Chard_freeze_r2

Global Summary

%DE = 0.17

genes with fdr < 0.2 = 1 (0 + / 1 −)

genes with fdr < 0.1 = 1 (0 + / 1 −)

genes with fdr < 0.05 = 0 (0 + / 0 −)

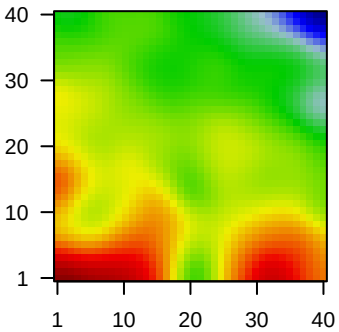
genes with fdr < 0.01 = 0 (0 + / 0 −)

<FC> = 0

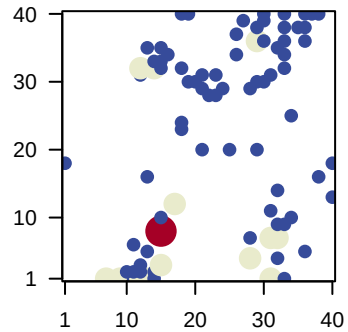
<p−value> = 0.32

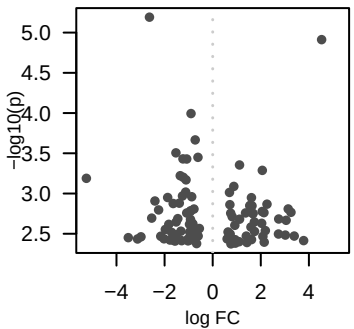
<fdr> = 0.83

Portrait



Top 100 DE genes





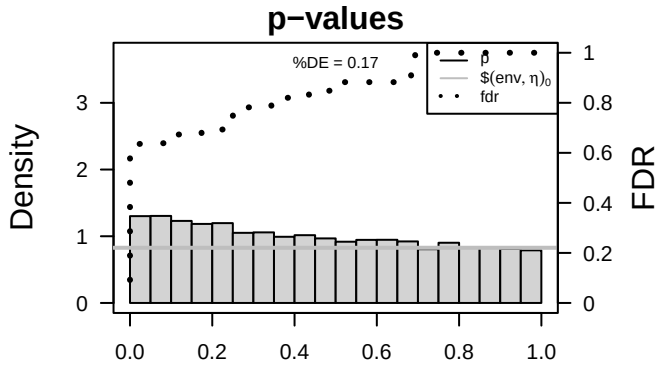
Differentially expressed genes

Rank	ID	log(FC)	p−value	fdr	Description / Metagene
Overexpressed					
1	Vitvi09g02008	4.53	1e−05	0.6	31 x 1	An intracellular non−membrane−bounded organelle comprisir
2	Vitvi16g00112	1.12	4e−04	0.6	32 x 7	Binding to ATP, adenosine 5'−triphosphate, a universally impc
3	Vitvi18g02819	2.06	5e−04	0.6	1 x 18	Catalysis of the hydrolysis of any ester bond.
4	Vitvi17g00730	0.88	8e−04	0.6	13 x 16	Catalysis of the transfer of ubiquitin from one protein to anoth
5	Vitvi10g00713	0.7	1e−03	0.6	31 x 11	Binding to a ribosome.
6	Vitvi03g00649	1.61	1e−03	0.6	28 x 4	
7	Vitvi11g01506	2.26	1e−03	0.6	17 x 12	A lipid bilayer along with all the proteins and protein complexe
8	Vitvi13g01650	0.71	1e−03	0.6	33 x 9	The action of a molecule that contributes to the structural inte
9	Vitvi00g00753	1.55	1e−03	0.6	15 x 3	
10	Vitvi00g01184	1.63	1e−03	0.6	32 x 4	
11	Vitvi07g03094	1.55	1e−03	0.6	15 x 3	
12	Vitvi19g01028	3.14	2e−03	0.6	7 x 1	Binding to a heme, a compound composed of iron complexed
13	Vitvi16g01882	2.06	2e−03	0.6	13 x 1	
14	Vitvi04g01233	3.25	2e−03	0.6	9 x 1	Catalysis of the transfer of a glycosyl group from a UDP−sug
15	Vitvi07g01333	2.13	2e−03	0.6	9 x 1	The chemical reactions and pathways involving lipids, compo
16	Vitvi04g00005	1.37	2e−03	0.6	31 x 7	
17	Vitvi06g01364	0.75	2e−03	0.6	15 x 8	The directed movement of proteins in a cell, including the mo
18	Vitvi11g00267	1.67	2e−03	0.6	12 x 3	The membrane surrounding a cell that separates the cell from
19	Vitvi11g00438	1.67	2e−03	0.6	13 x 5	The chemical reactions and pathways involving organic or inc
20	Vitvi05g02178	0.81	2e−03	0.6	25 x 20	
Underexpressed					
1	Vitvi07g01921	−2.63	6e−06	0.09	33 x 34	The component of a membrane consisting of the gene produc
2	Vitvi02g01272	−0.9	1e−04	0.60	12 x 32	Catalysis of the transfer of a group, e.g. a methyl group, glyco
3	Vitvi01g00070	−0.73	2e−04	0.60	23 x 28	Catalysis of the transfer of a methyl group to an acceptor mol
4	Vitvi14g01799	−1.53	3e−04	0.60	34 x 25	The component of a membrane consisting of the gene produc
5	Vitvi11g00483	−0.61	4e−04	0.60	22 x 28	The contents of a cell excluding the plasma membrane and n
6	Vitvi13g00747	−1.24	4e−04	0.60	21 x 29	Catalysis of a biochemical reaction at physiological temperatu
7	Vitvi02g00256	−1.08	4e−04	0.60	28 x 29	The component of a membrane consisting of the gene produc
8	Vitvi07g01280	−1.35	6e−04	0.60	21 x 31	Binding to ATP, adenosine 5'−triphosphate, a universally impc
9	Vitvi07g01930	−1.22	6e−04	0.60	18 x 40	Catalysis of the hydrolysis of internal, alpha−peptide bonds in
10	Vitvi07g02443	−5.25	6e−04	0.60	37 x 40	
11	Vitvi08g01792	−1.11	7e−04	0.60	16 x 34	The contents of a cell excluding the plasma membrane and n
12	Vitvi05g00437	−1.12	1e−03	0.60	40 x 13	The component of a membrane consisting of the gene produc
13	Vitvi06g01227	−1.26	1e−03	0.60	31 x 31	Catalysis of the transfer of a glycosyl group from one compou
14	Vitvi08g00174	−0.87	1e−03	0.60	30 x 30	A membrane−bounded organelle of eukaryotic cells in which
15	Vitvi18g00355	−1.87	1e−03	0.60	33 x 36	A closed structure, found only in eukaryotic cells, that is comp
16	Vitvi04g01481	−2.4	1e−03	0.60	35 x 38	The chemical reactions and pathways involving carbohydrates
17	Vitvi19g00276	−1.39	1e−03	0.60	26 x 37	The chemical reactions and pathways resulting in the formatic
18	Vitvi11g00401	−1.64	1e−03	0.60	32 x 35	The component of a membrane consisting of the gene produc
19	Vitvi01g01700	−0.78	2e−03	0.60	21 x 20	Binding to nicotinamide−adenine dinucleotide phosphate, a c
20	Vitvi18g01238	−2.25	2e−03	0.60	36 x 36	The space external to the outermost structure of a cell. For ce

