scaffold 00254 | 3 |
| AT1G31814 | Scaffold 00289 | 3 |
| AT4G08920 | Scaffold 00331 | 3 |
| AT2G06255 | Scaffold 00336 | 3 |
| AT1G30970 | Scaffold 00348 | 3 |
| AT2G25930 | Scaffold 00371 | 3 |
| AT3G21320 | Scaffold 00509 | 3 |
| AT5G58230 | Scaffold 00615 | 3 |
| AT1G04400 | Scaffold 00649 | 3 |
| AT5G39660 | Scaffold 00651 | 3 |
| AT5G23150 | Scaffold 00686 | 3 |
| AT2G42200 | Scaffold 00691 | 3 |
| AT5G17690 | Scaffold 00696 | 3 |
| AT2G19520 | Scaffold 00728 | 3 |
| AT5G61380 | Scaffold 00753 | 3 |
| AT3G18990 | Scaffold 00811 | 3 |
| AT3G07650 | Scaffold 00832 | 3 |
| AT1G77300 | Scaffold 00894 | 3 |
| AT5G37055 | Scaffold 00925 | 3 |
| AT5G08330 | Scaffold 00993 | 3 |
| AT4G11110 | Scaffold 01034 | 3 |
| AT2G47700 | Scaffold 01059 | 3 |
| AT5G35840 | Scaffold 01070 | 3 |
| AT5G62430 | Scaffold 01102 | 3 |
| AT3G46640 | Scaffold 01150 | 3 |
| AT4G34530 | Scaffold 01322 | 3 |
| AT3G04610 | Scaffold 01384 | 3 |
| AT3G20740 | Scaffold 01670 | 3 |
| AT2G43410 | Scaffold 01689 | 3 |
| AT5G60100 | Scaffold 02075 | 3 |
| AT1G20330 | Scaffold 02142 | 3 |
| AT5G24470/AT2G46790 | Scaffold 00001 | 3 |
| AT2G18915/AT5G57360 | Scaffold 00026 | 3 |
| AT1G53160/AT2G33810 | Scaffold 00062 | 3 |
| AT3G47500/AT1G26790 | Scaffold 00079 | 3 |
| AT1G66350/AT3G03450 | Scaffold 00134 | 3 |
| AT1G01060/AT2G46830 | Scaffold 00140 | 3 |
| AT4G11880/AT4G22950 | Scaffold 00249 | 3 |
| AT2G34140/AT1G29160 | Scaffold 00270 | 3 |
| AT1G65480/AT4G20370 | Scaffold 00357 | 3 |
| AT2G17770/AT4G35900 | Scaffold 00367 | 3 |
| AT3G24440/AT2G18870 | Scaffold 00396 | 3 |
| AT1G47250/AT5G42790 | Scaffold 00528 | 3 |
| AT2G22540/AT4G24540 | Scaffold 01187 | 3 |
| AT1G14920/AT2G01570 | Scaffold 01360 | 3 |
| AT2G18880/AT5G57380/AT4G30200 | Scaffold 00026 | 3 |
| AT2G23380/AT4G02020/AT1G02580 | Scaffold 00354 | 3 |
| AT2G18790/AT4G16250/AT4G18130 | Scaffold 00751 | 3 |
| AT5G51230/AT4G16845/AT2G35670 | Scaffold 00857 | 3 |
| AT3G02380/AT5G15840/AT5G15850 | Scaffold 01843 | 3 |
| AT2G32950/AT2G46340/AT1G53090/AT3G15354 | Scaffold 00734 | 3 |
| AT3G25730/AT1G13260/AT1G25560/AT1G68840 | Scaffold 00930 | 3 |
| AT5G24930/AT5G57660 | Scaffold 11225 | 1 |
| AT1G09570 | Scaffold 03861 | 0 |
| AT5G65060/AT5G65080/AT5G10140/AT5G65050/ AT5G65070/AT1G77080 | Scaffold 10765 | 0 |

**Table 1.** An abbreviated summary of the SSR results for the 72 *Vaccinium corymbosum* orthologs. The *Arabidopsis* gene locus identifies the particular *Arabidopsis* amino acid protein sequences that I analyzed via tBLASTn against the *Vaccinium* scaffolds. The best match *Vaccinium* scaffold and the number of SSRs identified are noted.

The age pathway enables a plant to flower upon reaching an adult age and prevents flowering during its juvenile phase. The age pathway centers on an interaction between miR156 and SPL that acts as an endogenous cue for the plant to undergo the transition from the vegetative phase to ﬂowering. Specifically, as the plant ages, miR156 decreases, which results in an increase in the SPL proteins. The SPL proteins promote the transition from the juvenile phase to the adult phase and ultimately result in ﬂowering through miR172, several *MADS* genes, and *LFY* (Yu *et al.*, 2012). Five *Arabidopsis* genes are involved in the age pathway (Amasino, 2010), and I successfully identified all genes in *Vaccinium* with three SSRs for each gene. The age pathway has significant implications on the time of flowering, as exemplified by *SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 3* (*SPL3*). The premature, or earlier than normal, presence of *SPL3* in a juvenile plant causes early flowering and can result in morphological abnormalities, as repression of *SPL3* is essential for normal vegetative growth (Gandikota *et al.*, 2007).

The ambient temperature pathway enables the plant to respond to daily high and low temperatures and either promote or repress flower development. Sixteen *Arabidopsis* genes are involved in the ambient temperature pathway (Jung *et al.*, 2012), and I successfully identified all genes in *Vaccinium* with three SSRs for ten of the genes. I identified zero SSRs for the other six genes because the SSR results did not include forward and reverse primers. The ambient temperature pathway is important for controlling flowering, as exemplified by *SHORT VEGETATIVE PHASE* (*SVP*). As seen with *SVP* under-expressed mutants, the decrease in transcription and translation of *SVP* results in a reduced response to colder temperatures, which causes the plant to flower earlier and in colder temperatures than normal. A loss of *SVP* would eliminate the plant’s normal response to cold temperature, which would result in extremely early flowering. Overexpression of *SVP*, on the other hand, resulted in late flowering, signifying that too much *SVP* keeps the plant stuck in the cold temperature response even after warmer weather has arrived (Lee *et al.*, 2007).

The autonomous pathway responds to endogenous changes, such as the plant's circadian rhythm (Jung *et al.*, 2012), and regulates flowering through epigenetic and post-transcriptional alteration (Simpson, 2004). Seventeen *Arabidopsis* genes are involved in the autonomous pathway (Jung *et al.*, 2012), and I successfully identified all genes in *Vaccinium* with three SSRs for each gene. The autonomous pathway has an important effect on the time of flowering, as exemplified by *FVE*. A mutation in *FVE*, which normally represses flowering using histone deacetylation (Ausín *et al.*, 2004), resulted in late flowering and an alteration in the normal clustering of flowers on a plant (Martínez-Zapater *et al.*, 1995).

The gibberellin pathway is dependent on the hormone gibberellic acid, which regulates growth and development in plants. Gibberellic acid promotes ﬂoral initiation under short-day conditions, and plants unable to properly synthesize gibberellic acid, such as those with a mutation in *GA1*, are incapable of ﬂowering. Five *Arabidopsis* genes are involved in the gibberellin pathway (Yu *et al.*, 2012), and I successfully identified all genes in *Vaccinium* with three SSRs for each gene. The gibberellin pathway has significant implications on the time of flowering, as exemplified by *GIBBERELLIC ACID INSENSITIVE* (*GAI*). A transformation mutation in *GAI* resulted in early flowering. The change in flowering time was due to an excess of gibberellic acid, which is connected with early flowering (Zhu *et al.*, 2007).

Light is the primary regulator and environmental factor that controls flowering. Plants recognize the time of day and the season by analyzing the duration and intensity of light. The light signaling pathway is comprised of the circadian clock components and the photoperiod/ photoreceptor genes. Forty-eight *Arabidopsis* genes are involved in the light signaling pathway (Jung *et al.*, 2012), and I successfully identified all genes in *Vaccinium* with three SSRs for 45 of the genes. I identified one SSR each for two genes and zero SSRs for one gene. The light signaling pathway has a great impact on controlling flowering, as exemplified by *CONSTANS* (*CO*). *CO* mutations down-regulate the meristem identity genes and the photochrome function, suggesting that *CO* promotes flowering (Putterill *et al.*, 1995).

The polycomb pathway responds to internal changes within the plant and centers on epigenetic repression of particular developmental and cellular routes through two protein complexes: *Polycomb Repressor Complex 1* (*PRC1*) and *Polycomb Repressor Complex 2* (*PRC2*). Ten *Arabidopsis* genes are involved in the polycomb pathway (Kim *et al.*, 2012), and I successfully identified all genes in *Vaccinium* with three SSRs for each gene. The polycomb pathway influences the time of flowering, as exemplified by *EMBRYONIC FLOWER 1* (*EMF1*). *EMF1* is essential for development in the vegetative stage, and individual plants with a mutation in *EMF1* skipped the vegetative stage and began flowering immediately after germination (Moon *et al.*, 2003).

The vernalization pathway is the response to an extended period of cold during the winter months. Thirty-two *Arabidopsis* genes are involved in the vernalization pathway (Jung *et al.*, 2012), and I successfully identified all genes in *Vaccinium* with three SSRs for 26 of the genes. Similar to the ambient temperature pathway, I identified zero SSRs for the remaining six genes. The vernalization pathway is essential in preventing flowering during the winter months and contains numerous core flowering control genes including *FRIGIDA* (*FRI*). A loss-of-function mutation in *FRI* resulted in early flowering (Werner *et al.*, 2005). In fact, up to 70% of variation in the time of flowering is due to *FRI* (Shindo *et al.*, 2005).

**Discussion**

In the study, I identified 72 potential *Vaccinium corymbosum* orthologs of 108 *Arabidopsis* genes that are involved in seven pathways controlling the time of flowering. Several paralogous *Arabidopsis* genes closely corresponded to a single *Vaccinium* gene, which is a consequence of only looking for one paralog in blueberry and resulted in 36 fewer *Vaccinium* genes than *Arabidopsis* genes. Noting the lack of a 1:1 ratio for *Arabidopsis* genes to *Vaccinium* orthologs, 68.1% of the examined *Vaccinium* orthologs corresponded with one *Arabidopsis* gene, 20.8% with two *Arabidopsis* genes, 6.9% with three *Arabidopsis* genes, 2.8% with four *Arabidopsis* genes, and 1.4% with five *Arabidopsis* genes (Table 1). To eliminate the statistical discrepancy and better assess all potential flowering control genes, future studies should select all ortholog matches of the tBLASTn that fall within the E value cutoff of 1e-04. By examining all ortholog matches, future studies will be able to better examine all possible genes, which was a limit of my study. Future studies should also search for *Vaccinium* paralogs of the currently identified 72 genes. Furthermore, since I only focused on the 108 condition pathway genes, additional research can examine the 99 flowering pathway integrators and meristem identity genes.

Breeders will use SSR markers to identify the alleles for the various genes that they want to breed. From the population of over 200 varieties with known phenotypes, the researchers will mix genomic DNA with the SSR forward and reverse primers as well as PCR cocktail to generate bands of variable sizes. The PCR amplicon will confirm whether the SSRs vary with the alleles for a particular gene. The PCR results will allow the breeders to select particular genotyhpes in the future. Therefore, rather than waiting for the seedlings to grow up and then examining their phenotypes, the scientists can first select the ones with the desired genotypes and cultivate them. They are not genetically modifying the plants but instead speeding up the screening process. Ultimately, utilization of the SSR strains will make traditional breeding methods more efficient and less random.

Flowering and the impetuses for flowering are important to study for a variety of reasons. First, engineering a crop to produce a greater number of flowers or enabling a plant to flower multiple times in a year can dramatically increase the crop output. Moreover, the time of flowering directly correlates with a plant’s ability to adapt to new environments since the majority of crops are outside of their ancestor’s ecogeographical boundaries (Higgins *et al.*, 2010). In fact, comparison of wild and domestic varieties of a plant in different environments can help isolate the changes in the domestic variety that allowed for a more expansive habitat. Understanding a plant’s mechanism for environmental adaptation will, in turn, help with the critical propagation of climate change resilient varieties (Jung *et al.*, 2012). As climate change alters the Earth, farmers and plants will need to adjust to new environments, be they colder/warmer or wetter/dryer. The study and future manipulation of the time of flowering will allow for greater plant adaptation to new environments and a changing climate.

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**Acknowledgements**

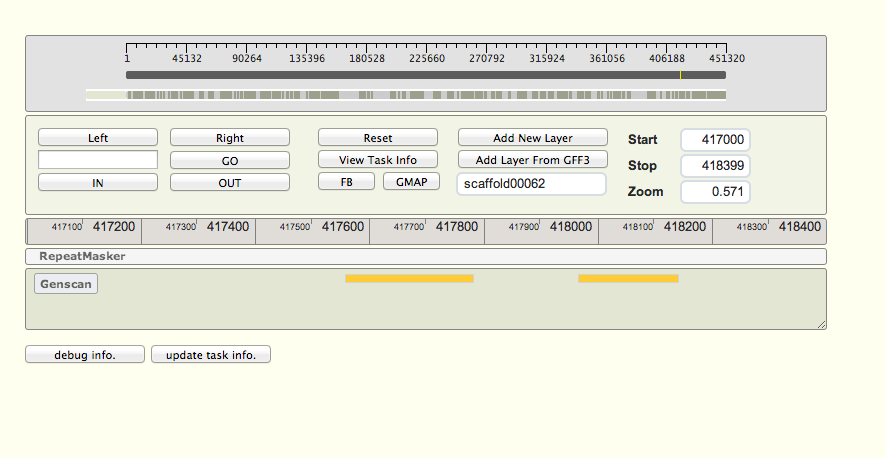
I would like to sincerely thank the following individuals: Allan Brown (NCSU), Jeannie Rowland (USDA), Doreen Main (WSU), and A. Malcolm Campbell (Davidson College).

