Supplementary material of the manuscript published in Vitis **60**, 141 – 149 (2021):

Global transcriptome analysis of heat stress response of grape variety 'Fantasy Seedless' under different irrigation regimens

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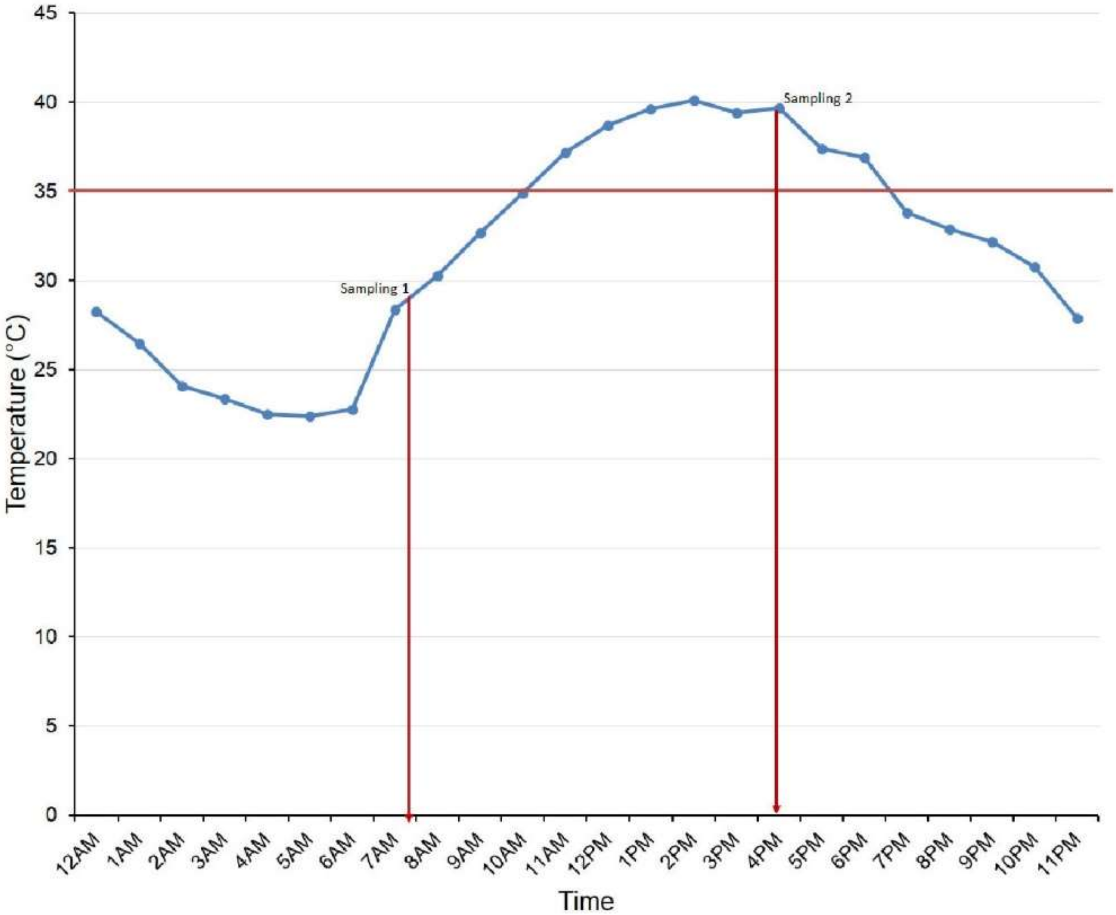
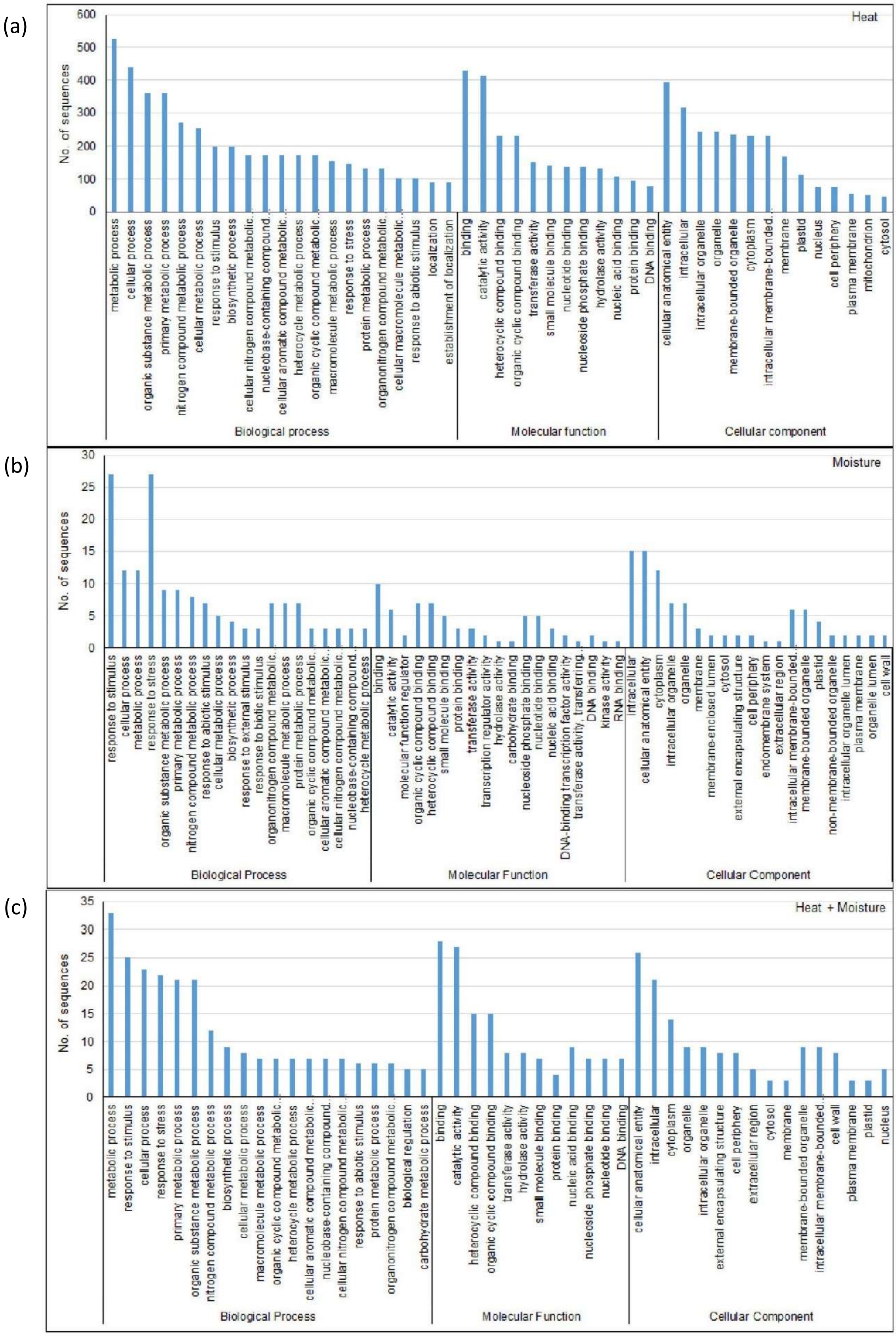
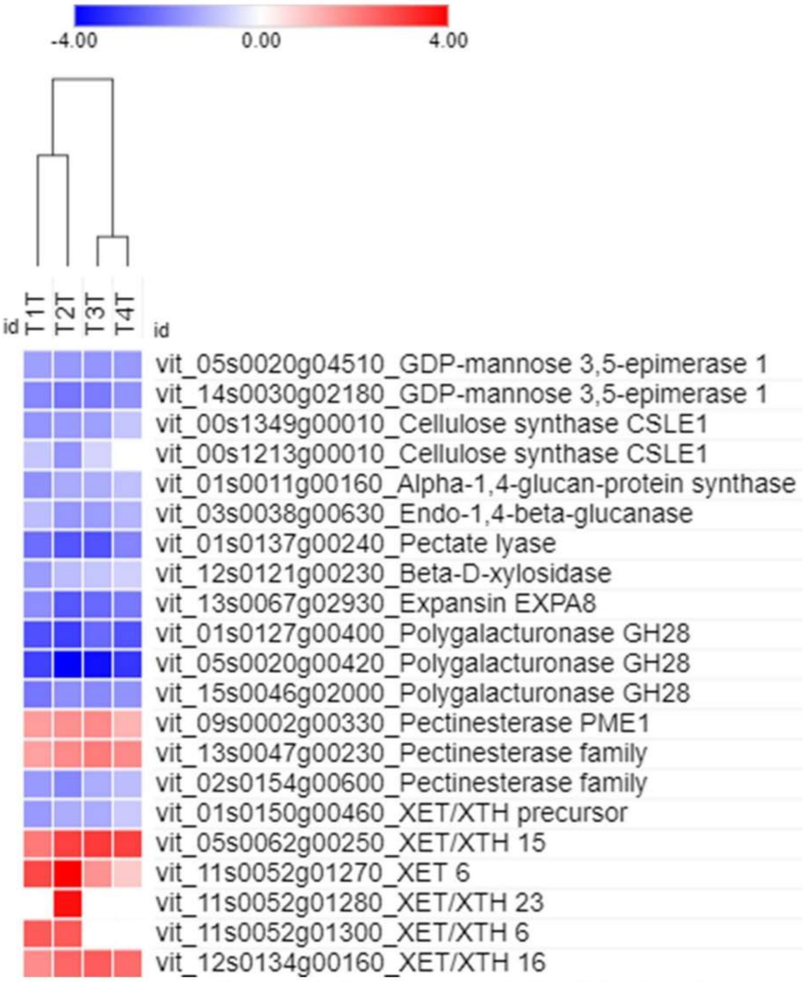


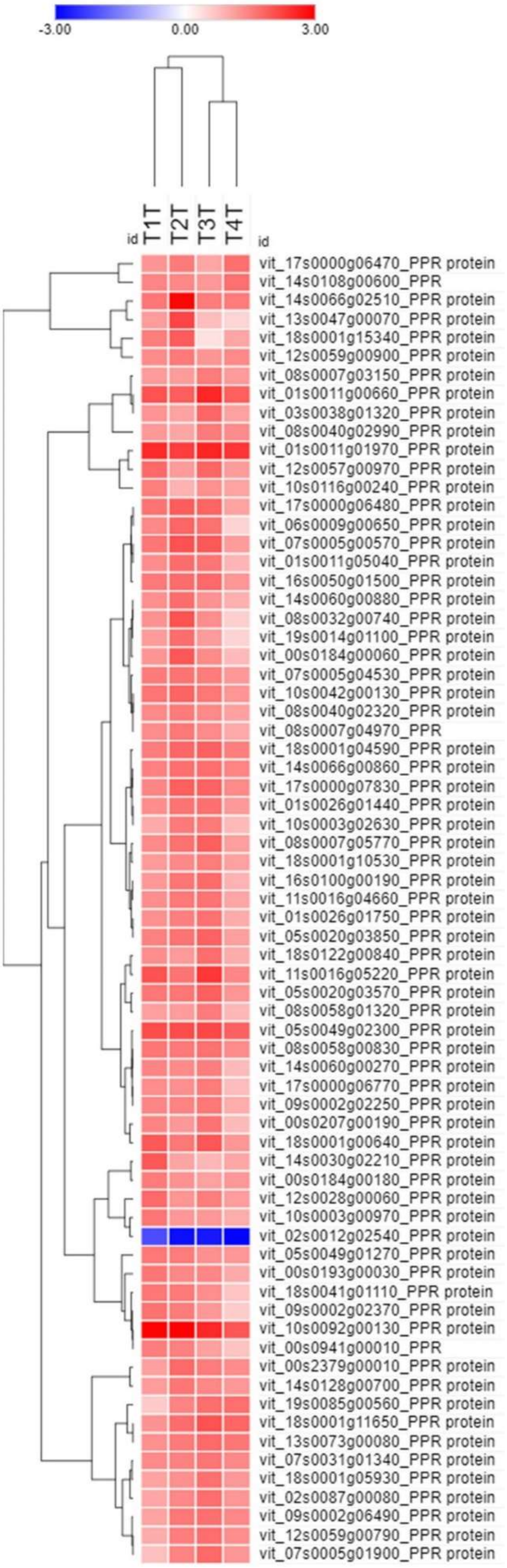
Supplementary Fig. 1: Temperature data during the experiment. The ambient temperature was 38-40 °C for more than 4 hours.



Supplementary Fig. 2: Bar chart of major GO terms belonging to Biological processes, Molecular functions and cellular component categories for different stresses. Large number of genes belonged to metabolic processes, molecular binding and cellular anatomical entity respectively under three categories.



Supplementary Fig. 3: Heat map of DEGs belonging to cell wall modification pathway. Majority of XET/XTH genes were upregulated, whereas those for polygalacturonase were downregulated in response to heat stress.



Supplementary Fig. 4: Heat map of significant DEGs belonging to PPR proteins category. Heat stress resulted in upregulation of large number of PPR protein genes.

Supplementary Table 1

Treatment	Transpiration rate	Assimilation rate	Leaf water potential
R	5.42^{ab}	9.89a	9.09b
R80%	5.41^{ab}	9.98a	9.25b
R50%	5.25^{b}	8.68b	10.53a
RS50%	5.56^{a}	10.68a	9.28b
P value	NS	0.007	< 0.001

Means with the same letter are not significantly different.

Supplementary Table 2

Heat stress responsive DEGs

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_09s0018g00310	-1,530	-1,345	-1,282	-1,297	MRP11, ABC transporter C member 1
VIT_08s0040g01620	2,284	1,412	1,825	2,050	ABC transporter G member 1,
VIT_08s0040g00790	1,788	1,497	2,395	2,028	FK506-binding protein 4/5,
VIT_12s0134g00590	-0,352	-1,052	-1,626	-1,166	Anthocyanidin 3-O-glucoside-6"-O-malonyltransferase
VIT_06s0004g06380	5,908	5,198	6,031	4,024	UDPGT domain-containing protein
VIT_01s0010g03590	1,356	1,607	1,090	1,183	Asynaptic 1 ASY1
VIT_14s0083g01200	1,617	1,511	1,922	1,871	Nitrilase
VIT_04s0008g00220	-2,000	-1,905	-1,928	-1,564	IAA6
VIT_05s0020g04680	-0,942	-1,049	-1,515	-0,704	Auxin-induced protein 22D
VIT_17s0000g06310	-0,829	-1,653	-0,859	-1,233	Cycling DOF factor 2
VIT_19s0090g01730	-0,736	-1,798	-0,934	-0,849	Zinc finger (C2H2 type) family
VIT_14s0030g02110	-0,677	-0,485	-1,522	-1,172	Ca2+-transporting ATPase type 2 isoform 8
VIT_16s0013g00330	1,119	0,667	1,559	0,596	Ribulose 1,5-bisphosphate carboxylase [Vitis aestivalis]
VIT_07s0129g00790	0,929	0,632	1,681	0,604	Ribulose bisphosphate carboxylase/oxygenase large subunit
VIT_00s0779g00020	-1,510	-1,442	-1,507	-0,790	CENTROMERERΕL
VIT_17s0000g04090	0,730	1,186	0,810	1,536	Cell division cycle associated 7
VIT_19s0090g01050	-0,363	-0,709	-1,200	-1,619	Endo-beta-1,4-glucanase
VIT_13s0067g00860	2,380	2,942	2,952	2,789	Early flowering 4
VIT_19s0015g00130	-1,171	-1,617	-0,840	-0,780	Serine acetyltransferase 3
VIT_16s0098g00900	2,915	2,735	3,219	2,346	Pseudo-response regulator 5 (APRR5)
VIT_06s0004g03650	3,401	2,921	2,626	2,311	Pseudo-response regulator 7 (APRR7)
VIT_15s0046g02550	0,000	0,460	0,667	1,938	Gibberellin 20-oxidase
VIT_05s0049g00230	1,731	1,167	0,810	1,343	E8 protein
VIT_06s0009g02810	1,596	0,446	1,233	0,798	TT7, Flavonoid 3',5'-hydroxylase,
VIT_17s0000g08960	0,054	-0,914	-1,685	-1,624	Raffinose synthase
VIT_00s0620g00010	2,551	2,025	2,175	1,368	Triacylglycerol lipase
VIT_01s0010g02460	-0,369	-0,840	-1,627	-0,076	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3
VIT_17s0000g02460	-1,541	-1,471	-0,705	-1,068	Wuschel related homeobox 1
VIT_03s0088g00810	-0,126	-0,928	-2,390	-0,333	Pathogenesis-related protein 1 precursor (PRP 1)
VIT_17s0000g08660	-1,828	-1,936	-1,945	-1,940	Anthranilate phosphoribosyltransferase
VIT_04s0008g01830	1,153	1,558	0,278	1,173	Myb domain protein 32
VIT_17s0000g09080	1,192	1,781	0,270	-0,141	Myb domain protein 4
VIT_19s0014g00330	0,961	0,852	1,171	1,522	NAD(H) kinase 3
VIT_00s0347g00030	1,186	1,820	1,351	0,912	Zinc finger (B-box type)
VIT_17s0000g01790	0,813	1,410	1,506	1,696	4-coumarate--CoA ligase
VIT_11s0052g01680	-1,333	2,491	1,136	0,482	Photosystem II protein D1
VIT_00s0275g00010	1,638	1,125	1,778	0,583	Photosystem II protein D2
VIT_11s0103g00110	1,316	1,087	1,686	0,767	Photosystem II protein D2
VIT_00s0396g00010	1,200	0,969	1,611	0,678	Photosystem II PsbC
VIT_06s0004g03920	1,773	2,259	2,099	1,681	Pto serine/threonine kinase
VIT_14s0030g00220	1,156	1,804	0,554	0,985	Sugar transporter ERD6-like 5
VIT_18s0041g01270	-1,373	-0,815	-1,996	-0,905	Amino acid permease 2
VIT_03s0038g02290	1,443	1,187	1,525	1,193	Amino acid permease 3
VIT_13s0019g04220	5,006	5,356	5,776	5,482	Tryptophan/tyrosine permease family
VIT_19s0177g00280	0,968	1,220	1,360	1,509	DNAJ heat shock N-terminal domain-containing
VIT_10s0003g01820	-1,558	-1,185	-1,181	-0,811	NLI interacting factor (NIF) family protein
VIT_19s0014g01820	0,963	1,689	0,700	0,387	RAB GTPase RABA1F
VIT_01s0011g02830	0,820	0,625	2,302	0,802	Signal peptidase I
VIT_15s0107g00280	3,015	2,933	2,558	2,684	TIR-NBS-LRR
VIT_15s0107g00290	3,266	3,250	2,903	2,681	TIR-NBS-LRR
VIT_15s0048g02290	-1,945	-1,597	-2,321	-2,292	CUC2_5, No apical meristem cup-shaped cotyledon2
VIT_18s0001g13580	1,609	1,279	1,680	1,058	Kinesin motor protein
VIT_15s0048g00860	1,905	1,945	2,042	1,813	Microtubule associated protein (MAP65/ASE1) pleiade
VIT_08s0040g00670	1,195	1,470	1,538	1,471	4-alpha-glucanotransferase
VIT_12s0059g02670	1,019	1,063	1,541	0,924	Beta-amylase
VIT_06s0004g06390	3,129	3,593	3,550	2,817	UDP-glucose glucosyltransferase

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_01s0146g00160	1,760	1,661	1,503	1,263	Exocyst subunit EXO70 family protein C1
VIT_00s0504g00010	0,274	-0,171	2,048	0,637	Photosystem II PsbD
VIT_13s0067g03390	2,246	2,036	1,625	1,726	Pseudo-response regulator 7 (APRR7)
VIT_07s0031g03000	0,772	0,504	1,596	0,479	Ribulose 1,5-bisphosphate carboxylase large subunit
VIT_08s0040g03120	-0,378	-0,539	-1,216	-1,614	Pseudo-response regulator 7 (APRR7)
VIT_11s0037g00010	-1,918	-1,610	-0,969	-0,513	RAV1-like ethylene-responsive transcription factor
VIT_11s0118g00490	-0,449	-1,104	-1,186	-1,723	Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein
VIT_18s0072g01220	-0,408	-0,919	-1,185	-1,634	ABC transporter G member 3
VIT_16s0098g01810	1,985	1,965	1,935	1,723	Histone H2B
VIT_00s0260g00070	1,721	1,032	0,591	0,869	Peptidyl-prolyl cis-trans isomerase, FKBP-type
VIT_11s0118g00310	0,000	-0,960	-2,262	0,000	1,2-diacylglycerol 3-beta-galactosyltransferase
VIT_02s0012g00400	2,347	2,554	2,213	2,710	1-aminocyclopropane-1-carboxylate oxidase
VIT_02s0012g00450	1,247	1,451	1,723	1,844	1-aminocyclopropane-1-carboxylate oxidase
VIT_15s0021g00960	0,868	1,713	0,442	1,363	1-aminocyclopropane-1-carboxylate oxidase
VIT_05s0049g00430	1,677	2,288	1,584	1,958	1-aminocyclopropane-1-carboxylate oxidase homolog 1
VIT_05s0049g00410	1,904	1,532	1,111	1,535	1-aminocyclopropane-1-carboxylate oxidase homolog 1 like
VIT_05s0049g00300	2,246	1,697	1,431	1,119	1-aminocyclopropane-1-carboxylate oxidase homolog 1 like
VIT_11s0016g02380	-1,819	-1,466	-1,121	-1,054	1-aminocyclopropane-1-carboxylate oxidase homolog 1 like
VIT_00s1764g00010	1,883	0,803	1,128	1,098	1-aminocyclopropane-1-carboxylate synthase
VIT_18s0001g05060	1,646	1,436	1,461	1,382	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase
VIT_18s0001g07320	1,837	1,469	1,543	1,193	2-oxoglutarate/malate carrier protein, Mitochondrial
VIT_04s0044g01480	-1,662	-1,482	-1,566	-0,998	3'(2'),5'-bisphosphate nucleotidase
VIT_17s0000g02140	-1,881	-1,666	-1,313	-1,586	3-hydroxyisobutyrate dehydrogenase
VIT_08s0007g07530	0,972	1,373	1,931	1,596	3-oxoacyl-[acyl-carrier-protein] reductase, chloroplast
VIT_08s0007g07520	1,367	1,540	0,629	0,442	3-oxoacyl-[acyl-carrier-protein] reductase, chloroplast
VIT_16s0050g00390	-2,432	-3,125	-2,826	-4,172	4-coumarate-CoA ligase
VIT_12s0028g00710	2,477	1,850	1,923	1,343	4-hydroxyphenylpyruvate dioxygenase
VIT_05s0020g00880	1,273	1,448	1,510	1,531	5-nucleotidase
VIT_02s0025g00900	1,461	1,217	1,818	0,972	6-phosphogluconate dehydrogenase
VIT_02s0087g00910	2,753	2,733	3,378	2,288	9-cis-epoxycarotenoid dioxygenase
VIT_14s0066g02060	-1,020	-1,529	-1,679	-0,523	AAA-type ATPase
VIT_05s0136g00140	-1,348	-1,456	-1,323	-1,625	AarF domain containing kinase
VIT_18s0001g10500	1,163	1,410	1,554	0,544	ABA 8'-hydroxylase CYP707A1
VIT_11s0052g00540	1,862	1,777	1,492	2,015	ABC protein 3 ATNAP3 non-intrinsic
VIT_10s0003g04460	-2,063	-1,697	-1,704	-1,387	ABC transporter C member 11
VIT_15s0021g00220	-1,167	-1,359	-1,568	-1,384	ABC transporter C member 15
VIT_15s0045g00090	1,022	2,195	1,667	1,009	ABC transporter C member 9
VIT_07s0031g01640	-0,649	-1,413	-1,105	-1,677	ABC transporter F member 8
VIT_09s0002g05570	0,591	1,288	1,281	1,880	ABC transporter g family pleiotropic drug resistance 12 PDR12
VIT_07s0031g02550	-1,840	-2,547	-2,725	-2,567	ABC transporter G member 14
VIT_16s0050g01620	-2,198	-1,531	-1,410	-1,410	ABC transporter G member 14
VIT_01s0011g04670	1,710	1,713	1,968	1,923	ABC transporter G member 2
VIT_18s0166g00080	-2,461	-2,271	-2,188	-1,738	ABC transporter G member 4
VIT_11s0016g03180	-0,681	-0,989	-1,176	-1,825	ABI1 (ABA insensitive 1)
VIT_02s0012g01270	-1,877	-1,575	-0,803	-1,048	abscisic acid receptor PYR1-like
VIT_06s0004g00610	-1,625	-2,073	-1,847	-1,971	Accelerated cell death 1 ACD1
VIT_13s0084g00310	-2,402	-2,951	-3,251	-3,163	ACI112
VIT_15s0046g01570	1,563	1,575	0,470	1,733	Acidic endochitinase (CHIB1)
VIT_01s0244g00030	-1,548	-1,510	-1,010	-0,826	ACP4 (Acyl carrier protein 4)
VIT_01s0011g05810	5,532	5,331	5,785	5,358	Adagio protein 1
VIT_09s0054g00910	-2,422	-2,271	-4,221	-2,468	Adenosinetriphosphatase
VIT_05s0020g02880	-1,358	-1,928	-1,085	-1,397	ADP-glucose pyrophosphorylase
VIT_03s0038g04570	2,121	1,625	1,589	1,331	ADP-glucose pyrophosphorylase large subunit 1
VIT_19s0027g00090	1,506	1,372	1,108	0,580	AERO1, AERO1
VIT_00s0225g00130	-1,657	-2,042	-1,515	-1,588	Alanine transaminase.
VIT_08s0007g07480	3,424	3,352	3,709	3,203	Aldose 1-epimerase
VIT_11s0016g05770	1,739	1,387	1,394	1,164	Alkaline alpha galactosidase 2
VIT_01s0011g00160	-1,734	-1,334	-1,294	-0,988	Alpha-1,4-glucan-protein synthase
VIT_01s0026g01660	1,736	2,093	2,207	2,161	Alpha-amylase isozyme C2 precursor
VIT_00s0270g00120	2,784	2,124	2,404	3,241	Alpha-amylase/subtilisin inhibitor

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_06s0004g06020	1,515	1,618	1,789	1,639	Alpha-glucan phosphorylase, H isozyme
VIT_16s0022g02170	-1,205	-1,857	-0,572	-1,912	Alpha-L-fucosidase
VIT_02s0012g01030	0,483	0,565	1,542	0,701	Aluminum-activated malate transporter 1
VIT_06s0004g00790	1,674	1,790	1,464	1,384	Amino acid permease
VIT_19s0015g01300	0,843	1,607	1,424	1,594	Amino acid permease 7
VIT_08s0007g00200	2,443	2,242	2,247	1,948	Ankyrin repeat
VIT_14s0081g00360	3,153	2,835	2,329	2,573	Ankyrin repeat
VIT_14s0081g00370	4,207	3,077	2,815	2,633	Ankyrin repeat
VIT_04s0008g03840	-1,700	-2,165	-2,424	-1,861	Ankyrin repeat
VIT_05s0029g01540	-1,408	-1,769	-1,508	-1,209	Ankyrin repeat
VIT_00s0411g00050	1,436	1,202	1,641	1,505	Ankyrin repeat
VIT_00s0901g00010	1,863	2,317	1,048	1,513	Ankyrin repeat
VIT_00s0228g00070	1,276	1,454	1,335	1,642	Ankyrin repeat
VIT_13s0106g00080	1,242	1,106	1,627	2,075	Ankyrin repeat
VIT_05s0029g01410	-0,863	-1,394	-1,173	-1,564	Ankyrin repeat
VIT_06s0004g06400	0,000	6,747	5,128	0,000	Anthocyanidin 3-O-glucosyltransferase
VIT_12s0034g00130	-0,826	-1,188	-1,565	-1,311	Anthocyanidin 3-O-glucosyltransferase
VIT_08s0056g01530	-1,510	-1,563	-1,274	-1,538	Anthranilate phosphoribosyltransferase
VIT_14s0108g00700	-1,365	-1,589	-1,139	-1,030	Aquaporin NIP1;2
VIT_08s0040g01890	-1,507	-1,927	-2,121	-1,883	Aquaporin PIP2;4
VIT_06s0004g02850	-1,229	-1,720	-1,186	-1,395	Aquaporin PIP2B
VIT_11s0016g03170	-0,864	-1,267	-1,618	-1,638	Arabidopsis histidine phosphotransfer AHP4
VIT_15s0048g01870	-1,545	-1,449	-1,625	-0,980	Arginine/serine-rich splicing factor RSP41
VIT_16s0100g00450	-1,507	-1,029	-0,649	-0,272	Arginine/serine-rich splicing factor RSP41
VIT_06s0004g05120	4,242	5,302	4,967	5,145	ARR1 typeB
VIT_08s0007g02780	1,133	0,395	1,528	0,650	Asp/Glu racemase
VIT_06s0004g07820	1,320	2,034	1,766	1,364	Aspartate-glutamate racemase
VIT_14s0006g00180	1,834	1,317	1,488	0,588	Aspartyl protease
VIT_08s0007g02470	1,083	1,120	2,156	0,915	Aspartyl protease
VIT_06s0080g01160	0,567	0,992	1,531	0,986	Aspartyl protease
VIT_08s0007g02450	1,655	0,942	4,320	2,769	Aspartyl protease
VIT_07s0031g01420	-1,173	-1,689	-1,323	-1,775	ATATH13
VIT_14s0066g01220	-1,366	-1,417	-1,667	-0,864	ATMYB66/WER/WER1 (WEREWOLF 1)
VIT_11s0016g01220	-2,034	-2,185	-1,065	-1,587	Auxin-binding protein ABP19a precursor
VIT_09s0002g06510	1,854	2,057	1,887	1,866	Auxin-independent growth promoter axi1
VIT_07s0141g00270	-1,686	-3,075	-1,889	-2,018	Auxin-induced protein 22D
VIT_05s0020g04670	-1,015	-1,147	-2,219	-0,657	auxin-responsive protein IAA4-like
VIT_02s0154g00010	0,957	1,733	1,141	0,330	Auxin-responsive SAUR11
VIT_03s0038g01110	-1,810	-1,981	-1,460	-1,194	Auxin-responsive SAUR31
VIT_05s0020g04620	2,021	1,991	2,126	2,130	Basic helix-loop-helix (bHLH) family
VIT_06s0004g07700	-1,897	-1,609	-0,962	-1,215	Basic helix-loop-helix (bHLH) family
VIT_08s0058g00960	-1,690	-0,916	-0,928	-1,025	Basic helix-loop-helix (bHLH) family
VIT_05s0049g00460	1,443	1,513	0,787	1,441	Basic helix-loop-helix ILR3
VIT_01s0146g00150	0,755	-1,244	0,461	2,440	BCL-2-associated athanogene 5
VIT_02s0025g00200	-1,811	-2,121	-0,979	-2,078	BEL1 (BELL 1)
VIT_08s0007g06040	1,606	1,854	1,365	1,900	Beta-1,3-glucanase
VIT_05s0077g00280	-1,844	-2,675	-2,501	-2,557	Beta-amylase
VIT_12s0121g00230	-1,546	-1,039	-0,909	-0,721	Beta-D-xylosidase
VIT_00s2527g00010	1,912	0,969	1,856	1,429	Beta-fructosidase (BFRUCT3)
VIT_10s0003g02190	1,754	1,665	1,811	1,343	Bidirectional sugar transporter SWEET
VIT_09s0002g06810	2,726	3,445	2,836	2,795	Binding
VIT_06s0004g06290	3,727	3,672	4,176	2,854	Binding
VIT_08s0007g08660	-1,679	-1,590	-1,608	-1,319	Binding
VIT_07s0129g00210	1,516	2,001	1,218	0,654	BT4 (BTB and TAZ Domain protein 4)
VIT_18s0122g01340	1,514	1,162	1,344	1,254	BTB/POZ domain-containing protein
VIT_19s0014g01780	0,673	1,643	0,814	0,090	BZIP transcription factor
VIT_14s0083g00700	2,988	1,655	1,333	1,752	BZIP transcription factor BZIP42
VIT_12s0057g00470	1,235	1,609	1,192	0,988	C2 domain containing protein
VIT_05s0020g04300	0,944	1,811	0,000	1,098	Ca2+-ATPase 13 ACA13, plasma membrane
VIT_03s0063g02040	1,128	0,982	1,649	0,961	Caffeine synthase

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_09s0002g08100	2,293	1,596	1,876	1,909	Calcineurin
VIT_02s0025g01640	1,676	1,379	1,661	1,782	Calcineurin B 4-1
VIT_06s0004g06030	1,345	1,709	2,141	1,938	Calcium/calmodulin-regulated receptor kinase
VIT_03s0038g01380	-1,189	-1,789	-1,617	-1,682	Calcium-binding EF hand
VIT_11s0118g00540	0,677	1,497	1,743	1,565	Calcium-binding EF hand
VIT_06s0080g01060	1,114	1,316	0,897	1,536	Calcium-binding EF hand
VIT_08s0056g00290	-1,839	-1,856	-2,559	-1,696	Calcium-binding protein CML
VIT_00s0992g00030	0,000	-1,921	-0,428	-0,713	Calmodulin-binding
VIT_00s0283g00030	2,377	1,875	1,128	0,983	Calnexin 1 (CNX1)
VIT_04s0023g00830	2,072	1,797	1,500	1,949	Calreticulin 3 (CRT3)
VIT_06s0004g00940	1,964	1,835	1,901	1,873	Carbamoyl-phosphate synthase, large subunit
VIT_14s0066g01210	-0,986	-2,048	-0,027	-2,116	Carbonic anhydrase, chloroplast precursor
VIT_03s0063g00800	5,097	5,494	5,037	4,904	Carboxyesterase 12; CXE12
VIT_08s0007g08050	-1,406	-1,772	-1,825	-1,840	Carboxyl-terminal processing protease
VIT_02s0025g03490	1,696	1,775	1,653	1,502	Carrier protein, Mitochondrial
VIT_04s0008g02860	-0,074	-0,187	1,545	1,342	Cation transport protein chaC
VIT_02s0025g00820	1,669	1,967	1,897	1,717	Cation/hydrogen exchanger (CHX18)
VIT_10s0003g04540	2,694	3,142	3,158	2,703	Cationic amino acid transporter 1
VIT_10s0003g01410	-3,459	-3,856	-3,925	-4,062	CBL-interacting protein kinase 20 (CIPK20)
VIT_06s0080g01090	-0,121	-0,846	-0,904	-1,516	CCR4-NOT transcription complex subunit 7/8
VIT_06s0004g07210	6,651	4,815	7,694	7,134	CCT motif constans-like
VIT_13s0019g01840	-1,556	-1,329	-1,585	-0,543	Cell division cycle 20-like protein 1
VIT_09s0002g02320	0,912	1,232	1,537	0,887	Cell wall apoplastic invertase
VIT_00s1349g00010	-1,656	-1,579	-1,506	-0,907	Cellulose synthase CSLE1
VIT_00s1213g00010	-0,904	-1,670	-0,667	0,000	Cellulose synthase CSLE1
VIT_04s0008g01290	-0,840	-1,085	-0,466	-1,659	CGA1 (cytokinin-responsive GATA factor 1)
VIT_14s0066g02040	-1,539	-1,205	-0,918	-0,861	Chaperone BCS1 mitochondrial
VIT_01s0010g00920	1,492	1,531	2,015	1,841	Chaperonin GroEL
VIT_05s0051g00340	1,517	1,192	0,784	0,791	Chaperonin GroEL
VIT_07s0130g00400	-1,226	-1,541	-1,586	-1,464	Chloride channel protein (CLC-c)
VIT_18s0001g02700	-1,309	-1,795	-1,717	-1,911	Chlorophyll a oxygenase (CAO)
VIT_09s0002g06980	2,189	2,104	2,561	2,333	Chloroplast post-illumination chlorophyll fluorescence increase protein
VIT_02s0025g00220	1,817	1,554	1,961	1,334	Chlororespiratory reduction 4 (CRR4)
VIT_19s0014g02970	1,219	1,546	1,554	1,411	Choline transporter
VIT_01s0011g02860	-1,998	-2,397	-1,745	-2,106	CHUP1 (chloroplast unusual positioning 1)
VIT_00s0640g00020	0,934	1,736	1,320	1,309	Cig3
VIT_04s0079g00410	-4,885	-5,216	-5,899	-4,928	CIR1/RVE2 (circadian 1)
VIT_07s0104g00350	3,541	3,029	3,755	3,378	Circadian clock coupling factor ZGT
VIT_08s0040g01470	-1,199	-1,891	-1,577	-2,436	Cis-zeatin O-beta-D-glucosyltransferase
VIT_14s0066g01480	1,022	1,061	1,578	0,696	Cis-zeatin O-beta-D-glucosyltransferase
VIT_04s0079g00810	-1,632	-1,736	-3,119	-2,146	Cold induced protein
VIT_03s0038g02130	-1,425	-1,459	-1,333	-2,061	Cold shock protein-1
VIT_07s0104g01480	-1,569	-1,740	-1,645	-1,906	Cold-induced thioredoxin domain
VIT_14s0083g00640	-2,245	-2,685	-3,015	-3,579	Constans 2 (COL2)
VIT_14s0068g01380	2,882	3,257	3,253	3,279	Constans-like 14
VIT_01s0146g00360	1,710	0,803	1,790	1,134	Constans-like 14
VIT_01s0011g03520	-1,444	-2,069	-1,569	-1,431	Constans-like 16
VIT_19s0014g03210	1,517	1,550	1,747	1,347	COP1-interacting protein 7
VIT_16s0098g00790	-1,413	-1,197	-1,700	-1,564	Copper-binding family protein
VIT_12s0142g00330	-2,859	-2,795	-2,709	-2,735	Copper-transporting ATPase PAA1
VIT_17s0000g10180	1,764	1,268	1,605	0,773	Coproporphyrinogen oxidase
VIT_14s0006g03210	0,757	1,190	1,581	1,682	COX assembly mitochondrial protein
VIT_02s0087g01020	-2,088	-1,945	-1,463	-1,121	CRK10 (cysteine-rich RLK10)
VIT_02s0087g01010	-0,793	-1,597	-1,560	-1,005	CRK10 (cysteine-rich RLK10)
VIT_01s0011g05310	3,219	3,085	2,938	2,681	CRR3 (chlororespiratory reduction 3)
VIT_04s0008g02670	-1,956	-2,194	-2,290	-2,099	Cryptochrome DASH
VIT_07s0031g02570	-1,511	-1,184	-1,159	-0,983	CTV.22
VIT_16s0050g00020	-1,247	-1,971	-1,588	-1,990	Cullin-4
VIT_19s0014g01360	1,968	2,865	2,942	2,914	Curculin (mannose-binding) lectin
VIT_13s0084g00130	-0,724	-1,216	-1,606	-1,346	CXE carboxylesterase

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_06s0009g02090	-1,946	-2,088	-1,732	-1,446	Cyclin CYCB1_2
VIT_18s0001g09160	1,217	1,537	0,817	0,593	Cyclin, N-terminal
VIT_14s0108g00980	-2,315	-3,359	-2,795	-2,980	Cycling DOF factor 1
VIT_01s0026g02580	-1,959	-2,381	-2,095	-2,382	Cycling DOF factor 2
VIT_08s0056g01230	-1,272	-1,605	-1,587	-1,631	Cycling DOF factor 2
VIT_15s0021g02680	1,607	1,905	2,214	1,841	Cyclin-U2-1 (CycU2;1) Cyclin-P3.1
VIT_07s0005g02490	-2,074	-1,472	-1,414	-1,343	CYP709B2
VIT_17s0000g09550	-1,636	-2,029	-0,854	-1,976	CYP71A26
VIT_17s0000g09540	0,000	-1,901	0,000	-2,394	CYP71A26
VIT_01s0137g00510	0,495	0,437	1,822	0,573	CYP71B10
VIT_10s0092g00370	3,933	3,483	4,277	4,118	CyP71D7
VIT_19s0015g02500	-1,178	-1,338	-1,026	-1,637	CYP72A1
VIT_04s0008g01860	-1,399	-1,353	-2,239	-1,087	CYP72A58
VIT_13s0074g00390	-1,962	-1,684	-0,623	-1,379	CYP77A2
VIT_07s0031g01570	1,461	1,922	1,221	1,078	CYP78A11
VIT_18s0001g09510	2,067	1,155	2,214	0,793	CYP81B2v1
VIT_18s0001g09520	-1,793	-1,733	-1,082	-2,242	CYP81B2v2
VIT_18s0001g09650	1,218	1,486	1,474	1,571	CYP81E1
VIT_00s0705g00010	2,709	2,752	2,444	2,609	CYP81E1 Isoflavone 2'-hydroxylase
VIT_07s0031g01680	0,450	1,353	1,699	1,638	CYP86A1
VIT_01s0137g00410	1,473	1,516	2,130	1,577	CYP86A2
VIT_16s0039g00880	-1,344	-1,741	-1,604	-1,531	CYP89H3
VIT_00s0187g00040	2,435	1,967	1,600	1,323	Cystatin
VIT_14s0006g00250	-1,091	-1,347	-1,319	-2,225	Cysteine-rich repeat secretory protein 60
VIT_00s0802g00010	-1,195	-1,704	-2,667	-2,130	CYSTM domain-containing protein
VIT_04s0008g01880	1,565	1,804	1,638	0,796	Cytokinin dehydrogenase 7
VIT_01s0244g00170	1,538	1,467	1,670	1,477	Cytokinin-repressed protein CR9
VIT_02s0025g00400	-1,484	-1,229	-1,505	-0,936	D111/G-patch domain-containing protein
VIT_19s0014g04710	1,308	1,145	1,629	1,487	DAG protein, chloroplast precursor
VIT_04s0023g00920	-1,964	-1,797	-2,252	-2,420	DCL2 (DICER 2)
VIT_12s0059g00280	2,249	2,280	2,214	1,701	Dehydration-responsive element-binding protein 16
VIT_13s0067g01960	2,364	2,088	2,272	2,909	Dehydration-responsive element-binding protein 2C
VIT_03s0063g02340	-2,252	-1,829	-0,866	-1,120	Dehydration-responsive protein (RD22)
VIT_04s0023g02480	3,171	2,795	1,929	1,513	Dehydrin 1b
VIT_05s0049g00400	1,080	1,044	0,901	1,637	Desacetoxyvindoline 4-hydroxylase
VIT_04s0008g02920	-2,169	-1,646	-2,117	-1,363	Desiccation protein PCC13-62 precursor
VIT_18s0041g00350	2,172	1,608	1,984	1,503	Dienelactone hydrolase
VIT_17s0000g06780	1,914	2,016	1,648	1,679	Dimethylaniline monooxygenase
VIT_03s0038g03140	2,190	1,920	1,130	0,777	Dimethylaniline monooxygenase, N-oxide-forming
VIT_00s0333g00050	-2,380	-3,078	-2,864	-2,825	DIR1 (defective IN induced resistance 1)
VIT_16s0039g02380	-1,190	-1,567	-1,729	-1,113	Disease resistance family protein
VIT_11s0118g00080	1,237	1,048	1,125	1,824	Disease resistance protein
VIT_03s0038g01770	-1,321	-1,634	-1,375	-1,256	Disease resistance protein (CC-NBS-LRR class)
VIT_05s0020g03810	1,032	1,098	1,759	1,094	Disease resistance protein (NBS-LRR class)
VIT_06s0004g00990	-1,569	-1,346	-1,282	-1,291	Disease resistance-responsive
VIT_05s0020g04630	1,227	1,280	1,588	1,300	DMI1 protein homologue
VIT_01s0011g03440	-0,409	-0,905	-0,936	-1,648	DNA mismatch repair protein
VIT_05s0049g00100	-2,618	-2,503	-3,309	-2,696	DNA-binding protein
VIT_00s0956g00030	1,063	1,550	1,020	1,067	DNA-binding protein
VIT_10s0042g00960	7,008	6,181	7,560	7,777	DNAJ heat shock N-terminal domain-containing protein
VIT_14s0060g01490	7,047	6,567	6,565	6,451	DnaJ homolog, subfamily A, member 5
VIT_10s0003g00260	0,014	-1,895	-2,303	-0,327	DnaJ homolog, subfamily B, member 4
VIT_09s0002g00690	3,434	1,769	1,541	2,060	DnaJ homolog, subfamily B, member 6
VIT_08s0007g00170	0,600	0,649	0,578	1,710	DPB-1 transcription factor (DPB)
VIT_01s0011g00560	2,313	2,275	2,105	1,934	DREPP plasma membrane polypeptide
VIT_06s0004g06630	0,502	0,909	1,251	1,885	DTA2 (downstream target of AGL15 2)
VIT_19s0014g03710	-2,756	-5,106	-5,413	-5,185	dynein light chain
VIT_08s0040g03270	1,525	1,192	1,092	0,762	E3 ubiquitin-protein ligase TRIP12
VIT_07s0104g00360	2,207	3,523	2,404	2,523	Early-responsive to dehydration
VIT_11s0037g01210	0,525	1,175	1,535	1,146	Eceriferum 1 (CER1 protein) Sterol desaturase

