

Table 2 Suppl. GO annotation of detected stress related modules.

Module	GO term	Ontology	Description	Number in input list	Number in BG/Ref	P-value	FDR
2							
	GO:0055114P		oxidation reduction	<u>6</u>	203	3.00E-07	1.50E-05
	GO:0046700P		heterocycle catabolic process	<u>4</u>	38	2.70E-07	1.50E-05
	GO:0008152P		metabolic process	<u>31</u>	10614	3.20E-07	1.50E-05
	GO:0043436P		oxoacid metabolic process	<u>2</u>	859	1.50E-06	2.30E-05
	GO:0009199P		ribonucleoside triphosphate metabolic process	<u>4</u>	61	1.60E-06	2.30E-05
	GO:0009205P		purine ribonucleoside triphosphate metabolic pr	<u>4</u>	61	1.60E-06	2.30E-05
	GO:0046034P		ATP metabolic process	<u>4</u>	59	1.40E-06	2.30E-05
	GO:0009141P		nucleoside triphosphate metabolic process	<u>4</u>	65	2.00E-06	2.30E-05
	GO:0009144P		purine nucleoside triphosphate metabolic proces	<u>4</u>	63	1.80E-06	2.30E-05
	GO:0006082P		organic acid metabolic process	<u>2</u>	860	1.50E-06	2.30E-05
	GO:0019752P		carboxylic acid metabolic process	<u>2</u>	859	1.50E-06	2.30E-05
	GO:0042180P		cellular ketone metabolic process	<u>2</u>	882	1.90E-06	2.30E-05
	GO:0009150P		purine ribonucleotide metabolic process	<u>4</u>	80	4.40E-06	4.00E-05
	GO:0009117P		nucleotide metabolic process	<u>5</u>	180	4.30E-06	4.00E-05
	GO:0006753P		nucleoside phosphate metabolic process	<u>5</u>	180	4.30E-06	4.00E-05
	GO:0006163P		purine nucleotide metabolic process	<u>4</u>	92	7.60E-06	6.40E-05
	GO:0009259P		ribonucleotide metabolic process	<u>4</u>	96	8.90E-06	7.10E-05
	GO:0006559P		L-phenylalanine catabolic process	<u>2</u>	2	9.90E-06	7.40E-05
	GO:0055086P		nucleobase, nucleoside and nucleotide metaboli	<u>5</u>	221	1.10E-05	8.00E-05
	GO:0009628P		response to abiotic stimulus	<u>10</u>	1471	1.70E-05	0.00011
	GO:0055085P		transmembrane transport	<u>5</u>	244	1.80E-05	0.00012
	GO:0009074P		aromatic amino acid family catabolic process	<u>2</u>	4	2.50E-05	0.00015
	GO:0044238P		primary metabolic process	<u>25</u>	8995	3.40E-05	0.0002
	GO:0044248P		cellular catabolic process	<u>7</u>	746	5.00E-05	0.00028
	GO:0044237P		cellular metabolic process	<u>24</u>	8722	6.70E-05	0.00036
	GO:0019439P		aromatic compound catabolic process	<u>2</u>	8	7.40E-05	0.00038
	GO:0009698P		phenylpropanoid metabolic process	<u>4</u>	175	8.70E-05	0.00044
	GO:0006558P		L-phenylalanine metabolic process	<u>2</u>	12	0.00015	0.00071
	GO:0032787P		monocarboxylic acid metabolic process	<u>5</u>	408	0.00019	0.00091