**Appendix A: GenSAS Results**

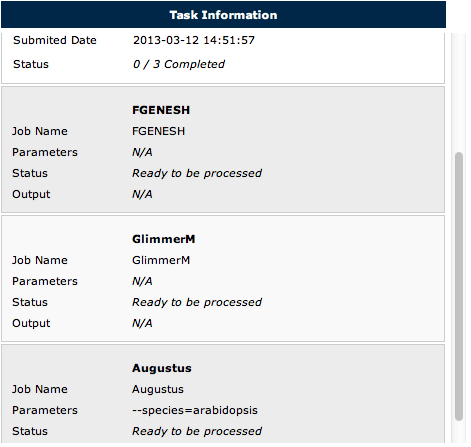
At the start of the experiment, I attempted to use GenSAS, an online genome annotation program from Washington State University. GenSAS was intended to offer a single interface with multiple tools for annotation and visualization of a genome’s structure and function (Lee *et al.*, 2011). After using GenSAS, however, it was not useful in its current iteration for my project. I particularly focused on the tool Genscan as well as running multiple jobs in one submission. Genscan is a tool that locates introns and exons within the genome. My run of the Genscan task was successfully completed, and the results were visualized (Figure 4).

I was less successful with running three jobs in one submission. I used the tools FGENESH, GlimmerM, and Augustus. FGENESH predicts the gene structure, GlimmerM locates exons within a genome, and Augustus finds genes with 3’ and 5’ untranslated region (UTR) sequences. Essentially, the three tasks were meant to determine the location of genes within the blueberry genome. The task, however, was not completed, as the jobs all said “Ready to be processed” more than 48 hours after submission (Figure 5). The GenSAS programmer responded to my error with the following:

**Figure 4.** Successful visualization of the Genscan results in GenSAS.



“I believe the problem with this is that the FgeneSH can only support uploading of results. FgeneSH is a commercial gene finder and we cannot offer the tool to be run for uploaded sequences. But, it is present in the event that someone has output from FgeneSH. They can upload the output to be included in GenSAS. This needs to be better stated on the page to keep folks from trying to use it if they don’t have output from it.” (personal communication; unreferenced)



**Figure 5.** Unsuccessful run of FGENESH, GlimmerM, and Augustus in GenSAS.

Therefore, although there were high hopes initially for using GenSAS to optimize the experiment, the practical application of GenSAS proved not yet up to the task.

In analysis of GenSAS, the 2013 Davidson College Laboratory Methods in Genomics course outlined an ideal program to optimize the blueberry experimentation, centering on three main changes to GenSAS. First, all of the *Vaccinium corymbosum* scaffolds would need to be pre-loaded onto GenSAS and accessible to multiple users. The optimal circumstance would be to pre-load multiple genomes, such as strawberry, grape, *Arabidopsis*, and tomato, so that the user can run multiple sequence alignments and readily compare specific genomes. Next, many of the tools that GenSAS offers should be pre-run on the *Vaccinium* genome. The desired pre-run tools include gene and exon predictions, BLAST results and annotations through comparison with the NCBI gene database using a set E-value cutoff, and SSRs. Therefore, the user would simply recall the results and readily confirm the annotation of the gene. Although the tasks are computation intensive processes, once they are completed a single time, they would not have to be repeated. Finally, GenSAS should be a more collective project. Researchers who identified a gene in a pathway, designated suitable SSR markers, or confirmed an annotation should be able to add new information to the genome so that all users can access the updated information (Davidson College Laboratory Methods in Genomics, 2013). The suggestions to GenSAS would promote a more community-based, open understanding of the *Vaccinium corymbosum* and other genomes.

