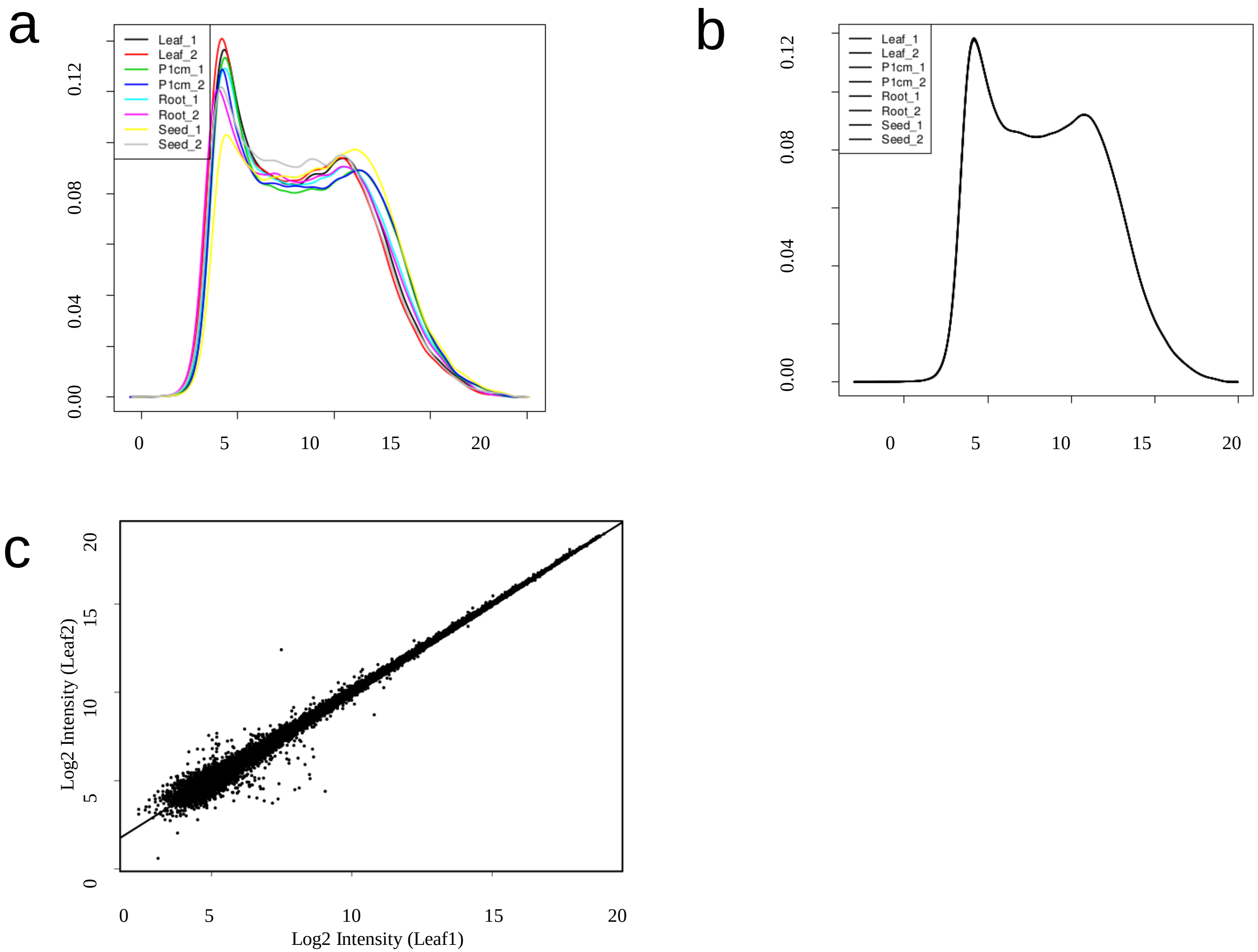
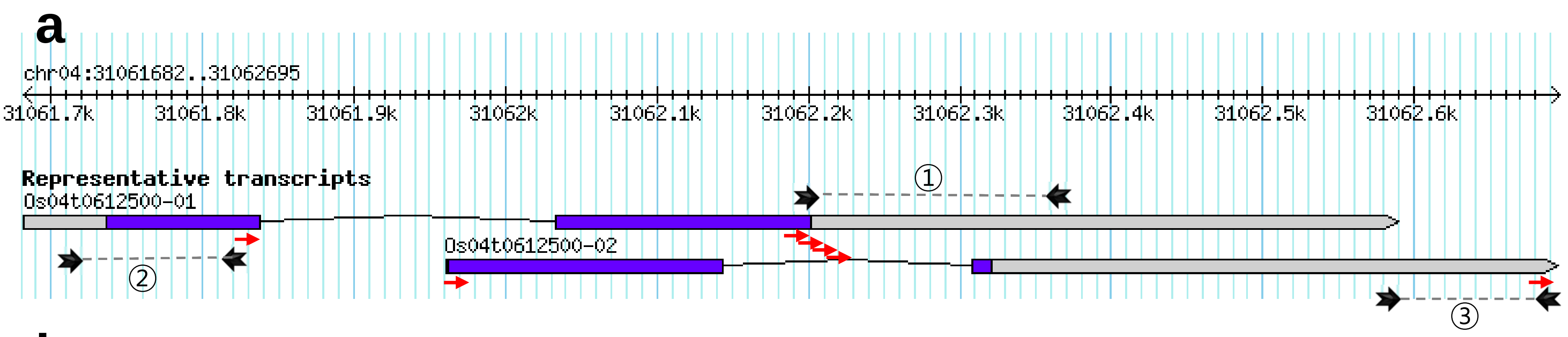


Fig. S1. Signal distribution of the rice ASDM after background correction (a), normalization between slides (b) and a consistency test between microarrays (c).

a, b The data were processed with limma package in R (http://www.bioconductor.org/) using backgroundCorrect and normalizeBetweenArrays functions, respectively. plotDensities functions were used to analyze the distribution of probe intensities from 8 microarray data. Frequency densities before and after normalization were plotted against log2-based intensities. **c** Log2-based intensities of 2 leaf samples were compared. The linear model was y=0.998x + 0.018, r2 = 0.996.



b

SEQ_ID (ASDM)	Leaf	Root	P1cm	S21DAP	CV
① Os04t0612500-01	33,864	309	1,348	5,214	1.6
② Os04t0612500-01_UE	7,667	135	325	1,045	1.6
③ Os04t0612500-02	41,814	273	2,979	5,436	1.6

SEQ_ID (RNA-Seq)	Leaf	Root	P1cm	Seed	CV
Os04t0612500-01_E004	2,274	13	44	144	1.8
Os04t0612500-02_E006	602	1	3	37	1.8

