

Supplementary Materials

Figure supplementary legends

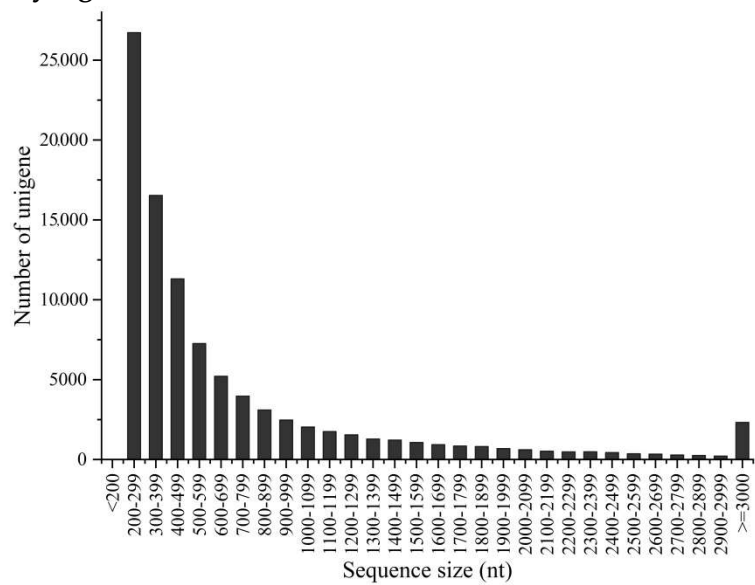


Figure S1. Length distribution of assembled unigenes.

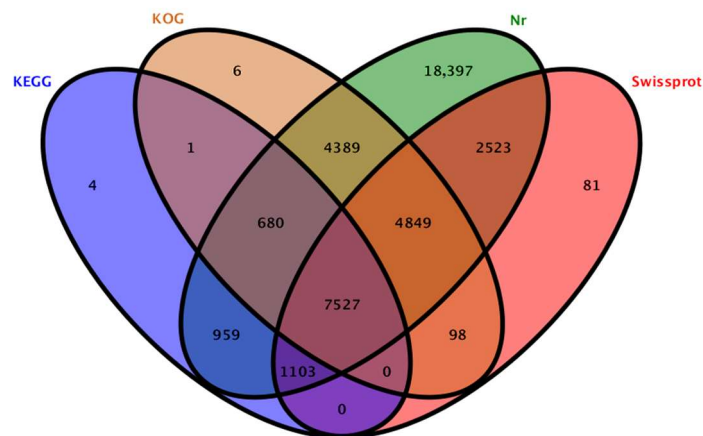


Figure S2. Basic annotation for all unigenes in *C. songaricum* on KEGG, KOG, Nr and Swissprot databases.

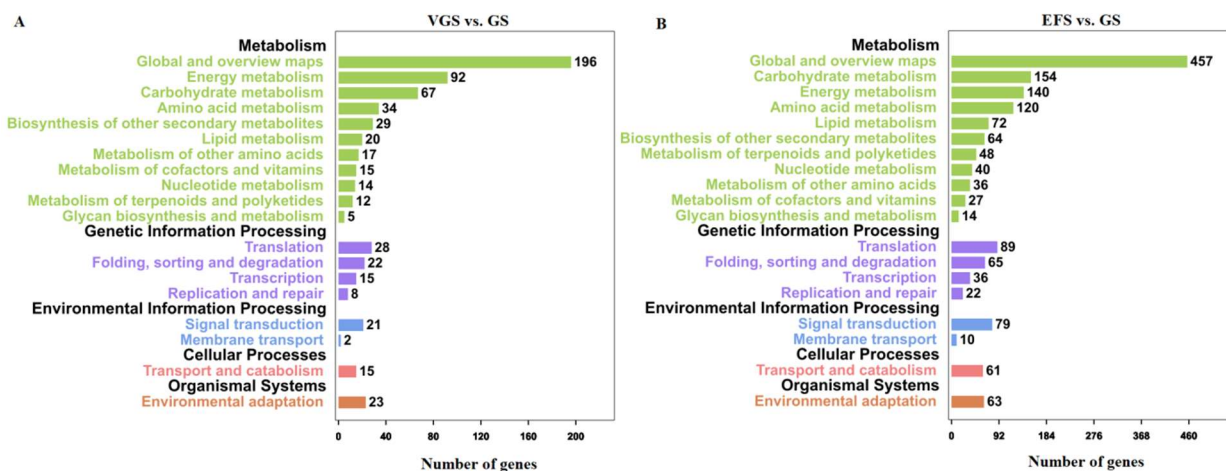
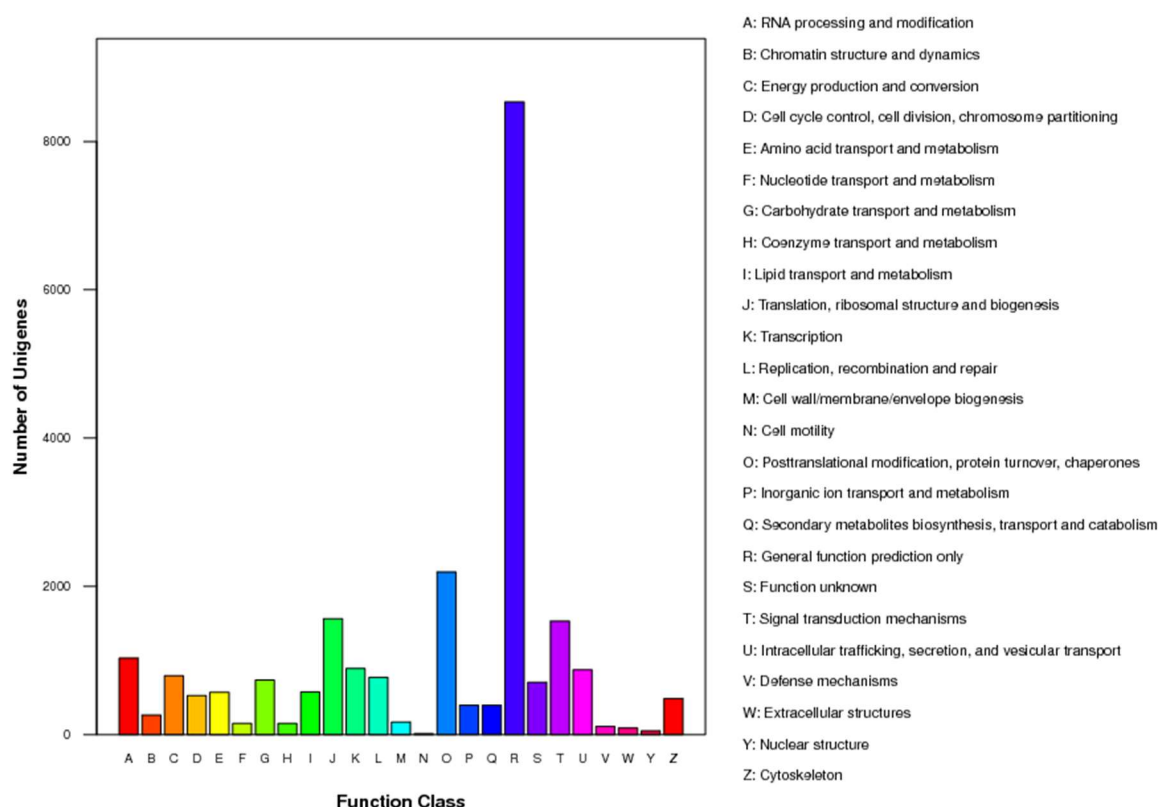
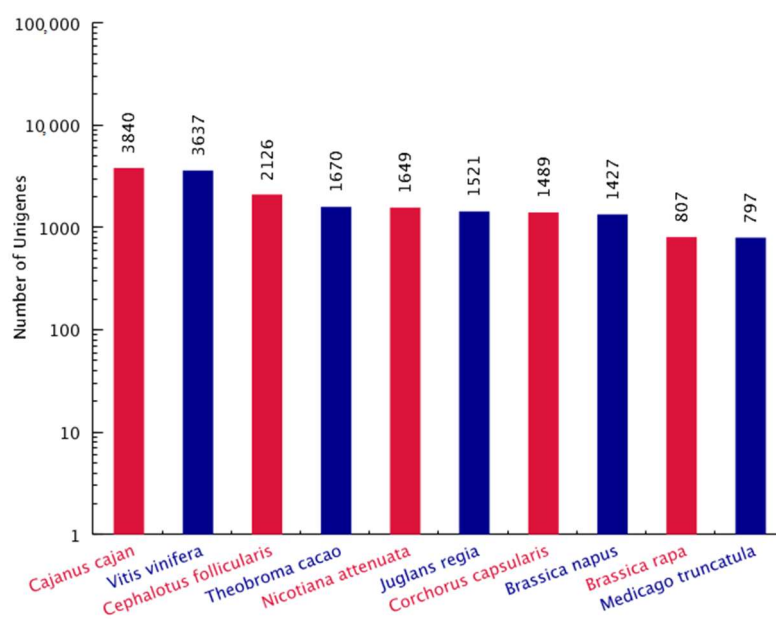


