

Table S6. Differentially expressed (DE) genes identified in the comparison between LB and SB segregants, in the FST stage (Cuffdiff2, $p < 0.01$).

Gene_ID	Chrom	log ₂ (FC)	p_value	Description
GSVIVG01024301001	16	4.12	0.00	Ca ²⁺ -dependent lipid-binding protein CLB1/vesicle protein vp115/Granuphilin A contains C2 domain
GSVIVG01016069001	9	4.05	0.00	Protein WAX2
GSVIVG01015141001	11	3.91	0.01	Ankyrin repeat-containing protein At3g12360
GSVIVG01011486001	14	3.56	0.01	Phosphatidylinositol-345-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN
GSVIVG01022448001	8	3.25	0.00	F-box/LRR-repeat protein At3g48880
GSVIVG01023110001	12	3.23	0.00	Glutathione S-transferase zeta class
GSVIVG01029491001	9	3.13	0.01	Lupeol synthase 5
GSVIVG01031484001	6	3.13	0.00	Vacuolar amino acid transporter 1
GSVIVG01029641001	9	2.74	0.00	60S ribosomal protein L7-3
GSVIVG01015194001	11	2.71	0.00	Cytokinin dehydrogenase 3
GSVIVG01011406001	14	2.60	0.00	Vacuolar amino acid transporter 1
GSVIVG01018891001	4	2.58	0.00	Abscisic acid 8'-hydroxylase 3
GSVIVG01012020001	1	2.43	0.01	Probable E3 ubiquitin-protein ligase RHA2B
GSVIVG01007745001	17	2.43	0.00	Carbonic anhydrase chloroplastic
GSVIVG01021134001	10	2.28	0.00	Isoflavone-7-O-methyltransferase 9
GSVIVG01026803001	15	2.23	0.01	Isoflavone-7-O-methyltransferase 6
GSVIVG01029525001	9	2.20	0.00	Camelliol C synthase
GSVIVG01029631001	9	2.17	0.00	60S ribosomal protein L7-4
GSVIVG01019570001	2	2.13	0.01	Cellulose synthase-like protein G3
GSVIVG01027716001	5	2.04	0.01	Cellulose synthase-like protein G2
GSVIVG01011401001	14	1.99	0.00	Vacuolar amino acid transporter 1
GSVIVG01024424001	16	1.98	0.01	LRR receptor-like serine/threonine-protein kinase ERECTA
GSVIVG01036853001	2	1.97	0.00	Cysteine-rich receptor-like protein kinase 10

GSVIVG01019490001	2	1.92	0.01	Unkown Protein Function
GSVIVG01030219001	8	1.86	0.00	Cationic peroxidase 1
GSVIVG01024885001	6	1.85	0.00	Tropinone reductase homolog At1g07440
GSVIVG01013763001	1	1.77	0.00	Glycosyl transferase family 8 - glycogenin
GSVIVG01035315001	4	1.74	0.00	Probable leucine-rich repeat receptor-like protein kinase At5g61480
GSVIVG01004877001	Un	1.74	0.01	TMV resistance protein N
GSVIVG01024892001	6	1.71	0.00	Tropinone reductase homolog At1g07440
GSVIVG01032425001	14	1.67	0.00	Galactinol--sucrose galactosyltransferase
GSVIVG01022171001	7	1.66	0.01	Unkown Protein Function
GSVIVG01014559001	19	1.63	0.01	Vacuolar H ⁺ -ATPase V0 sector subunit c"
GSVIVG01019452001	2	1.62	0.01	Unkown Protein Function
GSVIVG01010719001	13	1.51	0.01	Unkown Protein Function
GSVIVG01024879001	6	1.37	0.01	Tropinone reductase homolog At1g07440
GSVIVG01036279001	14	1.32	0.01	Pathogenesis-related protein PR- 4B
GSVIVG01027600001	15	1.28	0.01	Dihydroflavonol-4-reductase
GSVIVG01037055001	3	1.25	0.01	Unkown Protein Function
GSVIVG01022913001	12	-1.40	0.00	nutrient reservoir putative
GSVIVG01021609001	10	-1.41	0.00	Uncharacterized amino acid permease yfnA
GSVIVG01035059001	5	-1.49	0.00	Major allergen Pru av 1
GSVIVG01012363001	13_random	-1.52	0.01	Myrcene synthase chloroplastic
GSVIVG01000403001	12	-1.53	0.01	Isoprene synthase chloroplastic
GSVIVG01027790001	5	-1.61	0.01	Unkown Protein Function
GSVIVG01008910001	18	-1.66	0.00	Unkown Protein Function
GSVIVG01021724001	10	-1.79	0.01	Unkown Protein Function
GSVIVG01033484001	8	-1.92	0.00	Peroxidase 53
GSVIVG01015071001	11	-2.00	0.00	Cytochrome P450 71A1
GSVIVG01037077001	3	-2.06	0.00	Eugenol synthase 1
GSVIVG01015076001	11	-2.07	0.01	Flavonoid 3'5'-hydroxylase 1
GSVIVG01027568001	15	-2.07	0.01	Gibberellin receptor GID1
GSVIVG01037073001	3	-2.08	0.00	Eugenol synthase 1
GSVIVG01000567001	1	-2.13	0.00	Cytochrome P450 71B35
GSVIVG01021278001	10	-2.15	0.01	Probable LRR receptor-like serine/threonine-protein kinase At1g53430
GSVIVG01036885001	2	-2.17	0.00	Abscisic acid 8'-hydroxylase 1