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_13s0156g00120	3,629	3,194	3,415	3,293	EF hand
VIT_09s0018g01080	-1,826	-2,607	-1,889	-2,580	EFR (EF-TU receptor)
VIT_18s0076g00360	1,508	1,225	1,161	0,659	EMB1075 (embryo defective 1075) carboxy-lyase
VIT_06s0004g07840	-1,265	-1,182	-1,654	-0,960	Endo/excinuclease
VIT_03s0038g00630	-1,044	-1,629	-1,529	-1,170	Endo-1,4-beta-glucanase
VIT_15s0021g02470	1,377	1,891	1,513	1,445	Epoxide hydrolase-like protein
VIT_10s0003g00580	0,000	2,625	0,000	0,000	ERF/AP2 transcription factor sub B-3 (ATERF-2)
VIT_17s0000g02020	0,581	1,071	1,632	0,796	Erwinia induced protein 2
VIT_06s0080g00310	1,264	1,541	1,503	1,616	Esterase/lipase/thioesterase family protein
VIT_06s0004g08190	2,260	2,621	2,329	1,792	Ethylene-responsive transcription factor cytokinin response factor 1
VIT_06s0004g00490	1,523	1,542	1,473	1,292	Ethylene-responsive transcription factor related to APETALA2 11
VIT_04s0008g05440	-1,558	-1,581	-0,899	-1,332	Ethylene-responsive transcription factor SHINE 3
VIT_00s0317g00140	-1,901	-3,573	-3,430	-3,575	Exocyst subunit Exo70 family protein
VIT_18s0122g01400	1,360	1,701	1,539	0,654	Exostosin family protein
VIT_13s0067g02930	-1,773	-2,622	-2,357	-2,098	Expansin [Vitis labrusca x Vitis vinifera] EXPA8
VIT_17s0000g04490	-1,989	-2,030	-1,767	-1,881	Extracellular Ca2+ sensing receptor
VIT_03s0063g01780	1,863	2,433	1,736	1,454	Extra-large G-protein (XLG1)
VIT_08s0007g06450	2,296	2,374	2,553	2,326	FAD2, Omega-6 fatty acid desaturase#N/A
VIT_05s0077g01400	1,799	1,518	1,717	1,250	FAR1-related sequence 11
VIT_01s0011g01980	3,419	2,845	2,576	2,602	fasciclin arabinogalactan-protein (FLA21)
VIT_01s0011g06650	-3,066	-2,970	-1,529	-1,731	fasciclin arabinogalactan-protein (FLA21)
VIT_03s0038g03630	1,575	0,785	1,984	1,107	F-box domain containing protein
VIT_00s0181g00080	-0,593	-1,284	-1,531	-0,454	F-box domain containing protein
VIT_09s0002g08660	5,394	5,380	5,391	5,248	F-box protein (FBL14)
VIT_00s0214g00090	1,735	0,888	0,758	1,167	F-box protein PP2-B10 (Protein phloem protein 2-like B10)
VIT_09s0002g01000	-1,241	-1,920	-2,025	-1,384	Ferredoxin 4Fe-4S, iron-sulfur binding
VIT_18s0001g14450	-1,291	-1,670	-0,759	-1,296	Ferredoxin:nadp+ Oxidoreductase PETH
VIT_13s0064g00940	1,145	1,403	1,564	1,583	ferric reductase defective 3
VIT_16s0050g00980	1,684	1,568	1,907	2,198	ferric reduction oxidase 2
VIT_12s0035g02150	2,523	1,923	2,455	1,689	ferric reduction oxidase 7 FRO7
VIT_19s0014g01100	1,172	1,694	1,153	0,513	Fertility restorer homologue A,PPR
VIT_07s0031g01380	-1,752	-2,693	-1,946	-2,088	ferulate 5-hydroxylase
VIT_17s0000g03930	-0,646	-1,514	-1,908	-1,087	ferulate 5-hydroxylase
VIT_15s0021g02260	2,012	1,756	1,906	1,606	Fibrillin-11
VIT_00s0958g00020	1,782	1,165	0,603	0,826	FK506-binding protein 4/5 ROF1 (rotamase FKBP 1)
VIT_03s0038g03160	1,307	1,291	1,875	1,226	flavin-containing monooxygenase 1
VIT_03s0038g03190	3,151	2,583	3,269	2,835	flavin-containing monooxygenase 3
VIT_00s1682g00020	1,581	1,713	0,776	1,069	flavonoid 3'-hydroxylase cytochrome P450 (Flavonoid biosynthesis)
VIT_11s0016g01020	2,684	2,586	2,355	2,351	flavonoid 3-monooxygenase
VIT_09s0002g02980	1,815	2,144	2,280	2,042	FRK1 (FLG22-induced receptor-like kinase 1)
VIT_08s0007g01570	-1,811	-2,206	-1,785	-2,160	fructose 1,6-bisphosphatase
VIT_14s0108g00590	2,982	0,648	0,625	1,323	FtsH protease
VIT_14s0060g01700	1,762	1,782	1,305	1,089	fumarase (Reductive carboxylate cycle)
VIT_14s0060g01690	2,032	1,968	1,766	1,809	fumarase (Reductive carboxylate cycle)
VIT_07s0005g01970	8,150	5,320	5,147	5,111	Galactinol synthase
VIT_14s0060g00810	1,740	1,102	0,481	0,949	Galactinol synthase
VIT_14s0060g00790	2,153	1,149	0,465	1,306	Galactinol synthase
VIT_01s0010g02030	2,156	1,650	1,255	1,517	Gamma-thionin precursor
VIT_08s0007g05860	-1,951	-1,529	-1,008	-2,064	GASA like
VIT_14s0066g01790	0,976	2,034	1,548	2,010	GASA like
VIT_18s0001g09460	2,632	2,463	1,482	1,844	GASA5
VIT_03s0038g00490	2,010	2,331	1,545	1,431	GATA transcription factor 12
VIT_18s0041g01220	-2,101	-2,524	-2,532	-2,626	GCN5 N-acetyltransferase (GNAT)
VIT_14s0030g02180	-1,874	-2,154	-2,056	-1,695	GDP-mannose 3,5-epimerase 1
VIT_05s0020g04510	-1,492	-1,608	-1,656	-1,595	GDP-mannose 3,5-epimerase 1
VIT_02s0025g04880	1,968	2,168	2,664	2,360	Geraniol 10-hydroxylase
VIT_19s0014g04930	-0,218	-1,110	-2,005	0,542	Germacrene-D synthase
VIT_19s0140g00120	-0,888	-1,291	-1,753	-1,876	Gibberellin 2-beta-dioxygenase 1
VIT_06s0004g06790	0,956	0,210	1,680	0,971	Gibberellin 2-beta-dioxygenase 7
VIT_18s0157g00020	4,451	4,336	4,109	3,838	GIGANTEA protein

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_19s0090g01070	-1,481	-1,583	-1,609	-1,667	Glucan endo-1,3-beta-glucosidase 7 precursor
VIT_15s0024g01440	1,629	1,807	2,307	1,605	Glucose 6 phosphate/phosphate translocator-like protein
VIT_12s0057g01030	1,336	1,728	0,981	1,228	Glucose-6-phosphate 1-dehydrogenase 2, chloroplast precursor
VIT_04s0079g00600	-1,632	-1,378	-1,177	-1,092	Glutamate decarboxylase 1
VIT_19s0014g01830	2,163	2,001	2,346	1,295	Glutamate receptor 2.8
VIT_07s0104g00610	-1,236	-1,821	0,453	-1,477	Glutamine synthetase
VIT_03s0088g00570	0,000	0,000	2,128	0,000	Glutamine synthetase B1 GLB1
VIT_17s0000g01910	1,656	1,707	1,630	1,622	Glutamine synthetase cytosolic isozyme 1
VIT_19s0015g02690	3,832	2,976	0,000	0,000	Glutathione S-transferase 25 GSTU25
VIT_17s0000g02950	-1,581	-2,504	-3,367	-1,424	Glutathione S-transferase 25 GSTU7
VIT_07s0005g00030	2,329	1,409	0,900	1,572	Glutathione S-transferase 8 GSTF8
VIT_00s0153g00050	1,608	2,351	1,749	2,503	Glutathione S-transferase 8 GSTU8
VIT_12s0028g01330	-1,584	-0,927	-0,457	0,009	Glu-tRNA(Gln) amidotransferase subunit A
VIT_14s0219g00280	-0,956	-1,787	-1,179	-0,899	Glycerol-3-phosphate dehydrogenase (NAD+)
VIT_14s0068g01500	-0,893	-0,779	-1,564	-0,095	Glycerophosphoryl diester phosphodiesterase
VIT_10s0003g02160	-1,550	-1,929	-0,438	-0,529	Glyco_transf_20 domain-containing protein
VIT_04s0023g02510	1,914	2,451	2,556	1,824	Glycosyl transferase family 1 protein
VIT_19s0014g02650	0,992	0,976	1,714	1,029	Glycosyl transferase family 14 protein
VIT_07s0005g01980	8,291	7,685	5,700	4,939	Glycosyl transferase family 8 protein
VIT_01s0011g01910	1,193	1,098	1,596	0,656	Glycosyl transferase-related
VIT_05s0094g00990	3,613	3,240	5,128	3,819	Glycosyltransferase
VIT_13s0019g00240	0,981	1,559	1,128	1,089	Glycosyltransferase family 14 Beta-1-3-galactosyl-O-glycosyl-glycoprotein
VIT_12s0028g03100	-1,564	-1,595	-1,010	-1,290	GPRI1 (GOLDEN2 1)
VIT_09s0002g01350	-1,784	-1,182	-1,290	-0,926	Growth-regulating factor 5
VIT_08s0007g00320	1,118	1,706	0,630	0,961	GTP binding protein
VIT_18s0001g13120	1,615	1,301	1,645	1,508	GTP-binding protein hflX
VIT_16s0013g00130	1,215	1,217	1,220	1,661	GTP-binding protein HSR1
VIT_08s0007g08290	-2,233	-2,394	-2,194	-2,326	GTP-binding protein typA/bipA
VIT_11s0037g00860	1,526	1,068	0,921	0,579	Haemolysin-III related
VIT_12s0028g03470	1,983	2,040	1,626	1,673	Haloacid dehalogenase hydrolase
VIT_08s0007g00540	-1,991	-2,053	-1,775	-1,143	Haloacid dehalogenase hydrolase
VIT_02s0012g00760	-1,285	-1,520	-1,889	-1,681	Haloacid dehalogenase hydrolase
VIT_08s0007g05350	-1,170	-1,604	-1,536	-1,245	Haloacid dehalogenase hydrolase
VIT_05s0020g03190	1,281	1,717	1,831	2,110	Haloacid dehalogenase hydrolase
VIT_16s0039g00340	1,823	1,615	1,216	1,265	Harpin-induced protein-related
VIT_11s0016g04250	-1,943	-1,950	-1,328	-1,315	HCF101 (high-chlorophyll-fluorescence 101)
VIT_19s0014g05050	1,862	1,102	0,885	1,036	Heat shock HSP20 family protein
VIT_16s0022g00510	2,652	0,203	-1,082	-0,276	Heat shock 22 kDa protein
VIT_02s0154g00490	5,856	3,791	2,395	4,033	Heat shock 22 kDa protein mitochondrial
VIT_00s0992g00020	2,486	3,503	3,096	3,748	Heat shock protein (HSP26.5-P) 26.5 kDa class P
VIT_00s0707g00010	2,236	2,749	2,821	3,349	Heat shock protein (HSP26.5-P) 26.5 kDa class P
VIT_17s0000g07190	1,714	-0,598	-1,164	-0,963	Heat shock protein 101
VIT_13s0019g03170	3,203	1,567	1,219	0,969	Heat shock protein 16.9 kDa class I
VIT_06s0004g05770	2,192	3,048	1,097	1,695	Heat shock protein 17.6 kDa class I
VIT_13s0019g02760	3,015	-1,525	-0,838	1,396	Heat shock protein 17.6 kDa class I
VIT_13s0019g02770	2,594	0,000	-0,138	1,768	Heat shock protein 17.6 kDa class I
VIT_13s0019g02740	1,589	-1,380	-0,733	0,993	Heat shock protein 17.6 kDa class I
VIT_13s0019g02930	3,121	1,223	0,425	0,976	Heat shock protein 17.6 kDa class I
VIT_13s0019g02850	3,010	0,157	-0,479	0,836	Heat shock protein 17.6 kDa class I
VIT_13s0019g03000	1,657	-0,108	-0,786	0,062	Heat shock protein 17.6 kDa class I
VIT_13s0019g03160	3,548	0,921	0,345	0,805	Heat shock protein 17.6 kDa class I
VIT_19s0085g01050	0,000	0,000	0,000	3,048	Heat shock protein 17.6 kDa class I
VIT_04s0008g01490	4,454	2,767	1,881	1,599	Heat shock protein 17.6 kDa class II
VIT_04s0008g01520	4,727	2,367	1,766	1,654	Heat shock protein 17.6 kDa class II
VIT_04s0008g01510	5,817	2,157	0,638	1,800	Heat shock protein 17.6 kDa class II
VIT_04s0008g01590	4,328	1,988	1,113	1,051	Heat shock protein 17.6 kDa class II
VIT_04s0008g01580	4,508	2,016	1,192	1,318	Heat shock protein 17.6 kDa class II
VIT_04s0008g01570	2,450	-0,203	-1,346	-0,092	Heat shock protein 17.6 kDa class II
VIT_13s0019g02840	3,398	0,148	-0,114	1,751	Heat shock protein 18.2 kDa class I

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_12s0035g01910	6,301	5,312	4,907	4,648	Heat shock protein 18.2 kDa class II
VIT_01s0010g02290	2,304	0,603	-0,101	0,660	Heat shock protein 26a, chloroplast
VIT_14s0060g02340	3,635	3,014	2,399	1,756	Heat shock protein 70
VIT_05s0020g03330	2,406	1,875	1,110	0,813	Heat shock protein 70
VIT_16s0098g01580	2,378	1,725	1,309	0,831	Heat shock protein 70
VIT_02s0025g02140	1,981	1,275	0,826	0,553	Heat shock protein 70
VIT_06s0004g04470	4,124	1,277	0,274	0,636	Heat shock protein 70
VIT_18s0041g01230	1,889	0,200	0,007	-0,418	Heat shock protein 70
VIT_13s0019g00930	1,966	1,026	1,358	0,711	Heat shock protein 70
VIT_06s0004g04510	1,524	1,185	1,067	0,794	Heat shock protein 70
VIT_11s0037g00510	3,232	1,086	0,386	0,116	Heat shock protein 70
VIT_02s0025g00280	5,165	2,393	1,491	1,191	Heat shock protein 90-1
VIT_16s0050g01150	3,967	1,011	0,239	1,174	Heat shock protein 90-1
VIT_13s0019g03090	4,353	1,573	0,000	2,088	Heat shock protein class I (HSP17.8-CI)
VIT_02s0154g00480	2,442	0,481	-0,919	0,296	Heat shock protein MTSHP
VIT_18s0089g01270	5,750	3,826	2,338	2,298	Heat shock protein precursor 22.0 kDa class IV
VIT_04s0008g01110	4,894	3,026	2,160	2,332	Heat shock transcription factor A6B_2
VIT_00s0179g00150	3,122	1,412	0,986	1,083	Heat shock transcription factor A6B_4
VIT_16s0100g00720	-0,581	-1,953	-1,523	-0,180	Heat shock transcription factor B2A_1
VIT_02s0025g04170	-1,902	-3,910	-3,487	-2,279	Heat shock transcription factor B2B
VIT_01s0011g05970	2,522	2,961	2,657	2,620	Heat stress transcription factor A-8
VIT_15s0046g02230	-1,077	-1,558	-1,670	-1,128	Heavy-metal-associated domain-containing protein
VIT_09s0002g03390	2,644	2,380	2,503	1,935	Hexokinase
VIT_06s0061g00040	1,304	1,528	1,405	0,616	Hexokinase 6
VIT_18s0001g05570	1,607	1,477	1,686	1,483	Hexose transporter HT2
VIT_18s0001g00660	-1,256	-1,809	-1,160	-1,835	High mobility group (HMG1/2) family protein
VIT_18s0122g01190	-1,582	-1,340	-1,467	-0,972	HIGH MOBILITY GROUP B 3
VIT_08s0007g02200	-1,762	-1,630	-1,870	-1,351	High mobility group protein B1
VIT_14s0081g00500	-1,500	-1,381	-1,886	-1,412	Histone H1
VIT_14s0060g02360	-1,748	-2,210	-1,694	-1,307	Histone H2A.4 HTA12
VIT_06s0004g04300	-1,348	-1,396	-1,701	-0,846	Histone H2B
VIT_13s0064g01340	-1,646	-1,451	-1,283	-0,724	Histone H3
VIT_13s0067g03650	-1,825	-1,667	-1,676	-1,079	Histone H4
VIT_13s0019g00760	-1,533	-1,451	-1,625	-1,036	Histone H4
VIT_08s0007g07540	2,589	2,362	2,223	2,560	HNH endonuclease domain-containing protein
VIT_16s0100g00670	1,370	2,007	0,918	1,484	Homeodomain GLABROUS1
VIT_08s0007g03900	5,347	6,340	4,984	4,495	HSF A3
VIT_07s0151g00860	-1,873	-2,027	-1,310	-2,018	Hydrolase, alpha/beta fold
VIT_12s0059g01060	2,365	2,690	2,984	2,519	Hydroperoxide lyase (HPL1)
VIT_12s0057g00930	-1,452	-0,795	-1,525	-1,301	Hydroxycinnamoyl-CoA:shikimate hydroxycinnamoyltransferase
VIT_11s0016g05640	-1,326	-1,714	-1,964	-2,090	IAA29
VIT_04s0008g05560	-1,171	-1,357	-1,653	-1,498	IAA29
VIT_08s0058g00540	-1,864	-1,783	-1,698	-1,485	IMK2 (inflorescence meristem receptor-like kinase 2)
VIT_01s0011g03660	-2,022	-2,615	-2,243	-2,422	IMP dehydrogenase/GMP reductase
VIT_01s0010g02100	-2,223	-1,811	-1,187	-1,306	Indeterminate(ID)-domain 5
VIT_03s0180g00320	1,728	1,781	1,470	1,249	Indole-3-acetate beta-glucosyltransferase
VIT_06s0004g07310	0,767	1,222	1,590	0,365	Indole-3-acetate beta-glucosyltransferase
VIT_07s0129g00660	-1,840	-1,663	-1,902	-1,360	Indole-3-acetic acid-amido synthetase GH3.2
VIT_19s0027g00740	-1,261	-1,526	-0,602	-0,978	Inhibitor of apoptosis
VIT_07s0005g03290	1,187	2,256	0,635	1,312	Inorganic phosphate transporter 1-4
VIT_08s0040g02470	-1,659	-1,546	-1,555	-1,219	Inorganic pyrophosphatase
VIT_07s0031g00920	-1,333	-1,957	-1,874	-2,219	Inositol-3-phosphate synthase
VIT_03s0063g01910	-1,417	-1,605	-1,959	-1,379	Integral membrane protein
VIT_16s0022g00840	5,377	3,625	5,903	2,902	Invertase/pectin methylesterase inhibitor
VIT_14s0066g02270	0,165	1,433	1,747	1,848	IPPc domain-containing protein
VIT_03s0038g00360	2,172	2,831	2,934	3,266	Isochorismatase hydrolase
VIT_04s0008g05600	1,278	1,234	1,359	1,522	KEG (keep on going)
VIT_06s0009g02110	2,170	2,026	1,587	1,434	Kelch repeat-containing F-box family protein
VIT_05s0094g01590	-0,299	-1,649	-0,755	-1,646	Kelch repeat-containing F-box protein
VIT_01s0026g02270	1,944	1,536	2,049	1,093	Kinase

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_17s0000g03290	-1,736	-1,474	-1,383	-0,934	Kinesin motor HIK (HINKEL)
VIT_14s0128g00460	-1,798	-1,453	-1,313	-0,862	Kinesin motor protein
VIT_19s0090g01600	-1,674	-1,411	-1,001	-1,025	Kinesin motor protein
VIT_05s0029g00400	-1,600	-1,375	-1,164	-0,829	Kinesin PAKRP1L
VIT_17s0000g08710	-1,149	-0,718	-1,564	-0,903	KNAT2 (knotted1-like homeobox gene 6)
VIT_08s0040g00210	1,522	1,399	1,276	1,042	L-2-hydroxyglutarate dehydrogenase
VIT_08s0040g03150	1,989	1,996	1,523	1,632	L-ascorbate peroxidase 1, cytosolic (APX1)
VIT_14s0066g01240	-1,650	-1,456	-1,278	-0,968	L-aspartate oxidase
VIT_18s0001g09250	1,543	1,646	0,000	0,998	Lateral organ boundaries protein 38
VIT_08s0040g03220	-1,618	-1,672	-1,664	-1,550	LCL1 (LHY/CCA1-like 1)
VIT_18s0086g00200	1,441	1,565	1,740	1,098	Lectin protein kinase family
VIT_02s0025g01400	1,568	1,393	1,299	0,879	Leucine-rich repeat family protein
VIT_12s0057g00630	2,175	1,714	1,726	1,324	LHCB2.1 (Photosystem II light harvesting complex gene 2.1)
VIT_18s0072g00120	-1,195	-1,639	-1,577	-1,551	Light stress-responsive one-helix protein (OHP2)
VIT_03s0091g00040	1,556	1,700	1,858	1,165	Limonoid UDP-glucosyltransferase
VIT_09s0002g00140	-1,268	-1,506	-1,223	-1,110	Lipase class 3
VIT_14s0171g00110	1,792	1,743	1,416	1,530	Lipase family
VIT_10s0003g01010	1,792	1,346	2,154	1,832	Lipase GDSL
VIT_14s0066g00250	1,363	1,692	1,681	1,632	Lipase GDSL
VIT_18s0086g00220	1,408	2,156	1,173	1,554	Lipase GDSL
VIT_10s0003g02120	-1,607	-1,355	-0,946	-0,571	Lipase GDSL
VIT_18s0041g02160	-1,208	-2,058	-0,810	-1,216	Lipase GDSL
VIT_06s0004g01470	1,041	1,105	1,791	1,816	Lipoxygenase LOX1
VIT_06s0004g01480	1,245	1,007	2,090	1,419	Lipoxygenase LOX1
VIT_05s0051g00540	-1,582	-0,908	-0,899	-1,841	LRR receptor-like kinase 2
VIT_17s0000g07770	1,173	1,501	1,414	1,582	LTCOR11
VIT_04s0023g01080	0,938	1,583	1,088	0,696	Lys Motif-Type Receptor-Like Kinase LYK4
VIT_14s0171g00400	1,474	1,420	1,703	1,921	Lysine histidine transporter 1
VIT_01s0010g02640	0,711	1,157	0,906	1,544	Lysine histidine transporter 2
VIT_08s0058g00590	1,966	2,037	2,121	2,370	Macrophage migration inhibitory factor
VIT_05s0077g01670	2,185	0,903	2,932	1,351	Major cherry allergen Pru av 1.0202
VIT_19s0014g01640	1,593	1,097	0,624	0,508	Malate dehydrogenase
VIT_08s0058g00180	-1,713	-0,802	-0,685	-0,932	Male sterility 2 (MS2)
VIT_02s0025g04110	1,133	1,510	1,005	1,293	MAPKKK HA-tagged protein kinase
VIT_07s0031g00530	3,299	2,989	2,583	1,631	MAPKKK21
VIT_11s0016g03050	2,265	2,775	2,619	1,579	MATE efflux family protein
VIT_00s0225g00050	-1,517	-1,431	-0,904	-0,988	MATE efflux family protein
VIT_00s0332g00080	-1,809	-1,428	-1,047	-1,465	Maturase K
VIT_10s0092g00570	1,332	1,236	1,118	1,812	Mechanosensitive ion channel
VIT_09s0070g00210	-1,511	-0,945	-1,107	-0,691	Metal transporter Nramp1
VIT_01s0011g02440	1,561	1,467	1,021	0,948	Metal-dependent phosphohydrolase HD domain-containing protein-like
VIT_00s0253g00150	3,097	2,266	2,163	2,430	Methyl jasmonate esterase
VIT_00s0253g00110	1,113	1,635	1,444	1,022	Methyl jasmonate esterase
VIT_03s0132g00210	1,241	1,390	1,538	1,525	Methylmalonate semi-aldehyde dehydrogenase
VIT_08s0007g08540	-0,805	-1,261	-1,028	-1,699	Mg-chelatase subunit XANTHA-F
VIT_06s0004g06730	-2,105	-1,882	-1,729	-1,446	Microsomal omega-3 fatty acid desaturase
VIT_01s0010g02430	-1,668	-1,389	-1,629	-0,934	Mitotic spindle checkpoint protein (MAD2)
VIT_14s0066g01400	-1,739	-1,311	-1,556	-1,353	MLK/Raf-related protein kinase 1
VIT_01s0011g04820	3,626	2,614	2,815	3,576	Molecular chaperone DnaJ
VIT_17s0000g01070	-1,184	-2,034	-1,903	-2,017	Monoglyceride lipase
VIT_18s0001g01110	2,637	3,102	3,023	3,145	Monooxygenase (MO2)
VIT_05s0102g00450	-1,511	-1,659	-1,602	-1,777	MSS3 (multicopy suppressors of snf4 deficiency in yeast 3)
VIT_04s0210g00060	4,462	4,854	4,240	3,897	Mucin-like protein
VIT_19s0014g01260	1,590	1,121	0,589	1,044	Multiprotein-bridging factor 1a MBF1A
VIT_11s0016g04080	5,155	3,056	1,765	3,032	Multiprotein-bridging factor 1c MBF1C
VIT_15s0048g02410	-4,145	-4,598	-4,944	-4,474	Myb CCA1 (circadian clock associated 1)
VIT_14s0006g01620	1,602	0,649	0,163	0,372	Myb domain protein 4
VIT_04s0008g01810	-0,947	-1,227	-1,617	-1,184	Myb domain protein 4
VIT_02s0025g02210	2,214	2,069	1,366	0,800	MYB Domain protein 6
VIT_01s0011g03730	-2,295	-1,719	-2,541	-1,072	myb domain protein 62

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_07s0129g01050	1,784	1,918	1,148	0,357	Myb domain protein 73
VIT_18s0001g09850	1,525	1,661	0,593	-0,467	Myb domain protein R1
VIT_01s0026g01050	-1,801	-2,331	-2,142	-1,657	Myb family
VIT_08s0007g06180	1,594	1,500	0,537	1,460	Myb family G2-like (TF)
VIT_15s0046g00170	1,991	1,428	1,363	1,131	MYBPA1 protein [Vitis vinifera]
VIT_11s0016g02800	2,638	3,236	3,653	2,953	Myo-inositol oxygenase
VIT_09s0002g02940	1,290	0,978	1,677	1,894	Myo-inositol oxygenase 1
VIT_17s0000g06400	1,144	1,869	1,036	0,937	NAC domain containing protein 100
VIT_15s0048g02300	-1,436	-1,444	-2,271	-1,490	NAC transcription factor-like 9
VIT_15s0048g02310	-3,808	-1,869	-1,667	-2,121	NAC transcription factor-like 9 NTL9 (NAC TF)
VIT_18s0001g01660	-1,604	-1,899	-1,094	-1,289	NADH dehydrogenase I subunit M
VIT_11s0037g00070	-1,600	-2,190	-1,711	-2,036	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase
VIT_13s0084g00880	1,611	1,374	1,285	1,478	NADPH:quinone oxidoreductase
VIT_02s0012g00150	1,279	1,969	1,686	0,981	NAK-type protein kinase
VIT_02s0025g02960	-0,602	-1,543	-2,797	-1,125	Naringenin,2-oxoglutarate 3-dioxygenase
VIT_01s0026g00630	-3,849	-4,591	-4,388	-3,950	N-hydroxythioamide S-beta-glucosyltransferase
VIT_17s0000g09470	1,900	2,017	2,411	2,342	Nitrate transporter3.1
VIT_03s0063g00370	1,501	0,467	1,872	-0,168	Nitrite reductase
VIT_15s0048g02320	-1,527	-1,973	-3,155	-2,242	No apical meristem cup-shaped cotyledon2
VIT_15s0048g02270	-1,921	-1,658	-2,271	-2,153	No apical meristem cup-shaped cotyledon2
VIT_06s0061g00290	1,522	1,685	1,726	1,569	No hit
VIT_15s0048g02420	-4,066	-4,440	-4,765	-4,737	No hit
VIT_12s0035g01240	3,592	4,008	4,240	4,258	No hit
VIT_00s0189g00050	3,313	2,588	1,943	2,456	No hit
VIT_00s0125g00080	-1,556	-1,717	-2,097	-2,593	No hit
VIT_11s0016g03840	-2,215	-2,772	-2,619	-2,869	No hit
VIT_11s0037g00940	-2,893	-3,629	-2,980	-3,373	No hit
VIT_11s0016g05780	2,536	2,122	2,212	1,811	No hit
VIT_05s0062g01260	-2,235	-2,927	-3,089	-2,538	No hit
VIT_05s0049g00840	2,326	2,010	0,000	2,291	No hit
VIT_02s0025g04470	1,622	1,731	0,601	1,648	No hit
VIT_13s0067g02420	1,405	2,147	1,769	2,242	No hit
VIT_19s0015g00270	-1,115	-1,728	-1,701	-1,518	no hit
VIT_19s0014g03490	2,000	1,799	1,035	1,047	No hit
VIT_19s0027g00330	2,207	2,000	1,949	1,433	No hit
VIT_06s0004g04220	1,723	1,718	1,351	1,485	no hit
VIT_17s0000g08180	2,022	1,672	1,066	1,179	No hit
VIT_14s0083g00290	-1,627	-1,272	-2,411	-1,063	No hit
VIT_18s0001g04290	1,649	1,301	1,130	1,618	No hit
VIT_05s0049g00780	2,100	1,815	0,000	3,015	No hit
VIT_02s0025g04870	1,985	2,196	2,631	2,812	No hit
VIT_09s0002g00630	0,705	-2,182	-1,927	-0,137	No hit
VIT_17s0000g08090	1,186	1,661	0,556	1,793	No hit
VIT_15s0048g00090	1,614	0,941	1,132	1,134	No hit
VIT_13s0101g00060	1,575	1,332	0,876	0,975	No hit
VIT_14s0060g01730	1,765	0,988	1,175	0,689	No hit
VIT_03s0063g01770	1,592	0,733	0,099	1,150	No hit
VIT_05s0077g00540	-1,549	-1,380	-0,485	-1,039	No hit
VIT_13s0019g01030	1,520	1,267	1,491	1,496	No hit
VIT_00s0332g00100	-1,521	-1,476	-0,360	-1,152	No hit
VIT_07s0130g00160	1,816	1,175	1,177	1,322	No hit
VIT_16s0098g00600	-1,257	-1,726	0,171	0,210	No hit
VIT_01s0011g05980	2,169	2,795	2,141	1,587	No hit
VIT_17s0000g06720	-1,515	-1,898	-1,338	-1,072	No hit
VIT_06s0009g01410	-1,453	-1,730	-0,731	-0,990	No hit
VIT_17s0000g08190	0,922	2,229	0,000	0,982	No hit
VIT_05s0077g00310	-4,090	-6,182	-4,082	-7,058	No hit
VIT_00s0246g00020	-1,359	-1,554	-1,111	-1,242	No hit
VIT_16s0013g00390	-2,219	-2,781	-2,578	-2,581	No hit
VIT_07s0005g02070	-0,981	-1,578	-1,695	-1,566	No hit

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_01s0010g00570	1,648	1,795	1,720	1,155	No hit
VIT_06s0004g00440	0,680	1,239	1,659	0,837	No hit
VIT_02s0087g00780	-1,449	-1,296	-1,796	-1,238	No hit
VIT_19s0090g01340	-0,270	-0,924	-2,045	-0,146	No hit
VIT_17s0000g02850	-0,734	-1,093	-0,967	-1,610	No hit
VIT_19s0090g01360	1,446	1,286	0,304	1,980	No hit
VIT_01s0011g04100	-2,265	-2,163	-1,681	-2,195	no hit
VIT_14s0066g01640	1,977	2,474	2,273	2,235	Nodulin MtN21 family
VIT_01s0026g00530	-2,059	-2,275	-2,930	-1,335	Nodulin MtN21 family
VIT_18s0001g15330	-1,423	-1,641	-1,112	-1,187	Nodulin MtN3 family
VIT_14s0006g02550	0,000	3,713	4,977	0,000	Non-specific lipid-transfer protein 2 (LTP 2)
VIT_02s0012g00390	2,245	2,971	1,354	1,916	Norcoclaurine synthase
VIT_03s0091g00160	0,201	-1,045	-1,885	-0,313	NtPRp27 secretory protein
VIT_12s0059g01670	0,944	1,367	1,742	1,801	Nuclear ribonuclease Z
VIT_19s0015g00440	2,397	1,914	1,961	2,088	Nuclear transcription factor Y subunit B-3 (CCAAT)
VIT_00s0216g00060	-1,279	-1,799	-1,931	-1,712	Nuclear transport factor 2 (NTF2)
VIT_01s0011g00410	-1,316	-1,505	-1,811	-1,866	Nuclear transport factor 2 (NTF2)
VIT_14s0006g00300	-0,491	-1,562	-1,064	-1,639	Nudix hydrolase 18
VIT_06s0004g03990	-1,276	-0,865	-1,595	-1,289	Nudix hydrolase 9
VIT_00s0203g00140	-0,540	-1,767	-1,013	-1,750	Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein
VIT_17s0000g09000	1,543	1,722	1,443	1,423	Oleosin OLE-2
VIT_06s0004g04700	-2,020	-1,960	-2,606	-1,913	Outer envelope protein 16
VIT_08s0058g01110	0,954	1,177	1,687	0,011	Ovate family protein 4 OFP4
VIT_09s0002g08090	0,929	1,563	1,487	1,703	Oxidoreductase, 2OG-Fe(II) oxygenase
VIT_03s0063g01310	-0,088	-1,634	-0,702	-0,841	Oxidoreductase, 2OG-Fe(II) oxygenase family
VIT_06s0004g02120	-1,198	-1,447	-0,949	-1,538	Oxoglutarate/malate translocator
VIT_15s0046g02490	1,135	1,335	1,406	1,620	PAIR1 (Protein homologous pairing aberration in rice meiosis 1)
VIT_09s0002g06970	2,163	1,958	2,032	1,267	Palmitoyl-monogalactosyldiacylglycerol delta-7 desaturase, chloroplast
VIT_06s0004g01220	2,224	2,421	2,274	2,296	PAP/fibrillin family
VIT_07s0031g00830	1,751	1,617	1,288	1,330	Patatin-like protein
VIT_18s0041g00430	1,216	1,517	1,589	1,080	Patellin-1
VIT_18s0001g15650	-1,651	-2,252	-2,246	-1,437	Pathogenesis related protein
VIT_14s0081g00030	1,963	1,529	0,932	1,651	Pathogenesis-related protein-4 (Chitinase)
VIT_14s0066g01690	-2,023	-2,029	0,000	-1,416	Pathogen-inducible alpha-dioxygenase
VIT_01s0137g00240	-2,280	-2,646	-2,709	-1,906	Pectate lyase
VIT_13s0047g00230	1,484	1,845	2,049	1,840	Pectinesterase family
VIT_09s0002g00330	1,527	1,739	1,834	1,173	Pectinesterase PME1
VIT_00s0941g00010	1,515	1,482	1,108	0,712	Pentatricopeptide (PPR) repeat-containing
VIT_08s0007g04970	1,342	1,580	1,358	0,997	Pentatricopeptide (PPR) repeat-containing
VIT_14s0108g00600	1,420	1,404	1,204	1,676	Pentatricopeptide (PPR) repeat-containing
VIT_16s0050g00040	0,963	1,148	1,530	0,860	Pentatricopeptide (PPR) repeat-containing
VIT_01s0011g01970	2,509	2,269	2,563	2,364	Pentatricopeptide (PPR) repeat-containing protein
VIT_01s0011g00660	2,025	1,878	2,538	1,870	Pentatricopeptide (PPR) repeat-containing protein
VIT_18s0001g04590	1,519	1,783	1,854	1,501	Pentatricopeptide (PPR) repeat-containing protein
VIT_02s0012g02540	-2,099	-2,819	-2,703	-2,937	Pentatricopeptide (PPR) repeat-containing protein
VIT_05s0049g02300	2,082	2,099	2,141	1,845	Pentatricopeptide (PPR) repeat-containing protein
VIT_17s0000g06480	1,635	1,887	1,800	1,081	Pentatricopeptide (PPR) repeat-containing protein
VIT_16s0050g01500	1,548	1,712	1,751	1,218	Pentatricopeptide (PPR) repeat-containing protein
VIT_07s0005g04530	1,539	1,643	1,533	1,196	Pentatricopeptide (PPR) repeat-containing protein
VIT_10s0042g00130	1,611	1,814	1,593	1,231	Pentatricopeptide (PPR) repeat-containing protein
VIT_18s0001g00640	1,950	1,575	1,957	1,211	Pentatricopeptide (PPR) repeat-containing protein
VIT_05s0020g03570	1,589	1,600	1,866	1,242	Pentatricopeptide (PPR) repeat-containing protein
VIT_11s0016g05220	2,030	1,638	2,340	1,410	Pentatricopeptide (PPR) repeat-containing protein
VIT_08s0058g00830	1,600	1,574	1,663	1,348	Pentatricopeptide (PPR) repeat-containing protein
VIT_07s0005g00570	1,587	2,018	1,936	1,145	Pentatricopeptide (PPR) repeat-containing protein
VIT_18s0001g11650	1,260	1,696	2,024	1,798	Pentatricopeptide (PPR) repeat-containing protein
VIT_18s0041g01110	1,596	1,563	1,333	0,688	Pentatricopeptide (PPR) repeat-containing protein
VIT_05s0049g01270	1,577	1,534	1,294	1,216	Pentatricopeptide (PPR) repeat-containing protein
VIT_14s0066g02510	1,597	2,920	1,534	1,535	Pentatricopeptide (PPR) repeat-containing protein
VIT_09s0002g02370	1,649	1,532	1,204	0,600	Pentatricopeptide (PPR) repeat-containing protein

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_12s0028g00060	1,747	1,245	1,509	1,137	Pentatricopeptide (PPR) repeat-containing protein
VIT_16s0100g00190	1,200	1,611	1,728	0,891	Pentatricopeptide (PPR) repeat-containing protein
VIT_14s0066g00860	1,483	1,677	1,691	1,445	Pentatricopeptide (PPR) repeat-containing protein
VIT_01s0026g01440	1,320	1,638	1,673	1,187	Pentatricopeptide (PPR) repeat-containing protein
VIT_01s0026g01750	1,296	1,502	1,660	0,984	Pentatricopeptide (PPR) repeat-containing protein
VIT_17s0000g07830	1,420	1,874	1,826	1,370	Pentatricopeptide (PPR) repeat-containing protein
VIT_09s0002g06490	1,079	1,581	1,665	1,385	Pentatricopeptide (PPR) repeat-containing protein
VIT_08s0007g05770	1,372	1,648	1,874	1,133	Pentatricopeptide (PPR) repeat-containing protein
VIT_12s0059g00790	0,982	1,513	1,685	1,316	Pentatricopeptide (PPR) repeat-containing protein
VIT_13s0073g00080	1,297	1,540	1,741	1,595	Pentatricopeptide (PPR) repeat-containing protein
VIT_11s0016g04660	1,318	1,557	1,643	1,047	Pentatricopeptide (PPR) repeat-containing protein
VIT_01s0011g05040	1,320	1,707	1,610	0,864	Pentatricopeptide (PPR) repeat-containing protein
VIT_05s0020g03850	1,473	1,630	1,841	1,122	Pentatricopeptide (PPR) repeat-containing protein
VIT_06s0009g00650	1,387	1,800	1,655	0,516	Pentatricopeptide (PPR) repeat-containing protein
VIT_17s0000g06470	1,234	1,540	1,040	1,676	Pentatricopeptide (PPR) repeat-containing protein
VIT_19s0085g00560	0,622	1,438	1,694	1,682	Pentatricopeptide (PPR) repeat-containing protein
VIT_10s0116g00240	1,514	0,904	1,289	1,073	Pentatricopeptide (PPR) repeat-containing protein
VIT_14s0030g02210	1,973	1,063	0,839	1,037	Pentatricopeptide (PPR) repeat-containing protein
VIT_00s0193g00030	1,606	1,404	1,411	0,995	Pentatricopeptide (PPR) repeat-containing protein
VIT_00s0184g00180	1,541	1,271	1,097	1,206	Pentatricopeptide (PPR) repeat-containing protein
VIT_10s0003g00970	1,613	1,197	1,205	0,964	Pentatricopeptide (PPR) repeat-containing protein
VIT_14s0060g00880	1,307	1,702	1,279	0,928	Pentatricopeptide (PPR) repeat-containing protein
VIT_00s2379g00010	1,106	1,745	1,526	1,343	Pentatricopeptide (PPR) repeat-containing protein
VIT_00s0184g00060	1,242	1,966	1,372	0,801	Pentatricopeptide (PPR) repeat-containing protein
VIT_08s0040g02320	1,382	1,540	1,379	1,095	Pentatricopeptide (PPR) repeat-containing protein
VIT_18s0001g15340	1,507	1,905	0,346	1,050	Pentatricopeptide (PPR) repeat-containing protein
VIT_10s0003g02630	0,991	1,551	1,546	0,810	Pentatricopeptide (PPR) repeat-containing protein
VIT_13s0047g00070	1,170	2,192	0,762	0,499	Pentatricopeptide (PPR) repeat-containing protein
VIT_08s0032g00740	1,280	2,040	1,333	0,568	Pentatricopeptide (PPR) repeat-containing protein
VIT_14s0128g00700	1,150	1,595	1,399	1,207	Pentatricopeptide (PPR) repeat-containing protein
VIT_18s0001g10530	1,177	1,381	1,532	1,115	Pentatricopeptide (PPR) repeat-containing protein
VIT_00s0207g00190	1,432	1,205	1,640	0,801	Pentatricopeptide (PPR) repeat-containing protein
VIT_02s0087g00080	1,035	1,401	1,685	1,235	Pentatricopeptide (PPR) repeat-containing protein
VIT_08s0058g01320	1,123	1,155	1,543	0,827	Pentatricopeptide (PPR) repeat-containing protein
VIT_03s0038g01320	1,258	1,080	1,785	1,102	Pentatricopeptide (PPR) repeat-containing protein
VIT_07s0005g01900	0,741	1,443	1,754	1,223	Pentatricopeptide (PPR) repeat-containing protein
VIT_17s0000g06770	1,330	1,311	1,541	0,790	Pentatricopeptide (PPR) repeat-containing protein
VIT_18s0001g05930	1,084	1,297	1,666	1,210	Pentatricopeptide (PPR) repeat-containing protein
VIT_09s0002g02250	1,424	1,444	1,576	0,957	Pentatricopeptide (PPR) repeat-containing protein
VIT_14s0060g00270	1,426	1,375	1,525	0,796	Pentatricopeptide (PPR) repeat-containing protein
VIT_07s0031g01340	1,373	1,457	1,612	1,394	Pentatricopeptide (PPR) repeat-containing protein
VIT_08s0040g02990	1,189	1,037	1,543	1,340	Pentatricopeptide (PPR) repeat-containing protein
VIT_18s0122g00840	1,327	1,181	1,695	0,977	Pentatricopeptide (PPR) repeat-containing protein
VIT_08s0007g03150	1,179	1,148	1,541	1,184	Pentatricopeptide (PPR) repeat-containing protein
VIT_00s0369g00050	1,535	1,468	1,385	1,115	Pentatricopeptide (PPR) repeat-containing protein
VIT_18s0089g00300	1,089	1,563	0,714	0,753	Pentatricopeptide (PPR) repeat-containing protein
VIT_02s0087g00760	0,837	1,080	1,516	0,730	Pentatricopeptide (PPR) repeat-containing protein
VIT_06s0004g06420	0,924	0,625	2,007	0,611	Pentatricopeptide (PPR) repeat-containing protein
VIT_00s0593g00010	0,853	1,147	1,376	1,746	Pentatricopeptide (PPR) repeat-containing protein
VIT_18s0001g09690	1,203	1,375	1,541	1,068	Pentatricopeptide repeat protein
VIT_14s0068g02080	1,245	2,179	1,404	1,711	Pentatricopeptide repeat-containing protein
VIT_14s0068g02070	1,444	1,625	0,726	0,784	Peptidase M48
VIT_01s0150g00250	0,818	1,242	1,755	1,333	Peptide transporter PTR2-B
VIT_00s0769g00010	1,779	1,222	0,899	0,901	Peptidyl-prolyl cis-trans isomerase, FKBP-type
VIT_14s0006g02750	2,188	2,140	2,129	2,345	Peptidyl-tRNA hydrolase
VIT_00s0225g00170	1,817	2,072	1,363	1,391	Peroxidase
VIT_09s0002g04460	1,655	2,768	1,969	1,897	Peroxidase 48 (Atperox P48)
VIT_12s0059g02420	1,731	1,963	1,858	1,824	Peroxidase ATP11A (gb|X98802).
VIT_18s0001g06840	-2,994	-2,375	-1,745	-2,038	Peroxidase GvPx2b class III
VIT_14s0066g02300	2,136	2,046	2,169	1,191	P-glycoprotein 17

