Transcriptomic analysis of field-droughted sorghum from seedling to maturity reveals biotic and metabolic responses.
Supplementary Appendix

Contents

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1 Methods and Materials

1.1 Experimental protocols

Design experiment / Field set-up The field experiments were conducted in Parlier, CA (36.6008°N, 119.5109°W). The fields consist of sandy loam soils with a silky substratum and pH 7.37. We number the weeks according to the dates that plants were sampled. Week 0 was set to be June 1 to coincide with seedling emergence (June 1-3). All plots were pre-watered before planting. Three watering conditions were subsequently used on plots: I) Control, consisting of weekly watering five days before the sampling date, with the first irrigation starting before the sampling of Week 3 (June 18) and continuing until before the sampling of Week 17 (Sept 23) II) Pre-flowering drought, consisting of a complete lack of irrigation up through and including samples from Week 8, at which time regular watering resumed prior to the sampling of Week 9 (July 29), and III) Post-flowering drought, consisting of regular irrigation up through and including irrigation prior to Week 9 sampling (July 29) – at which point over 50% of the plants had reached flowering (anthesis) – and no irrigation after that date (Figure 1a). Plots receiving irrigation were irrigated at seven-day intervals using drip irrigation lines placed on the soil surface of each furrow. When irrigated, plots received 100% of the weekly calculated crop evapotranspiration for the 7 days prior to each irrigation. Crop evapotranspiration was determined based using potential evapotranspiration measured at an on-site CIMIS (CA Irrigation Management Information System) weather station multiplied by the crop coefficient, which was adjusted according to crop growth stage. See Xu *et al* (Xu et al., 2018) for details regarding estimation of evapotranspiration rates, irrigation management, and drought treatment measurements. For pre-flowering droughted plants, the first week in which the droughted plants differed from control in their water exposure when control samples first started receiving water in Week 3, so that Week 3 samples are considered the first samples with pre-flowering drought exposure. The pre-flowering droughted samples collected on Week 9 (Aug 3), 5 days after resumption of water, are the first samples collected pre-flowering droughted plants after they started receiving water. For post-flowering drought, the samples under post-flowering drought collected in Week 10 were collected 12 days after their last irrigation and 5 days after the weekly watering experienced by control plants, and thus are the first samples in post-flowering drought with different water exposure between control and droughted samples, so that Week 10 samples are considered the first samples with post-flowering drought exposure.

The treatment conditions were assigned via a randomized block design, where the fields were divided into 18 plots of 10 rows each ($\sim$ 1000 plants per plot). Each plot was randomly assigned a watering treatment (control, pre-flowering drought, or post-flowering drought) and genotype (RTx430 or BTx642), with 3 replicates, for a total of 18 plots. Within each plot individual plant samples of leaves and roots were manually collected weekly on the same day of the week and time of the day. At each week 10 plant samples from each plot were collected, leaves and roots (3^{rd} and 4^{th} leaves from each plant) separately and then pooled, to create a single leaf and root sample for each plot, except weeks 2-4 where more plants were used per replicate in order to obtain adequate tissue (Supplementary Table 7, 8).

Sample collection and processing. Individual sorghum plants were harvested at various developmental stages using a shovel to a depth of approximately 30 cm. Leaf tissue was collected by tearing off the third and fourth fully emerged leaf from the primary tiller, pooling material from 10 representative plants into an aluminum foil bag. The bags were then flash-frozen in liquid nitrogen. Root tissue from the same 10 individuals per sample was collected as previously described (Xu et al., 2018). Briefly, the top 30 cm of each individual's root system (avoiding brace roots) was cut using garden shears. This root sample consisted almost entirely of mature, differentiated roots with few if any growing root tips, to make this sample type more comparable to leaf tissue harvested at a similar developmental (mature) state. After isolation, roots were, vortexed for 2 minutes in epiphyte removal buffer (0.633% NaH2PO4·H2O, 1.65% Na2HP04.7H20, adding 200 μl Silwet-77/L, following autoclaving) to remove rhizosphere soil, then rinsed twice in root washing buffer, same as epiphyte removal buffer, omitting Silwet-77.

The washed roots were then gently dried, placed in aluminum foil bags, and quickly frozen in liquid nitrogen. Each week, all samples were collected at the same time of day (between 10am and 1pm) and the same day of the week for 16 weeks following seedling emergence (Week 2 to Week 17).

RNA extraction and sequencing. Harvested and frozen root and leaf tissue were ground in a cryogenic Freezer Mill (SPEX SamplePrep 6875D, Metuchen NJ USA) for 2-3 cycles of 2-3 minutes, with 1 minute cooling in between. Samples were then stored at -80°C. RNA was extracted using the QIAGEN miRNeasy Mini Kit (Cat. #AM217004) with modifications: 1 mL QIAzol (Cat #AM217004) and 100 μL 10% Sarkosyl solution were added to 100 mg of frozen tissue and placed in a vortex shaker adapter for 5 minutes. To these, 200 μL chloroform was added, and the samples were then vortexed and incubated for 3 minutes at room temperature before centrifugation at 12,000 xg for 15 minutes at 4°C. The aqueous phase was then transferred to a fresh tube, and ethanol was added to a final concentration of 60%. The remaining procedure was performed according to the kit manufacturer's recommendations. DNA contamination was removed from each sample using the TURBO DNA-free kit, (Cat. #AM1907, Invitrogen) according to the manufacturer's recommendations. Stranded cDNA libraries were generated using the Illumina Truseq Stranded RNA LT kitṁRNA was purified from 1 μg of total RNA using magnetic beads containing poly-T oligosṁRNA was fragmented and reversed transcribed using random hexamers and SSII (Invitrogen) followed by second strand synthesis. The fragmented cDNA was treated with end-pair, A-tailing, adapter ligation, and 8 cycles of PCR. qPCR was used to determine the concentration of the libraries. Libraries were sequenced on the Illumina HiSeq.

Protein extraction and western blotting For isolation of total protein, ground control and post-flowering drought leaf tissue from Week 11 was vigorously resuspended in a solution of 0.1 M EDTA pH 8.0, 0.12 M Tris-HCl pH 6.8, 0.1 M Na2CO3, 4% SDS, 12% sucrose, 0.2 M DTT, and 8 M Urea, and incubated in the dark at room temperature for 60 min. Tissue was pelleted and the proteinaceous supernatant was isolated. Total chlorophyll content of the supernatant was quantified as described (Porra et al., 1989). 2 μg of chlorophyll were loaded for each sample, excluding the 75% (1.5 μg), 50% (1 μg) and 25% (0.5 μg) dilution series. Proteins were resolved using pre-cast SDS-PAGE Any KD™ gels (BIO-RAD) and transferred to a polyvinylidene difluoride membrane (Immobilon-FL 0.45 mm, Millipore) via semi-dry transfer for immunodetection. Polyclonal antibodies raised against AtpB, PsaA, D1 (DE-loop), CP47, and Cyt b6 were obtained from Agrisera (Sweden) and visualized using the Western Lightning Plus-ECL chemiluminescent substrate system (PerkinElmer).

Spectrophometric metabolite and enzyme assays Proline was extracted from ground, frozen leaf tissue by boiling in 80% ethanol for 5 min. Material was pelleted, the supernatant removed, and then resuspended in 80% ethanol and boiled again. The second supernatant was combined with the first and then lyophilized to remove all ethanol. Following lyophilization, water-soluble molecules were separated from insoluble molecules by centrifuging and transferring the cleared supernatant to a new tube. Proline levels per unit fresh weight were quantified using a ninhydrin spectrometric assay (Bates et al., 1973).

Bulk glutathione S-transferase activity was measured using a 1-chloro-2,4-dinitrobenzene (CDNB) assay (Habig et al., 1974). Soluble proteins were extracted from ground, frozen leaf tissue by vortexing in 50 mM HEPES pH 7.5, 10% glycerol, 0.1% Triton X-100, 1 mM EDTA, 1 mM EGTA, 1 mM DTT, 10 mM MgCl2, and complete protease inhibitors (Roche) (Gibon et al., 2004). Total soluble protein was measured using a Bradford assay.

Leaf and root respiration measurements Respiration rates for leaves with no treatment and only leaves treated with 2.5 mM KCN were measured using a Clark-type oxygen electrode (Hansatech). Unlike all of the other experimental validation described here, the respiration rates for the leaf samples were measured on different samples from those used for the mRNA-Seq experiment because of the need for fresh material; these samples were collected from sorghum grown in the same field as the plants in the mRNA-Seq experiments, but in a different year. Fresh material was dark-adapted for over 1 hour and then dissected into pieces smaller than 5 mm and placed into air-saturated 20 mM MES, 20 mM HEPES pH 6.6, 0.2 mM CaCl2 with stirring and nylon mesh to prevent the plant material from contacting the electrode (Yoshida et al., 2007). We found that an effect of 2.5 mM KCN on leaves could only be observed when the cuticle was first damaged using sand paper. Respiration rates were collected over 5 min or longer when steady-state was not reached in the first 5 min.

High Performance Liquid Chromatography analysis of total chlorophyll Chlorophyll a and b levels were quantified by HPLC (1100 HPLC, Agilent) as described through a chlorophyll and carotenoid quantification procedure (Baroli et al., 2003), and were normalized by ground tissue weight. Frozen ground leaf tissue was weighed then mixed with 200 μl 100% HPLC-grade acetone. To extract most pigments, ground tissue was further pulverized in the acetone with lysing Matrix D beads through a FastPrep-24 5G™High-Speed Homogenizer (6.5 m s–1 for 2 x 60 s, MP Biomedical). Acetone supernatant was collected after centrifugation (2 min, 1500 g, 4°C). Extraction was repeated until the acetone extract was nearly clear to ensure full pigment extraction. Samples were held on ice in the dark throughout the extraction process to prevent pigment degradation.

Total fungal abundance (qPCR) & estimated AM fungal abundance A detailed description of the protocol used for measuring total fungal abundance can be found in our paper of sorghum mycobiome (Gao et al, in preparation). Briefly, fungal abundance was estimated by quantitative PCR (qPCR) of the fungal small subunit rRNA (SSU or 18S) using the FF2 and FR1 primers (Zhou et al., 2000). Analysis of qPCR mixtures was accomplished using a Real-Time PCR Detection System (Bio-Rad, Hercules, CA, USA) containing 1 μl of 5ng/μl genomic DNA, 10kμl iTAQ SYBR Green Supermix with ROX (Bio-Rad, Hercules, CA, USA), 0.2 μl of 100 mg ml-1 BSA, 0.15 μl of each 50 μM primer and water to 20 μl (Adams et al., 2013). Thermal cycling conditions consisted of an initial denaturation at 95°C for 3 min, followed by 40 cycles of 15 s of denaturation at 95°C and 1 min of annealing and extension at 60°C, finishing with a dissociation stage of 95°C for 15 s, 60°C for 30 s and 95°C for 15 s (Adams et al., 2013). Standard curves were developed using a series of 10-fold dilutions of plasmids containing a fragment of an insert of the 18S gene of Penicillium purpurogenum (Adams et al., 2013).

Let $q_{\text{TOTAL}}(t)$ be the total fungal abundance estimated with qPCR, $p_{\text{AMF}}(t)$ be the relative AM to all fungi abundance estimated with the 18S data. The estimated $\log_2$ abundance of AM fungi $q_{\text{AMF}}(t)$ is computed as follows:

$$q_{\text{AMF}}(t) = q_{\text{TOTAL}}(t) + \log_2(p_{\text{AMF}}(t))$$

1.2 Computational methods

1.2.1 Processing of Reads

Reference Genomes To increase read mapping rates for transcriptomic data, we generated custom SNP-corrected reference genome sequences for the two strains used in this study. We performed whole genome shotgun sequencing of DNA from each of the two strains (Tx642 or RTx430). We identified genome-wide SNPs between the sample and Sorghum bicolor v3.0 reference using samtools 0.1.19, then filtered with vcftools v 0.1.12a at default settings and for a maximum depth of 3 x average depth of the samples. After discarding indels, the remaining SNP calls were applied to the Sorghum bicolor v3.0 reference via bcftools consensus function to generate a custom reference sequence for each strain. These sequences are available at `https://www.stat.berkeley.edu/~epicon/publications/rnaseq/`[1] .

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[1] This page is currently password protected and will be made public upon acceptance. login: reviewer ; password: epicon

Transcriptomic sequence data analysis pipeline Raw fastq file reads were filtered and trimmed using the JGI QC pipeline resulting in the filtered fastq file (*.filter-RNA.gz files). Using BBDuk (bbd), raw reads were evaluated for artifact sequence by kmer matching (kmer=25), allowing 1 mismatch and detected artifact was trimmed from the 3' end of the reads. RNA spike-in reads, PhiX reads and reads containing any Ns were removed. Quality trimming was performed using the phred trimming method set at Q6. Finally, following trimming, reads under the length threshold were removed (minimum length 25 bases or 1/3 of the original read length - whichever is longer).

Filtered reads from each library were aligned to the reference genome (phytozome v3.1, supplemented with RTx430 and BTx642 SNP information) using HISAT version 2.1.0 (Kim et al., 2015) (BAMs/ directory). featureCounts (Liao et al., 2014) was used to generate the raw gene counts (counts.txt) file using gff3 annotations. Only primary hits assigned to the reverse strand were included in the raw gene counts (-s 2 -p –primary options).

Quality analysis and transformation of RNA-Seq data We performed quality analysis on the raw data and removed one sample of low-quality (low correlation to its replicates). We then applied the following normalization procedure: we filtered out low expressed genes and retained genes containing at least 20 reads in at least 3 samples and then applied upper-quartile normalization on the resulting set of genes to normalize using EDA-Seq (Bullard et al., 2010; Risso et al., 2011).

1.2.2 Differential expression analysis

Identifying genes differentially expressed across the time-course experiment We modeled the gene expression of gene i as a smooth function over time, with a different functional form estimated for each combination of genotype and watering condition.

Let y_{ij} be the log-expression level of gene i in sample j observed at time t_j, and C_j be the watering and genotype combination of a sample j (taking on six possible values for the three watering conditions and two genotypes). In what follows, we will drop the index i for gene, unless needed for clarity. We modeled the gene expression of sample j as:

$$y_j = g_{C_j}(t_j) + \epsilon_j \,, \tag{1}$$

where $g_C(t)$ is the smooth mean expression across time for the watering/genotype combination C, and ϵ_j are independent random variables with mean zero and variance σ_j^2.

We estimated the functional gene expression $g_C(t)$ for each combination C with B-splines basis (De Boor, 2001) separately for each sample type (leaf or root) and condition (pre- or post-flowering drought) using the package edge in R Storey et al. (2005). To accommodate the shift in expression at time T when there are watering changes – either water is re-established (pre-flowering drought, $T = 9$) or when drought commences (post-flowering drought, $T = 10$) – we estimated a different spline function on either side of T, which we refer to as a split-spline, so that the functional curve $g_C(t)$ can be written as follows:

$$g_C(t) = \begin{cases} \alpha_C^- + \sum_l \beta_{lC}^- \Phi_l(t) & \text{for } t < T \\ \alpha_C^+ + \sum_l \beta_{lC}^+ \Phi_l(t) & \text{for } t \geq T \end{cases} \,, \tag{2}$$

where Φ_l are B-splines basis of degree 3 with 3 degrees of freedom. This functional form captures both the smooth changes in gene expression from week to week, and the abrupt changes due to watering changes.

To allow for flexible comparisons of different treatments, we then extend the model implemented in edge Storey et al. (2005) to test hypotheses regarding linear combinations (contrasts) of the spline functions. We considered four different contrasts to identify the genes that are differentially expressed for the different possible comparisons of interest.

1. **Drought versus Control** For each genotype and drought regime, we tested if the functional gene expression was different between the watered and droughted conditions. The null hypotheses can be written for each genotype G:

   $$H_0 : g_{\text{Dght:G}}(t) = g_{\text{Cntrl:G}}(t),$$

   where "Dght" refers to one of the drought condition and "Cntrl" the control condition. Because there are two drought regimes (pre- and post-flowering drought) and two genotypes, this defines four separate contrasts each for leaf and root samples.

2. **Constitutive Genotype differences** We compared the functional gene expression for the two genotypes under watered conditions with the following null hypothesis:

$$H_0 : g_{\text{Dght:RTx430}}(t) = g_{\text{Cntrl:BTx642}}(t)$$

3. **Genotype-specific drought responses** For each drought regime, we tested whether the change in gene expression due to drought is the same in the two genotypes.

$$H_0 : g_{\text{Cntrl:RTx430}}(t) - g_{\text{Dght:RTx430}}(t) = g_{\text{Cntrl:BTx642}}(t) - g_{\text{Dght:BTx642}}(t)\,.$$

Identifying genes differentially expressed in specific weeks. We primarily relied on our holistic estimates of differential expression found using the functional splines methods. However, we also evaluated the number of genes differentially expressed in the first weeks of drought. To accomplish this, we used limma (Law et al., 2014) for differential expression (DE) analysis with the individual time points as factors in addition to our treatment combination (C) in the model, resulting in estimates of $\theta_C(t)$, the mean expression at week t for the combination C in the limma factorial model. We then isolated effects using similar contrasts as described above only applied to $\theta_C(t)$ in order to (1) identify genes DE between drought and control in a single week; (2) identify genes differentially expressed between the two genotypes with respect to drought in a single week. We also considered an additional contrast to identify genes whose expression abruptly changes between watering changes (either water resumption for pre-flowering or commencement of drought for post-flowering). We call this a "water change" analysis and test the following contrast:

$$H_0 : \theta_{\text{Cntrl:G}}(t-1) - \theta_{\text{Cntrl:G}}(t) = \theta_{\text{Dght:G}}(t-1) - \theta_{\text{Dght:G}}(t)\,,$$

where $t = 9$ for pre-flowering drought and $t = 10$ for post-flowering drought.

Computing a log-fold change across a time-course experiment To obtain a log-fold change between droughts across the whole time-course experiment, we first computed the log fold change using estimates from limma (Law et al., 2014) for each time point of the time-course experiment, obtaining a vector $L_i \in \mathbb{R}^T$ for each gene i. Then, we applied the following formula:

$$\text{lfc}_i = \text{sign}\left(\frac{1}{T}\sum_{t=1}^{T} L_i^t\right) \times \left(\frac{1}{T}\sum_{t=1}^{T} |L_i^t|\right)\,. \tag{3}$$

1.2.3 Clustering

We then applied a clustering strategy to group genes on their gene expression patterns. We performed this clustering routine separately for the four different combinations of sample types (leaf/root) and the drought conditions (pre- versus post-flowering droughted plants); note that control samples were used in defining the gene clusters for both the pre-flowering clusters and the post-flowering clusters.

First, we calculated the Fisher's combined probability (Fisher, 1925) based on the unadjusted p-values from three of the across-time DE analyses (drought versus control in RTx430, drought versus control in BTx642, and genotype-specific drought response) as well as the unadjusted p-value from the "water change" analysis. We then ranked the genes by their Fisher's combined probability. We selected the 5000 genes with the lowest Fisher's p-value, and that had a log fold change of at least 2 in at least a week. We then fitted a split-spline function to each gene and each condition, using Equation 2, to get estimates $\hat{g}_{iC}(t)$ for each watering condition and genotype combination, and gene i. For each genotype G we rescaled $\hat{g}_{iDght:G}(t)$ and $\hat{g}_{iCtrl:G}(t)$ by the same shift and scale constant per gene such that the functions range between 0 and 1; each genotype, however, was allowed separate rescaling constants to allowing clustering together genes with different levels of expression, but similar patterns in the two genotypes. Finally, we then applied k-means to the resulting fitted values at timepoints t_j, $\hat{g}_{iC}(t_j)$, with the number of clusters K set to 20 for pre-flowering drought stress, and 10 for post-flowering drought stress. We define for each cluster k and condition C the centroid at a time point t_j, $\hat{\mu}_k(t_j)$, as the average across the genes in the cluster of of the rescaled fitted values $\hat{g}_{iC}(t_j)$. This results in 60 centroid vectors.

Assigning a clustering score and label to all genes For each cluster k, we assigned a score to every gene that passed our expression cutoff (i.e. not only those used in defining the clusters) that determines its fit to the cluster centroid vector $\hat{\boldsymbol{\mu}}_k$, given by the following:

$$S(g, \hat{\boldsymbol{\mu}}_k) = \frac{1}{S_0(k)} \times \min_{a_{iG_j}, b_{iG_j}} \sum_j \left(b_{iG_j} y_{ij} + a_{iG_j} - \hat{\mu}_k(t_j) \right)^2 , \tag{4}$$

where $a_{iG} \geq 0$ and b_{iG} are scalars chosen per genotype that best rescale the gene's expression values y_{ij}, like that of the centroid $\hat{\mu}_k(t)$, and

$$S_0(k) = \min_{a_0 G_j} \sum_j \left(a_{0G_j} - \hat{\mu}_k(t_j) \right)^2 ,$$

to enforce the score $S(g, k)$ to be between 0 and 1. Note that the score is independent of the scale of the centroid and the scale of the gene.

We computed a score for each gene and each centroid and assign genes to the cluster that minimizes the score $S(g, \hat{\boldsymbol{\mu}}_k)$. We then separate the genes into "good" and "poor" matches, considering the top 50% percentile score over the whole set of clusters jointly between leaf and root as "good matches."

Visualizing cluster centroids For visualization of the cluster centroids, we fitted a split-spline to the centroid values, $\hat{\mu}_k(t_j)$, along with 20 and 80% percentile bands. To compute percentile bands, we use the estimates of a_{iG} and b_{iG} from Equation 4, and rescale the expression values y_{ij} for all "good-matched" genes i in cluster k. We then estimated the lower and higher bands by fitting a split-spline function onto the 20% and 80% percentile of the rescaled expression values.

1.2.4 Identification of motifs and transcription factors enriched in clusters

Annotating transcription factors We created a manually curated set of PFAM that are good predictors for the gene families defined in O'Malley et al. (2016) for Arabidopsis. We then used this mapping from PFAM to transcription families to annotate further the putative transcription factors from GrassTFDB.

Motif enrichment analysis We performed motif enrichment analysis in the promoters of each cluster. We considered the 500 bp downstream of each gene to be the promoter regions. For each cluster, we constructed a promoter sequence file, composed of promoter sequences of the "good-matched" genes of the cluster and a background file, composed of promoter sequences of "good-matched" genes from other clusters. We applied MEME-AME McLeay and Bailey (2010), using as *a priori* motifs of interest the database from O'Malley et al. (2016).

1.2.5 Gene set enrichment analysis in clusters

To facilitate interpretation of clusters, we performed KEGG pathway enrichment analysis and GO term enrichment analysis on the set of "good-matched" genes from each cluster independently from one another. To perform KEGG pathway enrichment analysis, we applied the R package `KEGGprofile`, which uses a hypergeometric tests to detect significant pathways. To detect GO terms highly enriched in each cluster, we applied gene set enrichment analysis (GSEA Subramanian et al. (2005)), which uses a Fisher test to detect significant GO terms. We then corrected for multiple tests using Benjamini-Hochberg.

1.2.6 Identifying shared patterns of expressions

The above enrichment analysis only detects enrichment of significant genes in functional gene sets, but does not imply that their temporal patterns are coordinated. To detect shared patterns of gene expression profile in a geneset, we applied an iterative method to identify inliers, by modifying the random sample consensus algorithm (RANSAC). RANSAC is widely used in vision to detect inliers, a set of data points whose distribution can be explained by a model with a fixed set of parameters, from outliers (data points that do not fit this model) (Fischler and Bolles, 1987). Let $\mathcal{G}$ be the geneset of interest, τ be a pre-defined threshold , m a pre-defined number of genes , and N the number of trials to consider. The procedure is as follows: for each iteration ℓ,

1. Select a random subset of genes $\mathcal{G}_\ell$ of size m, and estimate the set of mean centroids $\hat{\boldsymbol{\mu}}_\ell$ by the same procedure as in the clustering.
2. For all genes in the complete set $\mathcal{G}$, compute a score $S(g_i, \hat{\boldsymbol{\mu}}_\ell)$, as defined above in Equation 4 for scoring genes to clusters. Define I_ℓ to be the set of in-liers for trial ℓ as all genes with a score lower then the pre-defined threshold τ.

Once the pre-defined number of random trials has been reached, define the final set of inliers I_{inlier} as the largest set found through this procedure.

We applied this procedure with $\tau = 0.5$, $N = 1000$, $m = max(10, 0.3|\mathcal{G}|)$ on all gene sets defined by KEGG pathways, as well as pre-specified GO terms and gene sets of interest (total of 389 gene sets: 22 transcription factors families, 80 GO terms, 270 KEGG pathways, and 17 manually created gene sets of interest). We then rank these gene sets based on the proportion of their genes that are in I_{inlier}. Supplementary Table 9 shows all of those gene sets with proportions of in-liers greater than 50% of the gene set.

1.2.7 Longitudinal analysis of time course water potential

Let w_s be the s-th measurement water potential at time t_s, for replicate r_s, and C_s be the watering conditions, depth (6, 12, and 24 inches), and genotype combination of the measurement. In this analysis, we only considered measurements under drought conditions (before July, 28th for preflowering drought and after July, 28th for postflowering drought). Note that the water potential measurements are repeated observations of the same plot. We modeled the water potential as:

$$w_s = \mu_{C_s}(t_s) + \gamma_{r_s}(t_s) + \epsilon_s \,, \tag{5}$$

We modeled the average time curve water potential μ_{C_s} as a linearly related to time, with replicates deviating from the average time curve by a random effect intercept and slope through $\gamma_{r_s}(t_s)$. We fitted this model separately for pre- and post-flowering, using `lmer` (Bates et al., 2015), and performed significance testing on the slope of the models using `multcomp` (Hothorn et al., 2008).

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2 Supplementary Figures and Tables

Tables

Figures

2.1 Supplementary tables

2.1.1 Differential expression analyses

	Root		Leaf	
	Pre-flowering	Post-flowering	Pre-flowering	Post-flowering
Control-Drought RTx430	5977	4913	1889	2682
Control-Drought BTx642	5457	3247	3231	1393
Genotype specific drought	1180	466	340	713

Supplementary Table 1: **Time-course differential expression (DE) analysis.** The number of genes found significant for any difference in expression across the time points (based on hypothesis testing of contrasts in the spline estimate of expression, see Methods). Breakdowns in the number of DE genes are given for different conditions (leaf/root and drought regimes in the columns). The first two rows show the number of DE genes found when comparing between droughted and watered samples in each genotype, analyzed separately ("Drought versus Control" contrast), while the last row gives the number of DE genes found to have genotype-specific reactions to drought ("Genotype-specific drought responses" contrast). Genes are considered DE if their FDR-adjusted q-value is < 0.05 and at least a log-fold change of > 2.

	Root		Leaf	
	Pre-flowering	Post-flowering	Pre-flowering	Post-flowering
Control-Drought RTx430	939	1110	187	575
Control-Drought BTx642	1129	1112	766	106
Genotype specific drought	452	72	125	33

Supplementary Table 2: **Differential expression analysis of the first week of drought** The number of genes found significant during the first week of drought (defined as Week 3 for pre-flowering drought and Week 10 for post-flowering drought, see Methods for description of per-week analysis), with a FDR-corrected q-value < 0.05 and log fold change > 2.

	Leaf	Root
Upregulated in pre- and post-flowering drought	1086	1584
Downregulated in pre- and post-flowering drought	1038	1292
Upregulated in pre-flowering, downregulated in post-flowering	58	78
Downregulated in pre-flowering, upregulated in post-flowering	38	195

Supplementary Table 3: **Up and down regulation patterns in pre- and post-flowering drought.** The DE genes from Supplementary Table 1 are divided into different patterns of up and down regulation in pre and post-flowering drought. Genes found significant using the Fisher-combined q-value and which log-fold change is in the top or bottom 20% of significant genes are considered for this table.

	Root		Leaf	
	Pre-flowering	Post-flowering	Pre-flowering	Post-flowering
Total number of genotype different genes	480	799	2851	487
Genes expressed in only one of the genotypes	148 (30.83%)	105 (13.14%)	281 (9.86%)	97 (19.92%)
Genes DE in only one of the genotypes	147 (30.63%)	528 (66.08%)	547 (19.19%)	210 (43.12%)
Genes with much stronger reaction in one of the genotypes	199 (41.46%)	282 (35.29%)	795 (27.88%)	246 (50.51%)
Genes upregulated in one genotype and down-regulated in the other	43 (8.96%)	37 (4.63%)	316 (11.08%)	27 (5.54%)
Genes responding differently in recovery	174 (36.25%)	NA	1521 (53.35%)	NA

Supplementary Table 4: **Types of Genotype-specific reactions to drought.** The genes found to have genotype specific reactions to drought (Supplementary Table 1) are further broken down here by their comparative behavior in each genotype (rows). Note that the total of each row does not add to the total because not all of these categories are mutually exclusive.

	Number of genes	Unannotated	No homologs	No homologs in Ara	No name in Ara.
All genes	34211	14664 (42.86%)	5566 (16.27%)	8349 (24.40%)	22931 (67.03%)
Genes expressed in leaves	21668	7378 (34.05%)	1538 (7.10%)	2622 (12.10%)	13283 (61.30%)
Genes expressed in roots	23678	8174 (34.52%)	1684 (7.11%)	2924 (12.35%)	14602 (61.67%)
DE genes	10727	3923 (36.57%)	1059 (9.87%)	1870 (17.43%)	6537 (60.94%)
DE genes in leaves	5135	1787 (34.80%)	467 (9.09%)	861 (16.77%)	3040 (59.20%)
DE genes in roots	8899	3211 (36.08%)	807 (9.07%)	1490 (16.74%)	5414 (60.84%)

Supplementary Table 5: **Annotation of *S. bicolor* transcriptome** Number and proportion of *S. bicolor* genes that are, in the Phytozome v3.1 annotation, (1) unannotated (without GO annotation, KEGG information, nor a known homologue in Arabidopsis with a name); (2) with no homologs to Rice or arabidopsis; (3) with no homolog in Arabidopsis; (4) with no homolog to a named Arabidopsis gene.

Genotype	Treatment	Plot	Flowering day
BTx642	Control	2	62
BTx642	Control	11	62
BTx642	Control	19	62
BTx642	Post	4	62
BTx642	Post	15	62
BTx642	Post	21	62
BTx642	Pre	6	68
BTx642	Pre	9	68
BTx642	Pre	14	82
RTx430	Control	1	68
RTx430	Control	12	68
RTx430	Control	20	68
RTx430	Post	3	68
RTx430	Post	16	68
RTx430	Post	22	68
RTx430	Pre	5	82
RTx430	Pre	13	80
RTx430	Pre	18	80

Supplementary Table 6: **Flowering day per plot.** The day of flowering per plot. Day 0 corresponds to the day the seeds were planted (5/27/2016)

	Control		Post-flowering		Pre-flowering	
Week	BTx642	RTx430	BTx642	RTx430	BTx642	RTx430
2	3	3				
3	3	3			3	3
4	2	3			3	3
5	3	3			3	2
6	3	3			3	3
7	1	1			1	1
8	3	3			3	3
9	3	3	3	3	3	3
10	3	3	3	3	3	3
11	3	3	3	3	3	3
12	3	3	1	1	3	3
13	3	3	3	3	3	3
14	1	1	1	1	1	1
15	3	2	3	3	3	1
16		1	1		1	1
17	3	3	3	3	3	3

Supplementary Table 7: **Leaf Sampling Effort Per Week.** The number of mRNA-Seq leaf samples per week used in the analysis. Each sample consisted of a pool of plants per sample given above (usually 10, but in early weeks more plants were needed for sufficient tissue, see Methods). These numbers do not include the sample that was removed due to quality control (0629164L11).

	Control		Post-flowering		Pre-flowering	
Week	BTx642	RTx430	BTx642	RTx430	BTx642	RTx430
2	3	3				
3	3	3			3	3
4	3	3			3	3
5	3	3			3	3
6	3	3			3	3
7	1	1			1	1
8	3	3			2	3
9	3	3	3	3	3	3
10	3	3	3	3	3	3
11	3	3	3	3	3	3
12	3	2	1	1	3	3
13	3	3	3	3	3	3
14	1	1	1	1	1	1
15	2	3	3	3	2	2
16		1	1	1	1	1
17	3	3	3	3	3	3

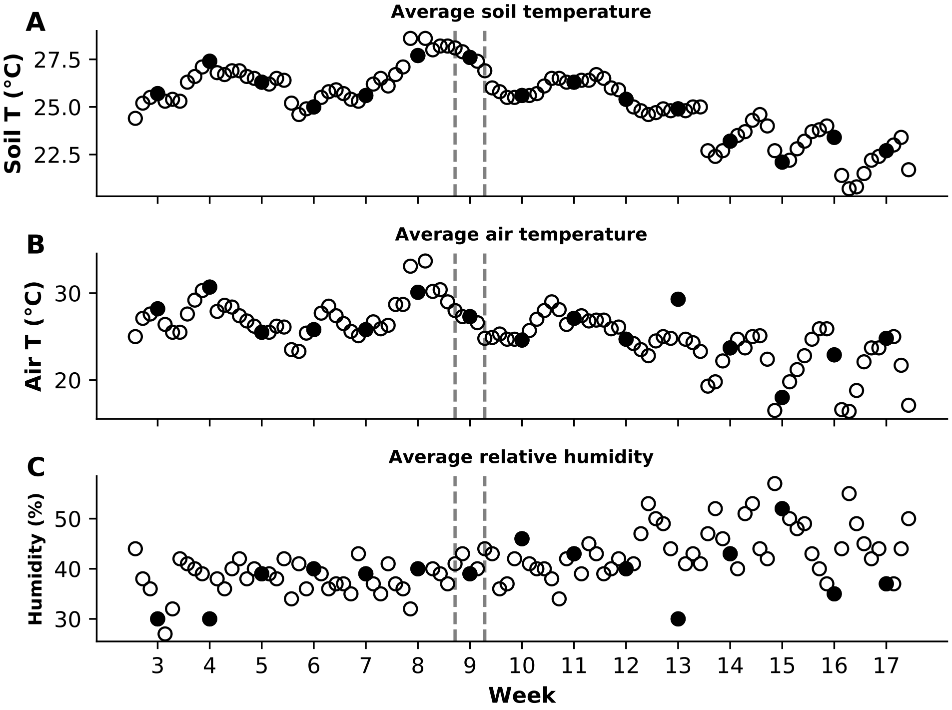
Supplementary Table 8: **Root Sampling Effort Per Week.** The number of mRNA-Seq root samples per week used in the analysis. Each sample consisted of a pool of plants per sample given above (usually 10, but in early weeks more plants were needed for sufficient tissue, see Methods). All root samples passed our quality control threshold and were considered for our analysis.

	Sample type	No. inliers	Perc. inliers	No. of genes
Genes annotated CAB in Rice	leaf	11	64.71%	17
DREB1 genes	root	5	62.50%	8
Genes annotated LHCB in Arabidopsis	leaf	6	60.00%	10
AMF-induced genes	root	171	70.95%	241
Chalcone and Stilben synthase genes	root	11	64.71%	17
Genes annotated LEA in Arabidopsis	root	5	71.43%	7
MCM genes	leaf	5	55.56%	9
MCM genes	root	8	72.73%	11
Pathway 00196 - Photosynthesis - light antenna	leaf	10	62.50%	16
Pathway 00531 - Glycan biosynthesis and metabolism	root	8	53.33%	15
Pathway 00603 - Glycosphingolipid biosynthesis ...	root	6	60.00%	10

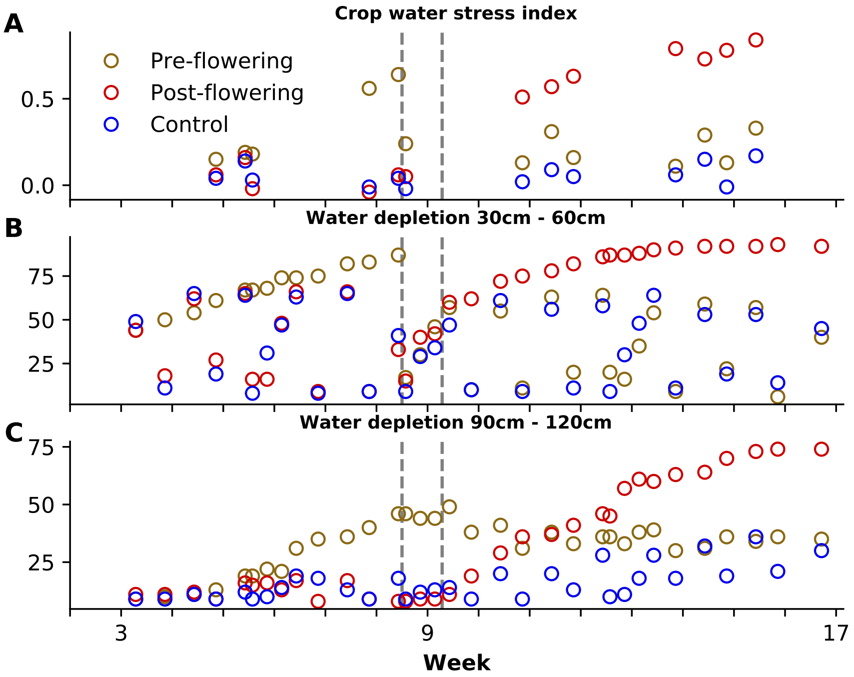
Supplementary Table 9: **Gene sets with highly shared gene expression patterns** We detected 9 gene sets with greater than 50% of the genes in the gene sets sharing similar gene expression patterns (MCM genes sharing expression patterns both in leaf and root samples). See Methods for description of how gene sets with similar patterns across time were identified.

2.2 Supplementary Figures

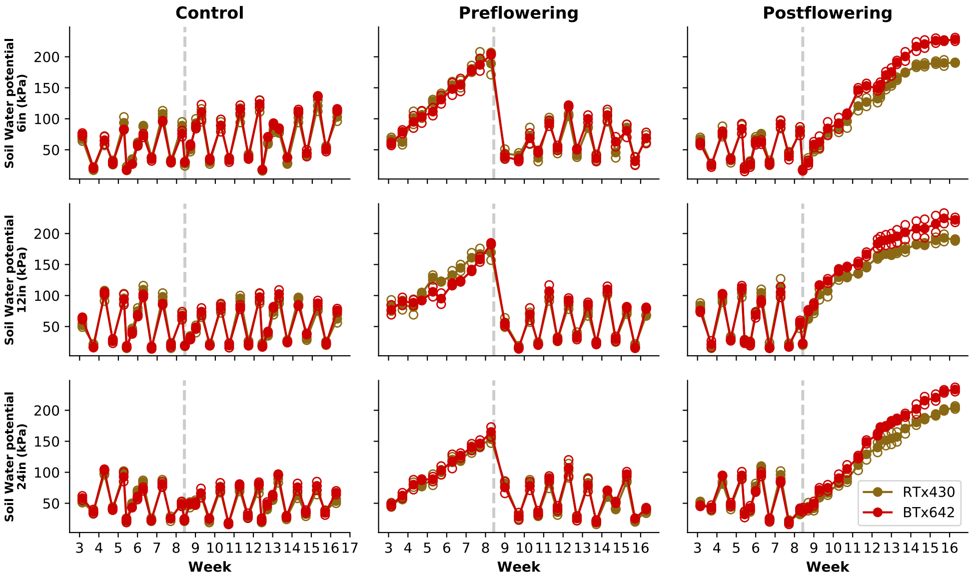
2.2.1 Weather data & crop stress index



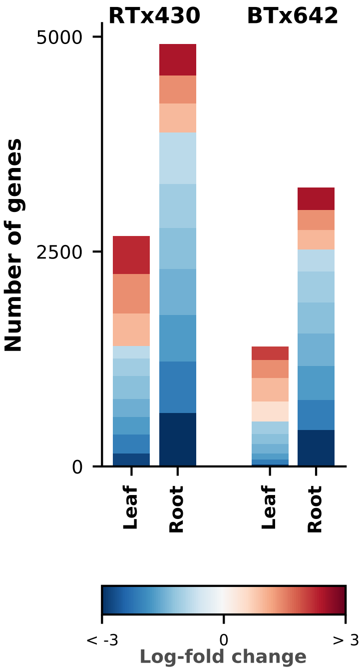
Supplementary Figure 1: **Weather during sampling** Y-axis shows the daily average soil temperature **(A)**, air temperature **(B)**, and relative humidity **(C)** plotted against the week of sampling (x-axis) as recorded by CIMIS (`https://cimis.water.ca.gov/`) at Station 39 (Parlier, CA) during the time of the field study. Black dots corresponds to sampling day. Dashed vertical lines correspond to watering changes for the two different drought regimes.



Supplementary Figure 2: **Crop stress index & Water depletion** Y-axis shows the crop water stress index (CWSI) **(A)**, soil water depletion at 30-60 cm **(B)**, and soil water depletion at 90-120cm **(C)** plotted against the week (x-axis). CWSI is a relative indicator of severity of plant water stress and indicates relative levels of plant water stress determined from the difference between air temperature and canopy/leaf temperatures, adjusted for vapor pressure deficit. Values of CWSI closer to 1.0 indicate a very severely water stressed plant, while values closer to 0.0 indicate non-water stressed condition. The measurements were not taken on the same days as the plant samples were collected; plant samples were collected at the points marked by ticks along the x-axis.

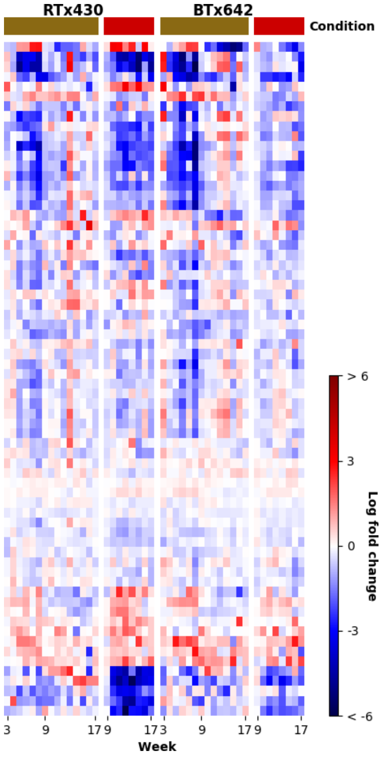


Supplementary Figure 3: Soil Water Potential: Soil water potential for two replicate plots for each condition and each genotype. Soil water potential for the two drought conditions show the decrease of water availability increasing during drought. A minor difference between the two genotypes can be observed at three different depths in post-flowering drought (p-values: 6in: 0.006, 12in: 0.044, 24in: 0.027), suggesting BTx642 is better able to extract water than RTx430. However, this difference is small (20kPa2̃5kPa), corresponding to only 1 or 2 days of ETc for a fully transpiring plant.

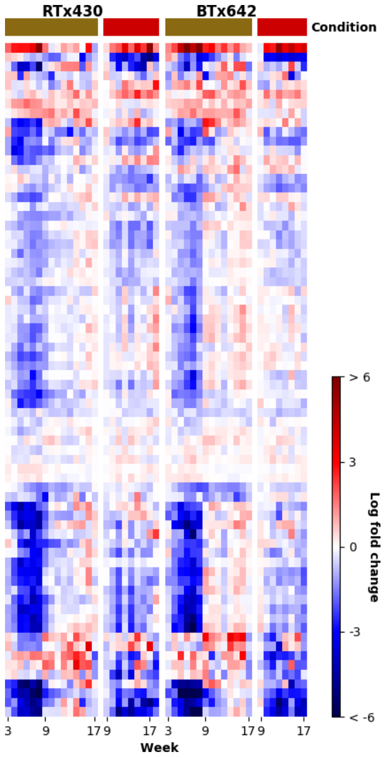


Supplementary Figure 4: **Root versus leaf in post-flowering** Barplot of significantly differentially expressed (DE) genes with at least a $\log_2$-fold difference in expression of 2 between drought and watered conditions in post-flowering drought.

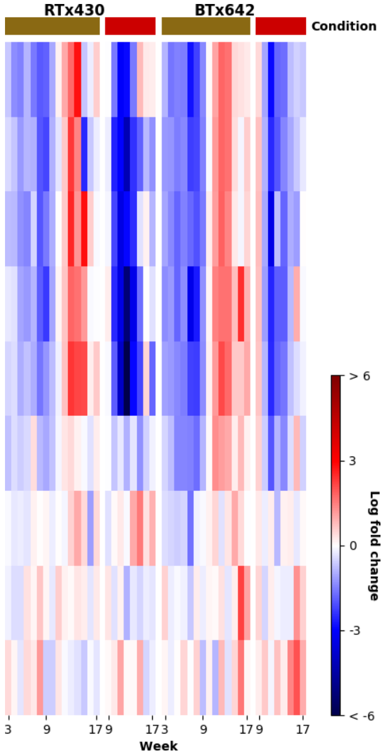
2.2.2 Heatmaps of the log-fold change of relevant gene sets



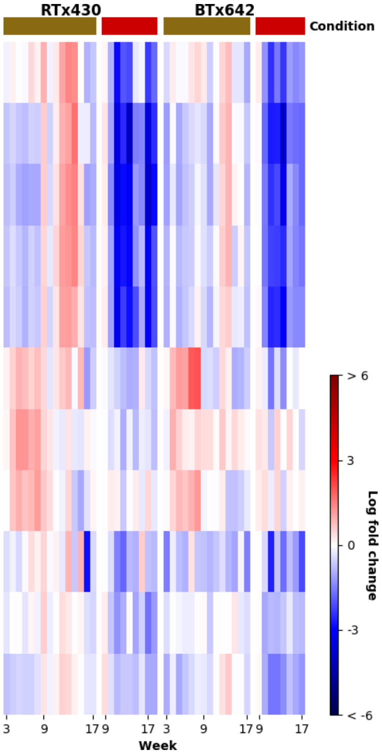
Supplementary Figure 5: **Log-fold change of WRKY Transcription factor family (leaf).** See methods for details on the annotation of putative transcription factors. The average difference in the log expression of drought and control is shown via a heatmap, where the color scale corresponds to log-fold change values indicated in the accompanying legend, with blue corresponding to lower expression under drought, and red higher expression under drought. The columns indicate the weeks of sampling, divided into groups based on the two genotypes and then further divided into pre-flowering (brown) and post-flowering drought (red).



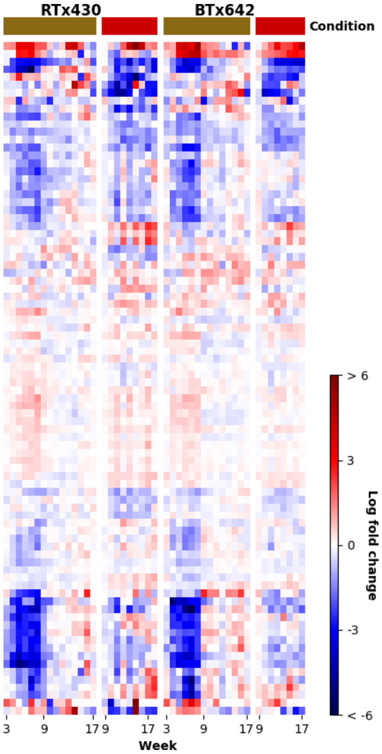
Supplementary Figure 6: **Log-fold change of WRKY Transcription factor family (root)**. See methods for details on the annotation of putative transcription factors. See caption of Supplementary Figure 5 for details.



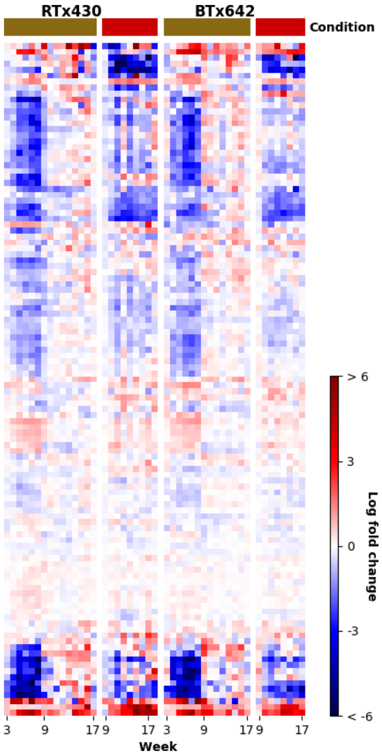
Supplementary Figure 7: **Log-fold change change of Mini Chromosome Repair protein family (leaf)** Known homologs to Arabidopsis MCM gene family. See caption of Supplementary Figure 5 for details.



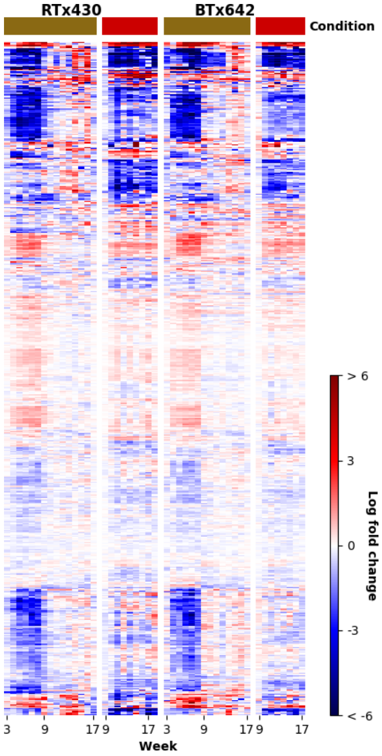
Supplementary Figure 8: **Log-fold change - Mini Chromosome Repair protein family (root)** Known homologs to Arabidopsis MCM gene family. See caption of Supplementary Figure 5 for details.



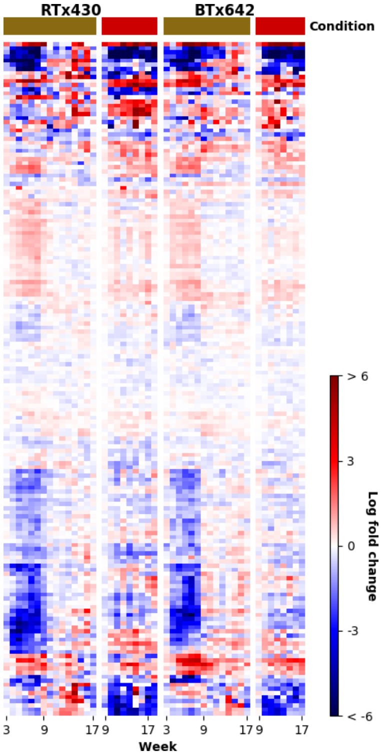
Supplementary Figure 9: **Log-fold change change of GO term "Response to Salicylic Acid" (GO:009751) in root.** See caption of Supplementary Figure 5 for details.



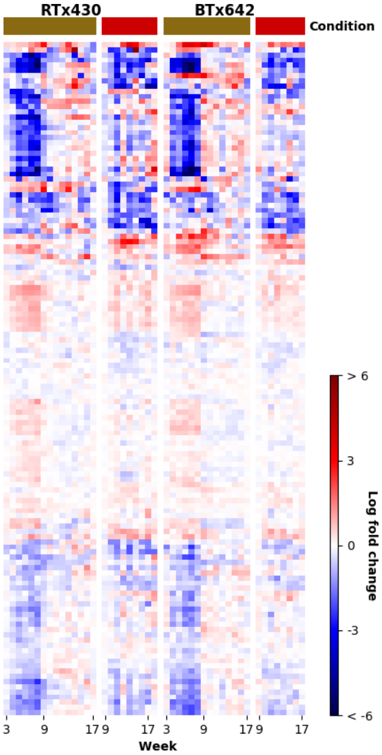
Supplementary Figure 10: **Log-fold change change of GO term "Response to Jasmonic Acid" (GO:009753) in root.** See caption of Supplementary Figure 5 for details.



Supplementary Figure 11: **Log-fold change change of GO term "Defense Response" (GO:006952) in root.** See caption of Supplementary Figure 5 for details.

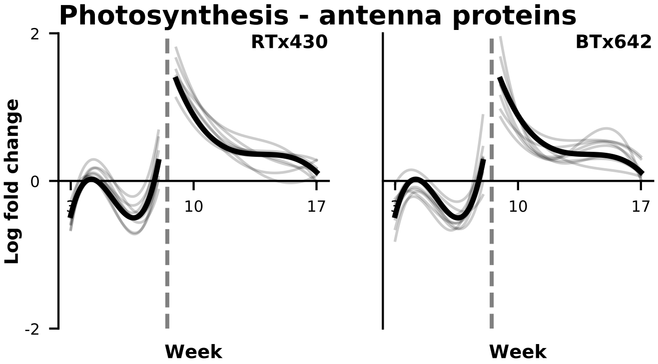


Supplementary Figure 12: **Log-fold change change of GO term "Response to fungus" (GO:006952) in root.** See caption of Supplementary Figure 5 for details.

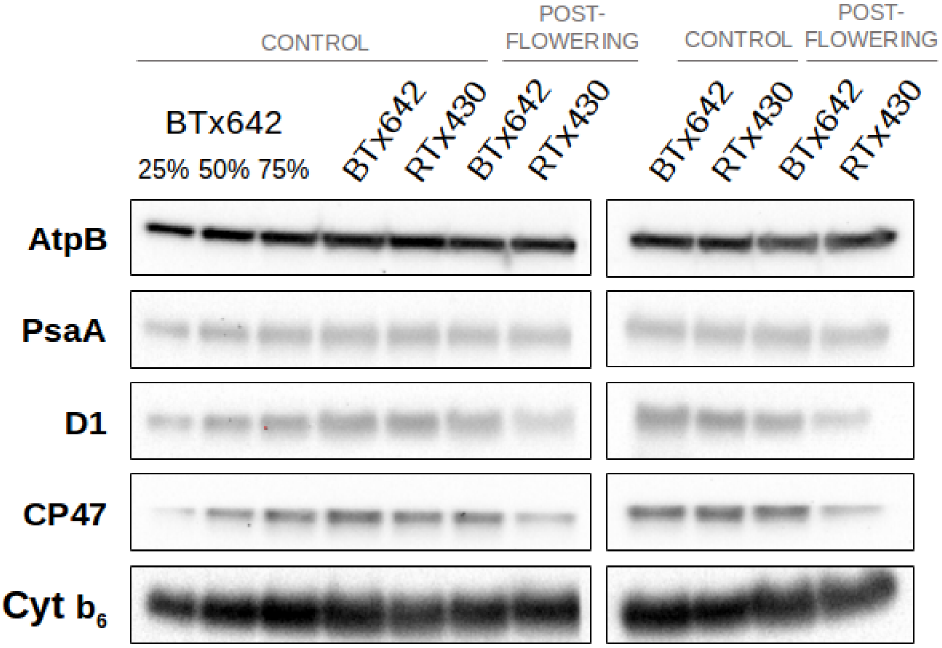


Supplementary Figure 13: **Log-fold change change of GO term "Regulation of defense response" (GO:031347) in root.** See caption of Supplementary Figure 5 for details.

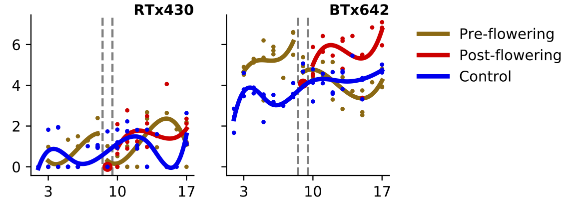
2.2.3 Photosynthesis



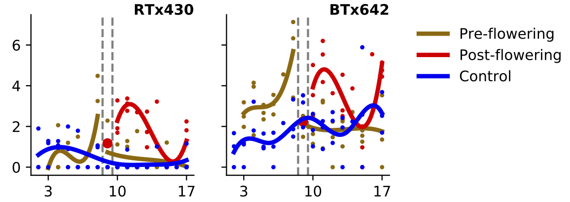
Supplementary Figure 14: **Photosynthesis antenna protein pathways shares common log fold change** Log-fold change between droughted and watered plants (y-axis) shown as a smoothed function over time (x-axis) (see Figure 2 in main text) for genes from the photosynthesis-antenna protein pathway in pre-flowering drought stress showing shared up-regulation after water resumption. Shown are the genes chosen as the "inlier" set I_{inlier} of genes in the photosynthesis-antenna protein pathway (see Methods). The photosynthesis-antenna protein pathway was chosen as one of the top pathways showing shared gene expression across the time course (Supplemental Table 9). The dark line corresponds to the average fold-change, averaged across the genes.



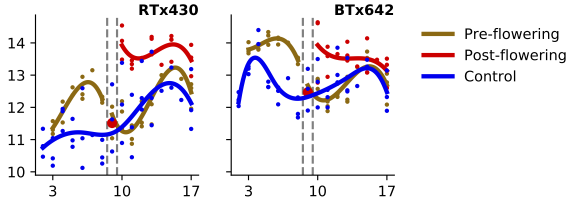
Supplementary Figure 15: **Western blot of photosynthesis proteins** Full results of the immunoblot analysis, including control, of representative subunits of photosynthetic complexes PSI (PsaA), PSII (D1, CP47), and cytochrome b6f complex (Cyt b6) under control and 3 weeks post-flowering drought (Week 11) with ATP synthase (AtpB) as a loading control.



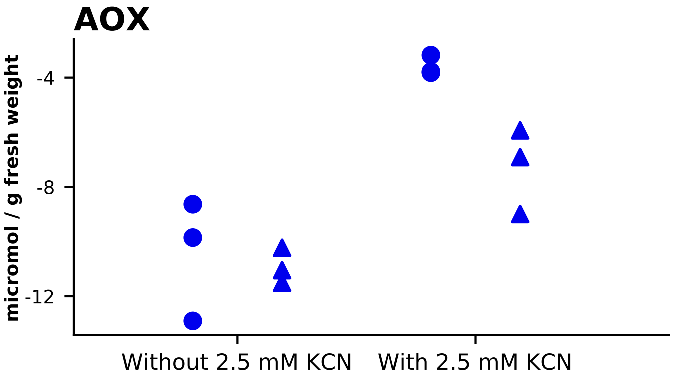
Supplementary Figure 16: **GST29 gene** Log-2 gene expression values (y-axis) against time (x-axis) of Sobic.003G264400, a homolog to GST29 with constitutive and drought differences between RTx430 (left) and BTx642 (right). Individual values are shown by dots, with a smooth split-splines showing the estimated functional forms.



Supplementary Figure 17: **FD3 gene** Log-2 gene expression values (y-axis) against time (x-axis) of Sobic.003G364400, a homolog to FD3 with constitutive and drought differences between RTx430 (left) and BTx642 (right). See caption of Supplementary Figure 16 for details.



Supplementary Figure 18: **P5SC2 gene** Log-2 gene expression values (y-axis) against time (x-axis) of Sobic.003G356000, a homolog to P5SC2 with constitutive and drought differences between RTx430 (left) and BTx642 (right). See caption of Supplementary Figure 16 for details.



Supplementary Figure 19: **Alternative Oxidase Capacity** Oxygraph measurements of respiration in week 5 in normally watered plants with and without treatment of 2.5 mM KCN show BTx642 maintaining AOX capacity better than RTx430.

3 Cluster Summaries

3.1 Overview

In what follows, we provide figures and summary information about the clusters found in our clustering analysis. We only provide information on the clusters that show clear differences in gene expression between drought and control watering regimes. See Methods for details of how the clusters were created.

For each cluster we provide

1. A visualization of the average gene expression of the cluster, plotted separately for drought (red/brown) versus control (blue), and separate plots for the two genotypes. See Methods in the main manuscript for how these visualizations were created.

2. An overview of the cluster, giving a our title of the cluster, the number of total genes assigned to the cluster, the number of "good" genes (i.e. with good fit to the cluster centroid), and a brief description of interesting features of the cluster.

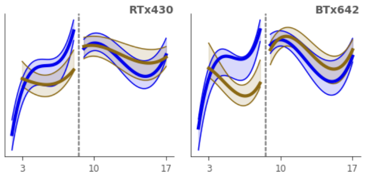
3. GO terms that are significantly enriched in the cluster, along with their adjusted p-value. Because of the large number of GO terms, we have for this summary filtered them to only show specific GO categories pre-specified to be of interest to drought. See Supplementary Note 2 "Full Cluster GO Annotation" for the complete GO annotation on all clusters.

4. All KEGG pathways that are enriched in the cluster, along with their adjusted p-value.

5. Transcription factors (TFs) whose motifs are found to be enriched in the promoter regions upstream of the genes in the cluster. Shown in the table are the number of motifs found enriched for the cluster, the total number of motifs association with that TF, and the percentage of the motifs found enriched.

3.2 Leaf Preflowering clusters

3.2.1 Leaf - Preflowering - Cluster 5 - Defense



Overview
Cluster 5: Defense
Number of genes: 1289
Number of "good" genes: 424
Description Contains 3 DREB1 genes. Contains mainy WRKY and AP2-EREBP transcription factors.

Pathway	Adj. p-value
Plant-pathogen interaction	0.000
MAPK signaling pathway - plant	0.008
Protein processing in endoplasmic reticulum	0.041

Supplementary Table 10: KEGG pathway enrichment - Leaf - Preflowering - Cluster 5 - Defense

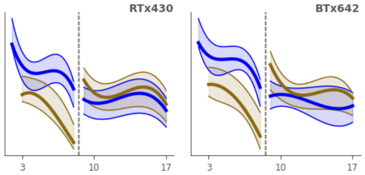
TF family	No. in cluster	Total number	Percentage
CAMTA	2	2	100.00
FAR1	2	2	100.00
HMG	2	2	100.00
mTERF	1	1	100.00
AP2EREBP	85	130	65.38
LOBAS2	6	13	46.15
E2FDP	2	7	28.57
TCP	6	23	26.09
bHLH	3	25	12.00
Trihelix	2	21	9.52
C2H2	2	38	5.26
NAC	3	86	3.49
MYB	2	86	2.33

Supplementary Table 11: Motif enrichment Leaf - Preflowering - Cluster 5 - Defense

GO type	GO ID	Description	Adj. p-value
BP	GO:0010468	regulation of gene expression	0.000
	GO:0009607	response to biotic stimulus	0.001
	GO:0009867	jasmonic acid mediated signaling pathway	0.002
	GO:0050832	defense response to fungus	0.006
	GO:0009812	flavonoid metabolic process	0.011
	GO:0031347	regulation of defense response	0.015
	GO:0009813	flavonoid biosynthetic process	0.018
	GO:0050793	regulation of developmental process	0.064
	GO:0002376	immune system process	0.076
	GO:0042742	defense response to bacterium	0.087
	GO:0009753	response to jasmonic acid	0.098
	GO:0006950	response to stress	0.099

Supplementary Table 13: GO term enrichment (filtered results) Leaf - Preflowering - Cluster 5 - Defense

3.2.2 Leaf - Preflowering - Cluster 6 - Photosynthesis



Overview
Cluster 6: Photosynthesis
Number of genes: 764
Number of "good" genes: 105
Description Many GO term related to photosynthesis enriched (light reaction, electron transport chain, regulation of photosynthesis, photosystem II repair)

Pathway	Adj. p-value
Metabolic pathways	0.021

Supplementary Table 14: KEGG pathway enrichment - Leaf - Preflowering - Cluster 6 - Photosynthesis

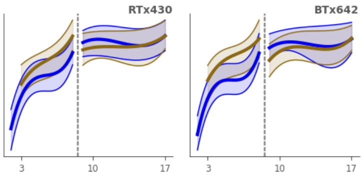
TF family	No. in cluster	Total number	Percentage
Trihelix	1	21	4.76

Supplementary Table 15: Motif enrichment Leaf - Preflowering - Cluster 6 - Photosynthesis

GO type	GO ID	Description	Adj. p-value
BP	GO:0019684	photosynthesis, light reaction	0.000
	GO:0022900	electron transport chain	0.000
	GO:0042546	cell wall biogenesis	0.000
	GO:0009628	response to abiotic stimulus	0.002
	GO:0010109	regulation of photosynthesis	0.003
MF	GO:0016787	hydrolase activity	0.000
	GO:0031072	heat shock protein binding	0.081

Supplementary Table 17: GO term enrichment (filtered results) Leaf - Preflowering - Cluster 6 - Photosynthesis

3.2.3 Leaf - Preflowering - Cluster 7 - Glutathione



Overview
Cluster 7: Glutathione
Number of genes: 1690
Number of "good" genes: 747
Description Contains many GST

Pathway	Adj. p-value
Protein processing in endoplasmic reticulum	0.001
Spliceosome	0.012
Ubiquitin mediated proteolysis	0.013

Supplementary Table 18: KEGG pathway enrichment - Leaf - Preflowering - Cluster 7 - Glutathione

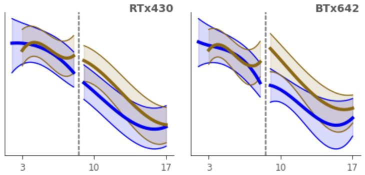
	No. in cluster	Total number	Percentage
TF family			
CPP	6	7	85.71
Orphan	1	3	33.33
ND	1	6	16.67
HSF	2	16	12.50
C2C2dof	3	39	7.69
MYB	1	86	1.16
NAC	1	86	1.16

Supplementary Table 19: Motif enrichment Leaf - Preflowering - Cluster 7 - Glutathione

		Description	Adj. p-value
GO type	GO ID		
BP	GO:0010468	regulation of gene expression	0.000
	GO:0006749	glutathione metabolic process	0.021
MF	GO:0004364	glutathione transferase activity	0.031
	GO:0015250	water channel activity	0.056

Supplementary Table 21: GO term enrichment (filtered results) Leaf - Preflowering - Cluster 7 - Glutathione

3.2.4 Leaf - Preflowering - Cluster 8 - Photosynthesis - light reaction



Overview
Cluster 8: Photosynthesis - light reaction
Number of genes: 1182
Number of "good" genes: 622

Pathway	Adj. p-value
Metabolic pathways	0.000
Biosynthesis of secondary metabolites	0.000
Fructose and mannose metabolism	0.018
Biosynthesis of amino acids	0.025
Phagosome	0.025
Cyanoamino acid metabolism	0.044

Supplementary Table 22: KEGG pathway enrichment - Leaf - Preflowering - Cluster 8 - Photosynthesis - light reaction

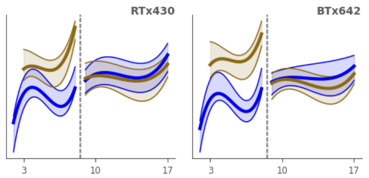
TF family	No. in cluster	Total number	Percentage
TCP	3	23	13.04
ABI3VP1	1	9	11.11
ZFHD	1	11	9.09
bZIP	3	51	5.88
C2H2	1	38	2.63
MYB	2	86	2.33
AP2EREBP	2	130	1.54

Supplementary Table 23: Motif enrichment Leaf - Preflowering - Cluster 8 - Photosynthesis - light reaction

GO type	GO ID	Description	Adj. p-value
BP	GO:0019684	photosynthesis, light reaction	0.000
	GO:0071554	cell wall organization or biogenesis	0.000
	GO:0022900	electron transport chain	0.000
	GO:0006629	lipid metabolic process	0.000
	GO:0008610	lipid biosynthetic process	0.000
	GO:0071555	cell wall organization	0.000
	GO:0042546	cell wall biogenesis	0.000
	GO:0009073	aromatic amino acid family biosynthetic ...	0.000
	GO:0042214	terpene metabolic process	0.009
	GO:0008652	cellular amino acid biosynthetic process	0.009
	GO:0010143	cutin biosynthetic process	0.017
	GO:0035336	long-chain fatty-acyl-CoA metabolic proc...	0.019
	GO:0104004	cellular response to environmental stimu...	0.021
	GO:0071214	cellular response to abiotic stimulus	0.021
	GO:0009628	response to abiotic stimulus	0.034
	GO:0010109	regulation of photosynthesis	0.034
	GO:0044550	secondary metabolite biosynthetic proces...	0.036
	GO:0009741	response to brassinosteroid	0.050
	GO:0009642	response to light intensity	0.056
	GO:0010345	suberin biosynthetic process	0.058
	GO:1901607	alpha-amino acid biosynthetic process	0.068
	GO:0034614	cellular response to reactive oxygen spe...	0.071
MF	GO:0016787	hydrolase activity	0.000
	GO:0016491	oxidoreductase activity	0.000

Supplementary Table 25: GO term enrichment (filtered results) Leaf - Preflowering - Cluster 8 - Photosynthesis - light reaction

3.2.5 Leaf - Preflowering - Cluster 9 - Response to hydrogene peroxide



Overview
Cluster 9: Response to hydrogene peroxide
Number of genes: 1189
Number of “good” genes: 192
Description Many motifs from the HSF transcription factor family.

Pathway	Adj. p-value
Protein processing in endoplasmic reticulum	0.002
Spliceosome	0.040

Supplementary Table 26: KEGG pathway enrichment - Leaf - Preflowering - Cluster 9 - Response to hydrogene peroxide

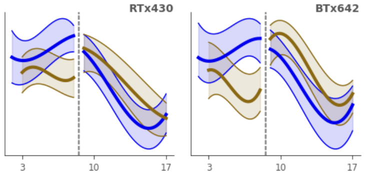
TF family	No. in cluster	Total number	Percentage
PLATZ	1	1	100.00
S1Falike	1	1	100.00
Orphan	2	3	66.67
HSF	9	16	56.25
ND	1	6	16.67
bZIP	7	51	13.73
C2C2dof	2	39	5.13
bHLH	1	25	4.00
C2H2	1	38	2.63
MYBrelated	1	47	2.13
AP2EREBP	1	130	0.77

Supplementary Table 27: Motif enrichment Leaf - Preflowering - Cluster 9 - Response to hydrogene peroxide

GO type	GO ID	Description	Adj. p-value
BP	GO:0042542	response to hydrogen peroxide	0.009
	GO:0010608	posttranscriptional regulation of gene e...	0.014
	GO:0009737	response to abscisic acid	0.078

Supplementary Table 29: GO term enrichment (filtered results) Leaf - Preflowering - Cluster 9 - Response to hydrogene peroxide

3.2.6 Leaf - Preflowering - Cluster 10 - DNA replication



Overview
Cluster 10: DNA replication
Number of genes: 622
Number of “good” genes: 98

Pathway	Adj. p-value
DNA replication	0.000

Supplementary Table 30: KEGG pathway enrichment - Leaf - Preflowering - Cluster 10 - DNA replication

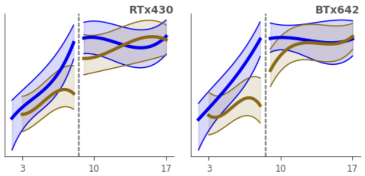
TF family	No. in cluster	Total number	Percentage
FAR1	2	2	100.00
mTERF	1	1	100.00
HMG	1	2	50.00
AP2EREBP	50	130	38.46
LOBAS2	3	13	23.08
bHLH	2	25	8.00
MYB	2	86	2.33

Supplementary Table 31: Motif enrichment Leaf - Preflowering - Cluster 10 - DNA replication

GO type	GO ID	Description	Adj. p-value
BP	GO:0071554	cell wall organization or biogenesis	0.000
	GO:0006629	lipid metabolic process	0.000
	GO:0006270	DNA replication initiation	0.003
	GO:0006631	fatty acid metabolic process	0.004
	GO:0006260	DNA replication	0.019
MF	GO:0016787	hydrolase activity	0.000

Supplementary Table 33: GO term enrichment (filtered results) Leaf - Preflowering - Cluster 10 - DNA replication

3.2.7 Leaf - Preflowering - Cluster 11 - Defense



Overview
Cluster 11: Defense
Number of genes: 1259
Number of “good” genes: 857

Pathway	Adj. p-value
Plant-pathogen interaction	0.016
Protein processing in endoplasmic reticulum	0.045

Supplementary Table 34: KEGG pathway enrichment - Leaf - Preflowering - Cluster 11 - Defense

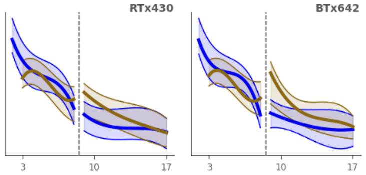
TF family	No. in cluster	Total number	Percentage
zfGRF	1	1	100.00
WRKY	11	60	18.33
E2FDP	1	7	14.29
G2like	1	29	3.45
bZIP	1	51	1.96

Supplementary Table 35: Motif enrichment Leaf - Preflowering - Cluster 11 - Defense

GO type	GO ID	Description	Adj. p-value
BP	GO:0009607	response to biotic stimulus	0.015
	GO:0006749	glutathione metabolic process	0.020
	GO:0006833	water transport	0.062
	GO:0050832	defense response to fungus	0.076
MF	GO:0004364	glutathione transferase activity	0.011
	GO:0015250	water channel activity	0.013

Supplementary Table 37: GO term enrichment (filtered results) Leaf - Preflowering - Cluster 11 - Defense

3.2.8 Leaf - Preflowering - Cluster 12 - Photosynthesis - light antenna



Overview
Cluster 12: Photosynthesis - light antenna
Number of genes: 1936
Number of "good" genes: 1295

Pathway	Adj. p-value
Metabolic pathways	0.000
Biosynthesis of secondary metabolites	0.000
Porphyrin and chlorophyll metabolism	0.000
Aminoacyl-tRNA biosynthesis	0.001
Carbon fixation in photosynthetic organisms	0.002
Oxidative phosphorylation	0.004
Phenylalanine, tyrosine and tryptophan biosynt...	0.005
Biosynthesis of amino acids	0.013
Carbon metabolism	0.034
Nitrogen metabolism	0.043

Supplementary Table 38: KEGG pathway enrichment - Leaf - Preflowering - Cluster 12 - Photosynthesis - light antenna

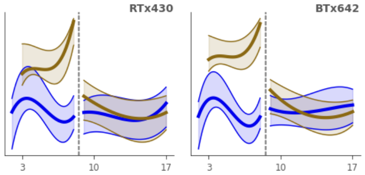
TF family	No. in cluster	Total number	Percentage
BBRBPC	1	5	20.00
ND	1	6	16.67
MYB	10	86	11.63
C2C2dof	2	39	5.13
AP2EREBP	5	130	3.85
C2H2	1	38	2.63

Supplementary Table 39: Motif enrichment Leaf - Preflowering - Cluster 12 - Photosynthesis - light antenna

GO type	GO ID	Description	Adj. p-value
BP	GO:0019684	photosynthesis, light reaction	0.000
	GO:0008610	lipid biosynthetic process	0.000
	GO:0022900	electron transport chain	0.000
	GO:0044255	cellular lipid metabolic process	0.000
	GO:0006629	lipid metabolic process	0.000
	GO:0006631	fatty acid metabolic process	0.000
	GO:0071555	cell wall organization	0.000
	GO:0015994	chlorophyll metabolic process	0.000
	GO:0010109	regulation of photosynthesis	0.002
	GO:0035336	long-chain fatty-acyl-CoA metabolic proc...	0.004
	GO:0042214	terpene metabolic process	0.004
	GO:0044550	secondary metabolite biosynthetic proces...	0.008
	GO:0010143	cutin biosynthetic process	0.009
	GO:0010345	suberin biosynthetic process	0.027
	GO:0034599	cellular response to oxidative stress	0.028
	GO:0009642	response to light intensity	0.028
	GO:1901607	alpha-amino acid biosynthetic process	0.029
	GO:0009628	response to abiotic stimulus	0.033
	GO:0104004	cellular response to environmental stimu...	0.049
	GO:0071214	cellular response to abiotic stimulus	0.049
	GO:0072593	reactive oxygen species metabolic proces...	0.089
MF	GO:0016491	oxidoreductase activity	0.000
	GO:0031072	heat shock protein binding	0.009

Supplementary Table 41: GO term enrichment (filtered results) Leaf - Preflowering - Cluster 12 - Photosynthesis - light antenna

3.2.9 Leaf - Preflowering - Cluster 13 - stress



Overview
Cluster 13: stress
Number of genes: 777
Number of "good" genes: 163
Description Many GO terms related to stress (response to abiotic stimulus, cellular response to oxidative stress, response to temperature stimulus)

Pathway	Adj. p-value
Metabolic pathways	0.028
Carbon metabolism	0.038

Supplementary Table 42: KEGG pathway enrichment - Leaf - Preflowering - Cluster 13 - stress

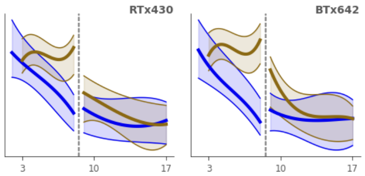
TF family	No. in cluster	Total number	Percentage
PLATZ	1	1	100.00
bHLH	11	25	44.00
C2C2COlike	1	3	33.33
C2C2gata	3	18	16.67
ND	1	6	16.67
bZIP	4	51	7.84
Homeobox	1	22	4.55
NAC	1	86	1.16
AP2EREBP	1	130	0.77

Supplementary Table 43: Motif enrichment Leaf - Preflowering - Cluster 13 - stress

GO type	GO ID	Description	Adj. p-value
BP	GO:0015979	photosynthesis	0.003
	GO:0003006	developmental process involved in reprod...	0.004
	GO:0009628	response to abiotic stimulus	0.007
	GO:0040029	regulation of gene expression, epigeneti...	0.026
	GO:0104004	cellular response to environmental stimu...	0.026
	GO:0071214	cellular response to abiotic stimulus	0.026
	GO:0009790	embryo development	0.029
	GO:0008652	cellular amino acid biosynthetic process	0.029
	GO:0048608	reproductive structure development	0.031
	GO:1901607	alpha-amino acid biosynthetic process	0.034
	GO:0009791	post-embryonic development	0.037
	GO:0009735	response to cytokinin	0.040
	GO:0034599	cellular response to oxidative stress	0.046
	GO:0016458	gene silencing	0.059
	GO:0048868	pollen tube development	0.090
	GO:0048316	seed development	0.094

Supplementary Table 45: GO term enrichment (filtered results) Leaf - Preflowering - Cluster 13 - stress

3.2.10 Leaf - Preflowering - Cluster 15 - Cell wall organization, aromatic acids



Overview
Cluster 15: Cell wall organization, aromatic acids
Number of genes: 1212
Number of "good" genes: 466

Pathway	Adj. p-value
Metabolic pathways	0.000
Biosynthesis of secondary metabolites	0.000
Biosynthesis of amino acids	0.032

Supplementary Table 46: KEGG pathway enrichment - Leaf - Preflowering - Cluster 15 - Cell wall organization, aromatic acids

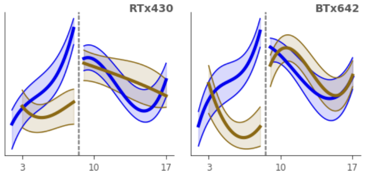
TF family	No. in cluster	Total number	Percentage
ZFHD	1	11	9.09

Supplementary Table 47: Motif enrichment Leaf - Preflowering - Cluster 15 - Cell wall organization, aromatic acids

GO type	GO ID	Description	Adj. p-value
BP	GO:0008610	lipid biosynthetic process	0.000
	GO:0006629	lipid metabolic process	0.000
	GO:0006631	fatty acid metabolic process	0.000
	GO:0009073	aromatic amino acid family biosynthetic ...	0.000
	GO:0071555	cell wall organization	0.000
	GO:0008652	cellular amino acid biosynthetic process	0.001
	GO:0042546	cell wall biogenesis	0.002
	GO:0009642	response to light intensity	0.002
	GO:0009832	plant-type cell wall biogenesis	0.003
	GO:0044550	secondary metabolite biosynthetic proces...	0.004
	GO:0009628	response to abiotic stimulus	0.005
	GO:0035336	long-chain fatty-acyl-CoA metabolic proc...	0.006
	GO:0010345	suberin biosynthetic process	0.010
	GO:0034599	cellular response to oxidative stress	0.011
	GO:1901607	alpha-amino acid biosynthetic process	0.032
	GO:0034614	cellular response to reactive oxygen spe...	0.046
	GO:0010143	cutin biosynthetic process	0.061
	GO:0104004	cellular response to environmental stimu...	0.066
	GO:0071214	cellular response to abiotic stimulus	0.066
	GO:0003006	developmental process involved in reprod...	0.098
CC	GO:0009523	photosystem II	0.000
MF	GO:0016787	hydrolase activity	0.000
	GO:0016491	oxidoreductase activity	0.000

Supplementary Table 49: GO term enrichment (filtered results) Leaf - Preflowering - Cluster 15 - Cell wall organization, aromatic acids

3.2.11 Leaf - Preflowering - Cluster 16 - Defense



Overview
Cluster 16: Defense
Number of genes: 500
Number of "good" genes: 99

Pathway	Adj. p-value
Plant-pathogen interaction	0.000

Supplementary Table 50: KEGG pathway enrichment - Leaf - Preflowering - Cluster 16 - Defense

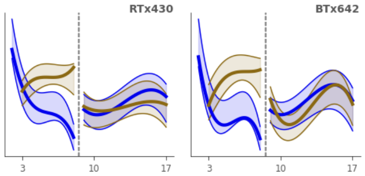
TF family	No. in cluster	Total number	Percentage
FAR1	1	2	50.00
bHLH	1	25	4.00
AP2EREBP	4	130	3.08
MYB	1	86	1.16

Supplementary Table 51: Motif enrichment Leaf - Preflowering - Cluster 16 - Defense

GO type	GO ID	Description	Adj. p-value
BP	GO:0009607	response to biotic stimulus	0.004
	GO:0050832	defense response to fungus	0.008
	GO:0031347	regulation of defense response	0.026
	GO:0006950	response to stress	0.052

Supplementary Table 53: GO term enrichment (filtered results) Leaf - Preflowering - Cluster 16 - Defense

3.2.12 Leaf - Preflowering - Cluster 19 - secondary metabolites



Overview
Cluster 19: secondary metabolites
Number of genes: 1020
Number of "good" genes: 63

Pathway	Adj. p-value
Metabolic pathways	0.015

Supplementary Table 54: KEGG pathway enrichment - Leaf - Preflowering - Cluster 19 - secondary metabolites

No motif found enriched

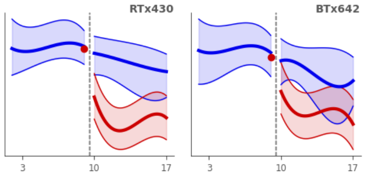
Supplementary Table 55: Motif enrichment Leaf - Preflowering - Cluster 19 - secondary metabolites

GO type	GO ID	Description	Adj. p-value
BP	GO:0006396	RNA processing	0.055
MF	GO:0016787	hydrolase activity	0.000

Supplementary Table 57: GO term enrichment (filtered results) Leaf - Preflowering - Cluster 19 - secondary metabolites

3.3 Leaf Postflowering clusters

3.3.1 Leaf - Postflowering - Cluster 1 - Photosynthesis light reaction



Overview
Cluster 1: Photosynthesis light reaction
Number of genes: 1856
Number of “good” genes: 756

Pathway	Adj. p-value
DNA replication	0.000
Metabolic pathways	0.000

Supplementary Table 58: KEGG pathway enrichment - Leaf - Postflowering - Cluster 1 - Photosynthesis light reaction

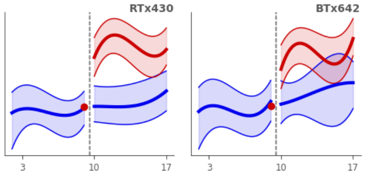
TF family	No. in cluster	Total number	Percentage
Homeobox	4	22	18.18
bHLH	3	25	12.00
HB	1	16	6.25
TCP	1	23	4.35

Supplementary Table 59: Motif enrichment Leaf - Postflowering - Cluster 1 - Photosynthesis light reaction

GO type	GO ID	Description	Adj. p-value
BP	GO:0019684	photosynthesis, light reaction	0.000
	GO:0006631	fatty acid metabolic process	0.005
	GO:0042546	cell wall biogenesis	0.008
	GO:0022900	electron transport chain	0.011
	GO:0104004	cellular response to environmental stimu...	0.026
	GO:0071214	cellular response to abiotic stimulus	0.026
	GO:0009888	tissue development	0.033
	GO:0009832	plant-type cell wall biogenesis	0.034
	GO:0015995	chlorophyll biosynthetic process	0.036
	GO:0006270	DNA replication initiation	0.049
	GO:0016116	carotenoid metabolic process	0.066
	GO:0009607	response to biotic stimulus	0.066
	GO:0009733	response to auxin	0.072

Supplementary Table 61: GO term enrichment (filtered results) Leaf - Postflowering - Cluster 1 - Photosynthesis light reaction

3.3.2 Leaf - Postflowering - Cluster 2 - Response to ROS



Overview
Cluster 2: Response to ROS
Number of genes: 1901
Number of “good” genes: 834

Pathway	Adj. p-value
Metabolic pathways	0.000
Carbon metabolism	0.000
Glyoxylate and dicarboxylate metabolism	0.001
Biosynthesis of secondary metabolites	0.004
Valine, leucine and isoleucine degradation	0.011
Ubiquinone and other terpenoid-quinone biosynt...	0.012
Biosynthesis of amino acids	0.017
Pyruvate metabolism	0.034
Galactose metabolism	0.036

Supplementary Table 62: KEGG pathway enrichment - Leaf - Postflowering - Cluster 2 - Response to ROS

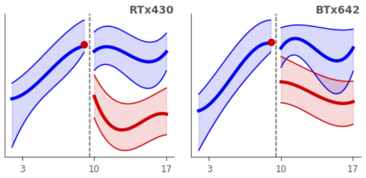
TF family	No. in cluster	Total number	Percentage
S1Falike	1	1	100.00
AP2EREBP	69	130	53.08
HMG	1	2	50.00
Orphan	1	3	33.33
LOBAS2	4	13	30.77
HSF	4	16	25.00
TCP	3	23	13.04
bZIP	6	51	11.76
C3H	1	10	10.00
NAC	3	86	3.49
MYB	2	86	2.33

Supplementary Table 63: Motif enrichment Leaf - Postflowering - Cluster 2 - Response to ROS

GO type	GO ID	Description	Adj. p-value
BP	GO:0000302	response to reactive oxygen species	0.092

Supplementary Table 65: GO term enrichment (filtered results) Leaf - Postflowering - Cluster 2 - Response to ROS

3.3.3 Leaf - Postflowering - Cluster 3 - Defense-post



Overview
Cluster 3: Defense-post
Number of genes: 1591
Number of "good" genes: 550
Description Strong enrichment in many response to biotic stimulus and defense GO terms. Contains members of the WRKY and GRAS Transcription Factor family

No pathways found enriched

Supplementary Table 66: KEGG pathway enrichment - Leaf - Postflowering - Cluster 3 - Defense-post

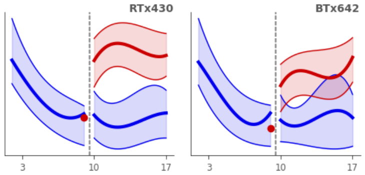
No motif found enriched

Supplementary Table 67: Motif enrichment Leaf - Postflowering - Cluster 3 - Defense-post

GO type	GO ID	Description	Adj. p-value
BP	GO:0009607	response to biotic stimulus	0.000
	GO:0009867	jasmonic acid mediated signaling pathway	0.000
	GO:0031347	regulation of defense response	0.002
	GO:0042742	defense response to bacterium	0.003
	GO:0009620	response to fungus	0.004
	GO:0009751	response to salicylic acid	0.010
	GO:0002376	immune system process	0.012
	GO:0006955	immune response	0.016
	GO:0050832	defense response to fungus	0.018
	GO:0009812	flavonoid metabolic process	0.030
	GO:0009813	flavonoid biosynthetic process	0.039
	GO:0060548	negative regulation of cell death	0.059

Supplementary Table 69: GO term enrichment (filtered results) Leaf - Postflowering - Cluster 3 - Defense-post

3.3.4 Leaf - Postflowering - Cluster 4 - Oxidative phosphorylation



Overview
Cluster 4: Oxidative phosphorylation
Number of genes: 1478
Number of “good” genes: 408
Description Enrichment in oxidation-reduction process, oxidoreductase activity, electron transport chain.

Pathway	Adj. p-value
Metabolic pathways	0.000
Oxidative phosphorylation	0.002
Biosynthesis of amino acids	0.039

Supplementary Table 70: KEGG pathway enrichment - Leaf - Postflowering - Cluster 4 - Oxidative phosphorylation

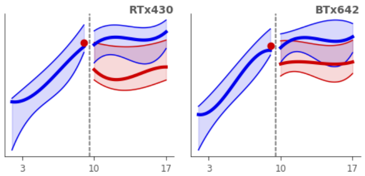
TF family	No. in cluster	Total number	Percentage
ARF	1	3	33.33
ABI3VP1	1	9	11.11
WRKY	6	60	10.00
ZFHD	1	11	9.09
Homeobox	1	22	4.55
MYB	2	86	2.33

Supplementary Table 71: Motif enrichment Leaf - Postflowering - Cluster 4 - Oxidative phosphorylation

GO type	GO ID	Description	Adj. p-value
BP	GO:0009628	response to abiotic stimulus	0.005
	GO:0022900	electron transport chain	0.013
	GO:0008652	cellular amino acid biosynthetic process	0.024
	GO:1901607	alpha-amino acid biosynthetic process	0.027
MF	GO:0016491	oxidoreductase activity	0.000

Supplementary Table 73: GO term enrichment (filtered results) Leaf - Postflowering - Cluster 4 - Oxidative phosphorylation

3.3.5 Leaf - Postflowering - Cluster 6 - Defense-post-2



Overview
Cluster 6: Defense-post-2
Number of genes: 2415
Number of "good" genes: 1196

Pathway	Adj. p-value
N-Glycan biosynthesis	0.000
Protein processing in endoplasmic reticulum	0.001

Supplementary Table 74: KEGG pathway enrichment - Leaf - Postflowering - Cluster 6 - Defense-post-2

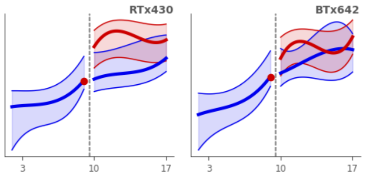
	No. in cluster	Total number	Percentage
TF family			
ZFHD	5	11	45.45
E2FDP	1	7	14.29
G2like	1	29	3.45
C2H2	1	38	2.63
bZIP	1	51	1.96

Supplementary Table 75: Motif enrichment Leaf - Postflowering - Cluster 6 - Defense-post-2

		Description	Adj. p-value
GO type	GO ID		
BP	GO:0006749	glutathione metabolic process	0.025
	GO:0009607	response to biotic stimulus	0.026
	GO:0009867	jasmonic acid mediated signaling pathway	0.079
MF	GO:0004364	glutathione transferase activity	0.014
	GO:0015250	water channel activity	0.045

Supplementary Table 77: GO term enrichment (filtered results) Leaf - Postflowering - Cluster 6 - Defense-post-2

3.3.6 Leaf - Postflowering - Cluster 8 - Glutathione



Overview
Cluster 8: Glutathione
Number of genes: 4197
Number of "good" genes: 2228

Pathway	Adj. p-value
Spliceosome	0.000
Ribosome	0.000
Basal transcription factors	0.021

Supplementary Table 78: KEGG pathway enrichment - Leaf - Postflowering - Cluster 8 - Glutathione

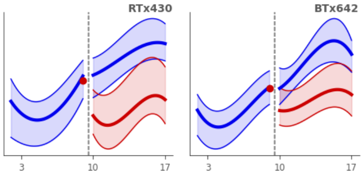
	No. in cluster	Total number	Percentage
TF family			
CPP	7	7	100.00
REM	2	2	100.00
ABI3VP1	3	9	33.33
Orphan	1	3	33.33
MYBrelated	15	47	31.91
C2C2dof	12	39	30.77
ND	1	6	16.67
C2H2	3	38	7.89
Trihelix	1	21	4.76

Supplementary Table 79: Motif enrichment Leaf - Postflowering - Cluster 8 - Glutathione

		Description	Adj. p-value
GO type	GO ID		
BP	GO:0006749	glutathione metabolic process	0.009
MF	GO:0004364	glutathione transferase activity	0.085

Supplementary Table 81: GO term enrichment (filtered results) Leaf - Postflowering - Cluster 8 - Glutathione

3.3.7 Leaf - Postflowering - Cluster 10 - Biosynthesis of secondary metabolites



Overview
Cluster 10: Biosynthesis of secondary metabolites
Number of genes: 1069
Number of "good" genes: 296

Pathway	Adj. p-value
Metabolic pathways	0.002

Supplementary Table 82: KEGG pathway enrichment - Leaf - Postflowering - Cluster 10 - Biosynthesis of secondary metabolites

TF family	No. in cluster	Total number	Percentage
WRKY	1	60	1.67

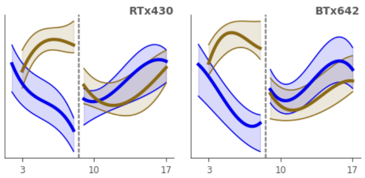
Supplementary Table 83: Motif enrichment Leaf - Postflowering - Cluster 10 - Biosynthesis of secondary metabolites

GO type	GO ID	Description	Adj. p-value
BP	GO:0044550	secondary metabolite biosynthetic proces...	0.014
	GO:0006820	anion transport	0.051
MF	GO:0016491	oxidoreductase activity	0.004
	GO:0010427	abscisic acid binding	0.035

Supplementary Table 85: GO term enrichment (filtered results) Leaf - Postflowering - Cluster 10 - Biosynthesis of secondary metabolites

3.4 Root Preflowering clusters

3.4.1 Root - Preflowering - Cluster 1 - Development



Overview
Cluster 1: Development
Number of genes: 1402
Number of "good" genes: 510

Pathway	Adj. p-value
Ribosome biogenesis in eukaryotes	0.006
Nucleotide excision repair	0.031

Supplementary Table 86: KEGG pathway enrichment - Root - Preflowering - Cluster 1 - Development

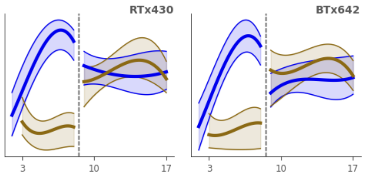
TF family	No. in cluster	Total number	Percentage
HMG	1	2	50.00
REM	1	2	50.00
ABI3VP1	4	9	44.44
CPP	3	7	42.86
C2C2dof	8	39	20.51
BBRBPC	1	5	20.00
TCP	4	23	17.39
LOBAS2	2	13	15.38
E2FDP	1	7	14.29
C2H2	3	38	7.89
AP2EREBP	8	130	6.15
Trihelix	1	21	4.76
MYB	1	86	1.16

Supplementary Table 87: Motif enrichment Root - Preflowering - Cluster 1 - Development

GO type	GO ID	Description	Adj. p-value
BP	GO:0003006	developmental process involved in reprod...	0.000
	GO:0009791	post-embryonic development	0.000
	GO:0048608	reproductive structure development	0.000
	GO:0016458	gene silencing	0.000
	GO:0048731	system development	0.000
	GO:0009790	embryo development	0.000
	GO:0010608	posttranscriptional regulation of gene e...	0.000
	GO:0050793	regulation of developmental process	0.000
	GO:0048869	cellular developmental process	0.000
	GO:0009908	flower development	0.000
	GO:0006342	chromatin silencing	0.000
	GO:0048868	pollen tube development	0.010
	GO:0104004	cellular response to environmental stimu...	0.028
	GO:0071214	cellular response to abiotic stimulus	0.028
	GO:0009642	response to light intensity	0.033
	GO:0042542	response to hydrogen peroxide	0.034
	GO:0000302	response to reactive oxygen species	0.041
	GO:0006950	response to stress	0.055
	GO:0034614	cellular response to reactive oxygen spe...	0.055

Supplementary Table 89: GO term enrichment (filtered results) Root - Preflowering - Cluster 1 - Development

3.4.2 Root - Preflowering - Cluster 2 - Defense, amino acid



Overview
Cluster 2: Defense, amino acid
Number of genes: 526
Number of "good" genes: 350

Pathway	Adj. p-value
Metabolic pathways	0.000
Biosynthesis of secondary metabolites	0.000

Supplementary Table 90: KEGG pathway enrichment - Root - Preflowering - Cluster 2 - Defense, amino acid

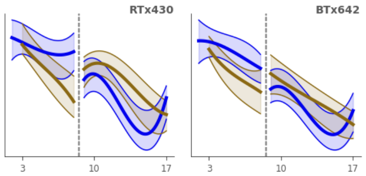
TF family	No. in cluster	Total number	Percentage
SBP	2	13	15.38
WRKY	7	60	11.67
ABI3VP1	1	9	11.11
MYB	3	86	3.49
AP2EREBP	1	130	0.77

Supplementary Table 91: Motif enrichment Root - Preflowering - Cluster 2 - Defense, amino acid

GO type	GO ID	Description	Adj. p-value
BP	GO:0009753	response to jasmonic acid	0.000
	GO:0006820	anion transport	0.007
	GO:0009607	response to biotic stimulus	0.007
	GO:0009073	aromatic amino acid family biosynthetic ...	0.009
	GO:0009751	response to salicylic acid	0.010

Supplementary Table 93: GO term enrichment (filtered results) Root - Preflowering - Cluster 2 - Defense, amino acid

3.4.3 Root - Preflowering - Cluster 3 - Cell wall



Overview
Cluster 3: Cell wall
Number of genes: 956
Number of "good" genes: 655

Pathway	Adj. p-value
Metabolic pathways	0.000
Biosynthesis of secondary metabolites	0.005
Amino sugar and nucleotide sugar metabolism	0.007
Flavonoid biosynthesis	0.038

Supplementary Table 94: KEGG pathway enrichment - Root - Preflowering - Cluster 3 - Cell wall

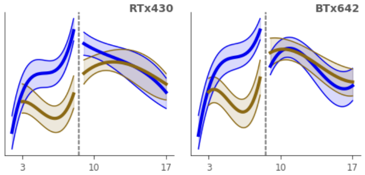
TF family	No. in cluster	Total number	Percentage
HMG	2	2	100.00
NLP	1	1	100.00
mTERF	1	1	100.00
AP2EREBP	61	130	46.92
MYB	23	86	26.74
LOBAS2	3	13	23.08
C2C2gata	1	18	5.56
bHLH	1	25	4.00
C2H2	1	38	2.63
NAC	2	86	2.33

Supplementary Table 95: Motif enrichment Root - Preflowering - Cluster 3 - Cell wall

GO type	GO ID	Description	Adj. p-value
BP	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0006631	fatty acid metabolic process	0.000
	GO:0048868	pollen tube development	0.000
	GO:0006979	response to oxidative stress	0.000
	GO:0006833	water transport	0.002
	GO:0044550	secondary metabolite biosynthetic proces...	0.003
	GO:0042545	cell wall modification	0.004
	GO:0044255	cellular lipid metabolic process	0.005
	GO:0006270	DNA replication initiation	0.011
	GO:0008610	lipid biosynthetic process	0.022
	GO:0071470	cellular response to osmotic stress	0.030
	GO:0010345	suberin biosynthetic process	0.040
	GO:0009741	response to brassinosteroid	0.067
MF	GO:0015250	water channel activity	0.001

Supplementary Table 97: GO term enrichment (filtered results) Root - Preflowering - Cluster 3 - Cell wall

3.4.4 Root - Preflowering - Cluster 4 - Defense



Overview
Cluster 4: Defense
Number of genes: 802
Number of "good" genes: 505
Description Enriched in many motifs from the AP2-EREBP TF family

Pathway	Adj. p-value
Plant hormone signal transduction	0.009
Plant-pathogen interaction	0.017

Supplementary Table 98: KEGG pathway enrichment - Root - Preflowering - Cluster 4 - Defense

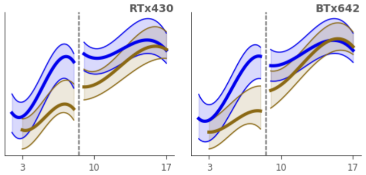
TF family	No. in cluster	Total number	Percentage
CAMTA	2	2	100.00
FAR1	2	2	100.00
HMG	2	2	100.00
mTERF	1	1	100.00
AP2EREBP	70	130	53.85
LOBAS2	5	13	38.46
Trihelix	3	21	14.29
TCP	1	23	4.35
bHLH	1	25	4.00
MYB	3	86	3.49
NAC	2	86	2.33

Supplementary Table 99: Motif enrichment Root - Preflowering - Cluster 4 - Defense

GO type	GO ID	Description	Adj. p-value
BP	GO:0009753	response to jasmonic acid	0.000
	GO:0009751	response to salicylic acid	0.000
	GO:0009867	jasmonic acid mediated signaling pathway	0.000
	GO:0010468	regulation of gene expression	0.004
	GO:0031347	regulation of defense response	0.005
	GO:0009620	response to fungus	0.019
	GO:0050832	defense response to fungus	0.030
MF	GO:0016491	oxidoreductase activity	0.007

Supplementary Table 101: GO term enrichment (filtered results) Root - Preflowering - Cluster 4 - Defense

3.4.5 Root - Preflowering - Cluster 6 - Lipid and cell wall biogenesis



Overview
Cluster 6: Lipid and cell wall biogenesis
Number of genes: 1642
Number of "good" genes: 1384

Pathway	Adj. p-value
Metabolic pathways	0.023
Phenylalanine, tyrosine and tryptophan biosynt...	0.048

Supplementary Table 102: KEGG pathway enrichment - Root - Preflowering - Cluster 6 - Lipid and cell wall biogenesis

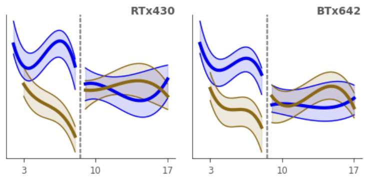
TF family	No. in cluster	Total number	Percentage
ARID	1	6	16.67
ND	1	6	16.67
ABI3VP1	1	9	11.11
ZFHD	1	11	9.09
Homeobox	1	22	4.55
C2H2	1	38	2.63
C2C2dof	1	39	2.56

Supplementary Table 103: Motif enrichment Root - Preflowering - Cluster 6 - Lipid and cell wall biogenesis

GO type	GO ID	Description	Adj. p-value
BP	GO:0006749	glutathione metabolic process	0.045
	GO:0006820	anion transport	0.049
MF	GO:0004364	glutathione transferase activity	0.022
	GO:0010427	abscisic acid binding	0.071

Supplementary Table 105: GO term enrichment (filtered results) Root - Preflowering - Cluster 6 - Lipid and cell wall biogenesis

3.4.6 Root - Preflowering - Cluster 8 - Lipid, suberin and secondary metabolite biosynthesis



Overview
Cluster 8: Lipid, suberin and secondary metabolite biosynthesis
Number of genes: 1108
Number of "good" genes: 501

Pathway	Adj. p-value
Metabolic pathways	0.000
Proteasome	0.000
Carbon metabolism	0.000
Biosynthesis of amino acids	0.000
Citrate cycle (TCA cycle)	0.003
Oxidative phosphorylation	0.006
Biosynthesis of secondary metabolites	0.007
Phenylalanine, tyrosine and tryptophan biosynt...	0.009
Cutin, suberine and wax biosynthesis	0.009

Supplementary Table 106: KEGG pathway enrichment - Root - Preflowering - Cluster 8 - Lipid, suberin and secondary metabolite biosynthesis

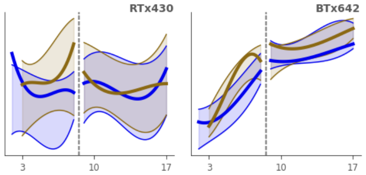
TF family	No. in cluster	Total number	Percentage
REM	2	2	100.00
MYB	10	86	11.63
ABI3VP1	1	9	11.11
C2C2dof	1	39	2.56

Supplementary Table 107: Motif enrichment Root - Preflowering - Cluster 8 - Lipid, suberin and secondary metabolite biosynthesis

GO type	GO ID	Description	Adj. p-value
BP	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0044550	secondary metabolite biosynthetic proces...	0.000
	GO:0006270	DNA replication initiation	0.004
	GO:0006833	water transport	0.006
	GO:0008610	lipid biosynthetic process	0.016
	GO:0010345	suberin biosynthetic process	0.016
	GO:0040007	growth	0.094
MF	GO:0016491	oxidoreductase activity	0.000
	GO:0004364	glutathione transferase activity	0.017

Supplementary Table 109: GO term enrichment (filtered results) Root - Preflowering - Cluster 8 - Lipid, suberin and secondary metabolite biosynthesis

3.4.7 Root - Preflowering - Cluster 9 - BTx642



Overview
Cluster 9: BTx642
Number of genes: 294
Number of “good” genes: 37
Description Enriched in C2C2dof

No pathways found enriched

Supplementary Table 110: KEGG pathway enrichment - Root - Preflowering - Cluster 9 - BTx642

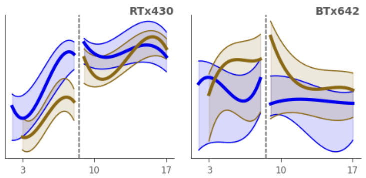
TF family	No. in cluster	Total number	Percentage
FAR1	2	2	100.00
C2C2COlike	2	3	66.67
bZIP	23	51	45.10
C2C2dof	16	39	41.03
TCP	8	23	34.78
Orphan	1	3	33.33
LOBAS2	3	13	23.08
C3H	2	10	20.00
Trihelix	4	21	19.05
BZR	1	7	14.29
ABI3VP1	1	9	11.11
bHLH	2	25	8.00
C2H2	3	38	7.89
NAC	3	86	3.49
AP2EREBP	3	130	2.31
MYB	1	86	1.16

Supplementary Table 111: Motif enrichment Root - Preflowering - Cluster 9 - BTx642

GO type	GO ID	Description	Adj. p-value
BP	GO:0006396	RNA processing	0.000
	GO:0006351	transcription, DNA-templated	0.000
	GO:0009812	flavonoid metabolic process	0.006
	GO:0050793	regulation of developmental process	0.069

Supplementary Table 113: GO term enrichment (filtered results) Root - Preflowering - Cluster 9 - BTx642

3.4.8 Root - Preflowering - Cluster 10 - RTx430



Overview
Cluster 10: RTx430
Number of genes: 220
Number of "good" genes: 21

No pathways found enriched

Supplementary Table 114: KEGG pathway enrichment - Root - Preflowering - Cluster 10 - RTx430

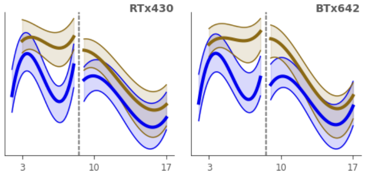
TF family	No. in cluster	Total number	Percentage
bZIP	1	51	1.96

Supplementary Table 115: Motif enrichment Root - Preflowering - Cluster 10 - RTx430

GO type	GO ID	Description	Adj. p-value
BP	GO:0010468	regulation of gene expression	0.007
	GO:0006351	transcription, DNA-templated	0.018
	GO:0006749	glutathione metabolic process	0.020
	GO:0044550	secondary metabolite biosynthetic proces...	0.023
	GO:0042742	defense response to bacterium	0.088
	GO:0009607	response to biotic stimulus	0.090
MF	GO:0004364	glutathione transferase activity	0.003

Supplementary Table 117: GO term enrichment (filtered results) Root - Preflowering - Cluster 10 - RTx430

3.4.9 Root - Preflowering - Cluster 11 - Stress



Overview
Cluster 11: Stress
Number of genes: 774
Number of "good" genes: 377
Description Enriched in response to water deprivation, and many motif from the AP2-EREBP transcription factor family

Pathway	Adj. p-value
Phosphatidylinositol signaling system	0.012
Protein processing in endoplasmic reticulum	0.044

Supplementary Table 118: KEGG pathway enrichment - Root - Preflowering - Cluster 11 - Stress

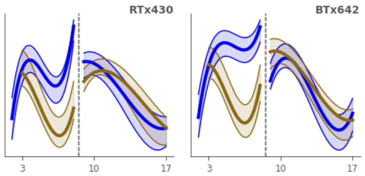
TF family	No. in cluster	Total number	Percentage
CAMTA	2	2	100.00
mTERF	1	1	100.00
FAR1	1	2	50.00
LOBAS2	3	13	23.08
AP2EREBP	25	130	19.23
E2FDP	1	7	14.29
MYBrelated	5	47	10.64
HSF	1	16	6.25
Trihelix	1	21	4.76
TCP	1	23	4.35
MYB	3	86	3.49
bZIP	1	51	1.96
NAC	1	86	1.16

Supplementary Table 119: Motif enrichment Root - Preflowering - Cluster 11 - Stress

GO type	GO ID	Description	Adj. p-value
BP	GO:0048868	pollen tube development	0.000
	GO:0009790	embryo development	0.000
	GO:0009791	post-embryonic development	0.002
	GO:0040029	regulation of gene expression, epigeneti...	0.003
	GO:0006979	response to oxidative stress	0.004
	GO:0048731	system development	0.007
	GO:0050793	regulation of developmental process	0.007
	GO:0009415	response to water	0.007
	GO:0009414	response to water deprivation	0.010
	GO:0009642	response to light intensity	0.013
	GO:0044255	cellular lipid metabolic process	0.018
	GO:0009888	tissue development	0.020
	GO:0048608	reproductive structure development	0.020
	GO:0009737	response to abscisic acid	0.024
	GO:0000302	response to reactive oxygen species	0.032
	GO:0071470	cellular response to osmotic stress	0.035
	GO:0104004	cellular response to environmental stimu...	0.047
	GO:0071214	cellular response to abiotic stimulus	0.047
	GO:0006631	fatty acid metabolic process	0.049
	GO:0006950	response to stress	0.051
	GO:0034614	cellular response to reactive oxygen spe...	0.053
	GO:0006833	water transport	0.059
	GO:0009741	response to brassinosteroid	0.064
MF	GO:0015250	water channel activity	0.040

Supplementary Table 121: GO term enrichment (filtered results) Root - Preflowering - Cluster 11 - Stress

3.4.10 Root - Preflowering - Cluster 12 - Defense response



Overview
Cluster 12: Defense response
Number of genes: 1188
Number of "good" genes: 725
Description Contains 8 DREB1 genes.

