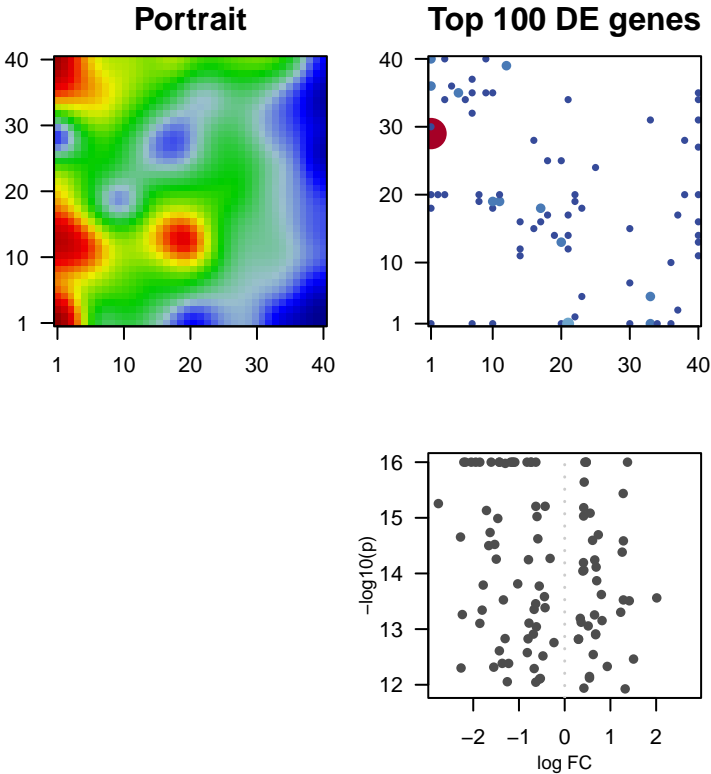


CabFra_accfreeze

Global Summary

%DE = NA
genes with $\text{fdr} < 0.2 = 7406$ (3868 + / 3538 -)
genes with $\text{fdr} < 0.1 = 4759$ (2482 + / 2277 -)
genes with $\text{fdr} < 0.05 = 3121$ (1624 + / 1497 -)
genes with $\text{fdr} < 0.01 = 1680$ (843 + / 837 -)

<FC> = 0
<p-value> = 0.04
<fdr> = 0.4



Differentially expressed genes

Rank	ID	log(FC)	fdr	Description		
		p-value		Metagene		
Overexpressed						
1	Vitv14g00111	0.44	1e-16	4e-14	21 x 17	The irregular network of unit membranes, visible only by elect
2	Vitv15g0093E	0.47	1e-16	4e-14	17 x 18	The component of a membrane consisting of the gene produc
3	Vitv18g0255C	0.47	1e-16	4e-14	14 x 16	The component of a membrane consisting of the gene produc
4	Vitv19g0231E	1.37	1e-16	4e-14	21 x 14	
5	Vitv06g00897	0.43	2e-16	6e-13	14 x 11	Binding to GTP, guanosine triphosphate.
6	Vitv01g02281	1.28	4e-16	6e-13	20 x 13	A lipid bilayer along with all the proteins and protein complex
7	Vitv07g01087	0.42	7e-16	6e-13	14 x 12	
8	Vitv14g01671	0.56	8e-16	6e-13	6 x 34	Catalysis of the transfer of ubiquitin to a substrate protein via
9	Vitv15g00707	0.41	9e-16	6e-13	9 x 35	
10	Vitv11g0027E	0.74	2e-15	2e-12	3 x 34	
11	Vitv06g01052	0.61	3e-15	2e-12	7 x 35	A conserved complex that contains a heterodimer of SMC prc
12	Vitv02g01474	1.28	3e-15	2e-12	4 x 36	Catalysis of an oxidation-reduction (redox) reaction, a reversi
13	Vitv19g00581	1.26	4e-15	4e-12	3 x 40	
14	Vitv09g0157E	0.66	6e-15	5e-12	1 x 20	
15	Vitv07g02497	0.41	6e-15	6e-12	7 x 32	
16	Vitv13g00031	0.69	8e-15	6e-12	1 x 36	A membrane-bounded organelle of eukaryotic cells in which
17	Vitv18g01157	0.42	9e-15	6e-12	3 x 20	Binding to a metal ion.
18	Vitv14g00674	0.4	9e-15	1e-11	22 x 20	A lipid bilayer along with all the proteins and protein complex
19	Vitv02g00073	0.7	1e-14	1e-11	18 x 17	The component of a membrane consisting of the gene produc
20	Vitv01g0198E	0.8	2e-14	2e-11	7 x 37	The contents of a cell excluding the plasma membrane and n
Underexpressed						
1	Vitv10g01211	-1.18	1e-16	4e-14	1 x 29	Binding to ATP, adenosine 5'-triphosphate, a universally impc
2	Vitv00g01044	-1.43	1e-16	4e-14	1 x 29	
3	Vitv15g01767	-1.43	1e-16	4e-14	1 x 29	Any molecular function by which a gene product interacts selc
4	Vitv00g0105E	-0.73	1e-16	4e-14	33 x 5	
5	Vitv02g01823	-0.74	1e-16	4e-14	33 x 5	A membrane-bounded organelle of eukaryotic cells in which
6	Vitv06g00202	-0.63	1e-16	4e-14	16 x 28	A chlorophyll-containing plastid with thylakoids organized intc
7	Vitv08g01703	-1.13	1e-16	4e-14	1 x 29	
8	Vitv09g01181	-1.86	1e-16	4e-14	1 x 29	Binding to a protein.
9	Vitv09g01812	-1.15	1e-16	4e-14	22 x 2	Binding to a protein.
10	Vitv12g02502	-1.09	1e-16	4e-14	1 x 29	
11	Vitv12g0089C	-1.95	1e-16	4e-14	1 x 28	
12	Vitv13g0200E	-2.04	1e-16	4e-14	40 x 35	Catalysis of the hydrolysis of internal, alpha-peptide bonds in
13	Vitv15g0103E	-2.21	1e-16	4e-14	21 x 1	
14	Vitv16g0008E	-0.82	1e-16	4e-14	37 x 3	Catalysis of the transfer of a phosphate group, usually from A
15	Vitv19g00154	-2.17	1e-16	4e-14	1 x 29	
16	Vitv19g01581	-1.61	1e-16	4e-14	1 x 29	
17	Vitv12g0019E	-1.3	1e-16	6e-13	1 x 28	
18	Vitv16g0078E	-2.76	6e-16	6e-13	1 x 29	Binding to a heme, a compound composed of iron complexed
19	Vitv19g02014	-0.43	6e-16	6e-13	23 x 5	A membrane-bounded organelle of eukaryotic cells in which
20	Vitv19g01577	-0.63	6e-16	6e-13	1 x 28	Binding to ADP, adenosine 5'-diphosphate.

Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	6.8	0.000	73	Transcription factor binding site (TFBS) - EREBP
2	6.29	0.000	140	Hormone signaling pathway - EREBP signaling
3	5.21	0.000	49	Transcription factor binding site (TFBS) - NAC
4	4.73	0.000	64	Transcription factor binding site (TFBS) - Other transcription factors
5	4.64	0.000	170	Transcription factor binding site (TFBS) - Other transcription factors
6	4.64	0.000	111	Hormone signaling pathway - EREBP signaling
7	4.22	0.000	48	Transcription factor binding site (TFBS) - WRKY
8	3.98	0.000	11	Biosynthesis of secondary metabolites - Biosynthesis
9	3.86	0.000	74	Transcription factor binding site (TFBS) - C2H2
10	3.17	0.002	128	Ubiquitin-proteasome pathway - Ubiquitin-proteasome pathway
11	2.74	0.008	29	Carotenoid biosynthesis
12	2.53	0.012	11	Zeatin biosynthesis
13	2.5	0.014	80	Transport system - Transport system
14	2.49	0.015	13	Peptidase family - Peptidase family
15	2.46	0.017	29	Transcription factor binding site (TFBS) - GRAS
16	2.32	0.023	26	Transcription factor binding site (TFBS) - G2-like
17	2.28	0.025	24	Inner membrane
18	2.14	0.036	238	Enzyme - Enzyme
19	2.07	0.043	27	Enzyme - Enzyme
20	1.96	0.055	51	Plant secondary metabolism - Plant secondary metabolism
<i>Underexpressed</i>				
1	-5.05	0e+00	211	Ribosome
2	-4.76	0e+00	219	Cell growth and division - Cell cycle
3	-4.47	0e+00	26	Flavonoid biosynthesis
4	-4.18	0e+00	78	Energy metabolism - Photosynthesis
5	-4.05	0e+00	38	Photosynthesis
6	-4.03	0e+00	24	Replication, recombination and repair - Replication
7	-3.87	0e+00	134	Hormone signaling pathway - Signaling
8	-3.8	0e+00	247	Translation - Translation
9	-3.68	2e-04	144	Ribosome
10	-3.57	4e-04	22	Fatty acid metabolism - Fatty acid metabolism
11	-3.49	6e-04	97	Ribosome
12	-3.48	6e-04	67	Ribosome
13	-3.34	1e-03	81	Enzyme - Enzyme
14	-3.32	1e-03	47	Transport system - Transport system
15	-3.27	2e-03	34	Peptidase family - Peptidase family
16	-3.26	2e-03	72	Ribosome
17	-3.24	2e-03	19	Cofactors and prosthetic groups - Cofactors and prosthetic groups
18	-3.2	2e-03	80	Cytoskeleton - Cytoskeleton
19	-3.02	4e-03	31	Chromatin organization and structure - Chromatin organization and structure
20	-2.99	4e-03	15	Stilbenoid, diarylheptanoid and lignan biosynthesis