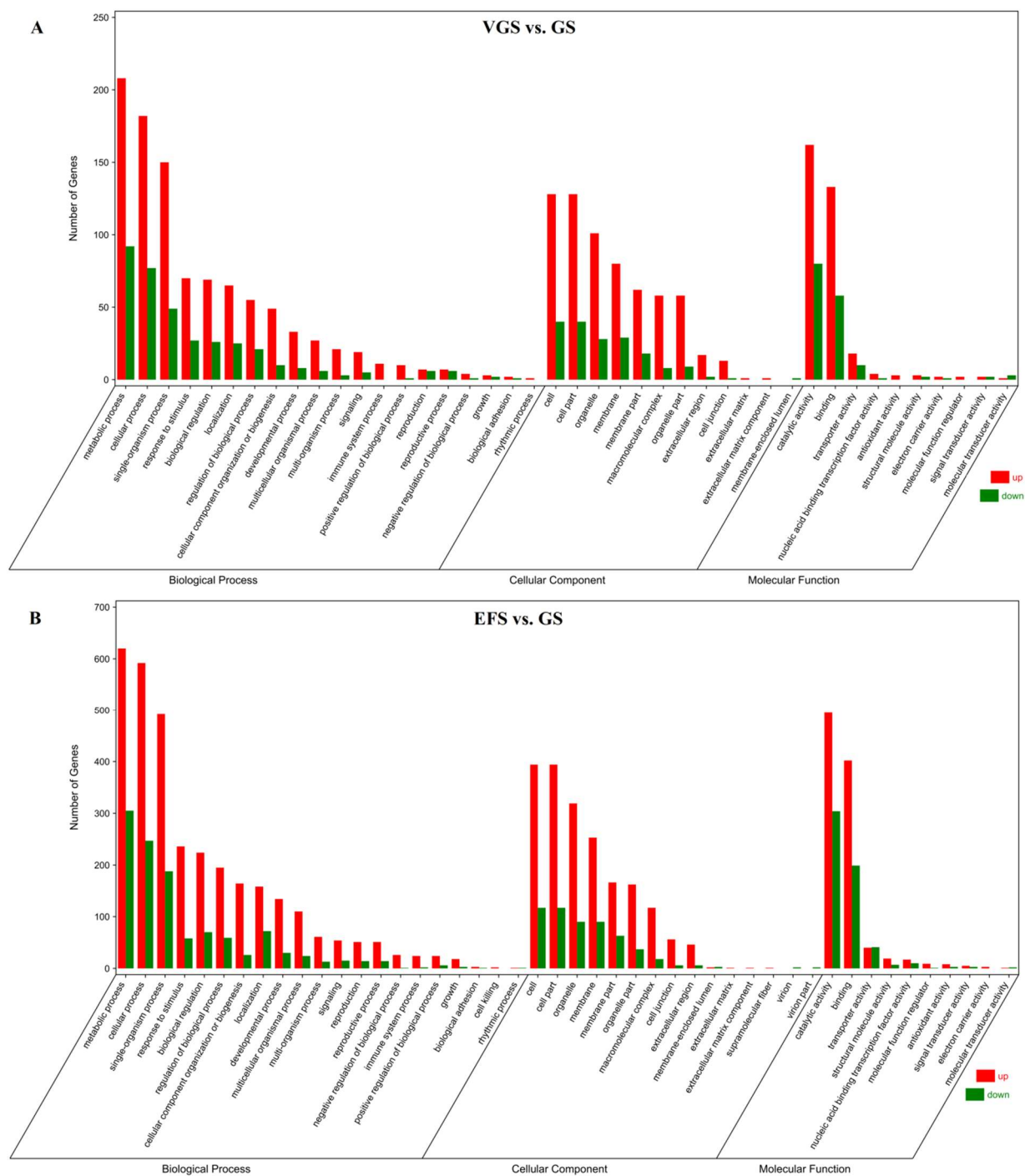
Figure S3. KEGG enrichment of DEGs at VGS vs. GS (A) and EFS vs. GS (B).



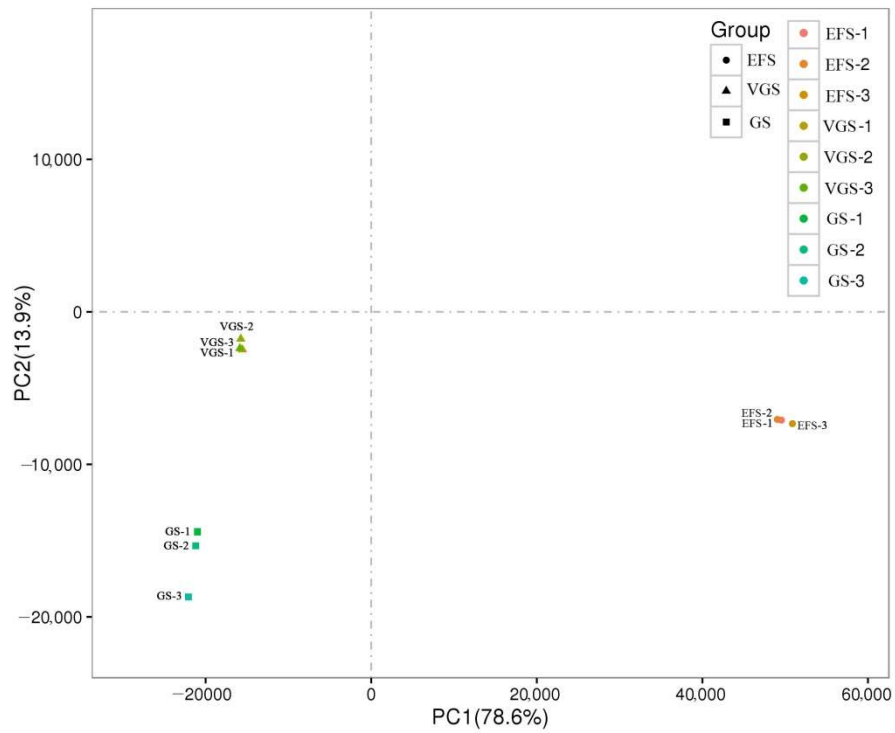
**Figure S4.** Distribution of unigenes in the transcriptome with KOG functional classification.



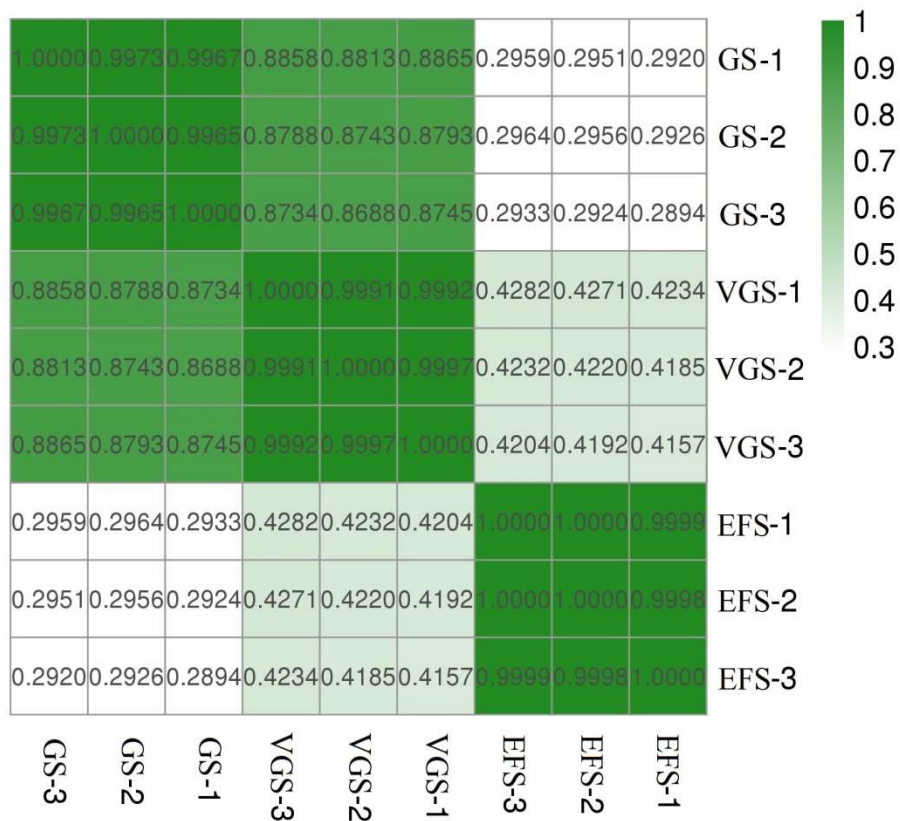
**Figure S5.** Annotation of unigenes on NR database and distribution of the top 10 species.



**Figure S6.** Annotation of unigenes on GO database and biological classification.



**Figure S7.** Principal component analysis (PCA) of GS, VGS and EFS.



**Figure S8.** Pearson correlation analysis of GS, VGS and EFS.



Figure S9. Growth characteristics of *C. songaricum* between the VGS and EFS.