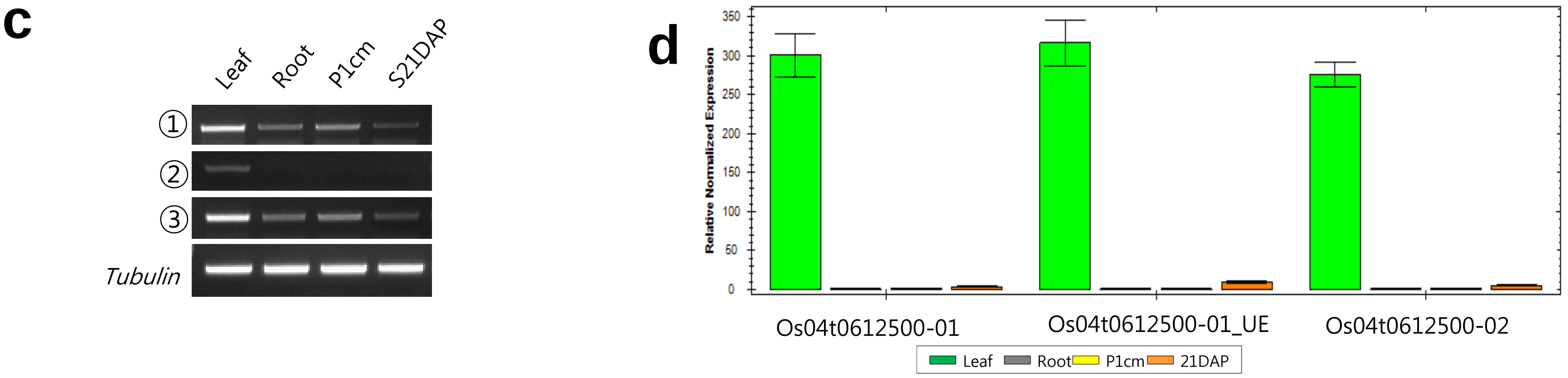
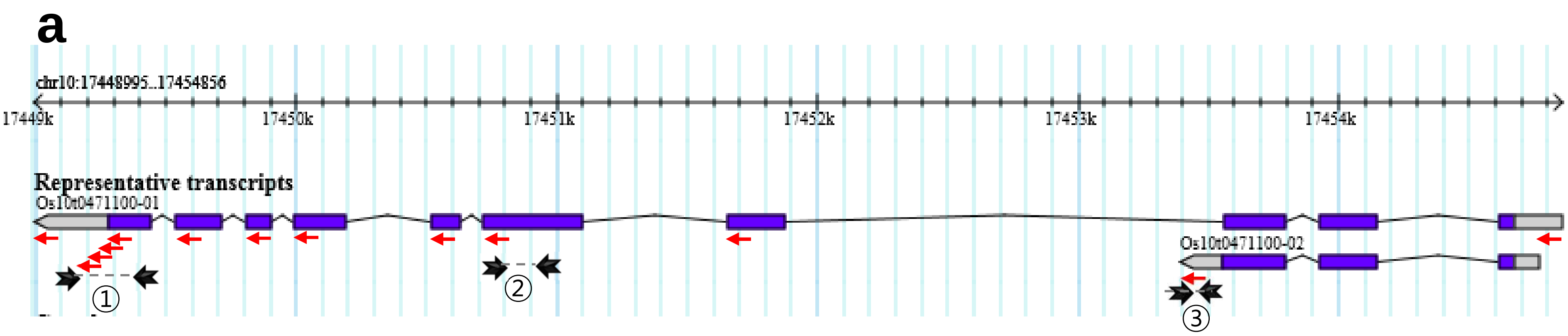


Fig. S2A. The analysis of a locus, Os04g0612500, which has two transcripts, Os04t0612500-01 and Os04t0612500-02 (proline-rich proteins). **a** Design of feature probes in ASDM. Feature probes and primers for PCR were indicated as single arrows and thick arrows, respectively. UniqExonJ was indicated as arrow heads in Os04t0612500-01 in the junctions of two spliced exons. **b** Intensities in ASDM (left) and counts in RNA-Seq (right). Exons in RNA-Seq are designated as in Fig. 1B. **c** Analysis by RT-PCR and **d** quantitative real-time PCR. A locus, Os04g0612500, was highly expressed in the leaf. The rice Tubulin gene was used as a control. The expression of the lowest stage in each transcript was set to 1.



b

SEQ_ID (ASDM)	Leaf	Root	P1cm	S21DAP	CV
① Os10t0471100-01	238	182	32,324	1,839	1.8
② Os10t0471100-01_UE	56	54	2,606	211	1.7
③ Os10t0471100-02	44	23	1,475	48	1.8

SEQ_ID (RNA-Seq)	Leaf	Root	P1cm	Seed	CV
Os10t0471100-01_E001	1	0	401	13	1.9
Os10t0471100-02_E008	0	0	244	5	1.9

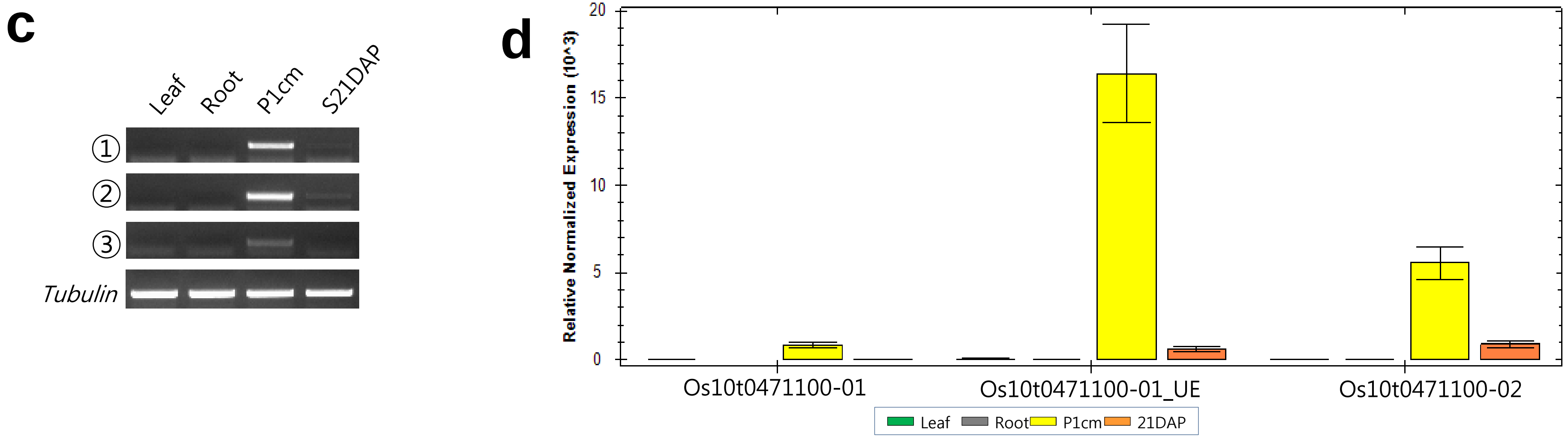
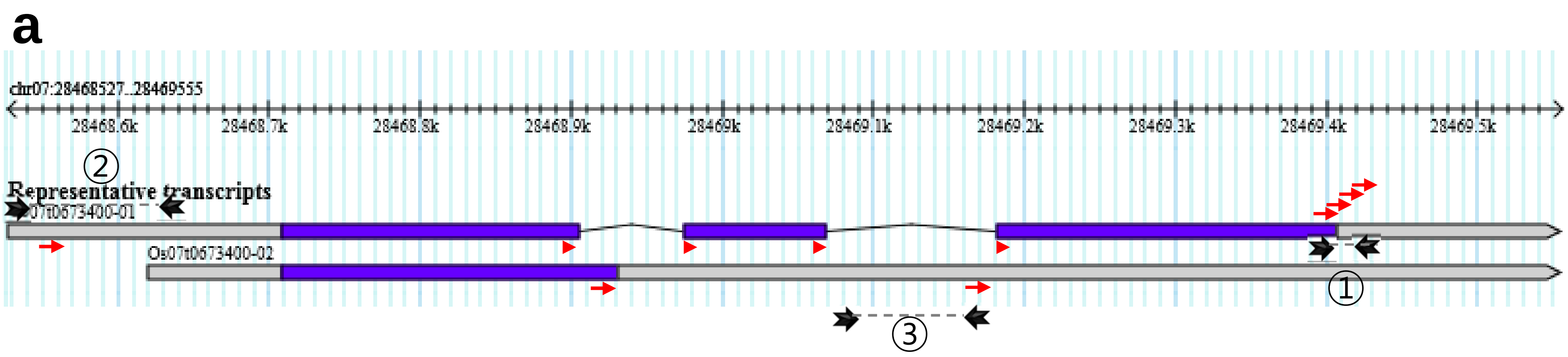


Fig. S2B. Os10g0471100 was active in the P1cm stage.