**Appendix B: All 108 Examined *Arabidopsis* Genes**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| ***Arabidopsis* Locus** | **Other Names** | **Pathway** | **Top Hit *Vaccinium* Scaffold** | **E Value** |
| AT1G01060 | LATE ELONGATED HYPOCOTYL, LATE ELONGATED HYPOCOTYL 1, LHY, LHY1 | Light Signaling | Scaffold00140 (length 354209) at 234299 | 2e-19 |
| AT1G02580 | EMB173, EMBRYO DEFECTIVE 173, FERTILIZATION INDEPENDENT SEED 1, FIS1, MEA, MEDEA, SDG5, SET DOMAIN-CONTAINING PROTEIN 5 | Polycomb | Scaffold00354 (length 215005) at 64805 | 4e-17 |
| AT1G04400 | AT-PHH1, ATCRY2, CRY2, CRYPTOCHROME 2, FHA, PHH1 | Light Signaling | Scaffold00649 (length 159319) at 28296 | 1e-119 |
| AT1G09570 | ELONGATED HYPOCOTYL 8, FAR RED ELONGATED 1, FAR RED ELONGATED HYPOCOTYL 2, FHY2, FRE1, HY8, PHYA, PHYTOCHROME A | Light Signaling | Scaffold03861 (length 7403) at 3771 | 0.0 |
| AT1G13260 | EDF4, ETHYLENE RESPONSE DNA BINDING FACTOR 4, RAV1, RELATED TO ABI3/VP1 1 | Light Signaling | Scaffold00930 (length 110378) at 63069 | 1e-103 |
| AT1G14920 | GAI, GIBBERELLIC ACID INSENSITIVE, RESTORATION ON GROWTH ON AMMONIA 2, RGA2 | Gibberellin | Scaffold01360 (length 81306) at 51382 | 0.0 |
| AT1G20330 | COTYLEDON VASCULAR PATTERN 1, CVP1, FRILL1, FRL1, SMT2, STEROL METHYLTRANSFERASE 2 | Vernalization | Scaffold02142 (length 46662) at 24743 | 9e-06 |
| AT1G22770 | FB, GI, GIGANTEA | Light Signaling | Scaffold00100 (length 346620) at 198329 | 0.0 |
| AT1G25560 | EDF1, ETHYLENE RESPONSE DNA BINDING FACTOR 1, TEM1, TEMPRANILLO 1 | Light Signaling | Scaffold00930 (length 110378) at 63096 | 3e-99 |
| AT1G26790 |  | Light Signaling | Scaffold00079 (length 471015) at 69048 | 6e-33 |
| AT1G27370 | SPL10, SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 10 | Age | Scaffold00127 (length 336847) at 165806 | 5e-33 |
| AT1G29160 |  | Light Signaling | Scaffold00270 (length 246371) at 215229 | 4e-50 |
| AT1G30970 | SUF4, SUPPRESSOR OF FRIGIDA4 | Vernalization | Scaffold00348 (length 210978) at 75279 | 1e-15 |
| AT1G31814 | FRIGIDA LIKE 2, FRL2 | Vernalization | Scaffold00289 (length 259591) at 150896 | 2e-19 |
| AT1G47250 | 20S PROTEASOME ALPHA SUBUNIT F2, PAF2 | Vernalization | Scaffold00528 (length 197283) at 110933 | 3e-64 |
| AT1G53090 | SPA1-RELATED 4, SPA4 | Light Signaling | Scaffold00734 (length 158513) at 143450 | 3e-129 |
| AT1G53160 | FLORAL TRANSITION AT THE MERISTEM6, FTM6, SPL4, SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 4 | Age | Scaffold00062 (length 451336) at 412489 | 1e-15 |
| AT1G65480 | FLOWERING LOCUS T, FT | Ambient Temperature | Scaffold00357 (length 260075) at 58774 | 6e-35 |
| AT1G66350 | RGA-LIKE 1, RGL, RGL1 | Gibberellin | Scaffold00134 (length 346346) at 174707 | 0.0 |
| AT1G68050 | "FLAVIN-BINDING, KELCH REPEAT, F BOX 1", ADO3, FKF1 | Light Signaling | Scaffold00110 (length 358202) at 120279 | 0.0 |
| AT1G68840 | ATRAV2, EDF2, ETHYLENE RESPONSE DNA BINDING FACTOR 2, RAP2.8, RAV2, RELATED TO ABI3/VP1 2, RELATED TO AP2 8, TEM2, TEMPRANILLO 2 | Light Signaling | Scaffold00930 (length 110378) at 63096 | 5e-102 |
| AT1G77080 | AGAMOUS-LIKE 27, AGL27, FLM, FLOWERING LOCUS M, MADS AFFECTING FLOWERING 1, MAF1 | Ambient Temperature, Vernalization | Scaffold10765 (length 2447) at 744 | 3e-13 |
| AT1G77300 | ASH1 HOMOLOG 2, ASHH2, CAROTENOID CHLOROPLAST REGULATORY1, CCR1, EARLY FLOWERING IN SHORT DAYS, EFS, LAZ2, LAZARUS 2, SDG8, SET DOMAIN GROUP 8 | Vernalization | Scaffold00894 (length 114877) at 89213 | 1e-27 |
| AT2G01570 | REPRESSOR OF GA, REPRESSOR OF GA1-3 1, RGA, RGA1 | Gibberellin | Scaffold01360 (length 81306) at 51382 | 0.0 |
| AT2G06255 | ELF4-L3, ELF4-LIKE 3 | Light Signaling | Scaffold00336 (length 230445) at 188137 | 1e-39 |
| AT2G17770 | ATBZIP27, BASIC REGION/LEUCINE ZIPPER MOTIF 27, BZIP27, FD PARALOG, FDP | Ambient Temperature | Scaffold00367 (length 240396) at 113139 | 7e-17 |
| AT2G18790 | HY3, OOP1, OUT OF PHASE 1, PHYB, PHYTOCHROME B | Light Signaling | Scaffold00751 (length 152548) at 83698 | 0.0 |
| AT2G18870 | VEL3, VERNALIZATION5/VIN3-LIKE 3, VIL4, VIN3-LIKE 4 | Autonomous | Scaffold00396 (length 187979) at 73810 | 7e-19 |
| AT2G18880 | VEL2, VERNALIZATION5/VIN3-LIKE 2, VIL3, VIN3-LIKE 3 | Autonomous | Scaffold00026 (length 499904) at 369396 | 6e-41 |
| AT2G18915 | ADAGIO 2, ADO2, LKP2, LOV KELCH PROTEIN 2 | Light Signaling | Scaffold00026 (length 499904) at 445582 | 0.0 |
| AT2G19520 | ACG1, ATMSI4, FVE, MSI4, MULTICOPY SUPPRESSOR OF IRA1 4, NFC04, NFC4 | Ambient Temperature, Autonomous | Scaffold00728 (length 157708) at 8716 | 6e-21 |
| AT2G22540 | AGAMOUS-LIKE 22, AGL22, SHORT VEGETATIVE PHASE, SVP | Ambient Temperature, Vernalization | Scaffold01187 (length 101153) at 47701 | 2e-24 |
| AT2G23380 | CLF, CURLY LEAF, ICU1, INCURVATA 1, SDG1, SET1, SETDOMAIN 1, SETDOMAIN GROUP 1 | Autonomous, Polycomb, Vernalization | Scaffold00354 (length 215005) at 64799 | 5e-41 |
| AT2G25930 | EARLY FLOWERING 3, ELF3, PYK20 | Light Signaling | Scaffold00371 (length 223748) at 73111 | 6e-19 |
| AT2G32950 | ARABIDOPSIS THALIANA CONSTITUTIVE PHOTOMORPHOGENIC 1, ATCOP1, CONSTITUTIVE PHOTOMORPHOGENIC 1, COP1, DEETIOLATED MUTANT 340, DET340, EMB168, EMBRYO DEFECTIVE 168, FUS1, FUSCA 1 | Light Signaling | Scaffold00734 (length 158513) at 142779 | 5e-62 |
| AT2G33810 | SPL3, SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 3 | Age | Scaffold00062 (length 451336) at 412489 | 2e-17 |
| AT2G33835 | FES1, FRIGIDA-ESSENTIAL 1 | Vernalization | Scaffold00102 (length 383343) at 88264 | 7e-17 |
| AT2G34140 |  | Light Signaling | Scaffold00270 (length 246371) at 215217 | 7e-49 |
| AT2G35670 | FERTILIZATION INDEPENDENT SEED 2, FERTILIZATION-INDEPENDENT ENDOSPERM 2, FIE2, FIS2 | Polycomb | Scaffold00857 (length 126644) at 55565 | 3e-04 |
| AT2G40080 | EARLY FLOWERING 4, ELF4 | Light Signaling | Scaffold00254 (length 265810) at 228805 | 4e-24 |
| AT2G42200 | ATSPL9, SPL9, SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 9 | Age | Scaffold00691 (length 141413) at 61795 | 5e-21 |
| AT2G43410 | FPA | Autonomous | Scaffold01689 (length 75472) at 47663 | 4e-45 |
| AT2G46340 | SPA1, SUPPRESSOR OF PHYA-105 1 | Light Signaling | Scaffold00734 (length 158513) at 142779 | 3e-69 |
| AT2G46790 | APRR9, ARABIDOPSIS PSEUDO-RESPONSE REGULATOR 9, PRR9, PSEUDO-RESPONSE REGULATOR 9, TL1, TOC1-LIKE PROTEIN 1 | Light Signaling | Scaffold00001 (length 1030549) at 322801 | 1e-36 |
| AT2G46830 | ATCCA1, CCA1, CIRCADIAN CLOCK ASSOCIATED 1 | Light Signaling | Scaffold00140 (length 354209) at 234299 | 7e-20 |
| AT2G47700 | RED AND FAR-RED INSENSITIVE 2, RFI2 | Light Signaling | Scaffold01059 (length 101143) at 96557 | 1e-19 |
| AT3G02380 | ATCOL2, B-BOX DOMAIN PROTEIN 3, BBX3, COL2, CONSTANS-LIKE 2 | Light Signaling | Scaffold01843 (length 51900) at 40767 | 3e-48 |
| AT3G03450 | RGA-LIKE 2, RGL2 | Gibberellin | Scaffold00134 (length 346346) at 174722 | 0.0 |
| AT3G04610 | FLK, FLOWERING LOCUS KH DOMAIN | Autonomous | Scaffold01384 (length 81068) at 28309 | 4e-29 |
| AT3G05120 | ATGID1A, GA INSENSITIVE DWARF1A, GID1A | Gibberellin | Scaffold00101 (length 425332) at 398762 | 4e-175 |
| AT3G07650 | B-BOX DOMAIN PROTEIN 7, BBX7, COL9, CONSTANS-LIKE 9 | Light Signaling | Scaffold00832 (length 123094) at 89599 | 1e-55 |
| AT3G10390 | FLD, FLOWERING LOCUS D | Ambient Temperature, Autonomous | Scaffold00232 (length 253418) at 139565 | 0.0 |
| AT3G12810 | CHR13, PHOTOPERIOD-INDEPENDENT EARLY FLOWERING 1, PIE1, SRCAP | Vernalization | Scaffold00147 (length 345970) at 30164 | 0.0 |
| AT3G15270 | SPL5, SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 5 | Age | Scaffold00105 (length 392037) at 147284 | 5e-16 |
| AT3G15354 | SPA1-RELATED 3, SPA3 | Light Signaling | Scaffold00734 (length 158513) at 143450 | 1e-144 |
| AT3G18990 | REDUCED VERNALIZATION RESPONSE 1, REM39, REPRODUCTIVE MERISTEM 39, VRN1 | Vernalization | Scaffold00811 (length 108354) at 96661 | 2e-25 |
| AT3G20740 | FERTILIZATION-INDEPENDENT ENDOSPERM, FERTILIZATION-INDEPENDENT ENDOSPERM 1, FIE, FIE1, FIS3 | Autonomous, Polycomb, Vernalization | Scaffold01670 (length 60304) at 9836 | 5e-20 |
| AT3G21320 |  | Light Signaling | Scaffold00509 (length 192554) at 181887 | 1e-21 |
| AT3G24440 | VERNALIZATION 5, VIL1, VIN3-LIKE 1, VRN5 | Autonomous, Vernalization | Scaffold00396 (length 187979) at 73795 | 2e-69 |
| AT3G25730 | EDF3, ETHYLENE RESPONSE DNA BINDING FACTOR 3 | Light Signaling | Scaffold00930 (length 110378) at 63060 | 5e-100 |
| AT3G33520 | ACTIN-RELATED PROTEIN 6, ARP6, ATARP6, EARLY IN SHORT DAYS 1, ESD1, SUF3, SUPPRESSOR OF FRI 3 | Ambient Temperature, Vernalization | Scaffold00246 (length 286612) at 268521 | 1e-53 |
| AT3G46640 | LUX, LUX ARRHYTHMO, PCL1, PHYTOCLOCK 1 | Light Signaling | Scaffold01150 (length 88293) at 80272 | 3e-34 |
| AT3G47500 | CDF3, CYCLING DOF FACTOR 3 | Light Signaling | Scaffold00079 (length 471015) at 68175 | 1e-85 |
| AT4G00650 | FLA, FLOWERING LOCUS A, FRI, FRIGIDA | Vernalization | Scaffold00039 (length 505275) at 216632 | 4e-50 |
| AT4G02020 | EZA1, SDG10, SET DOMAIN-CONTAINING PROTEIN 10, SWINGER, SWN | Autonomous, Polycomb, Vernalization | Scaffold00354 (length 215005) at 64799 | 2e-48 |
| AT4G02560 | LD, LUMINIDEPENDENS | Autonomous | Scaffold00002 (length 840149) at 158601 | 4e-28 |
| AT4G08920 | ATCRY1, BLU1, BLUE LIGHT UNINHIBITED 1, CRY1, CRYPTOCHROME 1, ELONGATED HYPOCOTYL 4, HY4, OOP2, OUT OF PHASE 2 | Light Signaling | Scaffold00331 (length 261439) at 124817 | 4e-128 |
| AT4G11110 | SPA1-RELATED 2, SPA2 | Light Signaling | Scaffold01034 (length 107107) at 19205 | 2e-62 |
| AT4G11880 | AGAMOUS-LIKE 14, AGL14 | Vernalization | Scaffold00249 (length 258199) at 131012 | 2e-29 |
| AT4G16250 | PHYD, PHYTOCHROME D | Light Signaling | Scaffold00751 (length 152548) at 83707 | 0.0 |
| AT4G16280 | FCA | Ambient Temperature, Autonomous | Scaffold00104 (length 360147) at 120318 | 5e-13 |
| AT4G16845 | REDUCED VERNALIZATION RESPONSE 2, VRN2 | Autonomous, Polycomb, Vernalization | Scaffold00857 (length 126644) at 55203 | 3e-07 |
| AT4G18130 | PHYE, PHYTOCHROME E | Light Signaling | Scaffold00751 (length 152548) at 83749 | 0.0 |
| AT4G20370 | TSF, TWIN SISTER OF FT | Ambient Temperature | Scaffold00357 (length 260075) at 58807 | 1e-33 |
| AT4G22950 | AGAMOUS-LIKE 19, AGL19, GL19 | Vernalization | Scaffold00249 (length 258199) at 131012 | 4e-28 |
| AT4G24540 | AGAMOUS-LIKE 24, AGL24 | Vernalization | Scaffold01187 (length 101153) at 47701 | 2e-25 |
| AT4G26000 | PEP, PEPPER | Vernalization | Scaffold00021 (length 527983) at 157278 | 3e-29 |
| AT4G30200 | VEL1, VERNALIZATION5/VIN3-LIKE 1, VIL2, VIN3-LIKE 2 | Autonomous, Vernalization | Scaffold00026 (length 499904) at 369417 | 7e-64 |
| AT4G34530 | CIB1, CRYPTOCHROME-INTERACTING BASIC-HELIX-LOOP-HELIX 1 | Light Signaling | Scaffold01322 (length 99420) at 82955 | 2e-29 |
| AT4G35900 | ATBZIP14, FD, FD-1 | Ambient Temperature | Scaffold00367 (length 240396) at 113139 | 1e-16 |
| AT5G02810 | APRR7, PRR7, PSEUDO-RESPONSE REGULATOR 7 | Light Signaling | Scaffold00125 (length 356885) at 276518 | 1e-33 |
| AT5G03840 | TERMINAL FLOWER 1, TFL1 | Ambient Temperature | Scaffold00181 (length 337602) at 12825 | 1e-28 |
| AT5G08330 | CCA1 HIKING EXPEDITION, CHE, TRANSCRIPTION FACTOR TCP21, TCP21 | Light Signaling | Scaffold00993 (length 109486) at 294 | 5e-27 |
| AT5G10140 | AGAMOUS-LIKE 25, AGL25, FLC, FLF, FLOWERING LOCUS C, FLOWERING LOCUS F | Ambient Temperature, Vernalization | Scaffold10765 (length 2447) at 708 | 8e-22 |
| AT5G11530 | EMBRYONIC FLOWER 1, EMF1 | Polycomb | Scaffold00253 (length 240879) at 11069 | 1e-06 |
| AT5G13480 | FY | Autonomous | Scaffold00166 (length 328538) at 74796 | 2e-43 |
| AT5G15840 | B-BOX DOMAIN PROTEIN 1, BBX1, CO, CONSTANS, FG | Light Signaling | Scaffold01843 (length 51900) at 40767 | 3e-29 |
| AT5G15850 | ATCOL1, B-BOX DOMAIN PROTEIN 2, BBX2, COL1, CONSTANS-LIKE 1 | Light Signaling | Scaffold01843 (length 51900) at 40767 | 5e-44 |
| AT5G17690 | ATLHP1, LHP1, LIKE HETEROCHROMATIN PROTEIN 1, TERMINAL FLOWER 2, TFL2 | Polycomb | Scaffold00696 (length 140617) at 128983 | 7e-13 |
| AT5G23150 | ENHANCER OF AG-4 2, HUA2 | Vernalization | Scaffold00686 (length 145647) at 102689 | 5e-42 |
| AT5G24470 | APRR5, PRR5, PSEUDO-RESPONSE REGULATOR 5 | Light Signaling | Scaffold00001 (length 1030549) at 322798 | 3e-40 |
| AT5G24930 | ATCOL4, B-BOX DOMAIN PROTEIN 5, BBX5, COL4, CONSTANS-LIKE 4 | Light Signaling | Scaffold11225 (length 3326) at 2816 | 8e-23 |
| AT5G35840 | PHYC, PHYTOCHROME C | Light Signaling | Scaffold01070 (length 102706) at 75395 | 0.0 |
| AT5G37055 | ATSWC6, SEF, SERRATED LEAVES AND EARLY FLOWERING | Vernalization | Scaffold00925 (length 141061) at 38143 | 4e-29 |
| AT5G39660 | CDF2, CYCLING DOF FACTOR 2 | Light Signaling | Scaffold00651 (length 145047) at 19066 | 1e-90 |
| AT5G42790 | ARS5, ARSENIC TOLERANCE 5, ATPSM30, PAF1, PROTEASOME ALPHA SUBUNIT F1 | Vernalization | Scaffold00528 (length 197283) at 110933 | 5e-64 |
| AT5G51230 | ATEMF2, CYR1, CYTOKININ RESISTANT 1, EMBRYONIC FLOWER 2, EMF2, VEF2 | Polycomb | Scaffold00857 (length 126644) at 44887 | 9e-19 |
| AT5G57360 | ADAGIO 1, ADO1, FKF1-LIKE PROTEIN 2, FKL2, LKP1, LOV KELCH PROTEIN 1, ZEITLUPE, ZTL | Light Signaling | Scaffold00026 (length 499904) at 445597 | 0.0 |
| AT5G57380 | VERNALIZATION INSENSITIVE 3, VIN3 | Autonomous, Vernalization | Scaffold00026 (length 499904) at 369405 | 3e-48 |
| AT5G57660 | ATCOL5, B-BOX DOMAIN PROTEIN 6, BBX6, COL5, CONSTANS-LIKE 5 | Light Signaling | Scaffold11225 (length 3326) at 2816 | 1e-25 |
| AT5G58230 | ARABIDOPSIS MULTICOPY SUPRESSOR OF IRA1, ATMSI1, MATERNAL EFFECT EMBRYO ARREST 70, MEE70, MSI1, MULTICOPY SUPRESSOR OF IRA1 | Autonomous, Polycomb, Vernalization | Scaffold00615 (length 179658) at 161081 | 2e-61 |
| AT5G60100 | APRR3, PRR3, PSEUDO-RESPONSE REGULATOR 3 | Light Signaling | Scaffold02075 (length 43325) at 14139 | 3e-25 |
| AT5G61380 | APRR1, ATTOC1, PRR1, PSEUDO-RESPONSE REGULATOR 1, TIMING OF CAB EXPRESSION 1, TOC1 | Light Signaling | Scaffold00753 (length 123742) at 70468 | 2e-47 |
| AT5G62430 | CDF1, CYCLING DOF FACTOR 1 | Light Signaling | Scaffold01102 (length 99830) at 51435 | 1e-59 |
| AT5G65050 | AGAMOUS-LIKE 31, AGL31, MADS AFFECTING FLOWERING 2, MAF2 | Ambient Temperature, Vernalization | Scaffold10765 (length 2447) at 723 | 4e-20 |
| AT5G65060 | AGAMOUS-LIKE 70, AGL70, FCL3, MADS AFFECTING FLOWERING 3, MAF3 | Ambient Temperature, Vernalization | Scaffold10765 (length 2447) at 639 | 7e-15 |
| AT5G65070 | AGAMOUS-LIKE 69, AGL69, FCL4, MADS AFFECTING FLOWERING 4, MAF4 | Ambient Temperature, Vernalization | Scaffold10765 (length 2447) at 723 | 6e-20 |
| AT5G65080 | AGAMOUS-LIKE 68, AGL68, MADS AFFECTING FLOWERING 5, MAF5 | Ambient Temperature, Vernalization | Scaffold10765 (length 2447) at 699 | 1e-18 |

