Riesl_acclim_r3

Global Summary

%DE = 0.12

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> = 0.39

<fdr> = 0.88

Differentially expressed genes

Overexpressed

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	Vitvi18g00953	0.85	0.002	0.8	26 x 22	The chemical reactions and pathways resulting in the breakdc
2	Vitvi06g00016	2.1	0.003	0.8	36 x 27	The space external to the outermost structure of a cell. For ce
3	Vitvi07g00597	0.84	0.003	0.8	27 x 22	A semiautonomous, self replicating organelle that occurs in va
4	Vitvi17g00032	0.52	0.003	0.8	25 x 22	Binding to an RNA molecule or a portion thereof.
5	Vitvi07g00807	2.43	0.003	0.8	36 x 26	Binding to a protein.
6	Vitvi06g01122	0.54	0.003	0.8	23 x 23	Catalysis of a biochemical reaction at physiological temperatu
7	Vitvi09g00007	1.34	0.004	0.8	13 x 29	The chemical reactions and pathways involving lipids, compou
8	Vitvi18g00059	0.76	0.005	0.8	27 x 28	The component of a membrane consisting of the gene produc
9	Vitvi05g01891	0.81	0.005	0.8	13 x 33	A lipid bilayer along with all the proteins and protein complexe
10	Vitvi18g01670	0.58	0.005	0.8	25 x 25	Catalysis of a biochemical reaction at physiological temperatu
11	Vitvi16g00077	0.52	0.005	0.8	29 x 18	A lipid bilayer along with all the proteins and protein complexe
12	Vitvi10g00012	0.92	0.005	0.8	29 x 24	Catalysis of the transfer of an acyl group to a nitrogen atom o
13	Vitvi16g00082	1.36	0.005	0.8	29 x 30	The part of the cytoplasm that does not contain organelles bu
14	Vitvi08g01962	1.29	0.006	0.8	10 x 40	Catalysis of an oxidation−reduction (redox) reaction, a reversi
15	Vitvi05g00765	0.48	0.006	0.8	25 x 24	The joining together of exons from one or more primary trans
16	Vitvi05g01573	1.7	0.006	0.8	1 x 28	The component of a membrane consisting of the gene produc
17	Vitvi04g01694	0.94	0.006	0.8	25 x 34	A lipid bilayer along with all the proteins and protein complexe
18	Vitvi13g01999	1.73	0.007	0.8	35 x 27	Catalysis of an oxidation−reduction (redox) reaction, a reversi
19	Vitvi08g01090	0.59	0.007	0.8	26 x 22	The action of a molecule that contributes to the structural inte
20	Vitvi04g01440	1.3	0.008	0.8	32 x 28	

Underexpressed

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	Vitvi19g00433	−0.98	2e−04	0.8	14 x 17	
2	Vitvi18g00220	−0.42	2e−03	0.8	16 x 21	A membrane−bounded organelle of eukaryotic cells in which
3	Vitvi04g00450	−0.53	2e−03	0.8	16 x 21	Catalysis of the reaction: peptidyl−proline (omega=180) = pep
4	Vitvi18g00167	−0.84	2e−03	0.8	7 x 24	Any molecular function by which a gene product interacts sele
5	Vitvi18g00368	−0.79	2e−03	0.8	23 x 7	Binding to a metal ion.
6	Vitvi13g02569	−1.29	3e−03	0.8	9 x 9	Binding to a protein.
7	Vitvi11g00458	−0.63	3e−03	0.8	14 x 22	A lipid bilayer along with all the proteins and protein complexe
8	Vitvi03g00059	−0.8	3e−03	0.8	14 x 22	Any process that modulates the frequency, rate or extent of ce
9	Vitvi01g00646	−1.41	3e−03	0.8	17 x 5	Binding to a protein.
10	Vitvi13g01348	−0.65	4e−03	0.8	15 x 21	Binding to ATP, adenosine 5'−triphosphate, a universally impc
11	Vitvi01g00676	−0.91	4e−03	0.8	15 x 18	
12	Vitvi03g01140	−0.7	4e−03	0.8	13 x 24	Cleavage of the 5'−cap of a nuclear mRNA triggered by short
13	Vitvi16g01086	−1.59	4e−03	0.8	9 x 4	A membrane−bounded organelle of eukaryotic cells in which
14	Vitvi18g00959	−0.67	5e−03	0.8	27 x 13	Binding to a metal ion.
15	Vitvi06g01476	−0.97	5e−03	0.8	22 x 16	A lipid bilayer along with all the proteins and protein complexe
16	Vitvi07g00267	−0.83	5e−03	0.8	13 x 12	Any molecular function by which a gene product interacts sele
17	Vitvi03g00355	−0.95	5e−03	0.8	19 x 6	Binding to a protein.
18	Vitvi01g00523	−0.81	5e−03	0.8	8 x 24	Any process involved in the conversion of a primary mRNA tra
19	Vitvi10g00301	−0.68	5e−03	0.8	14 x 17	
20	Vitvi13g00188	−0.5	6e−03	0.8	17 x 18	Binding to ATP, adenosine 5'−triphosphate, a universally impc