Os10t0471100-01 and Os10t0471100-02 encoded a protein with high similarity to proteins involved in wax production and CER1, respectively. **a** Feature probes and primers for PCR as indicated above. **b** Intensities in ASDM (left) and counts in RNA-Seq (right). **c** Analysis by RT-PCR and **d** quantitative real-time PCR.



b

SEQ_ID (ASDM)	Leaf	Root	P1cm	S21DAP	CV
① Os07t0673400-01	1,614	228	1,377	40,940	1.8
② Os07t0673400-01_UE	419	172	369	3,138	1.4
③ Os07t0673400-02	309	191	176	788	0.8

SEQ_ID (RNA-Seq)	Leaf	Root	P1cm	Seed	CV
Os07t0673400-01_E001	16	1	4	14	0.8
Os07t0673400-02_E003	1	0	1	10	1.6

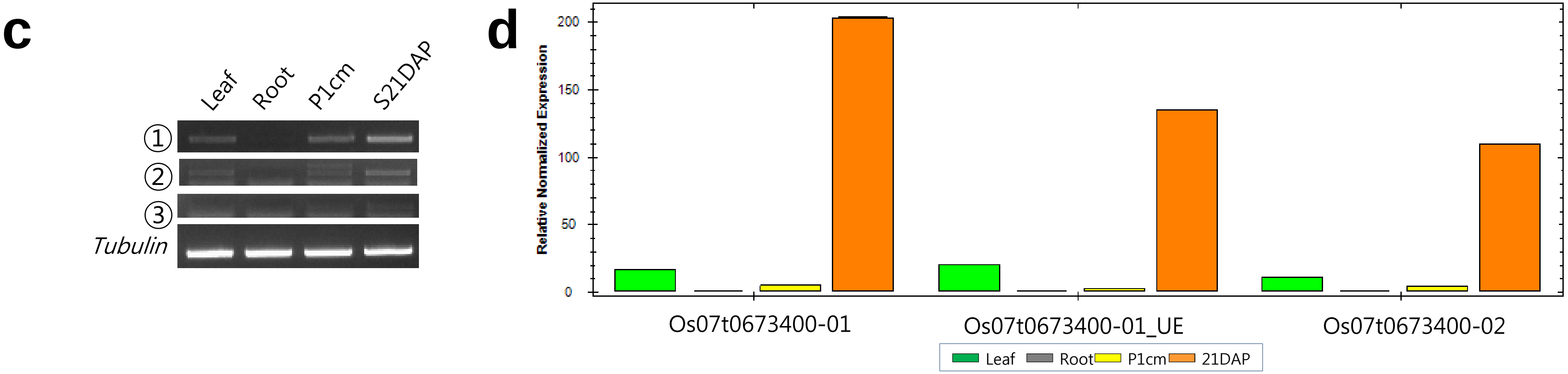


Fig. S2C. Os07g0673400 was active in the S21DAP stage.

Os07t0673400-01 and Os07t0673400-02 encoded a protein with high similarity to proteins involved in Rossmann-like alpha/beta/alpha sandwich fold domain containing protein and similar to universal stress protein, respectively. **a** Feature probes and primers for PCR as indicated above. **b** Intensities in ASDM (left) and counts in RNA-Seq (right). **c** Analysis by RT-PCR and **d** quantitative real-time PCR.

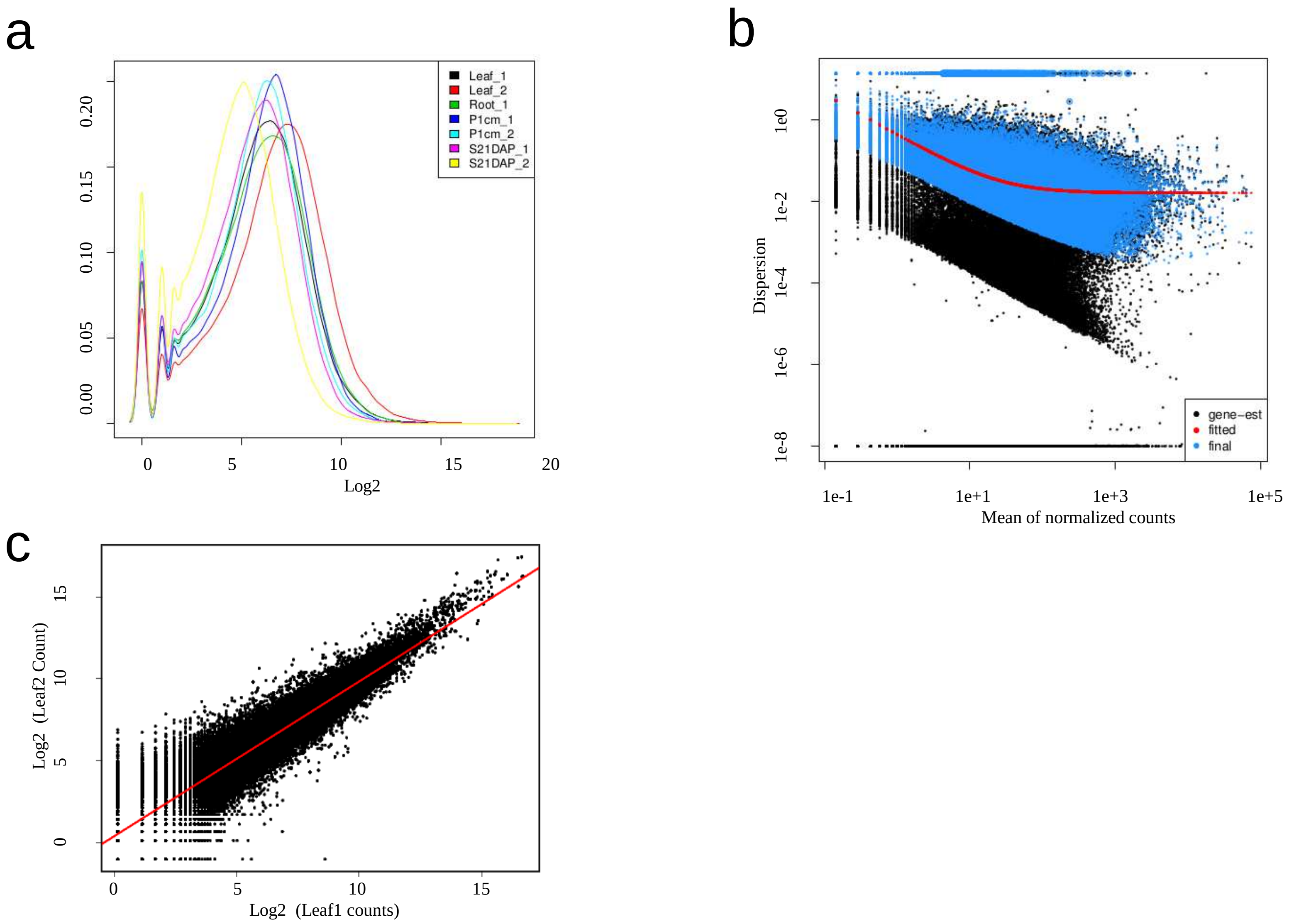


Fig. S3. Data distribution of raw RNA-Seq. Dispersion of raw (a) and normalized counts (b) and a consistency test between 2 independent RNA-seq using leaf samples (c).

a, The data was processed with density function of R. b The initial perData set was loaded and normalized with DEXSeqDataSetFromHTSeq and estimateSizeFactors, respectively in DEXSeq package. -exon dispersion estimates (shown by black points), the fitted mean-dispersion values function (red line), and the shrunken values in blue. c Log2-based intensities of 2 leaf samples were compared. The linear model was y=0.943x + 0.404, r2 = 0.889.