## Table supplementary legends

**Table S1.** Twenty-four genes involved in polysaccharide biosynthesis at VGS and EFS vs. GS.

Gene name	SwissProt ID	Protein name	log <sub>2</sub> FC (VGS vs. GS)	log <sub>2</sub> FC (EFS vs. GS)
<b>Glucose (5)</b>				
<i>BGLU23</i>	Q9SR37	Beta-glucosidase 23	9.74	9.87
<i>BGLU44</i>	Q9LV33	Beta-glucosidase 44	−1.51	−2.89
<i>At5g56590</i>	Q9FJU9	Glucan endo-1,3-beta-glucosidase 13	1.11	−2.73
<i>GAPA</i>	P09043	Glyceraldehyde-3-phosphate dehydrogenase A	9.00	9.25
<i>MTH_209</i>	O26311	Glyceraldehyde 3-phosphate phosphatase	1.07	1.35
<b>Sucrose (2)</b>				
<i>INVA</i>	P29001	Acid beta-fructofuranosidase	1.71	5.08
<i>BFRUCT3</i>	Q43348	Acid beta-fructofuranosidase 3	5.29	8.64
<b>Fructose (3)</b>				
<i>FBA2</i>	Q944G9	Fructose-bisphosphate aldolase 2, chloroplastic	6.70	5.85
<i>PFP-BETA</i>	P21343	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta	−1.41	−2.94
<i>At3g55800</i>	P46283	Sedoheptulose-1,7-bisphosphatase	7.54	7.29
<b>Xylan (6)</b>				
<i>BXL5</i>	Q9LJN4	Probable beta-D-xylosidase 5	1.76	1.29
<i>GT17</i>	Q9CA34	Probable xyloglucan galactosyltransferase GT17	−1.08	−2.43
<i>TBL19</i>	Q9LFT0	Protein trichome birefringence-like 19	1.14	2.45
<i>TBL31</i>	Q1PFD9	Protein trichome birefringence-like 31	1.78	2.50
<i>ESK1</i>	Q9LY46	Xylan O-acetyltransferase 1	1.25	2.34
<i>XTH9</i>	Q8LDW9	Xyloglucan endotransglucosylase/hydrolase protein 9	1.52	4.77
<b>Trehalose (1)</b>				
<i>TPPF</i>	Q9SU39	Probable trehalose-phosphate phosphatase F	1.46	4.05
<b>Pectin (7)</b>				
<i>PAE8</i>	Q6DBP4	Pectin acylesterase 8	1.05	3.55
<i>GAUT12</i>	Q9FH36	Probable galacturonosyltransferase 12	1.06	2.16
<i>At5g63180</i>	Q93Z25	Probable pectate lyase 22	3.02	1.32
<i>PME7</i>	Q9SRX4	Probable pectinesterase/pectinesterase inhibitor 7	1.31	1.73
<i>PMEI10</i>	Q9SI74	Pectinesterase inhibitor 10	−1.43	1.80
<i>PME15</i>	Q9ZQA3	Probable pectinesterase 15	1.32	−4.61
<i>PME40</i>	O81301	Probable pectinesterase/pectinesterase inhibitor 40	2.47	3.17

**Table S2.** Fifty-five genes involved in other primary metabolism at VGS and EFS vs. GS.

Gene name	SwissProt ID	Protein name	log <sub>2</sub> FC (VGS vs. GS)	log <sub>2</sub> FC (EFS vs. GS)
<b>Lipid and fatty acid catabolic process</b>				
<i>BEAT</i>	O64988	Acetyl-CoA-benzylalcohol acetyltransferase	1.84	− 5.09
<i>N/A</i>	O04353	Acyl-lipid (9-3)-desaturase	1.03	1.82
<i>AOC</i>	A2XID3	Allene oxide cyclase, chloroplastic	1.12	− 2.86
<i>At2g04020</i>	Q9SIF3	GDSL esterase/lipase At2g04020	− 1.54	− 2.06
<i>At3g26430</i>	Q9LIN2	GDSL esterase/lipase At3g26430	8.93	4.59
<i>At3g48460</i>	Q9STM6	GDSL esterase/lipase At3g48460	1.12	2.09
<i>At5g33370</i>	Q8LB81	GDSL esterase/lipase At5g33370	2.40	7.12
<i>GPAT5</i>	Q9CAY3	Glycerol-3-phosphate acyltransferase 5	2.86	2.39
<i>GDPD1</i>	Q9SGA2	Glycerophosphodiester phosphodiesterase GDPD1, chloroplastic	3.29	3.27
<i>NPC4</i>	Q9SRQ7	Non-specific phospholipase C4	2.51	2.31
<i>HB2</i>	Q93Y92	Non-symbiotic hemoglobin 2	− 1.34	− 1.19
<i>MATP6-A</i>	P29527	Oleosin 18.2 kDa	2.21	1.87
<i>At4g25140</i>	P29525	Oleosin 18.5 kDa	5.16	5.31
<i>MTM1</i>	F4J3T8	Phosphatidylinositol-3-phosphatase myotubularin-1	1.66	1.73
<i>At4g16820</i>	O23522	Phospholipase A1-Ibata2, chloroplastic	2.27	− 2.55

<i>NMT2</i>	Q944H0	Phosphomethylethanolamine N-methyltransferase	1.14	2.36
<i>At5g60760</i>	Q9FJH9	P-loop NTPase domain-containing protein LPA1 homolog 1	11.36	9.91
<i>LPPB</i>	Q9SUW4	Probable lipid phosphate phosphatase beta	-1.06	-1.48
<i>CER2</i>	Q39048	Protein ECERIFERUM 2	-1.45	-1.09
<i>At1g17710</i>	Q9FZ62	Inorganic pyrophosphatase 2	-1.38	-4.58
<b>Amino acid metabolism</b>				
<i>serA</i>	O29445	D-3-phosphoglycerate dehydrogenase	-6.41	-2.82
<i>GEK1</i>	Q9ZPQ3	D-aminoacyl-tRNA deacylase	9.41	7.71
<i>GGAT2</i>	Q9S7E9	Glutamate--glyoxylate aminotransferase 2	6.41	5.76
<i>GLN1-2</i>	Q8LCE1	Glutamine synthetase cytosolic isozyme 1-2	5.92	6.86
<i>GLN2</i>	O22506	Glutamine synthetase, chloroplastic	9.22	9.34
<i>GLN4</i>	P15102	Glutamine synthetase leaf isozyme, chloroplastic	9.84	9.84
<i>OVA9</i>	Q8W4F3	Glutamine--tRNA ligase, cytoplasmic	-1.23	-2.69
<i>GRXC3</i>	Q6K609	Glutaredoxin-C3	2.75	4.50
<i>GRXC6</i>	Q8L9S3	Glutaredoxin-C6	-1.04	1.10
<i>GGT3</i>	Q9M0G0	Glutathione hydrolase 3	-1.18	-5.02
<i>GSTF10</i>	P42761	Glutathione S-transferase F10	9.15	8.81
<i>GSTF12</i>	Q9FE46	Glutathione S-transferase F12	3.08	2.62
<i>DHAR2</i>	Q67UK9	Probable glutathione S-transferase DHAR2, chloroplastic	10.97	10.98
<i>At2g30660</i>	Q6NMB0	Probable 3-hydroxyisobutyryl-CoA hydrolase 3	1.30	2.55
<i>AGT1</i>	Q56YA5	Serine--glyoxylate aminotransferase	10.27	9.65
<i>GLYM1</i>	P49357	Serine hydroxymethyltransferase 1, mitochondrial	9.87	9.93
<i>GLYM2</i>	P49358	Serine hydroxymethyltransferase 2, mitochondrial	9.87	9.62
<b>Others associated with carbohydrate metabolism</b>				
<i>ADH2</i>	P04707	Alcohol dehydrogenase 2	-1.03	-1.78
<i>ACA7</i>	Q8L817	Alpha carbonic anhydrase 7	-2.56	-1.72
<i>CAHC</i>	P17067	Carbonic anhydrase, chloroplastic	11.10	10.83
<i>CTL2</i>	Q9LSP9	Chitinase-like protein 2	-1.13	-2.20
<i>ChiC</i>	O81862	Class V chitinase	-1.47	-2.53
<i>CYN</i>	A5BJL8	Cyanate hydratase	-1.34	-5.26
<i>CEL5</i>	Q2V4L8	Endoglucanase 3	1.62	1.43
<i>GH5FP</i>	C0HLA0	Glycosyl hydrolase 5 family protein	1.83	5.77
<i>HPPR</i>	Q65CJ7	Hydroxyphenylpyruvate reductase	8.21	9.74
<i>MDHG</i>	P46488	Malate dehydrogenase, glyoxysomal	9.08	9.08
<i>KPPR</i>	P27774	Phosphoribulokinase, chloroplastic	9.60	9.17
<i>At1g56190</i>	P50318	Phosphoglycerate kinase 2, chloroplastic	10.39	10.28
<i>At5g64460</i>	Q9FGF0	Phosphoglycerate mutase-like protein 1	1.09	1.26
<i>AKR1</i>	C6TBN2	Probable aldo-keto reductase 1	8.64	9.26
<i>PP2A10</i>	Q9SY57	Protein PHLOEM PROTEIN 2-LIKE A10	-12.07	-9.24
<i>SDR2b</i>	Q9ZUH5	Short-chain dehydrogenase/reductase 2b	1.06	1.13
<i>TKL-2</i>	F4IW47	Transketolase-2, chloroplastic	6.08	5.48
<i>TKT3</i>	Q42676	Transketolase, chloroplastic	8.79	9.38