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_01s0182g00130	1,141	1,254	1,520	1,279	PHO1-like protein
VIT_09s0002g02450	-1,406	-1,330	-2,343	-0,103	Phosphatase
VIT_14s0066g01000	-1,852	-1,781	-1,720	-1,410	Phosphate/phosphoenolpyruvate translocator
VIT_03s0038g03860	2,112	2,652	1,941	0,855	Phosphate-induced protein 1
VIT_18s0001g06170	1,072	2,055	0,000	0,000	Phosphate-induced protein 1
VIT_17s0000g08360	-1,256	-1,236	-1,530	-1,113	Phosphatidylinositol 3- and 4-kinase
VIT_11s0103g00190	-1,720	-1,142	-0,977	-0,534	Phospholipase A2 alpha
VIT_03s0038g02090	1,542	1,177	1,222	0,723	Phospholipase C.
VIT_02s0025g03600	1,559	1,331	1,177	1,353	Phospholipid hydroperoxide glutathione peroxidase
VIT_14s0060g02200	1,791	1,900	1,686	1,702	Phospholipid/glycerol acyltransferase
VIT_07s0151g01000	-0,743	-1,073	0,404	-1,682	Photosystem I reaction center subunit II (PSAD)
VIT_13s0019g02630	0,857	0,762	1,530	0,507	Photosystem II PsbA
VIT_18s0001g09110	1,040	0,899	1,669	0,729	Photosystem II PsbC protein
VIT_12s0055g00080	1,292	1,062	1,796	0,821	Photosystem II PsbD
VIT_01s0137g00820	-1,358	-1,519	-1,329	-1,522	Phototropic-responsive NPH3
VIT_12s0057g00510	-2,077	-0,595	-1,375	-0,923	Phototropic-responsive NPH3
VIT_06s0004g03700	-1,823	-1,693	-1,456	-1,518	Phototropin-1
VIT_12s0028g00960	-2,325	-2,471	-2,174	-2,075	Phytoene synthase, chloroplast precursor
VIT_01s0010g01710	1,758	1,294	1,419	0,626	Phytosulfokine receptor
VIT_03s0088g00290	-1,165	-1,952	-1,454	-1,085	Phytosulfokines PSK2
VIT_00s1328g00020	-0,649	0,735	-0,163	1,723	Phytosulfokines PSK4
VIT_05s0062g01190	-1,773	-1,419	-1,337	-1,217	Pirin
VIT_04s0008g06670	-1,465	-1,369	-1,555	-1,006	Plastocyanin domain-containing protein
VIT_12s0035g01420	-1,194	-1,531	-0,918	-1,510	Plus3 domain-containing protein
VIT_04s0044g01060	1,550	1,306	1,056	0,609	PMR5N domain-containing protein
VIT_14s0083g00980	-1,587	-1,432	-1,197	-1,730	Pollen Ole e 1 allergen and extensin
VIT_01s0127g00800	-1,442	-1,396	-1,634	-1,214	Polyamine oxidase precursor
VIT_15s0046g02000	-2,125	-1,760	-1,836	-1,703	Polygalacturonase GH28
VIT_01s0127g00400	-2,729	-3,014	-2,332	-2,683	Polygalacturonase GH28
VIT_05s0020g00420	-2,965	-4,093	-3,746	-3,149	Polygalacturonase GH28
VIT_00s0480g00030	-1,533	-1,667	-1,234	-1,186	Polyphenol oxidase
VIT_00s0480g00040	-1,390	-1,559	-0,972	-1,282	Polyphenol oxidase II, chloroplast precursor
VIT_11s0016g03340	0,963	1,779	1,054	0,998	PPR EMB2758 (embryo defective 2758)
VIT_14s0108g01530	1,520	0,840	1,211	0,864	PPR, Pentatricopeptide (PPR) repeat-containing
VIT_04s0023g01110	-2,220	-2,269	-1,656	-1,292	PQ-loop repeat protein
VIT_08s0058g00560	-1,101	-1,054	-0,957	-1,589	Prenylated rab acceptor (PRA1)
VIT_01s0011g00740	2,004	2,036	1,764	1,921	Processing peptidase beta subunit, mitochondrial
VIT_19s0090g01470	-1,967	-1,700	-2,208	-1,683	Protease inhibitor/seed storage/lipid transfer protein (LTP)
VIT_02s0154g00310	-2,391	-2,390	-2,999	-2,213	Protease inhibitor/seed storage/lipid transfer protein (LTP)
VIT_14s0006g02570	3,847	4,868	3,678	2,237	Protease inhibitor/seed storage/lipid transfer protein (LTP)
VIT_13s0156g00090	-1,501	-1,838	-2,605	-2,343	Protease inhibitor/seed storage/lipid transfer protein (LTP)
VIT_11s0016g05840	-1,828	-1,512	-1,284	-1,449	Protease inhibitor/seed storage/lipid transfer protein (LTP)
VIT_04s0008g05640	1,280	1,081	1,732	0,811	Protease inhibitor/seed storage/lipid transfer protein (LTP)
VIT_13s0019g02690	0,000	3,380	3,396	2,987	Protease inhibitor/seed storage/lipid transfer protein (LTP)
VIT_12s0059g01560	1,636	1,701	1,308	1,491	Protein disulfide-isomerase A6
VIT_11s0016g03830	-1,745	-2,316	-2,912	-2,802	Protein kinase
VIT_15s0024g01750	-0,596	-0,686	-1,755	-0,895	Protein kinase
VIT_17s0000g09290	1,070	1,501	1,192	1,813	Protein kinase ATN1
VIT_07s0031g01920	0,937	1,395	1,646	0,916	Protein kinase CRK1 CRK1 protein(Cdc2-related kinase 1)
VIT_00s0540g00020	2,036	1,958	1,466	1,636	Protein kinase domain-containing protein
VIT_17s0000g02410	2,628	2,380	2,760	1,990	Protein kinase domain-containing protein
VIT_13s0067g00420	2,440	2,274	2,261	1,913	Protein kinase Xa21
VIT_13s0067g00490	-1,982	-2,299	-1,358	-2,018	Protein kinase Xa21
VIT_13s0067g00440	1,566	2,303	2,378	0,000	Protein kinase Xa21
VIT_16s0050g02680	2,125	1,699	1,836	2,027	Protein phosphatase 2C
VIT_01s0137g00750	-1,740	-1,302	-1,500	-0,981	Protein phosphatase 2C
VIT_18s0001g09390	1,419	1,512	1,263	0,851	Protein phosphatase 2C
VIT_08s0007g00310	1,749	1,471	1,119	0,179	Protein phosphatase 2C POLTERGEIST-like 4
VIT_00s0250g00020	1,430	1,553	1,534	1,717	Protein tyrosine phosphatase
VIT_05s0049g01760	-1,983	-2,577	-2,485	-2,486	Proton gradient regulation 5 (PGR5)

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_18s0041g00580	-1,747	-1,812	-0,933	-1,200	Proton-dependent oligopeptide transport (POT) family protein
VIT_06s0004g03660	3,694	3,291	2,699	2,800	Pseudo-response regulator 7 (APRR7)
VIT_15s0048g02540	2,331	2,235	2,117	2,093	Pseudo-response regulator 9 (APRR9)
VIT_18s0001g06940	1,624	1,818	1,189	1,955	Purine permease 1 (PUP1)
VIT_18s0089g01410	1,916	1,595	2,176	1,480	Purine permease 4 PUP4
VIT_01s0011g06290	-0,867	-1,196	-1,824	-0,345	Purple acid phosphatase 3 ATPAP3/PAP3
VIT_08s0040g02440	1,567	1,365	0,858	0,819	PWWP domain-containing protein
VIT_06s0009g00680	1,384	0,785	1,636	1,077	Pyridine nucleotide-disulphide oxidoreductase
VIT_05s0020g02310	3,186	2,795	2,552	1,882	Pyruvate,orthophosphate dikinase
VIT_12s0034g02530	-1,326	-1,509	-1,350	-1,234	R protein disease resistance protein
VIT_13s0139g00340	-0,831	-0,930	-1,043	-1,532	R protein MLA10
VIT_00s0313g00050	1,265	1,487	1,804	1,492	RAB GDP dissociation inhibitor 1 ATGD1
VIT_02s0025g04060	2,850	1,650	0,477	1,055	Rab/Ypt GTPase Ara4-interacting protein
VIT_01s0011g05870	-1,401	-1,160	-1,222	-1,668	RDR1 (RNA-dependent RNA polymerase 1)
VIT_04s0008g05430	-1,603	-1,183	-1,186	-1,346	RDR6 (RNA-dependent RNA polymerase 6)
VIT_16s0098g00230	1,467	1,617	1,416	1,193	Receptor kinase homolog LRK10
VIT_06s0004g02640	-1,528	-1,543	-1,223	-1,005	Receptor protein kinase PERK1
VIT_06s0004g06430	-3,743	-3,484	-2,043	-3,282	Receptor ser/thr protein kinase
VIT_16s0098g00020	1,560	1,442	0,991	1,154	Receptor serine/threonine kinase
VIT_01s0011g04290	2,250	2,173	2,052	2,142	Receptor serine/threonine kinase PR5K
VIT_01s0011g04300	2,256	2,374	2,289	2,454	Receptor serine/threonine kinase PR5K
VIT_16s0050g01700	0,524	1,642	0,556	0,946	Receptor serine/threonine kinase PR5K
VIT_13s0073g00600	-1,439	-1,447	-1,584	-1,504	Receptor-like kinase 17
VIT_13s0019g02280	-2,899	-4,010	-4,517	-4,106	Regulator of chromosome condensation (RCC1)
VIT_14s0083g01020	2,309	1,836	1,780	1,755	Regulator of chromosome condensation (RCC1)
VIT_08s0007g00930	-0,753	-1,392	-1,774	-1,491	Regulator of chromosome condensation (RCC1)
VIT_12s0028g03190	-1,581	-1,322	-1,388	-0,845	Reticulon family protein
VIT_00s0438g00030	-2,450	-2,194	-1,913	-2,340	Retrotransposon protein, Unclassified
VIT_18s0075g00520	-1,150	-1,366	-1,063	-1,539	Retrotransposon protein, Unclassified
VIT_01s0010g02160	1,417	1,516	1,415	1,342	RGS1 (regulator of G-protein SIGNALING 1)
VIT_17s0000g08920	-1,420	-1,741	-1,574	-1,239	Ribitol dehydrogenase
VIT_13s0064g00170	-1,516	-1,525	-1,187	-1,090	Ribosomal protein L1
VIT_17s0000g02150	-2,390	-2,398	-3,082	-1,848	Ribosomal protein L19
VIT_17s0000g02610	-1,241	-1,567	-0,817	-1,264	Ribosomal protein L22 50S
VIT_13s0101g00220	-1,697	-1,357	-0,637	-1,805	Ribosomal RNA 16S
VIT_08s0058g01440	-1,495	-1,340	-1,694	-1,358	Ribosomal S6 kinase p90
VIT_13s0019g02050	-1,840	-2,611	-3,231	-2,981	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplast
VIT_06s0004g05180	-1,917	-2,448	-1,533	-2,429	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplast
VIT_18s0001g06720	-1,577	-1,726	-1,467	-1,386	Rieske [2Fe-2S] domain
VIT_07s0005g00710	1,574	1,595	1,333	1,475	Ring-H2 subgroup RHE protein
VIT_13s0047g00110	2,293	0,762	-0,097	0,829	Ripening regulated protein DDTFR8
VIT_19s0014g00680	1,113	1,753	2,192	1,670	RKF1 (receptor-like kinase in flowers 1)
VIT_13s0064g00190	2,607	1,776	2,585	2,129	RNA polymerase sigma subunit SigD
VIT_05s0049g01660	-0,926	-1,294	-0,968	-1,639	RNA-binding protein Musashi
VIT_19s0014g00360	1,438	1,728	1,464	1,372	Root initiation defective 3 RID3
VIT_06s0004g08230	-1,623	-1,785	-2,068	-2,106	Root phototropism protein 2
VIT_02s0087g00260	1,492	1,779	1,868	1,360	RPD1 (root primordium defective 1)
VIT_13s0067g03600	-1,587	-1,381	-1,489	-1,054	RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33)
VIT_04s0044g00060	1,467	1,851	1,493	1,837	RWP-RK domain-containing protein
VIT_19s0093g00510	-1,957	-2,163	-1,354	-1,766	S-2-hydroxy-acid oxidase, peroxisomal
VIT_10s0003g03830	-1,243	-1,561	-1,070	-1,310	S-2-hydroxy-acid oxidase, peroxisomal
VIT_01s0011g05930	1,690	2,276	3,188	2,758	S-adenosyl-L-methionine:carboxyl methyltransferase
VIT_04s0023g02230	-1,442	-1,946	-2,992	-1,936	S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase
VIT_01s0011g05920	-1,002	-1,686	-2,169	-2,260	S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase
VIT_11s0037g00950	-2,939	-4,134	-3,012	-3,885	S-adenosylmethionine decarboxylase proenzyme
VIT_03s0038g00340	6,732	7,771	6,726	7,093	Salt tolerance homolog2(zf-box)
VIT_07s0141g00190	0,509	1,296	1,627	1,005	SAM (and some other nucleotide) binding motif
VIT_04s0023g02210	-3,054	-2,935	-2,970	-1,859	SAM dependent carboxyl methyltransferase Methyltransf_7
VIT_04s0008g02800	-1,633	-0,836	-1,375	-1,278	SAUR_D
VIT_13s0019g01700	1,956	2,196	2,108	1,338	Scarecrow transcription factor 14 (SCL14_1)

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_02s0025g04000	-1,732	-1,679	-1,506	-1,251	Scarecrow transcription factor 29 (SCL29)
VIT_14s0066g00590	-1,274	-1,482	-1,411	-2,156	SCF E3 ubiquitin ligase complex F-box protein grrA
VIT_10s0003g05480	-1,368	-1,542	-1,115	-0,924	SEC14 cytosolic factor
VIT_13s0019g03350	-1,658	-1,892	-1,353	-1,558	Sedoheptulose-1,7-bisphosphatase (SBPase), Chloroplast
VIT_05s0077g01130	1,192	1,590	0,973	1,002	Seed maturation protein PM36
VIT_00s1003g00010	1,665	1,821	2,134	1,620	Senescence-associated protein
VIT_00s0357g00010	1,606	1,741	1,936	1,776	Senescence-associated protein
VIT_09s0002g00420	2,118	1,596	1,369	1,637	Senescence-associated protein
VIT_18s0001g01210	-1,214	-1,714	-1,444	-2,054	Senescence-inducible chloroplast stay-green protein 2
VIT_08s0040g01040	-1,878	-1,926	-2,069	-1,162	Serine carboxypeptidase II
VIT_03s0038g03600	0,607	0,678	1,584	0,716	Serine/threonine kinase
VIT_18s0041g01290	1,317	0,797	1,703	0,788	Serine/threonine-protein kinase CCR4
VIT_06s0009g03740	-1,645	-2,471	-1,907	-2,466	Serine-glyoxylate aminotransferase
VIT_04s0044g01260	1,457	1,553	1,782	1,244	SEU3B protein
VIT_07s0031g03150	-1,563	-1,617	-1,256	-1,296	S-glutathione dehydrogenase/class III alcohol dehydrogenase
VIT_18s0001g14500	2,115	1,852	1,544	1,601	SHD (shepherd)
VIT_07s0129g00340	-2,107	-1,579	-0,956	-2,072	Shoot gravitropism 7
VIT_06s0004g00260	-1,503	-1,901	-1,559	-1,859	Shoot1 protein
VIT_11s0016g03890	1,472	1,387	1,719	1,520	Short-chain dehydrogenase/reductase (SDR)
VIT_17s0000g08370	2,026	1,601	1,021	1,120	SIMILAR TO RCD ONE 2 (SRO2)
VIT_12s0134g00390	1,493	0,705	1,029	1,558	S-locus lectin protein kinase family
VIT_19s0014g04280	1,471	1,247	1,022	1,548	S-locus protein kinase
VIT_19s0014g04600	0,000	4,580	5,619	0,000	S-locus protein kinase
VIT_09s0002g06790	1,852	1,456	0,621	0,770	Small heat shock protein (HSP26.5-P) 26.5 kDa class I
VIT_12s0028g01390	5,723	6,024	5,969	5,851	Small heat shock protein ACD31
VIT_09s0002g00640	1,248	-1,520	-1,764	0,004	Small heat stress protein class CIII
VIT_13s0019g00860	3,157	1,775	0,580	1,302	Small heat-shock protein HSP17.5 Cytosolic class I
VIT_04s0008g01550	3,362	0,529	-0,950	0,283	Small molecular heat shock protein 17.5
VIT_04s0008g01530	4,878	1,295	0,468	0,877	Small molecular heat shock protein 17.5
VIT_02s0033g01370	1,317	1,420	1,794	1,546	Sodium:solute symporter family protein
VIT_05s0077g00810	-1,297	-1,612	-1,546	-1,864	Sodium-inducible calcium-binding protein (ACP1)
VIT_06s0004g07830	2,449	2,386	1,941	1,892	SOS2 (salt overly sensitive 2)
VIT_01s0150g00060	-1,559	-1,902	-2,230	-2,153	SOUL heme-binding
VIT_12s0028g03570	-1,604	-1,908	-2,021	-2,311	SPA3 (SPA1-related 3)
VIT_05s0020g03200	-1,575	-1,434	-1,405	-1,119	Spermine synthase
VIT_00s0611g00010	-1,508	-2,206	-1,679	-1,477	Splicing factor U2AF 65 kDa subunit
VIT_12s0142g00110	1,852	1,355	0,806	0,804	Splicing factor, arginine/serine-rich 2
VIT_04s0008g05730	2,264	2,128	3,572	1,567	SPS1, Sucrose-phosphate synthase
VIT_06s0080g00070	0,517	0,978	1,700	0,535	S-receptor kinase
VIT_00s1530g00010	-1,195	-1,873	-0,226	-0,851	Stachyose synthase precursor
VIT_00s0878g00020	-1,410	-1,728	-0,790	-1,357	Stachyose synthase precursor
VIT_15s0048g02600	-2,424	-3,555	-1,155	-2,721	Starch synthase
VIT_00s0586g00030	-1,502	-1,750	-1,146	-1,145	Stem-specific protein TSJT1
VIT_19s0014g00080	-1,182	-1,499	-1,467	-1,936	Steroid 5alpha-reductase
VIT_03s0063g01470	-1,487	-1,210	-1,864	-1,417	Steroid nuclear receptor, ligand-binding
VIT_00s1286g00010	-1,044	-1,576	-0,563	1,149	Stress-induced-phosphoprotein 1
VIT_08s0007g05360	3,613	3,971	3,372	3,908	Strictosidine synthase
VIT_10s0071g00250	-1,972	-1,138	-1,586	-0,595	Strictosidine synthase
VIT_04s0008g05820	2,770	2,190	2,090	2,162	Stromal cell-derived factor 2 protein precursor (SDF2 protein)
VIT_18s0001g10330	0,572	-0,187	1,644	0,558	Subtilisin protease
VIT_15s0048g01170	-1,210	-1,820	-1,154	-1,997	Subtilisin serine protease
VIT_02s0025g04780	-1,045	-0,659	-1,425	-1,502	Subtilisin stomatal density and distribution
VIT_07s0005g02020	1,082	1,044	1,232	1,727	Sulfate adenylyltransferase
VIT_05s0020g03930	-2,483	-3,093	-2,785	-3,089	Sulfate transporter 3.1 (AST12) (AtST1)
VIT_00s0227g00170	1,299	1,631	1,422	1,439	Syntaxin 52
VIT_12s0057g00880	-1,371	-1,512	-1,045	-1,355	TAF15b (TBP-associated factor 15b) zf-ranBP
VIT_14s0128g00440	-2,048	-1,672	-1,712	-1,454	Tangled
VIT_09s0002g01830	1,290	1,548	1,999	1,963	Tassel serine threonine kinase 1
VIT_06s0004g07650	-1,249	-1,446	-2,115	-2,147	Taxadien-5-alpha-ol-O-acetyltransferase
VIT_19s0090g00190	0,985	1,613	0,951	1,320	Taxane 10-beta-hydroxylase

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_12s0034g02390	-0,772	-1,498	-1,479	-1,656	T-complex protein 11
VIT_04s0008g03670	1,534	1,380	1,449	1,453	Tesmin/TSO1-like CXC domain-containing
VIT_11s0037g00840	-2,153	-2,342	-1,555	-2,209	Tetratricopeptide repeat (TPR)-containing
VIT_03s0063g00640	1,593	1,509	0,842	1,033	TF-B3 domain-containing protein
VIT_06s0004g06130	2,102	2,502	2,769	2,309	Thiamine biosynthesis protein ThiC
VIT_10s0116g00530	5,845	6,246	6,730	6,337	Thiazole biosynthetic enzyme, chloroplast (ARA6)
VIT_19s0177g00140	1,676	1,590	1,840	1,329	Thiazole biosynthetic enzyme, chloroplast (ARA6)
VIT_01s0011g03710	1,092	1,080	1,170	1,587	Thioesterase family
VIT_08s0007g07620	-1,401	-1,892	-1,346	-1,178	Thioredoxin 2
VIT_17s0000g06370	-1,041	-1,154	-1,320	-1,512	Thioredoxin 2
VIT_00s0532g00030	1,730	1,190	1,520	1,321	Thioredoxin H
VIT_18s0001g00820	1,431	1,244	1,705	1,439	Thioredoxin-like protein CDSP32
VIT_06s0004g06170	-1,543	-1,411	-0,983	-1,141	Thylakoid soluble phosphoprotein
VIT_18s0072g01090	-1,796	-1,715	-2,208	-1,958	TIR-NBS-LRR type R protein 7
VIT_14s0108g00070	1,352	1,792	1,137	1,005	Transcription initiation factor TFIID subunit 1-A
VIT_00s0388g00040	-1,509	-3,119	-2,203	-1,842	Transducin family protein / WD-40
VIT_19s0090g00420	1,948	1,477	1,118	2,393	Translation initiation factor eIF-1
VIT_13s0019g01850	1,880	1,561	1,040	1,300	Transposon protein, putative, CACTA
VIT_00s0233g00030	-1,859	-1,423	-1,120	-1,227	Trehalose-6-phosphate phosphatase (AtTPPA)
VIT_02s0154g00110	-1,936	-1,490	-1,100	-1,268	Trehalose-6-phosphate phosphatase (AtTPPA)
VIT_07s0005g01240	1,635	2,087	1,819	0,984	Triacylglycerol lipase
VIT_05s0020g01930	2,270	2,216	2,136	1,761	TUBBY like protein 3 TLP3
VIT_02s0025g03540	1,125	1,271	1,784	0,838	Tubulin beta-6 chain
VIT_12s0028g03210	1,569	1,338	1,600	1,900	Tyrosine aminotransferase
VIT_04s0043g00900	-1,293	-2,594	-2,624	-1,471	Tyrosine decarboxylase
VIT_12s0059g01400	-1,471	-1,568	-1,648	-0,647	Tyrosine specific protein phosphatase
VIT_04s0043g00930	-1,711	-2,363	-2,985	-1,445	Tyrosine/DOPA decarboxylase 2
VIT_04s0008g02240	2,015	1,963	1,232	1,187	Ubiquitin thiolesterase
VIT_06s0061g00070	-1,547	-1,137	-1,333	-0,729	Ubiquitin-conjugating enzyme E2 C
VIT_05s0077g00850	1,638	1,914	1,153	0,871	Ubiquitin-conjugating enzyme E2 O
VIT_19s0090g00120	-2,572	-3,414	-3,141	-3,448	Ubiquitin-conjugating enzyme E2 variant
VIT_18s0166g00190	1,529	0,814	0,123	0,098	U-box domain-containing protein
VIT_01s0026g01890	1,977	1,254	1,042	0,968	UDP-galactose transporter 3
VIT_06s0004g01670	-1,232	-1,737	-2,195	-0,743	UDP-glucoronosyl and UDP-glucosyl transferase
VIT_06s0004g01640	1,214	1,843	1,358	1,449	UDP-glucoronosyl and UDP-glucosyl transferase
VIT_16s0050g01680	-1,232	-2,015	-1,536	-1,892	UDP-glucose: anthocyanidin 5,3-O-glucosyltransferase
VIT_18s0041g00710	1,455	1,901	1,943	1,433	UDP-glucose: anthocyanidin 5,3-O-glucosyltransferase
VIT_16s0050g01580	0,859	1,436	1,981	1,207	UDP-glucose: anthocyanidin 5,3-O-glucosyltransferase
VIT_05s0062g00640	-1,657	-2,281	-1,456	-1,979	UDP-glucose:flavonoid 7-O-glucosyltransferase
VIT_03s0063g00050	-1,286	-1,298	-1,523	-1,609	UDP-glucuronosyl/UDP-glucosyltransferase
VIT_00s0324g00100	-1,272	-1,505	-0,721	-1,621	UDP-glycosyltransferase 85A1
VIT_17s0000g04750	-1,232	-0,977	-1,516	-1,776	UDP-glycosyltransferase 89B2
VIT_14s0060g01300	1,224	1,066	0,861	1,859	Universal stress protein (USP) family protein
VIT_02s0025g01710	-2,584	-3,318	-3,112	-3,771	Unknown
VIT_09s0002g08680	-1,825	-2,421	-1,630	-1,694	Unknown
VIT_06s0004g04620	2,096	1,875	2,002	1,021	Unknown
VIT_11s0065g01070	1,604	1,755	1,570	1,201	Unknown
VIT_03s0017g02210	-1,891	-1,977	-2,035	-0,666	Unknown
VIT_07s0031g01110	5,049	7,014	5,619	0,000	unknown
VIT_19s0014g01940	1,249	2,183	1,965	1,624	Unknown
VIT_18s0001g08870	-1,670	-0,601	-1,185	-1,089	Unknown
VIT_09s0002g04840	-1,986	-1,444	-0,928	-1,476	Unknown
VIT_06s0009g02670	-1,061	-0,873	-1,584	-0,513	Unknown
VIT_09s0002g05820	0,957	1,157	0,900	1,583	Unknown
VIT_00s0854g00030	-1,268	-1,437	-0,916	-1,682	Unknown
VIT_03s0063g00350	3,377	4,121	3,959	2,780	unknown
VIT_16s0100g00200	1,778	1,656	2,427	1,833	unknown
VIT_14s0068g00810	1,613	2,169	2,270	1,993	unknown
VIT_14s0108g01350	-3,941	-4,677	-4,715	-4,866	Unknown protein
VIT_05s0020g02770	-1,986	-2,332	-2,260	-2,030	Unknown protein

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_14s0108g00840	2,676	3,066	2,406	2,794	Unknown protein
VIT_00s2377g00010	-1,898	-2,182	-1,594	-2,158	Unknown protein
VIT_16s0050g00710	-2,041	-2,908	-2,237	-2,939	Unknown protein
VIT_16s0050g01260	2,527	2,535	2,699	2,473	Unknown protein
VIT_14s0066g00470	2,554	2,846	2,284	2,821	Unknown protein
VIT_07s0005g01830	-3,109	-2,891	-3,101	-2,948	Unknown protein
VIT_00s0225g00010	3,868	4,011	3,564	3,729	Unknown protein
VIT_02s0025g02640	-1,774	-2,534	-2,525	-2,538	Unknown protein
VIT_06s0004g05960	2,512	2,693	3,319	3,109	Unknown protein
VIT_15s0046g01560	3,049	2,495	2,591	2,080	Unknown protein
VIT_18s0001g10480	4,040	5,620	4,231	5,987	Unknown protein
VIT_17s0000g07950	2,266	3,201	2,185	2,160	Unknown protein
VIT_09s0054g01750	-1,939	-2,671	-2,360	-3,262	Unknown protein
VIT_15s0046g02050	3,281	3,588	2,820	2,937	Unknown protein
VIT_14s0068g02200	1,629	2,045	2,267	2,289	Unknown protein
VIT_03s0063g01380	2,055	1,650	1,728	2,423	Unknown protein
VIT_07s0104g00500	-1,684	-1,553	-1,660	-0,919	Unknown protein
VIT_11s0016g05430	2,027	2,242	1,965	1,236	Unknown protein
VIT_05s0062g01360	-2,277	-1,504	-2,227	-1,331	Unknown protein
VIT_18s0001g08810	4,357	5,269	5,166	4,700	Unknown protein
VIT_04s0008g02760	2,622	1,662	1,503	1,187	Unknown protein
VIT_00s1235g00010	-1,617	-1,646	-1,447	-1,531	Unknown protein
VIT_05s0049g00800	2,785	3,085	0,000	2,959	Unknown protein
VIT_00s0332g00090	-1,967	-1,559	-1,327	-1,856	Unknown protein
VIT_07s0129g00470	-1,220	-1,796	-1,901	-1,922	Unknown protein
VIT_03s0091g00230	-0,994	-2,021	-2,058	-2,655	Unknown protein
VIT_13s0067g02090	-0,820	-1,826	-1,791	-2,295	Unknown protein
VIT_13s0067g02560	-0,859	-1,788	-2,286	-2,344	Unknown protein
VIT_12s0059g01900	-1,305	-1,711	-1,650	-1,537	Unknown protein
VIT_07s0005g01080	-1,246	-2,691	-2,746	-2,340	Unknown protein
VIT_12s0028g00580	1,586	1,552	1,404	1,218	Unknown protein
VIT_19s0014g03500	2,136	1,592	1,079	0,938	Unknown protein
VIT_13s0139g00360	2,543	1,601	1,399	1,000	Unknown protein
VIT_09s0002g02060	1,563	1,523	1,249	1,282	Unknown protein
VIT_05s0051g00680	2,158	1,815	1,298	0,660	Unknown protein
VIT_19s0015g01440	2,740	2,865	2,285	2,002	Unknown protein
VIT_03s0091g01100	-1,761	-2,142	-0,841	-0,748	Unknown protein
VIT_11s0016g02920	1,760	2,298	1,424	-0,162	Unknown protein
VIT_06s0004g03910	1,516	1,523	1,057	0,358	Unknown protein
VIT_11s0016g02520	2,662	2,041	1,494	1,455	Unknown protein
VIT_00s2855g00010	-2,124	-1,819	-0,646	-1,247	Unknown protein
VIT_07s0031g01510	3,809	4,983	3,726	0,000	Unknown protein
VIT_16s0013g02030	1,935	1,763	1,333	1,448	Unknown protein
VIT_07s0031g01060	1,532	1,321	1,821	1,341	Unknown protein
VIT_04s0023g03360	-1,785	-1,442	-1,562	-1,178	Unknown protein
VIT_00s0302g00010	-1,735	-1,484	-1,690	-0,256	Unknown protein
VIT_17s0000g02160	1,579	1,398	1,475	1,959	Unknown protein
VIT_12s0028g03560	-1,434	-2,016	-2,324	-2,451	Unknown protein
VIT_03s0038g00660	0,000	5,965	5,503	5,761	Unknown protein
VIT_11s0016g05790	1,023	1,598	1,637	1,478	Unknown protein
VIT_19s0014g03220	1,230	1,602	1,400	1,562	Unknown protein
VIT_18s0001g00110	-1,368	-1,713	-1,029	-1,504	Unknown protein
VIT_16s0050g01990	-1,293	-1,087	-2,041	-1,787	Unknown protein
VIT_11s0016g05800	0,557	1,348	1,507	1,627	Unknown protein
VIT_03s0091g00550	-1,625	-1,474	-1,329	-1,008	Unknown protein
VIT_18s0001g07770	2,144	1,290	0,670	0,978	Unknown protein
VIT_18s0001g13080	-1,715	-0,871	-0,678	-0,792	Unknown protein
VIT_12s0057g01510	-1,813	-1,340	-1,237	-0,277	Unknown protein
VIT_17s0000g07600	1,570	1,144	1,300	0,845	Unknown protein
VIT_15s0048g02780	1,510	1,401	1,047	0,600	Unknown protein

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_05s0020g01270	-1,564	-1,448	-1,291	-1,037	Unknown protein
VIT_01s0010g03750	1,515	1,296	0,446	0,789	Unknown protein
VIT_02s0025g01470	-1,421	-1,644	-1,141	-1,325	Unknown protein
VIT_10s0116g00900	2,295	2,149	2,223	1,928	Unknown protein
VIT_03s0063g00340	3,930	3,106	4,421	0,000	Unknown protein
VIT_19s0090g01750	-0,753	-1,614	-0,557	-1,686	Unknown protein
VIT_01s0010g03680	1,474	1,582	0,892	0,996	Unknown protein
VIT_00s0323g00040	-1,410	-1,642	-1,443	-1,044	Unknown protein
VIT_13s0067g03180	-1,731	-2,713	-0,975	-2,213	Unknown protein
VIT_00s0317g00010	-1,651	-2,292	0,000	0,000	Unknown protein
VIT_17s0000g06760	1,377	1,238	1,576	0,966	Unknown protein
VIT_18s0001g09980	1,239	1,156	1,526	1,412	Unknown protein
VIT_14s0030g01710	1,313	1,310	1,647	1,181	Unknown protein
VIT_12s0028g00560	-1,860	-1,375	-2,288	-1,364	Unknown protein
VIT_17s0000g01800	1,087	1,288	1,520	0,913	Unknown protein
VIT_05s0020g02920	-1,123	-1,094	-1,774	-1,144	Unknown protein
VIT_15s0048g00910	0,124	0,879	1,557	0,861	Unknown protein
VIT_16s0039g02160	-1,151	-1,186	-1,755	-0,786	Unknown protein
VIT_14s0068g01020	1,468	1,416	1,744	1,384	Unknown protein
VIT_13s0019g01040	-1,275	-1,011	-1,774	-0,996	Unknown protein
VIT_03s0038g03690	1,340	1,409	1,187	1,673	Unknown protein
VIT_17s0000g03220	1,244	1,415	0,918	1,570	Unknown protein
VIT_09s0054g01760	-0,722	-1,249	-0,913	-1,752	Unknown protein
VIT_06s0004g00810	1,816	1,551	1,793	1,916	Unknown protein
VIT_11s0016g03760	1,251	1,641	1,485	1,602	VARLMGL domain-containing protein
VIT_08s0058g00040	1,771	1,080	2,269	1,387	Verticillium wilt disease resistance protein Ve2
VIT_03s0063g00120	1,704	1,105	0,994	1,247	Wax synthase
VIT_13s0019g01680	-1,496	-1,828	-0,760	-1,584	WD_REPEATS_REGION domain-containing protein
VIT_12s0057g00180	2,420	2,827	1,266	1,202	Wound-induced
VIT_12s0057g00100	2,348	1,282	0,452	1,279	Wound-responsive
VIT_18s0001g12960	1,666	1,324	1,440	1,505	Wound-responsive protein
VIT_04s0023g00470	1,573	1,601	1,606	1,504	WRKY DNA-binding protein 2 (WRKY)
VIT_07s0031g01710	-2,425	-2,457	-3,711	-1,677	WRKY DNA-binding protein 51
VIT_13s0067g03140	-1,368	-1,713	-1,436	-1,024	WRKY DNA-binding protein 70
VIT_08s0058g01390	-1,131	-1,368	-1,740	-1,220	WRKY DNA-binding protein 70
VIT_13s0067g02500	1,365	2,033	1,872	0,392	Xanthine/uracil permease
VIT_05s0062g00250	2,093	2,988	3,088	3,001	Xyloglucan endotransglucosylase/hydrolase 15
VIT_11s0052g01280	0,000	3,755	0,000	0,000	Xyloglucan endotransglucosylase/hydrolase 23
VIT_01s0150g00460	-1,575	-1,287	-1,305	-0,833	Xyloglucan endotransglucosylase/hydrolase precursor
VIT_11s0052g01300	2,575	2,566	0,000	0,000	Xyloglucan endotransglycosylase 6
VIT_12s0134g00160	1,790	2,390	2,545	2,300	Xyloglucan endotransglycosylase/hydrolase 16
VIT_12s0059g02510	-2,006	-2,590	-3,298	-2,965	Zinc finger (B-box type)
VIT_04s0023g03030	-1,212	-1,780	-1,931	-1,696	Zinc finger (B-box type)
VIT_19s0014g03960	-1,024	-1,752	-1,802	-1,836	Zinc finger (B-box type)
VIT_03s0038g00690	-1,084	-1,292	-1,626	-1,364	Zinc finger (B-box type)
VIT_06s0004g05850	2,114	2,282	2,141	2,043	Zinc finger (C3HC4-type ring finger)
VIT_15s0046g02070	1,738	2,544	1,612	2,029	Zinc finger (C3HC4-type ring finger)
VIT_06s0004g08080	4,356	3,832	4,006	4,911	Zinc finger (C3HC4-type ring finger)
VIT_17s0000g06610	-1,559	-1,664	-1,709	-1,756	Zinc finger (C3HC4-type ring finger)
VIT_01s0026g02540	2,001	1,203	1,567	2,459	Zinc finger (C3HC4-type ring finger)
VIT_02s0025g01990	1,536	1,636	1,587	1,229	Zinc finger (C3HC4-type ring finger)
VIT_04s0008g04480	2,099	1,804	1,319	1,432	Zinc finger (C3HC4-type ring finger)
VIT_07s0031g02250	1,299	1,718	1,519	1,442	Zinc finger (C3HC4-type ring finger)
VIT_14s0219g00040	-0,875	-1,082	-1,513	-1,682	Zinc finger (C3HC4-type ring finger)
VIT_14s0219g00030	-1,544	-1,205	-1,490	-1,026	Zinc finger (C3HC4-type ring finger)
VIT_09s0018g01220	-1,363	-1,124	-1,709	-1,354	Zinc finger (C3HC4-type ring finger)
VIT_19s0014g00340	1,020	1,199	1,368	1,575	Zinc finger (C3HC4-type ring finger)
VIT_08s0040g01950	1,462	1,396	1,285	1,535	Zinc finger (C3HC4-type ring finger)
VIT_01s0026g02460	0,922	1,103	1,800	1,490	Zinc finger homeobox 30
VIT_18s0166g00180	-1,583	-1,819	-1,659	-1,880	Zinc finger protein ATRZ-1A

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_13s0019g00720	1,951	1,597	1,393	1,463	Zinc knuckle
VIT_19s0015g00190	1,256	1,848	1,866	1,084	Zinc transporter ZIP11
VIT_01s0011g01280	-1,435	-1,446	-2,007	-1,665	Zinc transporter ZIP5
VIT_18s0001g02690	2,428	1,765	1,123	1,048	zinc_ribbon_15 domain-containing protein
VIT_12s0059g01410	-1,782	-1,770	-1,946	-1,539	Unknown
VIT_12s0142g00400	-1,869	-2,143	-1,925	-2,065	Unknown
VIT_15s0046g01380	-1,886	-1,873	-1,977	-1,728	Unknown
VIT_11s0065g01170	1,987	1,543	1,907	1,647	Unknown
VIT_04s0008g05860	1,544	1,866	1,872	1,917	Unknown
VIT_07s0104g01630	1,917	2,116	2,343	1,833	Unknown
VIT_18s0001g09290	2,339	2,043	1,720	1,658	Unknown
VIT_11s0037g00850	-2,383	-2,302	-1,704	-2,295	Unknown
VIT_01s0026g02740	3,651	4,511	4,256	3,764	Unknown
VIT_03s0038g01760	-1,543	-1,601	-1,521	-0,662	Unknown
VIT_00s0274g00050	2,695	2,182	2,215	1,197	Unknown
ENSRNA049996781	1,715	1,814	1,538	1,400	Unknown
VIT_03s0097g00210	-4,138	-4,790	2,332	-0,083	Unknown
VIT_09s0070g00710	2,257	2,129	2,496	1,493	Unknown
VIT_15s0021g02350	1,963	1,957	1,998	1,631	Unknown
VIT_12s0028g01380	2,540	1,813	2,480	0,000	Unknown
VIT_19s0090g00080	-2,115	-2,520	-1,696	-3,072	Unknown
VIT_14s0006g03100	-1,606	-2,231	-1,055	-2,657	Unknown
VIT_07s0141g00760	1,570	1,831	1,014	1,868	Unknown
VIT_08s0007g05630	2,377	1,830	1,918	2,807	Unknown
VIT_18s0089g01090	1,509	1,816	1,025	1,585	Unknown
VIT_12s0057g00120	2,325	3,222	1,609	2,680	Unknown
VIT_12s0059g01050	-1,855	-1,312	-2,203	-2,085	Unknown
ENSRNA049466084	5,167	-0,084	1,631	-2,649	Unknown
VIT_16s0022g01240	1,333	1,844	1,820	1,889	Unknown
VIT_05s0094g01260	-1,347	-1,960	-2,247	-1,855	Unknown
VIT_18s0117g00030	-1,828	-1,895	-1,404	-0,369	Unknown
VIT_19s0014g02800	2,170	1,998	1,448	1,255	Unknown
VIT_09s0018g00720	-1,938	-1,773	-1,563	-1,203	Unknown
VIT_06s0009g02450	2,151	1,525	1,382	1,386	Unknown
VIT_01s0137g00560	-1,576	-1,960	-1,216	-1,704	Unknown
VIT_18s0001g06150	2,158	2,792	1,190	-0,312	Unknown
VIT_00s0125g00040	-2,613	-2,751	-0,024	-1,271	Unknown
VIT_14s0036g01120	-2,008	-1,709	-1,236	-0,915	Unknown
VIT_11s0016g02190	1,611	1,435	1,728	1,354	Unknown
ENSRNA049469239	2,371	0,000	2,002	-1,236	Unknown
VIT_00s0396g00060	1,530	1,222	1,554	0,997	Unknown
VIT_18s0072g00270	-2,453	-1,498	-1,847	-1,028	Unknown
VIT_02s0025g04980	1,559	1,301	1,580	0,807	Unknown
ENSRNA049469936	2,992	0,882	1,206	-1,910	Unknown
ENSRNA049469319	2,130	1,033	0,748	-1,800	Unknown
ENSRNA049469358	2,782	0,858	1,047	-2,259	Unknown
VIT_18s0001g07900	1,223	1,985	1,748	1,262	Unknown
VIT_16s0100g00740	6,185	5,210	6,849	6,036	Unknown
VIT_00s1596g00010	0,000	6,734	0,000	-4,862	Unknown
VIT_17s0000g03780	-1,018	-1,300	-2,176	-2,287	Unknown
VIT_01s0113g00560	1,772	1,415	1,375	1,341	Unknown
VIT_05s0094g00510	-1,631	-1,025	-0,709	-0,786	Unknown
VIT_11s0016g05830	-1,631	-1,198	-0,975	-0,912	Unknown
VIT_03s0038g00130	-3,010	-1,960	-2,404	-2,052	Unknown
VIT_18s0117g00040	-1,642	-1,067	-0,870	-0,870	Unknown
VIT_00s0204g00010	1,639	0,691	0,993	0,513	Unknown
VIT_02s0025g00230	1,546	0,845	0,476	0,649	Unknown
VIT_05s0102g00620	1,605	-0,045	-0,710	0,171	Unknown
VIT_03s0088g01160	-1,558	-1,434	-1,363	-0,839	Unknown
VIT_11s0037g00610	-1,736	-1,451	-1,476	-1,204	Unknown