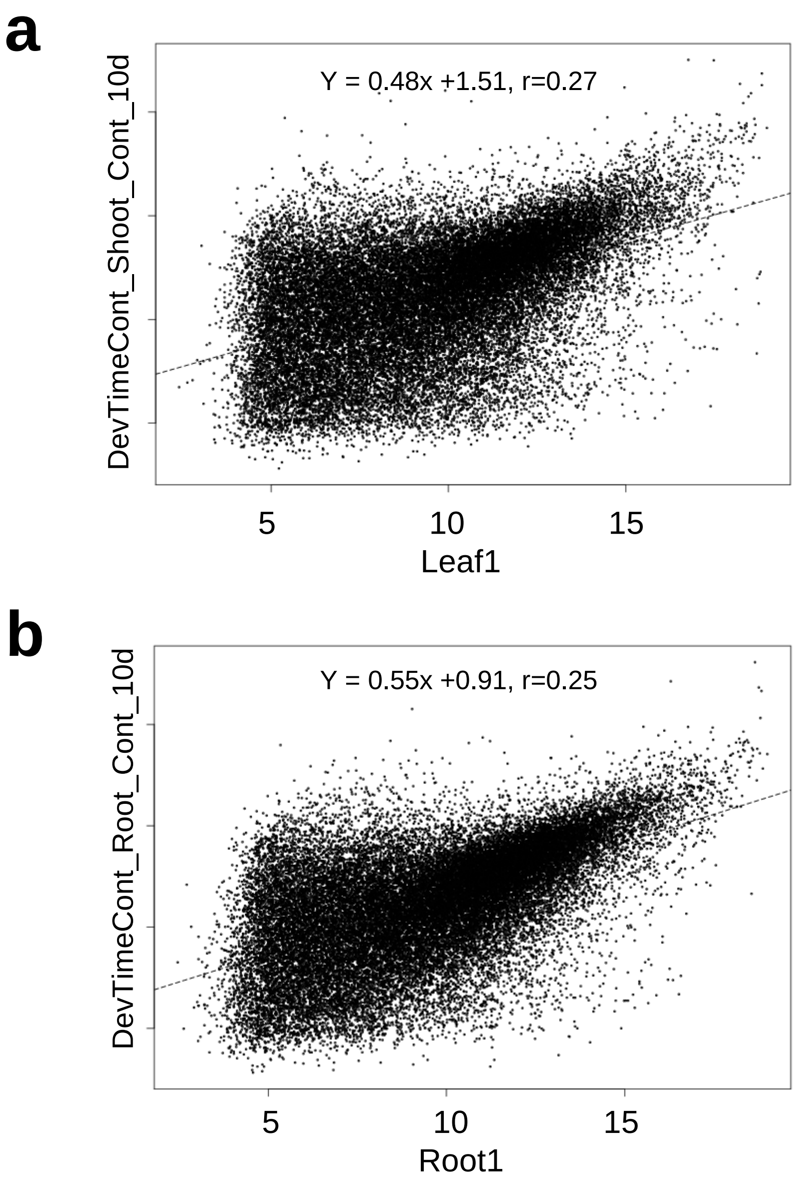


Fig. S4. Data comparison between the intensities of ASDM and the counts of RNA-seq in a public database, TENOR (http://tenor.dna.affrc.go.jp).

RNA-Seq data Soot_Count_10d and Root_Coun_10d were obtained from the TENOR database. The values are represented in x- and y-axes, respectively. The linear regression model gave slopes of 0.48 and 0.55 for the leaf (a) and root (b), respectively. Pearson correlation coefficients ranged 0.25-0.27.