**Table S3.** Eleven genes involved in flavonoid biosynthesis at VGS and EFS vs. GS.

Gene name	SwissProt ID	Protein name	log <sub>2</sub> FC (VGS vs. GS)	log <sub>2</sub> FC (EFS vs. GS)
<i>4CLL1</i>	Q9LQ12	4-coumarate-CoA ligase-like 1	1.45	1.73
<i>4CLL6</i>	Q84P24	4-coumarate-CoA ligase-like 6	3.33	8.48
<i>HST</i>	Q9FI78	Shikimate O-hydroxycinnamoyltransferase	1.67	2.09
<i>CHI3</i>	Q8VZW3	Probable chalcone--flavanone isomerase 3	1.57	1.24
<i>CAD9</i>	P42734	Probable cinnamyl alcohol dehydrogenase 9	1.10	-1.70
<i>CYP714C2</i>	Q2QYH7	Cytochrome P450 714C2	1.45	1.59
<i>CYP93B1</i>	P93149	Licodione synthase	1.22	1.42
<i>F6'H1</i>	Q9LHN8	Feruloyl CoA ortho-hydroxylase 1	2.11	-11.78
<i>UGT84A13</i>	V5LLZ9	Gallate 1-beta-glucosyltransferase	2.52	2.02
<i>UGT87A1</i>	O64732	UDP-glycosyltransferase 87A1	-1.97	-3.00
<i>UGT94E5</i>	F8WKW8	Beta-D-glucosyl crocetin beta-1,6-glucosyltransferase	1.09	-4.50

**Table S4.** Five genes involved in terpene biosynthesis at VGS and EFS vs. GS.

Gene name	SwissProt ID	Protein name	log <sub>2</sub> FC (VGS vs. GS)	log <sub>2</sub> FC (EFS vs. GS)
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<i>PINS</i>	O23945	(-)-alpha-pinene synthase	7.16	5.41
<i>CYP716A15</i>	F6H9N6	Beta-amyrin 28-monooxygenase	1.08	- 3.20
<i>CYP716A52v2</i>	I7C6E8	Beta-amyrin 28-monooxygenase	2.27	5.02
<i>GGR</i>	Q39108	Heterodimeric geranylgeranyl pyrophosphate synthase small subunit	1.38	2.55
<i>STPS1</i>	B5A435	Sesquiterpene synthase	8.57	6.09

**Table S5.** Twenty genes involved in cell growth and flower development at VGS and EFS vs. GS.

Gene name	SwissProt ID	Protein name	log <sub>2</sub> FC (VGS vs. GS)	log <sub>2</sub> FC (EFS vs. GS)
<b>Cell growth (9)</b>				
<i>AC58</i>	P30167	Actin-58	8.64	8.99
<i>ADF</i>	P30175	Actin-depolymerizing factor	1.06	1.65
<i>ATJ11</i>	Q9FYB5	Chaperone protein dnaJ 11	- 1.10	1.88
<i>CYCP3-1</i>	Q75HV0	Cyclin-P3-1	1.19	2.77
<i>SDS</i>	Q1PFW3	Cyclin-SDS	4.69	5.72
<i>LRX6</i>	Q9LUI1	Leucine-rich repeat extensin-like protein 6	1.51	1.85
<i>MIZ1</i>	O22227	Protein MIZU-KUSSEI 1	- 1.43	- 1.06
<i>PATROL1</i>	Q8RX56	Protein unc-13 homolog	- 1.16	- 1.35
<i>TBB7</i>	Q6VAF5	Tubulin beta-7 chain	9.49	9.43
<b>Flower development (11)</b>				
<i>CSLD4</i>	Q9SZL9	Cellulose synthase-like protein D4	- 3.38	- 1.88
<i>EXLB1</i>	O23547	Expansin-like B1	- 1.05	- 2.71
<i>AP1</i>	P35631	Floral homeotic protein APETALA 1	2.74	8.25
<i>ASOL</i>	P29162	L-ascorbate oxidase homolog	1.19	2.88
<i>AMP1</i>	Q9M1S8	Probable glutamate carboxypeptidase AMP1	- 1.02	- 4.74
<i>TKPR2</i>	Q9CA28	Tetraketide alpha-pyrone reductase 2	1.23	1.34
<i>TCTP1</i>	P31265	Translationally-controlled tumor protein 1	9.23	10.45
<i>CYP704B1</i>	Q9C788	Cytochrome P450 704B1	1.86	1.92
<i>HAT</i>	Q9M2N5	Zinc finger BED domain-containing protein DAYSLEEPER	- 7.25	- 4.08
<i>Os05g0239150</i>	B9FJG3	Zinc finger BED domain-containing protein RICESLEEPER 1	- 1.62	- 1.44
<i>Os05g0583200</i>	Q75HY5	Zinc finger BED domain-containing protein RICESLEEPER 3	2.13	2.50

**Table S6.** Eight genes involved in other cell morphogenesis at VGS and EFS vs. GS.

Gene name	SwissProt ID	Protein name	log <sub>2</sub> FC (VGS vs. GS)	log <sub>2</sub> FC (EFS vs. GS)
<i>N/A</i>	Q9XHP0	11S globulin seed storage protein 2	- 7.63	- 3.80
<i>AT2S1</i>	P15457	2S seed storage protein 1	10.08	10.97
<i>CRA1</i>	P15455	12S seed storage protein CRA1	3.64	4.26
<i>CRB</i>	P15456	12S seed storage protein CRB	4.49	5.13
<i>SOP1</i>	Q9SQ57	Peroxygenase	4.98	4.19
<i>SBT1.3</i>	Q9FLI4	Subtilisin-like protease SBT1.3	- 1.72	- 4.13
<i>SBT1.7</i>	O65351	Subtilisin-like protease SBT1.7	- 2.90	- 3.08
<i>CYSEP</i>	O65039	Vignain	2.27	4.59

**Table S7.** Twenty-two genes involved in hormone biosynthesis and signaling at VGS and EFS vs. GS.

Gene name	SwissProt ID	Protein name	log <sub>2</sub> FC (VGS vs. GS)	log <sub>2</sub> FC (EFS vs. GS)
<b>Hormone biosynthesis (7)</b>				
<i>YUC8</i>	Q9SVU0	Probable indole-3-pyruvate monooxygenase YUCCA8	1.31	1.72
<i>AIPT</i>	Q5GHF7	Adenylate isopentenyltransferase	1.94	2.73
		Cytokinin riboside 5'-monophosphate phosphoribohydrolase	1.30	1.14
<i>LOG5</i>	Q8LBB7	LOG5		
<i>LE</i>	O24648	Gibberellin 3-beta-dioxygenase 1	- 2.11	- 3.91
<i>ACO1</i>	Q9MB94	1-aminocyclopropane-1-carboxylate oxidase	1.01	- 3.54
<i>ACS1</i>	P31531	1-aminocyclopropane-1-carboxylate synthase	1.07	- 2.70
<i>CYP707A6</i>	Q09J78	Absciscic acid 8'-hydroxylase 2	- 1.07	- 2.02



<b>Hormone signaling (15)</b>				
<i>AUX22D</i>	Q24542	Auxin-induced protein 22D	1.18	3.68
<i>ARP12.5</i>	Q05349	Auxin-repressed 12.5 kDa protein	- 1.83	- 2.75
<i>SAUR71</i>	Q9SGU2	Auxin-responsive protein SAUR71	3.44	3.82
<i>GH3.6</i>	Q9LSQ4	Indole-3-acetic acid-amido synthetase GH3.6	2.43	2.58
<i>PILS2</i>	Q9C999	Protein PIN-LIKES 2	- 2.00	- 4.95
<i>AHK4</i>	Q9C5U0	Histidine kinase 4	4.25	3.47
<i>JOX2</i>	Q9FFF6	Jasmonate-induced oxygenase 2	1.52	- 7.98
<i>AIL1</i>	Q1PFE1	AP2-like ethylene-responsive transcription factor AIL1	- 1.63	1.23
<i>AIL6</i>	Q52QU2	AP2-like ethylene-responsive transcription factor AIL6	- 1.74	1.43
<i>ETR2</i>	Q0WPQ2	Ethylene receptor 2	- 1.03	- 1.95
<i>SHN3</i>	Q3E958	Ethylene-responsive transcription factor SHINE 3	- 1.10	- 1.97
<i>REF6</i>	Q9STM3	Lysine-specific demethylase REF6	4.79	3.80
<i>ERF010</i>	Q9FH94	Ethylene-responsive transcription factor ERF010	- 1.69	- 4.43
<i>ERF034</i>	Q8LBQ7	Ethylene-responsive transcription factor ERF034	- 1.12	1.49
<i>ERF114</i>	Q9FH54	Ethylene-responsive transcription factor ERF114	3.01	4.33

