CabFra_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

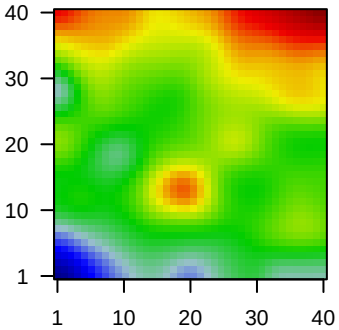
Differentially expressed genes

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
Overexpressed						
1	Vitvi07g01269	1.42	0.002	1	9 x 38	
2	Vitvi05g00733	1.62	0.004	1	7 x 39	The component of a membrane consisting of the gene produc
3	Vitvi15g01216	1.45	0.007	1	19 x 16	
4	Vitvi00g01858	1.84	0.007	1	20 x 14	
5	Vitvi10g02111	1.84	0.007	1	20 x 14	
6	Vitvi10g00418	0.95	0.008	1	7 x 31	
7	Vitvi15g01455	1.76	0.009	1	17 x 14	The series of molecular signals initiated upon sensing of blue
8	Vitvi09g00128	1.04	0.010	1	22 x 40	A membrane−bounded organelle of eukaryotic cells in which
9	Vitvi16g01740	1.83	0.010	1	20 x 13	
10	Vitvi02g00291	0.75	0.014	1	14 x 37	A membrane−bounded organelle of eukaryotic cells in which
11	Vitvi19g01643	1.52	0.014	1	35 x 27	Binding to ADP, adenosine 5'−diphosphate.
12	Vitvi10g00422	1.4	0.015	1	35 x 28	The component of a membrane consisting of the gene produc
13	Vitvi06g00650	1.09	0.015	1	28 x 32	The component of a membrane consisting of the gene produc
14	Vitvi07g01060	0.55	0.015	1	20 x 18	Binding to a protein.
15	Vitvi09g02101	1.16	0.016	1	9 x 40	
16	Vitvi00g01640	1.16	0.016	1	9 x 40	
17	Vitvi08g01656	1.75	0.017	1	29 x 33	The chemical reactions and pathways resulting in the formatic
18	Vitvi15g00396	2.65	0.018	1	37 x 25	Catalysis of the transfer of a methyl group to the oxygen atom
19	Vitvi07g01736	1.17	0.019	1	28 x 33	The component of a membrane consisting of the gene produc
20	Vitvi12g00211	1.07	0.020	1	8 x 31	The component of a membrane consisting of the gene produc
Underexpressed						
1	Vitvi07g00362	−1.09	0.002	1	31 x 15	A semiautonomous, self replicating organelle that occurs in va
2	Vitvi11g00796	−1.4	0.003	1	25 x 1	The component of a membrane consisting of the gene produc
3	Vitvi07g02313	−0.87	0.005	1	5 x 26	A lipid bilayer along with all the proteins and protein complexe
4	Vitvi16g02053	−1.26	0.005	1	12 x 4	
5	Vitvi10g00319	−0.99	0.006	1	27 x 25	
6	Vitvi05g01701	−0.58	0.006	1	28 x 11	Binding to ATP, adenosine 5'−triphosphate, a universally impo
7	Vitvi19g01338	−1.99	0.008	1	20 x 2	
8	Vitvi12g02722	−0.79	0.009	1	7 x 22	
9	Vitvi01g00365	−0.74	0.012	1	26 x 8	Binding to a protein.
10	Vitvi05g00288	−0.39	0.012	1	19 x 23	A membrane−bounded organelle of eukaryotic cells in which
11	Vitvi07g02621	−0.82	0.014	1	26 x 14	
12	Vitvi07g02025	−0.33	0.015	1	31 x 16	
13	Vitvi18g02691	−0.61	0.015	1	18 x 25	
14	Vitvi08g01759	−0.63	0.016	1	20 x 25	The leaflet the plasma membrane that faces the cytoplasm ar
15	Vitvi18g01254	−1.31	0.017	1	28 x 5	A membrane−bounded organelle of eukaryotic cells in which
16	Vitvi14g02421	−0.75	0.017	1	11 x 27	
17	Vitvi00g00983	−1.04	0.017	1	13 x 6	
18	Vitvi12g00340	−0.79	0.018	1	30 x 8	Catalysis of the transfer of an acetyl group to a nitrogen atom
19	Vitvi18g00336	−0.95	0.018	1	16 x 4	The part of the cytoplasm that does not contain organelles bu
20	Vitvi05g00056	−0.63	0.018	1	16 x 23	