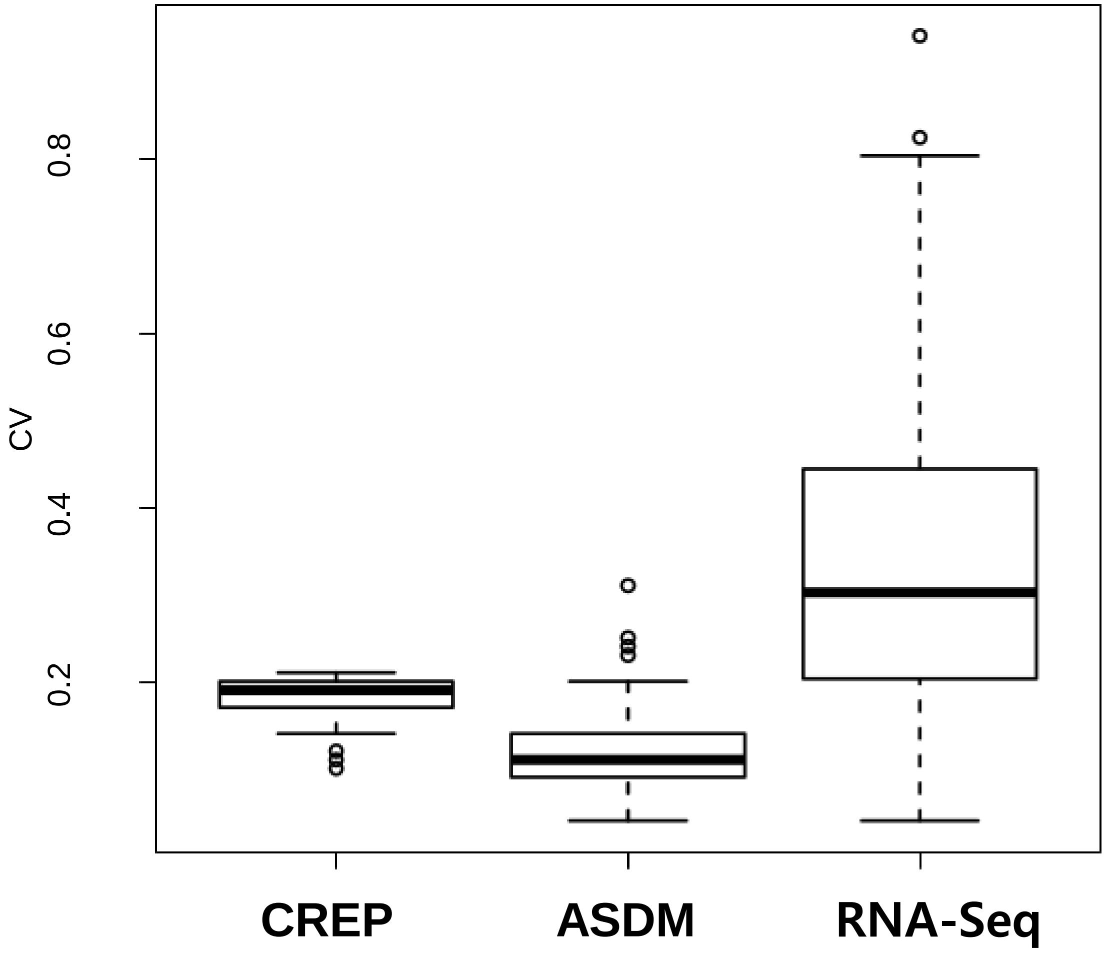
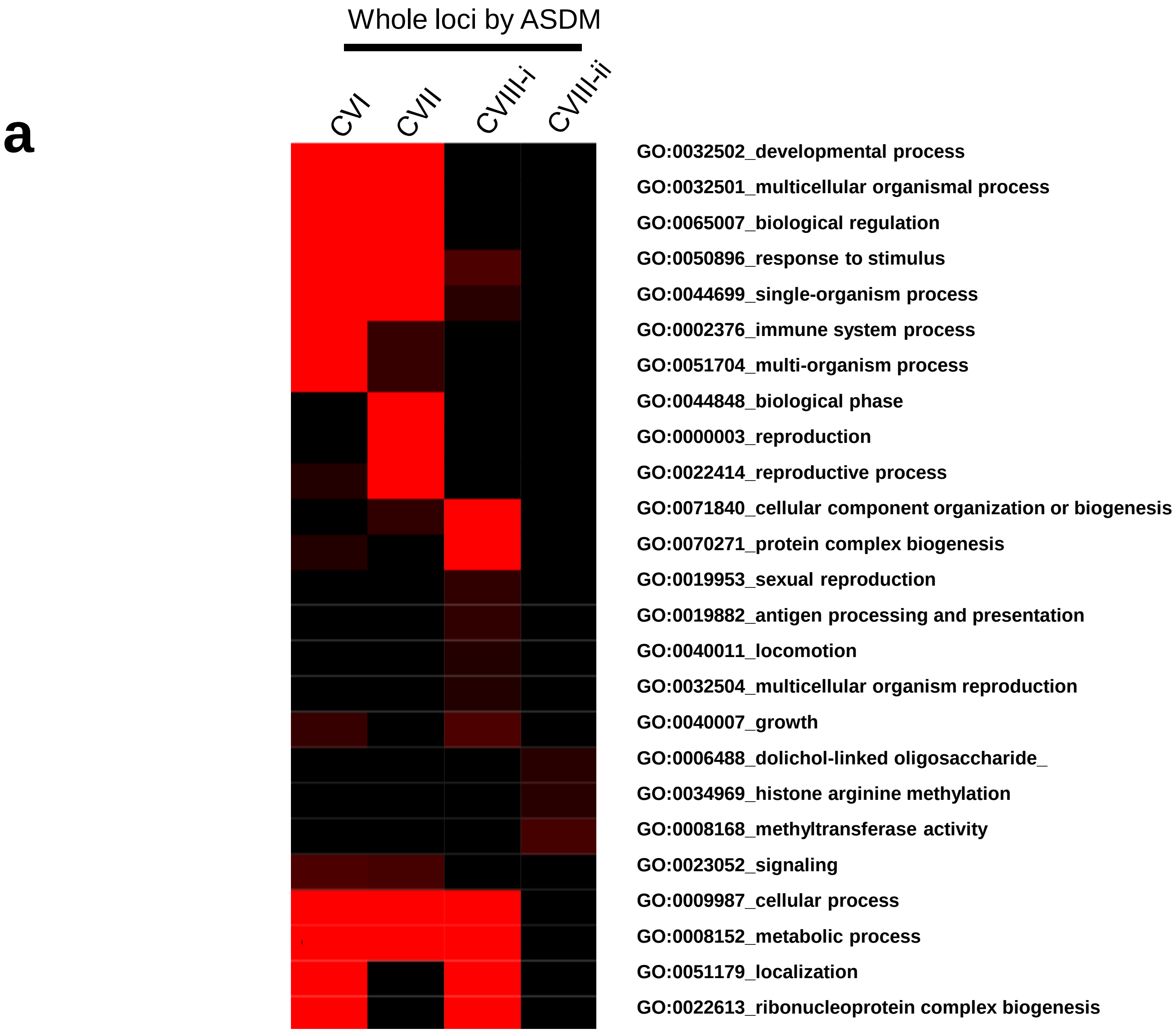
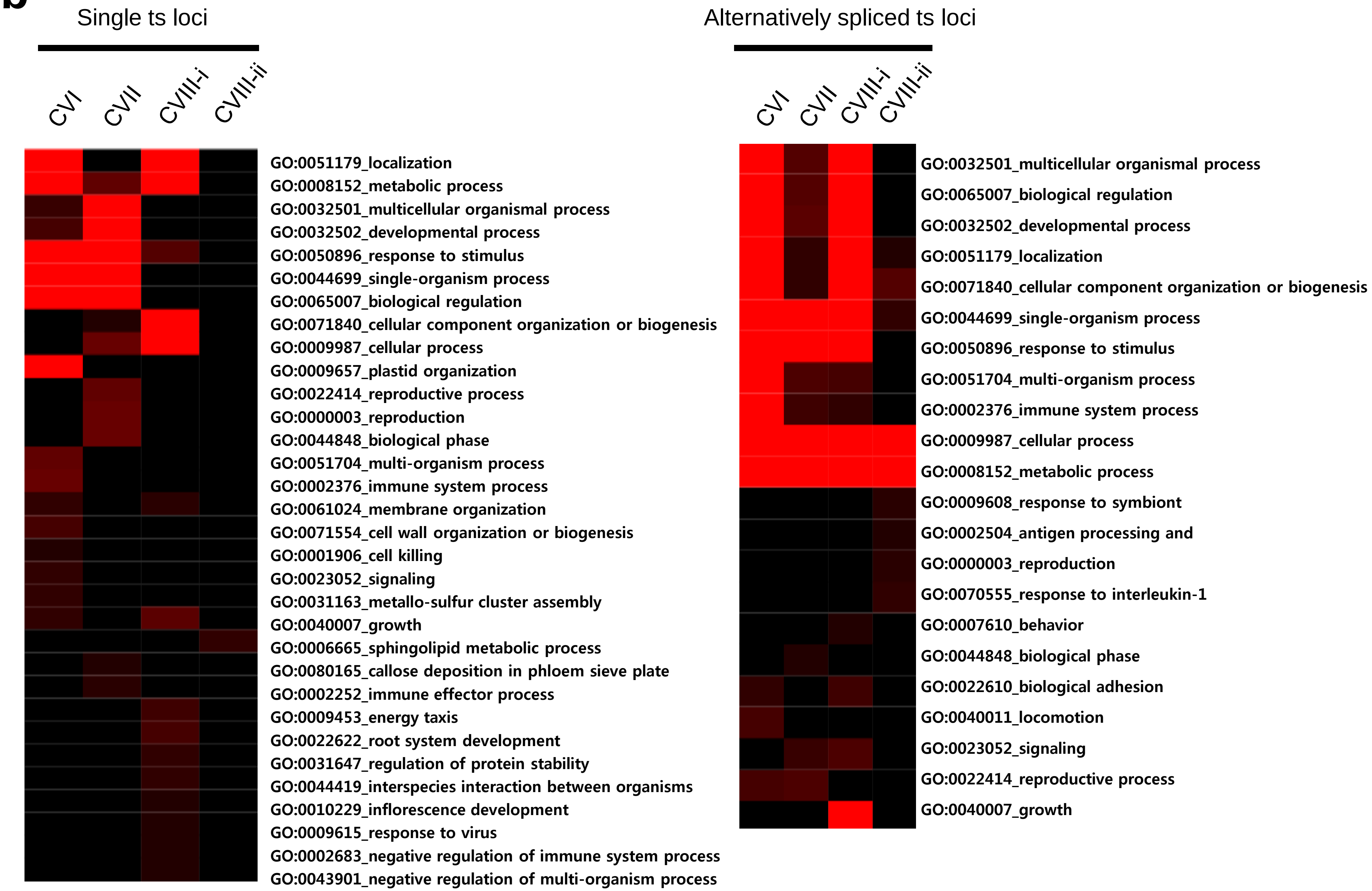


Fig. S5. The distribution of CVs of 100 constitutively expressed genes in CREP (mean = 0.18, sd 0.02) and their corresponding genes in ASDM (mean = 0.11, sd 0.05) and RNA-Seq (mean = 0.34, sd 0.19) datasets. The gene list was obtained from reported in Wang et al. (2010) and the values in the ASDM and RNA-Seq are retrieved in table S8 in this report.


a
Whole loci by ASDM
CVI
CVII
CVIII-i
CVIII-ii
GO:0032502_developmental process
GO:0032501_multicellular organismal process
GO:0065007_biological regulation
GO:0050896_response to stimulus
GO:0044699_single-organism process
GO:0002376_immune system process
GO:0051704_multi-organism process
GO:0044848_biological phase
GO:0000003_reproduction
GO:0022414_reproductive process
GO:0071840_cellular component organization or biogenesis
GO:0070271_protein complex biogenesis
GO:0019953_sexual reproduction
GO:0019882_antigen processing and presentation
GO:0040011_locomotion
GO:0032504_multicellular organism reproduction
GO:0040007_growth
GO:0006488_dolichol-linked oligosaccharide_
GO:0034969_histone arginine methylation
GO:0008168_methyltransferase activity
GO:0023052_signaling
GO:0009987_cellular process
GO:0008152_metabolic process
GO:0051179_localization
GO:0022613_ribonucleoprotein complex biogenesis

