CabFra_accfreeze_r3

Global Summary

%DE = 0.07

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> = 0.38

<fdr> = 0.93

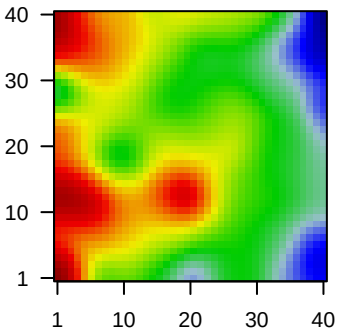
Differentially expressed genes

Rank	ID	log(FC)	p−value	fdr	Description	Metagene
Overexpressed						
1	Vitvi01g0207(	3.6	5e−06	0.9	20 x 13	The formation of a protein dimer, a macromolecular structure
2	Vitvi00g0060(	0.97	2e−03	0.9	14 x 36	
3	Vitvi07g0304(	0.97	2e−03	0.9	14 x 36	Binding to a protein.
4	Vitvi13g0193(	1.9	2e−03	0.9	7 x 13	A biological process whose specific outcome is the progressi
5	Vitvi13g0162(	2.51	2e−03	0.9	4 x 12	Binding to ADP, adenosine 5'−diphosphate.
6	Vitvi17g0003(	1.05	2e−03	0.9	6 x 13	Binding to ATP, adenosine 5'−triphosphate, a universally impo
7	Vitvi19g0070(	1.19	3e−03	0.9	4 x 14	
8	Vitvi12g0042(	0.51	3e−03	0.9	17 x 19	The cellular process in which a signal is conveyed to trigger a
9	Vitvi14g0297(	1.89	4e−03	0.9	19 x 15	
10	Vitvi04g0034(	3.59	4e−03	0.9	19 x 14	
11	Vitvi06g0175(	0.61	5e−03	0.9	23 x 18	Catalysis of the transfer of a phosphate group, usually from A
12	Vitvi06g0081(	1.08	5e−03	0.9	4 x 35	The movement of an organism, or part of an organism, in resp
13	Vitvi08g0217(	1.44	6e−03	0.9	20 x 15	
14	Vitvi08g0165(	0.59	6e−03	0.9	8 x 31	The irregular network of unit membranes, visible only by elect
15	Vitvi12g0057(	1.42	6e−03	0.9	7 x 12	A membrane−bounded organelle of eukaryotic cells in which
16	Vitvi18g0041(	0.77	6e−03	0.9	18 x 17	Binding to an RNA molecule or a portion thereof.
17	Vitvi18g0087(	2.56	6e−03	0.9	20 x 13	Binding to a heme, a compound composed of iron complexed
18	Vitvi19g0182(	1.24	6e−03	0.9	4 x 35	
19	Vitvi03g0054(	0.73	7e−03	0.9	5 x 34	The part of the cytoplasm that does not contain organelles bu
20	Vitvi16g0174(	1.93	7e−03	0.9	20 x 13	
Underexpressed						
1	Vitvi19g0176(	−0.78	0.002	0.9	24 x 30	
2	Vitvi13g0023(	−2.91	0.002	0.9	40 x 34	A lipid bilayer along with all the proteins and protein complexe
3	Vitvi18g0039(	−2.06	0.002	0.9	20 x 2	The component of a membrane consisting of the gene produc
4	Vitvi06g0015(	−3.08	0.002	0.9	40 x 2	Binding to a metal ion.
5	Vitvi03g0078(	−2.35	0.003	0.9	39 x 7	The contents of a cell excluding the plasma membrane and n
6	Vitvi17g0072(	−0.95	0.003	0.9	38 x 13	Binding to a protein.
7	Vitvi13g0054(	−1.1	0.003	0.9	30 x 8	Binding to a protein.
8	Vitvi02g0140(	−3.73	0.003	0.9	40 x 32	The space external to the outermost structure of a cell. For ce
9	Vitvi09g0055(	−1.33	0.004	0.9	37 x 7	The chemical reactions and pathways involving carbohydrate
10	Vitvi13g0177(	−0.61	0.004	0.9	30 x 9	Binding to a metal ion.
11	Vitvi03g0070(	−3.86	0.004	0.9	40 x 34	Catalysis of the transfer of an acyl group, other than amino−a
12	Vitvi04g0021(	−1.98	0.004	0.9	36 x 35	The component of a membrane consisting of the gene produc
13	Vitvi11g0083(	−1.13	0.004	0.9	32 x 5	The component of a membrane consisting of the gene produc
14	Vitvi15g0110(	−1.66	0.005	0.9	39 x 5	The component of a membrane consisting of the gene produc
15	Vitvi11g0046(	−1.32	0.006	0.9	38 x 7	
16	Vitvi05g0021(	−0.91	0.006	0.9	33 x 18	
17	Vitvi14g0144(	−3.34	0.006	0.9	40 x 4	
18	Vitvi18g0027(	−1.87	0.006	0.9	39 x 6	The component of a membrane consisting of the gene produc
19	Vitvi18g0008(	−1.22	0.006	0.9	40 x 14	Binding to a protein.
20	Vitvi03g0067(	−1.48	0.006	0.9	38 x 7	The component of a membrane consisting of the gene produc

