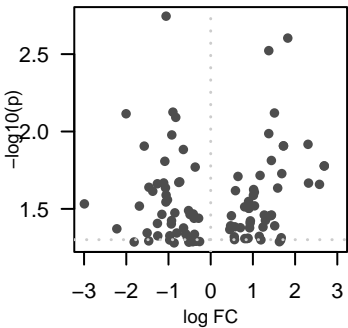
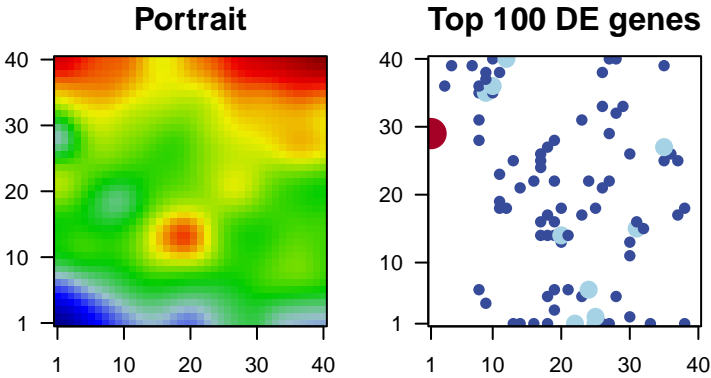


CabFra_acclim_r3

Global Summary

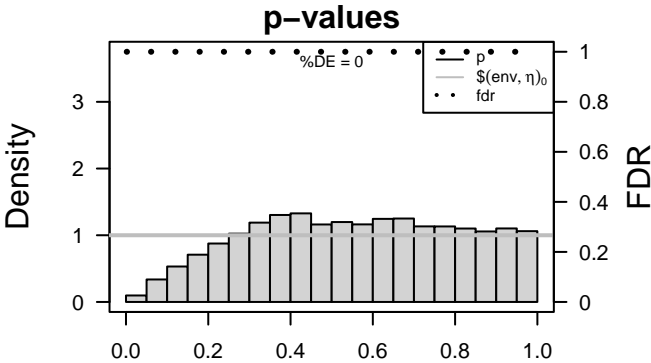
%DE = 0
genes with $fdr < 0.2 = 0$ (0 + / 0 -)
genes with $fdr < 0.1 = 0$ (0 + / 0 -)
genes with $fdr < 0.05 = 0$ (0 + / 0 -)
genes with $fdr < 0.01 = 0$ (0 + / 0 -)

<FC> = 0
<p-value> = 0.49
<fdr> = 1



Differentially expressed genes

Rank	ID	log(FC)	fdr	Description
		p-value		Metagene
Overexpressed				
1	Vitv01g01907	1.83	0.002	1 38 x 18 The membrane surrounding a cell that separates the cell from
2	Vitv03g00392	1.38	0.003	1 27 x 22 Binding to a heme, a compound composed of iron complexed
3	Vitv05g00733	1.51	0.008	1 7 x 39 The component of a membrane consisting of the gene produc
4	Vitv15g01216	1.38	0.010	1 19 x 16
5	Vitv08g02147	2.31	0.012	1 35 x 27 The membrane surrounding a cell that separates the cell from
6	Vitv10g02111	1.72	0.012	1 20 x 14
7	Vitv00g01858	1.72	0.012	1 20 x 14
8	Vitv08g0147C	1.44	0.015	1 10 x 35 A membrane-bounded organelle of eukaryotic cells in which
9	Vitv00g01655	2.69	0.017	1 12 x 40
10	Vitv10g02094	2.69	0.017	1 12 x 40
11	Vitv16g0174C	1.68	0.019	1 20 x 13
12	Vitv07g00435	1.17	0.019	1 18 x 14 The component of a membrane consisting of the gene produc
13	Vitv18g01696	0.65	0.020	1 26 x 33
14	Vitv17g00606	2.32	0.022	1 19 x 14 Catalysis of the hydrolysis of any ester bond.
15	Vitv15g0039E	2.58	0.022	1 37 x 25 Catalysis of the transfer of a methyl group to the oxygen atom
16	Vitv19g0231E	1.59	0.023	1 21 x 14
17	Vitv06g0065C	1.02	0.024	1 28 x 32 The component of a membrane consisting of the gene produc
18	Vitv17g01204	0.59	0.024	1 25 x 18 Binding to a protein.
19	Vitv12g00211	1.03	0.025	1 8 x 31 The component of a membrane consisting of the gene produc
20	Vitv02g0046C	1.01	0.026	1 30 x 26
Underexpressed				
1	Vitv18g0033E	-1.06	0.002	1 30 x 11 Binding to a zinc ion (Zn).
2	Vitv06g00477	-0.89	0.007	1 12 x 18 A small RNA-based gene silencing process in which small in
3	Vitv18g02077	-2	0.008	1 18 x 1 Binding to ADP, adenosine 5'-diphosphate.
4	Vitv17g00143	-0.83	0.008	1 25 x 2 Binding to a zinc ion (Zn).
5	Vitv07g00362	-0.92	0.011	1 31 x 15 A semiautonomous, self replicating organelle that occurs in vi
6	Vitv03g01727	-1.57	0.012	1 38 x 1 Binding to a zinc ion (Zn).
7	Vitv19g02014	-0.65	0.013	1 23 x 5 A membrane-bounded organelle of eukaryotic cells in which
8	Vitv11g00953	-1.09	0.016	1 11 x 18 The chemical reactions and pathways resulting in the formati
9	Vitv08g02135	-0.37	0.017	1 19 x 22 The membrane surrounding a cell that separates the cell from
10	Vitv07g0217C	-0.73	0.021	1 18 x 27
11	Vitv10g00461	-0.76	0.021	1 19 x 6 A lipid bilayer along with all the proteins and protein complex
12	Vitv15g0110E	-1.11	0.022	1 19 x 28 The component of a membrane consisting of the gene produc
13	Vitv18g01254	-1.26	0.022	1 28 x 5 A membrane-bounded organelle of eukaryotic cells in which
14	Vitv13g0235E	-1.46	0.023	1 1 x 29 A membrane-bounded organelle of eukaryotic cells in which
15	Vitv18g00335	-1.07	0.023	1 16 x 1 The component of a membrane consisting of the gene produc
16	Vitv01g0030E	-1.37	0.024	1 13 x 1
17	Vitv05g0061E	-1.06	0.026	1 30 x 2 A membrane-bounded organelle of eukaryotic cells in which
18	Vitv14g00791	-1.02	0.028	1 22 x 1 The contents of a cell excluding the plasma membrane and n
19	Vitv07g0147E	-1.06	0.029	1 19 x 3 The component of a membrane consisting of the gene produc
20	Vitv14g01657	-2.99	0.029	1 1 x 29 Binding to a heme, a compound composed of iron complexed



Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	8.49	0.000	18	Energy metabolism, Biosynthesis, Proteins
2	8.47	0.000	18	Photosynthesis, Proteins
3	8.1	0.000	47	Transport, Carbohydrate metabolism, Proteins
4	5.79	0.000	38	Photosynthesis
5	5.64	0.000	217	Cell motility, Regulation of cytoskeleton
6	5.58	0.000	78	Energy metabolism, Biosynthesis
7	5.12	0.000	10	Photosynthesis, Photosynthesis
8	4.78	0.000	80	Cytoskeleton, Microtubules
9	4.67	0.000	11	Transcription factors - GRF
10	3.08	0.002	28	Transcription factors - MTERF
11	2.72	0.008	18	Transcription factors - ARF
12	2.71	0.008	10	Peptidase, Peptidase inhibitors, Peptidase family
13	2.68	0.008	17	Kinase - Raf family, Kinase
14	2.63	0.009	219	Cell growth, Cell cycle
15	2.63	0.010	31	Fatty acid metabolism
16	2.63	0.010	101	Starch and carbohydrate metabolism
17	2.61	0.010	100	Plant specific signaling, Development
18	2.6	0.010	41	Porphyry metabolism
19	2.6	0.010	75	Mitochondrial transcription and translation factors
20	2.57	0.011	40	Transport, Glycolysis, Glycolysis pathway
<i>Underexpressed</i>				
1	-8.39	0e+00	48	Transcription factors - WRKY
2	-7.75	0e+00	162	Plant specific signaling, Plant-pathogen interaction
3	-5.73	0e+00	49	Transcription factors - NAC
4	-5.19	0e+00	153	Plant-pathogen interaction
5	-4.94	0e+00	26	Flavonoid biosynthesis
6	-4.82	0e+00	140	Hormone signaling, Signaling
7	-4.74	0e+00	73	Transcription factors - EREBP
8	-4.72	0e+00	45	Galactose metabolism
9	-4.2	0e+00	77	Pores ion channels [TC:1]
10	-3.84	8e-05	58	Other amino acid metabolism, Glutathione metabolism
11	-3.8	1e-04	26	Glycosyltransferase, Hydrolytic molecule
12	-3.7	1e-04	15	Stilbenoid, Coumarin, Anthraquinone biosynthesis
13	-3.67	3e-04	15	Chaperone, HSP70 / DNAK
14	-3.56	5e-04	24	Tropaeolum, Phytoalexin, Phytoalexin biosynthesis
15	-3.39	9e-04	71	Exosome, Exosome, Exosome, Exosome
16	-3.31	1e-03	64	Transcription factors - Other transcription factors
17	-3.19	2e-03	11	Biosynthesis, Biosynthesis, Biosynthesis
18	-3.17	2e-03	144	Ribosome, Ribosome, Ribosome
19	-3.13	2e-03	56	Hormone signaling, Signaling
20	-3.08	2e-03	38	Protein - Chaperone, Chaperone, Chaperone

