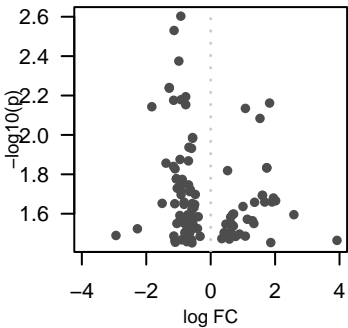
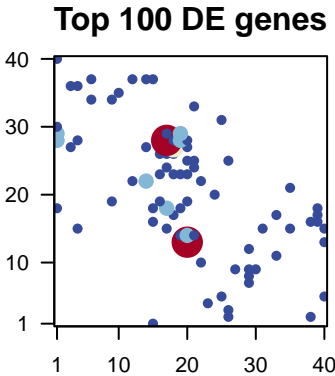
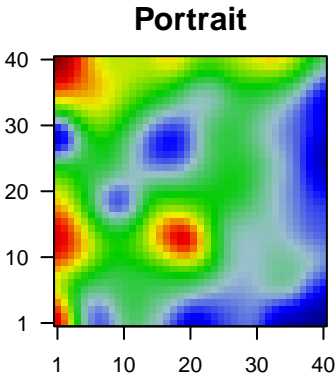


CabFra_accfreeze_r1

Global Summary

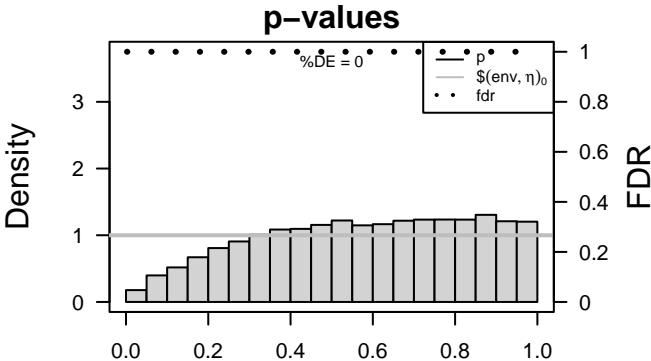
%DE = 0
genes with $fdr < 0.2 = 0$ (0 + / 0 -)
genes with $fdr < 0.1 = 0$ (0 + / 0 -)
genes with $fdr < 0.05 = 0$ (0 + / 0 -)
genes with $fdr < 0.01 = 0$ (0 + / 0 -)

