Chard_acclim_r1

Global Summary

%DE = 0

genes with fdr < 0.2 = 0 (0 + / 0 −)

genes with fdr < 0.1 = 0 (0 + / 0 −)

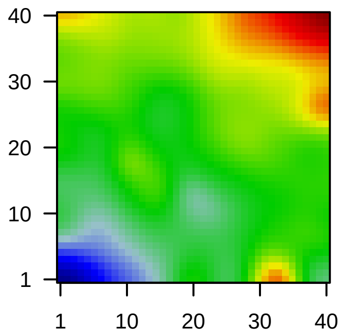
genes with fdr < 0.05 = 0 (0 + / 0 −)

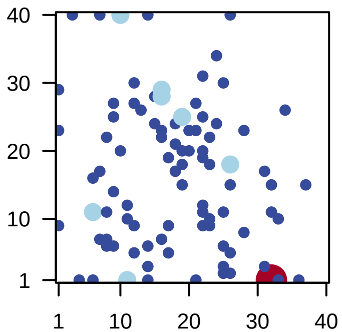
genes with fdr < 0.01 = 0 (0 + / 0 −)

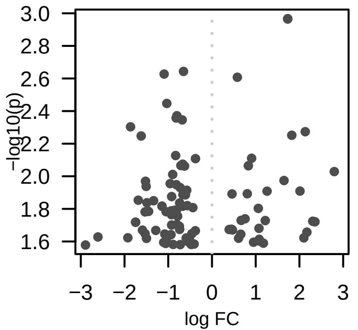
<FC> = 0

<p−value> = 0.46

<fdr> = 1







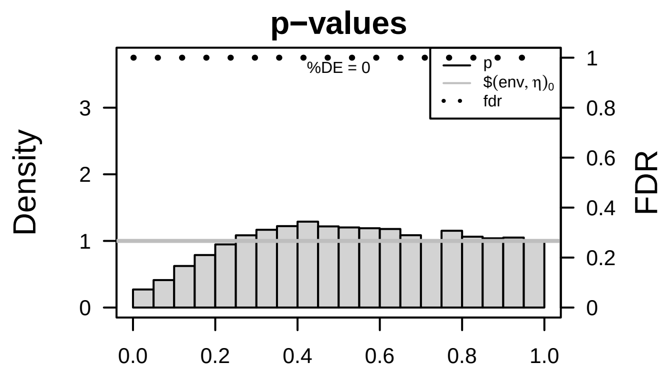
Differentially expressed genes

Overexpressed

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	Vitvi07g02817	1.73	0.001	1	32 x 1	
2	Vitvi00g00048	1.73	0.001	1	32 x 1	
3	Vitvi14g01213	0.58	0.002	1	23 x 22	Catalysis of an oxidation−reduction (redox) reaction, a reversi
4	Vitvi03g00936	2.13	0.005	1	21 x 1	Binding to a protein.
5	Vitvi17g00427	1.82	0.006	1	26 x 40	Catalysis of the reaction: H2O + L−arginyl− + NH4+, resulting
6	Vitvi04g00340	0.91	0.008	1	33 x 10	Catalysis of the reaction: N,N−dimethylaniline + NADPH + H+
7	Vitvi02g01177	0.83	0.009	1	24 x 34	Catalysis of the reaction: a phosphoprotein + H2O = a protein
8	Vitvi08g02122	2.8	0.009	1	14 x 40	
9	Vitvi05g02197	1.65	0.011	1	32 x 1	A lipid bilayer along with all the proteins and protein complexe
10	Vitvi18g03246	2.01	0.012	1	1 x 9	Binding to a protein.
11	Vitvi09g00331	1.26	0.012	1	34 x 26	Binding to a protein.
12	Vitvi14g02949	0.81	0.013	1	21 x 23	Reactions, triggered in response to the presence of a foreign
13	Vitvi08g00650	0.46	0.013	1	22 x 20	The part of the cytoplasm that does not contain organelles bu
14	Vitvi17g00576	1.06	0.016	1	7 x 40	
15	Vitvi04g01722	0.76	0.018	1	12 x 27	Binding to a protein.
16	Vitvi04g01750	0.67	0.019	1	9 x 25	Any process that modulates the frequency, rate or extent of ce
17	Vitvi14g00459	1.22	0.019	1	36 x 1	The component of a membrane consisting of the gene produc
18	Vitvi06g01100	2.3	0.019	1	1 x 29	Catalysis of the transfer of a glycosyl group from a UDP−suga
19	Vitvi06g01097	2.36	0.019	1	32 x 1	Catalysis of the transfer of a glycosyl group from a UDP−suga
20	Vitvi17g00662	1.07	0.021	1	37 x 15	

