CabFra_acclim

Global Summary

%DE = NA

genes with fdr < 0.2 = 11100 (6082 + / 5018 −)

genes with fdr < 0.1 = 10096 (5595 + / 4501 −)

genes with fdr < 0.05 = 8337 (4711 + / 3626 −)

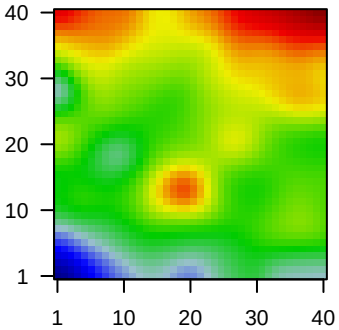
genes with fdr < 0.01 = 6218 (3588 + / 2630 −)

<FC> = 0

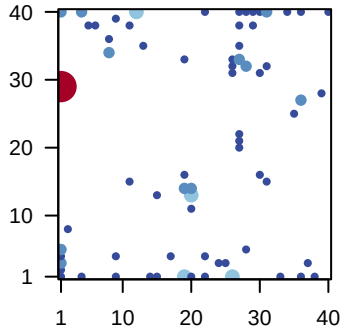
<p−value> = 0

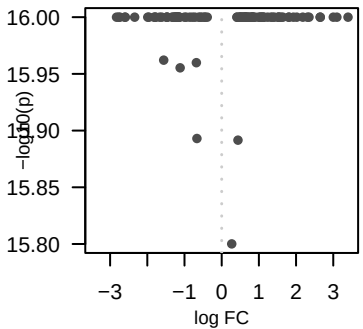
<fdr> = 0.27

Portrait



Top 100 DE genes

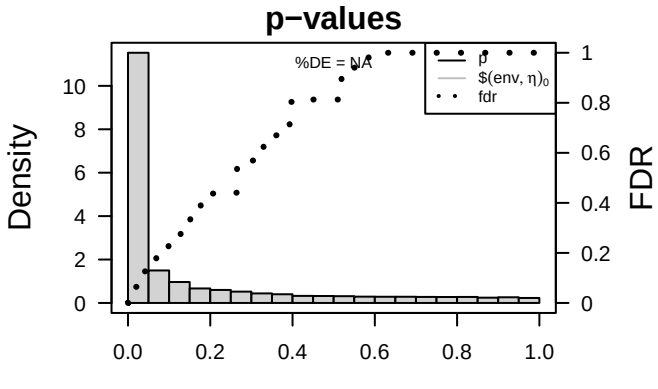




Differentially expressed genes

Rank	ID	log(FC)	p−value	fdr	Description Metagene
Overexpressed					
1	Vitvi00g01655	2.65	1e−16	2e−14	12 x 40
2	Vitvi10g02094	2.65	1e−16	2e−14	12 x 40
3	Vitvi00g00481	0.41	1e−16	2e−14	8 x 34
4	Vitvi02g0173(	0.41	1e−16	2e−14	8 x 34 Catalysis of the hydrolysis of phosphoric monoesters, releasi
5	Vitvi00g0185(	1.81	1e−16	2e−14	20 x 14
6	Vitvi10g02111	1.81	1e−16	2e−14	20 x 14
7	Vitvi00g0224(	3.1	1e−16	2e−14	40 x 40
8	Vitvi01g0014(	0.9	1e−16	2e−14	28 x 40 The contents of a cell excluding the plasma membrane and n
9	Vitvi02g00711	0.81	1e−16	2e−14	20 x 11 Any molecular function by which a gene product interacts sele
10	Vitvi02g00304	1.32	1e−16	2e−14	12 x 40 The component of a membrane consisting of the gene produc
11	Vitvi03g00432	1.37	1e−16	2e−14	35 x 25
12	Vitvi04g00163	0.57	1e−16	2e−14	31 x 32
13	Vitvi04g0034(	2.35	1e−16	2e−14	19 x 14
14	Vitvi04g00481	0.71	1e−16	2e−14	6 x 38
15	Vitvi05g0027(	0.48	1e−16	2e−14	28 x 32 Binding to ATP, adenosine 5'−triphosphate, a universally impo
16	Vitvi05g02122	2.02	1e−16	2e−14	36 x 40 The space external to the outermost structure of a cell. For ce
17	Vitvi06g0065(	1.04	1e−16	2e−14	28 x 32 The component of a membrane consisting of the gene produc
18	Vitvi07g0032(	2.18	1e−16	2e−14	20 x 13 Binding to ATP, adenosine 5'−triphosphate, a universally impo
19	Vitvi07g0188(	1.52	1e−16	2e−14	27 x 21 The action of a molecule that contributes to the structural inte
20	Vitvi07g01912	1.52	1e−16	2e−14	20 x 13
Underexpressed					
1	Vitvi10g00217	−0.95	1e−16	2e−14	26 x 1 Binding to ATP, adenosine 5'−triphosphate, a universally impo
2	Vitvi00g0051(	−1.16	1e−16	2e−14	19 x 1
3	Vitvi10g0213(	−1.16	1e−16	2e−14	19 x 1
4	Vitvi00g01044	−1.47	1e−16	2e−14	1 x 29
5	Vitvi15g01767	−1.47	1e−16	2e−14	1 x 29 Any molecular function by which a gene product interacts sele
6	Vitvi00g0114(	−2.77	1e−16	2e−14	1 x 29
7	Vitvi01g01981	−2.6	1e−16	2e−14	37 x 3 Reactions, triggered in response to the presence of a foreign
8	Vitvi02g00172	−1.34	1e−16	2e−14	1 x 28
9	Vitvi03g0181(	−1.67	1e−16	2e−14	9 x 4
10	Vitvi03g0049(	−0.72	1e−16	2e−14	26 x 1 A membrane−bounded organelle of eukaryotic cells in which
11	Vitvi03g01724	−2.59	1e−16	2e−14	1 x 1
12	Vitvi04g0162(	−1.18	1e−16	2e−14	20 x 1 Binding to ATP, adenosine 5'−triphosphate, a universally impo
13	Vitvi05g00551	−1.24	1e−16	2e−14	1 x 5 The chemical reactions and pathways resulting in the breakdo
14	Vitvi05g0067(	−2.74	1e−16	2e−14	1 x 2 The component of a membrane consisting of the gene produc
15	Vitvi05g0193(	−1.79	1e−16	2e−14	4 x 1 Binding to a metal ion.
16	Vitvi05g0004(	−1.21	1e−16	2e−14	36 x 1
17	Vitvi06g0052(	−1.96	1e−16	2e−14	14 x 1
18	Vitvi06g0116(	−0.46	1e−16	2e−14	11 x 15 A membrane−bounded organelle of eukaryotic cells in which
19	Vitvi06g0196(	−1.2	1e−16	2e−14	1 x 29 A lipid bilayer along with all the proteins and protein complexe
20	Vitvi07g0185(	−0.57	1e−16	2e−14	26 x 1 The process whose specific outcome is the progression of the