**Table S8.** Nineteen genes involved in other bio-signaling at VGS and EFS vs. GS.

Gene name	SwissProt ID	Protein name	log <sub>2</sub> FC (VGS vs. GS)	log <sub>2</sub> FC (EFS vs. GS)
<b>Protein kinase</b>				
<i>KRP7</i>	Q94CL9	Cyclin-dependent kinase inhibitor 7	1.04	3.62
<i>CRK36</i>	Q9XEC6	Cysteine-rich receptor-like protein kinase 36	2.31	3.69
<i>LECRK2</i>	A2XQD3	G-type lectin S-receptor-like serine/threonine-protein kinase LECRK2	- 2.01	- 7.27
<i>ERECTA</i>	Q42371	LRR receptor-like serine/threonine-protein kinase ERECTA	- 1.07	1.95
<i>SERPINE1</i>	P13909	Plasminogen activator inhibitor 1	- 9.18	- 9.18
<i>At1g35710</i>	Q9LP24	Probable leucine-rich repeat receptor-like protein kinase At1g35710	- 5.21	- 5.59
<i>At5g18500</i>	Q8LEB6	Probable receptor-like protein kinase At5g18500	1.26	2.95
<i>PERK4</i>	Q9ZNQ8	Proline-rich receptor-like protein kinase PERK4	- 1.11	- 3.82
<i>TMK4</i>	Q9LK43	Receptor-like kinase TMK4	1.98	1.07
<i>SCPL31</i>	O04084	Serine carboxypeptidase-like 31	- 2.83	- 3.04
<i>SCPL40</i>	Q0WRX3	Serine carboxypeptidase-like 40	- 4.44	- 6.83
<i>UNC</i>	Q9SYB9	Serine/threonine-protein kinase UCN	- 2.14	- 2.48
<b>Calcium</b>				
<i>RALFL4</i>	Q9FZA0	Protein RALF-like 4	1.59	1.20
<b>Others</b>				
<i>GF14C</i>	Q6ZKC0	14-3-3-like protein GF14-C	6.78	5.98
<i>CLE3</i>	Q3EDH8	CLAVATA3/ESR (CLE)-related protein 3	- 1.89	- 1.28
<i>CLE27</i>	Q9LUA1	CLAVATA3/ESR (CLE)-related protein 27	- 1.53	- 1.37
<i>TIMP1</i>	P20414	Metalloproteinase inhibitor 1	- 10.05	- 10.05
<i>ADM</i>	O62827	Pro-adrenomedullin	- 9.72	- 5.21
<i>At4g32285</i>	Q8S9J8	Probable clathrin assembly protein At4g32285	2.16	3.28

**Table S9.** Twenty-eight TFs involved in flavonoid biosynthesis as well as growth and development at VGS and EFS vs. GS.

Gene name	SwissProt ID	Protein name	log <sub>2</sub> FC (VGS vs. GS)	log <sub>2</sub> FC (EFS vs. GS)
<b>Flavonoid biosynthesis (12)</b>				
<b>MYB (6)</b>				
<i>LIMYB</i>	Q9FFJ8	L10-interacting MYB domain-containing protein	1.45	- 3.00
<i>MYB2</i>	Q10MB4	Transcription factor MYB2	- 5.00	- 11.58
<i>MYB14</i>	Q9SJX8	Transcription factor MYB14	2.21	- 2.24
<i>MYB52</i>	Q6R0C4	Transcription factor MYB52	1.66	2.56
<i>MYB83</i>	Q9C6U1	Transcription factor MYB83	1.22	2.58
<i>MYB306</i>	P81392	Myb-related protein 306	1.37	1.64
<b>bHLH (2)</b>				
<i>BHLH52</i>	Q9SA82	Transcription factor bHLH52	2.78	4.75
<i>BHLH94</i>	Q9SK91	Transcription factor bHLH94	1.31	- 1.83

<b>WRKY (4)</b>				
<i>WRKY6</i>	Q9C519	WRKY transcription factor 6	1.66	- 1.52
<i>WRKY53</i>	Q9SUP6	Probable WRKY transcription factor 53	1.57	2.26
<i>WRKY70</i>	Q9LY00	Probable WRKY transcription factor 70	- 1.20	- 3.28
<i>WRKY72</i>	Q9LXG8	Probable WRKY transcription factor 72	- 3.38	- 1.24
<b>Growth and development (16)</b>				
<b>Cell growth (8)</b>				
<i>DREB2D</i>	Q9LQZ2	Dehydration-responsive element-binding protein 2D	1.03	- 1.86
<i>DREB3</i>	Q9LYD3	Dehydration-responsive element-binding protein 3	1.82	2.40
<i>At2g01810</i>	Q9ZUA9	PHD finger protein At2g01810	- 1.74	- 3.64
<i>MMD1</i>	Q7X6Y7	PHD finger protein MALE MEIOCYTE DEATH 1	- 1.26	- 2.55
<i>PRE5</i>	Q9LJX1	Transcription factor PRE5	2.72	6.87
<i>TCP9</i>	O64647	Transcription factor TCP9	2.19	2.94
<i>TCP18</i>	A1YKT1	Transcription factor TCP18	- 1.07	- 1.29
<i>UPB1</i>	O22901	Transcription factor UPBEAT1	1.68	2.19
<b>Flower development (8)</b>				
<i>AHL17</i>	Q9LTA2	AT-hook motif nuclear-localized protein 17	- 1.00	- 4.88
<i>AHL20</i>	Q8GWQ2	AT-hook motif nuclear-localized protein 20	- 2.43	- 9.22
<i>AHL22</i>	O22130	AT-hook motif nuclear-localized protein 22	- 1.28	- 2.70
<i>AHL23</i>	O23620	AT-hook motif nuclear-localized protein 23	- 1.23	- 3.81
<i>MIP1B</i>	Q9LRM4	B-box domain protein 31	2.02	1.75
<i>HEC2</i>	Q9SND4	Transcription factor HEC2	- 2.58	- 4.44
<i>SCRM</i>	Q9LSE2	Transcription factor ICE1	1.46	3.35
<i>PAN</i>	Q9SX27	Transcription factor PERIANTHIA	- 2.45	- 2.20

**Table S10.** Ten genes involved in other TFs at VGS and EFS vs. GS.

Gene name	SwissProt ID	Protein name	log <sub>2</sub> FC (VGS vs. GS)	log <sub>2</sub> FC (EFS vs. GS)
<b>B3 domain-containing protein</b>				
<i>ARF31</i>	Q8GYJ2	B3 domain-containing protein At2g36080	- 2.26	- 1.67
<i>Os03g0120900</i>	Q8LMR9	B3 domain-containing protein Os03g0120900	1.85	2.19
<i>Os12g0591300</i>	Q2QMT7	B3 domain-containing protein Os12g0591400	1.19	- 1.91
<b>Transcription repressor</b>				
<i>OFPP7</i>	Q9ZU65	Transcription repressor OFP7	2.80	1.08
<i>OFPP11</i>	O23341	Transcription repressor OFP11	1.18	1.35
<i>OFPP14</i>	Q9S7T5	Transcription repressor OFP14	- 1.41	- 2.75
<b>Zipper protein</b>				
<i>ATHB-40</i>	O23208	Homeobox-leucine zipper protein ATHB-40	- 1.82	- 1.99
<i>At1g68200</i>	Q9C9F5	Zinc finger CCCH domain-containing protein 15	1.76	4.08
<i>At2g19810</i>	O82199	Zinc finger CCCH domain-containing protein 20	- 1.49	- 2.10
<i>ZHD1</i>	A2Z259	Zinc-finger homeodomain protein 1	- 2.82	2.22

**Table S11.** Six genes involved in polysaccharide transport at VGS and EFS vs. GS.

Gene name	SwissProt ID	Protein name	log <sub>2</sub> FC (VGS vs. GS)	log <sub>2</sub> FC (EFS vs. GS)
<b>Sugar transporter (3)</b>				
<i>SWEET5</i>	Q9FM10	Bidirectional sugar transporter SWEET5	6.27	7.12
<i>slc37a2</i>	Q7SY29	Glucose-6-phosphate exchanger SLC37A2	10.56	8.73
<i>At5g55950</i>	Q9FG70	Nucleotide-sugar uncharacterized transporter 2	1.03	1.13
<b>ABC transporter family (3)</b>				
<i>ABCB2</i>	Q8LPK2	ABC transporter B family member 2	6.70	3.86
<i>ABCG1</i>	O80946	ABC transporter G family member 1	- 1.08	- 1.08
<i>ABCG22</i>	Q93YS4	ABC transporter G family member 22	- 1.28	- 1.17

**Table S12.** Thirty-three genes involved in other transport at VGS and EFS vs. GS.

Gene name	SwissProt ID	Protein name	log <sub>2</sub> FC (VGS vs. GS)	log <sub>2</sub> FC (EFS vs. GS)
<b>Protein transport</b>				

