Riesl_warm

Global Summary

%DE = NA

genes with fdr < 0.2 = 4952 (2324 + / 2628 −)

genes with fdr < 0.1 = 4070 (1892 + / 2178 −)

genes with fdr < 0.05 = 3510 (1613 + / 1897 −)

genes with fdr < 0.01 = 2656 (1201 + / 1455 −)

<FC> = 0

<p−value> = 0.01

<fdr> = 0.4

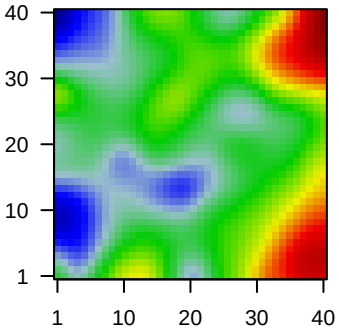
Differentially expressed genes

Rank	ID	log(FC)	p−value	fdr	Description Metagene
Overexpressed					
1	Vitvi01g00647	1.24	1e−16	2e−14	40 x 5 A lipid bilayer along with all the proteins and protein complexe
2	Vitvi07g01397	1.13	1e−16	2e−14	35 x 2
3	Vitvi01g00012	0.81	1e−16	2e−14	20 x 36 The membrane surrounding a cell that separates the cell from
4	Vitvi01g00288	1.01	1e−16	2e−14	32 x 33 A membrane−bounded organelle of eukaryotic cells in which
5	Vitvi01g00306	0.96	1e−16	2e−14	13 x 1
6	Vitvi01g00813	0.89	1e−16	2e−14	32 x 35 The component of a membrane consisting of the gene produc
7	Vitvi01g00867	1.36	1e−16	2e−14	39 x 4 A membrane−bounded organelle of eukaryotic cells in which
8	Vitvi01g00710	2.72	1e−16	2e−14	40 x 40 The chemical reactions and pathways involving carbohydrate
9	Vitvi01g01780	0.61	1e−16	2e−14	40 x 12 A chlorophyll−containing plastid with thylakoids organized into
10	Vitvi03g00573	0.54	1e−16	2e−14	35 x 16 The chemical reactions and pathways resulting in the formatio
11	Vitvi04g00284	0.81	1e−16	2e−14	14 x 1
12	Vitvi04g00974	0.9	1e−16	2e−14	39 x 7 A chlorophyll−containing plastid with thylakoids organized into
13	Vitvi04g01044	0.62	1e−16	2e−14	39 x 12 A membrane−bounded organelle of eukaryotic cells in which
14	Vitvi05g01924	1.25	1e−16	2e−14	33 x 33 Catalysis of an oxidation−reduction (redox) reaction, a reversi
15	Vitvi05g01648	0.46	1e−16	2e−14	30 x 12 Catalysis of the transfer of a glycosyl group from a UDP−suga
16	Vitvi06g00725	0.73	1e−16	2e−14	38 x 5 Catalysis of the hydrolysis of various bonds, e.g. C−O, C−N, (
17	Vitvi06g01410	2.18	1e−16	2e−14	40 x 33
18	Vitvi07g02226	1.65	1e−16	2e−14	37 x 1 The chemical reactions and pathways involving carbohydrate
19	Vitvi07g00509	1.56	1e−16	2e−14	1 x 29 Catalysis of the hydrolysis of various bonds, e.g. C−O, C−N, (
20	Vitvi07g00910	0.28	1e−16	2e−14	21 x 29 A transcription coregulator activity that represses or decrease
Underexpressed					
1	Vitvi10g01207	−1.16	1e−16	2e−14	2 x 10 The component of a membrane consisting of the gene produc
2	Vitvi10g01690	−1.77	1e−16	2e−14	29 x 40
3	Vitvi07g01266	−1.23	1e−16	2e−14	28 x 40 That part of a multicellular organism outside the cells proper,
4	Vitvi04g01535	−0.76	1e−16	2e−14	4 x 33 Binding to a metal ion.
5	Vitvi10g00317	−1.16	1e−16	2e−14	1 x 8
6	Vitvi00g00979	−0.44	1e−16	2e−14	28 x 24
7	Vitvi10g02255	−0.44	1e−16	2e−14	28 x 24 The contents of a cell excluding the plasma membrane and n
8	Vitvi00g01142	−1.58	1e−16	2e−14	19 x 14
9	Vitvi10g02400	−1.58	1e−16	2e−14	19 x 14
10	Vitvi01g01577	−0.4	1e−16	2e−14	21 x 18 A membrane−bounded organelle of eukaryotic cells in which
11	Vitvi01g01627	−0.46	1e−16	2e−14	17 x 16 The component of a membrane consisting of the gene produc
12	Vitvi01g00869	−0.34	1e−16	2e−14	11 x 14 The component of a membrane consisting of the gene produc
13	Vitvi01g00633	−0.53	1e−16	2e−14	10 x 33 Binding to messenger RNA (mRNA), an intermediate molecul
14	Vitvi01g01724	−0.45	1e−16	2e−14	11 x 14 Catalysis of a biochemical reaction at physiological temperatu
15	Vitvi01g01729	−0.81	1e−16	2e−14	25 x 40 Binding to a zinc ion (Zn).
16	Vitvi02g00073	−0.66	1e−16	2e−14	18 x 17 The component of a membrane consisting of the gene produc
17	Vitvi03g00303	−0.59	1e−16	2e−14	30 x 25 The action of a molecule that contributes to the structural inte
18	Vitvi03g00365	−0.94	1e−16	2e−14	1 x 11 Catalysis of an oxidation−reduction (redox) reaction, a reversi
19	Vitvi04g01835	−0.64	1e−16	2e−14	7 x 12 The series of molecular signals initiated by a ligand binding to
20	Vitvi04g01837	−0.91	1e−16	2e−14	25 x 40 Any process that results in a change in state or activity of a ce