**Appendix C: SSR Marker Details**

**AT5G24470 (APRR5, PRR5, PSEUDO-RESPONSE REGULATOR 5 of the Light Signaling pathway) found in Scaffold 00001 (query sequence starts at base 322798)**

**AT2G46790 (APRR9, ARABIDOPSIS PSEUDO-RESPONSE REGULATOR 9, PRR9, PSEUDO-RESPONSE REGULATOR 9, TL1, TOC1-LIKE PROTEIN 1 of the Light Signaling pathway) found in Scaffold 00001 (query sequence starts at base 322801)**

1)

For Primer GTCTTCTTGGCTTTCTCTTCCA  
Rev Primer CTTCCACCGCCACTAATATCTC  
Repeats (tc) x11 PCR product = 157 bp start at base 324273

2)

For Primer CGCCTTTTAATTCCTAGTGGTG  
Rev Primer TGTTGCCTTATTGTGAGCCTAA  
Repeats (tc) x15 PCR product = 153 bp start at base 324766

3)

For Primer AGCCAATAACCTTTCCTGTTGA  
Rev Primer GTGCCTATCAGCCACTCTTTTT  
Repeats (tc) x9 PCR product = 238 bp start at base 314842

**AT4G02560 (LD, LUMINIDEPENDENS of the Autonomous pathway) found in Scaffold 00002 (query sequence starts at base 158601)**

1)

For Primer ACTGGATCAGTCTCCGACTCTC  
Rev Primer GAGTTACGGCTAGGGTTAGGGT  
Repeats (tc) x11 PCR product = 204 bp start at base 155393

2)

For Primer TTTCACTTTTAGCCACCACCTT  
Rev Primer CGAATCCATCAGCTAAAAGGAC  
Repeats (tc) x11 PCR product = 190 bp start at base 166784

3)

For Primer GTATGCTGCTGCAAACAATGAT  
Rev Primer CTTGGAGAAGTGACAGAAAGCA  
Repeats (tc) x44 PCR product = 236 bp start at base 341579

**AT4G26000 (PEP, PEPPER of the Vernalization pathway) found in Scaffold 00021 (query sequence starts at base 157278)**

1)

For Primer CACAAGGATGCTCAAACCATAA  
Rev Primer AAATGGTTGGATACGAGCTGTT  
Repeats (at) x8 PCR product = 280 bp start at base 148634

2)

For Primer ACGAGGAGTGAGAGAGAAGTGG  
Rev Primer CAGACACAAATTGGAGAGCAAG  
Repeats (tc) x12 PCR product = 297 bp start at base 145700

3)

For Primer CTGGGACCAGATAATTCGAAAG  
Rev Primer TGACACATGTTGATTGGTCTGA  
Repeats (ga) x10 PCR product = 219 bp start at base 116906

**AT2G18880 (VEL2, VERNALIZATION5/VIN3-LIKE 2, VIL3, VIN3-LIKE 3 of the Autonomous pathway) found in Scaffold 00026 (query sequence starts at base 369396)**

**AT5G57380 (VERNALIZATION INSENSITIVE 3, VIN3 of the Autonomous and Vernalization pathways) found in Scaffold 00026 (query sequence starts at base 369405)**

**AT4G30200 (VEL1, VERNALIZATION5/VIN3-LIKE 1, VIL2, VIN3-LIKE 2 of the Autonomous and Vernalization pathways) found in Scaffold 00026 (query sequence starts at base 369417)**

1)

For Primer CGAGTCACCTATCACCAGATCA  
Rev Primer TCCTCCAAACCTTACAAAAGGA  
Repeats (ta) x10 PCR product = 244 bp start at base 362422

2)

For Primer AAAAAGGAAGAGGAAGAATCGG  
Rev Primer AGCCGACGACGACTCTATCTAA  
Repeats (ag) x19 PCR product = 260 bp start at base 362158

3)

For Primer CTGCTACTGTCACCATCAGAGG  
Rev Primer TCTTCCTCTCGTCTCATATGCC  
Repeats (ga) x11 PCR product = 297 bp start at base 344594

**AT2G18915 (ADAGIO 2, ADO2, LKP2, LOV KELCH PROTEIN 2 of the Light Signaling pathway) found in Scaffold 00026 (query sequence starts at base 445582)**

**AT5G57360 (ADAGIO 1, ADO1, FKF1-LIKE PROTEIN 2, FKL2, LKP1, LOV KELCH PROTEIN 1, ZEITLUPE, ZTL of the Light Signaling pathway) found in Scaffold 00026 (query sequence starts at base 445597)**

1)

For Primer CAGAGTAAATGGTGTGGACCAA  
Rev Primer AAACCGGAACATATCCTCTTCA  
Repeats (ga) x10 PCR product = 200 bp start at base 441957

2)

For Primer GTAGATCAGGGAGAGGAGGGAT  
Rev Primer GGTTTATGTGGACCGGAAATAA  
Repeats (ag) x11 PCR product = 250 bp start at base 429600

3)

For Primer TCGCTAAATTGTCTGGGAAAGT  
Rev Primer CCTACTTCGGGTAGGTACCTTTA  
Repeats (tc) x11 PCR product = 235 bp start at base 417206

**AT4G00650 (FLA, FLOWERING LOCUS A, FRI, FRIGIDA of the Vernalization pathway) found in Scaffold 00039 (query sequence starts at base 216632)**

1)

For Primer GGCTCCTTATTTCCCACTCTTT  
Rev Primer CAGCATTTCTCATAAGGGAAGG  
Repeats (ag) x13 PCR product = 229 bp start at base 202952

2)

For Primer GGGATTTTGAAGAGTGAAGACG  
Rev Primer TCTTCCTCCTCCTATTCCTTCC  
Repeats (tc) x10 PCR product = 297 bp start at base 235833

3)

For Primer CCGTCCAGACAAACTTCTCTTC  
Rev Primer GGATTTTAGTATGAGTTCGGCG  
Repeats (ctt) x11 PCR product = 299 bp start at base 257937

**AT1G53160 (FLORAL TRANSITION AT THE MERISTEM6, FTM6, SPL4, SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 4 of the Age pathway) found in Scaffold 00062 (query sequence starts at base 412489)**

**AT2G33810 (SPL3, SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 3 of the Age pathway) found in Scaffold 00062 (query sequence starts at base 412489)**

1)

For Primer CCAAACTCCAAGAATGAACTCC  
Rev Primer GATCTACGCATTGGAAACATCA  
Repeats (ga) x16 PCR product = 288 bp start at base 402970

2)

For Primer TTTTCTGCTGAAGTGAAGTGGA  
Rev Primer TCTTTGTCTGGACATTGTTTGG  
Repeats (ga) x10 PCR product = 180 bp start at base 392786

3)

For Primer AGCGGAAATTATAGGAGGGAAG  
Rev Primer GGAGAGAGGAGAGAGAGACGAG  
Repeats (tc) x28 PCR product = 205 bp start at base 423921

**AT3G47500 (CDF3, CYCLING DOF FACTOR 3 of the Light Signaling pathway) found in Scaffold 00079 (query sequence starts at base 68175)**

**AT1G26790 (of the Light Signaling pathway) found in Scaffold 00079 (query sequence starts at base 69048)**

1)

For Primer GTTTGACATATCGAGCTTGCAC  
Rev Primer TTGGTTGTAGAGGAGTGGGATT  
Repeats (aat) x6 PCR product = 292 bp start at base 69852

2)

For Primer CTCGATCCAATCCATAATCCAT  
Rev Primer GATCAAAAGCGCAAGTAGGAGT  
Repeats (ag) x8 PCR product = 270 bp start at base 71505

3)

For Primer TTTGGACTAAAGCGCTACCATT  
Rev Primer TACCACCACCCTTTATTTGGAG  
Repeats (tcc) x9 PCR product = 298 bp start at base 52487

**AT1G22770 (FB, GI, GIGANTEA of the Light Signaling pathway) found in Scaffold 00100 (query sequence starts at base 198329)**

1)

For Primer TTTTTGTTGACCCCAAGACTTC  
Rev Primer AGCAACTTCCTCATCACAGACA  
Repeats (ct) x11 PCR product = 257 bp start at base 196803

2)

For Primer TTTCGCTCAGTTATCTCTCTCTGA  
Rev Primer CCATCTTTAACTGCACAAACCA  
Repeats (ta) x12 PCR product = 225 bp start at base 207941

3)

For Primer TTTCGCTCAGTTATCTCTCTCTGA  
Rev Primer CCATCTTTAACTGCACAAACCA  
Repeats (ga) x11 PCR product = 225 bp start at base 207965

**AT3G05120 (ATGID1A, GA INSENSITIVE DWARF1A, GID1A of the Gibberellin pathway) found in Scaffold 00101 (query sequence starts at base 398762)**

1)

For Primer CATCAATCAACGTAACCACCAT  
Rev Primer ATCTGCTGTGAAGTGGAAAGGT  
Repeats (gaa) x15 PCR product = 293 bp start at base 400426

2)

For Primer CTGCTGTGCATATTACCGTTGT  
Rev Primer TAATGGTGGAGAATGTGTAGCG  
Repeats (ct) x11 PCR product = 219 bp start at base 389934

3)

For Primer ATGGGTAGTTGCTCCTAATTGC  
Rev Primer AACCTCACAACCGAAGAAACAT  
Repeats (ct) x10 PCR product = 279 bp start at base 420279

**AT2G33835 (FES1, FRIGIDA-ESSENTIAL 1 of the Vernalization pathway) found in Scaffold 00102 (query sequence starts at base 88264)**

1)

For Primer CACCCCTCCATCCATTAGTAAA  
Rev Primer ATGGAAAGGACTGGTGGTAAGA  
Repeats (tc) x10 PCR product = 163 bp start at base 113504

2)

For Primer TCTACAGCATCTCTCCCACTCA  
Rev Primer CCTCCAAATGATGAACACAAGA  
Repeats (tc) x13 PCR product = 250 bp start at base 52555

3)

For Primer TCTTTGATCCTTCTGGTTTGGT  
Rev Primer CAGCTCTCACCTACCTCACTCA  
Repeats (ga) x20 PCR product = 286 bp start at base 132341

**AT4G16280 (FCA of the Ambient Temperature and Autonomous pathways) found in Scaffold 00104 (query sequence starts at base 120318)**

1)

For Primer CATTCGGATTTCTTATCCATCC  
Rev Primer CTCCCTTTCACTGCTCTCTGAT  
Repeats (ga) x8 PCR product = 219 bp start at base 137168

2)

For Primer AACTCAAGCCCATTTACTCCAA  
Rev Primer TGTTTGTGACTATGAACCTGGG  
Repeats (tc) x10 PCR product = 209 bp start at base 150456

3)

For Primer ATAAAACCAACACTGACCACCC  
Rev Primer TAACCAAAACTCGTCGGAATCT  
Repeats (ct) x8 PCR product = 257 bp start at base 106905

**AT3G15270 (SPL5, SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 5 of the Age pathway) found in Scaffold 00105 (query sequence starts at base 147284)**

1)

For Primer TCCTCTTGCAAGGAATTGGTAT  
Rev Primer CCTAGGGGGAGAATAGTGCTTT  
Repeats (ga) x8 PCR product = 118 bp start at base 142051

2)

For Primer GAGCTTTCGTACCTCCGTAAAA  
Rev Primer TGACGTCGTAGAGTTGGTAGGA  
Repeats (tc) x13 PCR product = 299 bp start at base 139430

3)

For Primer TACTGTTATTCAGGGTGGCCTT  
Rev Primer AGCCTAGATCGTTTTGCTTCAA  
Repeats (ct) x12 PCR product = 268 bp start at base 123867

**AT1G68050 ("FLAVIN-BINDING, KELCH REPEAT, F BOX 1", ADO3, FKF1 of the Light Signaling pathway) found in Scaffold 00110 (query sequence starts at base 120279)**

1)

For Primer ATTCAGATGGCGGATAAAAGAG  
Rev Primer CCGCGTTTTCCAGTCTATATTC  
Repeats (ag) x8 PCR product = 242 bp start at base 126867

2)

For Primer GAGGTGAAGTGTAGATGAGGGG  
Rev Primer GAGAGAGAGCGACAAGACGAAT  
Repeats (ct) x14 PCR product = 274 bp start at base 136199

3)

For Primer TTTGCGCTCTCTCTCTCTCTCT  
Rev Primer GAAACTCGAAATCTTGAAACCG  
Repeats (ct) x15 PCR product = 260 bp start at base 136377

**AT5G02810 (APRR7, PRR7, PSEUDO-RESPONSE REGULATOR 7 of the Light Signaling pathway) found in Scaffold 00125 (query sequence starts at base 276518)**

1)

For Primer TAAGCAAGCTCGAACCCTAATC  
Rev Primer CGATGCTGTTAGTTCATTCCAA  
Repeats (tc) x11 PCR product = 263 bp start at base 278986

2)

For Primer GTCATTAGAGCAACAGCAGCAG  
Rev Primer TCGTCGTCGTTATCATCATCTC  
Repeats (ct) x8 PCR product = 291 bp start at base 290380