<i>ATG16L1</i>	Q5RAC9	Autophagy-related protein 16-1	1.04	1.67
<i>PEX12</i>	Q9M841	Peroxisome biogenesis protein 12	- 10.61	- 5.76
<i>SFH12</i>	Q9A434	Phosphatidylinositol/phosphatidylcholine transfer protein SFH12	2.04	1.69
<b>Lipid transport</b>				
<i>LTP</i>	Q39794	Non-specific lipid-transfer protein	- 3.61	- 1.36
<i>LTP4</i>	Q9LLR6	Non-specific lipid-transfer protein 4	9.47	9.93
<b>Amino acid transport</b>				
<i>CAT1</i>	Q84MA5	Cationic amino acid transporter 1	2.16	3.49
<i>BAC2</i>	Q9CA93	Mitochondrial arginine transporter BAC2	- 2.28	- 3.89
<b>Aquaporin</b>				
<i>PIP2-2</i>	P43287	Aquaporin PIP2-2	3.01	3.71
<i>TIP1-2</i>	Q41963	Aquaporin TIP1-2	8.55	9.36
<i>TIP2-1</i>	Q41951	Aquaporin TIP2-1	10.40	10.39
<i>TIP1-1</i>	P50156	Probable aquaporin TIP1-1	- 9.87	- 9.87
<b>Ion transport</b>				
<i>CHX17</i>	Q9SUQ7	Cation/H(+) antiporter 17	- 3.63	- 3.81
<i>IRT2</i>	Q6L8G1	Fe(2+) transport protein 2	- 4.54	- 1.87
<i>PHT1-4</i>	Q96303	Inorganic phosphate transporter 1-4	1.62	2.88
<i>MTP4</i>	Q10PP8	Metal tolerance protein 4	3.50	3.22
<i>MT4B</i>	Q42377	Metallothionein-like protein 4B	- 6.14	- 3.06
<i>MTI</i>	P30564	Metallothionein-like protein type 2	- 5.55	- 11.82
<i>NDT1</i>	Q22261	Nicotinamide adenine dinucleotide transporter 1	1.30	1.13
<i>CML18</i>	Q9M8U1	Probable calcium-binding protein CML18	- 2.77	- 4.27
<i>NHX1</i>	Q68KI4	Sodium/hydrogen exchanger 1	1.43	1.28
<i>CAX1</i>	Q39253	Vacuolar cation/proton exchanger 1	9.34	8.96
<i>ZIP3</i>	Q7XLD4	Zinc transporter 3	- 1.07	- 2.95
<b>Transmembrane transport</b>				
<i>DTX40</i>	Q9LVD9	Protein DETOXIFICATION 40	- 1.22	- 6.56
<i>DTX45</i>	Q9SVE7	Protein DETOXIFICATION 45	2.35	1.66
<i>At4g08290</i>	Q9SUF1	WAT1-related protein At4g08290	- 2.51	- 8.35
<b>Oligopeptide transport</b>				
<i>NPF4.3</i>	Q93VV5	Protein NRT1/ PTR FAMILY 4.3	- 1.01	- 5.37
<i>NPF5.6</i>	P0CI03	Protein NRT1/ PTR FAMILY 5.6	1.54	- 1.67
<i>NPF6.2</i>	Q9SZY4	Protein NRT1/ PTR FAMILY 6.2	- 1.01	- 1.22
<b>Virus transport</b>				
<i>POL</i>	P19199	Polyprotein P3	- 1.34	- 1.10
<i>POL2</i>	Q9YK98	RNA2 polyprotein	1.04	- 1.17
<b>Others</b>				
<i>XI-E</i>	F4HWY6	Myosin-11	- 1.12	- 1.33
<i>ORP1C</i>	Q8L751	Oxysterol-binding protein-related protein 1C	- 1.10	- 1.23
<i>At3g12180</i>	Q9C7D7	Protein cornichon homolog 1	1.76	1.62

**Table S13.** Forty-three genes involved in energy and photosynthesis at VGS and EFS vs. GS.

Gene name	SwissProt ID	Protein name	log <sub>2</sub> FC (VGS vs. GS)	log <sub>2</sub> FC (EFS vs. GS)
<b>Energy</b>				
<i>ATPD</i>	Q9SSS9	ATP synthase subunit delta, chloroplastic	10.03	9.44
<i>ATPC</i>	P29790	ATP synthase gamma chain, chloroplastic	9.33	8.37
<i>petC</i>	P26291	Cytochrome b6-f complex iron-sulfur subunit, chloroplastic	9.32	9.47
<i>MT-CO1</i>	Q6EMS9	Cytochrome c oxidase subunit 1	- 10.83	- 7.36
<i>COX6B-1</i>	Q9S7L9	Cytochrome c oxidase subunit 6b-1	11.01	10.41
<i>SEND33</i>	Q43517	Ferredoxin-1, chloroplastic	11.38	10.90
<i>PETH</i>	O04977	Ferredoxin--NADP reductase, leaf-type isozyme, chloroplastic	5.03	5.38
<i>GAPN</i>	P93338	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	2.27	1.16
<i>RCA1</i>	Q7X9A0	Ribulose biphosphate carboxylase/oxygenase activase 1, chloroplastic	8.75	8.31
<i>RCA2</i>	Q7X999	Ribulose biphosphate carboxylase/oxygenase activase 2, chloroplastic	12.79	12.35
<i>RBCS</i>	P31333	Ribulose biphosphate carboxylase small subunit, chloroplastic	14.83	14.67
<i>PETE</i>	P00299	Plastocyanin A, chloroplastic	12.18	12.32
<i>CYB561D</i>	Q9C540	Probable transmembrane ascorbate ferrereductase 4	1.29	2.57
<b>Photosynthesis</b>				
<i>LHCA4</i>	P27521	Chlorophyll a-b binding protein 4, chloroplastic	10.05	9.80
<i>LHCA1</i>	Q01667	Chlorophyll a-b binding protein 6, chloroplastic	10.22	9.89

<i>CAB7</i>	P10708	Chlorophyll a-b binding protein 7, chloroplastic	10.43	9.82
<i>CAB13</i>	P27489	Chlorophyll a-b binding protein 13, chloroplastic	8.91	8.90
<i>CAB21</i>	P27493	Chlorophyll a-b binding protein 21, chloroplastic	6.63	6.52
<i>CAB-151</i>	P27518	Chlorophyll a-b binding protein 151, chloroplastic	11.99	11.71
<i>CAP10A</i>	P27524	Chlorophyll a-b binding protein CP24 10A, chloroplastic	10.78	10.30
<i>LHCB4.1</i>	Q07473	Chlorophyll a-b binding protein CP29.1, chloroplastic	7.62	7.12
<i>HPR-A</i>	P13443	Glycerate dehydrogenase	8.85	9.18
<i>CRD1</i>	Q6SJV8	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic	9.23	8.96
<i>PSBO</i>	Q40459	Oxygen-evolving enhancer protein 1, chloroplastic	11.47	10.89
<i>PSBP1</i>	Q7DM39	Oxygen-evolving enhancer protein 2-1, chloroplastic	11.04	11.04
<i>PSBQ</i>	P12301	Oxygen-evolving enhancer protein 3, chloroplastic	10.66	10.44
<i>LHCA3</i>	Q9SY97	Photosystem I chlorophyll a/b-binding protein 3-1, chloroplastic	10.83	10.22
<i>psaD</i>	P12353	Photosystem I reaction center subunit II, chloroplastic	10.21	9.73
<i>PSAF</i>	Q9SHE8	Photosystem I reaction center subunit III, chloroplastic	10.06	9.48
<i>PSAE</i>	P13194	Photosystem I reaction center subunit IV, chloroplastic	10.20	9.66
<i>PSAEB</i>	Q41229	Photosystem I reaction center subunit IV B, chloroplastic	9.49	9.75
<i>PSAG</i>	Q9S7N7	Photosystem I reaction center subunit V, chloroplastic	10.61	9.96
<i>PSAH</i>	O04006	Photosystem I reaction center subunit VI, chloroplastic	6.73	7.06
<i>PSAN</i>	P49107	Photosystem I reaction center subunit N, chloroplastic	5.68	5.60
<i>PSAK</i>	Q9SUI5	Photosystem I reaction center subunit psaK, chloroplastic	10.93	10.79
<i>PSAO</i>	Q949Q5	Photosystem I subunit O	10.42	10.61
<i>PSBT</i>	P31336	Photosystem II 5 kDa protein, chloroplastic	10.35	10.40
<i>PSBR</i>	P06183	Photosystem II 10 kDa polypeptide, chloroplastic	11.50	11.23
<i>PSBY</i>	P80470	Photosystem II core complex proteins psbY, chloroplastic	10.39	9.83
<i>psbA</i>	Q7FNT3	Photosystem II protein D1	7.07	6.06
<i>PSY</i>	P49293	Phytoene synthase, chloroplastic	1.85	3.84
<i>CURT1A</i>	O04616	Protein CURVATURE THYLAKOID 1A, chloroplastic	9.37	9.38
<i>SPA3</i>	Q9LJR3	Protein SPA1-RELATED 3	2.61	4.04

