Tocai_accfreeze

Global Summary

%DE = NA

genes with fdr < 0.2 = 1645 (944 + / 701 −)

genes with fdr < 0.1 = 1085 (610 + / 475 −)

genes with fdr < 0.05 = 754 (416 + / 338 −)

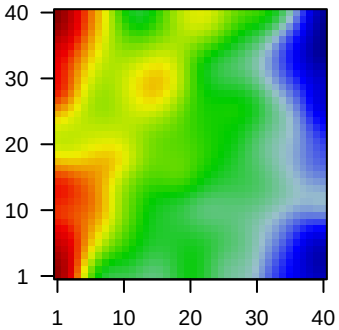
genes with fdr < 0.01 = 517 (271 + / 246 −)

<FC> = 0

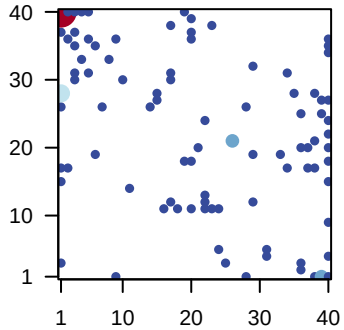
<p−value> = 0.13

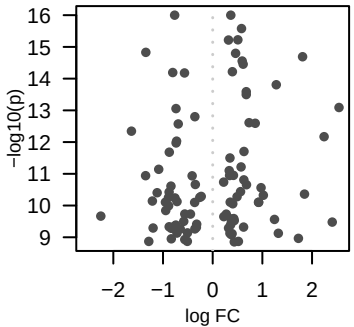
<fdr> = 0.54

Portrait



Top 100 DE genes





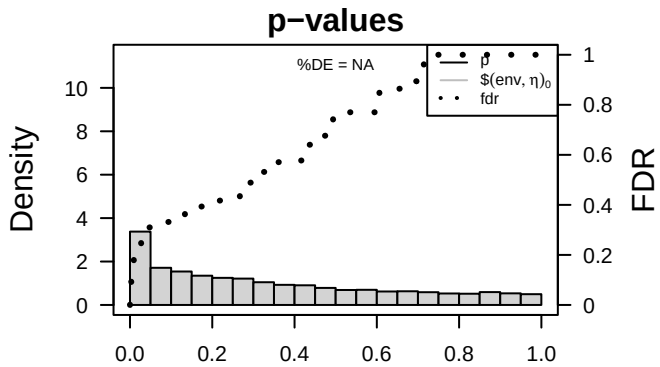
Differentially expressed genes

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
Overexpressed						
1	Vitvi12g01998	0.36	1e−16	2e−12	5 x 31	A membrane−bounded organelle of eukaryotic cells in which
2	Vitvi15g01635	0.58	3e−16	2e−12	3 x 30	
3	Vitvi09g00430	0.51	6e−16	2e−12	17 x 31	Binding to a protein.
4	Vitvi02g00458	0.32	6e−16	5e−12	7 x 26	
5	Vitvi07g01211	0.46	2e−15	5e−12	15 x 28	
6	Vitvi11g01268	1.81	2e−15	7e−12	1 x 40	The chemical reactions and pathways involving carbohydrate
7	Vitvi07g00686	0.59	3e−15	7e−12	6 x 35	
8	Vitvi18g01025	0.61	4e−15	1e−11	3 x 37	Binding to a protein.
9	Vitvi14g01636	0.4	6e−15	1e−11	20 x 18	Binding to a metal ion.
10	Vitvi02g00721	1.28	2e−14	8e−11	1 x 37	The chemical reactions and pathways involving carbohydrate
11	Vitvi07g02800	0.68	3e−14	8e−11	26 x 21	
12	Vitvi00g01897	0.68	3e−14	3e−10	26 x 21	
13	Vitvi17g00787	2.54	8e−14	3e−10	1 x 3	A membrane−bounded organelle of eukaryotic cells in which
14	Vitvi17g01221	0.73	2e−13	4e−10	19 x 40	Catalysis of the reaction: UDP−glucose + D−fructose = UDP
15	Vitvi18g00171	0.86	3e−13	4e−10	1 x 40	The directed movement of proteins in a cell, including the mo
16	Vitvi17g01380	2.24	7e−13	2e−09	1 x 28	The contents of a cell excluding the plasma membrane and n
17	Vitvi07g01978	0.63	2e−12	5e−09	23 x 38	The component of a membrane consisting of the gene produc
18	Vitvi13g01234	0.35	3e−12	1e−08	11 x 14	The component of a membrane consisting of the gene produc
19	Vitvi01g00824	0.57	6e−12	1e−08	20 x 39	Any molecular function by which a gene product interacts sel
20	Vitvi01g01700	0.33	8e−12	1e−08	21 x 20	Binding to nicotinamide−adenine dinucleotide phosphate, a c
Underexpressed						
1	Vitvi14g00623	−0.77	1e−16	2e−12	31 x 5	A membrane−bounded organelle of eukaryotic cells in which
2	Vitvi16g00501	−1.35	1e−15	5e−12	40 x 35	The component of a membrane consisting of the gene produc
3	Vitvi15g01621	−0.8	6e−15	1e−11	38 x 21	Any molecular function by which a gene product interacts sel
4	Vitvi15g00504	−0.57	7e−15	8e−11	18 x 11	Enables the synthesis of ATP from ADP and phosphate by the
5	Vitvi01g01946	−0.74	9e−14	4e−10	36 x 2	The formation of a protein dimer, a macromolecular structure
6	Vitvi19g00115	−0.36	2e−13	4e−10	37 x 17	The contents of a cell excluding the plasma membrane and n
7	Vitvi09g00358	−0.69	3e−13	2e−09	24 x 11	The part of the cytoplasm that does not contain organelles bu
8	Vitvi03g01760	−1.64	5e−13	2e−09	40 x 34	The component of a membrane consisting of the gene produc
9	Vitvi04g00670	−0.73	9e−13	2e−09	34 x 31	A lipid bilayer along with all the proteins and protein complexe
10	Vitvi05g01938	−0.74	1e−12	5e−09	37 x 20	
11	Vitvi11g01257	−0.87	2e−12	1e−08	39 x 1	Catalysis of the reaction: substrate + ATP + CoASH = AMP +
12	Vitvi19g00388	−1.09	7e−12	1e−08	40 x 4	Binding to a magnesium (Mg) ion.
13	Vitvi10g00164	−1.35	1e−11	1e−08	38 x 28	Binding to a calcium ion (Ca2+).
14	Vitvi11g00715	−0.41	1e−11	3e−08	16 x 11	Binding to a zinc ion (Zn).
15	Vitvi17g01001	−0.35	2e−11	3e−08	29 x 32	Catalysis of the transfer of a methyl group to an acceptor mol
16	Vitvi01g01999	−0.84	2e−11	3e−08	22 x 12	
17	Vitvi16g02059	−0.88	4e−11	3e−08	40 x 22	Binding to a metal ion.
18	Vitvi04g00641	−1.12	4e−11	3e−08	40 x 18	Catalysis of the hydrolysis of internal, alpha−peptide bonds in
19	Vitvi09g01352	−0.23	5e−11	3e−08	34 x 17	A membrane−bounded organelle of eukaryotic cells in which
20	Vitvi08g00201	−0.26	6e−11	3e−08	29 x 12	The action of a molecule that contributes to the structural inte