3)

For Primer CCTCAAAACTGGGGAAAATAGA  
Rev Primer GGGTATAAAAGGCAAGCAGATG  
Repeats (ga) x10 PCR product = 138 bp start at base 226349

**AT1G27370 (SPL10, SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 10 of the Age pathway) found in Scaffold 00127 (query sequence starts at base 165806)**

1)

For Primer CCAGAAATAACCTCGAAACAGC  
Rev Primer CCATGATTGATCAAAACAGCTC  
Repeats (ga) x12 PCR product = 281 bp start at base 169541

2)

For Primer AGTTAAGGGAGGCCTAGGGAC  
Rev Primer GGTCGCCCTTAGATAAGGATTC  
Repeats (at) x11 PCR product = 298 bp start at base 176760

3)

For Primer CAATTTTGTTCCCACCTCTCTC  
Rev Primer AATGAATGTAGCAAATCCCCAC  
Repeats (ac) x8 PCR product = 211 bp start at base 152171

**AT1G66350 (RGA-LIKE 1, RGL, RGL1 of the Gibberellin pathway) found in Scaffold 00134 (query sequence starts at base 174707)**

**AT3G03450 (RGA-LIKE 2, RGL2 of the Gibberellin pathway) found in Scaffold 00134 (query sequence starts at base 174722)**

1)

For Primer TGACAAGACGTGCGATATAAGG  
Rev Primer TCCTCGTCGAACATCTTTTTG  
Repeats (ttc) x5 PCR product = 250 bp start at base 174643

2)

For Primer TTCACACCAAATGGACTCTGAC  
Rev Primer GAGAATAATTTTGTCCCACCCA  
Repeats (tc) x9 PCR product = 237 bp start at base 135335

3)

For Primer AGATCACAATGGGCTTCAAACT  
Rev Primer AGGAGGACGTTGGAGACTGTAA  
Repeats (ca) x13 PCR product = 204 bp start at base 116959

**AT1G01060 (LATE ELONGATED HYPOCOTYL, LATE ELONGATED HYPOCOTYL 1, LHY, LHY1 of the Light Signaling pathway) found in Scaffold 00140 (query sequence starts at base 234299)**

**AT2G46830 (ATCCA1, CCA1, CIRCADIAN CLOCK ASSOCIATED 1 of the Light Signaling pathway) found in Scaffold 00140 (query sequence starts at base 234299)**

1)

For Primer GAAATTACCCTCTCTGACGTGG  
Rev Primer AGAAGATCCAGCTTTGAGTTGC  
Repeats (tc) x10 PCR product = 153 bp start at base 232252

2)

For Primer TTTGTTCCACTTCCCAAGTTCT  
Rev Primer GGGGACCATCTTCTTTGCTATT  
Repeats (ct) x8 PCR product = 230 bp start at base 262342

3)

For Primer CTAGGCAAAGCCGCTAATTACA  
Rev Primer CCCATGAGATTTCCTTTTGA  
Repeats (gaa) x10 PCR product = 203 bp start at base 264721

**AT3G12810 (CHR13, PHOTOPERIOD-INDEPENDENT EARLY FLOWERING 1, PIE1, SRCAP of the Vernalization pathway) found in Scaffold 00147 (query sequence starts at base 30164)**

1)

For Primer GGTTGGATGCTCTGTCACAATA  
Rev Primer CCTGCTGTTGTCATTCTCTTTG  
Repeats (gt) x14 PCR product = 195 bp start at base 36897

2)

For Primer GTGTGTGTGTGTGTGTGTGTGA  
Rev Primer AATCCTTCGAAAGTATGGCTCA  
Repeats (ag) x11 PCR product = 179 bp start at base 26112

3)

For Primer AGCCAACTACCGTACAAAGACC  
Rev Primer AATCCTTCGAAAGTATGGCTCA  
Repeats (tg) x15 PCR product = 239 bp start at base 26082

**AT5G13480 (FY of the Autonomous pathway) found in Scaffold 00166 (query sequence starts at base 74796)**

1)

For Primer CAGCTACAGCAACACCTTCAAT  
Rev Primer AAGGGGGTAAAAGCTGTACCAT  
Repeats (caa) x7 PCR product = 245 bp start at base 69326

2)

For Primer AAACCAATCTTCTCCTTCTCCC  
Rev Primer GGTGGTTGTTGTTGTTGTTGTT  
Repeats (gca) x6 PCR product = 282 bp start at base 69223

3)

For Primer GACATGGGAATCTTTGCCTTAG  
Rev Primer CACTTCATCAAATAACCAGCCA  
Repeats (ag) x19 PCR product = 266 bp start at base 119541

**AT5G03840 (TERMINAL FLOWER 1, TFL1 of the Ambient Temperature pathway) found in Scaffold 00181 (query sequence starts at base 12825)**

1)

For Primer TCTAGTAGCTGGGGTGCTTCTC  
Rev Primer AGCAGAAGGAAATAGCTCATGC  
Repeats (tc) x11 PCR product = 260 bp start at base 12778

2)

For Primer AGAATCATGCCAACAGAGGTTT  
Rev Primer TAGACGGATGGCCTATCAAGTT  
Repeats (ct) x9 PCR product = 111 bp start at base 13947

3)

For Primer TACCAGTTCACGATCTCTCCCT  
Rev Primer ACATCAACCCAACAACCTATCC  
Repeats (tc) x8 PCR product = 238 bp start at base 27256

**AT3G10390 (FLD, FLOWERING LOCUS D of the Ambient Temperature and Autonomous pathways) found in Scaffold 00232 (query sequence starts at base 139565)**

1)

For Primer CATAAACGGTTTTAGCAAGGCT  
Rev Primer TCTCTGGGTGACCTTACCATCT  
Repeats (ct) x8 PCR product = 207 bp start at base 132421

2)

For Primer CAGTCCATGGGTATGCTTGATA  
Rev Primer TTGCAATGATAAGTACCGCAAG  
Repeats (at) x11 PCR product = 273 bp start at base 113550

3)

For Primer CTTCTTGCTTTGCAGGCTTTAT  
Rev Primer TTAGAATGGGGTGTGTGTGTGT  
Repeats (tc) x12 PCR product = 299 bp start at base 153951

**AT3G33520 (ACTIN-RELATED PROTEIN 6, ARP6, ATARP6, EARLY IN SHORT DAYS 1, ESD1, SUF3, SUPPRESSOR OF FRI 3 of the Ambient Temperature and Vernalization pathways) found in Scaffold 00246 (query sequence starts at base 268521)**

1)

For Primer CGAGGTCTGGGTTTATGAGGTA  
Rev Primer GGGAAACAGAAGTCCAGAGAGA  
Repeats (tc) x10 PCR product = 265 bp start at base 268979

2)

For Primer TTCAACTGAGATGCGTTTAGGA  
Rev Primer AAGCAGGTAAATGAGCCCAATA  
Repeats (tg) x11 PCR product = 258 bp start at base 255772

3)

For Primer CACCTTAACAAATGTGGAGCAA  
Rev Primer CCCTCATTGATGTGTGTGTTCT  
Repeats (tc) x14 PCR product = 272 bp start at base 239356

**AT4G11880 (AGAMOUS-LIKE 14, AGL14 of the Vernalization pathway) found in Scaffold 00249 (query sequence starts at base 131012)**

**AT4G22950 (AGAMOUS-LIKE 19, AGL19, GL19 of the Vernalization pathway) found in Scaffold 00249 (query sequence starts at base 131012)**

1)

For Primer ACACTGTTCAGTTTCAAGGGGT  
Rev Primer ACGAAACACATCAAGCTAGCAA  
Repeats (at) x9 PCR product = 285 bp start at base 132095

2)

For Primer TCAAGAACCTGTGAATCTGGAA  
Rev Primer TAGGTTTTTCGGGTAACCTTGA  
Repeats (ag) x14 PCR product = 255 bp start at base 102031

3)

For Primer ATTGAACAACAGTTGGAGCAGA  
Rev Primer TCAGTGTCGTGTCTATGTCGTG  
Repeats (ga) x15 PCR product = 258 bp start at base 144337

**AT5G11530 (EMBRYONIC FLOWER 1, EMF1 of the Polycomb pathway) found in Scaffold 00253 (query sequence starts at base 11069)**

1)

For Primer CTCTAACACATTCTGGTTGCCA  
Rev Primer TGTATGAAGGTATCCATGCTGC  
Repeats (aga) x6 PCR product = 281 bp start at base 15630

2)

For Primer AAGCTTCACTTGGATTCTCCAC  
Rev Primer GCCTTTTATTACAACAAAGCCG  
Repeats (ag) x9 PCR product = 271 bp start at base 18170

3)

For Primer TTTTGATGATGTCAGCAGGTCT  
Rev Primer CCACTAGGCCTGATTTTCTCTG  
Repeats (ga) x10 PCR product = 243 bp start at base 34859

**AT2G40080 (EARLY FLOWERING 4, ELF4 of the Light Signaling pathway) found in Scaffold 00254 (query sequence starts at base 228805)**

1)

For Primer TGACCATCCCTTCTGAATTTCT  
Rev Primer TTTCGACAATGCCAACAGATAC  
Repeats (ct) x40 PCR product = 288 bp start at base 231757

2)

For Primer TACACCTCTTCTCTCTCCTGCC  
Rev Primer GACTGTTACAACTCCGCTTCCT  
Repeats (ca) x12 PCR product = 216 bp start at base 233794

3)

For Primer CCGTGTATCTATCTCCACTCCC  
Rev Primer AGTTTCGAACAGTGCTTTCACA  
Repeats (aga) x11 PCR product = 283 bp start at base 238558

**AT2G34140 (of the Light Signaling pathway) found in Scaffold 00270 (query sequence starts at base 215217)**

**AT1G29160 (of the Light Signaling pathway) found in Scaffold 00270 (query sequence starts at base 215229)**

1)

For Primer TGGGACCTGATCTTTTTCTTGT  
Rev Primer TGCCCGTTATTGTGTTTGTAAG  
Repeats (ga) x18 PCR product = 226 bp start at base 215694

2)

For Primer CGGATCTTCTCTGTCTGCTTCT  
Rev Primer CCCCCTCACCTACTCTTCTTCT  
Repeats (ct) x8 PCR product = 252 bp start at base 235137

3)

For Primer ATTTAACCCCCTCCAACATTCT  
Rev Primer GAATTGGCTGGAAATGCATAGT  
Repeats (ac) x11 PCR product = 237 bp start at base 146669

**AT1G31814 (FRIGIDA LIKE 2, FRL2 of the Vernalization pathway) found in Scaffold 00289 (query sequence starts at base 150896)**

1)

For Primer TTAGCAATAATCCACACGATGC  
Rev Primer TATGAAATCCCAAACAGGGAAC  
Repeats (at) x10 PCR product = 278 bp start at base 140291

2)

For Primer TACTATTGGGATAGTGGTGGGG  
Rev Primer CTTCCTTCATTCTTAGCTTGTTCTG  
Repeats (ct) x16 PCR product = 256 bp start at base 138109

3)

For Primer TATGCATTTGCTAACGGATGTC  
Rev Primer GCCTTCTGCGAATAGAAAAGAA  
Repeats (gt) x10 PCR product = 131 bp start at base 162744

**AT4G08920 (ATCRY1, BLU1, BLUE LIGHT UNINHIBITED 1, CRY1, CRYPTOCHROME 1, ELONGATED HYPOCOTYL 4, HY4, OOP2, OUT OF PHASE 2 of the Light Signaling pathway) found in Scaffold 00331 (query sequence starts at base 124817)**

1)

For Primer GACATTCAATACGCACCTACCA  
Rev Primer AAGGTGCATCGCTTACTACCTC  
Repeats (tc) x9 PCR product = 197 bp start at base 114263

2)

For Primer TTCTCGAACATTATTCCTCTGC  
Rev Primer TAGAGAAACCGAGAGAGGATGG  
Repeats (ga) x13 PCR product = 282 bp start at base 159723

3)

For Primer CAGTCGCAAACAAACCTACTCC  
Rev Primer TGCCCTAACTTCATTCTCCCTA  
Repeats (tcc) x6 PCR product = 276 bp start at base 61835

**AT2G06255 (ELF4-L3, ELF4-LIKE 3 of the Light Signaling pathway) found in Scaffold 00336 (query sequence starts at base 188137)**

1)

For Primer AAGTTGGGGTATTCTGTTGTGG  
Rev Primer ACTACAATCGTGTAGTGCGGTG  
Repeats (ag) x13 PCR product = 185 bp start at base 167935

2)

For Primer GAAAAACCAAACAAACCTCCAC  
Rev Primer CCACAACAGAATACCCCAACTT  
Repeats (ga) x10 PCR product = 277 bp start at base 167792

3)

For Primer AGGTGCAGGGTTCTTACTTGAG  
Rev Primer ACAAGCCGAGGTACAAAGAAAA  
Repeats (ct) x10 PCR product = 106 bp start at base 201634

**AT1G30970 (SUF4, SUPPRESSOR OF FRIGIDA4 of the Vernalization pathway) found in Scaffold 00348 (query sequence starts at base 75279)**

1)

