Sangio_warm_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> = 0.41

<fdr> = 1

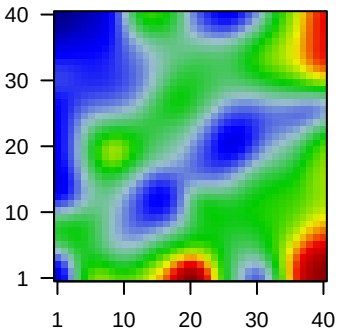
Differentially expressed genes

Rank	ID	log(FC)	p−value	fdr	Description	Metagene
Overexpressed						
1	Vitvi14g02722	3.67	5e−04	1	8 x 20	Any molecular function by which a gene product interacts sele
2	Vitvi16g01344	1.57	1e−03	1	22 x 1	Catalysis of the hydrolysis of internal, alpha−peptide bonds in
3	Vitvi14g01635	3.16	1e−03	1	40 x 22	Binding to a metal ion.
4	Vitvi07g00381	1.7	2e−03	1	40 x 10	A lipid bilayer along with all the proteins and protein complexe
5	Vitvi02g01507	1.91	2e−03	1	40 x 8	
6	Vitvi12g02315	1.43	2e−03	1	12 x 20	
7	Vitvi08g01904	2.56	3e−03	1	40 x 1	Catalysis of the transfer of a group, e.g. a methyl group, glyco
8	Vitvi12g02045	0.4	3e−03	1	20 x 25	The contents of a cell excluding the plasma membrane and n
9	Vitvi00g00915	2.65	3e−03	1	40 x 4	
10	Vitvi10g02309	2.65	3e−03	1	40 x 4	Binding to a metal ion.
11	Vitvi17g00347	3.01	3e−03	1	21 x 1	The component of a membrane consisting of the gene produc
12	Vitvi04g02118	2.72	4e−03	1	22 x 1	
13	Vitvi03g00936	2.22	4e−03	1	21 x 1	Binding to a protein.
14	Vitvi19g01677	1.94	4e−03	1	21 x 1	The membrane surrounding a cell that separates the cell from
15	Vitvi16g02072	2.49	4e−03	1	20 x 1	Catalysis of the hydrolysis of internal, alpha−peptide bonds in
16	Vitvi19g00835	1.47	5e−03	1	10 x 19	The contents of a cell excluding the plasma membrane and n
17	Vitvi19g02105	1.48	6e−03	1	17 x 2	
18	Vitvi01g01458	1.66	7e−03	1	40 x 1	
19	Vitvi03g00214	2.41	7e−03	1	40 x 1	A lipid bilayer along with all the proteins and protein complexe
20	Vitvi09g01556	2.58	8e−03	1	21 x 1	Binding to ATP, adenosine 5'−triphosphate, a universally impo
Underexpressed						
1	Vitvi07g01375	−1.3	4e−05	1	9 x 26	
2	Vitvi07g01466	−0.9	2e−04	1	11 x 30	
3	Vitvi04g02144	−1.46	3e−04	1	16 x 15	A lipid bilayer along with all the proteins and protein complexe
4	Vitvi18g01700	−0.62	4e−04	1	18 x 20	Catalysis of a biochemical reaction at physiological temperatu
5	Vitvi07g00322	−1.06	4e−04	1	25 x 21	The aggregation, arrangement and bonding together of a set
6	Vitvi18g00240	−1.13	6e−04	1	25 x 22	A membrane−bounded organelle of eukaryotic cells in which
7	Vitvi10g01325	−1.13	7e−04	1	25 x 31	The component of a membrane consisting of the gene produc
8	Vitvi00g01105	−1.05	9e−04	1	7 x 32	
9	Vitvi07g00906	−1.39	9e−04	1	21 x 40	A lipid bilayer along with all the proteins and protein complexe
10	Vitvi04g01129	−0.67	9e−04	1	21 x 22	The component of a membrane consisting of the gene produc
11	Vitvi07g02286	−1.02	1e−03	1	21 x 18	Any process that modulates the frequency, rate or extent of c
12	Vitvi08g01933	−1.21	1e−03	1	1 x 22	A semiautonomous, self replicating organelle that occurs in va
13	Vitvi17g00566	−1.19	1e−03	1	7 x 38	Binding to ATP, adenosine 5'−triphosphate, a universally impo
14	Vitvi12g00343	−1.24	2e−03	1	26 x 22	The membrane surrounding a cell that separates the cell from
15	Vitvi17g00240	−0.59	2e−03	1	9 x 29	The component of the peroxisomal membrane consisting of th
16	Vitvi11g00268	−1.04	2e−03	1	1 x 24	Catalysis of the transfer of a phosphoribosyl group from 5'−ph
17	Vitvi07g00262	−1.41	2e−03	1	1 x 20	Binding to a metal ion.
18	Vitvi08g00180	−1.04	2e−03	1	26 x 22	The process in which a methyl group is covalently attached to
19	Vitvi00g01897	−1.49	2e−03	1	26 x 21	
20	Vitvi07g02800	−1.49	2e−03	1	26 x 21	