Differentially expressed gene sets

Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	7.34	0e+00	49	Transcription factors − NAC
2	5.88	0e+00	48	Transcription factors − WRKY
3	5.51	0e+00	140	Hormone signaling − Ethylene signaling
4	4.94	0e+00	73	Transcription factors − AP2−EREBP
5	4.64	0e+00	64	Transcription factors − Other transcription factors
6	4.18	0e+00	62	Ribosome − Ribosome biogenesis in 80S particles
7	3.97	0e+00	238	Enzyme − Glycosyltransferases
8	3.73	2e−04	116	Ribosome − Ribosome biogenesis in 80S particles
9	3.62	2e−04	170	Transcription factors − C3HC4
10	3.31	1e−03	128	Ubiquitin system − Single ring type E3
11	3.06	3e−03	51	Plant specific signaling − Calcium rhythm
12	3.03	4e−03	31	Autophagy − other
13	3	4e−03	151	RNA polymerase II system
14	2.96	4e−03	11	Biosynthesis of secondary metabolites − ABA biosynthesis
15	2.95	4e−03	80	Transport − Tethering factors
16	2.92	4e−03	35	Mitophagy − factors
17	2.91	5e−03	409	Enzyme − Transferases − Phosphorus containing groups
18	2.91	5e−03	153	Plant−pathogen interaction
19	2.91	5e−03	89	MAPK signaling pathway − plant
20	2.82	6e−03	64	Ribosome biogenesis in eukaryotes
Underexpressed				
1	−11.05	0	78	Energy metabolism − Photosynthesis
2	−10.38	0	38	Photosynthesis
3	−8.7	0	47	Transport − Transporters − Electron carriers
4	−7.96	0	211	Ribosome
5	−7.87	0	18	Energy metabolism − Photosynthesis proteins
6	−7.78	0	247	Translation − Ribosome
7	−7.55	0	18	Photosynthesis proteins
8	−6.79	0	26	Flavonoid biosynthesis
9	−6.32	0	10	Photosynthesis proteins − Photosystem II (P700 chlorophyll a)
10	−6.1	0	144	Ribosome − Eukaryotes
11	−5.6	0	40	Transport − Thylakoid targeting pathway
12	−5.48	0	67	Ribosome − Bacteria
13	−5.43	0	97	Ribosome − Archaea
14	−5.26	0	72	Ribosome − Mitochondria − Chloroplast
15	−5.25	0	80	Cytoskeleton − Microtubules
16	−4.38	0	217	Cell motility − Regulation of cytoskeleton
17	−4.19	0	19	Aquaporins − Small and basic intrinsic subcluster [TC:1.A.8]
18	−4.07	0	72	Energy metabolism − Carbon fixation
19	−3.88	0	39	Pentose and glucuronate interconversions
20	−3.85	0	58	Carbohydrate metabolism − Fructose and mannose metabolism

p−values



p−values