	GO:0009414P		response to water deprivation	<u>4</u>	229	0.00024	0.0011
	GO:0009056P		catabolic process	<u>8</u>	1307	0.00027	0.0011
	GO:0008610P		lipid biosynthetic process	<u>5</u>	439	0.00027	0.0011
	GO:0009415P		response to water	<u>4</u>	240	0.00029	0.0012
	GO:0006575P		cellular amino acid derivative metabolic process	<u>4</u>	315	0.00078	0.003
	GO:0006629P		lipid metabolic process	<u>6</u>	841	0.00076	0.003
	GO:0006633P		fatty acid biosynthetic process	<u>3</u>	140	0.00086	0.0032
	GO:0046351P		disaccharide biosynthetic process	<u>2</u>	39	0.0013	0.0048
	GO:0009312P		oligosaccharide biosynthetic process	<u>2</u>	43	0.0016	0.0056
	GO:0034637P		cellular carbohydrate biosynthetic process	<u>3</u>	177	0.0017	0.0058
	GO:0005984P		disaccharide metabolic process	<u>2</u>	45	0.0017	0.0058
	GO:0009063P		cellular amino acid catabolic process	<u>2</u>	47	0.0019	0.006
	GO:0006725P		cellular aromatic compound metabolic process	<u>4</u>	399	0.0018	0.006
	GO:0006519P		cellular amino acid and derivative metabolic proc	<u>5</u>	682	0.0019	0.006
	GO:0009310P		amine catabolic process	<u>2</u>	49	0.0020	0.006
	GO:0006970P		response to osmotic stress	<u>4</u>	408	0.0020	0.006
	GO:0009311P		oligosaccharide metabolic process	<u>2</u>	52	0.0023	0.0066
	GO:0043086P		negative regulation of catalytic activity	<u>2</u>	53	0.0023	0.0067
	GO:0009987P		cellular process	<u>25</u>	11684	0.0027	0.0075
	GO:0006950P		response to stress	<u>9</u>	2320	0.0027	0.0075
	GO:0044092P		negative regulation of molecular function	<u>2</u>	61	0.0031	0.0081
	GO:0046483P		heterocycle metabolic process	<u>4</u>	460	0.0031	0.0081
	GO:0006631P		fatty acid metabolic process	<u>3</u>	225	0.0032	0.0084
	GO:0009072P		aromatic amino acid family metabolic process	<u>2</u>	68	0.0038	0.0095
	GO:0019748P		secondary metabolic process	<u>4</u>	489	0.0038	0.0095
	GO:0016051P		carbohydrate biosynthetic process	<u>3</u>	277	0.0058	0.014
	GO:0016054P		organic acid catabolic process	<u>2</u>	98	0.0075	0.018
	GO:0046395P		carboxylic acid catabolic process	<u>2</u>	98	0.0075	0.018

GO:0009416P	response to light stimulus	4	596	0.0076	0.018	
GO:0009314P	response to radiation	4	613	0.0083	0.019	
GO:0044255P	cellular lipid metabolic process	4	618	0.0086	0.019	
GO:0006807P	nitrogen compound metabolic process	11	3826	0.0089	0.020	
GO:0009409P	response to cold	3	328	0.0091	0.020	
