

Table S6 Key biological process and its associated genes differentially regulated in GLRaV-3-infected leaf and berry at E-L 31, 35, and 38 developmental stages.

**Degree of expressional change (fold change) and significant difference (FDR values) were calculated by differential expression analysis with DESeq2. For full list of differentially expressed genes (DEGs) and their associated fold change and FDR values at each developmental stages of leaf and berry, please refer to STable 4.*

**The genes included are DEGs that past FDR <0.05 threshold.*

**Gene ID and gene description were retrieved from Ensembl plants.*

**N/A indicates that no DEG was detected at FDR <0.05 threshold.*

A. Down-regulation						
Cellular process	Tissue	Developmental stage	Gene ID	Gene description	Fold change	FDR value
Photosynthesis	Leaf	E-L 31	VIT_08s0040g00850	PSBP domain-containing protein 6, chloroplastic	-1.99199599	0.033903241
			VIT_14s0128g00030	PSBP domain-containing protein	-1.650587644	0.017176662
			VIT_00s0181g00180	Chlorophyll a-b binding protein 13, chloroplastic	-1.431019538	0.003692198
			VIT_13s0019g00260	Putative oxygen evolving enhancer protein	-1.308234815	0.006368829
			VIT_13s0019g00320	Photosynthetic NDH subunit of lumenal location 1, chloroplastic	-1.2937063	0.020103386
			VIT_19s0014g05080	Uncharacterized protein	-1.292630128	0.000480496
			VIT_14s0081g00060	PSII 6.1 kDa protein	-1.211161416	0.002141469
			VIT_10s0003g02900	Chlorophyll a-b binding protein of LHCII type 1	-1.185162996	0.001994627

			VIT_00s09 04g00010	Oxygen- evolving enhancer protein 3, chloroplastic	- 1.168540939	0.0028 47964
			VIT_10s01 16g00900	Chaperonin- like RBCX protein 1, chloroplastic	- 1.063521336	0.0294 91686
			VIT_19s00 15g01760	PSI-G	- 0.829651289	0.0432 3668
			VIT_10s00 03g04350	PSI reaction center subunit psaK, chloroplastic	- 0.828464574	0.0206 85447
			VIT_11s00 16g01400	Uncharacteriz ed protein	- 0.780210214	0.0204 63039
			VIT_12s00 28g00320	Chlorophyll a- b binding protein 40, chloroplastic- like	- 0.773527941	0.0235 54993
	Lea f	E-L 35	*A total of 49 down-regulated DEGs were involved in photosynthesis, for detailed list of down-DEGs involved in photosynthesis, please refer to S Table 5, 'E-L 35 Leaf' subsheet			
	Ber ry	E-L 31	N/A	N/A	N/A	N/A
	Ber ry	E-L 35	N/A	N/A	N/A	N/A
	Ber ry	E-L 38	N/A	N/A	N/A	N/A
Chloroplast rRNA processing	Lea f	E-L 31	VIT_13s00 64g01430	30S ribosomal protein 2, chloroplastic	- 1.274681552	0.0161 61032
			VIT_17s00 00g09680	28 kDa ribonucleoprot ein, chloroplastic	- 1.161692835	0.0059 82332
			VIT_14s00 66g00140	28 kDa ribonucleoprot	- 0.874158366	0.0172 12347

				ein, chloroplastic		
				29 kDa		
				VIT_08s00 40g01760	ribonucleoprotein A, chloroplastic	- 0.866751862
						0.0116 1672
	Leaf	E-L 35	N/A	N/A	N/A	N/A
	Berry	E-L 31	N/A	N/A	N/A	N/A
	Berry	E-L 35	N/A	N/A	N/A	N/A
Plastid transcription	Berry	E-L 38	N/A	N/A	N/A	N/A
	Leaf	E-L 31	VIT_01s00 11g01080	Protein PLASTID TRANSCRIPTIONALLY ACTIVE 14	- 1.312743353	0.0444 36754
				Fructokinase-like 2, chloroplastic	- 1.116663713	0.0292 80554
				Transcription termination factor MTERF4, chloroplastic	- 0.918594687	0.0225 33095
	Leaf	E-L 35	N/A	N/A	N/A	N/A
	Berry	E-L 31	N/A	N/A	N/A	N/A
	Berry	E-L 35	N/A	N/A	N/A	N/A
	Berry	E-L 38	N/A	N/A	N/A	N/A
Chlorophyll biosynthetic process	Leaf	E-L 31	N/A	N/A	N/A	N/A
	Leaf	E-L 35	VIT_08s00 07g08540	CHLH magnesium	- 2.698812022	0.0006 1374