Pathway	Adj. p-value
Plant-pathogen interaction	0.036
Amino sugar and nucleotide sugar metabolism	0.036

Supplementary Table 122: KEGG pathway enrichment - Root - Preflowering - Cluster 12 - Defense response

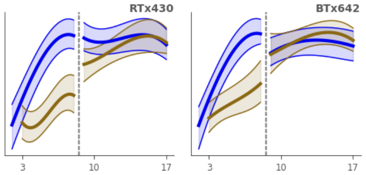
TF family	No. in cluster	Total number	Percentage
mTERF	1	1	100.00
FAR1	2	2	100.00
BZR	7	7	100.00
NLP	1	1	100.00
BES1	2	2	100.00
HMG	2	2	100.00
CAMTA	2	2	100.00
AP2EREBP	96	130	73.85
bHLH	15	25	60.00
LOBAS2	6	13	46.15
E2FDP	2	7	28.57
TCP	6	23	26.09
Trihelix	4	21	19.05
bZIP	7	51	13.73
MYB	9	86	10.47
C3H	1	10	10.00
C2C2gata	1	18	5.56
NAC	4	86	4.65
C2H2	1	38	2.63
MYBrelated	1	47	2.13

Supplementary Table 123: Motif enrichment Root - Preflowering - Cluster 12 - Defense response

GO type	GO ID	Description	Adj. p-value
BP	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0009753	response to jasmonic acid	0.000
	GO:0009867	jasmonic acid mediated signaling pathway	0.000
	GO:0009414	response to water deprivation	0.001
	GO:0009620	response to fungus	0.002
	GO:0006950	response to stress	0.002
	GO:0010345	suberin biosynthetic process	0.005
	GO:0031347	regulation of defense response	0.009
	GO:0006631	fatty acid metabolic process	0.009
	GO:0009695	jasmonic acid biosynthetic process	0.012
	GO:0010143	cutin biosynthetic process	0.015
	GO:0006820	anion transport	0.036
	GO:0009751	response to salicylic acid	0.037
	GO:0042545	cell wall modification	0.041
	GO:0050832	defense response to fungus	0.051
	GO:0006351	transcription, DNA-templated	0.080
CC	GO:0009523	photosystem II	0.096
MF	GO:0016491	oxidoreductase activity	0.000

Supplementary Table 125: GO term enrichment (filtered results) Root - Preflowering - Cluster 12 - Defense response

3.4.11 Root - Preflowering - Cluster 13 - Defense response



Overview
Cluster 13: Defense response
Number of genes: 1061
Number of "good" genes: 920
Description Contains many transcription factors and many motifs from the WRKY family

Pathway	Adj. p-value
Biosynthesis of secondary metabolites	0.002
Tyrosine metabolism	0.003
Metabolic pathways	0.003
Plant hormone signal transduction	0.046

Supplementary Table 126: KEGG pathway enrichment - Root - Preflowering - Cluster 13 - Defense response

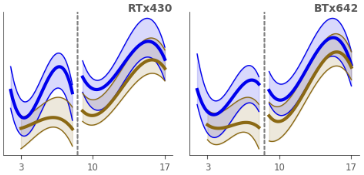
TF family	No. in cluster	Total number	Percentage
zfGRF	1	1	100.00
WRKY	48	60	80.00
ABI3VP1	1	9	11.11
bZIP	4	51	7.84
NAC	2	86	2.33

Supplementary Table 127: Motif enrichment Root - Preflowering - Cluster 13 - Defense response

GO type	GO ID	Description	Adj. p-value
BP	GO:0009751	response to salicylic acid	0.000
	GO:0009753	response to jasmonic acid	0.002
	GO:0006749	glutathione metabolic process	0.005
	GO:0009867	jasmonic acid mediated signaling pathway	0.008
	GO:0044550	secondary metabolite biosynthetic proces...	0.013
	GO:0006820	anion transport	0.061
MF	GO:0004364	glutathione transferase activity	0.002
	GO:0010427	abscisic acid binding	0.052
	GO:0016491	oxidoreductase activity	0.077

Supplementary Table 129: GO term enrichment (filtered results) Root - Preflowering - Cluster 13 - Defense response

3.4.12 Root - Preflowering - Cluster 14 - C2C2dof



Overview
Cluster 14: C2C2dof
Number of genes: 1654
Number of "good" genes: 713

Pathway	Adj. p-value
Ribosome	0.000
Spliceosome	0.008

Supplementary Table 130: KEGG pathway enrichment - Root - Preflowering - Cluster 14 - C2C2dof

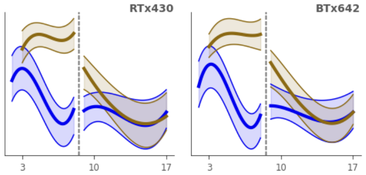
TF family	No. in cluster	Total number	Percentage
REM	2	2	100.00
C2C2YABBY	1	2	50.00
C2C2dof	15	39	38.46
C3H	2	10	20.00
ABI3VP1	1	9	11.11
TCP	1	23	4.35
NAC	2	86	2.33

Supplementary Table 131: Motif enrichment Root - Preflowering - Cluster 14 - C2C2dof

GO type	GO ID	Description	Adj. p-value
BP	GO:0006351	transcription, DNA-templated	0.010
	GO:0010468	regulation of gene expression	0.016
	GO:1901607	alpha-amino acid biosynthetic process	0.026
	GO:0008652	cellular amino acid biosynthetic process	0.057
	GO:0009073	aromatic amino acid family biosynthetic ...	0.077
MF	GO:0010427	abscisic acid binding	0.071
	GO:0004364	glutathione transferase activity	0.086

Supplementary Table 133: GO term enrichment (filtered results) Root - Preflowering - Cluster 14 - C2C2dof

3.4.13 Root - Preflowering - Cluster 15 - Stress



Overview
Cluster 15: Stress
Number of genes: 1426
Number of “good” genes: 1066
Description Enriched in motifs from the AP2/EREBP family

Pathway	Adj. p-value
Metabolic pathways	0.001

Supplementary Table 134: KEGG pathway enrichment - Root - Preflowering - Cluster 15 - Stress

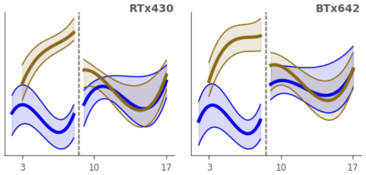
TF family	No. in cluster	Total number	Percentage
BSD	1	1.0	100.00
PLATZ	1	1.0	100.00
S1Falike	1	1.0	100.00
HSF	11	16.0	68.75
AP2EREBP	46	130.0	35.38
Orphan	1	3.0	33.33
CPP	2	7.0	28.57
Trihelix	4	21.0	19.05
ARID	1	6.0	16.67
ND	1	6.0	16.67
C2C2dof	4	39.0	10.26
C3H	1	10.0	10.00
bHLH	2	25.0	8.00
LOBAS2	1	13.0	7.69
TCP	1	23.0	4.35
MYBrelated	1	47.0	2.13
bZIP	1	51.0	1.96
NAC	1	86.0	1.16
ARF_ecoli	1	NaN	NaN

Supplementary Table 135: Motif enrichment Root - Preflowering - Cluster 15 - Stress

GO type	GO ID	Description	Adj. p-value
BP	GO:0003006	developmental process involved in reprod...	0.000
	GO:0009791	post-embryonic development	0.000
	GO:0040029	regulation of gene expression, epigeneti...	0.000
	GO:0006260	DNA replication	0.000
	GO:0048868	pollen tube development	0.000
	GO:0048608	reproductive structure development	0.000
	GO:0050793	regulation of developmental process	0.000
	GO:0042542	response to hydrogen peroxide	0.002
	GO:0006629	lipid metabolic process	0.003
	GO:0009888	tissue development	0.003
	GO:0006306	DNA methylation	0.004
	GO:0006342	chromatin silencing	0.005
	GO:0009642	response to light intensity	0.008
	GO:0044255	cellular lipid metabolic process	0.011
	GO:0000302	response to reactive oxygen species	0.020
	GO:0009741	response to brassinosteroid	0.021
	GO:0104004	cellular response to environmental stimu...	0.037
	GO:0071214	cellular response to abiotic stimulus	0.037
	GO:0009908	flower development	0.038
	GO:0009415	response to water	0.057
	GO:0010608	posttranscriptional regulation of gene e...	0.057
	GO:0006631	fatty acid metabolic process	0.068
	GO:0009414	response to water deprivation	0.073
	GO:0006979	response to oxidative stress	0.079
	GO:0006950	response to stress	0.083
MF	GO:0015250	water channel activity	0.074

Supplementary Table 137: GO term enrichment (filtered results) Root - Preflowering - Cluster 15 - Stress

3.4.14 Root - Preflowering - Cluster 16 - Stress and gene regulation



Overview

Cluster 16: Stress and gene regulation

Number of genes: 1683

Number of "good" genes: 952

Description Highly enriched in motfs from the C2C2-dof transcription factors family

Pathway	Adj. p-value
Spliceosome	0.000
Basal transcription factors	0.002
Ribosome biogenesis in eukaryotes	0.003
Aminoacyl-tRNA biosynthesis	0.006
Ubiquitin mediated proteolysis	0.011
RNA polymerase	0.014
Mismatch repair	0.017
Nucleotide excision repair	0.022

Supplementary Table 138: KEGG pathway enrichment - Root - Preflowering - Cluster 16 - Stress and gene regulation

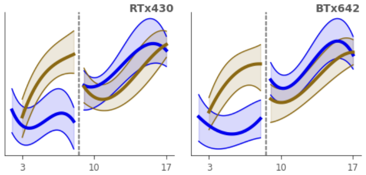
TF family	No. in cluster	Total number	Percentage
REM	2	2	100.00
C2C2dof	31	39	79.49
RAV	1	2	50.00
ARF	1	3	33.33
Orphan	1	3	33.33
ABI3VP1	2	9	22.22
CPP	1	7	14.29
C3H	1	10	10.00
MADS	1	14	7.14
MYBrelated	3	47	6.38
G2like	1	29	3.45
MYB	1	86	1.16
NAC	1	86	1.16

Supplementary Table 139: Motif enrichment Root - Preflowering - Cluster 16 - Stress and gene regulation

GO type	GO ID	Description	Adj. p-value
BP	GO:0040029	regulation of gene expression, epigeneti...	0.000
	GO:0003006	developmental process involved in reprod...	0.000
	GO:0009791	post-embryonic development	0.000
	GO:0010154	fruit development	0.000
	GO:0006306	DNA methylation	0.000
	GO:0006260	DNA replication	0.000
	GO:0009642	response to light intensity	0.000
	GO:0006342	chromatin silencing	0.001
	GO:0010468	regulation of gene expression	0.001
	GO:0043484	regulation of RNA splicing	0.002
	GO:0009908	flower development	0.002
	GO:0006950	response to stress	0.009
	GO:0009737	response to abscisic acid	0.012
	GO:0009414	response to water deprivation	0.032
	GO:0009415	response to water	0.035
MF	GO:0031072	heat shock protein binding	0.052

Supplementary Table 141: GO term enrichment (filtered results) Root - Preflowering - Cluster 16 - Stress and gene regulation

3.4.15 Root - Preflowering - Cluster 17 - Gene regulation



Overview
Cluster 17: Gene regulation
Number of genes: 2439
Number of "good" genes: 1412
Description Highly enriched in motfs from the C2C2-dof transcription factors family

Pathway	Adj. p-value
Spliceosome	0.000
RNA transport	0.010
Ribosome biogenesis in eukaryotes	0.013
Basal transcription factors	0.013
Nucleotide excision repair	0.022
Autophagy - other	0.022
Base excision repair	0.039

Supplementary Table 142: KEGG pathway enrichment - Root - Preflowering - Cluster 17 - Gene regulation

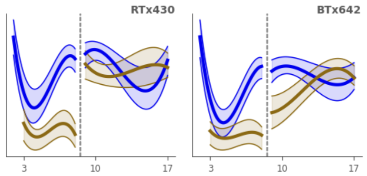
TF family	No. in cluster	Total number	Percentage
REM	2	2	100.00
C2C2dof	30	39	76.92
ABI3VP1	5	9	55.56
SRS	1	2	50.00
ARF	1	3	33.33
Orphan	1	3	33.33
MADS	4	14	28.57
BBRBPC	1	5	20.00
C3H	2	10	20.00
MYBrelated	5	47	10.64
C2H2	4	38	10.53
Trihelix	1	21	4.76
G2like	1	29	3.45
MYB	1	86	1.16
NAC	1	86	1.16

Supplementary Table 143: Motif enrichment Root - Preflowering - Cluster 17 - Gene regulation

GO type	GO ID	Description	Adj. p-value
BP	GO:0010468	regulation of gene expression	0.000
	GO:0010608	posttranscriptional regulation of gene e...	0.000
	GO:0016458	gene silencing	0.001
	GO:0015994	chlorophyll metabolic process	0.005
	GO:0040029	regulation of gene expression, epigeneti...	0.006
	GO:0015979	photosynthesis	0.033
	GO:0010109	regulation of photosynthesis	0.089

Supplementary Table 145: GO term enrichment (filtered results) Root - Preflowering - Cluster 17 - Gene regulation

3.4.16 Root - Preflowering - Cluster 19 - AMF-pre



Overview
Cluster 19: AMF-pre
Number of genes: 496
Number of "good" genes: 275

No pathways found enriched

Supplementary Table 146: KEGG pathway enrichment - Root - Preflowering - Cluster 19 - AMF-pre

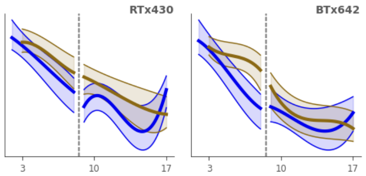
TF family	No. in cluster	Total number	Percentage
C2C2gata	1	18	5.56
MYB	3	86	3.49
G2like	1	29	3.45

Supplementary Table 147: Motif enrichment Root - Preflowering - Cluster 19 - AMF-pre

GO type	GO ID	Description	Adj. p-value
BP	GO:0009753	response to jasmonic acid	0.032
	GO:0009751	response to salicylic acid	0.049
	GO:0006820	anion transport	0.077
	GO:0006749	glutathione metabolic process	0.090
MF	GO:0004364	glutathione transferase activity	0.014
	GO:0010427	abscisic acid binding	0.029

Supplementary Table 149: GO term enrichment (filtered results) Root - Preflowering - Cluster 19 - AMF-pre

3.4.17 Root - Preflowering - Cluster 20 - Development



Overview
Cluster 20: Development
Number of genes: 2017
Number of "good" genes: 1604

Pathway	Adj. p-value
Metabolic pathways	0.000
Phagosome	0.000
Biosynthesis of secondary metabolites	0.000
Other glycan degradation	0.004
Steroid biosynthesis	0.020
2-Oxocarboxylic acid metabolism	0.040

Supplementary Table 150: KEGG pathway enrichment - Root - Preflowering - Cluster 20 - Development

TF family	No. in cluster	Total number	Percentage
BZR	5	7	71.43
ZFHD	7	11	63.64
FAR1	1	2	50.00
bHLH	12	25	48.00
SBP	2	13	15.38
bZIP	7	51	13.73
C2H2	3	38	7.89
HB	1	16	6.25
NAC	1	86	1.16

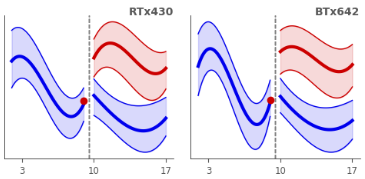
Supplementary Table 151: Motif enrichment Root - Preflowering - Cluster 20 - Development

GO type	GO ID	Description	Adj. p-value
BP	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0048868	pollen tube development	0.000
	GO:0040007	growth	0.000
	GO:0006260	DNA replication	0.000
	GO:0009790	embryo development	0.000
	GO:0009888	tissue development	0.000
	GO:0009791	post-embryonic development	0.000
	GO:0010154	fruit development	0.001
	GO:0048731	system development	0.002
	GO:0040029	regulation of gene expression, epigeneti...	0.002
	GO:0048608	reproductive structure development	0.003
	GO:0072593	reactive oxygen species metabolic proces...	0.003
	GO:0006631	fatty acid metabolic process	0.003
	GO:0006270	DNA replication initiation	0.004
	GO:0006833	water transport	0.006
	GO:0044255	cellular lipid metabolic process	0.008
	GO:0006979	response to oxidative stress	0.022
	GO:0009628	response to abiotic stimulus	0.023
	GO:0042542	response to hydrogen peroxide	0.035
	GO:0042545	cell wall modification	0.037
MF	GO:0016787	hydrolase activity	0.000
	GO:0015250	water channel activity	0.004

Supplementary Table 153: GO term enrichment (filtered results) Root - Preflowering - Cluster 20 - Development

3.5 Root Postflowering clusters

3.5.1 Root - Postflowering - Cluster 1 - Stress



Overview
Cluster 1: Stress
Number of genes: 1817
Number of "good" genes: 739
Description Highly enriched in heat-shock proteins

Pathway	Adj. p-value
Metabolic pathways	0.000
Valine, leucine and isoleucine degradation	0.007
Phagosome	0.007
Fatty acid degradation	0.010
Oxidative phosphorylation	0.010
Carbon metabolism	0.023
Terpenoid backbone biosynthesis	0.040
Arginine and proline metabolism	0.040

Supplementary Table 154: KEGG pathway enrichment - Root - Postflowering - Cluster 1 - Stress

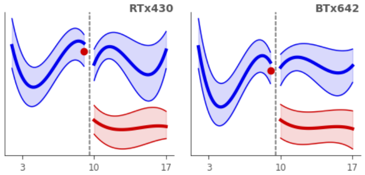
TF family	No. in cluster	Total number	Percentage
BSD	1	1	100.00
PLATZ	1	1	100.00
S1Falike	1	1	100.00
HSF	10	16	62.50
Orphan	1	3	33.33
BZR	2	7	28.57
bHLH	7	25	28.00
bZIP	9	51	17.65
ND	1	6	16.67
C3H	1	10	10.00
AP2EREBP	10	130	7.69

Supplementary Table 155: Motif enrichment Root - Postflowering - Cluster 1 - Stress

GO type	GO ID	Description	Adj. p-value
BP	GO:0003006	developmental process involved in reprod...	0.000
	GO:0009642	response to light intensity	0.000
	GO:0048608	reproductive structure development	0.000
	GO:0010154	fruit development	0.000
	GO:0048316	seed development	0.001
	GO:0006629	lipid metabolic process	0.004
	GO:0034599	cellular response to oxidative stress	0.004
	GO:0048868	pollen tube development	0.008
	GO:0044255	cellular lipid metabolic process	0.009
	GO:0006631	fatty acid metabolic process	0.018
	GO:0043484	regulation of RNA splicing	0.018
	GO:0034614	cellular response to reactive oxygen spe...	0.029
	GO:0009908	flower development	0.038
	GO:0009737	response to abscisic acid	0.040
MF	GO:0031072	heat shock protein binding	0.082

Supplementary Table 157: GO term enrichment (filtered results) Root - Postflowering - Cluster 1 - Stress

3.5.2 Root - Postflowering - Cluster 2 - AMF-post



Overview
Cluster 2: AMF-post
Number of genes: 807
Number of "good" genes: 565

Pathway	Adj. p-value
Metabolic pathways	0.021
Biosynthesis of secondary metabolites	0.035

Supplementary Table 158: KEGG pathway enrichment - Root - Postflowering - Cluster 2 - AMF-post

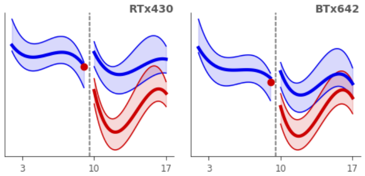
TF family	No. in cluster	Total number	Percentage
MYB	7	86	8.14
WRKY	1	60	1.67

Supplementary Table 159: Motif enrichment Root - Postflowering - Cluster 2 - AMF-post

GO type	GO ID	Description	Adj. p-value
BP	GO:0042546	cell wall biogenesis	0.000
	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0009733	response to auxin	0.041
	GO:0009813	flavonoid biosynthetic process	0.043
	GO:0010345	suberin biosynthetic process	0.057
	GO:0006629	lipid metabolic process	0.078
MF	GO:0016491	oxidoreductase activity	0.000
	GO:0010427	abscisic acid binding	0.042
	GO:0015250	water channel activity	0.099

Supplementary Table 161: GO term enrichment (filtered results) Root - Postflowering - Cluster 2 - AMF-post

3.5.3 Root - Postflowering - Cluster 3 - Cell wall biogenesis



Overview
Cluster 3: Cell wall biogenesis
Number of genes: 1607
Number of "good" genes: 888

Pathway	Adj. p-value
Metabolic pathways	0.000
Biosynthesis of amino acids	0.002
Ribosome	0.002
N-Glycan biosynthesis	0.004
DNA replication	0.004
Carbon metabolism	0.009
Biosynthesis of secondary metabolites	0.026
Pentose phosphate pathway	0.043
Glycine, serine and threonine metabolism	0.043
Proteasome	0.043

Supplementary Table 162: KEGG pathway enrichment - Root - Postflowering - Cluster 3 - Cell wall biogenesis

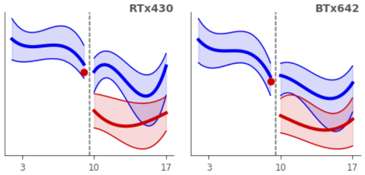
TF family	No. in cluster	Total number	Percentage
MYB	1	86	1.16

Supplementary Table 163: Motif enrichment Root - Postflowering - Cluster 3 - Cell wall biogenesis

GO type	GO ID	Description	Adj. p-value
BP	GO:0042546	cell wall biogenesis	0.000
	GO:0044550	secondary metabolite biosynthetic proces...	0.000
	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0006260	DNA replication	0.000
	GO:0042545	cell wall modification	0.004
	GO:0009888	tissue development	0.005
	GO:0048869	cellular developmental process	0.009
	GO:0006631	fatty acid metabolic process	0.015
	GO:0009733	response to auxin	0.066
	GO:0010345	suberin biosynthetic process	0.069
	GO:0006979	response to oxidative stress	0.094
MF	GO:0016491	oxidoreductase activity	0.000
	GO:0015250	water channel activity	0.035

Supplementary Table 165: GO term enrichment (filtered results) Root - Postflowering - Cluster 3 - Cell wall biogenesis

3.5.4 Root - Postflowering - Cluster 4 - Secondary metabolites



Overview
Cluster 4: Secondary metabolites
Number of genes: 2045
Number of "good" genes: 1447

Pathway	Adj. p-value
Metabolic pathways	0.000
Biosynthesis of secondary metabolites	0.001
Amino sugar and nucleotide sugar metabolism	0.001

Supplementary Table 166: KEGG pathway enrichment - Root - Postflowering - Cluster 4 - Secondary metabolites

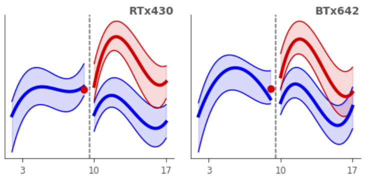
TF family	No. in cluster	Total number	Percentage
NLP	1	1	100.00
BZR	4	7	57.14
BES1	1	2	50.00
CAMTA	1	2	50.00
MYB	26	86	30.23
bHLH	4	25	16.00
TCP	1	23	4.35
C2H2	1	38	2.63

Supplementary Table 167: Motif enrichment Root - Postflowering - Cluster 4 - Secondary metabolites

GO type	GO ID	Description	Adj. p-value
BP	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0044550	secondary metabolite biosynthetic proces...	0.000
	GO:0006270	DNA replication initiation	0.002
	GO:0009888	tissue development	0.003
	GO:0008610	lipid biosynthetic process	0.004
	GO:0048869	cellular developmental process	0.011
	GO:0006260	DNA replication	0.014
	GO:0010345	suberin biosynthetic process	0.019
	GO:0006833	water transport	0.023
	GO:0009695	jasmonic acid biosynthetic process	0.028
	GO:0006979	response to oxidative stress	0.029
	GO:0060548	negative regulation of cell death	0.059
MF	GO:0016491	oxidoreductase activity	0.000
	GO:0015250	water channel activity	0.006
	GO:0004364	glutathione transferase activity	0.097

Supplementary Table 169: GO term enrichment (filtered results) Root - Postflowering - Cluster 4 - Secondary metabolites

3.5.5 Root - Postflowering - Cluster 6 - Response to ethylene



Overview
Cluster 6: Response to ethylene
Number of genes: 1427
Number of "good" genes: 293
Description Enriched in heat-shock proteins

Pathway	Adj. p-value
Metabolic pathways	0.000
Galactose metabolism	0.000
Biosynthesis of secondary metabolites	0.000
Carbon metabolism	0.020

Supplementary Table 170: KEGG pathway enrichment - Root - Postflowering - Cluster 6 - Response to ethylene

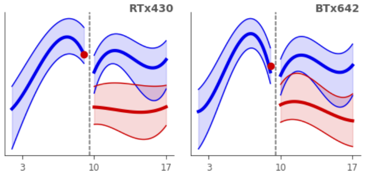
TF family	No. in cluster	Total number	Percentage
BSD	1	1	100.00
PLATZ	1	1	100.00
S1Falike	1	1	100.00
HSF	9	16	56.25
BES1	1	2	50.00
Orphan	1	3	33.33
BZR	2	7	28.57
E2FDP	2	7	28.57
bHLH	3	25	12.00
TCP	1	23	4.35
MYBrelated	2	47	4.26
bZIP	1	51	1.96

Supplementary Table 171: Motif enrichment Root - Postflowering - Cluster 6 - Response to ethylene

GO type	GO ID	Description	Adj. p-value
BP	GO:0009723	response to ethylene	0.013
	GO:0010150	leaf senescence	0.039
	GO:0050793	regulation of developmental process	0.047

Supplementary Table 173: GO term enrichment (filtered results) Root - Postflowering - Cluster 6 - Response to ethylene

3.5.6 Root - Postflowering - Cluster 7 - Defense



Overview
Cluster 7: Defense
Number of genes: 1451
Number of "good" genes: 762
Description Enriched in WRKY motifs., response to jasmonic acid, auxin, and biotic stimulus

Pathway	Adj. p-value
Metabolic pathways	0.018

Supplementary Table 174: KEGG pathway enrichment - Root - Postflowering - Cluster 7 - Defense

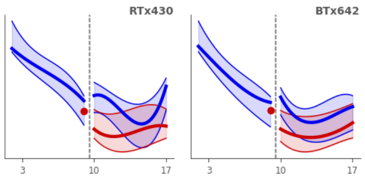
TF family	No. in cluster	Total number	Percentage
NLP	1	1	100.00
WRKY	25	60	41.67
SBP	3	13	23.08
ABI3VP1	1	9	11.11
bZIP	1	51	1.96

Supplementary Table 175: Motif enrichment Root - Postflowering - Cluster 7 - Defense

GO type	GO ID	Description	Adj. p-value
BP	GO:0071554	cell wall organization or biogenesis	0.000
	GO:0009753	response to jasmonic acid	0.001
	GO:0009809	lignin biosynthetic process	0.012
	GO:0006749	glutathione metabolic process	0.016
	GO:0009691	cytokinin biosynthetic process	0.021
	GO:0009733	response to auxin	0.038
	GO:0009607	response to biotic stimulus	0.091
MF	GO:0004364	glutathione transferase activity	0.002
	GO:0010427	abscisic acid binding	0.008

Supplementary Table 177: GO term enrichment (filtered results) Root - Postflowering - Cluster 7 - Defense

3.5.7 Root - Postflowering - Cluster 8 - Cell wall, and DNA replication



Overview
Cluster 8: Cell wall, and DNA replication
Number of genes: 3661
Number of “good” genes: 2694

Pathway	Adj. p-value
Metabolic pathways	0.000
Carbon metabolism	0.000
Biosynthesis of secondary metabolites	0.000
Citrate cycle (TCA cycle)	0.000
Oxidative phosphorylation	0.000
Phagosome	0.000
Amino sugar and nucleotide sugar metabolism	0.003
Glycolysis / Gluconeogenesis	0.005
Propanoate metabolism	0.006
Pentose phosphate pathway	0.007
Steroid biosynthesis	0.010
Fatty acid metabolism	0.010
Biosynthesis of amino acids	0.014
Galactose metabolism	0.023
Fatty acid biosynthesis	0.027
Glyoxylate and dicarboxylate metabolism	0.035

Supplementary Table 178: KEGG pathway enrichment - Root - Postflowering - Cluster 8 - Cell wall, and DNA replication

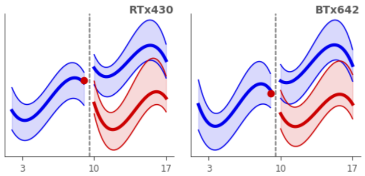
TF family	No. in cluster	Total number	Percentage
CCAATHAP3	1	2	50.00
bHLH	5	25	20.00
SBP	2	13	15.38
C2H2	2	38	5.26

Supplementary Table 179: Motif enrichment Root - Postflowering - Cluster 8 - Cell wall, and DNA replication

GO type	GO ID	Description	Adj. p-value
BP	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0044550	secondary metabolite biosynthetic proces...	0.000
	GO:0042545	cell wall modification	0.002
	GO:0006260	DNA replication	0.003
	GO:0009888	tissue development	0.005
	GO:0006833	water transport	0.007
	GO:0044255	cellular lipid metabolic process	0.011
	GO:0040007	growth	0.021
	GO:0006979	response to oxidative stress	0.021
	GO:0010345	suberin biosynthetic process	0.033
	GO:0048638	regulation of developmental growth	0.075
MF	GO:0016787	hydrolase activity	0.000
	GO:0016491	oxidoreductase activity	0.000
	GO:0015250	water channel activity	0.003

Supplementary Table 181: GO term enrichment (filtered results) Root - Postflowering - Cluster 8 - Cell wall, and DNA replication

3.5.8 Root - Postflowering - Cluster 9 - Gene regulation



Overview
Cluster 9: Gene regulation
Number of genes: 2004
Number of “good” genes: 615

Pathway	Adj. p-value
Metabolic pathways	0.038

Supplementary Table 182: KEGG pathway enrichment - Root - Postflowering - Cluster 9 - Gene regulation

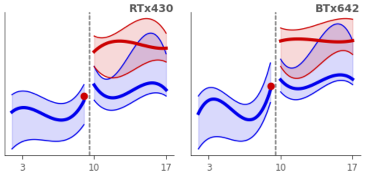
TF family	No. in cluster	Total number	Percentage
REM	1	2	50.00
C2C2dof	8	39	20.51
ABI3VP1	1	9	11.11

Supplementary Table 183: Motif enrichment Root - Postflowering - Cluster 9 - Gene regulation

GO type	GO ID	Description	Adj. p-value
BP	GO:0006351	transcription, DNA-templated	0.000
	GO:0010468	regulation of gene expression	0.000
	GO:0044550	secondary metabolite biosynthetic proces...	0.016
	GO:0009073	aromatic amino acid family biosynthetic ...	0.037
	GO:0006820	anion transport	0.080
MF	GO:0010427	abscisic acid binding	0.025

Supplementary Table 185: GO term enrichment (filtered results) Root - Postflowering - Cluster 9 - Gene regulation

3.5.9 Root - Postflowering - Cluster 10 - Gene regulation, and DNA replication



Overview
Cluster 10: Gene regulation, and DNA replication
Number of genes: 5725
Number of “good” genes: 3119
Description Enriched in many GO terms associated with gene silencing, epigenetic regulation, and regulation of gene expression. Highly enriched in C2C2dof motifs)

Pathway	Adj. p-value
Spliceosome	0.000
Basal transcription factors	0.000
Ribosome biogenesis in eukaryotes	0.000
RNA transport	0.000
Nucleotide excision repair	0.000
mRNA surveillance pathway	0.001
Porphyrin and chlorophyll metabolism	0.002
Aminoacyl-tRNA biosynthesis	0.007
Autophagy - other	0.008
Mismatch repair	0.042

Supplementary Table 186: KEGG pathway enrichment - Root - Postflowering - Cluster 10 - Gene regulation, and DNA replication

TF family	No. in cluster	Total number	Percentage
CPP	7	7	100.00
REM	2	2	100.00
C2C2dof	33	39	84.62
ABI3VP1	5	9	55.56
C3H	5	10	50.00
SRS	1	2	50.00
ARF	1	3	33.33
Orphan	1	3	33.33
MYBrelated	13	47	27.66
ARID	1	6	16.67
ND	1	6	16.67
MADS	2	14	14.29
ZFHD	1	11	9.09
C2H2	2	38	5.26
MYB	1	86	1.16
NAC	1	86	1.16

Supplementary Table 187: Motif enrichment Root - Postflowering - Cluster 10 - Gene regulation, and DNA replication

GO type	GO ID	Description	Adj. p-value
BP	GO:0010468	regulation of gene expression	0.000
	GO:0019684	photosynthesis, light reaction	0.000
	GO:0009628	response to abiotic stimulus	0.000
	GO:0006351	transcription, DNA-templated	0.000
	GO:0010608	posttranscriptional regulation of gene e...	0.000
	GO:0009642	response to light intensity	0.000
	GO:0015994	chlorophyll metabolic process	0.000
	GO:0010109	regulation of photosynthesis	0.000
	GO:0016458	gene silencing	0.001
	GO:0040029	regulation of gene expression, epigeneti...	0.001
	GO:0048608	reproductive structure development	0.004
	GO:0015995	chlorophyll biosynthetic process	0.004
	GO:0003006	developmental process involved in reprod...	0.007
	GO:0042742	defense response to bacterium	0.021
	GO:0050793	regulation of developmental process	0.024
	GO:1901607	alpha-amino acid biosynthetic process	0.047
	GO:0009908	flower development	0.049
	GO:0000302	response to reactive oxygen species	0.053
	GO:0009791	post-embryonic development	0.057
	GO:0034599	cellular response to oxidative stress	0.057
	GO:0048731	system development	0.100

Supplementary Table 189: GO term enrichment (filtered results) Root - Postflowering - Cluster 10 - Gene regulation, and DNA replication

4 All GO Terms per cluster

In what follows, we provide the list of all GO terms found enriched for all clusters.

4.1 Leaf Preflowering clusters

4.1.1 Leaf - Preflowering - Cluster 1

GO type	GO ID	Description	Adj. p-value
BP	GO:0051252	regulation of RNA metabolic process	0.000
	GO:0019748	secondary metabolic process	0.007
	GO:0006887	exocytosis	0.009
	GO:0097659	nucleic acid-templated transcription	0.009
	GO:0032774	RNA biosynthetic process	0.011
	GO:0019222	regulation of metabolic process	0.011
	GO:0006351	transcription, DNA-templated	0.013
	GO:0032940	secretion by cell	0.047
	GO:0016070	RNA metabolic process	0.059
	GO:0019941	modification-dependent protein catabolic...	0.059
	GO:0050794	regulation of cellular process	0.059
	GO:0046903	secretion	0.060
	GO:0043632	modification-dependent macromolecule cat...	0.073
	GO:0006511	ubiquitin-dependent protein catabolic pr...	0.083
	GO:0006575	cellular modified amino acid metabolic p...	0.098
CC	GO:0099023	tethering complex	0.001
	GO:0000145	exocyst	0.016
	GO:0005634	nucleus	0.034
	GO:0031226	intrinsic component of plasma membrane	0.034
	GO:0005886	plasma membrane	0.050
MF	GO:0005488	binding	0.000
	GO:0004497	monooxygenase activity	0.000
	GO:0016705	oxidoreductase activity, acting on paire...	0.001
	GO:0004672	protein kinase activity	0.001
	GO:0046527	glucosyltransferase activity	0.004
	GO:0004364	glutathione transferase activity	0.004
	GO:0032559	adenyl ribonucleotide binding	0.004
	GO:0016758	transferase activity, transferring hexos...	0.005
	GO:0030554	adenyl nucleotide binding	0.005
	GO:0008194	UDP-glycosyltransferase activity	0.005
	GO:0097367	carbohydrate derivative binding	0.005
	GO:0140110	transcription regulator activity	0.005
	GO:0003677	DNA binding	0.010
	GO:0017076	purine nucleotide binding	0.010
	GO:0032553	ribonucleotide binding	0.010
	GO:0046906	tetrapyrrole binding	0.010
	GO:0051213	dioxygenase activity	0.010

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GO type	GO ID	Description	Adj. p-value
	GO:0032555	purine ribonucleotide binding	0.010
	GO:0016773	phosphotransferase activity, alcohol gro...	0.013
	GO:0016757	transferase activity, transferring glyco...	0.015
	GO:0000166	nucleotide binding	0.029
	GO:1901265	nucleoside phosphate binding	0.029
	GO:0004674	protein serine/threonine kinase activity	0.030
	GO:0015291	secondary active transmembrane transport...	0.055
	GO:0035673	oligopeptide transmembrane transporter a...	0.075
	GO:0016740	transferase activity	0.093
	GO:0046914	transition metal ion binding	0.093

4.1.2 Leaf - Preflowering - Cluster 2

GO type	GO ID	Description	Adj. p-value
BP	GO:0015850	organic hydroxy compound transport	0.000
	GO:1901071	glucosamine-containing compound metaboli...	0.003
	GO:0006026	aminoglycan catabolic process	0.004
	GO:0006030	chitin metabolic process	0.004
	GO:0006032	chitin catabolic process	0.004
	GO:0046348	amino sugar catabolic process	0.004
	GO:1901072	glucosamine-containing compound cataboli...	0.004
	GO:0046323	glucose import	0.004
	GO:0015749	monosaccharide transmembrane transport	0.004
	GO:1904659	glucose transmembrane transport	0.004
	GO:0005996	monosaccharide metabolic process	0.005
	GO:0010200	response to chitin	0.005
	GO:0006022	aminoglycan metabolic process	0.006
	GO:0008645	hexose transmembrane transport	0.007
	GO:0015804	neutral amino acid transport	0.008
	GO:0006833	water transport	0.008
	GO:0042044	fluid transport	0.008
	GO:0006836	neurotransmitter transport	0.011
	GO:0009607	response to biotic stimulus	0.012
	GO:0030104	water homeostasis	0.013
	GO:0006810	transport	0.013
	GO:0007154	cell communication	0.013
	GO:0051234	establishment of localization	0.014
	GO:0015807	L-amino acid transport	0.014
	GO:0006040	amino sugar metabolic process	0.015
	GO:0006887	exocytosis	0.016
	GO:0051179	localization	0.017
	GO:0003333	amino acid transmembrane transport	0.019
	GO:0006487	protein N-linked glycosylation	0.021
	GO:0018196	peptidyl-asparagine modification	0.024
	GO:0018279	protein N-linked glycosylation via aspar...	0.024
	GO:0006865	amino acid transport	0.028
	GO:0007166	cell surface receptor signaling pathway	0.031
	GO:0008037	cell recognition	0.031
	GO:0071495	cellular response to endogenous stimulus	0.033
	GO:1902475	L-alpha-amino acid transmembrane transpo...	0.033
	GO:0043207	response to external biotic stimulus	0.034
	GO:0051707	response to other organism	0.034
	GO:0071577	zinc ion transmembrane transport	0.035
	GO:0009875	pollen-pistil interaction	0.038
	GO:0048544	recognition of pollen	0.041
	GO:0071229	cellular response to acid chemical	0.045
	GO:0008361	regulation of cell size	0.049
	GO:0032870	cellular response to hormone stimulus	0.049
	GO:0006575	cellular modified amino acid metabolic p...	0.049
	GO:0098542	defense response to other organism	0.049

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0055085	transmembrane transport	0.051
	GO:0008643	carbohydrate transport	0.054
	GO:0006855	drug transmembrane transport	0.077
	GO:0046903	secretion	0.077
	GO:0098754	detoxification	0.088
	GO:0010243	response to organonitrogen compound	0.090
	GO:0009873	ethylene-activated signaling pathway	0.091
	GO:0071310	cellular response to organic substance	0.091
	GO:0032940	secretion by cell	0.096
	GO:0006829	zinc ion transport	0.099
CC	GO:0000151	ubiquitin ligase complex	0.000
	GO:0005886	plasma membrane	0.000
	GO:0012505	endomembrane system	0.000
	GO:0005798	Golgi-associated vesicle	0.002
	GO:0044459	plasma membrane part	0.002
	GO:0031226	intrinsic component of plasma membrane	0.002
	GO:0005783	endoplasmic reticulum	0.004
	GO:0099023	tethering complex	0.010
	GO:0030120	vesicle coat	0.010
	GO:0030118	clathrin coat	0.012
	GO:0005773	vacuole	0.013
	GO:0030660	Golgi-associated vesicle membrane	0.016
	GO:0009506	plasmodesma	0.016
	GO:0055044	symplast	0.016
	GO:0005911	cell-cell junction	0.017
	GO:0030054	cell junction	0.017
	GO:0044433	cytoplasmic vesicle part	0.032
	GO:0005774	vacuolar membrane	0.053
	GO:0030662	coated vesicle membrane	0.053
	GO:0012506	vesicle membrane	0.057
	GO:0031410	cytoplasmic vesicle	0.061
	GO:0005794	Golgi apparatus	0.062
	GO:0009504	cell plate	0.067
	GO:0031982	vesicle	0.067
	GO:0097708	intracellular vesicle	0.067
	GO:0044437	vacuolar part	0.075
	GO:0030659	cytoplasmic vesicle membrane	0.089
	GO:0030135	coated vesicle	0.090
	GO:0004497	monooxygenase activity	0.000
	GO:0016705	oxidoreductase activity, acting on paire...	0.000
	GO:1901618	organic hydroxy compound transmembrane t...	0.000
	GO:0015166	polyol transmembrane transporter activit...	0.000
	GO:0015145	monosaccharide transmembrane transporter...	0.002
	GO:0140096	catalytic activity, acting on a protein	0.002
	GO:0005355	glucose transmembrane transporter activi...	0.002
	GO:0004568	chitinase activity	0.002
	GO:0097159	organic cyclic compound binding	0.002
	GO:0004364	glutathione transferase activity	0.002
	GO:1901363	heterocyclic compound binding	0.002

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		Description	Adj. p-value
GO type	GO ID		
	GO:0015149	hexose transmembrane transporter activit...	0.003
	GO:0005215	transporter activity	0.003
	GO:0051213	dioxygenase activity	0.003
	GO:0015179	L-amino acid transmembrane transporter a...	0.005
	GO:0015293	symporter activity	0.005
	GO:0005326	neurotransmitter transporter activity	0.006
	GO:0015174	basic amino acid transmembrane transport...	0.006
	GO:0016772	transferase activity, transferring phosp...	0.007
	GO:0003824	catalytic activity	0.011
	GO:0015294	solute:cation symporter activity	0.011
	GO:0001871	pattern binding	0.013
	GO:0030247	polysaccharide binding	0.013
	GO:0048037	cofactor binding	0.013
	GO:0015171	amino acid transmembrane transporter act...	0.014
	GO:0097367	carbohydrate derivative binding	0.014
	GO:0032559	adenyl ribonucleotide binding	0.015
	GO:0000166	nucleotide binding	0.015
	GO:1901265	nucleoside phosphate binding	0.015
	GO:0015295	solute:proton symporter activity	0.016
	GO:0030554	adenyl nucleotide binding	0.017
	GO:0015297	antiporter activity	0.019
	GO:0005351	carbohydrate:proton symporter activity	0.020
	GO:0005402	carbohydrate:cation symporter activity	0.020
	GO:0051119	sugar transmembrane transporter activity	0.025
	GO:0015144	carbohydrate transmembrane transporter a...	0.026
	GO:0032553	ribonucleotide binding	0.026
	GO:0022804	active transmembrane transporter activit...	0.029
	GO:0005385	zinc ion transmembrane transporter activ...	0.031
	GO:0036094	small molecule binding	0.032
	GO:0022857	transmembrane transporter activity	0.032
	GO:0032555	purine ribonucleotide binding	0.036
	GO:0017076	purine nucleotide binding	0.046
	GO:0015175	neutral amino acid transmembrane transpo...	0.048
	GO:0008144	drug binding	0.066
	GO:0008483	transaminase activity	0.083
	GO:0016769	transferase activity, transferring nitro...	0.083
	GO:0042562	hormone binding	0.095

4.1.3 Leaf - Preflowering - Cluster 3

GO type	GO ID	Description	Adj. p-value
BP	GO:0005975	carbohydrate metabolic process	0.000
	GO:1901071	glucosamine-containing compound metaboli...	0.006
	GO:0006855	drug transmembrane transport	0.008
	GO:0042743	hydrogen peroxide metabolic process	0.008
	GO:0006836	neurotransmitter transport	0.009
	GO:0015893	drug transport	0.015
	GO:0006022	aminoglycan metabolic process	0.016
	GO:0018196	peptidyl-asparagine modification	0.017
	GO:0018279	protein N-linked glycosylation via aspar...	0.017
	GO:1904659	glucose transmembrane transport	0.017
	GO:0005996	monosaccharide metabolic process	0.017
	GO:0015749	monosaccharide transmembrane transport	0.019
	GO:0051187	cofactor catabolic process	0.024
	GO:0008645	hexose transmembrane transport	0.025
	GO:0046323	glucose import	0.033
	GO:0003333	amino acid transmembrane transport	0.035
	GO:0006040	amino sugar metabolic process	0.035
	GO:1902475	L-alpha-amino acid transmembrane transpo...	0.035
	GO:0006633	fatty acid biosynthetic process	0.037
	GO:0009636	response to toxic substance	0.037
	GO:1990748	cellular detoxification	0.038
	GO:0044036	cell wall macromolecule metabolic proces...	0.038
	GO:0009058	biosynthetic process	0.040
	GO:0033692	cellular polysaccharide biosynthetic pro...	0.042
	GO:0098869	cellular oxidant detoxification	0.042
	GO:0016999	antibiotic metabolic process	0.044
	GO:0006865	amino acid transport	0.046
	GO:0071669	plant-type cell wall organization or bio...	0.053
	GO:0043412	macromolecule modification	0.056
	GO:0008037	cell recognition	0.060
	GO:0015807	L-amino acid transport	0.060
	GO:0048544	recognition of pollen	0.060
	GO:0017144	drug metabolic process	0.061
	GO:0007166	cell surface receptor signaling pathway	0.070
	GO:0009875	pollen-pistil interaction	0.070
	GO:0044281	small molecule metabolic process	0.075
	GO:0097237	cellular response to toxic substance	0.079
	GO:0006487	protein N-linked glycosylation	0.088
	GO:0044267	cellular protein metabolic process	0.090
CC	GO:0005886	plasma membrane	0.000
	GO:0044459	plasma membrane part	0.003
	GO:0031226	intrinsic component of plasma membrane	0.005
	GO:0008194	UDP-glycosyltransferase activity	0.000
	GO:0004497	monooxygenase activity	0.000
	GO:0016758	transferase activity, transferring hexos...	0.000
	GO:0016705	oxidoreductase activity, acting on paire...	0.000

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GO type	GO ID	Description	Adj. p-value
	GO:0003824	catalytic activity	0.000
	GO:0030246	carbohydrate binding	0.000
	GO:0032559	adenyl ribonucleotide binding	0.000
	GO:0004553	hydrolase activity, hydrolyzing O-glycos...	0.002
	GO:0016772	transferase activity, transferring phosp...	0.002
	GO:0005326	neurotransmitter transporter activity	0.004
	GO:0032553	ribonucleotide binding	0.006
	GO:0032555	purine ribonucleotide binding	0.006
	GO:0051213	dioxygenase activity	0.006
	GO:0015291	secondary active transmembrane transport...	0.006
	GO:0016684	oxidoreductase activity, acting on perox...	0.006
	GO:0017076	purine nucleotide binding	0.006
	GO:0004601	peroxidase activity	0.009
	GO:0016798	hydrolase activity, acting on glycosyl b...	0.009
	GO:0005355	glucose transmembrane transporter activi...	0.011
	GO:0015297	antiporter activity	0.011
	GO:0015145	monosaccharide transmembrane transporter...	0.012
	GO:0016209	antioxidant activity	0.016
	GO:0015149	hexose transmembrane transporter activit...	0.017
	GO:0015179	L-amino acid transmembrane transporter a...	0.018
	GO:0015238	drug transmembrane transporter activity	0.018
	GO:0015171	amino acid transmembrane transporter act...	0.021
	GO:0050662	coenzyme binding	0.024
	GO:0097159	organic cyclic compound binding	0.028
	GO:1901363	heterocyclic compound binding	0.029
	GO:0043168	anion binding	0.030
	GO:0005215	transporter activity	0.030
	GO:0015174	basic amino acid transmembrane transport...	0.032
	GO:0015293	symporter activity	0.034
	GO:0022804	active transmembrane transporter activit...	0.037
	GO:0003700	DNA binding transcription factor activit...	0.042
	GO:0008144	drug binding	0.042
	GO:0015295	solute:proton symporter activity	0.049
	GO:0016614	oxidoreductase activity, acting on CH-OH...	0.058
	GO:0015294	solute:cation symporter activity	0.058
	GO:0001871	pattern binding	0.060
	GO:0022857	transmembrane transporter activity	0.060
	GO:0030247	polysaccharide binding	0.060
	GO:0004364	glutathione transferase activity	0.068
	GO:0016747	transferase activity, transferring acyl ...	0.080
	GO:0043167	ion binding	0.088
	GO:0005524	ATP binding	0.089
	GO:0000166	nucleotide binding	0.099
	GO:1901265	nucleoside phosphate binding	0.099

4.1.4 Leaf - Preflowering - Cluster 4

GO type	GO ID	Description	Adj. p-value
	GO:0019684	photosynthesis, light reaction	0.000
	GO:0051188	cofactor biosynthetic process	0.000
	GO:0046394	carboxylic acid biosynthetic process	0.000
	GO:1901566	organonitrogen compound biosynthetic pro...	0.000
	GO:0022900	electron transport chain	0.000
	GO:0033014	tetrapyrrole biosynthetic process	0.000
	GO:0009108	coenzyme biosynthetic process	0.000
	GO:0006631	fatty acid metabolic process	0.000
	GO:0006629	lipid metabolic process	0.000
	GO:0009150	purine ribonucleotide metabolic process	0.000
	GO:0006778	porphyrin-containing compound metabolic ...	0.000
	GO:0009165	nucleotide biosynthetic process	0.000
	GO:0009161	ribonucleoside monophosphate metabolic p...	0.000
	GO:0009205	purine ribonucleoside triphosphate metab...	0.000
	GO:0071555	cell wall organization	0.000
	GO:0005975	carbohydrate metabolic process	0.000
	GO:0016052	carbohydrate catabolic process	0.000
	GO:0046034	ATP metabolic process	0.000
	GO:0009073	aromatic amino acid family biosynthetic ...	0.000
	GO:0005976	polysaccharide metabolic process	0.000
	GO:0009126	purine nucleoside monophosphate metaboli...	0.000
	GO:0009167	purine ribonucleoside monophosphate meta...	0.000
	GO:0009124	nucleoside monophosphate biosynthetic pr...	0.000
	GO:0072522	purine-containing compound biosynthetic ...	0.000
	GO:0009156	ribonucleoside monophosphate biosyntheti...	0.000
	GO:0046434	organophosphate catabolic process	0.000
	GO:0006164	purine nucleotide biosynthetic process	0.000
	GO:0006733	oxidoreduction coenzyme metabolic proces...	0.000
	GO:0008299	isoprenoid biosynthetic process	0.000
	GO:1902600	proton transmembrane transport	0.000
	GO:0043604	amide biosynthetic process	0.000
	GO:0072524	pyridine-containing compound metabolic p...	0.000
	GO:0007017	microtubule-based process	0.000
	GO:0046496	nicotinamide nucleotide metabolic proces...	0.000
	GO:0046939	nucleotide phosphorylation	0.000
	GO:0072525	pyridine-containing compound biosyntheti...	0.000
	GO:0019362	pyridine nucleotide metabolic process	0.000
	GO:0006090	pyruvate metabolic process	0.001
	GO:0043043	peptide biosynthetic process	0.001
	GO:0006412	translation	0.002
	GO:0009773	photosynthetic electron transport in pho...	0.002
	GO:0010109	regulation of photosynthesis	0.002
	GO:0006767	water-soluble vitamin metabolic process	0.002
	GO:0045333	cellular respiration	0.002
	GO:0045491	xylan metabolic process	0.002
	GO:0010206	photosystem II repair	0.002

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GO type	GO ID	Description	Adj. p-value
	GO:0046271	phenylpropanoid catabolic process	0.002
	GO:0006165	nucleoside diphosphate phosphorylation	0.003
	GO:0009664	plant-type cell wall organization	0.003
	GO:0042180	cellular ketone metabolic process	0.003
	GO:0032544	plastid translation	0.003
	GO:0044275	cellular carbohydrate catabolic process	0.003
	GO:0042168	heme metabolic process	0.003
	GO:0044249	cellular biosynthetic process	0.003
	GO:0042364	water-soluble vitamin biosynthetic proce...	0.003
	GO:0006783	heme biosynthetic process	0.003
	GO:0010383	cell wall polysaccharide metabolic proce...	0.003
	GO:0042435	indole-containing compound biosynthetic ...	0.004
	GO:0009166	nucleotide catabolic process	0.004
	GO:0016122	xanthophyll metabolic process	0.004
	GO:0017004	cytochrome complex assembly	0.005
	GO:0034404	nucleobase-containing small molecule bio...	0.005
	GO:0044282	small molecule catabolic process	0.006
	GO:0046274	lignin catabolic process	0.006
	GO:0009132	nucleoside diphosphate metabolic process	0.006
	GO:0043603	cellular amide metabolic process	0.006
	GO:0006096	glycolytic process	0.006
	GO:0006757	ATP generation from ADP	0.006
	GO:0009135	purine nucleoside diphosphate metabolic ...	0.006
	GO:0009179	purine ribonucleoside diphosphate metabo...	0.006
	GO:0009185	ribonucleoside diphosphate metabolic pro...	0.006
	GO:0009768	photosynthesis, light harvesting in phot...	0.006
	GO:0042866	pyruvate biosynthetic process	0.006
	GO:0046031	ADP metabolic process	0.006
	GO:1901292	nucleoside phosphate catabolic process	0.006
	GO:0009308	amine metabolic process	0.006
	GO:0015988	energy coupled proton transmembrane tran...	0.007
	GO:0015991	ATP hydrolysis coupled proton transport	0.007
	GO:0030091	protein repair	0.007
	GO:0090662	ATP hydrolysis coupled transmembrane tra...	0.007
	GO:0099131	ATP hydrolysis coupled ion transmembrane...	0.007
	GO:0099132	ATP hydrolysis coupled cation transmembr...	0.007
	GO:0006721	terpenoid metabolic process	0.007
	GO:0044042	glucan metabolic process	0.009
	GO:0043467	regulation of generation of precursor me...	0.009
	GO:2000652	regulation of secondary cell wall biogen...	0.009
	GO:1903338	regulation of cell wall organization or ...	0.009
	GO:0009409	response to cold	0.009
	GO:0019252	starch biosynthetic process	0.009
	GO:0006099	tricarboxylic acid cycle	0.009
	GO:0006081	cellular aldehyde metabolic process	0.010
	GO:0009060	aerobic respiration	0.010
	GO:0016114	terpenoid biosynthetic process	0.011
	GO:0016999	antibiotic metabolic process	0.011
	GO:0009416	response to light stimulus	0.011

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GO type	GO ID	Description	Adj. p-value
	GO:0017001	antibiotic catabolic process	0.011
	GO:0006073	cellular glucan metabolic process	0.012
	GO:0006518	peptide metabolic process	0.012
	GO:0019318	hexose metabolic process	0.012
	GO:0010410	hemicellulose metabolic process	0.013
	GO:0009314	response to radiation	0.013
	GO:0046364	monosaccharide biosynthetic process	0.013
	GO:1901605	alpha-amino acid metabolic process	0.015
	GO:0019748	secondary metabolic process	0.015
	GO:0043038	amino acid activation	0.015
	GO:0043039	tRNA aminoacylation	0.015
	GO:0046365	monosaccharide catabolic process	0.015
	GO:0000272	polysaccharide catabolic process	0.016
	GO:0006101	citrate metabolic process	0.016
	GO:0016311	dephosphorylation	0.017
	GO:0006760	folic acid-containing compound metabolic...	0.018
	GO:0044247	cellular polysaccharide catabolic proces...	0.018
	GO:0042558	pteridine-containing compound metabolic ...	0.018
	GO:0044036	cell wall macromolecule metabolic proces...	0.018
	GO:0005982	starch metabolic process	0.018
	GO:0015985	energy coupled proton transport, down el...	0.018
	GO:0015986	ATP synthesis coupled proton transport	0.018
	GO:0009251	glucan catabolic process	0.018
	GO:0006743	ubiquinone metabolic process	0.019
	GO:0006744	ubiquinone biosynthetic process	0.019
	GO:0072593	reactive oxygen species metabolic proces...	0.019
	GO:1901607	alpha-amino acid biosynthetic process	0.020
	GO:0045036	protein targeting to chloroplast	0.020
	GO:0072596	establishment of protein localization to...	0.020
	GO:0010345	suberin biosynthetic process	0.020
	GO:0016043	cellular component organization	0.020
	GO:0046185	aldehyde catabolic process	0.020
	GO:0043648	dicarboxylic acid metabolic process	0.020
	GO:0046184	aldehyde biosynthetic process	0.020
	GO:0009642	response to light intensity	0.020
	GO:0010143	cutin biosynthetic process	0.023
	GO:0042744	hydrogen peroxide catabolic process	0.024
	GO:0044085	cellular component biogenesis	0.024
	GO:0071482	cellular response to light stimulus	0.024
	GO:0032271	regulation of protein polymerization	0.024
	GO:0042726	flavin-containing compound metabolic pro...	0.024
	GO:0009058	biosynthetic process	0.024
	GO:0018298	protein-chromophore linkage	0.024
	GO:0006771	riboflavin metabolic process	0.025
	GO:0009231	riboflavin biosynthetic process	0.025
	GO:0042727	flavin-containing compound biosynthetic ...	0.025
	GO:0072350	tricarboxylic acid metabolic process	0.025
	GO:0005983	starch catabolic process	0.026
	GO:0072598	protein localization to chloroplast	0.027

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:1901137	carbohydrate derivative biosynthetic pro...	0.028
	GO:0006568	tryptophan metabolic process	0.028
	GO:0006586	indolalkylamine metabolic process	0.028
	GO:1901576	organic substance biosynthetic process	0.030
	GO:0042548	regulation of photosynthesis, light reac...	0.030
	GO:0071840	cellular component organization or bioge...	0.030
	GO:0006596	polyamine biosynthetic process	0.031
	GO:0045492	xylan biosynthetic process	0.032
	GO:0070592	cell wall polysaccharide biosynthetic pr...	0.035
	GO:0015672	monovalent inorganic cation transport	0.035
	GO:0009074	aromatic amino acid family catabolic pro...	0.035
	GO:0061024	membrane organization	0.035
	GO:0035336	long-chain fatty-acyl-CoA metabolic proc...	0.036
	GO:0009250	glucan biosynthetic process	0.036
	GO:0045037	protein import into chloroplast stroma	0.038
	GO:0006108	malate metabolic process	0.038
	GO:0030244	cellulose biosynthetic process	0.038
	GO:0071478	cellular response to radiation	0.038
	GO:0006637	acyl-CoA metabolic process	0.040
	GO:0035383	thioester metabolic process	0.040
	GO:1901463	regulation of tetrapyrrole biosynthetic ...	0.040
	GO:0009438	methylglyoxal metabolic process	0.042
	GO:0022411	cellular component disassembly	0.042
	GO:0042182	ketone catabolic process	0.042
	GO:0051596	methylglyoxal catabolic process	0.042
	GO:0030041	actin filament polymerization	0.047
	GO:0030243	cellulose metabolic process	0.047
	GO:0030833	regulation of actin filament polymerizat...	0.047
	GO:0008535	respiratory chain complex IV assembly	0.047
	GO:0044272	sulfur compound biosynthetic process	0.047
	GO:0031425	chloroplast RNA processing	0.047
	GO:1901568	fatty acid derivative metabolic process	0.050
	GO:0043624	cellular protein complex disassembly	0.051
	GO:0071806	protein transmembrane transport	0.052
	GO:1901401	regulation of tetrapyrrole metabolic pro...	0.052
	GO:0034599	cellular response to oxidative stress	0.053
	GO:1901135	carbohydrate derivative metabolic proces...	0.054
	GO:0008154	actin polymerization or depolymerization	0.059
	GO:0022607	cellular component assembly	0.059
	GO:0042743	hydrogen peroxide metabolic process	0.059
	GO:0006089	lactate metabolic process	0.061
	GO:0019243	methylglyoxal catabolic process to D-lac...	0.061
	GO:0022904	respiratory electron transport chain	0.061
	GO:0061727	methylglyoxal catabolic process to lacta...	0.061
	GO:0065002	intracellular protein transmembrane tran...	0.061
	GO:0098660	inorganic ion transmembrane transport	0.061
	GO:0071214	cellular response to abiotic stimulus	0.061
	GO:0104004	cellular response to environmental stimu...	0.061
	GO:0009628	response to abiotic stimulus	0.065

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0006418	tRNA aminoacylation for protein translat...	0.065
	GO:0051181	cofactor transport	0.071
	GO:0010103	stomatal complex morphogenesis	0.072
	GO:0048481	plant ovule development	0.072
	GO:0010380	regulation of chlorophyll biosynthetic p...	0.073
	GO:0044038	cell wall macromolecule biosynthetic pro...	0.078
	GO:0070589	cellular component macromolecule biosynt...	0.078
	GO:0051187	cofactor catabolic process	0.082
	GO:0032984	protein-containing complex disassembly	0.083
	GO:0019682	glyceraldehyde-3-phosphate metabolic pro...	0.085
	GO:0009395	phospholipid catabolic process	0.089
	GO:0035670	plant-type ovary development	0.089
	GO:0098754	detoxification	0.089
	GO:0008064	regulation of actin polymerization or de...	0.091
	GO:0030832	regulation of actin filament length	0.091
	GO:0032956	regulation of actin cytoskeleton organiz...	0.091
	GO:0032970	regulation of actin filament-based proce...	0.091
	GO:0110053	regulation of actin filament organizatio...	0.091
	GO:0032543	mitochondrial translation	0.093
	GO:0035337	fatty-acyl-CoA metabolic process	0.093
	GO:1901616	organic hydroxy compound catabolic proce...	0.095
	GO:0042775	mitochondrial ATP synthesis coupled elec...	0.096
	GO:0006399	tRNA metabolic process	0.097
CC	GO:0009521	photosystem	0.000
	GO:0044429	mitochondrial part	0.000
	GO:0005739	mitochondrion	0.000
	GO:1990204	oxidoreductase complex	0.000
	GO:0005740	mitochondrial envelope	0.000
	GO:0005576	extracellular region	0.000
	GO:0005743	mitochondrial inner membrane	0.000
	GO:0031969	chloroplast membrane	0.000
	GO:0098800	inner mitochondrial membrane protein com...	0.000
	GO:0098803	respiratory chain complex	0.000
	GO:0005746	mitochondrial respiratory chain	0.000
	GO:0005875	microtubule associated complex	0.000
	GO:0016469	proton-transporting two-sector ATPase co...	0.000
	GO:0009528	plastid inner membrane	0.000
	GO:0009295	nucleoid	0.000
	GO:0005618	cell wall	0.000
	GO:0005874	microtubule	0.000
	GO:0045259	proton-transporting ATP synthase complex	0.001
	GO:0009707	chloroplast outer membrane	0.001
	GO:0033178	proton-transporting two-sector ATPase co...	0.001
	GO:0009527	plastid outer membrane	0.001
	GO:0005881	cytoplasmic microtubule	0.002
	GO:0030863	cortical cytoskeleton	0.002
	GO:0030981	cortical microtubule cytoskeleton	0.002
	GO:0005840	ribosome	0.003
	GO:0009505	plant-type cell wall	0.003

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GO type	GO ID	Description	Adj. p-value
	GO:0005623	cell	0.005
	GO:0055028	cortical microtubule	0.008
	GO:0044464	cell part	0.008
	GO:0042644	chloroplast nucleoid	0.011
	GO:0033180	proton-transporting V-type ATPase, V1 do...	0.013
	GO:0031090	organelle membrane	0.023
	GO:0009508	plastid chromosome	0.031
	GO:0019867	outer membrane	0.043
	GO:0031968	organelle outer membrane	0.047
	GO:0045261	proton-transporting ATP synthase complex...	0.066
	GO:0000229	cytoplasmic chromosome	0.076
	GO:0005759	mitochondrial matrix	0.090
	GO:0016787	hydrolase activity	0.000
	GO:0016491	oxidoreductase activity	0.000
	GO:0016829	lyase activity	0.000
	GO:0016788	hydrolase activity, acting on ester bond...	0.000
	GO:0008092	cytoskeletal protein binding	0.000
	GO:0050662	coenzyme binding	0.000
	GO:0016651	oxidoreductase activity, acting on NAD(P...	0.000
	GO:0008236	serine-type peptidase activity	0.000
	GO:0017171	serine hydrolase activity	0.000
	GO:0016655	oxidoreductase activity, acting on NAD(P...	0.000
	GO:0016747	transferase activity, transferring acyl ...	0.000
	GO:0051536	iron-sulfur cluster binding	0.000
	GO:0051540	metal cluster binding	0.000
	GO:0016791	phosphatase activity	0.000
	GO:0016684	oxidoreductase activity, acting on perox...	0.002
	GO:0016830	carbon-carbon lyase activity	0.002
	GO:0016778	diphosphotransferase activity	0.003
	GO:0016853	isomerase activity	0.003
	GO:0019205	nucleobase-containing compound kinase ac...	0.003
	GO:0016838	carbon-oxygen lyase activity, acting on ...	0.003
	GO:0051539	4 iron, 4 sulfur cluster binding	0.003
	GO:0016614	oxidoreductase activity, acting on CH-OH...	0.004
	GO:0004601	peroxidase activity	0.005
	GO:0005198	structural molecule activity	0.006
	GO:0016462	pyrophosphatase activity	0.007
	GO:0019203	carbohydrate phosphatase activity	0.007
	GO:0010333	terpene synthase activity	0.008
	GO:0017111	nucleoside-triphosphatase activity	0.008
	GO:0050308	sugar-phosphatase activity	0.008
	GO:0016887	ATPase activity	0.008
	GO:0016616	oxidoreductase activity, acting on the C...	0.009
	GO:0052716	hydroquinone:oxygen oxidoreductase activ...	0.010
	GO:0016627	oxidoreductase activity, acting on the C...	0.010
	GO:0003993	acid phosphatase activity	0.010
	GO:0046933	proton-transporting ATP synthase activit...	0.011
	GO:0016866	intramolecular transferase activity	0.011
	GO:0016615	malate dehydrogenase activity	0.012

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GO type	GO ID	Description	Adj. p-value
	GO:0016817	hydrolase activity, acting on acid anhyd...	0.013
	GO:0050660	flavin adenine dinucleotide binding	0.013
	GO:0016818	hydrolase activity, acting on acid anhyd...	0.013
	GO:0046961	proton-transporting ATPase activity, rot...	0.014
	GO:0015399	primary active transmembrane transporter...	0.014
	GO:0015405	P-P-bond-hydrolysis-driven transmembrane...	0.014
	GO:0050661	NADP binding	0.014
	GO:0008374	O-acyltransferase activity	0.016
	GO:0016903	oxidoreductase activity, acting on the a...	0.017
	GO:0016836	hydro-lyase activity	0.018
	GO:0042626	ATPase activity, coupled to transmembran...	0.020
	GO:0016759	cellulose synthase activity	0.021
	GO:0016760	cellulose synthase (UDP-forming) activit...	0.021
	GO:0004175	endopeptidase activity	0.022
	GO:1901682	sulfur compound transmembrane transporte...	0.022
	GO:0016413	O-acetyltransferase activity	0.022
	GO:0016861	intramolecular oxidoreductase activity, ...	0.022
	GO:0051087	chaperone binding	0.023
	GO:0016620	oxidoreductase activity, acting on the a...	0.024
	GO:0016814	hydrolase activity, acting on carbon-nit...	0.025
	GO:0016765	transferase activity, transferring alkyl...	0.025
	GO:0036442	proton-exporting ATPase activity	0.025
	GO:0016741	transferase activity, transferring one-c...	0.026
	GO:0080019	fatty-acyl-CoA reductase (alcohol-formin...	0.026
	GO:0140101	catalytic activity, acting on a tRNA	0.030
	GO:0051287	NAD binding	0.033
	GO:0004812	aminoacyl-tRNA ligase activity	0.033
	GO:0016875	ligase activity, forming carbon-oxygen b...	0.033
	GO:0019201	nucleotide kinase activity	0.035
	GO:0016831	carboxy-lyase activity	0.035
	GO:0008574	ATP-dependent microtubule motor activity...	0.036
	GO:1990939	ATP-dependent microtubule motor activity	0.036
	GO:0019843	rRNA binding	0.037
	GO:0043492	ATPase activity, coupled to movement of ...	0.037
	GO:0019104	DNA N-glycosylase activity	0.040
	GO:0033764	steroid dehydrogenase activity, acting o...	0.041
	GO:0016717	oxidoreductase activity, acting on paire...	0.042
	GO:0016874	ligase activity	0.043
	GO:0070011	peptidase activity, acting on L-amino ac...	0.043
	GO:0016762	xyloglucan:xyloglucosyl transferase acti...	0.044
	GO:0004743	pyruvate kinase activity	0.045
	GO:0030955	potassium ion binding	0.045
	GO:0031420	alkali metal ion binding	0.045
	GO:0004312	fatty acid synthase activity	0.050
	GO:0031409	pigment binding	0.053
	GO:0016679	oxidoreductase activity, acting on diphe...	0.059
	GO:0004565	beta-galactosidase activity	0.060
	GO:0003779	actin binding	0.061
	GO:0008168	methyltransferase activity	0.061

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GO type	GO ID	Description	Adj. p-value
	GO:0016899	oxidoreductase activity, acting on the C...	0.063
	GO:0046556	alpha-L-arabinofuranosidase activity	0.066
	GO:0015925	galactosidase activity	0.067
	GO:0016405	CoA-ligase activity	0.067
	GO:0016878	acid-thiol ligase activity	0.067
	GO:0019238	cyclohydrolase activity	0.067
	GO:0019829	cation-transporting ATPase activity	0.067
	GO:0022853	active ion transmembrane transporter act...	0.067
	GO:0042625	ATPase coupled ion transmembrane transpo...	0.067
	GO:0016229	steroid dehydrogenase activity	0.070
	GO:0008233	peptidase activity	0.071
	GO:0004185	serine-type carboxypeptidase activity	0.073
	GO:0031072	heat shock protein binding	0.075
	GO:0016628	oxidoreductase activity, acting on the C...	0.076
	GO:0003854	3-beta-hydroxy-delta5-steroid dehydrogen...	0.078
	GO:0070008	serine-type exopeptidase activity	0.079
	GO:0008146	sulfotransferase activity	0.081
	GO:0016160	amylase activity	0.084
	GO:0071949	FAD binding	0.084
	GO:0019206	nucleoside kinase activity	0.085

4.1.5 Leaf - Preflowering - Cluster 5

GO type	GO ID	Description	Adj. p-value
	GO:0006464	cellular protein modification process	0.000
	GO:0036211	protein modification process	0.000
	GO:0060255	regulation of macromolecule metabolic pr...	0.000
	GO:0051171	regulation of nitrogen compound metaboli...	0.000
	GO:0080090	regulation of primary metabolic process	0.000
	GO:0019219	regulation of nucleobase-containing comp...	0.000
	GO:0051252	regulation of RNA metabolic process	0.000
	GO:1903506	regulation of nucleic acid-templated tra...	0.000
	GO:2001141	regulation of RNA biosynthetic process	0.000
	GO:0010468	regulation of gene expression	0.000
	GO:0010556	regulation of macromolecule biosynthetic...	0.000
	GO:0070647	protein modification by small protein co...	0.000
	GO:0048523	negative regulation of cellular process	0.000
	GO:0009892	negative regulation of metabolic process	0.000
	GO:0009607	response to biotic stimulus	0.001
	GO:0071395	cellular response to jasmonic acid stimu...	0.001
	GO:0009867	jasmonic acid mediated signaling pathway	0.002
	GO:0071495	cellular response to endogenous stimulus	0.003
	GO:0006022	aminoglycan metabolic process	0.004
	GO:0043161	proteasome-mediated ubiquitin-dependent ...	0.004
	GO:0006887	exocytosis	0.004
	GO:0018196	peptidyl-asparagine modification	0.004
	GO:0018279	protein N-linked glycosylation via aspar...	0.004
	GO:0019538	protein metabolic process	0.004
	GO:0031324	negative regulation of cellular metaboli...	0.004
	GO:0044267	cellular protein metabolic process	0.004
	GO:0032870	cellular response to hormone stimulus	0.005
	GO:0006026	aminoglycan catabolic process	0.005
	GO:0006030	chitin metabolic process	0.005
	GO:0006032	chitin catabolic process	0.005
	GO:0016192	vesicle-mediated transport	0.005
	GO:0046348	amino sugar catabolic process	0.005
	GO:1901072	glucosamine-containing compound cataboli...	0.005
	GO:0050832	defense response to fungus	0.006
	GO:0010629	negative regulation of gene expression	0.006
	GO:0051172	negative regulation of nitrogen compound...	0.006
	GO:0098542	defense response to other organism	0.006
	GO:0046903	secretion	0.007
	GO:0006487	protein N-linked glycosylation	0.007
	GO:1902679	negative regulation of RNA biosynthetic ...	0.007
	GO:1903507	negative regulation of nucleic acid-temp...	0.007
	GO:0010498	proteasomal protein catabolic process	0.008
	GO:0019941	modification-dependent protein catabolic...	0.010
	GO:0006511	ubiquitin-dependent protein catabolic pr...	0.011
	GO:0009812	flavonoid metabolic process	0.011
	GO:0009890	negative regulation of biosynthetic proc...	0.011

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GO type	GO ID	Description	Adj. p-value
	GO:0009755	hormone-mediated signaling pathway	0.011
	GO:0031327	negative regulation of cellular biosynth...	0.012
	GO:0032940	secretion by cell	0.012
	GO:0031146	SCF-dependent proteasomal ubiquitin-depe...	0.012
	GO:0043632	modification-dependent macromolecule cat...	0.012
	GO:0042493	response to drug	0.013
	GO:0031347	regulation of defense response	0.015
	GO:0010558	negative regulation of macromolecule bio...	0.017
	GO:1901698	response to nitrogen compound	0.018
	GO:0009813	flavonoid biosynthetic process	0.018
	GO:0045892	negative regulation of transcription, DN...	0.019
	GO:0071229	cellular response to acid chemical	0.024
	GO:0023051	regulation of signaling	0.025
	GO:0006040	amino sugar metabolic process	0.026
	GO:0045934	negative regulation of nucleobase-contai...	0.026
	GO:0009404	toxin metabolic process	0.026
	GO:0051253	negative regulation of RNA metabolic pro...	0.027
	GO:1901565	organonitrogen compound catabolic proces...	0.027
	GO:2000026	regulation of multicellular organismal d...	0.029
	GO:0009605	response to external stimulus	0.029
	GO:0009966	regulation of signal transduction	0.030
	GO:0031349	positive regulation of defense response	0.032
	GO:0051716	cellular response to stimulus	0.032
	GO:0050896	response to stimulus	0.033
	GO:0051239	regulation of multicellular organismal p...	0.035
	GO:0048507	meristem development	0.035
	GO:2000113	negative regulation of cellular macromol...	0.038
	GO:0009312	oligosaccharide biosynthetic process	0.040
	GO:1901700	response to oxygen-containing compound	0.042
	GO:0002684	positive regulation of immune system pro...	0.043
	GO:0023014	signal transduction by protein phosphory...	0.043
	GO:0050778	positive regulation of immune response	0.043
	GO:0048532	anatomical structure arrangement	0.048
	GO:0000209	protein polyubiquitination	0.048
	GO:0070085	glycosylation	0.048
	GO:0018193	peptidyl-amino acid modification	0.053
	GO:0009617	response to bacterium	0.055
	GO:0006139	nucleobase-containing compound metabolic...	0.057
	GO:1902531	regulation of intracellular signal trans...	0.058
	GO:0044238	primary metabolic process	0.063
	GO:0010646	regulation of cell communication	0.064
	GO:0050793	regulation of developmental process	0.064
	GO:0080134	regulation of response to stress	0.065
	GO:0048580	regulation of post-embryonic development	0.069
	GO:0048583	regulation of response to stimulus	0.074
	GO:0002376	immune system process	0.076
	GO:0009863	salicylic acid mediated signaling pathwa...	0.076
	GO:0051817	modification of morphology or physiology...	0.080
	GO:0045089	positive regulation of innate immune res...	0.080

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GO type	GO ID	Description	Adj. p-value
	GO:0071446	cellular response to salicylic acid stim...	0.080
	GO:0001101	response to acid chemical	0.083
	GO:0045087	innate immune response	0.086
	GO:0042742	defense response to bacterium	0.087
	GO:0010073	meristem maintenance	0.089
	GO:0009933	meristem structural organization	0.092
	GO:0009856	pollination	0.092
	GO:0044706	multi-multicellular organism process	0.092
	GO:0009753	response to jasmonic acid	0.098
	GO:0006950	response to stress	0.099
CC	GO:0005886	plasma membrane	0.000
	GO:0005911	cell-cell junction	0.007
	GO:0030054	cell junction	0.007
	GO:0009506	plasmodesma	0.008
	GO:0055044	symplast	0.008
	GO:0099023	tethering complex	0.010
	GO:0000145	exocyst	0.015
	GO:0044432	endoplasmic reticulum part	0.029
	GO:0030135	coated vesicle	0.034
	GO:0098827	endoplasmic reticulum subcompartment	0.051
	GO:0042175	nuclear outer membrane-endoplasmic retic...	0.055
	GO:0005789	endoplasmic reticulum membrane	0.058
MF	GO:0003677	DNA binding	0.000
	GO:0008061	chitin binding	0.002
	GO:0016757	transferase activity, transferring glyco...	0.002
	GO:0035251	UDP-glucosyltransferase activity	0.003
	GO:0005509	calcium ion binding	0.004
	GO:0008194	UDP-glycosyltransferase activity	0.005
	GO:0004568	chitinase activity	0.005
	GO:0016758	transferase activity, transferring hexos...	0.005
	GO:0051213	dioxygenase activity	0.035
	GO:0008408	3’-5’ exonuclease activity	0.078
	GO:0001067	regulatory region nucleic acid binding	0.085
	GO:0044212	transcription regulatory region DNA bind...	0.085
	GO:0005516	calmodulin binding	0.092

4.1.6 Leaf - Preflowering - Cluster 6

GO type	GO ID	Description	Adj. p-value
	GO:0019684	photosynthesis, light reaction	0.000
	GO:0044281	small molecule metabolic process	0.000
	GO:0051188	cofactor biosynthetic process	0.000
	GO:0022900	electron transport chain	0.000
	GO:0006732	coenzyme metabolic process	0.000
	GO:0016053	organic acid biosynthetic process	0.000
	GO:0046394	carboxylic acid biosynthetic process	0.000
	GO:0017144	drug metabolic process	0.000
	GO:0009108	coenzyme biosynthetic process	0.000
	GO:0033014	tetrapyrrole biosynthetic process	0.000
	GO:0009165	nucleotide biosynthetic process	0.000
	GO:0005975	carbohydrate metabolic process	0.000
	GO:0009150	purine ribonucleotide metabolic process	0.000
	GO:0006778	porphyrin-containing compound metabolic ...	0.000
	GO:0072522	purine-containing compound biosynthetic ...	0.000
	GO:0009124	nucleoside monophosphate biosynthetic pr...	0.000
	GO:0033013	tetrapyrrole metabolic process	0.000
	GO:0009123	nucleoside monophosphate metabolic proce...	0.000
	GO:0044262	cellular carbohydrate metabolic process	0.000
	GO:0006164	purine nucleotide biosynthetic process	0.000
	GO:0044264	cellular polysaccharide metabolic proces...	0.000
	GO:0042546	cell wall biogenesis	0.000
	GO:0009156	ribonucleoside monophosphate biosyntheti...	0.000
	GO:0009161	ribonucleoside monophosphate metabolic p...	0.000
	GO:0009152	purine ribonucleotide biosynthetic proce...	0.000
	GO:0009260	ribonucleotide biosynthetic process	0.000
	GO:0046390	ribose phosphate biosynthetic process	0.000
	GO:0016052	carbohydrate catabolic process	0.000
	GO:0016051	carbohydrate biosynthetic process	0.000
	GO:0010383	cell wall polysaccharide metabolic proce...	0.000
	GO:0000271	polysaccharide biosynthetic process	0.001
	GO:0046434	organophosphate catabolic process	0.001
	GO:1902600	proton transmembrane transport	0.001
	GO:0044275	cellular carbohydrate catabolic process	0.001
	GO:0072524	pyridine-containing compound metabolic p...	0.001
	GO:0016999	antibiotic metabolic process	0.002
	GO:0009628	response to abiotic stimulus	0.002
	GO:0018298	protein-chromophore linkage	0.002
	GO:0044036	cell wall macromolecule metabolic proces...	0.002
	GO:0044042	glucan metabolic process	0.002
	GO:0006733	oxidoreduction coenzyme metabolic proces...	0.003
	GO:0019318	hexose metabolic process	0.003
	GO:0006073	cellular glucan metabolic process	0.003
	GO:0010109	regulation of photosynthesis	0.003
	GO:0034637	cellular carbohydrate biosynthetic proce...	0.004
	GO:0009251	glucan catabolic process	0.004

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0044247	cellular polysaccharide catabolic proces...	0.004
	GO:0032787	monocarboxylic acid metabolic process	0.004
	GO:0010206	photosystem II repair	0.005
	GO:0006793	phosphorus metabolic process	0.005
	GO:0000272	polysaccharide catabolic process	0.006
	GO:0046496	nicotinamide nucleotide metabolic proces...	0.006
	GO:0072525	pyridine-containing compound biosyntheti...	0.006
	GO:0042180	cellular ketone metabolic process	0.007
	GO:0009664	plant-type cell wall organization	0.007
	GO:0006090	pyruvate metabolic process	0.008
	GO:0033692	cellular polysaccharide biosynthetic pro...	0.009
	GO:0046939	nucleotide phosphorylation	0.009
	GO:0019362	pyridine nucleotide metabolic process	0.009
	GO:0006783	heme biosynthetic process	0.011
	GO:0005983	starch catabolic process	0.011
	GO:0042168	heme metabolic process	0.013
	GO:0019359	nicotinamide nucleotide biosynthetic pro...	0.013
	GO:0009314	response to radiation	0.014
	GO:0043467	regulation of generation of precursor me...	0.015
	GO:0046365	monosaccharide catabolic process	0.015
	GO:0009416	response to light stimulus	0.016
	GO:0006767	water-soluble vitamin metabolic process	0.016
	GO:0015672	monovalent inorganic cation transport	0.017
	GO:0006796	phosphate-containing compound metabolic ...	0.017
	GO:0019363	pyridine nucleotide biosynthetic process	0.018
	GO:0090626	plant epidermis morphogenesis	0.019
	GO:0006520	cellular amino acid metabolic process	0.020
	GO:0042364	water-soluble vitamin biosynthetic proce...	0.021
	GO:0006165	nucleoside diphosphate phosphorylation	0.024
	GO:0010118	stomatal movement	0.025
	GO:0044282	small molecule catabolic process	0.027
	GO:0015980	energy derivation by oxidation of organi...	0.028
	GO:0042548	regulation of photosynthesis, light reac...	0.029
	GO:0010103	stomatal complex morphogenesis	0.029
	GO:0009132	nucleoside diphosphate metabolic process	0.030
	GO:0098754	detoxification	0.030
	GO:0019252	starch biosynthetic process	0.030
	GO:0006081	cellular aldehyde metabolic process	0.031
	GO:0045333	cellular respiration	0.032
	GO:0046364	monosaccharide biosynthetic process	0.032
	GO:0042594	response to starvation	0.034
	GO:0006108	malate metabolic process	0.037
	GO:0043648	dicarboxylic acid metabolic process	0.039
	GO:1901137	carbohydrate derivative biosynthetic pro...	0.041
	GO:0009166	nucleotide catabolic process	0.044
	GO:1901135	carbohydrate derivative metabolic proces...	0.047
	GO:0071496	cellular response to external stimulus	0.047
	GO:0030091	protein repair	0.050
	GO:0061024	membrane organization	0.054

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0090698	post-embryonic plant morphogenesis	0.057
	GO:0010119	regulation of stomatal movement	0.057
	GO:0034404	nucleobase-containing small molecule bio...	0.057
	GO:1901292	nucleoside phosphate catabolic process	0.057
	GO:0006096	glycolytic process	0.062
	GO:0006757	ATP generation from ADP	0.062
	GO:0009135	purine nucleoside diphosphate metabolic ...	0.062
	GO:0009179	purine ribonucleoside diphosphate metabo...	0.062
	GO:0009185	ribonucleoside diphosphate metabolic pro...	0.062
	GO:0009645	response to low light intensity stimulus	0.062
	GO:0042866	pyruvate biosynthetic process	0.062
	GO:0046031	ADP metabolic process	0.062
	GO:0009308	amine metabolic process	0.066
	GO:0009060	aerobic respiration	0.070
	GO:0009991	response to extracellular stimulus	0.073
	GO:0043038	amino acid activation	0.074
	GO:0043039	tRNA aminoacylation	0.074
	GO:0019682	glyceraldehyde-3-phosphate metabolic pro...	0.079
	GO:0042726	flavin-containing compound metabolic pro...	0.084
	GO:0015740	C4-dicarboxylate transport	0.086
	GO:0031668	cellular response to extracellular stimu...	0.088
	GO:0006099	tricarboxylic acid cycle	0.088
	GO:1901568	fatty acid derivative metabolic process	0.095
	GO:0009250	glucan biosynthetic process	0.097
CC	GO:0031977	thylakoid lumen	0.000
	GO:0009521	photosystem	0.000
	GO:0005576	extracellular region	0.000
	GO:1990204	oxidoreductase complex	0.000
	GO:0005740	mitochondrial envelope	0.000
	GO:0016469	proton-transporting two-sector ATPase co...	0.000
	GO:0070469	respiratory chain	0.000
	GO:0031969	chloroplast membrane	0.001
	GO:0042170	plastid membrane	0.002
	GO:0043227	membrane-bounded organelle	0.002
	GO:0043231	intracellular membrane-bounded organelle	0.004
	GO:0005739	mitochondrion	0.005
	GO:0009505	plant-type cell wall	0.005
	GO:0033178	proton-transporting two-sector ATPase co...	0.008
	GO:0045261	proton-transporting ATP synthase complex...	0.025
	GO:0043226	organelle	0.039
	GO:0043229	intracellular organelle	0.043
	GO:0005623	cell	0.048
	GO:0044425	membrane part	0.051
	GO:0044464	cell part	0.057
	GO:0009295	nucleoid	0.082
	GO:0009524	phragmoplast	0.082
	GO:0016787	hydrolase activity	0.000
	GO:0016798	hydrolase activity, acting on glycosyl b...	0.000
	GO:0016829	lyase activity	0.000