GO:0006810P	transport	7	1846	0.0095	0.020	
GO:0051234P	establishment of localization	7	1851	0.0096	0.020	
GO:0042545P	cell wall modification	2	123	0.0120	0.024	
GO:0009058P	biosynthetic process	13	5118	0.0120	0.024	
GO:0051179P	localization	7	1922	0.0120	0.024	
GO:0050896P	response to stimulus	11	4057	0.0130	0.027	
GO:0009699P	phenylpropanoid biosynthetic process	2	141	0.0150	0.029	
GO:0050790P	regulation of catalytic activity	2	141	0.0150	0.029	
GO:0016053P	organic acid biosynthetic process	3	417	0.0170	0.031	
GO:0044262P	cellular carbohydrate metabolic process	3	417	0.0170	0.031	
GO:0065009P	regulation of molecular function	2	153	0.0170	0.031	
GO:0046394P	carboxylic acid biosynthetic process	3	417	0.0170	0.031	
GO:0005976P	polysaccharide metabolic process	2	152	0.0170	0.031	
GO:0006520P	cellular amino acid metabolic process	3	430	0.0190	0.033	
GO:0044106P	cellular amine metabolic process	3	438	0.0200	0.034	
GO:0044249P	cellular biosynthetic process	12	4925	0.0210	0.037	
GO:0009266P	response to temperature stimulus	3	485	0.0250	0.043	
GO:0005975P	carbohydrate metabolic process	4	866	0.0260	0.044	
GO:0034641P	cellular nitrogen compound metabolic process	3	506	0.0280	0.047	
GO term	Ontology	Description	Number in input list	Number in BG/Ref	P-value	FDR
GO:0055114P		oxidation reduction	7	203	3.50E-10	4.10E-08
GO:0008152P		metabolic process	24	10614	1.80E-08	1.00E-06
GO:0044237P		cellular metabolic process	20	8722	1.10E-06	4.10E-05
GO:0046039P		GTP metabolic process	2	2	3.90E-06	0.00011
GO:0009199P		ribonucleoside triphosphate metabolic process	3	61	2.00E-05	0.00031
GO:0009205P		purine ribonucleoside triphosphate metabolic pr	3	61	2.00E-05	0.00031
GO:0006278P		RNA-dependent DNA replication	2	8	2.90E-05	0.00031
GO:0009141P		nucleoside triphosphate metabolic process	3	65	2.40E-05	0.00031
GO:0006807P		nitrogen compound metabolic process	12	3826	2.60E-05	0.00031
GO:0009144P		purine nucleoside triphosphate metabolic proces	3	63	2.20E-05	0.00031
GO:0009987P		cellular process	21	11684	2.70E-05	0.00031
GO:0055086P		nucleobase, nucleoside and nucleotide metaboli	4	221	3.40E-05	0.00033
GO:0009150P		purine ribonucleotide metabolic process	3	80	4.40E-05	0.0004
GO:0022900P		electron transport chain	3	88	5.80E-05	0.00048
GO:0006163P		purine nucleotide metabolic process	3	92	6.60E-05	0.00051
GO:0009259P		ribonucleotide metabolic process	3	96	7.40E-05	0.00054
