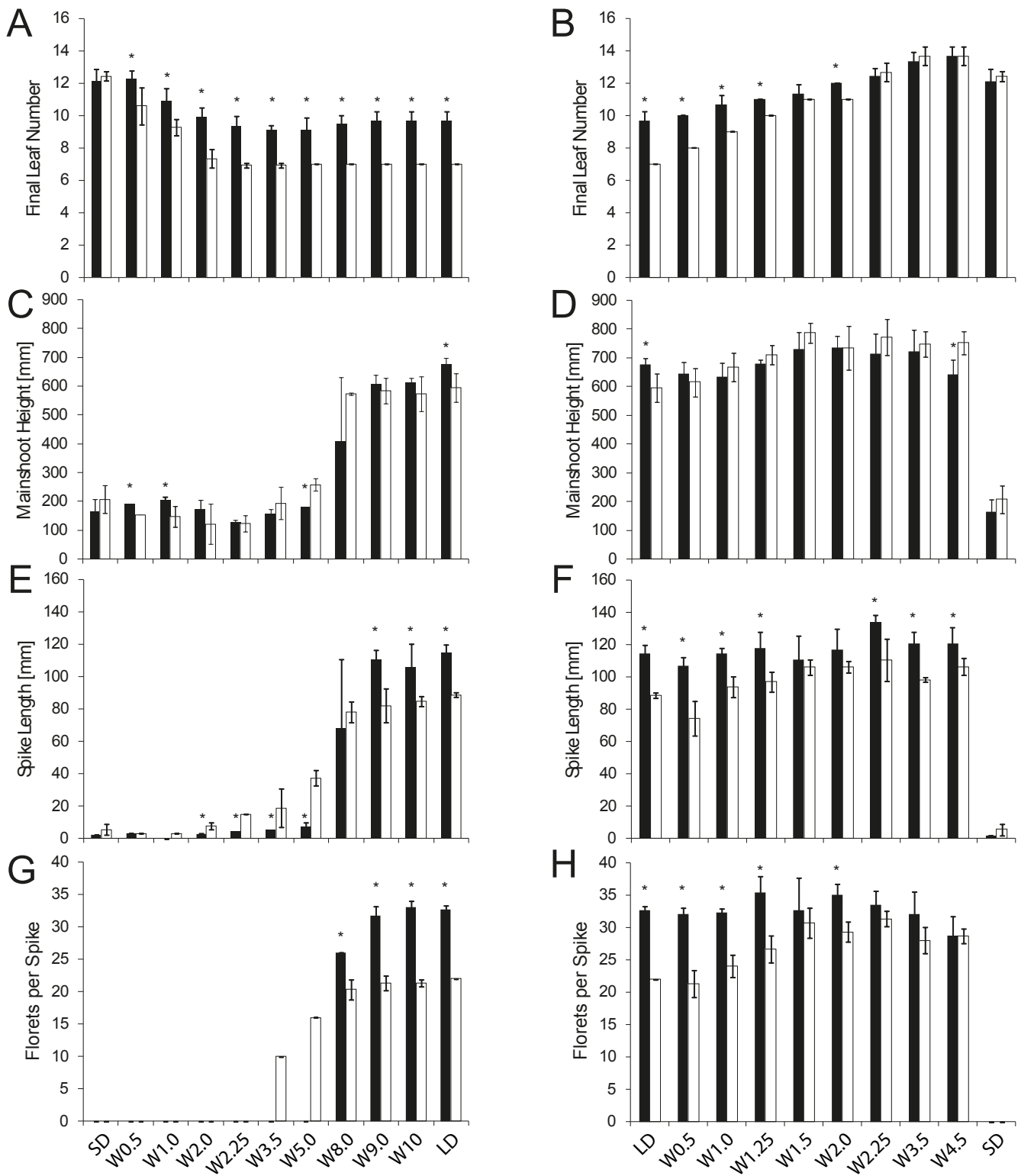


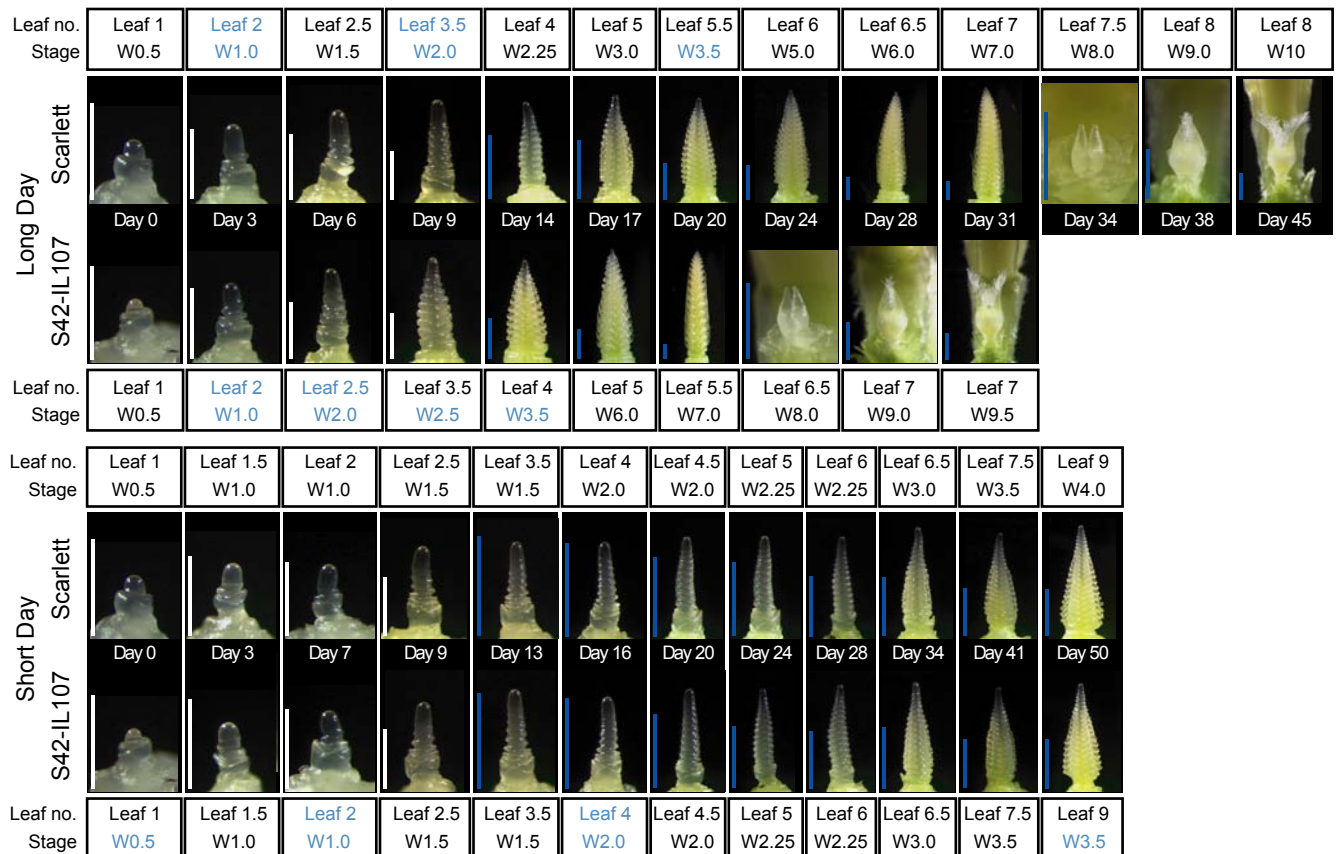
Supplemental Figure 1: Development related phenotypes of Scarlett/S42-IL107, Bowman/BW281 and Triumph/Triumph-IL

(A) Number of leaves emerged from the main shoot under long days (LDs) at the time of heading. **(B)** Phenotypes of the main shoot spike recorded at stamen primordium stage (W3.5, floret primordia per inflorescence) or at plant maturity (florets per spike, seeds per spike). Bars represent means \pm standard deviation over 5-15 plants. Significant differences ($p < 0.05$) between spring barleys and derived *Ppd-H1* introgression lines and between spike related phenotypes are indicated as asterisks and small letters on top of the charts, respectively.



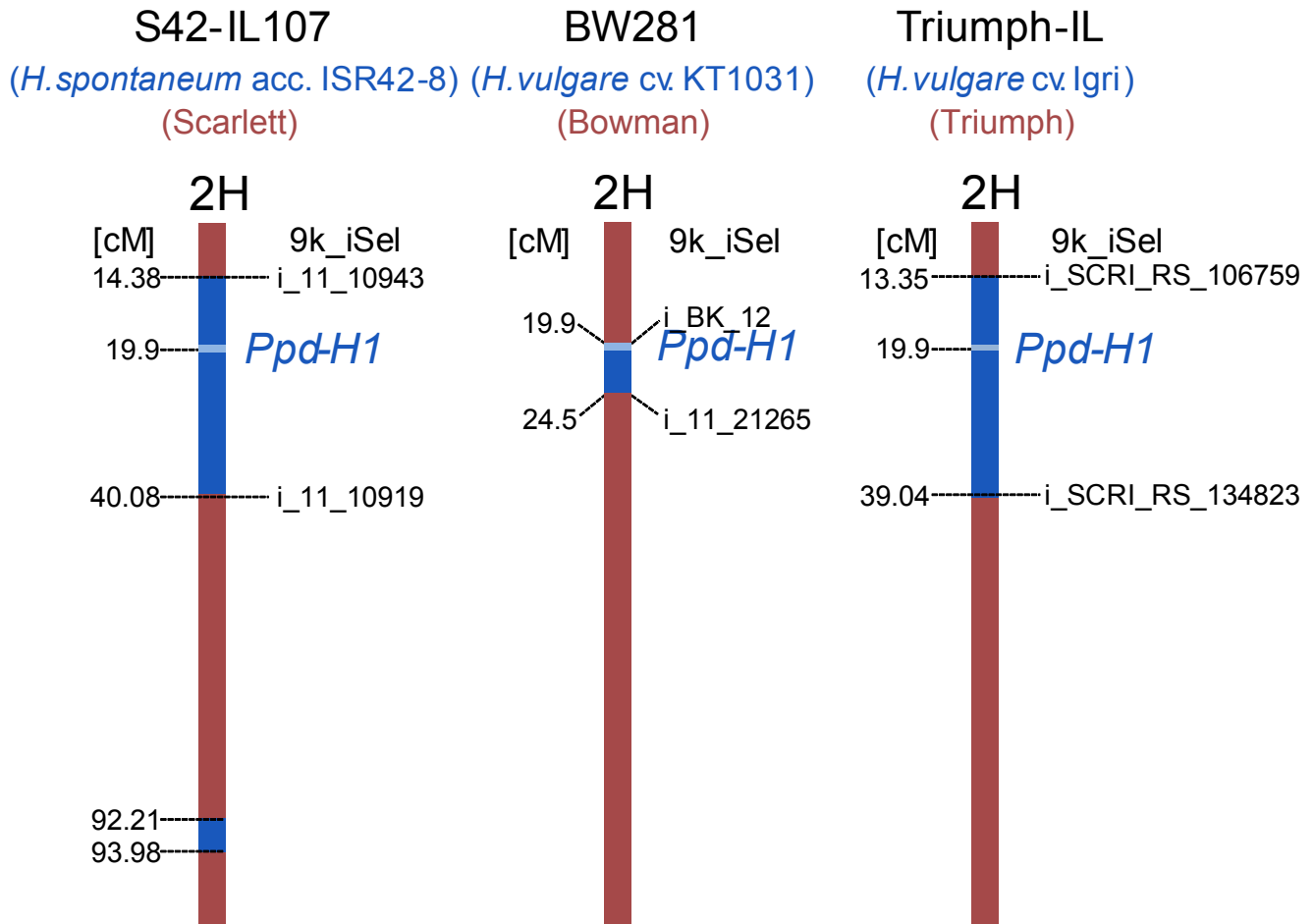
Supplemental Figure 2: Effects of the photoperiod during plant development on leaf emergence, stem elongation and spike traits of Scarlett and S42-IL107

Plants of Scarlett (black) and S42-IL107 (white) were grown under short-day (SD) or long-day (LD) conditions. At different stages of MSA development (W0.5 – W10), plants were transferred from (**left column**) LDs to SDs or from (**right column**) SDs to LDs and remained in the respective photoperiod until plant senescence. The following phenotypes of the main shoot were recorded for plants: (**A, B**) number of emerged leaves at heading or at main shoot senescence; (**C, D**) height; (**E, F**) spike length; (**G, H**) floret number per spike. Bars represent means \pm standard deviation over 3 plants. Significant differences ($p < 0.05$) between genotypes transferred from SDs to LDs and vice versa at the same developmental stage are indicated by asterisks above bar graphs.



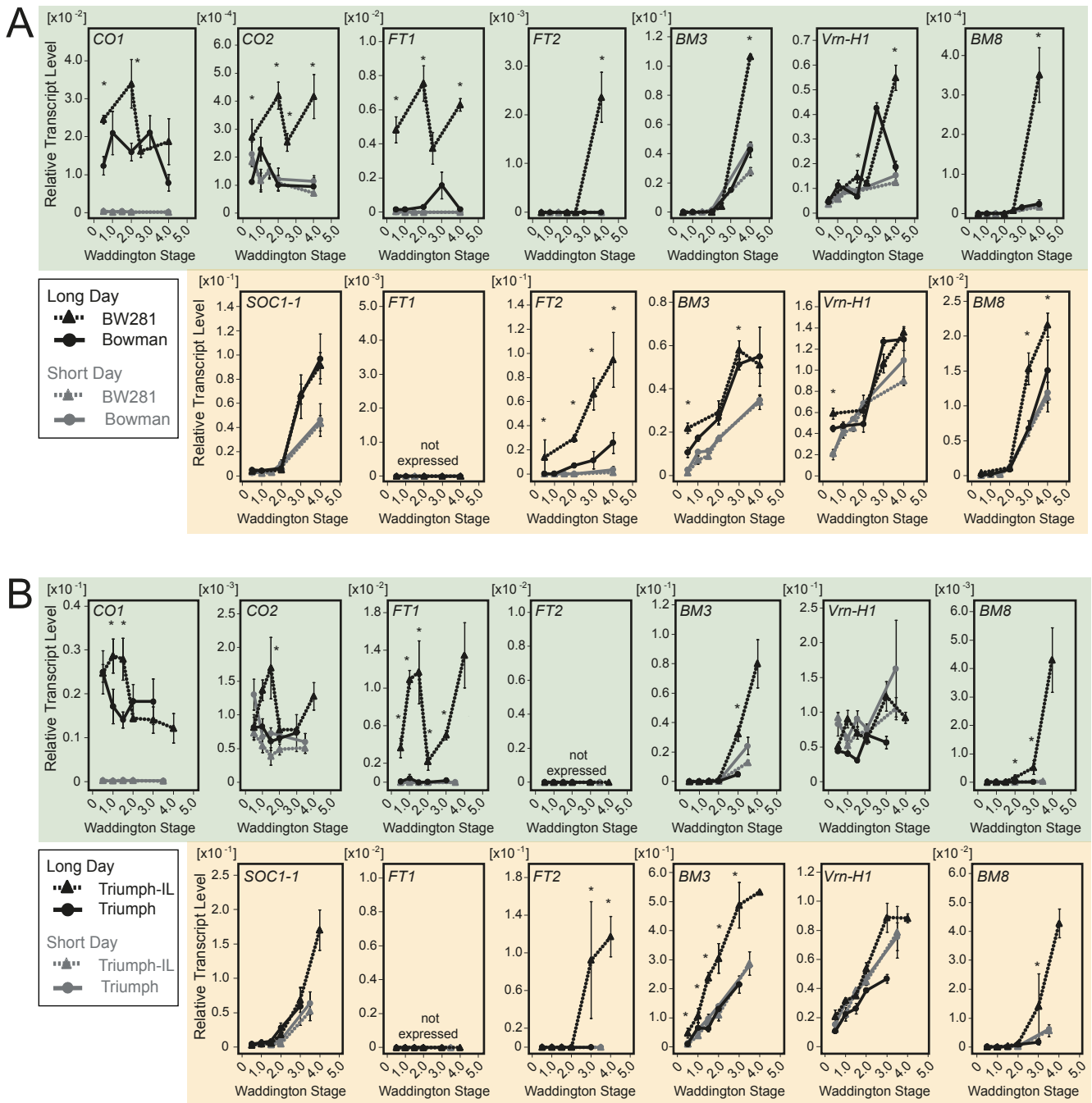
Supplemental Figure 3: Development of the main shoot apex of Scarlett and S42-IL107

Developmental stage of the apex (W: Waddington stage) and number of leaves emerged from the main shoot are reported. Plants were grown under short-day conditions (SD) or transferred to long days (LDs) seven days after germination (Day 0). Blue labels indicate stages, at which leaf and apex samples were harvested for transcriptome profiling using RNA sequencing. White bars (500µm), blue bars (1mm).