For Primer TTTACGGATATCATCACCCCTC  
Rev Primer TGTTTTGCAAGTTCTCCTCTCA  
Repeats (tg) x9 PCR product = 215 bp start at base 66541

2)

For Primer GATGCAGACATGCTAGGGATAC  
Rev Primer CAATATGTTGTGGACACCCAAG  
Repeats (ca) x10 PCR product = 297 bp start at base 65411

3)

For Primer GGGTTTATGGTGTTTGTGAAGG  
Rev Primer TTTAGAGTGTCTCGGAACACCA  
Repeats (ta) x10 PCR product = 292 bp start at base 122301

**AT2G23380 (CLF, CURLY LEAF, ICU1, INCURVATA 1, SDG1, SET1, SETDOMAIN 1, SETDOMAIN GROUP 1 of the Autonomous, Polycomb, and Vernalization pathways) found in Scaffold 00354 (query sequence starts at base 64799)**

**AT4G02020 (EZA1, SDG10, SET DOMAIN-CONTAINING PROTEIN 10, SWINGER, SWN of the Autonomous, Polycomb, and Vernalization pathways) found in Scaffold 00354 (query sequence starts at base 64799)**

**AT1G02580 (EMB173, EMBRYO DEFECTIVE 173, FERTILIZATION INDEPENDENT SEED 1, FIS1, MEA, MEDEA, SDG5, SET DOMAIN-CONTAINING PROTEIN 5 of the Polycomb pathway) found in Scaffold 00354 (query sequence starts at base 64805)**

1)

For Primer TCAGGAACATTGACTATGCAGG  
Rev Primer GTTAAAGAAACGATCCGACTGC  
Repeats (tc) x8 PCR product = 285 bp start at base 53913

2)

For Primer ATTTCAACTGATTTAGCTGGGC  
Rev Primer CTTGAGTTCAATCCCTCATCTACA  
Repeats (ct) x31 PCR product = 222 bp start at base 49463

3)

For Primer GTTGCCAGCTGAATATCCTTTC  
Rev Primer GTGTGTGTGTGTGTGTGTGTGA  
Repeats (tc) x14 PCR product = 163 bp start at base 81106

**AT1G65480 (FLOWERING LOCUS T, FT of the Ambient Temperature pathway) found in Scaffold 00357 (query sequence starts at base 58774)**

**AT4G20370 (TSF, TWIN SISTER OF FT of the Ambient Temperature pathway) found in Scaffold 00357 (query sequence starts at base 58807)**

1)

For Primer GCCCACCCTTAGTTATGTTGAC  
Rev Primer GAGAGACAGAAGACAGAGAAGAGG  
Repeats (ct) x11 PCR product = 225 bp start at base 76826

2)

For Primer CGCCACGGAAATATATAGGAGA  
Rev Primer TGCACGTTTCAAAGTATTGACC  
Repeats (at) x10 PCR product = 221 bp start at base 29021

3)

For Primer GCAATTGCGTAGATGACTTCAG  
Rev Primer CTCCAAAGATGTATGCCCTACC  
Repeats (tc) x13 PCR product = 197 bp start at base 83551

**AT2G17770 (ATBZIP27, BASIC REGION/LEUCINE ZIPPER MOTIF 27, BZIP27, FD PARALOG, FDP of the Ambient Temperature pathway) found in Scaffold 00367 (query sequence starts at base 113139)**

**AT4G35900 (ATBZIP14, FD, FD-1 of the Ambient Temperature pathway) found in Scaffold 00367 (query sequence starts at base 113139)**

1)

For Primer GTTTTTGTTGGAGAGGAAGTCG  
Rev Primer AGTACCAAATCCCCAAACACAC  
Repeats (ag) x9 PCR product = 188 bp start at base 113601

2)

For Primer GCTTTCTCAGAATGGAGCTGTT  
Rev Primer TCAGACAGAGCAGTTGGGTAGA  
Repeats (ca) x10 PCR product = 278 bp start at base 110027

3)

For Primer GATGAAGAGAAGTCTCGGGCTA  
Rev Primer GCACCATGCAAGGATTATAACA  
Repeats (ct) x10 PCR product = 243 bp start at base 100134

**AT2G25930 (EARLY FLOWERING 3, ELF3, PYK20 of the Light Signaling pathway) found in Scaffold 00371 (query sequence starts at base 73111)**

1)

For Primer GTGTGCGTGAGAGAGAGAGAGA  
Rev Primer ATCTGAAAAGAAAGGCTTGTGG  
Repeats (ag) x18 PCR product = 245 bp start at base 71081

2)

For Primer ATCCAGTTGAAGGCATCTGATT  
Rev Primer GGCAATGCCTTTTCTGTAGTTT  
Repeats (ga) x17 PCR product = 283 bp start at base 71026

3)

For Primer ATCCAGTTGAAGGCATCTGATT  
Rev Primer GGCAATGCCTTTTCTGTAGTTT  
Repeats (tg) x9 PCR product = 283 bp start at base 71005

**AT3G24440 (VERNALIZATION 5, VIL1, VIN3-LIKE 1, VRN5 of the Autonomous and Vernalization pathways) found in Scaffold 00396 (query sequence starts at base 73795)**

**AT2G18870 (VEL3, VERNALIZATION5/VIN3-LIKE 3, VIL4, VIN3-LIKE 4 of the Autonomous pathway) found in Scaffold 00396 (query sequence starts at base 73810)**

1)

For Primer CATCGGTCCATAGAGAACACAA  
Rev Primer GCAGAGTCGTGTCCTTTCTTTT  
Repeats (ag) x9 PCR product = 232 bp start at base 82383

2)

For Primer GGGGATGGTTACCTGTGAATAA  
Rev Primer TGACTCATCAGTCCCTCTCTCA  
Repeats (ct) x8 PCR product = 233 bp start at base 85845

3)

For Primer ATTTTTAGAACTGTGCCAAGCC  
Rev Primer CCTACTTGAACCGAACTGGTTT  
Repeats (tc) x9 PCR product = 298 bp start at base 50548

**AT3G21320 (of the Light Signaling pathway) found in Scaffold 00509 (query sequence starts at base 181887)**

1)

For Primer TCACGTAGGCAGTCAAAACAAC  
Rev Primer GGCAACATATGTCGGGTAATTT  
Repeats (ct) x26 PCR product = 259 bp start at base 189409

2)

For Primer AGCTCCTCCCATTACAATCTCA  
Rev Primer ATGAACTGCTTATGCAATGTGG  
Repeats (tg) x12 PCR product = 272 bp start at base 169832

3)

For Primer GAAATCAATGGAACTACCTCGG  
Rev Primer AAATACTACATGGCGCTGTTGA  
Repeats (at) x10 PCR product = 259 bp start at base 149049

**AT1G47250 (20S PROTEASOME ALPHA SUBUNIT F2, PAF2 of the Vernalization pathway) found in Scaffold 00528 (query sequence starts at base 110933)**

**AT5G42790 (ARS5, ARSENIC TOLERANCE 5, ATPSM30, PAF1, PROTEASOME ALPHA SUBUNIT F1 of the Vernalization pathway) found in Scaffold 00528 (query sequence starts at base 110933)**

1)

For Primer CACGAAAGTAGACGCTGTGAAA  
Rev Primer ATTTGAGCTGTCCAAAACACG  
Repeats (ata) x9 PCR product = 248 bp start at base 108589

2)

For Primer ACTTCCCTTAGTGCTGCTTGTC  
Rev Primer GGACTAGGTTTTCTTCCCCACT  
Repeats (tta) x7 PCR product = 165 bp start at base 112665

3)

For Primer GAGAGAGACTGTGCATACACGC  
Rev Primer AAAGGAAAAGAAGAACAAGGGG  
Repeats (ga) x10 PCR product = 223 bp start at base 124597

**AT5G58230 (ARABIDOPSIS MULTICOPY SUPRESSOR OF IRA1, ATMSI1, MATERNAL EFFECT EMBRYO ARREST 70, MEE70, MSI1, MULTICOPY SUPRESSOR OF IRA1 of the Autonomous, Polycomb, and Vernalization pathways) found in Scaffold 00615 (query sequence starts at base 161081)**

1)

For Primer GTGGGATCTTAGCAGGTTTGTC  
Rev Primer TACAGTGGGAGGTGGAGTTTTT  
Repeats (ct) x10 PCR product = 128 bp start at base 163332

2)

For Primer AGAACCATAGCATAACGGCCTA  
Rev Primer TATGGAGGGAAGAAATTTGGTG  
Repeats (tc) x12 PCR product = 145 bp start at base 158582

3)

For Primer TAGCACAGGCTCCCATTTTTAT  
Rev Primer GCTAGTCTGCAGAGCCAAAGAT  
Repeats (ag) x8 PCR product = 219 bp start at base 120273

**AT1G04400 (AT-PHH1, ATCRY2, CRY2, CRYPTOCHROME 2, FHA, PHH1 of the Light Signaling pathway) found in Scaffold 00649 (query sequence starts at base 28296)**

1)

For Primer TGGTGGTGGTATATGGGTAACA  
Rev Primer AATCAACAATCTCACTGCCGTT  
Repeats (gtg) x8 PCR product = 192 bp start at base 22759

2)

For Primer GTAGTGTGATGGTTATGGCGTG  
Rev Primer TATACCACCACCACTATTGCCA  
Repeats (tgg) x7 PCR product = 131 bp start at base 22555

3)

For Primer TTGTTTCGCCATTAGGAGAGAT  
Rev Primer CCTAAACCCAACTACCACTCCA  
Repeats (ga) x10 PCR product = 139 bp start at base 49549

**AT5G39660 (CDF2, CYCLING DOF FACTOR 2 of the Light Signaling pathway) found in Scaffold 00651 (query sequence starts at base 19066)**

1)

For Primer AAGTTGGTTTTGTGGCCTTAGA  
Rev Primer TTTTTGGGCTAACGAAGAGTGT  
Repeats (ct) x7 PCR product = 295 bp start at base 22514

2)

For Primer TCAAAAGCACACAGAATCAAGC  
Rev Primer TGCAAGAGCCAATCTCTCATAA  
Repeats (ga) x7 PCR product = 275 bp start at base 27722

3)

For Primer CCAGTTAGATTGGTGACATTGC  
Rev Primer GGACCCATCACTAGATCCTCTG  
Repeats (ct) x12 PCR product = 192 bp start at base 37067

**AT5G23150 (ENHANCER OF AG-4 2, HUA2 of the Vernalization pathway) found in Scaffold 00686 (query sequence starts at base 102689)**

1)

For Primer GATGAAGAGAAGGCATCAGGTC  
Rev Primer AATACCGATGTTTACCGGAGTG  
Repeats (ct) x14 PCR product = 221 bp start at base 106315

2)

For Primer GGATAATCAAAGATGCGAGAGG  
Rev Primer ATACACCTTTGGATTCTGTGGG  
Repeats (tg) x11 PCR product = 290 bp start at base 90834

3)

For Primer ACACAACCTGCAATACTCCTCC  
Rev Primer TACAAGGTGTGGTGAGTAACGG  
Repeats (ta) x12 PCR product = 284 bp start at base 117010

**AT2G42200 (ATSPL9, SPL9, SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 9 of the Age pathway) found in Scaffold 00691 (query sequence starts at base 61795)**

1)

For Primer TGTGGACCAACCAACATTAGAG  
Rev Primer GAGACTTTTTGTGGTAGGCACC  
Repeats (ta) x9 PCR product = 298 bp start at base 80542

2)

For Primer CACCTTGAGATCTCTCTCTCTCTC  
Rev Primer CCCAATCCACATTGAACAGAAT  
Repeats (tc) x16 PCR product = 300 bp start at base 36515

3)

For Primer GCACCATTCTTAATAACATTGCACC  
Rev Primer CACGAGAGAGAGAGAGAGAGAGAGA  
Repeats (tc) x11 PCR product = 298 bp start at base 36283

**AT5G17690 (ATLHP1, LHP1, LIKE HETEROCHROMATIN PROTEIN 1, TERMINAL FLOWER 2, TFL2 of the Polycomb pathway) found in Scaffold 00696 (query sequence starts at base 128983)**

1)

For Primer CCACCTAATCCATTCAAAAAGG  
Rev Primer TACCAAATCCCTCAATCCAAAG  
Repeats (ag) x9 PCR product = 293 bp start at base 127286

2)

For Primer GAGAGATGGGGCAACAAAAATA  
Rev Primer GCAGGCCTTAATATGCAAGAAC  
Repeats (ga) x8 PCR product = 143 bp start at base 81894

3)

For Primer GCTACAAACCAAAAAGAATCGG  
Rev Primer AAAAATCCTCCTTGACTGGGTT  
Repeats (ac) x8 PCR product = 298 bp start at base 45233

**AT2G19520 (ACG1, ATMSI4, FVE, MSI4, MULTICOPY SUPPRESSOR OF IRA1 4, NFC04, NFC4 of the Ambient Temperature and Autonomous pathways) found in Scaffold 00728 (query sequence starts at base 8716)**

1)

For Primer GCAGAAGGAAAACCAAAATCAC  
Rev Primer GAGAGGGAGAGAGAGAAGGGAC  
Repeats (ga) x11 PCR product = 263 bp start at base 2899

