Sangio_accfreeze_r1

Global Summary

%DE = 0.27

genes with fdr < 0.2 = 196 (82 + / 114 −)

genes with fdr < 0.1 = 19 (5 + / 14 −)

genes with fdr < 0.05 = 5 (0 + / 5 −)

genes with fdr < 0.01 = 2 (0 + / 2 −)

<FC> = 0

<p−value> = 0.26

<fdr> = 0.73

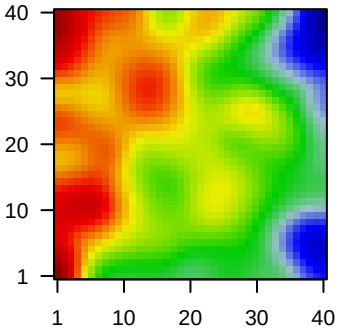
Differentially expressed genes

Rank	ID	log(FC)	p−value	fdr	Description / Metagene
Overexpressed					
1	Vitvi09g00149	1.41	2e−05	0.07	15 x 30 Binding to ATP, adenosine 5'−triphosphate, a universally impc
2	Vitvi10g01122	0.95	3e−05	0.07	11 x 32
3	Vitvi13g00010	0.46	3e−05	0.07	17 x 21 Binding to a metal ion.
4	Vitvi02g00954	1.04	5e−05	0.07	12 x 30 Binding to ATP, adenosine 5'−triphosphate, a universally impc
5	Vitvi17g00319	1.38	7e−05	0.09	2 x 25
6	Vitvi12g02175	0.81	1e−04	0.13	15 x 29 A membrane−bounded organelle of eukaryotic cells in which
7	Vitvi08g02220	2.66	1e−04	0.13	1 x 10 The component of a membrane consisting of the gene produc
8	Vitvi10g00937	1.22	2e−04	0.13	19 x 19 Binds to and increases the activity of a GTPase, an enzyme t
9	Vitvi01g01055	0.72	3e−04	0.13	27 x 12 Binding to ATP, adenosine 5'−triphosphate, a universally impc
10	Vitvi18g01090	1.26	3e−04	0.13	12 x 28 The initial step of transcription, consisting of the assembly of
11	Vitvi14g01895	1.01	3e−04	0.13	27 x 25 Catalysis of a biochemical reaction at physiological temperatu
12	Vitvi00g00533	1.04	3e−04	0.13	4 x 25
13	Vitvi10g02176	1.04	3e−04	0.13	4 x 25 Functions in the initiation of ribosome−mediated translation o
14	Vitvi15g00772	0.85	3e−04	0.13	13 x 26 Binding to an RNA molecule or a portion thereof.
15	Vitvi04g00279	0.75	4e−04	0.13	11 x 26 A membrane−bounded organelle of eukaryotic cells in which
16	Vitvi04g01201	1.05	4e−04	0.17	12 x 36 The contents of a cell excluding the plasma membrane and n
17	Vitvi01g00216	1.36	5e−04	0.17	14 x 27
18	Vitvi14g01530	2.06	5e−04	0.17	14 x 30 The component of a membrane consisting of the gene produc
19	Vitvi19g00111	3.06	5e−04	0.17	6 x 11
20	Vitvi08g00187	0.67	5e−04	0.17	12 x 30 The component of a membrane consisting of the gene produc
Underexpressed					
1	Vitvi05g00420	−1.18	6e−09	0.004	23 x 22 Any process involved in the maintenance of an internal steady
2	Vitvi10g00844	−1.21	3e−07	0.007	14 x 15 The component of a membrane consisting of the gene produc
3	Vitvi12g00905	−1.54	8e−07	0.025	24 x 4 Catalysis of the oxidation of ubiquinol by diverting electrons fr
4	Vitvi18g02574	−2.77	3e−06	0.025	40 x 5 Catalysis of a biochemical reaction at physiological temperatu
5	Vitvi07g02608	−3.03	6e−06	0.025	38 x 7 Catalysis of a biochemical reaction at physiological temperatu
6	Vitvi05g01091	−1.12	6e−06	0.052	35 x 15 The contents of a cell excluding the plasma membrane and n
7	Vitvi00g00770	−1.54	2e−05	0.052	36 x 7
8	Vitvi10g02218	−1.54	2e−05	0.052	36 x 7 The formation of a protein dimer, a macromolecular structure
9	Vitvi14g01339	−1.48	2e−05	0.052	34 x 8 Catalysis of an oxidation−reduction (redox) reaction, a reversi
10	Vitvi04g01902	−2.18	4e−05	0.073	37 x 8 Binding to a protein or a protein−containing complex to assist
11	Vitvi00g00610	−1.86	5e−05	0.073	33 x 8 A lipid bilayer along with all the proteins and protein complexe
12	Vitvi13g02504	−3.15	6e−05	0.073	38 x 7
13	Vitvi12g00084	−1.42	6e−05	0.073	35 x 8 Catalysis of the transfer of an alkyl or aryl (but not methyl) grc
14	Vitvi17g00927	−1.48	8e−05	0.094	35 x 6
15	Vitvi18g01674	−1.51	8e−05	0.111	37 x 8 Catalysis of the hydrolysis of internal, alpha−peptide bonds in
16	Vitvi18g01218	−2.02	9e−05	0.111	37 x 7 Binding to a calcium ion (Ca2+).
17	Vitvi11g00686	−2.95	1e−04	0.111	37 x 34 Catalysis of an oxidation−reduction (redox) reaction, a reversi
18	Vitvi18g00272	−2.52	1e−04	0.131	39 x 6 The component of a membrane consisting of the gene produc
19	Vitvi04g00112	−2.03	2e−04	0.131	36 x 7 Catalysis of a biochemical reaction at physiological temperatu
20	Vitvi01g01903	−1.5	2e−04	0.131	37 x 6 Catalysis of the reaction:a 2'−deoxyribonucleoside 5'−monopl