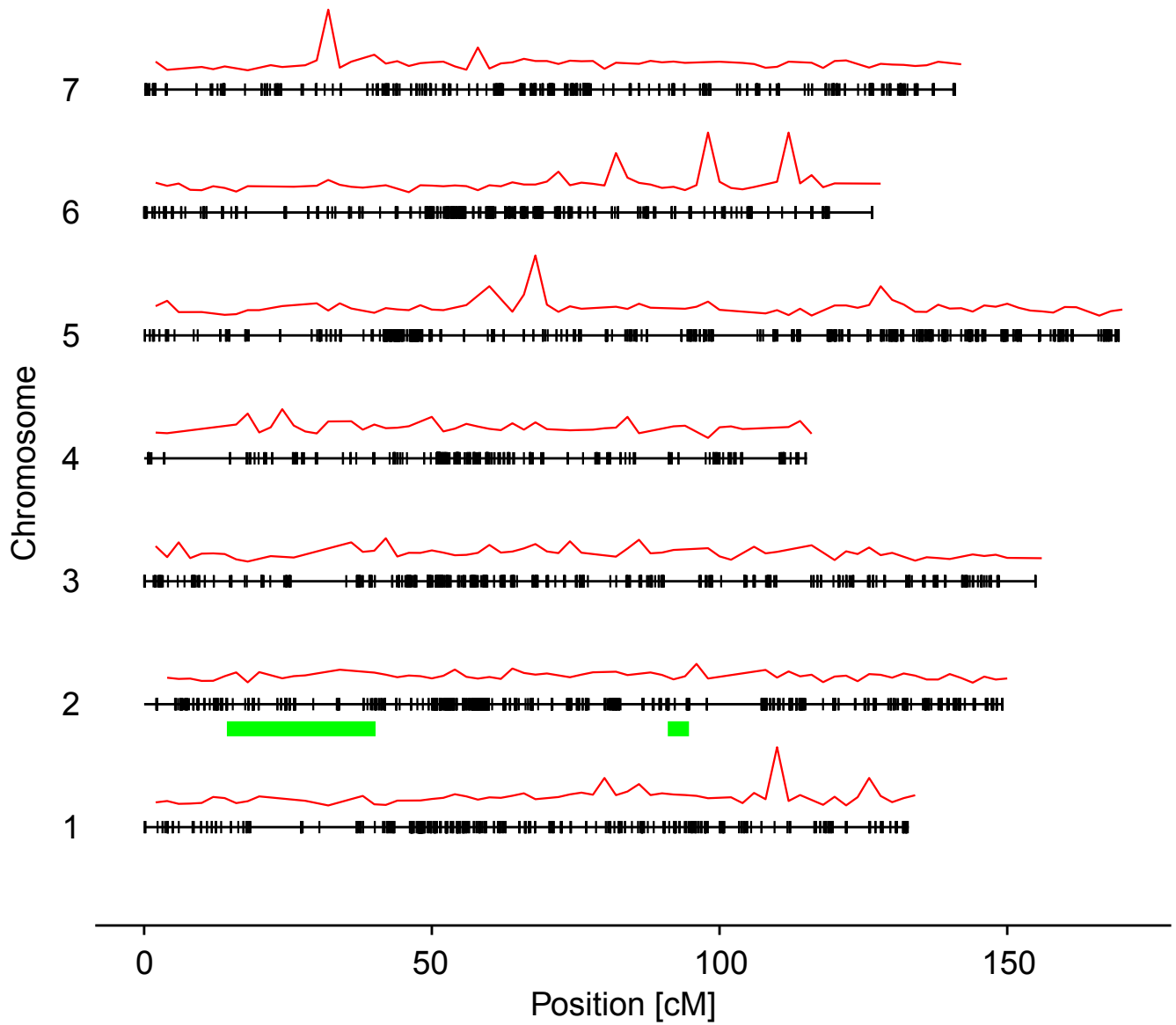
Supplemental Figure 4: Size and flanking markers of *Ppd-H1* introgressions on chromosome 2H.

Donor parents for the photoperiod-responsive *Ppd-H1* allele of the introgression lines and their respective spring barley background genotypes are indicated above each chart. Introgression lines were genotyped with the 9k-iSelect chip from Illumina. Flanking marker positions of the introgressions are given relative to the POPSEQ map (Marscher et al., 2013).



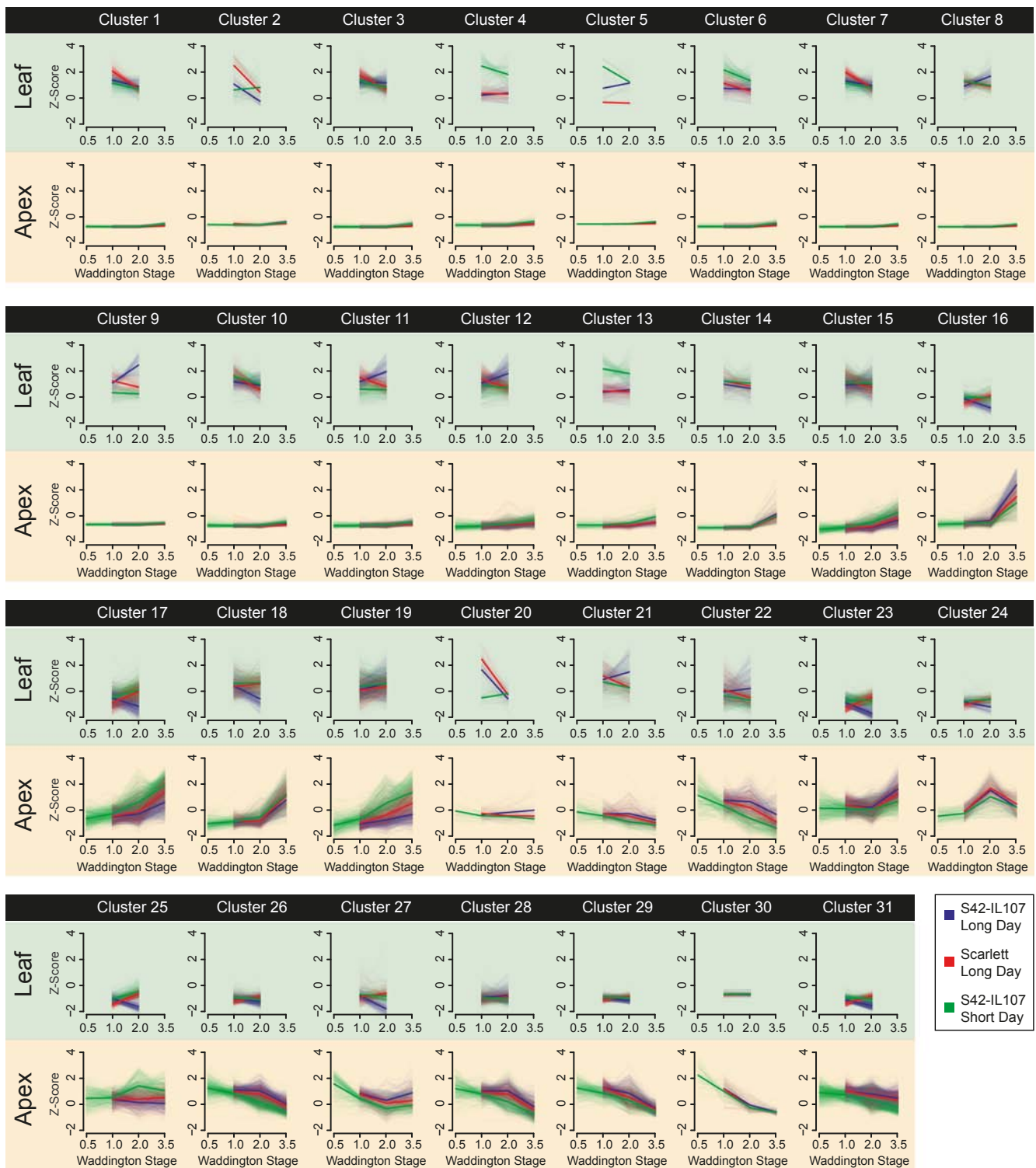
Supplemental Figure 5: Validation of transcript levels in leaves and shoot apices of Bowman/ BW281, Triumph/Triumph-IL

Quantification of transcript levels by quantitative real time PCR (RT-qPCR) in leaf samples (green) and samples enriched for apex tissue (orange) at different stages of plant development. Samples were harvested from the barley genotypes (A) Bowman and BW281 and (B) Triumph and Triumph-IL. Transcript levels are demonstrated relative to the transcript abundance of *Actin*. Error bars indicate the standard deviation over three biological and two technical replicates. Asterisks highlight significant differences ($p < 0.05$) between transcript levels of BW281 and Bowman or Triumph-IL and Triumph, respectively, when plants were at the same developmental stage and grown under long-day conditions.



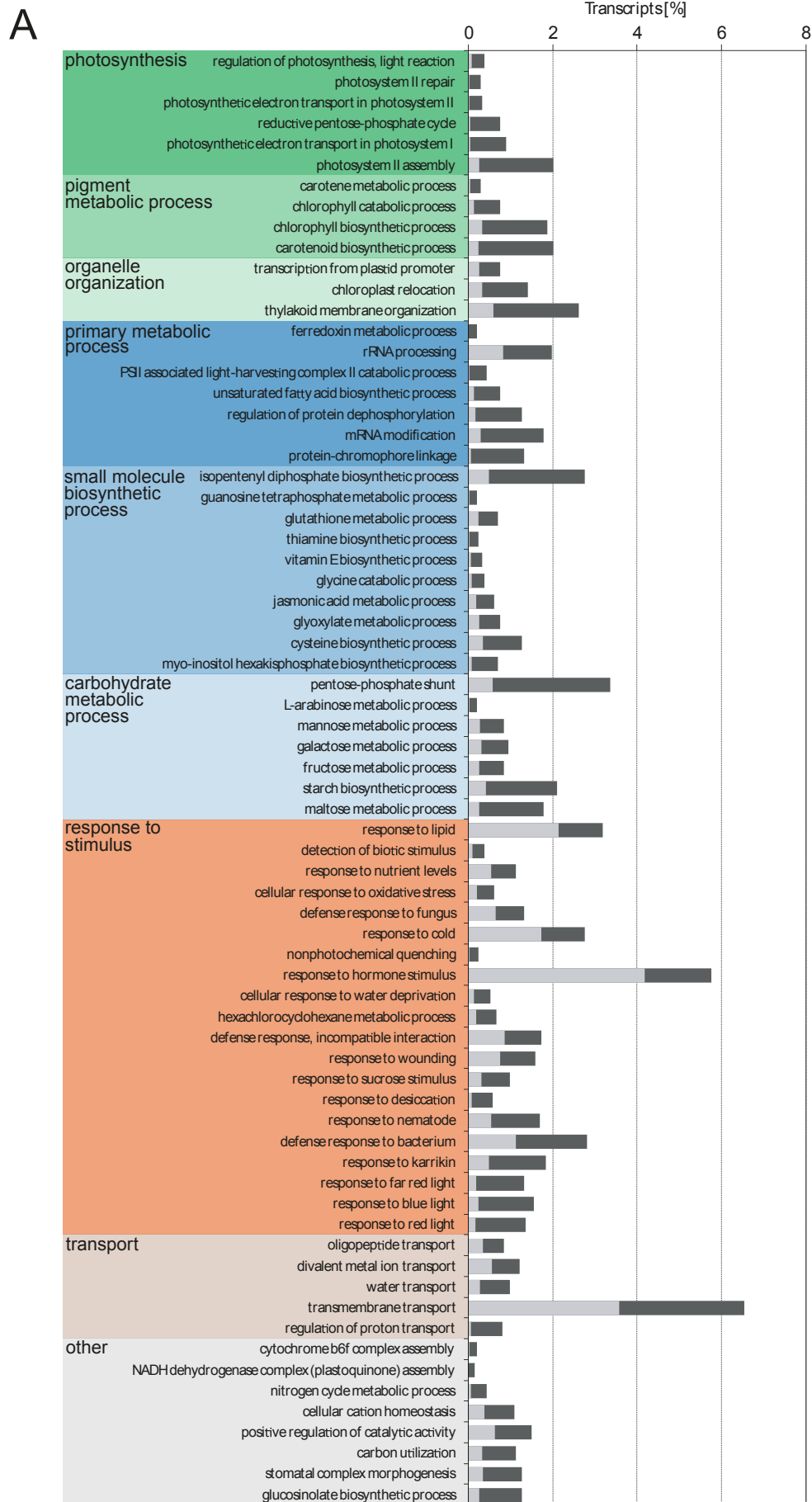
Supplemental Figure 6: Distribution and density of differentially expressed transcripts (DETs) along the barley chromosomes.

Seven barley chromosomes are depicted as horizontal black lines. The DETs are shown as vertical black lines plotted on the chromosomes. Location of the S42-IL107 introgression region is shown as green rectangles below the chromosome 2H. The density of the DETs is plotted as red lines above the chromosomes. Positions are given in centimorgans (cM) according to the PopSeq map (Mascher et al., 2013).



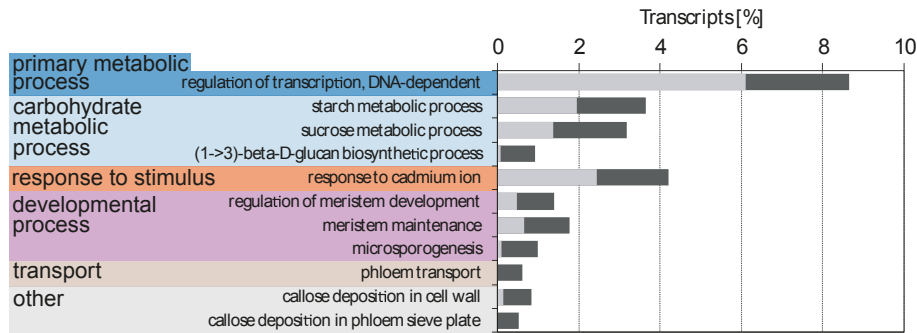
Supplemental Figure 7: Expression profiles of 7604 DETs in 31 coexpression clusters

Coexpression clusters of 7604 differentially expressed transcripts (DET). Expression levels for individual transcripts (light colors) and mean expression level across all transcripts within each cluster (bright color) were plotted. Coexpression plots depict transcript expression patterns in leaves (green) and apices (orange) as mean centered and scaled transcript levels (Z-Score). Detailed statistics for each cluster are presented in Supplemental Table 20.

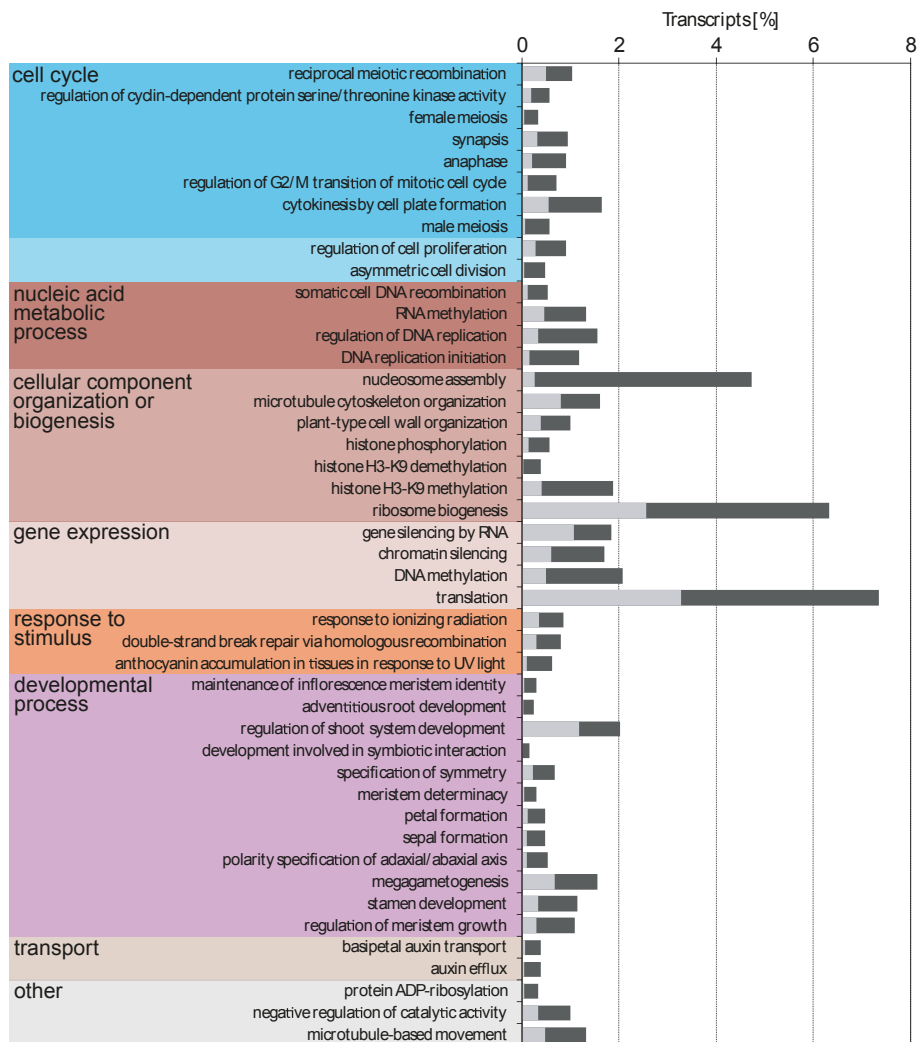


Supplemental Figure 8 (part 1): Overrepresentation of Gene Ontology (GO) terms among transcripts in coexpression clusters I-III
 Legend see next page

