

# Sangio\_acclim\_r3

## Global Summary

%DE = 0  
# genes with  $fdr < 0.2 = 0$  (0 + / 0 -)  
# genes with  $fdr < 0.1 = 0$  (0 + / 0 -)  
# genes with  $fdr < 0.05 = 0$  (0 + / 0 -)  
# genes with  $fdr < 0.01 = 0$  (0 + / 0 -)

<FC> = 0  
<p-value> = 0.48  
<fdr> = 1

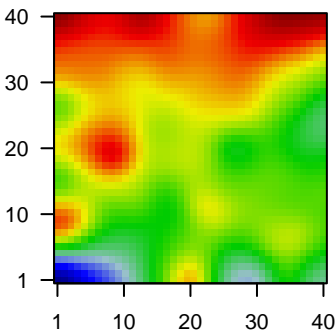
## Differentially expressed genes

Rank	ID	log(FC)	p-value	fdr	Description	Metagene
Overexpressed						
1	Vitv15g0161E	1.98	0.003	1	Catalysis of the transfer of a nucleotidyl group to a reactant.	13 x 40
2	Vitv14g0100C	0.62	0.005	1	The contents of a cell excluding the plasma membrane and n	14 x 34
3	Vitv18g00711	1.32	0.005	1	A transcription coregulator activity that represses or decrease	7 x 40
4	Vitv11g0151C	2.37	0.005	1	Binding to ATP, adenosine 5'-triphosphate, a universally impc	1 x 38
5	Vitv15g01667	2.05	0.006	1	Binding to ADP, adenosine 5'-diphosphate.	8 x 20
6	Vitv17g0024C	0.53	0.006	1	The component of the peroxisomal membrane consisting of th	9 x 29
7	Vitv16g0089E	0.52	0.008	1	The formation of a protein dimer, a macromolecular structure	23 x 27
8	Vitv04g0058Z	0.39	0.010	1	Binding to a carbohydrate, which includes monosaccharides,	11 x 23
9	Vitv10g0098E	1.74	0.010	1		10 x 20
10	Vitv04g0015E	0.98	0.012	1	A membrane-bound organelle of eukaryotic cells in which	24 x 33
11	Vitv18g0236I	1.19	0.012	1	Growth of pollen via tip extension of the intine wall.	12 x 38
12	Vitv09g0132C	0.68	0.015	1	The component of a membrane consisting of the gene produc	18 x 32
13	Vitv06g00547	1.55	0.016	1	Catalysis of the hydrolysis of internal, alpha-peptide bonds in	12 x 40
14	Vitv12g0076E	1.19	0.018	1	Catalysis of the hydrolysis of internal, alpha-peptide bonds in	28 x 38
15	Vitv19g0054E	0.76	0.019	1	The contents of a cell excluding the plasma membrane and n	25 x 32
16	Vitv02g0042E	0.38	0.019	1	A membrane-bound organelle of eukaryotic cells in which	22 x 27
17	Vitv01g0008E	1.64	0.020	1	Binding to ADP, adenosine 5'-diphosphate.	13 x 40
18	Vitv16g0151C	0.48	0.020	1	The component of a membrane consisting of the gene produc	14 x 35
19	Vitv19g00587	1.14	0.020	1	The component of a membrane consisting of the gene produc	9 x 21
20	Vitv10g0031E	0.96	0.021	1		8 x 21
Underexpressed						
1	Vitv18g0112E	-3.03	7e-04	1	Catalysis of the transfer of a group, e.g. a methyl group, glyco	29 x 1
2	Vitv15g0069E	-1.17	8e-04	1	A lipid bilayer along with all the proteins and protein comple	18 x 9
3	Vitv08g0173C	-0.68	3e-03	1	A membrane-bound organelle of eukaryotic cells in which	17 x 8
4	Vitv03g00514	-1.5	4e-03	1	The contents of a cell excluding the plasma membrane and n	26 x 1
5	Vitv04g0054C	-1	5e-03	1		15 x 8
6	Vitv09g0149I	-0.73	5e-03	1	The component of the mitochondrial inner membrane consisti	26 x 20
7	Vitv19g00557	-2.22	5e-03	1	The chemical reactions and pathways involving carbohydrate:	37 x 24
8	Vitv07g0205E	-0.83	5e-03	1		28 x 2
9	Vitv12g0031E	-0.92	6e-03	1	Catalysis of the reaction: a protein with reduced sulfide group	29 x 19
10	Vitv09g0148E	-1.16	7e-03	1		16 x 6
11	Vitv14g0000C	-1.33	9e-03	1		28 x 1
12	Vitv03g00454	-0.86	1e-02	1	A membrane-bound organelle of eukaryotic cells in which	33 x 9
13	Vitv14g0265C	-1.14	1e-02	1	The chemical reactions and pathways involving carbohydrate:	28 x 2
14	Vitv18g0274I	-1.31	1e-02	1	Binding to a heme, a compound composed of iron complexed	27 x 20
15	Vitv14g0169E	-0.77	1e-02	1	The component of a membrane consisting of the gene produc	30 x 6
16	Vitv05g0149E	-0.97	1e-02	1		18 x 6
17	Vitv08g0066E	-1.29	1e-02	1		11 x 7
18	Vitv07g01114	-0.55	1e-02	1	Binding to a nucleic acid.	27 x 16
19	Vitv01g00084	-1.1	1e-02	1		28 x 2
20	Vitv14g0198E	-0.85	1e-02	1	The action of a molecule that contributes to the structural inte	26 x 18