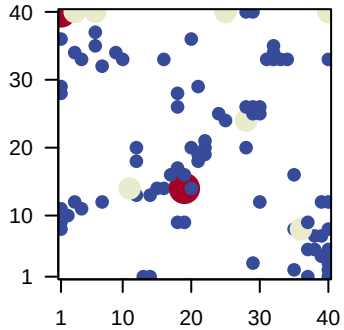
Differentially expressed gene sets

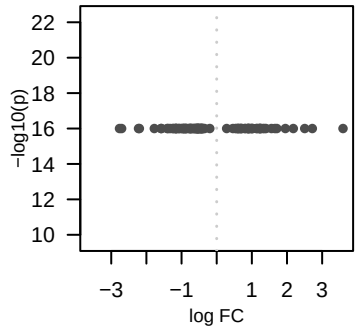
Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	7.87	0e+00	206	Cell growth and death Cell wall
2	6.85	0e+00	47	Transport catalysts Electron carriers
3	6.55	0e+00	18	Energy metabolism Photosynthesis proteins
4	6.37	0e+00	134	Hormone signaling Auxin signaling
5	6.21	0e+00	18	Photosynthesis proteins
6	5.9	0e+00	38	Photosynthesis
7	5.36	0e+00	39	Pentose and glucuronate interconversions
8	5.07	0e+00	78	Energy metabolism Photosynthesis
9	4.73	0e+00	19	Transcription factors Aux/IAA AUXIAA
10	4.52	0e+00	217	Cell motility Regulation of cytoskeleton
11	4.37	0e+00	80	Cytoskeleton Microtubules
12	4.36	0e+00	73	Transcription factors AP2/EREBP AP2 EREBP
13	4.35	0e+00	19	Aquaporins Small and basic intrinsic proteins [TC:1.A.8]
14	4.33	0e+00	78	Glycosyltransferases Starch and sucrose metabolism
15	4.13	0e+00	10	Photosynthesis Photosystem (P700 chlorophyll a)
16	3.67	2e−04	93	Transcription factors bHLH bHLH
17	3.49	6e−04	168	Plant hormone signal transduction
18	3.28	2e−03	34	Peptidases and inhibitors Family S10
19	3.2	2e−03	140	Hormone signaling Ethylene Ethylene signaling
20	3.09	3e−03	26	Steroid biosynthesis
Underexpressed				
1	−5.62	0e+00	116	Ribosome Ribosome biogenesis Pre−60S particles
2	−5.38	0e+00	64	Ribosome biogenesis eukaryotes
3	−5.34	0e+00	144	Ribosome Eukaryotes
4	−5.07	0e+00	62	Ribosome biogenesis 60S particles
5	−4.89	0e+00	247	Translation Ribosome
6	−4.67	0e+00	75	Translation Ribosome biogenesis Eukaryotes
7	−4.24	0e+00	211	Ribosome
8	−4.08	0e+00	24	Primary active transporters [TC:3]
9	−3.67	2e−04	44	Proteasome
10	−3.35	1e−03	165	Transcription Spliceosome
11	−3.31	1e−03	34	Tyrosine metabolism
12	−3.29	2e−03	42	Folding sorting and degradation Proteasome
13	−3.29	2e−03	126	Translation RNA transport
14	−3.22	2e−03	27	Enzyme 2.5.1 Transferring nitrogenous groups
15	−3.18	2e−03	43	Mitochondrial respiratory chain complex assembly factors
16	−3.17	2e−03	58	Other amino acid metabolism Glutathione metabolism
17	−3.03	3e−03	110	Ubiquitin system Ubiquitin E2 RING type ligase type E3
18	−2.86	5e−03	139	Spliceosome
19	−2.84	5e−03	151	RNA polymerase II system
20	−2.78	7e−03	36	DNA replication

Portrait

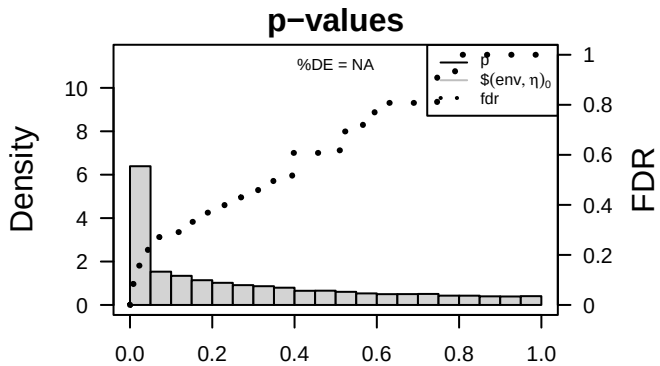


Top 100 DE genes





p−values



p−values