Elements	Log2FC(RC vs RT)	Log2FC(R80%C vs R80%T)	Log2FC(R50%C vs R50%T)	Log2FC(RS50%C vs RS50%T)	Description
VIT_09s0002g05680	-1,534	-1,497	-0,890	-0,939	Unknown
VIT_01s0011g03040	-1,616	-1,246	-1,286	-1,020	Unknown
VIT_05s0102g00600	2,017	0,144	0,049	0,371	Unknown
ENSRNA049469943	3,427	-0,478	1,458	-1,338	Unknown
VIT_00s0505g00020	-1,500	-0,975	-0,727	-1,067	Unknown
VIT_17s0000g06600	1,638	1,114	1,181	0,631	Unknown
VIT_12s0059g01640	1,529	0,625	0,591	0,471	Unknown
VIT_08s0007g02810	-2,153	-0,873	-0,157	-0,783	Unknown
VIT_01s0010g03410	1,529	1,006	1,333	0,709	Unknown
VIT_08s0007g05270	-1,671	-1,308	-1,410	-0,829	Unknown
VIT_00s0125g00050	-1,539	-1,246	-0,963	-1,405	Unknown
VIT_19s0015g00490	-2,207	-1,358	-1,155	-0,443	Unknown
VIT_07s0185g00080	1,981	1,177	1,757	1,513	Unknown
VIT_13s0067g00430	2,238	1,210	0,255	0,169	Unknown
VIT_00s0181g00050	1,394	1,711	1,101	1,067	Unknown
VIT_00s0411g00040	1,300	1,947	2,240	1,087	Unknown
VIT_07s0129g00420	1,334	1,603	1,298	1,283	Unknown
VIT_04s0044g00590	0,876	1,640	0,862	1,053	Unknown
VIT_17s0000g02040	-1,471	-1,542	-1,433	-0,719	Unknown
VIT_14s0036g00440	3,307	2,746	3,410	2,145	Unknown
VIT_00s0299g00090	0,845	1,567	0,671	1,373	Unknown
VIT_14s0219g00260	1,123	1,795	0,947	0,626	Unknown
VIT_18s0001g06920	1,051	1,572	1,200	1,258	Unknown
VIT_00s2424g00010	-2,502	-2,282	-2,522	-2,072	Unknown
VIT_07s0005g01070	0,000	-2,226	-0,764	-1,809	Unknown
VIT_03s0038g00570	1,050	0,714	1,521	0,937	Unknown
VIT_11s0016g03800	0,876	1,014	1,503	0,881	Unknown
VIT_02s0025g00870	-1,047	-0,532	-1,849	-0,945	Unknown
ENSRNA049469692	1,231	0,988	1,508	0,080	Unknown
VIT_18s0001g12330	-0,082	0,975	1,512	0,553	Unknown
VIT_07s0005g05180	0,110	-0,466	-0,649	-1,507	Unknown
VIT_02s0012g01350	-1,045	-1,434	-0,682	-1,942	Unknown
VIT_18s0001g02360	1,104	0,795	1,092	1,806	Unknown
VIT_12s0055g00380	0,532	1,103	0,788	1,537	Unknown
VIT_13s0158g00420	-1,362	-1,090	-1,494	-1,559	Unknown
VIT_00s0194g00060	1,228	2,052	1,022	1,702	Unknown

Supplementary Table 3a

Moisture stress responsive genes

Gene ID	Log2FC(RC vs R80%C)	Log2FC(RC vs R50%C)	Log2FC(RC vs RS50%C)	Description
VIT_11s0118g00310	1,234	2,039	0,405	1,2-diacylglycerol 3-beta-galactosyltransferase
ENSRNA049466933	0,000	4,094	0,000	5.8S ribosomal RNA
VIT_01s0146g00150	1,364	2,138	2,110	BCL-2-associated athanogene 5
VIT_18s0001g14990	0,663	1,657	-0,032	Dual-specific kinase DSK1
ENSRNA049469239	-1,892	1,260	1,352	Eukaryotic large subunit ribosomal RNA
ENSRNA049466084	-0,911	2,827	2,149	Eukaryotic small subunit ribosomal RNA
ENSRNA049469358	-1,666	1,704	1,398	Eukaryotic small subunit ribosomal RNA
ENSRNA049469319	-1,284	1,511	1,202	Eukaryotic small subunit ribosomal RNA
VIT_16s0022g00510	1,082	1,759	1,928	Heat shock 22 kDa protein
VIT_13s0019g02760	1,801	2,503	2,437	Heat shock protein 17.6 kDa class I
VIT_13s0019g02850	1,024	1,622	1,724	Heat shock protein 17.6 kDa class I
VIT_13s0019g02740	1,047	1,756	1,677	Heat shock protein 17.6 kDa class I
VIT_13s0019g02930	0,976	1,671	1,615	Heat shock protein 17.6 kDa class I
VIT_13s0019g02770	0,686	1,853	1,596	Heat shock protein 17.6 kDa class I
VIT_13s0019g03160	1,207	1,529	1,864	Heat shock protein 17.6 kDa class I
VIT_13s0019g02780	0,958	1,991	2,024	Heat shock protein 17.6 kDa class I
VIT_04s0008g01570	1,191	1,641	1,978	Heat shock protein 17.6 kDa class II
VIT_04s0008g01510	2,282	3,345	3,803	Heat shock protein 17.6 kDa class II
VIT_04s0008g01490	1,009	1,716	1,874	Heat shock protein 17.6 kDa class II
VIT_04s0008g01580	1,420	1,932	2,282	Heat shock protein 17.6 kDa class II
VIT_04s0008g01520	1,398	2,023	2,378	Heat shock protein 17.6 kDa class II
VIT_04s0008g01590	1,115	1,753	1,893	Heat shock protein 17.6 kDa class II
VIT_13s0019g02840	1,647	2,513	2,051	Heat shock protein 18.2 kDa class I
VIT_01s0010g02290	0,892	1,547	1,522	Heat shock protein 26a, chloroplast
VIT_16s0098g01060	1,125	1,562	1,359	Heat shock protein 26a, chloroplast
VIT_06s0004g04470	1,213	1,773	2,061	Heat shock protein 70
VIT_02s0025g00280	1,341	1,909	2,356	Heat shock protein 90-1
VIT_16s0050g01150	0,807	1,494	1,847	Heat shock protein 90-1
VIT_02s0154g00480	0,881	1,614	1,822	Heat shock protein MTSHP
VIT_18s0089g01270	0,872	2,009	1,938	Heat shock protein precursor 22.0 kDa class IV
VIT_04s0008g01110	0,897	1,948	1,898	Heat shock transcription factor A6B
VIT_05s0077g01670	1,793	0,235	1,340	Major cherry allergen Pru av 1.0202
VIT_11s0016g04080	0,797	1,915	2,054	Multiprotein-bridging factor 1c MBF1C
VIT_03s0063g00370	1,327	0,470	2,179	Nitrite reductase
VIT_09s0002g00630	1,056	1,468	1,628	No hit
VIT_18s0001g10210	-4,532	-0,469	-5,487	PAB8 (poly(A) binding protein 8)
VIT_09s0002g02450	0,913	1,569	-0,618	Phosphatase
VIT_11s0052g01680	-2,566	-2,571	-2,386	Photosystem II protein D1
VIT_09s0054g00210	1,588	1,808	1,070	Ribosomal protein L7 (RPL7D) 60S
VIT_04s0008g01530	2,542	2,964	2,922	Small molecular heat shock protein 17.5
VIT_04s0008g01550	1,460	2,158	2,373	Small molecular heat shock protein 17.5

Supplementary Table 3b

Moisture stress responsive genes with at least Log2(FC)=1.5or-1.5

Gene ID	Log2FC(RS50%C vs R50%C)	Description
VIT_15s0048g00190	-4,240	SPX (SYG1/Pho81/XPR1) domain-containing protein
ENSRNA049466933	-3,879	Ribosomal RNA
VIT_11s0037g00980	-2,534	Unknown
VIT_11s0016g05330	-2,401	SPX2 (SYG1/Pho81/XPR1) domain-containing protein SPX2
VIT_09s0002g02450	-2,186	Phosphatase
VIT_14s0068g01500	-2,018	Glycerophosphoryl diester phosphodiesterase
VIT_18s0001g14990	-1,689	Dual-specific kinase DSK1
VIT_11s0118g00310	-1,634	1,2-diacylglycerol 3-beta-galactosyltransferase
VIT_03s0063g00370	1,709	Nitrite reductase

Supplementary Table 4a

Effect of irrigation level on heat response

Gene ID	Log2FC(RT vs R80%T)	Log2FC(RT vs R50%T)	Log2FC(RT vs RS50%T)	Description
ENSRNA049466933	0,000	8,128	0,000	5.8S ribosomal RNA
VIT_10s0116g01650	0,369	2,087	1,897	5'-adenylylsulfate reductase (APR1)
VIT_12s0059g00760	0,144	1,235	1,730	Adenosine 5' phosphosulfate reductase
VIT_01s0146g00150	-0,668	1,876	3,808	BCL-2-associated athanogene 5
VIT_18s0122g00180	-0,310	0,171	1,905	Calmodulin CML37
VIT_04s0008g02860	0,417	1,920	1,789	Cation transport protein chaC
VIT_08s0058g00980	-0,538	-2,303	-0,545	Cationic peroxidase
VIT_16s0115g00190	-0,480	-0,708	-2,101	DNA-directed RNA Polymerase II subunit K
ENSRNA049469239	-5,667	0,415	-2,533	Eukaryotic large subunit ribosomal RNA
ENSRNA049466084	-6,339	-0,548	-5,250	Eukaryotic small subunit ribosomal RNA
ENSRNA049469358	-3,709	-0,104	-3,729	Eukaryotic small subunit ribosomal RNA
ENSRNA049469319	-2,397	0,095	-2,737	Eukaryotic small subunit ribosomal RNA
VIT_17s0000g03940	-1,446	-2,909	-0,929	ferulate 5-hydroxylase
VIT_17s0000g03930	-0,967	-1,651	-0,894	ferulate 5-hydroxylase
VIT_19s0014g04930	-0,999	-3,155	-0,309	Germacrene-D synthase
VIT_15s0046g02550	0,580	0,697	1,617	Gibberellin 20-oxidase
VIT_08s0007g05100	0,491	1,633	1,434	Glycosyl hydrolase family 31 protein
VIT_16s0022g00510	-1,378	-1,976	-0,999	Heat shock 22 kDa protein
VIT_02s0154g00490	-1,278	-1,975	-0,150	Heat shock 22 kDa protein mitochondrial
VIT_17s0000g07190	-1,687	-1,866	-1,434	Heat shock protein 101
VIT_13s0019g02850	-1,748	-1,894	-0,416	Heat shock protein 17.6 kDa class I
VIT_13s0019g02760	-2,718	-1,472	0,929	Heat shock protein 17.6 kDa class I
VIT_13s0019g02770	-1,528	-1,248	0,634	Heat shock protein 17.6 kDa class I
VIT_13s0019g02740	-2,049	-0,657	0,994	Heat shock protein 17.6 kDa class I
VIT_13s0019g03160	-1,425	-1,723	-0,901	Heat shock protein 17.6 kDa class I
VIT_13s0019g02780	-1,459	-1,510	-0,548	Heat shock protein 17.6 kDa class I
VIT_04s0008g01570	-1,524	-1,953	-0,582	Heat shock protein 17.6 kDa class II
VIT_04s0008g01510	-1,349	-1,751	-0,660	Heat shock protein 17.6 kDa class II
VIT_13s0019g02840	-1,747	-1,382	0,293	Heat shock protein 18.2 kDa class I
VIT_11s0037g00510	-1,551	-1,769	-1,716	Heat shock protein 70
VIT_06s0004g04470	-1,647	-2,088	-1,425	Heat shock protein 70
VIT_16s0050g01150	-2,203	-2,259	-0,935	Heat shock protein 90-1
VIT_02s0025g00280	-1,427	-1,766	-1,607	Heat shock protein 90-1
VIT_13s0019g03090	-1,231	-1,888	-0,359	Heat shock protein class I (HSP17.8-CI)
VIT_02s0154g00480	-1,071	-1,751	-0,271	Heat shock protein MTSHP
VIT_16s0100g00720	-0,895	-0,024	1,569	Heat shock transcription factor B2A
VIT_08s0058g00210	0,137	0,174	2,128	HSP17.4
VIT_11s0016g04490	-1,028	-1,600	-0,556	IAA16_3
VIT_09s0002g00570	-0,375	-1,720	-0,272	Lipase GDSL 1
VIT_07s0031g00530	-0,631	-1,028	-1,817	MAPKKK21
VIT_01s0011g04760	-0,333	-1,096	-1,705	Myb domain protein 4
VIT_07s0129g01050	-0,082	-1,005	-1,594	Myb domain protein 73

Gene ID	Log2FC(RT vs R80%T)	Log2FC(RT vs R50%T)	Log2FC(RT vs RS50%T)	Description
VIT_18s0001g09850	0,141	-0,849	-1,714	Myb domain protein R1
VIT_15s0048g02430	-0,662	-1,703	0,376	Naringenin,2-oxoglutarate 3-dioxygenase
VIT_02s0025g02960	-0,249	-1,601	0,243	Naringenin,2-oxoglutarate 3-dioxygenase
VIT_09s0002g00630	-1,954	-1,780	0,453	No hit
VIT_16s0098g00600	0,454	2,204	2,212	No hit
VIT_05s0049g00780	-0,831	-3,084	-0,117	No hit
VIT_19s0090g01360	-0,832	-2,193	-0,165	No hit
VIT_05s0049g00720	-1,254	-2,762	-0,256	No hit
VIT_05s0049g00770	-0,531	-4,512	-0,465	No hit
VIT_05s0049g00840	-0,832	-2,702	-0,695	No hit
VIT_19s0090g01340	-0,935	-2,139	-0,354	No hit
VIT_03s0091g00160	-0,422	-1,631	0,112	NtPRp27 secretory protein
VIT_18s0001g10210	-4,361	-3,984	-4,397	PAB8 (poly(A) binding protein 8)
VIT_03s0088g00810	-0,587	-2,177	-0,494	Pathogenesis-related protein 1 precursor (PRP 1)
VIT_18s0001g06150	0,564	-1,572	-2,539	Phosphate-induced protein 1
VIT_18s0001g06170	0,360	-2,685	-2,232	Phosphate-induced protein 1
ENSRNA049470361	0,000	5,550	4,890	Plant signal recognition particle RNA
ENSRNA049468680	0,000	3,408	2,560	Plant small nucleolar RNA U3
VIT_04s0023g02230	-0,824	-1,552	-0,340	S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase
VIT_09s0002g00640	-1,684	-1,431	0,436	Small heat stress protein class CIII
VIT_04s0008g01530	-0,766	-1,674	-0,977	Small molecular heat shock protein 17.5
VIT_04s0008g01550	-1,211	-2,072	-0,687	Small molecular heat shock protein 17.5
VIT_03s0088g00620	-0,588	-0,998	-2,046	Stress-induced
VIT_09s0002g03460	0,334	1,045	1,674	Taurine dioxygenase
VIT_15s0107g00550	0,590	1,805	1,934	Tetratricopeptide repeat domain male sterility MS5
VIT_07s0005g05720	0,514	1,183	1,914	Tetratricopeptide repeat domain male sterility MS5
VIT_04s0043g00900	-1,844	-2,010	-0,417	Tyrosine decarboxylase
VIT_04s0043g00930	-1,543	-2,028	-0,253	Tyrosine/DOPA decarboxylase 2
VIT_18s0166g00190	-0,273	-1,591	-1,263	U-box domain-containing protein
VIT_05s0049g00800	-0,924	-3,418	-0,536	Unknown protein
VIT_11s0016g02920	0,445	-0,786	-1,943	Unknown protein
VIT_10s0116g01200	-0,226	-1,858	-0,753	WRKY6_1
VIT_11s0052g01260	0,194	-2,315	-2,250	Xyloglucan endotransglucosylase/hydrolase 23
VIT_11s0052g01270	0,757	-1,527	-1,963	Xyloglucan endotransglycosylase 6
VIT_11s0052g01300	0,175	-3,093	-1,920	Xyloglucan endotransglycosylase 6
VIT_01s0026g02540	0,162	0,755	1,801	Zinc finger (C3HC4-type ring finger)
VIT_01s0127g00530	-1,836	-2,137	-1,114	No hit
VIT_03s0097g00210	0,000	7,732	6,611	No hit
VIT_07s0005g05180	-1,524	-0,586	-1,340	No hit
VIT_12s0028g01380	-0,764	-0,432	-1,800	No hit
VIT_13s0073g00590	-1,446	0,157	-1,849	Unknown protein

Supplementary Table 4b

Name	Log2FC(R50%T vs RS50%T)	Description	Pathway
VIT_18s0122g00180	1,733	Calmodulin CML37	Calcium signaling pathway /Plant-pathogen interaction
VIT_01s0146g00150	1,932	BCL-2-associated athanogene 5	Cellular process.Cell growth and death.Cell death
VIT_04s0043g00930	1,775	Tyrosine/DOPA decarboxylase 2	Metabolism.Primary metabolism.Amino acid metabolism.Aromatic amino acid metabolism.Tyrosine metabolism
VIT_03s0088g00570	-1,847	Glutamine synthetase B1 GLB1	Metabolism.Primary metabolism.Amino acid metabolism.Glutamine metabolism.Glutamine biosynthesis
VIT_02s0154g00490	1,825	Heat shock 22 kDa protein mitochondrial	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding. HSP-mediated protein folding
VIT_13s0019g02760	2,401	Heat shock protein 17.6 kDa class I	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding. HSP-mediated protein folding
VIT_13s0019g02770	1,882	Heat shock protein 17.6 kDa class I	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding. HSP-mediated protein folding
VIT_13s0019g02740	1,651	Heat shock protein 17.6 kDa class I	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding. HSP-mediated protein folding
VIT_19s0085g01050	3,670	Heat shock protein 17.6 kDa class I	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding. HSP-mediated protein folding
VIT_13s0019g02840	1,675	Heat shock protein 18.2 kDa class I	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding. HSP-mediated protein folding
VIT_04s0008g01500	2,260	Heat shock protein 17.6 kDa class II	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding. HSP-mediated protein folding
VIT_13s0019g02820	2,987	Heat shock protein 18.2 kDa class I	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding. HSP-mediated protein folding
VIT_13s0019g03090	1,529	Heat shock protein class I (HSP17.8-CI)	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding. HSP-mediated protein folding
VIT_09s0002g00640	1,866	Small heat stress protein class CIII	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding. HSP-mediated protein folding
VIT_10s0003g00260	2,141	DnaJ homolog, subfamily B, member 4	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding. HSP-mediated protein folding.HSP-mediated protein folding co-chaperone
VIT_02s0025g02960	1,844	Naringenin,2-oxoglutarate 3-dioxygenase	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Flavonoid metabolism.Flavonoid biosynthesis
VIT_15s0048g02430	2,079	Naringenin,2-oxoglutarate 3-dioxygenase	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Flavonoid metabolism.Flavonoid biosynthesis
VIT_17s0000g03940	1,979	ferulate 5-hydroxylase	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.phenylpropanoid biosynthesis
VIT_02s0025g00760	2,426	Pinoresinol forming dirigent protein	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.phenylpropanoid biosynthesis
VIT_19s0014g04930	2,845	Germacrene-D synthase	Metabolism.Secondary metabolism.Terpenoid metabolism.Sesquiterpenoid metabolism.Sesquiterpenoid biosynthesis
VIT_07s0129g00340	-1,504	Shoot gravitropism 7	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.GRAS family transcription factor
VIT_16s0100g00720	1,592	Heat shock transcription factor B2A	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.HSF family transcription factor
VIT_03s0091g00160	1,742	NtPRp27 secretory protein	Response to stimulus.Stress response.Biotic stress response
VIT_03s0088g00810	1,682	Pathogenesis-related protein 1 precursor (PRP 1)	Response to stimulus.Stress response.Biotic stress response
ENSRNA049469239	-2,949	5.8S ribosomal RNA	Ribosomal
ENSRNA049469319	-2,833	Eukaryotic small subunit ribosomal RNA	Ribosomal
ENSRNA049469358	-3,625	Eukaryotic small subunit ribosomal RNA	Ribosomal
ENSRNA049466084	-4,703	Eukaryotic small subunit ribosomal RNA	Ribosomal

Name	Log2FC(R50%T vs RS50%T)	Description	Pathway
VIT_09s0002g00550	1,536	Lipase GDSL 1	unknown
VIT_09s0002g00630	2,233	No hit	Unknown
VIT_05s0049g00840	2,006	No hit	Unknown
VIT_05s0049g00660	1,795	No hit	Unknown
VIT_05s0049g00730	1,811	No hit	Unknown
VIT_05s0049g00720	2,505	No hit	Unknown
VIT_05s0049g00780	2,967	No hit	Unknown
VIT_19s0090g01360	2,027	No hit	Unknown
VIT_19s0090g01340	1,785	No hit	Unknown
VIT_05s0049g00800	2,882	Unknown protein	Unknown
VIT_13s0073g00590	-2,007	Unknown protein	Unknown

Supplementary Table 5

Mapman analysis – Heat responsive DEGs

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
1.1.1	Cellular process.Cell growth and death.Cell death	vit_01s0146g00150	Transcript	BCL-2-associated athanogene 5	0,76	-1,24	0,46	2,44
1.1.1	Cellular process.Cell growth and death.Cell death	vit_01s0146g00150	Transcript	BCL-2-associated athanogene 5	0,76	-1,24	0,46	2,44
1.1.2	Cellular process.Cell growth and death.Cell death attenuation	vit_19s0027g00740	Transcript	Inhibitor of apoptosis	-1,26	-1,53	-0,6	-0,98
1.1.3	Cellular process.Cell growth and death.Cell division	vit_17s0000g03290	Transcript	Kinesin motor HIK (HINKEL)	-1,74	-1,47	-1,38	-0,93
1.1.4	Cellular process.Cell growth and death.Cell growth	vit_13s0067g02930	Transcript	Expansin [Vitis labrusca x Vitis vinifera] EXPA8	-1,77	-2,62	-2,36	-2,1
1.2.1.1.1.1	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall biosynthesis.Cell wall glycan monomers generation	vit_05s0020g04510	Transcript	GDP-mannose 3,5-epimerase 1	-1,49	-1,61	-1,66	-1,6
1.2.1.1.1.1	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall biosynthesis.Cell wall glycan monomers generation	vit_14s0030g02180	Transcript	GDP-mannose 3,5-epimerase 1	-1,87	-2,15	-2,06	-1,7
1.2.1.1.1.2	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall biosynthesis.Cellulose biosynthesis	vit_00s1349g00010	Transcript	Cellulose synthase CSLE1	-1,66	-1,58	-1,51	-0,91
1.2.1.1.1.2	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall biosynthesis.Cellulose biosynthesis	vit_00s1213g00010	Transcript	Cellulose synthase CSLE1	-0,9	-1,67	-0,67	0
1.2.1.1.1.2	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall biosynthesis.Cellulose biosynthesis	vit_01s0011g00160	Transcript	Alpha-1,4-glucan-protein synthase	-1,73	-1,33	-1,29	-0,99
1.2.1.1.2.2	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall catabolism.Cellulose catabolism	vit_03s0038g00630	Transcript	Endo-1,4-beta-glucanase	-1,04	-1,63	-1,53	-1,17
1.2.1.1.2.3	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall catabolism.Pectin catabolism	vit_01s0137g00240	Transcript	Pectate lyase	-2,28	-2,65	-2,71	-1,91
1.2.1.1.2.4	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall catabolism.Xylan catabolism	vit_12s0121g00230	Transcript	Beta-D-xylosidase	-1,55	-1,04	-0,91	-0,72
1.2.1.1.3	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall modification	vit_13s0067g02930	Transcript	Expansin [Vitis labrusca x Vitis vinifera] EXPA8	-1,77	-2,62	-2,36	-2,1
1.2.1.1.3.2	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall modification.Pectin modification	vit_01s0127g00400	Transcript	Polygalacturonase GH28	-2,73	-3,01	-2,33	-2,68
1.2.1.1.3.2	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall modification.Pectin modification	vit_13s0047g00230	Transcript	Pectinesterase family	1,48	1,84	2,05	1,84
1.2.1.1.3.2	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall modification.Pectin modification	vit_02s0154g00600	Transcript	Pectinesterase family	-1,57	-1,85	-1,28	-1,03
1.2.1.1.3.2	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall modification.Pectin modification	vit_05s0020g00420	Transcript	Polygalacturonase GH28	-2,97	-4,09	-3,75	-3,15

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
1.2.1.1.3.2	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall modification.Pectin modification	vit_09s0002g00330	Transcript	Pectinesterase PME1	1,53	1,74	1,83	1,17
1.2.1.1.3.2	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall modification.Pectin modification	vit_15s0046g02000	Transcript	Polygalacturonase GH28	-2,13	-1,76	-1,84	-1,7
1.2.1.1.3.4	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall modification.Xyloglucan modification	vit_01s0150g00460	Transcript	Xyloglucan endotransglucosylase/hydrolase precursor	-1,57	-1,29	-1,31	-0,83
1.2.1.1.3.4	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall modification.Xyloglucan modification	vit_05s0062g00250	Transcript	Xyloglucan endotransglucosylase/hydrolase 15	2,09	2,99	3,09	3
1.2.1.1.3.4	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall modification.Xyloglucan modification	vit_11s0052g01270	Transcript	Xyloglucan endotransglycosylase 6	2,87	4,12	1,69	0,83
1.2.1.1.3.4	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall modification.Xyloglucan modification	vit_11s0052g01280	Transcript	Xyloglucan endotransglucosylase/hydrolase 23	0	3,75	0	0
1.2.1.1.3.4	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall modification.Xyloglucan modification	vit_11s0052g01300	Transcript	Xyloglucan endotransglycosylase 6	2,58	2,57	0	0
1.2.1.1.3.4	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall metabolism.Cell wall modification.Xyloglucan modification	vit_12s0134g00160	Transcript	Xyloglucan endotransglycosylase/hydrolase 16	1,79	2,39	2,54	2,3
1.2.1.2	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall structural protein	vit_01s0011g06650	Transcript	fasciclin arabinogalactan-protein (FLA21)	-3,07	-2,97	-1,53	-1,73
1.2.1.2	Cellular process.Cellular component organization and biogenesis.Cell wall organization and biogenesis.Cell wall structural protein	vit_01s0011g01980	Transcript	fasciclin arabinogalactan-protein (FLA21)	3,42	2,84	2,58	2,6
1.2.2	Cellular process.Cellular component organization and biogenesis.Chromosome organization and biogenesis	vit_17s0000g03290	Transcript	Kinesin motor HIK (HINKEL)	-1,74	-1,47	-1,38	-0,93
1.2.2.1	Cellular process.Cellular component organization and biogenesis.Chromosome organization and biogenesis.Chromatin assembly	vit_13s0067g03650	Transcript	Histone H4	-1,82	-1,67	-1,68	-1,08
1.2.2.1	Cellular process.Cellular component organization and biogenesis.Chromosome organization and biogenesis.Chromatin assembly	vit_06s0004g04300	Transcript	Histone H2B	-1,35	-1,4	-1,7	-0,85
1.2.2.1	Cellular process.Cellular component organization and biogenesis.Chromosome organization and biogenesis.Chromatin assembly	vit_13s0019g00760	Transcript	Histone H4	-1,53	-1,45	-1,62	-1,04
1.2.2.1	Cellular process.Cellular component organization and biogenesis.Chromosome organization and biogenesis.Chromatin assembly	vit_13s0064g01340	Transcript	Histone H3	-1,65	-1,45	-1,28	-0,72
1.2.2.1	Cellular process.Cellular component organization and biogenesis.Chromosome organization and biogenesis.Chromatin assembly	vit_14s0060g02360	Transcript	Histone H2A.4 HTA12	-1,75	-2,21	-1,69	-1,31
1.2.2.1	Cellular process.Cellular component organization and biogenesis.Chromosome organization and biogenesis.Chromatin assembly	vit_14s0081g00500	Transcript	Histone H1	-1,5	-1,38	-1,89	-1,41
1.2.3.2	Cellular process.Cellular component organization and biogenesis.Cytoskeleton organization and biogenesis.Actin organization and biogenesis	vit_01s0011g02860	Transcript	CHUP1 (chloroplast unusual positioning 1)	-2	-2,4	-1,75	-2,11

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
1.2.3.3	Cellular process.Cellular component organization and biogenesis.Cytoskeleton organization and biogenesis.Microtubule organization and biogenesis	vit_02s0025g03540	Transcript	Tubulin beta-6 chain	1,13	1,27	1,78	0,84
1.2.3.3.1	Cellular process.Cellular component organization and biogenesis.Cytoskeleton organization and biogenesis.Microtubule organization and biogenesis.Microtubule-driven movement	vit_05s0029g00400	Transcript	Kinesin PAKRP1L	-1,6	-1,38	-1,16	-0,83
1.2.3.3.1	Cellular process.Cellular component organization and biogenesis.Cytoskeleton organization and biogenesis.Microtubule organization and biogenesis.Microtubule-driven movement	vit_19s0014g03710	Transcript	dynein light chain	-2,76	-5,11	-5,41	-5,18
1.2.3.3.1	Cellular process.Cellular component organization and biogenesis.Cytoskeleton organization and biogenesis.Microtubule organization and biogenesis.Microtubule-driven movement	vit_14s0128g00460	Transcript	Kinesin motor protein	-1,8	-1,45	-1,31	-0,86
1.2.3.3.1	Cellular process.Cellular component organization and biogenesis.Cytoskeleton organization and biogenesis.Microtubule organization and biogenesis.Microtubule-driven movement	vit_19s0090g01600	Transcript	Kinesin motor protein	-1,67	-1,41	-1	-1,03
1.2.5	Cellular process.Cellular component organization and biogenesis.Oil body organization and biogenesis	vit_17s0000g09000	Transcript	Oleosin OLE-2	1,54	1,72	1,44	1,42
1.2.6.4	Cellular process.Cellular component organization and biogenesis.Organelle organization and biogenesis.Plastid organization and biogenesis	vit_06s0004g04700	Transcript	Outer envelope protein 16	-2,02	-1,96	-2,61	-1,91
1.2.6.4	Cellular process.Cellular component organization and biogenesis.Organelle organization and biogenesis.Plastid organization and biogenesis	vit_14s0108g00590	Transcript	FtsH protease	2,98	0,65	0,63	1,32
1.3.1	Cellular process.Cellular homeostasis.Cell redox homeostasis	vit_00s0532g00030	Transcript	Thioredoxin H	1,73	1,19	1,52	1,32
1.3.1	Cellular process.Cellular homeostasis.Cell redox homeostasis	vit_08s0007g07620	Transcript	Thioredoxin 2	-1,4	-1,89	-1,35	-1,18
1.3.1	Cellular process.Cellular homeostasis.Cell redox homeostasis	vit_17s0000g06370	Transcript	Thioredoxin 2	-1,04	-1,15	-1,32	-1,51
1.3.1	Cellular process.Cellular homeostasis.Cell redox homeostasis	vit_18s0001g00820	Transcript	Thioredoxin-like protein CDSP32	1,43	1,24	1,71	1,44
1.3.2.1	Cellular process.Cellular homeostasis.Heavy metal ion homeostasis.Copper homeostasis	vit_12s0142g00330	Transcript	Copper-transporting ATPase PAA1	-2,86	-2,79	-2,71	-2,73
2	Development	vit_04s0044g01260	Transcript	SEU3B protein	1,46	1,55	1,78	1,24
2	Development	vit_08s0058g01110	Transcript	Ovate family protein 4 OFP4	0,95	1,18	1,69	0,01
2	Development	vit_12s0028g03570	Transcript	SPA3 (SPA1-related 3)	-1,6	-1,91	-2,02	-2,31
2	Development	vit_14s0066g01220	Transcript	ATMYB66/WER/WER1 (WEREWOLF 1)	-1,37	-1,42	-1,67	-0,86
2.2	Development.Reproductive development	vit_01s0011g03520	Transcript	Constans-like 16	-1,44	-2,07	-1,57	-1,43
2.2	Development.Reproductive development	vit_14s0083g00640	Transcript	Constans 2 (COL2)	-2,24	-2,69	-3,01	-3,58
2.2.1	Development.Reproductive development.Flowering	vit_01s0146g00360	Transcript	Constans-like 14	1,71	0,8	1,79	1,13
2.2.1	Development.Reproductive development.Flowering	vit_14s0068g01380	Transcript	Constans-like 14	2,88	3,26	3,25	3,28
2.2.1	Development.Reproductive development.Flowering	vit_18s0157g00020	Transcript	GIGANTEA protein	4,45	4,34	4,11	3,84
3.1.1	Diverse functions.Gene family with diverse functions.AAA-type ATPase domain family	vit_14s0066g02040	Transcript	Chaperone BCS1 mitochondrial	-1,54	-1,2	-0,92	-0,86
3.1.1	Diverse functions.Gene family with diverse functions.AAA-type ATPase domain family	vit_14s0066g02060	Transcript	AAA-type ATPase	-1,02	-1,53	-1,68	-0,52
3.1.2	Diverse functions.Gene family with diverse functions.Ankyrin domain family	vit_05s0029g01540	Transcript	Ankyrin repeat	-1,41	-1,77	-1,51	-1,21
3.1.2	Diverse functions.Gene family with diverse functions.Ankyrin domain family	vit_00s0228g00070	Transcript	Ankyrin repeat	1,28	1,45	1,34	1,64

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
3.1.2	Diverse functions.Gene family with diverse functions.Ankyrin domain family	vit_00s0411g00050	Transcript	Ankyrin repeat	1,44	1,2	1,64	1,51
3.1.2	Diverse functions.Gene family with diverse functions.Ankyrin domain family	vit_00s0901g00010	Transcript	Ankyrin repeat	1,86	2,32	1,05	1,51
3.1.2	Diverse functions.Gene family with diverse functions.Ankyrin domain family	vit_13s0106g00080	Transcript	Ankyrin repeat	1,24	1,11	1,63	2,07
3.1.2	Diverse functions.Gene family with diverse functions.Ankyrin domain family	vit_05s0029g01410	Transcript	Ankyrin repeat	-0,86	-1,39	-1,17	-1,56
3.1.2	Diverse functions.Gene family with diverse functions.Ankyrin domain family	vit_14s0081g00360	Transcript	Ankyrin repeat	3,15	2,83	2,33	2,57
3.1.2	Diverse functions.Gene family with diverse functions.Ankyrin domain family	vit_04s0008g03840	Transcript	Ankyrin repeat	-1,7	-2,17	-2,42	-1,86
3.1.2	Diverse functions.Gene family with diverse functions.Ankyrin domain family	vit_08s0007g00200	Transcript	Ankyrin repeat	2,44	2,24	2,25	1,95
3.1.2	Diverse functions.Gene family with diverse functions.Ankyrin domain family	vit_14s0081g00370	Transcript	Ankyrin repeat	4,21	3,08	2,82	2,63
3.1.4	Diverse functions.Gene family with diverse functions.GASA family	vit_08s0007g05860	Transcript	GASA like	-1,95	-1,53	-1,01	-2,06
3.1.4	Diverse functions.Gene family with diverse functions.GASA family	vit_14s0066g01790	Transcript	GASA like	0,98	2,03	1,55	2,01
3.1.4	Diverse functions.Gene family with diverse functions.GASA family	vit_17s0000g06210	Transcript	GASA like	-2,1	-1,36	-0,56	-0,81
3.1.4	Diverse functions.Gene family with diverse functions.GASA family	vit_18s0001g09460	Transcript	GASA5	2,63	2,46	1,48	1,84
3.1.5	Diverse functions.Gene family with diverse functions.NBS-LRR superfamily	vit_05s0020g03810	Transcript	Disease resistance protein (NBS-LRR class)	1,03	1,1	1,76	1,09
3.1.5	Diverse functions.Gene family with diverse functions.NBS-LRR superfamily	vit_18s0072g01090	Transcript	TIR-NBS-LRR type R protein 7	-1,8	-1,71	-2,21	-1,96
3.1.5	Diverse functions.Gene family with diverse functions.NBS-LRR superfamily	vit_03s0038g01770	Transcript	Disease resistance protein (CC-NBS-LRR class)	-1,32	-1,63	-1,37	-1,26
3.1.5	Diverse functions.Gene family with diverse functions.NBS-LRR superfamily	vit_02s0025g01400	Transcript	Leucine-rich repeat family protein	1,57	1,39	1,3	0,88
3.1.5	Diverse functions.Gene family with diverse functions.NBS-LRR superfamily	vit_11s0118g00080	Transcript	Disease resistance protein	1,24	1,05	1,12	1,82
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_17s0000g06470	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,23	1,54	1,04	1,68
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_08s0007g03150	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,18	1,15	1,54	1,18
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_14s0066g00860	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,48	1,68	1,69	1,45
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_18s0122g00840	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,33	1,18	1,69	0,98
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_00s2379g00010	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,11	1,75	1,53	1,34
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_07s0031g01340	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,37	1,46	1,61	1,39
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_01s0011g01970	Transcript	Pentatricopeptide (PPR) repeat-containing protein	2,51	2,27	2,56	2,36
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_05s0049g02300	Transcript	Pentatricopeptide (PPR) repeat-containing protein	2,08	2,1	2,14	1,85
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_05s0049g01270	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,58	1,53	1,29	1,22
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_17s0000g07830	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,42	1,87	1,83	1,37
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_14s0030g02210	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,97	1,06	0,84	1,04
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_14s0066g02510	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,6	2,92	1,53	1,54
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_07s0005g00570	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,59	2,02	1,94	1,15
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_14s0060g00880	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,31	1,7	1,28	0,93

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_05s0020g03570	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,59	1,6	1,87	1,24
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_18s0001g04590	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,52	1,78	1,85	1,5
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_16s0100g00190	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,2	1,61	1,73	0,89
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_08s0032g00740	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,28	2,04	1,33	0,57
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_12s0057g00970	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,74	1,17	1,79	1,17
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_17s0000g06480	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,64	1,89	1,8	1,08
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_01s0011g00660	Transcript	Pentatricopeptide (PPR) repeat-containing protein	2,02	1,88	2,54	1,87
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_12s0028g00060	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,75	1,24	1,51	1,14
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_00s0193g00030	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,61	1,4	1,41	1
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_06s0009g00650	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,39	1,8	1,66	0,52
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_16s0050g01500	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,55	1,71	1,75	1,22
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_03s0038g01320	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,26	1,08	1,79	1,1
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_09s0002g02370	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,65	1,53	1,2	0,6
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_01s0026g01440	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,32	1,64	1,67	1,19
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_08s0007g05770	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,37	1,65	1,87	1,13
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_10s0003g00970	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,61	1,2	1,2	0,96
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_08s0040g02990	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,19	1,04	1,54	1,34
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_07s0005g04530	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,54	1,64	1,53	1,2
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_09s0002g06490	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,08	1,58	1,67	1,39
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_01s0011g05040	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,32	1,71	1,61	0,86
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_13s0047g00070	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,17	2,19	0,76	0,5
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_08s0058g00830	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,6	1,57	1,66	1,35
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_00s0184g00060	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,24	1,97	1,37	0,8

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_00s0207g00190	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,43	1,21	1,64	0,8
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_10s0042g00130	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,61	1,81	1,59	1,23
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_18s0001g15340	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,51	1,91	0,35	1,05
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_10s0116g00240	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,51	0,9	1,29	1,07
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_19s0085g00560	Transcript	Pentatricopeptide (PPR) repeat-containing protein	0,62	1,44	1,69	1,68
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_17s0000g06770	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,33	1,31	1,54	0,79
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_18s0001g10530	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,18	1,38	1,53	1,11
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_18s0001g11650	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,26	1,7	2,02	1,8
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_14s0128g00700	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,15	1,6	1,4	1,21
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_18s0041g01110	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,6	1,56	1,33	0,69
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_14s0060g00270	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,43	1,37	1,52	0,8
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_08s0040g02320	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,38	1,54	1,38	1,1
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_13s0073g00080	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,3	1,54	1,74	1,59
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_08s0058g01320	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,12	1,15	1,54	0,83
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_10s0003g02630	Transcript	Pentatricopeptide (PPR) repeat-containing protein	0,99	1,55	1,55	0,81
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_12s0059g00790	Transcript	Pentatricopeptide (PPR) repeat-containing protein	0,98	1,51	1,69	1,32
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_11s0016g05220	Transcript	Pentatricopeptide (PPR) repeat-containing protein	2,03	1,64	2,34	1,41
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_07s0005g01900	Transcript	Pentatricopeptide (PPR) repeat-containing protein	0,74	1,44	1,75	1,22
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_12s0059g00900	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,35	1,56	1,23	1,38
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_09s0002g02250	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,42	1,44	1,58	0,96
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_11s0016g04660	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,32	1,56	1,64	1,05
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_02s0012g02540	Transcript	Pentatricopeptide (PPR) repeat-containing protein	-2,1	-2,82	-2,7	-2,94
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_10s0092g00130	Transcript	Pentatricopeptide (PPR) repeat-containing protein	2,96	2,97	2,53	1,98