p−values



Differentially expressed gene sets

Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	8.42	0.000	18	Energy metabolism − Photosynthesis, protein
2	8.38	0.000	18	Photosynthesis − proteins
3	8.28	0.000	47	Transporters − Electron carriers
4	6.13	0.000	38	Photosynthesis
5	5.99	0.000	78	Energy metabolism − Photosynthesis
6	5.48	0.000	217	Cell motility − Regulation of cytoskeleton
7	5.28	0.000	10	Photosynthesis − Photosystem II (P700 chlorophyll a)
8	4.79	0.000	80	Cytoskeleton − Microtubules
9	4.76	0.000	11	Transcription factors − GRF
10	3.02	0.004	206	Cell growth and death − Cell wall
11	2.98	0.004	28	Transcription factors − MTERF
12	2.92	0.005	40	Transporters − Sterol (ergosterol) biosynthesis pathway
13	2.86	0.005	10	Peptidases and inhibitors − Family A1 peptidase family
14	2.83	0.006	101	Starch and sucrose metabolism
15	2.74	0.008	219	Cell growth and death − Cell cycle
16	2.64	0.009	41	Porphyrin metabolism
17	2.64	0.009	18	Transcription factors − ARF
18	2.57	0.011	67	Ribosome − Bacteria
19	2.57	0.011	17	Kinase − RAF family
20	2.54	0.012	100	Plant specific signaling − Flavonoid development
Underexpressed				
1	−8.66	0e+00	48	Transcription factors − WRKY
2	−7.58	0e+00	162	Plant specific signaling − Plant−pathogen interaction
3	−6.45	0e+00	49	Transcription factors − NAC
4	−5.19	0e+00	140	Hormone signaling − Ethylene signaling
5	−5.14	0e+00	73	Transcription factors − AP2−EREBP
6	−5.11	0e+00	153	Plant−pathogen interaction
7	−4.93	0e+00	45	Galactose metabolism
8	−4.89	0e+00	26	Flavonoid biosynthesis
9	−4.6	0e+00	77	Pores ion channels [TC:1]
10	−4.23	0e+00	58	Other amino acid metabolism − Glutamine, Glutamate metabolism
11	−3.88	0e+00	15	Chaperones − HSP70 / DNAK
12	−3.74	0e+00	15	Stilbenoid, diarylheptanoid and gingerol biosynthesis
13	−3.74	2e−04	24	Tropane, piperidine and pyridine alkaloid biosynthesis
14	−3.69	2e−04	144	Ribosome − Eukaryotes
15	−3.64	2e−04	26	Glycosyltransferases − Hydrophobic molecule
16	−3.62	2e−04	64	Transcription factors − Other transcription factors
17	−3.61	4e−04	71	Exosome − Proteins found in most exosomes
18	−3.57	4e−04	56	Hormone signaling − Jasmonate signaling
19	−3.5	5e−04	38	Protein − Chaperone mediated autophagy (CMA)
20	−3.45	7e−04	11	Biosynthesis of secondary metabolites − ABA biosynthesis

p−values