Differentially expressed gene sets

Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	5.8	0e+00	64	Transcription factors − Other transcription factors
2	5.37	0e+00	73	Transcription factors − AP2 − EREBP
3	4.62	0e+00	140	Hormone signaling − Ethylene signaling
4	3.58	4e−04	26	Flavonoid biosynthesis
5	3.48	7e−04	45	Galactose metabolism
6	3.31	1e−03	42	Tryptophan metabolism
7	3.3	1e−03	11	Biosynthesis of secondary metabolites − ABA biosynthesis
8	3.25	1e−03	39	Enzyme − E2 − Acting on aldehyde or oxo group of donors
9	3.08	2e−03	92	Lipid metabolism − Glycerolipid metabolism
10	2.98	3e−03	48	Transcription factors − WRKY − WRKY
11	2.93	4e−03	18	Chaperone − HSP20 − HSP20
12	2.91	4e−03	29	Carotenoid biosynthesis
13	2.89	4e−03	108	Carbohydrate metabolism − Pyruvate metabolism
14	2.85	5e−03	57	Glyoxylate and dicarboxylate metabolism
15	2.83	5e−03	51	Carbon fixation in photosynthetic organisms
16	2.8	6e−03	26	Pantothenate and CoA biosynthesis
17	2.67	8e−03	12	SLC15: PTR Proton dipeptide/peptide transporter
18	2.64	9e−03	15	Chaperone − HSP70 / DNAK − HSP70 / DNAK
19	2.59	1e−02	38	Protein − Chaperone mediated autophagy (CMA)
20	2.47	1e−02	72	Ribosome − Ribosome − Mitochondrial − Chloroplast
Underexpressed				
1	−10.61	0e+00	206	Cell growth and death − Cell wall
2	−8.4	0e+00	217	Cell motility − Regulation of cytoskeleton
3	−7.82	0e+00	80	Cytoskeleton − Microtubules
4	−6.51	0e+00	10	Peptidases and inhibitors − Aspartic peptidase A1 family
5	−6.19	0e+00	78	Glycosyltransferases − Starch and sucrose metabolism
6	−5.89	0e+00	19	Aquaporin − Aquaporin-like subfamily [TC:1.A.8]
7	−5.41	0e+00	129	Enzyme − E3 − Glycosylases
8	−5.14	0e+00	219	Cell growth and death − Cell cycle
9	−4.52	0e+00	11	Transcription factors − GRF
10	−4.45	0e+00	134	Hormone signaling − Auxin signaling
11	−4.43	0e+00	66	Exosome − Exosome − Proteins of breast cancer cells
12	−4.26	0e+00	34	Peptidases and inhibitors − Family S10
13	−4.2	0e+00	18	Photosynthesis − Photosynthesis proteins
14	−4.19	0e+00	168	Plant hormone signal transduction
15	−4.17	0e+00	102	Amino sugar and nucleotide sugar metabolism
16	−4.15	0e+00	24	Replication − DNA Replication Factors
17	−4.08	0e+00	30	Glycan biosynthesis and metabolism − N-Glycan degradation
18	−4.02	0e+00	17	Kinase − IRAK4 family
19	−3.87	8e−05	113	Exosome − Exosome − Proteins of colorectal cancer cells
20	−3.83	8e−05	18	Energy metabolism − Photosynthesis proteins

p−values



p−values