				chelatase H subunit		
				Protochlorophyllide reductase, chloroplastic	- 2.655802771	1.3520 2E-06
				Uncharacterized protein	- 2.111207648	0.0014 93512
				Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic-like	- 2.064978918	0.0068 33531
				Protochlorophyllide reductase	- 1.918082208	0.0045 01822
				Probable 1-deoxy-D-xylulose-5-phosphate synthase, chloroplastic	- 1.627046679	0.0060 92146
				Uroporphyrinogen decarboxylase	- 1.341399694	0.0379 02476
	Berry	E-L 31	N/A	N/A	N/A	N/A
	Berry	E-L 35	N/A	N/A	N/A	N/A
	Berry	E-L 38	N/A	N/A	N/A	N/A
Carbohydrate metabolism	Leaf	E-L 31	VIT_11s0016g00470	Sucrose synthase (VvSUS)	- 1.548123753	0.0064 30004
			VIT_05s0077g00510	Neutral invertase (VvNIV)	- 1.308977202	0.0080 78829

Lea f	E-L 35	VIT_12s00 59g02670	Beta-amylase (VvBMY)	- 2.308800198	0.0421 86627		
		VIT_05s00 20g01910	Beta-amylase (VvBMY)	- 1.961451369	0.0003 20976		
		VIT_08s00 07g01570	Fructose bisphosphates (VvFBP)	- 1.839839925	0.0116 99588		
		VIT_05s00 77g00510	Neutral invertase (VvNIV)	- 1.764111238	0.0052 89888		
		VIT_02s01 09g00080	Phosphoribulo kinase (VvPRK)	- 1.759907347	0.0127 33449		
		VIT_03s00 38g00380	D-ribulose kinase (VvPSK)	-1.71631345	0.0408 54439		
		VIT_02s01 54g00100	Transaldolase (VvTALDO)	- 1.625053341	0.0113 84389		
		VIT_01s00 11g05210	Phosphogluco mutase (VvPGM)	- 1.453673213	0.0109 79642		
		VIT_17s00 00g02260	Aldose 1- epimerase	- 1.287142274	0.0499 04321		
		Ber ry	E-L 31	VIT_00s28 40g00010	Phosphoenolp yruvate carboxykinase (VvPEPCK)	- 0.526783839	0.0437 10289
				VIT_00s25 76g00010	Phosphoenolp yruvate carboxykinase (VvPEPCK)	-0.44549967	0.0428 61108
				VIT_00s19 95g00010	Phosphoenolp yruvate carboxykinase (VvPEPCK)	- 0.426019813	0.0128 55684
Ber ry	E-L 35			N/A	N/A	N/A	N/A
Ber ry	E-L 38	N/A	N/A	N/A	N/A		
Cell wall metabolism	Lea f	E-L 31	VIT_01s00 26g02620	Expansin	- 4.110101857	0.0119 63935	

			VIT_14s01 08g01020	Expansin	-3.80167402	3.20E-06
			VIT_13s00 67g02930	Expansin	-	0.046829039
			VIT_02s00 25g01330	Polygalacturonase	-	0.00578332
			VIT_13s00 64g01720	Beta-galactosidase	-	0.000436275
			VIT_13s00 67g02930	Expansin	-	1.0373E-06
			VIT_06s00 04g07970	Expansin	-	0.032065526
			VIT_07s00 31g02480	Beta-galactosidase	-	0.000630032
			VIT_02s00 25g01330	Polygalacturonase	-	0.01842931
			VIT_09s00 02g02120	Beta-galactosidase	-	0.014438646
	Leaf	E-L 35				
	Berry	E-L 31	N/A	N/A	N/A	N/A
	Berry	E-L 35	N/A	N/A	N/A	N/A
	Berry	E-L 38	N/A	N/A	N/A	N/A
	Leaf	E-L 31	N/A	N/A	N/A	N/A
			VIT_18s00 76g00220	Sucrose transporter 2 (VvSUT2)	-	0.026456582
			VIT_04s00 23g01500	Putative polyol/monosaccharide transporter (VvPMT3)	-	0.000909145
			VIT_18s00 76g00250	Sucrose transporter 27 (VvSUT27)	-	9.13414E-06
			VIT_11s01 49g00050	Hexose transporter 3/7 (VvHT3/7)	-	0.005609524
Sugar transport	Leaf	E-L 35				
	Berry	E-L 31	N/A	N/A	N/A	N/A