2)

For Primer TAACCGGTTTTACCGTTTTCC  
Rev Primer AGAACCAAGAATTCTGCATTGG  
Repeats (tc) x10 PCR product = 298 bp start at base 111

3)

For Primer CTTTATCATCTGCCTGCCTCTT  
Rev Primer CGTAATAAAGAAGGTGGTTCGG  
Repeats (tc) x16 PCR product = 162 bp start at base 36059

**AT2G32950 (ARABIDOPSIS THALIANA CONSTITUTIVE PHOTOMORPHOGENIC 1, ATCOP1, CONSTITUTIVE PHOTOMORPHOGENIC 1, COP1, DEETIOLATED MUTANT 340, DET340, EMB168, EMBRYO DEFECTIVE 168, FUS1, FUSCA 1 of the Light Signaling pathway) found in Scaffold 00734 (query sequence starts at base 142779)**

**AT2G46340 (SPA1, SUPPRESSOR OF PHYA-105 1 of the Light Signaling pathway) found in Scaffold 00734 (query sequence starts at base 142779)**

**AT1G53090 (SPA1-RELATED 4, SPA4 of the Light Signaling pathway) found in Scaffold 00734 (query sequence starts at base 143450)**

**AT3G15354 (SPA1-RELATED 3, SPA3 of the Light Signaling pathway) found in Scaffold 00734 (query sequence starts at base 143450)**

1)

For Primer GGAGGGGAAACAAGGATAGAAC  
Rev Primer ATATTGAGGCTGTGGTCGTCTT  
Repeats (aag) x8 PCR product = 186 bp start at base 148205

2)

For Primer TTACCCCCTCTCTCTCTCATACC  
Rev Primer AAACATCTTCAATCATGCTCCC  
Repeats (tc) x15 PCR product = 298 bp start at base 136748

3)

For Primer CCACAAAACAGCAGTAACCAAA  
Rev Primer TACGGTATGAGAGAGAGAGGGG  
Repeats (ga) x10 PCR product = 122 bp start at base 136457

**AT2G18790 (HY3, OOP1, OUT OF PHASE 1, PHYB, PHYTOCHROME B of the Light Signaling pathway) found in Scaffold 00751 (query sequence starts at base 83698)**

**AT4G16250 (PHYD, PHYTOCHROME D of the Light Signaling pathway) found in Scaffold 00751 (query sequence starts at base 83707)**

**AT4G18130 (PHYE, PHYTOCHROME E of the Light Signaling pathway) found in Scaffold 00751 (query sequence starts at base 83749)**

1)

For Primer CCCGAAAATACCCTTTCTCTCT  
Rev Primer GGCAATTACCAATTACGTGTCA  
Repeats (aga) x8 PCR product = 265 bp start at base 81899

2)

For Primer AAGAGGGGTAGACCAAAATTGA  
Rev Primer AATTTCACTCCAACCAAGAAGG  
Repeats (ag) x10 PCR product = 262 bp start at base 92356

3)

For Primer TCTCTCATGCATGGATGGTTAT  
Rev Primer CATTGAACATCTACCTGTGGGA  
Repeats (ct) x10 PCR product = 298 bp start at base 73385

**AT5G61380 (APRR1, ATTOC1, PRR1, PSEUDO-RESPONSE REGULATOR 1, TIMING OF CAB EXPRESSION 1, TOC1 of the Light Signaling pathway) found in Scaffold 00753 (query sequence starts at base 70468)**

1)

For Primer CACTACATCCAAACAAAACCCA  
Rev Primer TGCGTGCGATAATGGAGTATTA  
Repeats (gt) x11 PCR product = 284 bp start at base 98714

2)

For Primer CCTCGTGCACATACGAAAATTA  
Rev Primer TACGTTGCACATTTTTCTCCAC  
Repeats (ta) x8 PCR product = 266 bp start at base 52292

3)

For Primer ATTTCTACCCTGTCCACCAAGA  
Rev Primer GAGACAGAAGTGGCATCTGTGA  
Repeats (ga) x17 PCR product = 168 bp start at base 102220

**AT3G18990 (REDUCED VERNALIZATION RESPONSE 1, REM39, REPRODUCTIVE MERISTEM 39, VRN1 of the Vernalization pathway) found in Scaffold 00811 (query sequence starts at base 96661)**

1)

For Primer ACAGACCCTCCTGCCTTCAC  
Rev Primer TCTGAACTGCTCATACCCTGAA  
Repeats (ag) x21 PCR product = 251 bp start at base 89371

2)

For Primer TAAGGAGTGGGCACGGTATATT  
Rev Primer AATGTTTTGAGGTCTCTGGGAA  
Repeats (tc) x8 PCR product = 260 bp start at base 100084

3)

For Primer GACTTAACAGCAGCCTGGTACA  
Rev Primer AGTACCAATAAGTACCGCGTCG  
Repeats (ag) x8 PCR product = 112 bp start at base 100915

**AT3G07650 (B-BOX DOMAIN PROTEIN 7, BBX7, COL9, CONSTANS-LIKE 9 of the Light Signaling pathway) found in Scaffold 00832 (query sequence starts at base 89599)**

1)

For Primer TTATATGGTCGCTGATCCCTTT  
Rev Primer TGAAGGGGAGAAATAGCACCTA  
Repeats (tc) x7 PCR product = 233 bp start at base 58681

2)

For Primer GACCCTGTTCAAATTTTGCTTC  
Rev Primer TCAAAGGAGCGGAGAAGAATAG  
Repeats (ga) x9 PCR product = 212 bp start at base 21272

3)

For Primer GACCCTGTTCAAATTTTGCTTC  
Rev Primer TCAAAGGAGCGGAGAAGAATAG  
Repeats (ca) x8 PCR product = 212 bp start at base 21256

**AT5G51230 (ATEMF2, CYR1, CYTOKININ RESISTANT 1, EMBRYONIC FLOWER 2, EMF2, VEF2 of the Polycomb pathway) found in Scaffold 00857 (query sequence starts at base 44887)**

**AT4G16845 (REDUCED VERNALIZATION RESPONSE 2, VRN2 of the Autonomous, Polycomb, and Vernalization pathways) found in Scaffold 00857 (query sequence starts at base 55203)**

**AT2G35670 (FERTILIZATION INDEPENDENT SEED 2, FERTILIZATION-INDEPENDENT ENDOSPERM 2, FIE2, FIS2 of the Polycomb pathway) found in Scaffold 00857 (query sequence starts at base 55565)**

1)

For Primer CATGTGTGTGTGATCAAAGGTG  
Rev Primer ACGTATGACAGACGCAAAACAC  
Repeats (tc) x9 PCR product = 274 bp start at base 67373

2)

For Primer CCAAAGCCTTAAAAACGACACT  
Rev Primer ATGATTGGAAAGAAGGGAGTGA  
Repeats (ct) x11 PCR product = 204 bp start at base 113486

3)

For Primer CCCCCTCTATATATCCACCACA  
Rev Primer GAGGGTACTGGTGATGAAGGAG  
Repeats (cac) x8 PCR product = 214 bp start at base 125050

**AT1G77300 (ASH1 HOMOLOG 2, ASHH2, CAROTENOID CHLOROPLAST REGULATORY1, CCR1, EARLY FLOWERING IN SHORT DAYS, EFS, LAZ2, LAZARUS 2, SDG8, SET DOMAIN GROUP 8 of the Vernalization pathway) found in Scaffold 00894 (query sequence starts at base 89213)**

1)

For Primer GTAAAAGCGTTCGTATTTGCCT  
Rev Primer TTAAGGGTGGCTCTGATACCAT  
Repeats (ct) x10 PCR product = 295 bp start at base 77010

2)

For Primer AAACTGCTTACTTTCCGTTTGC  
Rev Primer TCATGTGCTGACCTACAAATCC  
Repeats (tag) x10 PCR product = 254 bp start at base 71796

3)

For Primer AAAGAAGCACCGAACTGGATAG  
Rev Primer CGGTTCCGGGTACATATAAAAA  
Repeats (ga) x10 PCR product = 293 bp start at base 92614

**AT5G37055 (ATSWC6, SEF, SERRATED LEAVES AND EARLY FLOWERING of the Vernalization pathway) found in Scaffold 00925 (query sequence starts at base 38143)**

1)

For Primer GCCTGATAGAAGGGACGTACAC  
Rev Primer TGCTGGATGTATCCTTCATTTG  
Repeats (ctt) x8 PCR product = 286 bp start at base 45585

2)

For Primer GAATGGCGACATTGTTAGATCA  
Rev Primer TAGAAATCCCACGATACGAAGG  
Repeats (tg) x11 PCR product = 173 bp start at base 17776

3)

For Primer CTTTCAGGATTCATTTTCCAGC  
Rev Primer TGTTGGCTTCACTCCATGTATC  
Repeats (ag) x8 PCR product = 204 bp start at base 5444

**AT3G25730 (EDF3, ETHYLENE RESPONSE DNA BINDING FACTOR 3 of the Light Signaling pathway) found in Scaffold 00930 (query sequence starts at base 63060)**

**AT1G13260 (EDF4, ETHYLENE RESPONSE DNA BINDING FACTOR 4, RAV1, RELATED TO ABI3/VP1 1 of the Light Signaling pathway) found in Scaffold 00930 (query sequence starts at base 63069)**

**AT1G25560 (EDF1, ETHYLENE RESPONSE DNA BINDING FACTOR 1, TEM1, TEMPRANILLO 1 of the Light Signaling pathway) found in Scaffold 00930 (query sequence starts at base 63096)**

**AT1G68840 (ATRAV2, EDF2, ETHYLENE RESPONSE DNA BINDING FACTOR 2, RAP2.8, RAV2, RELATED TO ABI3/VP1 2, RELATED TO AP2 8, TEM2, TEMPRANILLO 2 of the Light Signaling pathway) found in Scaffold 00930 (query sequence starts at base 63096)**

1)

For Primer ATTATGTGGAAAGCAAACCGAC  
Rev Primer TAGTTTGTGGCAAATGAGGATG  
Repeats (ct) x11 PCR product = 189 bp start at base 62365

2)

For Primer CCATGTGAAAAGGGATAAGCAT  
Rev Primer TTGTTTGGTGCTCCTCTACTCA  
Repeats (gat) x9 PCR product = 158 bp start at base 57313

3)

For Primer NGTTGCATGCTAATCTCTTTGG  
Rev Primer ATGAAATGTGGGACTCTGTTCC  
Repeats (ta) x11 PCR product = 214 bp start at base 54197

**AT5G08330 (CCA1 HIKING EXPEDITION, CHE, TRANSCRIPTION FACTOR TCP21, TCP21 of the Light Signaling pathway) found in Scaffold 00993 (query sequence starts at base 294)**

1)

For Primer ATCCACTCGATTGAAGCAAGAT  
Rev Primer GGTTTCTTCACAGTTAGGGCTC  
Repeats (aac) x7 PCR product = 190 bp start at base 261

2)

For Primer CCTCTTGCTGGTAAGCACTCTT  
Rev Primer ATGGTCTAGAACCAAACATGGG  
Repeats (gt) x11 PCR product = 208 bp start at base 13096

3)

For Primer ACATGTTCCAAACAAACCCTTC  
Rev Primer GCGTCTCCTCTCTCTCTCTCTC  
Repeats (ag) x12 PCR product = 292 bp start at base 18424

**AT4G11110 (SPA1-RELATED 2, SPA2 of the Light Signaling pathway) found in Scaffold 01034 (query sequence starts at base 19205)**

1)

For Primer CGGCCTAAAACACTTATCGAAC  
Rev Primer AACGGGCTTCCTCTACATACAA  
Repeats (ag) x9 PCR product = 222 bp start at base 14166

2)

For Primer CACGCCTCTCTCTCTCTCTCTC  
Rev Primer CTACAAAAGTCTCCAAACCCCA  
Repeats (ct) x20 PCR product = 180 bp start at base 3833

3)

For Primer ACTTCTTGTTTTGAGGGGGAAT  
Rev Primer TAGGTAACTCATGCTCTGGGGT  
Repeats (ct) x11 PCR product = 157 bp start at base 34735

**AT2G47700 (RED AND FAR-RED INSENSITIVE 2, RFI2 of the Light Signaling pathway) found in Scaffold 01059 (query sequence starts at base 96557)**

1)

For Primer TAACAGGAGCACAATGATCCAA  
Rev Primer TCTCTCTCCCTCTCTCGCTCTA  
Repeats (ga) x8 PCR product = 247 bp start at base 73538

2)

For Primer ACACATGGCTTGATCTACTTCG  
Rev Primer GCGAGGTAAGAGAGAAGGACAA  
Repeats (tc) x28 PCR product = 300 bp start at base 62959

3)

For Primer CCTCTCCAGTATTACTCACCCG  
Rev Primer TAAGAAAGGAACGAACCTTGGA  
Repeats (tc) x8 PCR product = 294 bp start at base 54451

**AT5G35840 (PHYC, PHYTOCHROME C of the Light Signaling pathway) found in Scaffold 01070 (query sequence starts at base 75395)**

1)