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_00s0184g00180	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,54	1,27	1,1	1,21
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_01s0026g01750	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,3	1,5	1,66	0,98
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_00s0941g00010	Transcript	Pentatricopeptide (PPR) repeat-containing	1,51	1,48	1,11	0,71
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_02s0087g00080	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,04	1,4	1,69	1,24
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_05s0020g03850	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,47	1,63	1,84	1,12
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_08s0007g04970	Transcript	Pentatricopeptide (PPR) repeat-containing	1,34	1,58	1,36	1
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_14s0108g00600	Transcript	Pentatricopeptide (PPR) repeat-containing	1,42	1,4	1,2	1,68
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_19s0014g01100	Transcript	Fertility restorer homologue A,PPR	1,17	1,69	1,15	0,51
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_18s0001g00640	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,95	1,58	1,96	1,21
3.1.6	Diverse functions.Gene family with diverse functions.Pentatricopeptide domain family	vit_18s0001g05930	Transcript	Pentatricopeptide (PPR) repeat-containing protein	1,08	1,3	1,67	1,21
4	Metabolism	vit_02s0012g00760	Transcript	Haloacid dehalogenase hydrolase	-1,29	-1,52	-1,89	-1,68
4	Metabolism	vit_05s0020g03190	Transcript	Haloacid dehalogenase hydrolase	1,28	1,72	1,83	2,11
4	Metabolism	vit_08s0007g00540	Transcript	Haloacid dehalogenase hydrolase	-1,99	-2,05	-1,77	-1,14
4	Metabolism	vit_08s0007g05350	Transcript	Haloacid dehalogenase hydrolase	-1,17	-1,6	-1,54	-1,24
4	Metabolism	vit_12s0028g03470	Transcript	Haloacid dehalogenase hydrolase	1,98	2,04	1,63	1,67
4	Metabolism	vit_18s0041g00350	Transcript	Dienelactone hydrolase	2,17	1,61	1,98	1,5
4.1.4	Metabolism.Cellular metabolism.Esterase activity	vit_03s0063g00800	Transcript	Carboxyesterase 12; CXE12	5,1	5,49	5,04	4,9
4.1.4	Metabolism.Cellular metabolism.Esterase activity	vit_13s0084g00130	Transcript	CXE carboxylesterase	-0,72	-1,22	-1,61	-1,35
4.1.5.1	Metabolism.Cellular metabolism.Iron metabolism.Iron assimilation	vit_16s0050g00980	Transcript	ferric reduction oxidase 2	1,68	1,57	1,91	2,2
4.1.5.1	Metabolism.Cellular metabolism.Iron metabolism.Iron assimilation	vit_12s0035g02150	Transcript	ferric reduction oxidase 7 FRO7	2,52	1,92	2,45	1,69
4.1.6	Metabolism.Cellular metabolism.Nitrogen metabolism	vit_17s0000g01910	Transcript	Glutamine synthetase cytosolic isozyme 1	1,66	1,71	1,63	1,62
4.1.6.2	Metabolism.Cellular metabolism.Nitrogen metabolism.Nitrogen assimilation	vit_03s0063g00370	Transcript	Nitrite reductase	1,5	0,47	1,87	-0,17
4.1.7	Metabolism.Cellular metabolism.One-carbon metabolism	vit_14s0066g01210	Transcript	Carbonic anhydrase, chloroplast precursor	-0,99	-2,05	-0,03	-2,12
4.1.8	Metabolism.Cellular metabolism.Oxidation reduction	vit_07s0031g03150	Transcript	S-glutathione dehydrogenase/class III alcohol dehydrogenase	-1,56	-1,62	-1,26	-1,3
4.1.8	Metabolism.Cellular metabolism.Oxidation reduction	vit_08s0007g07520	Transcript	3-oxoacyl-[acyl-carrier-protein] reductase, chloroplast	1,37	1,54	0,63	0,44
4.1.8	Metabolism.Cellular metabolism.Oxidation reduction	vit_08s0007g07530	Transcript	3-oxoacyl-[acyl-carrier-protein] reductase, chloroplast	0,97	1,37	1,93	1,6
4.1.8.1	Metabolism.Cellular metabolism.Oxidation reduction.2OG-Fe(II) oxygenase superfamily	vit_09s0002g08090	Transcript	Oxidoreductase, 2OG-Fe(II) oxygenase	0,93	1,56	1,49	1,7
4.1.8.2	Metabolism.Cellular metabolism.Oxidation reduction.Alcohol dehydrogenase superfamily	vit_04s0044g01110	Transcript	Alcohol dehydrogenase 6	-2,15	-2,26	-2	-1,52

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
4.1.8.2	Metabolism.Cellular metabolism.Oxidation reduction.Alcohol dehydrogenase superfamily	vit_11s0016g03890	Transcript	Short-chain dehydrogenase/reductase (SDR)	1,47	1,39	1,72	1,52
4.1.8.4	Metabolism.Cellular metabolism.Oxidation reduction.Cytochrome P450 oxidoreductase	vit_01s0137g00410	Transcript	CYP86A2	1,47	1,52	2,13	1,58
4.1.8.4	Metabolism.Cellular metabolism.Oxidation reduction.Cytochrome P450 oxidoreductase	vit_01s0137g00510	Transcript	CYP71B10	0,5	0,44	1,82	0,57
4.1.8.4	Metabolism.Cellular metabolism.Oxidation reduction.Cytochrome P450 oxidoreductase	vit_07s0031g01570	Transcript	CYP78A11	1,46	1,92	1,22	1,08
4.1.8.4	Metabolism.Cellular metabolism.Oxidation reduction.Cytochrome P450 oxidoreductase	vit_07s0031g01680	Transcript	CYP86A1	0,45	1,35	1,7	1,64
4.1.8.4	Metabolism.Cellular metabolism.Oxidation reduction.Cytochrome P450 oxidoreductase	vit_13s0074g00390	Transcript	CYP77A2	-1,96	-1,68	-0,62	-1,38
4.1.8.4	Metabolism.Cellular metabolism.Oxidation reduction.Cytochrome P450 oxidoreductase	vit_16s0039g00880	Transcript	CYP89H3	-1,34	-1,74	-1,6	-1,53
4.1.8.4	Metabolism.Cellular metabolism.Oxidation reduction.Cytochrome P450 oxidoreductase	vit_18s0001g09520	Transcript	CYP81B2v2	-1,79	-1,73	-1,08	-2,24
4.1.8.4	Metabolism.Cellular metabolism.Oxidation reduction.Cytochrome P450 oxidoreductase	vit_18s0001g09510	Transcript	CYP81B2v1	2,07	1,16	2,21	0,79
4.1.8.4	Metabolism.Cellular metabolism.Oxidation reduction.Cytochrome P450 oxidoreductase	vit_18s0001g09650	Transcript	CYP81E1	1,22	1,49	1,47	1,57
4.1.8.4	Metabolism.Cellular metabolism.Oxidation reduction.Cytochrome P450 oxidoreductase	vit_19s0015g02500	Transcript	CYP72A1	-1,18	-1,34	-1,03	-1,64
4.1.8.5	Metabolism.Cellular metabolism.Oxidation reduction.Flavin-containing monooxygenase	vit_17s0000g06780	Transcript	Dimethylaniline monooxygenase	1,91	2,02	1,65	1,68
4.1.8.5	Metabolism.Cellular metabolism.Oxidation reduction.Flavin-containing monooxygenase	vit_03s0038g03140	Transcript	Dimethylaniline monooxygenase, N-oxide-forming	2,19	1,92	1,13	0,78
4.1.8.5	Metabolism.Cellular metabolism.Oxidation reduction.Flavin-containing monooxygenase	vit_03s0038g03160	Transcript	flavin-containing monooxygenase 1	1,31	1,29	1,88	1,23
4.1.8.5	Metabolism.Cellular metabolism.Oxidation reduction.Flavin-containing monooxygenase	vit_03s0038g03190	Transcript	flavin-containing monooxygenase 3	3,15	2,58	3,27	2,83
4.1.9	Metabolism.Cellular metabolism.Phosphate metabolism	vit_01s0011g06290	Transcript	Purple acid phosphatase 3 ATPAP3/PAP3	-0,87	-1,2	-1,82	-0,34
4.1.9	Metabolism.Cellular metabolism.Phosphate metabolism	vit_05s0020g00880	Transcript	5-nucleotidase	1,27	1,45	1,51	1,53
4.1.10.1	Metabolism.Cellular metabolism.Phytoalexin metabolism.Phytoalexin biosynthesis	vit_03s0091g00040	Transcript	Limonoid UDP-glucosyltransferase	1,56	1,7	1,86	1,16
4.1.12	Metabolism.Cellular metabolism.Sulfur metabolism	vit_04s0044g01480	Transcript	3'(2'),5'-bisphosphate nucleotidase	-1,66	-1,48	-1,57	-1
4.1.12.1	Metabolism.Cellular metabolism.Sulfur metabolism.Sulfate assimilation	vit_07s0005g02020	Transcript	Sulfate adenylyltransferase	1,08	1,04	1,23	1,73
4.2.1.1	Metabolism.Primary metabolism.Amino acid metabolism.Alanine and aspartate metabolism	vit_06s0004g07820	Transcript	Aspartate-glutamate racemase	1,32	2,03	1,77	1,36
4.2.1.2	Metabolism.Primary metabolism.Amino acid metabolism.Alanine metabolism	vit_00s0225g00130	Transcript	Alanine transaminase.	-1,66	-2,04	-1,52	-1,59
4.2.1.3	Metabolism.Primary metabolism.Amino acid metabolism.Amino acid biosynthesis	vit_08s0056g01530	Transcript	Anthranilate phosphoribosyltransferase	-1,51	-1,56	-1,27	-1,54
4.2.1.3	Metabolism.Primary metabolism.Amino acid metabolism.Amino acid biosynthesis	vit_07s0104g00610	Transcript	Glutamine synthetase	-1,24	-1,82	0,45	-1,48
4.2.1.3	Metabolism.Primary metabolism.Amino acid metabolism.Amino acid biosynthesis	vit_17s0000g01910	Transcript	Glutamine synthetase cytosolic isozyme 1	1,66	1,71	1,63	1,62

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
4.2.1.4	Metabolism.Primary metabolism.Amino acid metabolism.Amino acid catabolism	vit_00s0480g00030	Transcript	Polyphenol oxidase	-1,53	-1,67	-1,23	-1,19
4.2.1.4	Metabolism.Primary metabolism.Amino acid metabolism.Amino acid catabolism	vit_04s0079g00600	Transcript	Glutamate decarboxylase 1	-1,63	-1,38	-1,18	-1,09
4.2.1.4	Metabolism.Primary metabolism.Amino acid metabolism.Amino acid catabolism	vit_04s0043g00900	Transcript	Tyrosine decarboxylase	-1,29	-2,59	-2,62	-1,47
4.2.1.4	Metabolism.Primary metabolism.Amino acid metabolism.Amino acid catabolism	vit_12s0028g00710	Transcript	4-hydroxyphenylpyruvate dioxygenase	2,48	1,85	1,92	1,34
4.2.1.4	Metabolism.Primary metabolism.Amino acid metabolism.Amino acid catabolism	vit_14s0066g01240	Transcript	L-aspartate oxidase	-1,65	-1,46	-1,28	-0,97
4.2.1.4	Metabolism.Primary metabolism.Amino acid metabolism.Amino acid catabolism	vit_17s0000g02140	Transcript	3-hydroxyisobutyrate dehydrogenase	-1,88	-1,67	-1,31	-1,59
4.2.1.6.2	Metabolism.Primary metabolism.Amino acid metabolism.Aromatic amino acid metabolism.Phenylalanine metabolism	vit_00s0225g00170	Transcript	Peroxidase	1,82	2,07	1,36	1,39
4.2.1.6.2	Metabolism.Primary metabolism.Amino acid metabolism.Aromatic amino acid metabolism.Phenylalanine metabolism	vit_09s0002g04460	Transcript	Peroxidase 48 (Atperox P48)	1,65	2,77	1,97	1,9
4.2.1.6.2	Metabolism.Primary metabolism.Amino acid metabolism.Aromatic amino acid metabolism.Phenylalanine metabolism	vit_12s0028g03210	Transcript	Tyrosine aminotransferase	1,57	1,34	1,6	1,9
4.2.1.6.4	Metabolism.Primary metabolism.Amino acid metabolism.Aromatic amino acid metabolism.Tyrosine metabolism	vit_00s0480g00040	Transcript	Polyphenol oxidase II, chloroplast precursor	-1,39	-1,56	-0,97	-1,28
4.2.1.6.4	Metabolism.Primary metabolism.Amino acid metabolism.Aromatic amino acid metabolism.Tyrosine metabolism	vit_04s0043g00930	Transcript	Tyrosine/DOPA decarboxylase 2	-1,71	-2,36	-2,98	-1,45
4.2.1.6.4	Metabolism.Primary metabolism.Amino acid metabolism.Aromatic amino acid metabolism.Tyrosine metabolism	vit_12s0028g03210	Transcript	Tyrosine aminotransferase	1,57	1,34	1,6	1,9
4.2.1.6.4.2	Metabolism.Primary metabolism.Amino acid metabolism.Aromatic amino acid metabolism.Tyrosine metabolism.Tyrosine catabolism	vit_00s0480g00030	Transcript	Polyphenol oxidase	-1,53	-1,67	-1,23	-1,19
4.2.1.6.4.2	Metabolism.Primary metabolism.Amino acid metabolism.Aromatic amino acid metabolism.Tyrosine metabolism.Tyrosine catabolism	vit_12s0028g00710	Transcript	4-hydroxyphenylpyruvate dioxygenase	2,48	1,85	1,92	1,34
4.2.1.8.1	Metabolism.Primary metabolism.Amino acid metabolism.Aspartate metabolism.Aspartate catabolism	vit_14s0066g01240	Transcript	L-aspartate oxidase	-1,65	-1,46	-1,28	-0,97
4.2.1.9.1	Metabolism.Primary metabolism.Amino acid metabolism.Beta-Alanine metabolism.Beta-Alanine biosynthesis	vit_04s0079g00600	Transcript	Glutamate decarboxylase 1	-1,63	-1,38	-1,18	-1,09
4.2.1.13.2	Metabolism.Primary metabolism.Amino acid metabolism.Glutamate metabolism.Glutamate catabolism	vit_04s0079g00600	Transcript	Glutamate decarboxylase 1	-1,63	-1,38	-1,18	-1,09
4.2.1.14	Metabolism.Primary metabolism.Amino acid metabolism.Glutamine metabolism	vit_06s0004g00940	Transcript	Carbamoyl-phosphate synthase, large subunit	1,96	1,84	1,9	1,87
4.2.1.14.1	Metabolism.Primary metabolism.Amino acid metabolism.Glutamine metabolism.Glutamine biosynthesis	vit_03s0088g00570	Transcript	Glutamine synthetase B1 GLB1	0	0	2,13	0
4.2.1.14.1	Metabolism.Primary metabolism.Amino acid metabolism.Glutamine metabolism.Glutamine biosynthesis	vit_07s0104g00610	Transcript	Glutamine synthetase	-1,24	-1,82	0,45	-1,48
4.2.1.14.1	Metabolism.Primary metabolism.Amino acid metabolism.Glutamine metabolism.Glutamine biosynthesis	vit_17s0000g01910	Transcript	Glutamine synthetase cytosolic isozyme 1	1,66	1,71	1,63	1,62
4.2.1.16	Metabolism.Primary metabolism.Amino acid metabolism.Glycine, serine, and threonine metabolism	vit_06s0009g03740	Transcript	Serine-glyoxylate aminotransferase	-1,64	-2,47	-1,91	-2,47
4.2.1.19	Metabolism.Primary metabolism.Amino acid metabolism.Methionine metabolism	vit_11s0037g00950	Transcript	S-adenosylmethionine decarboxylase proenzyme	-2,94	-4,13	-3,01	-3,89

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
4.2.1.19	Metabolism.Primary metabolism.Amino acid metabolism.Methionine metabolism	vit_12s0028g03210	Transcript	Tyrosine aminotransferase	1,57	1,34	1,6	1,9
4.2.1.24.2	Metabolism.Primary metabolism.Amino acid metabolism.Valine, leucine, and isoleucine metabolism.Valine, leucine, and isoleucine catabolism	vit_03s0132g00210	Transcript	Methylmalonate semi-aldehyde dehydrogenase	1,24	1,39	1,54	1,52
4.2.1.24.2	Metabolism.Primary metabolism.Amino acid metabolism.Valine, leucine, and isoleucine metabolism.Valine, leucine, and isoleucine catabolism	vit_17s0000g02140	Transcript	3-hydroxyisobutyrate dehydrogenase	-1,88	-1,67	-1,31	-1,59
4.2.2.1.1	Metabolism.Primary metabolism.Carbohydrate metabolism.Carbohydrate metabolism enzyme inhibitor.Invertase/pectin methylesterase inhibitor family	vit_16s0022g00840	Transcript	Invertase/pectin methylesterase inhibitor	5,38	3,63	5,9	2,9
4.2.2.3	Metabolism.Primary metabolism.Carbohydrate metabolism.Glycerol-3-P shuttle	vit_14s0219g00280	Transcript	Glycerol-3-phosphate dehydrogenase (NAD+)	-0,96	-1,79	-1,18	-0,9
4.2.2.4	Metabolism.Primary metabolism.Carbohydrate metabolism.Glycolysis and gluconeogenesis	vit_02s0025g00180	Transcript	Bisphosphoglycerate mutase	-1,36	-1,76	-1,68	-1,86
4.2.2.4	Metabolism.Primary metabolism.Carbohydrate metabolism.Glycolysis and gluconeogenesis	vit_18s0001g05060	Transcript	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	1,65	1,44	1,46	1,38
4.2.2.4	Metabolism.Primary metabolism.Carbohydrate metabolism.Glycolysis and gluconeogenesis	vit_09s0002g03390	Transcript	Hexokinase	2,64	2,38	2,5	1,93
4.2.2.4.1	Metabolism.Primary metabolism.Carbohydrate metabolism.Glycolysis and gluconeogenesis.Gluconeogenesis	vit_08s0007g01570	Transcript	fructose 1,6-bisphosphatase	-1,81	-2,21	-1,79	-2,16
4.2.2.4.2	Metabolism.Primary metabolism.Carbohydrate metabolism.Glycolysis and gluconeogenesis.Glycolysis	vit_06s0009g00680	Transcript	Pyridine nucleotide-disulphide oxidoreductase	1,38	0,79	1,64	1,08
4.2.2.4.2	Metabolism.Primary metabolism.Carbohydrate metabolism.Glycolysis and gluconeogenesis.Glycolysis	vit_11s0037g00070	Transcript	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	-1,6	-2,19	-1,71	-2,04
4.2.2.5	Metabolism.Primary metabolism.Carbohydrate metabolism.Glycosyl transference	vit_07s0005g01980	Transcript	Glycosyl transferase family 8 protein	8,29	7,68	5,7	4,94
4.2.2.5	Metabolism.Primary metabolism.Carbohydrate metabolism.Glycosyl transference	vit_04s0023g02510	Transcript	Glycosyl transferase family 1 protein	1,91	2,45	2,56	1,82
4.2.2.5	Metabolism.Primary metabolism.Carbohydrate metabolism.Glycosyl transference	vit_16s0050g01610	Transcript	UDP-glycosyltransferase 88A4	3,07	4,08	3,77	2,22
4.2.2.6	Metabolism.Primary metabolism.Carbohydrate metabolism.Monosaccharide metabolism	vit_08s0007g07480	Transcript	Aldose 1-epimerase	3,42	3,35	3,71	3,2
4.2.2.6.4	Metabolism.Primary metabolism.Carbohydrate metabolism.Monosaccharide metabolism.Galactose metabolism	vit_14s0060g00810	Transcript	Galactinol synthase	1,74	1,1	0,48	0,95
4.2.2.6.4	Metabolism.Primary metabolism.Carbohydrate metabolism.Monosaccharide metabolism.Galactose metabolism	vit_14s0060g00790	Transcript	Galactinol synthase	2,15	1,15	0,46	1,31
4.2.2.6.4	Metabolism.Primary metabolism.Carbohydrate metabolism.Monosaccharide metabolism.Galactose metabolism	vit_07s0005g01970	Transcript	Galactinol synthase	8,15	5,32	5,15	5,11
4.2.2.6.4	Metabolism.Primary metabolism.Carbohydrate metabolism.Monosaccharide metabolism.Galactose metabolism	vit_10s0071g01120	Transcript	Alpha-galactosidase	1,02	1,26	1,84	0,73
4.2.2.6.4	Metabolism.Primary metabolism.Carbohydrate metabolism.Monosaccharide metabolism.Galactose metabolism	vit_11s0016g05770	Transcript	Alkaline alpha galactosidase 2	1,74	1,39	1,39	1,16
4.2.2.6.5	Metabolism.Primary metabolism.Carbohydrate metabolism.Monosaccharide metabolism.Inositol phosphate metabolism	vit_07s0031g00920	Transcript	Inositol-3-phosphate synthase	-1,33	-1,96	-1,87	-2,22
4.2.2.6.6.1	Metabolism.Primary metabolism.Carbohydrate metabolism.Monosaccharide metabolism.Monosaccharide catabolism.Pentose-phosphate shunt	vit_02s0025g00900	Transcript	6-phosphogluconate dehydrogenase	1,46	1,22	1,82	0,97
4.2.2.6.6.1	Metabolism.Primary metabolism.Carbohydrate metabolism.Monosaccharide metabolism.Monosaccharide catabolism.Pentose-phosphate shunt	vit_12s0057g01030	Transcript	Glucose-6-phosphate 1-dehydrogenase 2, chloroplast precursor	1,34	1,73	0,98	1,23

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
4.2.2.6.7	Metabolism.Primary metabolism.Carbohydrate metabolism.Monosaccharide metabolism.Nucleotide sugar metabolism	vit_03s0038g04570	Transcript	ADP-glucose pyrophosphorylase large subunit 1	2,12	1,63	1,59	1,33
4.2.2.6.8	Metabolism.Primary metabolism.Carbohydrate metabolism.Monosaccharide metabolism.Pentose glucuronate interconversion	vit_03s0063g00050	Transcript	UDP-glucuronosyl/UDP-glucosyltransferase	-1,29	-1,3	-1,52	-1,61
4.2.2.6.8	Metabolism.Primary metabolism.Carbohydrate metabolism.Monosaccharide metabolism.Pentose glucuronate interconversion	vit_17s0000g04750	Transcript	UDP-glycosyltransferase 89B2	-1,23	-0,98	-1,52	-1,78
4.2.2.6.8	Metabolism.Primary metabolism.Carbohydrate metabolism.Monosaccharide metabolism.Pentose glucuronate interconversion	vit_17s0000g08920	Transcript	Ribitol dehydrogenase	-1,42	-1,74	-1,57	-1,24
4.2.2.7.1.1	Metabolism.Primary metabolism.Carbohydrate metabolism.Oligosaccharide metabolism.Glycan metabolism.Glycan catabolism	vit_08s0007g08310	Transcript	Alkaline alpha galactosidase	1,55	1,36	1,49	1
4.2.2.7.1.1	Metabolism.Primary metabolism.Carbohydrate metabolism.Oligosaccharide metabolism.Glycan metabolism.Glycan catabolism	vit_16s0022g02170	Transcript	Alpha-L-fucosidase	-1,2	-1,86	-0,57	-1,91
4.2.2.7.2.1	Metabolism.Primary metabolism.Carbohydrate metabolism.Oligosaccharide metabolism.N-Glycan metabolism.N-Glycan biosynthesis	vit_18s0122g01400	Transcript	Exostosin family protein	1,36	1,7	1,54	0,65
4.2.2.7.2.1	Metabolism.Primary metabolism.Carbohydrate metabolism.Oligosaccharide metabolism.N-Glycan metabolism.N-Glycan biosynthesis	vit_19s0014g02650	Transcript	Glycosyl transferase family 14 protein	0,99	0,98	1,71	1,03
4.2.2.7.5	Metabolism.Primary metabolism.Carbohydrate metabolism.Oligosaccharide metabolism.Raffinose metabolism	vit_00s1530g00010	Transcript	Stachyose synthase precursor	-1,19	-1,87	-0,23	-0,85
4.2.2.7.5	Metabolism.Primary metabolism.Carbohydrate metabolism.Oligosaccharide metabolism.Raffinose metabolism	vit_00s0878g00020	Transcript	Stachyose synthase precursor	-1,41	-1,73	-0,79	-1,36
4.2.2.7.6	Metabolism.Primary metabolism.Carbohydrate metabolism.Oligosaccharide metabolism.Trehalose metabolism	vit_00s0233g00030	Transcript	Trehalose-6-phosphate phosphatase (AtTPPA)	-1,86	-1,42	-1,12	-1,23
4.2.2.7.6	Metabolism.Primary metabolism.Carbohydrate metabolism.Oligosaccharide metabolism.Trehalose metabolism	vit_02s0154g00110	Transcript	Trehalose-6-phosphate phosphatase (AtTPPA)	-1,94	-1,49	-1,1	-1,27
4.2.2.8	Metabolism.Primary metabolism.Carbohydrate metabolism.Polysaccharide metabolism	vit_13s0019g00240	Transcript	Glycosyltransferase family 14 Beta-1-3-galactosyl-O-glycosyl-glycoprotein	0,98	1,56	1,13	1,09
4.2.2.8.1.1	Metabolism.Primary metabolism.Carbohydrate metabolism.Polysaccharide metabolism.Beta-1,3 glucan metabolism.Beta-1,3 glucan catabolism	vit_08s0007g06040	Transcript	Beta-1,3-glucanase	1,61	1,85	1,37	1,9
4.2.2.8.1.1	Metabolism.Primary metabolism.Carbohydrate metabolism.Polysaccharide metabolism.Beta-1,3 glucan metabolism.Beta-1,3 glucan catabolism	vit_19s0090g01070	Transcript	Glucan endo-1,3-beta-glucosidase 7 precursor	-1,48	-1,58	-1,61	-1,67
4.2.2.8.2	Metabolism.Primary metabolism.Carbohydrate metabolism.Polysaccharide metabolism.Starch and sucrose metabolism	vit_05s0020g02880	Transcript	ADP-glucose pyrophosphorylase	-1,36	-1,93	-1,08	-1,4
4.2.2.8.2.1.1	Metabolism.Primary metabolism.Carbohydrate metabolism.Polysaccharide metabolism.Starch and sucrose metabolism.Starch biosynthesis and catabolism.Starch biosynthesis	vit_15s0048g02600	Transcript	Starch synthase	-2,42	-3,55	-1,15	-2,72
4.2.2.8.2.1.3	Metabolism.Primary metabolism.Carbohydrate metabolism.Polysaccharide metabolism.Starch and sucrose metabolism.Starch biosynthesis and catabolism.Starch catabolism	vit_01s0026g01660	Transcript	Alpha-amylase isozyme C2 precursor	1,74	2,09	2,21	2,16
4.2.2.8.2.1.3	Metabolism.Primary metabolism.Carbohydrate metabolism.Polysaccharide metabolism.Starch and sucrose metabolism.Starch biosynthesis and catabolism.Starch catabolism	vit_05s0077g00280	Transcript	Beta-amylase	-1,84	-2,68	-2,5	-2,56
4.2.2.8.2.1.3	Metabolism.Primary metabolism.Carbohydrate metabolism.Polysaccharide metabolism.Starch and sucrose metabolism.Starch biosynthesis and catabolism.Starch catabolism	vit_06s0004g06020	Transcript	Alpha-glucan phosphorylase, H isozyme	1,52	1,62	1,79	1,64
4.2.2.8.2.1.4	Metabolism.Primary metabolism.Carbohydrate metabolism.Polysaccharide metabolism.Starch and sucrose metabolism.Starch biosynthesis and catabolism.Starch catabolism inhibitor	vit_00s0270g00120	Transcript	Alpha-amylase/subtilisin inhibitor	2,78	2,12	2,4	3,24

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
4.2.2.8.2.3	Metabolism.Primary metabolism.Carbohydrate metabolism.Polysaccharide metabolism.Starch and sucrose metabolism.Sucrose catabolism	vit_00s2527g00010	Transcript	Beta-fructosidase (BFRUCT3)	1,91	0,97	1,86	1,43
4.2.2.8.2.3	Metabolism.Primary metabolism.Carbohydrate metabolism.Polysaccharide metabolism.Starch and sucrose metabolism.Sucrose catabolism	vit_09s0002g02320	Transcript	Cell wall apoplastic invertase	0,91	1,23	1,54	0,89
4.2.3	Metabolism.Primary metabolism.Carbon fixation	vit_05s0020g02310	Transcript	Pyruvate,orthophosphate dikinase	3,19	2,8	2,55	1,88
4.2.4.4	Metabolism.Primary metabolism.Coenzyme and prosthetic group metabolism.Glutathione metabolism	vit_19s0015g02690	Transcript	Glutathione S-transferase 25 GSTU25	3,83	2,98	0	0
4.2.4.4	Metabolism.Primary metabolism.Coenzyme and prosthetic group metabolism.Glutathione metabolism	vit_00s0153g00050	Transcript	Glutathione S-transferase 8 GSTU8	1,61	2,35	1,75	2,5
4.2.4.4	Metabolism.Primary metabolism.Coenzyme and prosthetic group metabolism.Glutathione metabolism	vit_02s0025g03600	Transcript	Phospholipid hydroperoxide glutathione peroxidase	1,56	1,33	1,18	1,35
4.2.4.4	Metabolism.Primary metabolism.Coenzyme and prosthetic group metabolism.Glutathione metabolism	vit_07s0005g00030	Transcript	Glutathione S-transferase 8 GSTF8	2,33	1,41	0,9	1,57
4.2.4.4	Metabolism.Primary metabolism.Coenzyme and prosthetic group metabolism.Glutathione metabolism	vit_17s0000g02950	Transcript	Glutathione S-transferase 25 GSTU7	-1,58	-2,5	-3,37	-1,42
4.2.4.4	Metabolism.Primary metabolism.Coenzyme and prosthetic group metabolism.Glutathione metabolism	vit_19s0015g02590	Transcript	Glutathione S-transferase 25 GSTU25	2,63	2,93	3,04	2,93
4.2.4.10.1	Metabolism.Primary metabolism.Coenzyme and prosthetic group metabolism.Thiamine metabolism.Thiamine biosynthesis	vit_06s0004g06130	Transcript	Thiamine biosynthesis protein ThiC	2,1	2,5	2,77	2,31
4.2.4.10.1	Metabolism.Primary metabolism.Coenzyme and prosthetic group metabolism.Thiamine metabolism.Thiamine biosynthesis	vit_10s0116g00530	Transcript	Thiazole biosynthetic enzyme, chloroplast (ARA6)	5,85	6,25	6,73	6,34
4.2.4.10.1	Metabolism.Primary metabolism.Coenzyme and prosthetic group metabolism.Thiamine metabolism.Thiamine biosynthesis	vit_19s0177g00140	Transcript	Thiazole biosynthetic enzyme, chloroplast (ARA6)	1,68	1,59	1,84	1,33
4.2.5.2	Metabolism.Primary metabolism.Cofactor metabolism.Tetrapyrrole metabolism	vit_17s0000g10180	Transcript	Coproporphyrinogen oxidase	1,76	1,27	1,6	0,77
4.2.5.2.1.1	Metabolism.Primary metabolism.Cofactor metabolism.Tetrapyrrole metabolism.Chlorophyll metabolism.Chlorophyll biosynthesis	vit_08s0007g08540	Transcript	Mg-chelatase subunit XANTHA-F	-0,8	-1,26	-1,03	-1,7
4.2.5.2.1.1	Metabolism.Primary metabolism.Cofactor metabolism.Tetrapyrrole metabolism.Chlorophyll metabolism.Chlorophyll biosynthesis	vit_18s0001g02700	Transcript	Chlorophyll a oxygenase (CAO)	-1,31	-1,8	-1,72	-1,91
4.2.5.2.1.2	Metabolism.Primary metabolism.Cofactor metabolism.Tetrapyrrole metabolism.Chlorophyll metabolism.Chlorophyll catabolism	vit_06s0004g00610	Transcript	Accelerated cell death 1 ACD1	-1,62	-2,07	-1,85	-1,97
4.2.5.2.1.2	Metabolism.Primary metabolism.Cofactor metabolism.Tetrapyrrole metabolism.Chlorophyll metabolism.Chlorophyll catabolism	vit_18s0001g01210	Transcript	Senescence-inducible chloroplast stay-green protein 2	-1,21	-1,71	-1,44	-2,05
4.2.6.1	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Citric acid cycle	vit_06s0009g00680	Transcript	Pyridine nucleotide-disulphide oxidoreductase	1,38	0,79	1,64	1,08
4.2.6.1	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Citric acid cycle	vit_08s0040g00210	Transcript	L-2-hydroxyglutarate dehydrogenase	1,52	1,4	1,28	1,04
4.2.6.1	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Citric acid cycle	vit_19s0014g01640	Transcript	Malate dehydrogenase	1,59	1,1	0,62	0,51
4.2.6.2	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Electron transport	vit_04s0008g06670	Transcript	Plastocyanin domain-containing protein	-1,46	-1,37	-1,55	-1,01
4.2.6.2	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Electron transport	vit_18s0001g06720	Transcript	Rieske [2Fe-2S] domain	-1,58	-1,73	-1,47	-1,39
4.2.6.2	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Electron transport	vit_18s0001g14450	Transcript	Ferredoxin:nadp+ Oxidoreductase PETH	-1,29	-1,67	-0,76	-1,3
4.2.6.2	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Electron transport	vit_19s0014g02460	Transcript	Plastocyanin domain-containing protein	-2,85	-1,91	-2,13	-1,82

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
4.2.6.2.1	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Electron transport.Respiratory-chain phosphorylation	vit_06s0009g00680	Transcript	Pyridine nucleotide-disulphide oxidoreductase	1,38	0,79	1,64	1,08
4.2.6.2.1	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Electron transport.Respiratory-chain phosphorylation	vit_08s0040g02470	Transcript	Inorganic pyrophosphatase	-1,66	-1,55	-1,55	-1,22
4.2.6.2.1	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Electron transport.Respiratory-chain phosphorylation	vit_13s0084g00880	Transcript	NADPH:quinone oxidoreductase	1,61	1,37	1,29	1,48
4.2.6.2.1	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Electron transport.Respiratory-chain phosphorylation	vit_18s0001g01660	Transcript	NADH dehydrogenase I subunit M	-1,6	-1,9	-1,09	-1,29
4.2.6.3	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Glyoxylate and dicarboxylate metabolism	vit_10s0003g03830	Transcript	S-2-hydroxy-acid oxidase, peroxisomal	-1,24	-1,56	-1,07	-1,31
4.2.6.3	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Glyoxylate and dicarboxylate metabolism	vit_19s0093g00510	Transcript	S-2-hydroxy-acid oxidase, peroxisomal	-1,96	-2,16	-1,35	-1,77
4.2.6.5.1	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Photosynthesis.Antenna proteins	vit_12s0057g00630	Transcript	LHCB2.1 (Photosystem II light harvesting complex gene 2.1)	2,17	1,71	1,73	1,32
4.2.6.5.2	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Photosynthesis.Calvin cycle	vit_06s0004g05180	Transcript	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplast	-1,92	-2,45	-1,53	-2,43
4.2.6.5.2	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Photosynthesis.Calvin cycle	vit_13s0019g02050	Transcript	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplast	-1,84	-2,61	-3,23	-2,98
4.2.6.5.2	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Photosynthesis.Calvin cycle	vit_13s0019g03350	Transcript	Sedoheptulose-1,7-bisphosphatase (SBPase), Chloroplast	-1,66	-1,89	-1,35	-1,56
4.2.6.5.3	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Photosynthesis.Photosynthetic-chain phosphorylation	vit_04s0008g06670	Transcript	Plastocyanin domain-containing protein	-1,46	-1,37	-1,55	-1,01
4.2.6.5.3	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Photosynthesis.Photosynthetic-chain phosphorylation	vit_18s0001g14450	Transcript	Ferredoxin:nadp+ Oxidoreductase PETH	-1,29	-1,67	-0,76	-1,3
4.2.6.5.3	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Photosynthesis.Photosynthetic-chain phosphorylation	vit_19s0014g02460	Transcript	Plastocyanin domain-containing protein	-2,85	-1,91	-2,13	-1,82
4.2.6.5.4	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Photosynthesis.Photosystem I	vit_07s0151g01000	Transcript	Photosystem I reaction center subunit II (PSAD)	-0,74	-1,07	0,4	-1,68
4.2.6.5.5	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Photosynthesis.Photosystem II	vit_12s0055g00080	Transcript	Photosystem II PsbD	1,29	1,06	1,8	0,82
4.2.6.5.5	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Photosynthesis.Photosystem II	vit_13s0019g02630	Transcript	Photosystem II PsbA	0,86	0,76	1,53	0,51
4.2.6.5.5	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Photosynthesis.Photosystem II	vit_18s0001g09110	Transcript	Photosystem II PsbC protein	1,04	0,9	1,67	0,73
4.2.6.5.6	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Photosynthesis.Reaction center pigment biosynthesis	vit_08s0007g08540	Transcript	Mg-chelatase subunit XANTHA-F	-0,8	-1,26	-1,03	-1,7
4.2.6.5.6	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Photosynthesis.Reaction center pigment biosynthesis	vit_18s0001g02700	Transcript	Chlorophyll a oxygenase (CAO)	-1,31	-1,8	-1,72	-1,91
4.2.6.6	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Storage proteins	vit_07s0031g00830	Transcript	Patatin-like protein	1,75	1,62	1,29	1,33
4.2.6.6	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Storage proteins	vit_07s0005g03410	Transcript	Globulin 11S	-2,59	-3,66	-3,73	-4,83
4.2.6.6	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Storage proteins	vit_18s0041g00430	Transcript	Patellin-1	1,22	1,52	1,59	1,08
4.2.6.7	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Reductive_carboxylate_cycle	vit_14s0060g01700	Transcript	fumarase (Reductive carboxylate cycle)	1,76	1,78	1,31	1,09

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
4.2.6.7	Metabolism.Primary metabolism.Generation of metabolite precursors and energy.Reductive_carboxylate_cycle	vit_14s0060g01690	Transcript	fumarase (Reductive carboxylate cycle)	2,03	1,97	1,77	1,81
4.2.7.1	Metabolism.Primary metabolism.Lipid metabolism.Fatty acid metabolism	vit_01s0244g00030	Transcript	ACP4 (Acyl carrier protein 4)	-1,55	-1,51	-1,01	-0,83
4.2.7.1.1	Metabolism.Primary metabolism.Lipid metabolism.Fatty acid metabolism.Alpha-linolenic acid metabolism	vit_14s0066g01690	Transcript	Pathogen-inducible alpha-dioxygenase	-2,02	-2,03	0	-1,42
4.2.7.1.2.2	Metabolism.Primary metabolism.Lipid metabolism.Fatty acid metabolism.Fatty acid biosynthesis.Unsaturated fatty acid biosynthesis	vit_06s0004g06730	Transcript	Microsomal omega-3 fatty acid desaturase	-2,11	-1,88	-1,73	-1,45
4.2.7.1.2.2	Metabolism.Primary metabolism.Lipid metabolism.Fatty acid metabolism.Fatty acid biosynthesis.Unsaturated fatty acid biosynthesis	vit_09s0002g06970	Transcript	Palmitoyl-monogalactosyldiacylglycerol delta-7 desaturase, chloroplast	2,16	1,96	2,03	1,27
4.2.7.1.5	Metabolism.Primary metabolism.Lipid metabolism.Fatty acid metabolism.Oxylipin biosynthesis	vit_06s0004g01470	Transcript	Lipoxygenase LOX1	1,04	1,11	1,79	1,82
4.2.7.1.5	Metabolism.Primary metabolism.Lipid metabolism.Fatty acid metabolism.Oxylipin biosynthesis	vit_06s0004g01480	Transcript	Lipoxygenase LOX1	1,24	1,01	2,09	1,42
4.2.7.1.5	Metabolism.Primary metabolism.Lipid metabolism.Fatty acid metabolism.Oxylipin biosynthesis	vit_12s0059g01060	Transcript	Hydroperoxide lyase (HPL1)	2,36	2,69	2,98	2,52
4.2.7.2	Metabolism.Primary metabolism.Lipid metabolism.Glycerolipid metabolism	vit_08s0007g08310	Transcript	Alkaline alpha galactosidase	1,55	1,36	1,49	1
4.2.7.2	Metabolism.Primary metabolism.Lipid metabolism.Glycerolipid metabolism	vit_10s0071g01120	Transcript	Alpha-galactosidase	1,02	1,26	1,84	0,73
4.2.7.2	Metabolism.Primary metabolism.Lipid metabolism.Glycerolipid metabolism	vit_11s0016g05770	Transcript	Alkaline alpha galactosidase 2	1,74	1,39	1,39	1,16
4.2.7.2.1	Metabolism.Primary metabolism.Lipid metabolism.Glycerolipid metabolism.Glycerolipid biosynthesis	vit_11s0118g00310	Transcript	1,2-diacylglycerol 3-beta-galactosyltransferase	0	-0,96	-2,26	0
4.2.7.2.1	Metabolism.Primary metabolism.Lipid metabolism.Glycerolipid metabolism.Glycerolipid biosynthesis	vit_11s0118g00310	Transcript	1,2-diacylglycerol 3-beta-galactosyltransferase	0	-0,96	-2,26	0
4.2.7.2.2	Metabolism.Primary metabolism.Lipid metabolism.Glycerolipid metabolism.Glycerolipid catabolism	vit_07s0005g01240	Transcript	Triacylglycerol lipase	1,64	2,09	1,82	0,98
4.2.7.2.2	Metabolism.Primary metabolism.Lipid metabolism.Glycerolipid metabolism.Glycerolipid catabolism	vit_17s0000g01070	Transcript	Monoglyceride lipase	-1,18	-2,03	-1,9	-2,02
4.2.7.2.3	Metabolism.Primary metabolism.Lipid metabolism.Glycerolipid metabolism.Glycerophospholipid metabolism	vit_03s0038g02090	Transcript	Phospholipase C.	1,54	1,18	1,22	0,72
4.2.7.2.3	Metabolism.Primary metabolism.Lipid metabolism.Glycerolipid metabolism.Glycerophospholipid metabolism	vit_14s0068g01500	Transcript	Glycerophosphoryl diester phosphodiesterase	-0,89	-0,78	-1,56	-0,09
4.2.7.2.3	Metabolism.Primary metabolism.Lipid metabolism.Glycerolipid metabolism.Glycerophospholipid metabolism	vit_14s0068g01500	Transcript	Glycerophosphoryl diester phosphodiesterase	-0,89	-0,78	-1,56	-0,09
4.2.7.2.3.1	Metabolism.Primary metabolism.Lipid metabolism.Glycerolipid metabolism.Glycerophospholipid metabolism.Glycerophospholipid biosynthesis	vit_14s0060g02200	Transcript	Phospholipid/glycerol acyltransferase	1,79	1,9	1,69	1,7
4.2.7.2.3.1	Metabolism.Primary metabolism.Lipid metabolism.Glycerolipid metabolism.Glycerophospholipid metabolism.Glycerophospholipid biosynthesis	vit_14s0219g00280	Transcript	Glycerol-3-phosphate dehydrogenase (NAD+)	-0,96	-1,79	-1,18	-0,9
4.2.7.2.3.2	Metabolism.Primary metabolism.Lipid metabolism.Glycerolipid metabolism.Glycerophospholipid metabolism.Glycerophospholipid catabolism	vit_11s0103g00190	Transcript	Phospholipase A2 alpha	-1,72	-1,14	-0,98	-0,53
4.2.7.4	Metabolism.Primary metabolism.Lipid metabolism.Sphingolipid metabolism	vit_08s0007g08310	Transcript	Alkaline alpha galactosidase	1,55	1,36	1,49	1
4.2.7.4	Metabolism.Primary metabolism.Lipid metabolism.Sphingolipid metabolism	vit_10s0071g01120	Transcript	Alpha-galactosidase	1,02	1,26	1,84	0,73
4.2.7.4	Metabolism.Primary metabolism.Lipid metabolism.Sphingolipid metabolism	vit_11s0016g05770	Transcript	Alkaline alpha galactosidase 2	1,74	1,39	1,39	1,16
4.2.7.5	Metabolism.Primary metabolism.Lipid metabolism.Steroid metabolism	vit_19s0014g00080	Transcript	Steroid 5alpha-reductase	-1,18	-1,5	-1,47	-1,94
4.2.7.6.1	Metabolism.Primary metabolism.Lipid metabolism.Wax metabolism.Wax biosynthesis	vit_03s0063g00120	Transcript	Wax synthase	1,7	1,11	0,99	1,25