b


Single ts loci
CVI
CVII
CVIII-i
CVIII-ii
GO:0051179_localization
GO:0008152_metabolic process
GO:0032501_multicellular organismal process
GO:0032502_developmental process
GO:0050896_response to stimulus
GO:0044699_single-organism process
GO:0065007_biological regulation
GO:0071840_cellular component organization or biogenesis
GO:0009987_cellular process
GO:0009657_plastid organization
GO:0022414_reproductive process
GO:0000003_reproduction
GO:0044848_biological phase
GO:0051704_multi-organism process
GO:0002376_immune system process
GO:0061024_membrane organization
GO:0071554_cell wall organization or biogenesis
GO:0001906_cell killing
GO:0023052_signaling
GO:0031163_metallo-sulfur cluster assembly
GO:0040007_growth
GO:0006665_sphingolipid metabolic process
GO:0080165_callose deposition in phloem sieve plate
GO:0002252_immune effector process
GO:0009453_energy taxis
GO:0022622_root system development
GO:0031647_regulation of protein stability
GO:0044419_interspecies interaction between organisms
GO:0010229_inflorescence development
GO:0009615_response to virus
GO:0002683_negative regulation of immune system process
GO:0043901_negative regulation of multi-organism process
Alternatively spliced ts loci
CVI
CVII
CVIII-i
CVIII-ii
GO:0032501_multicellular organismal process
GO:0065007_biological regulation
GO:0032502_developmental process
GO:0051179_localization
GO:0071840_cellular component organization or biogenesis
GO:0044699_single-organism process
GO:0050896_response to stimulus
GO:0051704_multi-organism process
GO:0002376_immune system process
GO:0009987_cellular process
GO:0008152_metabolic process
GO:0009608_response to symbiont
GO:0002504_antigen processing and
GO:0000003_reproduction
GO:0070555_response to interleukin-1
GO:0007610_behavior
GO:0044848_biological phase
GO:0022610_biological adhesion
GO:0040011_locomotion
GO:0023052_signaling
GO:0022414_reproductive process
GO:0040007_growth

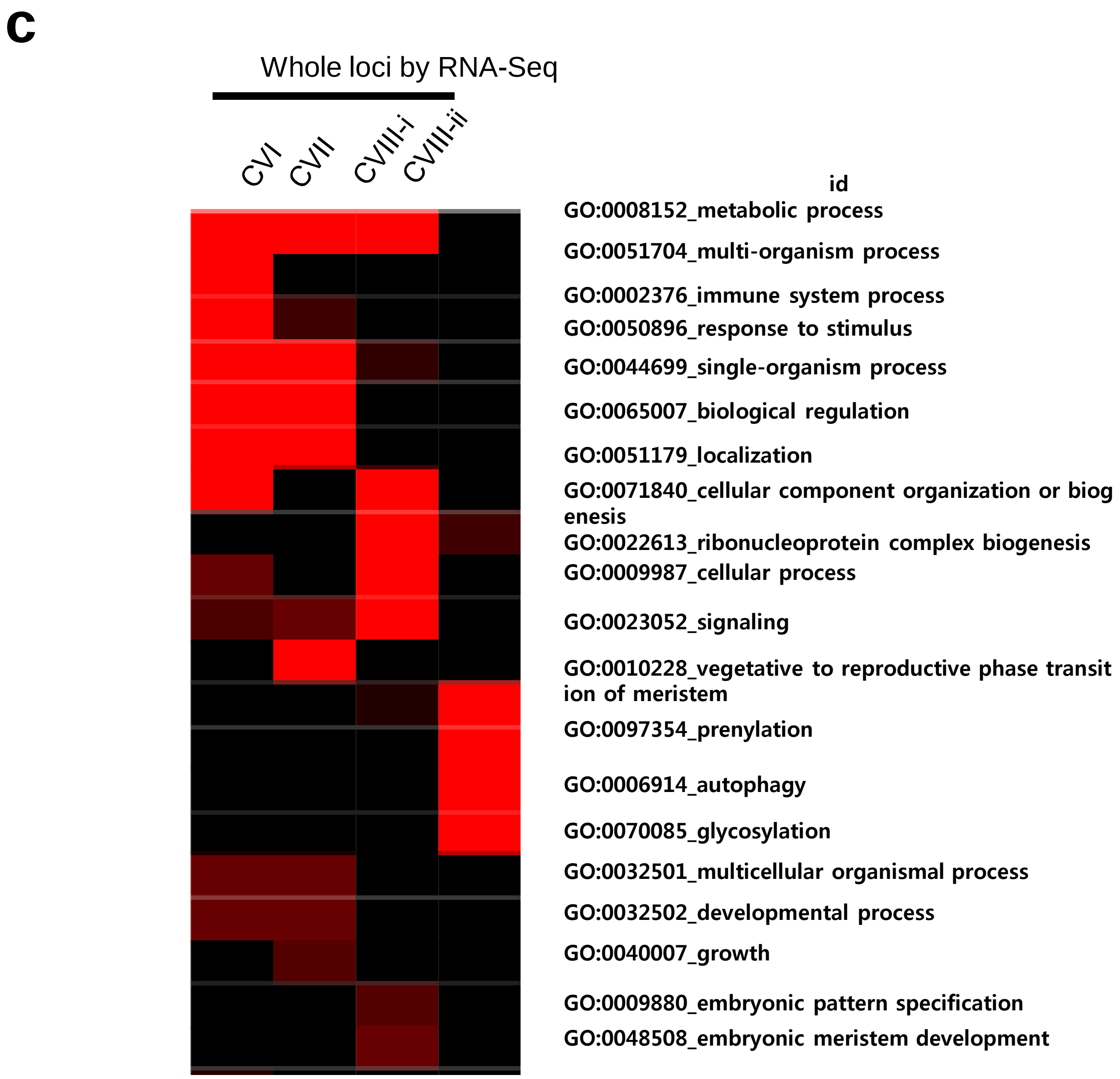

c
Whole loci by RNA-Seq
CVI
CVII
CVIII-i
CVIII-ii
id
GO:0008152_metabolic process
GO:0051704_multi-organism process
GO:0002376_immune system process
GO:0050896_response to stimulus
GO:0044699_single-organism process
GO:0065007_biological regulation
GO:0051179_localization
GO:0071840_cellular component organization or biogenesis
GO:0022613_ribonucleoprotein complex biogenesis
GO:0009987_cellular process
GO:0023052_signaling
GO:0010228_vegetative to reproductive phase transition of meristem
GO:0097354_prenylation
GO:0006914_autophagy
GO:0070085_glycosylation
GO:0032501_multicellular organismal process
GO:0032502_developmental process
GO:0040007_growth
GO:0009880_embryonic pattern specification
GO:0048508_embryonic meristem development