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0016788	hydrolase activity, acting on ester bond...	0.000
	GO:0016791	phosphatase activity	0.000
	GO:0016209	antioxidant activity	0.000
	GO:0016747	transferase activity, transferring acyl ...	0.000
	GO:0050662	coenzyme binding	0.001
	GO:0016684	oxidoreductase activity, acting on perox...	0.001
	GO:0016830	carbon-carbon lyase activity	0.001
	GO:0004601	peroxidase activity	0.002
	GO:0044769	ATPase activity, coupled to transmembran...	0.004
	GO:0016616	oxidoreductase activity, acting on the C...	0.005
	GO:0031409	pigment binding	0.005
	GO:0015399	primary active transmembrane transporter...	0.008
	GO:0015405	P-P-bond-hydrolysis-driven transmembrane...	0.008
	GO:0046983	protein dimerization activity	0.008
	GO:0022857	transmembrane transporter activity	0.012
	GO:0019203	carbohydrate phosphatase activity	0.013
	GO:0016615	malate dehydrogenase activity	0.014
	GO:0016776	phosphotransferase activity, phosphate g...	0.015
	GO:0016831	carboxy-lyase activity	0.016
	GO:0050308	sugar-phosphatase activity	0.017
	GO:0042626	ATPase activity, coupled to transmembran...	0.018
	GO:0016853	isomerase activity	0.019
	GO:0043492	ATPase activity, coupled to movement of ...	0.024
	GO:0015075	ion transmembrane transporter activity	0.025
	GO:0016861	intramolecular oxidoreductase activity, ...	0.025
	GO:0019829	cation-transporting ATPase activity	0.029
	GO:0022853	active ion transmembrane transporter act...	0.029
	GO:0042625	ATPase coupled ion transmembrane transpo...	0.029
	GO:0005215	transporter activity	0.041
	GO:0022804	active transmembrane transporter activit...	0.042
	GO:0051287	NAD binding	0.059
	GO:0015318	inorganic molecular entity transmembrane...	0.065
	GO:0015925	galactosidase activity	0.072
	GO:0016799	hydrolase activity, hydrolyzing N-glycos...	0.072
	GO:0015556	C4-dicarboxylate transmembrane transport...	0.076
	GO:0008289	lipid binding	0.081
	GO:0031072	heat shock protein binding	0.081
	GO:0019205	nucleobase-containing compound kinase ac...	0.082
	GO:0019842	vitamin binding	0.085
	GO:0016597	amino acid binding	0.092
	GO:0008509	anion transmembrane transporter activity	0.095
	GO:0016620	oxidoreductase activity, acting on the a...	0.095

4.1.7 Leaf - Preflowering - Cluster 7

GO type	GO ID	Description	Adj. p-value
BP	GO:0060255	regulation of macromolecule metabolic pr...	0.000
	GO:0051171	regulation of nitrogen compound metaboli...	0.000
	GO:0016070	RNA metabolic process	0.000
	GO:0080090	regulation of primary metabolic process	0.000
	GO:0019219	regulation of nucleobase-containing comp...	0.000
	GO:0051252	regulation of RNA metabolic process	0.000
	GO:0010468	regulation of gene expression	0.000
	GO:0010556	regulation of macromolecule biosynthetic...	0.000
	GO:2000112	regulation of cellular macromolecule bio...	0.000
	GO:0031326	regulation of cellular biosynthetic proc...	0.000
	GO:0097659	nucleic acid-templated transcription	0.000
	GO:0070647	protein modification by small protein co...	0.000
	GO:0010498	proteasomal protein catabolic process	0.000
	GO:0043161	proteasome-mediated ubiquitin-dependent ...	0.000
	GO:0019941	modification-dependent protein catabolic...	0.001
	GO:0043632	modification-dependent macromolecule cat...	0.001
	GO:0015850	organic hydroxy compound transport	0.002
	GO:1904659	glucose transmembrane transport	0.004
	GO:0006887	exocytosis	0.005
	GO:0046323	glucose import	0.006
	GO:0008645	hexose transmembrane transport	0.007
	GO:0015749	monosaccharide transmembrane transport	0.008
	GO:0046903	secretion	0.012
	GO:0046113	nucleobase catabolic process	0.015
	GO:0018196	peptidyl-asparagine modification	0.017
	GO:0018279	protein N-linked glycosylation via aspar...	0.017
	GO:0010629	negative regulation of gene expression	0.019
	GO:0032940	secretion by cell	0.019
	GO:0006749	glutathione metabolic process	0.021
	GO:0010243	response to organonitrogen compound	0.021
	GO:1901565	organonitrogen compound catabolic proces...	0.028
	GO:0015791	polyol transport	0.028
	GO:0006487	protein N-linked glycosylation	0.038
	GO:0051603	proteolysis involved in cellular protein...	0.043
	GO:0006829	zinc ion transport	0.047
	GO:0044257	cellular protein catabolic process	0.049
	GO:0006884	cell volume homeostasis	0.054
	GO:0009992	cellular water homeostasis	0.054
	GO:0015793	glycerol transport	0.054
	GO:0019748	secondary metabolic process	0.054
	GO:0009101	glycoprotein biosynthetic process	0.056
	GO:0044265	cellular macromolecule catabolic process	0.058
	GO:0008361	regulation of cell size	0.060
	GO:0071826	ribonucleoprotein complex subunit organi...	0.068
	GO:0034620	cellular response to unfolded protein	0.076
	GO:0035967	cellular response to topologically incor...	0.076

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GO type	GO ID	Description	Adj. p-value
	GO:0071577	zinc ion transmembrane transport	0.076
	GO:0016310	phosphorylation	0.076
	GO:0070085	glycosylation	0.088
	GO:0006505	GPI anchor metabolic process	0.091
	GO:0006506	GPI anchor biosynthetic process	0.091
	GO:0071705	nitrogen compound transport	0.093
CC	GO:0000151	ubiquitin ligase complex	0.000
	GO:0031461	cullin-RING ubiquitin ligase complex	0.000
	GO:0005681	spliceosomal complex	0.000
	GO:0030117	membrane coat	0.008
	GO:0048475	coated membrane	0.008
	GO:0005635	nuclear envelope	0.009
	GO:0099023	tethering complex	0.009
	GO:0012505	endomembrane system	0.011
	GO:0005798	Golgi-associated vesicle	0.014
	GO:0005684	U2-type spliceosomal complex	0.016
	GO:0030120	vesicle coat	0.016
	GO:0005783	endoplasmic reticulum	0.022
	GO:0071004	U2-type prespliceosome	0.036
	GO:0005911	cell-cell junction	0.038
	GO:0030054	cell junction	0.038
	GO:0009506	plasmodesma	0.041
	GO:0055044	symplast	0.041
	GO:0030660	Golgi-associated vesicle membrane	0.081
	GO:0071013	catalytic step 2 spliceosome	0.081
	GO:0030662	coated vesicle membrane	0.083
	GO:0071010	prespliceosome	0.083
MF	GO:0005488	binding	0.000
	GO:0004497	monooxygenase activity	0.000
	GO:0003676	nucleic acid binding	0.000
	GO:0004672	protein kinase activity	0.000
	GO:0016705	oxidoreductase activity, acting on paire...	0.000
	GO:0032559	adenyl ribonucleotide binding	0.003
	GO:0030554	adenyl nucleotide binding	0.004
	GO:0097367	carbohydrate derivative binding	0.004
	GO:0016773	phosphotransferase activity, alcohol gro...	0.005
	GO:0032553	ribonucleotide binding	0.005
	GO:0008061	chitin binding	0.007
	GO:0032555	purine ribonucleotide binding	0.007
	GO:0017076	purine nucleotide binding	0.007
	GO:0004674	protein serine/threonine kinase activity	0.008
	GO:0005355	glucose transmembrane transporter activi...	0.008
	GO:0000166	nucleotide binding	0.009
	GO:0008194	UDP-glycosyltransferase activity	0.009
	GO:1901265	nucleoside phosphate binding	0.009
	GO:1901618	organic hydroxy compound transmembrane t...	0.009
	GO:0015149	hexose transmembrane transporter activit...	0.016
	GO:0140096	catalytic activity, acting on a protein	0.017
	GO:0046527	glucosyltransferase activity	0.018

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0015145	monosaccharide transmembrane transporter...	0.018
	GO:0015166	polyol transmembrane transporter activit...	0.018
	GO:0016758	transferase activity, transferring hexos...	0.024
	GO:0051213	dioxygenase activity	0.028
	GO:0036094	small molecule binding	0.030
	GO:0004364	glutathione transferase activity	0.031
	GO:0015168	glycerol transmembrane transporter activ...	0.031
	GO:0046906	tetrapyrrole binding	0.043
	GO:0005372	water transmembrane transporter activity	0.056
	GO:0015250	water channel activity	0.056
	GO:0015254	glycerol channel activity	0.056
	GO:0030246	carbohydrate binding	0.056
	GO:0043168	anion binding	0.057
	GO:0015293	symporter activity	0.058
	GO:0001067	regulatory region nucleic acid binding	0.064
	GO:0044212	transcription regulatory region DNA bind...	0.064
	GO:0008536	Ran GTPase binding	0.068
	GO:0005385	zinc ion transmembrane transporter activ...	0.076
	GO:0015294	solute:cation symporter activity	0.079
	GO:0046914	transition metal ion binding	0.086
	GO:0016757	transferase activity, transferring glyco...	0.086
	GO:0031624	ubiquitin conjugating enzyme binding	0.086
	GO:0044390	ubiquitin-like protein conjugating enzym...	0.086

4.1.8 Leaf - Preflowering - Cluster 8

GO type	GO ID	Description	Adj. p-value
	GO:0019684	photosynthesis, light reaction	0.000
	GO:0051188	cofactor biosynthetic process	0.000
	GO:0044283	small molecule biosynthetic process	0.000
	GO:0019637	organophosphate metabolic process	0.000
	GO:0051186	cofactor metabolic process	0.000
	GO:0016053	organic acid biosynthetic process	0.000
	GO:0046394	carboxylic acid biosynthetic process	0.000
	GO:0006753	nucleoside phosphate metabolic process	0.000
	GO:0006732	coenzyme metabolic process	0.000
	GO:0005975	carbohydrate metabolic process	0.000
	GO:0009150	purine ribonucleotide metabolic process	0.000
	GO:0071554	cell wall organization or biogenesis	0.000
	GO:0009123	nucleoside monophosphate metabolic proce...	0.000
	GO:0022900	electron transport chain	0.000
	GO:0009699	phenylpropanoid biosynthetic process	0.000
	GO:0006629	lipid metabolic process	0.000
	GO:0008610	lipid biosynthetic process	0.000
	GO:0046434	organophosphate catabolic process	0.000
	GO:0033014	tetrapyrrole biosynthetic process	0.000
	GO:0046034	ATP metabolic process	0.000
	GO:0017144	drug metabolic process	0.000
	GO:0044262	cellular carbohydrate metabolic process	0.000
	GO:1901293	nucleoside phosphate biosynthetic proces...	0.000
	GO:0009165	nucleotide biosynthetic process	0.000
	GO:0071555	cell wall organization	0.000
	GO:0042546	cell wall biogenesis	0.000
	GO:0006090	pyruvate metabolic process	0.000
	GO:0090407	organophosphate biosynthetic process	0.000
	GO:0009145	purine nucleoside triphosphate biosynthe...	0.000
	GO:0009206	purine ribonucleoside triphosphate biosy...	0.000
	GO:0006164	purine nucleotide biosynthetic process	0.000
	GO:0019359	nicotinamide nucleotide biosynthetic pro...	0.000
	GO:0009201	ribonucleoside triphosphate biosynthetic...	0.000
	GO:0046939	nucleotide phosphorylation	0.000
	GO:0009152	purine ribonucleotide biosynthetic proce...	0.000
	GO:0009073	aromatic amino acid family biosynthetic ...	0.000
	GO:0008299	isoprenoid biosynthetic process	0.000
	GO:0010383	cell wall polysaccharide metabolic proce...	0.000
	GO:0000272	polysaccharide catabolic process	0.000
	GO:0015980	energy derivation by oxidation of organi...	0.001
	GO:0098869	cellular oxidant detoxification	0.001
	GO:0044275	cellular carbohydrate catabolic process	0.001
	GO:0006766	vitamin metabolic process	0.001
	GO:0034404	nucleobase-containing small molecule bio...	0.001
	GO:0016051	carbohydrate biosynthetic process	0.002
	GO:0016109	tetraterpenoid biosynthetic process	0.002

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GO type	GO ID	Description	Adj. p-value
	GO:0016117	carotenoid biosynthetic process	0.002
	GO:0006783	heme biosynthetic process	0.002
	GO:0010410	hemicellulose metabolic process	0.003
	GO:0009808	lignin metabolic process	0.003
	GO:0045333	cellular respiration	0.003
	GO:0006793	phosphorus metabolic process	0.003
	GO:0009110	vitamin biosynthetic process	0.003
	GO:0009664	plant-type cell wall organization	0.004
	GO:0046365	monosaccharide catabolic process	0.004
	GO:0016311	dephosphorylation	0.005
	GO:0010207	photosystem II assembly	0.005
	GO:0045491	xylan metabolic process	0.005
	GO:1901135	carbohydrate derivative metabolic proces...	0.005
	GO:0048235	pollen sperm cell differentiation	0.006
	GO:0009060	aerobic respiration	0.006
	GO:0016122	xanthophyll metabolic process	0.007
	GO:0034637	cellular carbohydrate biosynthetic proce...	0.008
	GO:0006520	cellular amino acid metabolic process	0.008
	GO:0030244	cellulose biosynthetic process	0.008
	GO:0044247	cellular polysaccharide catabolic proces...	0.008
	GO:0046185	aldehyde catabolic process	0.008
	GO:0009409	response to cold	0.008
	GO:0042214	terpene metabolic process	0.009
	GO:0008652	cellular amino acid biosynthetic process	0.009
	GO:0006006	glucose metabolic process	0.010
	GO:0030243	cellulose metabolic process	0.010
	GO:0030091	protein repair	0.010
	GO:2000652	regulation of secondary cell wall biogen...	0.011
	GO:0044036	cell wall macromolecule metabolic proces...	0.012
	GO:0032271	regulation of protein polymerization	0.012
	GO:0010114	response to red light	0.012
	GO:0006796	phosphate-containing compound metabolic ...	0.012
	GO:0009314	response to radiation	0.012
	GO:0010103	stomatal complex morphogenesis	0.012
	GO:0006081	cellular aldehyde metabolic process	0.013
	GO:0009416	response to light stimulus	0.016
	GO:0010143	cutin biosynthetic process	0.017
	GO:0017004	cytochrome complex assembly	0.017
	GO:0009773	photosynthetic electron transport in pho...	0.017
	GO:0035336	long-chain fatty-acyl-CoA metabolic proc...	0.019
	GO:0009251	glucan catabolic process	0.019
	GO:0000162	tryptophan biosynthetic process	0.021
	GO:0010206	photosystem II repair	0.021
	GO:0046219	indolalkylamine biosynthetic process	0.021
	GO:0071214	cellular response to abiotic stimulus	0.021
	GO:0104004	cellular response to environmental stimu...	0.021
	GO:0005983	starch catabolic process	0.021
	GO:0009250	glucan biosynthetic process	0.024
	GO:0009395	phospholipid catabolic process	0.024

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GO type	GO ID	Description	Adj. p-value
	GO:0042168	heme metabolic process	0.024
	GO:1901401	regulation of tetrapyrrole metabolic pro...	0.024
	GO:0007010	cytoskeleton organization	0.025
	GO:0098660	inorganic ion transmembrane transport	0.025
	GO:0006576	cellular biogenic amine metabolic proces...	0.027
	GO:0009309	amine biosynthetic process	0.027
	GO:0042401	cellular biogenic amine biosynthetic pro...	0.027
	GO:0032544	plastid translation	0.029
	GO:0009438	methylglyoxal metabolic process	0.033
	GO:0042182	ketone catabolic process	0.033
	GO:0046854	phosphatidylinositol phosphorylation	0.033
	GO:0051596	methylglyoxal catabolic process	0.033
	GO:0009628	response to abiotic stimulus	0.034
	GO:0030041	actin filament polymerization	0.034
	GO:0030833	regulation of actin filament polymerizat...	0.034
	GO:0043038	amino acid activation	0.034
	GO:0043039	tRNA aminoacylation	0.034
	GO:0019430	removal of superoxide radicals	0.034
	GO:0071450	cellular response to oxygen radical	0.034
	GO:0071451	cellular response to superoxide	0.034
	GO:0010109	regulation of photosynthesis	0.034
	GO:0044550	secondary metabolite biosynthetic proces...	0.036
	GO:0071478	cellular response to radiation	0.036
	GO:0035337	fatty-acyl-CoA metabolic process	0.037
	GO:0046184	aldehyde biosynthetic process	0.037
	GO:0048438	floral whorl development	0.038
	GO:1901137	carbohydrate derivative biosynthetic pro...	0.038
	GO:1901615	organic hydroxy compound metabolic proce...	0.042
	GO:0048481	plant ovule development	0.043
	GO:0006108	malate metabolic process	0.045
	GO:0019674	NAD metabolic process	0.047
	GO:0016114	terpenoid biosynthetic process	0.048
	GO:0071482	cellular response to light stimulus	0.049
	GO:0009741	response to brassinosteroid	0.050
	GO:0006721	terpenoid metabolic process	0.053
	GO:1901617	organic hydroxy compound biosynthetic pr...	0.053
	GO:0006284	base-excision repair	0.053
	GO:0015985	energy coupled proton transport, down el...	0.053
	GO:0015986	ATP synthesis coupled proton transport	0.053
	GO:0006644	phospholipid metabolic process	0.054
	GO:0006089	lactate metabolic process	0.056
	GO:0009074	aromatic amino acid family catabolic pro...	0.056
	GO:0019243	methylglyoxal catabolic process to D-lac...	0.056
	GO:0061727	methylglyoxal catabolic process to lacta...	0.056
	GO:0006558	L-phenylalanine metabolic process	0.056
	GO:1902221	erythrose 4-phosphate/phosphoenolpyruvat...	0.056
	GO:0006743	ubiquinone metabolic process	0.056
	GO:0006744	ubiquinone biosynthetic process	0.056
	GO:0009642	response to light intensity	0.056

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GO type	GO ID	Description	Adj. p-value
	GO:1901568	fatty acid derivative metabolic process	0.056
	GO:0035670	plant-type ovary development	0.057
	GO:0010345	suberin biosynthetic process	0.058
	GO:0008064	regulation of actin polymerization or de...	0.060
	GO:0030832	regulation of actin filament length	0.060
	GO:0032956	regulation of actin cytoskeleton organiz...	0.060
	GO:0032970	regulation of actin filament-based proce...	0.060
	GO:0110053	regulation of actin filament organizatio...	0.060
	GO:0098662	inorganic cation transmembrane transport	0.061
	GO:0045492	xylan biosynthetic process	0.061
	GO:0015672	monovalent inorganic cation transport	0.062
	GO:0051261	protein depolymerization	0.063
	GO:0090626	plant epidermis morphogenesis	0.063
	GO:0006637	acyl-CoA metabolic process	0.063
	GO:0018298	protein-chromophore linkage	0.063
	GO:0035383	thioester metabolic process	0.063
	GO:0044106	cellular amine metabolic process	0.064
	GO:0044249	cellular biosynthetic process	0.064
	GO:0046834	lipid phosphorylation	0.064
	GO:1902903	regulation of supramolecular fiber organ...	0.064
	GO:0008272	sulfate transport	0.068
	GO:0006418	tRNA aminoacylation for protein translat...	0.068
	GO:1901607	alpha-amino acid biosynthetic process	0.068
	GO:0051274	beta-glucan biosynthetic process	0.070
	GO:0098586	cellular response to virus	0.070
	GO:1903338	regulation of cell wall organization or ...	0.071
	GO:0034614	cellular response to reactive oxygen spe...	0.071
	GO:0008152	metabolic process	0.072
	GO:0051273	beta-glucan metabolic process	0.074
	GO:0010052	guard cell differentiation	0.074
	GO:1901566	organonitrogen compound biosynthetic pro...	0.076
	GO:0043244	regulation of protein complex disassembl...	0.077
	GO:0070592	cell wall polysaccharide biosynthetic pr...	0.079
	GO:0022904	respiratory electron transport chain	0.083
	GO:0043467	regulation of generation of precursor me...	0.086
	GO:0044038	cell wall macromolecule biosynthetic pro...	0.086
	GO:0070589	cellular component macromolecule biosynt...	0.086
	GO:0032259	methylation	0.089
	GO:0042335	cuticle development	0.091
	GO:0006119	oxidative phosphorylation	0.092
	GO:0042773	ATP synthesis coupled electron transport	0.092
	GO:0009308	amine metabolic process	0.096
	GO:0031977	thylakoid lumen	0.000
	GO:0005576	extracellular region	0.000
	GO:0016469	proton-transporting two-sector ATPase co...	0.000
	GO:0031969	chloroplast membrane	0.000
	GO:0005856	cytoskeleton	0.000
	GO:0044430	cytoskeletal part	0.000
	GO:1990204	oxidoreductase complex	0.000

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GO type	GO ID	Description	Adj. p-value
	GO:0005875	microtubule associated complex	0.000
	GO:0005743	mitochondrial inner membrane	0.000
	GO:0033176	proton-transporting V-type ATPase comple...	0.000
	GO:0009295	nucleoid	0.001
	GO:0009528	plastid inner membrane	0.001
	GO:0042646	plastid nucleoid	0.001
	GO:0046658	anchored component of plasma membrane	0.001
	GO:0070469	respiratory chain	0.001
	GO:0044455	mitochondrial membrane part	0.001
	GO:0016020	membrane	0.001
	GO:0010319	stromule	0.002
	GO:0005618	cell wall	0.002
	GO:0030312	external encapsulating structure	0.002
	GO:0005881	cytoplasmic microtubule	0.002
	GO:0030863	cortical cytoskeleton	0.002
	GO:0030981	cortical microtubule cytoskeleton	0.002
	GO:0009706	chloroplast inner membrane	0.003
	GO:0005753	mitochondrial proton-transporting ATP sy...	0.004
	GO:0098796	membrane protein complex	0.004
	GO:0042644	chloroplast nucleoid	0.004
	GO:0098803	respiratory chain complex	0.005
	GO:0009654	photosystem II oxygen evolving complex	0.006
	GO:0005746	mitochondrial respiratory chain	0.008
	GO:0009505	plant-type cell wall	0.008
	GO:0055028	cortical microtubule	0.009
	GO:0045259	proton-transporting ATP synthase complex	0.010
	GO:0098798	mitochondrial protein complex	0.010
	GO:0030964	NADH dehydrogenase complex	0.010
	GO:0045271	respiratory chain complex I	0.010
	GO:0005747	mitochondrial respiratory chain complex ...	0.018
	GO:0009524	phragmoplast	0.039
	GO:0000229	cytoplasmic chromosome	0.052
	GO:0009508	plastid chromosome	0.085
	GO:0016787	hydrolase activity	0.000
	GO:0016829	lyase activity	0.000
	GO:0016788	hydrolase activity, acting on ester bond...	0.000
	GO:0016491	oxidoreductase activity	0.000
	GO:0042578	phosphoric ester hydrolase activity	0.000
	GO:0016791	phosphatase activity	0.000
	GO:0016655	oxidoreductase activity, acting on NAD(P...	0.000
	GO:0003954	NADH dehydrogenase activity	0.000
	GO:0008168	methyltransferase activity	0.002
	GO:0050662	coenzyme binding	0.002
	GO:0016747	transferase activity, transferring acyl ...	0.002
	GO:0016168	chlorophyll binding	0.003
	GO:0016746	transferase activity, transferring acyl ...	0.003
	GO:0008236	serine-type peptidase activity	0.003
	GO:0016413	O-acetyltransferase activity	0.003
	GO:0016614	oxidoreductase activity, acting on CH-OH...	0.003

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0017171	serine hydrolase activity	0.003
	GO:0016762	xyloglucan:xyloglucosyl transferase acti...	0.003
	GO:0004252	serine-type endopeptidase activity	0.004
	GO:0008374	O-acyltransferase activity	0.004
	GO:0016759	cellulose synthase activity	0.004
	GO:0016760	cellulose synthase (UDP-forming) activit...	0.004
	GO:0016830	carbon-carbon lyase activity	0.004
	GO:0008137	NADH dehydrogenase (ubiquinone) activity	0.004
	GO:0016838	carbon-oxygen lyase activity, acting on ...	0.004
	GO:0048037	cofactor binding	0.004
	GO:0050136	NADH dehydrogenase (quinone) activity	0.004
	GO:0016836	hydro-lyase activity	0.004
	GO:0016620	oxidoreductase activity, acting on the a...	0.005
	GO:0016778	diphosphotransferase activity	0.007
	GO:0140097	catalytic activity, acting on DNA	0.008
	GO:0008574	ATP-dependent microtubule motor activity...	0.008
	GO:0046961	proton-transporting ATPase activity, rot...	0.008
	GO:1990939	ATP-dependent microtubule motor activity	0.008
	GO:0016790	thiolester hydrolase activity	0.009
	GO:0016866	intramolecular transferase activity	0.010
	GO:0016903	oxidoreductase activity, acting on the a...	0.010
	GO:2001070	starch binding	0.010
	GO:0016776	phosphotransferase activity, phosphate g...	0.012
	GO:0019203	carbohydrate phosphatase activity	0.013
	GO:0010333	terpene synthase activity	0.013
	GO:0016853	isomerase activity	0.015
	GO:0016840	carbon-nitrogen lyase activity	0.015
	GO:0016407	acetyltransferase activity	0.015
	GO:0016462	pyrophosphatase activity	0.016
	GO:0080019	fatty-acyl-CoA reductase (alcohol-formin...	0.016
	GO:0036442	proton-exporting ATPase activity	0.018
	GO:0016887	ATPase activity	0.019
	GO:0016616	oxidoreductase activity, acting on the C...	0.019
	GO:0019205	nucleobase-containing compound kinase ac...	0.019
	GO:0008757	S-adenosylmethionine-dependent methyltra...	0.020
	GO:0140101	catalytic activity, acting on a tRNA	0.023
	GO:0016818	hydrolase activity, acting on acid anhyd...	0.024
	GO:0017111	nucleoside-triphosphatase activity	0.025
	GO:0033764	steroid dehydrogenase activity, acting o...	0.031
	GO:0031409	pigment binding	0.034
	GO:0046933	proton-transporting ATP synthase activit...	0.034
	GO:0016817	hydrolase activity, acting on acid anhyd...	0.034
	GO:0051287	NAD binding	0.039
	GO:0016799	hydrolase activity, hydrolyzing N-glycos...	0.041
	GO:0019104	DNA N-glycosylase activity	0.042
	GO:0051015	actin filament binding	0.049
	GO:0016684	oxidoreductase activity, acting on perox...	0.049
	GO:0016615	malate dehydrogenase activity	0.050
	GO:0003779	actin binding	0.054

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0016740	transferase activity	0.054
	GO:0003854	3-beta-hydroxy-delta5-steroid dehydrogen...	0.059
	GO:0016229	steroid dehydrogenase activity	0.061
	GO:0050308	sugar-phosphatase activity	0.061
	GO:0004812	aminoacyl-tRNA ligase activity	0.064
	GO:0016875	ligase activity, forming carbon-oxygen b...	0.064
	GO:0004601	peroxidase activity	0.084
	GO:0016868	intramolecular transferase activity, pho...	0.085
	GO:0004185	serine-type carboxypeptidase activity	0.088
	GO:0070008	serine-type exopeptidase activity	0.093
	GO:0016874	ligase activity	0.095
	GO:0042349	guiding stereospecific synthesis activit...	0.095
	GO:0016774	phosphotransferase activity, carboxyl gr...	0.099
	GO:0050661	NADP binding	0.100

4.1.9 Leaf - Preflowering - Cluster 9

GO type	GO ID	Description	Adj. p-value
BP	GO:0060255	regulation of macromolecule metabolic pr...	0.000
	GO:0031323	regulation of cellular metabolic process	0.000
	GO:0009892	negative regulation of metabolic process	0.000
	GO:0018205	peptidyl-lysine modification	0.000
	GO:0022613	ribonucleoprotein complex biogenesis	0.000
	GO:0009451	RNA modification	0.000
	GO:0042493	response to drug	0.003
	GO:0032259	methylation	0.003
	GO:1901698	response to nitrogen compound	0.004
	GO:0010200	response to chitin	0.005
	GO:0018022	peptidyl-lysine methylation	0.005
	GO:0042254	ribosome biogenesis	0.005
	GO:0010243	response to organonitrogen compound	0.006
	GO:0048519	negative regulation of biological proces...	0.008
	GO:0031497	chromatin assembly	0.008
	GO:0006333	chromatin assembly or disassembly	0.008
	GO:0042542	response to hydrogen peroxide	0.009
	GO:0018193	peptidyl-amino acid modification	0.011
	GO:0006334	nucleosome assembly	0.011
	GO:0009266	response to temperature stimulus	0.011
	GO:0006323	DNA packaging	0.013
	GO:0010608	posttranscriptional regulation of gene e...	0.014
	GO:0031324	negative regulation of cellular metaboli...	0.015
	GO:0034728	nucleosome organization	0.020
	GO:0051603	proteolysis involved in cellular protein...	0.024
	GO:0044265	cellular macromolecule catabolic process	0.033
	GO:0001510	RNA methylation	0.034
	GO:0048523	negative regulation of cellular process	0.036
	GO:0048831	regulation of shoot system development	0.036
	GO:0044257	cellular protein catabolic process	0.039
	GO:0071103	DNA conformation change	0.044
	GO:0071826	ribonucleoprotein complex subunit organi...	0.056
	GO:0022618	ribonucleoprotein complex assembly	0.058
	GO:0046113	nucleobase catabolic process	0.063
	GO:0009966	regulation of signal transduction	0.066
	GO:0051246	regulation of protein metabolic process	0.071
	GO:0097305	response to alcohol	0.071
	GO:0032268	regulation of cellular protein metabolic...	0.077
	GO:0009737	response to abscisic acid	0.078
	GO:0023051	regulation of signaling	0.079
	GO:0009909	regulation of flower development	0.081
	GO:0006366	transcription by RNA polymerase II	0.097
CC	GO:0000151	ubiquitin ligase complex	0.000
	GO:0005622	intracellular	0.003
	GO:0000785	chromatin	0.004
	GO:0005694	chromosome	0.018

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GO type	GO ID	Description	Adj. p-value
	GO:0000228	nuclear chromosome	0.028
	GO:0043228	non-membrane-bounded organelle	0.056
	GO:0043232	intracellular non-membrane-bounded organ...	0.056
	GO:0044454	nuclear chromosome part	0.077
	GO:0044427	chromosomal part	0.091
MF	GO:0097159	organic cyclic compound binding	0.009
	GO:1901363	heterocyclic compound binding	0.010
	GO:0046914	transition metal ion binding	0.015
	GO:0051082	unfolded protein binding	0.032
	GO:0080043	quercetin 3-O-glucosyltransferase activi...	0.035
	GO:0080044	quercetin 7-O-glucosyltransferase activi...	0.035
	GO:0051213	dioxygenase activity	0.054

4.1.10 Leaf - Preflowering - Cluster 10

GO type	GO ID	Description	Adj. p-value
BP	GO:0071554	cell wall organization or biogenesis	0.000
	GO:0006793	phosphorus metabolic process	0.000
	GO:0005975	carbohydrate metabolic process	0.000
	GO:0072330	monocarboxylic acid biosynthetic process	0.000
	GO:0046394	carboxylic acid biosynthetic process	0.000
	GO:0016310	phosphorylation	0.000
	GO:0006629	lipid metabolic process	0.000
	GO:0000272	polysaccharide catabolic process	0.000
	GO:0030243	cellulose metabolic process	0.001
	GO:0006633	fatty acid biosynthetic process	0.001
	GO:0006270	DNA replication initiation	0.003
	GO:0006631	fatty acid metabolic process	0.004
	GO:0030244	cellulose biosynthetic process	0.004
	GO:0044275	cellular carbohydrate catabolic process	0.007
	GO:0051273	beta-glucan metabolic process	0.016
	GO:0006260	DNA replication	0.019
	GO:0070887	cellular response to chemical stimulus	0.021
	GO:0006468	protein phosphorylation	0.021
	GO:0044247	cellular polysaccharide catabolic proces...	0.021
	GO:0099402	plant organ development	0.028
	GO:0048438	floral whorl development	0.028
	GO:0006261	DNA-dependent DNA replication	0.030
	GO:0009251	glucan catabolic process	0.035
	GO:0048467	gynoecium development	0.035
	GO:0016311	dephosphorylation	0.042
	GO:0098662	inorganic cation transmembrane transport	0.042
	GO:0009653	anatomical structure morphogenesis	0.052
	GO:0009250	glucan biosynthetic process	0.054
	GO:0051274	beta-glucan biosynthetic process	0.062
	GO:0005982	starch metabolic process	0.075
	GO:0048827	phyllome development	0.079
CC	GO:0005618	cell wall	0.000
	GO:0016020	membrane	0.000
	GO:0005886	plasma membrane	0.000
	GO:0043596	nuclear replication fork	0.074
	GO:0044425	membrane part	0.078
	GO:0005657	replication fork	0.087
	GO:0016787	hydrolase activity	0.000
	GO:0016829	lyase activity	0.000
	GO:0016301	kinase activity	0.000
	GO:0016788	hydrolase activity, acting on ester bond...	0.000
	GO:0042578	phosphoric ester hydrolase activity	0.000
	GO:0016773	phosphotransferase activity, alcohol gro...	0.000
	GO:0016791	phosphatase activity	0.000
	GO:0016747	transferase activity, transferring acyl ...	0.002
	GO:0004674	protein serine/threonine kinase activity	0.003

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GO type	GO ID	Description	Adj. p-value
	GO:0017076	purine nucleotide binding	0.003
	GO:0032555	purine ribonucleotide binding	0.003
	GO:0032553	ribonucleotide binding	0.005
	GO:0097367	carbohydrate derivative binding	0.005
	GO:0016757	transferase activity, transferring glyco...	0.007
	GO:0043168	anion binding	0.007
	GO:0016746	transferase activity, transferring acyl ...	0.007
	GO:0008374	O-acyltransferase activity	0.010
	GO:0042626	ATPase activity, coupled to transmembran...	0.021
	GO:0015399	primary active transmembrane transporter...	0.024
	GO:0015405	P-P-bond-hydrolysis-driven transmembrane...	0.024
	GO:0043492	ATPase activity, coupled to movement of ...	0.031
	GO:0004185	serine-type carboxypeptidase activity	0.037
	GO:0004180	carboxypeptidase activity	0.037
	GO:0016887	ATPase activity	0.042
	GO:0008236	serine-type peptidase activity	0.047
	GO:0017171	serine hydrolase activity	0.047
	GO:0016462	pyrophosphatase activity	0.062
	GO:0016866	intramolecular transferase activity	0.062
	GO:0070008	serine-type exopeptidase activity	0.071
	GO:0008289	lipid binding	0.074
	GO:0017111	nucleoside-triphosphatase activity	0.074
	GO:0140097	catalytic activity, acting on DNA	0.074
	GO:0004683	calmodulin-dependent protein kinase acti...	0.077
	GO:0009931	calcium-dependent protein serine/threoni...	0.077
	GO:0010857	calcium-dependent protein kinase activit...	0.077
	GO:0016818	hydrolase activity, acting on acid anhyd...	0.090

4.1.11 Leaf - Preflowering - Cluster 11

GO type	GO ID	Description	Adj. p-value
BP	GO:0007165	signal transduction	0.000
	GO:0007154	cell communication	0.000
	GO:0023052	signaling	0.001
	GO:0071702	organic substance transport	0.001
	GO:0015850	organic hydroxy compound transport	0.002
	GO:0006022	aminoglycan metabolic process	0.003
	GO:0071705	nitrogen compound transport	0.003
	GO:0015791	polyol transport	0.005
	GO:0006040	amino sugar metabolic process	0.005
	GO:0046113	nucleobase catabolic process	0.005
	GO:0007166	cell surface receptor signaling pathway	0.006
	GO:0006887	exocytosis	0.007
	GO:0008361	regulation of cell size	0.008
	GO:0018196	peptidyl-asparagine modification	0.008
	GO:0018279	protein N-linked glycosylation via aspar...	0.008
	GO:0019748	secondary metabolic process	0.011
	GO:0071495	cellular response to endogenous stimulus	0.011
	GO:1904659	glucose transmembrane transport	0.011
	GO:0006796	phosphate-containing compound metabolic ...	0.012
	GO:0010243	response to organonitrogen compound	0.015
	GO:0009607	response to biotic stimulus	0.015
	GO:0032870	cellular response to hormone stimulus	0.017
	GO:0046323	glucose import	0.019
	GO:0006749	glutathione metabolic process	0.020
	GO:0006884	cell volume homeostasis	0.020
	GO:0008645	hexose transmembrane transport	0.020
	GO:0009992	cellular water homeostasis	0.020
	GO:0015749	monosaccharide transmembrane transport	0.020
	GO:0015793	glycerol transport	0.020
	GO:1902531	regulation of intracellular signal trans...	0.021
	GO:0071229	cellular response to acid chemical	0.021
	GO:0003333	amino acid transmembrane transport	0.021
	GO:0015807	L-amino acid transport	0.028
	GO:0006865	amino acid transport	0.028
	GO:0098542	defense response to other organism	0.028
	GO:0032940	secretion by cell	0.028
	GO:0006793	phosphorus metabolic process	0.028
	GO:0015804	neutral amino acid transport	0.035
	GO:0030104	water homeostasis	0.036
	GO:0071310	cellular response to organic substance	0.036
	GO:0046903	secretion	0.037
	GO:0006836	neurotransmitter transport	0.041
	GO:0005996	monosaccharide metabolic process	0.042
	GO:0006810	transport	0.042
	GO:0008037	cell recognition	0.042
	GO:0009755	hormone-mediated signaling pathway	0.042

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GO type	GO ID	Description	Adj. p-value
	GO:0043207	response to external biotic stimulus	0.042
	GO:0051707	response to other organism	0.042
	GO:0009875	pollen-pistil interaction	0.042
	GO:1902475	L-alpha-amino acid transmembrane transpo...	0.044
	GO:0071577	zinc ion transmembrane transport	0.047
	GO:0051234	establishment of localization	0.049
	GO:0006487	protein N-linked glycosylation	0.050
	GO:0048544	recognition of pollen	0.051
	GO:0051179	localization	0.056
	GO:0006833	water transport	0.062
	GO:0042044	fluid transport	0.062
	GO:0051704	multi-organism process	0.065
	GO:0006829	zinc ion transport	0.074
	GO:0010466	negative regulation of peptidase activit...	0.075
	GO:0010951	negative regulation of endopeptidase act...	0.075
	GO:0052547	regulation of peptidase activity	0.075
	GO:0052548	regulation of endopeptidase activity	0.075
	GO:0050832	defense response to fungus	0.076
	GO:0009057	macromolecule catabolic process	0.076
	GO:0042445	hormone metabolic process	0.080
	GO:0045087	innate immune response	0.085
	GO:0009738	abscisic acid-activated signaling pathwa...	0.094
	GO:0015893	drug transport	0.096
	GO:0045861	negative regulation of proteolysis	0.097
CC	GO:0005798	Golgi-associated vesicle	0.002
	GO:0005783	endoplasmic reticulum	0.002
	GO:0031226	intrinsic component of plasma membrane	0.003
	GO:0044459	plasma membrane part	0.003
	GO:0099023	tethering complex	0.003
	GO:0005911	cell-cell junction	0.005
	GO:0030054	cell junction	0.005
	GO:0030120	vesicle coat	0.005
	GO:0009506	plasmodesma	0.005
	GO:0055044	symplast	0.005
	GO:0005794	Golgi apparatus	0.008
	GO:0030660	Golgi-associated vesicle membrane	0.015
	GO:0000145	exocyst	0.023
	GO:0012506	vesicle membrane	0.026
	GO:0030662	coated vesicle membrane	0.041
	GO:0030659	cytoplasmic vesicle membrane	0.045
	GO:0031410	cytoplasmic vesicle	0.051
	GO:0097708	intracellular vesicle	0.060
	GO:0044433	cytoplasmic vesicle part	0.060
	GO:0005773	vacuole	0.061
	GO:0030118	clathrin coat	0.070
	GO:0031982	vesicle	0.077
	GO:0016607	nuclear speck	0.091
	GO:0030135	coated vesicle	0.091
	GO:0004497	monooxygenase activity	0.000

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GO type	GO ID	Description	Adj. p-value
	GO:0016705	oxidoreductase activity, acting on paire...	0.000
	GO:0016758	transferase activity, transferring hexos...	0.000
	GO:0016757	transferase activity, transferring glyco...	0.000
	GO:1901618	organic hydroxy compound transmembrane t...	0.001
	GO:0000166	nucleotide binding	0.001
	GO:1901265	nucleoside phosphate binding	0.001
	GO:0015166	polyol transmembrane transporter activit...	0.002
	GO:0051213	dioxygenase activity	0.003
	GO:0008144	drug binding	0.003
	GO:0005215	transporter activity	0.003
	GO:0015291	secondary active transmembrane transport...	0.004
	GO:0036094	small molecule binding	0.006
	GO:0005524	ATP binding	0.007
	GO:0003824	catalytic activity	0.008
	GO:0015168	glycerol transmembrane transporter activ...	0.009
	GO:0015297	antiporter activity	0.010
	GO:0004364	glutathione transferase activity	0.011
	GO:0001871	pattern binding	0.011
	GO:0015179	L-amino acid transmembrane transporter a...	0.011
	GO:0022857	transmembrane transporter activity	0.011
	GO:0030247	polysaccharide binding	0.011
	GO:0005355	glucose transmembrane transporter activi...	0.012
	GO:0005372	water transmembrane transporter activity	0.013
	GO:0015250	water channel activity	0.013
	GO:0015254	glycerol channel activity	0.013
	GO:0015171	amino acid transmembrane transporter act...	0.014
	GO:0015145	monosaccharide transmembrane transporter...	0.020
	GO:0015149	hexose transmembrane transporter activit...	0.020
	GO:0035639	purine ribonucleoside triphosphate bindi...	0.023
	GO:0005326	neurotransmitter transporter activity	0.025
	GO:0015174	basic amino acid transmembrane transport...	0.025
	GO:0005385	zinc ion transmembrane transporter activ...	0.033
	GO:0015293	symporter activity	0.033
	GO:0030414	peptidase inhibitor activity	0.038
	GO:0061134	peptidase regulator activity	0.038
	GO:0004866	endopeptidase inhibitor activity	0.048
	GO:0015144	carbohydrate transmembrane transporter a...	0.048
	GO:0061135	endopeptidase regulator activity	0.048
	GO:0015294	solute:cation symporter activity	0.049
	GO:0015295	solute:proton symporter activity	0.055
	GO:0022804	active transmembrane transporter activit...	0.062
	GO:0008417	fucosyltransferase activity	0.077
	GO:0005351	carbohydrate:proton symporter activity	0.099
	GO:0005402	carbohydrate:cation symporter activity	0.099
	GO:0051119	sugar transmembrane transporter activity	0.099
	GO:0072509	divalent inorganic cation transmembrane ...	0.099

4.1.12 Leaf - Preflowering - Cluster 12

GO type	GO ID	Description	Adj. p-value
	GO:0044281	small molecule metabolic process	0.000
	GO:0019684	photosynthesis, light reaction	0.000
	GO:0051188	cofactor biosynthetic process	0.000
	GO:0019637	organophosphate metabolic process	0.000
	GO:0046394	carboxylic acid biosynthetic process	0.000
	GO:0006732	coenzyme metabolic process	0.000
	GO:0008610	lipid biosynthetic process	0.000
	GO:0022900	electron transport chain	0.000
	GO:0044255	cellular lipid metabolic process	0.000
	GO:0006629	lipid metabolic process	0.000
	GO:0005975	carbohydrate metabolic process	0.000
	GO:0009108	coenzyme biosynthetic process	0.000
	GO:0009150	purine ribonucleotide metabolic process	0.000
	GO:0009259	ribonucleotide metabolic process	0.000
	GO:0019693	ribose phosphate metabolic process	0.000
	GO:0006163	purine nucleotide metabolic process	0.000
	GO:0033013	tetrapyrrole metabolic process	0.000
	GO:0016052	carbohydrate catabolic process	0.000
	GO:0033014	tetrapyrrole biosynthetic process	0.000
	GO:0006778	porphyrin-containing compound metabolic ...	0.000
	GO:0046034	ATP metabolic process	0.000
	GO:0046434	organophosphate catabolic process	0.000
	GO:0044262	cellular carbohydrate metabolic process	0.000
	GO:0009165	nucleotide biosynthetic process	0.000
	GO:0006631	fatty acid metabolic process	0.000
	GO:0009156	ribonucleoside monophosphate biosyntheti...	0.000
	GO:0009152	purine ribonucleotide biosynthetic proce...	0.000
	GO:0015994	chlorophyll metabolic process	0.000
	GO:0071555	cell wall organization	0.000
	GO:0009206	purine ribonucleoside triphosphate biosy...	0.000
	GO:0006090	pyruvate metabolic process	0.000
	GO:0072525	pyridine-containing compound biosyntheti...	0.000
	GO:0019359	nicotinamide nucleotide biosynthetic pro...	0.000
	GO:0008299	isoprenoid biosynthetic process	0.000
	GO:0046939	nucleotide phosphorylation	0.000
	GO:0006754	ATP biosynthetic process	0.000
	GO:0009127	purine nucleoside monophosphate biosynth...	0.000
	GO:0009168	purine ribonucleoside monophosphate bios...	0.000
	GO:0006165	nucleoside diphosphate phosphorylation	0.000
	GO:1902600	proton transmembrane transport	0.000
	GO:0098869	cellular oxidant detoxification	0.000
	GO:0009309	amine biosynthetic process	0.001
	GO:0042401	cellular biogenic amine biosynthetic pro...	0.001
	GO:0045491	xylan metabolic process	0.001
	GO:0006081	cellular aldehyde metabolic process	0.001
	GO:0009060	aerobic respiration	0.002

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0009768	photosynthesis, light harvesting in phot...	0.002
	GO:0010383	cell wall polysaccharide metabolic proce...	0.002
	GO:0034404	nucleobase-containing small molecule bio...	0.002
	GO:2000652	regulation of secondary cell wall biogen...	0.002
	GO:0006006	glucose metabolic process	0.002
	GO:0010109	regulation of photosynthesis	0.002
	GO:0016311	dephosphorylation	0.002
	GO:0044275	cellular carbohydrate catabolic process	0.002
	GO:0006520	cellular amino acid metabolic process	0.003
	GO:0006576	cellular biogenic amine metabolic proces...	0.003
	GO:0017004	cytochrome complex assembly	0.003
	GO:0010410	hemicellulose metabolic process	0.003
	GO:0015988	energy coupled proton transmembrane tran...	0.003
	GO:0015991	ATP hydrolysis coupled proton transport	0.003
	GO:0090662	ATP hydrolysis coupled transmembrane tra...	0.003
	GO:0099131	ATP hydrolysis coupled ion transmembrane...	0.003
	GO:0099132	ATP hydrolysis coupled cation transmembr...	0.003
	GO:0006783	heme biosynthetic process	0.003
	GO:0010206	photosystem II repair	0.004
	GO:0009664	plant-type cell wall organization	0.004
	GO:0035336	long-chain fatty-acyl-CoA metabolic proc...	0.004
	GO:1901566	organonitrogen compound biosynthetic pro...	0.004
	GO:0042214	terpene metabolic process	0.004
	GO:0006108	malate metabolic process	0.005
	GO:0006721	terpenoid metabolic process	0.005
	GO:0046365	monosaccharide catabolic process	0.005
	GO:0000272	polysaccharide catabolic process	0.005
	GO:0016122	xanthophyll metabolic process	0.006
	GO:0009773	photosynthetic electron transport in pho...	0.006
	GO:0044036	cell wall macromolecule metabolic proces...	0.006
	GO:0046184	aldehyde biosynthetic process	0.007
	GO:0042168	heme metabolic process	0.007
	GO:0032544	plastid translation	0.007
	GO:0044106	cellular amine metabolic process	0.007
	GO:0044550	secondary metabolite biosynthetic proces...	0.008
	GO:0010143	cutin biosynthetic process	0.009
	GO:0035337	fatty-acyl-CoA metabolic process	0.010
	GO:0032271	regulation of protein polymerization	0.010
	GO:0046185	aldehyde catabolic process	0.010
	GO:0019318	hexose metabolic process	0.010
	GO:0007010	cytoskeleton organization	0.011
	GO:0005983	starch catabolic process	0.011
	GO:1901137	carbohydrate derivative biosynthetic pro...	0.012
	GO:0000162	tryptophan biosynthetic process	0.013
	GO:0046219	indolalkylamine biosynthetic process	0.013
	GO:1901135	carbohydrate derivative metabolic proces...	0.013
	GO:0009074	aromatic amino acid family catabolic pro...	0.015
	GO:0046271	phenylpropanoid catabolic process	0.015
	GO:0010103	stomatal complex morphogenesis	0.015

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GO type	GO ID	Description	Adj. p-value
	GO:0009409	response to cold	0.015
	GO:0030091	protein repair	0.016
	GO:0043467	regulation of generation of precursor me...	0.017
	GO:0017001	antibiotic catabolic process	0.018
	GO:0030244	cellulose biosynthetic process	0.020
	GO:0016114	terpenoid biosynthetic process	0.021
	GO:0030041	actin filament polymerization	0.022
	GO:0030833	regulation of actin filament polymerizat...	0.022
	GO:0045492	xylan biosynthetic process	0.022
	GO:0070592	cell wall polysaccharide biosynthetic pr...	0.022
	GO:0030243	cellulose metabolic process	0.023
	GO:0044038	cell wall macromolecule biosynthetic pro...	0.023
	GO:0044247	cellular polysaccharide catabolic proces...	0.023
	GO:0070589	cellular component macromolecule biosynt...	0.023
	GO:0009250	glucan biosynthetic process	0.024
	GO:0033865	nucleoside bisphosphate metabolic proces...	0.024
	GO:0033875	ribonucleoside bisphosphate metabolic pr...	0.024
	GO:0034032	purine nucleoside bisphosphate metabolic...	0.024
	GO:0009438	methylglyoxal metabolic process	0.025
	GO:0042182	ketone catabolic process	0.025
	GO:0051596	methylglyoxal catabolic process	0.025
	GO:0043648	dicarboxylic acid metabolic process	0.025
	GO:1903338	regulation of cell wall organization or ...	0.025
	GO:0043244	regulation of protein complex disassembl...	0.026
	GO:0010345	suberin biosynthetic process	0.027
	GO:0009251	glucan catabolic process	0.027
	GO:0009642	response to light intensity	0.028
	GO:0034599	cellular response to oxidative stress	0.028
	GO:0018298	protein-chromophore linkage	0.029
	GO:0046274	lignin catabolic process	0.029
	GO:1901607	alpha-amino acid biosynthetic process	0.029
	GO:0010052	guard cell differentiation	0.030
	GO:0006743	ubiquinone metabolic process	0.032
	GO:0006744	ubiquinone biosynthetic process	0.032
	GO:0009628	response to abiotic stimulus	0.033
	GO:0006558	L-phenylalanine metabolic process	0.035
	GO:0006637	acyl-CoA metabolic process	0.035
	GO:0016999	antibiotic metabolic process	0.035
	GO:0035383	thioester metabolic process	0.035
	GO:1902221	erythrose 4-phosphate/phosphoenolpyruvat...	0.035
	GO:1901568	fatty acid derivative metabolic process	0.036
	GO:0009416	response to light stimulus	0.037
	GO:0006089	lactate metabolic process	0.038
	GO:0019243	methylglyoxal catabolic process to D-lac...	0.038
	GO:0061727	methylglyoxal catabolic process to lacta...	0.038
	GO:0009308	amine metabolic process	0.038
	GO:0006793	phosphorus metabolic process	0.039
	GO:0008064	regulation of actin polymerization or de...	0.040
	GO:0030832	regulation of actin filament length	0.040

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GO type	GO ID	Description	Adj. p-value
	GO:0032956	regulation of actin cytoskeleton organiz...	0.040
	GO:0032970	regulation of actin filament-based proce...	0.040
	GO:0090626	plant epidermis morphogenesis	0.040
	GO:0110053	regulation of actin filament organizatio...	0.040
	GO:0009314	response to radiation	0.041
	GO:0042435	indole-containing compound biosynthetic ...	0.041
	GO:0048438	floral whorl development	0.042
	GO:0000038	very long-chain fatty acid metabolic pro...	0.042
	GO:1901615	organic hydroxy compound metabolic proce...	0.042
	GO:0098660	inorganic ion transmembrane transport	0.043
	GO:0016043	cellular component organization	0.047
	GO:0071214	cellular response to abiotic stimulus	0.049
	GO:0104004	cellular response to environmental stimu...	0.049
	GO:1901605	alpha-amino acid metabolic process	0.052
	GO:0042744	hydrogen peroxide catabolic process	0.055
	GO:0019430	removal of superoxide radicals	0.058
	GO:0071450	cellular response to oxygen radical	0.058
	GO:0071451	cellular response to superoxide	0.058
	GO:1902903	regulation of supramolecular fiber organ...	0.058
	GO:0044282	small molecule catabolic process	0.059
	GO:0015672	monovalent inorganic cation transport	0.059
	GO:0042548	regulation of photosynthesis, light reac...	0.063
	GO:0006119	oxidative phosphorylation	0.063
	GO:0042773	ATP synthesis coupled electron transport	0.063
	GO:0009058	biosynthetic process	0.063
	GO:0045037	protein import into chloroplast stroma	0.063
	GO:1901617	organic hydroxy compound biosynthetic pr...	0.063
	GO:0071478	cellular response to radiation	0.064
	GO:0071482	cellular response to light stimulus	0.065
	GO:0009395	phospholipid catabolic process	0.067
	GO:0015985	energy coupled proton transport, down el...	0.068
	GO:0015986	ATP synthesis coupled proton transport	0.068
	GO:0046486	glycerolipid metabolic process	0.068
	GO:0008154	actin polymerization or depolymerization	0.069
	GO:1901401	regulation of tetrapyrrole metabolic pro...	0.070
	GO:0006595	polyamine metabolic process	0.075
	GO:0022904	respiratory electron transport chain	0.077
	GO:0051261	protein depolymerization	0.079
	GO:0019682	glyceraldehyde-3-phosphate metabolic pro...	0.081
	GO:1901463	regulation of tetrapyrrole biosynthetic ...	0.082
	GO:0006644	phospholipid metabolic process	0.083
	GO:0009943	adaxial/abaxial axis specification	0.086
	GO:0009944	polarity specification of adaxial/abaxia...	0.086
	GO:0044249	cellular biosynthetic process	0.086
	GO:0048235	pollen sperm cell differentiation	0.087
	GO:0009955	adaxial/abaxial pattern specification	0.089
	GO:0072593	reactive oxygen species metabolic proces...	0.089
	GO:0043038	amino acid activation	0.092
	GO:0043039	tRNA aminoacylation	0.092

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0051493	regulation of cytoskeleton organization	0.092
	GO:1901576	organic substance biosynthetic process	0.092
	GO:0046364	monosaccharide biosynthetic process	0.092
	GO:0061024	membrane organization	0.092
	GO:0080167	response to karrikin	0.099
CC	GO:0031977	thylakoid lumen	0.000
	GO:0009521	photosystem	0.000
	GO:1990204	oxidoreductase complex	0.000
	GO:0005856	cytoskeleton	0.000
	GO:0044430	cytoskeletal part	0.000
	GO:0005875	microtubule associated complex	0.000
	GO:0031969	chloroplast membrane	0.000
	GO:0005739	mitochondrion	0.000
	GO:0044429	mitochondrial part	0.000
	GO:0016469	proton-transporting two-sector ATPase co...	0.000
	GO:0005743	mitochondrial inner membrane	0.000
	GO:0005874	microtubule	0.000
	GO:0070469	respiratory chain	0.000
	GO:0033178	proton-transporting two-sector ATPase co...	0.000
	GO:0009295	nucleoid	0.000
	GO:0098803	respiratory chain complex	0.000
	GO:0009528	plastid inner membrane	0.000
	GO:0005746	mitochondrial respiratory chain	0.000
	GO:0009654	photosystem II oxygen evolving complex	0.001
	GO:0042646	plastid nucleoid	0.001
	GO:0009707	chloroplast outer membrane	0.001
	GO:0010319	stromule	0.001
	GO:0005618	cell wall	0.001
	GO:0030312	external encapsulating structure	0.001
	GO:0044424	intracellular part	0.001
	GO:0005622	intracellular	0.002
	GO:0009527	plastid outer membrane	0.002
	GO:0005753	mitochondrial proton-transporting ATP sy...	0.002
	GO:0009706	chloroplast inner membrane	0.002
	GO:0098798	mitochondrial protein complex	0.002
	GO:0005881	cytoplasmic microtubule	0.003
	GO:0030863	cortical cytoskeleton	0.003
	GO:0030981	cortical microtubule cytoskeleton	0.003
	GO:0030964	NADH dehydrogenase complex	0.003
	GO:0045271	respiratory chain complex I	0.003
	GO:0005747	mitochondrial respiratory chain complex ...	0.005
	GO:0045259	proton-transporting ATP synthase complex	0.005
	GO:0055028	cortical microtubule	0.010
	GO:0042644	chloroplast nucleoid	0.013
	GO:0009524	phragmoplast	0.013
	GO:0044464	cell part	0.019
	GO:0005623	cell	0.020
	GO:0009505	plant-type cell wall	0.024
	GO:0000229	cytoplasmic chromosome	0.077

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0009508	plastid chromosome	0.099
MF	GO:0016491	oxidoreductase activity	0.000
	GO:0016829	lyase activity	0.000
	GO:0016788	hydrolase activity, acting on ester bond...	0.000
	GO:0016655	oxidoreductase activity, acting on NAD(P...	0.000
	GO:0016791	phosphatase activity	0.000
	GO:0016747	transferase activity, transferring acyl ...	0.000
	GO:0050662	coenzyme binding	0.000
	GO:0003954	NADH dehydrogenase activity	0.000
	GO:0016614	oxidoreductase activity, acting on CH-OH...	0.001
	GO:0008236	serine-type peptidase activity	0.002
	GO:0017171	serine hydrolase activity	0.002
	GO:0016790	thiolester hydrolase activity	0.003
	GO:0016838	carbon-oxygen lyase activity, acting on ...	0.003
	GO:0016853	isomerase activity	0.003
	GO:0016830	carbon-carbon lyase activity	0.004
	GO:0044769	ATPase activity, coupled to transmembran...	0.004
	GO:0004252	serine-type endopeptidase activity	0.004
	GO:0016778	diphosphotransferase activity	0.004
	GO:0016616	oxidoreductase activity, acting on the C...	0.005
	GO:0080019	fatty-acyl-CoA reductase (alcohol-formin...	0.006
	GO:0016776	phosphotransferase activity, phosphate g...	0.006
	GO:0016866	intramolecular transferase activity	0.006
	GO:0016620	oxidoreductase activity, acting on the a...	0.006
	GO:0016615	malate dehydrogenase activity	0.006
	GO:0019203	carbohydrate phosphatase activity	0.007
	GO:0050308	sugar-phosphatase activity	0.008
	GO:0016887	ATPase activity	0.008
	GO:0008374	O-acyltransferase activity	0.009
	GO:0016759	cellulose synthase activity	0.009
	GO:0016760	cellulose synthase (UDP-forming) activit...	0.009
	GO:0016903	oxidoreductase activity, acting on the a...	0.009
	GO:0031072	heat shock protein binding	0.009
	GO:0051539	4 iron, 4 sulfur cluster binding	0.009
	GO:0010333	terpene synthase activity	0.009
	GO:0051536	iron-sulfur cluster binding	0.009
	GO:0051540	metal cluster binding	0.009
	GO:0016765	transferase activity, transferring alkyl...	0.010
	GO:0016413	O-acetyltransferase activity	0.010
	GO:0019205	nucleobase-containing compound kinase ac...	0.011
	GO:0140101	catalytic activity, acting on a tRNA	0.011
	GO:0016741	transferase activity, transferring one-c...	0.012
	GO:0016684	oxidoreductase activity, acting on perox...	0.012
	GO:0016762	xyloglucan:xyloglucosyl transferase acti...	0.013
	GO:0016836	hydro-lyase activity	0.014
	GO:0051087	chaperone binding	0.017
	GO:0016627	oxidoreductase activity, acting on the C...	0.017
	GO:0016407	acetyltransferase activity	0.017
	GO:0016814	hydrolase activity, acting on carbon-nit...	0.017

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GO type	GO ID	Description	Adj. p-value
	GO:0042349	guiding stereospecific synthesis activit...	0.017
	GO:0008574	ATP-dependent microtubule motor activity...	0.018
	GO:0050660	flavin adenine dinucleotide binding	0.018
	GO:1990939	ATP-dependent microtubule motor activity	0.018
	GO:0042623	ATPase activity, coupled	0.018
	GO:0008168	methyltransferase activity	0.021
	GO:0046961	proton-transporting ATPase activity, rot...	0.021
	GO:0051287	NAD binding	0.021
	GO:0016868	intramolecular transferase activity, pho...	0.021
	GO:0004601	peroxidase activity	0.024
	GO:0017111	nucleoside-triphosphatase activity	0.026
	GO:0016717	oxidoreductase activity, acting on paire...	0.029
	GO:0031409	pigment binding	0.031
	GO:0016462	pyrophosphatase activity	0.034
	GO:0036442	proton-exporting ATPase activity	0.036
	GO:0046556	alpha-L-arabinofuranosidase activity	0.036
	GO:0046933	proton-transporting ATP synthase activit...	0.036
	GO:0016799	hydrolase activity, hydrolyzing N-glycos...	0.037
	GO:0033764	steroid dehydrogenase activity, acting o...	0.038
	GO:0052716	hydroquinone:oxygen oxidoreductase activ...	0.039
	GO:0016861	intramolecular oxidoreductase activity, ...	0.040
	GO:0070011	peptidase activity, acting on L-amino ac...	0.042
	GO:2001070	starch binding	0.043
	GO:0004312	fatty acid synthase activity	0.044
	GO:0052689	carboxylic ester hydrolase activity	0.050
	GO:0016818	hydrolase activity, acting on acid anhyd...	0.058
	GO:0019104	DNA N-glycosylase activity	0.058
	GO:0051015	actin filament binding	0.058
	GO:0003779	actin binding	0.061
	GO:0008233	peptidase activity	0.061
	GO:0015399	primary active transmembrane transporter...	0.061
	GO:0015405	P-P-bond-hydrolysis-driven transmembrane...	0.061
	GO:0002161	aminoacyl-tRNA editing activity	0.063
	GO:0003854	3-beta-hydroxy-delta5-steroid dehydrogen...	0.064
	GO:0051537	2 iron, 2 sulfur cluster binding	0.067
	GO:0140097	catalytic activity, acting on DNA	0.070
	GO:0016817	hydrolase activity, acting on acid anhyd...	0.070
	GO:0008252	nucleotidase activity	0.074
	GO:0043022	ribosome binding	0.074
	GO:0050661	NADP binding	0.075
	GO:0004743	pyruvate kinase activity	0.078
	GO:0019829	cation-transporting ATPase activity	0.078
	GO:0022853	active ion transmembrane transporter act...	0.078
	GO:0030955	potassium ion binding	0.078
	GO:0031420	alkali metal ion binding	0.078
	GO:0042625	ATPase coupled ion transmembrane transpo...	0.078
	GO:0016229	steroid dehydrogenase activity	0.079
	GO:0019238	cyclohydrolase activity	0.080
	GO:0042626	ATPase activity, coupled to transmembran...	0.080

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GO type	GO ID	Description	Adj. p-value
	GO:0016899	oxidoreductase activity, acting on the C...	0.083
	GO:0016740	transferase activity	0.091

4.1.13 Leaf - Preflowering - Cluster 13

GO type	GO ID	Description	Adj. p-value
BP	GO:0006091	generation of precursor metabolites and ...	0.001
	GO:0018205	peptidyl-lysine modification	0.001
	GO:0006457	protein folding	0.001
	GO:0019637	organophosphate metabolic process	0.003
	GO:0015979	photosynthesis	0.003
	GO:0003006	developmental process involved in reprod...	0.004
	GO:0051188	cofactor biosynthetic process	0.004
	GO:0008202	steroid metabolic process	0.006
	GO:0046185	aldehyde catabolic process	0.007
	GO:0009628	response to abiotic stimulus	0.007
	GO:0009266	response to temperature stimulus	0.012
	GO:0016569	covalent chromatin modification	0.012
	GO:0016570	histone modification	0.012
	GO:0015980	energy derivation by oxidation of organi...	0.013
	GO:0006163	purine nucleotide metabolic process	0.013
	GO:0006732	coenzyme metabolic process	0.014
	GO:0006753	nucleoside phosphate metabolic process	0.014
	GO:0051276	chromosome organization	0.016
	GO:0006089	lactate metabolic process	0.017
	GO:0019243	methylglyoxal catabolic process to D-lac...	0.017
	GO:0061727	methylglyoxal catabolic process to lacta...	0.017
	GO:0009117	nucleotide metabolic process	0.019
	GO:0009259	ribonucleotide metabolic process	0.019
	GO:0009150	purine ribonucleotide metabolic process	0.019
	GO:0016053	organic acid biosynthetic process	0.020
	GO:0046394	carboxylic acid biosynthetic process	0.020
	GO:0040029	regulation of gene expression, epigeneti...	0.026
	GO:0071214	cellular response to abiotic stimulus	0.026
	GO:0104004	cellular response to environmental stimu...	0.026
	GO:0005977	glycogen metabolic process	0.028
	GO:0006112	energy reserve metabolic process	0.028
	GO:0008652	cellular amino acid biosynthetic process	0.029
	GO:0009790	embryo development	0.029
	GO:0048608	reproductive structure development	0.031
	GO:0061458	reproductive system development	0.031
	GO:0009438	methylglyoxal metabolic process	0.034
	GO:0042182	ketone catabolic process	0.034
	GO:0051596	methylglyoxal catabolic process	0.034
	GO:0055114	oxidation-reduction process	0.034
	GO:1901607	alpha-amino acid biosynthetic process	0.034
	GO:0018193	peptidyl-amino acid modification	0.035
	GO:0044281	small molecule metabolic process	0.036
	GO:0009791	post-embryonic development	0.037
	GO:0009108	coenzyme biosynthetic process	0.037
	GO:0022414	reproductive process	0.038
	GO:0000003	reproduction	0.040

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GO type	GO ID	Description	Adj. p-value
	GO:0009735	response to cytokinin	0.040
	GO:0009144	purine nucleoside triphosphate metabolic...	0.046
	GO:0009205	purine ribonucleoside triphosphate metab...	0.046
	GO:0034599	cellular response to oxidative stress	0.046
	GO:0019693	ribose phosphate metabolic process	0.046
	GO:0046434	organophosphate catabolic process	0.046
	GO:0048609	multicellular organismal reproductive pr...	0.047
	GO:0009199	ribonucleoside triphosphate metabolic pr...	0.047
	GO:0006473	protein acetylation	0.048
	GO:0005976	polysaccharide metabolic process	0.049
	GO:0043543	protein acylation	0.055
	GO:0016458	gene silencing	0.059
	GO:0006325	chromatin organization	0.059
	GO:0009123	nucleoside monophosphate metabolic proce...	0.059
	GO:0090407	organophosphate biosynthetic process	0.060
	GO:0009141	nucleoside triphosphate metabolic proces...	0.062
	GO:0051186	cofactor metabolic process	0.064
	GO:0072521	purine-containing compound metabolic pro...	0.070
	GO:1901362	organic cyclic compound biosynthetic pro...	0.073
	GO:0009793	embryo development ending in seed dorman...	0.075
	GO:0006520	cellular amino acid metabolic process	0.075
	GO:1901293	nucleoside phosphate biosynthetic proces...	0.075
	GO:1901605	alpha-amino acid metabolic process	0.079
	GO:0009161	ribonucleoside monophosphate metabolic p...	0.080
	GO:0006165	nucleoside diphosphate phosphorylation	0.082
	GO:0007275	multicellular organism development	0.082
	GO:2000113	negative regulation of cellular macromol...	0.084
	GO:0005978	glycogen biosynthetic process	0.088
	GO:0048868	pollen tube development	0.090
	GO:0005982	starch metabolic process	0.091
	GO:0016052	carbohydrate catabolic process	0.091
	GO:0034404	nucleobase-containing small molecule bio...	0.092
	GO:0006637	acyl-CoA metabolic process	0.094
	GO:0009126	purine nucleoside monophosphate metaboli...	0.094
	GO:0009165	nucleotide biosynthetic process	0.094
	GO:0009167	purine ribonucleoside monophosphate meta...	0.094
	GO:0035383	thioester metabolic process	0.094
	GO:0048316	seed development	0.094
	GO:0072330	monocarboxylic acid biosynthetic process	0.094
	GO:0000103	sulfate assimilation	0.100
	GO:0042180	cellular ketone metabolic process	0.100
CC	GO:0009579	thylakoid	0.000
	GO:0009526	plastid envelope	0.000
	GO:0009534	chloroplast thylakoid	0.000
	GO:0042651	thylakoid membrane	0.000
	GO:0042170	plastid membrane	0.006
	GO:0031969	chloroplast membrane	0.009
	GO:1990204	oxidoreductase complex	0.027
	GO:0031984	organelle subcompartment	0.036

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GO type	GO ID	Description	Adj. p-value
	GO:0031225	anchored component of membrane	0.043
	GO:0030532	small nuclear ribonucleoprotein complex	0.047
	GO:0097525	spliceosomal snRNP complex	0.047
	GO:0120114	Sm-like protein family complex	0.047
	GO:0046658	anchored component of plasma membrane	0.051
MF	GO:0016620	oxidoreductase activity, acting on the a...	0.019
	GO:0016903	oxidoreductase activity, acting on the a...	0.019
	GO:0016407	acetyltransferase activity	0.036
	GO:0003824	catalytic activity	0.047
	GO:0016774	phosphotransferase activity, carboxyl gr...	0.068
	GO:0008080	N-acetyltransferase activity	0.078
	GO:0043621	protein self-association	0.086
	GO:2001070	starch binding	0.086
	GO:0042393	histone binding	0.093
	GO:0051539	4 iron, 4 sulfur cluster binding	0.093

4.1.14 Leaf - Preflowering - Cluster 14

GO type	GO ID	Description	Adj. p-value
BP	GO:0060255	regulation of macromolecule metabolic pr...	0.000
	GO:0019219	regulation of nucleobase-containing comp...	0.000
	GO:0051252	regulation of RNA metabolic process	0.000
	GO:0043161	proteasome-mediated ubiquitin-dependent ...	0.000
	GO:0010498	proteasomal protein catabolic process	0.000
	GO:0006518	peptide metabolic process	0.000
	GO:0015850	organic hydroxy compound transport	0.001
	GO:0043603	cellular amide metabolic process	0.001
	GO:0000375	RNA splicing, via transesterification re...	0.003
	GO:0006749	glutathione metabolic process	0.003
	GO:0008645	hexose transmembrane transport	0.004
	GO:0046323	glucose import	0.005
	GO:0043632	modification-dependent macromolecule cat...	0.006
	GO:0031497	chromatin assembly	0.008
	GO:0005996	monosaccharide metabolic process	0.010
	GO:0019941	modification-dependent protein catabolic...	0.010
	GO:1901565	organonitrogen compound catabolic proces...	0.010
	GO:0006884	cell volume homeostasis	0.011
	GO:0009992	cellular water homeostasis	0.011
	GO:0015793	glycerol transport	0.011
	GO:0008361	regulation of cell size	0.016
	GO:0006334	nucleosome assembly	0.018
	GO:0030104	water homeostasis	0.018
	GO:0006511	ubiquitin-dependent protein catabolic pr...	0.022
	GO:0006836	neurotransmitter transport	0.022
	GO:0006333	chromatin assembly or disassembly	0.022
	GO:0006022	aminoglycan metabolic process	0.026
	GO:0006026	aminoglycan catabolic process	0.030
	GO:0006030	chitin metabolic process	0.030
	GO:0006032	chitin catabolic process	0.030
	GO:0044257	cellular protein catabolic process	0.030
	GO:0046348	amino sugar catabolic process	0.030
	GO:0051603	proteolysis involved in cellular protein...	0.030
	GO:1901072	glucosamine-containing compound cataboli...	0.030
	GO:1901071	glucosamine-containing compound metaboli...	0.030
	GO:0006952	defense response	0.032
	GO:0006323	DNA packaging	0.038
	GO:0044550	secondary metabolite biosynthetic proces...	0.038
	GO:0000466	maturation of 5.8S rRNA from tricistroni...	0.052
	GO:0044265	cellular macromolecule catabolic process	0.057
	GO:0000460	maturation of 5.8S rRNA	0.062
	GO:0006833	water transport	0.076
	GO:0042044	fluid transport	0.076
	GO:0034728	nucleosome organization	0.080
	GO:0010928	regulation of auxin mediated signaling p...	0.080
	GO:0006575	cellular modified amino acid metabolic p...	0.081

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0008643	carbohydrate transport	0.087
CC	GO:0000151	ubiquitin ligase complex	0.000
	GO:0005681	spliceosomal complex	0.000
	GO:0071013	catalytic step 2 spliceosome	0.003
	GO:0044425	membrane part	0.008
	GO:0030120	vesicle coat	0.035
	GO:0099023	tethering complex	0.038
	GO:0016591	DNA-directed RNA polymerase II, holoenzy...	0.038
	GO:0005798	Golgi-associated vesicle	0.050
	GO:0005852	eukaryotic translation initiation factor...	0.051
	GO:0080008	Cul4-RING E3 ubiquitin ligase complex	0.057
	GO:0044459	plasma membrane part	0.058
	GO:0005911	cell-cell junction	0.059
	GO:0030054	cell junction	0.059
	GO:0009506	plasmodesma	0.062
	GO:0055044	symplast	0.062
	GO:0005689	U12-type spliceosomal complex	0.066
	GO:0005886	plasma membrane	0.066
	GO:0030687	preribosome, large subunit precursor	0.066
	GO:0031226	intrinsic component of plasma membrane	0.066
	GO:0005686	U2 snRNP	0.085
	GO:0000786	nucleosome	0.096
MF	GO:0004497	monooxygenase activity	0.000
	GO:0016705	oxidoreductase activity, acting on paire...	0.000
	GO:1901618	organic hydroxy compound transmembrane t...	0.000
	GO:0005355	glucose transmembrane transporter activi...	0.005
	GO:0015145	monosaccharide transmembrane transporter...	0.006
	GO:0004364	glutathione transferase activity	0.007
	GO:0015149	hexose transmembrane transporter activit...	0.008
	GO:0015168	glycerol transmembrane transporter activ...	0.008
	GO:0097159	organic cyclic compound binding	0.008
	GO:1901363	heterocyclic compound binding	0.008
	GO:0005372	water transmembrane transporter activity	0.012
	GO:0015250	water channel activity	0.012
	GO:0015254	glycerol channel activity	0.012
	GO:0005326	neurotransmitter transporter activity	0.019
	GO:0015174	basic amino acid transmembrane transport...	0.019
	GO:0003677	DNA binding	0.025
	GO:0004568	chitinase activity	0.027
	GO:0015291	secondary active transmembrane transport...	0.029
	GO:0015293	symporter activity	0.030
	GO:0016757	transferase activity, transferring glyco...	0.030
	GO:0051213	dioxygenase activity	0.030
	GO:0030246	carbohydrate binding	0.033
	GO:0048037	cofactor binding	0.035
	GO:0015294	solute:cation symporter activity	0.054
	GO:0003700	DNA binding transcription factor activit...	0.070
	GO:0005351	carbohydrate:proton symporter activity	0.083
	GO:0005402	carbohydrate:cation symporter activity	0.083

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0015295	solute:proton symporter activity	0.083
	GO:0015179	L-amino acid transmembrane transporter a...	0.083

4.1.15 Leaf - Preflowering - Cluster 15

GO type	GO ID	Description	Adj. p-value
	GO:0051188	cofactor biosynthetic process	0.000
	GO:0046394	carboxylic acid biosynthetic process	0.000
	GO:0019637	organophosphate metabolic process	0.000
	GO:0009699	phenylpropanoid biosynthetic process	0.000
	GO:0006732	coenzyme metabolic process	0.000
	GO:0009117	nucleotide metabolic process	0.000
	GO:0008610	lipid biosynthetic process	0.000
	GO:0009150	purine ribonucleotide metabolic process	0.000
	GO:0016052	carbohydrate catabolic process	0.000
	GO:0009108	coenzyme biosynthetic process	0.000
	GO:0006629	lipid metabolic process	0.000
	GO:0046034	ATP metabolic process	0.000
	GO:0033014	tetrapyrrole biosynthetic process	0.000
	GO:0046434	organophosphate catabolic process	0.000
	GO:0006779	porphyrin-containing compound biosynthet...	0.000
	GO:0006778	porphyrin-containing compound metabolic ...	0.000
	GO:0090407	organophosphate biosynthetic process	0.000
	GO:0009165	nucleotide biosynthetic process	0.000
	GO:0006165	nucleoside diphosphate phosphorylation	0.000
	GO:0006631	fatty acid metabolic process	0.000
	GO:0009206	purine ribonucleoside triphosphate biosy...	0.000
	GO:0009073	aromatic amino acid family biosynthetic ...	0.000
	GO:0006164	purine nucleotide biosynthetic process	0.000
	GO:0046939	nucleotide phosphorylation	0.000
	GO:0044264	cellular polysaccharide metabolic proces...	0.000
	GO:0019359	nicotinamide nucleotide biosynthetic pro...	0.000
	GO:0009124	nucleoside monophosphate biosynthetic pr...	0.000
	GO:0009156	ribonucleoside monophosphate biosyntheti...	0.000
	GO:0009152	purine ribonucleotide biosynthetic proce...	0.000
	GO:0019363	pyridine nucleotide biosynthetic process	0.000
	GO:0009260	ribonucleotide biosynthetic process	0.000
	GO:0046390	ribose phosphate biosynthetic process	0.000
	GO:0071555	cell wall organization	0.000
	GO:1902600	proton transmembrane transport	0.000
	GO:0009834	plant-type secondary cell wall biogenesi...	0.000
	GO:0008299	isoprenoid biosynthetic process	0.000
	GO:0008652	cellular amino acid biosynthetic process	0.001
	GO:0009808	lignin metabolic process	0.002
	GO:0006081	cellular aldehyde metabolic process	0.002
	GO:0033692	cellular polysaccharide biosynthetic pro...	0.002
	GO:0005982	starch metabolic process	0.002
	GO:0042546	cell wall biogenesis	0.002
	GO:0009110	vitamin biosynthetic process	0.002
	GO:0010206	photosystem II repair	0.002
	GO:0006720	isoprenoid metabolic process	0.002
	GO:0006520	cellular amino acid metabolic process	0.002

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0009642	response to light intensity	0.002
	GO:0032787	monocarboxylic acid metabolic process	0.002
	GO:0016109	tetraterpenoid biosynthetic process	0.003
	GO:0016117	carotenoid biosynthetic process	0.003
	GO:0034404	nucleobase-containing small molecule bio...	0.003
	GO:0010207	photosystem II assembly	0.003
	GO:0009832	plant-type cell wall biogenesis	0.003
	GO:0044042	glucan metabolic process	0.003
	GO:0045037	protein import into chloroplast stroma	0.003
	GO:0000272	polysaccharide catabolic process	0.004
	GO:0044275	cellular carbohydrate catabolic process	0.004
	GO:0044249	cellular biosynthetic process	0.004
	GO:0044550	secondary metabolite biosynthetic proces...	0.004
	GO:2000652	regulation of secondary cell wall biogen...	0.005
	GO:0006073	cellular glucan metabolic process	0.005
	GO:0009628	response to abiotic stimulus	0.005
	GO:0035336	long-chain fatty-acyl-CoA metabolic proc...	0.006
	GO:0010114	response to red light	0.006
	GO:0017004	cytochrome complex assembly	0.007
	GO:0032259	methylation	0.007
	GO:0016051	carbohydrate biosynthetic process	0.009
	GO:0048235	pollen sperm cell differentiation	0.009
	GO:0097237	cellular response to toxic substance	0.009
	GO:0016122	xanthophyll metabolic process	0.009
	GO:0010345	suberin biosynthetic process	0.010
	GO:0046185	aldehyde catabolic process	0.010
	GO:0032544	plastid translation	0.011
	GO:0034599	cellular response to oxidative stress	0.011
	GO:1990748	cellular detoxification	0.011
	GO:0009309	amine biosynthetic process	0.015
	GO:0042401	cellular biogenic amine biosynthetic pro...	0.015
	GO:0098869	cellular oxidant detoxification	0.016
	GO:0045491	xylan metabolic process	0.017
	GO:0006743	ubiquinone metabolic process	0.019
	GO:0006744	ubiquinone biosynthetic process	0.019
	GO:0006399	tRNA metabolic process	0.019
	GO:0008152	metabolic process	0.021
	GO:0035337	fatty-acyl-CoA metabolic process	0.021
	GO:1901576	organic substance biosynthetic process	0.021
	GO:0006644	phospholipid metabolic process	0.023
	GO:0009409	response to cold	0.023
	GO:0009664	plant-type cell wall organization	0.023
	GO:0034637	cellular carbohydrate biosynthetic proce...	0.024
	GO:0000162	tryptophan biosynthetic process	0.024
	GO:0046219	indolalkylamine biosynthetic process	0.024
	GO:0043038	amino acid activation	0.024
	GO:0043039	tRNA aminoacylation	0.024
	GO:0006576	cellular biogenic amine metabolic proces...	0.025
	GO:0006783	heme biosynthetic process	0.026

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0009438	methylglyoxal metabolic process	0.026
	GO:0042182	ketone catabolic process	0.026
	GO:0051596	methylglyoxal catabolic process	0.026
	GO:0044247	cellular polysaccharide catabolic proces...	0.028
	GO:1901135	carbohydrate derivative metabolic proces...	0.028
	GO:0009768	photosynthesis, light harvesting in phot...	0.029
	GO:0009793	embryo development ending in seed dorman...	0.029
	GO:0010383	cell wall polysaccharide metabolic proce...	0.031
	GO:1901607	alpha-amino acid biosynthetic process	0.032
	GO:0006637	acyl-CoA metabolic process	0.035
	GO:0035383	thioester metabolic process	0.035
	GO:0006108	malate metabolic process	0.037
	GO:0044106	cellular amine metabolic process	0.038
	GO:0061077	chaperone-mediated protein folding	0.038
	GO:0009250	glucan biosynthetic process	0.039
	GO:0045489	pectin biosynthetic process	0.039
	GO:0071478	cellular response to radiation	0.039
	GO:0033108	mitochondrial respiratory chain complex ...	0.040
	GO:0006089	lactate metabolic process	0.040
	GO:0019243	methylglyoxal catabolic process to D-lac...	0.040
	GO:0061727	methylglyoxal catabolic process to lacta...	0.040
	GO:0043572	plastid fission	0.042
	GO:1901615	organic hydroxy compound metabolic proce...	0.042
	GO:1901617	organic hydroxy compound biosynthetic pr...	0.042
	GO:0006119	oxidative phosphorylation	0.043
	GO:0042773	ATP synthesis coupled electron transport	0.043
	GO:0005983	starch catabolic process	0.044
	GO:0046184	aldehyde biosynthetic process	0.044
	GO:1901137	carbohydrate derivative biosynthetic pro...	0.044
	GO:0034614	cellular response to reactive oxygen spe...	0.046
	GO:0010103	stomatal complex morphogenesis	0.046
	GO:0006721	terpenoid metabolic process	0.047
	GO:0006418	tRNA aminoacylation for protein translat...	0.049
	GO:1901605	alpha-amino acid metabolic process	0.051
	GO:0009058	biosynthetic process	0.051
	GO:0009251	glucan catabolic process	0.051
	GO:1901568	fatty acid derivative metabolic process	0.051
	GO:0042168	heme metabolic process	0.054
	GO:0051085	chaperone cofactor-dependent protein ref...	0.055
	GO:0016114	terpenoid biosynthetic process	0.057
	GO:0030244	cellulose biosynthetic process	0.058
	GO:0022904	respiratory electron transport chain	0.059
	GO:0044036	cell wall macromolecule metabolic proces...	0.059
	GO:0010143	cutin biosynthetic process	0.061
	GO:0010020	chloroplast fission	0.063
	GO:0042435	indole-containing compound biosynthetic ...	0.066
	GO:0071214	cellular response to abiotic stimulus	0.066
	GO:0104004	cellular response to environmental stimu...	0.066
	GO:0010410	hemicellulose metabolic process	0.067

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GO type	GO ID	Description	Adj. p-value
	GO:0009266	response to temperature stimulus	0.070
	GO:0006694	steroid biosynthetic process	0.070
	GO:0071482	cellular response to light stimulus	0.071
	GO:0016126	sterol biosynthetic process	0.071
	GO:0042775	mitochondrial ATP synthesis coupled elec...	0.074
	GO:0009644	response to high light intensity	0.074
	GO:0051261	protein depolymerization	0.076
	GO:0030243	cellulose metabolic process	0.076
	GO:0019430	removal of superoxide radicals	0.077
	GO:0071450	cellular response to oxygen radical	0.077
	GO:0071451	cellular response to superoxide	0.077
	GO:0043244	regulation of protein complex disassembl...	0.084
	GO:0009308	amine metabolic process	0.085
	GO:1903338	regulation of cell wall organization or ...	0.086
	GO:0045492	xylan biosynthetic process	0.087
	GO:0009943	adaxial/abaxial axis specification	0.093
	GO:0009944	polarity specification of adaxial/abaxia...	0.093
	GO:0019674	NAD metabolic process	0.097
	GO:0070592	cell wall polysaccharide biosynthetic pr...	0.097
	GO:0003006	developmental process involved in reprod...	0.098
	GO:0044038	cell wall macromolecule biosynthetic pro...	0.098
	GO:0070589	cellular component macromolecule biosynt...	0.098
	GO:0048481	plant ovule development	0.100
CC	GO:0031977	thylakoid lumen	0.000
	GO:0042170	plastid membrane	0.000
	GO:0031969	chloroplast membrane	0.000
	GO:0009523	photosystem II	0.000
	GO:0044429	mitochondrial part	0.000
	GO:1990204	oxidoreductase complex	0.000
	GO:0005875	microtubule associated complex	0.000
	GO:0033176	proton-transporting V-type ATPase comple...	0.000
	GO:0005740	mitochondrial envelope	0.000
	GO:0009295	nucleoid	0.000
	GO:0005743	mitochondrial inner membrane	0.000
	GO:0009528	plastid inner membrane	0.000
	GO:0005874	microtubule	0.000
	GO:0070469	respiratory chain	0.000
	GO:0044455	mitochondrial membrane part	0.001
	GO:0031225	anchored component of membrane	0.001
	GO:0098803	respiratory chain complex	0.001
	GO:0046658	anchored component of plasma membrane	0.001
	GO:0005746	mitochondrial respiratory chain	0.002
	GO:0042644	chloroplast nucleoid	0.002
	GO:0010319	stromule	0.002
	GO:0009654	photosystem II oxygen evolving complex	0.003
	GO:0016020	membrane	0.005
	GO:0009522	photosystem I	0.006
	GO:0005618	cell wall	0.008
	GO:0030312	external encapsulating structure	0.008

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GO type	GO ID	Description	Adj. p-value
	GO:0030964	NADH dehydrogenase complex	0.009
	GO:0045271	respiratory chain complex I	0.009
	GO:0098798	mitochondrial protein complex	0.012
	GO:0005753	mitochondrial proton-transporting ATP sy...	0.012
	GO:0005747	mitochondrial respiratory chain complex ...	0.013
	GO:0098796	membrane protein complex	0.019
	GO:0009527	plastid outer membrane	0.028
	GO:0009707	chloroplast outer membrane	0.028
	GO:0019898	extrinsic component of membrane	0.085
MF	GO:0016787	hydrolase activity	0.000
	GO:0016491	oxidoreductase activity	0.000
	GO:0016788	hydrolase activity, acting on ester bond...	0.000
	GO:0016829	lyase activity	0.000
	GO:0042578	phosphoric ester hydrolase activity	0.000
	GO:0016791	phosphatase activity	0.000
	GO:0016741	transferase activity, transferring one-c...	0.000
	GO:0003777	microtubule motor activity	0.000
	GO:0008168	methyltransferase activity	0.000
	GO:0016655	oxidoreductase activity, acting on NAD(P...	0.000
	GO:0050662	coenzyme binding	0.000
	GO:0003954	NADH dehydrogenase activity	0.001
	GO:0016620	oxidoreductase activity, acting on the a...	0.001
	GO:0016798	hydrolase activity, acting on glycosyl b...	0.001
	GO:0016747	transferase activity, transferring acyl ...	0.002
	GO:0051087	chaperone binding	0.003
	GO:0009055	electron transfer activity	0.004
	GO:0140101	catalytic activity, acting on a tRNA	0.004
	GO:0016413	O-acetyltransferase activity	0.004
	GO:0016853	isomerase activity	0.004
	GO:0016746	transferase activity, transferring acyl ...	0.004
	GO:0000287	magnesium ion binding	0.004
	GO:0016790	thiolester hydrolase activity	0.004
	GO:0019205	nucleobase-containing compound kinase ac...	0.004
	GO:0044769	ATPase activity, coupled to transmembran...	0.004
	GO:0046961	proton-transporting ATPase activity, rot...	0.004
	GO:0004553	hydrolase activity, hydrolyzing O-glycos...	0.004
	GO:0016209	antioxidant activity	0.004
	GO:0016776	phosphotransferase activity, phosphate g...	0.004
	GO:0016903	oxidoreductase activity, acting on the a...	0.004
	GO:0080019	fatty-acyl-CoA reductase (alcohol-formin...	0.006
	GO:0008374	O-acyltransferase activity	0.007
	GO:0016778	diphosphotransferase activity	0.007
	GO:0016866	intramolecular transferase activity	0.010
	GO:0140097	catalytic activity, acting on DNA	0.010
	GO:0008137	NADH dehydrogenase (ubiquinone) activity	0.011
	GO:0008757	S-adenosylmethionine-dependent methyltra...	0.011
	GO:0050136	NADH dehydrogenase (quinone) activity	0.011
	GO:2001070	starch binding	0.012
	GO:0036442	proton-exporting ATPase activity	0.012

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GO type	GO ID	Description	Adj. p-value
	GO:0016830	carbon-carbon lyase activity	0.013
	GO:0004252	serine-type endopeptidase activity	0.013
	GO:0008236	serine-type peptidase activity	0.013
	GO:0016614	oxidoreductase activity, acting on CH-OH...	0.013
	GO:0016887	ATPase activity	0.013
	GO:0017171	serine hydrolase activity	0.013
	GO:0016407	acetyltransferase activity	0.017
	GO:0016168	chlorophyll binding	0.018
	GO:0016759	cellulose synthase activity	0.018
	GO:0016760	cellulose synthase (UDP-forming) activit...	0.018
	GO:0016840	carbon-nitrogen lyase activity	0.021
	GO:0033764	steroid dehydrogenase activity, acting o...	0.021
	GO:0016774	phosphotransferase activity, carboxyl gr...	0.038
	GO:0016462	pyrophosphatase activity	0.039
	GO:0017111	nucleoside-triphosphatase activity	0.043
	GO:0016874	ligase activity	0.043
	GO:0016615	malate dehydrogenase activity	0.044
	GO:0003854	3-beta-hydroxy-delta5-steroid dehydrogen...	0.044
	GO:0016229	steroid dehydrogenase activity	0.045
	GO:0004812	aminoacyl-tRNA ligase activity	0.046
	GO:0016875	ligase activity, forming carbon-oxygen b...	0.046
	GO:0050660	flavin adenine dinucleotide binding	0.046
	GO:0004721	phosphoprotein phosphatase activity	0.047
	GO:0016817	hydrolase activity, acting on acid anhyd...	0.055
	GO:0016762	xyloglucan:xyloglucosyl transferase acti...	0.055
	GO:0016818	hydrolase activity, acting on acid anhyd...	0.055
	GO:0050661	NADP binding	0.062
	GO:0016838	carbon-oxygen lyase activity, acting on ...	0.064
	GO:0016616	oxidoreductase activity, acting on the C...	0.073
	GO:0050308	sugar-phosphatase activity	0.073
	GO:0019238	cyclohydrolase activity	0.081
	GO:0016861	intramolecular oxidoreductase activity, ...	0.084
	GO:0019203	carbohydrate phosphatase activity	0.099
	GO:0042349	guiding stereospecific synthesis activit...	0.099
	GO:0051015	actin filament binding	0.099

4.1.16 Leaf - Preflowering - Cluster 16

GO type	GO ID	Description	Adj. p-value
BP	GO:1903506	regulation of nucleic acid-templated tra...	0.000
	GO:2001141	regulation of RNA biosynthetic process	0.000
	GO:0051252	regulation of RNA metabolic process	0.000
	GO:0042493	response to drug	0.004
	GO:0009404	toxin metabolic process	0.004
	GO:0043207	response to external biotic stimulus	0.004
	GO:0051707	response to other organism	0.004
	GO:0009607	response to biotic stimulus	0.004
	GO:0051704	multi-organism process	0.005
	GO:0044267	cellular protein metabolic process	0.008
	GO:0050832	defense response to fungus	0.008
	GO:0050896	response to stimulus	0.009
	GO:0071229	cellular response to acid chemical	0.011
	GO:0019538	protein metabolic process	0.011
	GO:0098542	defense response to other organism	0.017
	GO:0006887	exocytosis	0.023
	GO:0023014	signal transduction by protein phosphory...	0.023
	GO:0032940	secretion by cell	0.023
	GO:1901700	response to oxygen-containing compound	0.023
	GO:0051716	cellular response to stimulus	0.023
	GO:0031347	regulation of defense response	0.026
	GO:0046903	secretion	0.028
	GO:0001101	response to acid chemical	0.031
	GO:1901698	response to nitrogen compound	0.032
	GO:0070887	cellular response to chemical stimulus	0.046
	GO:0006950	response to stress	0.052
	GO:0042737	drug catabolic process	0.052
	GO:0048523	negative regulation of cellular process	0.056
	GO:0009605	response to external stimulus	0.057
	GO:0042221	response to chemical	0.060
	GO:1902531	regulation of intracellular signal trans...	0.061
	GO:0010941	regulation of cell death	0.072
	GO:0009863	salicylic acid mediated signaling pathwa...	0.080
	GO:0071446	cellular response to salicylic acid stim...	0.084
CC	GO:0005911	cell-cell junction	0.005
	GO:0030054	cell junction	0.005
	GO:0009506	plasmodesma	0.005
	GO:0055044	symplast	0.005
	GO:0000145	exocyst	0.013
	GO:0099023	tethering complex	0.023
	GO:0030135	coated vesicle	0.066
MF	GO:0016757	transferase activity, transferring glyco...	0.000
	GO:0003677	DNA binding	0.000
	GO:0016758	transferase activity, transferring hexos...	0.000
	GO:0030246	carbohydrate binding	0.000
	GO:0008194	UDP-glycosyltransferase activity	0.001

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GO type	GO ID	Description	Adj. p-value
	GO:0046527	glucosyltransferase activity	0.001
	GO:0004871	signal transducer activity	0.005
	GO:0001871	pattern binding	0.028
	GO:0030247	polysaccharide binding	0.028
	GO:0004190	aspartic-type endopeptidase activity	0.039
	GO:0070001	aspartic-type peptidase activity	0.039
	GO:0051213	dioxygenase activity	0.040

4.1.17 Leaf - Preflowering - Cluster 17

GO type	GO ID	Description	Adj. p-value
BP	GO:0003333	amino acid transmembrane transport	0.002
	GO:1904659	glucose transmembrane transport	0.006
	GO:1903825	organic acid transmembrane transport	0.006
	GO:0006022	aminoglycan metabolic process	0.008
	GO:1905039	carboxylic acid transmembrane transport	0.009
	GO:0046323	glucose import	0.010
	GO:0008645	hexose transmembrane transport	0.010
	GO:0006836	neurotransmitter transport	0.010
	GO:0015749	monosaccharide transmembrane transport	0.011
	GO:0009875	pollen-pistil interaction	0.021
	GO:0006040	amino sugar metabolic process	0.024
	GO:0015807	L-amino acid transport	0.024
	GO:0042493	response to drug	0.024
	GO:0007166	cell surface receptor signaling pathway	0.024
	GO:0015849	organic acid transport	0.025
	GO:0015804	neutral amino acid transport	0.025
	GO:0098754	detoxification	0.028
	GO:0008037	cell recognition	0.029
	GO:0008643	carbohydrate transport	0.029
	GO:0046942	carboxylic acid transport	0.032
	GO:0048544	recognition of pollen	0.033
	GO:1902475	L-alpha-amino acid transmembrane transpo...	0.035
	GO:0010466	negative regulation of peptidase activit...	0.038
	GO:0010951	negative regulation of endopeptidase act...	0.038
	GO:0052547	regulation of peptidase activity	0.038
	GO:0052548	regulation of endopeptidase activity	0.038
	GO:0006855	drug transmembrane transport	0.038
	GO:0009607	response to biotic stimulus	0.038
	GO:0006820	anion transport	0.039
	GO:0006665	sphingolipid metabolic process	0.039
	GO:1901136	carbohydrate derivative catabolic proces...	0.041
	GO:0019748	secondary metabolic process	0.043
	GO:0015706	nitrate transport	0.048
	GO:0034219	carbohydrate transmembrane transport	0.049
	GO:0006796	phosphate-containing compound metabolic ...	0.056
	GO:0015850	organic hydroxy compound transport	0.056
	GO:0015893	drug transport	0.058
	GO:0098542	defense response to other organism	0.066
	GO:0006793	phosphorus metabolic process	0.073
	GO:0042737	drug catabolic process	0.080
	GO:0008361	regulation of cell size	0.083
	GO:0031348	negative regulation of defense response	0.083
	GO:0043207	response to external biotic stimulus	0.087
	GO:0051707	response to other organism	0.087
	GO:0045861	negative regulation of proteolysis	0.088
	GO:0005975	carbohydrate metabolic process	0.090

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0009617	response to bacterium	0.098
	GO:0015791	polyol transport	0.098
	GO:0006749	glutathione metabolic process	0.098
	GO:0006833	water transport	0.098
	GO:0042044	fluid transport	0.098
	GO:0098656	anion transmembrane transport	0.098
	GO:0009814	defense response, incompatible interacti...	0.099
CC	GO:0071944	cell periphery	0.000
	GO:0005773	vacuole	0.005
MF	GO:0005215	transporter activity	0.000
	GO:0016705	oxidoreductase activity, acting on paire...	0.000
	GO:0003824	catalytic activity	0.000
	GO:0004497	monooxygenase activity	0.000
	GO:0030246	carbohydrate binding	0.000
	GO:0015171	amino acid transmembrane transporter act...	0.000
	GO:0005355	glucose transmembrane transporter activi...	0.002
	GO:0015144	carbohydrate transmembrane transporter a...	0.002
	GO:0015293	symporter activity	0.002
	GO:0046527	glucosyltransferase activity	0.002
	GO:0005326	neurotransmitter transporter activity	0.002
	GO:0005524	ATP binding	0.002
	GO:0043168	anion binding	0.002
	GO:0030414	peptidase inhibitor activity	0.002
	GO:0061134	peptidase regulator activity	0.002
	GO:0015294	solute:cation symporter activity	0.003
	GO:0016758	transferase activity, transferring hexos...	0.003
	GO:0015149	hexose transmembrane transporter activit...	0.003
	GO:0015145	monosaccharide transmembrane transporter...	0.003
	GO:0004866	endopeptidase inhibitor activity	0.004
	GO:0005342	organic acid transmembrane transporter a...	0.004
	GO:0061135	endopeptidase regulator activity	0.004
	GO:0015179	L-amino acid transmembrane transporter a...	0.004
	GO:0022804	active transmembrane transporter activit...	0.005
	GO:0046943	carboxylic acid transmembrane transporte...	0.006
	GO:0008194	UDP-glycosyltransferase activity	0.007
	GO:0008514	organic anion transmembrane transporter ...	0.007
	GO:0035639	purine ribonucleoside triphosphate bindi...	0.007
	GO:0015297	antiporter activity	0.008
	GO:0051119	sugar transmembrane transporter activity	0.008
	GO:0015295	solute:proton symporter activity	0.008
	GO:0016757	transferase activity, transferring glyco...	0.010
	GO:0043167	ion binding	0.010
	GO:1901618	organic hydroxy compound transmembrane t...	0.010
	GO:0008324	cation transmembrane transporter activit...	0.012
	GO:0004871	signal transducer activity	0.013
	GO:0005351	carbohydrate:proton symporter activity	0.013
	GO:0005402	carbohydrate:cation symporter activity	0.013
	GO:0004364	glutathione transferase activity	0.013
	GO:0004857	enzyme inhibitor activity	0.016