	Berry	E-L 35	N/A	N/A	N/A	N/A
	Berry	E-L 38	N/A	N/A	N/A	N/A
	Leaf	E-L 31	N/A	N/A	N/A	N/A
Mitochondrion-associated	Leaf	E-L 35	VIT_16s0039g02750	Glutamate dehydrogenase (VvGDH)	-2.553537017	0.040452982
			VIT_00s1286g00020	Translation elongation factor	-2.197594459	0.001509423
			VIT_09s0002g04330	Mitochondrial ribosomal protein	-1.965057526	0.003534502
			VIT_19s0015g00140	Mitochondrial ribosomal protein	-1.917158837	0.005272773
			VIT_18s0001g03850	Mitochondrial ribosomal protein	-1.706629018	0.006407113
			VIT_00s0323g00080	Translation elongation factor	-1.681144532	0.008073655
			VIT_05s0049g00470	Electron transfer flavoprotein subunit beta	-1.40078102	0.037958832
			VIT_19s0014g04970	Mitochondrial ribosomal protein	-1.33398672	0.049830236
	Berry	E-L 31	N/A	N/A	N/A	N/A
	Berry	E-L 35	VIT_06s0009g03590	Reactive oxygen species modulator 1 (VvROMO1)	-1.034816368	0.038007393
			VIT_05s0020g02150	NADH dehydrogenase [ubiquinone] 1 alpha	-0.97007366	0.015243494

			subcomplex subunit 8-B		
		VIT_01s01 37g00340	Uncharacteriz ed protein	- 0.959519843	0.0327 10584
		VIT_02s00 25g02990	Mitochondrial import inner membrane translocase subunit TIM13 (VvTIM13)	- 0.955229294	0.0330 15689
		VIT_11s01 03g00270	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1	- 0.916141105	0.0334 55189
		VIT_06s00 80g00540	Uncharacteriz ed protein	- 0.783549942	0.0398 873
Ber ry	E-L 38	N/A	N/A	N/A	N/A

	Ber ry	E-L 38	N/A	N/A	N/A	N/A
Defense mechanism	Lea f	E-L 31	N/A	N/A	N/A	N/A
	Lea f	E-L 35	VIT_05s0077g01670	Pathogenesis-related protein 10.7 (VvPR-10.7)	-9.930153917	6.44732E-05
	Ber ry	E-L 31	N/A	N/A	N/A	N/A
	Ber ry	E-L 35	N/A	N/A	N/A	N/A
	Ber ry	E-L 38	VIT_05s0077g01670	Pathogenesis-related protein 10.7 (VvPR-10.7)	-1.134068074	0.000626765
Heat shock protein (HSP) and HSP co-chaperons	Lea f	E-L 31	N/A	N/A	N/A	N/A
	Lea f	E-L 35	VIT_15s0046g01560	BAG family molecular chaperone regulator 6 (BAG6)	-2.962246735	2.19805E-07
			VIT_18s0001g01570	16.9kDa HSP class I	-2.703856226	0.00012535
			VIT_02s0025g00280	HSP83	-1.967049793	0.016661365
			VIT_15s0021g00830	Chaperonin GroES	-1.704049014	0.006114618
			VIT_09s0002g03930	HSP60	-1.670062319	0.036612176
			Ber ry	E-L 31	N/A	N/A
	Ber ry	E-L 35	N/A	N/A	N/A	N/A
	Ber ry	E-L 38	N/A	N/A	N/A	N/A

Transcription factors	Leaf	E-L 31	N/A	N/A	N/A	N/A
			VIT_00s0226g00070	Protein SHORT ROOT/SHR	-10.74683952	1.69584E-07
		E-L 35	VIT_14s0108g00420	Transcription factor PRE2	-8.138166707	0.029248163
			VIT_04s0008g05560	IAA28	-7.66134994	6.61887E-06
			VIT_08s0056g00050	Protein SCARECROW/SCR	-6.384202169	0.023163259
			VIT_05s0020g04690	IAA14	-2.519923737	3.06575E-05
			VIT_15s0046g00290	ARF18	-1.982160394	0.002477448
			VIT_11s0016g03540	IAA27	-1.51840453	0.012627664
			VIT_02s0025g01740	ARF9	-1.333772382	0.037833687
			VIT_18s0001g08090	IAA	-1.296871905	0.024004196
	Berry	E-L 31	N/A	N/A	N/A	N/A
			VIT_11s0016g00660	ERF017	-5.759829656	0.001535734
		E-L 35	VIT_03s0063g00460	ERF109	-3.959097156	0.005743998
			VIT_16s0013g00950	ERF105	-3.939262956	0.024882223
			VIT_16s0013g01110	ERF005	-3.268995095	0.020280177
			VIT_16s0013g00990	ERF005	-2.643451912	0.044893097
			VIT_07s0141g00690	ERF011	-2.337779483	0.009044125
			VIT_01s0011g03070	ERF RAV1	-2.326366551	0.0453749
			VIT_12s0028g03270	ERF004	-2.144067757	0.011025863
			VIT_19s0014g02240	ERF004	-1.853191933	0.013494055
			VIT_18s0089g01030	ERF TINY	-1.755868123	0.003373735