Differentially expressed gene sets

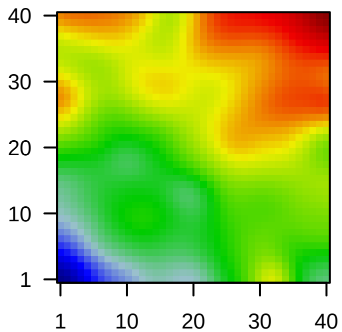
Overexpressed

Rank	GSZ	p−value	#all	Geneset
1	8.75	0e+00	211	Ribosome Ribosome
2	8.61	0e+00	247	Translation Translation − Ribosome
3	6.82	0e+00	144	Ribosome Ribosome − Eukaryotes
4	6.34	0e+00	217	Cell motility Cell motility − Regulation of actin cytoskeleton
5	6.16	0e+00	18	Energy metabolism Energy metabolism − Photosynthesis antenna proteins
6	6.01	0e+00	80	Cytoskeleton Cytoskeleton − Microtubules
7	5.89	0e+00	97	Ribosome Ribosome − Archaea
8	5.82	0e+00	18	Photosynthesis Photosynthesis − antenna proteins
9	5.74	0e+00	38	Photosynthesis Photosynthesis
10	5.68	0e+00	67	Ribosome Ribosome − Bacteria
11	5.64	0e+00	219	Cell growth and death Cell growth and death − Cell cycle
12	5.32	0e+00	72	Ribosome Ribosome − Mitochondria/Chloroplast
13	5.23	0e+00	47	Transporter catalog Transporter catalog − Electron carriers
14	5.15	0e+00	78	Energy metabolism Energy metabolism − Photosynthesis
15	4.46	0e+00	24	Replication protein Replication protein − DNA Replication Factors
16	4.1	0e+00	40	Transport system Transport system − Thylakoid targeting pathway
17	3.6	4e−04	41	Replication and repair Replication and repair − DNA replication
18	3.57	5e−04	66	Exosome Exosome − Exosomal proteins of bladder cancer cells
19	3.54	5e−04	36	DNA replication DNA replication
20	3.49	7e−04	10	Photosynthesis proteins Photosynthesis proteins − Photosystem I (P700 chlorophyll a)

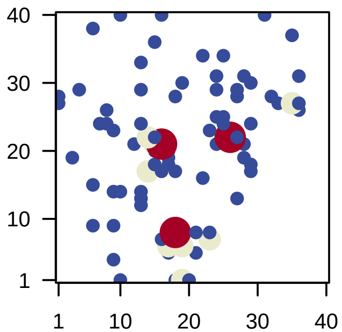
Underexpressed

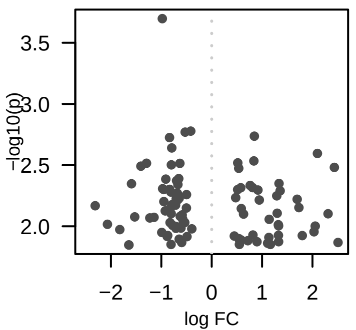
Rank	GSZ	p−value	#all	Geneset
1	−9.11	0e+00	48	Transcription factors Transcription factors − WRKY
2	−7.97	0e+00	73	Transcription factors Transcription factors − AP2 EREBP
3	−7.37	0e+00	140	Hormone signaling Hormone signaling − Ethylene signaling
4	−6.79	0e+00	64	Transcription factors Transcription factors − Other transcription factors
5	−6.59	0e+00	162	Plant specific signaling Plant specific signaling − Plant−pathogen interaction
6	−6.56	0e+00	49	Transcription factors Transcription factors − NAC
7	−6.06	0e+00	11	Biosynthesis of secondary metabolism Biosynthesis of secondary metabolism − ABA biosynthesis
8	−6.01	0e+00	26	Flavonoid biosynthesis Flavonoid biosynthesis
9	−5.59	0e+00	111	Hormone signaling Hormone signaling − ABA signaling
10	−4.89	0e+00	153	Plant−pathogen interaction Plant−pathogen interaction
11	−4.54	0e+00	29	Carotenoid biosynthesis Carotenoid biosynthesis
12	−4.35	0e+00	118	Transcription factors Transcription factors − Helix−turn−helix
13	−4.26	0e+00	28	Transcription factors Transcription factors − Basic leucine zipper (bZIP)
14	−4.13	0e+00	83	Transcription factors Transcription factors − MYB
15	−3.9	4e−05	43	Transcription factors Transcription factors − BZIP
16	−3.89	8e−05	45	Galactose metabolism Galactose metabolism
17	−3.81	1e−04	26	Glycosyltransferase Glycosyltransferase − Hydrophobic molecule
18	−3.53	5e−04	77	Pores ion channels Pores ion channels [TC:1]
19	−3.5	6e−04	56	Hormone signaling Hormone signaling − Jasmonate signaling
20	−3.35	1e−03	29	Transcription factors Transcription factors − GRAS

Portrait

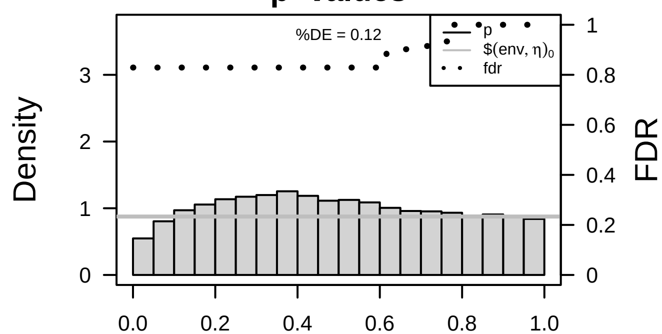


Top 100 DE genes





p−values



p−values