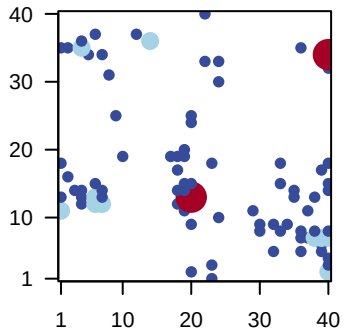
Differentially expressed gene sets

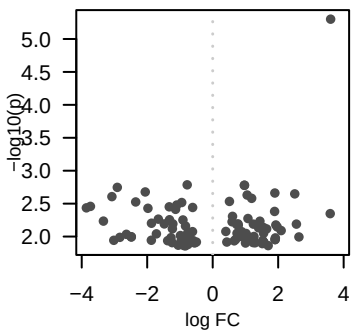
Rank	GSZ	p−value	#all	Geneset
Overexpressed				
1	5.2	0e+00	140	Hormone signaling − Ethylene signaling
2	4.82	0e+00	170	Transcription factors − Other C−HHC4f−C3HC4
3	4.33	0e+00	49	Transcription factors − NAC
4	4.3	0e+00	73	Transcription factors − AP2−ERF−AP2 EREBP
5	3.77	1e−04	74	Transcription factors − C2H2
6	3.59	4e−04	128	Ubiquitin system − Single Ring Finger type E3
7	3.4	9e−04	111	Hormone signaling − ABA signaling
8	3.3	1e−03	11	Zeatin biosynthesis
9	3.29	1e−03	26	Transcription factors − G2−like
10	3.24	1e−03	64	Transcription factors − Other transcription factors
11	3.17	2e−03	11	Biosynthesis of secondary metabolites − ABA biosynthesis
12	3.01	3e−03	48	Transcription factors − WRKY
13	2.73	8e−03	80	Transport − Systems − Tethering factors
14	2.7	8e−03	51	Plant specific signaling − Circadian rhythm
15	2.55	1e−02	29	Transcription factors − GRAS
16	2.44	2e−02	27	Enzyme − Transferases − Transferring glycosyl groups
17	2.44	2e−02	116	Ribosome biogenesis − 60S particles
18	2.31	2e−02	29	Carotenoid biosynthesis
19	2.29	2e−02	29	Transcription factors − Trihelix
20	2.28	2e−02	151	RNA polymerase II system
Underexpressed				
1	−10.74	0e+00	18	Energy metabolism − Photosynthesis − proteins
2	−10.54	0e+00	47	Transport − Transporter − Electron carriers
3	−9.94	0e+00	18	Photosynthesis − proteins
4	−8.52	0e+00	78	Energy metabolism − Photosynthesis
5	−8.51	0e+00	38	Photosynthesis
6	−8.37	0e+00	26	Flavonoid biosynthesis
7	−6.33	0e+00	10	Photosynthesis − Photosystem II (P700−chlorophyll a)
8	−6.24	0e+00	40	Transport − Systems − Thylakoid targeting pathway
9	−5.02	0e+00	80	Cytoskeleton − Microtubules
10	−4.85	0e+00	13	Cutin suberine and wax biosynthesis
11	−4.66	0e+00	34	Peptidases and inhibitors − Family S10
12	−4.5	0e+00	22	Fatty acid elongation
13	−4.44	0e+00	206	Cell growth and death − Cell wall
14	−4.32	0e+00	31	Biosynthesis of plant secondary metabolites
15	−4.26	0e+00	39	Pentose and glucuronate interconversions
16	−3.87	8e−05	81	Enzyme − Carbon−oxygen lyases
17	−3.7	1e−04	24	Tropane, piperidine and pyridine alkaloid biosynthesis
18	−3.51	6e−04	26	Steroid biosynthesis
19	−3.45	8e−04	217	Cell motility − Regulation of cytoskeleton
20	−3.44	8e−04	58	Carbohydrate metabolism − Fructose and mannose metabolism

Portrait

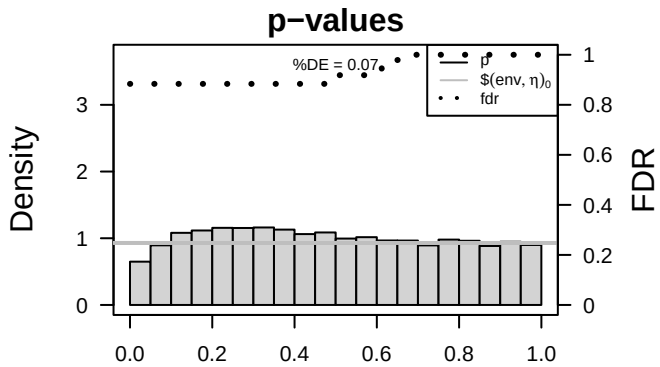


Top 100 DE genes





p−values



p−values