Tocai_accfreeze_r3

Global Summary

%DE = 0.25

genes with fdr < 0.2 = 9 (2 + / 7 −)

genes with fdr < 0.1 = 5 (0 + / 5 −)

genes with fdr < 0.05 = 0 (0 + / 0 −)

genes with fdr < 0.01 = 0 (0 + / 0 −)

<FC> = 0

<p−value> = 0.3

<fdr> = 0.75

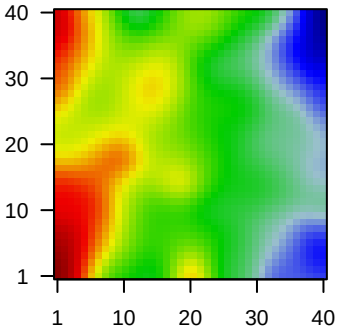
Differentially expressed genes

Rank	ID	log(FC)	p−value	fdr	Description / Metagene
Overexpressed					
1	Vitvi04g00467	2.21	3e−05	0.1	1 x 31
2	Vitvi09g0150(	0.97	4e−05	0.1	12 x 28 Catalysis of an oxidation−reduction (redox) reaction, a reversi
3	Vitvi07g0257(	1.52	1e−04	0.2	20 x 17
4	Vitvi18g00122	3.09	1e−04	0.2	1 x 38 The process whose specific outcome is the progression of the
5	Vitvi06g0092(	2.07	3e−04	0.5	2 x 37 The formation of a protein dimer, a macromolecular structure
6	Vitvi03g00243	0.48	5e−04	0.5	15 x 21 Binding to a calcium ion (Ca2+).
7	Vitvi08g00892	1.62	6e−04	0.5	8 x 15 The directed movement of proteins in a cell, including the mov
8	Vitvi16g00955	1.21	8e−04	0.5	10 x 20 A chlorophyll−containing plastid with thylakoids organized into
9	Vitvi01g00591	0.95	8e−04	0.5	8 x 14
10	Vitvi05g0002(	2	1e−03	0.5	1 x 36 Catalysis of an oxidation−reduction (redox) reaction, a reversi
11	Vitvi05g01427	2.07	1e−03	0.5	24 x 1
12	Vitvi08g0163(	0.76	1e−03	0.5	8 x 16 Any process that modulates the frequency, rate or extent of ce
13	Vitvi08g0135(	0.79	1e−03	0.5	9 x 28 Binding to ATP, adenosine 5'−triphosphate, a universally impo
14	Vitvi05g0175(	1.95	2e−03	0.5	9 x 17 A membrane−bounded organelle of eukaryotic cells in which
15	Vitvi08g00011	0.61	2e−03	0.5	18 x 20 The component of a membrane consisting of the gene produc
16	Vitvi18g0076(	1.68	2e−03	0.5	6 x 12 The formation of a protein dimer, a macromolecular structure
17	Vitvi18g0284(	3.07	2e−03	0.5	3 x 8
18	Vitvi11g00514	1.36	2e−03	0.5	15 x 29 A membrane−bounded organelle of eukaryotic cells in which
19	Vitvi02g00097	1.46	2e−03	0.5	13 x 18 The contents of a cell excluding the plasma membrane and n
20	Vitvi01g0065(	1.12	2e−03	0.5	8 x 12 The component of a membrane consisting of the gene produc
Underexpressed					
1	Vitvi15g01671	−1.64	5e−07	0.07	36 x 14
2	Vitvi17g0100(	−1.43	1e−05	0.07	38 x 15 Binding to a metal ion.
3	Vitvi03g01047	−0.92	2e−05	0.07	32 x 9 Binding to a zinc ion (Zn).
4	Vitvi05g00213	−1.33	2e−05	0.07	33 x 18
5	Vitvi16g01397	−1.31	3e−05	0.07	31 x 22
6	Vitvi11g00414	−1.58	5e−05	0.14	32 x 7 A part of a cellular organism that is either an immaterial entity
7	Vitvi18g0126(	−1.4	7e−05	0.14	35 x 17 The component of a membrane consisting of the gene produc
8	Vitvi05g00977	−1.37	7e−05	0.21	32 x 9 Catalysis of the geometric or structural changes within one m
9	Vitvi06g00019	−0.85	8e−05	0.22	24 x 29 The component of a membrane consisting of the gene produc
10	Vitvi09g01383	−1.26	1e−04	0.22	31 x 30 The pigmented membrane of a chloroplast thylakoid. An exan
11	Vitvi03g0009(	−0.94	2e−04	0.22	34 x 15 The formation of a protein dimer, a macromolecular structure
12	Vitvi12g0181(	−1.6	2e−04	0.22	28 x 28 A lipid bilayer along with all the proteins and protein complexes
13	Vitvi18g01677	−2.14	2e−04	0.22	39 x 32 The chemical reactions and pathways resulting in the formatic
14	Vitvi18g0275(	−1.43	2e−04	0.22	33 x 7 Catalysis of the reaction: a protein with reduced sulfide group
15	Vitvi18g00732	−1.57	2e−04	0.22	30 x 20 A process that is carried out at the cellular level which results
16	Vitvi15g01143	−0.82	2e−04	0.26	32 x 10
17	Vitvi12g0215(	−1.16	3e−04	0.26	35 x 10
18	Vitvi01g01083	−1.17	3e−04	0.52	31 x 30
19	Vitvi06g00514	−1.38	4e−04	0.52	37 x 8 The component of a membrane consisting of the gene produc
20	Vitvi10g0229(	−0.98	5e−04	0.52	32 x 10