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0051213	dioxygenase activity	0.017
	GO:0015168	glycerol transmembrane transporter activ...	0.018
	GO:0004553	hydrolase activity, hydrolyzing O-glycos...	0.020
	GO:0008483	transaminase activity	0.020
	GO:0016769	transferase activity, transferring nitro...	0.020
	GO:0015174	basic amino acid transmembrane transport...	0.023
	GO:0015166	polyol transmembrane transporter activit...	0.025
	GO:0038023	signaling receptor activity	0.026
	GO:0060089	molecular transducer activity	0.026
	GO:0005310	dicarboxylic acid transmembrane transpor...	0.030
	GO:0016491	oxidoreductase activity	0.030
	GO:0004867	serine-type endopeptidase inhibitor acti...	0.032
	GO:0005372	water transmembrane transporter activity	0.033
	GO:0015250	water channel activity	0.033
	GO:0015254	glycerol channel activity	0.033
	GO:0046983	protein dimerization activity	0.034
	GO:0015238	drug transmembrane transporter activity	0.038
	GO:0000166	nucleotide binding	0.043
	GO:0016798	hydrolase activity, acting on glycosyl b...	0.043
	GO:1901265	nucleoside phosphate binding	0.043
	GO:0036094	small molecule binding	0.045
	GO:0004970	ionotropic glutamate receptor activity	0.047
	GO:0005230	extracellular ligand-gated ion channel a...	0.047
	GO:0008066	glutamate receptor activity	0.047
	GO:0022824	transmitter-gated ion channel activity	0.047
	GO:0022835	transmitter-gated channel activity	0.047
	GO:0015175	neutral amino acid transmembrane transpo...	0.055
	GO:0022890	inorganic cation transmembrane transport...	0.074
	GO:0004888	transmembrane signaling receptor activit...	0.077
	GO:0003959	NADPH dehydrogenase activity	0.079
	GO:0030594	neurotransmitter receptor activity	0.085
	GO:0005102	signaling receptor binding	0.093

4.1.18 Leaf - Preflowering - Cluster 18

GO type	GO ID	Description	Adj. p-value
BP	GO:0071702	organic substance transport	0.000
	GO:0046323	glucose import	0.004
	GO:0042493	response to drug	0.005
	GO:0071705	nitrogen compound transport	0.005
	GO:0006833	water transport	0.005
	GO:0042044	fluid transport	0.005
	GO:0006575	cellular modified amino acid metabolic p...	0.007
	GO:0030104	water homeostasis	0.007
	GO:0005996	monosaccharide metabolic process	0.007
	GO:0006836	neurotransmitter transport	0.009
	GO:0006026	aminoglycan catabolic process	0.013
	GO:0006030	chitin metabolic process	0.013
	GO:0006032	chitin catabolic process	0.013
	GO:0008643	carbohydrate transport	0.013
	GO:0044550	secondary metabolite biosynthetic proces...	0.013
	GO:0046348	amino sugar catabolic process	0.013
	GO:1901071	glucosamine-containing compound metaboli...	0.013
	GO:1901072	glucosamine-containing compound cataboli...	0.013
	GO:0051179	localization	0.015
	GO:0006952	defense response	0.016
	GO:0006022	aminoglycan metabolic process	0.018
	GO:0051234	establishment of localization	0.018
	GO:0006810	transport	0.019
	GO:0015807	L-amino acid transport	0.024
	GO:0055114	oxidation-reduction process	0.025
	GO:0006040	amino sugar metabolic process	0.035
	GO:0015804	neutral amino acid transport	0.035
	GO:0006855	drug transmembrane transport	0.045
	GO:0044248	cellular catabolic process	0.045
	GO:0006665	sphingolipid metabolic process	0.053
	GO:1902475	L-alpha-amino acid transmembrane transpo...	0.055
	GO:0015893	drug transport	0.064
	GO:0010243	response to organonitrogen compound	0.089
	GO:0046149	pigment catabolic process	0.091
	GO:0072523	purine-containing compound catabolic pro...	0.091
	GO:0006468	protein phosphorylation	0.093
	GO:0034219	carbohydrate transmembrane transport	0.093
CC	GO:0005886	plasma membrane	0.000
	GO:0005773	vacuole	0.001
	GO:0044459	plasma membrane part	0.001
	GO:0098805	whole membrane	0.002
	GO:0030118	clathrin coat	0.006
	GO:0071944	cell periphery	0.006
	GO:0031226	intrinsic component of plasma membrane	0.010
	GO:0099023	tethering complex	0.010
	GO:0030120	vesicle coat	0.010

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0044433	cytoplasmic vesicle part	0.035
	GO:0098797	plasma membrane protein complex	0.056
	GO:0005852	eukaryotic translation initiation factor...	0.058
	GO:0017119	Golgi transport complex	0.073
	GO:0005777	peroxisome	0.090
	GO:0042579	microbody	0.090
MF	GO:0004497	monooxygenase activity	0.000
	GO:0016705	oxidoreductase activity, acting on paire...	0.000
	GO:1901618	organic hydroxy compound transmembrane t...	0.000
	GO:0005355	glucose transmembrane transporter activi...	0.002
	GO:0015145	monosaccharide transmembrane transporter...	0.003
	GO:0015293	symporter activity	0.003
	GO:0015149	hexose transmembrane transporter activit...	0.003
	GO:0030246	carbohydrate binding	0.003
	GO:0015144	carbohydrate transmembrane transporter a...	0.003
	GO:0016491	oxidoreductase activity	0.004
	GO:0015294	solute:cation symporter activity	0.004
	GO:0005326	neurotransmitter transporter activity	0.004
	GO:0015174	basic amino acid transmembrane transport...	0.004
	GO:0008483	transaminase activity	0.005
	GO:0016769	transferase activity, transferring nitro...	0.005
	GO:0015291	secondary active transmembrane transport...	0.007
	GO:0004568	chitinase activity	0.008
	GO:0042562	hormone binding	0.009
	GO:0015179	L-amino acid transmembrane transporter a...	0.010
	GO:0051213	dioxygenase activity	0.013
	GO:0004672	protein kinase activity	0.014
	GO:0005351	carbohydrate:proton symporter activity	0.016
	GO:0005402	carbohydrate:cation symporter activity	0.016
	GO:0015295	solute:proton symporter activity	0.016
	GO:0046914	transition metal ion binding	0.018
	GO:0005215	transporter activity	0.031
	GO:0051119	sugar transmembrane transporter activity	0.031
	GO:0004857	enzyme inhibitor activity	0.034
	GO:0016757	transferase activity, transferring glyco...	0.045
	GO:0016765	transferase activity, transferring alkyl...	0.046
	GO:0019840	isoprenoid binding	0.047
	GO:0035673	oligopeptide transmembrane transporter a...	0.057
	GO:0010427	abscisic acid binding	0.067
	GO:0004866	endopeptidase inhibitor activity	0.073
	GO:0061135	endopeptidase regulator activity	0.073
	GO:0016773	phosphotransferase activity, alcohol gro...	0.081
	GO:0015175	neutral amino acid transmembrane transpo...	0.083
	GO:0022857	transmembrane transporter activity	0.083
	GO:0030414	peptidase inhibitor activity	0.083
	GO:0061134	peptidase regulator activity	0.083
	GO:0015171	amino acid transmembrane transporter act...	0.089
	GO:0004867	serine-type endopeptidase inhibitor acti...	0.094

4.1.19 Leaf - Preflowering - Cluster 19

GO type	GO ID	Description	Adj. p-value
BP	GO:0044085	cellular component biogenesis	0.000
	GO:0034660	ncRNA metabolic process	0.000
	GO:0022607	cellular component assembly	0.000
	GO:0034470	ncRNA processing	0.000
	GO:0009451	RNA modification	0.002
	GO:0006399	tRNA metabolic process	0.003
	GO:0008152	metabolic process	0.009
	GO:0006396	RNA processing	0.055
	GO:0001510	RNA methylation	0.084
CC	GO:1902494	catalytic complex	0.009
	GO:0031090	organelle membrane	0.010
	GO:0046658	anchored component of plasma membrane	0.019
	GO:0031225	anchored component of membrane	0.019
	GO:0005576	extracellular region	0.068
MF	GO:0016787	hydrolase activity	0.000
	GO:0016798	hydrolase activity, acting on glycosyl b...	0.021
	GO:0008173	RNA methyltransferase activity	0.034
	GO:0140098	catalytic activity, acting on RNA	0.034
	GO:0016741	transferase activity, transferring one-c...	0.034
	GO:0004553	hydrolase activity, hydrolyzing O-glycos...	0.051

4.1.20 Leaf - Preflowering - Cluster 20

GO type	GO ID	Description	Adj. p-value
BP	GO:0032259	methylation	0.000
	GO:0051276	chromosome organization	0.000
	GO:0043414	macromolecule methylation	0.000
	GO:0006091	generation of precursor metabolites and ...	0.001
	GO:0018205	peptidyl-lysine modification	0.002
	GO:0006325	chromatin organization	0.003
	GO:0016570	histone modification	0.009
	GO:0019637	organophosphate metabolic process	0.010
	GO:0048235	pollen sperm cell differentiation	0.010
	GO:0016569	covalent chromatin modification	0.010
	GO:0019438	aromatic compound biosynthetic process	0.010
	GO:0006479	protein methylation	0.011
	GO:0008213	protein alkylation	0.011
	GO:0018193	peptidyl-amino acid modification	0.011
	GO:0009699	phenylpropanoid biosynthetic process	0.015
	GO:0009123	nucleoside monophosphate metabolic proce...	0.016
	GO:1901568	fatty acid derivative metabolic process	0.017
	GO:0018022	peptidyl-lysine methylation	0.018
	GO:0016571	histone methylation	0.020
	GO:0006694	steroid biosynthetic process	0.021
	GO:0009150	purine ribonucleotide metabolic process	0.021
	GO:1901362	organic cyclic compound biosynthetic pro...	0.021
	GO:0006163	purine nucleotide metabolic process	0.022
	GO:0051188	cofactor biosynthetic process	0.023
	GO:0048869	cellular developmental process	0.030
	GO:0009126	purine nucleoside monophosphate metaboli...	0.032
	GO:0009161	ribonucleoside monophosphate metabolic p...	0.032
	GO:0009167	purine ribonucleoside monophosphate meta...	0.032
	GO:0030154	cell differentiation	0.032
	GO:0035336	long-chain fatty-acyl-CoA metabolic proc...	0.034
	GO:0071555	cell wall organization	0.034
	GO:0046034	ATP metabolic process	0.038
	GO:0009259	ribonucleotide metabolic process	0.039
	GO:0090407	organophosphate biosynthetic process	0.039
	GO:0009144	purine nucleoside triphosphate metabolic...	0.040
	GO:0009205	purine ribonucleoside triphosphate metab...	0.040
	GO:0072330	monocarboxylic acid biosynthetic process	0.050
	GO:0044283	small molecule biosynthetic process	0.051
	GO:0009199	ribonucleoside triphosphate metabolic pr...	0.054
	GO:0016052	carbohydrate catabolic process	0.056
	GO:0009409	response to cold	0.059
	GO:0055114	oxidation-reduction process	0.069
	GO:0006629	lipid metabolic process	0.073
	GO:0016053	organic acid biosynthetic process	0.073
	GO:0045229	external encapsulating structure organiz...	0.073
	GO:0046394	carboxylic acid biosynthetic process	0.073

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GO type	GO ID	Description	Adj. p-value
	GO:0006637	acyl-CoA metabolic process	0.073
	GO:0035383	thioester metabolic process	0.073
	GO:0035337	fatty-acyl-CoA metabolic process	0.079
	GO:0006164	purine nucleotide biosynthetic process	0.092
	GO:0034968	histone lysine methylation	0.093
	GO:0008202	steroid metabolic process	0.094
	GO:0019359	nicotinamide nucleotide biosynthetic pro...	0.097
	GO:0009152	purine ribonucleotide biosynthetic proce...	0.099
	GO:0009698	phenylpropanoid metabolic process	0.099
	GO:0046434	organophosphate catabolic process	0.099
CC	GO:0009579	thylakoid	0.000
	GO:0009534	chloroplast thylakoid	0.000
	GO:0031976	plastid thylakoid	0.000
	GO:0005874	microtubule	0.001
	GO:0099080	supramolecular complex	0.003
	GO:0099081	supramolecular polymer	0.003
	GO:0099512	supramolecular fiber	0.003
	GO:0099513	polymeric cytoskeletal fiber	0.003
	GO:0005694	chromosome	0.006
	GO:0015630	microtubule cytoskeleton	0.007
	GO:0005881	cytoplasmic microtubule	0.008
	GO:0005634	nucleus	0.013
	GO:0055028	cortical microtubule	0.025
	GO:0030863	cortical cytoskeleton	0.039
	GO:0030981	cortical microtubule cytoskeleton	0.039
	GO:0005856	cytoskeleton	0.071
	GO:0044430	cytoskeletal part	0.071
	GO:0005739	mitochondrion	0.092
MF	GO:0003824	catalytic activity	0.001
	GO:0008757	S-adenosylmethionine-dependent methyltra...	0.001
	GO:0008276	protein methyltransferase activity	0.006
	GO:0016278	lysine N-methyltransferase activity	0.007
	GO:0016279	protein-lysine N-methyltransferase activ...	0.007
	GO:0016620	oxidoreductase activity, acting on the a...	0.011
	GO:0008170	N-methyltransferase activity	0.014
	GO:0140098	catalytic activity, acting on RNA	0.021
	GO:0042054	histone methyltransferase activity	0.021
	GO:0016903	oxidoreductase activity, acting on the a...	0.025
	GO:0042393	histone binding	0.038
	GO:0016788	hydrolase activity, acting on ester bond...	0.040
	GO:0016787	hydrolase activity	0.052
	GO:0080019	fatty-acyl-CoA reductase (alcohol-formin...	0.052
	GO:0018024	histone-lysine N-methyltransferase activ...	0.067
	GO:0016774	phosphotransferase activity, carboxyl gr...	0.075
	GO:0042578	phosphoric ester hydrolase activity	0.076

4.2 Leaf Postflowering clusters

4.2.1 Leaf - Postflowering - Cluster 1

GO type	GO ID	Description	Adj. p-value
	GO:0016310	phosphorylation	0.000
	GO:0019684	photosynthesis, light reaction	0.000
	GO:0044262	cellular carbohydrate metabolic process	0.000
	GO:0044281	small molecule metabolic process	0.000
	GO:0005975	carbohydrate metabolic process	0.000
	GO:0007165	signal transduction	0.000
	GO:0023052	signaling	0.000
	GO:0044264	cellular polysaccharide metabolic proces...	0.000
	GO:0007154	cell communication	0.000
	GO:0042737	drug catabolic process	0.000
	GO:0008299	isoprenoid biosynthetic process	0.000
	GO:0009767	photosynthetic electron transport chain	0.001
	GO:0044283	small molecule biosynthetic process	0.001
	GO:0072330	monocarboxylic acid biosynthetic process	0.003
	GO:0043436	oxoacid metabolic process	0.004
	GO:0005982	starch metabolic process	0.004
	GO:0050801	ion homeostasis	0.004
	GO:0006082	organic acid metabolic process	0.005
	GO:0006631	fatty acid metabolic process	0.005
	GO:0006721	terpenoid metabolic process	0.005
	GO:0051188	cofactor biosynthetic process	0.005
	GO:0009606	tropism	0.005
	GO:0030243	cellulose metabolic process	0.006
	GO:0009699	phenylpropanoid biosynthetic process	0.006
	GO:0019752	carboxylic acid metabolic process	0.007
	GO:0055065	metal ion homeostasis	0.007
	GO:0006633	fatty acid biosynthetic process	0.007
	GO:0042546	cell wall biogenesis	0.008
	GO:0050896	response to stimulus	0.009
	GO:0055080	cation homeostasis	0.009
	GO:0071482	cellular response to light stimulus	0.010
	GO:1990748	cellular detoxification	0.011
	GO:0009605	response to external stimulus	0.011
	GO:0022900	electron transport chain	0.011
	GO:0010383	cell wall polysaccharide metabolic proce...	0.011
	GO:0016052	carbohydrate catabolic process	0.012
	GO:0097237	cellular response to toxic substance	0.012
	GO:0016114	terpenoid biosynthetic process	0.013
	GO:0042445	hormone metabolic process	0.013
	GO:0098869	cellular oxidant detoxification	0.013
	GO:0009201	ribonucleoside triphosphate biosynthetic...	0.013
	GO:0006754	ATP biosynthetic process	0.014
	GO:0009142	nucleoside triphosphate biosynthetic pro...	0.014
	GO:0010410	hemicellulose metabolic process	0.014
	GO:0098771	inorganic ion homeostasis	0.014

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GO type	GO ID	Description	Adj. p-value
	GO:0007166	cell surface receptor signaling pathway	0.015
	GO:0009145	purine nucleoside triphosphate biosynthe...	0.016
	GO:0009206	purine ribonucleoside triphosphate biosy...	0.016
	GO:0051274	beta-glucan biosynthetic process	0.016
	GO:0006464	cellular protein modification process	0.017
	GO:0018298	protein-chromophore linkage	0.017
	GO:0036211	protein modification process	0.017
	GO:0009637	response to blue light	0.018
	GO:0010114	response to red light	0.019
	GO:0009072	aromatic amino acid family metabolic pro...	0.021
	GO:0015985	energy coupled proton transport, down el...	0.021
	GO:0015986	ATP synthesis coupled proton transport	0.021
	GO:0010817	regulation of hormone levels	0.021
	GO:0048467	gynoecium development	0.022
	GO:0046854	phosphatidylinositol phosphorylation	0.022
	GO:0006779	porphyrin-containing compound biosynthet...	0.023
	GO:0010118	stomatal movement	0.023
	GO:0090698	post-embryonic plant morphogenesis	0.025
	GO:0009698	phenylpropanoid metabolic process	0.026
	GO:0071214	cellular response to abiotic stimulus	0.026
	GO:0104004	cellular response to environmental stimu...	0.026
	GO:0034754	cellular hormone metabolic process	0.028
	GO:0009150	purine ribonucleotide metabolic process	0.029
	GO:0051273	beta-glucan metabolic process	0.029
	GO:0051716	cellular response to stimulus	0.029
	GO:0009888	tissue development	0.033
	GO:0033014	tetrapyrrole biosynthetic process	0.033
	GO:0010374	stomatal complex development	0.034
	GO:0009832	plant-type cell wall biogenesis	0.034
	GO:0019318	hexose metabolic process	0.034
	GO:0048440	carpel development	0.035
	GO:0071478	cellular response to radiation	0.035
	GO:0046834	lipid phosphorylation	0.035
	GO:0009152	purine ribonucleotide biosynthetic proce...	0.036
	GO:0015995	chlorophyll biosynthetic process	0.036
	GO:0023014	signal transduction by protein phosphory...	0.036
	GO:0010103	stomatal complex morphogenesis	0.037
	GO:0051186	cofactor metabolic process	0.037
	GO:0045944	positive regulation of transcription by ...	0.039
	GO:0007017	microtubule-based process	0.040
	GO:0046034	ATP metabolic process	0.040
	GO:0051128	regulation of cellular component organiz...	0.040
	GO:0006163	purine nucleotide metabolic process	0.041
	GO:0071495	cellular response to endogenous stimulus	0.041
	GO:0006952	defense response	0.041
	GO:0009141	nucleoside triphosphate metabolic proces...	0.041
	GO:0009074	aromatic amino acid family catabolic pro...	0.042
	GO:0019637	organophosphate metabolic process	0.042
	GO:0051701	interaction with host	0.042

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GO type	GO ID	Description	Adj. p-value
	GO:0090627	plant epidermal cell differentiation	0.042
	GO:0032870	cellular response to hormone stimulus	0.043
	GO:0000272	polysaccharide catabolic process	0.043
	GO:0051704	multi-organism process	0.044
	GO:0034762	regulation of transmembrane transport	0.046
	GO:0006164	purine nucleotide biosynthetic process	0.047
	GO:0031408	oxylipin biosynthetic process	0.048
	GO:0006753	nucleoside phosphate metabolic process	0.049
	GO:0006270	DNA replication initiation	0.049
	GO:0009416	response to light stimulus	0.049
	GO:0009629	response to gravity	0.050
	GO:0009630	gravitropism	0.050
	GO:0009734	auxin-activated signaling pathway	0.050
	GO:0072522	purine-containing compound biosynthetic ...	0.050
	GO:0071483	cellular response to blue light	0.052
	GO:0042440	pigment metabolic process	0.053
	GO:0006732	coenzyme metabolic process	0.053
	GO:0035670	plant-type ovary development	0.053
	GO:0009314	response to radiation	0.054
	GO:0016055	Wnt signaling pathway	0.055
	GO:0098656	anion transmembrane transport	0.055
	GO:0198738	cell-cell signaling by wnt	0.055
	GO:1905114	cell surface receptor signaling pathway ...	0.055
	GO:0009958	positive gravitropism	0.055
	GO:0007267	cell-cell signaling	0.059
	GO:0034765	regulation of ion transmembrane transpor...	0.059
	GO:1905392	plant organ morphogenesis	0.059
	GO:0009144	purine nucleoside triphosphate metabolic...	0.059
	GO:0009165	nucleotide biosynthetic process	0.059
	GO:0009199	ribonucleoside triphosphate metabolic pr...	0.059
	GO:0009205	purine ribonucleoside triphosphate metab...	0.059
	GO:1901293	nucleoside phosphate biosynthetic proces...	0.061
	GO:0009668	plastid membrane organization	0.061
	GO:0010027	thylakoid membrane organization	0.061
	GO:0009117	nucleotide metabolic process	0.062
	GO:0016109	tetraterpenoid biosynthetic process	0.062
	GO:0016117	carotenoid biosynthetic process	0.062
	GO:0070887	cellular response to chemical stimulus	0.063
	GO:0031407	oxylipin metabolic process	0.064
	GO:0009127	purine nucleoside monophosphate biosynth...	0.064
	GO:0009168	purine ribonucleoside monophosphate bios...	0.064
	GO:0018105	peptidyl-serine phosphorylation	0.064
	GO:0019693	ribose phosphate metabolic process	0.065
	GO:0016108	tetraterpenoid metabolic process	0.066
	GO:0016116	carotenoid metabolic process	0.066
	GO:0009607	response to biotic stimulus	0.066
	GO:0010218	response to far red light	0.066
	GO:0071365	cellular response to auxin stimulus	0.066
	GO:0043269	regulation of ion transport	0.066

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0009260	ribonucleotide biosynthetic process	0.067
	GO:0046390	ribose phosphate biosynthetic process	0.067
	GO:0048481	plant ovule development	0.070
	GO:0009124	nucleoside monophosphate biosynthetic pr...	0.071
	GO:0006897	endocytosis	0.071
	GO:0009126	purine nucleoside monophosphate metaboli...	0.071
	GO:0009167	purine ribonucleoside monophosphate meta...	0.071
	GO:0009639	response to red or far red light	0.071
	GO:0043207	response to external biotic stimulus	0.071
	GO:0051707	response to other organism	0.071
	GO:0072507	divalent inorganic cation homeostasis	0.071
	GO:0009733	response to auxin	0.072
	GO:0072521	purine-containing compound metabolic pro...	0.072
	GO:0008356	asymmetric cell division	0.073
	GO:0009259	ribonucleotide metabolic process	0.074
	GO:0046777	protein autophosphorylation	0.074
	GO:0010411	xyloglucan metabolic process	0.075
	GO:0035556	intracellular signal transduction	0.075
	GO:0018209	peptidyl-serine modification	0.078
	GO:0016998	cell wall macromolecule catabolic proces...	0.081
	GO:1901135	carbohydrate derivative metabolic proces...	0.083
	GO:0006816	calcium ion transport	0.088
	GO:0022604	regulation of cell morphogenesis	0.088
	GO:0009690	cytokinin metabolic process	0.092
	GO:0006108	malate metabolic process	0.094
	GO:0072524	pyridine-containing compound metabolic p...	0.094
	GO:0005984	disaccharide metabolic process	0.097
	GO:0072525	pyridine-containing compound biosyntheti...	0.097
	GO:0042168	heme metabolic process	0.098
CC	GO:0009534	chloroplast thylakoid	0.000
	GO:0016020	membrane	0.000
	GO:0031224	intrinsic component of membrane	0.000
	GO:0031977	thylakoid lumen	0.000
	GO:0009521	photosystem	0.000
	GO:0005618	cell wall	0.000
	GO:0030312	external encapsulating structure	0.000
	GO:0009505	plant-type cell wall	0.004
	GO:0048046	apoplast	0.004
	GO:0043596	nuclear replication fork	0.011
	GO:0005874	microtubule	0.015
	GO:0099080	supramolecular complex	0.019
	GO:0099081	supramolecular polymer	0.019
	GO:0099512	supramolecular fiber	0.019
	GO:0099513	polymeric cytoskeletal fiber	0.019
	GO:0009524	phragmoplast	0.032
	GO:0015629	actin cytoskeleton	0.043
	GO:0010319	stromule	0.045
	GO:0031225	anchored component of membrane	0.073
	GO:0000347	THO complex	0.099

Continued on next page

GO type	GO ID	Description	Adj. p-value
MF	GO:0016301	kinase activity	0.000
	GO:0016773	phosphotransferase activity, alcohol gro...	0.000
	GO:0032559	adenyl ribonucleotide binding	0.000
	GO:0043168	anion binding	0.000
	GO:0008144	drug binding	0.000
	GO:0016798	hydrolase activity, acting on glycosyl b...	0.000
	GO:0003774	motor activity	0.000
	GO:0003777	microtubule motor activity	0.000
	GO:0016829	lyase activity	0.000
	GO:0004871	signal transducer activity	0.000
	GO:0042626	ATPase activity, coupled to transmembran...	0.001
	GO:0005516	calmodulin binding	0.001
	GO:0015399	primary active transmembrane transporter...	0.001
	GO:0015405	P-P-bond-hydrolysis-driven transmembrane...	0.001
	GO:0042578	phosphoric ester hydrolase activity	0.002
	GO:0043492	ATPase activity, coupled to movement of ...	0.002
	GO:0016835	carbon-oxygen lyase activity	0.002
	GO:0001871	pattern binding	0.003
	GO:0003779	actin binding	0.003
	GO:0008236	serine-type peptidase activity	0.003
	GO:0017171	serine hydrolase activity	0.003
	GO:0022804	active transmembrane transporter activit...	0.003
	GO:0030247	polysaccharide binding	0.003
	GO:0031409	pigment binding	0.003
	GO:0008238	exopeptidase activity	0.006
	GO:0015923	mannosidase activity	0.007
	GO:0046933	proton-transporting ATP synthase activit...	0.011
	GO:0042349	guiding stereospecific synthesis activit...	0.013
	GO:0015085	calcium ion transmembrane transporter ac...	0.015
	GO:0016762	xyloglucan:xyloglucosyl transferase acti...	0.019
	GO:0005096	GTPase activator activity	0.020
	GO:0030246	carbohydrate binding	0.022
	GO:0016614	oxidoreductase activity, acting on CH-OH...	0.035
	GO:0016615	malate dehydrogenase activity	0.039
	GO:0016887	ATPase activity	0.050
	GO:0008422	beta-glucosidase activity	0.052
	GO:0030594	neurotransmitter receptor activity	0.052
	GO:0046910	pectinesterase inhibitor activity	0.056
	GO:0038023	signaling receptor activity	0.060
	GO:0060089	molecular transducer activity	0.060
	GO:2001070	starch binding	0.062
	GO:0030695	GTPase regulator activity	0.064
	GO:0016717	oxidoreductase activity, acting on paire...	0.064
	GO:0008134	transcription factor binding	0.068
	GO:0004970	ionotropic glutamate receptor activity	0.068
	GO:0005230	extracellular ligand-gated ion channel a...	0.068
	GO:0008066	glutamate receptor activity	0.068
	GO:0022824	transmitter-gated ion channel activity	0.068
	GO:0022835	transmitter-gated channel activity	0.068

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GO type	GO ID	Description	Adj. p-value
	GO:0001228	transcriptional activator activity, RNA ...	0.073
	GO:0016616	oxidoreductase activity, acting on the C...	0.074
	GO:0004659	prenyltransferase activity	0.074
	GO:0051015	actin filament binding	0.075
	GO:0004888	transmembrane signaling receptor activit...	0.076
	GO:0019901	protein kinase binding	0.077
	GO:0008171	O-methyltransferase activity	0.077
	GO:0015556	C4-dicarboxylate transmembrane transport...	0.080
	GO:0016462	pyrophosphatase activity	0.083
	GO:0015925	galactosidase activity	0.094
	GO:0016405	CoA-ligase activity	0.095
	GO:0016788	hydrolase activity, acting on ester bond...	0.095
	GO:0019829	cation-transporting ATPase activity	0.100
	GO:0022853	active ion transmembrane transporter act...	0.100
	GO:0042625	ATPase coupled ion transmembrane transpo...	0.100

4.2.2 Leaf - Postflowering - Cluster 2

GO type	GO ID	Description	Adj. p-value
BP	GO:0090305	nucleic acid phosphodiester bond hydroly...	0.000
	GO:0042255	ribosome assembly	0.000
	GO:1900864	mitochondrial RNA modification	0.001
	GO:0070925	organelle assembly	0.007
	GO:0019585	glucuronate metabolic process	0.008
	GO:0052695	cellular glucuronidation	0.008
	GO:0052696	flavonoid glucuronidation	0.008
	GO:0090502	RNA phosphodiester bond hydrolysis, endo...	0.009
	GO:0000959	mitochondrial RNA metabolic process	0.010
	GO:0006281	DNA repair	0.010
	GO:0016569	covalent chromatin modification	0.010
	GO:0019219	regulation of nucleobase-containing comp...	0.014
	GO:0006063	uronic acid metabolic process	0.015
	GO:0006974	cellular response to DNA damage stimulus	0.020
	GO:0071103	DNA conformation change	0.023
	GO:0000027	ribosomal large subunit assembly	0.023
	GO:0051252	regulation of RNA metabolic process	0.031
	GO:0006298	mismatch repair	0.032
	GO:0006560	proline metabolic process	0.032
	GO:0016570	histone modification	0.033
	GO:0006333	chromatin assembly or disassembly	0.033
	GO:0072528	pyrimidine-containing compound biosynthe...	0.033
	GO:0072527	pyrimidine-containing compound metabolic...	0.035
	GO:0045143	homologous chromosome segregation	0.037
	GO:0006308	DNA catabolic process	0.042
	GO:0031497	chromatin assembly	0.042
	GO:0006259	DNA metabolic process	0.045
	GO:0018205	peptidyl-lysine modification	0.052
	GO:0006323	DNA packaging	0.056
	GO:0002097	tRNA wobble base modification	0.070
	GO:1903506	regulation of nucleic acid-templated tra...	0.071
	GO:2001141	regulation of RNA biosynthetic process	0.071
	GO:0006334	nucleosome assembly	0.071
	GO:0019856	pyrimidine nucleobase biosynthetic proce...	0.072
	GO:0006355	regulation of transcription, DNA-templat...	0.073
	GO:0046700	heterocycle catabolic process	0.079
	GO:0045132	meiotic chromosome segregation	0.079
	GO:0002098	tRNA wobble uridine modification	0.091
	GO:0009407	toxin catabolic process	0.091
	GO:0034728	nucleosome organization	0.091
	GO:0006206	pyrimidine nucleobase metabolic process	0.091
	GO:0000302	response to reactive oxygen species	0.092
	GO:0007129	synapsis	0.092
	GO:0009266	response to temperature stimulus	0.095
	GO:0044270	cellular nitrogen compound catabolic pro...	0.097
CC	GO:0005759	mitochondrial matrix	0.000

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GO type	GO ID	Description	Adj. p-value
	GO:0000785	chromatin	0.001
	GO:0000315	organellar large ribosomal subunit	0.003
	GO:0005762	mitochondrial large ribosomal subunit	0.003
	GO:0005686	U2 snRNP	0.004
	GO:0005761	mitochondrial ribosome	0.009
	GO:0005694	chromosome	0.010
	GO:0005689	U12-type spliceosomal complex	0.010
	GO:0000786	nucleosome	0.010
	GO:0044815	DNA packaging complex	0.016
	GO:0044427	chromosomal part	0.023
	GO:0099023	tethering complex	0.023
	GO:0000313	organellar ribosome	0.024
	GO:0000228	nuclear chromosome	0.071
	GO:0044437	vacuolar part	0.091
	GO:0071011	precatalytic spliceosome	0.097
	GO:0032993	protein-DNA complex	0.098
MF	GO:0004519	endonuclease activity	0.022
	GO:0051082	unfolded protein binding	0.038
	GO:0080043	quercetin 3-O-glucosyltransferase activi...	0.060
	GO:0080044	quercetin 7-O-glucosyltransferase activi...	0.060
	GO:0003690	double-stranded DNA binding	0.076
	GO:0003677	DNA binding	0.081

4.2.3 Leaf - Postflowering - Cluster 3

GO type	GO ID	Description	Adj. p-value
BP	GO:0007165	signal transduction	0.000
	GO:0071495	cellular response to endogenous stimulus	0.000
	GO:0009607	response to biotic stimulus	0.000
	GO:0009867	jasmonic acid mediated signaling pathway	0.000
	GO:0016567	protein ubiquitination	0.001
	GO:0031347	regulation of defense response	0.002
	GO:0042742	defense response to bacterium	0.003
	GO:0042493	response to drug	0.004
	GO:0009620	response to fungus	0.004
	GO:1901701	cellular response to oxygen-containing c...	0.004
	GO:0018196	peptidyl-asparagine modification	0.005
	GO:0018279	protein N-linked glycosylation via aspar...	0.005
	GO:0009407	toxin catabolic process	0.006
	GO:0023014	signal transduction by protein phosphory...	0.006
	GO:0042737	drug catabolic process	0.007
	GO:0045087	innate immune response	0.008
	GO:0045088	regulation of innate immune response	0.010
	GO:0009751	response to salicylic acid	0.010
	GO:0002682	regulation of immune system process	0.010
	GO:0055085	transmembrane transport	0.011
	GO:0006022	aminoglycan metabolic process	0.011
	GO:0006026	aminoglycan catabolic process	0.011
	GO:0006030	chitin metabolic process	0.011
	GO:0006032	chitin catabolic process	0.011
	GO:0006487	protein N-linked glycosylation	0.011
	GO:0006829	zinc ion transport	0.011
	GO:0009404	toxin metabolic process	0.011
	GO:0035556	intracellular signal transduction	0.011
	GO:0046348	amino sugar catabolic process	0.011
	GO:1901072	glucosamine-containing compound cataboli...	0.011
	GO:0050776	regulation of immune response	0.012
	GO:0002376	immune system process	0.012
	GO:0036065	fucosylation	0.012
	GO:0009814	defense response, incompatible interacti...	0.016
	GO:0002237	response to molecule of bacterial origin	0.016
	GO:0006955	immune response	0.016
	GO:0071577	zinc ion transmembrane transport	0.017
	GO:0009627	systemic acquired resistance	0.018
	GO:0050832	defense response to fungus	0.018
	GO:0005975	carbohydrate metabolic process	0.020
	GO:0009863	salicylic acid mediated signaling pathwa...	0.020
	GO:0044267	cellular protein metabolic process	0.020
	GO:1901071	glucosamine-containing compound metaboli...	0.024
	GO:0019585	glucuronate metabolic process	0.026
	GO:0052695	cellular glucuronidation	0.026
	GO:0052696	flavonoid glucuronidation	0.026

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GO type	GO ID	Description	Adj. p-value
	GO:0080134	regulation of response to stress	0.026
	GO:0071446	cellular response to salicylic acid stim...	0.028
	GO:0008361	regulation of cell size	0.029
	GO:0009812	flavonoid metabolic process	0.030
	GO:0006063	uronic acid metabolic process	0.031
	GO:0002684	positive regulation of immune system pro...	0.031
	GO:0050778	positive regulation of immune response	0.031
	GO:0006665	sphingolipid metabolic process	0.033
	GO:0006040	amino sugar metabolic process	0.033
	GO:0044403	symbiont process	0.035
	GO:0015893	drug transport	0.035
	GO:0098655	cation transmembrane transport	0.037
	GO:0006811	ion transport	0.037
	GO:0006813	potassium ion transport	0.037
	GO:0006855	drug transmembrane transport	0.038
	GO:0009606	tropism	0.039
	GO:0035303	regulation of dephosphorylation	0.039
	GO:0009813	flavonoid biosynthetic process	0.039
	GO:0006836	neurotransmitter transport	0.040
	GO:0045089	positive regulation of innate immune res...	0.044
	GO:0048878	chemical homeostasis	0.049
	GO:0072507	divalent inorganic cation homeostasis	0.051
	GO:0034220	ion transmembrane transport	0.056
	GO:0010921	regulation of phosphatase activity	0.058
	GO:0035304	regulation of protein dephosphorylation	0.058
	GO:0072503	cellular divalent inorganic cation homeo...	0.058
	GO:0080163	regulation of protein serine/threonine p...	0.058
	GO:0060548	negative regulation of cell death	0.059
	GO:0009645	response to low light intensity stimulus	0.059
	GO:0030001	metal ion transport	0.062
	GO:0000209	protein polyubiquitination	0.077
	GO:0019538	protein metabolic process	0.080
	GO:0032535	regulation of cellular component size	0.080
	GO:0090066	regulation of anatomical structure size	0.080
	GO:0015804	neutral amino acid transport	0.081
	GO:0009862	systemic acquired resistance, salicylic ...	0.083
	GO:0043666	regulation of phosphoprotein phosphatase...	0.084
	GO:0015850	organic hydroxy compound transport	0.084
	GO:0042743	hydrogen peroxide metabolic process	0.087
	GO:0043069	negative regulation of programmed cell d...	0.098
CC	GO:0005798	Golgi-associated vesicle	0.000
	GO:0030660	Golgi-associated vesicle membrane	0.001
	GO:0044433	cytoplasmic vesicle part	0.003
	GO:0098827	endoplasmic reticulum subcompartment	0.036
	GO:0009522	photosystem I	0.037
	GO:0005789	endoplasmic reticulum membrane	0.043
	GO:0044432	endoplasmic reticulum part	0.047
	GO:0005576	extracellular region	0.072
	GO:0042175	nuclear outer membrane-endoplasmic retic...	0.076

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GO type	GO ID	Description	Adj. p-value
MF	GO:0030246	carbohydrate binding	0.000
	GO:0005215	transporter activity	0.000
	GO:0004842	ubiquitin-protein transferase activity	0.000
	GO:0004871	signal transducer activity	0.000
	GO:0046527	glucosyltransferase activity	0.002
	GO:0005506	iron ion binding	0.003
	GO:0015075	ion transmembrane transporter activity	0.003
	GO:0035251	UDP-glucosyltransferase activity	0.003
	GO:0015318	inorganic molecular entity transmembrane...	0.004
	GO:0046873	metal ion transmembrane transporter acti...	0.005
	GO:0016758	transferase activity, transferring hexos...	0.006
	GO:0015291	secondary active transmembrane transport...	0.006
	GO:0022804	active transmembrane transporter activit...	0.006
	GO:0004568	chitinase activity	0.006
	GO:0016757	transferase activity, transferring glyco...	0.006
	GO:0000981	RNA polymerase II transcription factor a...	0.006
	GO:0015923	mannosidase activity	0.007
	GO:0008417	fucosyltransferase activity	0.007
	GO:0008324	cation transmembrane transporter activit...	0.008
	GO:0005385	zinc ion transmembrane transporter activ...	0.008
	GO:0008194	UDP-glycosyltransferase activity	0.009
	GO:0072509	divalent inorganic cation transmembrane ...	0.022
	GO:0022890	inorganic cation transmembrane transport...	0.025
	GO:0015297	antiporter activity	0.027
	GO:0005326	neurotransmitter transporter activity	0.027
	GO:0015276	ligand-gated ion channel activity	0.038
	GO:0022834	ligand-gated channel activity	0.038
	GO:0031625	ubiquitin protein ligase binding	0.041
	GO:0044389	ubiquitin-like protein ligase binding	0.041
	GO:0004190	aspartic-type endopeptidase activity	0.042
	GO:0070001	aspartic-type peptidase activity	0.042
	GO:0004553	hydrolase activity, hydrolyzing O-glycos...	0.042
	GO:0080043	quercetin 3-O-glucosyltransferase activi...	0.045
	GO:0080044	quercetin 7-O-glucosyltransferase activi...	0.045
	GO:0004864	protein phosphatase inhibitor activity	0.057
	GO:0019212	phosphatase inhibitor activity	0.057
	GO:0004970	ionotropic glutamate receptor activity	0.058
	GO:0005230	extracellular ligand-gated ion channel a...	0.058
	GO:0008066	glutamate receptor activity	0.058
	GO:0022824	transmitter-gated ion channel activity	0.058
	GO:0022835	transmitter-gated channel activity	0.058
	GO:0005310	dicarboxylic acid transmembrane transpor...	0.059
	GO:0015238	drug transmembrane transporter activity	0.059
	GO:0038023	signaling receptor activity	0.059
	GO:0060089	molecular transducer activity	0.059
	GO:0015294	solute:cation symporter activity	0.063
	GO:0016709	oxidoreductase activity, acting on paire...	0.064
	GO:0046915	transition metal ion transmembrane trans...	0.068
	GO:0030594	neurotransmitter receptor activity	0.068

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GO type	GO ID	Description	Adj. p-value
	GO:0015166	polyol transmembrane transporter activit...	0.072
	GO:0015293	symporter activity	0.072
	GO:1901618	organic hydroxy compound transmembrane t...	0.088
	GO:0019208	phosphatase regulator activity	0.093
	GO:0019888	protein phosphatase regulator activity	0.093
	GO:0015149	hexose transmembrane transporter activit...	0.094
	GO:0015179	L-amino acid transmembrane transporter a...	0.094
	GO:0015295	solute:proton symporter activity	0.094

4.2.4 Leaf - Postflowering - Cluster 4

GO type	GO ID	Description	Adj. p-value
BP	GO:0006091	generation of precursor metabolites and ...	0.000
	GO:0044283	small molecule biosynthetic process	0.000
	GO:1902600	proton transmembrane transport	0.000
	GO:0009108	coenzyme biosynthetic process	0.000
	GO:0055114	oxidation-reduction process	0.000
	GO:1901663	quinone biosynthetic process	0.000
	GO:0006081	cellular aldehyde metabolic process	0.002
	GO:0034404	nucleobase-containing small molecule bio...	0.002
	GO:0090501	RNA phosphodiester bond hydrolysis	0.003
	GO:0006839	mitochondrial transport	0.003
	GO:0072522	purine-containing compound biosynthetic ...	0.003
	GO:0046034	ATP metabolic process	0.003
	GO:0006082	organic acid metabolic process	0.004
	GO:0019752	carboxylic acid metabolic process	0.004
	GO:0070925	organelle assembly	0.004
	GO:0043436	oxoacid metabolic process	0.004
	GO:0009628	response to abiotic stimulus	0.005
	GO:0090305	nucleic acid phosphodiester bond hydroly...	0.005
	GO:0006164	purine nucleotide biosynthetic process	0.005
	GO:0046434	organophosphate catabolic process	0.006
	GO:0046185	aldehyde catabolic process	0.006
	GO:0090502	RNA phosphodiester bond hydrolysis, endo...	0.006
	GO:0042440	pigment metabolic process	0.008
	GO:0009156	ribonucleoside monophosphate biosyntheti...	0.009
	GO:0016053	organic acid biosynthetic process	0.009
	GO:0046394	carboxylic acid biosynthetic process	0.009
	GO:0009124	nucleoside monophosphate biosynthetic pr...	0.011
	GO:0022900	electron transport chain	0.013
	GO:0034655	nucleobase-containing compound catabolic...	0.013
	GO:0009152	purine ribonucleotide biosynthetic proce...	0.014
	GO:0008652	cellular amino acid biosynthetic process	0.024
	GO:0046148	pigment biosynthetic process	0.024
	GO:0046939	nucleotide phosphorylation	0.025
	GO:0006733	oxidoreduction coenzyme metabolic proces...	0.026
	GO:0006743	ubiquinone metabolic process	0.026
	GO:0006744	ubiquinone biosynthetic process	0.026
	GO:0015672	monovalent inorganic cation transport	0.026
	GO:1901607	alpha-amino acid biosynthetic process	0.027
	GO:0042180	cellular ketone metabolic process	0.035
	GO:0009084	glutamine family amino acid biosynthetic...	0.038
	GO:0009201	ribonucleoside triphosphate biosynthetic...	0.045
	GO:0009145	purine nucleoside triphosphate biosynthe...	0.049
	GO:0009206	purine ribonucleoside triphosphate biosy...	0.049
	GO:0005977	glycogen metabolic process	0.054
	GO:0006112	energy reserve metabolic process	0.054
	GO:0009142	nucleoside triphosphate biosynthetic pro...	0.054

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GO type	GO ID	Description	Adj. p-value
	GO:0044282	small molecule catabolic process	0.057
	GO:0006637	acyl-CoA metabolic process	0.064
	GO:0035383	thioester metabolic process	0.064
	GO:0006605	protein targeting	0.066
	GO:0009064	glutamine family amino acid metabolic pr...	0.068
	GO:0006165	nucleoside diphosphate phosphorylation	0.069
	GO:0005978	glycogen biosynthetic process	0.070
	GO:0009132	nucleoside diphosphate metabolic process	0.070
	GO:1901605	alpha-amino acid metabolic process	0.073
	GO:0016052	carbohydrate catabolic process	0.074
	GO:0006520	cellular amino acid metabolic process	0.076
	GO:0006560	proline metabolic process	0.076
	GO:0019725	cellular homeostasis	0.076
	GO:0009127	purine nucleoside monophosphate biosynth...	0.078
	GO:0009168	purine ribonucleoside monophosphate bios...	0.078
	GO:0043648	dicarboxylic acid metabolic process	0.094
	GO:0006020	inositol metabolic process	0.094
CC	GO:0009526	plastid envelope	0.000
	GO:0098798	mitochondrial protein complex	0.000
	GO:0042651	thylakoid membrane	0.000
	GO:0070469	respiratory chain	0.000
	GO:0031966	mitochondrial membrane	0.000
	GO:0044455	mitochondrial membrane part	0.000
	GO:0005743	mitochondrial inner membrane	0.000
	GO:0033176	proton-transporting V-type ATPase comple...	0.000
	GO:0009528	plastid inner membrane	0.000
	GO:0042170	plastid membrane	0.000
	GO:0042646	plastid nucleoid	0.000
	GO:0070069	cytochrome complex	0.001
	GO:0031090	organelle membrane	0.001
	GO:0019867	outer membrane	0.003
	GO:0031968	organelle outer membrane	0.006
	GO:0031984	organelle subcompartment	0.037
	GO:0048046	apoplast	0.060
	GO:0042644	chloroplast nucleoid	0.071
	GO:0005741	mitochondrial outer membrane	0.090
MF	GO:0016491	oxidoreductase activity	0.000
	GO:0004519	endonuclease activity	0.001
	GO:0016741	transferase activity, transferring one-c...	0.001
	GO:0008168	methyltransferase activity	0.003
	GO:0016679	oxidoreductase activity, acting on diphe...	0.003
	GO:0016853	isomerase activity	0.003
	GO:0036442	proton-exporting ATPase activity	0.004
	GO:0004518	nuclease activity	0.008
	GO:0016829	lyase activity	0.028
	GO:0004540	ribonuclease activity	0.039
	GO:0004521	endoribonuclease activity	0.042
	GO:0016830	carbon-carbon lyase activity	0.061
	GO:0016788	hydrolase activity, acting on ester bond...	0.062

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GO type	GO ID	Description	Adj. p-value
	GO:0016407	acetyltransferase activity	0.084
	GO:0003824	catalytic activity	0.087

4.2.5 Leaf - Postflowering - Cluster 5

GO type	GO ID	Description	Adj. p-value
BP	GO:0006163	purine nucleotide metabolic process	0.000
	GO:0009165	nucleotide biosynthetic process	0.000
	GO:0046434	organophosphate catabolic process	0.000
	GO:0009161	ribonucleoside monophosphate metabolic p...	0.000
	GO:0006996	organelle organization	0.000
	GO:0044283	small molecule biosynthetic process	0.000
	GO:0051188	cofactor biosynthetic process	0.000
	GO:0009152	purine ribonucleotide biosynthetic proce...	0.000
	GO:0046034	ATP metabolic process	0.000
	GO:0009124	nucleoside monophosphate biosynthetic pr...	0.000
	GO:0006090	pyruvate metabolic process	0.001
	GO:1902600	proton transmembrane transport	0.001
	GO:0006165	nucleoside diphosphate phosphorylation	0.001
	GO:0009132	nucleoside diphosphate metabolic process	0.001
	GO:0009156	ribonucleoside monophosphate biosyntheti...	0.001
	GO:0016052	carbohydrate catabolic process	0.001
	GO:0009145	purine nucleoside triphosphate biosynthe...	0.002
	GO:0009206	purine ribonucleoside triphosphate biosy...	0.002
	GO:0046939	nucleotide phosphorylation	0.002
	GO:0009127	purine nucleoside monophosphate biosynth...	0.002
	GO:0009168	purine ribonucleoside monophosphate bios...	0.002
	GO:0019363	pyridine nucleotide biosynthetic process	0.002
	GO:0072525	pyridine-containing compound biosyntheti...	0.003
	GO:0034404	nucleobase-containing small molecule bio...	0.003
	GO:1901292	nucleoside phosphate catabolic process	0.003
	GO:0009201	ribonucleoside triphosphate biosynthetic...	0.003
	GO:0016053	organic acid biosynthetic process	0.003
	GO:0046394	carboxylic acid biosynthetic process	0.003
	GO:0034655	nucleobase-containing compound catabolic...	0.003
	GO:0051186	cofactor metabolic process	0.003
	GO:0009166	nucleotide catabolic process	0.003
	GO:0055086	nucleobase-containing small molecule met...	0.003
	GO:0048856	anatomical structure development	0.004
	GO:0006096	glycolytic process	0.004
	GO:0006757	ATP generation from ADP	0.004
	GO:0009135	purine nucleoside diphosphate metabolic ...	0.004
	GO:0009179	purine ribonucleoside diphosphate metabo...	0.004
	GO:0009185	ribonucleoside diphosphate metabolic pro...	0.004
	GO:0042866	pyruvate biosynthetic process	0.004
	GO:0046031	ADP metabolic process	0.004
	GO:0009142	nucleoside triphosphate biosynthetic pro...	0.005
	GO:1901661	quinone metabolic process	0.005
	GO:1901663	quinone biosynthetic process	0.005
	GO:1901137	carbohydrate derivative biosynthetic pro...	0.006
	GO:0007275	multicellular organism development	0.006
	GO:0006733	oxidoreduction coenzyme metabolic proces...	0.006

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0008610	lipid biosynthetic process	0.007
	GO:0006754	ATP biosynthetic process	0.008
	GO:0042181	ketone biosynthetic process	0.010
	GO:0006629	lipid metabolic process	0.010
	GO:0044255	cellular lipid metabolic process	0.011
	GO:0019439	aromatic compound catabolic process	0.014
	GO:0017144	drug metabolic process	0.014
	GO:0046496	nicotinamide nucleotide metabolic proces...	0.018
	GO:1901361	organic cyclic compound catabolic proces...	0.018
	GO:0072330	monocarboxylic acid biosynthetic process	0.019
	GO:0044270	cellular nitrogen compound catabolic pro...	0.020
	GO:0046700	heterocycle catabolic process	0.020
	GO:0072524	pyridine-containing compound metabolic p...	0.021
	GO:0032501	multicellular organismal process	0.023
	GO:0032502	developmental process	0.024
	GO:0033043	regulation of organelle organization	0.025
	GO:0019362	pyridine nucleotide metabolic process	0.025
	GO:0006743	ubiquinone metabolic process	0.028
	GO:0006744	ubiquinone biosynthetic process	0.028
	GO:0065002	intracellular protein transmembrane tran...	0.039
	GO:0048229	gametophyte development	0.041
	GO:0015672	monovalent inorganic cation transport	0.041
	GO:0071806	protein transmembrane transport	0.043
	GO:0055114	oxidation-reduction process	0.053
	GO:0005975	carbohydrate metabolic process	0.054
	GO:0048731	system development	0.059
	GO:0006644	phospholipid metabolic process	0.081
	GO:0042180	cellular ketone metabolic process	0.099
CC	GO:0043231	intracellular membrane-bounded organelle	0.000
	GO:0009579	thylakoid	0.000
	GO:0009534	chloroplast thylakoid	0.000
	GO:0019866	organelle inner membrane	0.000
	GO:0031966	mitochondrial membrane	0.000
	GO:0033176	proton-transporting V-type ATPase comple...	0.000
	GO:0005743	mitochondrial inner membrane	0.000
	GO:0099080	supramolecular complex	0.001
	GO:0099081	supramolecular polymer	0.001
	GO:0099512	supramolecular fiber	0.001
	GO:0099513	polymeric cytoskeletal fiber	0.001
	GO:0005874	microtubule	0.001
	GO:0033178	proton-transporting two-sector ATPase co...	0.005
	GO:0015630	microtubule cytoskeleton	0.010
	GO:0005634	nucleus	0.018
	GO:0044430	cytoskeletal part	0.031
	GO:0005856	cytoskeleton	0.036
	GO:0009574	preprophase band	0.052
	GO:0005881	cytoplasmic microtubule	0.087
	GO:0098796	membrane protein complex	0.087
	GO:0030863	cortical cytoskeleton	0.099

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GO type	GO ID	Description	Adj. p-value
	GO:0030981	cortical microtubule cytoskeleton	0.099
MF	GO:0003824	catalytic activity	0.000
	GO:0016817	hydrolase activity, acting on acid anhyd...	0.007
	GO:0016818	hydrolase activity, acting on acid anhyd...	0.007
	GO:0017111	nucleoside-triphosphatase activity	0.007
	GO:0016462	pyrophosphatase activity	0.008
	GO:0016866	intramolecular transferase activity	0.024
	GO:0016853	isomerase activity	0.026
	GO:0016651	oxidoreductase activity, acting on NAD(P...	0.031
	GO:0016887	ATPase activity	0.036
	GO:0003954	NADH dehydrogenase activity	0.066

4.2.6 Leaf - Postflowering - Cluster 6

GO type	GO ID	Description	Adj. p-value
BP	GO:0015850	organic hydroxy compound transport	0.002
	GO:0046323	glucose import	0.003
	GO:0008645	hexose transmembrane transport	0.003
	GO:0042493	response to drug	0.004
	GO:0015749	monosaccharide transmembrane transport	0.004
	GO:0006022	aminoglycan metabolic process	0.007
	GO:0018196	peptidyl-asparagine modification	0.008
	GO:0018279	protein N-linked glycosylation via aspar...	0.008
	GO:0007166	cell surface receptor signaling pathway	0.008
	GO:0007154	cell communication	0.009
	GO:0006487	protein N-linked glycosylation	0.010
	GO:0071577	zinc ion transmembrane transport	0.012
	GO:1901071	glucosamine-containing compound metaboli...	0.013
	GO:0019748	secondary metabolic process	0.014
	GO:0015791	polyol transport	0.015
	GO:1901565	organonitrogen compound catabolic proces...	0.019
	GO:0006829	zinc ion transport	0.021
	GO:0071495	cellular response to endogenous stimulus	0.021
	GO:0071705	nitrogen compound transport	0.021
	GO:0008037	cell recognition	0.022
	GO:0032870	cellular response to hormone stimulus	0.022
	GO:0071702	organic substance transport	0.022
	GO:0006887	exocytosis	0.025
	GO:0006749	glutathione metabolic process	0.025
	GO:0003333	amino acid transmembrane transport	0.026
	GO:0009607	response to biotic stimulus	0.026
	GO:0048544	recognition of pollen	0.028
	GO:0071310	cellular response to organic substance	0.028
	GO:0009875	pollen-pistil interaction	0.028
	GO:0006026	aminoglycan catabolic process	0.032
	GO:0006030	chitin metabolic process	0.032
	GO:0006032	chitin catabolic process	0.032
	GO:0046348	amino sugar catabolic process	0.032
	GO:1901072	glucosamine-containing compound cataboli...	0.032
	GO:0023051	regulation of signaling	0.032
	GO:1902531	regulation of intracellular signal trans...	0.033
	GO:0006865	amino acid transport	0.033
	GO:0043207	response to external biotic stimulus	0.035
	GO:0051707	response to other organism	0.035
	GO:0010243	response to organonitrogen compound	0.036
	GO:0006836	neurotransmitter transport	0.036
	GO:0009966	regulation of signal transduction	0.038
	GO:0015804	neutral amino acid transport	0.047
	GO:0006884	cell volume homeostasis	0.061
	GO:0009992	cellular water homeostasis	0.061
	GO:0015793	glycerol transport	0.061

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GO type	GO ID	Description	Adj. p-value
	GO:0009755	hormone-mediated signaling pathway	0.064
	GO:0071395	cellular response to jasmonic acid stimu...	0.064
	GO:0032940	secretion by cell	0.068
	GO:0098542	defense response to other organism	0.074
	GO:0009867	jasmonic acid mediated signaling pathway	0.079
	GO:0046903	secretion	0.085
	GO:0006904	vesicle docking involved in exocytosis	0.089
	GO:0140029	exocytic process	0.089
	GO:0008643	carbohydrate transport	0.092
	GO:0006857	oligopeptide transport	0.096
	GO:0010646	regulation of cell communication	0.096
	GO:0006040	amino sugar metabolic process	0.097
CC	GO:0000151	ubiquitin ligase complex	0.000
	GO:0005886	plasma membrane	0.001
	GO:0031226	intrinsic component of plasma membrane	0.003
	GO:0005783	endoplasmic reticulum	0.003
	GO:0071944	cell periphery	0.004
	GO:0030120	vesicle coat	0.007
	GO:0099023	tethering complex	0.007
	GO:0044459	plasma membrane part	0.008
	GO:0005911	cell-cell junction	0.014
	GO:0030054	cell junction	0.014
	GO:0009506	plasmodesma	0.015
	GO:0055044	symplast	0.015
	GO:0005798	Golgi-associated vesicle	0.016
	GO:0030660	Golgi-associated vesicle membrane	0.038
	GO:0000145	exocyst	0.068
MF	GO:0004497	monooxygenase activity	0.000
	GO:0016705	oxidoreductase activity, acting on paire...	0.000
	GO:0030246	carbohydrate binding	0.000
	GO:0043168	anion binding	0.002
	GO:0051213	dioxygenase activity	0.002
	GO:1901618	organic hydroxy compound transmembrane t...	0.002
	GO:0005355	glucose transmembrane transporter activi...	0.002
	GO:0046527	glucosyltransferase activity	0.003
	GO:0008194	UDP-glycosyltransferase activity	0.004
	GO:0016758	transferase activity, transferring hexos...	0.004
	GO:0043167	ion binding	0.004
	GO:0015149	hexose transmembrane transporter activit...	0.005
	GO:0015145	monosaccharide transmembrane transporter...	0.005
	GO:0036094	small molecule binding	0.005
	GO:0005385	zinc ion transmembrane transporter activ...	0.007
	GO:0015166	polyol transmembrane transporter activit...	0.007
	GO:0016757	transferase activity, transferring glyco...	0.007
	GO:0016772	transferase activity, transferring phosp...	0.009
	GO:0005215	transporter activity	0.009
	GO:0015293	symporter activity	0.011
	GO:0004364	glutathione transferase activity	0.014
	GO:0015294	solute:cation symporter activity	0.018

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GO type	GO ID	Description	Adj. p-value
	GO:0001871	pattern binding	0.019
	GO:0030247	polysaccharide binding	0.019
	GO:0005326	neurotransmitter transporter activity	0.021
	GO:0015174	basic amino acid transmembrane transport...	0.021
	GO:0072509	divalent inorganic cation transmembrane ...	0.021
	GO:0004568	chitinase activity	0.024
	GO:0015291	secondary active transmembrane transport...	0.025
	GO:0015168	glycerol transmembrane transporter activ...	0.028
	GO:0035673	oligopeptide transmembrane transporter a...	0.028
	GO:0015295	solute:proton symporter activity	0.035
	GO:0005372	water transmembrane transporter activity	0.045
	GO:0015250	water channel activity	0.045
	GO:0015254	glycerol channel activity	0.045
	GO:0015171	amino acid transmembrane transporter act...	0.045
	GO:0008144	drug binding	0.046
	GO:1990837	sequence-specific double-stranded DNA bi...	0.049
	GO:0005351	carbohydrate:proton symporter activity	0.052
	GO:0005402	carbohydrate:cation symporter activity	0.052
	GO:0015297	antiporter activity	0.052
	GO:0042562	hormone binding	0.053
	GO:0005524	ATP binding	0.055
	GO:0051119	sugar transmembrane transporter activity	0.060
	GO:0015179	L-amino acid transmembrane transporter a...	0.060
	GO:0015144	carbohydrate transmembrane transporter a...	0.069
	GO:0042887	amide transmembrane transporter activity	0.074
	GO:0046915	transition metal ion transmembrane trans...	0.099

4.2.7 Leaf - Postflowering - Cluster 7

GO type	GO ID	Description	Adj. p-value
	GO:0019684	photosynthesis, light reaction	0.000
	GO:0051188	cofactor biosynthetic process	0.000
	GO:0019637	organophosphate metabolic process	0.000
	GO:0046394	carboxylic acid biosynthetic process	0.000
	GO:0006732	coenzyme metabolic process	0.000
	GO:0009150	purine ribonucleotide metabolic process	0.000
	GO:0009123	nucleoside monophosphate metabolic proce...	0.000
	GO:0071554	cell wall organization or biogenesis	0.000
	GO:0009108	coenzyme biosynthetic process	0.000
	GO:0009161	ribonucleoside monophosphate metabolic p...	0.000
	GO:0008610	lipid biosynthetic process	0.000
	GO:0009165	nucleotide biosynthetic process	0.000
	GO:0033014	tetrapyrrole biosynthetic process	0.000
	GO:0046034	ATP metabolic process	0.000
	GO:0016052	carbohydrate catabolic process	0.000
	GO:0009124	nucleoside monophosphate biosynthetic pr...	0.000
	GO:0009156	ribonucleoside monophosphate biosyntheti...	0.000
	GO:0009145	purine nucleoside triphosphate biosynthe...	0.000
	GO:0009206	purine ribonucleoside triphosphate biosy...	0.000
	GO:0006164	purine nucleotide biosynthetic process	0.000
	GO:0006631	fatty acid metabolic process	0.000
	GO:0009152	purine ribonucleotide biosynthetic proce...	0.000
	GO:0009260	ribonucleotide biosynthetic process	0.000
	GO:0046390	ribose phosphate biosynthetic process	0.000
	GO:0042546	cell wall biogenesis	0.000
	GO:0019359	nicotinamide nucleotide biosynthetic pro...	0.000
	GO:0044262	cellular carbohydrate metabolic process	0.000
	GO:0071555	cell wall organization	0.000
	GO:0009201	ribonucleoside triphosphate biosynthetic...	0.000
	GO:0072525	pyridine-containing compound biosyntheti...	0.000
	GO:1902600	proton transmembrane transport	0.000
	GO:0006090	pyruvate metabolic process	0.000
	GO:0046939	nucleotide phosphorylation	0.000
	GO:0009073	aromatic amino acid family biosynthetic ...	0.000
	GO:0042401	cellular biogenic amine biosynthetic pro...	0.000
	GO:0015980	energy derivation by oxidation of organi...	0.000
	GO:0098869	cellular oxidant detoxification	0.000
	GO:0006165	nucleoside diphosphate phosphorylation	0.000
	GO:0008299	isoprenoid biosynthetic process	0.000
	GO:0045333	cellular respiration	0.001
	GO:0009060	aerobic respiration	0.001
	GO:0006081	cellular aldehyde metabolic process	0.001
	GO:0010383	cell wall polysaccharide metabolic proce...	0.001
	GO:0006006	glucose metabolic process	0.002
	GO:0006520	cellular amino acid metabolic process	0.002
	GO:0033692	cellular polysaccharide biosynthetic pro...	0.002

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GO type	GO ID	Description	Adj. p-value
	GO:0009768	photosynthesis, light harvesting in phot...	0.002
	GO:0010109	regulation of photosynthesis	0.002
	GO:0010410	hemicellulose metabolic process	0.002
	GO:0045491	xylan metabolic process	0.002
	GO:0016311	dephosphorylation	0.003
	GO:0000162	tryptophan biosynthetic process	0.003
	GO:0046219	indolalkylamine biosynthetic process	0.003
	GO:0019252	starch biosynthetic process	0.003
	GO:1901137	carbohydrate derivative biosynthetic pro...	0.003
	GO:0006108	malate metabolic process	0.003
	GO:0044275	cellular carbohydrate catabolic process	0.003
	GO:0009664	plant-type cell wall organization	0.004
	GO:0034637	cellular carbohydrate biosynthetic proce...	0.004
	GO:0006099	tricarboxylic acid cycle	0.004
	GO:0015988	energy coupled proton transmembrane tran...	0.004
	GO:0015991	ATP hydrolysis coupled proton transport	0.004
	GO:0090662	ATP hydrolysis coupled transmembrane tra...	0.004
	GO:0099131	ATP hydrolysis coupled ion transmembrane...	0.004
	GO:0099132	ATP hydrolysis coupled cation transmembr...	0.004
	GO:0042168	heme metabolic process	0.004
	GO:0006101	citrate metabolic process	0.005
	GO:0016122	xanthophyll metabolic process	0.006
	GO:0017004	cytochrome complex assembly	0.006
	GO:0046184	aldehyde biosynthetic process	0.006
	GO:0006783	heme biosynthetic process	0.007
	GO:0010206	photosystem II repair	0.007
	GO:0005983	starch catabolic process	0.007
	GO:0006721	terpenoid metabolic process	0.007
	GO:0010143	cutin biosynthetic process	0.007
	GO:0046271	phenylpropanoid catabolic process	0.007
	GO:0008652	cellular amino acid biosynthetic process	0.008
	GO:0044036	cell wall macromolecule metabolic proces...	0.008
	GO:0046365	monosaccharide catabolic process	0.008
	GO:0043467	regulation of generation of precursor me...	0.009
	GO:0015985	energy coupled proton transport, down el...	0.012
	GO:0015986	ATP synthesis coupled proton transport	0.012
	GO:0032271	regulation of protein polymerization	0.012
	GO:0009308	amine metabolic process	0.012
	GO:0044550	secondary metabolite biosynthetic proces...	0.012
	GO:0000272	polysaccharide catabolic process	0.012
	GO:0018298	protein-chromophore linkage	0.012
	GO:0035336	long-chain fatty-acyl-CoA metabolic proc...	0.013
	GO:0015672	monovalent inorganic cation transport	0.014
	GO:0009409	response to cold	0.014
	GO:0042214	terpene metabolic process	0.014
	GO:0046274	lignin catabolic process	0.016
	GO:0032544	plastid translation	0.016
	GO:0072350	tricarboxylic acid metabolic process	0.017
	GO:0019318	hexose metabolic process	0.017

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GO type	GO ID	Description	Adj. p-value
	GO:0007010	cytoskeleton organization	0.021
	GO:0016114	terpenoid biosynthetic process	0.021
	GO:0030091	protein repair	0.021
	GO:0098660	inorganic ion transmembrane transport	0.021
	GO:1901568	fatty acid derivative metabolic process	0.021
	GO:0046185	aldehyde catabolic process	0.021
	GO:0043038	amino acid activation	0.022
	GO:0043039	tRNA aminoacylation	0.022
	GO:0010345	suberin biosynthetic process	0.022
	GO:0016999	antibiotic metabolic process	0.022
	GO:0017001	antibiotic catabolic process	0.023
	GO:0044282	small molecule catabolic process	0.023
	GO:0044247	cellular polysaccharide catabolic proces...	0.024
	GO:0035337	fatty-acyl-CoA metabolic process	0.026
	GO:0009251	glucan catabolic process	0.028
	GO:0033865	nucleoside bisphosphate metabolic proces...	0.028
	GO:0033875	ribonucleoside bisphosphate metabolic pr...	0.028
	GO:0034032	purine nucleoside bisphosphate metabolic...	0.028
	GO:0019674	NAD metabolic process	0.029
	GO:0042435	indole-containing compound biosynthetic ...	0.029
	GO:0043244	regulation of protein complex disassembl...	0.031
	GO:1901615	organic hydroxy compound metabolic proce...	0.033
	GO:0030041	actin filament polymerization	0.033
	GO:0030833	regulation of actin filament polymerizat...	0.033
	GO:0006743	ubiquinone metabolic process	0.034
	GO:0006744	ubiquinone biosynthetic process	0.034
	GO:0098662	inorganic cation transmembrane transport	0.035
	GO:0008154	actin polymerization or depolymerization	0.037
	GO:0009628	response to abiotic stimulus	0.037
	GO:0030244	cellulose biosynthetic process	0.041
	GO:0045492	xylan biosynthetic process	0.042
	GO:1903338	regulation of cell wall organization or ...	0.043
	GO:0009250	glucan biosynthetic process	0.045
	GO:0044249	cellular biosynthetic process	0.045
	GO:0071482	cellular response to light stimulus	0.045
	GO:1901617	organic hydroxy compound biosynthetic pr...	0.045
	GO:0009438	methylglyoxal metabolic process	0.047
	GO:0042182	ketone catabolic process	0.047
	GO:0051596	methylglyoxal catabolic process	0.047
	GO:0044038	cell wall macromolecule biosynthetic pro...	0.049
	GO:0070589	cellular component macromolecule biosynt...	0.049
	GO:0006812	cation transport	0.049
	GO:0070592	cell wall polysaccharide biosynthetic pr...	0.049
	GO:0006637	acyl-CoA metabolic process	0.051
	GO:0035383	thioester metabolic process	0.051
	GO:0048438	floral whorl development	0.051
	GO:0009416	response to light stimulus	0.054
	GO:0046486	glycerolipid metabolic process	0.056
	GO:0080167	response to karrikin	0.056

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GO type	GO ID	Description	Adj. p-value
	GO:0009058	biosynthetic process	0.058
	GO:0006595	polyamine metabolic process	0.059
	GO:0045489	pectin biosynthetic process	0.059
	GO:0008064	regulation of actin polymerization or de...	0.060
	GO:0010393	galacturonan metabolic process	0.060
	GO:0030832	regulation of actin filament length	0.060
	GO:0032956	regulation of actin cytoskeleton organiz...	0.060
	GO:0032970	regulation of actin filament-based proce...	0.060
	GO:0033500	carbohydrate homeostasis	0.060
	GO:0045488	pectin metabolic process	0.060
	GO:0072593	reactive oxygen species metabolic proces...	0.060
	GO:0110053	regulation of actin filament organizatio...	0.060
	GO:0006568	tryptophan metabolic process	0.062
	GO:0006586	indolalkylamine metabolic process	0.062
	GO:0008152	metabolic process	0.063
	GO:0048481	plant ovule development	0.063
	GO:0006089	lactate metabolic process	0.064
	GO:0006418	tRNA aminoacylation for protein translat...	0.064
	GO:0019243	methylglyoxal catabolic process to D-lac...	0.064
	GO:0019430	removal of superoxide radicals	0.064
	GO:0061727	methylglyoxal catabolic process to lacta...	0.064
	GO:0071450	cellular response to oxygen radical	0.064
	GO:0071451	cellular response to superoxide	0.064
	GO:1902903	regulation of supramolecular fiber organ...	0.064
	GO:0042744	hydrogen peroxide catabolic process	0.065
	GO:0009395	phospholipid catabolic process	0.068
	GO:0000038	very long-chain fatty acid metabolic pro...	0.070
	GO:0006771	riboflavin metabolic process	0.070
	GO:0009231	riboflavin biosynthetic process	0.070
	GO:0042727	flavin-containing compound biosynthetic ...	0.070
	GO:0030243	cellulose metabolic process	0.072
	GO:0006694	steroid biosynthetic process	0.072
	GO:0010496	intercellular transport	0.074
	GO:1901607	alpha-amino acid biosynthetic process	0.075
	GO:0019682	glyceraldehyde-3-phosphate metabolic pro...	0.075
	GO:0007015	actin filament organization	0.076
	GO:0043254	regulation of protein complex assembly	0.082
	GO:0051261	protein depolymerization	0.085
	GO:0071478	cellular response to radiation	0.085
	GO:0046364	monosaccharide biosynthetic process	0.086
	GO:0006793	phosphorus metabolic process	0.090
	GO:0022904	respiratory electron transport chain	0.092
	GO:0042558	pteridine-containing compound metabolic ...	0.092
	GO:1901576	organic substance biosynthetic process	0.092
	GO:0043624	cellular protein complex disassembly	0.097
	GO:0035670	plant-type ovary development	0.099
	GO:0006119	oxidative phosphorylation	0.100
	GO:0042773	ATP synthesis coupled electron transport	0.100
	GO:0031977	thylakoid lumen	0.000

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GO type	GO ID	Description	Adj. p-value
	GO:0009521	photosystem	0.000
	GO:0044430	cytoskeletal part	0.000
	GO:0005576	extracellular region	0.000
	GO:0044429	mitochondrial part	0.000
	GO:0005875	microtubule associated complex	0.000
	GO:0005739	mitochondrion	0.000
	GO:0005740	mitochondrial envelope	0.000
	GO:0016469	proton-transporting two-sector ATPase co...	0.000
	GO:0005743	mitochondrial inner membrane	0.000
	GO:1990204	oxidoreductase complex	0.000
	GO:0031969	chloroplast membrane	0.000
	GO:0005874	microtubule	0.000
	GO:0044455	mitochondrial membrane part	0.000
	GO:0070469	respiratory chain	0.000
	GO:0098803	respiratory chain complex	0.000
	GO:0005618	cell wall	0.000
	GO:0005746	mitochondrial respiratory chain	0.000
	GO:0009528	plastid inner membrane	0.000
	GO:0033176	proton-transporting V-type ATPase comple...	0.000
	GO:0005753	mitochondrial proton-transporting ATP sy...	0.001
	GO:0046658	anchored component of plasma membrane	0.001
	GO:0009295	nucleoid	0.001
	GO:0098798	mitochondrial protein complex	0.001
	GO:0030964	NADH dehydrogenase complex	0.001
	GO:0045271	respiratory chain complex I	0.001
	GO:0033180	proton-transporting V-type ATPase, V1 do...	0.001
	GO:0005623	cell	0.001
	GO:0044464	cell part	0.001
	GO:0005747	mitochondrial respiratory chain complex ...	0.001
	GO:0009706	chloroplast inner membrane	0.001
	GO:0016020	membrane	0.002
	GO:0044424	intracellular part	0.002
	GO:0009654	photosystem II oxygen evolving complex	0.002
	GO:0055028	cortical microtubule	0.002
	GO:0042646	plastid nucleoid	0.006
	GO:0009524	phragmoplast	0.013
	GO:0009505	plant-type cell wall	0.017
	GO:0045261	proton-transporting ATP synthase complex...	0.042
	GO:0033177	proton-transporting two-sector ATPase co...	0.056
	GO:0000229	cytoplasmic chromosome	0.073
	GO:0009508	plastid chromosome	0.100
	GO:0016787	hydrolase activity	0.000
	GO:0016491	oxidoreductase activity	0.000
	GO:0016829	lyase activity	0.000
	GO:0003774	motor activity	0.000
	GO:0016788	hydrolase activity, acting on ester bond...	0.000
	GO:0048037	cofactor binding	0.000
	GO:0016655	oxidoreductase activity, acting on NAD(P...	0.000
	GO:0016651	oxidoreductase activity, acting on NAD(P...	0.000

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GO type	GO ID	Description	Adj. p-value
	GO:0050662	coenzyme binding	0.000
	GO:0016791	phosphatase activity	0.000
	GO:0003954	NADH dehydrogenase activity	0.001
	GO:0004553	hydrolase activity, hydrolyzing O-glycos...	0.001
	GO:0016887	ATPase activity	0.001
	GO:0008236	serine-type peptidase activity	0.002
	GO:0017171	serine hydrolase activity	0.002
	GO:0016776	phosphotransferase activity, phosphate g...	0.002
	GO:0016778	diphosphotransferase activity	0.002
	GO:0016830	carbon-carbon lyase activity	0.002
	GO:0016840	carbon-nitrogen lyase activity	0.002
	GO:0016462	pyrophosphatase activity	0.002
	GO:0008137	NADH dehydrogenase (ubiquinone) activity	0.003
	GO:0016853	isomerase activity	0.003
	GO:0050136	NADH dehydrogenase (quinone) activity	0.003
	GO:0050308	sugar-phosphatase activity	0.003
	GO:0016818	hydrolase activity, acting on acid anhyd...	0.004
	GO:0016413	O-acetyltransferase activity	0.004
	GO:0019203	carbohydrate phosphatase activity	0.004
	GO:0016615	malate dehydrogenase activity	0.004
	GO:0016616	oxidoreductase activity, acting on the C...	0.004
	GO:0016838	carbon-oxygen lyase activity, acting on ...	0.005
	GO:0016684	oxidoreductase activity, acting on perox...	0.005
	GO:0016866	intramolecular transferase activity	0.006
	GO:0046933	proton-transporting ATP synthase activit...	0.006
	GO:0016620	oxidoreductase activity, acting on the a...	0.008
	GO:0042349	guiding stereospecific synthesis activit...	0.008
	GO:0046961	proton-transporting ATPase activity, rot...	0.009
	GO:0010333	terpene synthase activity	0.009
	GO:0015399	primary active transmembrane transporter...	0.009
	GO:0015405	P-P-bond-hydrolysis-driven transmembrane...	0.009
	GO:0016759	cellulose synthase activity	0.009
	GO:0016760	cellulose synthase (UDP-forming) activit...	0.009
	GO:0016762	xyloglucan:xyloglucosyl transferase acti...	0.010
	GO:0016814	hydrolase activity, acting on carbon-nit...	0.010
	GO:0080019	fatty-acyl-CoA reductase (alcohol-formin...	0.011
	GO:0016836	hydro-lyase activity	0.011
	GO:0036442	proton-exporting ATPase activity	0.011
	GO:0070011	peptidase activity, acting on L-amino ac...	0.011
	GO:0042626	ATPase activity, coupled to transmembran...	0.012
	GO:0003993	acid phosphatase activity	0.013
	GO:0004601	peroxidase activity	0.013
	GO:0050660	flavin adenine dinucleotide binding	0.013
	GO:0003779	actin binding	0.013
	GO:0016741	transferase activity, transferring one-c...	0.014
	GO:0016903	oxidoreductase activity, acting on the a...	0.014
	GO:0019205	nucleobase-containing compound kinase ac...	0.016
	GO:0016874	ligase activity	0.018
	GO:0042623	ATPase activity, coupled	0.018

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GO type	GO ID	Description	Adj. p-value
	GO:0008233	peptidase activity	0.021
	GO:0052716	hydroquinone:oxygen oxidoreductase activ...	0.021
	GO:0016765	transferase activity, transferring alkyl...	0.021
	GO:0043492	ATPase activity, coupled to movement of ...	0.021
	GO:0140101	catalytic activity, acting on a tRNA	0.021
	GO:0043022	ribosome binding	0.024
	GO:0008168	methyltransferase activity	0.025
	GO:0016717	oxidoreductase activity, acting on paire...	0.025
	GO:0016861	intramolecular oxidoreductase activity, ...	0.025
	GO:0051537	2 iron, 2 sulfur cluster binding	0.025
	GO:0004175	endopeptidase activity	0.028
	GO:0004743	pyruvate kinase activity	0.028
	GO:0030955	potassium ion binding	0.028
	GO:0031420	alkali metal ion binding	0.028
	GO:0031409	pigment binding	0.029
	GO:0019104	DNA N-glycosylase activity	0.030
	GO:0016868	intramolecular transferase activity, pho...	0.038
	GO:0016799	hydrolase activity, hydrolyzing N-glycos...	0.039
	GO:0050661	NADP binding	0.040
	GO:0052689	carboxylic ester hydrolase activity	0.041
	GO:0004812	aminoacyl-tRNA ligase activity	0.046
	GO:0016875	ligase activity, forming carbon-oxygen b...	0.046
	GO:0019829	cation-transporting ATPase activity	0.046
	GO:0022853	active ion transmembrane transporter act...	0.046
	GO:0042625	ATPase coupled ion transmembrane transpo...	0.046
	GO:0046556	alpha-L-arabinofuranosidase activity	0.049
	GO:0051015	actin filament binding	0.056
	GO:0070008	serine-type exopeptidase activity	0.056
	GO:0016405	CoA-ligase activity	0.060
	GO:0016878	acid-thiol ligase activity	0.060
	GO:0004185	serine-type carboxypeptidase activity	0.061
	GO:2001070	starch binding	0.066
	GO:0033764	steroid dehydrogenase activity, acting o...	0.072
	GO:0019238	cyclohydrolase activity	0.076
	GO:0004659	prenyltransferase activity	0.081
	GO:0002161	aminoacyl-tRNA editing activity	0.082
	GO:0051087	chaperone binding	0.098

4.2.8 Leaf - Postflowering - Cluster 8

GO type	GO ID	Description	Adj. p-value
BP	GO:0016071	mRNA metabolic process	0.000
	GO:0008380	RNA splicing	0.000
	GO:0022618	ribonucleoprotein complex assembly	0.000
	GO:0042255	ribosome assembly	0.000
	GO:0051171	regulation of nitrogen compound metaboli...	0.000
	GO:0080090	regulation of primary metabolic process	0.000
	GO:0090501	RNA phosphodiester bond hydrolysis	0.000
	GO:0010556	regulation of macromolecule biosynthetic...	0.001
	GO:0051252	regulation of RNA metabolic process	0.001
	GO:0097659	nucleic acid-templated transcription	0.001
	GO:2000112	regulation of cellular macromolecule bio...	0.001
	GO:0031326	regulation of cellular biosynthetic proc...	0.002
	GO:1903506	regulation of nucleic acid-templated tra...	0.003
	GO:2001141	regulation of RNA biosynthetic process	0.003
	GO:0006355	regulation of transcription, DNA-templat...	0.003
	GO:0009889	regulation of biosynthetic process	0.003
	GO:0019941	modification-dependent protein catabolic...	0.004
	GO:0016074	snoRNA metabolic process	0.004
	GO:0043144	snoRNA processing	0.004
	GO:1900864	mitochondrial RNA modification	0.004
	GO:0006511	ubiquitin-dependent protein catabolic pr...	0.008
	GO:0006749	glutathione metabolic process	0.009
	GO:0000027	ribosomal large subunit assembly	0.009
	GO:0006333	chromatin assembly or disassembly	0.013
	GO:0031497	chromatin assembly	0.018
	GO:0090502	RNA phosphodiester bond hydrolysis, endo...	0.018
	GO:0070925	organelle assembly	0.027
	GO:0000959	mitochondrial RNA metabolic process	0.030
	GO:0006323	DNA packaging	0.030
	GO:0006334	nucleosome assembly	0.030
	GO:0010431	seed maturation	0.031
	GO:0046113	nucleobase catabolic process	0.031
	GO:0044265	cellular macromolecule catabolic process	0.031
	GO:0000463	maturation of LSU-rRNA from tricistronic...	0.035
	GO:0005996	monosaccharide metabolic process	0.041
	GO:0006457	protein folding	0.045
	GO:0034728	nucleosome organization	0.045
	GO:1904659	glucose transmembrane transport	0.050
	GO:0015749	monosaccharide transmembrane transport	0.052
	GO:0080156	mitochondrial mRNA modification	0.052
	GO:0046149	pigment catabolic process	0.058
	GO:0044257	cellular protein catabolic process	0.058
	GO:0051603	proteolysis involved in cellular protein...	0.059
	GO:0008645	hexose transmembrane transport	0.070
	GO:0015996	chlorophyll catabolic process	0.070
	GO:0015850	organic hydroxy compound transport	0.071

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GO type	GO ID	Description	Adj. p-value
	GO:0019748	secondary metabolic process	0.073
	GO:0006560	proline metabolic process	0.085
	GO:0000380	alternative mRNA splicing, via spliceoso...	0.085
	GO:0046323	glucose import	0.091
	GO:0006575	cellular modified amino acid metabolic p...	0.097
CC	GO:0005681	spliceosomal complex	0.000
	GO:0005829	cytosol	0.000
	GO:0030532	small nuclear ribonucleoprotein complex	0.001
	GO:0097525	spliceosomal snRNP complex	0.001
	GO:0120114	Sm-like protein family complex	0.001
	GO:0005684	U2-type spliceosomal complex	0.005
	GO:0000785	chromatin	0.005
	GO:0099023	tethering complex	0.005
	GO:0005686	U2 snRNP	0.006
	GO:0016607	nuclear speck	0.008
	GO:0000786	nucleosome	0.010
	GO:0005689	U12-type spliceosomal complex	0.011
	GO:0044815	DNA packaging complex	0.023
	GO:0017119	Golgi transport complex	0.025
	GO:0000315	organellar large ribosomal subunit	0.027
	GO:0005762	mitochondrial large ribosomal subunit	0.027
	GO:0055029	nuclear DNA-directed RNA polymerase comp...	0.034
	GO:0000428	DNA-directed RNA polymerase complex	0.042
	GO:0030880	RNA polymerase complex	0.042
	GO:0030118	clathrin coat	0.061
	GO:0071011	precatalytic spliceosome	0.100
MF	GO:0003676	nucleic acid binding	0.000
	GO:0004497	monooxygenase activity	0.006
	GO:0046914	transition metal ion binding	0.036
	GO:0043565	sequence-specific DNA binding	0.036
	GO:0016705	oxidoreductase activity, acting on paire...	0.042
	GO:0016709	oxidoreductase activity, acting on paire...	0.082
	GO:0003677	DNA binding	0.085
	GO:0004364	glutathione transferase activity	0.085
	GO:0035251	UDP-glucosyltransferase activity	0.085

4.2.9 Leaf - Postflowering - Cluster 9

GO type	GO ID	Description	Adj. p-value
	GO:0019684	photosynthesis, light reaction	0.000
	GO:0006091	generation of precursor metabolites and ...	0.000
	GO:0044281	small molecule metabolic process	0.000
	GO:0044283	small molecule biosynthetic process	0.000
	GO:0051188	cofactor biosynthetic process	0.000
	GO:0006796	phosphate-containing compound metabolic ...	0.000
	GO:0017144	drug metabolic process	0.000
	GO:0008299	isoprenoid biosynthetic process	0.000
	GO:0006629	lipid metabolic process	0.000
	GO:0016053	organic acid biosynthetic process	0.000
	GO:0046394	carboxylic acid biosynthetic process	0.000
	GO:0006732	coenzyme metabolic process	0.000
	GO:0005975	carbohydrate metabolic process	0.000
	GO:0005976	polysaccharide metabolic process	0.000
	GO:0009108	coenzyme biosynthetic process	0.000
	GO:0016999	antibiotic metabolic process	0.000
	GO:0009150	purine ribonucleotide metabolic process	0.000
	GO:0016310	phosphorylation	0.000
	GO:0044262	cellular carbohydrate metabolic process	0.000
	GO:0016114	terpenoid biosynthetic process	0.000
	GO:0009165	nucleotide biosynthetic process	0.000
	GO:0016052	carbohydrate catabolic process	0.000
	GO:1901293	nucleoside phosphate biosynthetic proces...	0.000
	GO:0009123	nucleoside monophosphate metabolic proce...	0.000
	GO:0009110	vitamin biosynthetic process	0.000
	GO:0009073	aromatic amino acid family biosynthetic ...	0.000
	GO:0009834	plant-type secondary cell wall biogenesi...	0.001
	GO:0046434	organophosphate catabolic process	0.001
	GO:0009832	plant-type cell wall biogenesis	0.002
	GO:0010383	cell wall polysaccharide metabolic proce...	0.002
	GO:0046854	phosphatidylinositol phosphorylation	0.002
	GO:0072525	pyridine-containing compound biosyntheti...	0.002
	GO:0033692	cellular polysaccharide biosynthetic pro...	0.003
	GO:0048438	floral whorl development	0.003
	GO:0051187	cofactor catabolic process	0.003
	GO:0071482	cellular response to light stimulus	0.003
	GO:0044036	cell wall macromolecule metabolic proces...	0.003
	GO:0055086	nucleobase-containing small molecule met...	0.003
	GO:0009808	lignin metabolic process	0.003
	GO:0016051	carbohydrate biosynthetic process	0.003
	GO:0048440	carpel development	0.003
	GO:0046939	nucleotide phosphorylation	0.003
	GO:0090407	organophosphate biosynthetic process	0.004
	GO:0072524	pyridine-containing compound metabolic p...	0.004
	GO:0009645	response to low light intensity stimulus	0.004
	GO:0006165	nucleoside diphosphate phosphorylation	0.005

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GO type	GO ID	Description	Adj. p-value
	GO:0006733	oxidoreduction coenzyme metabolic proces...	0.005
	GO:0046834	lipid phosphorylation	0.005
	GO:0034637	cellular carbohydrate biosynthetic proce...	0.005
	GO:0006090	pyruvate metabolic process	0.005
	GO:0007017	microtubule-based process	0.006
	GO:0019359	nicotinamide nucleotide biosynthetic pro...	0.006
	GO:0048467	gynoecium development	0.006
	GO:1901661	quinone metabolic process	0.006
	GO:1901663	quinone biosynthetic process	0.006
	GO:0006558	L-phenylalanine metabolic process	0.007
	GO:1902221	erythrose 4-phosphate/phosphoenolpyruvat...	0.007
	GO:0009074	aromatic amino acid family catabolic pro...	0.007
	GO:0009809	lignin biosynthetic process	0.007
	GO:0046496	nicotinamide nucleotide metabolic proces...	0.008
	GO:0010206	photosystem II repair	0.008
	GO:0010410	hemicellulose metabolic process	0.008
	GO:0019363	pyridine nucleotide biosynthetic process	0.008
	GO:0035670	plant-type ovary development	0.009
	GO:0009166	nucleotide catabolic process	0.009
	GO:0010109	regulation of photosynthesis	0.009
	GO:0032787	monocarboxylic acid metabolic process	0.009
	GO:0019362	pyridine nucleotide metabolic process	0.010
	GO:0035336	long-chain fatty-acyl-CoA metabolic proc...	0.010
	GO:1901135	carbohydrate derivative metabolic proces...	0.010
	GO:0009773	photosynthetic electron transport in pho...	0.011
	GO:0015985	energy coupled proton transport, down el...	0.011
	GO:0015986	ATP synthesis coupled proton transport	0.011
	GO:0009314	response to radiation	0.011
	GO:0042181	ketone biosynthetic process	0.011
	GO:0048481	plant ovule development	0.011
	GO:0071478	cellular response to radiation	0.012
	GO:1901292	nucleoside phosphate catabolic process	0.013
	GO:0042168	heme metabolic process	0.013
	GO:0006096	glycolytic process	0.013
	GO:0006757	ATP generation from ADP	0.013
	GO:0009135	purine nucleoside diphosphate metabolic ...	0.013
	GO:0009179	purine ribonucleoside diphosphate metabo...	0.013
	GO:0009185	ribonucleoside diphosphate metabolic pro...	0.013
	GO:0042866	pyruvate biosynthetic process	0.013
	GO:0046031	ADP metabolic process	0.013
	GO:0009132	nucleoside diphosphate metabolic process	0.013
	GO:0009416	response to light stimulus	0.014
	GO:0097435	supramolecular fiber organization	0.015
	GO:0006520	cellular amino acid metabolic process	0.016
	GO:0009308	amine metabolic process	0.016
	GO:0016122	xanthophyll metabolic process	0.017
	GO:0006783	heme biosynthetic process	0.018
	GO:0042214	terpene metabolic process	0.019
	GO:0006576	cellular biogenic amine metabolic proces...	0.019

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GO type	GO ID	Description	Adj. p-value
	GO:0042180	cellular ketone metabolic process	0.019
	GO:0043467	regulation of generation of precursor me...	0.019
	GO:0010103	stomatal complex morphogenesis	0.020
	GO:0071483	cellular response to blue light	0.020
	GO:0098754	detoxification	0.020
	GO:0006767	water-soluble vitamin metabolic process	0.020
	GO:1901568	fatty acid derivative metabolic process	0.020
	GO:0010118	stomatal movement	0.020
	GO:0030244	cellulose biosynthetic process	0.020
	GO:0000272	polysaccharide catabolic process	0.021
	GO:0042435	indole-containing compound biosynthetic ...	0.021
	GO:2000652	regulation of secondary cell wall biogen...	0.021
	GO:0009250	glucan biosynthetic process	0.022
	GO:1901617	organic hydroxy compound biosynthetic pr...	0.028
	GO:0035337	fatty-acyl-CoA metabolic process	0.028
	GO:0000038	very long-chain fatty acid metabolic pro...	0.029
	GO:0007015	actin filament organization	0.029
	GO:0017004	cytochrome complex assembly	0.031
	GO:0034220	ion transmembrane transport	0.031
	GO:0006637	acyl-CoA metabolic process	0.034
	GO:0035383	thioester metabolic process	0.034
	GO:0071214	cellular response to abiotic stimulus	0.034
	GO:0104004	cellular response to environmental stimu...	0.034
	GO:0030243	cellulose metabolic process	0.034
	GO:0032544	plastid translation	0.035
	GO:0042364	water-soluble vitamin biosynthetic proce...	0.036
	GO:0009789	positive regulation of abscisic acid-act...	0.036
	GO:1901421	positive regulation of response to alcoh...	0.036
	GO:1905959	positive regulation of cellular response...	0.036
	GO:1901615	organic hydroxy compound metabolic proce...	0.038
	GO:0005983	starch catabolic process	0.038
	GO:0015672	monovalent inorganic cation transport	0.040
	GO:0043648	dicarboxylic acid metabolic process	0.041
	GO:0008652	cellular amino acid biosynthetic process	0.041
	GO:0046486	glycerolipid metabolic process	0.042
	GO:0042548	regulation of photosynthesis, light reac...	0.044
	GO:1902600	proton transmembrane transport	0.045
	GO:0046364	monosaccharide biosynthetic process	0.048
	GO:0000162	tryptophan biosynthetic process	0.049
	GO:0046219	indolalkylamine biosynthetic process	0.049
	GO:0030036	actin cytoskeleton organization	0.050
	GO:0044275	cellular carbohydrate catabolic process	0.050
	GO:0009637	response to blue light	0.050
	GO:0046184	aldehyde biosynthetic process	0.050
	GO:0010143	cutin biosynthetic process	0.051
	GO:0006468	protein phosphorylation	0.051
	GO:0030029	actin filament-based process	0.052
	GO:0043038	amino acid activation	0.052
	GO:0043039	tRNA aminoacylation	0.052

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GO type	GO ID	Description	Adj. p-value
	GO:0046365	monosaccharide catabolic process	0.052
	GO:0022604	regulation of cell morphogenesis	0.055
	GO:0009642	response to light intensity	0.058
	GO:0006775	fat-soluble vitamin metabolic process	0.061
	GO:0010189	vitamin E biosynthetic process	0.061
	GO:0042360	vitamin E metabolic process	0.061
	GO:0042362	fat-soluble vitamin biosynthetic process	0.061
	GO:0042726	flavin-containing compound metabolic pro...	0.061
	GO:0009943	adaxial/abaxial axis specification	0.067
	GO:0009944	polarity specification of adaxial/abaxia...	0.067
	GO:0009741	response to brassinosteroid	0.067
	GO:0034754	cellular hormone metabolic process	0.067
	GO:0010119	regulation of stomatal movement	0.069
	GO:0010218	response to far red light	0.069
	GO:1901401	regulation of tetrapyrrole metabolic pro...	0.073
	GO:0010345	suberin biosynthetic process	0.079
	GO:0030091	protein repair	0.079
	GO:1901463	regulation of tetrapyrrole biosynthetic ...	0.079
	GO:0006568	tryptophan metabolic process	0.081
	GO:0006586	indolalkylamine metabolic process	0.081
	GO:0080167	response to karrikin	0.082
	GO:0051273	beta-glucan metabolic process	0.087
	GO:0009095	aromatic amino acid family biosynthetic ...	0.087
	GO:0009606	tropism	0.089
	GO:0051274	beta-glucan biosynthetic process	0.089
	GO:0009958	positive gravitropism	0.090
	GO:1903409	reactive oxygen species biosynthetic pro...	0.090
	GO:0006418	tRNA aminoacylation for protein translat...	0.095
	GO:0044550	secondary metabolite biosynthetic proces...	0.096
	GO:0009629	response to gravity	0.097
CC	GO:0031977	thylakoid lumen	0.000
	GO:0009521	photosystem	0.000
	GO:0016020	membrane	0.000
	GO:0005856	cytoskeleton	0.000
	GO:0044430	cytoskeletal part	0.000
	GO:0010319	stromule	0.002
	GO:0009505	plant-type cell wall	0.003
	GO:0045259	proton-transporting ATP synthase complex	0.005
	GO:0030863	cortical cytoskeleton	0.007
	GO:0030981	cortical microtubule cytoskeleton	0.007
	GO:0009654	photosystem II oxygen evolving complex	0.007
	GO:0031225	anchored component of membrane	0.010
	GO:0046658	anchored component of plasma membrane	0.011
	GO:0099080	supramolecular complex	0.015
	GO:0099081	supramolecular polymer	0.015
	GO:0099512	supramolecular fiber	0.015
	GO:0099513	polymeric cytoskeletal fiber	0.015
	GO:1990204	oxidoreductase complex	0.016
	GO:0005874	microtubule	0.018