Fig. S6. GO analysis of loci of whole genes (**a)** and the genes with single loci (**b**, left) or alternatively spliced transcripts (**b**, right) loci between CVI, CVII, CVIII-i and CVIII-ii based on ASDM. GO analysis of loci of whole genes by RNA-Seq is presented in (**c**). As the expression of the genes in CVIII-iii is very low, the group is disregard. GO terms that are enriched in CVI and CVII are GO:0032502_developmental process, GO:0032501_multicellular organismal process, GO:0065007_biological regulation, GO:0050896_response to stimulus, GO:0044699_single-organism process. GO:0009987_cellular process and GO:0008152_metabolic process are also enriched in CVIII-i. GO terms that are enriched in CVII are GO:0044848_biological phase, GO:0000003_reproduction, GO:0022414_reproductive process. GO terms that are enriched in CVIII-i are GO:0019953_sexual reproduction, GO:0019882_antigen processing and presentation, GO:0040011_locomotion, GO:0032504_multicellular organism reproduction, GO:0040007_growth. GO analysis of loci of single transcript loci (**b**, left) and alternatively spliced transcript loci (**b**, right) between CVI, CVII, CVIII-i and CVIII-ii. Next we tested GO enrichments of CV groups are affected by the loci with single or alternative spliced transcripts. The number of loci with single and alternative spliced transcripts are 16,999 and 5844, respectively. The number of loci with single transcript (16,999) are 4,172, 4,607, 3,154, 5,056 according to the groups of CVI, CVII, CVIII-I, and CVIII-ii, respectively. For these genes, GO enrichments are tested. GO:0009657_plastid organization is highly enriched by single transcript in CVI. GO terms that are moderately enriched by single transcript in CVI are GO:0051704_multi-organism process, GO:0002376_immune system process, GO:0061024_membrane organization, GO:0071554_cell wall organization or biogenesis, GO:0001906_cell killing, GO:0023052_signaling, GO:0031163_metallo-sulfur cluster assembly, GO:0040007_growth. GO terms that are moderately enriched by single transcript in CVII are GO:0009987_cellular process, GO:0000003_reproduction, GO:0044848_biological phase, GO:0080165_callose deposition in phloem sieve plate, GO:0002252_immune effector process. GO terms that are enriched by genes with single transcript in CVI and CVII are GO:0032501_multicellular organismal process, GO:0032502_developmental process, GO:0050896_response to stimulus, GO:0044699_single-organism process, GO:0065007_biological regulation. GO terms that are moderately enriched by single transcript in CVIII-i are GO:0009453_energy taxis, GO:0022622_root system development, GO:0031647_regulation of protein stability, GO:0044419_interspecies interaction between organisms, GO:0010229_inflorescence development, GO:0009615_response to virus, GO:0002683_negative regulation of immune system process, GO:0043901_negative regulation of multi-organism process. The number of loci with alternatively spliced transcripts (5844) are 690, 1276, 1632, 2246 according to the groups of CVI, CVII, CVIII-i, and CVIII-ii, respectively. In general the GO enrichement by the loci with alternative spliced transcripts are in agreement with those of the loci with single transcript. A exception is GO:0040007_growth. The term is highly enriched in this group while that of loci with single transcript is enriched a little bit. For these genes, GO enrichments are tested. GO terms are enrinched by CVI, CVII, CVIII-i are GO:0032501_multicellular organismal process, GO:0065007_biological regulation, GO:0032502_developmental process, GO:0051179_localization, GO:0071840_cellular component organization or biogenesis, GO:0044699_single-organism process, GO:0050896_response to stimulus, GO:0051704_multi-organism process, GO:0002376_immune system process, GO:0009987_cellular process, GO:0008152_metabolic process. GO:0040011_locomotion, GO:0044848_biological phase, GO:0007610_behavior are moderately enriched in CVI, CVII, CVIII-I, respectively.

c GO analysis of loci of whole genes between CVI, CVII, CVIII-i and CVIII-ii based on RNA-Seq dataset. In the analysis, 47 GO terms are enriched by RNA-Seq while 25 terms are by ASDM. Generally speaking, many terms are overlapped in both analyses such as GO:0032501_multicellular organismal process, GO:0065007_biological regulation, GO:0050896_response to stimulus, and GO:0009987_cellular process. Among 20 highly enriched processes by RNA-Seq 14 terms are found in ASDM. GO terms that are enriched in CVI and CVII are GO:0008152_metabolic process, GO:0050896_response to stimulus, GO:0044699_single-organism process, GO:0065007_biological regulation. GO:0071840_cellular component organization or biogenesis, GO:0022613_ribonucleoprotein complex biogenesis, GO:0009987_cellular process are also enriched in CVIII-i. GO:0010228_vegetative to reproductive phase transition of meristem GO:0097354_prenylation GO:0006914_autophagy GO:0070085_glycosylation are also enriched in CVIII-ii.

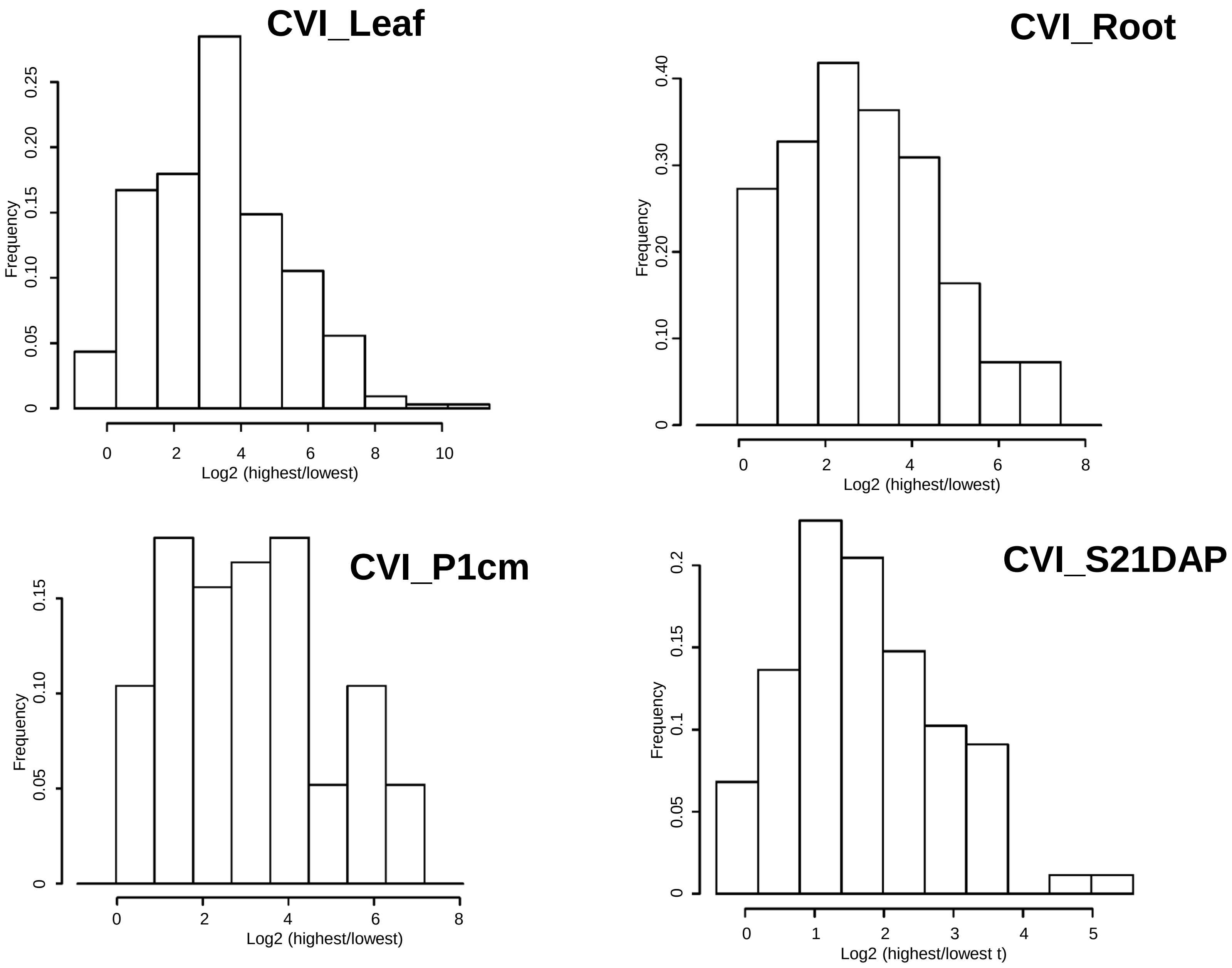


Fig. S7. Distribution of the highest and the lowest expression among alternatively spliced transcripts of the CVI: CVI_Leaf (f=323, mean=3.3, 9.9-fold , sd=1.9), CVI_Root (f=110, mean=2.9, 7.4- fold, sd=1.7), CVI_P1cm (f=78, mean=3.1, 8.5- fold, sd=1.8), and S21DAP (f=88, mean=3.4, 10.8- fold, sd=2.2).