GO:0006091P		generation of precursor metabolites and energy	4	285	8.90E-05	0.00062
GO:0006596P		polyamine biosynthetic process	2	21	0.0002	0.001
GO:0006139P		nucleobase, nucleoside, nucleotide and nucleic a	10	3198	0.0002	0.001
GO:0044238P		primary metabolic process	17	8995	0.0002	0.0012
GO:0006595P		polyamine metabolic process	2	26	0.0002	0.0014
GO:0006259P		DNA metabolic process	4	405	0.0003	0.0018
GO:0009117P		nucleotide metabolic process	3	180	0.0004	0.0022
GO:0006753P		nucleoside phosphate metabolic process	3	180	0.0004	0.0022
GO:0046700P		heterocycle catabolic process	2	38	0.0005	0.0023
GO:0022904P		respiratory electron transport chain	2	39	0.0005	0.0024
GO:0046483P		heterocycle metabolic process	4	460	0.0005	0.0024
GO:0009309P		amine biosynthetic process	3	229	0.0009	0.0037
GO:0042401P		cellular biogenic amine biosynthetic process	2	52	0.00091	0.0037
GO:0015992P		proton transport	2	59	0.0012	0.0044
GO:0006818P		hydrogen transport	2	59	0.0012	0.0044
GO:0044249P		cellular biosynthetic process	11	4925	0.0013	0.0045
GO:0006576P		cellular biogenic amine metabolic process	2	62	0.0013	0.0045
GO:0006119P		oxidative phosphorylation	2	69	0.0016	0.0054
GO:0016310P		phosphorylation	5	1079	0.0018	0.0057
GO:0009058P		biosynthetic process	11	5118	0.0018	0.0057
GO:0045333P		cellular respiration	2	85	0.0023	0.0072

Module
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	GO:0015980P		energy derivation by oxidation of organic compo	<u>2</u>	85	0.0023	0.0072
	GO:0006796P		phosphate metabolic process	<u>5</u>	1178	0.0026	0.0075
	GO:0006793P		phosphorus metabolic process	<u>5</u>	1179	0.0026	0.0075
	GO:0044271P		cellular nitrogen compound biosynthetic process	<u>3</u>	394	0.0042	0.012
	GO:0015672P		monovalent inorganic cation transport	<u>2</u>	115	0.0042	0.012
	GO:0006260P		DNA replication	<u>2</u>	117	0.0043	0.012
	GO:0016053P		organic acid biosynthetic process	<u>3</u>	417	0.0049	0.013
	GO:0046394P		carboxylic acid biosynthetic process	<u>3</u>	417	0.0049	0.013
	GO:0044106P		cellular amine metabolic process	<u>3</u>	438	0.0056	0.014
	GO:0042180P		cellular ketone metabolic process	<u>4</u>	882	0.0057	0.014
	GO:0009266P		response to temperature stimulus	<u>3</u>	485	0.0074	0.018
	GO:0043170P		macromolecule metabolic process	<u>12</u>	7127	0.0080	0.019
	GO:0034641P		cellular nitrogen compound metabolic process	<u>3</u>	506	0.0082	0.019
	GO:0009308P		amine metabolic process	<u>3</u>	521	0.0089	0.02