**Table S14.** Twenty-nine genes involved in polynucleotide metabolism at VGS and EFS vs. GS.

Gene name	SwissProt ID	Protein name	log <sub>2</sub> FC (VGS vs. GS)	log <sub>2</sub> FC (EFS vs. GS)
<b>DNA replication</b>				
<i>NRPB11</i>	Q38859	DNA-directed RNA polymerases II, IV and V subunit 11	2.24	- 10.83
<i>LIG1</i>	Q42572	DNA ligase 1	- 10.99	- 10.99
<i>ENDO4</i>	F4JJL0	Endonuclease 4	- 1.23	- 1.40
<i>gag-pol</i>	P08361	Gag-Pol polyprotein	- 1.07	- 2.14
<i>gag-pro-pol</i>	P07572	Gag-Pro-Pol polyprotein	- 1.46	- 1.46
<i>ORC5</i>	Q6EWX0	Origin of replication complex subunit 5	1.18	1.74
<i>ORC6</i>	Q9ZVH3	Origin of replication complex subunit 6	1.24	2.45
<i>RTEL1</i>	A0A0P0V4R0	Regulator of telomere elongation helicase 1 homolog	1.07	1.15
<i>top6A</i>	O05208	Type 2 DNA topoisomerase 6 subunit A	- 1.02	- 1.29
<b>DNA integration</b>				
<i>pol</i>	Q8I7P9	Retrovirus-related Pol polyprotein from transposon opus	- 1.36	- 1.45
<i>RE1</i>	Q94HW2	Retrovirus-related Pol polyprotein from transposon RE1	- 3.09	- 3.72
<i>R2</i>	Q03274	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2	1.76	1.39
<b>DNA recombination</b>				
<i>Pol</i>	P11369	LINE-1 retrotransposable element ORF2 protein	- 1.81	- 1.19
<b>DNA repair</b>				
<i>BARD1</i>	F4I443	BRCA1-associated RING domain protein 1	- 13.14	- 8.35
<i>EXO1</i>	Q8L6Z7	Exonuclease 1	1.47	2.89
<b>RNA processing</b>				
<i>XRN3</i>	Q9FQ03	5'-3' exoribonuclease 3	11.92	11.53
<i>CSP41B</i>	Q9SA52	Chloroplast stem-loop binding protein of 41 kDa b, chloroplastic	9.59	9.34
<i>At2g20020</i>	Q9SL79	CRS2-associated factor 1, chloroplastic	9.54	10.11
<i>PCMP-H12</i>	Q9LN01	Pentatricopeptide repeat-containing protein At1g08070, chloroplastic	- 1.10	- 1.30
<i>PCMP-H6</i>	P93011	Pentatricopeptide repeat-containing protein At2g33760	3.68	3.32
<i>At4g34730</i>	O65693	Probable ribosome-binding factor A, chloroplastic	- 10.94	- 3.99
<i>PEL1</i>	Q9ZT87	Protein PELOTA 1	9.38	8.11
<i>TE1</i>	O65001	Protein terminal ear1	- 1.61	3.17

<i>Os05g0571100</i>	Q65XL5	Protein WHAT'S THIS FACTOR 1 homolog, chloroplastic	- 1.17	- 1.07
<b>RNA replication</b>				
<i>RDRP</i>	O15925	RNA-directed RNA polymerase	- 1.23	- 1.81
<b>Others</b>				
<i>CID11</i>	Q9LPI5	Polyadenylate-binding protein-interacting protein 11	1.17	1.85
<i>PHN1</i>	Q69VD5	Protein argonaute PNH1	- 1.04	1.26
<i>DOGL3</i>	Q58FV0	Protein DOG1-like 3	- 1.43	- 3.34
<i>FRS5</i>	Q9SZL8	Protein FAR1-RELATED SEQUENCE 5	- 2.38	- 2.42

**Table S15.** Twenty-three genes involved in protein metabolism at VGS and EFS vs. GS.

Gene name	SwissProt ID	Protein name	log <sub>2</sub> FC (VGS vs. GS)	log <sub>2</sub> FC (EFS vs. GS)
<b>Ribosomal protein</b>				
<i>RPS16C</i>	Q42340	40S ribosomal protein S16-3	9.49	9.98
<i>RPS17</i>	P49215	40S ribosomal protein S17	- 8.31	- 8.31
<i>RPL22B</i>	Q9M9W1	60S ribosomal protein L22-2	10.90	10.87
<i>RPL9B</i>	P49209	60S ribosomal protein L9-1	5.27	5.71
<i>rnhA</i>	F9VN79	Ribonuclease HI	- 1.88	- 2.02
<i>RPL3</i>	O96774	Ribosomal protein L3	7.23	8.45
<b>Protein ubiquitination</b>				
<i>At2g24240</i>	Q9ZUH1	BTB/POZ domain-containing protein At2g24240	2.77	3.22
<i>At5g03250</i>	Q9LYW0	BTB/POZ domain-containing protein At5g03250	1.08	1.17
<i>At4g11680</i>	Q93Z92	E3 ubiquitin-protein ligase At4g11680	11.39	10.26
<i>ATL43</i>	Q5EAE9	RING-H2 finger protein ATL43	2.52	1.69
<i>ATL79</i>	Q9FGJ6	RING-H2 finger protein ATL79	- 1.03	- 1.38
<b>Protein folding</b>				
<i>CALR</i>	O81919	Calreticulin	1.24	1.30
<i>PBP1</i>	O04314	PYK10-binding protein 1	5.06	5.25
<b>Protein biosynthetic process</b>				
<i>fusA2</i>	I1K0K6	Elongation factor G-2, chloroplastic	8.95	8.96
<i>TUFB1</i>	P46280	Elongation factor Tu, chloroplastic	9.10	8.74
<i>IF5A</i>	Q9AXJ4	Eukaryotic translation initiation factor 5A	- 4.36	- 5.48
<b>Protein catabolic process</b>				
<i>MMP2</i>	Q9GLE5	72 kDa type IV collagenase	- 3.85	- 5.07
<i>VIT_05s0020g01830</i>	A7NW79	CASP-like protein 1D1	- 1.67	- 4.50
<i>COL1A2</i>	P02465	Collagen alpha-2(I) chain	- 4.02	- 6.03
<i>ASY1</i>	F4HRV8	Meiosis-specific protein ASY1	1.01	3.55
		Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine	- 2.60	- 2.75
<i>PNG1</i>	Q7F0R1	amidase		
<i>UBP12</i>	Q9FPT1	Ubiquitin C-terminal hydrolase 12	4.16	3.75
<i>UREG</i>	O64700	Urease accessory protein G	1.29	6.65

**Table S16.** Thirty-one genes involved in stress response at VGS and EFS vs. GS.

Gene name	SwissProt ID	Protein name	log <sub>2</sub> FC (VGS vs. GS)	log <sub>2</sub> FC (EFS vs. GS)
<b>Hydrogen peroxide catabolic process</b>				
<i>CAT2</i>	P30567	Catalase isozyme 2	10.60	10.13
<i>PER12</i>	Q96520	Peroxidase 12	1.13	1.12
<i>PER19</i>	O22959	Peroxidase 19	- 1.46	- 3.67
<i>PER42</i>	Q9SB81	Peroxidase 42	- 9.62	- 9.62
<i>PER69</i>	Q96511	Peroxidase 69	9.79	10.15
<i>RBOHE</i>	O81211	Respiratory burst oxidase homolog protein E	1.41	1.66
<b>Response to heat and cold</b>				
<i>HSP17.7</i>	P19242	17.1 kDa class II heat shock protein	3.76	5.41
<i>HSP70-1</i>	P22953	Heat shock 70 kDa protein 1	8.51	9.57
<i>ERD14</i>	P42763	Dehydrin ERD14	8.87	9.65
<i>ERD15</i>	Q39096	Protein EARLY RESPONSIVE TO DEHYDRATION 15	8.96	9.01
<b>Others</b>				
<i>CDR1</i>	Q6XBF8	Aspartic proteinase CDR1	- 1.83	- 1.59
<i>ML3</i>	P82683	Beta-galactoside-specific lectin 3	- 3.03	- 9.00
<i>BIG5</i>	F4IXW2	Brefeldin A-inhibited guanine nucleotide-exchange protein 5	- 9.42	- 1.90

<i>KRP1</i>	O81831	Calcium-binding protein KRP1	9.37	9.91
<i>CFB</i>	P81187	Complement factor B	− 9.76	− 9.76
<i>DEF</i>	A3FPF2	Defensin-like protein	3.24	8.68
<i>PI206</i>	P13240	Disease resistance response protein 206	1.13	2.26
<i>ephB</i>	I6YC03	Epoxide hydrolase B	2.05	1.45
<i>At5g07800</i>	Q9FF12	Flavin-containing monooxygenase FMO GS-OX-like 9	2.10	3.73
<i>HIPP37</i>	A2RVM8	Heavy metal-associated isoprenylated plant protein 37	1.58	3.66
<i>IQM3</i>	Q9LFA4	IQ domain-containing protein IQM3	− 1.28	− 3.27
<i>JOX1</i>	Q9SRM3	Jasmonate-induced oxygenase 1	− 1.03	− 5.49
<i>MO3</i>	Q9FLC2	Monoxygenase 3	− 1.67	− 3.08
<i>ATL24</i>	Q8LBA0	NEP1-interacting protein-like 2	7.23	10.95
<i>N/A</i>	Q41350	Osmotin-like protein	1.37	3.51
<i>PTX3</i>	Q0VCG9	Pentraxin-related protein PTX3	− 10.80	− 10.80
<i>EXO</i>	Q9ZPE7	Protein EXORDIUM	9.02	9.31
<i>EXL2</i>	Q9FE06	Protein EXORDIUM-like 2	− 1.29	− 1.40
<i>DLO2</i>	Q9ZSA7	Protein DMR6-LIKE OXYGENASE 2	− 2.25	− 4.25
<i>TSPO</i>	O82245	Translocator protein homolog	− 1.31	− 2.69
<i>AMP2-2</i>	Q9SPL4	Vicilin-like antimicrobial peptides 2-2	− 3.33	− 4.55