			VIT_10s00 03g00140	ERF004	- 1.589187054	0.0121 39086
			VIT_07s00 31g00190	ERF008	- 1.363387699	0.0114 03663
			VIT_02s02 34g00130	ERF002	- 1.284901335	0.0265 60263
Ber ry	E-L 38		N/A	N/A	N/A	N/A

B. Up-regulation						
Cellular process	Tis sue	Developme ntal stage	Gene ID	Gene description	Fold change	FDR value
	Lea f	E-L 31	N/A	N/A	N/A	N/A
	Lea f	E-L 35	N/A	N/A	N/A	N/A
Photosynthesi s	Ber ry	E-L 31	VIT_00s01 81g00180	Chlorophyll a-b binding protein, chloroplastic	0.9787612 74	2.5840 7E-05
			VIT_08s00 07g08540	Magnesium chelataase	0.9487021 86	0.0011 18541
			VIT_12s00 28g00320	Chlorophyll a-b binding protein, chloroplastic	0.8438033 66	0.0293 37049
			VIT_19s00 14g00160	Chlorophyll a-b binding protein, chloroplastic	0.8308056 31	0.0244 82006
			VIT_18s00 01g10550	Chlorophyll a-b binding protein, chloroplastic	0.6847704 52	0.0224 18583
			VIT_04s00 44g01410	Uncharacterized protein	0.6823044 47	0.0006 98058
			VIT_07s00 05g02220	Chlorophyll a-b binding protein, chloroplastic	0.6252855 18	0.0001 00081

		VIT_12s00 55g01110	Chlorophyll a-b binding protein, chloroplastic	0.6148984 66202	0.0089
		VIT_04s00 08g01730	Uncharacterized protein	0.5737578 64	0.0418 4377
		VIT_10s00 03g04350	PSI-K (Photosystem I subunit X)	0.5683601 69	0.0454 72904
		VIT_17s00 00g03690	Ribulose biphosphate carboxylase small subunit (RuBisCO small subunit)	0.5611542 96	0.0011 45619
		VIT_08s00 40g00390	Magnesium- protoporphyrin IX monomethyl ester (oxidative) cyclase	0.5597130 19	0.0029 28141
		VIT_07s00 05g04400	Photosystem II reaction center Psb28 protein	0.5362450 52	0.0218 64576
		VIT_10s00 03g02900	Chlorophyll a-b binding protein, chloroplastic	0.5252348 4	0.0007 40937
		VIT_19s00 14g03850	Plastoquinol-- plastocyanin reductase	0.5003339 08	0.0125 90557
		VIT_00s02 07g00210	Uncharacterized protein	0.4879670 68	0.0086 53088
		VIT_12s00 57g00020	Uncharacterized protein	0.4596435 08	0.0027 55571
		VIT_00s09 04g00010	Uncharacterized protein	0.4537288 05	0.0045 95422
		VIT_15s00 24g00040	Chlorophyll a-b binding protein, chloroplastic	0.4489625 62	0.0432 78122
		VIT_04s00 23g00410	PSI subunit V	0.4450055 61	0.0267 89559
Ber ry	E-L 35	N/A	N/A	N/A	N/A
Ber ry	E-L 38	N/A	N/A	N/A	N/A

	Leaf	E-L 31	N/A	N/A	N/A	N/A
Carbohydrate metabolism	Leaf	E-L 35	VIT_02s0025g02790	Granule-bound starch synthase 1, chloroplastic/amyloplastic (VvGBSS1)	2.432168517	0.029050767
			VIT_18s0001g00560	Alpha-amylase (VvAMY)	2.107962246	0.03403715
			VIT_03s0063g00400	Alpha-amylase (VvAMY)	1.865813776	0.002551314
			VIT_03s0038g00670	Aldolase and fructose biphosphatase (VvFBP)	1.127195337	0.000300258
			VIT_08s0007g01570	Aldolase and fructose biphosphatase (VvFBP)	1.041426285	8.76918E-06
	Berry	E-L 31	VIT_04s0023g03010	Aldolase and fructose biphosphatase (VvFBP)	0.730823016	0.006163961
			VIT_13s0019g03350	Aldolase and fructose biphosphatase (VvFBP)	0.67705116	0.003234988
			VIT_17s0000g03690	RuBisCO small subunit	0.561154296	0.001145619
			VIT_12s0028g02180	PEP carboxylase (VvPEPCase)	0.409252683	0.007891183
			VIT_01s0011g02740	PEP carboxylase (VvPEPCase)	0.387905072	0.021337078
		Berry	VIT_05s0077g01930	Sucrose synthase (VvSUS)	3.569665361	0.015715931
			VIT_11s0016g00470	Sucrose synthase (VvSUS)	0.980264567	6.03957E-06
Cell wall metabolism	Leaf	E-L 31	VIT_01s0026g00200	Xyloglucan endotransglucosylase/hydrolase	5.681804968	0.002130956