	GO:0044260P		cellular macromolecule metabolic process	<u>11</u>	6447	0.0110	0.024
	GO:0009611P		response to wounding	<u>2</u>	197	0.0120	0.026
	GO:0042398P		cellular amino acid derivative biosynthetic proces	<u>2</u>	233	0.0160	0.034
	GO:0006519P		cellular amino acid and derivative metabolic proc	<u>3</u>	682	0.0180	0.039
Module 12	GO term	Ontology	Description	Number in input list	Number in BG/Ref	P-value	FDR
	GO:0015074P		DNA integration	<u>2</u>	3	2.90E-06	0.00012
	GO:0008152P		metabolic process	<u>16</u>	10614	6.70E-06	0.00014
	GO:0055114P		oxidation reduction	<u>3</u>	203	0.0002	0.0028
	GO:0055085P		transmembrane transport	<u>3</u>	244	0.0003	0.0035
	GO:0044238P		primary metabolic process	<u>12</u>	8995	0.0011	0.009
	GO:0006259P		DNA metabolic process	<u>3</u>	405	0.0014	0.01
	GO:0009987P		cellular process	<u>13</u>	11684	0.0033	0.018
	GO:0044237P		cellular metabolic process	<u>11</u>	8722	0.0034	0.018
	GO:0005996P		monosaccharide metabolic process	<u>2</u>	168	0.0040	0.019
	GO:0009414P		response to water deprivation	<u>2</u>	229	0.0072	0.03
	GO:0009415P		response to water	<u>2</u>	240	0.0079	0.03
	GO:0006066P		alcohol metabolic process	<u>2</u>	270	0.0099	0.035
	GO:0005975P		carbohydrate metabolic process	<u>3</u>	866	0.0120	0.038
	GO:0009651P		response to salt stress	<u>2</u>	366	0.0180	0.047
	GO:0006810P		transport	<u>4</u>	1846	0.0180	0.047
	GO:0051234P		establishment of localization	<u>4</u>	1851	0.0180	0.047
	GO:0044262P		cellular carbohydrate metabolic process	<u>2</u>	417	0.0220	0.05
	GO:0051179P		localization	<u>4</u>	1922	0.0200	0.05
	GO:0006970P		response to osmotic stress	<u>2</u>	408	0.022	0.05
Module 22	GO term	Ontology	Description	Number in input list	Number in BG/Ref	P-value	FDR
	GO:0055114P		oxidation reduction	<u>4</u>	203	1.10E-06	4.30E-05
	GO:0008152P		metabolic process	<u>11</u>	10614	0.00036	0.0069
	GO:0006633P		fatty acid biosynthetic process	<u>2</u>	140	0.0014	0.018
	GO:0006631P		fatty acid metabolic process	<u>2</u>	225	0.0036	0.031
	GO:0016310P		phosphorylation	<u>3</u>	1079	0.0082	0.031
	GO:0006091P		generation of precursor metabolites and energy	<u>2</u>	285	0.0057	0.031
	GO:0006468P		protein amino acid phosphorylation	<u>3</u>	946	0.0057	0.031
	GO:0043687P		post-translational protein modification	<u>3</u>	1248	0.0120	0.031
	GO:0032787P		monocarboxylic acid metabolic process	<u>2</u>	408	0.0110	0.031