<FC> = 0
<p-value> = 0.5
<fdr> = 1



Differentially expressed genes

Rank	ID	log(FC)	fdr	Description		
		p-value		Metagene		
Overexpressed						
1	Vitv115g00812	1.83	0.007	1	4 x 15	Catalysis of an oxidation-reduction (redox) reaction, a reversi
2	Vitv01g00104	1.08	0.007	1	17 x 18	Catalysis of the random hydrolysis of (1->4)-alpha-D-galact
3	Vitv18g0154E	1.53	0.008	1	6 x 37	Binding to ATP, adenosine 5'-triphosphate, a universally impc
4	Vitv00g01872	1.74	0.015	1	20 x 13	
5	Vitv14g03131	1.74	0.015	1	20 x 13	
6	Vitv14g0102E	0.52	0.015	1	19 x 18	The part of the cytoplasm that does not contain organelles bu
7	Vitv10g02111	1.61	0.020	1	20 x 14	
8	Vitv00g0185E	1.61	0.020	1	20 x 14	
9	Vitv01g0207C	1.95	0.021	1	20 x 13	The formation of a protein dimer, a macromolecular structure
10	Vitv13g0193E	2.02	0.022	1	19 x 14	
11	Vitv17g0047C	1.9	0.022	1	3 x 36	The formation of a protein dimer, a macromolecular structure
12	Vitv12g0071C	1.68	0.022	1	1 x 18	Catalysis of the transfer of an acyl group, other than amino-a
13	Vitv08g0147C	1.36	0.022	1	10 x 35	A membrane-bound organelle of eukaryotic cells in which
14	Vitv18g01144	1	0.023	1	22 x 10	Binding to ATP, adenosine 5'-triphosphate, a universally impc
15	Vitv12g0017E	0.71	0.025	1	6 x 34	Catalysis of an oxidation-reduction (redox) reaction in which l
16	Vitv07g0202E	0.68	0.025	1	9 x 34	Binding to a metal ion.
17	Vitv16g0125E	2.58	0.025	1	20 x 13	
18	Vitv02g0012E	0.62	0.026	1	12 x 37	A lipid bilayer along with all the proteins and protein complex
19	Vitv03g01084	1.14	0.027	1	21 x 14	Reactions, triggered in response to the presence of a foreign
20	Vitv02g01474	1.3	0.027	1	4 x 36	Catalysis of an oxidation-reduction (redox) reaction, a reversi
Underexpressed						
1	Vitv11g0103E	-0.93	0.002	1	20 x 25	Binding to a protein.
2	Vitv01g0104E	-1.14	0.003	1	18 x 27	The component of a membrane consisting of the gene produc
3	Vitv03g0079E	-0.99	0.004	1	18 x 28	The component of a membrane consisting of the gene produc
4	Vitv02g01704	-1.29	0.006	1	17 x 28	
5	Vitv00g01904	-1.29	0.006	1	17 x 28	
6	Vitv17g0133C	-0.78	0.006	1	14 x 27	The component of a membrane consisting of the gene produc
7	Vitv14g0009E	-0.92	0.007	1	17 x 28	Binding to a protein.
8	Vitv11g0020E	-1.15	0.007	1	17 x 28	Binding to a zinc ion (Zn).
9	Vitv07g0122E	-0.77	0.007	1	19 x 28	Any process involved in the conversion of a primary ribosoma
10	Vitv03g00172	-1.83	0.007	1	38 x 2	A membrane-bound organelle of eukaryotic cells in which
11	Vitv00g0203E	-0.56	0.010	1	14 x 22	
12	Vitv07g0294E	-0.56	0.010	1	14 x 22	
13	Vitv03g0004E	-0.67	0.012	1	25 x 5	The chemical reactions and pathways resulting in the formati
14	Vitv03g0028E	-0.6	0.012	1	17 x 24	The process in which a SUMO protein (small ubiquitin-relate
15	Vitv05g0109C	-0.95	0.013	1	16 x 26	
16	Vitv05g0049E	-0.69	0.014	1	18 x 26	Binding to a metal ion.
17	Vitv01g01991	-1.39	0.014	1	18 x 27	
18	Vitv12g00027	-1.16	0.014	1	39 x 18	Catalysis of the reaction: phosphatidylglycerophosphate + H2
19	Vitv03g0025E	-1.11	0.015	1	26 x 2	Binding to an RNA molecule or a portion thereof.
20	Vitv00g0038E	-1.07	0.017	1	1 x 28	



Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
Overexpressed				
1	8.45	0e+00	73	Transcription factor A202-EREBP2 EREBP
2	7.63	0e+00	64	Transcription factor A202-EREBP2 EREBP
3	7.54	0e+00	140	Hormone signaling system signaling
4	4.61	0e+00	111	Hormone signaling system signaling
5	4.3	0e+00	170	Transcription factor A202-EREBP2 EREBP
6	4.07	0e+00	49	Transcription factor A202-EREBP2 EREBP
7	4.06	0e+00	11	Biosynthesis of secondary metabolites
8	4.06	0e+00	48	Transcription factor A202-EREBP2 EREBP
9	3.56	5e-04	18	Photosynthesis
10	3.13	2e-03	18	Energy metabolism
11	3.02	3e-03	74	Transcription factor A202-EREBP2 EREBP
12	2.59	1e-02	29	Carotenoid biosynthesis
13	2.56	1e-02	12	Transcription factor A202-EREBP2 EREBP
14	2.53	1e-02	29	Transcription factor A202-EREBP2 EREBP
15	2.45	2e-02	51	Plant specific signaling
16	2.33	2e-02	47	Transport
17	2.31	2e-02	128	Ubiquitin
18	2.19	3e-02	17	Kinase - RAK family
19	2.17	3e-02	10	Transcription factor A202-EREBP2 EREBP
20	2.12	4e-02	100	Plant specific signaling
Underexpressed				
1	-4.6	0e+00	211	Ribosome
2	-4.1	0e+00	219	Cell growth
3	-3.96	4e-05	26	Flavonoid biosynthesis
4	-3.89	8e-05	24	Tropene
5	-3.65	3e-04	15	Stilbenoid
6	-3.62	3e-04	45	Galactose
7	-3.49	7e-04	24	Replication
8	-3.46	8e-04	81	Enzyme
9	-3.35	1e-03	247	Translation
10	-3.32	1e-03	144	Ribosome
11	-3.25	1e-03	72	Ribosome
12	-3.23	1e-03	131	Enzyme
13	-3.23	1e-03	67	Ribosome
14	-3.19	2e-03	97	Ribosome
15	-3.13	2e-03	41	Replication
16	-3.12	2e-03	134	Hormone
17	-2.92	4e-03	11	Lipid
18	-2.74	7e-03	19	Cofactors
19	-2.53	1e-02	71	Amino acid
20	-2.52	1e-02	31	Chromosome