Leaf	E-L 35	VIT_02s00	Cellulose	4.8033665	0.0043
		25g01890	synthase	19	53587
		VIT_02s00	Cellulose	3.9855728	0.0493
		25g01920	synthase	3	77963
		VIT_02s00	Cellulose	1.5505311	0.0071
		25g01750	synthase	21	77193
		VIT_05s00	Cellulose	1.2528258	0.0135
		49g00010	synthase	21	75809
		VIT_19s00	Cellulose	1.2184423	2.78E-
		15g00730	synthase	3	05
		VIT_05s00	Cellulose	1.1559656	0.0132
		20g05050	synthase	74	62747
		VIT_05s00	Chitinase-related	10.658460	3.5421
		94g00330	protein	19	1E-05
			Xyloglucan		
		VIT_01s00	endotransglucosy	5.3745213	2.4667
		26g00200	lase/hydrolase	31	3E-05
			Xyloglucan		
		VIT_12s01	endotransglucosy	5.3217795	0.0037
		34g00160	lase/hydrolase	47	67351
			Xyloglucan		
		VIT_11s00	endotransglucosy	4.7124083	1.2678
		52g01200	lase/hydrolase	19	5E-05
		VIT_15s00		2.4615388	0.0056
		46g01570	Endochitinase	49	5505
		VIT_04s00	Chitinase-related	2.3100049	0.0002
		08g00140	protein	82	00818
Berry	E-L 31	VIT_15s00	Pectinesterase	2.3168209	0.0495
		48g00510	(VvPE)	98	79898
			Cytochrome		
		VIT_06s00	P450 86A1	1.4451834	0.0275
		04g06210	(VvCYP86A1)	46	94962
		VIT_09s00		1.1946447	0.0134
		02g08510	Expansion	22	55533
			Xyloglucan		
		VIT_05s00	endotransglucosy	0.9222265	0.0008
		62g00240	lase/hydrolase	33	34196
			Xyloglucan		
		VIT_08s00	endotransglucosy	0.9212874	0.0183
		07g04950	lase/hydrolase	29	37571
			Xyloglucan		
		VIT_11s00	endotransglucosy	0.8586837	0.0098
		52g01250	lase/hydrolase	69	14869
		VIT_11s00	Pectinesterase	0.7610273	0.0006
		16g00330	(VvPE)	32	98058

			VIT_19s00 14g00450	Protein trichome birefringence	0.7385530 35	0.0059 76317
			VIT_14s00 83g01100	UDP- arabinopyranose mutase 3	0.7036000 45	0.0021 34208
			VIT_14s01 08g01020	Expansion	0.6676046 26	0.0002 78588
			VIT_08s00 07g03990	Glucomannan 4- beta- mannosyltransfer ase	0.6248591 59	0.0148 92072
			VIT_05s00 29g00480	Eceriferum 26	0.4728219 32	0.0076 34942
			VIT_17s00 00g05070	COBRA	0.4423897 2	0.0150 22359
	Ber ry	E-L 35	N/A	N/A	N/A	N/A
	Ber ry	E-L 38	N/A	N/A	N/A	N/A
Sugar transport	Lea f	E-L 31	N/A	N/A	N/A	N/A
	Lea f	E-L 35	VIT_18s00 01g05570	Hexose transporter 2 (VvHT2)	2.6194118 57	0.0002 97238
			VIT_01s00 26g01890	UDP-galactose transporter 3-like (VvUTR3-like)	1.9822646 26	0.0059 63856
			VIT_05s00 20g03140	Hexose transporter 5 (VvHT5)	1.7083556 16	0.0016 92151
	Ber ry	E-L 31	VIT_03s00 63g02250	Polyol transporter 5 (VvPLT5)	0.9613009 85	0.0213 37078
			VIT_10s00 03g03930	Inositol transporter 2 (VvINT2)	0.5802449 01	0.0064 15565
			VIT_05s00 77g02260	Bidirectional sugar transporter SWEET17 (VvSWEET17)	0.4641261 35	0.0208 62053
			VIT_10s00 03g00300	Triose phosphate/phosp	0.3891036 26	0.0150 22359