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
4.2.7.6.1	Metabolism.Primary metabolism.Lipid metabolism.Wax metabolism.Wax biosynthesis	vit_11s0037g01210	Transcript	Eceriferum 1 (CER1 protein) Sterol desaturase	0,52	1,17	1,53	1,15
4.2.8.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism	vit_05s0020g04860	Transcript	Zinc knuckle	-1,69	-1,91	-2,01	-2,15
4.2.8.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism	vit_05s0049g01660	Transcript	RNA-binding protein Musashi	-0,93	-1,29	-0,97	-1,64
4.2.8.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism	vit_06s0080g01090	Transcript	CCR4-NOT transcription complex subunit 7/8	-0,12	-0,85	-0,9	-1,52
4.2.8.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism	vit_13s0019g00720	Transcript	Zinc knuckle	1,95	1,6	1,39	1,46
4.2.8.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism	vit_18s0166g00180	Transcript	Zinc finger protein ATRZ-1A	-1,58	-1,82	-1,66	-1,88
4.2.8.1.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.DNA metabolism	vit_00s0332g00080	Transcript	Maturase K	-1,81	-1,43	-1,05	-1,46
4.2.8.1.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.DNA metabolism	vit_05s0049g00100	Transcript	DNA-binding protein	-2,62	-2,5	-3,31	-2,7
4.2.8.1.1.4	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.DNA metabolism.DNA repair	vit_04s0008g02670	Transcript	Cryptochrome DASH	-1,96	-2,19	-2,29	-2,1
4.2.8.1.1.4	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.DNA metabolism.DNA repair	vit_18s0001g00660	Transcript	High mobility group (HMG1/2) family protein	-1,26	-1,81	-1,16	-1,84
4.2.8.1.1.4	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.DNA metabolism.DNA repair	vit_08s0007g02200	Transcript	High mobility group protein B1	-1,76	-1,63	-1,87	-1,35
4.2.8.1.1.4	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.DNA metabolism.DNA repair	vit_08s0007g07540	Transcript	HNH endonuclease domain-containing protein	2,59	2,36	2,22	2,56
4.2.8.1.3	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.RNA metabolism	vit_12s0059g01670	Transcript	Nuclear ribonuclease Z	0,94	1,37	1,74	1,8
4.2.8.1.3.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.RNA metabolism.RNA biosynthesis	vit_14s0108g00070	Transcript	Transcription initiation factor TFIID subunit 1-A	1,35	1,79	1,14	1
4.2.8.1.3.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.RNA metabolism.RNA biosynthesis	vit_13s0064g00190	Transcript	RNA polymerase sigma subunit SigD	2,61	1,78	2,58	2,13
4.2.8.1.3.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.RNA metabolism.RNA biosynthesis	vit_16s0050g02520	Transcript	RNA polymerase sigma subunit SigE (sigE)	-1,11	-1,81	-1,76	-1,73
4.2.8.1.3.3	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.RNA metabolism.RNA processing	vit_04s0008g05430	Transcript	RDR6 (RNA-dependent RNA polymerase 6)	-1,6	-1,18	-1,19	-1,35
4.2.8.1.3.3	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.RNA metabolism.RNA processing	vit_01s0011g05870	Transcript	RDR1 (RNA-dependent RNA polymerase 1)	-1,4	-1,16	-1,22	-1,67
4.2.8.1.3.3	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.RNA metabolism.RNA processing	vit_04s0008g05430	Transcript	RDR6 (RNA-dependent RNA polymerase 6)	-1,6	-1,18	-1,19	-1,35
4.2.8.1.3.3	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.RNA metabolism.RNA processing	vit_01s0011g05870	Transcript	RDR1 (RNA-dependent RNA polymerase 1)	-1,4	-1,16	-1,22	-1,67
4.2.8.1.3.3.1.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.RNA metabolism.RNA processing.mRNA processing.mRNA splicing	vit_00s0611g00010	Transcript	Splicing factor U2AF 65 kDa subunit	-1,51	-2,21	-1,68	-1,48
4.2.8.1.3.3.1.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.RNA metabolism.RNA processing.mRNA processing.mRNA splicing	vit_12s0142g00110	Transcript	Splicing factor, arginine/serine-rich 2	1,85	1,36	0,81	0,8

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
4.2.8.1.3.3.1.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.RNA metabolism.RNA processing.mRNA processing.mRNA splicing	vit_13s0067g03600	Transcript	RSZ33 (Arginine/serine-rich Zinc knuckle-containing protein 33)	-1,59	-1,38	-1,49	-1,05
4.2.8.1.3.3.1.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.RNA metabolism.RNA processing.mRNA processing.mRNA splicing	vit_15s0048g01870	Transcript	Arginine/serine-rich splicing factor RSP41	-1,55	-1,45	-1,62	-0,98
4.2.8.1.3.3.1.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.RNA metabolism.RNA processing.mRNA processing.mRNA splicing	vit_16s0100g00450	Transcript	Arginine/serine-rich splicing factor RSP41	-1,51	-1,03	-0,65	-0,27
4.2.8.2	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleotide metabolism	vit_05s0020g00880	Transcript	5-nucleotidase	1,27	1,45	1,51	1,53
4.2.8.2.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleotide metabolism.Purine metabolism	vit_01s0011g03660	Transcript	IMP dehydrogenase/GMP reductase	-2,02	-2,61	-2,24	-2,42
4.2.8.2.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleotide metabolism.Purine metabolism	vit_03s0063g02040	Transcript	Caffeine synthase	1,13	0,98	1,65	0,96
4.2.8.2.1	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleotide metabolism.Purine metabolism	vit_07s0005g02020	Transcript	Sulfate adenylyltransferase	1,08	1,04	1,23	1,73
4.2.8.2.2	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleotide metabolism.Pyrimidine metabolism	vit_06s0004g00940	Transcript	Carbamoyl-phosphate synthase, large subunit	1,96	1,84	1,9	1,87
4.2.8.3	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nudix hydrolase family	vit_06s0004g03990	Transcript	Nudix hydrolase 9	-1,28	-0,87	-1,59	-1,29
4.2.8.3	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nudix hydrolase family	vit_14s0006g00300	Transcript	Nudix hydrolase 18	-0,49	-1,56	-1,06	-1,64
4.2.9.1	Metabolism.Primary metabolism.Organic acid metabolism.Ascorbate and aldarate metabolism	vit_03s0063g00050	Transcript	UDP-glucuronosyl/UDP-glucosyltransferase	-1,29	-1,3	-1,52	-1,61
4.2.9.1	Metabolism.Primary metabolism.Organic acid metabolism.Ascorbate and aldarate metabolism	vit_05s0020g04510	Transcript	GDP-mannose 3,5-epimerase 1	-1,49	-1,61	-1,66	-1,6
4.2.9.1	Metabolism.Primary metabolism.Organic acid metabolism.Ascorbate and aldarate metabolism	vit_08s0040g03150	Transcript	L-ascorbate peroxidase 1, cytosolic (APX1)	1,99	2	1,52	1,63
4.2.9.1	Metabolism.Primary metabolism.Organic acid metabolism.Ascorbate and aldarate metabolism	vit_09s0002g02940	Transcript	Myo-inositol oxygenase 1	1,29	0,98	1,68	1,89
4.2.9.1	Metabolism.Primary metabolism.Organic acid metabolism.Ascorbate and aldarate metabolism	vit_11s0016g02800	Transcript	Myo-inositol oxygenase	2,64	3,24	3,65	2,95
4.2.9.1	Metabolism.Primary metabolism.Organic acid metabolism.Ascorbate and aldarate metabolism	vit_14s0030g02180	Transcript	GDP-mannose 3,5-epimerase 1	-1,87	-2,15	-2,06	-1,7
4.2.9.1	Metabolism.Primary metabolism.Organic acid metabolism.Ascorbate and aldarate metabolism	vit_17s0000g04750	Transcript	UDP-glycosyltransferase 89B2	-1,23	-0,98	-1,52	-1,78
4.2.9.2.1	Metabolism.Primary metabolism.Organic acid metabolism.Butanoate metabolism.Butanoate biosynthesis	vit_04s0079g00600	Transcript	Glutamate decarboxylase 1	-1,63	-1,38	-1,18	-1,09
4.2.9.5	Metabolism.Primary metabolism.Organic acid metabolism.Propanoate metabolism	vit_02s0012g00400	Transcript	1-aminocyclopropane-1-carboxylate oxidase	2,35	2,55	2,21	2,71
4.2.10.1.1	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding	vit_00s0283g00030	Transcript	Calnexin 1 (CNX1)	2,38	1,88	1,13	0,98
4.2.10.1.1.1	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.Chaperonin-mediated protein folding	vit_01s0010g00920	Transcript	Chaperonin GroEL	1,49	1,53	2,02	1,84

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
4.2.10.1.1.1	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.Chaperonin-mediated protein folding	vit_08s0040g01690	Transcript	T-complex protein 1 epsilon subunit	3,36	2,81	2,51	1,61
4.2.10.1.1.1	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.Chaperonin-mediated protein folding	vit_05s0051g00340	Transcript	Chaperonin GroEL	1,52	1,19	0,78	0,79
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g00930	Transcript	Heat shock protein 70	1,97	1,03	1,36	0,71
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02740	Transcript	Heat shock protein 17.6 kDa class I	1,59	-1,38	-0,73	0,99
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g03090	Transcript	Heat shock protein class I (HSP17.8-CI)	4,35	1,57	0	2,09
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_04s0008g01520	Transcript	Heat shock protein 17.6 kDa class II	4,73	2,37	1,77	1,65
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_18s0089g01270	Transcript	Heat shock protein precursor 22.0 kDa class IV	5,75	3,83	2,34	2,3
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_01s0010g02290	Transcript	Heat shock protein 26a, chloroplast	2,3	0,6	-0,1	0,66
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_02s0025g00280	Transcript	Heat shock protein 90-1	5,17	2,39	1,49	1,19
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_02s0025g02140	Transcript	Heat shock protein 70	1,98	1,27	0,83	0,55
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_02s0154g00480	Transcript	HSP23.6-MITO	2,44	0,48	-0,92	0,3
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_16s0022g00510	Transcript	Heat shock 22 kDa protein	2,65	0,2	-1,08	-0,28
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_02s0154g00490	Transcript	Heat shock 22 kDa protein mitochondrial	5,86	3,79	2,39	4,03
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_04s0008g01490	Transcript	Heat shock protein 17.6 kDa class II	4,45	2,77	1,88	1,6
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_04s0008g01510	Transcript	Heat shock protein 17.6 kDa class II	5,82	2,16	0,64	1,8
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_04s0008g01550	Transcript	Small molecular heat shock protein 17.5	3,36	0,53	-0,95	0,28
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_04s0008g01580	Transcript	Heat shock protein 17.6 kDa class II	4,51	2,02	1,19	1,32
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_04s0008g01590	Transcript	Heat shock protein 17.6 kDa class II	4,33	1,99	1,11	1,05
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_05s0020g03330	Transcript	Heat shock protein 70	2,41	1,88	1,11	0,81
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_06s0004g04470	Transcript	Heat shock protein 70	4,12	1,28	0,27	0,64
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_06s0004g04510	Transcript	Heat shock protein 70	1,52	1,19	1,07	0,79
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02850	Transcript	Heat shock protein 17.6 kDa class I	3,01	0,16	-0,48	0,84

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4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02740	Transcript	Heat shock protein 17.6 kDa class I	1,59	-1,38	-0,73	0,99
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02760	Transcript	Heat shock protein 17.6 kDa class I	3,01	-1,53	-0,84	1,4
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_04s0008g01570	Transcript	Heat shock protein 17.6 kDa class II	2,45	-0,2	-1,35	-0,09
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02840	Transcript	Heat shock protein 18.2 kDa class I	3,4	0,15	-0,11	1,75
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02820	Transcript	Heat shock protein 18.2 kDa class I	3,38	0	0	1,6
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_06s0004g05770	Transcript	Heat shock protein 17.6 kDa class I	2,19	3,05	1,1	1,7
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_09s0002g00640	Transcript	Small heat stress protein class CIII	1,25	-1,52	-1,76	0
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_09s0002g06790	Transcript	Small heat shock protein (HSP26.5-P) 26.5 kDa class I	1,85	1,46	0,62	0,77
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_11s0037g00510	Transcript	Heat shock protein 70	3,23	1,09	0,39	0,12
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_00s0992g00020	Transcript	Heat shock protein (HSP26.5-P) 26.5 kDa class P	2,49	3,5	3,1	3,75
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_00s0707g00010	Transcript	Heat shock protein (HSP26.5-P) 26.5 kDa class P	2,24	2,75	2,82	3,35
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g00860	Transcript	Small heat-shock protein HSP17.5 Cytosolic class I	3,16	1,78	0,58	1,3
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_12s0028g01390	Transcript	Small heat shock protein ACD31	5,72	6,02	5,97	5,85
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_12s0035g01910	Transcript	Heat shock protein 18.2 kDa class II	6,3	5,31	4,91	4,65
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_12s0059g01560	Transcript	Protein disulfide-isomerase A6	1,64	1,7	1,31	1,49
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02760	Transcript	Heat shock protein 17.6 kDa class I	3,01	-1,53	-0,84	1,4
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02770	Transcript	Heat shock protein 17.6 kDa class I	2,59	0	-0,14	1,77
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02780	Transcript	Heat shock protein 17.6 kDa class I	3,21	1,02	0,41	1,16
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02840	Transcript	Heat shock protein 18.2 kDa class I	3,4	0,15	-0,11	1,75
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02850	Transcript	Heat shock protein 17.6 kDa class I	3,01	0,16	-0,48	0,84
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02930	Transcript	Heat shock protein 17.6 kDa class I	3,12	1,22	0,42	0,98
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g03000	Transcript	Heat shock protein 17.6 kDa class I	1,66	-0,11	-0,79	0,06
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g03160	Transcript	Heat shock protein 17.6 kDa class I	3,55	0,92	0,35	0,81

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4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g03170	Transcript	Heat shock protein 16.9 kDa class I	3,2	1,57	1,22	0,97
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_14s0060g02340	Transcript	Heat shock protein 70	3,64	3,01	2,4	1,76
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_16s0050g01150	Transcript	Heat shock protein 90-1	3,97	1,01	0,24	1,17
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_01s0010g02290	Transcript	Heat shock protein 26a, chloroplast	2,3	0,6	-0,1	0,66
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_16s0098g01060	Transcript	Heat shock protein 26a, chloroplast	2,61	1,34	0,68	0,36
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_16s0098g01580	Transcript	Heat shock protein 70	2,38	1,73	1,31	0,83
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_17s0000g07190	Transcript	Heat shock protein 101	1,71	-0,6	-1,16	-0,96
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_18s0041g01230	Transcript	Heat shock protein 70	1,89	0,2	0,01	-0,42
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_19s0014g05050	Transcript	Heat shock HSP20 family protein	1,86	1,1	0,88	1,04
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_19s0085g01050	Transcript	Heat shock protein 17.6 kDa class I	0	0	0	3,05
4.2.10.1.1.2.1	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding.HSP-mediated protein folding co-chaperone	vit_01s0011g04820	Transcript	Molecular chaperone DnaJ	3,63	2,61	2,82	3,58
4.2.10.1.1.2.1	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding.HSP-mediated protein folding co-chaperone	vit_07s0005g01220	Transcript	DnaJ homolog, subfamily B, member 11	1,89	1,2	1,16	0,99
4.2.10.1.1.2.1	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding.HSP-mediated protein folding co-chaperone	vit_09s0002g00690	Transcript	DnaJ homolog, subfamily B, member 6	3,43	1,77	1,54	2,06
4.2.10.1.1.2.1	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding.HSP-mediated protein folding co-chaperone	vit_10s0003g00260	Transcript	DnaJ homolog, subfamily B, member 4	0,01	-1,9	-2,3	-0,33
4.2.10.1.1.2.1	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding.HSP-mediated protein folding co-chaperone	vit_10s0042g00960	Transcript	DNAJ heat shock N-terminal domain-containing protein	7,01	6,18	7,56	7,78
4.2.10.1.1.2.1	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding.HSP-mediated protein folding co-chaperone	vit_14s0060g01490	Transcript	DnaJ homolog, subfamily A, member 5	7,05	6,57	6,57	6,45
4.2.10.1.1.2.1	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding.HSP-mediated protein folding co-chaperone	vit_18s0001g14440	Transcript	Molecular chaperone DnaJ	-2,31	-2,77	-2,23	-1,77
4.2.10.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Disulfide bond rearrangement	vit_18s0001g01030	Transcript	Protein disulfide isomerase	-0,68	-1,11	-1,38	-1,65
4.2.10.1.3	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Peptidyl prolyl isomerase-mediated protein folding	vit_00s0769g00010	Transcript	Peptidyl-prolyl cis-trans isomerase, FKBP-type	1,78	1,22	0,9	0,9
4.2.10.1.3	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Peptidyl prolyl isomerase-mediated protein folding	vit_00s0958g00020	Transcript	FK506-binding protein 4/5 ROF1 (rotamase FKBP 1)	1,78	1,16	0,6	0,83

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4.2.10.3.2	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Peptidase-mediated proteolysis	vit_01s0011g00740	Transcript	Processing peptidase beta subunit, mitochondrial	2	2,04	1,76	1,92
4.2.10.3.2	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Peptidase-mediated proteolysis	vit_08s0040g01040	Transcript	Serine carboxypeptidase II	-1,88	-1,93	-2,07	-1,16
4.2.10.3.2	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Peptidase-mediated proteolysis	vit_06s0080g01160	Transcript	Aspartyl protease	0,57	0,99	1,53	0,99
4.2.10.3.2	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Peptidase-mediated proteolysis	vit_08s0007g02450	Transcript	Aspartyl protease	1,65	0,94	4,32	2,77
4.2.10.3.2	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Peptidase-mediated proteolysis	vit_08s0007g02470	Transcript	Aspartyl protease	1,08	1,12	2,16	0,91
4.2.10.3.2	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Peptidase-mediated proteolysis	vit_08s0007g08050	Transcript	Carboxyl-terminal processing protease	-1,41	-1,77	-1,83	-1,84
4.2.10.3.2	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Peptidase-mediated proteolysis	vit_14s0006g00180	Transcript	Aspartyl protease	1,83	1,32	1,49	0,59
4.2.10.3.2	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Peptidase-mediated proteolysis	vit_14s0068g02070	Transcript	Peptidase M48	1,44	1,63	0,73	0,78
4.2.10.3.2.1	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Peptidase-mediated proteolysis.Metallopeptidase-mediated proteolysis	vit_14s0108g00590	Transcript	FtsH protease	2,98	0,65	0,63	1,32
4.2.10.3.2.2	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Peptidase-mediated proteolysis.Subtilase-mediated proteolysis	vit_15s0048g01170	Transcript	Subtilisin serine protease	-1,21	-1,82	-1,15	-2
4.2.10.3.2.2	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Peptidase-mediated proteolysis.Subtilase-mediated proteolysis	vit_02s0025g04780	Transcript	Subtilisin stomatal density and distribution	-1,05	-0,66	-1,42	-1,5
4.2.10.3.2.2	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Peptidase-mediated proteolysis.Subtilase-mediated proteolysis	vit_18s0001g10330	Transcript	Subtilisin protease	0,57	-0,19	1,64	0,56
4.2.10.3.3	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Protease inhibition	vit_00s0187g00040	Transcript	Cystatin	2,44	1,97	1,6	1,32
4.2.10.3.3	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Protease inhibition	vit_00s0270g00120	Transcript	Alpha-amylase/subtilisin inhibitor	2,78	2,12	2,4	3,24
4.2.10.3.4	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Ubiquitin-mediated proteolysis	vit_00s0181g00080	Transcript	F-box domain containing protein	-0,59	-1,28	-1,53	-0,45
4.2.10.3.4	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Ubiquitin-mediated proteolysis	vit_00s0214g00090	Transcript	F-box protein PP2-B10 (Protein phloem protein 2-like B10)	1,73	0,89	0,76	1,17
4.2.10.3.4	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Ubiquitin-mediated proteolysis	vit_04s0008g02240	Transcript	Ubiquitin thiolesterase	2,01	1,96	1,23	1,19
4.2.10.3.4	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Ubiquitin-mediated proteolysis	vit_03s0038g03630	Transcript	F-box domain containing protein	1,58	0,79	1,98	1,11
4.2.10.3.4	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Ubiquitin-mediated proteolysis	vit_05s0077g00850	Transcript	Ubiquitin-conjugating enzyme E2 O	1,64	1,91	1,15	0,87
4.2.10.3.4	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Ubiquitin-mediated proteolysis	vit_19s0014g00340	Transcript	Zinc finger (C3HC4-type ring finger)	1,02	1,2	1,37	1,57
4.2.10.3.4	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Ubiquitin-mediated proteolysis	vit_06s0061g00070	Transcript	Ubiquitin-conjugating enzyme E2 C	-1,55	-1,14	-1,33	-0,73

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
4.2.10.3.4	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Ubiquitin-mediated proteolysis	vit_08s0040g03270	Transcript	E3 ubiquitin-protein ligase TRIP12	1,53	1,19	1,09	0,76
4.2.10.3.4	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Ubiquitin-mediated proteolysis	vit_09s0002g08660	Transcript	F-box protein (FBL14)	5,39	5,38	5,39	5,25
4.2.10.3.4	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Ubiquitin-mediated proteolysis	vit_13s0019g01840	Transcript	Cell division cycle 20-like protein 1	-1,56	-1,33	-1,58	-0,54
4.2.10.3.4	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Ubiquitin-mediated proteolysis	vit_12s0028g03570	Transcript	SPA3 (SPA1-related 3)	-1,6	-1,91	-2,02	-2,31
4.2.10.3.4	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Ubiquitin-mediated proteolysis	vit_14s0066g00590	Transcript	SCF E3 ubiquitin ligase complex F-box protein grrA	-1,27	-1,48	-1,41	-2,16
4.2.10.3.4	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Ubiquitin-mediated proteolysis	vit_16s0050g00020	Transcript	Cullin-4	-1,25	-1,97	-1,59	-1,99
4.2.10.3.4	Metabolism.Primary metabolism.Protein metabolism and modification.Proteolysis.Ubiquitin-mediated proteolysis	vit_18s0122g01340	Transcript	BTB/POZ domain-containing protein	1,51	1,16	1,34	1,25
4.2.10.4	Metabolism.Primary metabolism.Protein metabolism and modification.Translation	vit_17s0000g02610	Transcript	Ribosomal protein L22 50S	-1,24	-1,57	-0,82	-1,26
4.2.10.4	Metabolism.Primary metabolism.Protein metabolism and modification.Translation	vit_12s0028g01330	Transcript	Glu-tRNA(Gln) amidotransferase subunit A	-1,58	-0,93	-0,46	0,01
4.2.10.4	Metabolism.Primary metabolism.Protein metabolism and modification.Translation	vit_13s0064g00170	Transcript	Ribosomal protein L1	-1,52	-1,52	-1,19	-1,09
4.2.10.4	Metabolism.Primary metabolism.Protein metabolism and modification.Translation	vit_13s0101g00220	Transcript	Ribosomal RNA 16S	-1,7	-1,36	-0,64	-1,81
4.2.10.4	Metabolism.Primary metabolism.Protein metabolism and modification.Translation	vit_14s0006g02750	Transcript	Peptidyl-tRNA hydrolase	2,19	2,14	2,13	2,34
4.2.10.4.3	Metabolism.Primary metabolism.Protein metabolism and modification.Translation.Translational initiation	vit_19s0090g00420	Transcript	Translation initiation factor eIF-1	1,95	1,48	1,12	2,39
4.3.1.1	Metabolism.Secondary metabolism.Alkaloid metabolism.Alkaloid biosynthesis	vit_02s0012g00390	Transcript	Norcoclaurine synthase	2,25	2,97	1,35	1,92
4.3.1.1	Metabolism.Secondary metabolism.Alkaloid metabolism.Alkaloid biosynthesis	vit_12s0028g03210	Transcript	Tyrosine aminotransferase	1,57	1,34	1,6	1,9
4.3.1.1.3	Metabolism.Secondary metabolism.Alkaloid metabolism.Alkaloid biosynthesis.Monoterpenoid indole alkaloid biosynthesis	vit_05s0049g00400	Transcript	Desacetoxyvindoline 4-hydroxylase	1,08	1,04	0,9	1,64
4.3.1.1.3	Metabolism.Secondary metabolism.Alkaloid metabolism.Alkaloid biosynthesis.Monoterpenoid indole alkaloid biosynthesis	vit_08s0007g05360	Transcript	Strictosidine synthase	3,61	3,97	3,37	3,91
4.3.1.1.3	Metabolism.Secondary metabolism.Alkaloid metabolism.Alkaloid biosynthesis.Monoterpenoid indole alkaloid biosynthesis	vit_10s0071g00250	Transcript	Strictosidine synthase	-1,97	-1,14	-1,59	-0,59
4.3.1.1.3	Metabolism.Secondary metabolism.Alkaloid metabolism.Alkaloid biosynthesis.Monoterpenoid indole alkaloid biosynthesis	vit_10s0092g00370	Transcript	CyP71D7	3,93	3,48	4,28	4,12
4.3.1.1.3	Metabolism.Secondary metabolism.Alkaloid metabolism.Alkaloid biosynthesis.Monoterpenoid indole alkaloid biosynthesis	vit_17s0000g09550	Transcript	CYP71A26	-1,64	-2,03	-0,85	-1,98
4.3.2	Metabolism.Secondary metabolism.Aromatic compound metabolism	vit_01s0011g05920	Transcript	S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase	-1	-1,69	-2,17	-2,26
4.3.2	Metabolism.Secondary metabolism.Aromatic compound metabolism	vit_04s0023g02230	Transcript	S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase	-1,44	-1,95	-2,99	-1,94
4.3.2.5	Metabolism.Secondary metabolism.Aromatic compound metabolism.Rosmarinic acid biosynthesis	vit_00s0480g00030	Transcript	Polyphenol oxidase	-1,53	-1,67	-1,23	-1,19
4.3.3	Metabolism.Secondary metabolism.Glucosinolate metabolism	vit_01s0026g00630	Transcript	N-hydroxythioamide S-beta-glucosyltransferase	-3,85	-4,59	-4,39	-3,95

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4.3.4.1.1	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Flavonoid metabolism.Flavonoid biosynthesis	vit_00s1682g00020	Transcript	flavonoid 3'-hydroxylase cytochrome P450 (Flavonoid biosynthesis)	1,58	1,71	0,78	1,07
4.3.4.1.1	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Flavonoid metabolism.Flavonoid biosynthesis	vit_02s0025g02960	Transcript	Naringenin,2-oxoglutarate 3-dioxygenase	-0,6	-1,54	-2,8	-1,13
4.3.4.1.1	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Flavonoid metabolism.Flavonoid biosynthesis	vit_11s0016g01020	Transcript	flavonoid 3-monooxygenase	2,68	2,59	2,36	2,35
4.3.4.1.1.1.1	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Flavonoid metabolism.Flavonoid biosynthesis.Anthocyanin biosynthesis.Anthocyanin-glycoside biosynthesis	vit_06s0004g06400	Transcript	Anthocyanidin 3-O-glucosyltransferase	0	6,75	5,13	0
4.3.4.1.1.1.1	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Flavonoid metabolism.Flavonoid biosynthesis.Anthocyanin biosynthesis.Anthocyanin-glycoside biosynthesis	vit_12s0034g00130	Transcript	Anthocyanidin 3-O-glucosyltransferase	-0,83	-1,19	-1,57	-1,31
4.3.4.1.1.1.1	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Flavonoid metabolism.Flavonoid biosynthesis.Anthocyanin biosynthesis.Anthocyanin-glycoside biosynthesis	vit_16s0050g01580	Transcript	UDP-glucose: anthocyanidin 5,3-O-glucosyltransferase	0,86	1,44	1,98	1,21
4.3.4.1.1.1.1	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Flavonoid metabolism.Flavonoid biosynthesis.Anthocyanin biosynthesis.Anthocyanin-glycoside biosynthesis	vit_16s0050g01680	Transcript	UDP-glucose: anthocyanidin 5,3-O-glucosyltransferase	-1,23	-2,01	-1,54	-1,89
4.3.4.1.1.1.1	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Flavonoid metabolism.Flavonoid biosynthesis.Anthocyanin biosynthesis.Anthocyanin-glycoside biosynthesis	vit_18s0041g00710	Transcript	UDP-glucose: anthocyanidin 5,3-O-glucosyltransferase	1,46	1,9	1,94	1,43
4.3.4.1.1.2	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Flavonoid metabolism.Flavonoid biosynthesis.Flavonoid-glycoside biosynthesis	vit_05s0062g00640	Transcript	UDP-glucose:flavonoid 7-O-glucosyltransferase	-1,66	-2,28	-1,46	-1,98
4.3.4.1.2.1	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Flavonoid metabolism.Isoflavonoid metabolism.Isoflavonoid biosynthesis	vit_00s0705g00010	Transcript	CYP81E1 Isoflavone 2'-hydroxylase	2,71	2,75	2,44	2,61
4.3.4.4	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Phenylpropanoid biosynthesis	vit_17s0000g03930	Transcript	ferulate 5-hydroxylase	-0,65	-1,51	-1,91	-1,09
4.3.4.4	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Phenylpropanoid biosynthesis	vit_07s0031g01380	Transcript	ferulate 5-hydroxylase	-1,75	-2,69	-1,95	-2,09
4.3.4.4	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Phenylpropanoid biosynthesis	vit_03s0063g00140	Transcript	Caffeoyl-CoA O-methyltransferase	-1,58	-1,64	-1,6	-1,75
4.3.4.4	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Phenylpropanoid biosynthesis	vit_16s0050g00390	Transcript	4-coumarate-CoA ligase	-2,43	-3,12	-2,83	-4,17
4.3.4.4	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Phenylpropanoid biosynthesis	vit_12s0057g00930	Transcript	Hydroxycinnamoyl-CoA:shikimate hydroxycinnamoyltransferase	-1,45	-0,79	-1,52	-1,3
4.3.4.4.1	Metabolism.Secondary metabolism.Phenylpropanoid metabolism.Phenylpropanoid biosynthesis.Tannin biosynthesis	vit_03s0038g00360	Transcript	Isochorismatase hydrolase	2,17	2,83	2,93	3,27
4.3.5.1	Metabolism.Secondary metabolism.Polyamine metabolism.Polyamine biosynthesis	vit_05s0020g03200	Transcript	Spermine synthase	-1,58	-1,43	-1,4	-1,12
4.3.5.1	Metabolism.Secondary metabolism.Polyamine metabolism.Polyamine biosynthesis	vit_11s0037g00950	Transcript	S-adenosylmethionine decarboxylase proenzyme	-2,94	-4,13	-3,01	-3,89
4.3.5.2	Metabolism.Secondary metabolism.Polyamine metabolism.Polyamine catabolism	vit_01s0127g00800	Transcript	Polyamine oxidase precursor	-1,44	-1,4	-1,63	-1,21
4.3.6.1.1	Metabolism.Secondary metabolism.Terpenoid metabolism.Diterpenoid metabolism.Diterpenoid biosynthesis	vit_06s0004g06790	Transcript	Gibberellin 2-beta-dioxygenase 7	0,96	0,21	1,68	0,97
4.3.6.1.1	Metabolism.Secondary metabolism.Terpenoid metabolism.Diterpenoid metabolism.Diterpenoid biosynthesis	vit_19s0140g00120	Transcript	Gibberellin 2-beta-dioxygenase 1	-0,89	-1,29	-1,75	-1,88

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4.3.6.1.1.1	Metabolism.Secondary metabolism.Terpenoid metabolism.Diterpenoid metabolism.Diterpenoid biosynthesis.Taxol biosynthesis	vit_06s0004g07650	Transcript	Taxadien-5-alpha-ol-O-acetyltransferase	-1,25	-1,45	-2,12	-2,15
4.3.6.1.1.1	Metabolism.Secondary metabolism.Terpenoid metabolism.Diterpenoid metabolism.Diterpenoid biosynthesis.Taxol biosynthesis	vit_19s0090g00190	Transcript	Taxane 10-beta-hydroxylase	0,98	1,61	0,95	1,32
4.3.6.3.1	Metabolism.Secondary metabolism.Terpenoid metabolism.Monoterpenoid metabolism.Monoterpenoid biosynthesis	vit_02s0025g04880	Transcript	Geraniol 10-hydroxylase	1,97	2,17	2,66	2,36
4.3.6.3.1	Metabolism.Secondary metabolism.Terpenoid metabolism.Monoterpenoid metabolism.Monoterpenoid biosynthesis	vit_04s0008g01860	Transcript	CYP72A58	-1,4	-1,35	-2,24	-1,09
4.3.6.4.1	Metabolism.Secondary metabolism.Terpenoid metabolism.Sesquiterpenoid metabolism.Sesquiterpenoid biosynthesis	vit_19s0014g04930	Transcript	Germacrene-D synthase	-0,22	-1,11	-2	0,54
4.3.6.5.2	Metabolism.Secondary metabolism.Terpenoid metabolism.Terpenoid biosynthesis.Terpenoid-quinone biosynthesis	vit_12s0028g00710	Transcript	4-hydroxyphenylpyruvate dioxygenase	2,48	1,85	1,92	1,34
4.3.6.6	Metabolism.Secondary metabolism.Terpenoid metabolism.Tetranortriterpenoid metabolism	vit_03s0091g00040	Transcript	Limonoid UDP-glucosyltransferase	1,56	1,7	1,86	1,16
4.3.6.7.1.1	Metabolism.Secondary metabolism.Terpenoid metabolism.Tetraterpenoid metabolism.Tetraterpenoid biosynthesis.Carotenoid biosynthesis	vit_02s0087g00910	Transcript	9-cis-epoxycarotenoid dioxygenase	2,75	2,73	3,38	2,29
4.3.6.7.1.1	Metabolism.Secondary metabolism.Terpenoid metabolism.Tetraterpenoid metabolism.Tetraterpenoid biosynthesis.Carotenoid biosynthesis	vit_12s0028g00960	Transcript	Phytoene synthase, chloroplast precursor	-2,32	-2,47	-2,17	-2,07
4.3.6.7.1.1	Metabolism.Secondary metabolism.Terpenoid metabolism.Tetraterpenoid metabolism.Tetraterpenoid biosynthesis.Carotenoid biosynthesis	vit_18s0001g10500	Transcript	ABA 8'-hydroxylase CYP707A1	1,16	1,41	1,55	0,54
5.1	Regulation overview.Regulation of cell cycle	vit_06s0009g02090	Transcript	Cyclin CYCB1_2	-1,95	-2,09	-1,73	-1,45
5.1	Regulation overview.Regulation of cell cycle	vit_15s0021g02680	Transcript	Cyclin-U2-1 (CycU2;1) Cyclin-P3.1	1,61	1,91	2,21	1,84
5.1	Regulation overview.Regulation of cell cycle	vit_18s0001g09160	Transcript	Cyclin, N-terminal	1,22	1,54	0,82	0,59
5.1.2	Regulation overview.Regulation of cell cycle.Regulation of meiosis	vit_05s0020g04170	Transcript	RecA/Rad51/DMC1	0,73	1,27	1,29	1,55
5.1.3	Regulation overview.Regulation of cell cycle.Regulation of mitosis	vit_01s0010g02430	Transcript	Mitotic spindle checkpoint protein (MAD2)	-1,67	-1,39	-1,63	-0,93
5.1.3	Regulation overview.Regulation of cell cycle.Regulation of mitosis	vit_08s0007g00170	Transcript	DPB-1 transcription factor (DPB)	0,6	0,65	0,58	1,71
5.2.1.1.1	Regulation overview.Regulation of gene expression.Gene silencing.Posttranscriptional gene silencing by RNA.mRNA cleavage involved in gene silencing by miRNA	vit_04s0023g00920	Transcript	DCL2 (DICER 2)	-1,96	-1,8	-2,25	-2,42
5.2.2.1.3	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.AP2 family transcription factor	vit_06s0004g08190	Transcript	Ethylene-responsive transcription factor cytokinin response factor 1	2,26	2,62	2,33	1,79
5.2.2.1.3.2	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.AP2 family transcription factor.ERF subfamily transcription factor	vit_04s0008g05440	Transcript	Ethylene-responsive transcription factor SHINE 3	-1,56	-1,58	-0,9	-1,33
5.2.2.1.3.2	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.AP2 family transcription factor.ERF subfamily transcription factor	vit_12s0059g00280	Transcript	Dehydration-responsive element-binding protein 16	2,25	2,28	2,21	1,7
5.2.2.1.3.2	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.AP2 family transcription factor.ERF subfamily transcription factor	vit_06s0004g00490	Transcript	Ethylene-responsive transcription factor related to APETALA2 11	1,52	1,54	1,47	1,29
5.2.2.1.7	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.AS2 family transcription factor	vit_18s0001g09250	Transcript	Lateral organ boundaries protein 38	1,54	1,65	0	1
5.2.2.1.11	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.bHLH family transcription factor	vit_05s0020g04620	Transcript	Basic helix-loop-helix (bHLH) family	2,02	1,99	2,13	2,13

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5.2.2.1.11	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.bHLH family transcription factor	vit_05s0049g00460	Transcript	Basic helix-loop-helix ILR3	1,44	1,51	0,79	1,44
5.2.2.1.11	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.bHLH family transcription factor	vit_06s0004g07700	Transcript	Basic helix-loop-helix (bHLH) family	-1,9	-1,61	-0,96	-1,22
5.2.2.1.11	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.bHLH family transcription factor	vit_08s0058g00960	Transcript	Basic helix-loop-helix (bHLH) family	-1,69	-0,92	-0,93	-1,03
5.2.2.1.12	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.bZIP family transcription factor	vit_14s0083g00700	Transcript	BZIP transcription factor BZIP42	2,99	1,66	1,33	1,75
5.2.2.1.12	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.bZIP family transcription factor	vit_19s0014g01780	Transcript	BZIP transcription factor	0,67	1,64	0,81	0,09
5.2.2.1.14	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.CO-like / B-box family transcriprion factor	vit_01s0011g03520	Transcript	Constans-like 16	-1,44	-2,07	-1,57	-1,43
5.2.2.1.14	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.CO-like / B-box family transcriprion factor	vit_14s0083g00640	Transcript	Constans 2 (COL2)	-2,24	-2,69	-3,01	-3,58
5.2.2.1.15	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.C2C2-DOF family transcription factor	vit_01s0026g02580	Transcript	Cycling DOF factor 2	-1,96	-2,38	-2,09	-2,38
5.2.2.1.15	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.C2C2-DOF family transcription factor	vit_08s0056g01230	Transcript	Cycling DOF factor 2	-1,27	-1,6	-1,59	-1,63
5.2.2.1.15	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.C2C2-DOF family transcription factor	vit_14s0108g00980	Transcript	Cycling DOF factor 1	-2,32	-3,36	-2,79	-2,98
5.2.2.1.16	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.C2C2-GATA family transcription factor	vit_03s0038g00490	Transcript	GATA transcription factor 12	2,01	2,33	1,54	1,43
5.2.2.1.17	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.C2H2 family transcription factor	vit_01s0010g02100	Transcript	Indeterminate(ID)-domain 5	-2,22	-1,81	-1,19	-1,31
5.2.2.1.21.2	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.CCAAT family transcription factor.HAP2-type	vit_19s0015g00440	Transcript	Nuclear transcription factor Y subunit B-3 (CCAAT)	2,4	1,91	1,96	2,09
5.2.2.1.22	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.CPP family transcription factor	vit_04s0008g03670	Transcript	Tesmin/TSO1-like CXC domain-containing	1,53	1,38	1,45	1,45
5.2.2.1.23	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.CSD family transcription factor	vit_03s0038g02130	Transcript	Cold shock protein-1	-1,43	-1,46	-1,33	-2,06
5.2.2.1.26	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.E2F/DP family transcription factor	vit_08s0007g00170	Transcript	DPB-1 transcription factor (DPB)	0,6	0,65	0,58	1,71
5.2.2.1.29	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.G2-like family transcription factor	vit_12s0028g03100	Transcript	GPRI1 (GOLDEN2 1)	-1,56	-1,6	-1,01	-1,29
5.2.2.1.32	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.GRAS family transcription factor	vit_13s0019g01700	Transcript	Scarecrow transcription factor 14 (SCL14_1)	1,96	2,2	2,11	1,34
5.2.2.1.32	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.GRAS family transcription factor	vit_13s0019g01710	Transcript	Scarecrow transcription factor 14 (SCL14_9)	1,6	1,27	1,68	1,11
5.2.2.1.32	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.GRAS family transcription factor	vit_02s0025g04000	Transcript	Scarecrow transcription factor 29 (SCL29)	-1,73	-1,68	-1,51	-1,25
5.2.2.1.32	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.GRAS family transcription factor	vit_07s0129g00340	Transcript	Shoot gravitropism 7	-2,11	-1,58	-0,96	-2,07
5.2.2.1.33	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.GRF family transcription factor	vit_09s0002g01350	Transcript	Growth-regulating factor 5	-1,78	-1,18	-1,29	-0,93
5.2.2.1.34	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.HMG family transcription factor	vit_18s0122g01190	Transcript	HIGH MOBILITY GROUP B 3	-1,58	-1,34	-1,47	-0,97

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5.2.2.1.35	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Homeobox domain family transcription factor	vit_02s0025g00200	Transcript	BEL1 (BELL 1)	-1,81	-2,12	-0,98	-2,08
5.2.2.1.35	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Homeobox domain family transcription factor	vit_16s0100g00670	Transcript	Homeodomain GLABROUS1	1,37	2,01	0,92	1,48
5.2.2.1.37	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.HSF family transcription factor	vit_04s0008g01110	Transcript	Heat shock transcription factor A6B_2	4,89	3,03	2,16	2,33
5.2.2.1.37	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.HSF family transcription factor	vit_01s0011g05970	Transcript	Heat stress transcription factor A-8	2,52	2,96	2,66	2,62
5.2.2.1.37	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.HSF family transcription factor	vit_00s0179g00150	Transcript	Heat shock transcription factor A6B	3,12	1,41	0,99	1,08
5.2.2.1.37	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.HSF family transcription factor	vit_02s0025g04170	Transcript	Heat shock transcription factor B2B	-1,90	-3,91	-3,49	-2,28
5.2.2.1.37	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.HSF family transcription factor	VIT_16s0100g00720	Transcript	Heat shock transcription factor B2A_1	-0,581	-1,953	-1,523	-0,180
5.2.2.1.43	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.MBF	vit_19s0014g01260	Transcript	Multiprotein-bridging factor 1a MBF1A	1,59	1,12	0,59	1,04
5.2.2.1.44	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.MYB family transcription factor	vit_08s0007g06180	Transcript	Myb family G2-like (TF)	1,59	1,5	0,54	1,46
5.2.2.1.44	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.MYB family transcription factor	vit_02s0025g02210	Transcript	MYB Domain protein 6	2,21	2,07	1,37	0,8
5.2.2.1.44	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.MYB family transcription factor	vit_04s0008g01810	Transcript	Myb domain protein 4	-0,95	-1,23	-1,62	-1,18
5.2.2.1.44	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.MYB family transcription factor	vit_01s0011g03730	Transcript	myb domain protein 62	-2,3	-1,72	-2,54	-1,07
5.2.2.1.44	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.MYB family transcription factor	vit_04s0079g00410	Transcript	CIR1/RVE2 (circadian 1)	-4,88	-5,22	-5,9	-4,93
5.2.2.1.44	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.MYB family transcription factor	vit_07s0129g01050	Transcript	Myb domain protein 73	1,78	1,92	1,15	0,36
5.2.2.1.44	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.MYB family transcription factor	vit_08s0040g03220	Transcript	LCL1 (LHY/CCA1-like 1)	-1,62	-1,67	-1,66	-1,55
5.2.2.1.44	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.MYB family transcription factor	vit_14s0006g01620	Transcript	Myb domain protein 4	1,6	0,65	0,16	0,37
5.2.2.1.44	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.MYB family transcription factor	vit_14s0066g01220	Transcript	ATMYB66/WER/WER1 (WEREWOLF 1)	-1,37	-1,42	-1,67	-0,86
5.2.2.1.44	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.MYB family transcription factor	vit_15s0046g00170	Transcript	MYBPA1 protein [Vitis vinifera]	1,99	1,43	1,36	1,13
5.2.2.1.44	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.MYB family transcription factor	vit_15s0048g02410	Transcript	Myb CCA1 (circadian clock associated 1)	-4,14	-4,6	-4,94	-4,47
5.2.2.1.44	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.MYB family transcription factor	vit_18s0001g09850	Transcript	Myb domain protein R1	1,52	1,66	0,59	-0,47
5.2.2.1.44	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.MYB family transcription factor	vit_18s0001g11170	Transcript	Myb domain protein 73	2,18	3,62	1,84	0,91
5.2.2.1.45	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.MYB-related family transcription factor	vit_01s0026g01050	Transcript	Myb family	-1,8	-2,33	-2,14	-1,66