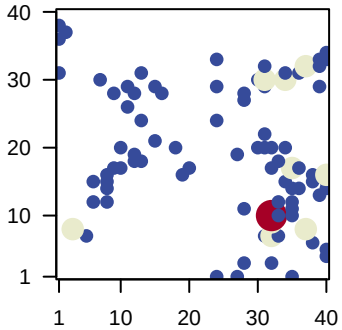
Differentially expressed gene sets

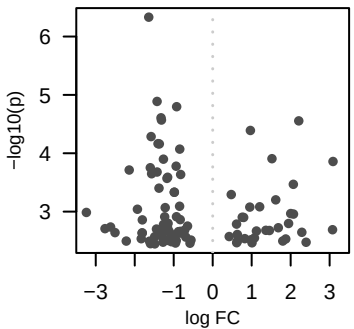
Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	7.69	0e+00	48	Transcription factors − WRKY
2	7.57	0e+00	49	Transcription factors − NAC
3	5.08	0e+00	140	Hormone signaling − Ethylene signaling
4	4.91	0e+00	162	Plant specific signaling pathway − Plant pathogen interaction
5	4.32	0e+00	153	Plant−pathogen interaction
6	4.2	0e+00	64	Transcription factors − Other transcription factors
7	4.15	0e+00	73	Transcription factors − AP2 EREBP
8	3.75	1e−04	170	Transcription factors − other − C3HC4
9	3.61	4e−04	128	Ubiquitin system − Single Ring type E3
10	3.58	4e−04	89	MAPK signaling pathway − plant
11	3.43	8e−04	86	Signal transduction − Calcium signaling pathway
12	3.4	9e−04	80	Transport − Tethering factors
13	3.3	1e−03	409	Enzyme − Transferring phosphorus−containing groups
14	3.18	2e−03	62	Ribosome biogenesis − 60S particles
15	3.01	3e−03	35	Mitophagy factors
16	2.99	3e−03	151	RNA polymerase II system
17	2.97	3e−03	31	Autophagy − other
18	2.93	4e−03	28	Transcription factors − Basic leucine zipper (bZIP)
19	2.89	4e−03	116	Ribosome biogenesis − 40S particles
20	2.78	6e−03	20	Protein − Autophagy − Autophagosome proteins
Underexpressed				
1	−11.72	0	78	Energy metabolism − Photosynthesis
2	−10.57	0	38	Photosynthesis
3	−9.59	0	211	Ribosome
4	−9.29	0	247	Translation − Ribosome
5	−9.12	0	47	Transport − Transporter − Catalog − Electron carriers
6	−8.27	0	18	Energy metabolism − Photosynthesis proteins
7	−7.94	0	18	Photosynthesis proteins
8	−7.24	0	144	Ribosome − Eukaryotes
9	−6.68	0	67	Ribosome − Bacteria
10	−6.58	0	10	Photosynthesis proteins − Photosystem II (P700 chlorophyll a)
11	−6.54	0	40	Transport − Thylakoid pathway
12	−6.44	0	97	Ribosome − Archaea
13	−6.4	0	72	Ribosome − Mitochondria − Chloroplast
14	−5.94	0	26	Flavonoid biosynthesis
15	−5.17	0	80	Cytoskeleton − Microtubules
16	−4.31	0	72	Energy metabolism − Carbon fixation
17	−4.29	0	41	Porphyrin metabolism
18	−4.17	0	13	Cutin suberine and wax biosynthesis
19	−4.15	0	217	Cell motility − Regulation of cytoskeleton
20	−4.05	0	41	Transport − Primary − P−type ATPase − Other cat D1

Portrait

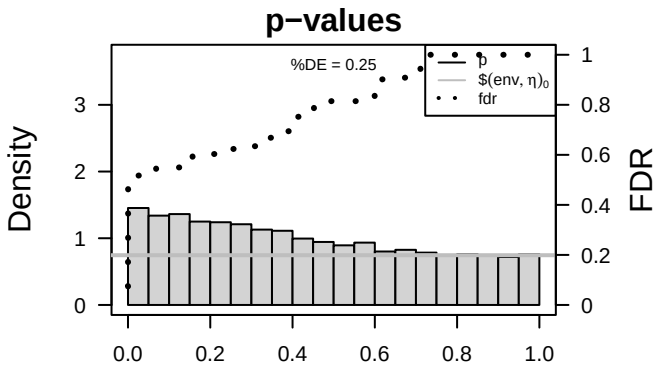


Top 100 DE genes





p−values



p−values