Sangio_acclim_r2

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> = 0.45

<fdr> = 1

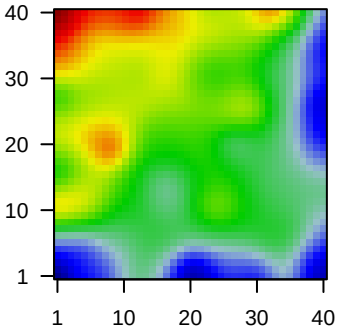
Differentially expressed genes

Rank	ID	log(FC)	p−value	fdr	Description	Metagene
Overexpressed						
1	Vitvi04g00474	0.68	8e−04	1	17 x 33	Binding to ATP, adenosine 5'−triphosphate, a universally impc
2	Vitvi15g00364	1.12	2e−03	1	5 x 30	The component of a membrane consisting of the gene produc
3	Vitvi18g00938	0.43	3e−03	1	11 x 32	The part of the cytoplasm that does not contain organelles bu
4	Vitvi18g02361	1.36	4e−03	1	12 x 38	Growth of pollen via tip extension of the intine wall.
5	Vitvi10g01508	0.67	5e−03	1	8 x 26	A ubiquitin ligase complex in which a cullin from the Cul1 sub
6	Vitvi08g01079	0.74	6e−03	1	25 x 24	
7	Vitvi07g01488	0.81	6e−03	1	15 x 36	A membrane−bounded organelle of eukaryotic cells in which
8	Vitvi05g00347	0.71	6e−03	1	11 x 23	Binding to a metal ion.
9	Vitvi17g01073	1.14	8e−03	1	11 x 32	Catalysis of the transfer of an acetyl group to an acceptor mo
10	Vitvi01g01765	0.95	8e−03	1	25 x 13	A membrane−bounded organelle of eukaryotic cells in which
11	Vitvi01g01019	1.81	9e−03	1	1 x 33	A lipid bilayer along with all the proteins and protein complexe
12	Vitvi01g00012	1.21	9e−03	1	20 x 36	The membrane surrounding a cell that separates the cell from
13	Vitvi19g02382	0.79	1e−02	1	7 x 22	
14	Vitvi00g00882	0.79	1e−02	1	7 x 22	
15	Vitvi07g01608	1.48	1e−02	1	6 x 37	Catalysis of the hydrolysis of any non−peptide carbon−nitroge
16	Vitvi06g00024	2.01	1e−02	1	1 x 38	Any molecular function by which a gene product interacts sele
17	Vitvi08g00923	0.59	1e−02	1	15 x 35	Catalysis of the transfer of ubiquitin to a substrate protein via
18	Vitvi15g01122	0.95	1e−02	1	9 x 30	Binding to a protein.
19	Vitvi01g00088	1.77	1e−02	1	13 x 40	Binding to ADP, adenosine 5'−diphosphate.
20	Vitvi10g01454	1.38	1e−02	1	2 x 26	
Underexpressed						
1	Vitvi14g01375	−1.01	8e−04	1	35 x 13	The component of a membrane consisting of the gene produc
2	Vitvi05g01500	−2.25	3e−03	1	38 x 22	Binding to a calcium ion (Ca2+).
3	Vitvi04g01937	−2.45	5e−03	1	23 x 1	Catalysis of the hydrolysis of internal, alpha−peptide bonds in
4	Vitvi14g00470	−1.05	5e−03	1	22 x 4	Binding to a calcium ion (Ca2+).
5	Vitvi18g00197	−1.69	5e−03	1	21 x 2	Binding to a calcium ion (Ca2+).
6	Vitvi18g01285	−2.02	7e−03	1	40 x 22	
7	Vitvi12g02334	−1.67	8e−03	1	40 x 6	Catalysis of a biochemical reaction at physiological temperatu
8	Vitvi05g00616	−1.24	1e−02	1	40 x 11	The component of a membrane consisting of the gene produc
9	Vitvi10g00680	−0.41	1e−02	1	20 x 20	The process in which relatively unspecialized cells, e.g. embr
10	Vitvi15g00593	−0.78	1e−02	1	29 x 3	The component of a membrane consisting of the gene produc
11	Vitvi01g02058	−2.95	1e−02	1	21 x 1	Catalysis of the reaction: NADP(+) + thioredoxin = H(+) + NAI
12	Vitvi04g01293	−1.28	1e−02	1	4 x 15	Catalysis of an oxidation−reduction (redox) reaction, a reversi
13	Vitvi09g00246	−2.24	1e−02	1	24 x 32	
14	Vitvi04g00794	−0.82	1e−02	1	25 x 22	
15	Vitvi18g03165	−0.97	2e−02	1	27 x 5	
16	Vitvi07g01688	−0.49	2e−02	1	19 x 18	The component of a membrane consisting of the gene produc
17	Vitvi16g01327	−1.3	2e−02	1	1 x 17	Any molecular function by which a gene product interacts sele
18	Vitvi06g00558	−1.3	2e−02	1	22 x 3	
19	Vitvi08g01022	−1.79	2e−02	1	40 x 1	
20	Vitvi02g01456	−1.76	2e−02	1	21 x 1	

