Riesl_accfreeze

Global Summary

%DE = NA

genes with fdr < 0.2 = 1543 (785 + / 758 −)

genes with fdr < 0.1 = 1140 (573 + / 567 −)

genes with fdr < 0.05 = 859 (421 + / 438 −)

genes with fdr < 0.01 = 571 (259 + / 312 −)

<FC> = 0

<p−value> = 0.14

<fdr> = 0.67

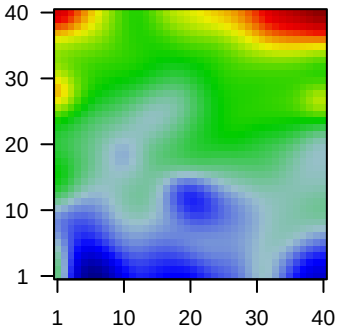
Differentially expressed genes

Rank	ID	log(FC)	p−value	fdr	Description Metagene
Overexpressed					
1	Vitvi13g00409	1.38	1e−16	4e−10	3 x 40 Any process that results in a change in state or activity of a c
2	Vitvi10g01886	1	4e−13	8e−09	3 x 40
3	Vitvi17g00843	0.39	1e−12	3e−08	27 x 27 Catalysis of the transfer of a glycosyl group from one compou
4	Vitvi14g01280	0.22	5e−12	3e−08	8 x 31 The process in which relatively unspecialized cells, e.g. embr
5	Vitvi02g00666	1.61	4e−11	1e−07	39 x 40 A membrane−bounded organelle of eukaryotic cells in which
6	Vitvi08g00930	0.81	6e−11	2e−07	1 x 40 The chemical reactions and pathways involving carbohydrate
7	Vitvi06g00578	1	1e−10	3e−07	35 x 40 Any process that results in a change in state or activity of a c
8	Vitvi18g00858	1.03	2e−10	3e−07	30 x 40 A membrane−bounded organelle of eukaryotic cells in which
9	Vitvi09g00327	0.56	2e−10	3e−07	4 x 40 The process in which a pre−tRNA molecule is converted to a
10	Vitvi17g00787	1.98	3e−10	3e−07	1 x 3 A membrane−bounded organelle of eukaryotic cells in which
11	Vitvi11g00657	1.47	4e−10	7e−07	1 x 40
12	Vitvi01g00064	1.35	1e−09	7e−07	35 x 40 The chemical reactions and pathways involving carbohydrate
13	Vitvi14g01805	0.98	1e−09	7e−07	33 x 40 The component of a membrane consisting of the gene produc
14	Vitvi07g03081	1.38	1e−09	7e−07	1 x 40
15	Vitvi00g01815	1.38	1e−09	8e−07	1 x 40
16	Vitvi13g01767	0.55	1e−09	8e−07	4 x 40 The space external to the outermost structure of a cell. For ce
17	Vitvi06g00579	1.51	2e−09	1e−06	1 x 40
18	Vitvi03g00200	0.36	4e−09	3e−06	6 x 37 Catalysis of the transfer of an acyl group to an oxygen atom c
19	Vitvi15g01672	0.34	5e−09	3e−06	5 x 37
20	Vitvi08g01497	0.89	5e−09	3e−06	1 x 40 The contents of a cell excluding the plasma membrane and n
Underexpressed					
1	Vitvi10g00590	−0.76	3e−14	9e−10	16 x 14
2	Vitvi03g01571	−1.17	1e−13	2e−09	21 x 12 Binding to a calcium ion (Ca2+).
3	Vitvi02g01424	−0.52	3e−13	2e−09	23 x 8
4	Vitvi14g01310	−0.27	3e−12	3e−08	7 x 24 Binding to a protein.
5	Vitvi02g01621	−0.84	9e−12	3e−08	6 x 6 Catalysis of a biochemical reaction at physiological temperatu
6	Vitvi06g00379	−0.71	2e−11	3e−08	25 x 1 Binding to a protein.
7	Vitvi02g00208	−0.35	2e−11	3e−08	31 x 13 Binding to a metal ion.
8	Vitvi01g02263	−0.77	2e−11	3e−08	40 x 20 Catalysis of the transfer of a methyl group to the oxygen atom
9	Vitvi10g01794	−0.33	2e−11	3e−08	16 x 7 A membrane−bounded organelle of eukaryotic cells in which
10	Vitvi19g01940	−1.26	2e−11	3e−08	34 x 1
11	Vitvi15g01469	−0.35	3e−11	3e−08	28 x 9
12	Vitvi13g01237	−0.31	3e−11	3e−08	17 x 5
13	Vitvi10g00178	−0.76	3e−11	1e−07	17 x 13 Binding to a chaperone protein, a class of proteins that bind t
14	Vitvi05g02086	−0.59	5e−11	1e−07	17 x 5
15	Vitvi07g01947	−0.4	6e−11	1e−07	32 x 7 A semiautonomous, self replicating organelle that occurs in va
16	Vitvi18g00191	−0.89	1e−10	2e−07	22 x 11 Catalysis of an oxidation−reduction (redox) reaction in which
17	Vitvi12g02046	−0.48	1e−10	2e−07	38 x 3 Catalysis of an oxidation−reduction (redox) reaction, a reversi
18	Vitvi09g00723	−0.35	2e−10	3e−07	28 x 5
19	Vitvi02g00466	−0.72	2e−10	3e−07	8 x 2 A lipid bilayer along with all the proteins and protein complexe
20	Vitvi16g01884	−0.58	3e−10	3e−07	31 x 4 Binding to a protein.