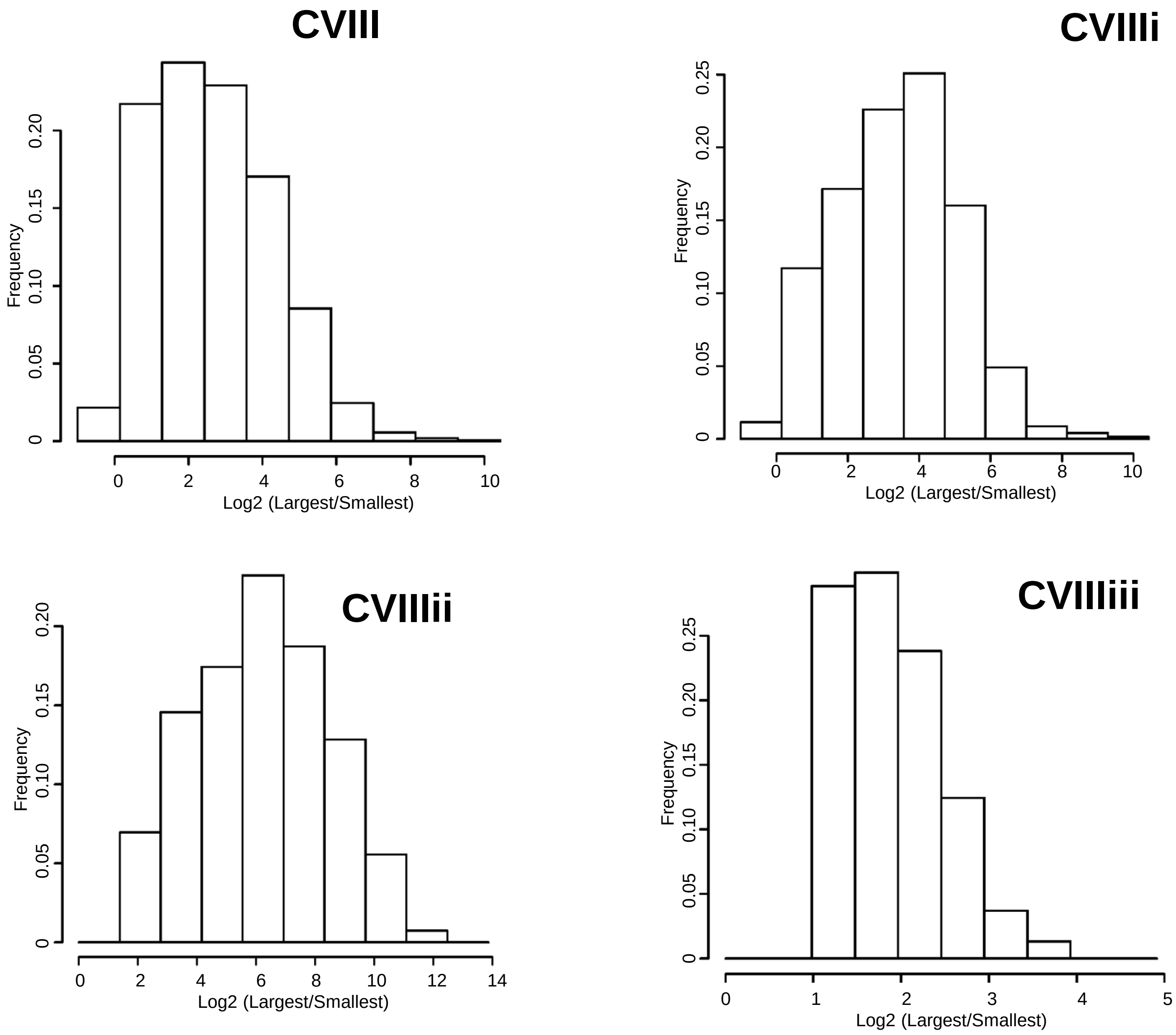


Fig. S8. Distribution of the highest and the lowest expression among alternatively spliced transcripts of the CVIII: CVIII (f=3382, mean=2.7, 6.3- fold, sd=1.6), CVIIIi (f=1488, mean=3.4, 10.5- fold, sd=1.7), CVIIIii (f=1244, mean=2.1, 4.3- fold, sd=1.1) and CVIIIiii (f=379, mean=0.9, 1.9- fold, sd=0.6)

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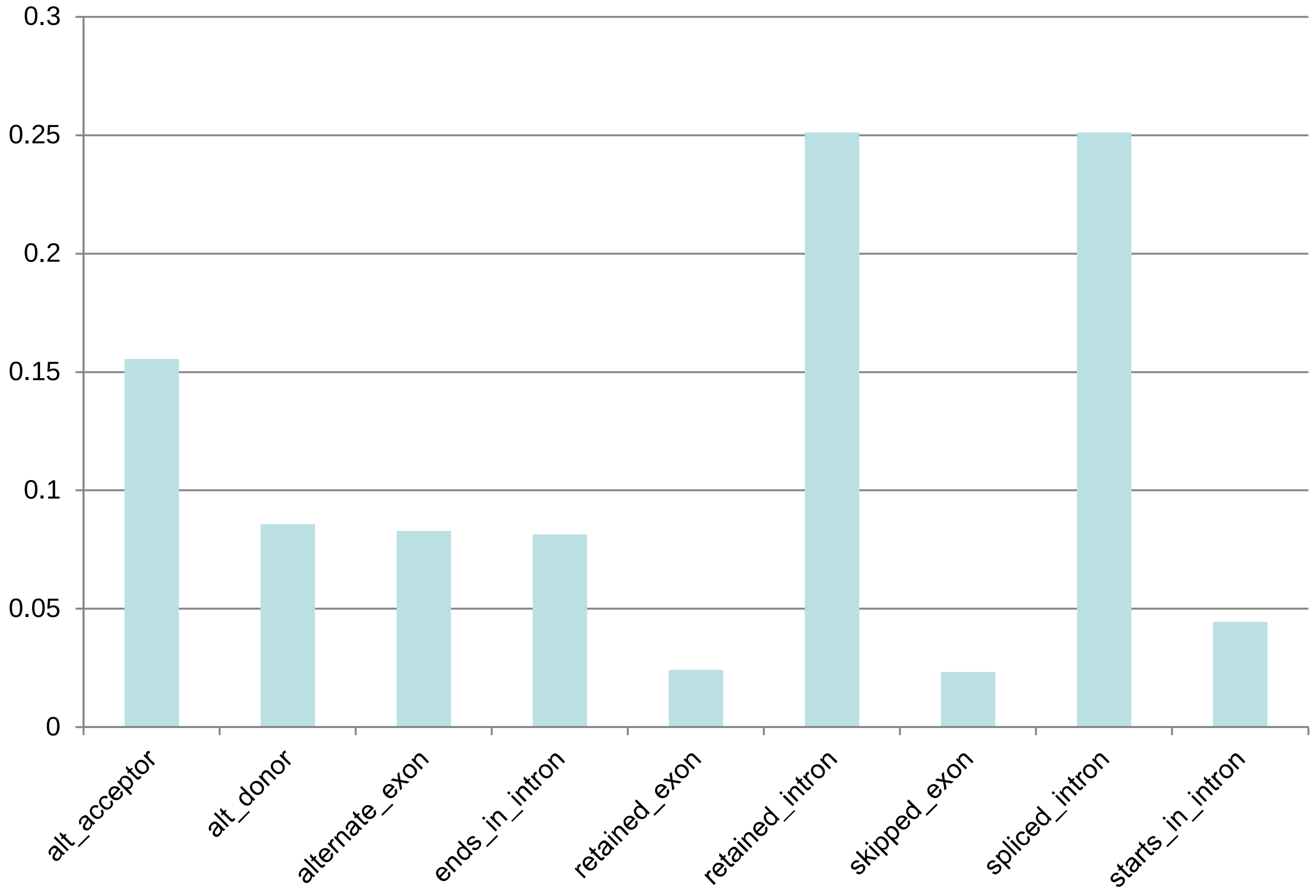

Fig. S9. Types of alternative splicing which affect the expression. Types are denoted as in Table S8
Campbell et al. classified the type of alternative splicing into 9 groups base on the results of the Program to Assemble Spliced Alignments (PASA, Campbell et al., 2006); Alternate Acceptor (AA), Alternate Donor (AD), Alternate Terminal Exon (ATE), Retained Exon and Skipped Exon (RE/SE), Initiation within an Intron (IWI), Termination within an Intron (TWI), and Spliced Intron and Retained Intron (RI/SI). PASA detected 5,028 alternative splicing from 2,438 loci .