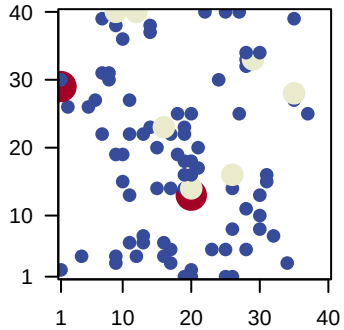
Differentially expressed gene sets

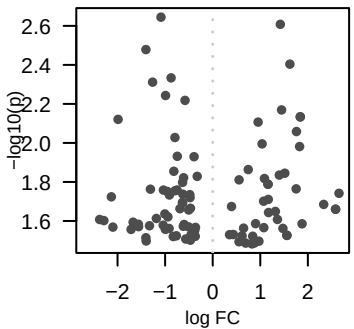
Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	8.46	0.000	18	Photosynthesis − proteins
2	8.39	0.000	18	Energy metabolism − Photosynthesis, proteins
3	8.26	0.000	47	Transporters − Electron carriers
4	6.25	0.000	38	Photosynthesis
5	5.92	0.000	78	Energy metabolism − Photosynthesis
6	5.29	0.000	10	Photosynthesis − Photosystem II (P700 chlorophyll a)
7	4.74	0.000	217	Cell motility − Regulation of cytoskeleton
8	4.37	0.000	11	Transcription factors − GRF
9	4.14	0.000	80	Cytoskeleton − Microtubules
10	4.07	0.000	206	Cell growth and death − Cell wall
11	3.13	0.002	10	Peptidases and inhibitors − Aspartic peptidase
12	3	0.003	101	Starch and sucrose metabolism
13	2.86	0.005	40	Transporters − Type I Protein exporting pathway
14	2.76	0.007	13	Cutin suberine and wax biosynthesis
15	2.74	0.007	100	Plant specific signaling − Flowering development
16	2.68	0.008	19	Aquaporins − Major intrinsic aquaporins [TC:1.A.8]
17	2.65	0.009	28	Transcription factors − MTERF
18	2.45	0.016	31	Fatty acid biosynthesis
19	2.41	0.017	67	Ribosome − Bacteria
20	2.38	0.019	19	Hormone signaling − Gibberellin signaling
Underexpressed				
1	−8.61	0e+00	48	Transcription factors − WRKY
2	−7.02	0e+00	162	Plant specific signaling − Plant pathogen interaction
3	−6.48	0e+00	49	Transcription factors − NAC
4	−4.97	0e+00	144	Ribosome − Eukaryotes
5	−4.93	0e+00	45	Galactose metabolism
6	−4.85	0e+00	153	Plant−pathogen interaction
7	−4.8	0e+00	140	Hormone signaling − Ethylene signaling
8	−4.69	0e+00	77	Pores ion channels [TC:1]
9	−4.52	0e+00	73	Transcription factors − AP2 EREBP
10	−4.34	0e+00	58	Other amino acid metabolism − Glutathione metabolism
11	−3.97	4e−05	15	Chaperones − HSP70 / DNAK
12	−3.79	1e−04	118	Transcription factors − Helix−turn−helix
13	−3.57	5e−04	64	Transcription factors − Other transcription factors
14	−3.51	6e−04	56	Hormone signaling − Jasmonic acid signaling
15	−3.41	9e−04	71	Exosome − Proteins found in exosomes
16	−3.38	9e−04	24	Tropane piperidine and pyridine alkaloid biosynthesis
17	−3.35	1e−03	38	Protein − Chaperone mediated autophagy (CMA)
18	−3.27	1e−03	17	Proteasome − Assembly factors
19	−3.18	2e−03	71	Glutathione metabolism
20	−3.15	2e−03	12	Endoplasmic reticulum membrane and cytosol

Portrait

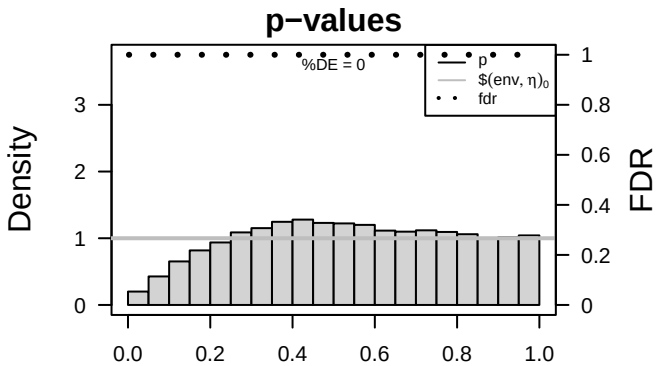


Top 100 DE genes





p−values



p−values