B

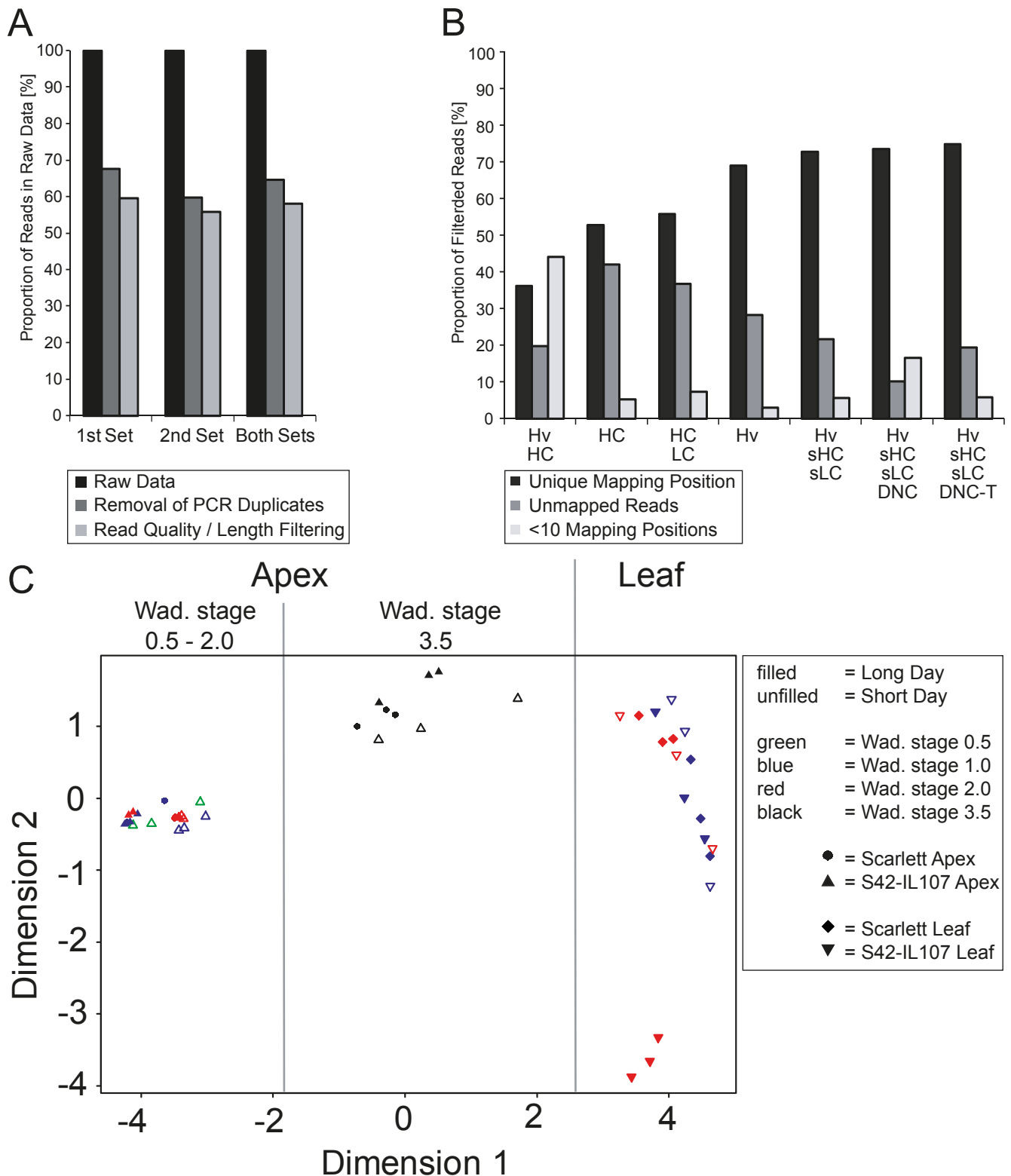


C



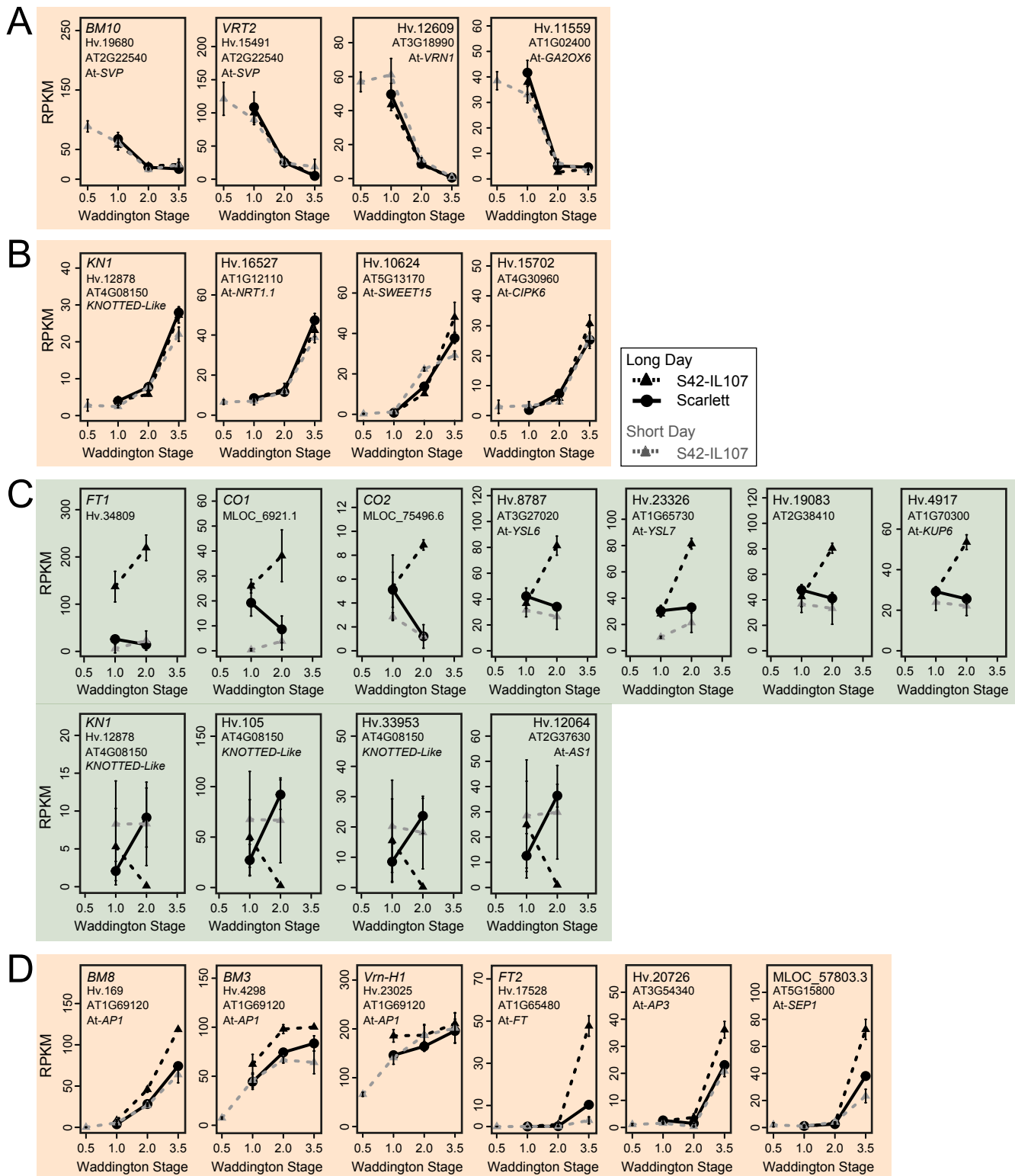
Supplemental Figure 8 (part 2): Overrepresentation of Gene Ontology (GO) terms among transcripts in coexpression clusters I-III

Overrepresented GO terms assigned to biological processes for transcripts coexpressed within (A) cluster I, (B) cluster II and (C) cluster III, respectively. Clusters represent transcripts predominantly expressed in leaves (cluster I), shoot apices (cluster III) or equally expressed in both tissues (cluster II). Significant (FDR<0.05) leaf nodes of the GO-tree were summarized to common parental GO-terms (colored). Bars indicate the relative abundance of transcripts assigned to the GO-terms in the test set (dark grey) and the reference set (light grey), respectively.



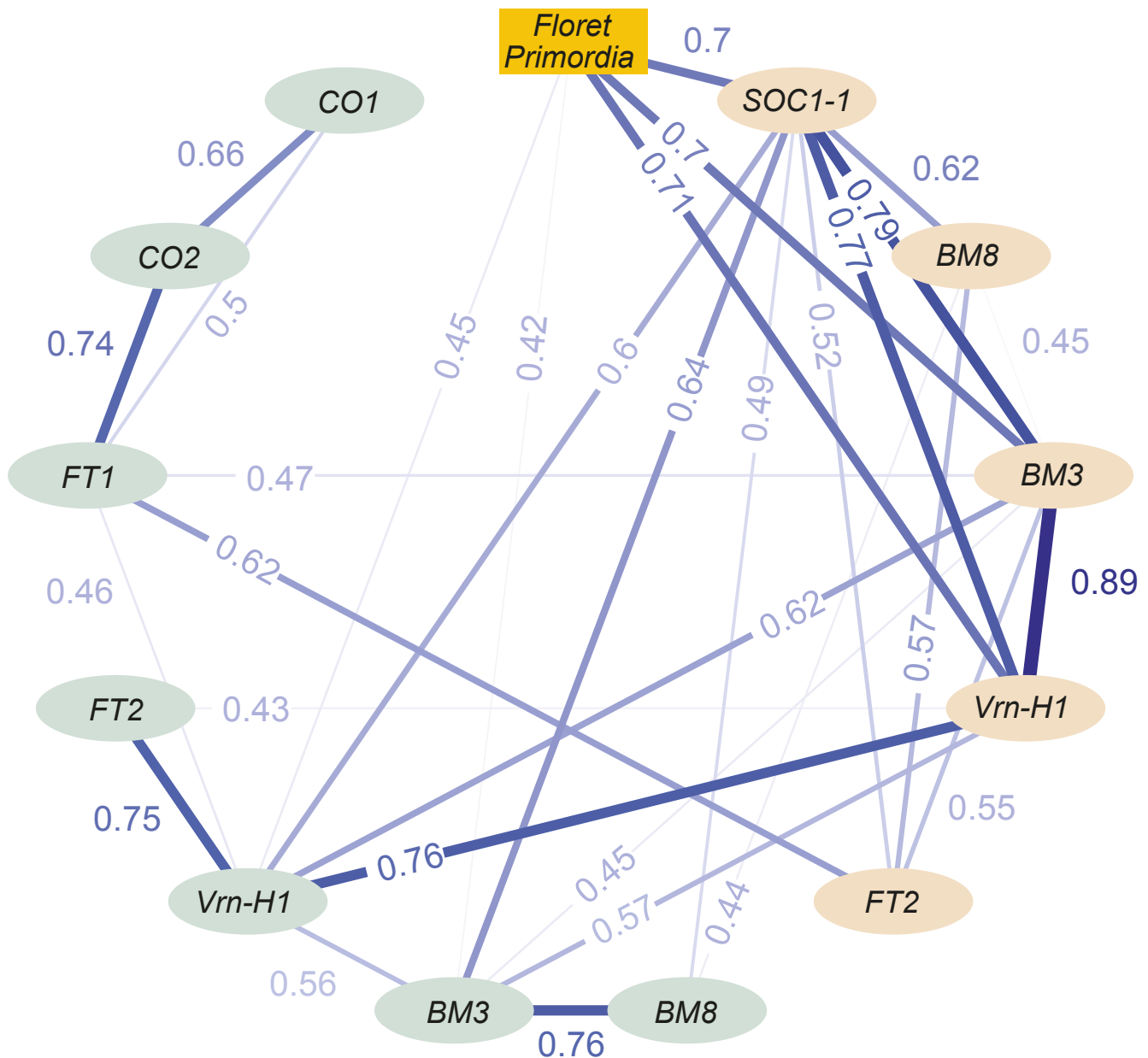
Supplemental Figure 9: Overview of RNA sequencing statistics

(A) Quality- and length-based filtering of raw sequencing reads (100bp, single-end, Illumina), derived from two independent sequencing runs. Reads of libraries A to X (1st set) and of libraries A1-AE1 (2nd set) retained after filtering. See Supplemental Table 18 for detailed information on the libraries. (B) Proportion of filtered reads mapping to the reference sets of different transcript combinations. Hv: barley NCBI UniGene set; HC: high confidence gene set; LC: low confidence gene set; sHC/sLC: selected subset of unique HC or LC; DNC, *de novo* contigs assembled from unmapped Illumina reads; DNC-T, selected *de novo* contigs with BLASTx hit in the Triticeae. (C) Unsupervised clustering of RNA samples in two dimensions by multidimensional scaling.



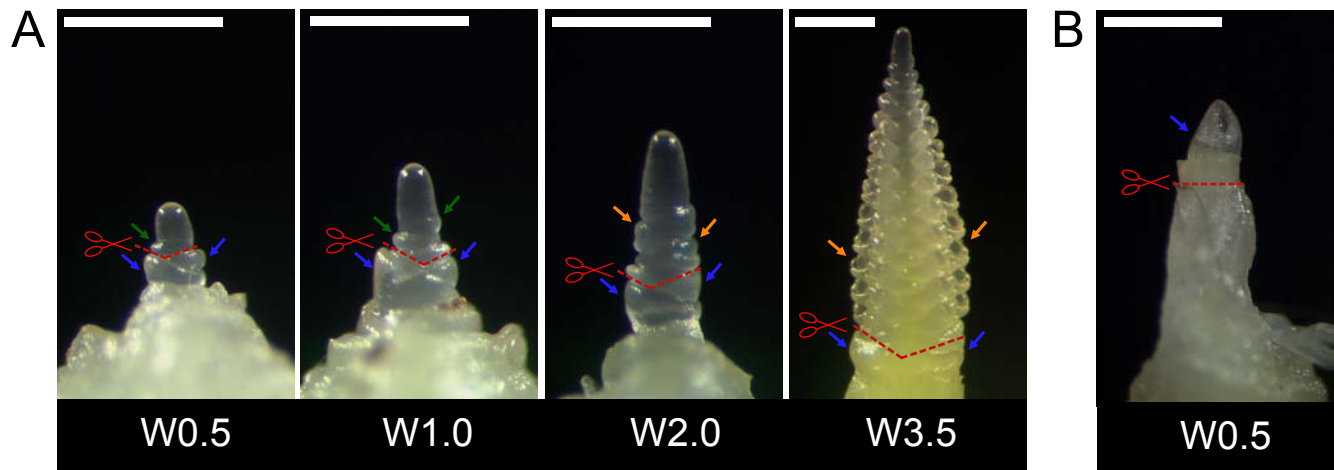
Supplemental Figure 10: Expression patterns of selected transcripts in leaves and shoot apices of Scarlett and S42-IL107 determined by RNA sequencing (RNA-seq)

RNA-seq derived expression data of transcripts (A) downregulated or (B) upregulated during MSA development independent of the genotype and photoperiod or differentially regulated between photoperiods and between genotypes in (C) leaves or (D) shoot apices. Normalized expression values are reported in reads per kilo base per million (RPKM). Error bars indicate standard deviation across two to three independent RNA samples.



Supplemental Figure 11: Correlation network for gene expression data in leaves and shoot apices

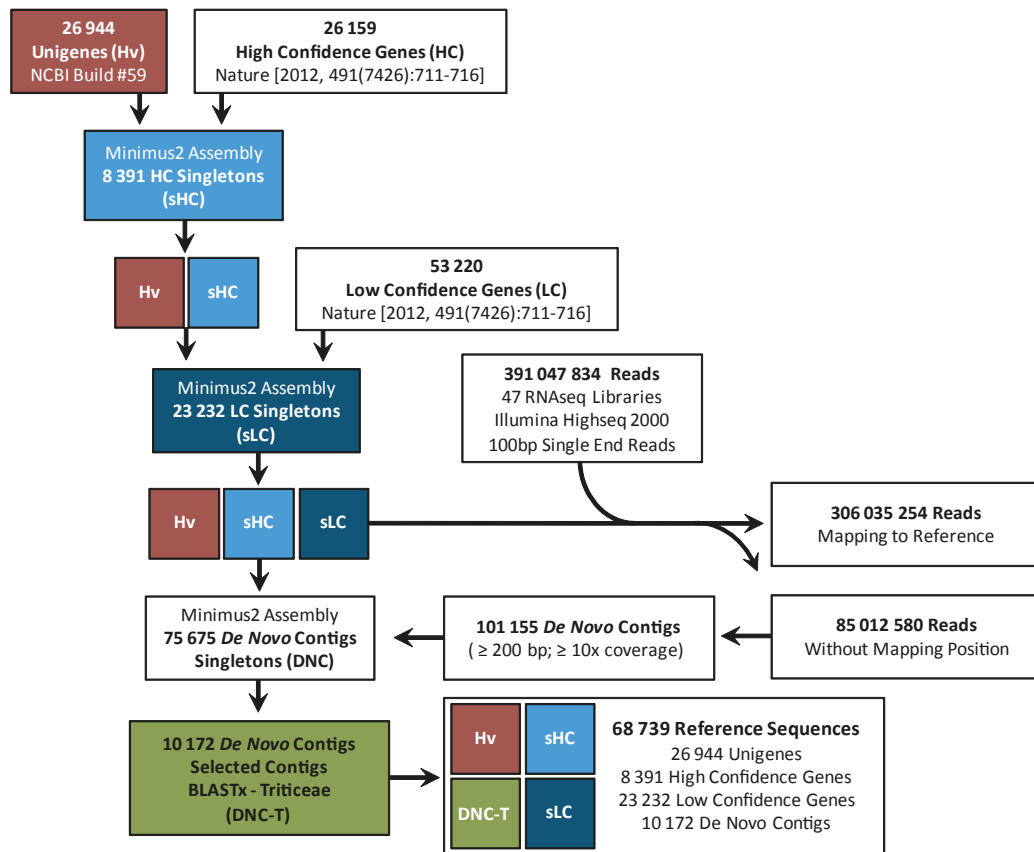
Correlation network between transcript levels of flowering time genes in leaf and shoot apex samples and number of floret primordia emerged at the shoot apex during early stages of shoot apex development. Transcript abundance was determined by RT-qPCR in leaves (green ellipses) and shoot apex enriched tissue (orange ellipses) of Scarlett, Bowman, Triumph and their derived *Ppd-H1* introgression lines (see also Figure 3D+E and Supplemental Figure 5). Pearson correlation coefficients of $r > |0.4|$ and $FDR < 0.05$ are indicated as blue lines connecting the individual transcripts.



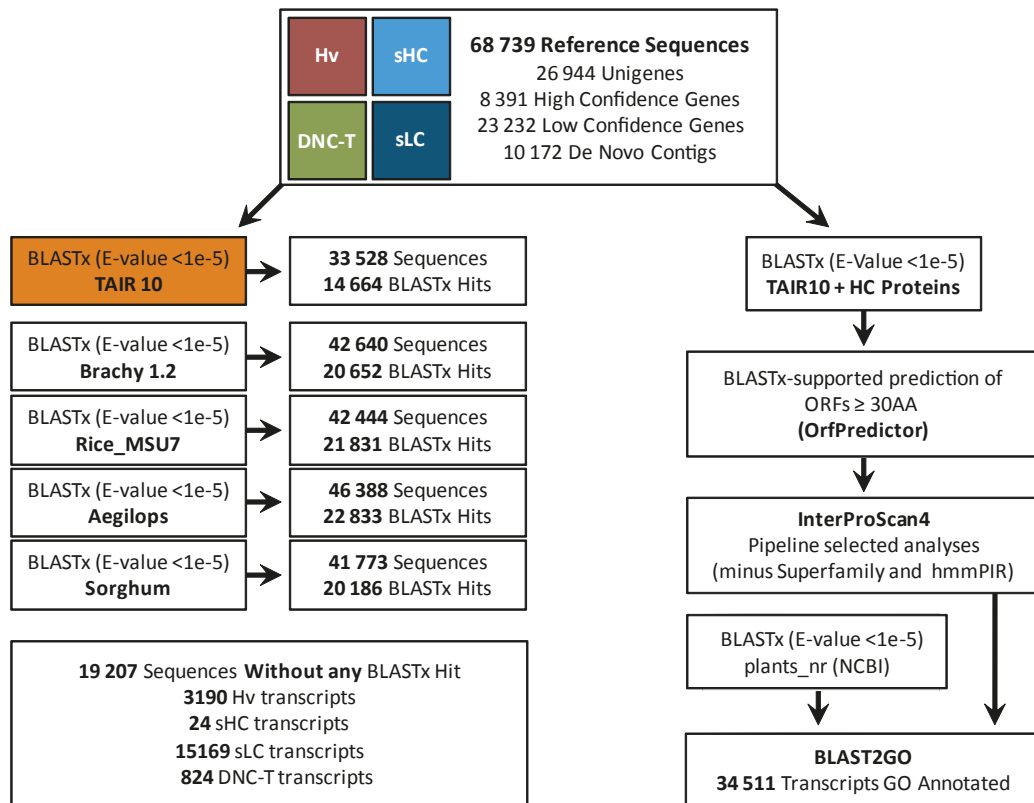
Supplemental Figure 12: Representative main shoot apices dissected for RNA extraction

Total RNA was extracted from pools of isolated shoot apices including the tissue above the red dashed lines. Waddington stages (W) of harvested shoot apices are indicated below the pictures. White bars represent 500µm. **(A)** Shoot apex samples harvested for RNA sequencing comprised dissected tissues of the apical dome, young leaf primordia (green arrows) and floret primordia (orange arrows). Older leaf primordia (blue arrows) and basal parts of the shoot apex were excluded. **(B)** Apex enriched tissue harvested for RT-qPCR analysis at different stages of development also included older leaf primordia and basal parts of the shoot apex as indicated for a vegetative shoot apex at W0.5.