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GO type	GO ID	Description	Adj. p-value
	GO:0055028	cortical microtubule	0.019
	GO:0019866	organelle inner membrane	0.025
	GO:0042170	plastid membrane	0.025
	GO:0044425	membrane part	0.025
	GO:0005881	cytoplasmic microtubule	0.030
	GO:0031969	chloroplast membrane	0.038
	GO:0045261	proton-transporting ATP synthase complex...	0.058
	GO:0042575	DNA polymerase complex	0.062
	GO:0005740	mitochondrial envelope	0.066
	GO:0098796	membrane protein complex	0.073
	GO:0016787	hydrolase activity	0.000
	GO:0016829	lyase activity	0.000
	GO:0016491	oxidoreductase activity	0.000
	GO:0016209	antioxidant activity	0.000
	GO:0008144	drug binding	0.000
	GO:0016791	phosphatase activity	0.000
	GO:0042578	phosphoric ester hydrolase activity	0.000
	GO:0016838	carbon-oxygen lyase activity, acting on ...	0.000
	GO:0016773	phosphotransferase activity, alcohol gro...	0.000
	GO:0016788	hydrolase activity, acting on ester bond...	0.000
	GO:0050662	coenzyme binding	0.000
	GO:0016835	carbon-oxygen lyase activity	0.000
	GO:0004672	protein kinase activity	0.002
	GO:0046933	proton-transporting ATP synthase activit...	0.002
	GO:0043167	ion binding	0.002
	GO:0042626	ATPase activity, coupled to transmembran...	0.002
	GO:0016746	transferase activity, transferring acyl ...	0.003
	GO:0015399	primary active transmembrane transporter...	0.003
	GO:0015405	P-P-bond-hydrolysis-driven transmembrane...	0.003
	GO:0003779	actin binding	0.003
	GO:0016830	carbon-carbon lyase activity	0.003
	GO:0016747	transferase activity, transferring acyl ...	0.004
	GO:0005215	transporter activity	0.004
	GO:0022857	transmembrane transporter activity	0.004
	GO:0043492	ATPase activity, coupled to movement of ...	0.004
	GO:0050308	sugar-phosphatase activity	0.006
	GO:0005216	ion channel activity	0.006
	GO:0080019	fatty-acyl-CoA reductase (alcohol-formin...	0.006
	GO:0019203	carbohydrate phosphatase activity	0.007
	GO:0003993	acid phosphatase activity	0.010
	GO:0008574	ATP-dependent microtubule motor activity...	0.010
	GO:1990939	ATP-dependent microtubule motor activity	0.010
	GO:0016762	xyloglucan:xyloglucosyl transferase acti...	0.011
	GO:0022839	ion gated channel activity	0.011
	GO:0016616	oxidoreductase activity, acting on the C...	0.012
	GO:0016651	oxidoreductase activity, acting on NAD(P...	0.013
	GO:0015103	inorganic anion transmembrane transporte...	0.020
	GO:0022836	gated channel activity	0.021
	GO:0016620	oxidoreductase activity, acting on the a...	0.021

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0016853	isomerase activity	0.022
	GO:0036094	small molecule binding	0.023
	GO:0009055	electron transfer activity	0.024
	GO:0003954	NADH dehydrogenase activity	0.024
	GO:0004252	serine-type endopeptidase activity	0.028
	GO:0008252	nucleotidase activity	0.028
	GO:0008266	poly(U) RNA binding	0.028
	GO:0016778	diphosphotransferase activity	0.028
	GO:0016799	hydrolase activity, hydrolyzing N-glycos...	0.028
	GO:0050661	NADP binding	0.028
	GO:1901682	sulfur compound transmembrane transporte...	0.028
	GO:0016776	phosphotransferase activity, phosphate g...	0.030
	GO:2001070	starch binding	0.031
	GO:0016840	carbon-nitrogen lyase activity	0.031
	GO:0001871	pattern binding	0.031
	GO:0016717	oxidoreductase activity, acting on paire...	0.031
	GO:0030247	polysaccharide binding	0.031
	GO:0016887	ATPase activity	0.041
	GO:0005509	calcium ion binding	0.042
	GO:0044769	ATPase activity, coupled to transmembran...	0.048
	GO:0000166	nucleotide binding	0.048
	GO:0008374	O-acyltransferase activity	0.048
	GO:1901265	nucleoside phosphate binding	0.048
	GO:0004674	protein serine/threonine kinase activity	0.050
	GO:0005244	voltage-gated ion channel activity	0.050
	GO:0022832	voltage-gated channel activity	0.050
	GO:0043022	ribosome binding	0.053
	GO:0004659	prenyltransferase activity	0.055
	GO:0004812	aminoacyl-tRNA ligase activity	0.055
	GO:0008238	exopeptidase activity	0.055
	GO:0016744	transferase activity, transferring aldeh...	0.055
	GO:0016875	ligase activity, forming carbon-oxygen b...	0.055
	GO:0016307	phosphatidylinositol phosphate kinase ac...	0.057
	GO:0016413	O-acetyltransferase activity	0.057
	GO:0051015	actin filament binding	0.057
	GO:0019829	cation-transporting ATPase activity	0.060
	GO:0022853	active ion transmembrane transporter act...	0.060
	GO:0042625	ATPase coupled ion transmembrane transpo...	0.060
	GO:0070011	peptidase activity, acting on L-amino ac...	0.060
	GO:0019104	DNA N-glycosylase activity	0.062
	GO:0008146	sulfotransferase activity	0.064
	GO:0008233	peptidase activity	0.064
	GO:0005507	copper ion binding	0.065
	GO:0016874	ligase activity	0.070
	GO:0042623	ATPase activity, coupled	0.070
	GO:0016615	malate dehydrogenase activity	0.072
	GO:0015556	C4-dicarboxylate transmembrane transport...	0.074
	GO:0022804	active transmembrane transporter activit...	0.076
	GO:0051539	4 iron, 4 sulfur cluster binding	0.079

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0004743	pyruvate kinase activity	0.079
	GO:0016405	CoA-ligase activity	0.079
	GO:0016878	acid-thiol ligase activity	0.079
	GO:0030955	potassium ion binding	0.079
	GO:0031420	alkali metal ion binding	0.079
	GO:0016861	intramolecular oxidoreductase activity, ...	0.087
	GO:0017111	nucleoside-triphosphatase activity	0.087
	GO:0050660	flavin adenine dinucleotide binding	0.087
	GO:0019842	vitamin binding	0.088
	GO:0016462	pyrophosphatase activity	0.089

4.2.10 Leaf - Postflowering - Cluster 10

GO type	GO ID	Description	Adj. p-value
BP	GO:0042493	response to drug	0.002
	GO:0003333	amino acid transmembrane transport	0.004
	GO:0015807	L-amino acid transport	0.005
	GO:0055085	transmembrane transport	0.006
	GO:1902475	L-alpha-amino acid transmembrane transpo...	0.007
	GO:0051234	establishment of localization	0.008
	GO:1901071	glucosamine-containing compound metaboli...	0.008
	GO:0006810	transport	0.012
	GO:0051179	localization	0.012
	GO:0071702	organic substance transport	0.012
	GO:0006022	aminoglycan metabolic process	0.013
	GO:0044550	secondary metabolite biosynthetic proces...	0.014
	GO:0015893	drug transport	0.018
	GO:0034219	carbohydrate transmembrane transport	0.018
	GO:1905039	carboxylic acid transmembrane transport	0.019
	GO:0010200	response to chitin	0.020
	GO:0035303	regulation of dephosphorylation	0.020
	GO:0005996	monosaccharide metabolic process	0.021
	GO:0080163	regulation of protein serine/threonine p...	0.023
	GO:1903825	organic acid transmembrane transport	0.023
	GO:0015804	neutral amino acid transport	0.027
	GO:0000209	protein polyubiquitination	0.030
	GO:0006665	sphingolipid metabolic process	0.030
	GO:0010243	response to organonitrogen compound	0.032
	GO:0010921	regulation of phosphatase activity	0.034
	GO:0035304	regulation of protein dephosphorylation	0.034
	GO:0007166	cell surface receptor signaling pathway	0.034
	GO:0015706	nitrate transport	0.034
	GO:0055114	oxidation-reduction process	0.036
	GO:0006040	amino sugar metabolic process	0.039
	GO:0006829	zinc ion transport	0.040
	GO:0006575	cellular modified amino acid metabolic p...	0.042
	GO:1901564	organonitrogen compound metabolic proces...	0.049
	GO:0043412	macromolecule modification	0.050
	GO:0006887	exocytosis	0.051
	GO:0006820	anion transport	0.051
	GO:0043666	regulation of phosphoprotein phosphatase...	0.056
	GO:0006857	oligopeptide transport	0.065
	GO:0046942	carboxylic acid transport	0.067
	GO:0008037	cell recognition	0.069
	GO:0030148	sphingolipid biosynthetic process	0.073
	GO:0036065	fucosylation	0.079
	GO:0015849	organic acid transport	0.081
	GO:0009875	pollen-pistil interaction	0.085
	GO:0048544	recognition of pollen	0.088
	GO:0006796	phosphate-containing compound metabolic ...	0.099

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0019740	nitrogen utilization	0.099
CC	GO:0005886	plasma membrane	0.000
	GO:0099023	tethering complex	0.013
	GO:0000145	exocyst	0.065
MF	GO:0004497	monooxygenase activity	0.000
	GO:0016705	oxidoreductase activity, acting on paire...	0.000
	GO:0030246	carbohydrate binding	0.000
	GO:0015294	solute:cation symporter activity	0.000
	GO:0032559	adenyl ribonucleotide binding	0.001
	GO:0030554	adenyl nucleotide binding	0.001
	GO:0043168	anion binding	0.001
	GO:0015318	inorganic molecular entity transmembrane...	0.001
	GO:0015171	amino acid transmembrane transporter act...	0.002
	GO:0032553	ribonucleotide binding	0.002
	GO:0015295	solute:proton symporter activity	0.002
	GO:0042562	hormone binding	0.002
	GO:0015174	basic amino acid transmembrane transport...	0.002
	GO:0016491	oxidoreductase activity	0.004
	GO:0032555	purine ribonucleotide binding	0.004
	GO:0017076	purine nucleotide binding	0.005
	GO:0005351	carbohydrate:proton symporter activity	0.006
	GO:0005402	carbohydrate:cation symporter activity	0.006
	GO:0016757	transferase activity, transferring glyco...	0.007
	GO:0051119	sugar transmembrane transporter activity	0.007
	GO:0001871	pattern binding	0.007
	GO:0030247	polysaccharide binding	0.007
	GO:0022804	active transmembrane transporter activit...	0.008
	GO:0043167	ion binding	0.008
	GO:0005385	zinc ion transmembrane transporter activ...	0.008
	GO:0015297	antiporter activity	0.010
	GO:0015075	ion transmembrane transporter activity	0.012
	GO:0019208	phosphatase regulator activity	0.014
	GO:0019888	protein phosphatase regulator activity	0.014
	GO:0004857	enzyme inhibitor activity	0.015
	GO:0019840	isoprenoid binding	0.020
	GO:0003959	NADPH dehydrogenase activity	0.021
	GO:0004864	protein phosphatase inhibitor activity	0.025
	GO:0008483	transaminase activity	0.025
	GO:0016769	transferase activity, transferring nitro...	0.025
	GO:0019212	phosphatase inhibitor activity	0.025
	GO:0046943	carboxylic acid transmembrane transporte...	0.029
	GO:0038023	signaling receptor activity	0.030
	GO:0060089	molecular transducer activity	0.030
	GO:0072509	divalent inorganic cation transmembrane ...	0.033
	GO:0061630	ubiquitin protein ligase activity	0.034
	GO:0005342	organic acid transmembrane transporter a...	0.034
	GO:0008417	fucosyltransferase activity	0.034
	GO:0030414	peptidase inhibitor activity	0.034
	GO:0061134	peptidase regulator activity	0.034

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GO type	GO ID	Description	Adj. p-value
	GO:0010427	abscisic acid binding	0.035
	GO:0015238	drug transmembrane transporter activity	0.035
	GO:0043178	alcohol binding	0.035
	GO:0015276	ligand-gated ion channel activity	0.041
	GO:0022834	ligand-gated channel activity	0.041
	GO:0004866	endopeptidase inhibitor activity	0.044
	GO:0061135	endopeptidase regulator activity	0.044
	GO:0004970	ionotropic glutamate receptor activity	0.045
	GO:0005230	extracellular ligand-gated ion channel a...	0.045
	GO:0008066	glutamate receptor activity	0.045
	GO:0022824	transmitter-gated ion channel activity	0.045
	GO:0022835	transmitter-gated channel activity	0.045
	GO:0036094	small molecule binding	0.045
	GO:0008144	drug binding	0.047
	GO:0061659	ubiquitin-like protein ligase activity	0.050
	GO:0004867	serine-type endopeptidase inhibitor acti...	0.051
	GO:0015175	neutral amino acid transmembrane transpo...	0.058
	GO:0000166	nucleotide binding	0.059
	GO:1901265	nucleoside phosphate binding	0.059
	GO:0004888	transmembrane signaling receptor activit...	0.065
	GO:0035673	oligopeptide transmembrane transporter a...	0.065
	GO:0046915	transition metal ion transmembrane trans...	0.071
	GO:0046983	protein dimerization activity	0.076
	GO:0030594	neurotransmitter receptor activity	0.092

4.3 Root Preflowering clusters

4.3.1 Root - Preflowering - Cluster 1

GO type	GO ID	Description	Adj. p-value
	GO:0051276	chromosome organization	0.000
	GO:0034660	ncRNA metabolic process	0.000
	GO:0034470	ncRNA processing	0.000
	GO:0022613	ribonucleoprotein complex biogenesis	0.000
	GO:0006974	cellular response to DNA damage stimulus	0.000
	GO:0016071	mRNA metabolic process	0.000
	GO:0003006	developmental process involved in reprod...	0.000
	GO:0048856	anatomical structure development	0.000
	GO:0022607	cellular component assembly	0.000
	GO:0009791	post-embryonic development	0.000
	GO:0007049	cell cycle	0.000
	GO:0048608	reproductive structure development	0.000
	GO:0061458	reproductive system development	0.000
	GO:0033554	cellular response to stress	0.000
	GO:0016458	gene silencing	0.000
	GO:0010629	negative regulation of gene expression	0.000
	GO:0048731	system development	0.000
	GO:0009790	embryo development	0.000
	GO:0031047	gene silencing by RNA	0.000
	GO:0006399	tRNA metabolic process	0.000
	GO:1903047	mitotic cell cycle process	0.000
	GO:0000278	mitotic cell cycle	0.000
	GO:0010608	posttranscriptional regulation of gene e...	0.000
	GO:0006304	DNA modification	0.000
	GO:0044728	DNA methylation or demethylation	0.000
	GO:0016441	posttranscriptional gene silencing	0.000
	GO:0006261	DNA-dependent DNA replication	0.000
	GO:0006479	protein methylation	0.000
	GO:0035194	posttranscriptional gene silencing by RN...	0.000
	GO:0001510	RNA methylation	0.000
	GO:0016571	histone methylation	0.000
	GO:0018205	peptidyl-lysine modification	0.000
	GO:0033043	regulation of organelle organization	0.000
	GO:0007059	chromosome segregation	0.000
	GO:0050793	regulation of developmental process	0.000
	GO:0018022	peptidyl-lysine methylation	0.000
	GO:0051052	regulation of DNA metabolic process	0.000
	GO:0051641	cellular localization	0.000
	GO:2000113	negative regulation of cellular macromol...	0.000
	GO:0022618	ribonucleoprotein complex assembly	0.000
	GO:0090501	RNA phosphodiester bond hydrolysis	0.000
	GO:0010212	response to ionizing radiation	0.000
	GO:0048869	cellular developmental process	0.000
	GO:0009553	embryo sac development	0.000
	GO:0051726	regulation of cell cycle	0.000

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0009653	anatomical structure morphogenesis	0.000
	GO:0009908	flower development	0.000
	GO:0042274	ribosomal small subunit biogenesis	0.000
	GO:0006342	chromatin silencing	0.000
	GO:0010564	regulation of cell cycle process	0.000
	GO:0006417	regulation of translation	0.000
	GO:2000026	regulation of multicellular organismal d...	0.000
	GO:0007276	gamete generation	0.000
	GO:0006886	intracellular protein transport	0.000
	GO:0048367	shoot system development	0.000
	GO:0070192	chromosome organization involved in meio...	0.000
	GO:0000902	cell morphogenesis	0.000
	GO:0006400	tRNA modification	0.000
	GO:0005977	glycogen metabolic process	0.000
	GO:0006112	energy reserve metabolic process	0.000
	GO:0048580	regulation of post-embryonic development	0.000
	GO:0070925	organelle assembly	0.000
	GO:0045132	meiotic chromosome segregation	0.000
	GO:0030490	maturation of SSU-rRNA	0.000
	GO:0071824	protein-DNA complex subunit organization	0.000
	GO:0061077	chaperone-mediated protein folding	0.000
	GO:0000154	rRNA modification	0.000
	GO:0065004	protein-DNA complex assembly	0.001
	GO:0048831	regulation of shoot system development	0.001
	GO:0000281	mitotic cytokinesis	0.001
	GO:0000469	cleavage involved in rRNA processing	0.001
	GO:0032984	protein-containing complex disassembly	0.001
	GO:0000245	spliceosomal complex assembly	0.001
	GO:0005978	glycogen biosynthetic process	0.001
	GO:0009890	negative regulation of biosynthetic proc...	0.001
	GO:0045934	negative regulation of nucleobase-contai...	0.001
	GO:0048518	positive regulation of biological proces...	0.001
	GO:0009266	response to temperature stimulus	0.001
	GO:0051168	nuclear export	0.001
	GO:0009314	response to radiation	0.001
	GO:0009161	ribonucleoside monophosphate metabolic p...	0.001
	GO:0009123	nucleoside monophosphate metabolic proce...	0.001
	GO:0007346	regulation of mitotic cell cycle	0.002
	GO:0009909	regulation of flower development	0.002
	GO:0046185	aldehyde catabolic process	0.002
	GO:2000241	regulation of reproductive process	0.002
	GO:0000819	sister chromatid segregation	0.002
	GO:0006298	mismatch repair	0.002
	GO:0061640	cytoskeleton-dependent cytokinesis	0.002
	GO:0031935	regulation of chromatin silencing	0.002
	GO:0045143	homologous chromosome segregation	0.002
	GO:1901987	regulation of cell cycle phase transitio...	0.002
	GO:0006611	protein export from nucleus	0.002
	GO:0015833	peptide transport	0.002

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0042886	amide transport	0.002
	GO:0000373	Group II intron splicing	0.002
	GO:0030488	tRNA methylation	0.002
	GO:0007129	synapsis	0.002
	GO:0016573	histone acetylation	0.002
	GO:0018393	internal peptidyl-lysine acetylation	0.002
	GO:0018394	peptidyl-lysine acetylation	0.002
	GO:0006323	DNA packaging	0.003
	GO:0010228	vegetative to reproductive phase transit...	0.003
	GO:0007033	vacuole organization	0.003
	GO:0044770	cell cycle phase transition	0.003
	GO:0055046	microgametogenesis	0.003
	GO:0071478	cellular response to radiation	0.003
	GO:1901990	regulation of mitotic cell cycle phase t...	0.003
	GO:0051567	histone H3-K9 methylation	0.003
	GO:0061647	histone H3-K9 modification	0.003
	GO:0022411	cellular component disassembly	0.003
	GO:0044786	cell cycle DNA replication	0.003
	GO:0031060	regulation of histone methylation	0.004
	GO:0042255	ribosome assembly	0.004
	GO:0006475	internal protein amino acid acetylation	0.004
	GO:0035195	gene silencing by miRNA	0.004
	GO:0071407	cellular response to organic cyclic comp...	0.004
	GO:0044249	cellular biosynthetic process	0.004
	GO:0051094	positive regulation of developmental pro...	0.004
	GO:0035196	production of miRNAs involved in gene si...	0.005
	GO:0048284	organelle fusion	0.005
	GO:0090502	RNA phosphodiester bond hydrolysis, endo...	0.005
	GO:0006405	RNA export from nucleus	0.005
	GO:0072528	pyrimidine-containing compound biosynthe...	0.005
	GO:0048232	male gamete generation	0.005
	GO:0000460	maturation of 5.8S rRNA	0.005
	GO:0009126	purine nucleoside monophosphate metaboli...	0.006
	GO:0009167	purine ribonucleoside monophosphate meta...	0.006
	GO:0010639	negative regulation of organelle organiz...	0.006
	GO:0043624	cellular protein complex disassembly	0.006
	GO:0051172	negative regulation of nitrogen compound...	0.006
	GO:0030154	cell differentiation	0.006
	GO:0006406	mRNA export from nucleus	0.006
	GO:0071427	mRNA-containing ribonucleoprotein comple...	0.006
	GO:0043038	amino acid activation	0.007
	GO:0043039	tRNA aminoacylation	0.007
	GO:0044772	mitotic cell cycle phase transition	0.007
	GO:0006403	RNA localization	0.007
	GO:0031167	rRNA methylation	0.007
	GO:0009893	positive regulation of metabolic process	0.007
	GO:0000466	maturation of 5.8S rRNA from tricistroni...	0.007
	GO:0048437	floral organ development	0.007
	GO:0006284	base-excision repair	0.007

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GO type	GO ID	Description	Adj. p-value
	GO:0019953	sexual reproduction	0.007
	GO:0015980	energy derivation by oxidation of organi...	0.007
	GO:0050657	nucleic acid transport	0.007
	GO:0050658	RNA transport	0.007
	GO:0051236	establishment of RNA localization	0.007
	GO:0009156	ribonucleoside monophosphate biosyntheti...	0.007
	GO:0006289	nucleotide-excision repair	0.008
	GO:0009117	nucleotide metabolic process	0.008
	GO:0031497	chromatin assembly	0.008
	GO:0009124	nucleoside monophosphate biosynthetic pr...	0.008
	GO:0031056	regulation of histone modification	0.008
	GO:0017148	negative regulation of translation	0.008
	GO:0009845	seed germination	0.008
	GO:0009438	methylglyoxal metabolic process	0.008
	GO:0042182	ketone catabolic process	0.008
	GO:0051596	methylglyoxal catabolic process	0.008
	GO:0034728	nucleosome organization	0.009
	GO:0045037	protein import into chloroplast stroma	0.009
	GO:0071166	ribonucleoprotein complex localization	0.009
	GO:0071426	ribonucleoprotein complex export from nu...	0.009
	GO:0090351	seedling development	0.009
	GO:0033365	protein localization to organelle	0.009
	GO:0048868	pollen tube development	0.010
	GO:0006753	nucleoside phosphate metabolic process	0.010
	GO:0010332	response to gamma radiation	0.010
	GO:0048523	negative regulation of cellular process	0.010
	GO:0006376	mRNA splice site selection	0.010
	GO:0031324	negative regulation of cellular metaboli...	0.010
	GO:0048582	positive regulation of post-embryonic de...	0.010
	GO:0006333	chromatin assembly or disassembly	0.011
	GO:0006418	tRNA aminoacylation for protein translat...	0.011
	GO:0045036	protein targeting to chloroplast	0.011
	GO:0072596	establishment of protein localization to...	0.011
	GO:0048522	positive regulation of cellular process	0.012
	GO:0051240	positive regulation of multicellular org...	0.012
	GO:0016192	vesicle-mediated transport	0.012
	GO:0051253	negative regulation of RNA metabolic pro...	0.012
	GO:0034249	negative regulation of cellular amide me...	0.012
	GO:0010604	positive regulation of macromolecule met...	0.012
	GO:0006334	nucleosome assembly	0.013
	GO:0006366	transcription by RNA polymerase II	0.013
	GO:0009860	pollen tube growth	0.013
	GO:0009165	nucleotide biosynthetic process	0.013
	GO:2000242	negative regulation of reproductive proc...	0.015
	GO:1901293	nucleoside phosphate biosynthetic proces...	0.015
	GO:0044260	cellular macromolecule metabolic process	0.015
	GO:0000027	ribosomal large subunit assembly	0.015
	GO:0010073	meristem maintenance	0.016
	GO:0007292	female gamete generation	0.016

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GO type	GO ID	Description	Adj. p-value
	GO:0006415	translational termination	0.017
	GO:0016074	snoRNA metabolic process	0.017
	GO:0016973	poly(A)+ mRNA export from nucleus	0.017
	GO:0043144	snoRNA processing	0.017
	GO:0005983	starch catabolic process	0.017
	GO:0031503	protein-containing complex localization	0.017
	GO:0072598	protein localization to chloroplast	0.018
	GO:0006271	DNA strand elongation involved in DNA re...	0.018
	GO:0022616	DNA strand elongation	0.018
	GO:0048438	floral whorl development	0.018
	GO:0043543	protein acylation	0.019
	GO:2001251	negative regulation of chromosome organi...	0.019
	GO:0006221	pyrimidine nucleotide biosynthetic proce...	0.019
	GO:0000478	endonucleolytic cleavage involved in rRN...	0.019
	GO:0006089	lactate metabolic process	0.019
	GO:0006273	lagging strand elongation	0.019
	GO:0019243	methylglyoxal catabolic process to D-lac...	0.019
	GO:0051129	negative regulation of cellular componen...	0.019
	GO:0061727	methylglyoxal catabolic process to lacta...	0.019
	GO:0006338	chromatin remodeling	0.019
	GO:0072594	establishment of protein localization to...	0.019
	GO:1902679	negative regulation of RNA biosynthetic ...	0.019
	GO:1903507	negative regulation of nucleic acid-temp...	0.019
	GO:1905268	negative regulation of chromatin organiz...	0.019
	GO:0006473	protein acetylation	0.019
	GO:0044703	multi-organism reproductive process	0.020
	GO:0051028	mRNA transport	0.020
	GO:0032268	regulation of cellular protein metabolic...	0.020
	GO:0140014	mitotic nuclear division	0.020
	GO:0051246	regulation of protein metabolic process	0.021
	GO:0009259	ribonucleotide metabolic process	0.021
	GO:0009911	positive regulation of flower developmen...	0.022
	GO:0048581	negative regulation of post-embryonic de...	0.024
	GO:0051304	chromosome separation	0.024
	GO:0019252	starch biosynthetic process	0.024
	GO:0019693	ribose phosphate metabolic process	0.024
	GO:0032784	regulation of DNA-templated transcriptio...	0.024
	GO:0000904	cell morphogenesis involved in different...	0.025
	GO:0006913	nucleocytoplasmic transport	0.026
	GO:0032270	positive regulation of cellular protein ...	0.026
	GO:0051169	nuclear transport	0.026
	GO:0051247	positive regulation of protein metabolic...	0.026
	GO:0009218	pyrimidine ribonucleotide metabolic proc...	0.027
	GO:0009220	pyrimidine ribonucleotide biosynthetic p...	0.027
	GO:0006413	translational initiation	0.028
	GO:0006075	(1-¿3)-beta-D-glucan biosynthetic proces...	0.028
	GO:0009629	response to gravity	0.028
	GO:0070828	heterochromatin organization	0.028
	GO:0060627	regulation of vesicle-mediated transport	0.028

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0140053	mitochondrial gene expression	0.028
	GO:0071214	cellular response to abiotic stimulus	0.028
	GO:0104004	cellular response to environmental stimu...	0.028
	GO:0042023	DNA endoreduplication	0.029
	GO:0048825	cotyledon development	0.029
	GO:0009127	purine nucleoside monophosphate biosynth...	0.029
	GO:0009168	purine ribonucleoside monophosphate bios...	0.029
	GO:0006220	pyrimidine nucleotide metabolic process	0.030
	GO:0051053	negative regulation of DNA metabolic pro...	0.031
	GO:0048444	floral organ morphogenesis	0.031
	GO:0007140	male meiotic nuclear division	0.031
	GO:0009910	negative regulation of flower developmen...	0.032
	GO:0009642	response to light intensity	0.033
	GO:1900140	regulation of seedling development	0.034
	GO:0042542	response to hydrogen peroxide	0.034
	GO:0006605	protein targeting	0.036
	GO:0017038	protein import	0.037
	GO:0009416	response to light stimulus	0.037
	GO:0006775	fat-soluble vitamin metabolic process	0.039
	GO:0010189	vitamin E biosynthetic process	0.039
	GO:0042360	vitamin E metabolic process	0.039
	GO:0042362	fat-soluble vitamin biosynthetic process	0.039
	GO:0009743	response to carbohydrate	0.040
	GO:0071482	cellular response to light stimulus	0.040
	GO:0000075	cell cycle checkpoint	0.041
	GO:0000302	response to reactive oxygen species	0.041
	GO:0006207	'de novo' pyrimidine nucleobase biosynth...	0.041
	GO:0008360	regulation of cell shape	0.041
	GO:0031338	regulation of vesicle fusion	0.041
	GO:0051640	organelle localization	0.041
	GO:0006188	IMP biosynthetic process	0.042
	GO:0017004	cytochrome complex assembly	0.042
	GO:0009615	response to virus	0.043
	GO:0042180	cellular ketone metabolic process	0.044
	GO:0010030	positive regulation of seed germination	0.045
	GO:0072527	pyrimidine-containing compound metabolic...	0.046
	GO:0051307	meiotic chromosome separation	0.047
	GO:0090174	organelle membrane fusion	0.048
	GO:0048440	carpel development	0.048
	GO:0009260	ribonucleotide biosynthetic process	0.048
	GO:0046390	ribose phosphate biosynthetic process	0.048
	GO:0009630	gravitropism	0.049
	GO:0046132	pyrimidine ribonucleoside biosynthetic p...	0.051
	GO:0046134	pyrimidine nucleoside biosynthetic proce...	0.051
	GO:0051241	negative regulation of multicellular org...	0.052
	GO:0035670	plant-type ovary development	0.052
	GO:0048481	plant ovule development	0.052
	GO:0031325	positive regulation of cellular metaboli...	0.052
	GO:0006357	regulation of transcription by RNA polym...	0.053

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GO type	GO ID	Description	Adj. p-value
	GO:0006950	response to stress	0.055
	GO:0034614	cellular response to reactive oxygen spe...	0.055
	GO:0048507	meristem development	0.057
	GO:0010029	regulation of seed germination	0.057
	GO:0009060	aerobic respiration	0.057
	GO:0022406	membrane docking	0.058
	GO:0046040	IMP metabolic process	0.058
	GO:0140056	organelle localization by membrane tethe...	0.058
	GO:0051716	cellular response to stimulus	0.058
	GO:0006906	vesicle fusion	0.059
	GO:0006352	DNA-templated transcription, initiation	0.062
	GO:0043632	modification-dependent macromolecule cat...	0.063
	GO:0009555	pollen development	0.063
	GO:0043647	inositol phosphate metabolic process	0.064
	GO:0045787	positive regulation of cell cycle	0.064
	GO:0007267	cell-cell signaling	0.065
	GO:0048468	cell development	0.065
	GO:2001020	regulation of response to DNA damage sti...	0.066
	GO:0048598	embryonic morphogenesis	0.066
	GO:0008283	cell proliferation	0.068
	GO:0044003	modification by symbiont of host morphol...	0.068
	GO:0007093	mitotic cell cycle checkpoint	0.069
	GO:0048278	vesicle docking	0.072
	GO:0006354	DNA-templated transcription, elongation	0.073
	GO:0048467	gynoecium development	0.078
	GO:0000959	mitochondrial RNA metabolic process	0.082
	GO:0015931	nucleobase-containing compound transport	0.083
	GO:0051817	modification of morphology or physiology...	0.083
	GO:0070816	phosphorylation of RNA polymerase II C-t...	0.085
	GO:0006904	vesicle docking involved in exocytosis	0.086
	GO:0032543	mitochondrial translation	0.086
	GO:0140029	exocytic process	0.086
	GO:0006383	transcription by RNA polymerase III	0.086
	GO:0009932	cell tip growth	0.088
	GO:0090626	plant epidermis morphogenesis	0.088
	GO:0009129	pyrimidine nucleoside monophosphate meta...	0.091
	GO:0009130	pyrimidine nucleoside monophosphate bios...	0.091
	GO:0010948	negative regulation of cell cycle proces...	0.091
	GO:0042127	regulation of cell proliferation	0.092
	GO:0035265	organ growth	0.092
	GO:0065002	intracellular protein transmembrane tran...	0.092
	GO:0051173	positive regulation of nitrogen compound...	0.093
	GO:0019856	pyrimidine nucleobase biosynthetic proce...	0.093
	GO:0030036	actin cytoskeleton organization	0.093
	GO:0043254	regulation of protein complex assembly	0.093
	GO:0009904	chloroplast accumulation movement	0.093
	GO:0009163	nucleoside biosynthetic process	0.093
	GO:0042455	ribonucleoside biosynthetic process	0.093
	GO:0071806	protein transmembrane transport	0.094

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0045737	positive regulation of cyclin-dependent ...	0.097
	GO:0090329	regulation of DNA-dependent DNA replicat...	0.097
	GO:0033108	mitochondrial respiratory chain complex ...	0.099
CC	GO:1902494	catalytic complex	0.000
	GO:0005634	nucleus	0.000
	GO:0044427	chromosomal part	0.000
	GO:1990904	ribonucleoprotein complex	0.000
	GO:1990234	transferase complex	0.000
	GO:0000228	nuclear chromosome	0.000
	GO:0044454	nuclear chromosome part	0.000
	GO:0005654	nucleoplasm	0.000
	GO:0009526	plastid envelope	0.000
	GO:0009579	thylakoid	0.000
	GO:0061695	transferase complex, transferring phosph...	0.000
	GO:0000785	chromatin	0.000
	GO:0000151	ubiquitin ligase complex	0.000
	GO:0031461	cullin-RING ubiquitin ligase complex	0.000
	GO:0016604	nuclear body	0.000
	GO:0000428	DNA-directed RNA polymerase complex	0.000
	GO:0030880	RNA polymerase complex	0.000
	GO:0000793	condensed chromosome	0.000
	GO:0055029	nuclear DNA-directed RNA polymerase comp...	0.001
	GO:0042646	plastid nucleoid	0.001
	GO:0005657	replication fork	0.001
	GO:0005663	DNA replication factor C complex	0.001
	GO:0000229	cytoplasmic chromosome	0.001
	GO:0009528	plastid inner membrane	0.001
	GO:0000123	histone acetyltransferase complex	0.001
	GO:0000790	nuclear chromatin	0.002
	GO:0009295	nucleoid	0.002
	GO:0005684	U2-type spliceosomal complex	0.002
	GO:0009706	chloroplast inner membrane	0.003
	GO:0009508	plastid chromosome	0.003
	GO:0030532	small nuclear ribonucleoprotein complex	0.004
	GO:0097525	spliceosomal snRNP complex	0.004
	GO:0120114	Sm-like protein family complex	0.004
	GO:0009707	chloroplast outer membrane	0.004
	GO:0031984	organelle subcompartment	0.004
	GO:0071010	prespliceosome	0.005
	GO:0009524	phragmoplast	0.005
	GO:0016607	nuclear speck	0.007
	GO:0009527	plastid outer membrane	0.008
	GO:0031248	protein acetyltransferase complex	0.009
	GO:1902493	acetyltransferase complex	0.009
	GO:0005643	nuclear pore	0.012
	GO:0071004	U2-type prespliceosome	0.016
	GO:0030687	preribosome, large subunit precursor	0.020
	GO:0019867	outer membrane	0.021
	GO:0031977	thylakoid lumen	0.021

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0000148	1,3-beta-D-glucan synthase complex	0.023
	GO:0031968	organelle outer membrane	0.025
	GO:0000313	organellar ribosome	0.038
	GO:0015030	Cajal body	0.042
	GO:0098805	whole membrane	0.050
	GO:0005761	mitochondrial ribosome	0.056
	GO:0005666	DNA-directed RNA polymerase III complex	0.057
	GO:0042644	chloroplast nucleoid	0.060
MF	GO:0140098	catalytic activity, acting on RNA	0.000
	GO:0003676	nucleic acid binding	0.000
	GO:0004386	helicase activity	0.000
	GO:0008094	DNA-dependent ATPase activity	0.000
	GO:0008173	RNA methyltransferase activity	0.000
	GO:0003724	RNA helicase activity	0.000
	GO:0003678	DNA helicase activity	0.000
	GO:0008170	N-methyltransferase activity	0.000
	GO:0008276	protein methyltransferase activity	0.000
	GO:0004519	endonuclease activity	0.000
	GO:0042054	histone methyltransferase activity	0.000
	GO:0016278	lysine N-methyltransferase activity	0.000
	GO:0016279	protein-lysine N-methyltransferase activ...	0.000
	GO:0019783	ubiquitin-like protein-specific protease...	0.001
	GO:0044877	protein-containing complex binding	0.001
	GO:0051082	unfolded protein binding	0.001
	GO:0003899	DNA-directed 5'-3' RNA polymerase activi...	0.002
	GO:0016866	intramolecular transferase activity	0.002
	GO:0019843	rRNA binding	0.003
	GO:0003689	DNA clamp loader activity	0.003
	GO:0033170	protein-DNA loading ATPase activity	0.003
	GO:0036459	thiol-dependent ubiquitinyl hydrolase ac...	0.003
	GO:0101005	ubiquitinyl hydrolase activity	0.003
	GO:0016423	tRNA (guanine) methyltransferase activit...	0.003
	GO:0016893	endonuclease activity, active with eithe...	0.004
	GO:0016853	isomerase activity	0.004
	GO:0004527	exonuclease activity	0.004
	GO:0043021	ribonucleoprotein complex binding	0.004
	GO:0004536	deoxyribonuclease activity	0.005
	GO:0003690	double-stranded DNA binding	0.006
	GO:0003684	damaged DNA binding	0.006
	GO:0016796	exonuclease activity, active with either...	0.008
	GO:0016891	endoribonuclease activity, producing 5'-...	0.008
	GO:0030983	mismatched DNA binding	0.008
	GO:0036094	small molecule binding	0.008
	GO:0008135	translation factor activity, RNA binding	0.009
	GO:0008649	rRNA methyltransferase activity	0.009
	GO:0140102	catalytic activity, acting on a rRNA	0.009
	GO:0008175	tRNA methyltransferase activity	0.009
	GO:0043621	protein self-association	0.011
	GO:0003924	GTPase activity	0.011

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0008408	3’-5’ exonuclease activity	0.011
	GO:0004540	ribonuclease activity	0.014
	GO:0000166	nucleotide binding	0.020
	GO:1901265	nucleoside phosphate binding	0.020
	GO:0005527	macrolide binding	0.021
	GO:0005528	FK506 binding	0.021
	GO:0003729	mRNA binding	0.021
	GO:0016874	ligase activity	0.023
	GO:0003713	transcription coactivator activity	0.025
	GO:0051087	chaperone binding	0.025
	GO:1901363	heterocyclic compound binding	0.025
	GO:0097159	organic cyclic compound binding	0.026
	GO:0004520	endodeoxyribonuclease activity	0.029
	GO:0004812	aminoacyl-tRNA ligase activity	0.029
	GO:0016875	ligase activity, forming carbon-oxygen b...	0.029
	GO:0004521	endoribonuclease activity	0.033
	GO:0042162	telomeric DNA binding	0.034
	GO:0051536	iron-sulfur cluster binding	0.037
	GO:0051540	metal cluster binding	0.037
	GO:0008138	protein tyrosine/serine/threonine phosph...	0.037
	GO:0016884	carbon-nitrogen ligase activity, with gl...	0.039
	GO:0004529	exodeoxyribonuclease activity	0.042
	GO:0016895	exodeoxyribonuclease activity, producing...	0.042
	GO:0004549	tRNA-specific ribonuclease activity	0.043
	GO:0004526	ribonuclease P activity	0.045
	GO:0042803	protein homodimerization activity	0.045
	GO:0003843	1,3-beta-D-glucan synthase activity	0.048
	GO:0017069	snRNA binding	0.061
	GO:0060589	nucleoside-triphosphatase regulator acti...	0.064
	GO:0016774	phosphotransferase activity, carboxyl gr...	0.078
	GO:0030695	GTPase regulator activity	0.086
	GO:0004402	histone acetyltransferase activity	0.096
	GO:0061733	peptide-lysine-N-acetyltransferase activ...	0.096
	GO:0003697	single-stranded DNA binding	0.098

4.3.2 Root - Preflowering - Cluster 2

GO type	GO ID	Description	Adj. p-value
BP	GO:0009404	toxin metabolic process	0.000
	GO:0055085	transmembrane transport	0.000
	GO:0009753	response to jasmonic acid	0.000
	GO:0098754	detoxification	0.000
	GO:0009636	response to toxic substance	0.001
	GO:0042430	indole-containing compound metabolic pro...	0.001
	GO:0009072	aromatic amino acid family metabolic pro...	0.002
	GO:0003333	amino acid transmembrane transport	0.002
	GO:0010243	response to organonitrogen compound	0.004
	GO:0008645	hexose transmembrane transport	0.004
	GO:0015749	monosaccharide transmembrane transport	0.004
	GO:0051346	negative regulation of hydrolase activit...	0.004
	GO:0043412	macromolecule modification	0.004
	GO:0006040	amino sugar metabolic process	0.005
	GO:0006575	cellular modified amino acid metabolic p...	0.005
	GO:1904659	glucose transmembrane transport	0.006
	GO:0006820	anion transport	0.007
	GO:0009312	oligosaccharide biosynthetic process	0.007
	GO:0098542	defense response to other organism	0.007
	GO:0001666	response to hypoxia	0.007
	GO:0009607	response to biotic stimulus	0.007
	GO:0043086	negative regulation of catalytic activit...	0.008
	GO:0009627	systemic acquired resistance	0.008
	GO:0071229	cellular response to acid chemical	0.008
	GO:0009308	amine metabolic process	0.008
	GO:0046323	glucose import	0.008
	GO:0009073	aromatic amino acid family biosynthetic ...	0.009
	GO:0044092	negative regulation of molecular functio...	0.009
	GO:1905039	carboxylic acid transmembrane transport	0.009
	GO:0006568	tryptophan metabolic process	0.009
	GO:0006586	indolalkylamine metabolic process	0.009
	GO:0046351	disaccharide biosynthetic process	0.009
	GO:0009751	response to salicylic acid	0.010
	GO:0046942	carboxylic acid transport	0.011
	GO:1901136	carbohydrate derivative catabolic proces...	0.013
	GO:0070482	response to oxygen levels	0.015
	GO:0009593	detection of chemical stimulus	0.015
	GO:0051704	multi-organism process	0.015
	GO:0043207	response to external biotic stimulus	0.016
	GO:0051707	response to other organism	0.016
	GO:0009862	systemic acquired resistance, salicylic ...	0.018
	GO:1903825	organic acid transmembrane transport	0.019
	GO:0098656	anion transmembrane transport	0.022
	GO:0015849	organic acid transport	0.022
	GO:0036293	response to decreased oxygen levels	0.023
	GO:0042537	benzene-containing compound metabolic pr...	0.025

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0000162	tryptophan biosynthetic process	0.026
	GO:0016143	S-glycoside metabolic process	0.026
	GO:0019757	glycosinolate metabolic process	0.026
	GO:0019760	glucosinolate metabolic process	0.026
	GO:0042435	indole-containing compound biosynthetic ...	0.026
	GO:0046219	indolalkylamine biosynthetic process	0.026
	GO:0030162	regulation of proteolysis	0.027
	GO:0009309	amine biosynthetic process	0.031
	GO:0042401	cellular biogenic amine biosynthetic pro...	0.031
	GO:0042445	hormone metabolic process	0.034
	GO:1902022	L-lysine transport	0.034
	GO:1903401	L-lysine transmembrane transport	0.034
	GO:0017001	antibiotic catabolic process	0.034
	GO:0009856	pollination	0.037
	GO:0044706	multi-multicellular organism process	0.037
	GO:0009056	catabolic process	0.038
	GO:0009698	phenylpropanoid metabolic process	0.038
	GO:0042447	hormone catabolic process	0.039
	GO:0044248	cellular catabolic process	0.047
	GO:0034219	carbohydrate transmembrane transport	0.048
	GO:0006790	sulfur compound metabolic process	0.055
	GO:0043666	regulation of phosphoprotein phosphatase...	0.076
	GO:0006465	signal peptide processing	0.080
	GO:0015706	nitrate transport	0.080
	GO:0051187	cofactor catabolic process	0.080
	GO:0042744	hydrogen peroxide catabolic process	0.084
	GO:0080163	regulation of protein serine/threonine p...	0.084
CC	GO:0071944	cell periphery	0.000
	GO:0000323	lytic vacuole	0.000
	GO:0031226	intrinsic component of plasma membrane	0.004
	GO:0044421	extracellular region part	0.004
	GO:0044459	plasma membrane part	0.030
	GO:0046906	tetrapyrrole binding	0.000
	GO:0016705	oxidoreductase activity, acting on paire...	0.000
	GO:0022857	transmembrane transporter activity	0.000
	GO:0005215	transporter activity	0.000
	GO:0030414	peptidase inhibitor activity	0.000
	GO:0061134	peptidase regulator activity	0.000
	GO:0015291	secondary active transmembrane transport...	0.000
	GO:0022804	active transmembrane transporter activit...	0.000
	GO:0043565	sequence-specific DNA binding	0.000
	GO:0015149	hexose transmembrane transporter activit...	0.001
	GO:0015171	amino acid transmembrane transporter act...	0.001
	GO:0015145	monosaccharide transmembrane transporter...	0.001
	GO:0016829	lyase activity	0.002
	GO:0005355	glucose transmembrane transporter activi...	0.002
	GO:0004190	aspartic-type endopeptidase activity	0.002
	GO:0070001	aspartic-type peptidase activity	0.002
	GO:0015075	ion transmembrane transporter activity	0.002

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GO type	GO ID	Description	Adj. p-value
	GO:0008194	UDP-glycosyltransferase activity	0.003
	GO:0001067	regulatory region nucleic acid binding	0.003
	GO:0044212	transcription regulatory region DNA bind...	0.003
	GO:0046527	glucosyltransferase activity	0.003
	GO:0016765	transferase activity, transferring alkyl...	0.003
	GO:0015295	solute:proton symporter activity	0.004
	GO:0005351	carbohydrate:proton symporter activity	0.004
	GO:0005402	carbohydrate:cation symporter activity	0.004
	GO:0051119	sugar transmembrane transporter activity	0.004
	GO:0015172	acidic amino acid transmembrane transpor...	0.005
	GO:0016682	oxidoreductase activity, acting on diphe...	0.005
	GO:0015318	inorganic molecular entity transmembrane...	0.010
	GO:0015293	symporter activity	0.011
	GO:0015181	arginine transmembrane transporter activ...	0.013
	GO:0015189	L-lysine transmembrane transporter activ...	0.013
	GO:0001046	core promoter sequence-specific DNA bind...	0.014
	GO:0003959	NADPH dehydrogenase activity	0.014
	GO:0015294	solute:cation symporter activity	0.014
	GO:0016863	intramolecular oxidoreductase activity, ...	0.020
	GO:0046943	carboxylic acid transmembrane transporte...	0.022
	GO:0001047	core promoter binding	0.023
	GO:0042562	hormone binding	0.024
	GO:0016679	oxidoreductase activity, acting on diphe...	0.025
	GO:0004864	protein phosphatase inhibitor activity	0.029
	GO:0019212	phosphatase inhibitor activity	0.029
	GO:0016841	ammonia-lyase activity	0.031
	GO:0008233	peptidase activity	0.032
	GO:0036094	small molecule binding	0.033
	GO:0016838	carbon-oxygen lyase activity, acting on ...	0.034
	GO:0005342	organic acid transmembrane transporter a...	0.038
	GO:0015174	basic amino acid transmembrane transport...	0.042
	GO:0001228	transcriptional activator activity, RNA ...	0.046
	GO:0015297	antiporter activity	0.047
	GO:0070008	serine-type exopeptidase activity	0.048
	GO:0019208	phosphatase regulator activity	0.049
	GO:0019888	protein phosphatase regulator activity	0.049
	GO:0070011	peptidase activity, acting on L-amino ac...	0.050
	GO:0008324	cation transmembrane transporter activit...	0.053
	GO:0015144	carbohydrate transmembrane transporter a...	0.053
	GO:0016746	transferase activity, transferring acyl ...	0.054
	GO:0005326	neurotransmitter transporter activity	0.057
	GO:0000166	nucleotide binding	0.060
	GO:1901265	nucleoside phosphate binding	0.060
	GO:0000981	RNA polymerase II transcription factor a...	0.061
	GO:0008483	transaminase activity	0.065
	GO:0008514	organic anion transmembrane transporter ...	0.065
	GO:0016769	transferase activity, transferring nitro...	0.065
	GO:0052716	hydroquinone:oxygen oxidoreductase activ...	0.065
	GO:0004871	signal transducer activity	0.075

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GO type	GO ID	Description	Adj. p-value
	GO:0004185	serine-type carboxypeptidase activity	0.081
	GO:0005385	zinc ion transmembrane transporter activ...	0.081
	GO:0008509	anion transmembrane transporter activity	0.081
	GO:0019840	isoprenoid binding	0.090
	GO:0016758	transferase activity, transferring hexos...	0.092
	GO:0046915	transition metal ion transmembrane trans...	0.092
	GO:0030594	neurotransmitter receptor activity	0.094

4.3.3 Root - Preflowering - Cluster 3

GO type	GO ID	Description	Adj. p-value
	GO:0010383	cell wall polysaccharide metabolic proce...	0.000
	GO:0044262	cellular carbohydrate metabolic process	0.000
	GO:0007017	microtubule-based process	0.000
	GO:0097237	cellular response to toxic substance	0.000
	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0072330	monocarboxylic acid biosynthetic process	0.000
	GO:0000902	cell morphogenesis	0.000
	GO:0007010	cytoskeleton organization	0.000
	GO:0006754	ATP biosynthetic process	0.000
	GO:0016049	cell growth	0.000
	GO:0030243	cellulose metabolic process	0.000
	GO:1902600	proton transmembrane transport	0.000
	GO:0051273	beta-glucan metabolic process	0.000
	GO:0046434	organophosphate catabolic process	0.000
	GO:0070592	cell wall polysaccharide biosynthetic pr...	0.000
	GO:0009699	phenylpropanoid biosynthetic process	0.000
	GO:0019318	hexose metabolic process	0.000
	GO:1903047	mitotic cell cycle process	0.000
	GO:0000281	mitotic cytokinesis	0.000
	GO:0016053	organic acid biosynthetic process	0.000
	GO:0046394	carboxylic acid biosynthetic process	0.000
	GO:0006631	fatty acid metabolic process	0.000
	GO:0046496	nicotinamide nucleotide metabolic proces...	0.000
	GO:0000910	cytokinesis	0.000
	GO:0019362	pyridine nucleotide metabolic process	0.000
	GO:0009826	unidimensional cell growth	0.000
	GO:0006733	oxidoreduction coenzyme metabolic proces...	0.000
	GO:0044283	small molecule biosynthetic process	0.000
	GO:0048468	cell development	0.000
	GO:0090558	plant epidermis development	0.000
	GO:0045492	xylan biosynthetic process	0.000
	GO:0048868	pollen tube development	0.000
	GO:0051301	cell division	0.000
	GO:0006633	fatty acid biosynthetic process	0.000
	GO:0044247	cellular polysaccharide catabolic proces...	0.000
	GO:0006979	response to oxidative stress	0.000
	GO:0097435	supramolecular fiber organization	0.000
	GO:0000904	cell morphogenesis involved in different...	0.000
	GO:0048193	Golgi vesicle transport	0.001
	GO:0008154	actin polymerization or depolymerization	0.001
	GO:0019748	secondary metabolic process	0.001
	GO:0072525	pyridine-containing compound biosyntheti...	0.001
	GO:0006090	pyruvate metabolic process	0.001
	GO:0009225	nucleotide-sugar metabolic process	0.001
	GO:0006884	cell volume homeostasis	0.002
	GO:0009992	cellular water homeostasis	0.002

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0010103	stomatal complex morphogenesis	0.002
	GO:0015793	glycerol transport	0.002
	GO:0051186	cofactor metabolic process	0.002
	GO:0098660	inorganic ion transmembrane transport	0.002
	GO:0006833	water transport	0.002
	GO:0042044	fluid transport	0.002
	GO:0009251	glucan catabolic process	0.002
	GO:0008064	regulation of actin polymerization or de...	0.003
	GO:0030832	regulation of actin filament length	0.003
	GO:0032956	regulation of actin cytoskeleton organiz...	0.003
	GO:0032970	regulation of actin filament-based proce...	0.003
	GO:0110053	regulation of actin filament organizatio...	0.003
	GO:0090627	plant epidermal cell differentiation	0.003
	GO:0006119	oxidative phosphorylation	0.003
	GO:0042773	ATP synthesis coupled electron transport	0.003
	GO:0071840	cellular component organization or bioge...	0.003
	GO:0048856	anatomical structure development	0.003
	GO:0048588	developmental cell growth	0.003
	GO:0006101	citrate metabolic process	0.003
	GO:0007015	actin filament organization	0.003
	GO:0015791	polyol transport	0.003
	GO:0098662	inorganic cation transmembrane transport	0.003
	GO:0030029	actin filament-based process	0.003
	GO:0030245	cellulose catabolic process	0.003
	GO:0030258	lipid modification	0.003
	GO:0034404	nucleobase-containing small molecule bio...	0.003
	GO:0006732	coenzyme metabolic process	0.003
	GO:0044550	secondary metabolite biosynthetic proces...	0.003
	GO:0010374	stomatal complex development	0.004
	GO:0010052	guard cell differentiation	0.004
	GO:0051493	regulation of cytoskeleton organization	0.004
	GO:0022603	regulation of anatomical structure morph...	0.004
	GO:0030036	actin cytoskeleton organization	0.004
	GO:0042545	cell wall modification	0.004
	GO:0080147	root hair cell development	0.005
	GO:0051235	maintenance of location	0.005
	GO:0051258	protein polymerization	0.005
	GO:0030041	actin filament polymerization	0.005
	GO:0030833	regulation of actin filament polymerizat...	0.005
	GO:0051275	beta-glucan catabolic process	0.005
	GO:0044255	cellular lipid metabolic process	0.005
	GO:0009808	lignin metabolic process	0.006
	GO:0042775	mitochondrial ATP synthesis coupled elec...	0.006
	GO:0034220	ion transmembrane transport	0.007
	GO:0000226	microtubule cytoskeleton organization	0.007
	GO:0008361	regulation of cell size	0.007
	GO:0090407	organophosphate biosynthetic process	0.007
	GO:0022904	respiratory electron transport chain	0.008
	GO:0030154	cell differentiation	0.008

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0035556	intracellular signal transduction	0.008
	GO:0022604	regulation of cell morphogenesis	0.008
	GO:0006099	tricarboxylic acid cycle	0.008
	GO:0007049	cell cycle	0.008
	GO:1902903	regulation of supramolecular fiber organ...	0.008
	GO:1903338	regulation of cell wall organization or ...	0.009
	GO:0009060	aerobic respiration	0.009
	GO:0048469	cell maturation	0.009
	GO:0048764	trichoblast maturation	0.009
	GO:0048765	root hair cell differentiation	0.009
	GO:0022622	root system development	0.011
	GO:0048767	root hair elongation	0.011
	GO:0018105	peptidyl-serine phosphorylation	0.011
	GO:0010413	glucuronoxylan metabolic process	0.011
	GO:0010417	glucuronoxylan biosynthetic process	0.011
	GO:0006270	DNA replication initiation	0.011
	GO:0010191	mucilage metabolic process	0.012
	GO:0005984	disaccharide metabolic process	0.012
	GO:0065008	regulation of biological quality	0.012
	GO:0015980	energy derivation by oxidation of organi...	0.012
	GO:0010054	trichoblast differentiation	0.013
	GO:0010026	trichome differentiation	0.013
	GO:0032502	developmental process	0.013
	GO:0048278	vesicle docking	0.013
	GO:0010215	cellulose microfibril organization	0.013
	GO:0019321	pentose metabolic process	0.014
	GO:0019752	carboxylic acid metabolic process	0.014
	GO:0016042	lipid catabolic process	0.014
	GO:0006891	intra-Golgi vesicle-mediated transport	0.014
	GO:0052546	cell wall pectin metabolic process	0.014
	GO:0048364	root development	0.014
	GO:2000652	regulation of secondary cell wall biogen...	0.014
	GO:0009250	glucan biosynthetic process	0.017
	GO:0008643	carbohydrate transport	0.017
	GO:0006644	phospholipid metabolic process	0.017
	GO:0018209	peptidyl-serine modification	0.017
	GO:0051510	regulation of unidimensional cell growth	0.017
	GO:0046470	phosphatidylcholine metabolic process	0.018
	GO:0046854	phosphatidylinositol phosphorylation	0.018
	GO:0009934	regulation of meristem structural organi...	0.018
	GO:0044703	multi-organism reproductive process	0.018
	GO:0010214	seed coat development	0.019
	GO:0032271	regulation of protein polymerization	0.019
	GO:0009108	coenzyme biosynthetic process	0.020
	GO:0006006	glucose metabolic process	0.021
	GO:0009932	cell tip growth	0.021
	GO:0022406	membrane docking	0.021
	GO:0140056	organelle localization by membrane tethe...	0.021
	GO:0008610	lipid biosynthetic process	0.022

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0009056	catabolic process	0.022
	GO:0010192	mucilage biosynthetic process	0.023
	GO:0051129	negative regulation of cellular componen...	0.023
	GO:0006811	ion transport	0.023
	GO:0043436	oxoacid metabolic process	0.025
	GO:0009395	phospholipid catabolic process	0.025
	GO:0006082	organic acid metabolic process	0.025
	GO:0019953	sexual reproduction	0.026
	GO:0046486	glycerolipid metabolic process	0.027
	GO:0070726	cell wall assembly	0.027
	GO:0071668	plant-type cell wall assembly	0.027
	GO:0043647	inositol phosphate metabolic process	0.027
	GO:0009860	pollen tube growth	0.028
	GO:0006812	cation transport	0.030
	GO:0015850	organic hydroxy compound transport	0.030
	GO:0006650	glycerophospholipid metabolic process	0.030
	GO:0071470	cellular response to osmotic stress	0.030
	GO:1901615	organic hydroxy compound metabolic proce...	0.030
	GO:0072350	tricarboxylic acid metabolic process	0.031
	GO:0031407	oxylipin metabolic process	0.032
	GO:0070887	cellular response to chemical stimulus	0.032
	GO:0010053	root epidermal cell differentiation	0.032
	GO:0010256	endomembrane system organization	0.033
	GO:0009555	pollen development	0.038
	GO:0019751	polyol metabolic process	0.038
	GO:0009100	glycoprotein metabolic process	0.038
	GO:0055082	cellular chemical homeostasis	0.038
	GO:0009226	nucleotide-sugar biosynthetic process	0.039
	GO:0044770	cell cycle phase transition	0.039
	GO:0010090	trichome morphogenesis	0.040
	GO:0007030	Golgi organization	0.040
	GO:0090698	post-embryonic plant morphogenesis	0.040
	GO:0010345	suberin biosynthetic process	0.040
	GO:0046834	lipid phosphorylation	0.042
	GO:0019566	arabinose metabolic process	0.042
	GO:0048359	mucilage metabolic process involved in s...	0.045
	GO:0030198	extracellular matrix organization	0.045
	GO:0043062	extracellular structure organization	0.045
	GO:0046173	polyol biosynthetic process	0.047
	GO:0098655	cation transmembrane transport	0.048
	GO:0010564	regulation of cell cycle process	0.051
	GO:0031408	oxylipin biosynthetic process	0.051
	GO:0019915	lipid storage	0.052
	GO:1901617	organic hydroxy compound biosynthetic pr...	0.052
	GO:0021700	developmental maturation	0.053
	GO:0044772	mitotic cell cycle phase transition	0.054
	GO:0046365	monosaccharide catabolic process	0.058
	GO:0015985	energy coupled proton transport, down el...	0.060
	GO:0015986	ATP synthesis coupled proton transport	0.060

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0048878	chemical homeostasis	0.064
	GO:0034765	regulation of ion transmembrane transpor...	0.064
	GO:0051716	cellular response to stimulus	0.065
	GO:0009741	response to brassinosteroid	0.067
	GO:0030641	regulation of cellular pH	0.070
	GO:0051453	regulation of intracellular pH	0.070
	GO:0018904	ether metabolic process	0.075
	GO:0006108	malate metabolic process	0.080
	GO:0010639	negative regulation of organelle organiz...	0.082
	GO:0030004	cellular monovalent inorganic cation hom...	0.083
	GO:0005996	monosaccharide metabolic process	0.084
	GO:0008356	asymmetric cell division	0.087
	GO:0044248	cellular catabolic process	0.091
	GO:0046835	carbohydrate phosphorylation	0.091
	GO:0070085	glycosylation	0.091
	GO:0071695	anatomical structure maturation	0.091
	GO:0006793	phosphorus metabolic process	0.098
	GO:0006536	glutamate metabolic process	0.098
CC	GO:0016020	membrane	0.000
	GO:0098791	Golgi subcompartment	0.000
	GO:0044425	membrane part	0.000
	GO:0005773	vacuole	0.000
	GO:0031225	anchored component of membrane	0.000
	GO:0044437	vacuolar part	0.000
	GO:0033178	proton-transporting two-sector ATPase co...	0.000
	GO:0005768	endosome	0.000
	GO:0033180	proton-transporting V-type ATPase, V1 do...	0.001
	GO:0044433	cytoplasmic vesicle part	0.001
	GO:0030660	Golgi-associated vesicle membrane	0.001
	GO:0009504	cell plate	0.002
	GO:0005769	early endosome	0.002
	GO:0070069	cytochrome complex	0.003
	GO:0005876	spindle microtubule	0.003
	GO:0005881	cytoplasmic microtubule	0.004
	GO:0030863	cortical cytoskeleton	0.004
	GO:0030981	cortical microtubule cytoskeleton	0.004
	GO:0005819	spindle	0.004
	GO:0055028	cortical microtubule	0.005
	GO:0005753	mitochondrial proton-transporting ATP sy...	0.007
	GO:0030136	clathrin-coated vesicle	0.008
	GO:0009705	plant-type vacuole membrane	0.015
	GO:0033177	proton-transporting two-sector ATPase co...	0.016
	GO:0030658	transport vesicle membrane	0.023
	GO:0009574	preprophase band	0.023
	GO:0000325	plant-type vacuole	0.030
	GO:0000775	chromosome, centromeric region	0.033
	GO:0030133	transport vesicle	0.036
	GO:0005798	Golgi-associated vesicle	0.052
	GO:0045259	proton-transporting ATP synthase complex	0.070

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0042995	cell projection	0.079
	GO:0120025	plasma membrane bounded cell projection	0.079
	GO:0090406	pollen tube	0.086
MF	GO:0016757	transferase activity, transferring glyco...	0.000
	GO:0015077	monovalent inorganic cation transmembran...	0.000
	GO:0015078	proton transmembrane transporter activit...	0.000
	GO:0005372	water transmembrane transporter activity	0.001
	GO:0015250	water channel activity	0.001
	GO:0015254	glycerol channel activity	0.001
	GO:0015926	glucosidase activity	0.001
	GO:0046906	tetrapyrrole binding	0.001
	GO:0004567	beta-mannosidase activity	0.002
	GO:0009055	electron transfer activity	0.002
	GO:0005085	guanyl-nucleotide exchange factor activi...	0.002
	GO:0015168	glycerol transmembrane transporter activ...	0.002
	GO:0016758	transferase activity, transferring hexos...	0.002
	GO:0016759	cellulose synthase activity	0.002
	GO:0016760	cellulose synthase (UDP-forming) activit...	0.002
	GO:0008146	sulfotransferase activity	0.003
	GO:0015267	channel activity	0.003
	GO:0015318	inorganic molecular entity transmembrane...	0.003
	GO:0016788	hydrolase activity, acting on ester bond...	0.003
	GO:0022803	passive transmembrane transporter activi...	0.003
	GO:0022838	substrate-specific channel activity	0.003
	GO:0020037	heme binding	0.003
	GO:0046910	pectinesterase inhibitor activity	0.003
	GO:0015166	polyol transmembrane transporter activit...	0.003
	GO:0016857	racemase and epimerase activity, acting ...	0.003
	GO:0005088	Ras guanyl-nucleotide exchange factor ac...	0.004
	GO:0015144	carbohydrate transmembrane transporter a...	0.004
	GO:0030276	clathrin binding	0.004
	GO:0030599	pectinesterase activity	0.004
	GO:0008810	cellulase activity	0.005
	GO:1901618	organic hydroxy compound transmembrane t...	0.006
	GO:0008422	beta-glucosidase activity	0.007
	GO:0008324	cation transmembrane transporter activit...	0.008
	GO:0016717	oxidoreductase activity, acting on paire...	0.008
	GO:0015923	mannosidase activity	0.008
	GO:0008081	phosphoric diester hydrolase activity	0.009
	GO:0051020	GTPase binding	0.010
	GO:0016307	phosphatidylinositol phosphate kinase ac...	0.013
	GO:0042285	xylosyltransferase activity	0.013
	GO:0016854	racemase and epimerase activity	0.013
	GO:1901681	sulfur compound binding	0.014
	GO:0042349	guiding stereospecific synthesis activit...	0.016
	GO:0005509	calcium ion binding	0.016
	GO:0016722	oxidoreductase activity, oxidizing metal...	0.017
	GO:0019203	carbohydrate phosphatase activity	0.019
	GO:0046527	glucosyltransferase activity	0.020

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0070569	uridylyltransferase activity	0.021
	GO:0016791	phosphatase activity	0.021
	GO:0016835	carbon-oxygen lyase activity	0.022
	GO:0015020	glucuronosyltransferase activity	0.025
	GO:0016615	malate dehydrogenase activity	0.025
	GO:0005215	transporter activity	0.025
	GO:0098772	molecular function regulator	0.029
	GO:0019200	carbohydrate kinase activity	0.029
	GO:0051015	actin filament binding	0.030
	GO:0004743	pyruvate kinase activity	0.042
	GO:0015018	galactosylgalactosylxylosylprotein 3-bet...	0.042
	GO:0030955	potassium ion binding	0.042
	GO:0031420	alkali metal ion binding	0.042
	GO:0017016	Ras GTPase binding	0.043
	GO:0031267	small GTPase binding	0.043
	GO:0016417	S-acyltransferase activity	0.050
	GO:0046933	proton-transporting ATP synthase activit...	0.052
	GO:0005200	structural constituent of cytoskeleton	0.058
	GO:0008194	UDP-glycosyltransferase activity	0.058
	GO:0008378	galactosyltransferase activity	0.060
	GO:0008047	enzyme activator activity	0.067
	GO:0016740	transferase activity	0.071
	GO:0043168	anion binding	0.076
	GO:0052716	hydroquinone:oxygen oxidoreductase activ...	0.076
	GO:0004620	phospholipase activity	0.097
	GO:0008171	O-methyltransferase activity	0.100

4.3.4 Root - Preflowering - Cluster 4

GO type	GO ID	Description	Adj. p-value
BP	GO:1903506	regulation of nucleic acid-templated tra...	0.000
	GO:0009753	response to jasmonic acid	0.000
	GO:0071229	cellular response to acid chemical	0.000
	GO:0009751	response to salicylic acid	0.000
	GO:0009867	jasmonic acid mediated signaling pathway	0.000
	GO:0009312	oligosaccharide biosynthetic process	0.001
	GO:0042537	benzene-containing compound metabolic pr...	0.002
	GO:0019538	protein metabolic process	0.003
	GO:0005992	trehalose biosynthetic process	0.003
	GO:0042447	hormone catabolic process	0.003
	GO:0009862	systemic acquired resistance, salicylic ...	0.004
	GO:0034654	nucleobase-containing compound biosynthe...	0.004
	GO:0044267	cellular protein metabolic process	0.004
	GO:0003333	amino acid transmembrane transport	0.004
	GO:0006865	amino acid transport	0.004
	GO:0007165	signal transduction	0.004
	GO:0010468	regulation of gene expression	0.004
	GO:0031347	regulation of defense response	0.005
	GO:0001101	response to acid chemical	0.005
	GO:0005991	trehalose metabolic process	0.005
	GO:0046351	disaccharide biosynthetic process	0.005
	GO:1901701	cellular response to oxygen-containing c...	0.005
	GO:0019222	regulation of metabolic process	0.005
	GO:0023052	signaling	0.005
	GO:0009814	defense response, incompatible interacti...	0.006
	GO:0019438	aromatic compound biosynthetic process	0.006
	GO:0042445	hormone metabolic process	0.009
	GO:0009072	aromatic amino acid family metabolic pro...	0.010
	GO:0071215	cellular response to abscisic acid stimu...	0.010
	GO:0097306	cellular response to alcohol	0.010
	GO:0009696	salicylic acid metabolic process	0.011
	GO:0046677	response to antibiotic	0.011
	GO:0071446	cellular response to salicylic acid stim...	0.012
	GO:0009605	response to external stimulus	0.014
	GO:0051704	multi-organism process	0.014
	GO:0009863	salicylic acid mediated signaling pathwa...	0.014
	GO:0009617	response to bacterium	0.015
	GO:0032787	monocarboxylic acid metabolic process	0.015
	GO:1901362	organic cyclic compound biosynthetic pro...	0.015
	GO:0006040	amino sugar metabolic process	0.017
	GO:0043648	dicarboxylic acid metabolic process	0.018
	GO:0042737	drug catabolic process	0.018
	GO:0009636	response to toxic substance	0.019
	GO:1901698	response to nitrogen compound	0.019
	GO:0009620	response to fungus	0.019
	GO:0018130	heterocycle biosynthetic process	0.020

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GO type	GO ID	Description	Adj. p-value
	GO:0046942	carboxylic acid transport	0.024
	GO:0043436	oxoacid metabolic process	0.025
	GO:0006082	organic acid metabolic process	0.030
	GO:0050832	defense response to fungus	0.030
	GO:1905039	carboxylic acid transmembrane transport	0.032
	GO:0002831	regulation of response to biotic stimulu...	0.033
	GO:0009755	hormone-mediated signaling pathway	0.033
	GO:0006575	cellular modified amino acid metabolic p...	0.034
	GO:0055114	oxidation-reduction process	0.035
	GO:0015893	drug transport	0.037
	GO:0015849	organic acid transport	0.039
	GO:0035304	regulation of protein dephosphorylation	0.040
	GO:1901700	response to oxygen-containing compound	0.042
	GO:0055081	anion homeostasis	0.046
	GO:0032101	regulation of response to external stimu...	0.048
	GO:1903825	organic acid transmembrane transport	0.052
	GO:0080163	regulation of protein serine/threonine p...	0.057
	GO:0002237	response to molecule of bacterial origin	0.058
	GO:0001666	response to hypoxia	0.060
	GO:0015711	organic anion transport	0.061
	GO:0009311	oligosaccharide metabolic process	0.062
	GO:0043666	regulation of phosphoprotein phosphatase...	0.070
	GO:0071236	cellular response to antibiotic	0.071
	GO:0009991	response to extracellular stimulus	0.077
	GO:0009698	phenylpropanoid metabolic process	0.078
	GO:0050896	response to stimulus	0.080
	GO:0035303	regulation of dephosphorylation	0.080
	GO:0070482	response to oxygen levels	0.080
	GO:0006811	ion transport	0.081
	GO:0071396	cellular response to lipid	0.091
CC	GO:0005576	extracellular region	0.003
	GO:0044421	extracellular region part	0.018
	GO:0022857	transmembrane transporter activity	0.000
	GO:0016831	carboxy-lyase activity	0.000
	GO:0022804	active transmembrane transporter activit...	0.000
	GO:0044212	transcription regulatory region DNA bind...	0.000
	GO:0000166	nucleotide binding	0.001
	GO:0016830	carbon-carbon lyase activity	0.001
	GO:0036094	small molecule binding	0.001
	GO:1901265	nucleoside phosphate binding	0.001
	GO:0004190	aspartic-type endopeptidase activity	0.001
	GO:0070001	aspartic-type peptidase activity	0.001
	GO:0015171	amino acid transmembrane transporter act...	0.002
	GO:0004871	signal transducer activity	0.005
	GO:0001047	core promoter binding	0.006
	GO:0016491	oxidoreductase activity	0.007
	GO:0001046	core promoter sequence-specific DNA bind...	0.009
	GO:0003959	NADPH dehydrogenase activity	0.011
	GO:0016682	oxidoreductase activity, acting on diphe...	0.011

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MF

GO type	GO ID	Description	Adj. p-value
	GO:0003714	transcription corepressor activity	0.017
	GO:0046943	carboxylic acid transmembrane transporte...	0.020
	GO:0016829	lyase activity	0.028
	GO:0005342	organic acid transmembrane transporter a...	0.034
	GO:0004864	protein phosphatase inhibitor activity	0.037
	GO:0019212	phosphatase inhibitor activity	0.037
	GO:0042562	hormone binding	0.042
	GO:0001228	transcriptional activator activity, RNA ...	0.046
	GO:0016841	ammonia-lyase activity	0.048
	GO:0046872	metal ion binding	0.049
	GO:0016765	transferase activity, transferring alkyl...	0.055
	GO:0000976	transcription regulatory region sequence...	0.056
	GO:0008509	anion transmembrane transporter activity	0.059
	GO:0043169	cation binding	0.065
	GO:0004702	signal transducer, downstream of recepto...	0.072
	GO:0005057	signal transducer activity, downstream o...	0.072
	GO:0004805	trehalose-phosphatase activity	0.072
	GO:0019208	phosphatase regulator activity	0.072
	GO:0019888	protein phosphatase regulator activity	0.072
	GO:0016679	oxidoreductase activity, acting on diphe...	0.072
	GO:0008514	organic anion transmembrane transporter ...	0.078
	GO:0016840	carbon-nitrogen lyase activity	0.078
	GO:0019203	carbohydrate phosphatase activity	0.078
	GO:0016757	transferase activity, transferring glyco...	0.085
	GO:0016298	lipase activity	0.086

4.3.5 Root - Preflowering - Cluster 5

GO type	GO ID	Description	Adj. p-value
BP	GO:0060255	regulation of macromolecule metabolic pr...	0.000
	GO:0031323	regulation of cellular metabolic process	0.000
	GO:0051171	regulation of nitrogen compound metaboli...	0.000
	GO:0010468	regulation of gene expression	0.000
	GO:0080090	regulation of primary metabolic process	0.000
	GO:0019219	regulation of nucleobase-containing comp...	0.000
	GO:0031326	regulation of cellular biosynthetic proc...	0.000
	GO:0009889	regulation of biosynthetic process	0.000
	GO:0010556	regulation of macromolecule biosynthetic...	0.000
	GO:0051252	regulation of RNA metabolic process	0.000
	GO:0044267	cellular protein metabolic process	0.000
	GO:0032446	protein modification by small protein co...	0.000
	GO:0008033	tRNA processing	0.000
	GO:0043161	proteasome-mediated ubiquitin-dependent ...	0.000
	GO:0090305	nucleic acid phosphodiester bond hydroly...	0.000
	GO:0010498	proteasomal protein catabolic process	0.000
	GO:0006952	defense response	0.002
	GO:0042752	regulation of circadian rhythm	0.003
	GO:0006796	phosphate-containing compound metabolic ...	0.004
	GO:0065007	biological regulation	0.004
	GO:0002097	tRNA wobble base modification	0.004
	GO:0010501	RNA secondary structure unwinding	0.004
	GO:0044265	cellular macromolecule catabolic process	0.005
	GO:0016226	iron-sulfur cluster assembly	0.005
	GO:0031163	metallo-sulfur cluster assembly	0.005
	GO:0090501	RNA phosphodiester bond hydrolysis	0.005
	GO:0006063	uronic acid metabolic process	0.005
	GO:0006511	ubiquitin-dependent protein catabolic pr...	0.007
	GO:0007623	circadian rhythm	0.007
	GO:0048511	rhythmic process	0.007
	GO:0009813	flavonoid biosynthetic process	0.007
	GO:0009627	systemic acquired resistance	0.007
	GO:0009909	regulation of flower development	0.008
	GO:1904659	glucose transmembrane transport	0.010
	GO:0015749	monosaccharide transmembrane transport	0.011
	GO:0008645	hexose transmembrane transport	0.014
	GO:0006793	phosphorus metabolic process	0.015
	GO:0019941	modification-dependent protein catabolic...	0.015
	GO:2000241	regulation of reproductive process	0.018
	GO:0043632	modification-dependent macromolecule cat...	0.018
	GO:0046323	glucose import	0.018
	GO:0031425	chloroplast RNA processing	0.018
	GO:0009751	response to salicylic acid	0.031
	GO:0006836	neurotransmitter transport	0.033
	GO:0000373	Group II intron splicing	0.038
	GO:0044257	cellular protein catabolic process	0.048

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GO type	GO ID	Description	Adj. p-value
	GO:0006568	tryptophan metabolic process	0.054
	GO:0006586	indolalkylamine metabolic process	0.054
	GO:0015995	chlorophyll biosynthetic process	0.054
	GO:0098542	defense response to other organism	0.058
	GO:0000162	tryptophan biosynthetic process	0.062
	GO:0046219	indolalkylamine biosynthetic process	0.062
	GO:0051603	proteolysis involved in cellular protein...	0.063
	GO:0009607	response to biotic stimulus	0.067
	GO:0006281	DNA repair	0.071
	GO:0006289	nucleotide-excision repair	0.071
	GO:0043207	response to external biotic stimulus	0.071
	GO:0051707	response to other organism	0.071
	GO:0051606	detection of stimulus	0.072
	GO:1902022	L-lysine transport	0.079
	GO:1903401	L-lysine transmembrane transport	0.079
	GO:0009987	cellular process	0.082
	GO:0042430	indole-containing compound metabolic pro...	0.083
	GO:0006974	cellular response to DNA damage stimulus	0.087
	GO:0006379	mRNA cleavage	0.096
CC	GO:0044451	nucleoplasm part	0.000
	GO:1990234	transferase complex	0.000
	GO:0009507	chloroplast	0.000
	GO:0043227	membrane-bounded organelle	0.001
	GO:0061695	transferase complex, transferring phosph...	0.004
	GO:0016604	nuclear body	0.005
	GO:0016592	mediator complex	0.006
	GO:1902494	catalytic complex	0.007
	GO:0042651	thylakoid membrane	0.007
	GO:0034357	photosynthetic membrane	0.010
	GO:0044436	thylakoid part	0.013
	GO:0009579	thylakoid	0.024
	GO:0044435	plastid part	0.024
	GO:0009534	chloroplast thylakoid	0.026
	GO:0031976	plastid thylakoid	0.026
	GO:0080008	Cul4-RING E3 ubiquitin ligase complex	0.027
	GO:0055035	plastid thylakoid membrane	0.028
	GO:0009535	chloroplast thylakoid membrane	0.039
	GO:0044434	chloroplast part	0.046
	GO:0009508	plastid chromosome	0.055
	GO:0016607	nuclear speck	0.064
	GO:0003677	DNA binding	0.000
	GO:0004672	protein kinase activity	0.000
	GO:0140098	catalytic activity, acting on RNA	0.000
	GO:0004518	nuclease activity	0.004
	GO:0043167	ion binding	0.004
	GO:0004540	ribonuclease activity	0.004
	GO:0008408	3'-5' exonuclease activity	0.006
	GO:0035639	purine ribonucleoside triphosphate bindi...	0.008
	GO:0005524	ATP binding	0.009

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GO type	GO ID	Description	Adj. p-value
	GO:0005506	iron ion binding	0.009
	GO:0003725	double-stranded RNA binding	0.010
	GO:0003724	RNA helicase activity	0.011
	GO:0004532	exoribonuclease activity	0.014
	GO:0008026	ATP-dependent helicase activity	0.014
	GO:0070035	purine NTP-dependent helicase activity	0.014
	GO:0008173	RNA methyltransferase activity	0.017
	GO:0080043	quercetin 3-O-glucosyltransferase activi...	0.021
	GO:0080044	quercetin 7-O-glucosyltransferase activi...	0.021
	GO:0016896	exoribonuclease activity, producing 5'-p...	0.023
	GO:0016705	oxidoreductase activity, acting on paire...	0.025
	GO:0008144	drug binding	0.025
	GO:0004004	ATP-dependent RNA helicase activity	0.025
	GO:0008186	RNA-dependent ATPase activity	0.025
	GO:0005355	glucose transmembrane transporter activi...	0.026
	GO:0004527	exonuclease activity	0.026
	GO:0015145	monosaccharide transmembrane transporter...	0.027
	GO:0005326	neurotransmitter transporter activity	0.030
	GO:0051213	dioxygenase activity	0.035
	GO:0015149	hexose transmembrane transporter activit...	0.035
	GO:0004497	monooxygenase activity	0.043
	GO:0072509	divalent inorganic cation transmembrane ...	0.043
	GO:0030246	carbohydrate binding	0.072
	GO:0015172	acidic amino acid transmembrane transpor...	0.077
	GO:0015181	arginine transmembrane transporter activ...	0.077
	GO:0015189	L-lysine transmembrane transporter activ...	0.077
	GO:0030983	mismatched DNA binding	0.080
	GO:0004519	endonuclease activity	0.089
	GO:0046915	transition metal ion transmembrane trans...	0.097
	GO:0015291	secondary active transmembrane transport...	0.099

4.3.6 Root - Preflowering - Cluster 6

GO type	GO ID	Description	Adj. p-value
BP	GO:0051171	regulation of nitrogen compound metaboli...	0.000
	GO:0032446	protein modification by small protein co...	0.000
	GO:0060255	regulation of macromolecule metabolic pr...	0.000
	GO:0080090	regulation of primary metabolic process	0.000
	GO:0055085	transmembrane transport	0.000
	GO:0043161	proteasome-mediated ubiquitin-dependent ...	0.000
	GO:0010498	proteasomal protein catabolic process	0.001
	GO:0042430	indole-containing compound metabolic pro...	0.006
	GO:0044257	cellular protein catabolic process	0.007
	GO:0000162	tryptophan biosynthetic process	0.008
	GO:0006511	ubiquitin-dependent protein catabolic pr...	0.008
	GO:0046219	indolalkylamine biosynthetic process	0.008
	GO:0051603	proteolysis involved in cellular protein...	0.009
	GO:1901565	organonitrogen compound catabolic proces...	0.009
	GO:0050794	regulation of cellular process	0.010
	GO:1902022	L-lysine transport	0.010
	GO:1903401	L-lysine transmembrane transport	0.010
	GO:0010921	regulation of phosphatase activity	0.011
	GO:0043632	modification-dependent macromolecule cat...	0.011
	GO:0044265	cellular macromolecule catabolic process	0.011
	GO:0019438	aromatic compound biosynthetic process	0.013
	GO:0006857	oligopeptide transport	0.014
	GO:1901362	organic cyclic compound biosynthetic pro...	0.015
	GO:0019941	modification-dependent protein catabolic...	0.017
	GO:0080163	regulation of protein serine/threonine p...	0.020
	GO:0035303	regulation of dephosphorylation	0.022
	GO:0009627	systemic acquired resistance	0.023
	GO:0043666	regulation of phosphoprotein phosphatase...	0.024
	GO:0030163	protein catabolic process	0.026
	GO:0006836	neurotransmitter transport	0.033
	GO:0006749	glutathione metabolic process	0.045
	GO:0008643	carbohydrate transport	0.046
	GO:0006508	proteolysis	0.049
	GO:0006820	anion transport	0.049
	GO:0035304	regulation of protein dephosphorylation	0.049
	GO:0043648	dicarboxylic acid metabolic process	0.053
	GO:0009308	amine metabolic process	0.066
	GO:0009072	aromatic amino acid family metabolic pro...	0.067
	GO:0000041	transition metal ion transport	0.071
	GO:0015802	basic amino acid transport	0.078
	GO:0010243	response to organonitrogen compound	0.081
	GO:0071577	zinc ion transmembrane transport	0.096
	GO:0042364	water-soluble vitamin biosynthetic proce...	0.099
CC	GO:0000323	lytic vacuole	0.004
	GO:0031226	intrinsic component of plasma membrane	0.010
	GO:0031461	cullin-RING ubiquitin ligase complex	0.010

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GO type	GO ID	Description	Adj. p-value
	GO:0005764	lysosome	0.015
	GO:0071013	catalytic step 2 spliceosome	0.019
	GO:0016591	DNA-directed RNA polymerase II, holoenzy...	0.021
	GO:0044459	plasma membrane part	0.021
	GO:0090575	RNA polymerase II transcription factor c...	0.026
	GO:0000151	ubiquitin ligase complex	0.031
	GO:0005886	plasma membrane	0.050
	GO:0071944	cell periphery	0.070
	GO:0044798	nuclear transcription factor complex	0.072
MF	GO:0019787	ubiquitin-like protein transferase activ...	0.000
	GO:0004497	monooxygenase activity	0.000
	GO:0016705	oxidoreductase activity, acting on paire...	0.000
	GO:0015291	secondary active transmembrane transport...	0.000
	GO:0022857	transmembrane transporter activity	0.001
	GO:0044212	transcription regulatory region DNA bind...	0.001
	GO:0017076	purine nucleotide binding	0.002
	GO:0005351	carbohydrate:proton symporter activity	0.002
	GO:0005402	carbohydrate:cation symporter activity	0.002
	GO:0015295	solute:proton symporter activity	0.002
	GO:0032553	ribonucleotide binding	0.002
	GO:0015294	solute:cation symporter activity	0.002
	GO:0001047	core promoter binding	0.003
	GO:0003677	DNA binding	0.003
	GO:0035639	purine ribonucleoside triphosphate bindi...	0.003
	GO:0046906	tetrapyrrole binding	0.003
	GO:0001046	core promoter sequence-specific DNA bind...	0.005
	GO:0001871	pattern binding	0.005
	GO:0030247	polysaccharide binding	0.005
	GO:1901363	heterocyclic compound binding	0.005
	GO:0035251	UDP-glucosyltransferase activity	0.005
	GO:0097159	organic cyclic compound binding	0.005
	GO:0015181	arginine transmembrane transporter activ...	0.006
	GO:0015189	L-lysine transmembrane transporter activ...	0.006
	GO:0015172	acidic amino acid transmembrane transpor...	0.006
	GO:0043531	ADP binding	0.006
	GO:0016830	carbon-carbon lyase activity	0.009
	GO:0015318	inorganic molecular entity transmembrane...	0.010
	GO:0003824	catalytic activity	0.011
	GO:0015075	ion transmembrane transporter activity	0.011
	GO:0004864	protein phosphatase inhibitor activity	0.013
	GO:0019212	phosphatase inhibitor activity	0.013
	GO:0008324	cation transmembrane transporter activit...	0.015
	GO:0008061	chitin binding	0.016
	GO:0005326	neurotransmitter transporter activity	0.019
	GO:0015174	basic amino acid transmembrane transport...	0.019
	GO:0061630	ubiquitin protein ligase activity	0.021
	GO:0004364	glutathione transferase activity	0.022
	GO:0061659	ubiquitin-like protein ligase activity	0.022
	GO:0036094	small molecule binding	0.023

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GO type	GO ID	Description	Adj. p-value
	GO:0001228	transcriptional activator activity, RNA ...	0.023
	GO:0019208	phosphatase regulator activity	0.026
	GO:0019888	protein phosphatase regulator activity	0.026
	GO:0004857	enzyme inhibitor activity	0.032
	GO:0030414	peptidase inhibitor activity	0.033
	GO:0061134	peptidase regulator activity	0.033
	GO:0005385	zinc ion transmembrane transporter activ...	0.035
	GO:0008194	UDP-glycosyltransferase activity	0.036
	GO:0004866	endopeptidase inhibitor activity	0.039
	GO:0016765	transferase activity, transferring alkyl...	0.039
	GO:0061135	endopeptidase regulator activity	0.039
	GO:0015144	carbohydrate transmembrane transporter a...	0.041
	GO:0042562	hormone binding	0.047
	GO:0046527	glucosyltransferase activity	0.047
	GO:0022890	inorganic cation transmembrane transport...	0.050
	GO:0000166	nucleotide binding	0.054
	GO:1901265	nucleoside phosphate binding	0.054
	GO:0008483	transaminase activity	0.059
	GO:0016769	transferase activity, transferring nitro...	0.059
	GO:0046915	transition metal ion transmembrane trans...	0.064
	GO:0004970	ionotropic glutamate receptor activity	0.066
	GO:0005230	extracellular ligand-gated ion channel a...	0.066
	GO:0008066	glutamate receptor activity	0.066
	GO:0022824	transmitter-gated ion channel activity	0.066
	GO:0022835	transmitter-gated channel activity	0.066
	GO:0072509	divalent inorganic cation transmembrane ...	0.066
	GO:0010427	abscisic acid binding	0.071
	GO:0000976	transcription regulatory region sequence...	0.074
	GO:0019840	isoprenoid binding	0.075
	GO:0004568	chitinase activity	0.081

4.3.7 Root - Preflowering - Cluster 7

GO type	GO ID	Description	Adj. p-value
	GO:0007017	microtubule-based process	0.000
	GO:0010383	cell wall polysaccharide metabolic proce...	0.000
	GO:0044036	cell wall macromolecule metabolic proces...	0.000
	GO:0046034	ATP metabolic process	0.000
	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0032989	cellular component morphogenesis	0.000
	GO:0000902	cell morphogenesis	0.000
	GO:1903047	mitotic cell cycle process	0.000
	GO:0009145	purine nucleoside triphosphate biosynthe...	0.000
	GO:0009206	purine ribonucleoside triphosphate biosy...	0.000
	GO:0009142	nucleoside triphosphate biosynthetic pro...	0.000
	GO:0046434	organophosphate catabolic process	0.000
	GO:0016049	cell growth	0.000
	GO:1902600	proton transmembrane transport	0.000
	GO:0000910	cytokinesis	0.000
	GO:0009156	ribonucleoside monophosphate biosyntheti...	0.000
	GO:0098754	detoxification	0.000
	GO:0009124	nucleoside monophosphate biosynthetic pr...	0.000
	GO:0044038	cell wall macromolecule biosynthetic pro...	0.000
	GO:0070589	cellular component macromolecule biosynt...	0.000
	GO:0046496	nicotinamide nucleotide metabolic proces...	0.000
	GO:0046939	nucleotide phosphorylation	0.000
	GO:0016192	vesicle-mediated transport	0.000
	GO:0070592	cell wall polysaccharide biosynthetic pr...	0.000
	GO:0046394	carboxylic acid biosynthetic process	0.000
	GO:0019318	hexose metabolic process	0.000
	GO:0034637	cellular carbohydrate biosynthetic proce...	0.000
	GO:0048193	Golgi vesicle transport	0.000
	GO:0009699	phenylpropanoid biosynthetic process	0.000
	GO:0000226	microtubule cytoskeleton organization	0.000
	GO:0006629	lipid metabolic process	0.000
	GO:0000904	cell morphogenesis involved in different...	0.000
	GO:0097435	supramolecular fiber organization	0.000
	GO:0051273	beta-glucan metabolic process	0.000
	GO:0006631	fatty acid metabolic process	0.000
	GO:0006260	DNA replication	0.000
	GO:0006101	citrate metabolic process	0.001
	GO:0048868	pollen tube development	0.001
	GO:0006261	DNA-dependent DNA replication	0.001
	GO:0032502	developmental process	0.001
	GO:0006119	oxidative phosphorylation	0.001
	GO:0042773	ATP synthesis coupled electron transport	0.001
	GO:0006633	fatty acid biosynthetic process	0.001
	GO:0044703	multi-organism reproductive process	0.001
	GO:0006099	tricarboxylic acid cycle	0.001
	GO:0010052	guard cell differentiation	0.001

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		Description	Adj. p-value
GO type	GO ID		
	GO:0090626	plant epidermis morphogenesis	0.001
	GO:0008154	actin polymerization or depolymerization	0.002
	GO:0019953	sexual reproduction	0.002
	GO:0030244	cellulose biosynthetic process	0.002
	GO:0032535	regulation of cellular component size	0.002
	GO:0090066	regulation of anatomical structure size	0.002
	GO:0015791	polyol transport	0.002
	GO:0044247	cellular polysaccharide catabolic proces...	0.002
	GO:0045493	xylan catabolic process	0.002
	GO:0006650	glycerophospholipid metabolic process	0.002
	GO:0010564	regulation of cell cycle process	0.002
	GO:0090627	plant epidermal cell differentiation	0.002
	GO:0098662	inorganic cation transmembrane transport	0.002
	GO:0008064	regulation of actin polymerization or de...	0.002
	GO:0030832	regulation of actin filament length	0.002
	GO:0032956	regulation of actin cytoskeleton organiz...	0.002
	GO:0032970	regulation of actin filament-based proce...	0.002
	GO:0110053	regulation of actin filament organizatio...	0.002
	GO:0048588	developmental cell growth	0.003
	GO:0052546	cell wall pectin metabolic process	0.003
	GO:0009225	nucleotide-sugar metabolic process	0.003
	GO:0044255	cellular lipid metabolic process	0.003
	GO:0010374	stomatal complex development	0.003
	GO:0051274	beta-glucan biosynthetic process	0.003
	GO:0015985	energy coupled proton transport, down el...	0.003
	GO:0015986	ATP synthesis coupled proton transport	0.003
	GO:0042775	mitochondrial ATP synthesis coupled elec...	0.003
	GO:0051258	protein polymerization	0.003
	GO:0015980	energy derivation by oxidation of organi...	0.004
	GO:0008361	regulation of cell size	0.004
	GO:0051129	negative regulation of cellular componen...	0.004
	GO:0072350	tricarboxylic acid metabolic process	0.004
	GO:0009056	catabolic process	0.004
	GO:0009809	lignin biosynthetic process	0.004
	GO:0030041	actin filament polymerization	0.004
	GO:0030833	regulation of actin filament polymerizat...	0.004
	GO:0051179	localization	0.004
	GO:0006012	galactose metabolic process	0.005
	GO:0006644	phospholipid metabolic process	0.005
	GO:0048469	cell maturation	0.005
	GO:0048764	trichoblast maturation	0.005
	GO:0048765	root hair cell differentiation	0.005
	GO:0022904	respiratory electron transport chain	0.005
	GO:0010026	trichome differentiation	0.005
	GO:0051493	regulation of cytoskeleton organization	0.005
	GO:0080147	root hair cell development	0.006
	GO:0048278	vesicle docking	0.006
	GO:0046486	glycerolipid metabolic process	0.006
	GO:0010054	trichoblast differentiation	0.006

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GO type	GO ID	Description	Adj. p-value
	GO:0019321	pentose metabolic process	0.007
	GO:0044275	cellular carbohydrate catabolic process	0.008
	GO:0006810	transport	0.008
	GO:0044770	cell cycle phase transition	0.008
	GO:0034220	ion transmembrane transport	0.008
	GO:0007015	actin filament organization	0.008
	GO:0032787	monocarboxylic acid metabolic process	0.008
	GO:0051234	establishment of localization	0.009
	GO:1902903	regulation of supramolecular fiber organ...	0.009
	GO:0009100	glycoprotein metabolic process	0.009
	GO:0030029	actin filament-based process	0.009
	GO:0018105	peptidyl-serine phosphorylation	0.011
	GO:0030036	actin cytoskeleton organization	0.011
	GO:0051188	cofactor biosynthetic process	0.011
	GO:0022622	root system development	0.012
	GO:0009934	regulation of meristem structural organi...	0.013
	GO:0022406	membrane docking	0.013
	GO:0140056	organelle localization by membrane tethe...	0.013
	GO:0009226	nucleotide-sugar biosynthetic process	0.013
	GO:0019722	calcium-mediated signaling	0.013
	GO:0008610	lipid biosynthetic process	0.014
	GO:0006486	protein glycosylation	0.014
	GO:0043413	macromolecule glycosylation	0.014
	GO:0015850	organic hydroxy compound transport	0.015
	GO:0044772	mitotic cell cycle phase transition	0.015
	GO:0048364	root development	0.015
	GO:0051235	maintenance of location	0.015
	GO:0006812	cation transport	0.016
	GO:0045490	pectin catabolic process	0.016
	GO:0018209	peptidyl-serine modification	0.016
	GO:0010053	root epidermal cell differentiation	0.016
	GO:0010639	negative regulation of organelle organiz...	0.017
	GO:1903338	regulation of cell wall organization or ...	0.017
	GO:0070085	glycosylation	0.018
	GO:0007275	multicellular organism development	0.018
	GO:0022604	regulation of cell morphogenesis	0.020
	GO:0006006	glucose metabolic process	0.021
	GO:0031122	cytoplasmic microtubule organization	0.021
	GO:0043547	positive regulation of GTPase activity	0.022
	GO:0019752	carboxylic acid metabolic process	0.022
	GO:0048229	gametophyte development	0.022
	GO:0046470	phosphatidylcholine metabolic process	0.022
	GO:0009808	lignin metabolic process	0.024
	GO:0022603	regulation of anatomical structure morph...	0.024
	GO:0006979	response to oxidative stress	0.024
	GO:0009932	cell tip growth	0.025
	GO:0051345	positive regulation of hydrolase activit...	0.025
	GO:0009860	pollen tube growth	0.025
	GO:0030198	extracellular matrix organization	0.025

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GO type	GO ID	Description	Adj. p-value
	GO:0043062	extracellular structure organization	0.025
	GO:0046835	carbohydrate phosphorylation	0.026
	GO:0032501	multicellular organismal process	0.027
	GO:0030004	cellular monovalent inorganic cation hom...	0.028
	GO:0006888	ER to Golgi vesicle-mediated transport	0.029
	GO:0097164	ammonium ion metabolic process	0.032
	GO:0000280	nuclear division	0.032
	GO:0007051	spindle organization	0.035
	GO:2000652	regulation of secondary cell wall biogen...	0.035
	GO:0032271	regulation of protein polymerization	0.035
	GO:0055082	cellular chemical homeostasis	0.035
	GO:0043087	regulation of GTPase activity	0.037
	GO:0010345	suberin biosynthetic process	0.037
	GO:0048826	cotyledon morphogenesis	0.038
	GO:0051640	organelle localization	0.038
	GO:0051726	regulation of cell cycle	0.038
	GO:0030258	lipid modification	0.040
	GO:0043647	inositol phosphate metabolic process	0.041
	GO:0046854	phosphatidylinositol phosphorylation	0.041
	GO:0030148	sphingolipid biosynthetic process	0.041
	GO:0000086	G2/M transition of mitotic cell cycle	0.041
	GO:0042545	cell wall modification	0.041
	GO:0051275	beta-glucan catabolic process	0.041
	GO:1901617	organic hydroxy compound biosynthetic pr...	0.041
	GO:1901990	regulation of mitotic cell cycle phase t...	0.043
	GO:0030245	cellulose catabolic process	0.044
	GO:0019915	lipid storage	0.044
	GO:0030641	regulation of cellular pH	0.048
	GO:0051453	regulation of intracellular pH	0.048
	GO:0098655	cation transmembrane transport	0.048
	GO:0031109	microtubule polymerization or depolymeri...	0.051
	GO:0035556	intracellular signal transduction	0.051
	GO:0006536	glutamate metabolic process	0.051
	GO:0009101	glycoprotein biosynthetic process	0.052
	GO:0007030	Golgi organization	0.052
	GO:0019932	second-messenger-mediated signaling	0.052
	GO:0009629	response to gravity	0.053
	GO:0043254	regulation of protein complex assembly	0.053
	GO:1901987	regulation of cell cycle phase transitio...	0.054
	GO:0006970	response to osmotic stress	0.055
	GO:0048825	cotyledon development	0.057
	GO:0009250	glucan biosynthetic process	0.058
	GO:1903046	meiotic cell cycle process	0.058
	GO:0044839	cell cycle G2/M phase transition	0.059
	GO:0044248	cellular catabolic process	0.059
	GO:0016050	vesicle organization	0.059
	GO:0000819	sister chromatid segregation	0.060
	GO:0009395	phospholipid catabolic process	0.060
	GO:0051651	maintenance of location in cell	0.060