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5.2.2.1.46	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.NAC family transcription factor	vit_15s0048g02270	Transcript	No apical meristem cup-shaped cotyledon2	-1,92	-1,66	-2,27	-2,15
5.2.2.1.46	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.NAC family transcription factor	vit_15s0048g02310	Transcript	NAC transcription factor-like 9 NTL9 (NAC TF)	-3,81	-1,87	-1,67	-2,12
5.2.2.1.46	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.NAC family transcription factor	vit_15s0048g02320	Transcript	No apical meristem cup-shaped cotyledon2	-1,53	-1,97	-3,15	-2,24
5.2.2.1.46	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.NAC family transcription factor	vit_15s0048g02270	Transcript	No apical meristem cup-shaped cotyledon2	-1,92	-1,66	-2,27	-2,15
5.2.2.1.46	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.NAC family transcription factor	vit_15s0048g02300	Transcript	NAC transcription factor-like 9	-1,44	-1,44	-2,27	-1,49
5.2.2.1.46	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.NAC family transcription factor	vit_17s0000g06400	Transcript	NAC domain containing protein 100	1,14	1,87	1,04	0,94
5.2.2.1.52	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.RWP-RK family transcription factor	vit_04s0044g00060	Transcript	RWP-RK domain-containing protein	1,47	1,85	1,49	1,84
5.2.2.1.60	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.TAZ family transcription factor	vit_07s0129g00210	Transcript	BT4 (BTB and TAZ Domain protein 4)	1,52	2	1,22	0,65
5.2.2.1.61	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.TCP family transcription factor	vit_12s0028g02520	Transcript	TCP family transcription factor 4	-2,03	-2,17	-1,69	-1,53
5.2.2.1.62	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Trihelix family transcription factor	vit_00s0956g00030	Transcript	DNA-binding protein	1,06	1,55	1,02	1,07
5.2.2.1.63	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.TUBBY-like family transcription factor	vit_05s0020g01930	Transcript	TUBBY like protein 3 TLP3	2,27	2,22	2,14	1,76
5.2.2.1.66	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.WRKY family transcription factor	vit_04s0023g00470	Transcript	WRKY DNA-binding protein 2 (WRKY)	1,57	1,6	1,61	1,5
5.2.2.1.66	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.WRKY family transcription factor	vit_07s0031g01710	Transcript	WRKY DNA-binding protein 51	-2,42	-2,46	-3,71	-1,68
5.2.2.1.66	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.WRKY family transcription factor	vit_08s0058g01390	Transcript	WRKY DNA-binding protein 70	-1,13	-1,37	-1,74	-1,22
5.2.2.1.66	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.WRKY family transcription factor	vit_13s0067g03140	Transcript	WRKY DNA-binding protein 70	-1,37	-1,71	-1,44	-1,02
5.2.2.1.68	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.zf-HD family transcription factor	vit_01s0026g02460	Transcript	Zinc finger homeobox 30	0,92	1,1	1,8	1,49
5.2.2.1.68	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.zf-HD family transcription factor	vit_17s0000g08710	Transcript	KNAT2 (knotted1-like homeobox gene 6)	-1,15	-0,72	-1,56	-0,9
5.2.2.1.70	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.CCT family transcription factor	vit_06s0004g07210	Transcript	CCT motif constans-like	6,65	4,82	7,69	7,13
5.2.2.1.71	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.FAR1-like family transcription factor	vit_05s0077g01400	Transcript	FAR1-related sequence 11	1,8	1,52	1,72	1,25
5.2.2.1.73	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger B-box family transcription factor	vit_03s0038g00340	Transcript	Salt tolerance homolog2(zf-box)	6,73	7,77	6,73	7,09
5.2.2.1.73	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger B-box family transcription factor	vit_03s0038g00690	Transcript	Zinc finger (B-box type)	-1,08	-1,29	-1,63	-1,36
5.2.2.1.73	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger B-box family transcription factor	vit_12s0059g02510	Transcript	Zinc finger (B-box type)	-2,01	-2,59	-3,3	-2,97

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
5.2.2.1.73	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger B-box family transcription factor	vit_04s0023g03030	Transcript	Zinc finger (B-box type)	-1,21	-1,78	-1,93	-1,7
5.2.2.1.73	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger B-box family transcription factor	vit_19s0014g03960	Transcript	Zinc finger (B-box type)	-1,02	-1,75	-1,8	-1,84
5.2.2.1.77	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger AN1 family transcription factor	vit_13s0064g01210	Transcript	Zf A20 and AN1 domain-containing stress-associated protein 2	1,51	1,65	1,36	1,41
5.2.2.1.78	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger C3HC4 family transcription factor	vit_02s0025g01990	Transcript	Zinc finger (C3HC4-type ring finger)	1,54	1,64	1,59	1,23
5.2.2.1.78	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger C3HC4 family transcription factor	vit_15s0046g02070	Transcript	Zinc finger (C3HC4-type ring finger)	1,74	2,54	1,61	2,03
5.2.2.1.78	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger C3HC4 family transcription factor	vit_01s0026g02540	Transcript	Zinc finger (C3HC4-type ring finger)	2	1,2	1,57	2,46
5.2.2.1.78	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger C3HC4 family transcription factor	vit_04s0008g04480	Transcript	Zinc finger (C3HC4-type ring finger)	2,1	1,8	1,32	1,43
5.2.2.1.78	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger C3HC4 family transcription factor	vit_06s0004g05850	Transcript	Zinc finger (C3HC4-type ring finger)	2,11	2,28	2,14	2,04
5.2.2.1.78	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger C3HC4 family transcription factor	vit_06s0004g08080	Transcript	Zinc finger (C3HC4-type ring finger)	4,36	3,83	4,01	4,91
5.2.2.1.78	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger C3HC4 family transcription factor	vit_07s0031g02250	Transcript	Zinc finger (C3HC4-type ring finger)	1,3	1,72	1,52	1,44
5.2.2.1.78	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger C3HC4 family transcription factor	vit_08s0040g01950	Transcript	Zinc finger (C3HC4-type ring finger)	1,46	1,4	1,28	1,54
5.2.2.1.78	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger C3HC4 family transcription factor	vit_09s0018g01220	Transcript	Zinc finger (C3HC4-type ring finger)	-1,36	-1,12	-1,71	-1,35
5.2.2.1.78	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger C3HC4 family transcription factor	vit_14s0219g00030	Transcript	Zinc finger (C3HC4-type ring finger)	-1,54	-1,21	-1,49	-1,03
5.2.2.1.78	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger C3HC4 family transcription factor	vit_14s0219g00040	Transcript	Zinc finger (C3HC4-type ring finger)	-0,87	-1,08	-1,51	-1,68
5.2.2.1.78	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.Zinc finger C3HC4 family transcription factor	vit_17s0000g06610	Transcript	Zinc finger (C3HC4-type ring finger)	-1,56	-1,66	-1,71	-1,76
5.2.2.1.96	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.GATA family transcription factor	vit_04s0008g01290	Transcript	CGA1 (cytokinin-responsive GATA factor 1)	-0,84	-1,09	-0,47	-1,66

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
5.2.2.1.96	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.GATA family transcription factor	vit_19s0014g03210	Transcript	COP1-interacting protein 7	1,52	1,55	1,75	1,35
5.2.2.2	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factors adaptation	vit_04s0044g01260	Transcript	SEU3B protein	1,46	1,55	1,78	1,24
5.2.2.3	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcriptional co-activation	vit_11s0016g04080	Transcript	Multiprotein-bridging factor 1c MBF1C	5,16	3,06	1,77	3,03
5.2.3	Regulation overview.Regulation of gene expression.Regulation of translation	vit_05s0049g01660	Transcript	RNA-binding protein Musashi	-0,93	-1,29	-0,97	-1,64
6.2	Response to stimulus.Stress response	vit_05s0094g00360	Transcript	Chitinase class IV	2,35	1,27	1,83	2,11
6.2	Response to stimulus.Stress response	vit_11s0016g04080	Transcript	Multiprotein-bridging factor 1c MBF1C	5,16	3,06	1,77	3,03
6.2	Response to stimulus.Stress response	vit_14s0060g01300	Transcript	Universal stress protein (USP) family protein	1,22	1,07	0,86	1,86
6.2	Response to stimulus.Stress response	vit_14s0081g00030	Transcript	Pathogenesis-related protein-4 (Chitinase)	1,96	1,53	0,93	1,65
6.2	Response to stimulus.Stress response	vit_15s0046g01570	Transcript	Acidic endochitinase (CHIB1)	1,56	1,58	0,47	1,73
6.2.1	Response to stimulus.Stress response.Abiotic stress response	vit_17s0000g07770	Transcript	LTCOR11	1,17	1,5	1,41	1,58
6.2.1	Response to stimulus.Stress response.Abiotic stress response	vit_07s0104g00360	Transcript	Early-responsive to dehydration	2,21	3,52	2,4	2,52
6.2.1.1	Response to stimulus.Stress response.Abiotic stress response.Desiccation stress response	vit_04s0008g02920	Transcript	Desiccation protein PCC13-62 precursor	-2,17	-1,65	-2,12	-1,36
6.2.1.1	Response to stimulus.Stress response.Abiotic stress response.Desiccation stress response	vit_04s0023g02480	Transcript	Dehydrin 1b	3,17	2,8	1,93	1,51
6.2.1.2	Response to stimulus.Stress response.Abiotic stress response.Drought stress response	vit_03s0063g02340	Transcript	Dehydration-responsive protein (RD22)	-2,25	-1,83	-0,87	-1,12
6.2.1.3.1	Response to stimulus.Stress response.Abiotic stress response.Heavy metal stress response.Aluminium stress response	vit_02s0012g01030	Transcript	Aluminum-activated malate transporter 1	0,48	0,56	1,54	0,7
6.2.1.5	Response to stimulus.Stress response.Abiotic stress response.Light stress response	vit_18s0072g00120	Transcript	Light stress-responsive one-helix protein (OHP2)	-1,19	-1,64	-1,58	-1,55
6.2.1.7	Response to stimulus.Stress response.Abiotic stress response.Oxidative stress response	vit_00s0153g00050	Transcript	Glutathione S-transferase 8 GSTU8	1,61	2,35	1,75	2,5
6.2.1.7	Response to stimulus.Stress response.Abiotic stress response.Oxidative stress response	vit_00s0480g00030	Transcript	Polyphenol oxidase	-1,53	-1,67	-1,23	-1,19
6.2.1.7	Response to stimulus.Stress response.Abiotic stress response.Oxidative stress response	vit_02s0025g03600	Transcript	Phospholipid hydroperoxide glutathione peroxidase	1,56	1,33	1,18	1,35
6.2.1.7	Response to stimulus.Stress response.Abiotic stress response.Oxidative stress response	vit_07s0005g00030	Transcript	Glutathione S-transferase 8 GSTF8	2,33	1,41	0,9	1,57
6.2.1.7	Response to stimulus.Stress response.Abiotic stress response.Oxidative stress response	vit_08s0040g03150	Transcript	L-ascorbate peroxidase 1, cytosolic (APX1)	1,99	2	1,52	1,63
6.2.1.7	Response to stimulus.Stress response.Abiotic stress response.Oxidative stress response	vit_12s0059g02420	Transcript	Peroxidase ATP11A (gb|X98802).	1,73	1,96	1,86	1,82
6.2.1.7	Response to stimulus.Stress response.Abiotic stress response.Oxidative stress response	vit_17s0000g02950	Transcript	Glutathione S-transferase 25 GSTU7	-1,58	-2,5	-3,37	-1,42
6.2.1.7	Response to stimulus.Stress response.Abiotic stress response.Oxidative stress response	vit_18s0001g06840	Transcript	Peroxidase GvPx2b class III	-2,99	-2,37	-1,74	-2,04
6.2.1.7	Response to stimulus.Stress response.Abiotic stress response.Oxidative stress response	vit_19s0015g02590	Transcript	Glutathione S-transferase 25 GSTU25	2,63	2,93	3,04	2,93
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_00s0179g00150	Transcript	Heat shock transcription factor A6B	3,12	1,41	0,99	1,08

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_00s0958g00020	Transcript	FK506-binding protein 4/5 ROF1 (rotamase FKBP 1)	1,78	1,16	0,6	0,83
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_01s0010g02290	Transcript	Heat shock protein 26a, chloroplast	2,3	0,6	-0,1	0,66
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_02s0025g02140	Transcript	Heat shock protein 70	1,98	1,27	0,83	0,55
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_02s0025g04170	Transcript	Heat shock transcription factor B2B	-1,9	-3,91	-3,49	-2,28
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_05s0020g03330	Transcript	Heat shock protein 70	2,41	1,88	1,11	0,81
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_06s0004g04470	Transcript	Heat shock protein 70	4,12	1,28	0,27	0,64
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_06s0004g04510	Transcript	Heat shock protein 70	1,52	1,19	1,07	0,79
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_11s0037g00510	Transcript	Heat shock protein 70	3,23	1,09	0,39	0,12
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_13s0019g03000	Transcript	Heat shock protein 17.6 kDa class I	1,66	-0,11	-0,79	0,06
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_13s0019g03160	Transcript	Heat shock protein 17.6 kDa class I	3,55	0,92	0,35	0,81
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_14s0060g02340	Transcript	Heat shock protein 70	3,64	3,01	2,4	1,76
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_16s0098g01060	Transcript	Heat shock protein 26a, chloroplast	2,61	1,34	0,68	0,36
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_16s0098g01580	Transcript	Heat shock protein 70	2,38	1,73	1,31	0,83
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_18s0041g01230	Transcript	Heat shock protein 70	1,89	0,2	0,01	-0,42
6.2.2	Response to stimulus.Stress response.Biotic stress response	vit_08s0058g00040	Transcript	Verticillium wilt disease resistance protein Ve2	1,77	1,08	2,27	1,39
6.2.2	Response to stimulus.Stress response.Biotic stress response	vit_01s0010g02030	Transcript	Gamma-thionin precursor	2,16	1,65	1,25	1,52
6.2.2	Response to stimulus.Stress response.Biotic stress response	vit_02s0025g00280	Transcript	Heat shock protein 90-1	5,17	2,39	1,49	1,19
6.2.2	Response to stimulus.Stress response.Biotic stress response	vit_03s0038g01770	Transcript	Disease resistance protein (CC-NBS-LRR class)	-1,32	-1,63	-1,37	-1,26
6.2.2	Response to stimulus.Stress response.Biotic stress response	vit_03s0091g00160	Transcript	NtPRp27 secretory protein	0,2	-1,04	-1,88	-0,31
6.2.2	Response to stimulus.Stress response.Biotic stress response	vit_05s0102g00450	Transcript	MSS3 (multicopy suppressors of snf4 deficiency in yeast 3)	-1,51	-1,66	-1,6	-1,78
6.2.2	Response to stimulus.Stress response.Biotic stress response	vit_06s0004g00990	Transcript	Disease resistance-responsive	-1,57	-1,35	-1,28	-1,29
6.2.2	Response to stimulus.Stress response.Biotic stress response	vit_08s0056g00290	Transcript	Calcium-binding protein CML	-1,84	-1,86	-2,56	-1,7
6.2.2	Response to stimulus.Stress response.Biotic stress response	vit_11s0118g00080	Transcript	Disease resistance protein	1,24	1,05	1,12	1,82
6.2.2	Response to stimulus.Stress response.Biotic stress response	vit_12s0034g02530	Transcript	R protein disease resistance protein	-1,33	-1,51	-1,35	-1,23
6.2.2	Response to stimulus.Stress response.Biotic stress response	vit_13s0139g00340	Transcript	R protein MLA10	-0,83	-0,93	-1,04	-1,53
6.2.2	Response to stimulus.Stress response.Biotic stress response	vit_18s0001g14500	Transcript	SHD (shepherd)	2,12	1,85	1,54	1,6
6.2.2.2	Response to stimulus.Stress response.Biotic stress response.Virus stress response	vit_16s0039g00340	Transcript	Harpin-induced protein-related	1,82	1,62	1,22	1,27
6.2.2.3	Response to stimulus.Stress response.Biotic stress response.Plant-pathogen_interaction	vit_09s0018g01080	Transcript	EFR (EF-TU receptor)	-1,83	-2,61	-1,89	-2,58

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
6.2.2.3	Response to stimulus.Stress response.Biotic stress response.Plant-pathogen_interaction	vit_13s0067g00420	Transcript	Protein kinase Xa21	2,44	2,27	2,26	1,91
6.2.2.3	Response to stimulus.Stress response.Biotic stress response.Plant-pathogen_interaction	vit_13s0067g00490	Transcript	Protein kinase Xa21	-1,98	-2,3	-1,36	-2,02
6.2.2.3	Response to stimulus.Stress response.Biotic stress response.Plant-pathogen_interaction	vit_13s0067g00440	Transcript	Protein kinase Xa21	1,57	2,3	2,38	0
7.1.1.1.1	Signalling.Hormone signalling.ABA signalling.ABA metabolism.ABA biosynthesis	vit_02s0087g00910	Transcript	9-cis-epoxycarotenoid dioxygenase	2,75	2,73	3,38	2,29
7.1.1.1.2	Signalling.Hormone signalling.ABA signalling.ABA metabolism.ABA catabolism	vit_18s0001g10500	Transcript	ABA 8'-hydroxylase CYP707A1	1,16	1,41	1,55	0,54
7.1.1.2	Signalling.Hormone signalling.ABA signalling.ABA-mediated signalling pathway	vit_02s0012g01270	Transcript	abscisic acid receptor PYR1-like	-1,88	-1,57	-0,8	-1,05
7.1.1.2	Signalling.Hormone signalling.ABA signalling.ABA-mediated signalling pathway	vit_04s0008g05600	Transcript	KEG (keep on going)	1,28	1,23	1,36	1,52
7.1.1.2	Signalling.Hormone signalling.ABA signalling.ABA-mediated signalling pathway	vit_11s0016g03180	Transcript	ABI1 (ABA insensitive 1)	-0,68	-0,99	-1,18	-1,82
7.1.2.1.2	Signalling.Hormone signalling.Auxin signalling.Auxin metabolism.Auxin inactivation by conjugation	vit_03s0180g00320	Transcript	Indole-3-acetate beta-glucosyltransferase	1,73	1,78	1,47	1,25
7.1.2.1.2	Signalling.Hormone signalling.Auxin signalling.Auxin metabolism.Auxin inactivation by conjugation	vit_06s0004g07310	Transcript	Indole-3-acetate beta-glucosyltransferase	0,77	1,22	1,59	0,37
7.1.2.1.2	Signalling.Hormone signalling.Auxin signalling.Auxin metabolism.Auxin inactivation by conjugation	vit_07s0129g00660	Transcript	Indole-3-acetic acid-amido synthetase GH3.2	-1,84	-1,66	-1,9	-1,36
7.1.2.2	Signalling.Hormone signalling.Auxin signalling.Auxin responsive	vit_07s0005g00090	Transcript	Auxin-responsive GH3	1,45	1,85	2,04	1,24
7.1.2.2	Signalling.Hormone signalling.Auxin signalling.Auxin responsive	vit_02s0154g00010	Transcript	Auxin-responsive SAUR11	0,96	1,73	1,14	0,33
7.1.2.2	Signalling.Hormone signalling.Auxin signalling.Auxin responsive	vit_03s0038g01110	Transcript	Auxin-responsive SAUR31	-1,81	-1,98	-1,46	-1,19
7.1.2.2	Signalling.Hormone signalling.Auxin signalling.Auxin responsive	vit_04s0008g02800	Transcript	SAUR_D	-1,63	-0,84	-1,38	-1,28
7.1.2.4	Signalling.Hormone signalling.Auxin signalling.Auxin-mediated signalling pathway	vit_05s0020g04670	Transcript	auxin-responsive protein IAA4-like	-1,02	-1,15	-2,22	-0,66
7.1.2.4	Signalling.Hormone signalling.Auxin signalling.Auxin-mediated signalling pathway	vit_04s0008g05560	Transcript	IAA29	-1,17	-1,36	-1,65	-1,5
7.1.2.4	Signalling.Hormone signalling.Auxin signalling.Auxin-mediated signalling pathway	vit_07s0141g00270	Transcript	Auxin-induced protein 22D	-1,69	-3,08	-1,89	-2,02
7.1.2.4	Signalling.Hormone signalling.Auxin signalling.Auxin-mediated signalling pathway	vit_11s0016g01220	Transcript	Auxin-binding protein ABP19a precursor	-2,03	-2,19	-1,06	-1,59
7.1.2.4	Signalling.Hormone signalling.Auxin signalling.Auxin-mediated signalling pathway	vit_11s0016g05640	Transcript	IAA29	-1,33	-1,71	-1,96	-2,09
7.1.3.1.1	Signalling.Hormone signalling.Brassinosteroid signalling.Brassinosteroid metabolism.Brassinosteroid biosynthesis	vit_19s0014g00080	Transcript	Steroid 5alpha-reductase	-1,18	-1,5	-1,47	-1,94
7.1.4	Signalling.Hormone signalling.Cytokinin signalling	vit_00s0640g00020	Transcript	Cig3	0,93	1,74	1,32	1,31
7.1.4.1.2	Signalling.Hormone signalling.Cytokinin signalling.Cytokinin metabolism.Cytokinin catabolism	vit_04s0008g01880	Transcript	Cytokinin dehydrogenase 7	1,56	1,8	1,64	0,8
7.1.4.1.3	Signalling.Hormone signalling.Cytokinin signalling.Cytokinin metabolism.Cytokinin inactivation by glycosylation	vit_08s0040g01470	Transcript	Cis-zeatin O-beta-D-glucosyltransferase	-1,2	-1,89	-1,58	-2,44
7.1.4.1.3	Signalling.Hormone signalling.Cytokinin signalling.Cytokinin metabolism.Cytokinin inactivation by glycosylation	vit_14s0066g01480	Transcript	Cis-zeatin O-beta-D-glucosyltransferase	1,02	1,06	1,58	0,7

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
7.1.4.2	Signalling.Hormone signalling.Cytokinin signalling.Cytokinin transport	vit_18s0001g06940	Transcript	Purine permease 1 (PUP1)	1,62	1,82	1,19	1,96
7.1.4.3	Signalling.Hormone signalling.Cytokinin signalling.Cytokinin-mediated signalling pathway	vit_06s0004g05120	Transcript	ARR1 typeB	4,24	5,3	4,97	5,15
7.1.4.3	Signalling.Hormone signalling.Cytokinin signalling.Cytokinin-mediated signalling pathway	vit_11s0016g03170	Transcript	Arabidopsis histidine phosphotransfer AHP4	-0,86	-1,27	-1,62	-1,64
7.1.5.1.1	Signalling.Hormone signalling.Ethylene signalling.Ethylene metabolism.Ethylene biosynthesis	vit_00s1764g00010	Transcript	1-aminocyclopropane-1-carboxylate synthase	1,88	0,8	1,13	1,1
7.1.5.1.1	Signalling.Hormone signalling.Ethylene signalling.Ethylene metabolism.Ethylene biosynthesis	vit_02s0012g00450	Transcript	1-aminocyclopropane-1-carboxylate oxidase	1,25	1,45	1,72	1,84
7.1.5.1.1	Signalling.Hormone signalling.Ethylene signalling.Ethylene metabolism.Ethylene biosynthesis	vit_11s0016g02380	Transcript	1-aminocyclopropane-1-carboxylate oxidase homolog 1 like	-1,82	-1,47	-1,12	-1,05
7.1.5.1.1	Signalling.Hormone signalling.Ethylene signalling.Ethylene metabolism.Ethylene biosynthesis	vit_05s0049g00410	Transcript	1-aminocyclopropane-1-carboxylate oxidase homolog 1 like	1,9	1,53	1,11	1,53
7.1.5.1.1	Signalling.Hormone signalling.Ethylene signalling.Ethylene metabolism.Ethylene biosynthesis	vit_05s0049g00300	Transcript	1-aminocyclopropane-1-carboxylate oxidase homolog 1 like	2,25	1,7	1,43	1,12
7.1.5.1.1	Signalling.Hormone signalling.Ethylene signalling.Ethylene metabolism.Ethylene biosynthesis	vit_05s0049g00430	Transcript	1-aminocyclopropane-1-carboxylate oxidase homolog 1	1,68	2,29	1,58	1,96
7.1.5.1.1	Signalling.Hormone signalling.Ethylene signalling.Ethylene metabolism.Ethylene biosynthesis	vit_15s0021g00960	Transcript	1-aminocyclopropane-1-carboxylate oxidase	0,87	1,71	0,44	1,36
7.1.5.2	Signalling.Hormone signalling.Ethylene signalling.Ethylene responsive	vit_12s0059g00280	Transcript	Dehydration-responsive element-binding protein 16	2,25	2,28	2,21	1,7
7.1.5.2	Signalling.Hormone signalling.Ethylene signalling.Ethylene responsive	vit_13s0067g01960	Transcript	Dehydration-responsive element-binding protein 2C	2,36	2,09	2,27	2,91
7.1.5.2	Signalling.Hormone signalling.Ethylene signalling.Ethylene responsive	vit_10s0003g00580	Transcript	ERF/AP2 transcription factor sub B-3 (ATERF-2)	0	2,63	0	0
7.1.6.1.2	Signalling.Hormone signalling.Gibberellic acid signalling.Gibberellic acid metabolism.Gibberellic acid catabolism	vit_06s0004g06790	Transcript	Gibberellin 2-beta-dioxygenase 7	0,96	0,21	1,68	0,97
7.1.6.1.2	Signalling.Hormone signalling.Gibberellic acid signalling.Gibberellic acid metabolism.Gibberellic acid catabolism	vit_19s0140g00120	Transcript	Gibberellin 2-beta-dioxygenase 1	-0,89	-1,29	-1,75	-1,88
7.1.7.1	Signalling.Hormone signalling.Jasmonate signalling.Jasmonate metabolism	vit_00s0253g00110	Transcript	Methyl jasmonate esterase	1,11	1,64	1,44	1,02
7.1.7.1	Signalling.Hormone signalling.Jasmonate signalling.Jasmonate metabolism	vit_00s0253g00150	Transcript	Methyl jasmonate esterase	3,1	2,27	2,16	2,43
7.1.7.1	Signalling.Hormone signalling.Jasmonate signalling.Jasmonate metabolism	vit_01s0011g05900	Transcript	Jasmonate O-methyltransferase	-1,24	-1,67	-1,8	-1,94
7.2.2	Signalling.Signalling pathway.Calcium sensors and signalling	vit_00s0283g00030	Transcript	Calnexin 1 (CNX1)	2,38	1,88	1,13	0,98
7.2.2	Signalling.Signalling pathway.Calcium sensors and signalling	vit_02s0025g01640	Transcript	Calcineurin B 4-1	1,68	1,38	1,66	1,78
7.2.2	Signalling.Signalling pathway.Calcium sensors and signalling	vit_04s0023g00830	Transcript	Calreticulin 3 (CRT3)	2,07	1,8	1,5	1,95
7.2.2	Signalling.Signalling pathway.Calcium sensors and signalling	vit_05s0077g00810	Transcript	Sodium-inducible calcium-binding protein (ACP1)	-1,3	-1,61	-1,55	-1,86
7.2.2	Signalling.Signalling pathway.Calcium sensors and signalling	vit_06s0004g06030	Transcript	Calcium/calmodulin-regulated receptor kinase	1,34	1,71	2,14	1,94
7.2.2	Signalling.Signalling pathway.Calcium sensors and signalling	vit_09s0002g08100	Transcript	Calcineurin	2,29	1,6	1,88	1,91
7.2.2	Signalling.Signalling pathway.Calcium sensors and signalling	vit_13s0156g00120	Transcript	EF hand	3,63	3,19	3,41	3,29
7.2.2	Signalling.Signalling pathway.Calcium sensors and signalling	vit_17s0000g04490	Transcript	Extracellular Ca2+ sensing receptor	-1,99	-2,03	-1,77	-1,88
7.2.3	Signalling.Signalling pathway.Circadian clock signalling	vit_01s0011g05810	Transcript	Adagio protein 1	5,53	5,33	5,79	5,36
7.2.3	Signalling.Signalling pathway.Circadian clock signalling	vit_04s0079g00410	Transcript	CIR1/RVE2 (circadian 1)	-4,88	-5,22	-5,9	-4,93
7.2.3	Signalling.Signalling pathway.Circadian clock signalling	vit_06s0004g03660	Transcript	Pseudo-response regulator 7 (APRR7)	3,69	3,29	2,7	2,8

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
7.2.3	Signalling.Signalling pathway.Circadian clock signalling	vit_08s0040g03220	Transcript	LCL1 (LHY/CCA1-like 1)	-1,62	-1,67	-1,66	-1,55
7.2.3	Signalling.Signalling pathway.Circadian clock signalling	vit_15s0048g02410	Transcript	Myb CCA1 (circadian clock associated 1)	-4,14	-4,6	-4,94	-4,47
7.2.3	Signalling.Signalling pathway.Circadian clock signalling	vit_15s0048g02540	Transcript	Pseudo-response regulator 9 (APRR9)	2,33	2,23	2,12	2,09
7.2.3	Signalling.Signalling pathway.Circadian clock signalling	vit_18s0157g00020	Transcript	GIGANTEA protein	4,45	4,34	4,11	3,84
7.2.4	Signalling.Signalling pathway.G-protein signalling pathway	vit_16s0013g00130	Transcript	GTP-binding protein HSR1	1,21	1,22	1,22	1,66
7.2.4	Signalling.Signalling pathway.G-protein signalling pathway	vit_01s0010g02160	Transcript	RGS1 (regulator of G-protein SIGNALING 1)	1,42	1,52	1,41	1,34
7.2.4	Signalling.Signalling pathway.G-protein signalling pathway	vit_03s0063g01780	Transcript	Extra-large G-protein (XLG1)	1,86	2,43	1,74	1,45
7.2.4	Signalling.Signalling pathway.G-protein signalling pathway	vit_08s0007g08290	Transcript	GTP-binding protein typA/bipA	-2,23	-2,39	-2,19	-2,33
7.2.4	Signalling.Signalling pathway.G-protein signalling pathway	vit_18s0001g13120	Transcript	GTP-binding protein hflX	1,61	1,3	1,65	1,51
7.2.4.1	Signalling.Signalling pathway.G-protein signalling pathway.RAB-GTPase regulation	vit_02s0025g04060	Transcript	Rab/Ypt GTPase Ara4-interacting protein	2,85	1,65	0,48	1,05
7.2.4.2	Signalling.Signalling pathway.G-protein signalling pathway.RCC1 superfamily protein	vit_08s0007g00930	Transcript	Regulator of chromosome condensation (RCC1)	-0,75	-1,39	-1,77	-1,49
7.2.4.2	Signalling.Signalling pathway.G-protein signalling pathway.RCC1 superfamily protein	vit_13s0019g02280	Transcript	Regulator of chromosome condensation (RCC1)	-2,9	-4,01	-4,52	-4,11
7.2.4.2	Signalling.Signalling pathway.G-protein signalling pathway.RCC1 superfamily protein	vit_14s0083g01020	Transcript	Regulator of chromosome condensation (RCC1)	2,31	1,84	1,78	1,75
7.2.5	Signalling.Signalling pathway.Light signalling	vit_01s0137g00820	Transcript	Phototropic-responsive NPH3	-1,36	-1,52	-1,33	-1,52
7.2.5	Signalling.Signalling pathway.Light signalling	vit_06s0004g08230	Transcript	Root phototropism protein 2	-1,62	-1,78	-2,07	-2,11
7.2.5	Signalling.Signalling pathway.Light signalling	vit_12s0028g03570	Transcript	SPA3 (SPA1-related 3)	-1,6	-1,91	-2,02	-2,31
7.2.5	Signalling.Signalling pathway.Light signalling	vit_18s0157g00020	Transcript	GIGANTEA protein	4,45	4,34	4,11	3,84
7.2.5.1	Signalling.Signalling pathway.Light signalling.Blue light signalling	vit_06s0004g03700	Transcript	Phototropin-1	-1,82	-1,69	-1,46	-1,52
7.2.6	Signalling.Signalling pathway.Phosphatidylinositol signalling	vit_10s0003g05480	Transcript	SEC14 cytosolic factor	-1,37	-1,54	-1,11	-0,92
7.2.7	Signalling.Signalling pathway.Phospholipid signalling	vit_03s0038g02090	Transcript	Phospholipase C.	1,54	1,18	1,22	0,72
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_17s0000g09290	Transcript	Protein kinase ATN1	1,07	1,5	1,19	1,81
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_16s0098g00020	Transcript	Receptor serine/threonine kinase	1,56	1,44	0,99	1,15
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_19s0014g04280	Transcript	S-locus protein kinase	1,47	1,25	1,02	1,55
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_18s0041g01290	Transcript	Serine/threonine-protein kinase CCR4	1,32	0,8	1,7	0,79
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_16s0098g00230	Transcript	Receptor kinase homolog LRK10	1,47	1,62	1,42	1,19
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_01s0011g04290	Transcript	Receptor serine/threonine kinase PR5K	2,25	2,17	2,05	2,14
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_18s0086g00200	Transcript	Lectin protein kinase family	1,44	1,56	1,74	1,1
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_01s0026g02270	Transcript	Kinase	1,94	1,54	2,05	1,09
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_02s0087g01020	Transcript	CRK10 (cysteine-rich RLK10)	-2,09	-1,94	-1,46	-1,12
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_05s0020g03870	Transcript	MLK/Raf-related protein kinase 1	0,64	2,07	1,02	1,16
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_05s0136g00140	Transcript	AarF domain containing kinase	-1,35	-1,46	-1,32	-1,63
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_06s0004g06430	Transcript	Receptor ser/thr protein kinase	-3,74	-3,48	-2,04	-3,28
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_06s0004g07830	Transcript	SOS2 (salt overly sensitive 2)	2,45	2,39	1,94	1,89
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_06s0080g00070	Transcript	S-receptor kinase	0,52	0,98	1,7	0,53
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_08s0058g00540	Transcript	IMK2 (inflorescence meristem receptor-like kinase 2)	-1,86	-1,78	-1,7	-1,48
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_09s0002g01830	Transcript	Tassel serine threonine kinase 1	1,29	1,55	2	1,96

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_06s0004g02640	Transcript	Receptor protein kinase PERK1	-1,53	-1,54	-1,22	-1
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_09s0018g01390	Transcript	STE20/SPS1 proline-alanine-rich protein kinase	1,24	1,05	1,54	0,96
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_10s0003g01410	Transcript	CBL-interacting protein kinase 20 (CIPK20)	-3,46	-3,86	-3,93	-4,06
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_19s0014g00680	Transcript	RKF1 (receptor-like kinase in flowers 1)	1,11	1,75	2,19	1,67
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_11s0016g03830	Transcript	Protein kinase	-1,74	-2,32	-2,91	-2,8
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_13s0073g00600	Transcript	Receptor-like kinase 17	-1,44	-1,45	-1,58	-1,5
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_14s0006g00250	Transcript	Cysteine-rich repeat secretory protein 60	-1,09	-1,35	-1,32	-2,23
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_14s0066g01400	Transcript	MLK/Raf-related protein kinase 1	-1,74	-1,31	-1,56	-1,35
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_01s0011g04300	Transcript	Receptor serine/threonine kinase PR5K	2,26	2,37	2,29	2,45
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_17s0000g08360	Transcript	Phosphatidylinositol 3- and 4-kinase	-1,26	-1,24	-1,53	-1,11
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_05s0051g00540	Transcript	LRR receptor-like kinase 2	-1,58	-0,91	-0,9	-1,84
7.2.9.1	Signalling.Signalling pathway.Protein kinase.MAPK cascade	vit_07s0031g00530	Transcript	MAPKKK21	3,3	2,99	2,58	1,63
7.2.9.1	Signalling.Signalling pathway.Protein kinase.MAPK cascade	vit_02s0025g04110	Transcript	MAPKKK HA-tagged protein kinase	1,13	1,51	1	1,29
7.2.9.2	Signalling.Signalling pathway.Protein kinase.Ribosomal protein kinase	vit_08s0058g01440	Transcript	Ribosomal S6 kinase p90	-1,5	-1,34	-1,69	-1,36
7.2.10	Signalling.Signalling pathway.Protein phosphatase	vit_00s0250g00020	Transcript	Protein tyrosine phosphatase	1,43	1,55	1,53	1,72
7.2.10	Signalling.Signalling pathway.Protein phosphatase	vit_09s0002g02450	Transcript	Phosphatase	-1,41	-1,33	-2,34	-0,1
7.2.10	Signalling.Signalling pathway.Protein phosphatase	vit_03s0063g02700	Transcript	CPL4 (C-Terminal Domain Phosphatase-like 4)	1,98	1,78	1,37	2,02
7.2.10	Signalling.Signalling pathway.Protein phosphatase	vit_03s0063g02700	Transcript	CPL4 (C-Terminal Domain Phosphatase-like 4)	1,98	1,78	1,37	2,02
7.2.10	Signalling.Signalling pathway.Protein phosphatase	vit_11s0016g03180	Transcript	ABI1 (ABA insensitive 1)	-0,68	-0,99	-1,18	-1,82
7.2.10	Signalling.Signalling pathway.Protein phosphatase	vit_12s0059g01400	Transcript	Tyrosine specific protein phosphatase	-1,47	-1,57	-1,65	-0,65
7.2.10.2	Signalling.Signalling pathway.Protein phosphatase.PP2C	vit_01s0137g00750	Transcript	Protein phosphatase 2C	-1,74	-1,3	-1,5	-0,98
7.2.10.2	Signalling.Signalling pathway.Protein phosphatase.PP2C	vit_16s0050g02680	Transcript	Protein phosphatase 2C	2,12	1,7	1,84	2,03
7.2.10.2	Signalling.Signalling pathway.Protein phosphatase.PP2C	vit_18s0001g09390	Transcript	Protein phosphatase 2C	1,42	1,51	1,26	0,85
7.2.11.2.1	Signalling.Signalling pathway.Signalling molecules.Signalling peptide.Ligand peptide	vit_00s1328g00020	Transcript	Phytosulfokines PSK4	-0,65	0,73	-0,16	1,72
7.2.11.2.1	Signalling.Signalling pathway.Signalling molecules.Signalling peptide.Ligand peptide	vit_01s0010g01710	Transcript	Phytosulfokine receptor	1,76	1,29	1,42	0,63
7.2.11.2.1	Signalling.Signalling pathway.Signalling molecules.Signalling peptide.Ligand peptide	vit_03s0088g00290	Transcript	Phytosulfokines PSK2	-1,16	-1,95	-1,45	-1,08
7.2.13.2	Signalling.Signalling pathway.Stress response signalling.Salt stress response signalling	vit_06s0004g07830	Transcript	SOS2 (salt overly sensitive 2)	2,45	2,39	1,94	1,89
7.2.14	Signalling.Signalling pathway.TOR signalling pathway	vit_08s0058g01440	Transcript	Ribosomal S6 kinase p90	-1,5	-1,34	-1,69	-1,36
8.1.1.23	Transport overview.Channels and pores.Alpha-type channels.Small Conductance Mechanosensitive Ion Channel	vit_10s0092g00570	Transcript	Mechanosensitive ion channel	1,33	1,24	1,12	1,81
8.2.1.21	Transport overview.Electrochemical Potential-driven Transporters.Porters.Solute:Sodium Symporter	vit_02s0033g01370	Transcript	Sodium:solute symporter family protein	1,32	1,42	1,79	1,55
8.2.1.92	Transport overview.Electrochemical Potential-driven Transporters.Porters.Choline Transporter Like	vit_19s0014g02970	Transcript	Choline transporter	1,22	1,55	1,55	1,41
8.13	Transport overview.Ion transport	vit_05s0020g04630	Transcript	DMI1 protein homologue	1,23	1,28	1,59	1,3
8.13.1.1	Transport overview.Ion transport.Anion transport.Chloride transport	vit_07s0130g00400	Transcript	Chloride channel protein (CLC-c)	-1,23	-1,54	-1,59	-1,46
8.13.1.2	Transport overview.Ion transport.Anion transport.Nitrate transport	vit_17s0000g09470	Transcript	Nitrate transporter3.1	1,9	2,02	2,41	2,34
8.13.1.3	Transport overview.Ion transport.Anion transport.Phosphate transport	vit_07s0005g03290	Transcript	Inorganic phosphate transporter 1-4	1,19	2,26	0,64	1,31

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
8.13.1.3	Transport overview.Ion transport.Anion transport.Phosphate transport	vit_15s0024g01440	Transcript	Glucose 6 phosphate/phosphate translocator-like protein	1,63	1,81	2,31	1,61
8.13.1.3	Transport overview.Ion transport.Anion transport.Phosphate transport	vit_14s0066g01000	Transcript	Phosphate/phosphoenolpyruvate translocator	-1,85	-1,78	-1,72	-1,41
8.13.1.4	Transport overview.Ion transport.Anion transport.Sulfate transport	vit_05s0020g03930	Transcript	Sulfate transporter 3.1 (AST12) (AtST1)	-2,48	-3,09	-2,78	-3,09
8.13.2	Transport overview.Ion transport.Cation transport	vit_02s0025g00820	Transcript	Cation/hydrogen exchanger (CHX18)	1,67	1,97	1,9	1,72
8.13.2	Transport overview.Ion transport.Cation transport	vit_04s0008g02860	Transcript	Cation transport protein chaC	-0,07	-0,19	1,54	1,34
8.13.2.3	Transport overview.Ion transport.Cation transport.Glutamate activated channel	vit_19s0014g01830	Transcript	Glutamate receptor 2.8	2,16	2	2,35	1,29
8.13.2.4	Transport overview.Ion transport.Cation transport.Heavy metal ion transport	vit_09s0070g00210	Transcript	Metal transporter Nramp1	-1,51	-0,95	-1,11	-0,69
8.13.2.4.2	Transport overview.Ion transport.Cation transport.Heavy metal ion transport.Copper transport	vit_12s0142g00330	Transcript	Copper-transporting ATPase PAA1	-2,86	-2,79	-2,71	-2,73
8.13.2.4.4	Transport overview.Ion transport.Cation transport.Heavy metal ion transport.Zinc transport	vit_01s0011g01280	Transcript	Zinc transporter ZIP5	-1,43	-1,45	-2,01	-1,67
8.13.2.4.4	Transport overview.Ion transport.Cation transport.Heavy metal ion transport.Zinc transport	vit_19s0015g00190	Transcript	Zinc transporter ZIP11	1,26	1,85	1,87	1,08
8.13.2.7	Transport overview.Ion transport.Cation transport.Proton transport	vit_02s0025g00820	Transcript	Cation/hydrogen exchanger (CHX18)	1,67	1,97	1,9	1,72
8.13.2.7	Transport overview.Ion transport.Cation transport.Proton transport	vit_08s0040g02470	Transcript	Inorganic pyrophosphatase	-1,66	-1,55	-1,55	-1,22
8.14	Transport overview.Macromolecule transport	vit_11s0016g04250	Transcript	HCF101 (high-chlorophyll-fluorescence 101)	-1,94	-1,95	-1,33	-1,32
8.14.1	Transport overview.Macromolecule transport.Amino acid transport	vit_01s0010g02640	Transcript	Lysine histidine transporter 2	0,71	1,16	0,91	1,54
8.14.1	Transport overview.Macromolecule transport.Amino acid transport	vit_06s0004g00790	Transcript	Amino acid permease	1,67	1,79	1,46	1,38
8.14.1	Transport overview.Macromolecule transport.Amino acid transport	vit_10s0003g04540	Transcript	Cationic amino acid transporter 1	2,69	3,14	3,16	2,7
8.14.1	Transport overview.Macromolecule transport.Amino acid transport	vit_14s0171g00400	Transcript	Lysine histidine transporter 1	1,47	1,42	1,7	1,92
8.14.1	Transport overview.Macromolecule transport.Amino acid transport	vit_19s0015g01300	Transcript	Amino acid permease 7	0,84	1,61	1,42	1,59
8.14.2.2	Transport overview.Macromolecule transport.Carbohydrate transport.Sugar transport	vit_01s0026g01890	Transcript	UDP-galactose transporter 3	1,98	1,25	1,04	0,97
8.14.2.2	Transport overview.Macromolecule transport.Carbohydrate transport.Sugar transport	vit_15s0024g01440	Transcript	Glucose 6 phosphate/phosphate translocator-like protein	1,63	1,81	2,31	1,61
8.14.2.2	Transport overview.Macromolecule transport.Carbohydrate transport.Sugar transport	vit_18s0001g05570	Transcript	Hexose transporter HT2	1,61	1,48	1,69	1,48
8.14.4	Transport overview.Macromolecule transport.Heme prostetic groups trafficking	vit_01s0150g00060	Transcript	SOUL heme-binding	-1,56	-1,9	-2,23	-2,15
8.14.5	Transport overview.Macromolecule transport.Lipid transport	vit_14s0006g02550	Transcript	Non-specific lipid-transfer protein 2 (LTP 2)	0	3,71	4,98	0
8.14.5	Transport overview.Macromolecule transport.Lipid transport	vit_02s0154g00310	Transcript	Protease inhibitor/seed storage/lipid transfer protein (LTP)	-2,39	-2,39	-3	-2,21
8.14.5	Transport overview.Macromolecule transport.Lipid transport	vit_04s0008g05640	Transcript	Protease inhibitor/seed storage/lipid transfer protein (LTP)	1,28	1,08	1,73	0,81
8.14.5	Transport overview.Macromolecule transport.Lipid transport	vit_11s0016g05840	Transcript	Protease inhibitor/seed storage/lipid transfer protein (LTP)	-1,83	-1,51	-1,28	-1,45
8.14.5	Transport overview.Macromolecule transport.Lipid transport	vit_13s0156g00090	Transcript	Protease inhibitor/seed storage/lipid transfer protein (LTP)	-1,5	-1,84	-2,61	-2,34
8.14.5	Transport overview.Macromolecule transport.Lipid transport	vit_14s0006g02570	Transcript	Protease inhibitor/seed storage/lipid transfer protein (LTP)	3,85	4,87	3,68	2,24
8.14.5	Transport overview.Macromolecule transport.Lipid transport	vit_19s0090g01470	Transcript	Protease inhibitor/seed storage/lipid transfer protein (LTP)	-1,97	-1,7	-2,21	-1,68