	GO:0009409P		response to cold	<u>2</u>	328	0.0074	0.031
	GO:0008610P		lipid biosynthetic process	<u>2</u>	439	0.0130	0.031
	GO:0016053P		organic acid biosynthetic process	<u>2</u>	417	0.0120	0.031
	GO:0044237P		cellular metabolic process	<u>8</u>	8722	0.0110	0.031
	GO:0046394P		carboxylic acid biosynthetic process	<u>2</u>	417	0.0120	0.031
	GO:0006796P		phosphate metabolic process	<u>3</u>	1178	0.0100	0.031
	GO:0006793P		phosphorus metabolic process	<u>3</u>	1179	0.0100	0.031
	GO:0009266P		response to temperature stimulus	<u>2</u>	485	0.0160	0.035
	GO:0009628P		response to abiotic stimulus	<u>3</u>	1471	0.0190	0.038
	GO:0006464P		protein modification process	<u>3</u>	1474	0.0190	0.038
	GO:0043412P		macromolecule modification	<u>3</u>	1636	0.0250	0.045
	GO:0044255P		cellular lipid metabolic process	<u>2</u>	618	0.0250	0.045

Table 3 Suppl. List of connected nodes to MYB12 (Contig10499) and ADC (Contig6762).

MYB12		
Related genes	HRR values	Description
Contig13152	1/25	tr K4BDI2 K4BDI2_SOLLC:Uncharacterized protein OS=Solanum lycopersicum GN=Solyc02g093860.2 PE=4 SV=1
Contig13664	1/5	tr Q767C8 Q767C8_IRIHO:Anthocyanin 5-O-glucosyltransferase OS=Iris hollandica GN=Ih5GT PE=2 SV=1
Contig14863	1/15	tr G7JRA5 G7JRA5_MEDTR:Heme-binding-like protein OS=Medicago truncatula GN=MTR_4g019150 PE=4 SV=1
Contig15051	1/15	tr K3ZD75 K3ZD75_SETIT:Uncharacterized protein OS=Setaria italica GN=Si024509m.g PE=3 SV=1
Contig16261	1/5	tr Q9AWZ5 Q9AWZ5_ORYSJ:Os01g0225600 protein OS=Oryza sativa subsp. japonica GN=P0492F05.18 PE=4 SV=1
Contig16553	1/15	tr D7TCF5 D7TCF5_VITVI:Putative uncharacterized protein OS=Vitis vinifera GN=VIT_11s0016g01160 PE=4 SV=1
Contig17121	1/25	tr B9N581 B9N581_POPTR:Predicted protein OS=Populus trichocarpa GN=POPTRDRAFT_811252 PE=4 SV=1
Contig17282	1/25	tr J7RA23 J7RA23_HORVU:Putative general amino acid permease (Fragment) OS=Hordeum vulgare GN=HvAAP11 PE=2 SV=1
Contig23289	1/25	tr B9SYV7 B9SYV7_RICCO:"Nucleic acid binding protein, putative OS=Ricinus communis GN=RCOM_0042390 PE=4 SV=1"
Contig24610	1/15	tr I1HU19 I1HU19_BRADI:Uncharacterized protein OS=Brachypodium distachyon GN=BRADI2G57100 PE=4 SV=1
Contig26338	1/25	tr D7TNF6 D7TNF6_VITVI:Putative uncharacterized protein OS=Vitis vinifera GN=VIT_01s0026g01490 PE=4 SV=1
Contig28519	1/15	tr C5WVF0 C5WVF0_SORBI:Putative uncharacterized protein Sb01g017180 OS=Sorghum bicolor GN=Sb01g017180 PE=3 SV=1