A

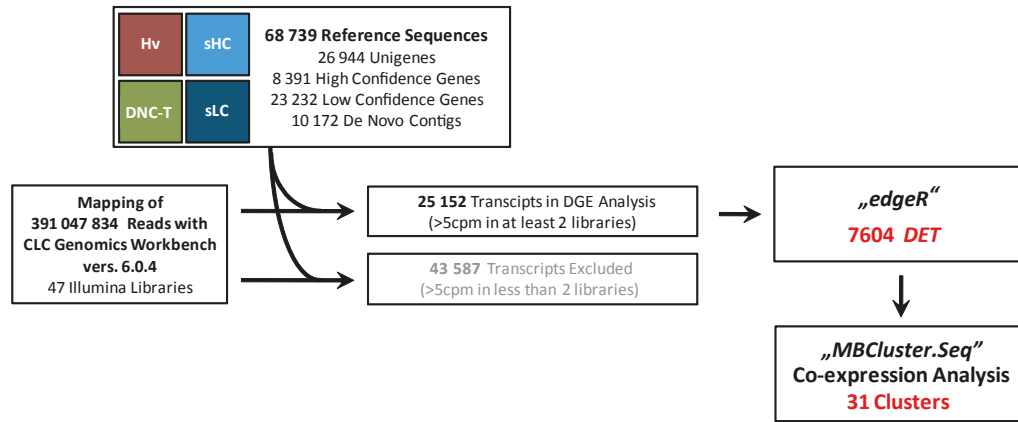


B



Supplemental Figure 13 (part 1): Schematic representation of the RNA sequencing pipeline Legend see next page

C



Supplemental Figure 13 (part 2): Schematic representation of the RNA sequencing pipeline

(A) Selection of transcripts used as reference sequences in the read mapping step prior to differential gene expression analysis. **(B)** Annotation of transcripts in the reference set is based on BLASTx results against different plant protein databases (left panel) and retrieval of Gene Ontology terms with Blast2GO software (right panel). **(C)** Summary of the differential gene expression and coexpression analysis using the edgeR- and MBCluster.Seq-packages of the R statistical software, respectively. DET: Differentially expressed transcripts; Hv, Unigenes: Barley NCBI UniGene set; HC: High confidence gene set; LC: Low confidence gene set; sHC/sLC: selected subset of unique HC or LC.

Supplemental Table 1: Slopes of broken-line regressions performed on MSA development and floret primordia induction in Scarlett and S42-IL107 under SD and LD

Phenotype	Photoperiod	Genotype	Segment of Regression Line	Slope	St.Err.	Upper 95%-CI ¹	Lower 95%-CI ¹
Shoot apex development (see Fig. 1C)	Long day	Scarlett	segment 1	0.118	0.010	0.098	0.138
			segment 2	0.246	0.006	0.234	0.258
			segment 3	0.057	0.019	0.019	0.094
	Short day	S42-IL017	segment 1	0.207	0.015	0.176	0.237
			segment 2	0.440	0.012	0.416	0.463
			segment 3	0.026	0.006	0.014	0.038
Induction of floret primordia (see Fig. 1D)	Long day	Scarlett	segment 1	-0.005	0.332	-0.660	0.651
			segment 2	2.107	0.040	2.027	2.187
			segment 3	0.098	0.069	-0.038	0.235
	Short day	S42-IL017	segment 1	-0.109	0.491	-1.081	0.863
			segment 2	2.683	0.087	2.510	2.856
			segment 3	-0.080	0.039	-0.158	-0.002
Induction of floret primordia (see Fig. 1D)	Long day	Scarlett	segment 1	0.095	0.095	-0.093	0.283
			segment 2	1.247	0.045	1.158	1.336
			segment 3	0.557	0.035	0.487	0.628
	Short day	S42-IL017	segment 1	0.135	0.098	-0.059	0.330
			segment 2	1.206	0.041	1.125	1.286
			segment 3	0.509	0.041	0.427	0.591

¹Upper and lower 95%-Confidence Interval of the slope

Broken-line regressions performed with the 'segmented'-package in R (Muggeo et al. 2003 and 2008).

Supplemental Table 2: Average differences* in expression levels (RPKM) between transcripts in coexpression clusters I-III

Tissue	Wad. Stage	Cluster I	Cluster II	Cluster III
Leaf	1.0 - 2.0	1.34	0.03	-1.07
Apex	3.5	-1.48	0.18	0.19
Apex	0.5 - 2.0	-3.10	-0.24	0.47

*Average over RPKM log₂-fold changes per transcript between leaf samples at stage W1.0-2.0, apex samples at W3.5 and apex samples at W0.5-W2.0, respectively.

Supplemental Table 3: GO-term enrichment for 3299 transcripts specifically upregulated at stamen primordium stage

GO-ID	GO-Term ¹	FDR	GO-ID	GO-Term ¹	FDR
GO:0015979	photosynthesis	1.95E-88	GO:0044724	single-organism carbohydrate catabolic process	1.76E-08
GO:0019684	photosynthesis, light reaction	1.79E-69	GO:0044723	single-organism carbohydrate metabolic process	2.66E-08
GO:0006091	generation of precursor metabolites and energy	1.94E-35	GO:0010218	response to far red light	2.66E-08
GO:0009765	photosynthesis, light harvesting	3.62E-32	GO:0035304	regulation of protein dephosphorylation	5.34E-08
GO:0055114	oxidation-reduction process	1.67E-26	GO:0008152	metabolic process	5.34E-08
GO:0009767	photosynthetic electron transport chain	2.92E-23	GO:0005996	monosaccharide metabolic process	5.77E-08
GO:0006740	NADPH regeneration	7.61E-20	GO:0006721	terpenoid metabolic process	6.00E-08
GO:0006098	pentose-phosphate shunt	2.55E-19	GO:0008654	phospholipid biosynthetic process	1.02E-07
GO:0006739	NADP metabolic process	1.24E-18	GO:0006007	glucose catabolic process	1.05E-07
GO:0019362	pyridine nucleotide metabolic process	2.37E-18	GO:0046365	monosaccharide catabolic process	1.05E-07
GO:0046496	nicotinamide nucleotide metabolic process	3.43E-18	GO:0019320	hexose catabolic process	1.05E-07
GO:0042440	pigment metabolic process	4.84E-18	GO:0019685	photosynthesis, dark reaction	1.62E-07
GO:0072524	pyridine-containing compound metabolic process	8.76E-17	GO:0010155	regulation of proton transport	1.69E-07
GO:0006733	oxidoreduction coenzyme metabolic process	4.20E-16	GO:0035303	regulation of dephosphorylation	4.78E-07
GO:0051186	cofactor metabolic process	9.48E-16	GO:0016114	terpenoid biosynthetic process	5.09E-07
GO:0019288	isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway	1.51E-15	GO:0005984	disaccharide metabolic process	8.95E-07
GO:0009240	isopentenyl diphosphate biosynthetic process	2.10E-15	GO:0019318	hexose metabolic process	1.34E-06
GO:0046490	isopentenyl diphosphate metabolic process	2.10E-15	GO:0016143	S-glycoside metabolic process	1.48E-06
GO:0019682	glyceraldehyde-3-phosphate metabolic process	2.10E-15	GO:0019760	glucosinolate metabolic process	1.48E-06
GO:0015994	chlorophyll metabolic process	2.54E-15	GO:0019757	glucosinolate metabolic process	1.48E-06
GO:0016116	carotenoid metabolic process	4.87E-15	GO:0009311	oligosaccharide metabolic process	1.51E-06
GO:0016108	tetraterpenoid metabolic process	4.87E-15	GO:0019253	reductive pentose-phosphate cycle	1.78E-06
GO:0018298	protein-chromophore linkage	5.75E-15	GO:0006118	electron transport	2.23E-06
GO:0046148	pigment biosynthetic process	6.57E-15	GO:0005982	starch metabolic process	3.13E-06
GO:0008299	isoprenoid biosynthetic process	1.61E-14	GO:0051667	establishment of plastid localization	7.53E-06
GO:0016117	carotenoid biosynthetic process	2.38E-14	GO:0009902	chloroplast relocation	7.53E-06
GO:0016109	tetraterpenoid biosynthetic process	2.38E-14	GO:0051644	plastid localization	1.00E-05
GO:0006778	porphyrin-containing compound metabolic process	5.30E-14	GO:0006006	glucose metabolic process	1.11E-05
GO:0033013	tetrapyrrole metabolic process	5.30E-14	GO:0006073	cellular glucan metabolic process	1.48E-05
GO:0022900	electron transport chain	7.40E-14	GO:0044042	glucan metabolic process	1.48E-05
GO:0006720	isoprenoid metabolic process	9.64E-14	GO:0044262	cellular carbohydrate metabolic process	1.61E-05
GO:0006090	pyruvate metabolic process	3.56E-13	GO:0009250	glucan biosynthetic process	1.74E-05
GO:0010207	photosystem II assembly	1.07E-12	GO:0032787	monocarboxylic acid metabolic process	1.88E-05
GO:0006081	cellular aldehyde metabolic process	2.53E-12	GO:0044802	single-organism membrane organization	4.26E-05
GO:0000023	maltose metabolic process	2.07E-11	GO:0008610	lipid biosynthetic process	4.43E-05
GO:0015995	chlorophyll biosynthetic process	5.89E-11	GO:0006766	vitamin metabolic process	5.58E-05
GO:0019252	starch biosynthetic process	1.09E-10	GO:0051188	cofactor biosynthetic process	6.98E-05
GO:0044710	single-organism metabolic process	1.42E-10	GO:0009617	response to bacterium	8.06E-05
GO:0005975	carbohydrate metabolic process	2.45E-10	GO:0016144	S-glycoside biosynthetic process	8.52E-05
GO:0009657	plastid organization	3.63E-10	GO:0019761	glucosinolate biosynthetic process	8.52E-05
GO:0006732	coenzyme metabolic process	3.81E-10	GO:0019758	glucosinolate biosynthetic process	8.52E-05
GO:0010114	response to red light	1.01E-09	GO:0006629	lipid metabolic process	1.03E-04
GO:0033014	tetrapyrrole biosynthetic process	1.15E-09	GO:0006805	xenobiotic metabolic process	1.44E-04
GO:0010027	thylakoid membrane organization	1.57E-09	GO:0071466	cellular response to xenobiotic stimulus	1.44E-04
GO:0009668	plastid membrane organization	1.57E-09	GO:0010109	regulation of photosynthesis	1.44E-04
GO:0006779	porphyrin-containing compound biosynthetic process	1.69E-09	GO:0051656	establishment of organelle localization	1.52E-04
GO:0009773	photosynthetic electron transport in photosystem I	2.78E-09	GO:0010304	PSII associated light-harvesting complex II catabolic process	1.70E-04
GO:0016556	mRNA modification	6.14E-09	GO:0006636	unsaturated fatty acid biosynthetic process	1.71E-04
GO:0009637	response to blue light	6.14E-09	GO:0042742	defense response to bacterium	1.93E-04
GO:0016052	carbohydrate catabolic process	1.47E-08			

(table continued on next page)

¹ Only GO-terms assigned to biological processes are shown

Supplemental Table 3: continued

GO-ID	GO-Term ¹	FDR	GO-ID	GO-Term ¹	FDR
(table continued from previous page)			GO:0043467	regulation of generation of precursor metabolites and energy	6.88E-03
GO:0006644	phospholipid metabolic process	2.13E-04	GO:0009314	response to radiation	6.97E-03
GO:0016051	carbohydrate biosynthetic process	2.18E-04	GO:0019748	secondary metabolic process	7.14E-03
GO:0044255	cellular lipid metabolic process	2.21E-04	GO:0030091	protein repair	7.22E-03
GO:0006787	porphyrin-containing compound catabolic process	3.62E-04	GO:0009772	photosynthetic electron transport in photosystem II	7.22E-03
GO:0033015	tetrapyrrole catabolic process	3.62E-04	GO:0010206	photosystem II repair	7.22E-03
GO:0051187	cofactor catabolic process	3.62E-04	GO:0033692	cellular polysaccharide biosynthetic process	7.31E-03
GO:0005976	polysaccharide metabolic process	3.62E-04	GO:0043647	inositol phosphate metabolic process	7.59E-03
GO:0042197	halogenated hydrocarbon metabolic process	3.85E-04	GO:0006124	ferredoxin metabolic process	7.60E-03
GO:0042196	chlorinated hydrocarbon metabolic process	3.85E-04	GO:0016072	rRNA metabolic process	7.77E-03
GO:0006790	sulfur compound metabolic process	4.26E-04	GO:0009070	serine family amino acid biosynthetic process	8.11E-03
GO:0009416	response to light stimulus	4.60E-04	GO:0006749	glutathione metabolic process	8.28E-03
GO:0006804	peroxidase reaction	4.80E-04	GO:0071496	cellular response to external stimulus	9.08E-03
GO:0009607	response to biotic stimulus	6.25E-04	GO:0031668	cellular response to extracellular stimulus	9.08E-03
GO:0061024	membrane organization	6.34E-04	GO:0010374	stomatal complex development	9.44E-03
GO:0019497	hexachlorocyclohexane metabolic process	6.35E-04	GO:0009744	response to sucrose stimulus	9.74E-03
GO:0015996	chlorophyll catabolic process	7.37E-04	GO:0034285	response to disaccharide stimulus	9.74E-03
GO:0046149	pigment catabolic process	7.37E-04	GO:0070887	cellular response to chemical stimulus	1.05E-02
GO:0000271	polysaccharide biosynthetic process	7.98E-04	GO:0071214	cellular response to abiotic stimulus	1.05E-02
GO:0044264	cellular polysaccharide metabolic process	7.98E-04	GO:1901659	glycosyl compound biosynthetic process	1.38E-02
GO:0080167	response to karrikin	8.85E-04	GO:0006534	cysteine metabolic process	1.47E-02
GO:0033559	unsaturated fatty acid metabolic process	9.63E-04	GO:0044272	sulfur compound biosynthetic process	1.52E-02
GO:0009410	response to xenobiotic stimulus	1.02E-03	GO:0050896	response to stimulus	1.64E-02
GO:0019637	organophosphate metabolic process	1.06E-03	GO:0051640	organelle localization	1.72E-02
GO:0051707	response to other organism	1.06E-03	GO:0006518	peptide metabolic process	1.99E-02
GO:0009414	response to water deprivation	1.08E-03	GO:0006818	hydrogen transport	2.02E-02
GO:0006803	glutathione conjugation reaction	1.60E-03	GO:0015992	proton transport	2.02E-02
GO:1901700	response to oxygen-containing compound	1.70E-03	GO:0009695	jasmonic acid biosynthetic process	2.08E-02
GO:0009658	chloroplast organization	1.78E-03	GO:0006952	defense response	2.16E-02
GO:0006979	response to oxidative stress	2.27E-03	GO:0046173	polyol biosynthetic process	2.37E-02
GO:0033517	myo-inositol hexakisphosphate metabolic process	2.41E-03	GO:0055080	cation homeostasis	2.42E-02
GO:0010264	myo-inositol hexakisphosphate biosynthetic process	2.41E-03	GO:0042631	cellular response to water deprivation	2.42E-02
GO:0006767	water-soluble vitamin metabolic process	2.42E-03	GO:0071462	cellular response to water stimulus	2.42E-02
GO:0006771	riboflavin metabolic process	2.42E-03	GO:0043269	regulation of ion transport	2.60E-02
GO:0042726	flavin-containing compound metabolic process	2.42E-03	GO:0042221	response to chemical stimulus	2.60E-02
GO:0034637	cellular carbohydrate biosynthetic process	2.56E-03	GO:0043155	negative regulation of photosynthesis, light reaction	2.68E-02
GO:0009639	response to red or far red light	2.88E-03	GO:0010205	photoinhibition	2.68E-02
GO:0009415	response to water stimulus	3.06E-03	GO:0042724	thiamine-containing compound biosynthetic process	3.17E-02
GO:0032958	inositol phosphate biosynthetic process	3.47E-03	GO:1990066	energy quenching	3.17E-02
GO:0009694	jasmonic acid metabolic process	3.56E-03	GO:0009228	thiamine biosynthetic process	3.17E-02
GO:0090407	organophosphate biosynthetic process	3.82E-03	GO:0010196	nonphotochemical quenching	3.17E-02
GO:0019725	cellular homeostasis	4.35E-03	GO:0006546	glycine catabolic process	3.20E-02
GO:0015977	carbon fixation	4.62E-03	GO:0009071	serine family amino acid catabolic process	3.20E-02
GO:0046487	glyoxylate metabolic process	4.62E-03	GO:0009743	response to carbohydrate stimulus	3.69E-02
GO:0044550	secondary metabolite biosynthetic process	4.67E-03	GO:0009814	defense response, incompatible interaction	4.32E-02
GO:0009628	response to abiotic stimulus	4.78E-03	GO:0006812	cation transport	4.43E-02
GO:0010103	stomatal complex morphogenesis	5.33E-03	GO:0030003	cellular cation homeostasis	4.51E-02
GO:0006364	rRNA processing	5.77E-03	GO:0006013	mannose metabolic process	4.52E-02
GO:0006950	response to stress	6.23E-03	GO:0006753	nucleoside phosphate metabolic process	4.60E-02
GO:0009991	response to extracellular stimulus	6.28E-03	GO:0009117	nucleotide metabolic process	4.74E-02
GO:0019344	cysteine biosynthetic process	6.31E-03	GO:0010258	NADH dehydrogenase complex (plastoquinone) assembly	4.74E-02
GO:0042548	regulation of photosynthesis, light reaction	6.88E-03			