Underexpressed

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	Vitvi14g00557	−0.65	0.002	1	11 x 12	
2	Vitvi14g01005	−1.09	0.002	1	6 x 16	The contents of a cell excluding the plasma membrane and nu
3	Vitvi10g00116	−1.03	0.004	1	8 x 22	A lipid bilayer along with all the proteins and protein complexe
4	Vitvi13g01803	−0.8	0.004	1	22 x 19	Binding to a metal ion.
5	Vitvi14g00256	−0.82	0.004	1	16 x 23	
6	Vitvi01g00414	−0.68	0.005	1	26 x 18	A lipid bilayer along with all the proteins and protein complexe
7	Vitvi19g00256	−1.86	0.005	1	22 x 12	The membrane surrounding a cell that separates the cell from
8	Vitvi10g00288	−1.62	0.006	1	14 x 3	The component of a membrane consisting of the gene produc
9	Vitvi19g00319	−0.83	0.007	1	28 x 8	A membrane−bounded organelle of eukaryotic cells in which
10	Vitvi14g00608	−0.38	0.008	1	20 x 23	The component of a membrane consisting of the gene produc
11	Vitvi02g00735	−0.67	0.008	1	12 x 30	A small, dense body one or more of which are present in the
12	Vitvi16g00012	−0.71	0.009	1	23 x 18	
13	Vitvi18g00073	−0.63	0.009	1	32 x 15	
14	Vitvi14g00478	−0.9	0.010	1	24 x 24	Catalysis of the elimination of hydrogen sulfide or substituted
15	Vitvi18g02603	−1.52	0.011	1	8 x 6	
16	Vitvi04g01212	−0.96	0.011	1	15 x 28	Binding to a protein.
17	Vitvi09g00345	−0.82	0.011	1	11 x 10	The component of a membrane consisting of the gene produc
18	Vitvi13g02024	−1.51	0.012	1	12 x 5	Any process that results in a change in state or activity of a ce
19	Vitvi16g01875	−0.73	0.012	1	16 x 22	
20	Vitvi06g01140	−0.58	0.012	1	17 x 19	The chemical reactions and pathways involving organic or ino



Differentially expressed gene sets

Overexpressed

Rank	GSZ	p−value	#all	Geneset
1	7.29	0.000	18	Energy metabolism − Photosynthesis antenna proteins
2	6.72	0.000	18	Photosynthesis − antenna proteins
3	6.31	0.000	47	Transporter catalog − Transport electron carriers
4	6.12	0.000	78	Energy metabolism − Photosynthesis
5	5.96	0.000	80	Cytoskeleton − Microtubules
6	5.95	0.000	38	Photosynthesis
7	5.76	0.000	217	Cell motility − Regulation of actin cytoskeleton
8	5.43	0.000	219	Cell growth and death − Cell cycle
9	4.93	0.000	10	Peptidases and inhibitors − Family A1: pepsin family
10	4.66	0.000	10	Photosynthesis proteins − Photosystem I (P700 chlorophyll a)
11	4.57	0.000	24	Replication protein − DNA Replication Initiation Factors
12	4.51	0.000	40	Transport system − Thylakoid targeting pathway
13	4.4	0.000	26	Steroid biosynthesis
14	3.3	0.001	66	Exosome − Exosomal proteins of bladder cancer cells
15	3.2	0.001	36	DNA replication
16	3.16	0.002	31	Chromosome and associated proteins − Gene silencing
17	3.13	0.002	41	Porphyrin metabolism
18	3	0.003	113	Exosome − Exosomal proteins of colorectal cancer cells
19	2.94	0.004	11	Transcription factors − GRF
20	2.82	0.006	22	Fatty acid elongation

Underexpressed

Rank	GSZ	p−value	#all	Geneset
1	−7.41	0e+00	140	Hormone signaling − Ethylene signaling
2	−7.03	0e+00	73	Transcription factors − AP2 EREBP
3	−6.06	0e+00	49	Transcription factors − NAC
4	−5.01	0e+00	48	Transcription factors − WRKY
5	−4.8	0e+00	64	Transcription factors − Other transcription factors
6	−4.44	0e+00	45	Galactose metabolism
7	−4.37	0e+00	26	Transcription factors − G2−like
8	−3.76	1e−04	153	Plant−pathogen interaction
9	−3.32	1e−03	77	Carbohydrate metabolism − Galactose metabolism
10	−3.05	2e−03	58	Other amino acids metabolism − Glutathione metabolism
11	−2.91	4e−03	32	Carbohydrate metabolism − Propanoate metabolism
12	−2.86	5e−03	18	Chaperone − HSP20
13	−2.8	6e−03	15	Chaperone − HSP70 / DNAK
14	−2.51	1e−02	111	Hormone signaling − ABA signaling
15	−2.5	1e−02	28	Transcription factors − Basic leucine zipper (bZIP)
16	−2.5	1e−02	29	Other amino acids metabolism − Beta−alanine metabolism
17	−2.44	2e−02	16	Transcription factors − HSF
18	−2.43	2e−02	77	Pores ion channels [TC:1]
19	−2.4	2e−02	71	Exosome − Proteins found in most exosomes
20	−2.4	2e−02	162	Plant specific signaling − Plant−pathogen interaction