Contig3366	1/15	tr Q7XB37 Q7XB37_MAZPU:Chalcone synthase OS=Mazus pumilus GN=CHS PE=2 SV=1
Contig343	1/5	tr B9I4W8 B9I4W8_POPTR:Predicted protein OS=Populus trichocarpa GN=POPTRDRAFT_569405 PE=3 SV=1
Contig3879	1/5	tr Q84TM1 Q84TM1_ALLCE:Flavonol synthase OS=Allium cepa PE=2 SV=1
Contig4269	1/15	tr Q2YGU1 Q2YGU1_LILDA:Phosphatidylinositol-specific phospholipase C 2 (Fragment) OS=Lilium davidii GN=PLC2 PE=2 SV=1
Contig4359	1/15	tr J7FPQ8 J7FPQ8_COFA:4-hydroxycinnamoyl-CoA ligase 2 OS=Coffea arabica GN=4CL2 PE=2 SV=1
Contig4670	1/5	tr D7L2F8 D7L2F8_ARALL:Early light-inducable protein OS=Arabidopsis lyrata subsp. lyrata GN=ELIP1 PE=4 SV=1
Contig4828	1/25	tr K3XDS0 K3XDS0_SETIT:Uncharacterized protein OS=Setaria italica GN=Si000037m.g PE=3 SV=1
Contig8008	1/25	tr I7HB59 I7HB59_9LILI:Phenylalanine ammonia-lyase OS=Lilium hybrid division I GN=LhPAL1 PE=2 SV=1
Contig9513	1/25	tr B9RUV8 B9RUV8_RICCO:"ATP-dependent transporter, putative OS=Ricinus communis GN=RCOM_0894930 PE=3 SV=1"
Contig9753	1/25	tr I1IK70 I1IK70_BRADI:Uncharacterized protein OS=Brachypodium distachyon GN=BRADI4G12990 PE=4 SV=1
First_Contig158	1/15	tr I1IR19 I1IR19_BRADI:Uncharacterized protein OS=Brachypodium distachyon GN=BRADI4G33080 PE=4 SV=1
First_Contig438	1/5	tr Q17UC0 Q17UC0_CUUSA:Cinnamate-4-hydroxylase OS=Cucumis sativus GN=c4H PE=2 SV=1
ADC		
Related genes	HRR values	Description
Contig10973	1/25	tr B7FLI8 B7FLI8_MEDTR:Putative uncharacterized protein (Fragment) OS=Medicago truncatula PE=2 SV=1
Contig11099	1/25	tr F2CW19 F2CW19_HORVD:UDP-glucose 6-dehydrogenase (Fragment) OS=Hordeum vulgare var. distichum PE=2 SV=1
Contig11664	1/5	tr B0LK18 B0LK18_ASPOF:Zinc finger-homeodomain protein 1 OS=Asparagus officinalis GN=ZHD1 PE=2 SV=1
Contig12017	1/25	tr B7TYB8 B7TYB8_ACYPI:Cytochrome c oxidase subunit 3 OS=Acyrtosiphon pisum GN=cox3 PE=3 SV=1
Contig1356	1/5	tr K3Z6P5 K3Z6P5_SETIT:3-isopropylmalate dehydrogenase OS=Setaria italica GN=Si022214m.g PE=3 SV=1
Contig14700	1/25	tr D9YV74 D9YV74_9HEMI:Elongation factor 1 alpha (Fragment) OS=Aphis sedi PE=4 SV=1
Contig15052	1/25	tr K3ZD75 K3ZD75_SETIT:Uncharacterized protein OS=Setaria italica GN=Si024509m.g PE=3 SV=1

Contig15487	1/5	tr D7SSM5 D7SSM5_VITVI:Putative uncharacterized protein OS=Vitis vinifera GN=VIT_00s0274g00070 PE=4 SV=1
Contig1592	1/5	tr K3Y7T9 K3Y7T9_SETIT:S-adenosylmethionine decarboxylase proenzyme OS=Setaria italica GN=Si010282m.g PE=3 SV=1