¹Only GO-terms assigned to biological processes are shown

Supplemental Table 4: GO-term enrichment for 798 transcripts upregulated during floral transition

GO-ID	GO-Term ¹	FDR
GO:0045449	regulation of transcription, DNA-dependent	1.34E-03
GO:0044262	cellular carbohydrate metabolic process	5.25E-03
GO:0005985	sucrose metabolic process	5.25E-03
GO:0009725	response to hormone stimulus	8.60E-03
GO:0032870	cellular response to hormone stimulus	9.46E-03
GO:0071495	cellular response to endogenous stimulus	9.46E-03
GO:0006073	cellular glucan metabolic process	9.46E-03
GO:0044042	glucan metabolic process	9.46E-03
GO:0009719	response to endogenous stimulus	9.46E-03
GO:0005976	polysaccharide metabolic process	1.10E-02
GO:0044264	cellular polysaccharide metabolic process	1.10E-02
GO:0005975	carbohydrate metabolic process	1.14E-02
GO:0033993	response to lipid	1.14E-02
GO:0009556	microsporogenesis	1.33E-02
GO:0048236	plant-type spore development	1.33E-02
GO:0005982	starch metabolic process	1.33E-02
GO:0005984	disaccharide metabolic process	2.38E-02
GO:0071396	cellular response to lipid	2.72E-02
GO:0071310	cellular response to organic substance	2.98E-02
GO:0006075	(1->3)-beta-D-glucan biosynthetic process	2.98E-02
GO:0006074	(1->3)-beta-D-glucan metabolic process	2.98E-02
GO:0009624	response to nematode	3.34E-02
GO:0009311	oligosaccharide metabolic process	3.35E-02
GO:0010233	phloem transport	3.68E-02
GO:0010232	vascular transport	3.68E-02
GO:0010033	response to organic substance	3.81E-02
GO:0006355	regulation of transcription, DNA-dependent	4.65E-02
GO:0044723	single-organism carbohydrate metabolic process	4.90E-02

¹Only GO-terms assigned to biological processes are shown

Supplemental Table 5: GO-term enrichment for 1434 DETs commonly expressed during floral transition and at stamen primordium stage

GO-ID	GO-Term ¹	FDR	GO-ID	GO-Term ¹	FDR
GO:0045449	regulation of transcription, DNA-dependent	2.56E-08	GO:0009624	response to nematode	9.93E-03
GO:0071824	protein-DNA complex subunit organization	1.51E-05	GO:0042221	response to chemical stimulus	1.03E-02
GO:0065004	protein-DNA complex assembly	1.51E-05	GO:0005976	polysaccharide metabolic process	1.17E-02
GO:0031497	chromatin assembly	1.51E-05	GO:0005982	starch metabolic process	1.36E-02
GO:0006334	nucleosome assembly	1.54E-05	GO:0044264	cellular polysaccharide metabolic process	1.50E-02
GO:0034728	nucleosome organization	1.54E-05	GO:0009059	macromolecule biosynthetic process	1.66E-02
GO:0006323	DNA packaging	5.63E-05	GO:0034645	cellular macromolecule biosynthetic process	1.78E-02
GO:0006333	chromatin assembly or disassembly	1.59E-04	GO:0071704	organic substance metabolic process	1.99E-02
GO:0071103	DNA conformation change	8.83E-04	GO:0009058	biosynthetic process	2.00E-02
GO:0005985	sucrose metabolic process	1.27E-03	GO:0010582	floral meristem determinacy	2.01E-02
GO:0009725	response to hormone stimulus	1.29E-03	GO:0005984	disaccharide metabolic process	2.03E-02
GO:0009719	response to endogenous stimulus	1.29E-03	GO:0044249	cellular biosynthetic process	2.46E-02
GO:2001141	regulation of RNA biosynthetic process	3.22E-03	GO:0048509	regulation of meristem development	2.62E-02
GO:0043086	negative regulation of catalytic activity	3.88E-03	GO:0033993	response to lipid	3.19E-02
GO:0006073	cellular glucan metabolic process	3.95E-03	GO:0010073	meristem maintenance	3.19E-02
GO:0044042	glucan metabolic process	3.95E-03	GO:0010556	regulation of macromolecule biosynthetic process	3.19E-02
GO:0010022	meristem determinacy	3.95E-03	GO:2000112	regulation of cellular macromolecule biosynthetic process	3.19E-02
GO:0010077	maintenance of inflorescence meristem identity	6.69E-03	GO:0019219	regulation of nucleobase-containing compound metabolic process	3.52E-02
GO:0044262	cellular carbohydrate metabolic process	6.69E-03	GO:0032870	cellular response to hormone stimulus	3.68E-02
GO:0006355	regulation of transcription, DNA-dependent	6.69E-03	GO:0071495	cellular response to endogenous stimulus	3.68E-02
GO:0008152	metabolic process	8.82E-03	GO:0010033	response to organic substance	3.82E-02
GO:0042254	ribosome biogenesis	8.82E-03	GO:0009311	oligosaccharide metabolic process	3.82E-02
GO:1901576	organic substance biosynthetic process	8.82E-03	GO:1901700	response to oxygen-containing compound	3.82E-02
GO:0044092	negative regulation of molecular function	8.82E-03	GO:0031326	regulation of cellular biosynthetic process	3.82E-02
GO:0010076	maintenance of floral meristem identity	8.85E-03	GO:0051171	regulation of nitrogen compound metabolic process	3.82E-02
GO:0051252	regulation of RNA metabolic process	9.21E-03	GO:0034654	nucleobase-containing compound biosynthetic process	3.82E-02
GO:0032774	RNA biosynthetic process	9.76E-03	GO:0005975	carbohydrate metabolic process	4.12E-02
GO:0006351	transcription, DNA-dependent	9.76E-03	GO:0009889	regulation of biosynthetic process	4.20E-02
GO:0022613	ribonucleoprotein complex biogenesis	9.93E-03	GO:0071836	nectar secretion	4.20E-02
GO:0006412	translation	9.93E-03	GO:0042545	cell wall modification	4.74E-02

¹ Only GO-terms assigned to biological processes are shown

SupplementalTable 6: Selected* transcripts downregulated during MSA development independent of the photoperiod and genotype

Transcript	Reference Set ¹	Coexpression Cluster	logFC ²	Barley Gene Identifier	Arabidopsis Gene Model ³	Arabidopsis Gene Identifier	Description ⁴
Flowering, floral organ and meristem development							
Hv.110	Hv	21	-4.33	<i>BM1</i>	AT2G22540.1	<i>SVP</i>	Short vegetative phase
Hv.19680	Hv	21	-1.79	<i>BM10</i>			
Hv.15491	Hv	21	-2.61	<i>VRT2</i>			
Hv.8782	Hv	21	-1.60		AT2G30140.1	<i>UGT87A2</i>	UDP-Glucosyl transferase 87A2
MLOC_14596.3	sHC	29	-1.54		AT1G68640.1	<i>PAN</i>	Perianthia
contig_10845	DNC-T	29	-3.48		AT3G26120.1	<i>TEL1</i>	Terminal EAR1-like 1
MLOC_51836.1	sLC	29	-2.24				
MLOC_56117.1	sHC	29	-2.37		AT1G10120.1	<i>CIB4</i>	CRY2-interacting bHLH 4
Hv.35135	Hv	30	-3.64	<i>AP2-2L</i>	AT4G36920.2	<i>AP2</i>	Apetala 2
contig_22204	DNC-T	30	-6.11		AT4G33280.1		AP2/B3-like transcriptional factor
Hv.12609	Hv	30	-5.96		AT3G18990.1	<i>VRN1</i>	Reduced vernalization response 1
contig_3763	DNC-T	30	-6.25		AT3G23290.2	<i>LSH4</i>	Light sensitive
MLOC_10221.2	sHC	31	-1.03		AT4G37750.1	<i>ANT</i>	Aintegumenta
Hormones and signalling							
MLOC_52145.1	sHC	21	-5.25		AT2G41510.1	<i>CKX1</i>	Cytokinin oxidase/dehydrogenase
Hv.31348	Hv	29	-1.61		AT3G16500.1	<i>PAP1</i>	Phytochrome-associated protein 1
Hv.33734	Hv	30	-4.48		AT4G35390.1	<i>AGF1</i>	At-hook protein of GA feedback 1
Hv.11559	Hv	30	-3.46		AT1G02400	<i>ATGA2OX6</i>	Gibberellin-2-oxidase-6
Others							
Hv.12175	Hv	29	-2.83		AT3G04290.1	<i>LTL1</i>	Li-tolerant lipase 1
MLOC_44910.1	sHC	29	-1.31		AT2G39760.1	<i>BPM3</i>	BTB/POZ/MATH-domains containing protein
MLOC_14316.1	sHC	29	-2.22		AT4G09510.2	<i>CINV2</i>	Cytosolic invertase 2
contig_4243	DNC-T	30	-5.24		AT1G15910.1	<i>FDM1</i>	Factor of DNA methylation 1
MLOC_68447.1	sLC	30	-3.16		AT5G24280.1	<i>GMI1</i>	Gamma-irradiation and mitomycin c induced 1

*Transcripts represent the expression profiles of 154 DETs downregulated during MSA development independent of the

¹Set of reference transcripts:

²log₂ fold change of transcript abundance in shoot apices of S42-IL107 at W3.5 as compared to W0.5 under short-day conditions.

³Arabidopsis gene model (Best BLASTx hit)

⁴Annotation of Arabidopsis gene model (TAIR 10)

Supplemental Table 7: Coexpression clusters enriched for transcripts downregulated during MSA development independent of the photoperiod and genotype

Cluster ID	Cluster Size	Number of DETs in Cluster	Expected Number of DETs	Enrichment ¹
Cluster 30	55	31	1.11	27.83 ***
Cluster 29	319	46	6.46	7.12 ***
Cluster 21	141	12	2.86	4.20 ***
Cluster 31	716	24	14.50	1.66 *
Cluster 26	521	16	10.55	1.52
Cluster 22	260	9	5.27	1.71
Cluster 11	217	4	4.39	0.91
Cluster 28	333	6	6.74	0.89
Cluster 27	218	3	4.42	0.68
Cluster 12	345	2	6.99	0.29
Cluster 25	302	1	6.12	0.16
SUM		154		

¹Chi-squared test: *p<0.05, **p<0.01, ***p<0.001

Supplemental Table 8: Selected* transcripts upregulated during MSA development independent of the photoperiod and genotype

Transcript	Reference Set ¹	Coexpression Cluster	logFC ²	Barley Gene Identifier	Arabidopsis Gene Model ³	Arabidopsis Gene Identifier	Description ⁴
Flowering, floral organ and meristem development							
Hv.12878	Hv	16	3.13	<i>KN1</i>	AT4G08150.1	<i>BP1</i>	Brevipedicellus 1
Hv.20746	Hv	16	9.53	<i>AG1</i>	AT4G18960.1	<i>AG</i>	Agamous
Hv.11508	Hv	16	2.57		AT2G41370.1	<i>BOP2</i>	Blade on Petiole 2
Hv.16012	Hv	16	3.36		AT3G61880.2	<i>CYP78A9</i>	Cytochrome P450 78A9
MLOC_13032.1	sHC	16	6.02		AT1G53160.1	<i>SPL4</i>	Squamosa promoter binding protein-like 4
MLOC_65676.1	sHC	16	3.54		AT5G59810.1	<i>SBT5.4</i>	Serine-type endopeptidase activity
Hv.36753	Hv	11	4.79		AT4G29100.1	<i>EPFL6</i>	EPF1-like 6
Hv.11726	Hv	13	2.09		AT2G27230.2	<i>LHW</i>	Lonesome highway
Hv.8895	Hv	17	1.44		AT5G62100.2	<i>BAG2</i>	BCL2-associated athanogene 2
Hv.32892	Hv	18	1.55		AT4G29900.1	<i>ACA10</i>	Autoinhibited Ca(2+)-ATPase 10
MLOC_70653.1	sHC	24	1.33		AT4G00180.1	<i>YAB3</i>	Yabby 3
Hormones and signalling							
Hv.2397	Hv	16	5.51		AT1G17290.1	<i>ALAAT1</i>	Alanine aminotransferase
Hv.32781	Hv	16	3.34		AT4G11530.1	<i>CRK34</i>	Cysteine-rich RLK (receptor-like protein kinase) 34
Hv.15702	Hv	11	3.33		AT4G30960.1	<i>CIPK6</i>	CBL-interacting protein kinase 6
Hv.31377	Hv	14	5.60		AT1G48480.1	<i>RKL1</i>	Receptor-like kinase 1
Hv.32577	Hv	17	1.86		AT3G45860.1	<i>CRK4</i>	Cysteine-rich RLK (receptor-like protein kinase) 4
Hv.32275	Hv	18	4.75		AT1G05010.1	<i>EFE</i>	Ethylene forming enzyme
Carbohydrate metabolism							
Hv.8649	Hv	24	5.56		AT2G15480.2	<i>UGT73B5</i>	UDP-glucosyl transferase 73B5
Hv.10624	Hv	16	7.35		AT5G13170.1	<i>SWEET15</i>	Senescence-associated gene 29
Others							
MLOC_36809.2	sHC	18	2.31		AT1G06490.1	<i>CALS7</i>	Callose synthase 7
MLOC_50471.2	sLC	18	3.40		AT3G59100.1	<i>GSL11</i>	Glucan synthase-like 11
Hv.16527	Hv	16	2.57		AT1G12110.1	<i>NRT1.1</i>	Nitrate Transporter 1.1
Hv.10047	Hv	3	1.79		AT2G42005		Transmembrane amino acid transporter family protein

*Transcripts represent the expression profiles of 245 DETs upregulated during MSA development independent of the photoperiod and genotype

¹Set of reference transcripts: Hv: NCBI Barley UniGenes; sHC: selected Barley High Confidence Genes; sLC: selected Barley Low Confidence Genes; DNC-T: selected *de novo* contigs

²log₂ fold change of transcript abundance in shoot apices of S42-IL107 at W3.5 as compared to W0.5 under short-day conditions.

³Arabidopsis gene model (Best BLASTx hit)

⁴Annotation of Arabidopsis gene model (TAIR 10)

Supplemental Table 9: Coexpression clusters enriched for transcripts upregulated during MSA development independent of the photoperiod and genotype

Cluster ID	Cluster Size	Number of DETs in Cluster	Expected Number of DETs	Enrichment ¹
Cluster 24	139	23	4.48	5.14 ***
Cluster 16	210	21	6.77	3.10 ***
Cluster 17	568	34	18.30	1.86 ***
Cluster 11	217	17	6.99	2.43 **
Cluster 13	134	12	4.32	2.78 **
Cluster 14	105	10	3.38	2.96 **
Cluster 18	311	18	10.02	1.80 *
Cluster 19	454	22	14.63	1.50
Cluster 12	345	17	11.12	1.53
Cluster 15	361	17	11.63	1.46
Cluster 4	79	4	2.55	1.57
Cluster 20	38	2	1.22	1.63
Cluster 6	157	6	5.06	1.19
Cluster 23	414	14	13.34	1.05
Cluster 10	247	7	7.96	0.88
Cluster 2	40	1	1.29	0.78
Cluster 3	296	7	9.54	0.73
Cluster 1	180	4	5.80	0.69
Cluster 25	302	5	9.73	0.51
Cluster 8	125	2	4.03	0.50
Cluster 7	214	2	6.90	0.29
	SUM	245		

¹Chi-squared test: *p<0.05, **p<0.01, ***p<0.001

Supplemental Table 10: Coexpression clusters enriched for transcripts upregulated in leaves by long photoperiods and in S42-IL107

Cluster ID	Cluster Size	Number of DETs in Cluster	Expected Number of DETs	Enrichment ¹
Cluster 9	95	59	2.41	24.47 ***
Cluster 11	217	53	5.51	9.62 ***
Cluster 21	141	20	3.58	5.59 ***
Cluster 12	345	41	8.76	4.68 ***
Cluster 8	125	7	3.17	2.21 *
Cluster 5	10	1	0.25	3.94
Cluster 22	260	7	6.60	1.06
Cluster 3	296	2	7.51	0.27
Cluster 7	214	1	5.43	0.18
Cluster 10	247	1	6.27	0.16
Cluster 19	454	1	11.52	0.09
	SUM	193		

¹Chi-squared test: *p<0.05, **p<0.01, ***p<0.001

Supplemental Table 11: Selected* transcripts upregulated in leaves by long photoperiods and in S42-IL107