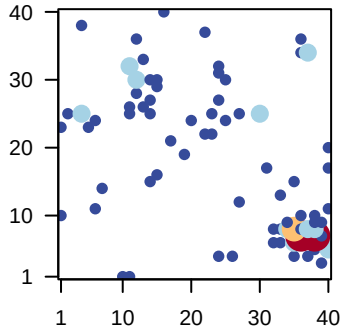
Differentially expressed gene sets

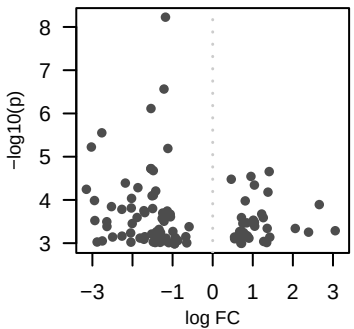
Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	6.16	0e+00	62	Ribosome Ribosome biogenesis 60S particles
2	5.84	0e+00	116	Ribosome Ribosome biogenesis 40S particles
3	5.56	0e+00	140	Hormone signaling Ethylene signaling
4	5.25	0e+00	75	Translation Ribosome Ribosome biogenesis eukaryotes
5	5.07	0e+00	64	Ribosome biogenesis eukaryotes
6	5.03	0e+00	73	Transcription factors AP2−EREBP EREBP
7	4.75	0e+00	144	Ribosome Eukaryotes
8	4.69	0e+00	64	Transcription factors Other transcription factors
9	4.57	0e+00	151	RNA polymerase II system
10	4.35	0e+00	49	Transcription factors NAC
11	3.91	4e−05	48	Transcription factors WRKY
12	3.74	1e−04	165	Transcription Spliceosome
13	3.63	3e−04	126	Translation RNA transport
14	3.26	1e−03	115	Enzyme Acting on acid anhydrides
15	3.25	1e−03	99	mRNA surveillance pathway
16	3.2	1e−03	81	Translation mRNA surveillance pathway
17	3.15	2e−03	36	Ribosome Ribosome biogenesis 40S particles
18	3.15	2e−03	67	Replication and Repair RNA degradation
19	3.05	2e−03	85	Nucleocytoplasmic transport
20	3.02	3e−03	128	Ubiquitin System Ring finger type E3
Underexpressed				
1	−14.86	0	47	Transporters Electron carriers
2	−14.74	0	18	Energy metabolism Photosynthesis proteins
3	−14.49	0	18	Photosynthesis proteins
4	−12.24	0	78	Energy metabolism Photosynthesis
5	−11.84	0	38	Photosynthesis
6	−9.2	0	10	Photosynthesis Photosystem I (P700 chlorophyll a)
7	−8.33	0	26	Flavonoid biosynthesis
8	−6.78	0	40	Transporters Vesicle trafficking pathway
9	−6.21	0	80	Cytoskeleton Microtubules
10	−6.18	0	57	Glyoxylate and dicarboxylate metabolism
11	−5.26	0	206	Cell growth and death Cell wall
12	−5.24	0	25	Nitrogen metabolism
13	−4.93	0	217	Cell motility Regulation of cytoskeleton
14	−4.47	0	13	Cutin suberine and wax biosynthesis
15	−4.46	0	31	Biosynthesis of plant secondary metabolites
16	−4.43	0	51	Carbon fixation photosynthetic organisms
17	−4.21	0	24	Carbohydrate metabolism Ascorbate and aldarate metabolism
18	−4.09	0	72	Energy metabolism Carbon fixation
19	−4.08	0	63	Phenylpropanoid biosynthesis
20	−4.06	0	47	ABC transporters

Portrait

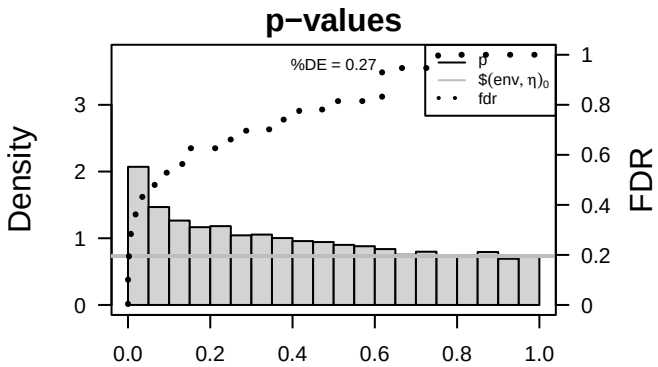


Top 100 DE genes





p−values



p−values