hate translocator (VvTPT)					
Ber ry	E-L 35	N/A	N/A	N/A	N/A
Ber ry	E-L 38	VIT_18s00 76g00250	Sucrose transporter 27 (VvSUT27)	1.0270534 23	0.0255 98535
Phenylpropan oids and flavonoids biosynthesis	Lea f	E-L 31	N/A	N/A	N/A
			VIT_01s00 11g02960	Leucoanthocyani din reductase 1 (VvLAR1)	10.481070 95
			VIT_16s00 39g02230	Anthocyanidin 3- O- glucosyltransfera se (VvUFGT)	9.3709845 19
			VIT_02s00 25g04720	Anthocyanidin synthase (VvANS)	7.8265689 24
	Lea f	E-L 35	VIT_04s00 23g03370	Flavonol synthase/flavano ne 3-hydroxylase (VvFLS)	6.2557544 92
			VIT_18s00 01g12800	Dihydroflavonol 4-reductase (VvDFR)	4.1529283 18
			VIT_18s00 01g03430	Flavonol synthase/flavano ne 3-hydroxylase (VvFLS)	3.4640272 9
			VIT_00s03 61g00040	Anthocyanidin reductase (VvANR)	2.9498240 18
	Ber ry	E-L 31	N/A	N/A	N/A
	Ber ry	E-L 35	N/A	N/A	N/A
	Ber ry	E-L 38	VIT_00s06 15g00020	Mannitol dehydrogenase (VvCAD7)	2.8978293 19
					0.0003 85188

VIT_16s00 39g01360	Phenylalanine ammonia lyase (VvPAL)	2.6848393 42	0.0435 59059
VIT_16s00 39g01170	Phenylalanine ammonia lyase (VvPAL)	2.5203450 1	5.1784 9E-07
VIT_00s06 15g00030	Mannitol dehydrogenase (VvCAD7)	2.3824163 67	0.0025 17939
VIT_16s00 39g01300	Phenylalanine ammonia lyase (VvPAL)	2.3538362 95	0.0010 25274
VIT_16s00 39g01110	Phenylalanine ammonia lyase (VvPAL)	2.2655609 34	0.0223 09729
VIT_16s01 00g01000	Stilbene synthase 4-like (VvSTS4- like)	2.0222343 37	0.0020 41952
VIT_16s01 00g00850	Stilbene synthase 4-like (VvSTS4- like)	1.9896973 88	0.0308 74368
VIT_12s00 34g00130	Anthocyanidin 3- O- glucosyltransferase 2 (VvUFGT)	1.8427016 47	0.0014 64303
VIT_04s00 44g00210	Mannitol dehydrogenase (VvCAD7)	1.2128976 54	0.0261 16134
VIT_06s00 04g08150	Trans-cinnamate 4- monooxygenase (VvC4H)	1.0717790 28	0.0176 4136
VIT_07s00 31g00350	Caffeoyl-CoA O- methyltransferase (VvCCOAMT)	1.0071612 4	0.0006 26765
VIT_17s00 00g04150	Leucoanthocyanidin reductase 2 (VvLAR2)	0.9204836 88	0.0488 38407
VIT_08s00 40g03040	Glutathione S- transferase L3 (VvGSTL3)	0.7482006 55	0.0060 85753

Defense mechanism	Leaf	E-L 31	VIT_06s00 61g00100	Beta-1,3- glucanase (VvPR-2)	4.5958606 38	0.0333 20268
			VIT_05s00 77g01550	Pathogenesis- related protein 10.3 (VvPR- 10.3)	1.3388433 05	0.0355 79663
	Leaf	E-L 35	VIT_02s00 25g04300	Thaumatococcus-like protein (VvPR-5)	7.1316377 72	0.0449 4005
			VIT_02s00 25g04290	Thaumatococcus-like protein (VvPR-5)	6.3967096 59	4.1640 5E-05
			VIT_06s00 61g00120	Beta-1,3- glucanase (VvPR-2)	3.9389118 73	0.0013 83384
			VIT_00s01 84g00120	Toll/interleukin- 1 receptor/resistanc e (TIR) domain- containing protein	3.8859115 64	0.0184 65883
			VIT_02s00 25g04230	Thaumatococcus-like protein (VvPR-5)	3.2836616 65	0.0203 21187
			VIT_14s00 81g00030	Pathogenesis- related protein 4A (VvPR-4A)	3.1817123 48	0.0210 84037
			VIT_02s00 25g04250	Thaumatococcus-like protein (VvPR-5)	3.1488409 94	0.0091 86248
			VIT_18s00 01g03710	Toll/interleukin- 1 receptor/resistanc e (TIR) domain- containing protein	2.8951838 45	0.0033 91152
			VIT_05s00 29g00880	NB-ARC domain- containing protein	2.5114879 26	0.0355 42064
			VIT_05s00 77g01570	Pathogenesis- related protein 10.3 (VvPR- 10.3)	2.1433730 36	0.0241 44198
			VIT_05s00 77g01550	Pathogenesis- related protein 10.3 (VvPR- 10.3)	1.633264	0.0154 67