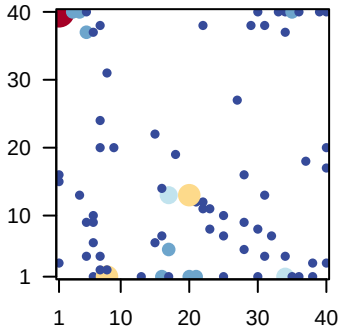
Differentially expressed gene sets

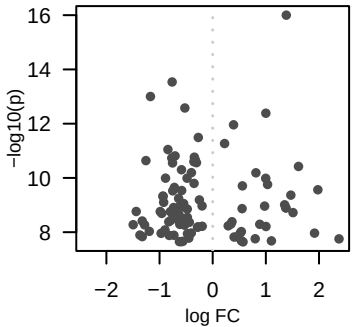
Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	8.83	0e+00	18	Photosynthesis − proteins
2	8.64	0e+00	18	Energy metabolism − Photosynthesis, proteins
3	7.98	0e+00	47	Transporters − Electron carriers
4	7.77	0e+00	80	Cytoskeleton − Microtubules
5	7.3	0e+00	206	Cell growth and death − Cell wall
6	6.42	0e+00	64	Transcription factors − Other transcription factors
7	6.15	0e+00	217	Cell motility − Regulation of cytoskeleton
8	5.99	0e+00	73	Transcription factors − AP2 EREBP
9	5.75	0e+00	11	Transcription factors − GRF
10	5.04	0e+00	10	Peptidases − Aspartic peptidases, A1 family
11	4.87	0e+00	10	Photosynthesis − Photosystem II (PSII)
12	3.76	0e+00	113	Exosome − Exosome proteins
13	3.75	0e+00	140	Hormone signaling − Ethylene signaling
14	3.65	2e−04	38	Photosynthesis
15	3.56	5e−04	66	Exosome − Exosome proteins
16	3.36	1e−03	219	Cell growth and death − Cell cycle
17	3.12	3e−03	40	Transporters − Type I Type II pathway
18	3.06	3e−03	78	Glycosyltransferases − Sphingolipid
19	2.93	4e−03	238	Enzyme − Glycosyltransferases
20	2.75	7e−03	21	Thiamine metabolism
Underexpressed				
1	−5.3	0e+00	45	Galactose metabolism
2	−3.9	0e+00	92	Lipid metabolism − Glycerolipid metabolism
3	−3.7	2e−04	44	Energy metabolism − Nitrogen metabolism
4	−3.51	5e−04	28	Transcription factors − Basic leucine zipper (bZIP)
5	−3.28	2e−03	45	Valine leucine and isoleucine degradation
6	−3.27	2e−03	79	Transporters − Proteins 31 to 64
7	−3.26	2e−03	77	Carbohydrate metabolism − Galactose metabolism
8	−3.05	3e−03	42	Tryptophan metabolism
9	−2.93	4e−03	77	Pores ion channels [TC:1]
10	−2.88	5e−03	68	Amino acid metabolism − Aspartate asparagine metabolism
11	−2.86	5e−03	11	Lipid metabolism − Steroid metabolism
12	−2.85	5e−03	25	Lysine degradation
13	−2.84	5e−03	41	Cofactors and vitamins metabolism − Riboflavin metabolism
14	−2.84	6e−03	56	Glycine serine and threonine metabolism
15	−2.8	6e−03	43	Transcription factors − BZIP
16	−2.76	7e−03	26	Pantothenate and CoA biosynthesis
17	−2.72	8e−03	51	Biosynthesis of secondary metabolites − Isoquinoline alkaloid biosynthesis
18	−2.66	9e−03	43	Alanine aspartate and glutamate metabolism
19	−2.64	9e−03	11	Vitamin B6 metabolism
20	−2.63	1e−02	58	Other amino acid metabolism − Glutamine glutamate metabolism

Portrait

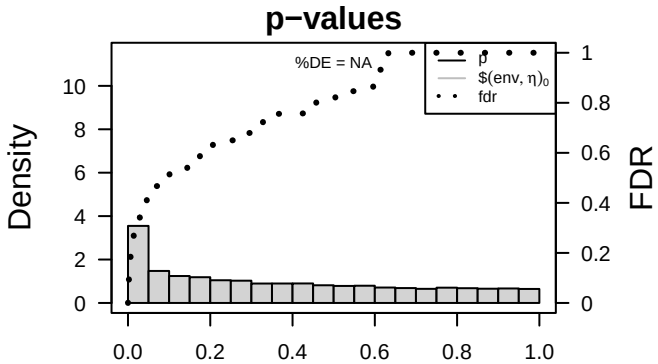


Top 100 DE genes





p−values



p−values