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GO type	GO ID	Description	Adj. p-value
	GO:0016482	cytosolic transport	0.061
	GO:0048878	chemical homeostasis	0.063
	GO:0065008	regulation of biological quality	0.063
	GO:0042147	retrograde transport, endosome to Golgi	0.063
	GO:0048316	seed development	0.066
	GO:0021700	developmental maturation	0.066
	GO:0008643	carbohydrate transport	0.067
	GO:0051321	meiotic cell cycle	0.070
	GO:0009555	pollen development	0.070
	GO:0071103	DNA conformation change	0.073
	GO:0051716	cellular response to stimulus	0.074
	GO:0010215	cellulose microfibril organization	0.074
	GO:0000003	reproduction	0.076
	GO:0008356	asymmetric cell division	0.076
	GO:0010090	trichome morphogenesis	0.076
	GO:0043244	regulation of protein complex disassembl...	0.076
	GO:0048285	organelle fission	0.081
	GO:0016042	lipid catabolic process	0.081
	GO:0022900	electron transport chain	0.082
	GO:0046834	lipid phosphorylation	0.087
	GO:0006811	ion transport	0.091
	GO:0007346	regulation of mitotic cell cycle	0.092
	GO:0098813	nuclear chromosome segregation	0.093
	GO:0033043	regulation of organelle organization	0.095
	GO:0022414	reproductive process	0.096
	GO:0051510	regulation of unidimensional cell growth	0.096
	GO:0098657	import into cell	0.096
	GO:0003006	developmental process involved in reprod...	0.097
CC	GO:0044430	cytoskeletal part	0.000
	GO:0016020	membrane	0.000
	GO:0070469	respiratory chain	0.000
	GO:0005740	mitochondrial envelope	0.000
	GO:0031225	anchored component of membrane	0.000
	GO:0044429	mitochondrial part	0.000
	GO:0044437	vacuolar part	0.000
	GO:0044425	membrane part	0.000
	GO:0033178	proton-transporting two-sector ATPase co...	0.000
	GO:0005819	spindle	0.000
	GO:0005768	endosome	0.000
	GO:0030660	Golgi-associated vesicle membrane	0.001
	GO:0005881	cytoplasmic microtubule	0.001
	GO:0030863	cortical cytoskeleton	0.001
	GO:0030981	cortical microtubule cytoskeleton	0.001
	GO:0055028	cortical microtubule	0.001
	GO:0033177	proton-transporting two-sector ATPase co...	0.001
	GO:0033180	proton-transporting V-type ATPase, V1 do...	0.001
	GO:0009504	cell plate	0.001
	GO:0044815	DNA packaging complex	0.002
	GO:0032993	protein-DNA complex	0.002

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0044433	cytoplasmic vesicle part	0.002
	GO:0045259	proton-transporting ATP synthase complex	0.002
	GO:0031224	intrinsic component of membrane	0.003
	GO:0000786	nucleosome	0.005
	GO:0070069	cytochrome complex	0.005
	GO:0005838	proteasome regulatory particle	0.005
	GO:0022624	proteasome accessory complex	0.005
	GO:0000775	chromosome, centromeric region	0.006
	GO:0005769	early endosome	0.007
	GO:0030118	clathrin coat	0.008
	GO:0009574	preprophase band	0.014
	GO:0005798	Golgi-associated vesicle	0.015
	GO:0030133	transport vesicle	0.017
	GO:0030658	transport vesicle membrane	0.017
	GO:0000325	plant-type vacuole	0.022
	GO:0030136	clathrin-coated vesicle	0.024
	GO:0044427	chromosomal part	0.027
	GO:0000793	condensed chromosome	0.029
	GO:0009705	plant-type vacuole membrane	0.033
	GO:0042575	DNA polymerase complex	0.033
	GO:0043596	nuclear replication fork	0.056
	GO:0000794	condensed nuclear chromosome	0.062
	GO:0016021	integral component of membrane	0.079
	GO:0017119	Golgi transport complex	0.079
	GO:0000347	THO complex	0.081
	GO:0005657	replication fork	0.082
	GO:0005938	cell cortex	0.085
	GO:0000228	nuclear chromosome	0.087
	GO:0019867	outer membrane	0.095
	GO:0031201	SNARE complex	0.096
	GO:0044454	nuclear chromosome part	0.096
	GO:0003824	catalytic activity	0.000
	GO:0016787	hydrolase activity	0.000
	GO:0016491	oxidoreductase activity	0.000
	GO:0015077	monovalent inorganic cation transmembran...	0.001
	GO:0005085	guanyl-nucleotide exchange factor activi...	0.001
	GO:0009044	xylan 1,4-beta-xylosidase activity	0.001
	GO:0097599	xylanase activity	0.001
	GO:0042349	guiding stereospecific synthesis activit...	0.002
	GO:0016462	pyrophosphatase activity	0.002
	GO:0015166	polyol transmembrane transporter activit...	0.002
	GO:0016853	isomerase activity	0.002
	GO:0016817	hydrolase activity, acting on acid anhyd...	0.002
	GO:0015078	proton transmembrane transporter activit...	0.003
	GO:1901618	organic hydroxy compound transmembrane t...	0.003
	GO:0046933	proton-transporting ATP synthase activit...	0.003
	GO:0016747	transferase activity, transferring acyl ...	0.003
	GO:0016620	oxidoreductase activity, acting on the a...	0.004
	GO:0042578	phosphoric ester hydrolase activity	0.004

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0015318	inorganic molecular entity transmembrane...	0.005
	GO:0022890	inorganic cation transmembrane transport...	0.005
	GO:0051020	GTPase binding	0.006
	GO:0140097	catalytic activity, acting on DNA	0.006
	GO:0004567	beta-mannosidase activity	0.006
	GO:0016759	cellulose synthase activity	0.006
	GO:0016760	cellulose synthase (UDP-forming) activit...	0.006
	GO:0016788	hydrolase activity, acting on ester bond...	0.008
	GO:0016776	phosphotransferase activity, phosphate g...	0.010
	GO:0016887	ATPase activity	0.010
	GO:0015926	glucosidase activity	0.011
	GO:0016857	racemase and epimerase activity, acting ...	0.012
	GO:0045330	aspartyl esterase activity	0.013
	GO:0098772	molecular function regulator	0.015
	GO:1901681	sulfur compound binding	0.015
	GO:0015923	mannosidase activity	0.016
	GO:0030276	clathrin binding	0.018
	GO:0003678	DNA helicase activity	0.019
	GO:0004743	pyruvate kinase activity	0.019
	GO:0005200	structural constituent of cytoskeleton	0.019
	GO:0008047	enzyme activator activity	0.019
	GO:0008081	phosphoric diester hydrolase activity	0.019
	GO:0008324	cation transmembrane transporter activit...	0.019
	GO:0015267	channel activity	0.019
	GO:0016722	oxidoreductase activity, oxidizing metal...	0.019
	GO:0022803	passive transmembrane transporter activi...	0.019
	GO:0022838	substrate-specific channel activity	0.019
	GO:0030955	potassium ion binding	0.019
	GO:0031420	alkali metal ion binding	0.019
	GO:0042285	xylosyltransferase activity	0.019
	GO:0046906	tetrapyrrole binding	0.019
	GO:0070569	uridylyltransferase activity	0.019
	GO:0008289	lipid binding	0.022
	GO:0016868	intramolecular transferase activity, pho...	0.022
	GO:0017016	Ras GTPase binding	0.023
	GO:0031267	small GTPase binding	0.023
	GO:0008378	galactosyltransferase activity	0.024
	GO:0019201	nucleotide kinase activity	0.024
	GO:0016758	transferase activity, transferring hexos...	0.025
	GO:0016417	S-acyltransferase activity	0.029
	GO:0015144	carbohydrate transmembrane transporter a...	0.030
	GO:0030599	pectinesterase activity	0.032
	GO:0020037	heme binding	0.032
	GO:0005215	transporter activity	0.035
	GO:0035639	purine ribonucleoside triphosphate bindi...	0.035
	GO:0016854	racemase and epimerase activity	0.040
	GO:0019205	nucleobase-containing compound kinase ac...	0.041
	GO:0016679	oxidoreductase activity, acting on diphe...	0.044
	GO:0015154	disaccharide transmembrane transporter a...	0.049

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0015157	oligosaccharide transmembrane transporte...	0.049
	GO:0019200	carbohydrate kinase activity	0.049
	GO:0097367	carbohydrate derivative binding	0.049
	GO:0016791	phosphatase activity	0.049
	GO:0043138	3'-5' DNA helicase activity	0.049
	GO:0008810	cellulase activity	0.050
	GO:0016836	hydro-lyase activity	0.050
	GO:0032553	ribonucleotide binding	0.050
	GO:0032555	purine ribonucleotide binding	0.050
	GO:0016835	carbon-oxygen lyase activity	0.051
	GO:0015075	ion transmembrane transporter activity	0.051
	GO:0017076	purine nucleotide binding	0.051
	GO:0052716	hydroquinone:oxygen oxidoreductase activ...	0.057
	GO:0060589	nucleoside-triphosphatase regulator acti...	0.059
	GO:0016717	oxidoreductase activity, acting on paire...	0.061
	GO:0005524	ATP binding	0.062
	GO:0016615	malate dehydrogenase activity	0.062
	GO:0051015	actin filament binding	0.062
	GO:0019899	enzyme binding	0.066
	GO:0046910	pectinesterase inhibitor activity	0.069
	GO:0051087	chaperone binding	0.072
	GO:0015020	glucuronosyltransferase activity	0.079
	GO:0019104	DNA N-glycosylase activity	0.079
	GO:0046527	glucosyltransferase activity	0.081
	GO:0030234	enzyme regulator activity	0.084
	GO:0016651	oxidoreductase activity, acting on NAD(P...	0.084
	GO:0043168	anion binding	0.084
	GO:0004129	cytochrome-c oxidase activity	0.085
	GO:0015002	heme-copper terminal oxidase activity	0.085
	GO:0016675	oxidoreductase activity, acting on a hem...	0.085
	GO:0016676	oxidoreductase activity, acting on a hem...	0.085
	GO:0004185	serine-type carboxypeptidase activity	0.089
	GO:0032559	adenyl ribonucleotide binding	0.089
	GO:0001883	purine nucleoside binding	0.090
	GO:0005525	GTP binding	0.090
	GO:0019001	guanyl nucleotide binding	0.090
	GO:0030554	adenyl nucleotide binding	0.090
	GO:0032550	purine ribonucleoside binding	0.090
	GO:0032561	guanyl ribonucleotide binding	0.090
	GO:0008144	drug binding	0.091
	GO:0005096	GTPase activator activity	0.092
	GO:0016829	lyase activity	0.092
	GO:0001882	nucleoside binding	0.093
	GO:0046983	protein dimerization activity	0.099

4.3.8 Root - Preflowering - Cluster 8

GO type	GO ID	Description	Adj. p-value
	GO:0042737	drug catabolic process	0.000
	GO:0010383	cell wall polysaccharide metabolic proce...	0.000
	GO:0044036	cell wall macromolecule metabolic proces...	0.000
	GO:0019748	secondary metabolic process	0.000
	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0044281	small molecule metabolic process	0.000
	GO:0043436	oxoacid metabolic process	0.000
	GO:0006082	organic acid metabolic process	0.000
	GO:0055086	nucleobase-containing small molecule met...	0.000
	GO:0007017	microtubule-based process	0.000
	GO:0044550	secondary metabolite biosynthetic proces...	0.000
	GO:0070592	cell wall polysaccharide biosynthetic pr...	0.000
	GO:0016053	organic acid biosynthetic process	0.000
	GO:0046394	carboxylic acid biosynthetic process	0.000
	GO:0043648	dicarboxylic acid metabolic process	0.000
	GO:0010038	response to metal ion	0.000
	GO:0009808	lignin metabolic process	0.000
	GO:0006732	coenzyme metabolic process	0.001
	GO:0045489	pectin biosynthetic process	0.002
	GO:0006810	transport	0.002
	GO:0019722	calcium-mediated signaling	0.002
	GO:1902600	proton transmembrane transport	0.002
	GO:0006811	ion transport	0.002
	GO:0051179	localization	0.003
	GO:0006884	cell volume homeostasis	0.003
	GO:0009992	cellular water homeostasis	0.003
	GO:0015793	glycerol transport	0.003
	GO:0019637	organophosphate metabolic process	0.003
	GO:0051234	establishment of localization	0.003
	GO:0030148	sphingolipid biosynthetic process	0.003
	GO:0006270	DNA replication initiation	0.004
	GO:0009060	aerobic respiration	0.004
	GO:0015985	energy coupled proton transport, down el...	0.004
	GO:0015986	ATP synthesis coupled proton transport	0.004
	GO:0000910	cytokinesis	0.005
	GO:0006091	generation of precursor metabolites and ...	0.005
	GO:0034404	nucleobase-containing small molecule bio...	0.005
	GO:0030104	water homeostasis	0.005
	GO:1903047	mitotic cell cycle process	0.006
	GO:0006833	water transport	0.006
	GO:0042044	fluid transport	0.006
	GO:0009225	nucleotide-sugar metabolic process	0.006
	GO:0019932	second-messenger-mediated signaling	0.006
	GO:0009108	coenzyme biosynthetic process	0.006
	GO:0009404	toxin metabolic process	0.006
	GO:0060560	developmental growth involved in morphog...	0.007

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0006101	citrate metabolic process	0.007
	GO:0007010	cytoskeleton organization	0.008
	GO:0016049	cell growth	0.009
	GO:0055082	cellular chemical homeostasis	0.010
	GO:0046364	monosaccharide biosynthetic process	0.011
	GO:0006099	tricarboxylic acid cycle	0.011
	GO:0022904	respiratory electron transport chain	0.012
	GO:0009407	toxin catabolic process	0.012
	GO:0000278	mitotic cell cycle	0.012
	GO:0009826	unidimensional cell growth	0.013
	GO:0048468	cell development	0.015
	GO:0061640	cytoskeleton-dependent cytokinesis	0.016
	GO:0008610	lipid biosynthetic process	0.016
	GO:0010345	suberin biosynthetic process	0.016
	GO:1903338	regulation of cell wall organization or ...	0.017
	GO:0015791	polyol transport	0.017
	GO:0072350	tricarboxylic acid metabolic process	0.020
	GO:0008643	carbohydrate transport	0.020
	GO:0018209	peptidyl-serine modification	0.020
	GO:2000652	regulation of secondary cell wall biogen...	0.021
	GO:0000281	mitotic cytokinesis	0.022
	GO:0010413	glucuronoxylan metabolic process	0.023
	GO:0010417	glucuronoxylan biosynthetic process	0.023
	GO:0034220	ion transmembrane transport	0.023
	GO:0019953	sexual reproduction	0.030
	GO:0018105	peptidyl-serine phosphorylation	0.030
	GO:0010026	trichome differentiation	0.032
	GO:0005996	monosaccharide metabolic process	0.035
	GO:0044703	multi-organism reproductive process	0.035
	GO:0009395	phospholipid catabolic process	0.036
	GO:0008361	regulation of cell size	0.038
	GO:0090376	seed trichome differentiation	0.038
	GO:0009074	aromatic amino acid family catabolic pro...	0.039
	GO:0007154	cell communication	0.039
	GO:0015980	energy derivation by oxidation of organi...	0.040
	GO:0032989	cellular component morphogenesis	0.041
	GO:0046274	lignin catabolic process	0.042
	GO:0055085	transmembrane transport	0.043
	GO:0090407	organophosphate biosynthetic process	0.046
	GO:0042221	response to chemical	0.048
	GO:1901575	organic substance catabolic process	0.053
	GO:0006888	ER to Golgi vesicle-mediated transport	0.054
	GO:0000902	cell morphogenesis	0.055
	GO:0015850	organic hydroxy compound transport	0.059
	GO:0019321	pentose metabolic process	0.059
	GO:0006575	cellular modified amino acid metabolic p...	0.060
	GO:0000904	cell morphogenesis involved in different...	0.061
	GO:0006812	cation transport	0.061
	GO:0035556	intracellular signal transduction	0.064

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GO type	GO ID	Description	Adj. p-value
	GO:0019439	aromatic compound catabolic process	0.068
	GO:0006793	phosphorus metabolic process	0.069
	GO:0000911	cytokinesis by cell plate formation	0.070
	GO:0009226	nucleotide-sugar biosynthetic process	0.070
	GO:0090378	seed trichome elongation	0.079
	GO:0051235	maintenance of location	0.084
	GO:0010043	response to zinc ion	0.093
	GO:0006665	sphingolipid metabolic process	0.094
	GO:0060260	regulation of transcription initiation f...	0.094
	GO:0060261	positive regulation of transcription ini...	0.094
	GO:1901361	organic cyclic compound catabolic proces...	0.094
	GO:2000142	regulation of DNA-templated transcriptio...	0.094
	GO:2000144	positive regulation of DNA-templated tra...	0.094
	GO:0040007	growth	0.094
	GO:0051261	protein depolymerization	0.099
	GO:0016054	organic acid catabolic process	0.099
	GO:0033866	nucleoside bisphosphate biosynthetic pro...	0.099
	GO:0034030	ribonucleoside bisphosphate biosynthetic...	0.099
	GO:0034033	purine nucleoside bisphosphate biosynthe...	0.099
	GO:0046271	phenylpropanoid catabolic process	0.099
	GO:0046395	carboxylic acid catabolic process	0.099
	GO:1901264	carbohydrate derivative transport	0.099
CC	GO:0070469	respiratory chain	0.000
	GO:0098800	inner mitochondrial membrane protein com...	0.000
	GO:0044445	cytosolic part	0.000
	GO:0005740	mitochondrial envelope	0.000
	GO:0031225	anchored component of membrane	0.000
	GO:1990204	oxidoreductase complex	0.000
	GO:0044431	Golgi apparatus part	0.000
	GO:0000502	proteasome complex	0.000
	GO:0044437	vacuolar part	0.000
	GO:0005839	proteasome core complex	0.000
	GO:0005829	cytosol	0.000
	GO:0032993	protein-DNA complex	0.001
	GO:0070069	cytochrome complex	0.002
	GO:0005838	proteasome regulatory particle	0.002
	GO:0019773	proteasome core complex, alpha-subunit c...	0.002
	GO:0022624	proteasome accessory complex	0.002
	GO:0033176	proton-transporting V-type ATPase comple...	0.002
	GO:0009524	phragmoplast	0.003
	GO:0005876	spindle microtubule	0.003
	GO:0005739	mitochondrion	0.006
	GO:0008540	proteasome regulatory particle, base sub...	0.017
	GO:0031595	nuclear proteasome complex	0.022
	GO:0030120	vesicle coat	0.036
	GO:0030662	coated vesicle membrane	0.037
	GO:0030135	coated vesicle	0.043
	GO:0031597	cytosolic proteasome complex	0.048
	GO:0030659	cytoplasmic vesicle membrane	0.050

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		Description	Adj. p-value
GO type	GO ID		
	GO:0044444	cytoplasmic part	0.055
	GO:0000788	nuclear nucleosome	0.058
	GO:0030660	Golgi-associated vesicle membrane	0.060
	GO:0044432	endoplasmic reticulum part	0.060
	GO:0033178	proton-transporting two-sector ATPase co...	0.067
	GO:0030136	clathrin-coated vesicle	0.077
	GO:0009504	cell plate	0.078
	GO:0044433	cytoplasmic vesicle part	0.080
	GO:0005737	cytoplasm	0.084
	GO:0000325	plant-type vacuole	0.097
	GO:0000347	THO complex	0.097
	GO:0012506	vesicle membrane	0.100
	GO:0016798	hydrolase activity, acting on glycosyl b...	0.000
	GO:0016491	oxidoreductase activity	0.000
	GO:0005215	transporter activity	0.000
	GO:0022857	transmembrane transporter activity	0.000
	GO:0016830	carbon-carbon lyase activity	0.000
	GO:0016831	carboxy-lyase activity	0.000
	GO:0050662	coenzyme binding	0.000
	GO:0015318	inorganic molecular entity transmembrane...	0.000
	GO:0005088	Ras guanyl-nucleotide exchange factor ac...	0.001
	GO:0004650	polygalacturonase activity	0.001
	GO:0015075	ion transmembrane transporter activity	0.001
	GO:0046933	proton-transporting ATP synthase activit...	0.001
	GO:0016857	racemase and epimerase activity, acting ...	0.001
	GO:0008194	UDP-glycosyltransferase activity	0.002
	GO:0015144	carbohydrate transmembrane transporter a...	0.002
	GO:0016679	oxidoreductase activity, acting on diphe...	0.002
	GO:0005085	guanyl-nucleotide exchange factor activi...	0.002
	GO:0008238	exopeptidase activity	0.002
	GO:0015077	monovalent inorganic cation transmembran...	0.002
	GO:0030276	clathrin binding	0.002
	GO:0000287	magnesium ion binding	0.003
	GO:0036442	proton-exporting ATPase activity	0.003
	GO:0046961	proton-transporting ATPase activity, rot...	0.003
	GO:0004565	beta-galactosidase activity	0.003
	GO:0017048	Rho GTPase binding	0.004
	GO:0015078	proton transmembrane transporter activit...	0.004
	GO:0008374	O-acyltransferase activity	0.004
	GO:0015925	galactosidase activity	0.004
	GO:0016835	carbon-oxygen lyase activity	0.004
	GO:0016682	oxidoreductase activity, acting on diphe...	0.005
	GO:1901618	organic hydroxy compound transmembrane t...	0.006
	GO:0004683	calmodulin-dependent protein kinase acti...	0.006
	GO:0009931	calcium-dependent protein serine/threoni...	0.006
	GO:0010857	calcium-dependent protein kinase activit...	0.006
	GO:0005089	Rho guanyl-nucleotide exchange factor ac...	0.006
	GO:0015166	polyol transmembrane transporter activit...	0.006
	GO:0015020	glucuronosyltransferase activity	0.007

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MF

GO type	GO ID	Description	Adj. p-value
	GO:0022890	inorganic cation transmembrane transport...	0.007
	GO:0005200	structural constituent of cytoskeleton	0.008
	GO:0008081	phosphoric diester hydrolase activity	0.008
	GO:0022804	active transmembrane transporter activit...	0.009
	GO:0008324	cation transmembrane transporter activit...	0.009
	GO:0022838	substrate-specific channel activity	0.009
	GO:0046982	protein heterodimerization activity	0.012
	GO:0001883	purine nucleoside binding	0.012
	GO:0005525	GTP binding	0.012
	GO:0016854	racemase and epimerase activity	0.012
	GO:0019001	guanyl nucleotide binding	0.012
	GO:0032550	purine ribonucleoside binding	0.012
	GO:0032561	guanyl ribonucleotide binding	0.012
	GO:0052716	hydroquinone:oxygen oxidoreductase activ...	0.012
	GO:0015267	channel activity	0.014
	GO:0022803	passive transmembrane transporter activi...	0.014
	GO:0051287	NAD binding	0.014
	GO:0032549	ribonucleoside binding	0.015
	GO:0004427	inorganic diphosphatase activity	0.016
	GO:0001882	nucleoside binding	0.017
	GO:0004364	glutathione transferase activity	0.017
	GO:0008509	anion transmembrane transporter activity	0.021
	GO:0004743	pyruvate kinase activity	0.025
	GO:0030955	potassium ion binding	0.025
	GO:0031420	alkali metal ion binding	0.025
	GO:0015103	inorganic anion transmembrane transporte...	0.025
	GO:0003779	actin binding	0.026
	GO:0042578	phosphoric ester hydrolase activity	0.027
	GO:0046912	transferase activity, transferring acyl ...	0.027
	GO:0016651	oxidoreductase activity, acting on NAD(P...	0.029
	GO:0047372	acylglycerol lipase activity	0.030
	GO:0016782	transferase activity, transferring sulfu...	0.037
	GO:0016838	carbon-oxygen lyase activity, acting on ...	0.044
	GO:0016836	hydro-lyase activity	0.044
	GO:0030170	pyridoxal phosphate binding	0.047
	GO:0070279	vitamin B6 binding	0.047
	GO:0070569	uridylyltransferase activity	0.049
	GO:0019842	vitamin binding	0.050
	GO:0016407	acetyltransferase activity	0.065
	GO:1901505	carbohydrate derivative transmembrane tr...	0.083
	GO:0016799	hydrolase activity, hydrolyzing N-glycos...	0.091
	GO:0019829	cation-transporting ATPase activity	0.096
	GO:0022853	active ion transmembrane transporter act...	0.096
	GO:0042625	ATPase coupled ion transmembrane transpo...	0.096

4.3.9 Root - Preflowering - Cluster 9

GO type	GO ID	Description	Adj. p-value
BP	GO:0006396	RNA processing	0.000
	GO:0006464	cellular protein modification process	0.000
	GO:0006351	transcription, DNA-templated	0.000
	GO:0034470	ncRNA processing	0.000
	GO:0009451	RNA modification	0.000
	GO:0006259	DNA metabolic process	0.000
	GO:0008033	tRNA processing	0.000
	GO:0051276	chromosome organization	0.000
	GO:0006400	tRNA modification	0.002
	GO:0006399	tRNA metabolic process	0.004
	GO:0006793	phosphorus metabolic process	0.004
	GO:0034654	nucleobase-containing compound biosynthe...	0.005
	GO:0009812	flavonoid metabolic process	0.006
	GO:2000241	regulation of reproductive process	0.008
	GO:0002098	tRNA wobble uridine modification	0.014
	GO:0070192	chromosome organization involved in meio...	0.014
	GO:0140013	meiotic nuclear division	0.014
	GO:0048285	organelle fission	0.014
	GO:2000026	regulation of multicellular organismal d...	0.016
	GO:0007127	meiosis I	0.016
	GO:0061982	meiosis I cell cycle process	0.016
	GO:1903046	meiotic cell cycle process	0.017
	GO:0044267	cellular protein metabolic process	0.018
	GO:0022414	reproductive process	0.018
	GO:0051321	meiotic cell cycle	0.021
	GO:0006310	DNA recombination	0.023
	GO:0000280	nuclear division	0.023
	GO:0048580	regulation of post-embryonic development	0.024
	GO:0002097	tRNA wobble base modification	0.026
	GO:0019538	protein metabolic process	0.027
	GO:0000003	reproduction	0.030
	GO:0051239	regulation of multicellular organismal p...	0.030
	GO:0009736	cytokinin-activated signaling pathway	0.036
	GO:0007131	reciprocal meiotic recombination	0.042
	GO:0035825	homologous recombination	0.042
	GO:0071368	cellular response to cytokinin stimulus	0.057
	GO:0033554	cellular response to stress	0.068
	GO:0050793	regulation of developmental process	0.069
	GO:0022402	cell cycle process	0.074
	GO:0000160	phosphorelay signal transduction system	0.080
CC	GO:0005654	nucleoplasm	0.000
	GO:0043231	intracellular membrane-bounded organelle	0.067
	GO:0043227	membrane-bounded organelle	0.098
	GO:0000166	nucleotide binding	0.000
	GO:0042623	ATPase activity, coupled	0.000
	GO:0016887	ATPase activity	0.000

Continued on next page

MF

GO type	GO ID	Description	Adj. p-value
	GO:0017111	nucleoside-triphosphatase activity	0.000
	GO:0004519	endonuclease activity	0.001
	GO:0003677	DNA binding	0.001
	GO:0016817	hydrolase activity, acting on acid anhyd...	0.001
	GO:0016462	pyrophosphatase activity	0.002
	GO:0008094	DNA-dependent ATPase activity	0.002
	GO:0016818	hydrolase activity, acting on acid anhyd...	0.002
	GO:0140097	catalytic activity, acting on DNA	0.032
	GO:0005506	iron ion binding	0.042
	GO:0043565	sequence-specific DNA binding	0.058
	GO:0004497	monooxygenase activity	0.067
	GO:0016740	transferase activity	0.067
	GO:0016705	oxidoreductase activity, acting on paire...	0.070
	GO:0051213	dioxygenase activity	0.074
	GO:0003700	DNA binding transcription factor activit...	0.094

4.3.10 Root - Preflowering - Cluster 10

GO type	GO ID	Description	Adj. p-value
BP	GO:0042493	response to drug	0.000
	GO:0019219	regulation of nucleobase-containing comp...	0.005
	GO:2000112	regulation of cellular macromolecule bio...	0.006
	GO:0010468	regulation of gene expression	0.007
	GO:0055114	oxidation-reduction process	0.007
	GO:1903506	regulation of nucleic acid-templated tra...	0.007
	GO:2001141	regulation of RNA biosynthetic process	0.007
	GO:0009627	systemic acquired resistance	0.009
	GO:0010556	regulation of macromolecule biosynthetic...	0.018
	GO:0006351	transcription, DNA-templated	0.018
	GO:0006749	glutathione metabolic process	0.020
	GO:0044550	secondary metabolite biosynthetic proces...	0.023
	GO:0031326	regulation of cellular biosynthetic proc...	0.027
	GO:0032446	protein modification by small protein co...	0.029
	GO:0009617	response to bacterium	0.030
	GO:0009889	regulation of biosynthetic process	0.034
	GO:0006855	drug transmembrane transport	0.034
	GO:0015893	drug transport	0.034
	GO:0046677	response to antibiotic	0.045
	GO:0097659	nucleic acid-templated transcription	0.050
	GO:0010243	response to organonitrogen compound	0.051
	GO:0032774	RNA biosynthetic process	0.061
	GO:0016567	protein ubiquitination	0.086
	GO:0042742	defense response to bacterium	0.088
	GO:0006829	zinc ion transport	0.090
	GO:0009607	response to biotic stimulus	0.090
CC	GO:0044459	plasma membrane part	0.018
MF	GO:0004497	monooxygenase activity	0.000
	GO:0016705	oxidoreductase activity, acting on paire...	0.000
	GO:0015291	secondary active transmembrane transport...	0.000
	GO:0022857	transmembrane transporter activity	0.000
	GO:0005215	transporter activity	0.000
	GO:0022804	active transmembrane transporter activit...	0.001
	GO:0046527	glucosyltransferase activity	0.002
	GO:0035639	purine ribonucleoside triphosphate bindi...	0.002
	GO:0008194	UDP-glycosyltransferase activity	0.002
	GO:0015318	inorganic molecular entity transmembrane...	0.002
	GO:0051213	dioxygenase activity	0.002
	GO:0004364	glutathione transferase activity	0.003
	GO:0043167	ion binding	0.004
	GO:0019787	ubiquitin-like protein transferase activ...	0.010
	GO:0015075	ion transmembrane transporter activity	0.010
	GO:0048037	cofactor binding	0.015
	GO:0001871	pattern binding	0.017
	GO:0030247	polysaccharide binding	0.017
	GO:0016758	transferase activity, transferring hexos...	0.028

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0003677	DNA binding	0.031
	GO:0004842	ubiquitin-protein transferase activity	0.033
	GO:0046914	transition metal ion binding	0.043
	GO:0005385	zinc ion transmembrane transporter activ...	0.056
	GO:0008324	cation transmembrane transporter activit...	0.057
	GO:0015238	drug transmembrane transporter activity	0.073
	GO:0016829	lyase activity	0.091

4.3.11 Root - Preflowering - Cluster 11

GO type	GO ID	Description	Adj. p-value
	GO:0005976	polysaccharide metabolic process	0.000
	GO:0044264	cellular polysaccharide metabolic proces...	0.000
	GO:0044042	glucan metabolic process	0.000
	GO:0006073	cellular glucan metabolic process	0.000
	GO:0005975	carbohydrate metabolic process	0.000
	GO:0016052	carbohydrate catabolic process	0.000
	GO:0000272	polysaccharide catabolic process	0.000
	GO:0044247	cellular polysaccharide catabolic proces...	0.000
	GO:0007010	cytoskeleton organization	0.000
	GO:0033043	regulation of organelle organization	0.000
	GO:0048868	pollen tube development	0.000
	GO:0044275	cellular carbohydrate catabolic process	0.000
	GO:0009790	embryo development	0.000
	GO:1903047	mitotic cell cycle process	0.000
	GO:0097237	cellular response to toxic substance	0.001
	GO:0005982	starch metabolic process	0.001
	GO:0051128	regulation of cellular component organiz...	0.002
	GO:0051273	beta-glucan metabolic process	0.002
	GO:0009791	post-embryonic development	0.002
	GO:0009555	pollen development	0.002
	GO:0009636	response to toxic substance	0.003
	GO:0030258	lipid modification	0.003
	GO:0040029	regulation of gene expression, epigeneti...	0.003
	GO:0032506	cytokinetic process	0.004
	GO:1902410	mitotic cytokinetic process	0.004
	GO:0006979	response to oxidative stress	0.004
	GO:0009793	embryo development ending in seed dorman...	0.004
	GO:0098869	cellular oxidant detoxification	0.004
	GO:0010393	galacturonan metabolic process	0.004
	GO:0045488	pectin metabolic process	0.004
	GO:0005983	starch catabolic process	0.004
	GO:0031935	regulation of chromatin silencing	0.004
	GO:0032535	regulation of cellular component size	0.004
	GO:0090066	regulation of anatomical structure size	0.004
	GO:0009826	unidimensional cell growth	0.005
	GO:0045489	pectin biosynthetic process	0.005
	GO:0048731	system development	0.007
	GO:0050793	regulation of developmental process	0.007
	GO:0009415	response to water	0.007
	GO:0051276	chromosome organization	0.007
	GO:0098657	import into cell	0.008
	GO:0009414	response to water deprivation	0.010
	GO:0006012	galactose metabolic process	0.010
	GO:0015988	energy coupled proton transmembrane tran...	0.010
	GO:0015991	ATP hydrolysis coupled proton transport	0.010
	GO:0090662	ATP hydrolysis coupled transmembrane tra...	0.010

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0099131	ATP hydrolysis coupled ion transmembrane...	0.010
	GO:0099132	ATP hydrolysis coupled cation transmembr...	0.010
	GO:0009845	seed germination	0.010
	GO:0008361	regulation of cell size	0.012
	GO:0055046	microgametogenesis	0.012
	GO:0000226	microtubule cytoskeleton organization	0.012
	GO:0000726	non-recombinational repair	0.012
	GO:0006303	double-strand break repair via nonhomolo...	0.012
	GO:0009932	cell tip growth	0.012
	GO:0009642	response to light intensity	0.013
	GO:0097305	response to alcohol	0.014
	GO:0001101	response to acid chemical	0.015
	GO:0006897	endocytosis	0.015
	GO:0022406	membrane docking	0.015
	GO:0140056	organelle localization by membrane tethe...	0.015
	GO:0072330	monocarboxylic acid biosynthetic process	0.016
	GO:0048468	cell development	0.016
	GO:0048229	gametophyte development	0.017
	GO:0048278	vesicle docking	0.018
	GO:0044255	cellular lipid metabolic process	0.018
	GO:0016042	lipid catabolic process	0.019
	GO:0090351	seedling development	0.019
	GO:0006986	response to unfolded protein	0.019
	GO:0009888	tissue development	0.020
	GO:0048608	reproductive structure development	0.020
	GO:0061458	reproductive system development	0.020
	GO:0010033	response to organic substance	0.020
	GO:0006457	protein folding	0.022
	GO:0030104	water homeostasis	0.022
	GO:0009737	response to abscisic acid	0.024
	GO:0033993	response to lipid	0.024
	GO:0019915	lipid storage	0.026
	GO:0022603	regulation of anatomical structure morph...	0.026
	GO:0051567	histone H3-K9 methylation	0.026
	GO:0061647	histone H3-K9 modification	0.026
	GO:0046486	glycerolipid metabolic process	0.026
	GO:0065008	regulation of biological quality	0.027
	GO:0010035	response to inorganic substance	0.027
	GO:0010191	mucilage metabolic process	0.028
	GO:0006075	(1-¿3)-beta-D-glucan biosynthetic proces...	0.028
	GO:0046434	organophosphate catabolic process	0.028
	GO:0009644	response to high light intensity	0.029
	GO:0008154	actin polymerization or depolymerization	0.030
	GO:0010029	regulation of seed germination	0.030
	GO:0046854	phosphatidylinositol phosphorylation	0.030
	GO:0019637	organophosphate metabolic process	0.031
	GO:1900140	regulation of seedling development	0.031
	GO:0000302	response to reactive oxygen species	0.032
	GO:0018205	peptidyl-lysine modification	0.032

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GO type	GO ID	Description	Adj. p-value
	GO:0050826	response to freezing	0.034
	GO:0071470	cellular response to osmotic stress	0.035
	GO:0048193	Golgi vesicle transport	0.038
	GO:0006644	phospholipid metabolic process	0.038
	GO:0009123	nucleoside monophosphate metabolic proce...	0.038
	GO:0043647	inositol phosphate metabolic process	0.038
	GO:0010192	mucilage biosynthetic process	0.038
	GO:0006884	cell volume homeostasis	0.039
	GO:0009161	ribonucleoside monophosphate metabolic p...	0.039
	GO:0009992	cellular water homeostasis	0.039
	GO:0015791	polyol transport	0.039
	GO:0015793	glycerol transport	0.039
	GO:0051274	beta-glucan biosynthetic process	0.039
	GO:0006089	lactate metabolic process	0.040
	GO:0019243	methylglyoxal catabolic process to D-lac...	0.040
	GO:0061727	methylglyoxal catabolic process to lacta...	0.040
	GO:0008064	regulation of actin polymerization or de...	0.041
	GO:0030832	regulation of actin filament length	0.041
	GO:0032956	regulation of actin cytoskeleton organiz...	0.041
	GO:0032970	regulation of actin filament-based proce...	0.041
	GO:0034968	histone lysine methylation	0.041
	GO:0110053	regulation of actin filament organizatio...	0.041
	GO:0005984	disaccharide metabolic process	0.041
	GO:0007389	pattern specification process	0.041
	GO:0000723	telomere maintenance	0.041
	GO:0032200	telomere organization	0.041
	GO:0033044	regulation of chromosome organization	0.041
	GO:0030245	cellulose catabolic process	0.041
	GO:0042180	cellular ketone metabolic process	0.042
	GO:0071214	cellular response to abiotic stimulus	0.047
	GO:0104004	cellular response to environmental stimu...	0.047
	GO:0050896	response to stimulus	0.048
	GO:0005985	sucrose metabolic process	0.049
	GO:0006631	fatty acid metabolic process	0.049
	GO:0006970	response to osmotic stress	0.049
	GO:0030029	actin filament-based process	0.049
	GO:0060968	regulation of gene silencing	0.049
	GO:1902275	regulation of chromatin organization	0.050
	GO:0006650	glycerophospholipid metabolic process	0.050
	GO:0048359	mucilage metabolic process involved in s...	0.050
	GO:0097435	supramolecular fiber organization	0.050
	GO:0016579	protein deubiquitination	0.051
	GO:0046834	lipid phosphorylation	0.051
	GO:0046185	aldehyde catabolic process	0.051
	GO:0006950	response to stress	0.051
	GO:0034614	cellular response to reactive oxygen spe...	0.053
	GO:0009438	methylglyoxal metabolic process	0.054
	GO:0042182	ketone catabolic process	0.054
	GO:0051596	methylglyoxal catabolic process	0.054

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0009126	purine nucleoside monophosphate metaboli...	0.054
	GO:0009167	purine ribonucleoside monophosphate meta...	0.054
	GO:0042391	regulation of membrane potential	0.055
	GO:0030041	actin filament polymerization	0.055
	GO:0030833	regulation of actin filament polymerizat...	0.055
	GO:0009259	ribonucleotide metabolic process	0.056
	GO:0006074	(1-¿3)-beta-D-glucan metabolic process	0.057
	GO:0006833	water transport	0.059
	GO:0009166	nucleotide catabolic process	0.059
	GO:0042044	fluid transport	0.059
	GO:0035966	response to topologically incorrect prot...	0.060
	GO:0051275	beta-glucan catabolic process	0.060
	GO:0030004	cellular monovalent inorganic cation hom...	0.062
	GO:0060249	anatomical structure homeostasis	0.062
	GO:0051493	regulation of cytoskeleton organization	0.064
	GO:0009741	response to brassinosteroid	0.064
	GO:0016570	histone modification	0.065
	GO:0034404	nucleobase-containing small molecule bio...	0.065
	GO:0009725	response to hormone	0.065
	GO:0033554	cellular response to stress	0.065
	GO:0046034	ATP metabolic process	0.067
	GO:0009719	response to endogenous stimulus	0.067
	GO:0015850	organic hydroxy compound transport	0.067
	GO:1901292	nucleoside phosphate catabolic process	0.067
	GO:0010876	lipid localization	0.068
	GO:0019359	nicotinamide nucleotide biosynthetic pro...	0.071
	GO:0048878	chemical homeostasis	0.071
	GO:0006096	glycolytic process	0.071
	GO:0006757	ATP generation from ADP	0.071
	GO:0009135	purine nucleoside diphosphate metabolic ...	0.071
	GO:0009179	purine ribonucleoside diphosphate metabo...	0.071
	GO:0009185	ribonucleoside diphosphate metabolic pro...	0.071
	GO:0042866	pyruvate biosynthetic process	0.071
	GO:0046031	ADP metabolic process	0.071
	GO:0009127	purine nucleoside monophosphate biosynth...	0.075
	GO:0009168	purine ribonucleoside monophosphate bios...	0.075
	GO:0010214	seed coat development	0.077
	GO:0006002	fructose 6-phosphate metabolic process	0.080
	GO:0030036	actin cytoskeleton organization	0.081
	GO:0003002	regionalization	0.082
	GO:0018022	peptidyl-lysine methylation	0.086
	GO:1902903	regulation of supramolecular fiber organ...	0.086
	GO:0016571	histone methylation	0.086
	GO:0051085	chaperone cofactor-dependent protein ref...	0.086
	GO:0009201	ribonucleoside triphosphate biosynthetic...	0.089
	GO:1901000	regulation of response to salt stress	0.089
	GO:0009260	ribonucleotide biosynthetic process	0.091
	GO:0046390	ribose phosphate biosynthetic process	0.091
	GO:0021700	developmental maturation	0.094

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GO type	GO ID	Description	Adj. p-value
	GO:0006816	calcium ion transport	0.095
	GO:0019363	pyridine nucleotide biosynthetic process	0.097
	GO:0022604	regulation of cell morphogenesis	0.098
CC	GO:0030117	membrane coat	0.002
	GO:0048475	coated membrane	0.002
	GO:0033176	proton-transporting V-type ATPase comple...	0.003
	GO:0098588	bounding membrane of organelle	0.005
	GO:0031982	vesicle	0.009
	GO:0005819	spindle	0.012
	GO:0005886	plasma membrane	0.015
	GO:0005773	vacuole	0.018
	GO:0005802	trans-Golgi network	0.019
	GO:0005811	lipid droplet	0.020
	GO:0097708	intracellular vesicle	0.021
	GO:0000148	1,3-beta-D-glucan synthase complex	0.022
	GO:0030135	coated vesicle	0.023
	GO:0031410	cytoplasmic vesicle	0.023
	GO:0030659	cytoplasmic vesicle membrane	0.030
	GO:0005911	cell-cell junction	0.039
	GO:0009506	plasmodesma	0.039
	GO:0030054	cell junction	0.039
	GO:0030662	coated vesicle membrane	0.039
	GO:0031984	organelle subcompartment	0.039
	GO:0044459	plasma membrane part	0.039
	GO:0055044	symplast	0.039
	GO:0090406	pollen tube	0.039
	GO:0012506	vesicle membrane	0.045
	GO:0044437	vacuolar part	0.048
	GO:0005774	vacuolar membrane	0.050
	GO:0009705	plant-type vacuole membrane	0.056
	GO:0000782	telomere cap complex	0.056
	GO:0000783	nuclear telomere cap complex	0.056
	GO:0044433	cytoplasmic vesicle part	0.063
	GO:0030120	vesicle coat	0.070
	GO:0031226	intrinsic component of plasma membrane	0.070
	GO:0098805	whole membrane	0.072
	GO:0000781	chromosome, telomeric region	0.073
	GO:0030133	transport vesicle	0.075
	GO:0009504	cell plate	0.077
	GO:0033178	proton-transporting two-sector ATPase co...	0.083
	GO:0000325	plant-type vacuole	0.093
	GO:0004553	hydrolase activity, hydrolyzing O-glycos...	0.000
	GO:0017111	nucleoside-triphosphatase activity	0.000
	GO:0019783	ubiquitin-like protein-specific protease...	0.001
	GO:0043168	anion binding	0.003
	GO:0003824	catalytic activity	0.004
	GO:0016407	acetyltransferase activity	0.004
	GO:0016307	phosphatidylinositol phosphate kinase ac...	0.005
	GO:0030554	adenyl nucleotide binding	0.006

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GO type	GO ID	Description	Adj. p-value
	GO:0036094	small molecule binding	0.006
	GO:0005515	protein binding	0.007
	GO:0032559	adenyl ribonucleotide binding	0.007
	GO:0017076	purine nucleotide binding	0.008
	GO:0051087	chaperone binding	0.009
	GO:0032553	ribonucleotide binding	0.010
	GO:0032555	purine ribonucleotide binding	0.010
	GO:0097367	carbohydrate derivative binding	0.011
	GO:0008289	lipid binding	0.011
	GO:0005524	ATP binding	0.014
	GO:0015925	galactosidase activity	0.014
	GO:0005261	cation channel activity	0.015
	GO:0043167	ion binding	0.016
	GO:0035639	purine ribonucleoside triphosphate bindi...	0.019
	GO:0008144	drug binding	0.026
	GO:0004567	beta-mannosidase activity	0.027
	GO:0016757	transferase activity, transferring glyco...	0.027
	GO:0008270	zinc ion binding	0.027
	GO:0018024	histone-lysine N-methyltransferase activ...	0.027
	GO:0016788	hydrolase activity, acting on ester bond...	0.027
	GO:0015923	mannosidase activity	0.028
	GO:0003843	1,3-beta-D-glucan synthase activity	0.030
	GO:0060589	nucleoside-triphosphatase regulator acti...	0.030
	GO:0016903	oxidoreductase activity, acting on the a...	0.035
	GO:0051082	unfolded protein binding	0.040
	GO:0005372	water transmembrane transporter activity	0.040
	GO:0015250	water channel activity	0.040
	GO:0015254	glycerol channel activity	0.040
	GO:0015267	channel activity	0.040
	GO:0022803	passive transmembrane transporter activi...	0.040
	GO:0022838	substrate-specific channel activity	0.040
	GO:0036459	thiol-dependent ubiquitinyl hydrolase ac...	0.046
	GO:0101005	ubiquitinyl hydrolase activity	0.046
	GO:1901681	sulfur compound binding	0.046
	GO:0015166	polyol transmembrane transporter activit...	0.052
	GO:0004650	polygalacturonase activity	0.053
	GO:0015168	glycerol transmembrane transporter activ...	0.053
	GO:0035091	phosphatidylinositol binding	0.056
	GO:0005488	binding	0.057
	GO:0050661	NADP binding	0.058
	GO:1901618	organic hydroxy compound transmembrane t...	0.059
	GO:0015926	glucosidase activity	0.068
	GO:0016620	oxidoreductase activity, acting on the a...	0.068
	GO:0008810	cellulase activity	0.080
	GO:0043621	protein self-association	0.081
	GO:0015085	calcium ion transmembrane transporter ac...	0.088
	GO:0036442	proton-exporting ATPase activity	0.090
	GO:0008443	phosphofructokinase activity	0.092
	GO:0022843	voltage-gated cation channel activity	0.095

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GO type	GO ID	Description	Adj. p-value
	GO:0051015	actin filament binding	0.095
	GO:0004565	beta-galactosidase activity	0.095
	GO:0016278	lysine N-methyltransferase activity	0.095
	GO:0016279	protein-lysine N-methyltransferase activ...	0.095

4.3.12 Root - Preflowering - Cluster 12

GO type	GO ID	Description	Adj. p-value
	GO:0019748	secondary metabolic process	0.000
	GO:0009698	phenylpropanoid metabolic process	0.000
	GO:0010383	cell wall polysaccharide metabolic proce...	0.000
	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0072330	monocarboxylic acid biosynthetic process	0.000
	GO:0001101	response to acid chemical	0.000
	GO:0046351	disaccharide biosynthetic process	0.000
	GO:0009753	response to jasmonic acid	0.000
	GO:0045492	xylan biosynthetic process	0.000
	GO:0071229	cellular response to acid chemical	0.000
	GO:0006063	uronic acid metabolic process	0.000
	GO:0009867	jasmonic acid mediated signaling pathway	0.000
	GO:0009725	response to hormone	0.000
	GO:0009414	response to water deprivation	0.001
	GO:0071495	cellular response to endogenous stimulus	0.002
	GO:0009620	response to fungus	0.002
	GO:0032870	cellular response to hormone stimulus	0.002
	GO:0006950	response to stress	0.002
	GO:0031407	oxylipin metabolic process	0.002
	GO:1903506	regulation of nucleic acid-templated tra...	0.003
	GO:2001141	regulation of RNA biosynthetic process	0.003
	GO:0048878	chemical homeostasis	0.003
	GO:0051273	beta-glucan metabolic process	0.004
	GO:0048544	recognition of pollen	0.004
	GO:0034220	ion transmembrane transport	0.004
	GO:0055082	cellular chemical homeostasis	0.005
	GO:0009311	oligosaccharide metabolic process	0.005
	GO:0009755	hormone-mediated signaling pathway	0.005
	GO:0010345	suberin biosynthetic process	0.005
	GO:0031408	oxylipin biosynthetic process	0.005
	GO:0042445	hormone metabolic process	0.005
	GO:0008037	cell recognition	0.005
	GO:0050794	regulation of cellular process	0.005
	GO:0033692	cellular polysaccharide biosynthetic pro...	0.007
	GO:0051252	regulation of RNA metabolic process	0.007
	GO:0030244	cellulose biosynthetic process	0.007
	GO:0043207	response to external biotic stimulus	0.007
	GO:0051707	response to other organism	0.007
	GO:0009875	pollen-pistil interaction	0.008
	GO:0007264	small GTPase mediated signal transductio...	0.009
	GO:0031347	regulation of defense response	0.009
	GO:0006631	fatty acid metabolic process	0.009
	GO:0046777	protein autophosphorylation	0.011
	GO:0009695	jasmonic acid biosynthetic process	0.012
	GO:0071310	cellular response to organic substance	0.012
	GO:0065007	biological regulation	0.012

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BP

GO type	GO ID	Description	Adj. p-value
	GO:0050789	regulation of biological process	0.014
	GO:0010817	regulation of hormone levels	0.014
	GO:0010143	cutin biosynthetic process	0.015
	GO:0019219	regulation of nucleobase-containing comp...	0.016
	GO:0097659	nucleic acid-templated transcription	0.017
	GO:0032774	RNA biosynthetic process	0.018
	GO:0051716	cellular response to stimulus	0.018
	GO:0006355	regulation of transcription, DNA-templat...	0.018
	GO:0009969	xyloglucan biosynthetic process	0.018
	GO:0009605	response to external stimulus	0.018
	GO:0044281	small molecule metabolic process	0.018
	GO:0055081	anion homeostasis	0.021
	GO:0016053	organic acid biosynthetic process	0.022
	GO:0046394	carboxylic acid biosynthetic process	0.022
	GO:0051275	beta-glucan catabolic process	0.022
	GO:0010646	regulation of cell communication	0.023
	GO:0010215	cellulose microfibril organization	0.025
	GO:0009966	regulation of signal transduction	0.025
	GO:0009694	jasmonic acid metabolic process	0.026
	GO:0023051	regulation of signaling	0.027
	GO:0010556	regulation of macromolecule biosynthetic...	0.030
	GO:0080134	regulation of response to stress	0.031
	GO:0009617	response to bacterium	0.031
	GO:0009269	response to desiccation	0.032
	GO:0035556	intracellular signal transduction	0.033
	GO:0051704	multi-organism process	0.033
	GO:0046686	response to cadmium ion	0.034
	GO:0006820	anion transport	0.036
	GO:0048268	clathrin coat assembly	0.036
	GO:0009751	response to salicylic acid	0.037
	GO:0098542	defense response to other organism	0.040
	GO:0009889	regulation of biosynthetic process	0.040
	GO:0042545	cell wall modification	0.041
	GO:0031326	regulation of cellular biosynthetic proc...	0.043
	GO:0006633	fatty acid biosynthetic process	0.043
	GO:0050832	defense response to fungus	0.051
	GO:0009863	salicylic acid mediated signaling pathwa...	0.052
	GO:0070726	cell wall assembly	0.059
	GO:0071668	plant-type cell wall assembly	0.059
	GO:0046677	response to antibiotic	0.061
	GO:0071446	cellular response to salicylic acid stim...	0.062
	GO:0050801	ion homeostasis	0.068
	GO:0009856	pollination	0.068
	GO:0044706	multi-multicellular organism process	0.068
	GO:0046364	monosaccharide biosynthetic process	0.070
	GO:0051274	beta-glucan biosynthetic process	0.070
	GO:0010214	seed coat development	0.073
	GO:0065008	regulation of biological quality	0.074
	GO:0019438	aromatic compound biosynthetic process	0.077

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0009690	cytokinin metabolic process	0.080
	GO:0006351	transcription, DNA-templated	0.080
	GO:0036065	fucosylation	0.082
	GO:0006970	response to osmotic stress	0.089
	GO:0006790	sulfur compound metabolic process	0.090
	GO:0009069	serine family amino acid metabolic proce...	0.091
	GO:0071215	cellular response to abscisic acid stimu...	0.099
	GO:0097306	cellular response to alcohol	0.099
CC	GO:0031225	anchored component of membrane	0.000
	GO:0044421	extracellular region part	0.000
	GO:0009521	photosystem	0.004
	GO:0005769	early endosome	0.014
	GO:0005768	endosome	0.019
	GO:0090406	pollen tube	0.044
	GO:0012505	endomembrane system	0.063
	GO:0009523	photosystem II	0.096
MF	GO:0016491	oxidoreductase activity	0.000
	GO:0016773	phosphotransferase activity, alcohol gro...	0.000
	GO:0030246	carbohydrate binding	0.000
	GO:0016705	oxidoreductase activity, acting on paire...	0.000
	GO:0015318	inorganic molecular entity transmembrane...	0.000
	GO:0004805	trehalose-phosphatase activity	0.001
	GO:0015075	ion transmembrane transporter activity	0.001
	GO:0016791	phosphatase activity	0.002
	GO:0015020	glucuronosyltransferase activity	0.002
	GO:0008081	phosphoric diester hydrolase activity	0.003
	GO:0019203	carbohydrate phosphatase activity	0.004
	GO:0030276	clathrin binding	0.004
	GO:0005516	calmodulin binding	0.004
	GO:0022838	substrate-specific channel activity	0.005
	GO:0016759	cellulose synthase activity	0.005
	GO:0016760	cellulose synthase (UDP-forming) activit...	0.005
	GO:0008422	beta-glucosidase activity	0.005
	GO:0043565	sequence-specific DNA binding	0.005
	GO:0008236	serine-type peptidase activity	0.005
	GO:0017171	serine hydrolase activity	0.005
	GO:0042285	xylosyltransferase activity	0.006
	GO:0008107	galactoside 2-alpha-L-fucosyltransferase...	0.006
	GO:0031127	alpha-(1,2)-fucosyltransferase activity	0.006
	GO:0004871	signal transducer activity	0.006
	GO:0015018	galactosylgalactosylxylosylprotein 3-bet...	0.007
	GO:0015267	channel activity	0.009
	GO:0022803	passive transmembrane transporter activi...	0.009
	GO:0016838	carbon-oxygen lyase activity, acting on ...	0.010
	GO:0004602	glutathione peroxidase activity	0.013
	GO:0015926	glucosidase activity	0.014
	GO:0003677	DNA binding	0.015
	GO:0005545	1-phosphatidylinositol binding	0.016
	GO:0004683	calmodulin-dependent protein kinase acti...	0.018

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0009931	calcium-dependent protein serine/threoni...	0.018
	GO:0010857	calcium-dependent protein kinase activit...	0.018
	GO:0022890	inorganic cation transmembrane transport...	0.021
	GO:0010333	terpene synthase activity	0.022
	GO:0097367	carbohydrate derivative binding	0.023
	GO:0043168	anion binding	0.026
	GO:0015077	monovalent inorganic cation transmembran...	0.026
	GO:0004702	signal transducer, downstream of recepto...	0.030
	GO:0005057	signal transducer activity, downstream o...	0.030
	GO:0008417	fucosyltransferase activity	0.034
	GO:0016717	oxidoreductase activity, acting on paire...	0.034
	GO:0032559	adenyl ribonucleotide binding	0.036
	GO:0001067	regulatory region nucleic acid binding	0.040
	GO:0044212	transcription regulatory region DNA bind...	0.040
	GO:0008509	anion transmembrane transporter activity	0.041
	GO:0030554	adenyl nucleotide binding	0.046
	GO:0016835	carbon-oxygen lyase activity	0.049
	GO:0015079	potassium ion transmembrane transporter ...	0.051
	GO:0008378	galactosyltransferase activity	0.055
	GO:0032553	ribonucleotide binding	0.071
	GO:0032555	purine ribonucleotide binding	0.085
	GO:0050662	coenzyme binding	0.088
	GO:0008144	drug binding	0.094

4.3.13 Root - Preflowering - Cluster 13

GO type	GO ID	Description	Adj. p-value
BP	GO:0032446	protein modification by small protein co...	0.000
	GO:0055085	transmembrane transport	0.000
	GO:0009751	response to salicylic acid	0.000
	GO:0009753	response to jasmonic acid	0.002
	GO:0042430	indole-containing compound metabolic pro...	0.003
	GO:0006026	aminoglycan catabolic process	0.005
	GO:0006030	chitin metabolic process	0.005
	GO:0006032	chitin catabolic process	0.005
	GO:0043207	response to external biotic stimulus	0.005
	GO:0046348	amino sugar catabolic process	0.005
	GO:0051707	response to other organism	0.005
	GO:1901072	glucosamine-containing compound cataboli...	0.005
	GO:0006749	glutathione metabolic process	0.005
	GO:0009627	systemic acquired resistance	0.005
	GO:0098542	defense response to other organism	0.005
	GO:0006022	aminoglycan metabolic process	0.007
	GO:0009867	jasmonic acid mediated signaling pathway	0.008
	GO:0071395	cellular response to jasmonic acid stimu...	0.011
	GO:0043666	regulation of phosphoprotein phosphatase...	0.013
	GO:0006857	oligopeptide transport	0.013
	GO:0080163	regulation of protein serine/threonine p...	0.013
	GO:0006568	tryptophan metabolic process	0.013
	GO:0006586	indolalkylamine metabolic process	0.013
	GO:0044550	secondary metabolite biosynthetic proces...	0.013
	GO:1901071	glucosamine-containing compound metaboli...	0.013
	GO:0003333	amino acid transmembrane transport	0.017
	GO:0010466	negative regulation of peptidase activit...	0.018
	GO:0010951	negative regulation of endopeptidase act...	0.018
	GO:0052547	regulation of peptidase activity	0.018
	GO:0052548	regulation of endopeptidase activity	0.018
	GO:1902022	L-lysine transport	0.018
	GO:1903401	L-lysine transmembrane transport	0.018
	GO:0043648	dicarboxylic acid metabolic process	0.019
	GO:0010921	regulation of phosphatase activity	0.024
	GO:0035304	regulation of protein dephosphorylation	0.024
	GO:0015893	drug transport	0.026
	GO:0035303	regulation of dephosphorylation	0.026
	GO:0009617	response to bacterium	0.027
	GO:0045861	negative regulation of proteolysis	0.027
	GO:0009862	systemic acquired resistance, salicylic ...	0.028
	GO:0007154	cell communication	0.028
	GO:0008643	carbohydrate transport	0.028
	GO:0000162	tryptophan biosynthetic process	0.034
	GO:0005996	monosaccharide metabolic process	0.034
	GO:0046219	indolalkylamine biosynthetic process	0.034
	GO:0006865	amino acid transport	0.040

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GO type	GO ID	Description	Adj. p-value
	GO:0006575	cellular modified amino acid metabolic p...	0.043
	GO:0009611	response to wounding	0.048
	GO:0044092	negative regulation of molecular functio...	0.048
	GO:0010112	regulation of systemic acquired resistan...	0.054
	GO:1905039	carboxylic acid transmembrane transport	0.054
	GO:0042447	hormone catabolic process	0.055
	GO:0006836	neurotransmitter transport	0.056
	GO:0006820	anion transport	0.061
	GO:0071229	cellular response to acid chemical	0.075
	GO:0042537	benzene-containing compound metabolic pr...	0.076
	GO:0043086	negative regulation of catalytic activit...	0.076
	GO:0046942	carboxylic acid transport	0.076
	GO:1901698	response to nitrogen compound	0.078
	GO:0009814	defense response, incompatible interacti...	0.086
	GO:0009072	aromatic amino acid family metabolic pro...	0.087
	GO:1903825	organic acid transmembrane transport	0.092
	GO:0051346	negative regulation of hydrolase activit...	0.096
CC	GO:0005886	plasma membrane	0.000
	GO:0031226	intrinsic component of plasma membrane	0.003
	GO:0044459	plasma membrane part	0.013
	GO:0044421	extracellular region part	0.098
	GO:0016705	oxidoreductase activity, acting on paire...	0.000
	GO:0019787	ubiquitin-like protein transferase activ...	0.000
	GO:0015291	secondary active transmembrane transport...	0.000
	GO:0022804	active transmembrane transporter activit...	0.000
	GO:0022857	transmembrane transporter activity	0.000
	GO:0035251	UDP-glucosyltransferase activity	0.001
	GO:0000166	nucleotide binding	0.002
	GO:1901265	nucleoside phosphate binding	0.002
	GO:0004364	glutathione transferase activity	0.002
	GO:0015293	symporter activity	0.002
	GO:0003677	DNA binding	0.002
	GO:0004568	chitinase activity	0.002
	GO:0005351	carbohydrate:proton symporter activity	0.003
	GO:0005402	carbohydrate:cation symporter activity	0.003
	GO:0015295	solute:proton symporter activity	0.003
	GO:0015294	solute:cation symporter activity	0.004
	GO:0004857	enzyme inhibitor activity	0.005
	GO:0030414	peptidase inhibitor activity	0.005
	GO:0061134	peptidase regulator activity	0.005
	GO:0004864	protein phosphatase inhibitor activity	0.006
	GO:0019212	phosphatase inhibitor activity	0.006
	GO:0004866	endopeptidase inhibitor activity	0.006
	GO:0061135	endopeptidase regulator activity	0.006
	GO:0016830	carbon-carbon lyase activity	0.007
	GO:0015318	inorganic molecular entity transmembrane...	0.007
	GO:0015181	arginine transmembrane transporter activ...	0.009
	GO:0015189	L-lysine transmembrane transporter activ...	0.009
	GO:0046527	glucosyltransferase activity	0.009

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MF

GO type	GO ID	Description	Adj. p-value
	GO:0019208	phosphatase regulator activity	0.011
	GO:0019888	protein phosphatase regulator activity	0.011
	GO:0015075	ion transmembrane transporter activity	0.012
	GO:0001047	core promoter binding	0.015
	GO:0015172	acidic amino acid transmembrane transpor...	0.015
	GO:0004867	serine-type endopeptidase inhibitor acti...	0.018
	GO:0042562	hormone binding	0.020
	GO:0015297	antiporter activity	0.021
	GO:0016765	transferase activity, transferring alkyl...	0.025
	GO:0019840	isoprenoid binding	0.025
	GO:0008194	UDP-glycosyltransferase activity	0.025
	GO:0001046	core promoter sequence-specific DNA bind...	0.025
	GO:0015144	carbohydrate transmembrane transporter a...	0.026
	GO:0004190	aspartic-type endopeptidase activity	0.027
	GO:0070001	aspartic-type peptidase activity	0.027
	GO:0005326	neurotransmitter transporter activity	0.027
	GO:0008324	cation transmembrane transporter activit...	0.032
	GO:0015174	basic amino acid transmembrane transport...	0.032
	GO:0015238	drug transmembrane transporter activity	0.042
	GO:0001228	transcriptional activator activity, RNA ...	0.043
	GO:0008483	transaminase activity	0.049
	GO:0016769	transferase activity, transferring nitro...	0.049
	GO:0015171	amino acid transmembrane transporter act...	0.050
	GO:0010427	abscisic acid binding	0.052
	GO:0048037	cofactor binding	0.065
	GO:0005385	zinc ion transmembrane transporter activ...	0.073
	GO:0016758	transferase activity, transferring hexos...	0.076
	GO:0046915	transition metal ion transmembrane trans...	0.077
	GO:0016491	oxidoreductase activity	0.077
	GO:0004970	ionotropic glutamate receptor activity	0.086
	GO:0005230	extracellular ligand-gated ion channel a...	0.086
	GO:0008066	glutamate receptor activity	0.086
	GO:0022824	transmitter-gated ion channel activity	0.086
	GO:0022835	transmitter-gated channel activity	0.086

4.3.14 Root - Preflowering - Cluster 14

GO type	GO ID	Description	Adj. p-value
	GO:0010467	gene expression	0.000
	GO:0043603	cellular amide metabolic process	0.000
	GO:1901564	organonitrogen compound metabolic proces...	0.000
	GO:0042254	ribosome biogenesis	0.000
	GO:0042273	ribosomal large subunit biogenesis	0.000
	GO:0043161	proteasome-mediated ubiquitin-dependent ...	0.000
	GO:0032446	protein modification by small protein co...	0.000
	GO:0010498	proteasomal protein catabolic process	0.001
	GO:0055085	transmembrane transport	0.002
	GO:0051603	proteolysis involved in cellular protein...	0.002
	GO:0044257	cellular protein catabolic process	0.002
	GO:0043632	modification-dependent macromolecule cat...	0.003
	GO:0031323	regulation of cellular metabolic process	0.004
	GO:0006511	ubiquitin-dependent protein catabolic pr...	0.004
	GO:0006355	regulation of transcription, DNA-templat...	0.004
	GO:0006568	tryptophan metabolic process	0.004
	GO:0006586	indolalkylamine metabolic process	0.004
	GO:0019941	modification-dependent protein catabolic...	0.004
	GO:0015749	monosaccharide transmembrane transport	0.005
	GO:0043412	macromolecule modification	0.005
	GO:0046483	heterocycle metabolic process	0.005
	GO:0051171	regulation of nitrogen compound metaboli...	0.005
	GO:2000112	regulation of cellular macromolecule bio...	0.005
	GO:0008645	hexose transmembrane transport	0.006
	GO:0042364	water-soluble vitamin biosynthetic proce...	0.006
	GO:0060255	regulation of macromolecule metabolic pr...	0.006
	GO:1901565	organonitrogen compound catabolic proces...	0.007
	GO:0000027	ribosomal large subunit assembly	0.007
	GO:0010921	regulation of phosphatase activity	0.007
	GO:1904659	glucose transmembrane transport	0.007
	GO:0031326	regulation of cellular biosynthetic proc...	0.008
	GO:0080090	regulation of primary metabolic process	0.008
	GO:1903506	regulation of nucleic acid-templated tra...	0.008
	GO:2001141	regulation of RNA biosynthetic process	0.008
	GO:0006836	neurotransmitter transport	0.008
	GO:0010556	regulation of macromolecule biosynthetic...	0.009
	GO:0030163	protein catabolic process	0.009
	GO:0006351	transcription, DNA-templated	0.010
	GO:0000162	tryptophan biosynthetic process	0.010
	GO:0046219	indolalkylamine biosynthetic process	0.010
	GO:0009889	regulation of biosynthetic process	0.011
	GO:0070647	protein modification by small protein co...	0.011
	GO:1901360	organic cyclic compound metabolic proces...	0.012
	GO:0019222	regulation of metabolic process	0.014
	GO:0046323	glucose import	0.014
BP	GO:0080163	regulation of protein serine/threonine p...	0.014

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0035303	regulation of dephosphorylation	0.014
	GO:0051252	regulation of RNA metabolic process	0.014
	GO:0009593	detection of chemical stimulus	0.014
	GO:0043666	regulation of phosphoprotein phosphatase...	0.015
	GO:0015802	basic amino acid transport	0.015
	GO:0010468	regulation of gene expression	0.016
	GO:0006508	proteolysis	0.016
	GO:0019748	secondary metabolic process	0.017
	GO:0006725	cellular aromatic compound metabolic pro...	0.019
	GO:0042430	indole-containing compound metabolic pro...	0.019
	GO:0006464	cellular protein modification process	0.020
	GO:0036211	protein modification process	0.020
	GO:0044265	cellular macromolecule catabolic process	0.020
	GO:0006857	oligopeptide transport	0.021
	GO:0097659	nucleic acid-templated transcription	0.021
	GO:0019219	regulation of nucleobase-containing comp...	0.023
	GO:0006952	defense response	0.023
	GO:0032774	RNA biosynthetic process	0.025
	GO:1901607	alpha-amino acid biosynthetic process	0.026
	GO:1905039	carboxylic acid transmembrane transport	0.027
	GO:0035304	regulation of protein dephosphorylation	0.028
	GO:0003333	amino acid transmembrane transport	0.032
	GO:0000041	transition metal ion transport	0.033
	GO:1903825	organic acid transmembrane transport	0.039
	GO:0006414	translational elongation	0.044
	GO:0009110	vitamin biosynthetic process	0.047
	GO:0006767	water-soluble vitamin metabolic process	0.057
	GO:0008652	cellular amino acid biosynthetic process	0.057
	GO:0000470	maturation of LSU-rRNA	0.058
	GO:0034219	carbohydrate transmembrane transport	0.059
	GO:0042274	ribosomal small subunit biogenesis	0.062
	GO:0045047	protein targeting to ER	0.063
	GO:0072599	establishment of protein localization to...	0.063
	GO:0071577	zinc ion transmembrane transport	0.069
	GO:0009309	amine biosynthetic process	0.076
	GO:0042401	cellular biogenic amine biosynthetic pro...	0.076
	GO:0009073	aromatic amino acid family biosynthetic ...	0.077
	GO:0006829	zinc ion transport	0.082
	GO:0008037	cell recognition	0.087
	GO:0009072	aromatic amino acid family metabolic pro...	0.089
	GO:0006913	nucleocytoplasmic transport	0.091
	GO:0051169	nuclear transport	0.091
	GO:0006790	sulfur compound metabolic process	0.095
	GO:0006865	amino acid transport	0.099
	GO:0033365	protein localization to organelle	0.100
CC	GO:0005839	proteasome core complex	0.001
	GO:0016021	integral component of membrane	0.002
	GO:0097526	spliceosomal tri-snRNP complex	0.003
	GO:0031224	intrinsic component of membrane	0.005

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0005761	mitochondrial ribosome	0.007
	GO:0000313	organellar ribosome	0.010
	GO:0005887	integral component of plasma membrane	0.012
	GO:0000315	organellar large ribosomal subunit	0.014
	GO:0005762	mitochondrial large ribosomal subunit	0.014
	GO:0044452	nucleolar part	0.014
	GO:0005686	U2 snRNP	0.015
	GO:0019773	proteasome core complex, alpha-subunit c...	0.018
	GO:0046540	U4/U6 x U5 tri-snRNP complex	0.028
	GO:0071011	precatalytic spliceosome	0.028
	GO:0005682	U5 snRNP	0.034
	GO:0005732	small nucleolar ribonucleoprotein comple...	0.035
	GO:0016591	DNA-directed RNA polymerase II, holoenzy...	0.035
	GO:0030532	small nuclear ribonucleoprotein complex	0.035
	GO:0097525	spliceosomal snRNP complex	0.035
	GO:0120114	Sm-like protein family complex	0.035
	GO:0000323	lytic vacuole	0.036
	GO:0030684	preribosome	0.036
	GO:0005764	lysosome	0.092
	GO:0004672	protein kinase activity	0.000
	GO:0019787	ubiquitin-like protein transferase activ...	0.001
	GO:0019843	rRNA binding	0.002
	GO:0004497	monooxygenase activity	0.003
	GO:0016705	oxidoreductase activity, acting on paire...	0.003
	GO:0016709	oxidoreductase activity, acting on paire...	0.003
	GO:0015174	basic amino acid transmembrane transport...	0.005
	GO:0015145	monosaccharide transmembrane transporter...	0.006
	GO:0003700	DNA binding transcription factor activit...	0.007
	GO:0005326	neurotransmitter transporter activity	0.007
	GO:0015149	hexose transmembrane transporter activit...	0.007
	GO:0022857	transmembrane transporter activity	0.008
	GO:0015291	secondary active transmembrane transport...	0.008
	GO:0001047	core promoter binding	0.010
	GO:0005355	glucose transmembrane transporter activi...	0.011
	GO:0004864	protein phosphatase inhibitor activity	0.012
	GO:0019212	phosphatase inhibitor activity	0.012
	GO:0140110	transcription regulator activity	0.012
	GO:0005506	iron ion binding	0.014
	GO:0001067	regulatory region nucleic acid binding	0.016
	GO:0044212	transcription regulatory region DNA bind...	0.016
	GO:0015293	symporter activity	0.017
	GO:0020037	heme binding	0.017
	GO:0001046	core promoter sequence-specific DNA bind...	0.017
	GO:0051213	dioxygenase activity	0.017
	GO:0016765	transferase activity, transferring alkyl...	0.019
	GO:0016830	carbon-carbon lyase activity	0.020
	GO:0019208	phosphatase regulator activity	0.020
	GO:0019888	protein phosphatase regulator activity	0.020
	GO:0051119	sugar transmembrane transporter activity	0.023
MF			Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0015295	solute:proton symporter activity	0.025
	GO:0005215	transporter activity	0.025
	GO:0005351	carbohydrate:proton symporter activity	0.025
	GO:0005402	carbohydrate:cation symporter activity	0.025
	GO:0015294	solute:cation symporter activity	0.025
	GO:0046982	protein heterodimerization activity	0.026
	GO:0016773	phosphotransferase activity, alcohol gro...	0.027
	GO:0046906	tetrapyrrole binding	0.030
	GO:0035251	UDP-glucosyltransferase activity	0.032
	GO:0005385	zinc ion transmembrane transporter activ...	0.035
	GO:0030246	carbohydrate binding	0.036
	GO:0043565	sequence-specific DNA binding	0.036
	GO:0016740	transferase activity	0.039
	GO:0016301	kinase activity	0.039
	GO:0008134	transcription factor binding	0.045
	GO:0008483	transaminase activity	0.045
	GO:0016769	transferase activity, transferring nitro...	0.045
	GO:0043178	alcohol binding	0.047
	GO:0015175	neutral amino acid transmembrane transpo...	0.048
	GO:0001228	transcriptional activator activity, RNA ...	0.054
	GO:0016772	transferase activity, transferring phosp...	0.063
	GO:0010427	abscisic acid binding	0.071
	GO:0008061	chitin binding	0.071
	GO:0046915	transition metal ion transmembrane trans...	0.071
	GO:0072509	divalent inorganic cation transmembrane ...	0.074
	GO:0008097	5S rRNA binding	0.079
	GO:0004364	glutathione transferase activity	0.086
	GO:0061630	ubiquitin protein ligase activity	0.088
	GO:0004857	enzyme inhibitor activity	0.090
	GO:0015144	carbohydrate transmembrane transporter a...	0.092
	GO:0061659	ubiquitin-like protein ligase activity	0.097

4.3.15 Root - Preflowering - Cluster 15

GO type	GO ID	Description	Adj. p-value
	GO:0051276	chromosome organization	0.000
	GO:0022402	cell cycle process	0.000
	GO:0009653	anatomical structure morphogenesis	0.000
	GO:0003006	developmental process involved in reprod...	0.000
	GO:0007010	cytoskeleton organization	0.000
	GO:1903047	mitotic cell cycle process	0.000
	GO:0033043	regulation of organelle organization	0.000
	GO:0016049	cell growth	0.000
	GO:0009791	post-embryonic development	0.000
	GO:0040029	regulation of gene expression, epigeneti...	0.000
	GO:0006073	cellular glucan metabolic process	0.000
	GO:0006281	DNA repair	0.000
	GO:0000910	cytokinesis	0.000
	GO:0006260	DNA replication	0.000
	GO:0006310	DNA recombination	0.000
	GO:0048589	developmental growth	0.000
	GO:0048868	pollen tube development	0.000
	GO:0048608	reproductive structure development	0.000
	GO:0061458	reproductive system development	0.000
	GO:0006325	chromatin organization	0.000
	GO:0048229	gametophyte development	0.000
	GO:0016052	carbohydrate catabolic process	0.000
	GO:0050793	regulation of developmental process	0.000
	GO:0070646	protein modification by small protein re...	0.000
	GO:0000272	polysaccharide catabolic process	0.000
	GO:0009826	unidimensional cell growth	0.000
	GO:0010564	regulation of cell cycle process	0.000
	GO:0033554	cellular response to stress	0.000
	GO:0010639	negative regulation of organelle organiz...	0.000
	GO:0048609	multicellular organismal reproductive pr...	0.000
	GO:0000904	cell morphogenesis involved in different...	0.001
	GO:0044247	cellular polysaccharide catabolic proces...	0.001
	GO:0009123	nucleoside monophosphate metabolic proce...	0.001
	GO:0009161	ribonucleoside monophosphate metabolic p...	0.002
	GO:0009860	pollen tube growth	0.002
	GO:0006261	DNA-dependent DNA replication	0.002
	GO:0021700	developmental maturation	0.002
	GO:0009555	pollen development	0.002
	GO:0042542	response to hydrogen peroxide	0.002
	GO:0060249	anatomical structure homeostasis	0.002
	GO:0032259	methylation	0.003
	GO:0097435	supramolecular fiber organization	0.003
	GO:0045814	negative regulation of gene expression, ...	0.003
	GO:0048468	cell development	0.003
	GO:0099402	plant organ development	0.003
	GO:0009126	purine nucleoside monophosphate metaboli...	0.003

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0009167	purine ribonucleoside monophosphate meta...	0.003
	GO:0009259	ribonucleotide metabolic process	0.003
	GO:0009657	plastid organization	0.003
	GO:0006629	lipid metabolic process	0.003
	GO:0007131	reciprocal meiotic recombination	0.003
	GO:0034968	histone lysine methylation	0.003
	GO:0035825	homologous recombination	0.003
	GO:0046034	ATP metabolic process	0.003
	GO:0009888	tissue development	0.003
	GO:0005982	starch metabolic process	0.003
	GO:0009932	cell tip growth	0.004
	GO:0030154	cell differentiation	0.004
	GO:0061077	chaperone-mediated protein folding	0.004
	GO:0010393	galacturonan metabolic process	0.004
	GO:0045488	pectin metabolic process	0.004
	GO:0006305	DNA alkylation	0.004
	GO:0006306	DNA methylation	0.004
	GO:0007127	meiosis I	0.004
	GO:0061982	meiosis I cell cycle process	0.004
	GO:0016579	protein deubiquitination	0.005
	GO:0045489	pectin biosynthetic process	0.005
	GO:0006091	generation of precursor metabolites and ...	0.005
	GO:0035194	posttranscriptional gene silencing by RN...	0.005
	GO:0060968	regulation of gene silencing	0.005
	GO:0010052	guard cell differentiation	0.005
	GO:0008154	actin polymerization or depolymerization	0.005
	GO:1900140	regulation of seedling development	0.005
	GO:0006342	chromatin silencing	0.005
	GO:0018022	peptidyl-lysine methylation	0.006
	GO:0044786	cell cycle DNA replication	0.006
	GO:0046185	aldehyde catabolic process	0.006
	GO:0015980	energy derivation by oxidation of organi...	0.006
	GO:0090626	plant epidermis morphogenesis	0.006
	GO:0007059	chromosome segregation	0.006
	GO:0071103	DNA conformation change	0.006
	GO:0009845	seed germination	0.006
	GO:0005983	starch catabolic process	0.007
	GO:0006304	DNA modification	0.007
	GO:0044728	DNA methylation or demethylation	0.007
	GO:2001251	negative regulation of chromosome organi...	0.007
	GO:0031047	gene silencing by RNA	0.007
	GO:0022603	regulation of anatomical structure morph...	0.007
	GO:0009438	methylglyoxal metabolic process	0.007
	GO:0016571	histone methylation	0.007
	GO:0042182	ketone catabolic process	0.007
	GO:0051052	regulation of DNA metabolic process	0.007
	GO:0051596	methylglyoxal catabolic process	0.007
	GO:0090627	plant epidermal cell differentiation	0.007
	GO:0010029	regulation of seed germination	0.008

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GO type	GO ID	Description	Adj. p-value
	GO:0032504	multicellular organism reproduction	0.008
	GO:0010629	negative regulation of gene expression	0.008
	GO:0008064	regulation of actin polymerization or de...	0.008
	GO:0009150	purine ribonucleotide metabolic process	0.008
	GO:0030832	regulation of actin filament length	0.008
	GO:0032956	regulation of actin cytoskeleton organiz...	0.008
	GO:0032970	regulation of actin filament-based proce...	0.008
	GO:0110053	regulation of actin filament organizatio...	0.008
	GO:0009642	response to light intensity	0.008
	GO:0033692	cellular polysaccharide biosynthetic pro...	0.008
	GO:0051239	regulation of multicellular organismal p...	0.008
	GO:0048588	developmental cell growth	0.008
	GO:0009251	glucan catabolic process	0.009
	GO:0010212	response to ionizing radiation	0.009
	GO:0071695	anatomical structure maturation	0.010
	GO:0044839	cell cycle G2/M phase transition	0.010
	GO:1905268	negative regulation of chromatin organiz...	0.010
	GO:0009144	purine nucleoside triphosphate metabolic...	0.010
	GO:0009205	purine ribonucleoside triphosphate metab...	0.010
	GO:0051567	histone H3-K9 methylation	0.011
	GO:0061647	histone H3-K9 modification	0.011
	GO:0018193	peptidyl-amino acid modification	0.011
	GO:0006207	'de novo' pyrimidine nucleobase biosynth...	0.011
	GO:1902600	proton transmembrane transport	0.011
	GO:0090351	seedling development	0.011
	GO:0044255	cellular lipid metabolic process	0.011
	GO:2000113	negative regulation of cellular macromol...	0.012
	GO:0051493	regulation of cytoskeleton organization	0.012
	GO:1901987	regulation of cell cycle phase transitio...	0.012
	GO:0030041	actin filament polymerization	0.012
	GO:0030833	regulation of actin filament polymerizat...	0.012
	GO:0098813	nuclear chromosome segregation	0.012
	GO:0030036	actin cytoskeleton organization	0.012
	GO:0009199	ribonucleoside triphosphate metabolic pr...	0.013
	GO:0005978	glycogen biosynthetic process	0.013
	GO:0019318	hexose metabolic process	0.013
	GO:0019693	ribose phosphate metabolic process	0.013
	GO:0046486	glycerolipid metabolic process	0.013
	GO:1901137	carbohydrate derivative biosynthetic pro...	0.013
	GO:0006650	glycerophospholipid metabolic process	0.014
	GO:0030029	actin filament-based process	0.014
	GO:0051302	regulation of cell division	0.014
	GO:0010103	stomatal complex morphogenesis	0.014
	GO:0016441	posttranscriptional gene silencing	0.014
	GO:0022622	root system development	0.015
	GO:1901661	quinone metabolic process	0.015
	GO:1901663	quinone biosynthetic process	0.015
	GO:0007015	actin filament organization	0.016
	GO:0051640	organelle localization	0.016

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GO type	GO ID	Description	Adj. p-value
	GO:0009124	nucleoside monophosphate biosynthetic pr...	0.016
	GO:1902749	regulation of cell cycle G2/M phase tran...	0.017
	GO:0022406	membrane docking	0.017
	GO:0140056	organelle localization by membrane tethe...	0.017
	GO:0090407	organophosphate biosynthetic process	0.017
	GO:0051273	beta-glucan metabolic process	0.017
	GO:0048364	root development	0.017
	GO:0043647	inositol phosphate metabolic process	0.018
	GO:0022604	regulation of cell morphogenesis	0.018
	GO:1902903	regulation of supramolecular fiber organ...	0.018
	GO:0097237	cellular response to toxic substance	0.018
	GO:0006089	lactate metabolic process	0.018
	GO:0009141	nucleoside triphosphate metabolic proces...	0.018
	GO:0009260	ribonucleotide biosynthetic process	0.018
	GO:0019243	methylglyoxal catabolic process to D-lac...	0.018
	GO:0046390	ribose phosphate biosynthetic process	0.018
	GO:0061727	methylglyoxal catabolic process to lacta...	0.018
	GO:0009250	glucan biosynthetic process	0.018
	GO:0009156	ribonucleoside monophosphate biosyntheti...	0.019
	GO:0051716	cellular response to stimulus	0.019
	GO:0042180	cellular ketone metabolic process	0.019
	GO:0055046	microgametogenesis	0.019
	GO:0000302	response to reactive oxygen species	0.020
	GO:0006986	response to unfolded protein	0.020
	GO:0044770	cell cycle phase transition	0.020
	GO:0006458	'de novo' protein folding	0.021
	GO:0019915	lipid storage	0.021
	GO:0032535	regulation of cellular component size	0.021
	GO:0051084	'de novo' posttranslational protein fold...	0.021
	GO:0090066	regulation of anatomical structure size	0.021
	GO:0010332	response to gamma radiation	0.021
	GO:0048278	vesicle docking	0.021
	GO:0006012	galactose metabolic process	0.021
	GO:0070828	heterochromatin organization	0.021
	GO:0009741	response to brassinosteroid	0.021
	GO:0090698	post-embryonic plant morphogenesis	0.022
	GO:0010431	seed maturation	0.022
	GO:0031050	dsRNA fragmentation	0.023
	GO:0043331	response to dsRNA	0.023
	GO:0070918	production of small RNA involved in gene...	0.023
	GO:0071359	cellular response to dsRNA	0.023
	GO:0042181	ketone biosynthetic process	0.024
	GO:0016246	RNA interference	0.024
	GO:0007276	gamete generation	0.025
	GO:0034637	cellular carbohydrate biosynthetic proce...	0.025
	GO:0006644	phospholipid metabolic process	0.025
	GO:0016051	carbohydrate biosynthetic process	0.025
	GO:0048367	shoot system development	0.026
	GO:0006284	base-excision repair	0.027

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GO type	GO ID	Description	Adj. p-value
	GO:0009165	nucleotide biosynthetic process	0.027
	GO:2000026	regulation of multicellular organismal d...	0.027
	GO:1901293	nucleoside phosphate biosynthetic proces...	0.028
	GO:0051094	positive regulation of developmental pro...	0.028
	GO:0006479	protein methylation	0.029
	GO:0008213	protein alkylation	0.029
	GO:0090558	plant epidermis development	0.029
	GO:0009127	purine nucleoside monophosphate biosynth...	0.030
	GO:0009168	purine ribonucleoside monophosphate bios...	0.030
	GO:0000184	nuclear-transcribed mRNA catabolic proce...	0.030
	GO:0030104	water homeostasis	0.031
	GO:0010030	positive regulation of seed germination	0.032
	GO:0044093	positive regulation of molecular functio...	0.033
	GO:1990748	cellular detoxification	0.034
	GO:0051085	chaperone cofactor-dependent protein ref...	0.036
	GO:0071214	cellular response to abiotic stimulus	0.037
	GO:0104004	cellular response to environmental stimu...	0.037
	GO:0048232	male gamete generation	0.038
	GO:0009908	flower development	0.038
	GO:0006754	ATP biosynthetic process	0.039
	GO:0009553	embryo sac development	0.039
	GO:0046434	organophosphate catabolic process	0.039
	GO:0005977	glycogen metabolic process	0.040
	GO:0006112	energy reserve metabolic process	0.040
	GO:1901699	cellular response to nitrogen compound	0.041
	GO:0019566	arabinose metabolic process	0.041
	GO:0042023	DNA endoreduplication	0.041
	GO:0098657	import into cell	0.041
	GO:0045132	meiotic chromosome segregation	0.042
	GO:0043085	positive regulation of catalytic activit...	0.043
	GO:0043624	cellular protein complex disassembly	0.043
	GO:0098869	cellular oxidant detoxification	0.044
	GO:0030422	production of siRNA involved in RNA inte...	0.045
	GO:0019359	nicotinamide nucleotide biosynthetic pro...	0.045
	GO:0009142	nucleoside triphosphate biosynthetic pro...	0.045
	GO:0009145	purine nucleoside triphosphate biosynthe...	0.046
	GO:0009206	purine ribonucleoside triphosphate biosy...	0.046
	GO:0006206	pyrimidine nucleobase metabolic process	0.047
	GO:0043244	regulation of protein complex disassembl...	0.047
	GO:0016573	histone acetylation	0.048
	GO:0018393	internal peptidyl-lysine acetylation	0.048
	GO:0018394	peptidyl-lysine acetylation	0.048
	GO:0009117	nucleotide metabolic process	0.048
	GO:0006884	cell volume homeostasis	0.050
	GO:0009992	cellular water homeostasis	0.050
	GO:0015793	glycerol transport	0.050
	GO:0090567	reproductive shoot system development	0.050
	GO:0030004	cellular monovalent inorganic cation hom...	0.052
	GO:0006970	response to osmotic stress	0.053

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GO type	GO ID	Description	Adj. p-value
	GO:0044282	small molecule catabolic process	0.053
	GO:0009201	ribonucleoside triphosphate biosynthetic...	0.054
	GO:0048580	regulation of post-embryonic development	0.055
	GO:0051240	positive regulation of multicellular org...	0.056
	GO:0042592	homeostatic process	0.056
	GO:0006753	nucleoside phosphate metabolic process	0.056
	GO:0007267	cell-cell signaling	0.056
	GO:0009415	response to water	0.057
	GO:0010608	posttranscriptional regulation of gene e...	0.057
	GO:0046165	alcohol biosynthetic process	0.057
	GO:0046488	phosphatidylinositol metabolic process	0.058
	GO:0032271	regulation of protein polymerization	0.059
	GO:0051274	beta-glucan biosynthetic process	0.059
	GO:0009644	response to high light intensity	0.060
	GO:0006075	(1-¿3)-beta-D-glucan biosynthetic proces...	0.061
	GO:0019363	pyridine nucleotide biosynthetic process	0.061
	GO:0009225	nucleotide-sugar metabolic process	0.062
	GO:0009636	response to toxic substance	0.062
	GO:0055082	cellular chemical homeostasis	0.062
	GO:0019252	starch biosynthetic process	0.063
	GO:0006801	superoxide metabolic process	0.063
	GO:0015791	polyol transport	0.064
	GO:0051258	protein polymerization	0.065
	GO:0048443	stamen development	0.065
	GO:0048466	androecium development	0.065
	GO:0048825	cotyledon development	0.065
	GO:0048827	phyllome development	0.068
	GO:0006631	fatty acid metabolic process	0.068
	GO:0010162	seed dormancy process	0.069
	GO:0022611	dormancy process	0.069
	GO:0006743	ubiquinone metabolic process	0.069
	GO:0006744	ubiquinone biosynthetic process	0.069
	GO:0070192	chromosome organization involved in meio...	0.069
	GO:0006475	internal protein amino acid acetylation	0.069
	GO:0032875	regulation of DNA endoreduplication	0.070
	GO:0009414	response to water deprivation	0.073
	GO:1901135	carbohydrate derivative metabolic proces...	0.073
	GO:0006006	glucose metabolic process	0.073
	GO:0051701	interaction with host	0.073
	GO:0006733	oxidoreduction coenzyme metabolic proces...	0.074
	GO:0010090	trichome morphogenesis	0.074
	GO:0030838	positive regulation of actin filament po...	0.077
	GO:0045010	actin nucleation	0.077
	GO:0016071	mRNA metabolic process	0.079
	GO:0006979	response to oxidative stress	0.079
	GO:0018208	peptidyl-proline modification	0.079
	GO:0046854	phosphatidylinositol phosphorylation	0.079
	GO:0045892	negative regulation of transcription, DN...	0.080
	GO:0048598	embryonic morphogenesis	0.080

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GO type	GO ID	Description	Adj. p-value
	GO:0008361	regulation of cell size	0.083
	GO:0017148	negative regulation of translation	0.083
	GO:0031060	regulation of histone methylation	0.083
	GO:0006950	response to stress	0.083
	GO:0009904	chloroplast accumulation movement	0.084
	GO:0006074	(1-¿3)-beta-D-glucan metabolic process	0.084
	GO:0010558	negative regulation of macromolecule bio...	0.085
	GO:0010638	positive regulation of organelle organiz...	0.089
	GO:0008360	regulation of cell shape	0.089
	GO:0010948	negative regulation of cell cycle proces...	0.089
	GO:0015672	monovalent inorganic cation transport	0.089
	GO:0009934	regulation of meristem structural organi...	0.089
	GO:1903311	regulation of mRNA metabolic process	0.091
	GO:0031338	regulation of vesicle fusion	0.092
	GO:0072528	pyrimidine-containing compound biosynthe...	0.092
	GO:0048437	floral organ development	0.095
	GO:0009166	nucleotide catabolic process	0.096
	GO:1901700	response to oxygen-containing compound	0.097
	GO:0010035	response to inorganic substance	0.099
	GO:0048438	floral whorl development	0.099
	GO:0009629	response to gravity	0.100
	GO:0035966	response to topologically incorrect prot...	0.100
	GO:0044430	cytoskeletal part	0.000
	GO:0044444	cytoplasmic part	0.000
	GO:0044427	chromosomal part	0.000
	GO:0005794	Golgi apparatus	0.000
	GO:0005819	spindle	0.000
	GO:0033176	proton-transporting V-type ATPase comple...	0.000
	GO:0009507	chloroplast	0.001
	GO:0012505	endomembrane system	0.001
	GO:0000139	Golgi membrane	0.001
	GO:0044454	nuclear chromosome part	0.001
	GO:0009524	phragmoplast	0.001
	GO:0000228	nuclear chromosome	0.001
	GO:0098687	chromosomal region	0.001
	GO:0098588	bounding membrane of organelle	0.002
	GO:0009526	plastid envelope	0.002
	GO:0009941	chloroplast envelope	0.003
	GO:0031090	organelle membrane	0.005
	GO:0048046	apoplast	0.007
	GO:0000784	nuclear chromosome, telomeric region	0.007
	GO:0042170	plastid membrane	0.007
	GO:0033178	proton-transporting two-sector ATPase co...	0.010
	GO:0031969	chloroplast membrane	0.011
	GO:0044435	plastid part	0.013
	GO:0005811	lipid droplet	0.013
	GO:0031982	vesicle	0.014
	GO:0031984	organelle subcompartment	0.021
	GO:0000781	chromosome, telomeric region	0.021

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GO type	GO ID	Description	Adj. p-value
	GO:0044434	chloroplast part	0.022
	GO:0030659	cytoplasmic vesicle membrane	0.022
	GO:0005802	trans-Golgi network	0.023
	GO:0019867	outer membrane	0.029
	GO:0044437	vacuolar part	0.029
	GO:0009705	plant-type vacuole membrane	0.030
	GO:0097708	intracellular vesicle	0.031
	GO:0030662	coated vesicle membrane	0.033
	GO:0031410	cytoplasmic vesicle	0.034
	GO:0000782	telomere cap complex	0.035
	GO:0000783	nuclear telomere cap complex	0.035
	GO:0005774	vacuolar membrane	0.035
	GO:0005881	cytoplasmic microtubule	0.035
	GO:0012506	vesicle membrane	0.035
	GO:0016469	proton-transporting two-sector ATPase co...	0.035
	GO:0044433	cytoplasmic vesicle part	0.035
	GO:0000325	plant-type vacuole	0.036
	GO:0005773	vacuole	0.038
	GO:0009506	plasmodesma	0.038
	GO:0055044	symplast	0.038
	GO:0015629	actin cytoskeleton	0.045
	GO:0000790	nuclear chromatin	0.046
	GO:0000148	1,3-beta-D-glucan synthase complex	0.047
	GO:0030120	vesicle coat	0.048
	GO:0098805	whole membrane	0.048
	GO:0009504	cell plate	0.051
	GO:0016459	myosin complex	0.051
	GO:0055028	cortical microtubule	0.053
	GO:0005657	replication fork	0.057
	GO:0030863	cortical cytoskeleton	0.057
	GO:0030981	cortical microtubule cytoskeleton	0.057
	GO:0030133	transport vesicle	0.057
	GO:0031968	organelle outer membrane	0.060
	GO:0009528	plastid inner membrane	0.070
	GO:0030658	transport vesicle membrane	0.070
	GO:0042646	plastid nucleoid	0.072
	GO:0042575	DNA polymerase complex	0.089
	GO:0030660	Golgi-associated vesicle membrane	0.089
	GO:0005768	endosome	0.099
	GO:0009706	chloroplast inner membrane	0.099
	GO:0009707	chloroplast outer membrane	0.100
	GO:0003774	motor activity	0.000
	GO:0017111	nucleoside-triphosphatase activity	0.000
	GO:0004553	hydrolase activity, hydrolyzing O-glycos...	0.000
	GO:0005515	protein binding	0.000
	GO:0004386	helicase activity	0.000
	GO:0003678	DNA helicase activity	0.000
	GO:0019783	ubiquitin-like protein-specific protease...	0.001
	GO:0016278	lysine N-methyltransferase activity	0.003

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GO type	GO ID	Description	Adj. p-value
	GO:0016279	protein-lysine N-methyltransferase activ...	0.003
	GO:0005524	ATP binding	0.003
	GO:0008270	zinc ion binding	0.004
	GO:0008574	ATP-dependent microtubule motor activity...	0.004
	GO:1990939	ATP-dependent microtubule motor activity	0.004
	GO:0036442	proton-exporting ATPase activity	0.004
	GO:0016407	acetyltransferase activity	0.005
	GO:0008144	drug binding	0.006
	GO:0042054	histone methyltransferase activity	0.009
	GO:0042623	ATPase activity, coupled	0.010
	GO:0016307	phosphatidylinositol phosphate kinase ac...	0.010
	GO:0036094	small molecule binding	0.012
	GO:0015925	galactosidase activity	0.015
	GO:0030554	adenyl nucleotide binding	0.015
	GO:0000166	nucleotide binding	0.015
	GO:0005488	binding	0.015
	GO:0008170	N-methyltransferase activity	0.015
	GO:0015923	mannosidase activity	0.015
	GO:0036459	thiol-dependent ubiquitinyl hydrolase ac...	0.015
	GO:0101005	ubiquitinyl hydrolase activity	0.015
	GO:1901265	nucleoside phosphate binding	0.015
	GO:0008094	DNA-dependent ATPase activity	0.016
	GO:0004567	beta-mannosidase activity	0.016
	GO:0003824	catalytic activity	0.017
	GO:0003954	NADH dehydrogenase activity	0.017
	GO:0015926	glucosidase activity	0.017
	GO:0032559	adenyl ribonucleotide binding	0.017
	GO:0035639	purine ribonucleoside triphosphate bindi...	0.017
	GO:0044769	ATPase activity, coupled to transmembran...	0.017
	GO:0046961	proton-transporting ATPase activity, rot...	0.017
	GO:0051082	unfolded protein binding	0.018
	GO:0046556	alpha-L-arabinofuranosidase activity	0.019
	GO:0008276	protein methyltransferase activity	0.020
	GO:0008026	ATP-dependent helicase activity	0.021
	GO:0070035	purine NTP-dependent helicase activity	0.021
	GO:0004003	ATP-dependent DNA helicase activity	0.022
	GO:0008047	enzyme activator activity	0.022
	GO:0043168	anion binding	0.022
	GO:0008289	lipid binding	0.025
	GO:0017076	purine nucleotide binding	0.035
	GO:0050661	NADP binding	0.036
	GO:0008168	methyltransferase activity	0.039
	GO:0060589	nucleoside-triphosphatase regulator acti...	0.039
	GO:0019829	cation-transporting ATPase activity	0.045
	GO:0022853	active ion transmembrane transporter act...	0.045
	GO:0042625	ATPase coupled ion transmembrane transpo...	0.045
	GO:0016209	antioxidant activity	0.046
	GO:0043167	ion binding	0.046
	GO:0032555	purine ribonucleotide binding	0.046