		VIT_17s00	protein EDS1-	1.6328241	0.0367
		00g07400	related	73	83159
		VIT_17s00	protein EDS1-	1.3680620	0.0452
		00g07560	related	09	5429
Ber ry	E-L 31	N/A	N/A	N/A	N/A
Ber ry	E-L 35	VIT_13s00	RN_N domain- containing protein	2.7538953	0.0393
		47g00950		28	94598
		VIT_05s00	Pathogenesis- related protein 10.3 (VvPR- 10.3)	2.4900385	0.0409
		77g01590		46	53162
		VIT_00s04	RN_N domain- containing protein	2.4778947	0.0167
		67g00010		5	59386
		VIT_13s01	RN_N domain- containing protein	2.4141975	0.0253
		01g00300		28	70541
		VIT_13s01	RN_N domain- containing protein	2.3034668	0.0125
		58g00210		38	6742
		VIT_13s01	RN_N domain- containing protein	2.0975768	0.0372
		58g00260		95	0172
		VIT_07s01	RN_N domain- containing protein	2.0710842	0.0185
		41g01030		94	34408
		VIT_12s00	RN_N domain- containing protein	1.9758983	0.0199
		34g01490		03	77404
		VIT_17s00	Thaumatococcus-like protein (VvPR-5)	1.9631178	0.0264
		00g02470		01	76649
		VIT_04s00	Endoribonucleas e dicer 2 (VvDcr2)	1.8713291	0.0004
		23g00920		89	18918
		VIT_13s00	RN_N domain- containing protein	1.8144500	0.0271
		19g01880		47	00125
		VIT_00s04	RN_N domain- containing protein	1.7586197	0.0402
		67g00030		74	36181
		VIT_18s00	Toll/interleukin- 1 receptor/resistanc e (TIR) domain-	1.5649799	0.0038
		01g03900		72	39959

	containing protein		
VIT_13s00 84g00420	RN_N domain- containing protein	1.5483449 19	0.0235 1503
VIT_05s00 77g01540	Pathogenesis- related protein 10.3 (VvPR- 10.3)	1.4780089 18	4.2663 9E-07
VIT_12s00 34g00910	Toll/interleukin- 1 receptor/resistanc e (TIR) domain- containing protein	1.4578679 85	0.0027 38712
VIT_18s00 41g02120	Toll/interleukin- 1 receptor/resistanc e (TIR) domain- containing protein	1.3974128 17	0.0100 65127
VIT_13s00 19g04940	Protein RNA- directed DNA methylation 3 (VvRDM3)	1.3469322 52	0.0038 39959
VIT_18s00 89g00100	Toll/interleukin- 1 receptor/resistanc e (TIR) domain- containing protein	1.3022250 64	0.0122 75989
VIT_12s00 34g01030	RN_N domain- containing protein	1.2835628 21	0.0075 84517
VIT_18s00 01g12390	Beta-1,3- glucanase (VvPR-2)	1.2363637 55	0.0016 66823
VIT_11s01 49g00120	Dicer-like protein 4 (VvDCL4)	1.1611201 3	0.0381 83156
VIT_08s00 40g00070	Protein argonaute 4A (VvAGO4A)	1.1335097 45	0.0395 92633
VIT_06s00 61g01040	Protein argonaute 5 (VvAGO5)	1.1323988 29	0.0148 19184

Heat shock protein (HSP) and HSP co-chaperons	Leaf	E-L 31	VIT_12s0059g01320	Beta-1,3-glucanase (VvPR-2)	1.125450533	0.035729415
			VIT_04s0008g05430	RNA dependent RNA polymerase 6 (VvRdRp6)	1.105707065	0.008590499
			VIT_01s0011g05880	RNA dependent RNA polymerase 1 (VvRdRp1)	0.961610426	0.020025787
			VIT_18s0041g01750	NB-ARC domain-containing protein	0.837814871	0.039394598
			VIT_05s0077g01530	Pathogenesis-related protein 10.3 (VvPR-10.3)	1.864331635	0.000211093
			VIT_13s0019g01180	Beta-1,3-glucanase (VvPR-2)	1.039286395	6.09535E-05
			VIT_04s0008g01570	17.3 kDa HSP class II	9.226044184	9.22E-05
			VIT_04s0008g01550	17.3 kDa HSP class II	7.603957955	0.012837145
			VIT_04s0008g01510	17.3 kDa HSP class II	6.424988963	0.002138398
			VIT_02s0025g00280	HSP90	3.025376811	0.002847964
			VIT_13s0019g02850	18.2kDa HSP class I	2.377512808	0.023444084
			VIT_13s0019g02740	18.2kDa HSP class I	2.125954671	0.008010291
			VIT_10s0003g00260	DNAJ/Hsp40 protein	1.314887474	0.040859804
			VIT_00s1569g00010	HSP90	1.208769929	0.026300316
			VIT_13s0019g01430	HSP70	1.185124836	0.010733371
			VIT_09s0070g00380	HSP90 activator	1.045716007	0.033708586
			VIT_13s0019g03170	18.2kDa HSP class I	0.957458782	0.000238353