**Table S17.** Sequences of primer used in qRT-PCR validation.

Genes	Sequences (5' to 3')	Amplicon size (bp)
ACT	Forward: CTAAACCGCTTGTTGCTGGC	104
	Reverse: GGGGAGCTCACACGAAAGAT	
Polysaccharide biosynthesis (12)		
BGLU23	Forward: TCGTCGGCAAGCGGTATTTTC	106
	Reverse: CGACAACCTAACGACGATGC	
GAPA	Forward: GATTGGACGGATAGCCCACG	134
	Reverse: TGTCATCCGGCGCAATTCT	
INVA	Forward: TGGTGATGGTTAGACTGGTTG	105
	Reverse: TTAACCGTTTCCACACTGCC	
FBA2	Forward: TGTTGAGGTGGATGTGTGGT	183
	Reverse: GCCTTGCCGTAATAGTCTCAC	
At3g55800	Forward: AATGGTGGGCAATAAGCAGG	114
	Reverse: TTCGGCCTATATGCACCCTC	
BXL5	Forward: AACCTCAGCGGCTAATAAGG	159
	Reverse: ACAACGCCTGGACTTCATCTT	
TBL31	Forward: GAGGGAGGGTTAGGCATTAC	149
	Reverse: GTTTTGGTGTCCCACTGCTC	
XTH9	Forward: ATTGCCCAGCACTCACTACC	114
	Reverse: GGTACGCCTGAGAATAGGGC	
TPPF	Forward: ACTTCTCAAGTTGCCCCACC	187
	Reverse: GACTCGAAGAGTGGGAGTGC	
PAE8	Forward: ACAAGTGTGCTCGGAAAAGG	111
	Reverse: AGTTGACCTCGTCGTGTGTT	
PME7	Forward: TCTGTGCTGGAAGGCAAATC	142
	Reverse: ATCACCATCACCACATGCAC	
PMEI10	Forward: GGCAGCCAGATTGACTCTTTTC	100
	Reverse: GTTGGGTAATGGGTGGCACG	
Flavonoid biosynthesis (11)		
4CLL1	Forward primer: TGTATTGAGGTGGATGTGTGGT	124
	Reverse primer: ATCGAACAACCTCAAATGGTTCT	
4CLL6	Forward: CTCAAAGGACAAGGAGGCGT	195
	Reverse: TGATCCACCACTCATCTCCG	
HST	Forward: CCAGAAAATGGGCCTGACAC	139
	Reverse: CACAGTCATCTGCGAGGTTT	
CHI3	Forward: GGTCATCCAGTAACGAACGC	104
	Reverse: ATTCAGCGTCTGCTAACCGC	
CAD9	Forward: TCCACTCGTCTAGGCACTCT	169
	Reverse: TGCTCCGGCCAGCTTTATG	
CYP714C2	Forward: TGACCATGTCTAAAAGAGGTGGT	111
	Reverse: AATTGAGTTACGGCGGGGC	
CYP93B1	Forward: CGCTCTGAAGGCGAGTAATG	178
	Reverse: ATCGGAATCGAATCGTGTGTT	

<i>F6'H1</i>	Forward: ATCCACCAAAATGGCACTCC Reverse: ATTGACGAGACTAGAAAGTGGCG	121
<i>UGT84A13</i>	Forward: CCTCGACTGTTACATGCCCCG Reverse: GAGAGGAGGTGTTCTGTCGTC	161
<i>UGT87A1</i>	Forward: TGACCTAGATTGCCACCCCT Reverse: AAGCACCCCGAAATACCGTT	200
<i>UGT94E5</i>	Forward: TGGTTTGCCCATAGCACCTT Reverse: CGGCACTACACATTTGACCT	161
<b>Cell growth and flower development (8)</b>		
<i>AC58</i>	Forward: ATTTGCCCCATGCTTCCACT Reverse: TGTGCAAGTGGTTGAAGATCC	122
<i>CYCP3-1</i>	Forward: TCCTCGACCCTACTTCTGCT Reverse: AGTGGTGTGCGAAATGTGGT	167
<i>MIZ1</i>	Forward: TGCCACAATGGCCCAAGATT Reverse: TAGTGGTCCACCCTTACCGC	200
<i>TBB7</i>	Forward: TTCCGAGTCTTGCTTGTTGTT Reverse: GCCCCATATGTGATATGAGTAAAGC	131
<i>AP1</i>	Forward: ACCATCGAGACCGACACATC Reverse: TCCAAGTCCGAATAGCCTCG	160
<i>AMP1</i>	Forward: CATCGTCACCGCTAGTCTCC Reverse: CCGGGATTGGCATAGTTGGT	165
<i>TKPR2</i>	Forward: CAAGGGTTCAAATGAGGGTGG Reverse: AATTTTCTCCAGCACTCCGT	162
<i>HAT</i>	Forward: ATGTGGGCAGAGGACTGATT Reverse: GCTGAGAAATCGCCCATATTGTG	146
<b>Hormone Biosynthesis and Signaling (15)</b>		
<i>YUC8</i>	Forward: TGATCTCCTAGGTGCGCTTC Reverse: ATTATACGCCGTCGCCATCC	114
<i>AIPT</i>	Forward: GAGGTTGCTTTTGCTGGAC Reverse: AACTGATCCGCTGTTACC	179
<i>LOG5</i>	Forward: GACCGCCCTGAGGGTAATTC Reverse: GAGGAGGAGCGTACAACCAC	186
<i>LE</i>	Forward: CTACGGCGTCACGAATTGC Reverse: CCACGACGCGAAAAATTGTG	117
<i>ACO1</i>	Forward: CCCGTGCAAATACCACAAGC Reverse: TTGGATTTGGTCGGAGGAGC	172
<i>ACS1</i>	Forward: ACAGCAAGGAGCACGGATAG Reverse: AAACACGGTTGTGTGACTCG	121
<i>CYP707A6</i>	Forward: GTCGGTTTTCTGGTTCGGTT Reverse: ACCACGACTCGACCAACCT	102
<i>AUX22D</i>	Forward: TTTTGGTTGCTTGGCTCACG Reverse: TAAGCTTTGGACTTGCCGCT	108
<i>SAUR71</i>	Forward: GATAGTCCCGGAGGCAAGGT Reverse: ACCTATGCACGAAAGTCGAGG	100
<i>GH3.6</i>	Forward: AGTCGACCCTTTTGAGGAC Reverse: GCTCGTTCACATTCCCTCT	170
<i>AHK4</i>	Forward: CAAGAACCCAAGGGCCAAGT Reverse: CGGAAAAGCACCCAGTCTCC	100
<i>JOX2</i>	Forward: CCTTCAGTCCAAAAGTGTTGGC Reverse: GTCGAGTCAACCAAGGGATGT	149
<i>AIL1</i>	Forward: ATGGATGTGCGTGAGAGAGGT Reverse: CTATCTGTCACTGGGGCAACT	148
<i>ERF010</i>	Forward: AGGGTTTGATTTCCAGGTTGG Reverse: TGTTCGCGCACTGTCTACC	139
<i>ERF114</i>	Forward: AGGAGGTCCACGAAGGAGTT Reverse: ATCGGCGAACCTTTGTCACT	150
<b>Transcription factor (12)</b>		
<b>Flavonoid biosynthesis (6)</b>		
<i>MYB2</i>	Forward: TAAGGAATAAGAACAACGGGGC Reverse: AGCGATGATGCACGAATGTT	100
<i>MYB14</i>	Forward: TGAGGATAGTGCTAGAGGCAAC Reverse: AGGGGTAAACTATGCCGATGG	100
<i>MYB83</i>	Forward: TGGTGTGTGGGCTCTTTTAC Reverse: GTGGTGGTTGTAATGGGTGG	192

<i>BHLH52</i>	Forward: TTGGCATGAGATGAGCTGCG Reverse: GGTCCTCAGACAGCCAGAATG	101
<i>WRKY6</i>	Forward: TTCAACTGGCCTCCTCGAAC Reverse: CAACCTTTTCCACCGATGCC	190
<i>WRKY53</i>	Forward: TTGGGCGAATTGTCCAGTC Reverse: GGGGGCTTAGACTAGGGTTG	125
<i>WRKY72</i>	Forward: GGCTCGGTATTATCCTCCGC Reverse: CGACAGCAACTCCGCAAAAT	132
<b>Growth and development (6)</b>		
<i>DREB2D</i>	Forward: GGTGTTTCGTCTGTACGTCT Reverse: TCGTCGTTCCCAATCTCGTC	195
<i>At2g01810</i>	Forward: TCGGCACCCCTAAAACTGC Reverse: AGGGTGAGGAGTGCAAAGAC	109
<i>TCP9</i>	Forward: AGCTTCTTTGGATTGCGCCT Reverse: TGGCTCTGACACCATGAAGAC	130
<i>UPB1</i>	Forward: GAAGGGGGTTCGGTTGGTC Reverse: CGAGCAGTAGCCCAAAACAAT	195
<i>AHL20</i>	Forward: TCACCAGGCGTGAATGTCT Reverse: GAGAAGGACAAGAGGTGCGT	200
<b>Polysaccharide transport (6)</b>		
<i>SWEET5</i>	Forward: CTCCTTCGCCCAGCCATTAC Reverse: AGCAACATGAGGCCAAAAGTC	192
<i>slc37a2</i>	Forward: GGTGGCATCGTAGCTGGATT Reverse: TCCATTACGAGAGCACCAC	171
<i>At5g55950</i>	Forward: TGAGTTGGTACCCTCTTGGTG Reverse: TCAGGACCTCCTCCTCGATAC	104
<i>ABC2</i>	Forward: AAAGGTTCCACATGCCTCCAC Reverse: ACTACTTCCCAGCGTTCCTT	132
<i>ABCG1</i>	Forward: TTCTGACGGACTTCTAAACTCTT Reverse: GTATGCGTGCTGGCCTTTTC	156
<i>ABCG22</i>	Forward: GGCGCTCGTCATAGATGGTT Reverse: AACTTCCTTCCAGTGTCCCG	161