Chard_acclim_r3

Global Summary

%DE = 0

genes with fdr < 0.2 = 0 (0 + / 0 −)

genes with fdr < 0.1 = 0 (0 + / 0 −)

genes with fdr < 0.05 = 0 (0 + / 0 −)

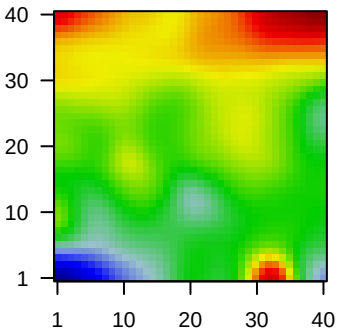
genes with fdr < 0.01 = 0 (0 + / 0 −)

<FC> = 0

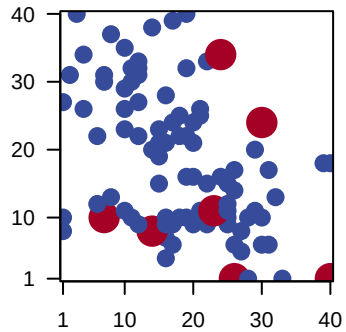
<p−value> = 0.45

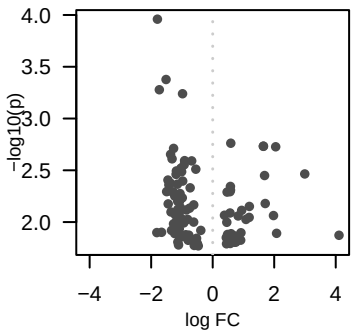
<fdr> = 1

Portrait



Top 100 DE genes





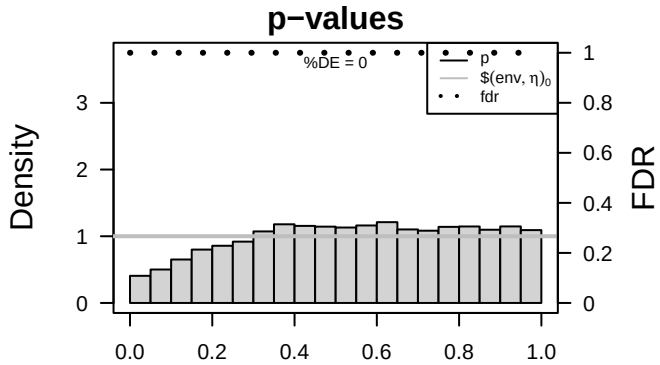
Differentially expressed genes

Rank	ID	log(FC)	p−value	fdr	Description	Metagene
Overexpressed						
1	Vitvi03g00307	0.59	0.002	1	10 x 26	The component of a membrane consisting of the gene produc
2	Vitvi07g03061	1.65	0.002	1	30 x 24	The component of a membrane consisting of the gene produc
3	Vitvi00g00589	1.65	0.002	1	30 x 24	
4	Vitvi09g00172	2.05	0.002	1	4 x 34	The component of a membrane consisting of the gene produc
5	Vitvi05g01760	2.99	0.003	1	1 x 8	A membrane−bounded organelle of eukaryotic cells in which
6	Vitvi18g02592	1.69	0.004	1	2 x 31	The space external to the outermost structure of a cell. For ce
7	Vitvi09g01020	0.58	0.005	1	15 x 19	
8	Vitvi04g01434	0.58	0.005	1	7 x 30	
9	Vitvi17g01553	0.56	0.005	1	31 x 17	A semiautonomous, self replicating organelle that occurs in va
10	Vitvi02g00737	0.47	0.005	1	12 x 31	A lipid bilayer along with all the proteins and protein complexe
11	Vitvi14g02885	1.71	0.007	1	24 x 34	
12	Vitvi19g01375	1.19	0.007	1	24 x 34	Binding to a protein.
13	Vitvi15g01052	0.94	0.008	1	29 x 20	A macromolecular complex that contains both RNA and prote
14	Vitvi08g01512	0.56	0.008	1	26 x 17	A small, dense body one or more of which are present in the
15	Vitvi01g00669	0.38	0.009	1	21 x 25	Organized structure of distinctive morphology and function, be
16	Vitvi10g01886	1.98	0.009	1	3 x 40	
17	Vitvi07g02014	0.83	0.009	1	8 x 37	The directed movement of substances to, from or across the p
18	Vitvi04g00346	1.19	0.009	1	12 x 27	Binding to a nucleic acid.
19	Vitvi16g00784	1.08	0.009	1	7 x 31	
20	Vitvi11g00057	0.46	0.010	1	19 x 22	
Underexpressed						
1	Vitvi06g01418	−1.8	1e−04	1	26 x 1	The contents of a cell excluding the plasma membrane and n
2	Vitvi06g00366	−1.52	4e−04	1	19 x 10	A semiautonomous, self replicating organelle that occurs in va
3	Vitvi19g00532	−1.73	5e−04	1	27 x 5	
4	Vitvi18g00176	−0.98	6e−04	1	23 x 11	Binding to ATP, adenosine 5'−triphosphate, a universally impo
5	Vitvi14g02465	−1.27	2e−03	1	17 x 9	The component of a membrane consisting of the gene produc
6	Vitvi11g00435	−1.37	2e−03	1	27 x 8	A membrane−bounded organelle of eukaryotic cells in which
7	Vitvi18g00515	−1.32	2e−03	1	24 x 16	
8	Vitvi08g01120	−0.91	3e−03	1	32 x 13	A multisubunit protein complex that contains the Ino80p ATPa
9	Vitvi12g00656	−0.68	3e−03	1	29 x 11	Binding to a nucleic acid.
10	Vitvi11g01656	−0.93	3e−03	1	25 x 15	A membrane−bounded organelle of eukaryotic cells in which
11	Vitvi04g01787	−1.03	3e−03	1	26 x 6	The component of a membrane consisting of the gene produc
12	Vitvi06g00167	−0.55	3e−03	1	20 x 24	Catalysis of the transfer of a methyl group to an acceptor mol
13	Vitvi06g01505	−1.18	3e−03	1	15 x 21	Any process that results in a change in state or activity of a ce
14	Vitvi18g00637	−1.01	3e−03	1	10 x 11	A lipid bilayer along with all the proteins and protein complexe
15	Vitvi07g00824	−1.19	3e−03	1	26 x 14	Binding to ATP, adenosine 5'−triphosphate, a universally impo
16	Vitvi13g01817	−1.45	4e−03	1	6 x 12	Binding to the oxidized form, FAD, of flavin−adenine dinucleot
17	Vitvi03g00279	−0.98	4e−03	1	22 x 9	
18	Vitvi08g02251	−1.37	4e−03	1	19 x 16	A lipid bilayer along with all the proteins and protein complexe
19	Vitvi04g00081	−1.15	4e−03	1	8 x 13	The component of a membrane consisting of the gene produc
20	Vitvi13g02287	−1.42	4e−03	1	40 x 18	