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GO type	GO ID	Description	Adj. p-value
	GO:0097367	carbohydrate derivative binding	0.052
	GO:2001070	starch binding	0.053
	GO:0008757	S-adenosylmethionine-dependent methyltra...	0.056
	GO:0005527	macrolide binding	0.062
	GO:0005528	FK506 binding	0.062
	GO:0016903	oxidoreductase activity, acting on the a...	0.072
	GO:0005372	water transmembrane transporter activity	0.074
	GO:0015250	water channel activity	0.074
	GO:0015254	glycerol channel activity	0.074
	GO:0032553	ribonucleotide binding	0.075
	GO:0042393	histone binding	0.075
	GO:0019200	carbohydrate kinase activity	0.076
	GO:0042803	protein homodimerization activity	0.080
	GO:0008422	beta-glucosidase activity	0.082
	GO:0004650	polygalacturonase activity	0.084
	GO:0003682	chromatin binding	0.085
	GO:0003843	1,3-beta-D-glucan synthase activity	0.085
	GO:0004176	ATP-dependent peptidase activity	0.085
	GO:0042162	telomeric DNA binding	0.085
	GO:0043621	protein self-association	0.085
	GO:0015085	calcium ion transmembrane transporter ac...	0.089
	GO:0016741	transferase activity, transferring one-c...	0.089
	GO:0016788	hydrolase activity, acting on ester bond...	0.090
	GO:0035091	phosphatidylinositol binding	0.090
	GO:0016620	oxidoreductase activity, acting on the a...	0.092
	GO:0004565	beta-galactosidase activity	0.094
	GO:0070569	uridylyltransferase activity	0.094
	GO:0015168	glycerol transmembrane transporter activ...	0.095

4.3.16 Root - Preflowering - Cluster 16

		Description	Adj. p-value
GO type	GO ID		
	GO:0006259	DNA metabolic process	0.000
	GO:0034660	ncRNA metabolic process	0.000
	GO:0043414	macromolecule methylation	0.000
	GO:0009451	RNA modification	0.000
	GO:0040029	regulation of gene expression, epigeneti...	0.000
	GO:0003006	developmental process involved in reprod...	0.000
	GO:0009791	post-embryonic development	0.000
	GO:0009657	plastid organization	0.000
	GO:0016569	covalent chromatin modification	0.000
	GO:0016570	histone modification	0.000
	GO:0022613	ribonucleoprotein complex biogenesis	0.000
	GO:0006310	DNA recombination	0.000
	GO:0031047	gene silencing by RNA	0.000
	GO:2000113	negative regulation of cellular macromol...	0.000
	GO:0018022	peptidyl-lysine methylation	0.000
	GO:0035194	posttranscriptional gene silencing by RN...	0.000
	GO:0006304	DNA modification	0.000
	GO:0044728	DNA methylation or demethylation	0.000
	GO:0051239	regulation of multicellular organismal p...	0.000
	GO:0010154	fruit development	0.000
	GO:0033043	regulation of organelle organization	0.000
	GO:0006401	RNA catabolic process	0.000
	GO:0051052	regulation of DNA metabolic process	0.000
	GO:0048580	regulation of post-embryonic development	0.000
	GO:0090501	RNA phosphodiester bond hydrolysis	0.000
	GO:0006306	DNA methylation	0.000
	GO:0005982	starch metabolic process	0.000
	GO:0034249	negative regulation of cellular amide me...	0.000
	GO:0016246	RNA interference	0.000
	GO:0006417	regulation of translation	0.000
	GO:0017148	negative regulation of translation	0.000
	GO:0006400	tRNA modification	0.000
	GO:0007049	cell cycle	0.000
	GO:0006302	double-strand break repair	0.000
	GO:0045892	negative regulation of transcription, DN...	0.000
	GO:0071478	cellular response to radiation	0.000
	GO:0035196	production of miRNAs involved in gene si...	0.000
	GO:0006260	DNA replication	0.000
	GO:0045814	negative regulation of gene expression, ...	0.000
	GO:0048518	positive regulation of biological proces...	0.000
	GO:0006402	mRNA catabolic process	0.000
	GO:0009642	response to light intensity	0.000
	GO:0007033	vacuole organization	0.000
	GO:0016556	mRNA modification	0.000
	GO:0070192	chromosome organization involved in meio...	0.000
	GO:2000241	regulation of reproductive process	0.000

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:1903311	regulation of mRNA metabolic process	0.001
	GO:0048831	regulation of shoot system development	0.001
	GO:0006342	chromatin silencing	0.001
	GO:0006886	intracellular protein transport	0.001
	GO:0005977	glycogen metabolic process	0.001
	GO:0006112	energy reserve metabolic process	0.001
	GO:0009416	response to light stimulus	0.001
	GO:0009893	positive regulation of metabolic process	0.001
	GO:0051253	negative regulation of RNA metabolic pro...	0.001
	GO:0071482	cellular response to light stimulus	0.001
	GO:0010468	regulation of gene expression	0.001
	GO:0031056	regulation of histone modification	0.001
	GO:0006312	mitotic recombination	0.001
	GO:0006261	DNA-dependent DNA replication	0.001
	GO:0043484	regulation of RNA splicing	0.002
	GO:0009908	flower development	0.002
	GO:0019252	starch biosynthetic process	0.002
	GO:0009909	regulation of flower development	0.002
	GO:0044260	cellular macromolecule metabolic process	0.002
	GO:1902679	negative regulation of RNA biosynthetic ...	0.002
	GO:1903507	negative regulation of nucleic acid-temp...	0.002
	GO:0006289	nucleotide-excision repair	0.002
	GO:0045132	meiotic chromosome segregation	0.002
	GO:0009668	plastid membrane organization	0.003
	GO:0010027	thylakoid membrane organization	0.003
	GO:0046907	intracellular transport	0.003
	GO:0098813	nuclear chromosome segregation	0.003
	GO:0000245	spliceosomal complex assembly	0.003
	GO:0009845	seed germination	0.003
	GO:0051649	establishment of localization in cell	0.003
	GO:0010604	positive regulation of macromolecule met...	0.003
	GO:0071407	cellular response to organic cyclic comp...	0.003
	GO:0045036	protein targeting to chloroplast	0.003
	GO:0072596	establishment of protein localization to...	0.003
	GO:0048609	multicellular organismal reproductive pr...	0.003
	GO:0071704	organic substance metabolic process	0.003
	GO:0050684	regulation of mRNA processing	0.004
	GO:0000956	nuclear-transcribed mRNA catabolic proce...	0.004
	GO:0090502	RNA phosphodiester bond hydrolysis, endo...	0.004
	GO:0005978	glycogen biosynthetic process	0.004
	GO:0051567	histone H3-K9 methylation	0.005
	GO:0061647	histone H3-K9 modification	0.005
	GO:0090351	seedling development	0.005
	GO:0090567	reproductive shoot system development	0.005
	GO:0072598	protein localization to chloroplast	0.005
	GO:0006366	transcription by RNA polymerase II	0.005
	GO:0048522	positive regulation of cellular process	0.006
	GO:0006273	lagging strand elongation	0.006
	GO:0033993	response to lipid	0.006

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0045143	homologous chromosome segregation	0.006
	GO:0005983	starch catabolic process	0.006
	GO:0030488	tRNA methylation	0.006
	GO:0031325	positive regulation of cellular metaboli...	0.006
	GO:0051168	nuclear export	0.006
	GO:0006611	protein export from nucleus	0.007
	GO:0043038	amino acid activation	0.007
	GO:0043039	tRNA aminoacylation	0.007
	GO:0044030	regulation of DNA methylation	0.008
	GO:0032270	positive regulation of cellular protein ...	0.008
	GO:0006284	base-excision repair	0.008
	GO:0097305	response to alcohol	0.008
	GO:0006376	mRNA splice site selection	0.009
	GO:0006950	response to stress	0.009
	GO:0042752	regulation of circadian rhythm	0.009
	GO:0071897	DNA biosynthetic process	0.009
	GO:0007129	synapsis	0.010
	GO:0051173	positive regulation of nitrogen compound...	0.010
	GO:0008104	protein localization	0.010
	GO:0006338	chromatin remodeling	0.010
	GO:0006378	mRNA polyadenylation	0.010
	GO:0006418	tRNA aminoacylation for protein translat...	0.010
	GO:0009910	negative regulation of flower developmen...	0.011
	GO:2000242	negative regulation of reproductive proc...	0.011
	GO:0006379	mRNA cleavage	0.011
	GO:0000725	recombinational repair	0.012
	GO:0009737	response to abscisic acid	0.012
	GO:0051247	positive regulation of protein metabolic...	0.012
	GO:0006403	RNA localization	0.012
	GO:0045184	establishment of protein localization	0.012
	GO:0071826	ribonucleoprotein complex subunit organi...	0.012
	GO:0000045	autophagosome assembly	0.013
	GO:1905037	autophagosome organization	0.013
	GO:0043572	plastid fission	0.013
	GO:0043631	RNA polyadenylation	0.013
	GO:0016236	macroautophagy	0.013
	GO:0015031	protein transport	0.014
	GO:0048232	male gamete generation	0.015
	GO:0031323	regulation of cellular metabolic process	0.015
	GO:0000959	mitochondrial RNA metabolic process	0.015
	GO:0000724	double-strand break repair via homologou...	0.015
	GO:0006405	RNA export from nucleus	0.015
	GO:0009615	response to virus	0.015
	GO:0010267	production of ta-siRNAs involved in RNA ...	0.016
	GO:0006265	DNA topological change	0.016
	GO:0031401	positive regulation of protein modificat...	0.016
	GO:0031123	RNA 3'-end processing	0.017
	GO:0050657	nucleic acid transport	0.017
	GO:0050658	RNA transport	0.017

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GO type	GO ID	Description	Adj. p-value
	GO:0051236	establishment of RNA localization	0.017
	GO:0010020	chloroplast fission	0.017
	GO:0031053	primary miRNA processing	0.018
	GO:0006913	nucleocytoplasmic transport	0.018
	GO:0051169	nuclear transport	0.018
	GO:0051094	positive regulation of developmental pro...	0.019
	GO:0071166	ribonucleoprotein complex localization	0.019
	GO:0071426	ribonucleoprotein complex export from nu...	0.019
	GO:0006271	DNA strand elongation involved in DNA re...	0.019
	GO:0022616	DNA strand elongation	0.019
	GO:0048583	regulation of response to stimulus	0.019
	GO:0031124	mRNA 3'-end processing	0.022
	GO:0048581	negative regulation of post-embryonic de...	0.023
	GO:0006352	DNA-templated transcription, initiation	0.023
	GO:0032544	plastid translation	0.024
	GO:0045037	protein import into chloroplast stroma	0.024
	GO:0007018	microtubule-based movement	0.025
	GO:0030258	lipid modification	0.025
	GO:0000380	alternative mRNA splicing, via spliceoso...	0.026
	GO:0031627	telomeric loop formation	0.028
	GO:0048582	positive regulation of post-embryonic de...	0.028
	GO:0051171	regulation of nitrogen compound metaboli...	0.028
	GO:0060147	regulation of posttranscriptional gene s...	0.029
	GO:0032392	DNA geometric change	0.030
	GO:0032508	DNA duplex unwinding	0.030
	GO:0050789	regulation of biological process	0.030
	GO:0070828	heterochromatin organization	0.030
	GO:0051053	negative regulation of DNA metabolic pro...	0.031
	GO:0080090	regulation of primary metabolic process	0.031
	GO:0000460	maturation of 5.8S rRNA	0.031
	GO:0033036	macromolecule localization	0.031
	GO:0051026	chiasma assembly	0.031
	GO:0009414	response to water deprivation	0.032
	GO:0080188	RNA-directed DNA methylation	0.032
	GO:0031338	regulation of vesicle fusion	0.033
	GO:0009415	response to water	0.035
	GO:0022618	ribonucleoprotein complex assembly	0.035
	GO:2001020	regulation of response to DNA damage sti...	0.035
	GO:0098586	cellular response to virus	0.035
	GO:0015833	peptide transport	0.036
	GO:0046185	aldehyde catabolic process	0.036
	GO:0070816	phosphorylation of RNA polymerase II C-t...	0.036
	GO:0042886	amide transport	0.037
	GO:0031399	regulation of protein modification proce...	0.037
	GO:0009438	methylglyoxal metabolic process	0.037
	GO:0042182	ketone catabolic process	0.037
	GO:0051596	methylglyoxal catabolic process	0.037
	GO:0043933	protein-containing complex subunit organ...	0.038
	GO:0017038	protein import	0.039

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GO type	GO ID	Description	Adj. p-value
	GO:0031503	protein-containing complex localization	0.039
	GO:0051640	organelle localization	0.039
	GO:0051240	positive regulation of multicellular org...	0.040
	GO:1901700	response to oxygen-containing compound	0.040
	GO:0031058	positive regulation of histone modificat...	0.040
	GO:2001252	positive regulation of chromosome organi...	0.043
	GO:0061024	membrane organization	0.044
	GO:0009743	response to carbohydrate	0.045
	GO:0071103	DNA conformation change	0.046
	GO:0006089	lactate metabolic process	0.046
	GO:0019243	methylglyoxal catabolic process to D-lac...	0.046
	GO:0061727	methylglyoxal catabolic process to lacta...	0.046
	GO:0007062	sister chromatid cohesion	0.047
	GO:0051248	negative regulation of protein metabolic...	0.047
	GO:0051130	positive regulation of cellular componen...	0.051
	GO:0009894	regulation of catabolic process	0.051
	GO:0006928	movement of cell or subcellular componen...	0.051
	GO:0031329	regulation of cellular catabolic process	0.055
	GO:0009637	response to blue light	0.056
	GO:0009630	gravitropism	0.057
	GO:0035601	protein deacylation	0.057
	GO:0006476	protein deacetylation	0.058
	GO:0006406	mRNA export from nucleus	0.059
	GO:0071427	mRNA-containing ribonucleoprotein comple...	0.059
	GO:0090503	RNA phosphodiester bond hydrolysis, exon...	0.060
	GO:0009581	detection of external stimulus	0.062
	GO:0009582	detection of abiotic stimulus	0.062
	GO:0009911	positive regulation of flower developmen...	0.062
	GO:0032269	negative regulation of cellular protein ...	0.064
	GO:0000160	phosphorelay signal transduction system	0.066
	GO:0016973	poly(A)+ mRNA export from nucleus	0.066
	GO:0006904	vesicle docking involved in exocytosis	0.069
	GO:0140029	exocytic process	0.069
	GO:0048229	gametophyte development	0.072
	GO:0009787	regulation of abscisic acid-activated si...	0.073
	GO:1901419	regulation of response to alcohol	0.073
	GO:1905957	regulation of cellular response to alcoh...	0.073
	GO:0043085	positive regulation of catalytic activit...	0.073
	GO:1905269	positive regulation of chromatin organiz...	0.077
	GO:0000478	endonucleolytic cleavage involved in rRN...	0.078
	GO:0044093	positive regulation of molecular functio...	0.080
	GO:0010431	seed maturation	0.080
	GO:0008284	positive regulation of cell proliferatio...	0.080
	GO:0019953	sexual reproduction	0.080
	GO:0014070	response to organic cyclic compound	0.080
	GO:0000469	cleavage involved in rRNA processing	0.085
	GO:0032436	positive regulation of proteasomal ubiqu...	0.085
	GO:2000060	positive regulation of ubiquitin-depende...	0.085
	GO:0006383	transcription by RNA polymerase III	0.089

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GO type	GO ID	Description	Adj. p-value
	GO:0007389	pattern specification process	0.089
	GO:0006914	autophagy	0.097
	GO:0061919	process utilizing autophagic mechanism	0.097
	GO:0071806	protein transmembrane transport	0.097
	GO:0009553	embryo sac development	0.098
	GO:0071489	cellular response to red or far red ligh...	0.099
CC	GO:0044428	nuclear part	0.000
	GO:0044435	plastid part	0.000
	GO:0005654	nucleoplasm	0.000
	GO:0044451	nucleoplasm part	0.000
	GO:0005737	cytoplasm	0.000
	GO:0009526	plastid envelope	0.000
	GO:0000151	ubiquitin ligase complex	0.000
	GO:0031461	cullin-RING ubiquitin ligase complex	0.000
	GO:0005694	chromosome	0.000
	GO:0009532	plastid stroma	0.000
	GO:0005681	spliceosomal complex	0.000
	GO:0061695	transferase complex, transferring phosph...	0.000
	GO:0016604	nuclear body	0.000
	GO:0042646	plastid nucleoid	0.000
	GO:0009295	nucleoid	0.000
	GO:0042170	plastid membrane	0.000
	GO:0000428	DNA-directed RNA polymerase complex	0.000
	GO:0030880	RNA polymerase complex	0.000
	GO:0042651	thylakoid membrane	0.000
	GO:0005684	U2-type spliceosomal complex	0.000
	GO:0030684	preribosome	0.001
	GO:0031248	protein acetyltransferase complex	0.001
	GO:1902493	acetyltransferase complex	0.001
	GO:0000794	condensed nuclear chromosome	0.001
	GO:0016607	nuclear speck	0.001
	GO:0000229	cytoplasmic chromosome	0.002
	GO:0030686	90S preribosome	0.002
	GO:0030532	small nuclear ribonucleoprotein complex	0.002
	GO:0071004	U2-type prespliceosome	0.002
	GO:0071010	prespliceosome	0.002
	GO:0097525	spliceosomal snRNP complex	0.002
	GO:0120114	Sm-like protein family complex	0.002
	GO:0000793	condensed chromosome	0.002
	GO:0005643	nuclear pore	0.002
	GO:0032991	protein-containing complex	0.002
	GO:0009508	plastid chromosome	0.003
	GO:0032040	small-subunit processome	0.006
	GO:0043228	non-membrane-bounded organelle	0.006
	GO:0043232	intracellular non-membrane-bounded organ...	0.006
	GO:0044798	nuclear transcription factor complex	0.006
	GO:0044454	nuclear chromosome part	0.009
	GO:0016592	mediator complex	0.010
	GO:0005663	DNA replication factor C complex	0.011

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GO type	GO ID	Description	Adj. p-value
	GO:0016591	DNA-directed RNA polymerase II, holoenzy...	0.013
	GO:0005739	mitochondrion	0.015
	GO:0044427	chromosomal part	0.015
	GO:0005635	nuclear envelope	0.017
	GO:0090575	RNA polymerase II transcription factor c...	0.021
	GO:0005667	transcription factor complex	0.021
	GO:0019898	extrinsic component of membrane	0.022
	GO:0098687	chromosomal region	0.022
	GO:0009707	chloroplast outer membrane	0.031
	GO:0000243	commitment complex	0.033
	GO:0009527	plastid outer membrane	0.033
	GO:0005666	DNA-directed RNA polymerase III complex	0.034
	GO:0030117	membrane coat	0.038
	GO:0048475	coated membrane	0.038
	GO:0044452	nucleolar part	0.045
	GO:0030677	ribonuclease P complex	0.046
	GO:0000782	telomere cap complex	0.049
	GO:0000783	nuclear telomere cap complex	0.049
	GO:1902555	endoribonuclease complex	0.058
	GO:1905348	endonuclease complex	0.058
	GO:0033180	proton-transporting V-type ATPase, V1 do...	0.062
	GO:0030687	preribosome, large subunit precursor	0.068
	GO:0005686	U2 snRNP	0.076
	GO:1902554	serine/threonine protein kinase complex	0.089
	GO:1902911	protein kinase complex	0.089
	GO:0005685	U1 snRNP	0.094
	GO:0017053	transcriptional repressor complex	0.094
	GO:0080008	Cul4-RING E3 ubiquitin ligase complex	0.096
	GO:0030119	AP-type membrane coat adaptor complex	0.097
	GO:0140097	catalytic activity, acting on DNA	0.000
	GO:0003724	RNA helicase activity	0.000
	GO:0008094	DNA-dependent ATPase activity	0.000
	GO:0008173	RNA methyltransferase activity	0.000
	GO:0036459	thiol-dependent ubiquitinyl hydrolase ac...	0.000
	GO:0016893	endonuclease activity, active with eithe...	0.000
	GO:0140101	catalytic activity, acting on a tRNA	0.000
	GO:0016779	nucleotidyltransferase activity	0.001
	GO:0016891	endoribonuclease activity, producing 5'-...	0.001
	GO:0004540	ribonuclease activity	0.001
	GO:0016796	exonuclease activity, active with either...	0.002
	GO:0017076	purine nucleotide binding	0.003
	GO:0003682	chromatin binding	0.003
	GO:0008168	methyltransferase activity	0.003
	GO:0051082	unfolded protein binding	0.003
	GO:0030554	adenyl nucleotide binding	0.003
	GO:0043022	ribosome binding	0.003
	GO:0032555	purine ribonucleotide binding	0.004
	GO:0032559	adenyl ribonucleotide binding	0.004
	GO:0140102	catalytic activity, acting on a rRNA	0.005

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GO type	GO ID	Description	Adj. p-value
	GO:0051536	iron-sulfur cluster binding	0.005
	GO:0051540	metal cluster binding	0.005
	GO:0032553	ribonucleotide binding	0.005
	GO:0003924	GTPase activity	0.005
	GO:0004176	ATP-dependent peptidase activity	0.005
	GO:0008649	rRNA methyltransferase activity	0.005
	GO:0008757	S-adenosylmethionine-dependent methyltra...	0.006
	GO:0004402	histone acetyltransferase activity	0.006
	GO:0061733	peptide-lysine-N-acetyltransferase activ...	0.006
	GO:0016896	exoribonuclease activity, producing 5'-p...	0.006
	GO:0097159	organic cyclic compound binding	0.006
	GO:1901363	heterocyclic compound binding	0.007
	GO:0004521	endoribonuclease activity	0.008
	GO:0016423	tRNA (guanine) methyltransferase activit...	0.008
	GO:0008409	5'-3' exonuclease activity	0.009
	GO:0004536	deoxyribonuclease activity	0.009
	GO:0042162	telomeric DNA binding	0.010
	GO:0004532	exoribonuclease activity	0.010
	GO:0042393	histone binding	0.010
	GO:0016741	transferase activity, transferring one-c...	0.011
	GO:0003690	double-stranded DNA binding	0.011
	GO:0016874	ligase activity	0.015
	GO:0044877	protein-containing complex binding	0.017
	GO:0097367	carbohydrate derivative binding	0.018
	GO:0004520	endodeoxyribonuclease activity	0.018
	GO:0003678	DNA helicase activity	0.020
	GO:0034212	peptide N-acetyltransferase activity	0.021
	GO:0004843	thiol-dependent ubiquitin-specific prote...	0.022
	GO:0008080	N-acetyltransferase activity	0.023
	GO:0004525	ribonuclease III activity	0.026
	GO:0032296	double-stranded RNA-specific ribonucleas...	0.026
	GO:0008175	tRNA methyltransferase activity	0.026
	GO:0034061	DNA polymerase activity	0.026
	GO:0003916	DNA topoisomerase activity	0.031
	GO:0003689	DNA clamp loader activity	0.033
	GO:0033170	protein-DNA loading ATPase activity	0.033
	GO:0043021	ribonucleoprotein complex binding	0.036
	GO:0003887	DNA-directed DNA polymerase activity	0.037
	GO:0034062	5'-3' RNA polymerase activity	0.040
	GO:0097747	RNA polymerase activity	0.040
	GO:0016884	carbon-nitrogen ligase activity, with gl...	0.041
	GO:0031072	heat shock protein binding	0.052
	GO:0003691	double-stranded telomeric DNA binding	0.058
	GO:0004812	aminoacyl-tRNA ligase activity	0.058
	GO:0016875	ligase activity, forming carbon-oxygen b...	0.058
	GO:0042803	protein homodimerization activity	0.058
	GO:0000175	3'-5'-exoribonuclease activity	0.065
	GO:0004526	ribonuclease P activity	0.065
	GO:0003950	NAD+ ADP-ribosyltransferase activity	0.065

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GO type	GO ID	Description	Adj. p-value
	GO:0008234	cysteine-type peptidase activity	0.068
	GO:0015631	tubulin binding	0.068
	GO:0019899	enzyme binding	0.068
	GO:0060589	nucleoside-triphosphatase regulator acti...	0.068
	GO:0000049	tRNA binding	0.069
	GO:0003712	transcription cofactor activity	0.069
	GO:0017069	snRNA binding	0.074
	GO:0003899	DNA-directed 5'-3' RNA polymerase activi...	0.075
	GO:0003729	mRNA binding	0.076
	GO:0016774	phosphotransferase activity, carboxyl gr...	0.077
	GO:0016866	intramolecular transferase activity	0.085
	GO:0016410	N-acyltransferase activity	0.087
	GO:0043168	anion binding	0.088

4.3.17 Root - Preflowering - Cluster 17

GO type	GO ID	Description	Adj. p-value
	GO:0016071	mRNA metabolic process	0.000
	GO:0042254	ribosome biogenesis	0.000
	GO:0009451	RNA modification	0.000
	GO:0043412	macromolecule modification	0.000
	GO:0019222	regulation of metabolic process	0.000
	GO:0010468	regulation of gene expression	0.000
	GO:0031323	regulation of cellular metabolic process	0.000
	GO:0080090	regulation of primary metabolic process	0.000
	GO:0006259	DNA metabolic process	0.000
	GO:0006399	tRNA metabolic process	0.000
	GO:2000112	regulation of cellular macromolecule bio...	0.000
	GO:0043414	macromolecule methylation	0.000
	GO:0019219	regulation of nucleobase-containing comp...	0.000
	GO:0043161	proteasome-mediated ubiquitin-dependent ...	0.000
	GO:0001510	RNA methylation	0.000
	GO:0070647	protein modification by small protein co...	0.000
	GO:0006400	tRNA modification	0.000
	GO:0032446	protein modification by small protein co...	0.000
	GO:0042273	ribosomal large subunit biogenesis	0.000
	GO:0051276	chromosome organization	0.000
	GO:0006366	transcription by RNA polymerase II	0.000
	GO:0006996	organelle organization	0.000
	GO:0090501	RNA phosphodiester bond hydrolysis	0.000
	GO:0042274	ribosomal small subunit biogenesis	0.000
	GO:0071826	ribonucleoprotein complex subunit organi...	0.000
	GO:0000154	rRNA modification	0.000
	GO:0022618	ribonucleoprotein complex assembly	0.000
	GO:0009909	regulation of flower development	0.000
	GO:0000245	spliceosomal complex assembly	0.000
	GO:0010629	negative regulation of gene expression	0.000
	GO:0006310	DNA recombination	0.000
	GO:0009658	chloroplast organization	0.000
	GO:0018205	peptidyl-lysine modification	0.000
	GO:0030490	maturation of SSU-rRNA	0.000
	GO:0010608	posttranscriptional regulation of gene e...	0.000
	GO:0051173	positive regulation of nitrogen compound...	0.000
	GO:0000470	maturation of LSU-rRNA	0.000
	GO:0016458	gene silencing	0.001
	GO:0031167	rRNA methylation	0.001
	GO:0010604	positive regulation of macromolecule met...	0.001
	GO:0016569	covalent chromatin modification	0.001
	GO:0031325	positive regulation of cellular metaboli...	0.001
	GO:0042255	ribosome assembly	0.001
	GO:0048518	positive regulation of biological proces...	0.001
	GO:0051603	proteolysis involved in cellular protein...	0.001
	GO:1901362	organic cyclic compound biosynthetic pro...	0.001

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0002097	tRNA wobble base modification	0.002
	GO:0072598	protein localization to chloroplast	0.002
	GO:0000373	Group II intron splicing	0.002
	GO:0006352	DNA-templated transcription, initiation	0.002
	GO:0031047	gene silencing by RNA	0.002
	GO:0000462	maturation of SSU-rRNA from tricistronic...	0.002
	GO:0065003	protein-containing complex assembly	0.002
	GO:0006401	RNA catabolic process	0.002
	GO:0007127	meiosis I	0.002
	GO:0061982	meiosis I cell cycle process	0.002
	GO:0006379	mRNA cleavage	0.003
	GO:0010605	negative regulation of macromolecule met...	0.003
	GO:0048522	positive regulation of cellular process	0.004
	GO:0006479	protein methylation	0.004
	GO:0008213	protein alkylation	0.004
	GO:0031123	RNA 3'-end processing	0.004
	GO:0016441	posttranscriptional gene silencing	0.004
	GO:0006338	chromatin remodeling	0.004
	GO:0016556	mRNA modification	0.004
	GO:0015994	chlorophyll metabolic process	0.005
	GO:0051168	nuclear export	0.005
	GO:0035196	production of miRNAs involved in gene si...	0.005
	GO:0043572	plastid fission	0.005
	GO:0007623	circadian rhythm	0.005
	GO:0048511	rhythmic process	0.005
	GO:0000460	maturation of 5.8S rRNA	0.006
	GO:0040029	regulation of gene expression, epigeneti...	0.006
	GO:2000026	regulation of multicellular organismal d...	0.006
	GO:0010228	vegetative to reproductive phase transit...	0.006
	GO:0009314	response to radiation	0.006
	GO:0006611	protein export from nucleus	0.007
	GO:0048285	organelle fission	0.007
	GO:0071806	protein transmembrane transport	0.007
	GO:0006298	mismatch repair	0.007
	GO:0006302	double-strand break repair	0.007
	GO:0051028	mRNA transport	0.007
	GO:0090502	RNA phosphodiester bond hydrolysis, endo...	0.008
	GO:0000956	nuclear-transcribed mRNA catabolic proce...	0.009
	GO:0016570	histone modification	0.009
	GO:0010020	chloroplast fission	0.010
	GO:0033554	cellular response to stress	0.010
	GO:0006417	regulation of translation	0.010
	GO:0070925	organelle assembly	0.011
	GO:0043628	ncRNA 3'-end processing	0.011
	GO:0006402	mRNA catabolic process	0.012
	GO:0071166	ribonucleoprotein complex localization	0.013
	GO:0071426	ribonucleoprotein complex export from nu...	0.013
	GO:0034248	regulation of cellular amide metabolic p...	0.013
	GO:0006403	RNA localization	0.013

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0045143	homologous chromosome segregation	0.014
	GO:0010628	positive regulation of gene expression	0.015
	GO:0009416	response to light stimulus	0.015
	GO:0016073	snRNA metabolic process	0.015
	GO:0007059	chromosome segregation	0.018
	GO:0006383	transcription by RNA polymerase III	0.018
	GO:0009648	photoperiodism	0.018
	GO:0000469	cleavage involved in rRNA processing	0.019
	GO:0031328	positive regulation of cellular biosynth...	0.020
	GO:0007131	reciprocal meiotic recombination	0.020
	GO:0035825	homologous recombination	0.020
	GO:0000160	phosphorelay signal transduction system	0.021
	GO:0051053	negative regulation of DNA metabolic pro...	0.021
	GO:0051052	regulation of DNA metabolic process	0.021
	GO:0009891	positive regulation of biosynthetic proc...	0.022
	GO:0065002	intracellular protein transmembrane tran...	0.022
	GO:0045132	meiotic chromosome segregation	0.023
	GO:2000024	regulation of leaf development	0.023
	GO:0007129	synapsis	0.025
	GO:0070192	chromosome organization involved in meio...	0.026
	GO:0006413	translational initiation	0.027
	GO:0035303	regulation of dephosphorylation	0.027
	GO:0033013	tetrapyrrole metabolic process	0.028
	GO:0048573	photoperiodism, flowering	0.029
	GO:0051246	regulation of protein metabolic process	0.029
	GO:0006779	porphyrin-containing compound biosynthet...	0.030
	GO:0090056	regulation of chlorophyll metabolic proc...	0.030
	GO:0098813	nuclear chromosome segregation	0.030
	GO:0032268	regulation of cellular protein metabolic...	0.030
	GO:0140013	meiotic nuclear division	0.030
	GO:0032784	regulation of DNA-templated transcriptio...	0.031
	GO:0031050	dsRNA fragmentation	0.032
	GO:0043331	response to dsRNA	0.032
	GO:0070918	production of small RNA involved in gene...	0.032
	GO:0071359	cellular response to dsRNA	0.032
	GO:0071478	cellular response to radiation	0.033
	GO:0015979	photosynthesis	0.033
	GO:0018193	peptidyl-amino acid modification	0.035
	GO:1901401	regulation of tetrapyrrole metabolic pro...	0.035
	GO:0018022	peptidyl-lysine methylation	0.036
	GO:0006778	porphyrin-containing compound metabolic ...	0.037
	GO:0048581	negative regulation of post-embryonic de...	0.037
	GO:0051241	negative regulation of multicellular org...	0.037
	GO:0006913	nucleocytoplasmic transport	0.037
	GO:0010921	regulation of phosphatase activity	0.037
	GO:0051169	nuclear transport	0.037
	GO:2001020	regulation of response to DNA damage sti...	0.039
	GO:0000027	ribosomal large subunit assembly	0.040
	GO:0031124	mRNA 3'-end processing	0.040

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0031399	regulation of protein modification proce...	0.040
	GO:0033014	tetrapyrrole biosynthetic process	0.041
	GO:0071482	cellular response to light stimulus	0.041
	GO:0065007	biological regulation	0.042
	GO:0009736	cytokinin-activated signaling pathway	0.042
	GO:0016074	snoRNA metabolic process	0.042
	GO:0043144	snoRNA processing	0.042
	GO:0071103	DNA conformation change	0.043
	GO:0006470	protein dephosphorylation	0.043
	GO:0006304	DNA modification	0.044
	GO:0044728	DNA methylation or demethylation	0.044
	GO:0090503	RNA phosphodiester bond hydrolysis, exon...	0.044
	GO:0006568	tryptophan metabolic process	0.045
	GO:0006586	indolalkylamine metabolic process	0.045
	GO:2000113	negative regulation of cellular macromol...	0.045
	GO:0016043	cellular component organization	0.045
	GO:0000478	endonucleolytic cleavage involved in rRN...	0.046
	GO:0032544	plastid translation	0.048
	GO:0010212	response to ionizing radiation	0.048
	GO:0000280	nuclear division	0.049
	GO:2000242	negative regulation of reproductive proc...	0.050
	GO:0009910	negative regulation of flower developmen...	0.050
	GO:0010224	response to UV-B	0.051
	GO:0000725	recombinational repair	0.052
	GO:0000463	maturation of LSU-rRNA from tricistronic...	0.052
	GO:0033365	protein localization to organelle	0.052
	GO:0000466	maturation of 5.8S rRNA from tricistroni...	0.052
	GO:0000184	nuclear-transcribed mRNA catabolic proce...	0.053
	GO:0006354	DNA-templated transcription, elongation	0.053
	GO:0015931	nucleobase-containing compound transport	0.053
	GO:0010380	regulation of chlorophyll biosynthetic p...	0.056
	GO:0000162	tryptophan biosynthetic process	0.057
	GO:0046219	indolalkylamine biosynthetic process	0.057
	GO:0070475	rRNA base methylation	0.058
	GO:0009668	plastid membrane organization	0.058
	GO:0010027	thylakoid membrane organization	0.058
	GO:1901699	cellular response to nitrogen compound	0.058
	GO:0007062	sister chromatid cohesion	0.061
	GO:0009411	response to UV	0.063
	GO:0051321	meiotic cell cycle	0.064
	GO:0071824	protein-DNA complex subunit organization	0.064
	GO:0008284	positive regulation of cell proliferatio...	0.064
	GO:0017038	protein import	0.067
	GO:0035194	posttranscriptional gene silencing by RN...	0.069
	GO:0000122	negative regulation of transcription by ...	0.069
	GO:0048571	long-day photoperiodism	0.071
	GO:0030163	protein catabolic process	0.075
	GO:0000724	double-strand break repair via homologou...	0.077
	GO:0043574	peroxisomal transport	0.077

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0006368	transcription elongation from RNA polyme...	0.077
	GO:0031053	primary miRNA processing	0.077
	GO:1902022	L-lysine transport	0.081
	GO:1903401	L-lysine transmembrane transport	0.081
	GO:0044743	protein transmembrane import into intrac...	0.083
	GO:0051193	regulation of cofactor metabolic process	0.083
	GO:2000030	regulation of response to red or far red...	0.087
	GO:0010109	regulation of photosynthesis	0.089
	GO:1903046	meiotic cell cycle process	0.091
	GO:0009583	detection of light stimulus	0.092
	GO:0071368	cellular response to cytokinin stimulus	0.092
CC	GO:1990904	ribonucleoprotein complex	0.000
	GO:1990234	transferase complex	0.000
	GO:0005654	nucleoplasm	0.000
	GO:0044451	nucleoplasm part	0.000
	GO:0044435	plastid part	0.000
	GO:0044434	chloroplast part	0.000
	GO:0031461	cullin-RING ubiquitin ligase complex	0.000
	GO:0000151	ubiquitin ligase complex	0.000
	GO:0005684	U2-type spliceosomal complex	0.000
	GO:0009534	chloroplast thylakoid	0.000
	GO:0042651	thylakoid membrane	0.000
	GO:0016604	nuclear body	0.000
	GO:0055035	plastid thylakoid membrane	0.000
	GO:0071010	prespliceosome	0.000
	GO:0005694	chromosome	0.000
	GO:0016607	nuclear speck	0.001
	GO:0009295	nucleoid	0.001
	GO:0080008	Cul4-RING E3 ubiquitin ligase complex	0.001
	GO:0009508	plastid chromosome	0.001
	GO:0000228	nuclear chromosome	0.002
	GO:0000229	cytoplasmic chromosome	0.003
	GO:0030687	preribosome, large subunit precursor	0.003
	GO:0005732	small nucleolar ribonucleoprotein comple...	0.004
	GO:0005689	U12-type spliceosomal complex	0.004
	GO:0005759	mitochondrial matrix	0.005
	GO:0008023	transcription elongation factor complex	0.005
	GO:0042646	plastid nucleoid	0.005
	GO:0000123	histone acetyltransferase complex	0.005
	GO:0015030	Cajal body	0.006
	GO:0005685	U1 snRNP	0.007
	GO:0005666	DNA-directed RNA polymerase III complex	0.012
	GO:0000178	exosome (RNase complex)	0.013
	GO:1905354	exoribonuclease complex	0.013
	GO:0031248	protein acetyltransferase complex	0.013
	GO:1902493	acetyltransferase complex	0.013
	GO:0097526	spliceosomal tri-snRNP complex	0.018
	GO:1902555	endoribonuclease complex	0.018
	GO:1905348	endonuclease complex	0.018

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0005643	nuclear pore	0.019
	GO:0009706	chloroplast inner membrane	0.020
	GO:0044454	nuclear chromosome part	0.024
	GO:0009528	plastid inner membrane	0.024
	GO:0000176	nuclear exosome (RNase complex)	0.028
	GO:0005665	DNA-directed RNA polymerase II, core com...	0.030
	GO:0046540	U4/U6 x U5 tri-snRNP complex	0.033
	GO:0000784	nuclear chromosome, telomeric region	0.037
	GO:0005682	U5 snRNP	0.037
	GO:0000243	commitment complex	0.043
	GO:1902554	serine/threonine protein kinase complex	0.043
	GO:1902911	protein kinase complex	0.043
	GO:0044427	chromosomal part	0.051
	GO:0000793	condensed chromosome	0.053
	GO:0000781	chromosome, telomeric region	0.057
	GO:0000794	condensed nuclear chromosome	0.068
	GO:0030677	ribonuclease P complex	0.080
	GO:0000785	chromatin	0.083
MF	GO:0140098	catalytic activity, acting on RNA	0.000
	GO:0004518	nuclease activity	0.000
	GO:0004519	endonuclease activity	0.000
	GO:0003677	DNA binding	0.000
	GO:0003724	RNA helicase activity	0.000
	GO:0140101	catalytic activity, acting on a tRNA	0.000
	GO:0016893	endonuclease activity, active with eithe...	0.000
	GO:0008094	DNA-dependent ATPase activity	0.001
	GO:0003697	single-stranded DNA binding	0.004
	GO:0016891	endoribonuclease activity, producing 5'-...	0.005
	GO:0030983	mismatched DNA binding	0.009
	GO:0004536	deoxyribonuclease activity	0.012
	GO:0043021	ribonucleoprotein complex binding	0.012
	GO:0003684	damaged DNA binding	0.012
	GO:0004532	exoribonuclease activity	0.012
	GO:0003725	double-stranded RNA binding	0.013
	GO:0004521	endoribonuclease activity	0.014
	GO:0003682	chromatin binding	0.015
	GO:0140102	catalytic activity, acting on a rRNA	0.017
	GO:0016896	exoribonuclease activity, producing 5'-p...	0.017
	GO:0042393	histone binding	0.018
	GO:0008170	N-methyltransferase activity	0.018
	GO:0004520	endodeoxyribonuclease activity	0.020
	GO:0140097	catalytic activity, acting on DNA	0.020
	GO:0044877	protein-containing complex binding	0.021
	GO:0019843	rRNA binding	0.023
	GO:0004003	ATP-dependent DNA helicase activity	0.029
	GO:0016779	nucleotidyltransferase activity	0.029
	GO:0008097	5S rRNA binding	0.032
	GO:0017069	snRNA binding	0.032
	GO:0003729	mRNA binding	0.034

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GO type	GO ID	Description	Adj. p-value
	GO:0004549	tRNA-specific ribonuclease activity	0.050
	GO:0003727	single-stranded RNA binding	0.050
	GO:0035064	methylated histone binding	0.078
	GO:0140034	methylation-dependent protein binding	0.078
	GO:0043022	ribosome binding	0.088
	GO:0140030	modification-dependent protein binding	0.091

4.3.18 Root - Preflowering - Cluster 18

GO type	GO ID	Description	Adj. p-value
BP	GO:0019748	secondary metabolic process	0.000
	GO:0009404	toxin metabolic process	0.000
	GO:0042430	indole-containing compound metabolic pro...	0.002
	GO:0003333	amino acid transmembrane transport	0.002
	GO:0015749	monosaccharide transmembrane transport	0.005
	GO:0008645	hexose transmembrane transport	0.006
	GO:1904659	glucose transmembrane transport	0.011
	GO:0009072	aromatic amino acid family metabolic pro...	0.011
	GO:0009073	aromatic amino acid family biosynthetic ...	0.014
	GO:0008152	metabolic process	0.014
	GO:0006575	cellular modified amino acid metabolic p...	0.015
	GO:0005996	monosaccharide metabolic process	0.016
	GO:0046323	glucose import	0.018
	GO:0006508	proteolysis	0.020
	GO:0042493	response to drug	0.020
	GO:1902022	L-lysine transport	0.020
	GO:1903401	L-lysine transmembrane transport	0.020
	GO:0006811	ion transport	0.020
	GO:0007154	cell communication	0.022
	GO:0046942	carboxylic acid transport	0.024
	GO:0006568	tryptophan metabolic process	0.032
	GO:0006586	indolalkylamine metabolic process	0.032
	GO:1905039	carboxylic acid transmembrane transport	0.034
	GO:0006820	anion transport	0.034
	GO:0042445	hormone metabolic process	0.036
	GO:0015849	organic acid transport	0.042
	GO:0032787	monocarboxylic acid metabolic process	0.047
	GO:0071577	zinc ion transmembrane transport	0.047
	GO:0006026	aminoglycan catabolic process	0.050
	GO:0006030	chitin metabolic process	0.050
	GO:0006032	chitin catabolic process	0.050
	GO:0009308	amine metabolic process	0.050
	GO:0046348	amino sugar catabolic process	0.050
	GO:1901072	glucosamine-containing compound cataboli...	0.050
	GO:1903825	organic acid transmembrane transport	0.054
	GO:0072523	purine-containing compound catabolic pro...	0.055
	GO:0030163	protein catabolic process	0.061
	GO:0098754	detoxification	0.065
	GO:0051603	proteolysis involved in cellular protein...	0.065
	GO:0098656	anion transmembrane transport	0.067
	GO:0034219	carbohydrate transmembrane transport	0.072
	GO:0006810	transport	0.073
	GO:0045861	negative regulation of proteolysis	0.073
	GO:0010466	negative regulation of peptidase activit...	0.077
	GO:0010951	negative regulation of endopeptidase act...	0.077
	GO:0052547	regulation of peptidase activity	0.077

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0052548	regulation of endopeptidase activity	0.077
	GO:0015706	nitrate transport	0.078
	GO:0044257	cellular protein catabolic process	0.078
	GO:0000162	tryptophan biosynthetic process	0.081
	GO:0046219	indolalkylamine biosynthetic process	0.081
	GO:0080163	regulation of protein serine/threonine p...	0.081
	GO:0006829	zinc ion transport	0.083
	GO:0051234	establishment of localization	0.083
	GO:1901071	glucosamine-containing compound metaboli...	0.083
	GO:0006022	aminoglycan metabolic process	0.087
	GO:0042737	drug catabolic process	0.092
	GO:0009611	response to wounding	0.093
	GO:0043666	regulation of phosphoprotein phosphatase...	0.093
	GO:0015802	basic amino acid transport	0.094
	GO:0000041	transition metal ion transport	0.097
	GO:0015698	inorganic anion transport	0.098
	GO:0015711	organic anion transport	0.098
	GO:0006040	amino sugar metabolic process	0.099
	GO:1902475	L-alpha-amino acid transmembrane transpo...	0.099
	GO:0006836	neurotransmitter transport	0.100
CC	GO:0071944	cell periphery	0.000
	GO:0000323	lytic vacuole	0.000
	GO:1905368	peptidase complex	0.001
	GO:0005839	proteasome core complex	0.002
	GO:0005576	extracellular region	0.010
	GO:0019773	proteasome core complex, alpha-subunit c...	0.029
	GO:0044421	extracellular region part	0.036
	GO:0005615	extracellular space	0.064
	GO:0004672	protein kinase activity	0.000
	GO:0005215	transporter activity	0.000
	GO:0022857	transmembrane transporter activity	0.000
	GO:0016705	oxidoreductase activity, acting on paire...	0.000
	GO:0015291	secondary active transmembrane transport...	0.000
	GO:0030246	carbohydrate binding	0.000
	GO:0016829	lyase activity	0.002
	GO:0004298	threonine-type endopeptidase activity	0.002
	GO:0015145	monosaccharide transmembrane transporter...	0.002
	GO:0070003	threonine-type peptidase activity	0.002
	GO:0001067	regulatory region nucleic acid binding	0.002
	GO:0015149	hexose transmembrane transporter activit...	0.002
	GO:0015172	acidic amino acid transmembrane transpor...	0.002
	GO:0044212	transcription regulatory region DNA bind...	0.002
	GO:0051213	dioxygenase activity	0.002
	GO:0043565	sequence-specific DNA binding	0.002
	GO:0015171	amino acid transmembrane transporter act...	0.002
	GO:0001871	pattern binding	0.002
	GO:0030247	polysaccharide binding	0.002
	GO:0004197	cysteine-type endopeptidase activity	0.002
	GO:0015318	inorganic molecular entity transmembrane...	0.002

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GO type	GO ID	Description	Adj. p-value
	GO:0004867	serine-type endopeptidase inhibitor acti...	0.003
	GO:0005355	glucose transmembrane transporter activi...	0.003
	GO:0051119	sugar transmembrane transporter activity	0.004
	GO:0008144	drug binding	0.004
	GO:0015181	arginine transmembrane transporter activ...	0.004
	GO:0015189	L-lysine transmembrane transporter activ...	0.004
	GO:0015075	ion transmembrane transporter activity	0.006
	GO:0004190	aspartic-type endopeptidase activity	0.007
	GO:0070001	aspartic-type peptidase activity	0.007
	GO:0015144	carbohydrate transmembrane transporter a...	0.009
	GO:0061630	ubiquitin protein ligase activity	0.009
	GO:0015295	solute:proton symporter activity	0.010
	GO:0004568	chitinase activity	0.011
	GO:0005351	carbohydrate:proton symporter activity	0.012
	GO:0005402	carbohydrate:cation symporter activity	0.012
	GO:0046527	glucosyltransferase activity	0.012
	GO:0015293	symporter activity	0.012
	GO:0005385	zinc ion transmembrane transporter activ...	0.013
	GO:0016765	transferase activity, transferring alkyl...	0.013
	GO:0015174	basic amino acid transmembrane transport...	0.013
	GO:0008194	UDP-glycosyltransferase activity	0.015
	GO:0008233	peptidase activity	0.022
	GO:0015294	solute:cation symporter activity	0.023
	GO:0070011	peptidase activity, acting on L-amino ac...	0.025
	GO:0004185	serine-type carboxypeptidase activity	0.026
	GO:0003959	NADPH dehydrogenase activity	0.026
	GO:0070008	serine-type exopeptidase activity	0.027
	GO:0004864	protein phosphatase inhibitor activity	0.029
	GO:0005524	ATP binding	0.029
	GO:0019212	phosphatase inhibitor activity	0.029
	GO:0016682	oxidoreductase activity, acting on diphe...	0.034
	GO:0004180	carboxypeptidase activity	0.034
	GO:0005326	neurotransmitter transporter activity	0.034
	GO:0016863	intramolecular oxidoreductase activity, ...	0.034
	GO:0015112	nitrate transmembrane transporter activi...	0.035
	GO:0046943	carboxylic acid transmembrane transporte...	0.036
	GO:0072509	divalent inorganic cation transmembrane ...	0.037
	GO:0046915	transition metal ion transmembrane trans...	0.039
	GO:0008483	transaminase activity	0.044
	GO:0016769	transferase activity, transferring nitro...	0.044
	GO:0015179	L-amino acid transmembrane transporter a...	0.045
	GO:0016679	oxidoreductase activity, acting on diphe...	0.048
	GO:0019208	phosphatase regulator activity	0.048
	GO:0019888	protein phosphatase regulator activity	0.048
	GO:0016838	carbon-oxygen lyase activity, acting on ...	0.050
	GO:0005509	calcium ion binding	0.053
	GO:0008509	anion transmembrane transporter activity	0.054
	GO:0005342	organic acid transmembrane transporter a...	0.057
	GO:0008324	cation transmembrane transporter activit...	0.068

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GO type	GO ID	Description	Adj. p-value
	GO:0005315	inorganic phosphate transmembrane transp...	0.083
	GO:0043167	ion binding	0.085
	GO:0015297	antiporter activity	0.087
	GO:0052716	hydroquinone:oxygen oxidoreductase activ...	0.089
	GO:0015175	neutral amino acid transmembrane transpo...	0.097
	GO:0016746	transferase activity, transferring acyl ...	0.098
	GO:0032559	adenyl ribonucleotide binding	0.099
	GO:0042887	amide transmembrane transporter activity	0.099

4.3.19 Root - Preflowering - Cluster 19

GO type	GO ID	Description	Adj. p-value
BP	GO:0006865	amino acid transport	0.006
	GO:0006857	oligopeptide transport	0.007
	GO:0005996	monosaccharide metabolic process	0.007
	GO:0006810	transport	0.007
	GO:0003333	amino acid transmembrane transport	0.008
	GO:0051234	establishment of localization	0.010
	GO:0019752	carboxylic acid metabolic process	0.011
	GO:0080163	regulation of protein serine/threonine p...	0.013
	GO:0030163	protein catabolic process	0.016
	GO:0046942	carboxylic acid transport	0.020
	GO:0051179	localization	0.020
	GO:0009753	response to jasmonic acid	0.032
	GO:0015849	organic acid transport	0.036
	GO:0044257	cellular protein catabolic process	0.042
	GO:1905039	carboxylic acid transmembrane transport	0.048
	GO:0009751	response to salicylic acid	0.049
	GO:0055114	oxidation-reduction process	0.056
	GO:0043666	regulation of phosphoprotein phosphatase...	0.057
	GO:0051603	proteolysis involved in cellular protein...	0.063
	GO:0006508	proteolysis	0.071
	GO:0034219	carbohydrate transmembrane transport	0.077
	GO:0006820	anion transport	0.077
	GO:1903825	organic acid transmembrane transport	0.079
	GO:0044092	negative regulation of molecular functio...	0.080
	GO:0072523	purine-containing compound catabolic pro...	0.080
	GO:0008643	carbohydrate transport	0.080
	GO:0006575	cellular modified amino acid metabolic p...	0.083
	GO:0010921	regulation of phosphatase activity	0.089
	GO:0035304	regulation of protein dephosphorylation	0.089
	GO:0006749	glutathione metabolic process	0.090
	GO:0006811	ion transport	0.090
	GO:0006817	phosphate ion transport	0.090
	GO:1901264	carbohydrate derivative transport	0.090
CC	GO:0005886	plasma membrane	0.000
	GO:0000323	lytic vacuole	0.000
	GO:0004672	protein kinase activity	0.000
	GO:0005215	transporter activity	0.000
	GO:0022857	transmembrane transporter activity	0.000
	GO:0016705	oxidoreductase activity, acting on paire...	0.000
	GO:0015291	secondary active transmembrane transport...	0.000
	GO:0022804	active transmembrane transporter activit...	0.000
	GO:0043565	sequence-specific DNA binding	0.000
	GO:0001067	regulatory region nucleic acid binding	0.002
	GO:0044212	transcription regulatory region DNA bind...	0.002
	GO:0004175	endopeptidase activity	0.002
	GO:0015144	carbohydrate transmembrane transporter a...	0.004

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0015295	solute:proton symporter activity	0.004
	GO:0005351	carbohydrate:proton symporter activity	0.004
	GO:0005402	carbohydrate:cation symporter activity	0.004
	GO:0015171	amino acid transmembrane transporter act...	0.004
	GO:0015293	symporter activity	0.005
	GO:0030414	peptidase inhibitor activity	0.005
	GO:0061134	peptidase regulator activity	0.005
	GO:0015075	ion transmembrane transporter activity	0.005
	GO:0070011	peptidase activity, acting on L-amino ac...	0.007
	GO:0004866	endopeptidase inhibitor activity	0.009
	GO:0061135	endopeptidase regulator activity	0.009
	GO:0015294	solute:cation symporter activity	0.009
	GO:0004190	aspartic-type endopeptidase activity	0.009
	GO:0070001	aspartic-type peptidase activity	0.009
	GO:0008233	peptidase activity	0.010
	GO:0004867	serine-type endopeptidase inhibitor acti...	0.012
	GO:0051213	dioxygenase activity	0.013
	GO:0016765	transferase activity, transferring alkyl...	0.013
	GO:0004864	protein phosphatase inhibitor activity	0.013
	GO:0019212	phosphatase inhibitor activity	0.013
	GO:0004185	serine-type carboxypeptidase activity	0.014
	GO:0004364	glutathione transferase activity	0.014
	GO:0046527	glucosyltransferase activity	0.015
	GO:0070008	serine-type exopeptidase activity	0.017
	GO:0004197	cysteine-type endopeptidase activity	0.017
	GO:0004180	carboxypeptidase activity	0.019
	GO:0016829	lyase activity	0.019
	GO:0008144	drug binding	0.019
	GO:0019208	phosphatase regulator activity	0.022
	GO:0019888	protein phosphatase regulator activity	0.022
	GO:0010427	abscisic acid binding	0.029
	GO:0008324	cation transmembrane transporter activit...	0.032
	GO:0008194	UDP-glycosyltransferase activity	0.033
	GO:0042887	amide transmembrane transporter activity	0.033
	GO:0015238	drug transmembrane transporter activity	0.036
	GO:0019840	isoprenoid binding	0.040
	GO:0008061	chitin binding	0.041
	GO:0046943	carboxylic acid transmembrane transporte...	0.055
	GO:0015112	nitrate transmembrane transporter activi...	0.057
	GO:1904680	peptide transmembrane transporter activi...	0.057
	GO:0043178	alcohol binding	0.058
	GO:0052716	hydroquinone:oxygen oxidoreductase activ...	0.061
	GO:0004568	chitinase activity	0.063
	GO:0042562	hormone binding	0.070
	GO:0003959	NADPH dehydrogenase activity	0.072
	GO:0001871	pattern binding	0.084
	GO:0005342	organic acid transmembrane transporter a...	0.084
	GO:0008509	anion transmembrane transporter activity	0.084
	GO:0030247	polysaccharide binding	0.084

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0016746	transferase activity, transferring acyl ...	0.084
	GO:0008236	serine-type peptidase activity	0.085
	GO:0017171	serine hydrolase activity	0.085
	GO:0005315	inorganic phosphate transmembrane transp...	0.090

4.3.20 Root - Preflowering - Cluster 20

		Description	Adj. p-value
GO type	GO ID		
	GO:0007017	microtubule-based process	0.000
	GO:0005975	carbohydrate metabolic process	0.000
	GO:0044264	cellular polysaccharide metabolic proces...	0.000
	GO:0016052	carbohydrate catabolic process	0.000
	GO:0044036	cell wall macromolecule metabolic proces...	0.000
	GO:0000902	cell morphogenesis	0.000
	GO:1903047	mitotic cell cycle process	0.000
	GO:0048856	anatomical structure development	0.000
	GO:0046034	ATP metabolic process	0.000
	GO:0010383	cell wall polysaccharide metabolic proce...	0.000
	GO:0016049	cell growth	0.000
	GO:0019637	organophosphate metabolic process	0.000
	GO:0000910	cytokinesis	0.000
	GO:0000271	polysaccharide biosynthetic process	0.000
	GO:0044042	glucan metabolic process	0.000
	GO:0097237	cellular response to toxic substance	0.000
	GO:0007010	cytoskeleton organization	0.000
	GO:0000272	polysaccharide catabolic process	0.000
	GO:0006073	cellular glucan metabolic process	0.000
	GO:0006996	organelle organization	0.000
	GO:0000281	mitotic cytokinesis	0.000
	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0009826	unidimensional cell growth	0.000
	GO:0048868	pollen tube development	0.000
	GO:0022402	cell cycle process	0.000
	GO:1901137	carbohydrate derivative biosynthetic pro...	0.000
	GO:0009206	purine ribonucleoside triphosphate biosy...	0.000
	GO:1902600	proton transmembrane transport	0.000
	GO:0006754	ATP biosynthetic process	0.000
	GO:0009156	ribonucleoside monophosphate biosyntheti...	0.000
	GO:0009124	nucleoside monophosphate biosynthetic pr...	0.000
	GO:0034637	cellular carbohydrate biosynthetic proce...	0.000
	GO:0040007	growth	0.000
	GO:0007275	multicellular organism development	0.000
	GO:0033692	cellular polysaccharide biosynthetic pro...	0.000
	GO:0051273	beta-glucan metabolic process	0.000
	GO:0000904	cell morphogenesis involved in different...	0.000
	GO:0009165	nucleotide biosynthetic process	0.000
	GO:0044038	cell wall macromolecule biosynthetic pro...	0.000
	GO:0070589	cellular component macromolecule biosynt...	0.000
	GO:0019318	hexose metabolic process	0.000
	GO:0006101	citrate metabolic process	0.000
	GO:0090558	plant epidermis development	0.000
	GO:0006260	DNA replication	0.000
	GO:0009790	embryo development	0.000
	GO:0009888	tissue development	0.000

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GO type	GO ID	Description	Adj. p-value
	GO:0009791	post-embryonic development	0.000
	GO:0006457	protein folding	0.000
	GO:0008154	actin polymerization or depolymerization	0.000
	GO:0000226	microtubule cytoskeleton organization	0.000
	GO:0044275	cellular carbohydrate catabolic process	0.000
	GO:0070592	cell wall polysaccharide biosynthetic pr...	0.001
	GO:0044247	cellular polysaccharide catabolic proces...	0.001
	GO:0048278	vesicle docking	0.001
	GO:0009699	phenylpropanoid biosynthetic process	0.001
	GO:0030833	regulation of actin filament polymerizat...	0.001
	GO:0022406	membrane docking	0.001
	GO:0140056	organelle localization by membrane tethe...	0.001
	GO:0000003	reproduction	0.001
	GO:0006259	DNA metabolic process	0.001
	GO:0048193	Golgi vesicle transport	0.001
	GO:0010154	fruit development	0.001
	GO:0019359	nicotinamide nucleotide biosynthetic pro...	0.001
	GO:0022622	root system development	0.001
	GO:0090407	organophosphate biosynthetic process	0.001
	GO:0006119	oxidative phosphorylation	0.002
	GO:0042773	ATP synthesis coupled electron transport	0.002
	GO:0072350	tricarboxylic acid metabolic process	0.002
	GO:0090627	plant epidermal cell differentiation	0.002
	GO:0098754	detoxification	0.002
	GO:0009793	embryo development ending in seed dorman...	0.002
	GO:0048731	system development	0.002
	GO:0022904	respiratory electron transport chain	0.002
	GO:0048364	root development	0.002
	GO:0051493	regulation of cytoskeleton organization	0.002
	GO:0022414	reproductive process	0.002
	GO:0030154	cell differentiation	0.002
	GO:0042737	drug catabolic process	0.002
	GO:0010639	negative regulation of organelle organiz...	0.002
	GO:0019363	pyridine nucleotide biosynthetic process	0.002
	GO:0040029	regulation of gene expression, epigeneti...	0.002
	GO:0042743	hydrogen peroxide metabolic process	0.002
	GO:0051274	beta-glucan biosynthetic process	0.002
	GO:0048229	gametophyte development	0.002
	GO:0080147	root hair cell development	0.002
	GO:0048608	reproductive structure development	0.003
	GO:0061458	reproductive system development	0.003
	GO:0072593	reactive oxygen species metabolic proces...	0.003
	GO:1902903	regulation of supramolecular fiber organ...	0.003
	GO:0006884	cell volume homeostasis	0.003
	GO:0009932	cell tip growth	0.003
	GO:0009992	cellular water homeostasis	0.003
	GO:0015791	polyol transport	0.003
	GO:0015793	glycerol transport	0.003
	GO:0099402	plant organ development	0.003

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0006631	fatty acid metabolic process	0.003
	GO:0006270	DNA replication initiation	0.004
	GO:0009251	glucan catabolic process	0.004
	GO:0006090	pyruvate metabolic process	0.004
	GO:0006891	intra-Golgi vesicle-mediated transport	0.004
	GO:0006732	coenzyme metabolic process	0.004
	GO:0006261	DNA-dependent DNA replication	0.004
	GO:0051186	cofactor metabolic process	0.004
	GO:0009266	response to temperature stimulus	0.004
	GO:0007015	actin filament organization	0.004
	GO:0015672	monovalent inorganic cation transport	0.004
	GO:0030244	cellulose biosynthetic process	0.004
	GO:0090626	plant epidermis morphogenesis	0.004
	GO:0022603	regulation of anatomical structure morph...	0.005
	GO:0030104	water homeostasis	0.005
	GO:0072524	pyridine-containing compound metabolic p...	0.005
	GO:0010564	regulation of cell cycle process	0.005
	GO:0051258	protein polymerization	0.006
	GO:0006633	fatty acid biosynthetic process	0.006
	GO:0042221	response to chemical	0.006
	GO:0010103	stomatal complex morphogenesis	0.006
	GO:0030258	lipid modification	0.006
	GO:0006833	water transport	0.006
	GO:0042044	fluid transport	0.006
	GO:0048469	cell maturation	0.006
	GO:0048764	trichoblast maturation	0.006
	GO:0048765	root hair cell differentiation	0.006
	GO:0022604	regulation of cell morphogenesis	0.007
	GO:0010054	trichoblast differentiation	0.007
	GO:0048767	root hair elongation	0.007
	GO:0030036	actin cytoskeleton organization	0.007
	GO:0043254	regulation of protein complex assembly	0.007
	GO:0019953	sexual reproduction	0.008
	GO:0044255	cellular lipid metabolic process	0.008
	GO:0034404	nucleobase-containing small molecule bio...	0.008
	GO:0044703	multi-organism reproductive process	0.008
	GO:0072525	pyridine-containing compound biosyntheti...	0.008
	GO:0009250	glucan biosynthetic process	0.009
	GO:0009555	pollen development	0.009
	GO:0098657	import into cell	0.009
	GO:0030029	actin filament-based process	0.010
	GO:0051716	cellular response to stimulus	0.010
	GO:0015850	organic hydroxy compound transport	0.010
	GO:0030838	positive regulation of actin filament po...	0.010
	GO:0045010	actin nucleation	0.010
	GO:0016053	organic acid biosynthetic process	0.011
	GO:0046394	carboxylic acid biosynthetic process	0.011
	GO:0045493	xylan catabolic process	0.012
	GO:0046185	aldehyde catabolic process	0.012

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GO type	GO ID	Description	Adj. p-value
	GO:0032271	regulation of protein polymerization	0.012
	GO:0009698	phenylpropanoid metabolic process	0.012
	GO:0046486	glycerolipid metabolic process	0.013
	GO:0006897	endocytosis	0.013
	GO:0051276	chromosome organization	0.013
	GO:0044283	small molecule biosynthetic process	0.014
	GO:0008361	regulation of cell size	0.014
	GO:0021700	developmental maturation	0.015
	GO:0009934	regulation of meristem structural organi...	0.015
	GO:0090698	post-embryonic plant morphogenesis	0.015
	GO:0005982	starch metabolic process	0.015
	GO:0010374	stomatal complex development	0.015
	GO:0005984	disaccharide metabolic process	0.016
	GO:0061077	chaperone-mediated protein folding	0.017
	GO:0044839	cell cycle G2/M phase transition	0.019
	GO:0015766	disaccharide transport	0.019
	GO:0015770	sucrose transport	0.019
	GO:0015772	oligosaccharide transport	0.019
	GO:0045492	xylan biosynthetic process	0.019
	GO:0048825	cotyledon development	0.020
	GO:0006650	glycerophospholipid metabolic process	0.021
	GO:0010038	response to metal ion	0.021
	GO:0006979	response to oxidative stress	0.022
	GO:0010053	root epidermal cell differentiation	0.022
	GO:0006006	glucose metabolic process	0.023
	GO:0009628	response to abiotic stimulus	0.023
	GO:0052546	cell wall pectin metabolic process	0.023
	GO:1903338	regulation of cell wall organization or ...	0.023
	GO:0043647	inositol phosphate metabolic process	0.024
	GO:0046854	phosphatidylinositol phosphorylation	0.024
	GO:0006986	response to unfolded protein	0.024
	GO:0009108	coenzyme biosynthetic process	0.024
	GO:0065008	regulation of biological quality	0.026
	GO:0006284	base-excision repair	0.026
	GO:0098660	inorganic ion transmembrane transport	0.026
	GO:0006904	vesicle docking involved in exocytosis	0.026
	GO:0010026	trichome differentiation	0.026
	GO:0140029	exocytic process	0.026
	GO:0009225	nucleotide-sugar metabolic process	0.027
	GO:0044770	cell cycle phase transition	0.027
	GO:1905392	plant organ morphogenesis	0.028
	GO:2001251	negative regulation of chromosome organi...	0.029
	GO:0051640	organelle localization	0.029
	GO:0031122	cytoplasmic microtubule organization	0.030
	GO:0032504	multicellular organism reproduction	0.031
	GO:0007030	Golgi organization	0.031
	GO:0071695	anatomical structure maturation	0.031
	GO:0033554	cellular response to stress	0.031
	GO:0006207	'de novo' pyrimidine nucleobase biosynth...	0.032

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GO type	GO ID	Description	Adj. p-value
	GO:0010876	lipid localization	0.034
	GO:0046686	response to cadmium ion	0.034
	GO:0048826	cotyledon morphogenesis	0.034
	GO:0015985	energy coupled proton transport, down el...	0.034
	GO:0015986	ATP synthesis coupled proton transport	0.034
	GO:0042542	response to hydrogen peroxide	0.035
	GO:0051235	maintenance of location	0.035
	GO:0051275	beta-glucan catabolic process	0.037
	GO:0042545	cell wall modification	0.037
	GO:0010035	response to inorganic substance	0.037
	GO:0007264	small GTPase mediated signal transductio...	0.039
	GO:0006644	phospholipid metabolic process	0.039
	GO:0034968	histone lysine methylation	0.039
	GO:0030245	cellulose catabolic process	0.039
	GO:0051510	regulation of unidimensional cell growth	0.039
	GO:0006310	DNA recombination	0.040
	GO:0051726	regulation of cell cycle	0.041
	GO:0045490	pectin catabolic process	0.041
	GO:0055082	cellular chemical homeostasis	0.043
	GO:0042180	cellular ketone metabolic process	0.043
	GO:0016042	lipid catabolic process	0.044
	GO:0046835	carbohydrate phosphorylation	0.045
	GO:0042592	homeostatic process	0.046
	GO:0030004	cellular monovalent inorganic cation hom...	0.046
	GO:0000086	G2/M transition of mitotic cell cycle	0.048
	GO:0034220	ion transmembrane transport	0.048
	GO:1901661	quinone metabolic process	0.048
	GO:1901663	quinone biosynthetic process	0.048
	GO:1902749	regulation of cell cycle G2/M phase tran...	0.048
	GO:0046834	lipid phosphorylation	0.051
	GO:0005983	starch catabolic process	0.053
	GO:0055046	microgametogenesis	0.053
	GO:0009629	response to gravity	0.053
	GO:1905268	negative regulation of chromatin organiz...	0.054
	GO:0048598	embryonic morphogenesis	0.055
	GO:0035966	response to topologically incorrect prot...	0.056
	GO:0030641	regulation of cellular pH	0.056
	GO:0043244	regulation of protein complex disassembl...	0.056
	GO:0051453	regulation of intracellular pH	0.056
	GO:0071103	DNA conformation change	0.057
	GO:0044087	regulation of cellular component biogene...	0.057
	GO:0098662	inorganic cation transmembrane transport	0.058
	GO:0019321	pentose metabolic process	0.060
	GO:0046470	phosphatidylcholine metabolic process	0.061
	GO:0031109	microtubule polymerization or depolymeri...	0.061
	GO:0019751	polyol metabolic process	0.063
	GO:0006458	'de novo' protein folding	0.064
	GO:0051084	'de novo' posttranslational protein fold...	0.064
	GO:0032392	DNA geometric change	0.064

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GO type	GO ID	Description	Adj. p-value
	GO:0032508	DNA duplex unwinding	0.064
	GO:0009438	methylglyoxal metabolic process	0.070
	GO:0042182	ketone catabolic process	0.070
	GO:0051596	methylglyoxal catabolic process	0.070
	GO:0055067	monovalent inorganic cation homeostasis	0.070
	GO:0018022	peptidyl-lysine methylation	0.070
	GO:0000280	nuclear division	0.072
	GO:0010191	mucilage metabolic process	0.072
	GO:0044772	mitotic cell cycle phase transition	0.072
	GO:0019915	lipid storage	0.076
	GO:0051085	chaperone cofactor-dependent protein ref...	0.076
	GO:0034976	response to endoplasmic reticulum stress	0.077
	GO:0008356	asymmetric cell division	0.077
	GO:0051651	maintenance of location in cell	0.077
	GO:0006970	response to osmotic stress	0.078
	GO:0051495	positive regulation of cytoskeleton orga...	0.079
	GO:1902905	positive regulation of supramolecular fi...	0.079
	GO:0032787	monocarboxylic acid metabolic process	0.080
	GO:0009630	gravitropism	0.081
	GO:0018208	peptidyl-proline modification	0.082
	GO:0019566	arabinose metabolic process	0.082
	GO:0043622	cortical microtubule organization	0.085
	GO:0010015	root morphogenesis	0.088
	GO:0018105	peptidyl-serine phosphorylation	0.089
	GO:0043547	positive regulation of GTPase activity	0.089
	GO:0006075	(1-¿3)-beta-D-glucan biosynthetic proces...	0.091
	GO:0044786	cell cycle DNA replication	0.091
	GO:0042181	ketone biosynthetic process	0.091
	GO:0010215	cellulose microfibril organization	0.096
	GO:0044282	small molecule catabolic process	0.098
	GO:0006812	cation transport	0.099
	GO:0008202	steroid metabolic process	0.099
	GO:0044089	positive regulation of cellular componen...	0.099
	GO:0048609	multicellular organismal reproductive pr...	0.100
	GO:0044430	cytoskeletal part	0.000
	GO:0012505	endomembrane system	0.000
	GO:0044431	Golgi apparatus part	0.000
	GO:0016020	membrane	0.000
	GO:0033176	proton-transporting V-type ATPase comple...	0.000
	GO:0005773	vacuole	0.000
	GO:0033178	proton-transporting two-sector ATPase co...	0.000
	GO:0005886	plasma membrane	0.000
	GO:0031410	cytoplasmic vesicle	0.000
	GO:0005819	spindle	0.000
	GO:0044427	chromosomal part	0.000
	GO:0030662	coated vesicle membrane	0.000
	GO:0012506	vesicle membrane	0.001
	GO:0044425	membrane part	0.001
	GO:0005876	spindle microtubule	0.001

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CC

GO type	GO ID	Description	Adj. p-value
	GO:0000775	chromosome, centromeric region	0.002
	GO:0030863	cortical cytoskeleton	0.002
	GO:0030981	cortical microtubule cytoskeleton	0.002
	GO:0009504	cell plate	0.002
	GO:0055028	cortical microtubule	0.003
	GO:0044433	cytoplasmic vesicle part	0.003
	GO:0005881	cytoplasmic microtubule	0.004
	GO:0030660	Golgi-associated vesicle membrane	0.004
	GO:0030133	transport vesicle	0.009
	GO:0009705	plant-type vacuole membrane	0.010
	GO:0005753	mitochondrial proton-transporting ATP sy...	0.011
	GO:0005768	endosome	0.011
	GO:0015629	actin cytoskeleton	0.011
	GO:0031224	intrinsic component of membrane	0.014
	GO:0030658	transport vesicle membrane	0.015
	GO:0009574	preprophase band	0.020
	GO:0042575	DNA polymerase complex	0.020
	GO:0005769	early endosome	0.024
	GO:0000325	plant-type vacuole	0.031
	GO:0033177	proton-transporting two-sector ATPase co...	0.043
	GO:0044454	nuclear chromosome part	0.051
	GO:0005657	replication fork	0.053
	GO:0005811	lipid droplet	0.053
	GO:0000228	nuclear chromosome	0.060
	GO:0000148	1,3-beta-D-glucan synthase complex	0.062
	GO:0098687	chromosomal region	0.071
	GO:0000793	condensed chromosome	0.088
	GO:0030134	COPII-coated ER to Golgi transport vesic...	0.090
	GO:0003824	catalytic activity	0.000
	GO:0016787	hydrolase activity	0.000
	GO:0015925	galactosidase activity	0.000
	GO:0016887	ATPase activity	0.001
	GO:0140097	catalytic activity, acting on DNA	0.002
	GO:0008374	O-acyltransferase activity	0.003
	GO:0004567	beta-mannosidase activity	0.003
	GO:0016757	transferase activity, transferring glyco...	0.004
	GO:0005372	water transmembrane transporter activity	0.004
	GO:0015250	water channel activity	0.004
	GO:0015254	glycerol channel activity	0.004
	GO:0005524	ATP binding	0.004
	GO:0008144	drug binding	0.005
	GO:0008289	lipid binding	0.005
	GO:0003954	NADH dehydrogenase activity	0.005
	GO:1901618	organic hydroxy compound transmembrane t...	0.005
	GO:0015166	polyol transmembrane transporter activit...	0.005
	GO:0015168	glycerol transmembrane transporter activ...	0.006
	GO:0016903	oxidoreductase activity, acting on the a...	0.008
	GO:0003678	DNA helicase activity	0.009
	GO:0035639	purine ribonucleoside triphosphate bindi...	0.009

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GO type	GO ID	Description	Adj. p-value
	GO:0015078	proton transmembrane transporter activit...	0.010
	GO:0016307	phosphatidylinositol phosphate kinase ac...	0.010
	GO:0016620	oxidoreductase activity, acting on the a...	0.010
	GO:0030554	adenyl nucleotide binding	0.010
	GO:0043168	anion binding	0.010
	GO:0051020	GTPase binding	0.010
	GO:0051087	chaperone binding	0.010
	GO:1901681	sulfur compound binding	0.010
	GO:0032559	adenyl ribonucleotide binding	0.010
	GO:0008146	sulfotransferase activity	0.012
	GO:0009044	xylan 1,4-beta-xylosidase activity	0.013
	GO:0097599	xylanase activity	0.013
	GO:0015077	monovalent inorganic cation transmembran...	0.013
	GO:0008047	enzyme activator activity	0.014
	GO:0005085	guanyl-nucleotide exchange factor activi...	0.015
	GO:0009055	electron transfer activity	0.015
	GO:0015926	glucosidase activity	0.015
	GO:0018024	histone-lysine N-methyltransferase activ...	0.016
	GO:0045330	aspartyl esterase activity	0.016
	GO:0008422	beta-glucosidase activity	0.016
	GO:0017076	purine nucleotide binding	0.016
	GO:0032555	purine ribonucleotide binding	0.018
	GO:0004650	polygalacturonase activity	0.018
	GO:0005088	Ras guanyl-nucleotide exchange factor ac...	0.020
	GO:0097367	carbohydrate derivative binding	0.021
	GO:0032553	ribonucleotide binding	0.023
	GO:0003993	acid phosphatase activity	0.027
	GO:0015154	disaccharide transmembrane transporter a...	0.027
	GO:0015157	oligosaccharide transmembrane transporte...	0.027
	GO:0016853	isomerase activity	0.027
	GO:0016788	hydrolase activity, acting on ester bond...	0.035
	GO:0016615	malate dehydrogenase activity	0.035
	GO:0000287	magnesium ion binding	0.036
	GO:0060589	nucleoside-triphosphatase regulator acti...	0.039
	GO:0019783	ubiquitin-like protein-specific protease...	0.042
	GO:0030599	pectinesterase activity	0.042
	GO:0005200	structural constituent of cytoskeleton	0.042
	GO:0019104	DNA N-glycosylase activity	0.042
	GO:0042578	phosphoric ester hydrolase activity	0.043
	GO:0016774	phosphotransferase activity, carboxyl gr...	0.043
	GO:0046933	proton-transporting ATP synthase activit...	0.043
	GO:0008378	galactosyltransferase activity	0.044
	GO:0016759	cellulose synthase activity	0.047
	GO:0016760	cellulose synthase (UDP-forming) activit...	0.047
	GO:0022838	substrate-specific channel activity	0.047
	GO:0015267	channel activity	0.050
	GO:0022803	passive transmembrane transporter activi...	0.050
	GO:0016758	transferase activity, transferring hexos...	0.051
	GO:0015318	inorganic molecular entity transmembrane...	0.056

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GO type	GO ID	Description	Adj. p-value
	GO:0015144	carbohydrate transmembrane transporter a...	0.059
	GO:0051082	unfolded protein binding	0.061
	GO:0019200	carbohydrate kinase activity	0.065
	GO:0016746	transferase activity, transferring acyl ...	0.065
	GO:0017016	Ras GTPase binding	0.067
	GO:0031267	small GTPase binding	0.067
	GO:0051539	4 iron, 4 sulfur cluster binding	0.067
	GO:0051015	actin filament binding	0.072
	GO:0008810	cellulase activity	0.077
	GO:0005543	phospholipid binding	0.077
	GO:0016747	transferase activity, transferring acyl ...	0.077
	GO:0003843	1,3-beta-D-glucan synthase activity	0.079
	GO:0042054	histone methyltransferase activity	0.083
	GO:0070569	uridylyltransferase activity	0.084
	GO:0005527	macrolide binding	0.086
	GO:0005528	FK506 binding	0.086
	GO:0016857	racemase and epimerase activity, acting ...	0.086
	GO:0004029	aldehyde dehydrogenase (NAD) activity	0.087
	GO:0016417	S-acyltransferase activity	0.092
	GO:0008443	phosphofructokinase activity	0.093
	GO:0043138	3'-5' DNA helicase activity	0.093
	GO:0003755	peptidyl-prolyl cis-trans isomerase acti...	0.096

4.4 Root Postflowering clusters

4.4.1 Root - Postflowering - Cluster 1

GO type	GO ID	Description	Adj. p-value
	GO:0009266	response to temperature stimulus	0.000
	GO:0003006	developmental process involved in reprod...	0.000
	GO:0009642	response to light intensity	0.000
	GO:0016071	mRNA metabolic process	0.000
	GO:0048608	reproductive structure development	0.000
	GO:0008380	RNA splicing	0.000
	GO:0019637	organophosphate metabolic process	0.000
	GO:0010154	fruit development	0.000
	GO:0046034	ATP metabolic process	0.001
	GO:0005982	starch metabolic process	0.001
	GO:0006397	mRNA processing	0.001
	GO:0048316	seed development	0.001
	GO:0006970	response to osmotic stress	0.001
	GO:0007034	vacuolar transport	0.001
	GO:0061077	chaperone-mediated protein folding	0.001
	GO:0030258	lipid modification	0.001
	GO:0033365	protein localization to organelle	0.001
	GO:0000398	mRNA splicing, via spliceosome	0.002
	GO:0009141	nucleoside triphosphate metabolic proces...	0.003
	GO:0009416	response to light stimulus	0.003
	GO:0072594	establishment of protein localization to...	0.003
	GO:0034440	lipid oxidation	0.003
	GO:0050896	response to stimulus	0.004
	GO:0090351	seedling development	0.004
	GO:0000413	protein peptidyl-prolyl isomerization	0.004
	GO:0000184	nuclear-transcribed mRNA catabolic proce...	0.004
	GO:0006623	protein targeting to vacuole	0.004
	GO:0009081	branched-chain amino acid metabolic proc...	0.004
	GO:0009117	nucleotide metabolic process	0.004
	GO:0006629	lipid metabolic process	0.004
	GO:0034599	cellular response to oxidative stress	0.004
	GO:0044282	small molecule catabolic process	0.004
	GO:0009260	ribonucleotide biosynthetic process	0.005
	GO:0046390	ribose phosphate biosynthetic process	0.005
	GO:0006753	nucleoside phosphate metabolic process	0.005
	GO:0015672	monovalent inorganic cation transport	0.005
	GO:0005983	starch catabolic process	0.006
	GO:0009124	nucleoside monophosphate biosynthetic pr...	0.006
	GO:0006551	leucine metabolic process	0.006
	GO:0007033	vacuole organization	0.006
	GO:0006206	pyrimidine nucleobase metabolic process	0.006
	GO:0009156	ribonucleoside monophosphate biosyntheti...	0.006
	GO:0010256	endomembrane system organization	0.007
	GO:0006892	post-Golgi vesicle-mediated transport	0.007
	GO:0044270	cellular nitrogen compound catabolic pro...	0.007

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0046700	heterocycle catabolic process	0.007
	GO:0072666	establishment of protein localization to...	0.008
	GO:0048868	pollen tube development	0.008
	GO:0009845	seed germination	0.008
	GO:0044255	cellular lipid metabolic process	0.009
	GO:0051085	chaperone cofactor-dependent protein ref...	0.009
	GO:0022411	cellular component disassembly	0.010
	GO:0019395	fatty acid oxidation	0.011
	GO:0009062	fatty acid catabolic process	0.011
	GO:0009127	purine nucleoside monophosphate biosynth...	0.011
	GO:0009168	purine ribonucleoside monophosphate bios...	0.011
	GO:0030091	protein repair	0.011
	GO:0006089	lactate metabolic process	0.011
	GO:0019243	methylglyoxal catabolic process to D-lac...	0.011
	GO:0061727	methylglyoxal catabolic process to lacta...	0.011
	GO:0046185	aldehyde catabolic process	0.012
	GO:0090407	organophosphate biosynthetic process	0.013
	GO:0006635	fatty acid beta-oxidation	0.013
	GO:0009201	ribonucleoside triphosphate biosynthetic...	0.013
	GO:0016052	carbohydrate catabolic process	0.015
	GO:0009145	purine nucleoside triphosphate biosynthe...	0.015
	GO:0009206	purine ribonucleoside triphosphate biosy...	0.015
	GO:0044247	cellular polysaccharide catabolic proces...	0.015
	GO:0072521	purine-containing compound metabolic pro...	0.016
	GO:0009152	purine ribonucleotide biosynthetic proce...	0.016
	GO:0072329	monocarboxylic acid catabolic process	0.017
	GO:0009860	pollen tube growth	0.017
	GO:0006754	ATP biosynthetic process	0.017
	GO:0009409	response to cold	0.017
	GO:1901700	response to oxygen-containing compound	0.017
	GO:0006631	fatty acid metabolic process	0.018
	GO:0043484	regulation of RNA splicing	0.018
	GO:0043624	cellular protein complex disassembly	0.019
	GO:0072528	pyrimidine-containing compound biosynthe...	0.019
	GO:0009932	cell tip growth	0.019
	GO:1901661	quinone metabolic process	0.020
	GO:1901663	quinone biosynthetic process	0.020
	GO:0034655	nucleobase-containing compound catabolic...	0.020
	GO:0006401	RNA catabolic process	0.021
	GO:0006402	mRNA catabolic process	0.021
	GO:0009142	nucleoside triphosphate biosynthetic pro...	0.021
	GO:0051179	localization	0.023
	GO:0008154	actin polymerization or depolymerization	0.023
	GO:0019856	pyrimidine nucleobase biosynthetic proce...	0.023
	GO:0016054	organic acid catabolic process	0.024
	GO:0046395	carboxylic acid catabolic process	0.024
	GO:0051261	protein depolymerization	0.024
	GO:0033993	response to lipid	0.024
	GO:0006164	purine nucleotide biosynthetic process	0.024

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0006810	transport	0.024
	GO:0009438	methylglyoxal metabolic process	0.024
	GO:0042182	ketone catabolic process	0.024
	GO:0051596	methylglyoxal catabolic process	0.024
	GO:0006458	'de novo' protein folding	0.026
	GO:0051084	'de novo' posttranslational protein fold...	0.026
	GO:0097305	response to alcohol	0.026
	GO:0051234	establishment of localization	0.026
	GO:0042181	ketone biosynthetic process	0.027
	GO:0009165	nucleotide biosynthetic process	0.028
	GO:0034614	cellular response to reactive oxygen spe...	0.029
	GO:0006012	galactose metabolic process	0.029
	GO:0006896	Golgi to vacuole transport	0.029
	GO:1901293	nucleoside phosphate biosynthetic proces...	0.029
	GO:0008064	regulation of actin polymerization or de...	0.032
	GO:0030832	regulation of actin filament length	0.032
	GO:0032956	regulation of actin cytoskeleton organiz...	0.032
	GO:0032970	regulation of actin filament-based proce...	0.032
	GO:0045037	protein import into chloroplast stroma	0.032
	GO:0046486	glycerolipid metabolic process	0.032
	GO:0061025	membrane fusion	0.032
	GO:0110053	regulation of actin filament organizatio...	0.032
	GO:0006733	oxidoreduction coenzyme metabolic proces...	0.033
	GO:0032984	protein-containing complex disassembly	0.034
	GO:0009651	response to salt stress	0.034
	GO:0006207	'de novo' pyrimidine nucleobase biosynth...	0.035
	GO:0090174	organelle membrane fusion	0.035
	GO:0006644	phospholipid metabolic process	0.035
	GO:0042221	response to chemical	0.035
	GO:0044281	small molecule metabolic process	0.036
	GO:0009908	flower development	0.038
	GO:0009737	response to abscisic acid	0.040
	GO:0001101	response to acid chemical	0.041
	GO:0006972	hyperosmotic response	0.042
	GO:0034404	nucleobase-containing small molecule bio...	0.042
	GO:0055086	nucleobase-containing small molecule met...	0.043
	GO:0030041	actin filament polymerization	0.045
	GO:0030833	regulation of actin filament polymerizat...	0.045
	GO:0008643	carbohydrate transport	0.048
	GO:0044275	cellular carbohydrate catabolic process	0.051
	GO:1901135	carbohydrate derivative metabolic proces...	0.051
	GO:0072527	pyrimidine-containing compound metabolic...	0.051
	GO:0051493	regulation of cytoskeleton organization	0.053
	GO:0006906	vesicle fusion	0.054
	GO:0006108	malate metabolic process	0.055
	GO:0048284	organelle fusion	0.055
	GO:0009064	glutamine family amino acid metabolic pr...	0.057
	GO:0042335	cuticle development	0.058
	GO:0009063	cellular amino acid catabolic process	0.060

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0046488	phosphatidylinositol metabolic process	0.061
	GO:0006560	proline metabolic process	0.062
	GO:0046434	organophosphate catabolic process	0.063
	GO:0090567	reproductive shoot system development	0.065
	GO:0006650	glycerophospholipid metabolic process	0.068
	GO:0006090	pyruvate metabolic process	0.070
	GO:0048468	cell development	0.071
	GO:0000904	cell morphogenesis involved in different...	0.072
	GO:1902903	regulation of supramolecular fiber organ...	0.073
	GO:1900140	regulation of seedling development	0.075
	GO:1901575	organic substance catabolic process	0.075
	GO:0006743	ubiquinone metabolic process	0.077
	GO:0006744	ubiquinone biosynthetic process	0.077
	GO:0051188	cofactor biosynthetic process	0.078
	GO:0046496	nicotinamide nucleotide metabolic proces...	0.079
	GO:0048443	stamen development	0.079
	GO:0048466	androecium development	0.079
	GO:0044242	cellular lipid catabolic process	0.080
	GO:0046854	phosphatidylinositol phosphorylation	0.083
	GO:0046365	monosaccharide catabolic process	0.085
	GO:0019362	pyridine nucleotide metabolic process	0.085
	GO:0019359	nicotinamide nucleotide biosynthetic pro...	0.087
	GO:0072598	protein localization to chloroplast	0.089
	GO:0031338	regulation of vesicle fusion	0.090
	GO:1901606	alpha-amino acid catabolic process	0.090
	GO:0033043	regulation of organelle organization	0.090
	GO:0055046	microgametogenesis	0.092
	GO:0043244	regulation of protein complex disassembl...	0.093
	GO:0072524	pyridine-containing compound metabolic p...	0.093
	GO:0000956	nuclear-transcribed mRNA catabolic proce...	0.095
	GO:0098660	inorganic ion transmembrane transport	0.095
	GO:0042180	cellular ketone metabolic process	0.097
	GO:0019674	NAD metabolic process	0.097
	GO:0010029	regulation of seed germination	0.100
CC	GO:0009536	plastid	0.000
	GO:0009579	thylakoid	0.000
	GO:0009532	plastid stroma	0.000
	GO:0005746	mitochondrial respiratory chain	0.000
	GO:0098803	respiratory chain complex	0.000
	GO:0031977	thylakoid lumen	0.000
	GO:0016469	proton-transporting two-sector ATPase co...	0.000
	GO:0005773	vacuole	0.000
	GO:0044437	vacuolar part	0.000
	GO:0033178	proton-transporting two-sector ATPase co...	0.000
	GO:0019898	extrinsic component of membrane	0.001
	GO:0042170	plastid membrane	0.001
	GO:0009528	plastid inner membrane	0.002
	GO:0031969	chloroplast membrane	0.003
	GO:0009706	chloroplast inner membrane	0.010

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0030135	coated vesicle	0.013
	GO:0005681	spliceosomal complex	0.013
	GO:0070069	cytochrome complex	0.016
	GO:0031968	organelle outer membrane	0.021
	GO:0000325	plant-type vacuole	0.031
	GO:0009705	plant-type vacuole membrane	0.041
	GO:0005684	U2-type spliceosomal complex	0.053
	GO:0048046	apoplast	0.068
MF	GO:0044769	ATPase activity, coupled to transmembran...	0.000
	GO:0003713	transcription coactivator activity	0.007
	GO:0003755	peptidyl-prolyl cis-trans isomerase acti...	0.009
	GO:0016859	cis-trans isomerase activity	0.009
	GO:0008047	enzyme activator activity	0.011
	GO:0003954	NADH dehydrogenase activity	0.011
	GO:0051087	chaperone binding	0.011
	GO:0016874	ligase activity	0.011
	GO:0003779	actin binding	0.015
	GO:0008092	cytoskeletal protein binding	0.016
	GO:0051539	4 iron, 4 sulfur cluster binding	0.016
	GO:2001070	starch binding	0.016
	GO:0019829	cation-transporting ATPase activity	0.019
	GO:0022853	active ion transmembrane transporter act...	0.019
	GO:0042625	ATPase coupled ion transmembrane transpo...	0.019
	GO:0004553	hydrolase activity, hydrolyzing O-glycos...	0.026
	GO:0016307	phosphatidylinositol phosphate kinase ac...	0.026
	GO:0016627	oxidoreductase activity, acting on the C...	0.026
	GO:0016903	oxidoreductase activity, acting on the a...	0.026
	GO:0005507	copper ion binding	0.029
	GO:0005527	macrolide binding	0.029
	GO:0005528	FK506 binding	0.029
	GO:0008237	metallopeptidase activity	0.029
	GO:0016774	phosphotransferase activity, carboxyl gr...	0.030
	GO:0008289	lipid binding	0.037
	GO:0016798	hydrolase activity, acting on glycosyl b...	0.039
	GO:0060589	nucleoside-triphosphatase regulator acti...	0.051
	GO:0015144	carbohydrate transmembrane transporter a...	0.054
	GO:0019200	carbohydrate kinase activity	0.057
	GO:0016667	oxidoreductase activity, acting on a sul...	0.061
	GO:0016853	isomerase activity	0.068
	GO:0016671	oxidoreductase activity, acting on a sul...	0.074
	GO:0009055	electron transfer activity	0.076
	GO:0051020	GTPase binding	0.078
	GO:0031072	heat shock protein binding	0.082
	GO:0035091	phosphatidylinositol binding	0.084
	GO:0015267	channel activity	0.094
	GO:0022803	passive transmembrane transporter activi...	0.094

4.4.2 Root - Postflowering - Cluster 2

GO type	GO ID	Description	Adj. p-value
BP	GO:0042737	drug catabolic process	0.000
	GO:0019748	secondary metabolic process	0.000
	GO:0009698	phenylpropanoid metabolic process	0.000
	GO:0005975	carbohydrate metabolic process	0.000
	GO:0042546	cell wall biogenesis	0.000
	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0009808	lignin metabolic process	0.000
	GO:0030243	cellulose metabolic process	0.000
	GO:0042445	hormone metabolic process	0.001
	GO:0010817	regulation of hormone levels	0.003
	GO:0045490	pectin catabolic process	0.003
	GO:0042446	hormone biosynthetic process	0.005
	GO:0009734	auxin-activated signaling pathway	0.007
	GO:0055085	transmembrane transport	0.007
	GO:2000652	regulation of secondary cell wall biogen...	0.009
	GO:0006694	steroid biosynthetic process	0.010
	GO:0009074	aromatic amino acid family catabolic pro...	0.010
	GO:0046274	lignin catabolic process	0.012
	GO:0015706	nitrate transport	0.013
	GO:0006810	transport	0.014
	GO:0008202	steroid metabolic process	0.014
	GO:0006811	ion transport	0.016
	GO:0034637	cellular carbohydrate biosynthetic proce...	0.016
	GO:0009694	jasmonic acid metabolic process	0.017
	GO:0051274	beta-glucan biosynthetic process	0.017
	GO:0018209	peptidyl-serine modification	0.020
	GO:0046271	phenylpropanoid catabolic process	0.021
	GO:0051234	establishment of localization	0.027
	GO:0018105	peptidyl-serine phosphorylation	0.033
	GO:0046777	protein autophosphorylation	0.033
	GO:0071365	cellular response to auxin stimulus	0.033
	GO:0051179	localization	0.039
	GO:0032787	monocarboxylic acid metabolic process	0.041
	GO:0009733	response to auxin	0.041
	GO:0009813	flavonoid biosynthetic process	0.043
	GO:0009056	catabolic process	0.045
	GO:0048878	chemical homeostasis	0.048
	GO:0010374	stomatal complex development	0.056
	GO:0010345	suberin biosynthetic process	0.057
	GO:1903338	regulation of cell wall organization or ...	0.058
	GO:0006082	organic acid metabolic process	0.063
	GO:0009404	toxin metabolic process	0.063
	GO:0009850	auxin metabolic process	0.063
	GO:0043436	oxoacid metabolic process	0.063
	GO:1901136	carbohydrate derivative catabolic proces...	0.063
	GO:0050801	ion homeostasis	0.066

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0010200	response to chitin	0.068
	GO:0098771	inorganic ion homeostasis	0.068
	GO:0006558	L-phenylalanine metabolic process	0.069
	GO:1902221	erythrose 4-phosphate/phosphoenolpyruvat...	0.069
	GO:0048544	recognition of pollen	0.071
	GO:0008037	cell recognition	0.074
	GO:0016143	S-glycoside metabolic process	0.075
	GO:0019757	glycosinolate metabolic process	0.075
	GO:0019760	glucosinolate metabolic process	0.075
	GO:0006629	lipid metabolic process	0.078
	GO:0055076	transition metal ion homeostasis	0.083
	GO:0055080	cation homeostasis	0.083
	GO:0030001	metal ion transport	0.090
	GO:0009308	amine metabolic process	0.098
	GO:0009875	pollen-pistil interaction	0.098
	GO:0000323	lytic vacuole	0.000
CC	GO:0005773	vacuole	0.084
	GO:0005615	extracellular space	0.093
	GO:0016491	oxidoreductase activity	0.000
	GO:0016798	hydrolase activity, acting on glycosyl b...	0.000
	GO:0016705	oxidoreductase activity, acting on paire...	0.000
	GO:0022857	transmembrane transporter activity	0.000
	GO:0022804	active transmembrane transporter activit...	0.000
	GO:0003993	acid phosphatase activity	0.001
	GO:0046527	glucosyltransferase activity	0.001
	GO:0008233	peptidase activity	0.002
	GO:0008374	O-acyltransferase activity	0.002
	GO:0015075	ion transmembrane transporter activity	0.003
	GO:0016830	carbon-carbon lyase activity	0.003
	GO:0004565	beta-galactosidase activity	0.003
	GO:0015318	inorganic molecular entity transmembrane...	0.003
	GO:0070011	peptidase activity, acting on L-amino ac...	0.004
	GO:0052716	hydroquinone:oxygen oxidoreductase activ...	0.004
	GO:0005544	calcium-dependent phospholipid binding	0.006
	GO:0008194	UDP-glycosyltransferase activity	0.007
	GO:0008238	exopeptidase activity	0.009
	GO:0001046	core promoter sequence-specific DNA bind...	0.009
	GO:0004197	cysteine-type endopeptidase activity	0.013
	GO:0016614	oxidoreductase activity, acting on CH-OH...	0.013
	GO:0098772	molecular function regulator	0.014
	GO:0016682	oxidoreductase activity, acting on diphe...	0.014
	GO:0016829	lyase activity	0.014
	GO:0016838	carbon-oxygen lyase activity, acting on ...	0.014
	GO:0003854	3-beta-hydroxy-delta5-steroid dehydrogen...	0.014
	GO:0015925	galactosidase activity	0.015
	GO:0016229	steroid dehydrogenase activity	0.016
	GO:0016854	racemase and epimerase activity	0.018
	GO:0030234	enzyme regulator activity	0.018
	GO:0001047	core promoter binding	0.019