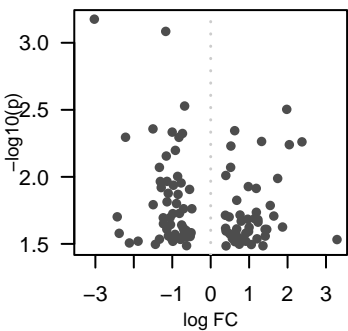
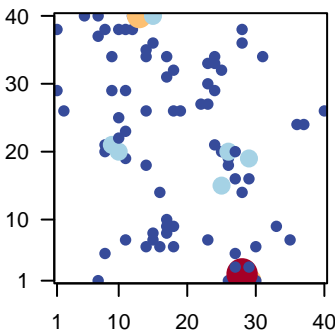
## Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
Overexpressed				
1	3.77	1e-04	32	Circadian rhythm - plant
2	3.35	1e-03	51	Plant species-specific signaling pathway
3	3.27	1e-03	12	Channel - CNG
4	3.22	1e-03	129	Enzyme - G2E
5	3.12	2e-03	111	Transporter - G2E
6	2.91	4e-03	18	Photosynthesis - proteins
7	2.9	4e-03	100	Plant species-specific signaling pathway
8	2.81	6e-03	110	Ubiquitin - G2E
9	2.75	7e-03	26	Flavonoid - G2E
10	2.69	8e-03	18	Transcription factor - ARF
11	2.69	8e-03	18	Energy metabolism - G2E
12	2.68	8e-03	31	Chromatin - G2E
13	2.63	1e-02	10	Peptidase - G2E
14	2.59	1e-02	62	Ribosome - G2E
15	2.58	1e-02	223	Enzyme - G2E
16	2.53	1e-02	13	Cofactors - G2E
17	2.38	2e-02	11	Transcription factor - GRF
18	2.37	2e-02	26	Sphingolipid - G2E
19	2.37	2e-02	217	Cell motility - G2E
20	2.3	2e-02	10	Transcription factor - G2E
Underexpressed				
1	-5.77	0e+00	73	Transcription factor - EREBP
2	-5.71	0e+00	45	Galactose - G2E
3	-5.7	0e+00	211	Ribosome - G2E
4	-5.34	0e+00	247	Translation - G2E
5	-5.28	0e+00	144	Ribosome - G2E
6	-4.96	0e+00	140	Hormone - G2E
7	-4.58	0e+00	49	Transcription factor - NAC
8	-3.83	6e-05	64	Transcription factor - G2E
9	-3.52	6e-04	97	Ribosome - G2E
10	-3.42	9e-04	77	Cysteine - G2E
11	-3.35	1e-03	77	Carbohydrate - G2E
12	-3.17	2e-03	26	Transcription factor - G2E
13	-3.08	2e-03	11	Biosynthesis - G2E
14	-2.98	3e-03	43	Alanine - G2E
15	-2.97	3e-03	37	Chaperone - G2E
16	-2.74	7e-03	51	Other - G2E
17	-2.62	1e-02	10	Transcription factor - AS2
18	-2.59	1e-02	44	Energy metabolism - G2E
19	-2.59	1e-02	18	Chaperone - G2E
20	-2.47	1e-02	29	Transcription factor - GRAS

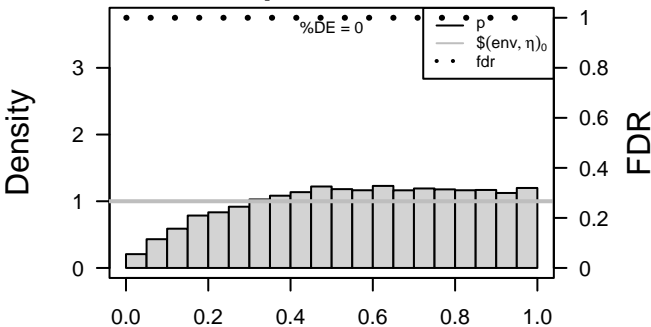
Portrait



Top 100 DE genes



p-values



p-values