GSVIVG01024292001	16	-2.17	0.00	Phenylalanine ammonia-lyase
GSVIVG01027558001	15	-2.30	0.00	Cytochrome P450 76C2
GSVIVG01026810001	15	-2.37	0.00	Protein WAX2
GSVIVG01025391001	6	-2.37	0.01	Unkown Protein Function
GSVIVG01027785001	5	-2.41	0.00	Unkown Protein Function
GSVIVG01018990001	4	-2.43	0.00	Flavin-containing monooxygenase YUCCA6
GSVIVG01032091001	13	-2.48	0.01	Uncharacterized membrane protein predicted efflux pump
GSVIVG01018142001	5	-2.55	0.00	PR6 protease inhibitor
GSVIVG01010565001	16	-2.57	0.00	Stilbene synthase 2
GSVIVG01025394001	6	-2.62	0.00	Unkown Protein Function
GSVIVG01010561001	16	-2.73	0.00	Stilbene synthase 1
GSVIVG01035076001	5	-2.78	0.00	Pathogenesis-related protein STH-2
GSVIVG01036322001	18_random	-2.79	0.00	(+)-delta-cadinene synthase isozyme A
GSVIVG01026220001	10	-2.89	0.00	Stilbene synthase 3
GSVIVG01025284001	6	-3.00	0.00	Unkown Protein Function
GSVIVG01010580001	16	-3.04	0.00	Stilbene synthase 2
GSVIVG01010591001	16	-3.07	0.00	Unkown Protein Function
GSVIVG01010584001	16	-3.12	0.00	Stilbene synthase 4
GSVIVG01029110001	11	-3.14	0.00	Proteasome subunit alpha type-2-B
GSVIVG01010583001	16	-3.16	0.00	Stilbene synthase 4
GSVIVG01038414001	9	-3.17	0.00	Omega-hydroxypalmitate O-feruloyl transferase
GSVIVG01010590001	16	-3.18	0.00	Stilbene synthase 3
GSVIVG01024305001	16	-3.20	0.01	Phenylalanine ammonia-lyase 2
GSVIVG01032256001	11	-3.20	0.00	Trans-cinnamate 4-monooxygenase
GSVIVG01024295001	16	-3.20	0.01	Phenylalanine ammonia-lyase 2
GSVIVG01010579001	16	-3.22	0.00	Stilbene synthase 4
GSVIVG01025287001	6	-3.28	0.00	Unkown Protein Function
GSVIVG01024294001	16	-3.31	0.00	Phenylalanine ammonia-lyase
GSVIVG01010578001	16	-3.34	0.00	Stilbene synthase 4
GSVIVG01024315001	16	-3.37	0.01	Phenylalanine ammonia-lyase
GSVIVG01010589001	16	-3.45	0.00	Stilbene synthase 3
GSVIVG01024293001	16	-3.49	0.01	Phenylalanine ammonia-lyase G2B
GSVIVG01024306001	16	-3.64	0.00	Phenylalanine ammonia-lyase
GSVIVG01010556001	16	-3.72	0.00	Stilbene synthase 1
GSVIVG01010582001	16	-3.88	0.00	Stilbene synthase 3
GSVIVG01024299001	16	-3.89	0.00	Phenylalanine ammonia-lyase 2

GSVIVG01024756001	6	-3.96	0.00	4-hydroxyphenylacetaldehyde oxime monooxygenase
GSVIVG01010585001	16	-3.99	0.00	Stilbene synthase 4
GSVIVG01010568001	16	-4.17	0.00	Stilbene synthase 6
GSVIVG01028606001	7	-4.41	0.00	Unkown Protein Function
GSVIVG01010581001	16	-4.48	0.00	Stilbene synthase 4
GSVIVG01028618001	7	-4.61	0.00	Pore-forming toxin-like protein Hfr-2
GSVIVG01026213001	10	-4.79	0.00	Stilbene synthase 1
GSVIVG01010557001	16	-4.90	0.00	Stilbene synthase 4
GSVIVG01031746001	3	-6.32	0.00	Alpha-amylase

Gene_ID= Gene code nomenclature based on reference genome annotation PN40024 (12X.v1); $\log_2(\text{FC})$ = log base 2 of fold change; p_value = differential expression significance.