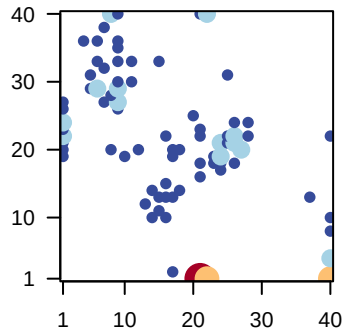
Differentially expressed gene sets

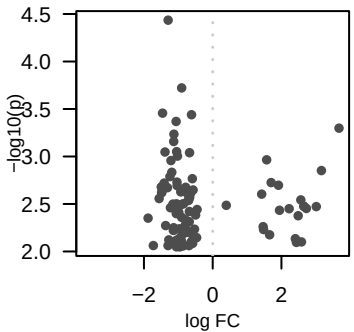
Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	6.03	0e+00	206	Cell growth and death − Cell wall
2	5.84	0e+00	39	Pentose and glucuronate interconversions
3	5.46	0e+00	47	Transporters − Electron carriers
4	4.93	0e+00	197	Transporters − Channels and pores
5	4.82	0e+00	40	Energy metabolism − Methane metabolism
6	4.81	0e+00	38	Photosynthesis
7	4.79	0e+00	19	Aquaporins [TC:1.A.8]
8	4.78	0e+00	18	Energy metabolism − Photosynthesis, proteins
9	4.76	0e+00	78	Energy metabolism − Photosynthesis
10	4.59	0e+00	134	Hormone signaling − Auxin signaling
11	4.51	0e+00	26	Flavonoid biosynthesis
12	4.34	0e+00	162	Plant pathogen interaction
13	4.34	0e+00	18	Photosynthesis − proteins
14	4.26	0e+00	47	ABC transporters
15	4.07	0e+00	44	Enzyme − Acyltransferases
16	3.96	4e−05	27	ABCG (White) subfamily
17	3.96	4e−05	129	Enzyme − Glycosylases
18	3.93	4e−05	56	Hormone signaling − Jasmonic acid signaling
19	3.9	4e−05	168	Plant hormone signal transduction
20	3.85	8e−05	30	Glycan biosynthesis and metabolism − N−Glycan degradation
Underexpressed				
1	−6.31	0e+00	73	Transcription factors − AP2−EREBP
2	−6.19	0e+00	64	Transcription factors − Other transcription factors
3	−4.99	0e+00	36	DNA replication
4	−4.96	0e+00	41	Replication and repair − DNA replication
5	−4.3	0e+00	11	Transcription factors − GRF
6	−4.17	0e+00	116	Ribosome biogenesis − 40S particles
7	−4.15	0e+00	29	Base excision repair
8	−3.97	4e−05	140	Hormone signaling − Ethylene signaling
9	−3.93	4e−05	44	Replication and repair − DNA Replication Factors
10	−3.8	1e−04	22	Replication and repair − Homologous recombination
11	−3.67	3e−04	64	Ribosome biogenesis − eukaryotes
12	−3.63	3e−04	75	Translation − Ribosome biogenesis − Eukaryotes
13	−3.51	6e−04	21	Replication and repair − Mismatch repair
14	−3.4	9e−04	25	Replication and repair − Base excision repair
15	−3.36	1e−03	219	Cell growth and death − Cell cycle
16	−3.28	1e−03	62	Ribosome biogenesis − 60S particles
17	−3.24	1e−03	37	Homologous recombination
18	−3.24	1e−03	38	Transcription factors − Basal transcription factors
19	−3.21	1e−03	247	Translation − Ribosome
20	−3.21	1e−03	165	Transcription − Spliceosome

Portrait

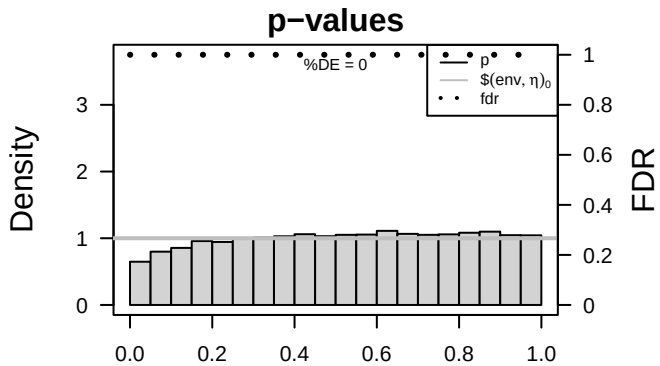


Top 100 DE genes





p−values



p−values