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MF

GO type	GO ID	Description	Adj. p-value
	GO:0035251	UDP-glucosyltransferase activity	0.020
	GO:0004867	serine-type endopeptidase inhibitor acti...	0.020
	GO:0050662	coenzyme binding	0.022
	GO:0010333	terpene synthase activity	0.022
	GO:0008422	beta-glucosidase activity	0.022
	GO:0001228	transcriptional activator activity, RNA ...	0.023
	GO:0015112	nitrate transmembrane transporter activi...	0.023
	GO:0033764	steroid dehydrogenase activity, acting o...	0.028
	GO:0004499	N,N-dimethylaniline monooxygenase activi...	0.033
	GO:0016298	lipase activity	0.036
	GO:0080043	quercetin 3-O-glucosyltransferase activi...	0.036
	GO:0080044	quercetin 7-O-glucosyltransferase activi...	0.036
	GO:0042285	xylosyltransferase activity	0.037
	GO:0016840	carbon-nitrogen lyase activity	0.038
	GO:0008398	sterol 14-demethylase activity	0.039
	GO:0010427	abscisic acid binding	0.042
	GO:0047372	acylglycerol lipase activity	0.042
	GO:0016782	transferase activity, transferring sulfu...	0.044
	GO:0005516	calmodulin binding	0.045
	GO:0004857	enzyme inhibitor activity	0.045
	GO:0015926	glucosidase activity	0.046
	GO:0015399	primary active transmembrane transporter...	0.047
	GO:0015405	P-P-bond-hydrolysis-driven transmembrane...	0.047
	GO:0043492	ATPase activity, coupled to movement of ...	0.052
	GO:0042626	ATPase activity, coupled to transmembran...	0.057
	GO:0016679	oxidoreductase activity, acting on diphe...	0.058
	GO:0015168	glycerol transmembrane transporter activ...	0.066
	GO:0004866	endopeptidase inhibitor activity	0.069
	GO:0061135	endopeptidase regulator activity	0.069
	GO:0008107	galactoside 2-alpha-L-fucosyltransferase...	0.073
	GO:0016799	hydrolase activity, hydrolyzing N-glycos...	0.073
	GO:0030414	peptidase inhibitor activity	0.073
	GO:0031127	alpha-(1,2)-fucosyltransferase activity	0.073
	GO:0061134	peptidase regulator activity	0.073
	GO:0003700	DNA binding transcription factor activit...	0.076
	GO:0016616	oxidoreductase activity, acting on the C...	0.076
	GO:0000976	transcription regulatory region sequence...	0.078
	GO:0019840	isoprenoid binding	0.078
	GO:0008061	chitin binding	0.078
	GO:0015179	L-amino acid transmembrane transporter a...	0.093
	GO:0005372	water transmembrane transporter activity	0.099
	GO:0015250	water channel activity	0.099
	GO:0015254	glycerol channel activity	0.099
	GO:0000981	RNA polymerase II transcription factor a...	0.100

4.4.3 Root - Postflowering - Cluster 3

GO type	GO ID	Description	Adj. p-value
	GO:0005975	carbohydrate metabolic process	0.000
	GO:0007017	microtubule-based process	0.000
	GO:0042546	cell wall biogenesis	0.000
	GO:0098754	detoxification	0.000
	GO:0019748	secondary metabolic process	0.000
	GO:0044550	secondary metabolite biosynthetic proces...	0.000
	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0070592	cell wall polysaccharide biosynthetic pr...	0.000
	GO:0030243	cellulose metabolic process	0.000
	GO:0007010	cytoskeleton organization	0.000
	GO:0006260	DNA replication	0.000
	GO:0006694	steroid biosynthetic process	0.001
	GO:0009225	nucleotide-sugar metabolic process	0.001
	GO:1903047	mitotic cell cycle process	0.002
	GO:0009150	purine ribonucleotide metabolic process	0.002
	GO:0000272	polysaccharide catabolic process	0.002
	GO:1901293	nucleoside phosphate biosynthetic proces...	0.002
	GO:0019953	sexual reproduction	0.003
	GO:0034637	cellular carbohydrate biosynthetic proce...	0.003
	GO:0030244	cellulose biosynthetic process	0.003
	GO:0042545	cell wall modification	0.004
	GO:0072522	purine-containing compound biosynthetic ...	0.004
	GO:0009166	nucleotide catabolic process	0.004
	GO:0009056	catabolic process	0.004
	GO:0044042	glucan metabolic process	0.004
	GO:0010411	xyloglucan metabolic process	0.004
	GO:0046434	organophosphate catabolic process	0.004
	GO:0044703	multi-organism reproductive process	0.005
	GO:0009165	nucleotide biosynthetic process	0.005
	GO:0009888	tissue development	0.005
	GO:1901137	carbohydrate derivative biosynthetic pro...	0.005
	GO:0000278	mitotic cell cycle	0.005
	GO:0022402	cell cycle process	0.006
	GO:0006073	cellular glucan metabolic process	0.006
	GO:0006165	nucleoside diphosphate phosphorylation	0.006
	GO:0019693	ribose phosphate metabolic process	0.006
	GO:0009074	aromatic amino acid family catabolic pro...	0.006
	GO:0006096	glycolytic process	0.006
	GO:0006757	ATP generation from ADP	0.006
	GO:0008202	steroid metabolic process	0.006
	GO:0009135	purine nucleoside diphosphate metabolic ...	0.006
	GO:0009179	purine ribonucleoside diphosphate metabo...	0.006
	GO:0009185	ribonucleoside diphosphate metabolic pro...	0.006
	GO:0042866	pyruvate biosynthetic process	0.006
	GO:0044283	small molecule biosynthetic process	0.006
	GO:0046031	ADP metabolic process	0.006

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:1901292	nucleoside phosphate catabolic process	0.006
	GO:0035556	intracellular signal transduction	0.006
	GO:0000910	cytokinesis	0.007
	GO:0010374	stomatal complex development	0.008
	GO:0045493	xylan catabolic process	0.008
	GO:0032989	cellular component morphogenesis	0.008
	GO:0010026	trichome differentiation	0.009
	GO:0000902	cell morphogenesis	0.009
	GO:0009260	ribonucleotide biosynthetic process	0.009
	GO:0046390	ribose phosphate biosynthetic process	0.009
	GO:0006261	DNA-dependent DNA replication	0.009
	GO:0048869	cellular developmental process	0.009
	GO:0009734	auxin-activated signaling pathway	0.010
	GO:0030148	sphingolipid biosynthetic process	0.010
	GO:0016126	sterol biosynthetic process	0.010
	GO:0009259	ribonucleotide metabolic process	0.011
	GO:0007049	cell cycle	0.012
	GO:2000652	regulation of secondary cell wall biogen...	0.012
	GO:0019359	nicotinamide nucleotide biosynthetic pro...	0.013
	GO:0046496	nicotinamide nucleotide metabolic proces...	0.013
	GO:0090627	plant epidermal cell differentiation	0.013
	GO:0010038	response to metal ion	0.013
	GO:0046274	lignin catabolic process	0.013
	GO:0051274	beta-glucan biosynthetic process	0.013
	GO:0006631	fatty acid metabolic process	0.015
	GO:0018209	peptidyl-serine modification	0.016
	GO:0006559	L-phenylalanine catabolic process	0.017
	GO:0019363	pyridine nucleotide biosynthetic process	0.017
	GO:1902222	erythrose 4-phosphate/phosphoenolpyruvat...	0.017
	GO:0010016	shoot system morphogenesis	0.017
	GO:0019362	pyridine nucleotide metabolic process	0.017
	GO:0061640	cytoskeleton-dependent cytokinesis	0.020
	GO:0000226	microtubule cytoskeleton organization	0.021
	GO:0046271	phenylpropanoid catabolic process	0.021
	GO:0018105	peptidyl-serine phosphorylation	0.023
	GO:1903338	regulation of cell wall organization or ...	0.024
	GO:0019318	hexose metabolic process	0.025
	GO:0022622	root system development	0.026
	GO:0000281	mitotic cytokinesis	0.026
	GO:0009226	nucleotide-sugar biosynthetic process	0.028
	GO:0060560	developmental growth involved in morphog...	0.028
	GO:0032787	monocarboxylic acid metabolic process	0.028
	GO:0042775	mitochondrial ATP synthesis coupled elec...	0.028
	GO:0010043	response to zinc ion	0.028
	GO:0016125	sterol metabolic process	0.030
	GO:0048364	root development	0.032
	GO:0010103	stomatal complex morphogenesis	0.032
	GO:0051716	cellular response to stimulus	0.033
	GO:0016049	cell growth	0.035

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GO type	GO ID	Description	Adj. p-value
	GO:0070887	cellular response to chemical stimulus	0.035
	GO:0000904	cell morphogenesis involved in different...	0.037
	GO:0046777	protein autophosphorylation	0.040
	GO:0043436	oxoacid metabolic process	0.040
	GO:0006082	organic acid metabolic process	0.042
	GO:0072524	pyridine-containing compound metabolic p...	0.044
	GO:0006732	coenzyme metabolic process	0.044
	GO:0009826	unidimensional cell growth	0.044
	GO:1905392	plant organ morphogenesis	0.044
	GO:0009694	jasmonic acid metabolic process	0.044
	GO:0051510	regulation of unidimensional cell growth	0.044
	GO:0090626	plant epidermis morphogenesis	0.047
	GO:0051301	cell division	0.056
	GO:0015985	energy coupled proton transport, down el...	0.058
	GO:0015986	ATP synthesis coupled proton transport	0.058
	GO:0008356	asymmetric cell division	0.066
	GO:0006119	oxidative phosphorylation	0.066
	GO:0009733	response to auxin	0.066
	GO:0042773	ATP synthesis coupled electron transport	0.066
	GO:0072525	pyridine-containing compound biosyntheti...	0.066
	GO:0097435	supramolecular fiber organization	0.066
	GO:0010564	regulation of cell cycle process	0.066
	GO:0019321	pentose metabolic process	0.067
	GO:0006733	oxidoreduction coenzyme metabolic proces...	0.067
	GO:0007051	spindle organization	0.068
	GO:0009072	aromatic amino acid family metabolic pro...	0.068
	GO:0055082	cellular chemical homeostasis	0.068
	GO:0006090	pyruvate metabolic process	0.069
	GO:0010315	auxin efflux	0.069
	GO:0000911	cytokinesis by cell plate formation	0.069
	GO:0019637	organophosphate metabolic process	0.069
	GO:0010345	suberin biosynthetic process	0.069
	GO:0010413	glucuronoxylan metabolic process	0.069
	GO:0010417	glucuronoxylan biosynthetic process	0.069
	GO:0030154	cell differentiation	0.069
	GO:0006637	acyl-CoA metabolic process	0.071
	GO:0035383	thioester metabolic process	0.071
	GO:0071365	cellular response to auxin stimulus	0.071
	GO:0009958	positive gravitropism	0.073
	GO:0023052	signaling	0.074
	GO:0007165	signal transduction	0.077
	GO:0046364	monosaccharide biosynthetic process	0.083
	GO:0019752	carboxylic acid metabolic process	0.086
	GO:0044772	mitotic cell cycle phase transition	0.086
	GO:0006884	cell volume homeostasis	0.089
	GO:0009992	cellular water homeostasis	0.089
	GO:0015793	glycerol transport	0.089
	GO:0006558	L-phenylalanine metabolic process	0.092
	GO:1902221	erythrose 4-phosphate/phosphoenolpyruvat...	0.092

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GO type	GO ID	Description	Adj. p-value
	GO:0006979	response to oxidative stress	0.094
	GO:0090378	seed trichome elongation	0.095
CC	GO:0005856	cytoskeleton	0.000
	GO:0031225	anchored component of membrane	0.000
	GO:0044431	Golgi apparatus part	0.000
	GO:0031226	intrinsic component of plasma membrane	0.000
	GO:0044459	plasma membrane part	0.000
	GO:0000786	nucleosome	0.001
	GO:0009524	phragmoplast	0.001
	GO:0045259	proton-transporting ATP synthase complex	0.001
	GO:0005881	cytoplasmic microtubule	0.001
	GO:0055028	cortical microtubule	0.001
	GO:0005768	endosome	0.002
	GO:0032993	protein-DNA complex	0.003
	GO:0000139	Golgi membrane	0.003
	GO:0005819	spindle	0.006
	GO:0030863	cortical cytoskeleton	0.007
	GO:0030981	cortical microtubule cytoskeleton	0.007
	GO:0043228	non-membrane-bounded organelle	0.008
	GO:0043232	intracellular non-membrane-bounded organ...	0.008
	GO:0044427	chromosomal part	0.012
	GO:0000228	nuclear chromosome	0.018
	GO:0000347	THO complex	0.020
	GO:0005764	lysosome	0.025
	GO:0000775	chromosome, centromeric region	0.034
	GO:0000323	lytic vacuole	0.036
	GO:0044454	nuclear chromosome part	0.036
	GO:0000788	nuclear nucleosome	0.045
	GO:0009574	preprophase band	0.047
	GO:0005694	chromosome	0.095
	GO:0043596	nuclear replication fork	0.096
	GO:0000790	nuclear chromatin	0.097
	GO:0016491	oxidoreductase activity	0.000
	GO:0016798	hydrolase activity, acting on glycosyl b...	0.000
	GO:0016757	transferase activity, transferring glyco...	0.000
	GO:0016614	oxidoreductase activity, acting on CH-OH...	0.000
	GO:0050662	coenzyme binding	0.000
	GO:0016616	oxidoreductase activity, acting on the C...	0.000
	GO:0005088	Ras guanyl-nucleotide exchange factor ac...	0.001
	GO:0016709	oxidoreductase activity, acting on paire...	0.001
	GO:0005085	guanyl-nucleotide exchange factor activi...	0.002
	GO:0008171	O-methyltransferase activity	0.002
	GO:0016762	xyloglucan:xyloglucosyl transferase acti...	0.002
	GO:0008236	serine-type peptidase activity	0.002
	GO:0017171	serine hydrolase activity	0.002
	GO:0030599	pectinesterase activity	0.002
	GO:0016758	transferase activity, transferring hexos...	0.002
	GO:0004565	beta-galactosidase activity	0.002
	GO:0008238	exopeptidase activity	0.002

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GO type	GO ID	Description	Adj. p-value
	GO:0008422	beta-glucosidase activity	0.003
	GO:0015926	glucosidase activity	0.003
	GO:0016705	oxidoreductase activity, acting on paire...	0.003
	GO:0009044	xylan 1,4-beta-xylosidase activity	0.004
	GO:0097599	xylanase activity	0.004
	GO:0016740	transferase activity	0.004
	GO:0052716	hydroquinone:oxygen oxidoreductase activ...	0.004
	GO:0000287	magnesium ion binding	0.006
	GO:0004497	monooxygenase activity	0.007
	GO:0047372	acylglycerol lipase activity	0.008
	GO:0016682	oxidoreductase activity, acting on diphe...	0.009
	GO:0016841	ammonia-lyase activity	0.010
	GO:0016857	racemase and epimerase activity, acting ...	0.010
	GO:0015562	efflux transmembrane transporter activit...	0.011
	GO:0015925	galactosidase activity	0.011
	GO:0016679	oxidoreductase activity, acting on diphe...	0.011
	GO:0009055	electron transfer activity	0.011
	GO:0017048	Rho GTPase binding	0.011
	GO:0016773	phosphotransferase activity, alcohol gro...	0.012
	GO:0046910	pectinesterase inhibitor activity	0.012
	GO:0004683	calmodulin-dependent protein kinase acti...	0.013
	GO:0009931	calcium-dependent protein serine/threoni...	0.013
	GO:0010857	calcium-dependent protein kinase activit...	0.013
	GO:0005089	Rho guanyl-nucleotide exchange factor ac...	0.014
	GO:0003854	3-beta-hydroxy-delta5-steroid dehydrogen...	0.016
	GO:0005506	iron ion binding	0.016
	GO:0008398	sterol 14-demethylase activity	0.016
	GO:0016407	acetyltransferase activity	0.016
	GO:0080161	auxin transmembrane transporter activity	0.018
	GO:0098772	molecular function regulator	0.018
	GO:0042285	xylosyltransferase activity	0.019
	GO:0016854	racemase and epimerase activity	0.019
	GO:0046527	glucosyltransferase activity	0.020
	GO:0051287	NAD binding	0.022
	GO:0016301	kinase activity	0.024
	GO:0003779	actin binding	0.026
	GO:0052689	carboxylic ester hydrolase activity	0.032
	GO:0033764	steroid dehydrogenase activity, acting o...	0.034
	GO:0005200	structural constituent of cytoskeleton	0.035
	GO:0005372	water transmembrane transporter activity	0.035
	GO:0015250	water channel activity	0.035
	GO:0015254	glycerol channel activity	0.035
	GO:0016229	steroid dehydrogenase activity	0.035
	GO:0046933	proton-transporting ATP synthase activit...	0.035
	GO:0016799	hydrolase activity, hydrolyzing N-glycos...	0.036
	GO:0005516	calmodulin binding	0.045
	GO:0019104	DNA N-glycosylase activity	0.047
	GO:0016782	transferase activity, transferring sulfu...	0.050
	GO:0008810	cellulase activity	0.051

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GO type	GO ID	Description	Adj. p-value
	GO:0016772	transferase activity, transferring phosp...	0.051
	GO:0004672	protein kinase activity	0.053
	GO:0010329	auxin efflux transmembrane transporter a...	0.053
	GO:0015168	glycerol transmembrane transporter activ...	0.053
	GO:0016838	carbon-oxygen lyase activity, acting on ...	0.054
	GO:0016405	CoA-ligase activity	0.060
	GO:0016878	acid-thiol ligase activity	0.060
	GO:0031406	carboxylic acid binding	0.060
	GO:0043177	organic acid binding	0.060
	GO:0016298	lipase activity	0.060
	GO:0004567	beta-mannosidase activity	0.063
	GO:0015020	glucuronosyltransferase activity	0.065
	GO:0008194	UDP-glycosyltransferase activity	0.066
	GO:0004650	polygalacturonase activity	0.073
	GO:0016829	lyase activity	0.073
	GO:0016899	oxidoreductase activity, acting on the C...	0.073
	GO:0016717	oxidoreductase activity, acting on paire...	0.078
	GO:0016620	oxidoreductase activity, acting on the a...	0.087
	GO:0003678	DNA helicase activity	0.090
	GO:0005544	calcium-dependent phospholipid binding	0.090
	GO:0004674	protein serine/threonine kinase activity	0.092
	GO:0016776	phosphotransferase activity, phosphate g...	0.095
	GO:0019201	nucleotide kinase activity	0.098

4.4.4 Root - Postflowering - Cluster 4

		Description	Adj. p-value
GO type	GO ID		
	GO:0010383	cell wall polysaccharide metabolic proce...	0.000
	GO:0007017	microtubule-based process	0.000
	GO:0019748	secondary metabolic process	0.000
	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0044550	secondary metabolite biosynthetic proces...	0.000
	GO:0070592	cell wall polysaccharide biosynthetic pr...	0.000
	GO:0030243	cellulose metabolic process	0.000
	GO:0009808	lignin metabolic process	0.000
	GO:0006793	phosphorus metabolic process	0.000
	GO:0006694	steroid biosynthetic process	0.001
	GO:0007165	signal transduction	0.001
	GO:0007010	cytoskeleton organization	0.001
	GO:0009694	jasmonic acid metabolic process	0.002
	GO:0009117	nucleotide metabolic process	0.002
	GO:0019359	nicotinamide nucleotide biosynthetic pro...	0.002
	GO:0072522	purine-containing compound biosynthetic ...	0.002
	GO:0006270	DNA replication initiation	0.002
	GO:0009132	nucleoside diphosphate metabolic process	0.002
	GO:0009888	tissue development	0.003
	GO:0006165	nucleoside diphosphate phosphorylation	0.003
	GO:0008202	steroid metabolic process	0.003
	GO:0009152	purine ribonucleotide biosynthetic proce...	0.003
	GO:0019363	pyridine nucleotide biosynthetic process	0.003
	GO:1901137	carbohydrate derivative biosynthetic pro...	0.003
	GO:1903047	mitotic cell cycle process	0.003
	GO:0009225	nucleotide-sugar metabolic process	0.003
	GO:0009074	aromatic amino acid family catabolic pro...	0.003
	GO:0016310	phosphorylation	0.003
	GO:0006164	purine nucleotide biosynthetic process	0.004
	GO:0008610	lipid biosynthetic process	0.004
	GO:0000910	cytokinesis	0.004
	GO:0010026	trichome differentiation	0.004
	GO:2000652	regulation of secondary cell wall biogen...	0.004
	GO:0044283	small molecule biosynthetic process	0.004
	GO:0046939	nucleotide phosphorylation	0.004
	GO:0045493	xylan catabolic process	0.004
	GO:0009124	nucleoside monophosphate biosynthetic pr...	0.004
	GO:0055082	cellular chemical homeostasis	0.004
	GO:1901293	nucleoside phosphate biosynthetic proces...	0.006
	GO:0009404	toxin metabolic process	0.006
	GO:1903338	regulation of cell wall organization or ...	0.007
	GO:0009156	ribonucleoside monophosphate biosyntheti...	0.007
	GO:0019953	sexual reproduction	0.007
	GO:0090627	plant epidermal cell differentiation	0.007
	GO:0009407	toxin catabolic process	0.007
	GO:0052546	cell wall pectin metabolic process	0.007

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GO type	GO ID	Description	Adj. p-value
	GO:0006090	pyruvate metabolic process	0.008
	GO:0043436	oxoacid metabolic process	0.008
	GO:0046496	nicotinamide nucleotide metabolic proces...	0.008
	GO:0006082	organic acid metabolic process	0.008
	GO:0010374	stomatal complex development	0.009
	GO:0009165	nucleotide biosynthetic process	0.010
	GO:0019362	pyridine nucleotide metabolic process	0.011
	GO:0048869	cellular developmental process	0.011
	GO:0006559	L-phenylalanine catabolic process	0.011
	GO:0046274	lignin catabolic process	0.011
	GO:1902222	erythrose 4-phosphate/phosphoenolpyruvat...	0.011
	GO:0019693	ribose phosphate metabolic process	0.011
	GO:0000278	mitotic cell cycle	0.011
	GO:0051716	cellular response to stimulus	0.012
	GO:0072525	pyridine-containing compound biosyntheti...	0.013
	GO:0009259	ribonucleotide metabolic process	0.013
	GO:0048468	cell development	0.013
	GO:0006260	DNA replication	0.014
	GO:0070085	glycosylation	0.015
	GO:0010413	glucuronoxylan metabolic process	0.015
	GO:0010417	glucuronoxylan biosynthetic process	0.015
	GO:0090626	plant epidermis morphogenesis	0.015
	GO:0050801	ion homeostasis	0.015
	GO:0006811	ion transport	0.016
	GO:0061640	cytoskeleton-dependent cytokinesis	0.016
	GO:0022402	cell cycle process	0.016
	GO:0044703	multi-organism reproductive process	0.016
	GO:0046364	monosaccharide biosynthetic process	0.016
	GO:0032989	cellular component morphogenesis	0.016
	GO:0046271	phenylpropanoid catabolic process	0.017
	GO:0042445	hormone metabolic process	0.017
	GO:0019752	carboxylic acid metabolic process	0.017
	GO:0044248	cellular catabolic process	0.018
	GO:0000226	microtubule cytoskeleton organization	0.018
	GO:0019637	organophosphate metabolic process	0.018
	GO:0042221	response to chemical	0.018
	GO:0010345	suberin biosynthetic process	0.019
	GO:0000902	cell morphogenesis	0.019
	GO:0070887	cellular response to chemical stimulus	0.019
	GO:0006884	cell volume homeostasis	0.019
	GO:0009992	cellular water homeostasis	0.019
	GO:0015793	glycerol transport	0.019
	GO:0000281	mitotic cytokinesis	0.022
	GO:0030148	sphingolipid biosynthetic process	0.023
	GO:0006833	water transport	0.023
	GO:0042044	fluid transport	0.023
	GO:0006261	DNA-dependent DNA replication	0.025
	GO:0010053	root epidermal cell differentiation	0.027
	GO:0010817	regulation of hormone levels	0.027

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GO type	GO ID	Description	Adj. p-value
	GO:0009260	ribonucleotide biosynthetic process	0.027
	GO:0046390	ribose phosphate biosynthetic process	0.027
	GO:0009826	unidimensional cell growth	0.028
	GO:0010103	stomatal complex morphogenesis	0.028
	GO:0009695	jasmonic acid biosynthetic process	0.028
	GO:0006979	response to oxidative stress	0.029
	GO:0034404	nucleobase-containing small molecule bio...	0.029
	GO:0009934	regulation of meristem structural organi...	0.033
	GO:0010038	response to metal ion	0.034
	GO:0072524	pyridine-containing compound metabolic p...	0.035
	GO:0016125	sterol metabolic process	0.035
	GO:0010016	shoot system morphogenesis	0.035
	GO:0016049	cell growth	0.038
	GO:0051275	beta-glucan catabolic process	0.039
	GO:0030104	water homeostasis	0.039
	GO:0060560	developmental growth involved in morphog...	0.040
	GO:0007049	cell cycle	0.041
	GO:0055080	cation homeostasis	0.043
	GO:0022622	root system development	0.043
	GO:0098771	inorganic ion homeostasis	0.044
	GO:0043069	negative regulation of programmed cell d...	0.046
	GO:0019321	pentose metabolic process	0.047
	GO:0055065	metal ion homeostasis	0.049
	GO:0048364	root development	0.050
	GO:0006732	coenzyme metabolic process	0.050
	GO:0022603	regulation of anatomical structure morph...	0.051
	GO:0019318	hexose metabolic process	0.051
	GO:0019722	calcium-mediated signaling	0.055
	GO:0016043	cellular component organization	0.056
	GO:0051301	cell division	0.056
	GO:0032535	regulation of cellular component size	0.059
	GO:0048193	Golgi vesicle transport	0.059
	GO:0060548	negative regulation of cell death	0.059
	GO:0090066	regulation of anatomical structure size	0.059
	GO:0097435	supramolecular fiber organization	0.059
	GO:0006873	cellular ion homeostasis	0.061
	GO:0051510	regulation of unidimensional cell growth	0.067
	GO:0006733	oxidoreduction coenzyme metabolic proces...	0.069
	GO:0008356	asymmetric cell division	0.069
	GO:0051235	maintenance of location	0.069
	GO:0009395	phospholipid catabolic process	0.074
	GO:0010564	regulation of cell cycle process	0.074
	GO:0015985	energy coupled proton transport, down el...	0.075
	GO:0015986	ATP synthesis coupled proton transport	0.075
	GO:0031407	oxylipin metabolic process	0.075
	GO:0006468	protein phosphorylation	0.076
	GO:0046686	response to cadmium ion	0.077
	GO:0048826	cotyledon morphogenesis	0.080
	GO:0030245	cellulose catabolic process	0.080

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0010043	response to zinc ion	0.082
	GO:0015791	polyol transport	0.089
	GO:0065008	regulation of biological quality	0.090
	GO:0015850	organic hydroxy compound transport	0.095
	GO:0043648	dicarboxylic acid metabolic process	0.099
CC	GO:0031225	anchored component of membrane	0.000
	GO:0044431	Golgi apparatus part	0.000
	GO:0005753	mitochondrial proton-transporting ATP sy...	0.001
	GO:0044815	DNA packaging complex	0.003
	GO:0005876	spindle microtubule	0.004
	GO:0000323	lytic vacuole	0.005
	GO:0000786	nucleosome	0.007
	GO:0005819	spindle	0.008
	GO:0005887	integral component of plasma membrane	0.012
	GO:0030135	coated vesicle	0.017
	GO:0005881	cytoplasmic microtubule	0.019
	GO:0030863	cortical cytoskeleton	0.019
	GO:0030981	cortical microtubule cytoskeleton	0.019
	GO:0045259	proton-transporting ATP synthase complex	0.019
	GO:0055028	cortical microtubule	0.019
	GO:0009574	preprophase band	0.025
	GO:0042575	DNA polymerase complex	0.036
	GO:0030136	clathrin-coated vesicle	0.053
	GO:0032993	protein-DNA complex	0.053
	GO:0000347	THO complex	0.062
	GO:0030173	integral component of Golgi membrane	0.083
	GO:0031228	intrinsic component of Golgi membrane	0.083
	GO:0000775	chromosome, centromeric region	0.085
	GO:0005769	early endosome	0.085
	GO:0016491	oxidoreductase activity	0.000
	GO:0016757	transferase activity, transferring glyco...	0.000
	GO:0016773	phosphotransferase activity, alcohol gro...	0.000
	GO:0005088	Ras guanyl-nucleotide exchange factor ac...	0.000
	GO:0005085	guanyl-nucleotide exchange factor activi...	0.000
	GO:0004672	protein kinase activity	0.000
	GO:0016614	oxidoreductase activity, acting on CH-OH...	0.000
	GO:0005089	Rho guanyl-nucleotide exchange factor ac...	0.001
	GO:0016616	oxidoreductase activity, acting on the C...	0.002
	GO:0008171	O-methyltransferase activity	0.002
	GO:0016759	cellulose synthase activity	0.002
	GO:0016760	cellulose synthase (UDP-forming) activit...	0.002
	GO:0009044	xylan 1,4-beta-xylosidase activity	0.002
	GO:0097599	xylanase activity	0.002
	GO:0008374	O-acyltransferase activity	0.002
	GO:0016788	hydrolase activity, acting on ester bond...	0.003
	GO:0022838	substrate-specific channel activity	0.003
	GO:0098772	molecular function regulator	0.003
	GO:0016709	oxidoreductase activity, acting on paire...	0.003
	GO:0052716	hydroquinone:oxygen oxidoreductase activ...	0.004

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0015318	inorganic molecular entity transmembrane...	0.004
	GO:0008422	beta-glucosidase activity	0.004
	GO:0004497	monooxygenase activity	0.005
	GO:0015168	glycerol transmembrane transporter activ...	0.005
	GO:0015267	channel activity	0.005
	GO:0015926	glucosidase activity	0.005
	GO:0022803	passive transmembrane transporter activi...	0.005
	GO:0043492	ATPase activity, coupled to movement of ...	0.006
	GO:0016705	oxidoreductase activity, acting on paire...	0.006
	GO:0003779	actin binding	0.006
	GO:0004674	protein serine/threonine kinase activity	0.006
	GO:0016682	oxidoreductase activity, acting on diphe...	0.006
	GO:0003854	3-beta-hydroxy-delta5-steroid dehydrogen...	0.006
	GO:0005372	water transmembrane transporter activity	0.006
	GO:0015250	water channel activity	0.006
	GO:0015254	glycerol channel activity	0.006
	GO:0005516	calmodulin binding	0.008
	GO:0016679	oxidoreductase activity, acting on diphe...	0.008
	GO:0050662	coenzyme binding	0.009
	GO:0000287	magnesium ion binding	0.010
	GO:0016841	ammonia-lyase activity	0.010
	GO:0016790	thiolester hydrolase activity	0.011
	GO:0046527	glucosyltransferase activity	0.011
	GO:0008081	phosphoric diester hydrolase activity	0.011
	GO:0042578	phosphoric ester hydrolase activity	0.011
	GO:0042626	ATPase activity, coupled to transmembran...	0.012
	GO:0042285	xylosyltransferase activity	0.014
	GO:0033764	steroid dehydrogenase activity, acting o...	0.015
	GO:0016857	racemase and epimerase activity, acting ...	0.015
	GO:0008398	sterol 14-demethylase activity	0.015
	GO:0052689	carboxylic ester hydrolase activity	0.017
	GO:0004197	cysteine-type endopeptidase activity	0.018
	GO:0008810	cellulase activity	0.018
	GO:0004650	polygalacturonase activity	0.019
	GO:0008194	UDP-glycosyltransferase activity	0.020
	GO:0015020	glucuronosyltransferase activity	0.024
	GO:0009055	electron transfer activity	0.024
	GO:0015144	carbohydrate transmembrane transporter a...	0.024
	GO:0043168	anion binding	0.024
	GO:0005200	structural constituent of cytoskeleton	0.026
	GO:0016229	steroid dehydrogenase activity	0.030
	GO:0015399	primary active transmembrane transporter...	0.031
	GO:0015405	P-P-bond-hydrolysis-driven transmembrane...	0.031
	GO:0016298	lipase activity	0.031
	GO:0015166	polyol transmembrane transporter activit...	0.033
	GO:0016799	hydrolase activity, hydrolyzing N-glycos...	0.038
	GO:0030234	enzyme regulator activity	0.039
	GO:0015562	efflux transmembrane transporter activit...	0.043
	GO:0051287	NAD binding	0.043

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:1901618	organic hydroxy compound transmembrane t...	0.043
	GO:0016854	racemase and epimerase activity	0.047
	GO:0047372	acylglycerol lipase activity	0.055
	GO:0032451	demethylase activity	0.057
	GO:0015077	monovalent inorganic cation transmembran...	0.061
	GO:0010329	auxin efflux transmembrane transporter a...	0.071
	GO:0080161	auxin transmembrane transporter activity	0.073
	GO:0016838	carbon-oxygen lyase activity, acting on ...	0.078
	GO:0004567	beta-mannosidase activity	0.082
	GO:0008144	drug binding	0.083
	GO:0004871	signal transducer activity	0.085
	GO:0030276	clathrin binding	0.086
	GO:0016717	oxidoreductase activity, acting on paire...	0.086
	GO:0016791	phosphatase activity	0.086
	GO:0070569	uridylyltransferase activity	0.086
	GO:0015018	galactosylgalactosylxylosylprotein 3-bet...	0.091
	GO:0004364	glutathione transferase activity	0.097
	GO:0016829	lyase activity	0.097
	GO:0030246	carbohydrate binding	0.097
	GO:0010333	terpene synthase activity	0.098

4.4.5 Root - Postflowering - Cluster 5

GO type	GO ID	Description	Adj. p-value
BP	GO:0002098	tRNA wobble uridine modification	0.003
	GO:0008037	cell recognition	0.003
	GO:0000162	tryptophan biosynthetic process	0.003
	GO:0046219	indolalkylamine biosynthetic process	0.003
	GO:0009407	toxin catabolic process	0.003
	GO:0048544	recognition of pollen	0.003
	GO:0009875	pollen-pistil interaction	0.004
	GO:0015749	monosaccharide transmembrane transport	0.005
	GO:0008645	hexose transmembrane transport	0.006
	GO:0098542	defense response to other organism	0.007
	GO:0002097	tRNA wobble base modification	0.009
	GO:1904659	glucose transmembrane transport	0.010
	GO:1902022	L-lysine transport	0.011
	GO:1903401	L-lysine transmembrane transport	0.011
	GO:0006568	tryptophan metabolic process	0.013
	GO:0006586	indolalkylamine metabolic process	0.013
	GO:0048831	regulation of shoot system development	0.014
	GO:0009607	response to biotic stimulus	0.016
	GO:0043207	response to external biotic stimulus	0.016
	GO:0051707	response to other organism	0.016
	GO:0006836	neurotransmitter transport	0.017
	GO:0046323	glucose import	0.018
	GO:0009404	toxin metabolic process	0.019
	GO:0009814	defense response, incompatible interacti...	0.021
	GO:0035303	regulation of dephosphorylation	0.030
	GO:0009627	systemic acquired resistance	0.031
	GO:0042430	indole-containing compound metabolic pro...	0.033
	GO:1901698	response to nitrogen compound	0.039
	GO:0010243	response to organonitrogen compound	0.041
	GO:0055085	transmembrane transport	0.042
	GO:0051606	detection of stimulus	0.045
	GO:0010921	regulation of phosphatase activity	0.053
	GO:0035304	regulation of protein dephosphorylation	0.053
	GO:0009309	amine biosynthetic process	0.061
	GO:0009583	detection of light stimulus	0.061
	GO:0042401	cellular biogenic amine biosynthetic pro...	0.061
	GO:0046677	response to antibiotic	0.061
	GO:0080163	regulation of protein serine/threonine p...	0.073
	GO:0015802	basic amino acid transport	0.073
	GO:0009909	regulation of flower development	0.085
	GO:0043648	dicarboxylic acid metabolic process	0.085
	GO:0019748	secondary metabolic process	0.087
	GO:0043666	regulation of phosphoprotein phosphatase...	0.090
	GO:0002376	immune system process	0.091
	GO:0042447	hormone catabolic process	0.098
CC	GO:0016020	membrane	0.005

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0005887	integral component of plasma membrane	0.011
	GO:0000323	lytic vacuole	0.028
	GO:0005764	lysosome	0.050
MF	GO:0030246	carbohydrate binding	0.000
	GO:0080043	quercetin 3-O-glucosyltransferase activi...	0.006
	GO:0080044	quercetin 7-O-glucosyltransferase activi...	0.006
	GO:0016831	carboxy-lyase activity	0.008
	GO:0015172	acidic amino acid transmembrane transpor...	0.010
	GO:0015181	arginine transmembrane transporter activ...	0.010
	GO:0015189	L-lysine transmembrane transporter activ...	0.010
	GO:0001871	pattern binding	0.014
	GO:0030247	polysaccharide binding	0.014
	GO:0015145	monosaccharide transmembrane transporter...	0.015
	GO:0015291	secondary active transmembrane transport...	0.016
	GO:0015149	hexose transmembrane transporter activit...	0.017
	GO:0005326	neurotransmitter transporter activity	0.018
	GO:0015174	basic amino acid transmembrane transport...	0.020
	GO:0005355	glucose transmembrane transporter activi...	0.024
	GO:0004497	monooxygenase activity	0.036
	GO:0022804	active transmembrane transporter activit...	0.039
	GO:0016830	carbon-carbon lyase activity	0.043
	GO:0046914	transition metal ion binding	0.043
	GO:0051213	dioxygenase activity	0.043
	GO:0072509	divalent inorganic cation transmembrane ...	0.046
	GO:0035251	UDP-glucosyltransferase activity	0.056
	GO:0016705	oxidoreductase activity, acting on paire...	0.068
	GO:0051119	sugar transmembrane transporter activity	0.075
	GO:0022857	transmembrane transporter activity	0.077
	GO:0015297	antiporter activity	0.097
	GO:0005506	iron ion binding	0.099

4.4.6 Root - Postflowering - Cluster 6

GO type	GO ID	Description	Adj. p-value
BP	GO:0016070	RNA metabolic process	0.000
	GO:1903506	regulation of nucleic acid-templated tra...	0.000
	GO:0042493	response to drug	0.000
	GO:0006970	response to osmotic stress	0.000
	GO:1901701	cellular response to oxygen-containing c...	0.003
	GO:0070647	protein modification by small protein co...	0.003
	GO:0046483	heterocycle metabolic process	0.006
	GO:0048583	regulation of response to stimulus	0.006
	GO:0048580	regulation of post-embryonic development	0.006
	GO:0071229	cellular response to acid chemical	0.006
	GO:2000026	regulation of multicellular organismal d...	0.009
	GO:0006139	nucleobase-containing compound metabolic...	0.010
	GO:0051239	regulation of multicellular organismal p...	0.010
	GO:0009723	response to ethylene	0.013
	GO:0071310	cellular response to organic substance	0.022
	GO:0005984	disaccharide metabolic process	0.027
	GO:0009651	response to salt stress	0.027
	GO:0071495	cellular response to endogenous stimulus	0.028
	GO:0032870	cellular response to hormone stimulus	0.029
	GO:0009311	oligosaccharide metabolic process	0.035
	GO:0010150	leaf senescence	0.039
	GO:0090693	plant organ senescence	0.039
	GO:0009611	response to wounding	0.043
	GO:0009873	ethylene-activated signaling pathway	0.044
	GO:0046351	disaccharide biosynthetic process	0.044
	GO:0005992	trehalose biosynthetic process	0.046
	GO:0050793	regulation of developmental process	0.047
	GO:0010467	gene expression	0.049
	GO:0032446	protein modification by small protein co...	0.051
	GO:0009312	oligosaccharide biosynthetic process	0.054
	GO:0016567	protein ubiquitination	0.056
	GO:0010646	regulation of cell communication	0.059
	GO:0007568	aging	0.059
	GO:0051241	negative regulation of multicellular org...	0.059
	GO:0006972	hyperosmotic response	0.069
	GO:0009966	regulation of signal transduction	0.073
	GO:2000241	regulation of reproductive process	0.074
	GO:0007165	signal transduction	0.075
	GO:0071369	cellular response to ethylene stimulus	0.075
	GO:0005991	trehalose metabolic process	0.077
	GO:0009755	hormone-mediated signaling pathway	0.077
	GO:0023051	regulation of signaling	0.085
	GO:0023052	signaling	0.085
	GO:0019438	aromatic compound biosynthetic process	0.089
	GO:0010029	regulation of seed germination	0.093
	GO:1900140	regulation of seedling development	0.099

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GO type	GO ID	Description	Adj. p-value
CC	GO:0009507	chloroplast	0.000
	GO:0005634	nucleus	0.002
	GO:0044434	chloroplast part	0.002
	GO:0005777	peroxisome	0.048
	GO:0042579	microbody	0.048
	GO:0009532	plastid stroma	0.050
	GO:0005623	cell	0.064
	GO:0044464	cell part	0.091
MF	GO:0043565	sequence-specific DNA binding	0.008
	GO:0003676	nucleic acid binding	0.016
	GO:0016671	oxidoreductase activity, acting on a sul...	0.019
	GO:0004721	phosphoprotein phosphatase activity	0.026
	GO:0016667	oxidoreductase activity, acting on a sul...	0.031
	GO:0003677	DNA binding	0.067
	GO:0019787	ubiquitin-like protein transferase activ...	0.091

4.4.7 Root - Postflowering - Cluster 7

GO type	GO ID	Description	Adj. p-value
BP	GO:0071554	cell wall organization or biogenesis	0.000
	GO:0010410	hemicellulose metabolic process	0.000
	GO:0009808	lignin metabolic process	0.000
	GO:0042445	hormone metabolic process	0.000
	GO:0007165	signal transduction	0.000
	GO:0023052	signaling	0.000
	GO:0055085	transmembrane transport	0.000
	GO:0010411	xyloglucan metabolic process	0.001
	GO:0009753	response to jasmonic acid	0.001
	GO:0042537	benzene-containing compound metabolic pr...	0.003
	GO:0009690	cytokinin metabolic process	0.003
	GO:0034754	cellular hormone metabolic process	0.004
	GO:0006559	L-phenylalanine catabolic process	0.004
	GO:1902222	erythrose 4-phosphate/phosphoenolpyruvat...	0.004
	GO:0015706	nitrate transport	0.005
	GO:0009074	aromatic amino acid family catabolic pro...	0.005
	GO:0006811	ion transport	0.006
	GO:0015698	inorganic anion transport	0.008
	GO:0098656	anion transmembrane transport	0.008
	GO:1905039	carboxylic acid transmembrane transport	0.008
	GO:0003333	amino acid transmembrane transport	0.010
	GO:0080163	regulation of protein serine/threonine p...	0.012
	GO:0009809	lignin biosynthetic process	0.012
	GO:0034637	cellular carbohydrate biosynthetic proce...	0.013
	GO:1903825	organic acid transmembrane transport	0.015
	GO:0071229	cellular response to acid chemical	0.015
	GO:0006749	glutathione metabolic process	0.016
	GO:1901136	carbohydrate derivative catabolic proces...	0.016
	GO:0009056	catabolic process	0.018
	GO:0042447	hormone catabolic process	0.021
	GO:0009691	cytokinin biosynthetic process	0.021
	GO:0009694	jasmonic acid metabolic process	0.022
	GO:0006857	oligopeptide transport	0.026
	GO:0006865	amino acid transport	0.028
	GO:0043086	negative regulation of catalytic activit...	0.031
	GO:0006575	cellular modified amino acid metabolic p...	0.035
	GO:0015711	organic anion transport	0.035
	GO:0006026	aminoglycan catabolic process	0.038
	GO:0006030	chitin metabolic process	0.038
	GO:0006032	chitin catabolic process	0.038
	GO:0010167	response to nitrate	0.038
	GO:0046348	amino sugar catabolic process	0.038
	GO:1901072	glucosamine-containing compound cataboli...	0.038
	GO:0009733	response to auxin	0.038
	GO:0045861	negative regulation of proteolysis	0.039
	GO:0010466	negative regulation of peptidase activit...	0.043

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0010951	negative regulation of endopeptidase act...	0.043
	GO:0051704	multi-organism process	0.043
	GO:0052547	regulation of peptidase activity	0.043
	GO:0052548	regulation of endopeptidase activity	0.043
	GO:0006694	steroid biosynthetic process	0.045
	GO:0006558	L-phenylalanine metabolic process	0.046
	GO:0009969	xyloglucan biosynthetic process	0.046
	GO:1902221	erythrose 4-phosphate/phosphoenolpyruvat...	0.046
	GO:0045490	pectin catabolic process	0.046
	GO:0016143	S-glycoside metabolic process	0.050
	GO:0019757	glycosinolate metabolic process	0.050
	GO:0019760	glucosinolate metabolic process	0.050
	GO:0043666	regulation of phosphoprotein phosphatase...	0.050
	GO:0015780	nucleotide-sugar transmembrane transport	0.051
	GO:0055076	transition metal ion homeostasis	0.061
	GO:1901071	glucosamine-containing compound metaboli...	0.062
	GO:0009856	pollination	0.064
	GO:0044706	multi-multicellular organism process	0.064
	GO:0010243	response to organonitrogen compound	0.070
	GO:0002237	response to molecule of bacterial origin	0.077
	GO:0044092	negative regulation of molecular functio...	0.077
	GO:0046777	protein autophosphorylation	0.084
	GO:0009607	response to biotic stimulus	0.091
	GO:0009734	auxin-activated signaling pathway	0.091
	GO:0010921	regulation of phosphatase activity	0.092
	GO:0035304	regulation of protein dephosphorylation	0.092
CC	GO:0031225	anchored component of membrane	0.000
	GO:0044421	extracellular region part	0.005
	GO:0005615	extracellular space	0.035
	GO:0005911	cell-cell junction	0.058
	GO:0030054	cell junction	0.058
	GO:0009506	plasmodesma	0.059
	GO:0055044	symplast	0.059
	GO:0005215	transporter activity	0.000
	GO:0022857	transmembrane transporter activity	0.000
	GO:0030246	carbohydrate binding	0.000
	GO:0015291	secondary active transmembrane transport...	0.000
	GO:0016747	transferase activity, transferring acyl ...	0.000
	GO:0044212	transcription regulatory region DNA bind...	0.000
	GO:0004175	endopeptidase activity	0.001
	GO:0016841	ammonia-lyase activity	0.001
	GO:0004364	glutathione transferase activity	0.002
	GO:0008238	exopeptidase activity	0.002
	GO:0008509	anion transmembrane transporter activity	0.002
	GO:0043565	sequence-specific DNA binding	0.002
	GO:0004867	serine-type endopeptidase inhibitor acti...	0.002
	GO:0004857	enzyme inhibitor activity	0.002
	GO:0016838	carbon-oxygen lyase activity, acting on ...	0.002
	GO:0030414	peptidase inhibitor activity	0.004

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GO type	GO ID	Description	Adj. p-value
	GO:0061134	peptidase regulator activity	0.004
	GO:0051213	dioxygenase activity	0.004
	GO:0010333	terpene synthase activity	0.005
	GO:0004866	endopeptidase inhibitor activity	0.007
	GO:0061135	endopeptidase regulator activity	0.007
	GO:0046872	metal ion binding	0.007
	GO:0010427	abscisic acid binding	0.008
	GO:0015171	amino acid transmembrane transporter act...	0.008
	GO:0008233	peptidase activity	0.009
	GO:0043169	cation binding	0.009
	GO:0004683	calmodulin-dependent protein kinase acti...	0.010
	GO:0004805	trehalose-phosphatase activity	0.010
	GO:0005516	calmodulin binding	0.010
	GO:0009931	calcium-dependent protein serine/threoni...	0.010
	GO:0010857	calcium-dependent protein kinase activit...	0.010
	GO:0016679	oxidoreductase activity, acting on diphe...	0.010
	GO:0004568	chitinase activity	0.010
	GO:0045330	aspartyl esterase activity	0.010
	GO:0046943	carboxylic acid transmembrane transporte...	0.010
	GO:0004871	signal transducer activity	0.010
	GO:0001228	transcriptional activator activity, RNA ...	0.013
	GO:0030599	pectinesterase activity	0.013
	GO:0008236	serine-type peptidase activity	0.014
	GO:0017171	serine hydrolase activity	0.014
	GO:0004864	protein phosphatase inhibitor activity	0.014
	GO:0019212	phosphatase inhibitor activity	0.014
	GO:0019840	isoprenoid binding	0.014
	GO:0070011	peptidase activity, acting on L-amino ac...	0.015
	GO:0005342	organic acid transmembrane transporter a...	0.015
	GO:0008061	chitin binding	0.015
	GO:0008107	galactoside 2-alpha-L-fucosyltransferase...	0.017
	GO:0031127	alpha-(1,2)-fucosyltransferase activity	0.017
	GO:0042626	ATPase activity, coupled to transmembran...	0.022
	GO:0043492	ATPase activity, coupled to movement of ...	0.026
	GO:0043178	alcohol binding	0.026
	GO:0019208	phosphatase regulator activity	0.028
	GO:0019888	protein phosphatase regulator activity	0.028
	GO:0016854	racemase and epimerase activity	0.031
	GO:0008398	sterol 14-demethylase activity	0.032
	GO:0005544	calcium-dependent phospholipid binding	0.040
	GO:0030234	enzyme regulator activity	0.040
	GO:0003854	3-beta-hydroxy-delta5-steroid dehydrogen...	0.045
	GO:0098772	molecular function regulator	0.045
	GO:0016765	transferase activity, transferring alkyl...	0.051
	GO:0003959	NADPH dehydrogenase activity	0.053
	GO:0016229	steroid dehydrogenase activity	0.055
	GO:0042562	hormone binding	0.057
	GO:0015399	primary active transmembrane transporter...	0.059
	GO:0015405	P-P-bond-hydrolysis-driven transmembrane...	0.059

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GO type	GO ID	Description	Adj. p-value
	GO:0016614	oxidoreductase activity, acting on CH-OH...	0.066
	GO:0000981	RNA polymerase II transcription factor a...	0.068
	GO:0033293	monocarboxylic acid binding	0.073
	GO:0031406	carboxylic acid binding	0.076
	GO:0043177	organic acid binding	0.076
	GO:0015112	nitrate transmembrane transporter activi...	0.086
	GO:0015276	ligand-gated ion channel activity	0.086
	GO:0022834	ligand-gated channel activity	0.086
	GO:0048038	quinone binding	0.086
	GO:0000976	transcription regulatory region sequence...	0.087
	GO:0033764	steroid dehydrogenase activity, acting o...	0.089
	GO:0030594	neurotransmitter receptor activity	0.091
	GO:0008417	fucosyltransferase activity	0.093

4.4.8 Root - Postflowering - Cluster 8

GO type	GO ID	Description	Adj. p-value
	GO:0007017	microtubule-based process	0.000
	GO:0010383	cell wall polysaccharide metabolic proce...	0.000
	GO:0042737	drug catabolic process	0.000
	GO:0009832	plant-type cell wall biogenesis	0.000
	GO:0070592	cell wall polysaccharide biosynthetic pr...	0.000
	GO:0019748	secondary metabolic process	0.000
	GO:0044550	secondary metabolite biosynthetic proces...	0.000
	GO:0055086	nucleobase-containing small molecule met...	0.000
	GO:0007010	cytoskeleton organization	0.000
	GO:1903047	mitotic cell cycle process	0.000
	GO:0006694	steroid biosynthetic process	0.000
	GO:0000910	cytokinesis	0.000
	GO:0009225	nucleotide-sugar metabolic process	0.001
	GO:0048193	Golgi vesicle transport	0.001
	GO:0008202	steroid metabolic process	0.001
	GO:0019318	hexose metabolic process	0.001
	GO:0000281	mitotic cytokinesis	0.002
	GO:0006119	oxidative phosphorylation	0.002
	GO:0016126	sterol biosynthetic process	0.002
	GO:0042773	ATP synthesis coupled electron transport	0.002
	GO:0052546	cell wall pectin metabolic process	0.002
	GO:0009808	lignin metabolic process	0.002
	GO:0006261	DNA-dependent DNA replication	0.002
	GO:0019363	pyridine nucleotide biosynthetic process	0.002
	GO:0000226	microtubule cytoskeleton organization	0.002
	GO:0071840	cellular component organization or bioge...	0.002
	GO:0019953	sexual reproduction	0.002
	GO:0042545	cell wall modification	0.002
	GO:0016049	cell growth	0.003
	GO:0044283	small molecule biosynthetic process	0.003
	GO:0000911	cytokinesis by cell plate formation	0.003
	GO:0006260	DNA replication	0.003
	GO:0006891	intra-Golgi vesicle-mediated transport	0.003
	GO:0046777	protein autophosphorylation	0.003
	GO:0006090	pyruvate metabolic process	0.003
	GO:0042775	mitochondrial ATP synthesis coupled elec...	0.004
	GO:0009888	tissue development	0.005
	GO:0046496	nicotinamide nucleotide metabolic proces...	0.005
	GO:0030244	cellulose biosynthetic process	0.005
	GO:0032506	cytokinetic process	0.005
	GO:0032787	monocarboxylic acid metabolic process	0.005
	GO:1902410	mitotic cytokinetic process	0.005
	GO:0035556	intracellular signal transduction	0.005
	GO:0060560	developmental growth involved in morphog...	0.005
	GO:0051301	cell division	0.006
	GO:0010054	trichoblast differentiation	0.006

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GO type	GO ID	Description	Adj. p-value
	GO:0006733	oxidoreduction coenzyme metabolic proces...	0.007
	GO:0006101	citrate metabolic process	0.007
	GO:0019362	pyridine nucleotide metabolic process	0.007
	GO:0097435	supramolecular fiber organization	0.007
	GO:0006833	water transport	0.007
	GO:0006884	cell volume homeostasis	0.007
	GO:0009992	cellular water homeostasis	0.007
	GO:0015793	glycerol transport	0.007
	GO:0042044	fluid transport	0.007
	GO:0044703	multi-organism reproductive process	0.007
	GO:0090626	plant epidermis morphogenesis	0.007
	GO:0010053	root epidermal cell differentiation	0.008
	GO:0010374	stomatal complex development	0.008
	GO:0009826	unidimensional cell growth	0.009
	GO:0019321	pentose metabolic process	0.009
	GO:1902600	proton transmembrane transport	0.010
	GO:0051274	beta-glucan biosynthetic process	0.011
	GO:0010038	response to metal ion	0.011
	GO:0019722	calcium-mediated signaling	0.011
	GO:0048878	chemical homeostasis	0.011
	GO:0044255	cellular lipid metabolic process	0.011
	GO:0010103	stomatal complex morphogenesis	0.012
	GO:0009226	nucleotide-sugar biosynthetic process	0.012
	GO:0030104	water homeostasis	0.012
	GO:0010026	trichome differentiation	0.013
	GO:0015985	energy coupled proton transport, down el...	0.013
	GO:0015986	ATP synthesis coupled proton transport	0.013
	GO:0072525	pyridine-containing compound biosyntheti...	0.013
	GO:0010564	regulation of cell cycle process	0.014
	GO:0000904	cell morphogenesis involved in different...	0.014
	GO:0048469	cell maturation	0.014
	GO:0048764	trichoblast maturation	0.014
	GO:0048765	root hair cell differentiation	0.014
	GO:0015988	energy coupled proton transmembrane tran...	0.015
	GO:0015991	ATP hydrolysis coupled proton transport	0.015
	GO:0030148	sphingolipid biosynthetic process	0.015
	GO:0090662	ATP hydrolysis coupled transmembrane tra...	0.015
	GO:0099131	ATP hydrolysis coupled ion transmembrane...	0.015
	GO:0099132	ATP hydrolysis coupled cation transmembr...	0.015
	GO:1903338	regulation of cell wall organization or ...	0.015
	GO:0009060	aerobic respiration	0.015
	GO:0044275	cellular carbohydrate catabolic process	0.015
	GO:0006006	glucose metabolic process	0.018
	GO:0008154	actin polymerization or depolymerization	0.018
	GO:0022622	root system development	0.019
	GO:2000652	regulation of secondary cell wall biogen...	0.020
	GO:0010052	guard cell differentiation	0.020
	GO:0022603	regulation of anatomical structure morph...	0.021
	GO:0040007	growth	0.021

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0046686	response to cadmium ion	0.021
	GO:0006979	response to oxidative stress	0.021
	GO:0010016	shoot system morphogenesis	0.021
	GO:0006099	tricarboxylic acid cycle	0.022
	GO:0032535	regulation of cellular component size	0.022
	GO:0090066	regulation of anatomical structure size	0.022
	GO:0072524	pyridine-containing compound metabolic p...	0.022
	GO:0051261	protein depolymerization	0.022
	GO:0016125	sterol metabolic process	0.023
	GO:0048364	root development	0.023
	GO:0008064	regulation of actin polymerization or de...	0.024
	GO:0030832	regulation of actin filament length	0.024
	GO:0032956	regulation of actin cytoskeleton organiz...	0.024
	GO:0032970	regulation of actin filament-based proce...	0.024
	GO:0110053	regulation of actin filament organizatio...	0.024
	GO:0009934	regulation of meristem structural organi...	0.024
	GO:0034404	nucleobase-containing small molecule bio...	0.024
	GO:0045333	cellular respiration	0.024
	GO:0006732	coenzyme metabolic process	0.025
	GO:0010413	glucuronoxylan metabolic process	0.025
	GO:0010417	glucuronoxylan biosynthetic process	0.025
	GO:0015791	polyol transport	0.025
	GO:0007051	spindle organization	0.027
	GO:0055082	cellular chemical homeostasis	0.027
	GO:0044247	cellular polysaccharide catabolic proces...	0.027
	GO:0022904	respiratory electron transport chain	0.028
	GO:0051275	beta-glucan catabolic process	0.029
	GO:0044248	cellular catabolic process	0.029
	GO:0048589	developmental growth	0.030
	GO:0051235	maintenance of location	0.030
	GO:0007015	actin filament organization	0.030
	GO:0030041	actin filament polymerization	0.032
	GO:0030833	regulation of actin filament polymerizat...	0.032
	GO:0010345	suberin biosynthetic process	0.033
	GO:0006811	ion transport	0.033
	GO:1905392	plant organ morphogenesis	0.034
	GO:0015672	monovalent inorganic cation transport	0.035
	GO:0030154	cell differentiation	0.035
	GO:0007154	cell communication	0.040
	GO:0009251	glucan catabolic process	0.040
	GO:1901615	organic hydroxy compound metabolic proce...	0.040
	GO:0072350	tricarboxylic acid metabolic process	0.042
	GO:0044770	cell cycle phase transition	0.043
	GO:0034220	ion transmembrane transport	0.044
	GO:0019752	carboxylic acid metabolic process	0.046
	GO:0048826	cotyledon morphogenesis	0.046
	GO:0009694	jasmonic acid metabolic process	0.048
	GO:0009074	aromatic amino acid family catabolic pro...	0.049
	GO:0009395	phospholipid catabolic process	0.049

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0009100	glycoprotein metabolic process	0.049
	GO:0016482	cytosolic transport	0.049
	GO:0030036	actin cytoskeleton organization	0.049
	GO:0006486	protein glycosylation	0.050
	GO:0006637	acyl-CoA metabolic process	0.050
	GO:0030029	actin filament-based process	0.050
	GO:0035383	thioester metabolic process	0.050
	GO:0043413	macromolecule glycosylation	0.050
	GO:0043436	oxoacid metabolic process	0.050
	GO:0070085	glycosylation	0.050
	GO:0044772	mitotic cell cycle phase transition	0.051
	GO:0051716	cellular response to stimulus	0.051
	GO:0009629	response to gravity	0.052
	GO:0006793	phosphorus metabolic process	0.053
	GO:0043547	positive regulation of GTPase activity	0.053
	GO:0019566	arabinose metabolic process	0.053
	GO:1901617	organic hydroxy compound biosynthetic pr...	0.053
	GO:0046364	monosaccharide biosynthetic process	0.054
	GO:0006082	organic acid metabolic process	0.055
	GO:0009108	coenzyme biosynthetic process	0.055
	GO:0023052	signaling	0.055
	GO:0051258	protein polymerization	0.055
	GO:0051726	regulation of cell cycle	0.055
	GO:0046274	lignin catabolic process	0.056
	GO:0030245	cellulose catabolic process	0.057
	GO:0006812	cation transport	0.057
	GO:0007165	signal transduction	0.058
	GO:0000280	nuclear division	0.062
	GO:0070887	cellular response to chemical stimulus	0.064
	GO:0048825	cotyledon development	0.064
	GO:0046835	carbohydrate phosphorylation	0.065
	GO:0051510	regulation of unidimensional cell growth	0.065
	GO:0030004	cellular monovalent inorganic cation hom...	0.065
	GO:0090378	seed trichome elongation	0.073
	GO:0048638	regulation of developmental growth	0.075
	GO:0043647	inositol phosphate metabolic process	0.077
	GO:0046271	phenylpropanoid catabolic process	0.077
	GO:0010215	cellulose microfibril organization	0.078
	GO:0006559	L-phenylalanine catabolic process	0.082
	GO:1902222	erythrose 4-phosphate/phosphoenolpyruvat...	0.082
	GO:0046854	phosphatidylinositol phosphorylation	0.083
	GO:0080147	root hair cell development	0.086
	GO:0098662	inorganic cation transmembrane transport	0.087
	GO:0008356	asymmetric cell division	0.088
	GO:0019932	second-messenger-mediated signaling	0.093
	GO:0006012	galactose metabolic process	0.093
	GO:0051129	negative regulation of cellular componen...	0.094
	GO:0009250	glucan biosynthetic process	0.094
	GO:0015850	organic hydroxy compound transport	0.094

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GO type	GO ID	Description	Adj. p-value
	GO:0043087	regulation of GTPase activity	0.098
CC	GO:0005856	cytoskeleton	0.000
	GO:0031225	anchored component of membrane	0.000
	GO:0044431	Golgi apparatus part	0.000
	GO:0044459	plasma membrane part	0.000
	GO:0005819	spindle	0.001
	GO:0030120	vesicle coat	0.001
	GO:0044815	DNA packaging complex	0.001
	GO:0030135	coated vesicle	0.001
	GO:0030660	Golgi-associated vesicle membrane	0.002
	GO:0000786	nucleosome	0.002
	GO:0005881	cytoplasmic microtubule	0.002
	GO:0030662	coated vesicle membrane	0.003
	GO:0055028	cortical microtubule	0.004
	GO:0030863	cortical cytoskeleton	0.004
	GO:0030981	cortical microtubule cytoskeleton	0.004
	GO:0033177	proton-transporting two-sector ATPase co...	0.004
	GO:0030659	cytoplasmic vesicle membrane	0.006
	GO:0045259	proton-transporting ATP synthase complex	0.006
	GO:0032993	protein-DNA complex	0.014
	GO:0009574	preprophase band	0.015
	GO:0030117	membrane coat	0.017
	GO:0048475	coated membrane	0.017
	GO:0033176	proton-transporting V-type ATPase comple...	0.018
	GO:0042575	DNA polymerase complex	0.018
	GO:0044427	chromosomal part	0.018
	GO:0030136	clathrin-coated vesicle	0.022
	GO:0000775	chromosome, centromeric region	0.022
	GO:0012506	vesicle membrane	0.025
	GO:0005769	early endosome	0.041
	GO:0030173	integral component of Golgi membrane	0.044
	GO:0031228	intrinsic component of Golgi membrane	0.044
	GO:0000347	THO complex	0.048
	GO:0000228	nuclear chromosome	0.048
	GO:0005798	Golgi-associated vesicle	0.048
	GO:0005694	chromosome	0.058
	GO:0044433	cytoplasmic vesicle part	0.061
	GO:0005838	proteasome regulatory particle	0.062
	GO:0022624	proteasome accessory complex	0.062
	GO:0009504	cell plate	0.062
	GO:0000793	condensed chromosome	0.062
	GO:0044454	nuclear chromosome part	0.077
	GO:0008540	proteasome regulatory particle, base sub...	0.078
	GO:0033178	proton-transporting two-sector ATPase co...	0.078
	GO:0005657	replication fork	0.095
	GO:0016787	hydrolase activity	0.000
	GO:0016491	oxidoreductase activity	0.000
	GO:0046906	tetrapyrrole binding	0.000
	GO:0016757	transferase activity, transferring glyco...	0.000

Continued on next page

GO type	GO ID	Description	Adj. p-value
	GO:0016614	oxidoreductase activity, acting on CH-OH...	0.000
	GO:0005215	transporter activity	0.000
	GO:0016747	transferase activity, transferring acyl ...	0.000
	GO:0005085	guanyl-nucleotide exchange factor activi...	0.000
	GO:0005088	Ras guanyl-nucleotide exchange factor ac...	0.000
	GO:0050662	coenzyme binding	0.000
	GO:0098772	molecular function regulator	0.001
	GO:0046910	pectinesterase inhibitor activity	0.001
	GO:0051287	NAD binding	0.001
	GO:0046983	protein dimerization activity	0.002
	GO:0008374	O-acyltransferase activity	0.002
	GO:0016758	transferase activity, transferring hexos...	0.002
	GO:0042285	xylosyltransferase activity	0.003
	GO:0003854	3-beta-hydroxy-delta5-steroid dehydrogen...	0.003
	GO:0016407	acetyltransferase activity	0.003
	GO:0005372	water transmembrane transporter activity	0.003
	GO:0015250	water channel activity	0.003
	GO:0015254	glycerol channel activity	0.003
	GO:0004683	calmodulin-dependent protein kinase acti...	0.003
	GO:0009931	calcium-dependent protein serine/threoni...	0.003
	GO:0010857	calcium-dependent protein kinase activit...	0.003
	GO:0004650	polygalacturonase activity	0.003
	GO:0009055	electron transfer activity	0.004
	GO:0008422	beta-glucosidase activity	0.004
	GO:0008171	O-methyltransferase activity	0.004
	GO:0015926	glucosidase activity	0.004
	GO:0015267	channel activity	0.004
	GO:0022803	passive transmembrane transporter activi...	0.004
	GO:0022838	substrate-specific channel activity	0.005
	GO:0015168	glycerol transmembrane transporter activ...	0.005
	GO:0015318	inorganic molecular entity transmembrane...	0.006
	GO:0042578	phosphoric ester hydrolase activity	0.007
	GO:0016759	cellulose synthase activity	0.007
	GO:0016760	cellulose synthase (UDP-forming) activit...	0.007
	GO:0033764	steroid dehydrogenase activity, acting o...	0.007
	GO:0036442	proton-exporting ATPase activity	0.007
	GO:0005516	calmodulin binding	0.009
	GO:0008081	phosphoric diester hydrolase activity	0.009
	GO:0016740	transferase activity	0.012
	GO:0044769	ATPase activity, coupled to transmembran...	0.012
	GO:0016773	phosphotransferase activity, alcohol gro...	0.012
	GO:0016679	oxidoreductase activity, acting on diphe...	0.015
	GO:0016868	intramolecular transferase activity, pho...	0.015
	GO:0016301	kinase activity	0.016
	GO:0016857	racemase and epimerase activity, acting ...	0.017
	GO:0016229	steroid dehydrogenase activity	0.017
	GO:0046933	proton-transporting ATP synthase activit...	0.017
	GO:0004567	beta-mannosidase activity	0.018
	GO:0015166	polyol transmembrane transporter activit...	0.019

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GO type	GO ID	Description	Adj. p-value
	GO:0016620	oxidoreductase activity, acting on the a...	0.019
	GO:1901618	organic hydroxy compound transmembrane t...	0.021
	GO:0015144	carbohydrate transmembrane transporter a...	0.024
	GO:0052689	carboxylic ester hydrolase activity	0.027
	GO:0070569	uridylyltransferase activity	0.027
	GO:0005200	structural constituent of cytoskeleton	0.027
	GO:0008398	sterol 14-demethylase activity	0.028
	GO:0052716	hydroquinone:oxygen oxidoreductase activ...	0.030
	GO:0015075	ion transmembrane transporter activity	0.031
	GO:0016705	oxidoreductase activity, acting on paire...	0.033
	GO:0016709	oxidoreductase activity, acting on paire...	0.036
	GO:0046527	glucosyltransferase activity	0.037
	GO:0046961	proton-transporting ATPase activity, rot...	0.038
	GO:0004620	phospholipase activity	0.039
	GO:0015018	galactosylgalactosylxylosylprotein 3-bet...	0.041
	GO:0019829	cation-transporting ATPase activity	0.041
	GO:0022853	active ion transmembrane transporter act...	0.041
	GO:0042625	ATPase coupled ion transmembrane transpo...	0.041
	GO:0016682	oxidoreductase activity, acting on diphe...	0.042
	GO:0008194	UDP-glycosyltransferase activity	0.042
	GO:0016903	oxidoreductase activity, acting on the a...	0.042
	GO:0008810	cellulase activity	0.046
	GO:0015077	monovalent inorganic cation transmembran...	0.047
	GO:0016854	racemase and epimerase activity	0.048
	GO:0015020	glucuronosyltransferase activity	0.050
	GO:0030276	clathrin binding	0.051
	GO:0140097	catalytic activity, acting on DNA	0.051
	GO:0016298	lipase activity	0.054
	GO:0047372	acylglycerol lipase activity	0.054
	GO:0016717	oxidoreductase activity, acting on paire...	0.057
	GO:0017111	nucleoside-triphosphatase activity	0.059
	GO:0030234	enzyme regulator activity	0.061
	GO:0016772	transferase activity, transferring phosp...	0.062
	GO:0015154	disaccharide transmembrane transporter a...	0.063
	GO:0015157	oligosaccharide transmembrane transporte...	0.063
	GO:0016782	transferase activity, transferring sulfu...	0.067
	GO:0008324	cation transmembrane transporter activit...	0.073
	GO:0015078	proton transmembrane transporter activit...	0.077
	GO:0016878	acid-thiol ligase activity	0.077
	GO:0051015	actin filament binding	0.077
	GO:0022890	inorganic cation transmembrane transport...	0.080
	GO:0015923	mannosidase activity	0.086
	GO:0016790	thiolester hydrolase activity	0.087
	GO:0016818	hydrolase activity, acting on acid anhyd...	0.091
	GO:0015399	primary active transmembrane transporter...	0.095
	GO:0015405	P-P-bond-hydrolysis-driven transmembrane...	0.095
	GO:0080161	auxin transmembrane transporter activity	0.095
	GO:0032451	demethylase activity	0.095
	GO:0043492	ATPase activity, coupled to movement of ...	0.096

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GO type	GO ID	Description	Adj. p-value
	GO:0004743	pyruvate kinase activity	0.099
	GO:0030955	potassium ion binding	0.099
	GO:0031420	alkali metal ion binding	0.099

4.4.9 Root - Postflowering - Cluster 9

GO type	GO ID	Description	Adj. p-value
BP	GO:0090304	nucleic acid metabolic process	0.000
	GO:0060255	regulation of macromolecule metabolic pr...	0.000
	GO:0051171	regulation of nitrogen compound metaboli...	0.000
	GO:2000112	regulation of cellular macromolecule bio...	0.000
	GO:0006351	transcription, DNA-templated	0.000
	GO:0010468	regulation of gene expression	0.000
	GO:0080090	regulation of primary metabolic process	0.000
	GO:0008645	hexose transmembrane transport	0.000
	GO:0055085	transmembrane transport	0.000
	GO:0019748	secondary metabolic process	0.003
	GO:0018130	heterocycle biosynthetic process	0.003
	GO:0080163	regulation of protein serine/threonine p...	0.003
	GO:0042430	indole-containing compound metabolic pro...	0.003
	GO:0032446	protein modification by small protein co...	0.006
	GO:0006511	ubiquitin-dependent protein catabolic pr...	0.006
	GO:0010921	regulation of phosphatase activity	0.006
	GO:0043632	modification-dependent macromolecule cat...	0.006
	GO:1902022	L-lysine transport	0.007
	GO:1903401	L-lysine transmembrane transport	0.007
	GO:0016567	protein ubiquitination	0.007
	GO:0034654	nucleobase-containing compound biosynthe...	0.008
	GO:0006568	tryptophan metabolic process	0.011
	GO:0006586	indolalkylamine metabolic process	0.011
	GO:0019941	modification-dependent protein catabolic...	0.011
	GO:0035303	regulation of dephosphorylation	0.011
	GO:0043666	regulation of phosphoprotein phosphatase...	0.015
	GO:0044550	secondary metabolite biosynthetic proces...	0.016
	GO:0009072	aromatic amino acid family metabolic pro...	0.018
	GO:0006796	phosphate-containing compound metabolic ...	0.028
	GO:0000162	tryptophan biosynthetic process	0.028
	GO:0046219	indolalkylamine biosynthetic process	0.028
	GO:0070647	protein modification by small protein co...	0.028
	GO:0035304	regulation of protein dephosphorylation	0.028
	GO:0009073	aromatic amino acid family biosynthetic ...	0.037
	GO:0051603	proteolysis involved in cellular protein...	0.040
	GO:0044257	cellular protein catabolic process	0.042
	GO:0006974	cellular response to DNA damage stimulus	0.046
	GO:0015802	basic amino acid transport	0.054
	GO:0006281	DNA repair	0.055
	GO:0009110	vitamin biosynthetic process	0.060
	GO:0042364	water-soluble vitamin biosynthetic proce...	0.070
	GO:0003333	amino acid transmembrane transport	0.070
	GO:0006508	proteolysis	0.070
	GO:0006793	phosphorus metabolic process	0.070
	GO:0009407	toxin catabolic process	0.071
	GO:0030163	protein catabolic process	0.071

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GO type	GO ID	Description	Adj. p-value
	GO:1902475	L-alpha-amino acid transmembrane transpo...	0.075
	GO:0006820	anion transport	0.080
	GO:0019740	nitrogen utilization	0.088
	GO:0000041	transition metal ion transport	0.089
	GO:0006836	neurotransmitter transport	0.089
	GO:0010200	response to chitin	0.089
	GO:1905039	carboxylic acid transmembrane transport	0.093
	GO:0009308	amine metabolic process	0.095
	GO:0051276	chromosome organization	0.098
	GO:0006259	DNA metabolic process	0.100
	GO:0006811	ion transport	0.100
CC	GO:0044425	membrane part	0.002
	GO:0031226	intrinsic component of plasma membrane	0.007
	GO:0044798	nuclear transcription factor complex	0.033
	GO:0090575	RNA polymerase II transcription factor c...	0.035
	GO:0044459	plasma membrane part	0.037
	GO:0016020	membrane	0.085
	GO:0005886	plasma membrane	0.090
MF	GO:0004672	protein kinase activity	0.000
	GO:0015075	ion transmembrane transporter activity	0.002
	GO:0003700	DNA binding transcription factor activit...	0.003
	GO:0043565	sequence-specific DNA binding	0.003
	GO:0005215	transporter activity	0.003
	GO:0022804	active transmembrane transporter activit...	0.004
	GO:0051119	sugar transmembrane transporter activity	0.004
	GO:0015181	arginine transmembrane transporter activ...	0.005
	GO:0015189	L-lysine transmembrane transporter activ...	0.005
	GO:0015297	antiporter activity	0.008
	GO:0015172	acidic amino acid transmembrane transpor...	0.009
	GO:0003690	double-stranded DNA binding	0.010
	GO:0015174	basic amino acid transmembrane transport...	0.010
	GO:0019787	ubiquitin-like protein transferase activ...	0.010
	GO:0001047	core promoter binding	0.011
	GO:0004864	protein phosphatase inhibitor activity	0.011
	GO:0019212	phosphatase inhibitor activity	0.011
	GO:0015318	inorganic molecular entity transmembrane...	0.011
	GO:0004842	ubiquitin-protein transferase activity	0.012
	GO:0051213	dioxygenase activity	0.014
	GO:0020037	heme binding	0.016
	GO:0001046	core promoter sequence-specific DNA bind...	0.017
	GO:0008324	cation transmembrane transporter activit...	0.019
	GO:0019208	phosphatase regulator activity	0.019
	GO:0019888	protein phosphatase regulator activity	0.019
	GO:0035251	UDP-glucosyltransferase activity	0.021
	GO:0010427	abscisic acid binding	0.025
	GO:0140110	transcription regulator activity	0.028
	GO:0046915	transition metal ion transmembrane trans...	0.029
	GO:0046906	tetrapyrrole binding	0.031
	GO:0046983	protein dimerization activity	0.031

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GO type	GO ID	Description	Adj. p-value
	GO:0072509	divalent inorganic cation transmembrane ...	0.040
	GO:0019840	isoprenoid binding	0.042
	GO:0042562	hormone binding	0.050
	GO:0005326	neurotransmitter transporter activity	0.055
	GO:0001228	transcriptional activator activity, RNA ...	0.060
	GO:1990837	sequence-specific double-stranded DNA bi...	0.072
	GO:0015238	drug transmembrane transporter activity	0.075
	GO:0000976	transcription regulatory region sequence...	0.084
	GO:0005385	zinc ion transmembrane transporter activ...	0.100

4.4.10 Root - Postflowering - Cluster 10

GO type	GO ID	Description	Adj. p-value
	GO:0034660	ncRNA metabolic process	0.000
	GO:0034470	ncRNA processing	0.000
	GO:0022613	ribonucleoprotein complex biogenesis	0.000
	GO:0042254	ribosome biogenesis	0.000
	GO:0009451	RNA modification	0.000
	GO:0009657	plastid organization	0.000
	GO:0006996	organelle organization	0.000
	GO:0006259	DNA metabolic process	0.000
	GO:0010468	regulation of gene expression	0.000
	GO:0070647	protein modification by small protein co...	0.000
	GO:0043414	macromolecule methylation	0.000
	GO:0019684	photosynthesis, light reaction	0.000
	GO:0001510	RNA methylation	0.000
	GO:0010629	negative regulation of gene expression	0.000
	GO:0009628	response to abiotic stimulus	0.000
	GO:0051171	regulation of nitrogen compound metaboli...	0.000
	GO:0032446	protein modification by small protein co...	0.000
	GO:0006351	transcription, DNA-templated	0.000
	GO:0080090	regulation of primary metabolic process	0.000
	GO:0006401	RNA catabolic process	0.000
	GO:0009266	response to temperature stimulus	0.000
	GO:0009314	response to radiation	0.000
	GO:0010608	posttranscriptional regulation of gene e...	0.000
	GO:0000245	spliceosomal complex assembly	0.000
	GO:0022607	cellular component assembly	0.000
	GO:0009416	response to light stimulus	0.000
	GO:0009642	response to light intensity	0.000
	GO:0042273	ribosomal large subunit biogenesis	0.000
	GO:0071826	ribonucleoprotein complex subunit organi...	0.000
	GO:0051276	chromosome organization	0.000
	GO:0019219	regulation of nucleobase-containing comp...	0.000
	GO:2000112	regulation of cellular macromolecule bio...	0.000
	GO:0042274	ribosomal small subunit biogenesis	0.000
	GO:0048580	regulation of post-embryonic development	0.000
	GO:0000154	rRNA modification	0.000
	GO:0000956	nuclear-transcribed mRNA catabolic proce...	0.000
	GO:0018205	peptidyl-lysine modification	0.000
	GO:0015994	chlorophyll metabolic process	0.000
	GO:0009909	regulation of flower development	0.000
	GO:0010109	regulation of photosynthesis	0.000
	GO:0022618	ribonucleoprotein complex assembly	0.000
	GO:0006400	tRNA modification	0.000
	GO:0051252	regulation of RNA metabolic process	0.000
	GO:0065002	intracellular protein transmembrane tran...	0.000
	GO:0090501	RNA phosphodiester bond hydrolysis	0.001
	GO:0006406	mRNA export from nucleus	0.001

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GO type	GO ID	Description	Adj. p-value
	GO:0010228	vegetative to reproductive phase transit...	0.001
	GO:0006357	regulation of transcription by RNA polym...	0.001
	GO:0016458	gene silencing	0.001
	GO:0040029	regulation of gene expression, epigeneti...	0.001
	GO:0006417	regulation of translation	0.001
	GO:0030490	maturation of SSU-rRNA	0.001
	GO:0034622	cellular protein-containing complex asse...	0.001
	GO:0006355	regulation of transcription, DNA-templat...	0.001
	GO:0048518	positive regulation of biological proces...	0.001
	GO:0071478	cellular response to radiation	0.001
	GO:0034248	regulation of cellular amide metabolic p...	0.002
	GO:0072594	establishment of protein localization to...	0.002
	GO:0000460	maturation of 5.8S rRNA	0.002
	GO:0044743	protein transmembrane import into intrac...	0.002
	GO:0065003	protein-containing complex assembly	0.002
	GO:0006325	chromatin organization	0.002
	GO:0006605	protein targeting	0.002
	GO:0006518	peptide metabolic process	0.002
	GO:0032259	methylation	0.002
	GO:0042440	pigment metabolic process	0.003
	GO:2000024	regulation of leaf development	0.003
	GO:0000380	alternative mRNA splicing, via spliceoso...	0.003
	GO:0033554	cellular response to stress	0.003
	GO:2000113	negative regulation of cellular macromol...	0.003
	GO:0009648	photoperiodism	0.003
	GO:0009668	plastid membrane organization	0.003
	GO:0010027	thylakoid membrane organization	0.003
	GO:0032784	regulation of DNA-templated transcriptio...	0.004
	GO:0005982	starch metabolic process	0.004
	GO:0006289	nucleotide-excision repair	0.004
	GO:0048608	reproductive structure development	0.004
	GO:0061458	reproductive system development	0.004
	GO:0015995	chlorophyll biosynthetic process	0.004
	GO:0031503	protein-containing complex localization	0.004
	GO:0006415	translational termination	0.004
	GO:0031167	rRNA methylation	0.004
	GO:0016569	covalent chromatin modification	0.004
	GO:0051028	mRNA transport	0.004
	GO:1903311	regulation of mRNA metabolic process	0.004
	GO:0006354	DNA-templated transcription, elongation	0.004
	GO:0019252	starch biosynthetic process	0.005
	GO:0006778	porphyrin-containing compound metabolic ...	0.005
	GO:0051641	cellular localization	0.005
	GO:0032984	protein-containing complex disassembly	0.006
	GO:0000413	protein peptidyl-prolyl isomerization	0.006
	GO:0018208	peptidyl-proline modification	0.006
	GO:0050789	regulation of biological process	0.006
	GO:0016441	posttranscriptional gene silencing	0.006
	GO:0006310	DNA recombination	0.006

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GO type	GO ID	Description	Adj. p-value
	GO:0009617	response to bacterium	0.006
	GO:1903506	regulation of nucleic acid-templated tra...	0.006
	GO:2001141	regulation of RNA biosynthetic process	0.006
	GO:0034654	nucleobase-containing compound biosynthe...	0.007
	GO:0003006	developmental process involved in reprod...	0.007
	GO:0051168	nuclear export	0.007
	GO:0006405	RNA export from nucleus	0.007
	GO:0043603	cellular amide metabolic process	0.007
	GO:0002098	tRNA wobble uridine modification	0.007
	GO:0031047	gene silencing by RNA	0.007
	GO:0009893	positive regulation of metabolic process	0.007
	GO:0051246	regulation of protein metabolic process	0.007
	GO:0031123	RNA 3'-end processing	0.008
	GO:1905156	negative regulation of photosynthesis	0.008
	GO:0071482	cellular response to light stimulus	0.008
	GO:0045037	protein import into chloroplast stroma	0.008
	GO:0045184	establishment of protein localization	0.008
	GO:0010207	photosystem II assembly	0.008
	GO:0030488	tRNA methylation	0.009
	GO:0006479	protein methylation	0.009
	GO:0008213	protein alkylation	0.009
	GO:0035196	production of miRNAs involved in gene si...	0.010
	GO:0016570	histone modification	0.010
	GO:0051649	establishment of localization in cell	0.010
	GO:0031324	negative regulation of cellular metaboli...	0.011
	GO:0006383	transcription by RNA polymerase III	0.011
	GO:0015031	protein transport	0.011
	GO:0016573	histone acetylation	0.011
	GO:0018393	internal peptidyl-lysine acetylation	0.011
	GO:0018394	peptidyl-lysine acetylation	0.011
	GO:0031124	mRNA 3'-end processing	0.011
	GO:0002097	tRNA wobble base modification	0.012
	GO:0000122	negative regulation of transcription by ...	0.012
	GO:0033014	tetrapyrrole biosynthetic process	0.013
	GO:0032268	regulation of cellular protein metabolic...	0.013
	GO:0050657	nucleic acid transport	0.013
	GO:0050658	RNA transport	0.013
	GO:0051236	establishment of RNA localization	0.013
	GO:0007623	circadian rhythm	0.013
	GO:0048511	rhythmic process	0.013
	GO:0006413	translational initiation	0.013
	GO:0042548	regulation of photosynthesis, light reac...	0.013
	GO:0006475	internal protein amino acid acetylation	0.014
	GO:0016556	mRNA modification	0.015
	GO:1901566	organonitrogen compound biosynthetic pro...	0.015
	GO:0008104	protein localization	0.015
	GO:0015833	peptide transport	0.015
	GO:0046907	intracellular transport	0.015
	GO:0043038	amino acid activation	0.015

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GO type	GO ID	Description	Adj. p-value
	GO:0043039	tRNA aminoacylation	0.015
	GO:0016973	poly(A)+ mRNA export from nucleus	0.016
	GO:0006403	RNA localization	0.017
	GO:0048573	photoperiodism, flowering	0.017
	GO:0000469	cleavage involved in rRNA processing	0.017
	GO:0006298	mismatch repair	0.017
	GO:0042886	amide transport	0.017
	GO:0022411	cellular component disassembly	0.018
	GO:2000242	negative regulation of reproductive proc...	0.018
	GO:1900864	mitochondrial RNA modification	0.021
	GO:0032436	positive regulation of proteasomal ubiqu...	0.021
	GO:0042742	defense response to bacterium	0.021
	GO:2000060	positive regulation of ubiquitin-depende...	0.021
	GO:0030091	protein repair	0.021
	GO:0032502	developmental process	0.021
	GO:0032544	plastid translation	0.022
	GO:0006379	mRNA cleavage	0.022
	GO:0009890	negative regulation of biosynthetic proc...	0.023
	GO:0006779	porphyrin-containing compound biosynthet...	0.024
	GO:0050793	regulation of developmental process	0.024
	GO:0051247	positive regulation of protein metabolic...	0.025
	GO:0008284	positive regulation of cell proliferatio...	0.025
	GO:0032270	positive regulation of cellular protein ...	0.025
	GO:0006368	transcription elongation from RNA polyme...	0.026
	GO:0031325	positive regulation of cellular metaboli...	0.026
	GO:0018193	peptidyl-amino acid modification	0.027
	GO:0045143	homologous chromosome segregation	0.029
	GO:0005977	glycogen metabolic process	0.030
	GO:0006112	energy reserve metabolic process	0.030
	GO:2000030	regulation of response to red or far red...	0.030
	GO:0000478	endonucleolytic cleavage involved in rRN...	0.030
	GO:0031050	dsRNA fragmentation	0.030
	GO:0043331	response to dsRNA	0.030
	GO:0070918	production of small RNA involved in gene...	0.030
	GO:0071359	cellular response to dsRNA	0.030
	GO:0010604	positive regulation of macromolecule met...	0.030
	GO:0000462	maturation of SSU-rRNA from tricistronic...	0.031
	GO:0051052	regulation of DNA metabolic process	0.031
	GO:0046148	pigment biosynthetic process	0.034
	GO:0048522	positive regulation of cellular process	0.034
	GO:0005978	glycogen biosynthetic process	0.034
	GO:0035194	posttranscriptional gene silencing by RN...	0.034
	GO:0031327	negative regulation of cellular biosynth...	0.034
	GO:0018022	peptidyl-lysine methylation	0.034
	GO:0051173	positive regulation of nitrogen compound...	0.034
	GO:0006913	nucleocytoplasmic transport	0.035
	GO:0007275	multicellular organism development	0.035
	GO:0009910	negative regulation of flower developmen...	0.035
	GO:0051169	nuclear transport	0.035

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GO type	GO ID	Description	Adj. p-value
	GO:0022414	reproductive process	0.035
	GO:0070192	chromosome organization involved in meio...	0.035
	GO:0140053	mitochondrial gene expression	0.035
	GO:0032501	multicellular organismal process	0.036
	GO:0007127	meiosis I	0.037
	GO:0061982	meiosis I cell cycle process	0.037
	GO:0045934	negative regulation of nucleobase-contai...	0.037
	GO:0045132	meiotic chromosome segregation	0.038
	GO:0032434	regulation of proteasomal ubiquitin-depe...	0.041
	GO:2000058	regulation of ubiquitin-dependent protei...	0.041
	GO:0007129	synapsis	0.041
	GO:0071483	cellular response to blue light	0.042
	GO:0033036	macromolecule localization	0.042
	GO:0000003	reproduction	0.042
	GO:0006378	mRNA polyadenylation	0.042
	GO:0010558	negative regulation of macromolecule bio...	0.043
	GO:0019438	aromatic compound biosynthetic process	0.045
	GO:0035265	organ growth	0.046
	GO:0048581	negative regulation of post-embryonic de...	0.047
	GO:1901607	alpha-amino acid biosynthetic process	0.047
	GO:0051241	negative regulation of multicellular org...	0.048
	GO:0007059	chromosome segregation	0.049
	GO:0070475	rRNA base methylation	0.049
	GO:0009908	flower development	0.049
	GO:0043572	plastid fission	0.049
	GO:0006879	cellular iron ion homeostasis	0.053
	GO:0006418	tRNA aminoacylation for protein translat...	0.053
	GO:0032543	mitochondrial translation	0.053
	GO:0000302	response to reactive oxygen species	0.053
	GO:0016246	RNA interference	0.053
	GO:0048856	anatomical structure development	0.053
	GO:0009894	regulation of catabolic process	0.056
	GO:0010206	photosystem II repair	0.056
	GO:0009791	post-embryonic development	0.057
	GO:0034599	cellular response to oxidative stress	0.057
	GO:0034249	negative regulation of cellular amide me...	0.059
	GO:1901362	organic cyclic compound biosynthetic pro...	0.062
	GO:0015931	nucleobase-containing compound transport	0.063
	GO:0006091	generation of precursor metabolites and ...	0.065
	GO:0007006	mitochondrial membrane organization	0.065
	GO:0017148	negative regulation of translation	0.066
	GO:0043467	regulation of generation of precursor me...	0.067
	GO:0006560	proline metabolic process	0.068
	GO:0080156	mitochondrial mRNA modification	0.069
	GO:0071369	cellular response to ethylene stimulus	0.069
	GO:0031053	primary miRNA processing	0.070
	GO:0051050	positive regulation of transport	0.070
	GO:0051172	negative regulation of nitrogen compound...	0.070
	GO:0090503	RNA phosphodiester bond hydrolysis, exon...	0.070

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GO type	GO ID	Description	Adj. p-value
	GO:0048523	negative regulation of cellular process	0.074
	GO:0009911	positive regulation of flower developmen...	0.076
	GO:0090056	regulation of chlorophyll metabolic proc...	0.079
	GO:0018198	peptidyl-cysteine modification	0.081
	GO:0043631	RNA polyadenylation	0.083
	GO:0010020	chloroplast fission	0.085
	GO:0060249	anatomical structure homeostasis	0.085
	GO:0045892	negative regulation of transcription, DN...	0.087
	GO:0031056	regulation of histone modification	0.089
	GO:0007005	mitochondrion organization	0.090
	GO:0051253	negative regulation of RNA metabolic pro...	0.090
	GO:0009640	photomorphogenesis	0.090
	GO:0016109	tetraterpenoid biosynthetic process	0.091
	GO:0016117	carotenoid biosynthetic process	0.091
	GO:0050794	regulation of cellular process	0.091
	GO:0016114	terpenoid biosynthetic process	0.091
	GO:0031329	regulation of cellular catabolic process	0.095
	GO:0043624	cellular protein complex disassembly	0.097
	GO:0090567	reproductive shoot system development	0.099
	GO:0048731	system development	0.100
CC	GO:0005654	nucleoplasm	0.000
	GO:1990234	transferase complex	0.000
	GO:0044451	nucleoplasm part	0.000
	GO:0000151	ubiquitin ligase complex	0.000
	GO:0005681	spliceosomal complex	0.000
	GO:0016604	nuclear body	0.000
	GO:0009295	nucleoid	0.000
	GO:0042646	plastid nucleoid	0.000
	GO:0071010	prespliceosome	0.000
	GO:0042170	plastid membrane	0.000
	GO:0031969	chloroplast membrane	0.000
	GO:0016591	DNA-directed RNA polymerase II, holoenzy...	0.001
	GO:0009521	photosystem	0.001
	GO:0071011	precatalytic spliceosome	0.001
	GO:0005686	U2 snRNP	0.001
	GO:0043228	non-membrane-bounded organelle	0.002
	GO:0043232	intracellular non-membrane-bounded organ...	0.002
	GO:0000243	commitment complex	0.003
	GO:0005739	mitochondrion	0.003
	GO:0005666	DNA-directed RNA polymerase III complex	0.004
	GO:0016592	mediator complex	0.004
	GO:0030686	90S preribosome	0.004
	GO:0030687	preribosome, large subunit precursor	0.004
	GO:0005694	chromosome	0.005
	GO:0080008	Cul4-RING E3 ubiquitin ligase complex	0.011
	GO:0000784	nuclear chromosome, telomeric region	0.012
	GO:0000123	histone acetyltransferase complex	0.014
	GO:0000228	nuclear chromosome	0.014
	GO:0031984	organelle subcompartment	0.015

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GO type	GO ID	Description	Adj. p-value
	GO:0005689	U12-type spliceosomal complex	0.018
	GO:0044452	nucleolar part	0.019
	GO:0048500	signal recognition particle	0.020
	GO:0008023	transcription elongation factor complex	0.021
	GO:0000781	chromosome, telomeric region	0.023
	GO:0005759	mitochondrial matrix	0.031
	GO:0005777	peroxisome	0.031
	GO:0042579	microbody	0.031
	GO:0005667	transcription factor complex	0.033
	GO:0044454	nuclear chromosome part	0.036
	GO:0009654	photosystem II oxygen evolving complex	0.044
	GO:0000178	exosome (RNase complex)	0.051
	GO:1905354	exoribonuclease complex	0.051
	GO:0000176	nuclear exosome (RNase complex)	0.080
	GO:1902554	serine/threonine protein kinase complex	0.087
	GO:1902911	protein kinase complex	0.087
	GO:0000152	nuclear ubiquitin ligase complex	0.091
	GO:0015030	Cajal body	0.091
	GO:0031248	protein acetyltransferase complex	0.091
	GO:1902493	acetyltransferase complex	0.091
	GO:0009527	plastid outer membrane	0.095
	GO:0031968	organelle outer membrane	0.097
	GO:0140098	catalytic activity, acting on RNA	0.000
	GO:0003724	RNA helicase activity	0.000
	GO:0004518	nuclease activity	0.000
	GO:0008173	RNA methyltransferase activity	0.000
	GO:0051536	iron-sulfur cluster binding	0.000
	GO:0044877	protein-containing complex binding	0.001
	GO:0004540	ribonuclease activity	0.001
	GO:0140101	catalytic activity, acting on a tRNA	0.004
	GO:0003690	double-stranded DNA binding	0.006
	GO:0003677	DNA binding	0.008
	GO:0003713	transcription coactivator activity	0.008
	GO:0008649	rRNA methyltransferase activity	0.008
	GO:0140102	catalytic activity, acting on a rRNA	0.008
	GO:2001070	starch binding	0.008
	GO:0008408	3'-5' exonuclease activity	0.012
	GO:0004003	ATP-dependent DNA helicase activity	0.012
	GO:0051537	2 iron, 2 sulfur cluster binding	0.012
	GO:0016896	exoribonuclease activity, producing 5'-p...	0.012
	GO:0016893	endonuclease activity, active with eithe...	0.013
	GO:0003924	GTPase activity	0.013
	GO:0046914	transition metal ion binding	0.015
	GO:0004532	exoribonuclease activity	0.017
	GO:0008094	DNA-dependent ATPase activity	0.017
	GO:0016796	exonuclease activity, active with either...	0.017
	GO:0003755	peptidyl-prolyl cis-trans isomerase acti...	0.023
	GO:0004527	exonuclease activity	0.023
	GO:0016859	cis-trans isomerase activity	0.023
MF			

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GO type	GO ID	Description	Adj. p-value
	GO:0016817	hydrolase activity, acting on acid anhyd...	0.030
	GO:0003684	damaged DNA binding	0.034
	GO:0017111	nucleoside-triphosphatase activity	0.034
	GO:0032549	ribonucleoside binding	0.037
	GO:0001882	nucleoside binding	0.042
	GO:0008170	N-methyltransferase activity	0.047
	GO:0003725	double-stranded RNA binding	0.052
	GO:0042162	telomeric DNA binding	0.052
	GO:0000049	tRNA binding	0.053
	GO:0016462	pyrophosphatase activity	0.053
	GO:0008276	protein methyltransferase activity	0.054
	GO:0016818	hydrolase activity, acting on acid anhyd...	0.054
	GO:0042802	identical protein binding	0.054
	GO:0000988	transcription factor activity, protein b...	0.054
	GO:0001883	purine nucleoside binding	0.054
	GO:0005525	GTP binding	0.054
	GO:0016891	endoribonuclease activity, producing 5'-...	0.054
	GO:0019001	guanyl nucleotide binding	0.054
	GO:0032550	purine ribonucleoside binding	0.054
	GO:0032561	guanyl ribonucleotide binding	0.054
	GO:0000175	3'-5'-exoribonuclease activity	0.064
	GO:0004525	ribonuclease III activity	0.066
	GO:0032296	double-stranded RNA-specific ribonucleas...	0.066
	GO:0003747	translation release factor activity	0.067
	GO:0008079	translation termination factor activity	0.067
	GO:0008198	ferrous iron binding	0.067
	GO:0030983	mismatched DNA binding	0.067
	GO:0003712	transcription cofactor activity	0.070
	GO:0001056	RNA polymerase III activity	0.098