

Riesl_freeze_r1

Global Summary

%DE = 0.14
genes with $\text{fdr} < 0.2 = 1 \text{ (0 + / 1 -)}$
genes with $\text{fdr} < 0.1 = 0 \text{ (0 + / 0 -)}$
genes with $\text{fdr} < 0.05 = 0 \text{ (0 + / 0 -)}$
genes with $\text{fdr} < 0.01 = 0 \text{ (0 + / 0 -)}$

<FC> = 0
<p-value> = 0.34
<fdr> = 0.86

Differentially expressed genes

Rank	ID	log(FC)	fdr	Description	
		p-value		Metagene	
Overexpressed					
1	Vitv10g0134E	1.48	2e-04	0.7	15 x 4 Binding to a nucleic acid.
2	Vitv10g0191E	1.64	3e-04	0.7	30 x 5 A membrane-bounded organelle of eukaryotic cells in which
3	Vitv10g0049E	2.12	5e-04	0.7	12 x 4 The process of assisting in the covalent and noncovalent assi
4	Vitv10g0144E	2.69	5e-04	0.7	29 x 1
5	Vitv11g0168E	2.48	6e-04	0.7	1 x 17
6	Vitv10g0218E	2.15	6e-04	0.7	38 x 1 The contents of a cell excluding the plasma membrane and n
7	Vitv13g0049C	1.75	7e-04	0.7	15 x 6 The process of assisting in the covalent and noncovalent assi
8	Vitv16g0110E	2.39	9e-04	0.7	27 x 1 Binding to ATP, adenosine 5'-triphosphate, a universally impc
9	Vitv16g0068E	2.5	9e-04	0.7	5 x 24
10	Vitv13g0256E	1.45	1e-03	0.7	29 x 3
11	Vitv12g0196E	0.55	1e-03	0.7	21 x 25 The component of a membrane consisting of the gene produ
12	Vitv10g0151E	0.54	1e-03	0.7	17 x 22 Binding to messenger RNA (mRNA), an intermediate molecu
13	Vitv17g0069E	2.01	2e-03	0.7	36 x 5 The contents of a cell excluding the plasma membrane and n
14	Vitv10g0123A	0.92	2e-03	0.7	1 x 20 Binding to a protein.
15	Vitv01g0155E	0.55	2e-03	0.7	16 x 23 A membrane-bounded organelle of eukaryotic cells in which
16	Vitv10g0095A	1.06	2e-03	0.7	16 x 6 Catalysis of a biochemical reaction at physiological temperat
17	Vitv10g0068E	1.82	2e-03	0.7	11 x 3 Catalysis of an oxidation-reduction (redox) reaction, a reversi
18	Vitv10g0021E	1.35	2e-03	0.7	26 x 1 Binding to ATP, adenosine 5'-triphosphate, a universally impc
19	Vitv03g0037E	2.35	3e-03	0.7	12 x 6 Binding to a heme, a compound composed of iron complexed
20	Vitv15g0011C	2.01	3e-03	0.7	30 x 3 A lipid bilayer along with all the proteins and protein complex
Underexpressed					
1	Vitv18g0102C	-2.09	2e-06	0.2	30 x 31 Binding to a zinc ion (Zn).
2	Vitv04g0143C	-1.5	1e-05	0.4	24 x 31 Any molecular function by which a gene product interacts sele
3	Vitv10g0097E	-1.64	6e-05	0.4	33 x 13 A semiautonomous, self replicating organelle that occurs in vi
4	Vitv10g0006E	-0.55	8e-05	0.4	21 x 21 Any process involved in the conversion of a primary mRNA tra
5	Vitv13g0206E	-1.04	9e-05	0.7	18 x 20
6	Vitv16g0051E	-1.85	3e-04	0.7	35 x 26 Binding to a protein.
7	Vitv07g0053E	-0.69	3e-04	0.7	17 x 21 A membrane-bounded organelle of eukaryotic cells in which
8	Vitv04g0014E	-1.58	4e-04	0.7	27 x 37 Catalysis of a biochemical reaction at physiological temperat
9	Vitv10g0022E	-1.41	7e-04	0.7	13 x 33 Any process that modulates the frequency, rate or extent of pl
10	Vitv10g0041E	-1.22	8e-04	0.7	21 x 40 Binding to a metal ion.
11	Vitv10g0184E	-1.63	8e-04	0.7	28 x 38
12	Vitv07g0263E	-0.99	9e-04	0.7	22 x 17
13	Vitv15g0024E	-1.01	9e-04	0.7	12 x 36 Binding to a calcium ion (Ca2+).
14	Vitv07g0241E	-1.01	1e-03	0.7	16 x 16
15	Vitv10g0156E	-0.61	1e-03	0.7	19 x 19 A membrane-bounded organelle of eukaryotic cells in which
16	Vitv13g0003E	-0.86	1e-03	0.7	12 x 15 A lipid bilayer along with all the proteins and protein complex
17	Vitv10g0203E	-1.56	1e-03	0.7	25 x 40
18	Vitv14g0251E	-1.92	2e-03	0.7	30 x 38 Binding to a calcium ion (Ca2+).
19	Vitv01g0172E	-1.55	2e-03	0.7	25 x 40 Binding to a zinc ion (Zn).
20	Vitv13g0190C	-2.94	2e-03	0.7	1 x 40

Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	6.46	0e+00	64	Transcription factors
2	6.39	0e+00	157	Protein processing in endoplasmic reticulum
3	6.31	0e+00	73	Transcription factor AP2, EREBP2, EREBP
4	6.23	0e+00	140	Hormone signaling pathway
5	6.16	0e+00	17	Proteasome assembly
6	6.11	0e+00	15	Chaperone HSP70 - DSKK0 / DNAK
7	5.92	0e+00	18	Chaperone HSP20 - HSP20
8	5.92	0e+00	12	Endoplasmic reticulum chaperone
9	5.56	0e+00	48	Transcription factor WRKY - WRKY
10	5.2	0e+00	38	Protein - Chaperone mediated autophagy (CMA)
11	4.98	0e+00	71	Exosome
12	4.46	0e+00	45	Galactose metabolism
13	3.88	8e-05	162	Plant specific signaling pathway
14	3.64	3e-04	153	Plant-pathogen interaction
15	3.28	1e-03	38	Protein - Clathrin-mediated endocytosis
16	3.23	1e-03	49	Transcription factor NACs - NAC
17	3.22	1e-03	16	Transcription factor HSFs - HSF
18	3.04	2e-03	116	Ribosome biogenesis
19	3.03	2e-03	35	Mitochondrial factors
20	2.96	3e-03	165	Transcription factor Spliceosome
<i>Underexpressed</i>				
1	-7.74	0e+00	217	Cell motility
2	-7.69	0e+00	80	Cytoskeleton
3	-6.97	0e+00	18	Energy metabolism
4	-6.53	0e+00	18	Photosynthesis
5	-6.48	0e+00	47	Transport
6	-6.37	0e+00	78	Energy metabolism
7	-5.93	0e+00	219	Cell growth
8	-5.85	0e+00	38	Photosynthesis
9	-4.96	0e+00	10	Photosynthesis
10	-4.48	0e+00	41	Replication
11	-4.46	0e+00	11	Transcription factors - GRF
12	-4.34	0e+00	36	DNA replication
13	-4.13	0e+00	40	Transport
14	-4.03	0e+00	24	Replication
15	-3.78	1e-04	34	Peptidase
16	-3.78	1e-04	13	Cutin subunit
17	-3.59	4e-04	41	Porphyryr
18	-3.49	7e-04	129	Enzyme
19	-3.24	1e-03	39	Pentose
20	-3.07	2e-03	101	Starch