Transcript	Reference Set ¹	Coexpression Cluster	logFC ²	logFC ³	Barley Gene Identifier	Arabidopsis Gene Model ⁴	Arabidopsis Gene Identifier	Description ⁵
Flowering, light response								
Hv.34809	Hv	9	3.15	3.99	<i>FT1</i>	AT1G65480.1	<i>FT</i>	Flow ering locus T
MLOC_6921.1	sHC	9	1.24	4.68	<i>CO1</i>	AT5G15850.1	<i>COL1</i>	CONSTANS-like 1
Hv.29120	Hv	9	0.45	3.29		AT4G38180.1	<i>FRS5</i>	FAR1-related sequence 5
Hv.37168	Hv	9	1.27	1.01		AT3G04030.3	<i>MYR2</i>	Homeodomain-like superfamily protein
MLOC_75496.6	sHC	11	1.38	1.93	<i>CO2</i>	AT3G02380.1	<i>COL2</i>	CONSTANS-like 2
Hv.18604	Hv	11	0.46	3.19		AT5G48250.1	<i>BBX8</i>	B-box type zinc finger protein with CCT domain
MLOC_51314.1	sHC	11				AT3G07500.1		Far-red impaired responsive (FAR1) family protein
contig_38668	DNC-T	11	0.67	0.50				
			0.63	1.02		AT1G53090.2	<i>SPA4</i>	SPA1-related 4
Disease resistance								
Hv.10174	Hv	9	0.69	0.83				
MLOC_66826.2	sLC	9	0.48	1.77		AT5G20480.1	<i>EFR</i>	EF-TU receptor
Hv.10217	Hv	9				AT2G34930.1		Disease resistance family protein / LRR family protein
Hv.30969	Hv	9	0.50	0.76				
			0.68	0.76		AT2G37710.1	<i>RLK</i>	Receptor lectin kinase
MLOC_66610.1	sHC	9	0.66	0.88				LRR and NB-ARC domains containing disease resistance protein
contig_388521	DNC-T	9				AT3G14460.1		
			0.66	1.18				
MLOC_1192.1	sHC	9				AT3G07040.1	<i>RPM1</i>	Resistance to <i>P. syringae</i> pv. <i>maculicola</i> 1
			0.74	1.05				
MLOC_14723.1	sLC	9				AT3G46730.1		NB-ARC domain-containing disease resistance protein
			0.55	1.19				
contig_385738	DNC-T	9	0.74	0.92		AT5G46330.1	<i>FLS2</i>	Flagellin-sensitive 2
contig_385733	DNC-T	9	0.60	0.87		AT1G47890.1	<i>RLP7</i>	Receptor like protein 7

(table continued on next page)

*Transcripts represent the expression profiles of 193 DETs upregulated in a *Ppd-H1* dependent manner in leaves¹Set of reference transcripts: Hv: NCBI Barley UniGenes; sHC: selected Barley High Confidence Genes; sLC: selected Barley Low Confidence Genes; DNC-T: selected *de novo* contigs²Arabidopsis gene model (Best BLASTx hit)³log₂-fold change of transcript abundance in leaves of S42-IL107 as compared to Scarlett across the developmental stages W1.0 and W2.0 under long-day conditions⁴log₂-fold change of transcript abundance comparing leaves of S42-IL107 under long and short photoperiods across the developmental stages W1.0 and W2.0⁵Annotation of Arabidopsis gene model (TAIR 10)

Supplemental Table 11: continued

Transcript	Reference Set ¹	Coexpression Cluster	logFC ²	logFC ³	Barley Gene Identifier	Arabidopsis Gene Model ⁴	Arabidopsis Gene Identifier	Description ⁵
(table continued from previous page)								
Transport								
Hv.8671	Hv	9	0.46	1.97	YS1	AT5G53550.2	YSL3	YELLOW STRIPE-like 3
Hv.8787	Hv	12	0.51	0.96		AT3G27020.1	YSL6	YELLOW STRIPE-like 6
Hv.23326	Hv	12	0.56	1.73		AT1G65730.1	YSL7	YELLOW STRIPE-like 7
Hv.35529	Hv	9	1.92	2.26		AT1G05300.1	ZIP5	Zinc transporter 5 precursor
Hv.10430	Hv	9	0.21	1.06		AT2G16120.1	PMT1	Polyol/monosaccharide transporter 1
MLOC_10758.2	sHC	9	1.36	2.03		AT4G13420.1	HAK5	High affinity K ⁺ transporter 5
Hv.22725	Hv	11	0.58	0.78		AT1G15520.1	PDR12	Pleiotropic drug resistance 12
Hv.27044	Hv	11	0.49	1.26		AT1G64890.1		Major facilitator superfamily protein
Hv.19083	Hv	11	0.38	0.79		AT2G38410.1		ENTH/VHS/GAT family protein
Hv.4917	Hv	12	0.52	0.82		AT1G70300.1	KUP6	K ⁺ uptake permease 6
Cell differentiation, floral organ development								
Hv.34198	Hv	9	0.74	1.43		AT1G54510.3	NEK1	NIMA-related serine/threonine kinase 1
contig_144168	DNC-T	9	0.77	0.97		AT3G11980.1	MS2	Male sterility 2
contig_332463	DNC-T	9	1.29	1.61		AT3G02000.1	ROXY1	Thioredoxin superfamily protein
MLOC_6537.1	sHC	11	0.33	1.16		AT5G49660.1	XIP1	Xylem intermixed with phloem 1
MLOC_43403.1	sHC	11	0.62	2.30		AT2G03140.2		Alpha/beta-Hydrolases superfamily protein

*Transcripts represent the expression profiles of 193 DETs upregulated in a *Ppd-H1* dependent manner in leaves

¹Set of reference transcripts: Hv: NCBI Barley UniGenes; sHC: selected Barley High Confidence Genes; sLC: selected Barley Low Confidence Genes; DNC-T: selected *de novo* contigs

²Arabidopsis gene model (Best BLASTx hit)

³log₂-fold change of transcript abundance in leaves of S42-IL107 as compared to Scarlett across the developmental stages W1.0 and W2.0 under long-day conditions

⁴log₂-fold change of transcript abundance comparing leaves of S42-IL107 under long and short photoperiods across the developmental stages W1.0 and W2.0

⁵Annotation of Arabidopsis gene model (TAIR 10)

Supplemental Table 12: GO-term enrichment of transcripts in coexpression clusters 9, 11 and 12

GO-ID	GO-Term¹	FDR
GO:0055085	transmembrane transport	2.06E-05
GO:0046373	L-arabinose metabolic process	1.28E-02
GO:0009624	response to nematode	3.66E-02

¹Only GO-terms assigned to biological processes are shown

Supplemental Table 13: GO-term enrichment for 1205 transcripts downregulated in leaves by long photoperiods and in S42-IL107

GO-ID	GO-Term ¹	FDR	GO-ID	GO-Term ¹	FDR
GO:0006334	nucleosome assembly	3.08E-28	(table continued from previous page)		
GO:0034728	nucleosome organization	3.08E-28	GO:0048367	shoot system development	3.67E-03
GO:0071824	protein-DNA complex subunit organization	1.16E-27	GO:0005976	polysaccharide metabolic process	4.32E-03
GO:0065004	protein-DNA complex assembly	1.16E-27	GO:0006073	cellular glucan metabolic process	4.83E-03
GO:0031497	chromatin assembly	1.16E-27	GO:0044042	glucan metabolic process	4.83E-03
GO:0006333	chromatin assembly or disassembly	1.64E-26	GO:0048731	system development	5.11E-03
GO:0071103	DNA conformation change	2.10E-26	GO:0010073	meristem maintenance	7.31E-03
GO:0006323	DNA packaging	2.10E-26	GO:0048856	anatomical structure development	1.21E-02
GO:0006325	chromatin organization	1.64E-18	GO:0005975	carbohydrate metabolic process	1.39E-02
GO:0051276	chromosome organization	7.59E-14	GO:0032502	developmental process	1.57E-02
GO:0034622	cellular macromolecular complex assembly	7.75E-11	GO:0009734	auxin mediated signaling pathway	1.57E-02
GO:0006259	DNA metabolic process	2.78E-10	GO:0043170	macromolecule metabolic process	1.61E-02
GO:0065003	macromolecular complex assembly	6.89E-10	GO:0043481	anthocyanin accumulation in tissues in response to UV light	1.61E-02
GO:0043933	macromolecular complex subunit organization	1.00E-08	GO:0043480	pigment accumulation in tissues	1.61E-02
GO:0008283	cell proliferation	4.40E-08	GO:0043479	pigment accumulation in tissues in response to UV light	1.61E-02
GO:0048466	androecium development	7.22E-08	GO:0043478	pigment accumulation in response to UV light	1.61E-02
GO:0048443	stamen development	7.22E-08	GO:0043476	pigment accumulation	1.61E-02
GO:0022607	cellular component assembly	2.35E-07	GO:0043473	pigmentation	1.61E-02
GO:0010315	auxin efflux	1.49E-05	GO:0044085	cellular component biogenesis	1.68E-02
GO:0006996	organelle organization	4.43E-05	GO:0071840	cellular component organization or biogenesis	1.68E-02
GO:0048437	floral organ development	4.68E-05	GO:0005984	disaccharide metabolic process	1.70E-02
GO:0048513	organ development	5.20E-05	GO:0071365	cellular response to auxin stimulus	1.82E-02
GO:0016043	cellular component organization	7.06E-05	GO:0006139	nucleobase-containing compound metabolic process	2.06E-02
GO:0008356	asymmetric cell division	8.55E-05	GO:0044262	cellular carbohydrate metabolic process	2.27E-02
GO:0048827	phyllome development	8.63E-05	GO:0044260	cellular macromolecule metabolic process	2.64E-02
GO:0048438	floral whorl development	1.14E-04	GO:0009311	oligosaccharide metabolic process	2.64E-02
GO:0090304	nucleic acid metabolic process	1.34E-04	GO:0044264	cellular polysaccharide metabolic process	2.78E-02
GO:0048569	post-embryonic organ development	3.22E-04	GO:0009926	auxin polar transport	3.10E-02
GO:0009908	flower development	5.99E-04	GO:0051322	anaphase	3.41E-02
GO:0010541	acropetal auxin transport	5.99E-04	GO:0007275	multicellular organismal development	3.63E-02
GO:0044699	single-organism process	7.97E-04	GO:0005982	starch metabolic process	3.63E-02
GO:0044767	single-organism developmental process	1.00E-03	GO:0007010	cytoskeleton organization	3.72E-02
GO:0005985	sucrose metabolic process	1.15E-03	GO:2001141	regulation of RNA biosynthetic process	3.75E-02
GO:0060918	auxin transport	1.75E-03	GO:0006355	regulation of transcription, DNA-dependent	3.75E-02
GO:0009914	hormone transport	1.75E-03	GO:0009733	response to auxin stimulus	3.88E-02
GO:0051301	cell division	1.77E-03	GO:0000911	cytokinesis by cell plate formation	4.43E-02
GO:0010540	basipetal auxin transport	1.87E-03	GO:0000279	M phase	4.65E-02
GO:0009958	positive gravitropism	1.87E-03			

¹Only GO-terms assigned to biological processes are shown

Supplemental Table 14: Selected* transcripts upregulated in shoot apices by long photoperiods and in S42-IL107

Transcript	Reference Set ¹	Coexpression Cluster	logFC ²	logFC ³	Barley Gene Identifier	Arabidopsis Gene Model ⁴	Arabidopsis Gene Identifier	Description ⁵
Flowering, floral organ and meristem development								
Hv.17528	Hv	16	1.72	2.70	<i>FT2</i>	AT1G65480.1	<i>FT</i>	Flowering locus T
Hv.169	Hv	16	0.81	0.74	<i>BM8</i>	AT1G69120.1	<i>AP1</i>	Apetala 1
Hv.4298	Hv	24	0.38	0.54	<i>BM3</i>			
MLOC_44160.1	sHC	29	1.65	2.45	<i>CEN</i>	AT2G27550.1	<i>ATC</i>	Centroradialis
Hv.20726	Hv	16	0.62	1.50		AT3G54340.1	<i>AP3</i>	Apetala 3
MLOC_57803.3	sLC	16	0.19	0.34		AT5G15800.1	<i>Sep 01</i>	Sepallata 1
Hv.29973	Hv	16	0.09	0.43		AT1G24260.1	<i>Sep 03</i>	Sepallata 3
Hv.20696	Hv	16	0.26	0.69		AT5G20240.1	<i>PI</i>	Pistillata
Hv.15352	Hv	16	0.40	1.20		AT5G65700.2	<i>BAM1</i>	Barely any meristem 1
MLOC_68900.1	sHC	16	0.86	1.00		AT2G26170.1	<i>MAX1</i>	More axillary branches 1
Hv.12185	Hv	16	1.00	2.53		AT1G69780.1	<i>HB13</i>	Homeobox-leucine zipper protein family
Hv.18425	Hv	11	1.17	1.42		AT2G46680.1	<i>HB7</i>	Homeobox domain 7
Hv.15611	Hv	15	1.10	1.79		AT2G38090.1		Duplicated homeodomain-like superfamily protein
Hormone signalling								
Hv.21105	Hv	10	1.68	2.30	<i>GA20ox1</i>	AT4G25420.1	<i>GA20ox1</i>	Gibberellin 20-oxidase 1
Hv.23094	Hv	21	1.03	2.06		AT3G19000.1		2-oxoglutarate and Fe(II)-dependent oxygenase superfamily protein
Hv.5860	Hv	16	0.65	1.15		AT1G75500.1	<i>WAT1</i>	Walls are thin 1
Hv.821	Hv	3	0.01	0.32		AT4G14550.1	<i>IAA14</i>	Indole-3-acetic acid inducible 14
Hv.6142	Hv	18	0.57	1.2		AT1G51950.1	<i>IAA18</i>	Indole-3-acetic acid inducible 18
Hv.11413	Hv	12	0.31	0.57		AT2G38120.1	<i>AUX1</i>	Auxin resistant 1
Hv.11504	Hv	23	0.63	0.53		AT2G39540.1		Gibberellin-regulated family protein
Hv.17614	Hv	23	0.56	0.75		AT4G30610.1	<i>BRS1</i>	BR1 supressor 1
Hv.3674	Hv	27	0.27	0.66		AT1G61870.1	<i>PPR336</i>	Pentatricopeptide repeat 336
Metabolism								
Hv.15994	Hv	14	0.13	1.12		AT1G09610.1	<i>GXM3</i>	Glucuronoxylan methyltransferase 3
Hv.10982	Hv	14	1.00	0.81		AT1G08650.1	<i>PPCK1</i>	Phosphoenolpyruvate carboxylase kinase 1
Hv.18832	Hv	14	1.21	1.07		AT2G01770.1	<i>VIT1</i>	Vacuolar iron transporter 1
Hv.15635	Hv	16	0.58	0.98		AT3G48360.1	<i>BT2</i>	BTB and TAZ domain protein 2
MLOC_62899.1	sLC	16	0.55	2.54		AT2G18950.1	<i>HPT1</i>	Homogentisate phytyltransferase 1
Hv.354	Hv	16	0.45	1.70		AT1G21680.1		DPP6 N-terminal domain-like protein
Hv.15809	Hv	16	0.22	0.86		AT1G22440.1		Zinc-binding alcohol dehydrogenase family protein
contig_287828	DNC-T	16	2.45	3.67		AT3G26380.1		Melibiase family protein
Hv.9784	Hv	16	3.06	2.40				
Hv.4237	Hv	21	0.49	1.42		AT4G34230.1	<i>CAD5</i>	Cinnamyl alcohol dehydrogenase 5
Hv.8796	Hv	21	0.75	1.75		AT1G19600.1		pfkB-like carbohydrate kinase family protein
MLOC_74713.2	sHC	21	0.87	1.92				
Hv.24746	Hv	22	0.32	0.70		AT1G62640.2	<i>KASIII</i>	3-ketoacyl-acyl carrier protein synthase III

(table continued on next page)

Supplemental Table 14: continued

Transcript	Reference Set ¹	Coexpression Cluster	logFC ²	logFC ³	Barley Gene Identifier	Arabidopsis Gene Model ⁴	Arabidopsis Gene Identifier	Description ⁵
(table continued from previous page)								
Metabolism								
Hv.3916	Hv	22	0.27	0.71		AT1G30120.1		Pyruvate dehydrogenase E1 beta
Hv.6110	Hv	22	0.38	0.95		AT1G63000.1	<i>UER1</i>	Nucleotide-rhamnose synthase/epimerase-reductase
Hv.16152	Hv	23	1.07	1.46		AT3G23510.1		Cyclopropane-fatty-acyl-phospholipid synthase
Hv.20490	Hv	23	2.35	2.02		AT1G19715.3		Mannose-binding lectin superfamily protein
MLOC_24654.2	sHC	23	2.84	1.63				
contig_63792	DNC-T	23	3.60	1.73				
Hv.12805	Hv	27	0.29	0.48		AT3G18080.1	<i>BGLU44</i>	B-S glucosidase 44
Disease resistance								
Hv.11447	Hv	16	0.57	1.23		AT3G50930.1	<i>BCS1</i>	Cytochrome BC1 synthesis
Hv.17743	Hv	16	0.34	0.51		AT1G19250.1	<i>FMO1</i>	Flavin-dependent monooxygenase 1
contig_125109	DNC-T	16	1.26	2.67		AT5G25930.1		LRR receptor-like protein kinase family protein
contig_80125	DNC-T	16	1.66	2.39				
Hv.10484	Hv	23	1.63	1.95		AT3G22400.1	<i>LOX5</i>	Lipoxygenase 5
Chromatin modification, nucleosome assembly								
Hv.11786	Hv	31	0.29	0.91		AT5G58230.1	<i>MSI1</i>	Multicopy suppressor of IRA1
MLOC_71372.1	sHC	31	0.29	0.67		AT2G31270.1	<i>CDT1</i>	Homolog of yeast CDT1 A
Hv.15834	Hv	31	0.52	1.10		AT5G02560.1	<i>HTA12</i>	Histone H2A 12
MLOC_43244.1	sHC	31	0.59	1.04				
Hv.29208	Hv	23	0.38	0.57		AT5G22880.1	<i>H2B</i>	Histone B2
Hv.32211	Hv	31	0.38	1.03				
Hv.32725	Hv	31	0.38	0.90				
MLOC_75262.1	sLC	31	0.31	0.72				
MLOC_6467.1	sLC	23	0.77	1.32		AT5G59870.1	<i>HTA6</i>	Histone H2A 6
Hv.24307	Hv	31	0.38	0.78				
Hv.26391	Hv	31	0.32	0.83				
Hv.31863	Hv	31	0.33	0.84				
MLOC_37489.1	sLC	31	0.45	1.28		AT5G59970.1		Histone superfamily protein
Hv.22959	Hv	31	0.33	0.93				
Hv.26322	Hv	31	0.28	0.66				
Hv.31856	Hv	31	0.37	0.87				
Hv.32004	Hv	31	0.42	1.00				
Hv.32904	Hv	31	0.35	0.72				
MLOC_9919.1	sLC	31	0.35	0.76				
Hv.26128	Hv	23	0.36	0.78				
Hv.34411	Hv	27	0.43	0.74				

*Transcripts represent the expression profiles of 266 DETs upregulated in a *Ppd-H1* dependent manner in shoot apices