Leaf	E-L 35	VIT_06s00 80g01230	DNAJ/Hsp40 protein	0.8412589 72	0.0116 73479
		VIT_18s00 01g14500	HSP90	3.1563345 41	2.7276 1E-05
			BAG family molecular chaperone regulator 3 (BAG3)		
		VIT_10s00 03g04270		2.9655739 19	0.0241 44198
		VIT_09s00 96g00090	HSP70	2.8880060 12	8.4524 9E-07
		VIT_11s01 18g00490	HSP-interacting protein (HIP)	2.4650389 67	0.0436 7104
		VIT_07s00 05g01220	DNAJ/Hsp40 protein	2.2855709 7	0.0113 53252
		VIT_00s15 69g00010	HSP90	1.2874258 34	0.0411 07782
Berry	E-L 31	N/A	N/A	N/A	N/A
Berry	E-L 35	VIT_02s00 25g00280	HSP83	1.1584791 87	0.0077 10556
		VIT_00s04 15g00030	HSP70, mitochondrial	0.8257416 03	0.0199 77404
		VIT_01s00 10g00680	HSP90-5, chloroplastic	0.7507808 25	0.0463 97019
Berry	E-L 38	VIT_16s00 98g01060	HSP21	1.8302948 01	0.0003 08544
		VIT_06s00 04g05770	17.3kDa class III	1.5748981 65	0.0073 65313
		VIT_13s00 19g03000	18.1kDa class I	1.5517807 55	0.0009 17532
		VIT_18s00 89g01270	22.0 kDa class IV	1.3600462 04	1.8690 9E-06
		VIT_18s00 01g01610	17.3kDa class I	1.2995696 6	0.0068 48919
		VIT_18s00 01g01570	17.3kDa class I	1.1217704 31	0.0004 5774
		VIT_11s00 37g00510	HSP70	1.0964140 66	0.0136 0204
		VIT_04s00 08g01610	17.3kDa class II	1.0031441 23	0.0294 37963

Transcription factors	Leaf	E-L 31	VIT_16s00 13g01090	ERF005	5.0639221 51	0.0302 28975
			VIT_09s00 18g00240	WRKY 40	2.0924757 14	0.0149 90795
			VIT_01s00 26g01550	Homeobox-leucin zipper protein ATHB1	1.6127787 83	0.0188 90721
			VIT_01s00 11g00720	WRKY 57	1.3657492 17	7.60E-05
			VIT_05s00 77g00730	WRKY 48	1.1393154 63	0.0410 01274
			VIT_19s00 14g01680	Transcription factor TCP4	1.1276926 28	1.35E-08
			VIT_07s00 31g00080	WRKY 7	0.9963259 44	0.0296 1563
			VIT_18s00 01g03240	ERF004	8.2445717 53	0.0379 02476
			VIT_17s00 00g01280	WRKY53	7.0994956 32	0.0172 85867
			VIT_14s00 81g00670	AT-hook motif nuclear-localized protein 19 (AHL19)	6.2673039 56	0.0091 59622
Leaf	E-L 35		VIT_09s00 02g09120	ERF003	4.6628480 83	0.0421 86627
			VIT_02s00 12g01040	NAC domain-containing protein 86	4.5254162 8	5.0777 1E-10
			VIT_08s00 07g07670	NAC transcription factor 47	4.1060768 88	0.0012 43178
			VIT_04s00 08g06000	ERF045	3.7040483 87	0.0098 72403
			VIT_19s00 90g00840	WRKY 31	2.8208232 82	0.0202 45924
			VIT_17s00 00g03370	Protein SAR DEFICIENT 1 (SARD1)	2.5843241 83	0.0265 30846
			VIT_04s00 08g05750	WRKY 18	2.4024093 44	0.0184 2931
			VIT_17s00 00g03390	Protein SAR DEFICIENT 1 (SARD1)	2.3140281 31	0.0219 51318
			VIT_07s00 31g01710	WRKY51	1.8845668 09	0.0035 13756

Ber ry	E-L 31	N/A	N/A	N/A	N/A
Ber ry	E-L 35	N/A	N/A	N/A	N/A
Ber ry	E-L 38	VIT_14s00	ERF113	2.3070120	0.0020
		68g01040		83	41952
		VIT_01s00	ERF RAV1	1.8278040	2.1948
		11g03070		33	1E-05
		VIT_19s00	ERF004	1.3609655	0.0063
		14g02240		23	48559
		VIT_18s00	ERF110	1.1804801	0.0297
		72g00260		96	58167
		VIT_12s00	ERF004	0.7872631	0.0038
		28g03270		01	57149