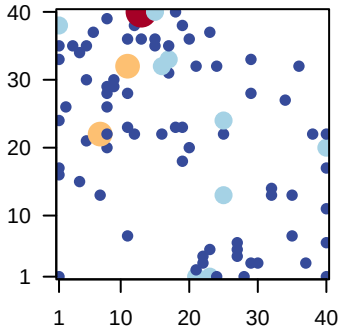
Differentially expressed gene sets

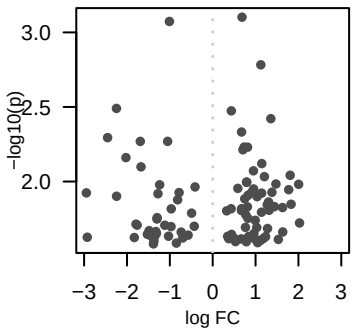
Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	5.02	0e+00	62	Ribosome Ribosome biogenesis 60S particles
2	4.55	0e+00	116	Ribosome Ribosome biogenesis Pre−60S Particles 60S particles
3	4.48	0e+00	51	Plant circadian rhythm Circadian rhythm
4	4.25	0e+00	64	Ribosome Ribosome biogenesis eukaryotes
5	4.19	0e+00	75	Translation Translation Ribosome biogenesis eukaryotes
6	3.86	8e−05	75	Mitochondrial transcription and translation factors
7	3.82	1e−04	110	Ubiquitin system Ubiquitin mediated proteolysis RING−type E3
8	3.75	1e−04	165	Transcription Transcription Spliceosome
9	3.75	1e−04	67	Replication and repair RNA degradation
10	3.6	4e−04	151	RNA polymerase RNA polymerase II system
11	3.47	8e−04	99	mRNA surveillance pathway
12	3.41	9e−04	21	Replication and repair Mismatch repair
13	3.28	1e−03	13	Cofactors and vitamins metabolism Thiamine metabolism
14	3.13	2e−03	63	Messenger RNA biogenesis RNA degradation factors
15	3.12	2e−03	21	Thiamine metabolism
16	3.1	2e−03	81	Translation mRNA surveillance pathway
17	3.07	2e−03	85	Nucleocytoplasmic transport
18	3	3e−03	37	Homologous recombination
19	2.92	4e−03	83	RNA degradation
20	2.9	4e−03	34	Transcription factors SETS PCG
Underexpressed				
1	−7.35	0e+00	26	Flavonoid biosynthesis
2	−6.69	0e+00	73	Transcription factors AP2 EREBP
3	−6.34	0e+00	48	Transcription factors WRKY
4	−5.35	0e+00	153	Plant−pathogen interaction
5	−5.2	0e+00	63	Phenylpropanoid biosynthesis
6	−4.9	0e+00	162	Plant signaling Plant−pathogen interaction
7	−4.45	0e+00	206	Cell growth and death Cell wall
8	−4.15	0e+00	15	Stilbenoid diarylheptanoid and gingerol biosynthesis
9	−3.89	4e−05	10	Linoleic acid metabolism
10	−3.83	8e−05	47	Transporters Transporter Electron carriers
11	−3.76	1e−04	39	Pentose and glucuronate interconversions
12	−3.76	1e−04	140	Hormone signaling Ethylene signaling
13	−3.58	4e−04	81	Enzyme Carbon−oxygen lyases
14	−3.52	6e−04	22	Fatty acid elongation
15	−3.43	8e−04	64	Transcription factors Other transcription factors
16	−3.35	1e−03	35	Lipid metabolism Alpha−linolenic acid metabolism
17	−3.28	1e−03	25	Nitrogen metabolism
18	−3.21	1e−03	26	Glycosyltransferases Hydrophobic molecule
19	−3.18	2e−03	40	Transporters Terpenoid backbone pathway
20	−3.16	2e−03	33	alpha−Linolenic acid metabolism

Portrait

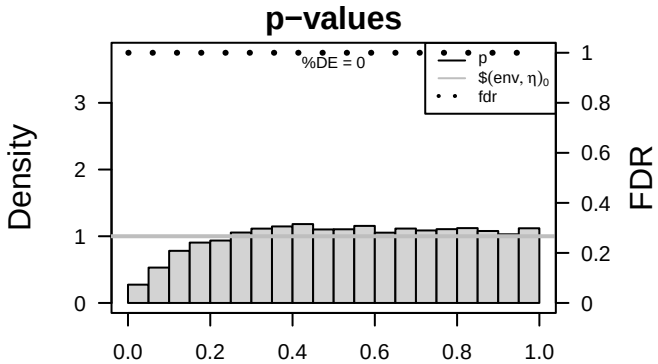


Top 100 DE genes





p−values



p−values