¹Set of reference transcripts: Hv: NCBI Barley UniGenes; sHC: selected Barley High Confidence Genes; sLC: selected Barley Low Confidence Genes; DNC-T: selected *de novo* contigs

²Arabidopsis gene model (Best BLASTx hit)

³log₂-fold change of transcript abundance in shoot apices of S42-IL107 as compared to Scarlett across the developmental stages W1.0-W3.5 under long-day conditions

⁴log₂-fold change of transcript abundance comparing shoot apices of S42-IL107 under long and short photoperiods across the developmental stages W1.0-W3.5

⁵Annotation of Arabidopsis gene model (TAIR 10)

Supplemental Table 15: Coexpression clusters enriched for transcripts upregulated in shoot apices by long photoperiods and in S42-IL107

Cluster ID	Cluster Size	Number of DETs in Cluster	Expected Number of DETs	Enrichment ¹
Cluster 16	210	39	7.35	5.31 ***
Cluster 21	141	17	4.93	3.45 ***
Cluster 22	260	23	9.10	2.53 ***
Cluster 31	716	43	25.05	1.72 ***
Cluster 20	38	6	1.33	4.51 **
Cluster 14	105	11	3.67	2.99 **
Cluster 23	414	26	14.48	1.80 **
Cluster 27	218	15	7.63	1.97 *
Cluster 29	319	15	11.16	1.34
Cluster 30	55	2	1.92	1.04
Cluster 11	217	7	7.59	0.92
Cluster 28	333	10	11.65	0.86
Cluster 12	345	9	12.07	0.75
Cluster 2	40	1	1.40	0.71
Cluster 26	521	12	18.23	0.66
Cluster 24	139	3	4.86	0.62
Cluster 15	361	7	12.63	0.55
Cluster 3	296	5	10.35	0.48
Cluster 10	247	4	8.64	0.46
Cluster 18	311	3	10.88	0.28
Cluster 17	568	5	19.87	0.25
Cluster 13	134	1	4.69	0.21
Cluster 1	180	1	6.30	0.16
Cluster 19	454	1	15.88	0.06
	SUM	266		

¹Chi-squared test: *p<0.05, **p<0.01, ***p<0.001

Supplemental Table 16: GO-term enrichment for transcripts in coexpression cluster 16

GO-ID	GO-Term ¹	FDR	GO-ID	GO-Term ¹	FDR
GO:0045449	regulation of transcription, DNA-dependent	3E-10	GO:0065007	biological regulation	4.25E-03
GO:0006355	regulation of transcription, DNA-dependent	9.4E-07	GO:0048507	meristem development	4.87E-03
GO:0048466	androecium development	1.1E-06	GO:0048509	regulation of meristem development	5.33E-03
GO:0048443	stamen development	1.1E-06	GO:0048569	post-embryonic organ development	6.85E-03
GO:2001141	regulation of RNA biosynthetic process	1.3E-06	GO:0019438	aromatic compound biosynthetic process	1.03E-02
GO:0051252	regulation of RNA metabolic process	1.3E-06	GO:0018130	heterocycle biosynthetic process	1.03E-02
GO:0051171	regulation of nitrogen compound metabolic process	1.1E-05	GO:0010321	regulation of vegetative phase change	1.14E-02
GO:0019219	regulation of nucleobase-containing compound metabolic process	2.4E-05	GO:0048827	phyllome development	1.54E-02
GO:0010556	regulation of macromolecule biosynthetic process	2.4E-05	GO:0061458	reproductive system development	1.94E-02
GO:2000112	regulation of cellular macromolecule biosynthetic process	2.4E-05	GO:0048608	reproductive structure development	1.94E-02
GO:0032774	RNA biosynthetic process	2.7E-05	GO:0046351	disaccharide biosynthetic process	2.05E-02
GO:0006351	transcription, DNA-dependent	2.7E-05	GO:0009059	macromolecule biosynthetic process	2.37E-02
GO:0031326	regulation of cellular biosynthetic process	3.1E-05	GO:0050793	regulation of developmental process	2.48E-02
GO:0009889	regulation of biosynthetic process	4.2E-05	GO:0016070	RNA metabolic process	2.64E-02
GO:0019222	regulation of metabolic process	4.8E-05	GO:0000024	maltose biosynthetic process	2.66E-02
GO:0010073	meristem maintenance	9.1E-05	GO:0048497	maintenance of floral organ identity	2.66E-02
GO:0010468	regulation of gene expression	0.00012	GO:0048496	maintenance of organ identity	2.66E-02
GO:0031323	regulation of cellular metabolic process	0.00016	GO:0045595	regulation of cell differentiation	2.81E-02
GO:0080090	regulation of primary metabolic process	0.0003	GO:0048653	anther development	3.41E-02
GO:0034654	nucleobase-containing compound biosynthetic process	0.00039	GO:1901362	organic cyclic compound biosynthetic process	3.44E-02
GO:0009908	flower development	0.00064	GO:0009312	oligosaccharide biosynthetic process	3.65E-02
GO:0048437	floral organ development	0.0007	GO:0010075	regulation of meristem growth	3.96E-02
GO:0060255	regulation of macromolecule metabolic process	0.00096	GO:0044767	single-organism developmental process	4.13E-02
GO:0048367	shoot system development	0.00182	GO:0048833	specification of floral organ number	4.70E-02
GO:0044271	cellular nitrogen compound biosynthetic process	0.00218	GO:0005983	starch catabolic process	4.70E-02
GO:0048438	floral whorl development	0.00264	GO:0043086	negative regulation of catalytic activity	4.70E-02
GO:0045596	negative regulation of cell differentiation	0.0028	GO:0035266	meristem growth	4.70E-02
GO:0050789	regulation of biological process	0.00306			

¹Only GO-terms assigned to biological processes are shown

Supplemental Table 17: GO-term enrichment for transcripts in coexpression cluster 31

GO-ID	GO-Term ¹	FDR	GO-ID	GO-Term ¹	FDR
GO:0006259	DNA metabolic process	1.34E-55	GO:0071840	cellular component organization or biogenesis	2.73E-12
GO:0051276	chromosome organization	2.77E-45	GO:0046483	heterocycle metabolic process	3.24E-12
GO:0071103	DNA conformation change	1.56E-40	GO:0006725	cellular aromatic compound metabolic process	3.76E-12
GO:0006325	chromatin organization	1.56E-40	GO:0016568	chromatin modification	3.92E-12
GO:0031497	chromatin assembly	6.31E-36	GO:0034641	cellular nitrogen compound metabolic process	5.96E-12
GO:0006323	DNA packaging	2.94E-35	GO:0006974	response to DNA damage stimulus	8.76E-12
GO:0008283	cell proliferation	2.94E-35	GO:0044260	cellular macromolecule metabolic process	1.44E-11
GO:0071824	protein-DNA complex subunit organization	5.80E-35	GO:1901360	organic cyclic compound metabolic process	1.46E-10
GO:0065004	protein-DNA complex assembly	5.80E-35	GO:0044772	mitotic cell cycle phase transition	2.29E-10
GO:0006333	chromatin assembly or disassembly	3.83E-34	GO:0044770	cell cycle phase transition	2.29E-10
GO:0006334	nucleosome assembly	8.37E-34	GO:0000086	G2/M transition of mitotic cell cycle	2.52E-10
GO:0034728	nucleosome organization	8.37E-34	GO:0000281	mitotic cytokinesis	4.55E-10
GO:0007049	cell cycle	3.86E-29	GO:1902410	mitotic cytokinetic process	4.55E-10
GO:0006996	organelle organization	3.97E-27	GO:0000911	cytokinesis by cell plate formation	4.55E-10
GO:0090304	nucleic acid metabolic process	9.00E-25	GO:0006281	DNA repair	5.76E-10
GO:0006260	DNA replication	1.64E-24	GO:1901990	regulation of mitotic cell cycle phase transition	8.78E-10
GO:0022402	cell cycle process	4.30E-24	GO:1901987	regulation of cell cycle phase transition	8.78E-10
GO:0006261	DNA-dependent DNA replication	7.96E-20	GO:0032506	cytokinetic process	1.10E-09
GO:0051301	cell division	3.44E-19	GO:0043170	macromolecule metabolic process	1.10E-09
GO:0016043	cellular component organization	2.02E-18	GO:0006807	nitrogen compound metabolic process	1.24E-09
GO:0051567	histone H3-K9 methylation	1.00E-17	GO:0000003	reproduction	1.49E-09
GO:0006139	nucleobase-containing compound metabolic process	4.86E-17	GO:0043414	macromolecule methylation	1.54E-09
GO:0022607	cellular component assembly	1.06E-16	GO:0010389	regulation of G2/M transition of mitotic cell cycle	1.96E-09
GO:0044728	DNA methylation or demethylation	2.39E-16	GO:0007018	microtubule-based movement	6.62E-09
GO:0006304	DNA modification	2.39E-16	GO:0007010	cytoskeleton organization	8.64E-09
GO:0006306	DNA methylation	1.52E-15	GO:0042127	regulation of cell proliferation	1.19E-08
GO:0006305	DNA alkylation	1.52E-15	GO:0019219	regulation of nucleobase-containing compound metabolic process	1.24E-08
GO:0051052	regulation of DNA metabolic process	1.86E-15	GO:0060255	regulation of macromolecule metabolic process	1.54E-08
GO:0065003	macromolecular complex assembly	2.12E-15	GO:0010564	regulation of cell cycle process	1.54E-08
GO:0000910	cytokinesis	5.41E-15	GO:0000226	microtubule cytoskeleton organization	1.92E-08
GO:0043933	macromolecular complex subunit organization	6.13E-15	GO:0051171	regulation of nitrogen compound metabolic process	2.52E-08
GO:0034622	cellular macromolecular complex assembly	6.38E-15	GO:0006928	cellular component movement	3.35E-08
GO:0034968	histone lysine methylation	7.43E-15	GO:0009908	flower development	9.03E-08
GO:0044763	single-organism cellular process	8.25E-15	GO:0051322	anaphase	9.94E-08
GO:0044699	single-organism process	1.15E-14	GO:0007346	regulation of mitotic cell cycle	1.45E-07
GO:0007017	microtubule-based process	3.08E-14	GO:0070192	chromosome organization involved in meiosis	1.70E-07
GO:0006461	protein complex assembly	3.26E-14	GO:0000279	M phase	2.54E-07
GO:0070271	protein complex biogenesis	3.47E-14	GO:0006342	chromatin silencing	3.90E-07
GO:0016570	histone modification	4.80E-14	GO:0045814	negative regulation of gene expression, epigenetic	3.90E-07
GO:0006270	DNA replication initiation	4.89E-14	GO:0048437	floral organ development	5.46E-07
GO:0016571	histone methylation	7.77E-14	GO:0007129	synapsis	5.61E-07
GO:0071822	protein complex subunit organization	8.80E-14	GO:0050794	regulation of cellular process	7.22E-07
GO:0000278	mitotic cell cycle	1.23E-13	GO:0044085	cellular component biogenesis	7.93E-07
GO:0051726	regulation of cell cycle	1.55E-13	GO:0051321	meiotic cell cycle	1.20E-06
GO:0016569	covalent chromatin modification	2.21E-13	GO:0080090	regulation of primary metabolic process	1.32E-06
GO:0006275	regulation of DNA replication	2.35E-13	GO:0019222	regulation of metabolic process	1.32E-06
GO:0006479	protein methylation	5.13E-13	GO:0048466	androecium development	1.81E-06
GO:0008213	protein alkylation	5.13E-13	GO:0048443	stamen development	1.81E-06
GO:0040029	regulation of gene expression, epigenetic	2.47E-12			

(table continued on next page)¹Only GO-terms assigned to biological processes are shown

Supplemental Table 17: continued

GO-ID	GO-Term ¹	FDR	GO-ID	GO-Term ¹	FDR
(table continued from previous page)			GO:0010332	response to gamma radiation	0.00011
GO:0048443	stamen development	1.81E-06	GO:0009059	macromolecule biosynthetic process	0.00012
GO:0061458	reproductive system development	2.39E-06	GO:0048827	phyllome development	0.00012
GO:0048608	reproductive structure development	2.39E-06	GO:0034645	cellular macromolecule biosynthetic process	0.00012
GO:0048569	post-embryonic organ development	2.91E-06	GO:0010605	negative regulation of macromolecule metabolic process	0.00013
GO:0016458	gene silencing	3.28E-06	GO:0044767	single-organism developmental process	0.00014
GO:0050789	regulation of biological process	4.5E-06	GO:0009892	negative regulation of metabolic process	0.00014
GO:0031323	regulation of cellular metabolic process	5.1E-06	GO:0009791	post-embryonic development	0.00018
GO:0007126	meiosis	5.7E-06	GO:0007131	reciprocal meiotic recombination	0.00018
GO:0048438	floral whorl development	6E-06	GO:0035825	reciprocal DNA recombination	0.00018
GO:0022414	reproductive process	7.4E-06	GO:0032508	DNA duplex unwinding	0.00033
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	7.9E-06	GO:0006355	regulation of transcription, DNA-dependent	0.00035
GO:0051172	negative regulation of nitrogen compound metabolic process	7.9E-06	GO:0016444	somatic cell DNA recombination	0.00041
GO:0048367	shoot system development	8.7E-06	GO:0051252	regulation of RNA metabolic process	0.00042
GO:0006302	double-strand break repair	1E-05	GO:0009653	anatomical structure morphogenesis	0.00043
GO:0010556	regulation of macromolecule biosynthetic process	1.4E-05	GO:0036211	protein modification process	0.00043
GO:2000112	regulation of cellular macromolecule biosynthetic process	1.4E-05	GO:0006464	cellular protein modification process	0.00043
GO:0003006	developmental process involved in reproduction	1.5E-05	GO:0032392	DNA geometric change	0.00044
GO:0022403	cell cycle phase	1.6E-05	GO:0044707	single-multicellular organism process	0.0005
GO:0031327	negative regulation of cellular biosynthetic process	1.7E-05	GO:2001141	regulation of RNA biosynthetic process	0.00053
GO:0007127	meiosis I	2E-05	GO:0007349	cellularization	0.0006
GO:0009890	negative regulation of biosynthetic process	2E-05	GO:0048610	cellular process involved in reproduction	0.00074
GO:0048646	anatomical structure formation involved in morphogenesis	2E-05	GO:0042138	meiotic DNA double-strand break formation	0.00076
GO:0032259	methylation	2E-05	GO:0044238	primary metabolic process	0.00083
GO:0031326	regulation of cellular biosynthetic process	2.7E-05	GO:0007059	chromosome segregation	0.00111
GO:0048731	system development	3.6E-05	GO:0016572	histone phosphorylation	0.00115
GO:0010212	response to ionizing radiation	3.7E-05	GO:0006468	protein phosphorylation	0.00176
GO:0045892	negative regulation of transcription, DNA-dependent	3.7E-05	GO:0009887	organ morphogenesis	0.00186
GO:0051253	negative regulation of RNA metabolic process	4E-05	GO:0006346	methylation-dependent chromatin silencing	0.00188
GO:0009889	regulation of biosynthetic process	4.4E-05	GO:0009886	post-embryonic morphogenesis	0.002
GO:0031324	negative regulation of cellular metabolic process	4.6E-05	GO:0048653	anther development	0.00235
GO:0033554	cellular response to stress	4.6E-05	GO:0008356	asymmetric cell division	0.00243
GO:0010468	regulation of gene expression	4.6E-05	GO:0048563	post-embryonic organ morphogenesis	0.00248
GO:0010558	negative regulation of macromolecule biosynthetic process	5E-05	GO:0048444	floral organ morphogenesis	0.00248
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	5E-05	GO:0048513	organ development	0.00254
GO:0007275	multicellular organismal development	5E-05	GO:0032774	RNA biosynthetic process	0.00289
GO:0006310	DNA recombination	5.2E-05	GO:0006351	transcription, DNA-dependent	0.00289
GO:0010629	negative regulation of gene expression	5.7E-05	GO:0044237	cellular metabolic process	0.00338
GO:0032502	developmental process	6.3E-05	GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	0.00373
GO:0000725	recombinational repair	6.3E-05	GO:0031047	gene silencing by RNA	0.00379
GO:0000724	double-strand break repair via homologous recombination	6.3E-05	GO:0031048	chromatin silencing by small RNA	0.00447
GO:0009987	cellular process	6.4E-05	GO:0043412	macromolecule modification	0.00451
GO:0032501	multicellular organismal process	8.5E-05	GO:0048523	negative regulation of cellular process	0.0046
GO:0048856	anatomical structure development	0.0001	GO:0048509	regulation of meristem development	0.00482
GO:0065007	biological regulation	0.00011	(table continued on next page)		

¹Only GO-terms assigned to biological processes are shown

Supplemental Table 17: continued

GO-ID	GO-Term ¹	FDR	GO-ID	GO-Term ¹	FDR
(table continued from previous page)			GO:0071900	regulation of protein serine/threonine kinase activity	2.04E-02
GO:0048449	floral organ formation	0.00628	GO:0010075	regulation of meristem growth	2.19E-02
GO:0051225	spindle assembly	0.00667	GO:0048507	meristem development	2.37E-02
GO:0048645	organ formation	0.00688	GO:0051026	chiasma assembly	2.71E-02
GO:2000026	regulation of multicellular organismal development	0.00713	GO:0034654	nucleobase-containing compound biosynthetic process	2.74E-02
GO:0000280	nuclear division	0.00721	GO:0009558	embryo sac cellularization	2.74E-02
GO:0033044	regulation of chromosome organization	0.00736	GO:0035266	meristem growth	3.06E-02
GO:0006471	protein ADP-ribosylation	0.00988	GO:0050793	regulation of developmental process	3.16E-02
GO:0071704	organic substance metabolic process	0.01107	GO:0071514	genetic imprinting	3.28E-02
GO:0051239	regulation of multicellular organismal process	0.01166	GO:0006349	regulation of gene expression by genetic imprinting	3.28E-02
GO:0007051	spindle organization	0.01255	GO:0048519	negative regulation of biological process	3.50E-02
GO:0007062	sister chromatid cohesion	0.0155	GO:0043247	telomere maintenance in response to DNA damage	3.57E-02
GO:0010639	negative regulation of organelle organization	0.01728	GO:0048638	regulation of developmental growth	3.60E-02
GO:0051129	negative regulation of cellular component organization	0.01728	GO:0031032	actomyosin structure organization	3.81E-02
GO:0070925	organelle assembly	0.01784	GO:0032776	DNA methylation on cytosine	3.81E-02
GO:0048285	organelle fission	0.01834	GO:1902407	assembly of actomyosin apparatus involved in mitotic cytokinesis	3.81E-02
GO:0090305	nucleic acid phosphodiester bond hydrolysis	0.01834	GO:0000914	phragmoplast assembly	3.81E-02
GO:0006268	DNA unwinding involved in DNA replication	1.84E-02	GO:0000912	assembly of actomyosin apparatus involved in cytokinesis	3.81E-02
GO:0007112	male meiosis cytokinesis	2.03E-02	GO:0010073	meristem maintenance	4.34E-02
GO:0033206	meiotic cytokinesis	2.03E-02	GO:0007140	male meiosis	4.70E-02
GO:0010245	radial microtubular system formation	2.03E-02	GO:0040008	regulation of growth	4.81E-02