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
8.14.5.1	Transport overview.Macromolecule transport.Lipid transport.Phosphatidylinositol/Phosphatidyl choline transport	vit_10s0003g05480	Transcript	SEC14 cytosolic factor	-1,37	-1,54	-1,11	-0,92
8.14.6	Transport overview.Macromolecule transport.Multidrug transport	vit_11s0016g03050	Transcript	MATE efflux family protein	2,26	2,78	2,62	1,58
8.14.6	Transport overview.Macromolecule transport.Multidrug transport	vit_00s0225g00050	Transcript	MATE efflux family protein	-1,52	-1,43	-0,9	-0,99
8.14.6.2	Transport overview.Macromolecule transport.Multidrug transport.Multidrug ABC transport	vit_14s0066g02300	Transcript	P-glycoprotein 17	2,14	2,05	2,17	1,19
8.14.6.2	Transport overview.Macromolecule transport.Multidrug transport.Multidrug ABC transport	vit_10s0003g04460	Transcript	ABC transporter C member 11	-2,06	-1,7	-1,7	-1,39
8.14.6.2	Transport overview.Macromolecule transport.Multidrug transport.Multidrug ABC transport	vit_15s0045g00090	Transcript	ABC transporter C member 9	1,02	2,2	1,67	1,01
8.14.6.2	Transport overview.Macromolecule transport.Multidrug transport.Multidrug ABC transport	vit_18s0166g00080	Transcript	ABC transporter G member 4	-2,46	-2,27	-2,19	-1,74
8.14.6.2	Transport overview.Macromolecule transport.Multidrug transport.Multidrug ABC transport	vit_01s0011g04670	Transcript	ABC transporter G member 2	1,71	1,71	1,97	1,92
8.14.6.2	Transport overview.Macromolecule transport.Multidrug transport.Multidrug ABC transport	vit_07s0031g01420	Transcript	ATATH13	-1,17	-1,69	-1,32	-1,78
8.14.6.2	Transport overview.Macromolecule transport.Multidrug transport.Multidrug ABC transport	vit_07s0031g01640	Transcript	ABC transporter F member 8	-0,65	-1,41	-1,11	-1,68
8.14.6.2	Transport overview.Macromolecule transport.Multidrug transport.Multidrug ABC transport	vit_07s0031g02550	Transcript	ABC transporter G member 14	-1,84	-2,55	-2,73	-2,57
8.14.6.2	Transport overview.Macromolecule transport.Multidrug transport.Multidrug ABC transport	vit_09s0002g05570	Transcript	ABC transporter g family pleiotropic drug resistance 12 PDR12	0,59	1,29	1,28	1,88
8.14.6.2	Transport overview.Macromolecule transport.Multidrug transport.Multidrug ABC transport	vit_11s0052g00540	Transcript	ABC protein 3 ATNAP3 non-intrinsic	1,86	1,78	1,49	2,02
8.14.6.2	Transport overview.Macromolecule transport.Multidrug transport.Multidrug ABC transport	vit_15s0021g00220	Transcript	ABC transporter C member 15	-1,17	-1,36	-1,57	-1,38
8.14.6.2	Transport overview.Macromolecule transport.Multidrug transport.Multidrug ABC transport	vit_16s0050g01620	Transcript	ABC transporter G member 14	-2,2	-1,53	-1,41	-1,41
8.14.8	Transport overview.Macromolecule transport.Nucleotide transport	vit_13s0067g02500	Transcript	Xanthine/uracil permease	1,36	2,03	1,87	0,39
8.14.8	Transport overview.Macromolecule transport.Nucleotide transport	vit_18s0001g06940	Transcript	Purine permease 1 (PUP1)	1,62	1,82	1,19	1,96
8.14.10	Transport overview.Macromolecule transport.Oligopeptide transport	vit_18s0041g00580	Transcript	Proton-dependent oligopeptide transport (POT) family protein	-1,75	-1,81	-0,93	-1,2
8.14.10	Transport overview.Macromolecule transport.Oligopeptide transport	vit_01s0150g00250	Transcript	Peptide transporter PTR2-B	0,82	1,24	1,76	1,33
8.14.10	Transport overview.Macromolecule transport.Oligopeptide transport	vit_12s0035g01820	Transcript	Proton-dependent oligopeptide transport (POT) family protein	-2,25	-2,54	-1,9	-2,31
8.14.11	Transport overview.Macromolecule transport.Protein transport	vit_06s0004g04700	Transcript	Outer envelope protein 16	-2,02	-1,96	-2,61	-1,91
8.14.12.1	Transport overview.Macromolecule transport.Organic ion transport.Organic anion transport	vit_13s0064g00940	Transcript	ferric reductase defective 3	1,14	1,4	1,56	1,58
8.14.12.1.1	Transport overview.Macromolecule transport.Organic ion transport.Organic anion transport.Malate transport	vit_06s0004g02120	Transcript	Oxoglutarate/malate translocator	-1,2	-1,45	-0,95	-1,54
8.15	Transport overview.Mitochondrial membrane transport	vit_02s0025g03490	Transcript	Carrier protein, Mitochondrial	1,7	1,77	1,65	1,5
8.15.2	Transport overview.Mitochondrial membrane transport.Mitochondrial membrane carbon compound transport	vit_18s0001g07320	Transcript	2-oxoglutarate/malate carrier protein, Mitochondrial	1,84	1,47	1,54	1,19
8.16	Transport overview.Nucleocytoplasmic transport	vit_00s0216g00060	Transcript	Nuclear transport factor 2 (NTF2)	-1,28	-1,8	-1,93	-1,71

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
8.16	Transport overview.Nucleocytoplasmic transport	vit_01s0011g00410	Transcript	Nuclear transport factor 2 (NTF2)	-1,32	-1,5	-1,81	-1,87
8.16.1	Transport overview.Nucleocytoplasmic transport.Nuclear pore complex	vit_08s0040g00230	Transcript	Exportin 7	-2	-1,81	-2,02	-1,65
8.17.1.2	Transport overview.Water transport.Aquaporins.PIP	vit_06s0004g02850	Transcript	Aquaporin PIP2B	-1,23	-1,72	-1,19	-1,39
8.17.1.2	Transport overview.Water transport.Aquaporins.PIP	vit_08s0040g01890	Transcript	Aquaporin PIP2;4	-1,51	-1,93	-2,12	-1,88
8.17.1.2	Transport overview.Water transport.Aquaporins.PIP	vit_14s0108g00700	Transcript	Aquaporin NIP1;2	-1,37	-1,59	-1,14	-1,03
9	Unknown	vit_07s0031g01110	Transcript	unknown	5,05	7,01	5,62	0
9	Unknown	vit_09s0002g00630	Transcript	No hit	0,7	-2,18	-1,93	-0,14
9	Unknown	vit_17s0000g08190	Transcript	No hit	0,92	2,23	0	0,98
9	Unknown	vit_11s0016g05780	Transcript	No hit	2,54	2,12	2,21	1,81
9	Unknown	vit_09s0002g00140	Transcript	Lipase class 3	-1,27	-1,51	-1,22	-1,11
9	Unknown	vit_19s0027g00330	Transcript	No hit	2,21	2	1,95	1,43
9	Unknown	vit_17s0000g08090	Transcript	No hit	1,19	1,66	0,56	1,79
9	Unknown	vit_07s0005g02070	Transcript	No hit	-0,98	-1,58	-1,69	-1,57
9	Unknown	vit_17s0000g09020	Transcript	No hit	1,08	1,92	1,32	1,54
9	Unknown	vit_11s0037g00940	Transcript	No hit	-2,89	-3,63	-2,98	-3,37
9	Unknown	vit_17s0000g02850	Transcript	No hit	-0,73	-1,09	-0,97	-1,61
9	Unknown	vit_02s0025g04870	Transcript	No hit	1,98	2,2	2,63	2,81
9	Unknown	vit_01s0011g05980	Transcript	No hit	2,17	2,8	2,14	1,59
9	Unknown	vit_19s0014g03490	Transcript	No hit	2	1,8	1,04	1,05
9	Unknown	vit_00s0332g00100	Transcript	No hit	-1,52	-1,48	-0,36	-1,15
9	Unknown	vit_06s0061g00290	Transcript	No hit	1,52	1,68	1,73	1,57
9	Unknown	vit_11s0016g03840	Transcript	No hit	-2,22	-2,77	-2,62	-2,87
9	Unknown	vit_02s0025g04470	Transcript	No hit	1,62	1,73	0,6	1,65
9	Unknown	vit_13s0067g02420	Transcript	No hit	1,41	2,15	1,77	2,24
9	Unknown	vit_01s0010g00570	Transcript	No hit	1,65	1,8	1,72	1,15
9	Unknown	vit_00s0246g00020	Transcript	No hit	-1,36	-1,55	-1,11	-1,24
9	Unknown	vit_00s0125g00080	Transcript	No hit	-1,56	-1,72	-2,1	-2,59
9	Unknown	vit_13s0019g01030	Transcript	No hit	1,52	1,27	1,49	1,5
9	Unknown	vit_17s0000g06720	Transcript	No hit	-1,52	-1,9	-1,34	-1,07
9	Unknown	vit_12s0028g00560	Transcript	Unknown protein	-1,86	-1,37	-2,29	-1,36
9	Unknown	vit_11s0016g05800	Transcript	Unknown protein	0,56	1,35	1,51	1,63
9	Unknown	vit_11s0016g05790	Transcript	Unknown protein	1,02	1,6	1,64	1,48
9	Unknown	vit_18s0001g09980	Transcript	Unknown protein	1,24	1,16	1,53	1,41
9	Unknown	vit_16s0050g01260	Transcript	Unknown protein	2,53	2,54	2,7	2,47
9	Unknown	vit_12s0028g03560	Transcript	Unknown protein	-1,43	-2,02	-2,32	-2,45
9	Unknown	vit_14s0068g02200	Transcript	Unknown protein	1,63	2,04	2,27	2,29
9	Unknown	vit_07s0031g01060	Transcript	Unknown protein	1,53	1,32	1,82	1,34
9	Unknown	vit_02s0033g01190	Transcript	Unknown protein	1,62	1,7	1,45	1,5
9	Unknown	vit_00s0317g00010	Transcript	Unknown protein	-1,65	-2,29	0	0
9	Unknown	vit_00s2855g00010	Transcript	Unknown protein	-2,12	-1,82	-0,65	-1,25

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
9	Unknown	vit_19s0015g01440	Transcript	Unknown protein	2,74	2,86	2,29	2
9	Unknown	vit_16s0050g01990	Transcript	Unknown protein	-1,29	-1,09	-2,04	-1,79
9	Unknown	vit_00s0189g00050	Transcript	No hit	3,31	2,59	1,94	2,46
9	Unknown	vit_06s0009g02110	Transcript	Kelch repeat-containing F-box family protein	2,17	2,03	1,59	1,43
9	Unknown	vit_00s0225g00010	Transcript	Unknown protein	3,87	4,01	3,56	3,73
9	Unknown	vit_00s0246g00040	Transcript	No hit	-1,4	-1,7	-1,15	-1,64
9	Unknown	vit_00s0302g00010	Transcript	Unknown protein	-1,73	-1,48	-1,69	-0,26
9	Unknown	vit_00s0323g00040	Transcript	Unknown protein	-1,41	-1,64	-1,44	-1,04
9	Unknown	vit_00s0332g00090	Transcript	Unknown protein	-1,97	-1,56	-1,33	-1,86
9	Unknown	vit_00s0357g00010	Transcript	Senescence-associated protein	1,61	1,74	1,94	1,78
9	Unknown	vit_14s0083g00980	Transcript	Pollen Ole e 1 allergen and extensin	-1,59	-1,43	-1,2	-1,73
9	Unknown	vit_16s0039g02160	Transcript	Unknown protein	-1,15	-1,19	-1,76	-0,79
9	Unknown	vit_03s0063g00340	Transcript	Unknown protein	3,93	3,11	4,42	0
9	Unknown	vit_06s0004g04220	Transcript	no hit	1,72	1,72	1,35	1,48
9	Unknown	vit_17s0000g02160	Transcript	Unknown protein	1,58	1,4	1,47	1,96
9	Unknown	vit_00s0586g00030	Transcript	Stem-specific protein TSJT1	-1,5	-1,75	-1,15	-1,15
9	Unknown	vit_00s0854g00030	Transcript	Unknown	-1,27	-1,44	-0,92	-1,68
9	Unknown	vit_00s1235g00010	Transcript	Unknown protein	-1,62	-1,65	-1,45	-1,53
9	Unknown	vit_00s2377g00010	Transcript	Unknown protein	-1,9	-2,18	-1,59	-2,16
9	Unknown	vit_01s0010g03680	Transcript	Unknown protein	1,47	1,58	0,89	1
9	Unknown	vit_01s0010g03750	Transcript	Unknown protein	1,52	1,3	0,45	0,79
9	Unknown	vit_01s0011g00560	Transcript	DREPP plasma membrane polypeptide	2,31	2,28	2,11	1,93
9	Unknown	vit_01s0011g05290	Transcript	Inorganic carbon transport protein	-1,25	-1,6	-0,94	-1,49
9	Unknown	vit_01s0011g05310	Transcript	CRR3 (chlororespiratory reduction 3)	3,22	3,08	2,94	2,68
9	Unknown	vit_01s0011g05930	Transcript	S-adenosyl-L-methionine:carboxyl methyltransferase	1,69	2,28	3,19	2,76
9	Unknown	vit_01s0026g00530	Transcript	Nodulin MtN21 family	-2,06	-2,28	-2,93	-1,34
9	Unknown	vit_01s0182g00130	Transcript	PHO1-like protein	1,14	1,25	1,52	1,28
9	Unknown	vit_01s0244g00170	Transcript	Cytokinin-repressed protein CR9	1,54	1,47	1,67	1,48
9	Unknown	vit_02s0012g00150	Transcript	NAK-type protein kinase	1,28	1,97	1,69	0,98
9	Unknown	vit_07s0005g00710	Transcript	Ring-H2 subgroup RHE protein	1,57	1,59	1,33	1,48
9	Unknown	vit_02s0025g00220	Transcript	Chlororespiratory reduction 4 (CRR4)	1,82	1,55	1,96	1,33
9	Unknown	vit_02s0025g00400	Transcript	D111/G-patch domain-containing protein	-1,48	-1,23	-1,51	-0,94
9	Unknown	vit_02s0025g01470	Transcript	Unknown protein	-1,42	-1,64	-1,14	-1,32
9	Unknown	vit_02s0025g01710	Transcript	Unknown	-2,58	-3,32	-3,11	-3,77
9	Unknown	vit_02s0025g02640	Transcript	Unknown protein	-1,77	-2,53	-2,53	-2,54
9	Unknown	vit_02s0087g00780	Transcript	No hit	-1,45	-1,3	-1,8	-1,24
9	Unknown	vit_03s0017g02210	Transcript	Unknown	-1,89	-1,98	-2,04	-0,67
9	Unknown	vit_03s0038g00660	Transcript	Unknown protein	0	5,97	5,5	5,76
9	Unknown	vit_11s0118g00540	Transcript	Calcium-binding EF hand	0,68	1,5	1,74	1,56

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
9	Unknown	vit_03s0038g01380	Transcript	Calcium-binding EF hand	-1,19	-1,79	-1,62	-1,68
9	Unknown	vit_03s0038g03690	Transcript	Unknown protein	1,34	1,41	1,19	1,67
9	Unknown	vit_03s0038g03860	Transcript	Phosphate-induced protein 1	2,11	2,65	1,94	0,86
9	Unknown	vit_03s0063g01380	Transcript	Unknown protein	2,06	1,65	1,73	2,42
9	Unknown	vit_03s0063g01910	Transcript	Integral membrane protein	-1,42	-1,61	-1,96	-1,38
9	Unknown	vit_03s0091g00230	Transcript	Unknown protein	-0,99	-2,02	-2,06	-2,66
9	Unknown	vit_03s0091g00550	Transcript	Unknown protein	-1,63	-1,47	-1,33	-1,01
9	Unknown	vit_03s0091g01100	Transcript	Unknown protein	-1,76	-2,14	-0,84	-0,75
9	Unknown	vit_04s0008g02760	Transcript	Unknown protein	2,62	1,66	1,5	1,19
9	Unknown	vit_04s0008g05820	Transcript	Stromal cell-derived factor 2 protein precursor (SDF2 protein)	2,77	2,19	2,09	2,16
9	Unknown	vit_06s0004g07840	Transcript	Endo/excinuclease	-1,26	-1,18	-1,65	-0,96
9	Unknown	vit_04s0023g01110	Transcript	PQ-loop repeat protein	-2,22	-2,27	-1,66	-1,29
9	Unknown	vit_04s0023g02210	Transcript	SAM dependent carboxyl methyltransferase Methyltransf_7	-3,05	-2,93	-2,97	-1,86
9	Unknown	vit_04s0023g03360	Transcript	Unknown protein	-1,79	-1,44	-1,56	-1,18
9	Unknown	vit_04s0044g00130	Transcript	Unknown protein	-1,58	-0,86	-1,11	-1,09
9	Unknown	vit_04s0079g00810	Transcript	Cold induced protein	-1,63	-1,74	-3,12	-2,15
9	Unknown	vit_04s0210g00060	Transcript	Mucin-like protein	4,46	4,85	4,24	3,9
9	Unknown	vit_05s0020g01270	Transcript	Unknown protein	-1,56	-1,45	-1,29	-1,04
9	Unknown	vit_05s0020g02770	Transcript	Unknown protein	-1,99	-2,33	-2,26	-2,03
9	Unknown	vit_05s0020g02920	Transcript	Unknown protein	-1,12	-1,09	-1,77	-1,14
9	Unknown	vit_05s0049g00800	Transcript	Unknown protein	2,79	3,08	0	2,96
9	Unknown	vit_05s0049g00840	Transcript	No hit	2,33	2,01	0	2,29
9	Unknown	vit_05s0049g01760	Transcript	Proton gradient regulation 5 (PGR5)	-1,98	-2,58	-2,48	-2,49
9	Unknown	vit_05s0051g00680	Transcript	Unknown protein	2,16	1,81	1,3	0,66
9	Unknown	vit_05s0051g00700	Transcript	No hit	1,91	0,93	1,26	0,42
9	Unknown	vit_05s0062g01190	Transcript	Pirin	-1,77	-1,42	-1,34	-1,22
9	Unknown	vit_05s0062g01260	Transcript	No hit	-2,24	-2,93	-3,09	-2,54
9	Unknown	vit_05s0062g01360	Transcript	Unknown protein	-2,28	-1,5	-2,23	-1,33
9	Unknown	vit_05s0077g00310	Transcript	No hit	-4,09	-6,18	-4,08	-7,06
9	Unknown	vit_05s0077g01130	Transcript	Seed maturation protein PM36	1,19	1,59	0,97	1
9	Unknown	vit_00s0388g00040	Transcript	Transducin family protein / WD-40	-1,51	-3,12	-2,2	-1,84
9	Unknown	vit_05s0077g01670	Transcript	Major cherry allergen Pru av 1.0202	2,19	0,9	2,93	1,35
9	Unknown	vit_05s0094g01590	Transcript	Kelch repeat-containing F-box protein	-0,3	-1,65	-0,75	-1,65
9	Unknown	vit_19s0014g00360	Transcript	Root initiation defective 3 RID3	1,44	1,73	1,46	1,37
9	Unknown	vit_02s0087g00260	Transcript	RPD1 (root primordium defective 1)	1,49	1,78	1,87	1,36
9	Unknown	vit_06s0004g00260	Transcript	Shoot1 protein	-1,5	-1,9	-1,56	-1,86
9	Unknown	vit_06s0004g00440	Transcript	No hit	0,68	1,24	1,66	0,84
9	Unknown	vit_06s0004g01220	Transcript	PAP/fibrillin family	2,22	2,42	2,27	2,3
9	Unknown	vit_06s0004g03910	Transcript	Unknown protein	1,52	1,52	1,06	0,36
9	Unknown	vit_06s0004g04620	Transcript	Unknown	2,1	1,88	2	1,02

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
9	Unknown	vit_06s0004g05960	Transcript	Unknown protein	2,51	2,69	3,32	3,11
9	Unknown	vit_06s0009g01410	Transcript	No hit	-1,45	-1,73	-0,73	-0,99
9	Unknown	vit_10s0003g01010	Transcript	Lipase GDSL	1,79	1,35	2,15	1,83
9	Unknown	vit_06s0009g02670	Transcript	Unknown	-1,06	-0,87	-1,58	-0,51
9	Unknown	vit_06s0080g00310	Transcript	Esterase/lipase/thioesterase family protein	1,26	1,54	1,5	1,62
9	Unknown	vit_07s0005g01080	Transcript	Unknown protein	-1,25	-2,69	-2,75	-2,34
9	Unknown	vit_07s0005g01830	Transcript	Unknown protein	-3,11	-2,89	-3,1	-2,95
9	Unknown	vit_00s0333g00050	Transcript	DIR1 (defective IN induced resistance 1)	-2,38	-3,08	-2,86	-2,82
9	Unknown	vit_07s0031g01510	Transcript	Unknown protein	3,81	4,98	3,73	0
9	Unknown	vit_07s0031g02780	Transcript	Cyclase/dehydrase	-1,17	-1,62	-1,48	-1,64
9	Unknown	vit_07s0104g00500	Transcript	Unknown protein	-1,68	-1,55	-1,66	-0,92
9	Unknown	vit_07s0104g01480	Transcript	Cold-induced thioredoxin domain	-1,57	-1,74	-1,64	-1,91
9	Unknown	vit_07s0129g00470	Transcript	Unknown protein	-1,22	-1,8	-1,9	-1,92
9	Unknown	vit_07s0130g00160	Transcript	No hit	1,82	1,17	1,18	1,32
9	Unknown	vit_07s0151g00860	Transcript	Hydrolase, alpha/beta fold	-1,87	-2,03	-1,31	-2,02
9	Unknown	vit_08s0007g06500	Transcript	Unknown protein	-2,11	-1,71	-1,78	-1,66
9	Unknown	vit_08s0058g00590	Transcript	Macrophage migration inhibitory factor	1,97	2,04	2,12	2,37
9	Unknown	vit_09s0002g00420	Transcript	Senescence-associated protein	2,12	1,6	1,37	1,64
9	Unknown	vit_09s0002g01000	Transcript	Ferredoxin 4Fe-4S, iron-sulfur binding	-1,24	-1,92	-2,02	-1,38
9	Unknown	vit_09s0002g02060	Transcript	Unknown protein	1,56	1,52	1,25	1,28
9	Unknown	vit_09s0002g04840	Transcript	Unknown	-1,99	-1,44	-0,93	-1,48
9	Unknown	vit_09s0002g05820	Transcript	Unknown	0,96	1,16	0,9	1,58
9	Unknown	vit_09s0002g06510	Transcript	Auxin-independent growth promoter axi1	1,85	2,06	1,89	1,87
9	Unknown	vit_09s0002g06810	Transcript	Binding	2,73	3,44	2,84	2,8
9	Unknown	vit_09s0002g06980	Transcript	Chloroplast post-illumination chlorophyll fluorescence increase protein	2,19	2,1	2,56	2,33
9	Unknown	vit_09s0002g08680	Transcript	Unknown	-1,82	-2,42	-1,63	-1,69
9	Unknown	vit_09s0018g01680	Transcript	Unknown protein	-0,44	-2,14	-2,31	-1,36
9	Unknown	vit_09s0054g01750	Transcript	Unknown protein	-1,94	-2,67	-2,36	-3,26
9	Unknown	vit_09s0054g01760	Transcript	Unknown protein	-0,72	-1,25	-0,91	-1,75
9	Unknown	vit_10s0003g02120	Transcript	Lipase GDSL	-1,61	-1,35	-0,95	-0,57
9	Unknown	vit_10s0116g00900	Transcript	Unknown protein	2,29	2,15	2,22	1,93
9	Unknown	vit_11s0016g02520	Transcript	Unknown protein	2,66	2,04	1,49	1,45
9	Unknown	vit_11s0016g02920	Transcript	Unknown protein	1,76	2,3	1,42	-0,16
9	Unknown	vit_11s0016g03710	Transcript	Abl interactor protein 1 (ABIL1)	-3	-2,85	-2,7	-1,96
9	Unknown	vit_11s0016g05430	Transcript	Unknown protein	2,03	2,24	1,96	1,24
9	Unknown	vit_11s0037g00840	Transcript	Tetratricopeptide repeat (TPR)-containing	-2,15	-2,34	-1,56	-2,21
9	Unknown	vit_11s0037g00860	Transcript	Haemolysin-III related	1,53	1,07	0,92	0,58
9	Unknown	vit_11s0065g00370	Transcript	Senescence-associated protein	1,57	1,43	1,45	1,43
9	Unknown	vit_11s0065g01070	Transcript	Unknown	1,6	1,76	1,57	1,2

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
9	Unknown	vit_12s0028g00580	Transcript	Unknown protein	1,59	1,55	1,4	1,22
9	Unknown	vit_12s0028g03190	Transcript	Reticulon family protein	-1,58	-1,32	-1,39	-0,85
9	Unknown	vit_12s0034g02390	Transcript	T-complex protein 11	-0,77	-1,5	-1,48	-1,66
9	Unknown	vit_12s0035g01240	Transcript	No hit	3,59	4,01	4,24	4,26
9	Unknown	vit_12s0057g00100	Transcript	Wound-responsive	2,35	1,28	0,45	1,28
9	Unknown	vit_12s0057g00180	Transcript	Wound-induced	2,42	2,83	1,27	1,2
9	Unknown	vit_12s0057g00470	Transcript	C2 domain containing protein	1,23	1,61	1,19	0,99
9	Unknown	vit_12s0057g00880	Transcript	TAF15b (TBP-associated factor 15b) zf-ranBP	-1,37	-1,51	-1,04	-1,36
9	Unknown	vit_12s0057g01510	Transcript	Unknown protein	-1,81	-1,34	-1,24	-0,28
9	Unknown	vit_14s0171g00110	Transcript	Lipase family	1,79	1,74	1,42	1,53
9	Unknown	vit_12s0059g01900	Transcript	Unknown protein	-1,3	-1,71	-1,65	-1,54
9	Unknown	vit_13s0019g01040	Transcript	Unknown protein	-1,27	-1,01	-1,77	-1
9	Unknown	vit_13s0047g00110	Transcript	Ripening regulated protein DDTFR8	2,29	0,76	-0,1	0,83
9	Unknown	vit_07s0031g02570	Transcript	CTV.22	-1,51	-1,18	-1,16	-0,98
9	Unknown	vit_13s0067g02090	Transcript	Unknown protein	-0,82	-1,83	-1,79	-2,3
9	Unknown	vit_13s0067g02560	Transcript	Unknown protein	-0,86	-1,79	-2,29	-2,34
9	Unknown	vit_13s0067g03180	Transcript	Unknown protein	-1,73	-2,71	-0,97	-2,21
9	Unknown	vit_13s0084g00310	Transcript	ACI112	-2,4	-2,95	-3,25	-3,16
9	Unknown	vit_13s0101g00060	Transcript	No hit	1,57	1,33	0,88	0,97
9	Unknown	vit_13s0139g00360	Transcript	Unknown protein	2,54	1,6	1,4	1
9	Unknown	vit_14s0030g01710	Transcript	Unknown protein	1,31	1,31	1,65	1,18
9	Unknown	vit_14s0060g01730	Transcript	No hit	1,77	0,99	1,18	0,69
9	Unknown	vit_14s0066g00250	Transcript	Lipase GDSL	1,36	1,69	1,68	1,63
9	Unknown	vit_14s0066g00470	Transcript	Unknown protein	2,55	2,85	2,28	2,82
9	Unknown	vit_14s0066g01640	Transcript	Nodulin MtN21 family	1,98	2,47	2,27	2,23
9	Unknown	vit_14s0068g01020	Transcript	Unknown protein	1,47	1,42	1,74	1,38
9	Unknown	vit_14s0083g00290	Transcript	No hit	-1,63	-1,27	-2,41	-1,06
9	Unknown	vit_14s0108g00840	Transcript	Unknown protein	2,68	3,07	2,41	2,79
9	Unknown	vit_14s0108g01350	Transcript	Unknown protein	-3,94	-4,68	-4,71	-4,87
9	Unknown	vit_14s0128g00440	Transcript	Tangled	-2,05	-1,67	-1,71	-1,45
9	Unknown	vit_15s0021g02260	Transcript	Fibrillin-11	2,01	1,76	1,91	1,61
9	Unknown	vit_15s0046g01560	Transcript	Unknown protein	3,05	2,49	2,59	2,08
9	Unknown	vit_15s0046g02050	Transcript	Unknown protein	3,28	3,59	2,82	2,94
9	Unknown	vit_15s0046g02230	Transcript	Heavy-metal-associated domain-containing protein	-1,08	-1,56	-1,67	-1,13
9	Unknown	vit_15s0048g00090	Transcript	No hit	1,61	0,94	1,13	1,13
9	Unknown	vit_15s0048g00910	Transcript	Unknown protein	0,12	0,88	1,56	0,86
9	Unknown	vit_15s0048g02420	Transcript	No hit	-4,07	-4,44	-4,77	-4,74
9	Unknown	vit_15s0048g02780	Transcript	Unknown protein	1,51	1,4	1,05	0,6
9	Unknown	vit_16s0013g02030	Transcript	Unknown protein	1,94	1,76	1,33	1,45

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
9	Unknown	vit_16s0050g00710	Transcript	Unknown protein	-2,04	-2,91	-2,24	-2,94
9	Unknown	vit_16s0098g00600	Transcript	No hit	-1,26	-1,73	0,17	0,21
9	Unknown	vit_16s0098g00790	Transcript	Copper-binding family protein	-1,41	-1,2	-1,7	-1,56
9	Unknown	vit_17s0000g01800	Transcript	Unknown protein	1,09	1,29	1,52	0,91
9	Unknown	vit_17s0000g02020	Transcript	Erwinia induced protein 2	0,58	1,07	1,63	0,8
9	Unknown	vit_17s0000g03220	Transcript	Unknown protein	1,24	1,42	0,92	1,57
9	Unknown	vit_17s0000g06760	Transcript	Unknown protein	1,38	1,24	1,58	0,97
9	Unknown	vit_17s0000g07600	Transcript	Unknown protein	1,57	1,14	1,3	0,84
9	Unknown	vit_17s0000g07950	Transcript	Unknown protein	2,27	3,2	2,19	2,16
9	Unknown	vit_17s0000g08370	Transcript	SIMILAR TO RCD ONE 2 (SRO2)	2,03	1,6	1,02	1,12
9	Unknown	vit_18s0001g00110	Transcript	Unknown protein	-1,37	-1,71	-1,03	-1,5
9	Unknown	vit_18s0001g01110	Transcript	Monooxygenase (MO2)	2,64	3,1	3,02	3,15
9	Unknown	vit_18s0001g04290	Transcript	No hit	1,65	1,3	1,13	1,62
9	Unknown	vit_18s0001g06170	Transcript	Phosphate-induced protein 1	1,07	2,06	0	0
9	Unknown	vit_18s0001g07640	Transcript	Eceriferum 2 (CER2)	1,65	1,28	2,36	0,98
9	Unknown	vit_18s0001g07770	Transcript	Unknown protein	2,14	1,29	0,67	0,98
9	Unknown	vit_18s0001g08810	Transcript	Unknown protein	4,36	5,27	5,17	4,7
9	Unknown	vit_18s0001g08870	Transcript	Unknown	-1,67	-0,6	-1,18	-1,09
9	Unknown	vit_00s0227g00170	Transcript	Syntaxin 52	1,3	1,63	1,42	1,44
9	Unknown	vit_18s0001g10480	Transcript	Unknown protein	4,04	5,62	4,23	5,99
9	Unknown	vit_18s0001g13080	Transcript	Unknown protein	-1,71	-0,87	-0,68	-0,79
9	Unknown	vit_18s0001g15330	Transcript	Nodulin MtN3 family	-1,42	-1,64	-1,11	-1,19
9	Unknown	vit_18s0001g15650	Transcript	Pathogenesis related protein	-1,65	-2,25	-2,25	-1,44
9	Unknown	vit_18s0041g01220	Transcript	GCN5 N-acetyltransferase (GNAT)	-2,1	-2,52	-2,53	-2,63
9	Unknown	vit_18s0041g02160	Transcript	Lipase GDSL	-1,21	-2,06	-0,81	-1,22
9	Unknown	vit_18s0076g00360	Transcript	EMB1075 (embryo defective 1075) carboxy-lyase	1,51	1,22	1,16	0,66
9	Unknown	vit_18s0086g00220	Transcript	Lipase GDSL	1,41	2,16	1,17	1,55
9	Unknown	vit_18s0089g01410	Transcript	Purine permease 4 PUP4	1,92	1,59	2,18	1,48
9	Unknown	vit_18s0166g00190	Transcript	U-box domain-containing protein	1,53	0,81	0,12	0,1
9	Unknown	vit_19s0014g01360	Transcript	Curculin (mannose-binding) lectin	1,97	2,86	2,94	2,91
9	Unknown	vit_19s0014g01940	Transcript	Unknown	1,25	2,18	1,96	1,62
9	Unknown	vit_19s0014g03220	Transcript	Unknown protein	1,23	1,6	1,4	1,56
9	Unknown	vit_19s0014g03500	Transcript	Unknown protein	2,14	1,59	1,08	0,94
9	Unknown	vit_19s0014g04710	Transcript	DAG protein, chloroplast precursor	1,31	1,15	1,63	1,49
9	Unknown	vit_19s0090g01340	Transcript	No hit	-0,27	-0,92	-2,04	-0,15
9	Unknown	vit_19s0090g01360	Transcript	No hit	1,45	1,29	0,3	1,98
9	Unknown	vit_19s0090g01750	Transcript	Unknown protein	-0,75	-1,61	-0,56	-1,69
9	Unknown	vit_08s0007g08660	Transcript	Binding	-1,68	-1,59	-1,61	-1,32
9	Unknown	vit_06s0004g06290	Transcript	Binding	3,73	3,67	4,18	2,85

BinCode	BinName	ID	Type	Description	T1T	T2T	T3T	T4T
9	Unknown	vit_05s0049g00780	Transcript	No hit	2,1	1,82	0	3,02
9	Unknown	vit_03s0063g01770	Transcript	No hit	1,59	0,73	0,1	1,15
9	Unknown	vit_16s0013g00390	Transcript	No hit	-2,22	-2,78	-2,58	-2,58
9	Unknown	vit_05s0077g00540	Transcript	No hit	-1,55	-1,38	-0,48	-1,04
9	Unknown	vit_19s0015g00270	Transcript	no hit	-1,11	-1,73	-1,7	-1,52
9	Unknown	vit_17s0000g08180	Transcript	No hit	2,02	1,67	1,07	1,18
10.1	Xenoprotein.Protein from transposable element	vit_00s0438g00030	Transcript	Retrotransposon protein, Unclassified	-2,45	-2,19	-1,91	-2,34
10.1	Xenoprotein.Protein from transposable element	vit_13s0019g01850	Transcript	Transposon protein, putative, CACTA	1,88	1,56	1,04	1,3
10.1	Xenoprotein.Protein from transposable element	vit_18s0075g00520	Transcript	Retrotransposon protein, Unclassified	-1,15	-1,37	-1,06	-1,54

	T1T	T2T	T3T	T4T
Pectinesterase family	1,48	1,84	2,05	1,84
Pectinesterase family	-1,57	-1,85	-1,28	-1,03
Polygalacturonase GH28	-2,97	-4,09	-3,75	-3,15
Pectinesterase PME1	1,53	1,74	1,83	1,17
Polygalacturonase GH28	-2,13	-1,76	-1,84	-1,7
Xyloglucan endotransglucosylase/hydrolase precursor (EXGT-A4)	-1,57	-1,29	-1,31	-0,83
Xyloglucan endotransglucosylase/hydrolase 15	2,09	2,99	3,09	3
Xyloglucan endotransglycosylase 6(XTR6)	2,87	4,12	1,69	0,83
Xyloglucan endotransglucosylase/hydrolase 23	0	3,75	0	0
Xyloglucan endotransglycosylase 6	2,58	2,57	0	0
Xyloglucan endotransglycosylase/hydrolase 16	1,79	2,39	2,54	2,3

Supplementary Table 6

Mapman pathway analysis moisture stress responsive genes

BinCode	BinName	ID	Type	Description	RCvsR80%C	RcvsR50%C	RcvsRs50%C
1.1.1	Cellular process.Cell growth and death.Cell death	vit_01s0146g00150	Transcript	BCL-2-associated athanogene 5	1,364	2,138	2,11
4.1.6.2	Metabolism.Cellular metabolism.Nitrogen metabolism.Nitrogen assimilation	vit_03s0063g00370	Transcript	Nitrite reductase	1,327	0,47	2,179
4.2.7.2.1	Metabolism.Primary metabolism.Lipid metabolism.Glycerolipid metabolism.Glycerolipid biosynthesis	vit_11s0118g00310	Transcript	1,2-diacylglycerol 3-beta-galactosyltransferase	1,234	2,039	0,405
4.2.7.2.1	Metabolism.Primary metabolism.Lipid metabolism.Glycerolipid metabolism.Glycerolipid biosynthesis	vit_11s0118g00310	Transcript	1,2-diacylglycerol 3-beta-galactosyltransferase	1,234	2,039	0,405
4.2.8.1.3.3	Metabolism.Primary metabolism.Nucleobase, nucleoside, nucleotide, nucleic acid metabolism.Nucleic acid metabolism.RNA metabolism.RNA processing	vit_18s0001g10210	Transcript	PAB8 (poly(A) binding protein 8)	-4,532	-0,469	-5,487
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02740	Transcript	Heat shock protein 17.6 kDa class I	1,047	1,756	1,677
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_04s0008g01520	Transcript	Heat shock protein 17.6 kDa class II	1,398	2,023	2,378
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_18s0089g01270	Transcript	Heat shock protein precursor 22.0 kDa class IV	0,872	2,009	1,938
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_01s0010g02290	Transcript	Heat shock protein 26a, chloroplast	0,892	1,547	1,522
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_02s0025g00280	Transcript	Heat shock protein 90-1	1,341	1,909	2,356
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_02s0154g00480	Transcript	Heat shock protein MTSHP	0,881	1,614	1,822
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_16s0022g00510	Transcript	Heat shock 22 kDa protein	1,082	1,759	1,928
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_04s0008g01490	Transcript	Heat shock protein 17.6 kDa class II	1,009	1,716	1,874
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_04s0008g01510	Transcript	Heat shock protein 17.6 kDa class II	2,282	3,345	3,803
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_04s0008g01550	Transcript	Small molecular heat shock protein 17.5	1,46	2,158	2,373
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_04s0008g01580	Transcript	Heat shock protein 17.6 kDa class II	1,42	1,932	2,282
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_04s0008g01590	Transcript	Heat shock protein 17.6 kDa class II	1,115	1,753	1,893
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_06s0004g04470	Transcript	Heat shock protein 70	1,213	1,773	2,061
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02850	Transcript	Heat shock protein 17.6 kDa class I	1,024	1,622	1,724
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02740	Transcript	Heat shock protein 17.6 kDa class I	1,047	1,756	1,677
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02760	Transcript	Heat shock protein 17.6 kDa class I	1,801	2,503	2,437

BinCode	BinName	ID	Type	Description	RCvsR80%C	RcvsR50%C	RcvsRs50%C
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_04s0008g01570	Transcript	Heat shock protein 17.6 kDa class II	1,191	1,641	1,978
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_09s0002g00640	Transcript	Small heat stress protein class CIII	1,081	1,564	1,65
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02760	Transcript	Heat shock protein 17.6 kDa class I	1,801	2,503	2,437
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02770	Transcript	Heat shock protein 17.6 kDa class I	0,686	1,853	1,596
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02780	Transcript	Heat shock protein 17.6 kDa class I	0,958	1,991	2,024
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02840	Transcript	Heat shock protein 18.2 kDa class I	1,647	2,513	2,051
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02850	Transcript	Heat shock protein 17.6 kDa class I	1,024	1,622	1,724
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g02930	Transcript	Heat shock protein 17.6 kDa class I	0,976	1,671	1,615
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_13s0019g03160	Transcript	Heat shock protein 17.6 kDa class I	1,207	1,529	1,864
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_16s0050g01150	Transcript	Heat shock protein 90-1	0,807	1,494	1,847
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_01s0010g02290	Transcript	Heat shock protein 26a, chloroplast	0,892	1,547	1,522
4.2.10.1.1.2	Metabolism.Primary metabolism.Protein metabolism and modification.Protein folding.Chaperone-mediated protein folding.HSP-mediated protein folding	vit_16s0098g01060	Transcript	Heat shock protein 26a, chloroplast	1,125	1,562	1,359
5.2.2.1.37	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcription factor.HSF family transcription factor	vit_04s0008g01110	Transcript	Heat shock transcription factor A6B_2	0,897	1,948	1,898
5.2.2.3	Regulation overview.Regulation of gene expression.Regulation of transcription.Transcriptional co-activation	vit_11s0016g04080	Transcript	Multiprotein-bridging factor 1c MBF1C	0,797	1,915	2,054
6.2	Response to stimulus.Stress response	vit_11s0016g04080	Transcript	Multiprotein-bridging factor 1c MBF1C	0,797	1,915	2,054
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_01s0010g02290	Transcript	Heat shock protein 26a, chloroplast	0,892	1,547	1,522
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_06s0004g04470	Transcript	Heat shock protein 70	1,213	1,773	2,061
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_13s0019g03160	Transcript	Heat shock protein 17.6 kDa class I	1,207	1,529	1,864
6.2.1.8	Response to stimulus.Stress response.Abiotic stress response.Temperature stress response	vit_16s0098g01060	Transcript	Heat shock protein 26a, chloroplast	1,125	1,562	1,359
6.2.2	Response to stimulus.Stress response.Biotic stress response	vit_02s0025g00280	Transcript	Heat shock protein 90-1	1,341	1,909	2,356
7.2.9	Signalling.Signalling pathway.Protein kinase	vit_18s0001g14990	Transcript	Dual-specific kinase DSK1	0,663	1,657	-0,032
7.2.10	Signalling.Signalling pathway.Protein phosphatase	vit_09s0002g02450	Transcript	Phosphatase	0,913	1,569	-0,618
9	Unknown	vit_09s0002g00630	Transcript	No hit	1,056	1,468	1,628
9	Unknown	vit_05s0077g01670	Transcript	Major cherry allergen Pru av 1.0202	1,793	0,235	1,34