Differentially expressed gene sets

Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	6.59	0e+00	18	Photosynthesis − proteins
2	6.47	0e+00	18	Energy metabolism − Photosynthesis, proteins
3	5.05	0e+00	47	Transporters − Major Facilitator Superfamily (MFS)
4	4.61	0e+00	134	Hormone signaling − Auxin signaling
5	4.36	0e+00	66	Exosome − Eukaryota, proteins
6	4.35	0e+00	206	Cell growth and death − Cell cycle
7	3.8	1e−04	10	Photosynthesis − Photosystem II (PSII)
8	3.71	1e−04	113	Exosome − Eukaryota, proteins
9	3.54	5e−04	38	Photosynthesis
10	3.48	7e−04	26	Steroid biosynthesis
11	3.34	1e−03	17	Kinase − MAPK family
12	3.22	1e−03	78	Glycosyltransferases − Glycosyltransferases
13	3.15	2e−03	78	Energy metabolism − Photosynthesis
14	2.98	3e−03	42	Folding, sorting and degradation − Proteasome
15	2.93	4e−03	44	Proteasome
16	2.81	6e−03	13	Cofactors and vitamins metabolism − Thiamine metabolism
17	2.72	8e−03	75	Translation − Ribosome − Ribosomes in eukaryotes
18	2.67	8e−03	62	Ribosome − Ribosomes, 80S particles
19	2.67	8e−03	40	Transport − Thylakoid targeting pathway
20	2.63	1e−02	64	Ribosome − Ribosomes in eukaryotes
Underexpressed				
1	−5.09	0e+00	49	Transcription factors − NAC
2	−5.08	0e+00	10	Linoleic acid metabolism
3	−4.01	0e+00	73	Transcription factors − AP2−EREBP
4	−3.85	8e−05	29	Transcription factors − GRAS
5	−3.84	8e−05	140	Hormone signaling − Ethylene signaling
6	−3.79	1e−04	48	Transcription factors − WRKY
7	−3.46	8e−04	153	Plant−pathogen interaction
8	−3.35	1e−03	45	Galactose metabolism
9	−3.02	3e−03	51	Other metabolism − Single reactions
10	−2.85	5e−03	170	Transcription factors − C3HC4
11	−2.82	6e−03	33	alpha−Linolenic acid metabolism
12	−2.81	6e−03	29	Carotenoid biosynthesis
13	−2.79	6e−03	44	Energy metabolism − Nitrogen metabolism
14	−2.78	6e−03	38	Enzyme − Enzymes of unknown specificity
15	−2.76	7e−03	28	Transcription factors − Basic leucine zipper (bZIP)
16	−2.73	8e−03	11	Cofactors and vitamins metabolism − Vitamin B6 metabolism
17	−2.61	1e−02	25	Transcription factors − GNAT
18	−2.58	1e−02	18	Chaperones − HSP20
19	−2.56	1e−02	56	Hormone signaling − Jasmonate signaling
20	−2.51	1e−02	77	Carbohydrate metabolism − Galactose metabolism

p−values



p−values