For Primer TGAACGGGTCCAGTCTATTCTT  
Rev Primer TTTGGTGTCTCTTCTGGGTTTT  
Repeats (ag) x14 PCR product = 182 bp start at base 56787

2)

For Primer AATCCCATGTCGACACCTATTC  
Rev Primer TGCCTTCAAATCAGACTAAGCA  
Repeats (gca) x6 PCR product = 186 bp start at base 97674

3)

For Primer GGGAGGAAATCCACTAAAAAGG  
Rev Primer CCTGTTGGTGGTCTTGCATATT  
Repeats (tg) x17 PCR product = 298 bp start at base 16459

**AT5G62430 (CDF1, CYCLING DOF FACTOR 1 of the Light Signaling pathway) found in Scaffold 01102 (query sequence starts at base 51435)**

1)

For Primer AGGATGAGTGAAAGAGCGTACC  
Rev Primer CCAGATTTTTCAGAGAATTGGC  
Repeats (ag) x12 PCR product = 253 bp start at base 45392

2)

For Primer TTCTCCATCTTTAACGTCAGCA  
Rev Primer GATTGCACGTACTTCACCAAGA  
Repeats (ga) x32 PCR product = 260 bp start at base 78317

3)

For Primer GTGTGTAATGGGACAAGCCTTT  
Rev Primer GCTAAAATAGGCCCAGTAGGCT  
Repeats (ac) x11 PCR product = 289 bp start at base 81642

**AT3G46640 (LUX, LUX ARRHYTHMO, PCL1, PHYTOCLOCK 1 of the Light Signaling pathway) found in Scaffold 01150 (query sequence starts at base 80272)**

1)

For Primer CCTTGTCTGCACACTTAGCATC  
Rev Primer AAATTGAGTGAGATAAGCCCCA  
Repeats (gaa) x8 PCR product = 197 bp start at base 72111

2)

For Primer ACATATGGTTTCTATGTGCCCC  
Rev Primer TTGTTCGATTACAGGAGCAGAA  
Repeats (ga) x9 PCR product = 277 bp start at base 64622

3)

For Primer CTTTCAGCAACTTCTCCTTCGT  
Rev Primer TGAGATCCCAACCACAATGTTA  
Repeats (tc) x18 PCR product = 242 bp start at base 30081

**AT2G22540 (AGAMOUS-LIKE 22, AGL22, SHORT VEGETATIVE PHASE, SVP of the Ambient Temperature and Vernalization pathways) found in Scaffold 01187 (query sequence starts at base 47701)**

**AT4G24540 (AGAMOUS-LIKE 24, AGL24 of the Vernalization pathway) found in Scaffold 01187 (query sequence starts at base 47701)**

1)

For Primer CAAATGGTGATAGCAAACATGG  
Rev Primer CTCAAAGAAAATTCCCAAGACG  
Repeats (tta) x7 PCR product = 274 bp start at base 57880

2)

For Primer GCTACTGTTCTCGTCTCCTCGT  
Rev Primer TCAATAGAACCTTCCACCGACT  
Repeats (ct) x13 PCR product = 116 bp start at base 78977

3)

For Primer AATGTTTTGTGTCTCCCAATCC  
Rev Primer GGCACAACGCTAGTTGATAAAG  
Repeats (ga) x12 PCR product = 275 bp start at base 95120

**AT4G34530 (CIB1, CRYPTOCHROME-INTERACTING BASIC-HELIX-LOOP-HELIX 1 of the Light Signaling pathway) found in Scaffold 01322 (query sequence starts at base 82955)**

1)

For Primer ACCTTTTCCCGGAACTATGATT  
Rev Primer GGTTAAAACCGTAAACGACAGC  
Repeats (gt) x20 PCR product = 243 bp start at base 88042

2)

For Primer AAGATGGAGATAAGCAGGTCCC  
Rev Primer TTCTAGTCTTAGCGTGGATGGC  
Repeats (ag) x11 PCR product = 290 bp start at base 75518

3)

For Primer TCAAAGAGCTTGTTCTGCTGTG  
Rev Primer CCCTCAACCCTCTTCTTCTTTT  
Repeats (ga) x9 PCR product = 143 bp start at base 61574

**AT1G14920 (GAI, GIBBERELLIC ACID INSENSITIVE, RESTORATION ON GROWTH ON AMMONIA 2, RGA2 of the Gibberellin pathway) found in Scaffold 01360 (query sequence starts at base 51382)**

**AT2G01570 (REPRESSOR OF GA, REPRESSOR OF GA1-3 1, RGA, RGA1 of the Gibberellin pathway) found in Scaffold 01360 (query sequence starts at base 51382)**

1)

For Primer CCCTCTCCCTCATTCTAACCTT  
Rev Primer GTGCCTTAGGGTACCAAATCAA  
Repeats (tc) x11 PCR product = 252 bp start at base 68499

2)

For Primer ACCCACTTTCAGAGAAATTCCA  
Rev Primer ACGGAGTCTTTATCGGTTGAAA  
Repeats (ct) x18 PCR product = 267 bp start at base 39593

3)

For Primer TTCTAGTACCGCGCTTTTTCTC  
Rev Primer ATCAACAAAGGGTTTCAGGCTA  
Repeats (tc) x17 PCR product = 286 bp start at base 75242

**AT3G04610 (FLK, FLOWERING LOCUS KH DOMAIN of the Autonomous pathway) found in Scaffold 01384 (query sequence starts at base 28309)**

1)

For Primer GCAAAAATGGGTAGGTCTTCTG  
Rev Primer CCACGTGTTACATTTGTCTTGG  
Repeats (ag) x9 PCR product = 226 bp start at base 27550

2)

For Primer GGAATTGGGATGAAATGAGAAG  
Rev Primer CGGAACAATTATCTTCCTCGTC  
Repeats (ta) x10 PCR product = 258 bp start at base 46362

3)

For Primer CGAGTAATATTTCCGAAGCACA  
Rev Primer ATTAAAAGCGTGAGAGGCAGAG  
Repeats (aat) x10 PCR product = 266 bp start at base 49252

**AT3G20740 (FERTILIZATION-INDEPENDENT ENDOSPERM, FERTILIZATION-INDEPENDENT ENDOSPERM 1, FIE, FIE1, FIS3 of the Autonomous, Polycomb, and Vernalization pathways) found in Scaffold 01670 (query sequence starts at base 9836)**

1)

For Primer CCTCTCCCTCAATTCTCTCTCA  
Rev Primer CTTGTTCTCGTTGTCGAGTTTG  
Repeats (cgg) x5 PCR product = 287 bp start at base 4993

2)

For Primer GCGATGCAGAAGTTGTTGATAG  
Rev Primer ACACCTTACCGATTCAAGTGCT  
Repeats (ta) x6 PCR product = 223 bp start at base 31113

3)

For Primer GCAATTTCATCTTCGCTCTCTT  
Rev Primer GAGCGTTTGTATGGAGTGAATG  
Repeats (ct) x5 PCR product = 298 bp start at base 59874

**AT2G43410 (FPA of the Autonomous pathway) found in Scaffold 01689 (query sequence starts at base 47663)**

1)

For Primer AGAATTTAAGGGGGTTTGGTGT  
Rev Primer CGTGTAAACTGTAAAGTAGTTGGG  
Repeats (ac) x10 PCR product = 111 bp start at base 45530

2)

For Primer TACGGCGAAGACCAGATTTATT  
Rev Primer AAAAACTTGGGGTCTGTAGGGT  
Repeats (ct) x9 PCR product = 135 bp start at base 25148

3)

For Primer TATGGGCCAGCGTTTACTTACT  
Rev Primer CAGTTCCTGCTTGTCAAGTGTC  
Repeats (gt) x14 PCR product = 255 bp start at base 10708

**AT3G02380 (ATCOL2, B-BOX DOMAIN PROTEIN 3, BBX3, COL2, CONSTANS-LIKE 2 of the Light Signaling pathway) found in Scaffold 01843 (query sequence starts at base 40767)**

**AT5G15840 (B-BOX DOMAIN PROTEIN 1, BBX1, CO, CONSTANS, FG of the Light Signaling pathway) found in Scaffold 01843 (query sequence starts at base 40767)**

**AT5G15850 (ATCOL1, B-BOX DOMAIN PROTEIN 2, BBX2, COL1, CONSTANS-LIKE 1 of the Light Signaling pathway) found in Scaffold 01843 (query sequence starts at base 40767)**

1)

For Primer GAAACAGATGGCATGGTGAGTA  
Rev Primer CTCCAAAACCCTATGAAAGTGC  
Repeats (tc) x11 PCR product = 275 bp start at base 48319

2)

For Primer GTCATCCTCGAAGAAAGACACC  
Rev Primer TCGACTGGAATTGTCTCCCTAT  
Repeats (ct) x7 PCR product = 287 bp start at base 48872

3)

For Primer AGGGAAGTAGCAGCAAAGACAT  
Rev Primer AGAACCCTGATGAGTTGAGGAA  
Repeats (ca) x11 PCR product = 133 bp start at base 18196

**AT5G60100 (APRR3, PRR3, PSEUDO-RESPONSE REGULATOR 3 of the Light Signaling pathway) found in Scaffold 02075 (query sequence starts at base 14139)**

1)

For Primer GCATGTTAAAAGGTGCTGTTGA  
Rev Primer ACTTCGACTTTCTCTTGTTCCG  
Repeats (ct) x7 PCR product = 238 bp start at base 14277

2)

For Primer GATCACCATTTCACAAGCTGAG  
Rev Primer ATACATTTCAGATATGCGCGTG  
Repeats (ga) x7 PCR product = 263 bp start at base 14887

3)

For Primer CCTTTCTCTTATTCTCTCGCCA  
Rev Primer AGCCATAGAGTGAGGACGGTTA  
Repeats (ct) x8 PCR product = 293 bp start at base 20948

**AT1G20330 (COTYLEDON VASCULAR PATTERN 1, CVP1, FRILL1, FRL1, SMT2, STEROL METHYLTRANSFERASE 2 of the Vernalization pathway) found in Scaffold 02142 (query sequence starts at base 24743)**

1)

For Primer TATCAGAAGACGTCCCAGAGGT  
Rev Primer GGTCGAGATGCACAATTAGACA  
Repeats (ct) x10 PCR product = 182 bp start at base 35782

2)

For Primer CGTTTTGGGTGAGTACAAGTGA  
Rev Primer CCACATTCCCGATCTTATTGTT  
Repeats (tc) x6 PCR product = 235 bp start at base 23016

3)

For Primer CGAATCTTGTTGTCGTATTGGA  
Rev Primer ATCAGCACATTCTCAGAAAGCA  
Repeats (ct) x5 PCR product = 252 bp start at base 22648

**AT1G09570 (ELONGATED HYPOCOTYL 8, FAR RED ELONGATED 1, FAR RED ELONGATED HYPOCOTYL 2, FHY2, FRE1, HY8, PHYA, PHYTOCHROME A of the Light Signaling pathway) found in Scaffold 03861 (query sequence starts at base 3771)**

No adequate SSRs could be found

**AT5G65060 (AGAMOUS-LIKE 70, AGL70, FCL3, MADS AFFECTING FLOWERING 3, MAF3 of the Ambient Temperature and Vernalization pathways) found in Scaffold 10765 (query sequence starts at base 639)**

**AT5G65080 (AGAMOUS-LIKE 68, AGL68, MADS AFFECTING FLOWERING 5, MAF5 of the Ambient Temperature and Vernalization pathways) found in Scaffold 10765 (query sequence starts at base 699)**

**AT5G10140 (AGAMOUS-LIKE 25, AGL25, FLC, FLF, FLOWERING LOCUS C, FLOWERING LOCUS F of the Ambient Temperature and Vernalization pathways) found in Scaffold 10765 (query sequence starts at base 708)**

**AT5G65050 (AGAMOUS-LIKE 31, AGL31, MADS AFFECTING FLOWERING 2, MAF2 of the Ambient Temperature and Vernalization pathways) found in Scaffold 10765 (query sequence starts at base 723)**

**AT5G65070 (AGAMOUS-LIKE 69, AGL69, FCL4, MADS AFFECTING FLOWERING 4, MAF4 of the Ambient Temperature and Vernalization pathways) found in Scaffold 10765 (query sequence starts at base 723)**

**AT1G77080 (AGAMOUS-LIKE 27, AGL27, FLM, FLOWERING LOCUS M, MADS AFFECTING FLOWERING 1, MAF1 of the Ambient Temperature and Vernalization pathways) found in Scaffold 10765 (query sequence starts at base 744)**

No adequate SSRs could be found

**AT5G24930 (ATCOL4, B-BOX DOMAIN PROTEIN 5, BBX5, COL4, CONSTANS-LIKE 4 of the Light Signaling pathway) found in Scaffold 11225 (query sequence starts at base 2816)**

**AT5G57660 (ATCOL5, B-BOX DOMAIN PROTEIN 6, BBX6, COL5, CONSTANS-LIKE 5 of the Light Signaling pathway) found in Scaffold 11225 (query sequence starts at base 2816)**

1)

For Primer CTCCGTTCCAAAATAAGTGTCC  
Rev Primer ACGTACTACTCCCTCCATTCCA  
Repeats (ag) x5 PCR product = 240 bp start at base 442

Only one adequate SSR could be found