Contig16924	1/5	tr B9GU14 B9GU14_POPTR:"NAC domain protein, IPR003441 OS=Populus trichocarpa GN=NAC030 PE=4 SV=1"
Contig17396	1/25	tr F6GYH6 F6GYH6_VITVI:Putative uncharacterized protein OS=Vitis vinifera GN=VIT_09s0054g01740 PE=4 SV=1
Contig17644	1/25	tr Q2AA50 Q2AA50_ASPOF:Retrotransposon gag protein OS=Asparagus officinalis GN=19.t00014 PE=4 SV=1
Contig17952	1/15	tr H6U1F0 H6U1F0_CITSI:Polyprotein OS=Citrus sinensis GN=Tcs2 PE=4 SV=1
Contig18211	1/15	tr Q2AA50 Q2AA50_ASPOF:Retrotransposon gag protein OS=Asparagus officinalis GN=19.t00014 PE=4 SV=1
Contig20456	1/5	tr A9CBE7 A9CBE7_APHGL:Cytochrome c oxidase subunit 2 OS=Aphis glycines GN=COII PE=3 SV=1
Contig20954	1/25	tr D7TNB9 D7TNB9_VITVI:Putative uncharacterized protein OS=Vitis vinifera GN=VIT_01s0026g01910 PE=4 SV=1
Contig21761	1/25	tr F6H4G8 F6H4G8_VITVI:Putative uncharacterized protein OS=Vitis vinifera GN=VIT_07s0031g02900 PE=3 SV=1
Contig24832	1/5	tr J9K1S3 J9K1S3_ACYPI:Elongation factor 1-alpha OS=Acyrtosiphon pisum PE=3 SV=1
Contig26473	1/25	tr Q9B6I1 Q9B6I1_9HEMI:ATP synthase subunit a OS=Pterocomma populeum GN=ATP6 PE=3 SV=1
Contig2704	1/25	tr F6I089 F6I089_VITVI:Putative uncharacterized protein OS=Vitis vinifera GN=VIT_02s0033g01120 PE=4 SV=1
Contig3758	1/15	tr A5B9L0 A5B9L0_VITVI:Putative uncharacterized protein OS=Vitis vinifera GN=VITISV_035274 PE=3 SV=1
Contig4930	1/5	tr I7K8K8 I7K8K8_9ROSA:T4.5 protein OS=Malus x robusta GN=T4.5 PE=4 SV=1
Contig5879	1/15	tr B9MY09 B9MY09_POPTR:Predicted protein OS=Populus trichocarpa GN=POPTRDRAFT_920990 PE=4 SV=1
Contig6127	1/15	tr E5DLB2 E5DLB2_9MAGN:NADH-ubiquinone oxidoreductase chain 5 (Fragment) OS=Decaisnea fargesii GN=nad5 PE=3 SV=1
Contig8521	1/15	tr Q6L4X8 Q6L4X8_ORYSJ:Putative polyprotein OS=Oryza sativa subsp. japonica GN=OSJNBb0108E17.1 PE=4 SV=1
First_Contig2 81	1/25	tr E7CCN3 E7CCN3_SOLHA:Arginine decarboxylase (Fragment) OS=Solanum habrochaites PE=3 SV=1
First_Contig3 45	1/25	tr C4P7S7 C4P7S7_SORBI:CBL-interacting protein kinase 25 OS=Sorghum bicolor GN=CIPK25 PE=2 SV=1

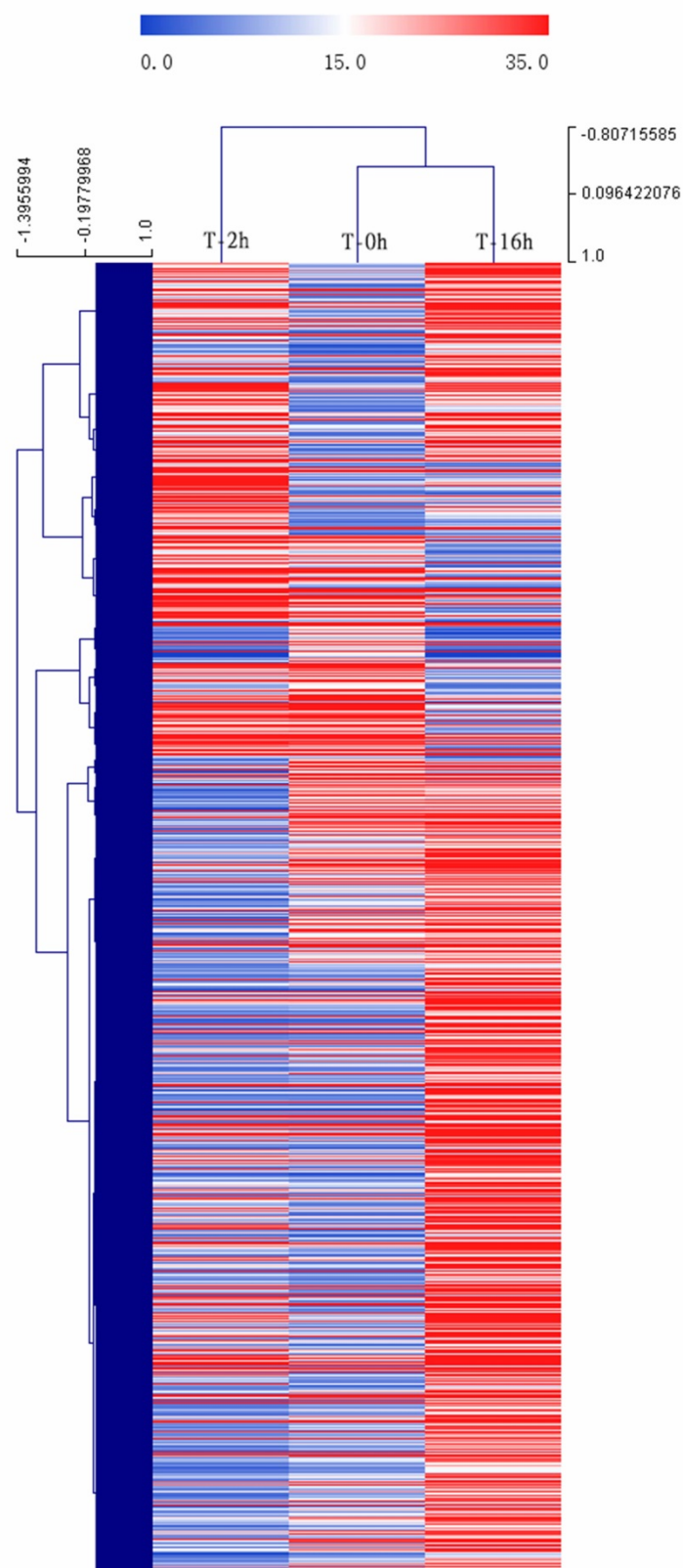


Fig. 1 Suppl. The heat-map of the differentially expressed genes (DEGs). Columns and rows in the heat maps represent samples and genes, respectively. T-0h - controls, T-2h and T-16h - cold treatment for 2 and 16 h, respectively. Colour scale indicates RPKM value of gene expression.