¹Only GO-terms assigned to biological processes are shown

Supplemental Table 18: Overview of RNA samples and sequencing statistics

Tissue	Photoperiod	Genotype	Wad. Stage	Timepoint ¹	Library	Raw Data Read Number	Filtered Data Read Number	Total Mapped Reads	Uniquely Mapped Reads	Mapped Reads (<10 Positions)	Unmapped Reads	% Total Mapped Reads ¹	% Uniquely Mapped Reads ¹	% Mapped Reads ² (<10 Positions)	% Unmapped Reads ¹
Apex	Short day	S42-IL107	0.5	0	A	16459061	9893302	8074964	7604962	470002	1818338	81.62	76.87	4.75	18.38
Apex	Short day	S42-IL107	0.5	0	B	7474058	4219953	3486797	3276316	210481	733156	82.63	77.64	4.99	17.37
Apex	Short day	S42-IL107	0.5	0	C	10626845	2642659	2082591	1953507	129084	560068	78.81	73.92	4.88	21.19
Apex	Long day	Scarlett	1.0	3	D	17104663	9738819	5369553	5046743	322810	4369266	55.14	51.82	3.31	44.86
Apex	Long day	Scarlett	1.0	3	E	14897387	9397113	7723833	7278930	444903	1673280	82.19	77.46	4.73	17.81
Apex	Long day	Scarlett	1.0	3	F	17730966	11537432	9579412	9033763	545649	1958020	83.03	78.30	4.73	16.97
Apex	Long day	S42-IL107	1.0	3	G	19358313	10951141	8969982	8445259	524723	1981159	81.91	77.12	4.79	18.09
Apex	Long day	S42-IL107	1.0	3	H	17092440	10071274	8000971	7537109	463862	2070303	79.44	74.84	4.61	20.56
Apex	Long day	S42-IL107	1.0	3	I	16566298	9109101	7535252	7099987	435265	1573849	82.72	77.94	4.78	17.28
Apex	Long day	S42-IL107	2.0	6	J	32563534	18201818	1.1E+07	14085315	846588	3269915	82.04	77.38	4.65	17.96
Apex	Long day	S42-IL107	2.0	6	K	23951610	14142385	1.1E+07	10187863	602323	3352199	76.30	72.04	4.26	23.70
Apex	Long day	S42-IL107	2.0	6	(L)	-	-	-	-	-	-	-	-	-	-
Leaf	Long day	S42-IL107	2.0	6	M	17760086	9100127	7598589	6795801	802788	1501538	83.50	74.68	8.82	16.50
Leaf	Long day	S42-IL107	2.0	6	N	21814456	11176202	9382236	8423041	959195	1793966	83.95	75.37	8.58	16.05
Leaf	Long day	S42-IL107	2.0	6	O	20289165	11362454	9504470	8624381	880089	1857984	83.65	75.90	7.75	16.35
Apex	Long day	Scarlett	2.0	9	P	14359218	9911948	8200558	7735749	464809	1711390	82.73	78.04	4.69	17.27
Apex	Long day	Scarlett	2.0	9	Q	20007830	12535122	1E+07	9666980	573298	2294844	81.69	77.12	4.57	18.31
Apex	Long day	Scarlett	2.0	9	R	21999556	14020216	1.1E+07	10837222	649945	2533049	81.93	77.30	4.64	18.07
Apex	Short day	S42-IL107	2.0	16	S	18856390	12755506	1.1E+07	9919814	612186	2223506	82.57	77.77	4.80	17.43
Apex	Short day	S42-IL107	2.0	16	T	17899889	12181159	1E+07	9428186	576210	2176763	82.13	77.40	4.73	17.87
Apex	Short day	S42-IL107	2.0	16	U	13652340	9440970	7869896	7406957	462939	1571074	83.36	78.46	4.90	16.64
Apex	Short day	S42-IL107	1.0	7	V	21151250	13207739	1.1E+07	10435541	647039	2125159	83.91	79.01	4.90	16.09
Apex	Short day	S42-IL107	1.0	7	W	14840256	9907029	8187503	7711492	476011	1719526	82.64	77.84	4.80	17.36
Apex	Short day	S42-IL107	1.0	7	X	17692798	11220700	9302660	8762766	539894	1918040	82.91	78.09	4.81	17.09
Leaf	Long day	Scarlett	1.0	3	A1	9026797	5432759	3185557	2828665	356892	2247202	58.64	52.07	6.57	41.36
Leaf	Long day	Scarlett	1.0	3	B1	9895345	4829142	3239058	2876667	362391	1590084	67.07	59.57	7.50	32.93
Leaf	Long day	Scarlett	1.0	3	C1	8040428	4686020	2850797	2535253	315544	1835223	60.84	54.10	6.73	39.16
Leaf	Long day	S42-IL107	1.0	3	D1	9475973	5380083	3907323	3523777	383546	1472760	72.63	65.50	7.13	27.37
Leaf	Long day	S42-IL107	1.0	3	E1	8876566	4646223	3713020	3314891	398129	933203	79.91	71.35	8.57	20.09
Leaf	Long day	S42-IL107	1.0	3	F1	24420300	10662510	8223394	7468010	755384	2439116	77.12	70.04	7.08	22.88
Leaf	Long day	Scarlett	2.0	9	G1	9299840	5336032	4592336	4157580	434756	743696	86.06	77.92	8.15	13.94
Leaf	Long day	Scarlett	2.0	9	H1	7859909	4607638	3677568	3319688	357880	930070	79.81	72.05	7.77	20.19
Leaf	Long day	Scarlett	2.0	9	I1	12377623	7455485	6276388	5731061	545327	1179097	84.18	76.87	7.31	15.82
Apex	Long day	S42-IL107	3.5	14	J1	9050764	6141815	5143688	4799701	343987	998127	83.75	78.15	5.60	16.25
Apex	Long day	S42-IL107	3.5	14	K1	9570762	6339239	5331268	4963348	367920	1007971	84.10	78.30	5.80	15.90
Apex	Long day	S42-IL107	3.5	14	L1	5162724	3936287	3336398	3112804	223594	599889	84.76	79.08	5.68	15.24
Leaf	Short day	S42-IL107	2.0	16	M1	10116020	5391320	4624600	4151410	473190	766720	85.78	77.00	8.78	14.22
Leaf	Short day	S42-IL107	2.0	16	N1	12074847	6675503	5723413	5184815	538598	952090	85.74	77.67	8.07	14.26
Leaf	Short day	S42-IL107	2.0	16	O1	9963482	6130135	5248033	4789203	458830	882102	85.61	78.13	7.48	14.39
Apex	Long day	Scarlett	3.5	20	P1	9581977	6883431	5746021	5378877	367144	1137410	83.48	78.14	5.33	16.52
Apex	Long day	Scarlett	3.5	20	X1	6427149	4848100	3928855	3680523	248332	919245	81.04	75.92	5.12	18.96
Apex	Long day	Scarlett	3.5	20	Y1	12725456	8450127	6829176	6404370	424806	1620951	80.82	75.79	5.03	19.18
Leaf	Short day	S42-IL107	1.0	7	Z1	11063884	6040842	4537274	4100767	436507	1503568	75.11	67.88	7.23	24.89
Leaf	Short day	S42-IL107	1.0	7	AA1	8988461	4958127	4163623	3762488	401135	794504	83.98	75.89	8.09	16.02
Leaf	Short day	S42-IL107	1.0	7	AB1	11010676	5172688	4344558	3893009	451549	828130	83.99	75.26	8.73	16.01
Apex	Short day	S42-IL107	3.5	50	AC1	23918237	7202925	5797197	5368935	428262	1405728	80.48	74.54	5.95	19.52
Apex	Short day	S42-IL107	3.5	50	AD1	9282564	6444967	5295853	4945492	350361	1149114	82.17	76.73	5.44	17.83
Apex	Short day	S42-IL107	3.5	50	AE1	10104901	6672267	5455680	5110588	345092	1216587	81.77	76.59	5.17	18.23
Average 1st Set						18006453	10727138	8692947	8143378	549569	2034191	80.90	75.75	5.15	19.10
Average 2nd Set						10763134	6013486	4798795	4391747	407048	1214691	79.53	72.69	6.85	20.47
Average						14307737	8320167	6704444	6227651	476793	1615723	80.20	74.19	6.02	19.80

¹Days after separation of plants into short-day or long-day conditions²Proportion relative to the number of filtered reads

Supplemental Table 19: Correlation analysis for quality control of biological replicates used for RNA sequencing

Tissue	Photoperiod	Genotype	Waddington Stage	Rep1 vs. Rep2 *	Rep1 vs. Rep3 *	Rep2 vs. Rep3 *
Apex	Short day	S42-IL107	0.5	0.99	0.96	0.98
Apex	Short day	S42-IL107	1	0.99	0.99	0.98
Apex	Long day	Scarlett	1	0.95	0.94	0.99
Apex	Long day	S42-IL107	1	0.99	0.99	0.99
Apex	Short day	S42-IL107	2	1.00	0.99	0.99
Apex	Long day	Scarlett	2	0.98	0.99	0.98
Apex	Long day	S42-IL107	2	0.98	-	-
Apex	Short day	S42-IL107	3.5	0.86	0.85	0.98
Apex	Long day	Scarlett	3.5	0.99	0.99	0.99
Apex	Long day	S42-IL107	3.5	0.99	0.99	0.99
Leaf	Short day	S42-IL107	1	0.99	0.97	0.97
Leaf	Long day	Scarlett	1	0.99	0.92	0.92
Leaf	Long day	S42-IL107	1	0.97	0.96	0.97
Leaf	Short day	S42-IL107	2	0.98	0.92	0.97
Leaf	Long day	Scarlett	2	0.95	0.98	0.94
Leaf	Long day	S42-IL107	2	0.99	0.97	0.98

*r, Pearson's correlation coefficient for RPKM expression levels of 25152 transcripts between biological replicates, $p < 10^{-8}$

Supplemental Table 20: Statistics of coexpression clustering

Cluster ID	Average Probability¹	StDev Probability¹	Cluster Size²
1	0.967	0.095	180
2	0.998	0.008	40
3	0.975	0.083	296
4	0.970	0.108	79
5	0.998	0.007	10
6	0.982	0.074	157
7	0.979	0.069	214
8	0.950	0.115	125
9	0.969	0.095	95
10	0.964	0.100	247
11	0.966	0.095	217
12	0.966	0.096	345
13	0.977	0.083	134
14	0.978	0.063	105
15	0.952	0.112	361
16	0.976	0.087	210
17	0.949	0.117	568
18	0.936	0.131	311
19	0.942	0.123	454
20	0.953	0.119	38
21	0.965	0.105	141
22	0.965	0.101	260
23	0.962	0.096	414
24	0.954	0.117	139
25	0.951	0.113	302
26	0.932	0.133	521
27	0.955	0.122	218
28	0.936	0.127	333
29	0.942	0.129	319
30	0.982	0.068	55
31	0.960	0.108	716
1-31	0.963	0.031	245 ± 167

¹Average probability and standard deviation for all DETs grouping into the respective coexpression cluster

²Number of DETs in coexpression cluster

Supplemental Table 21: Oligonucleotide sequences used in RT-qPCR assays

Gene	Transcript ID ¹	5' -> 3' fwd - Primer Sequence	5' -> 3' rev - Primer Sequence	Reference
<i>Actin</i>	Hv.23088	CGTGTGGATTCTGGTGATG	AGCCACATATGCGAGCTTCT	Campoli et al. 2012b
<i>BM3</i>	Hv.4298	GCCGTCAACAGCACAAGCAA	CCCCATTCAACCCTGTAGCAAAGA	this study
<i>Vrn-H1</i>	Hv.23025	CTGAAAGCGAAGGTTGAGAC	TTCTCCTCCTGCAGTGACCT	Campoli et al. 2012b
<i>BM8</i>	Hv.169	CCACAGCAGCCGACACCTA	TGCCTTTGGGGGAGAAGACG	this study
<i>CO1</i>	MLOC_6921.1	CTGCTGGGGCTAGTGCTTAC	CCTTGTTGCATAACGTGTGG	Campoli et al. 2012a
<i>CO2</i>	MLOC_75496.6	AGTGGA CTCTTGGCTCCTCA	CATGCTGCTGTTCTTGCA TT	Campoli et al. 2012b
<i>FT1</i>	Hv.34809	GGTAGACCCAGATGCTCCAA	TCGTAGCACA TCACCTCCTG	fw d primer in Campoli et al. 2012a
<i>FT2</i>	Hv.17258	TACCGAGGTTGTGTGCTACG	TCACATCCTTCTCCGCCGG	this study
<i>SOC1-1</i>	Hv.32986	TTTGACGCAAGTCAAAGCTG	CCTCTGATGATGCGGAGACT	this study

¹Transcript Sequences available at the National Center for Biotechnology Information (NCBI: <http://www.ncbi.nlm.nih.gov>) and at the PGSB barley genome database (<http://pgsb.helmholtz-muenchen.de/plant/barley>), respectively.

Supplemental methods

Design of the reference sequence

To obtain a comprehensive reference sequence, we compared the mapping efficiency of the filtered reads against two sets of transcript clusters available for barley.

Recently, the International Barley Genome Sequencing Consortium (IBGSC) published the draft genome sequence of barley including the transcribed gene space assigned to a set of 26,159 annotated high-confidence genes (HC) and a set of 53,220 low-confidence genes (LC) (IBGSC, Nature 2012). Sequences of the HC and LC were downloaded from the Barley project webpage (ftp://ftpmips.helmholtz-muenchen.de/plants/barley/public_data/genes/, sequence version of March 23rd, 2012). Secondly, a cluster of 26,944 barley UniGenes (UniGene build #59 at NCBI), henceforth referred to as unigenes, was downloaded from NCBI (ftp://ftp.ncbi.nih.gov/repository/UniGene/Hordeum_vulgare/) and used for comparison.

Filtered reads of all libraries were combined and mapped against the respective reference sequences using the RNA-Seq Analysis function of CLC with default parameters. Test mappings were performed on the unigenes, HC and LC sets alone and on various combinations of those. In addition, we assembled *de novo* contigs using CLC *de novo* assemble tool.

To determine the appropriate core reference set for our study, we estimated the extent of sequence redundancy within the different reference sets using BLASTn. Redundancy was defined as a proportion of blast hits longer than 100bp with 97% identity. Furthermore, as an estimate for sequence redundancy, we extracted the proportion of reads with multiple mapping positions (≤ 10 positions) within a respective reference set. In addition to low sequence redundancy, we expected a comprehensive set of reference sequences to yield a high proportion of reads with unique mapping positions and a low percentage of reads assigned as unmapped, i.e. reads without mapping position or mapped to more than ten locations.

The unigenes were selected as a core set due to its lowest sequence redundancy and highest proportion of uniquely mapping reads as compared to the HC and LC datasets (Supplemental Fig. 9B), e.g. in total we mapped 280,871,398 reads against the unigene set, of which 269,468,960 reads had unique and 11,402,438 reads had multiple mapping positions. Against transcripts of the HC dataset, we mapped 226,964,864 reads in total with unique and multiple mapping positions for 206,228,484 reads and 20,736,380 reads, respectively. Thus, other datasets were added to transcripts of the unigene set in the following order of priority: HC, LC, *de novo* contigs.

Redundancy in the combined datasets was eliminated using Minimus2 software with parameters set to 130bp overlap and 97% minimum identity. Filtering transcripts appropriately yielded 8,391 HC (sHC) and 23,232 LC (sLC) progressively added to the unigenes.

To allow the identification of new transcripts specific for shoot apex tissue used in our study, we used CLC *de novo* assembly tool with default parameters to construct a set of 473,651 *de novo* contigs (DNC) from 85,0125,80 reads, which did not map to a reference sequence constructed from unigenes, sHC and sLC. Contigs were filtered for a minimum length of 200bp and a 10X average coverage. A set of 10,172 DNC with BLASTx hits in the *Triticeae* family (E-value $\leq 10^{-5}$), henceforth DNC-T, was selected from the 75,675 DNC identified as Minimus2 singletons. A schematic representation of the pipeline used to construct the reference sequence is presented in Supplemental Fig. 13A.

In summary, a final set of 68,739 transcripts, consisting of 26,944 unigenes, 8,391 sHC, 23,232 sLC and 10,172 DNC-T, was used as a custom reference for the RNA-sequencing analysis. Using this as reference set, 80.6% (315,108,855 reads) of the quality filtered reads could be mapped in total with 74.9% (292,699,606 reads) having unique and 5.7% (22,409,249 reads) multiple mapping positions.

The reference set was annotated using BLASTx against protein databases of *Arabidopsis* (TAIR version 10), *Brachypodium* (*Brachypodium distachyon*, Project version 1.2), Rice (MSU Rice Genome Annotation Project release 7) and *Sorghum* (1.4, Paterson et al., 2009) with cut-off E-value 10^{-5} .

The open reading frames (ORF) of barley transcripts were predicted using the OrfPredictor software guided by the BLASTx results against TAIR (≥ 30 aa, Min et al., 2005). Conserved domain annotation of the translated ORFs was performed using InterProScan4 software (Hunter et al., 2011). These data together with the top 20 BLASTx hits against the *Viridiplantae* sub-set of NCBI 'nr' database were used to determine gene ontology (GO) terms for the reference barley transcripts using Blast2GO pipe 2.5.0 (Conesa et al., 2005). An overview the reference sequence annotation pipeline is depicted in Supplemental Fig. 13B.

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