

# CabFra\_warm

## Global Summary

%DE = NA

```
# genes with fdr < 0.2 = 11561 ( 5499 + / 6062 -)
```

# genes with  $\text{fdr} < 0.1 = 9685$  ( 4791 + / 4894 - )

```
# genes with fdr < 0.05 = 8041 ( 4213 + / 3828 -)
```

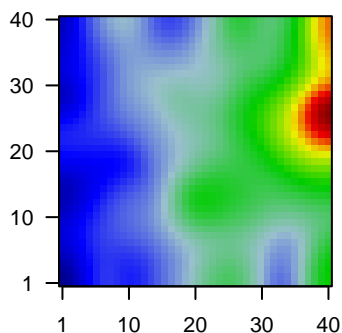
# genes with  $\text{fdr} < 0.01 = 5130$  ( 2969 + / 2161 - )

$$\langle FC \rangle = 0$$

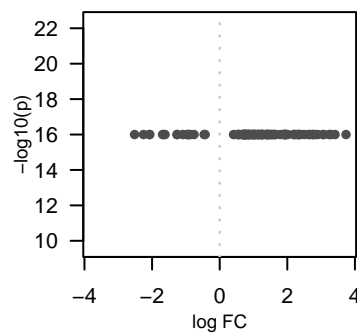
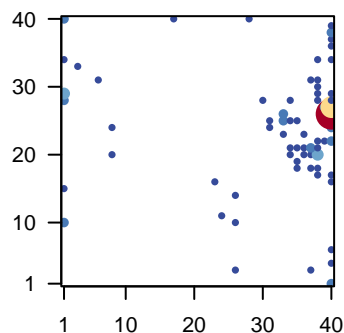
$\langle p\text{-value} \rangle = 0$

$\langle \text{fdr} \rangle = 0.24$

## Portrait



### Top 100 DE genes



## Differentially expressed genes

Rank	ID	log(FC)	fdr	Description		
			p-value	Metagene		
<i>Overexpressed</i>						
1	Vitvi07g02483	0.82	1e-16	1e-14	34 x 20	
2	Vitvi07g02097	3.41	1e-16	1e-14	40 x 27	A membrane-bounded organelle of eukaryotic cells in which
3	Vitvi10g000232	1.05	1e-16	1e-14	34 x 28	A chlorophyll-containing plastid with thylakoids organized into
4	Vitvi07g01219	1.02	1e-16	1e-14	23 x 16	Catalysis of a biochemical reaction at physiological temperature
5	Vitvi07g01433	1.91	1e-16	1e-14	40 x 24	
6	Vitvi07g01439	0.86	1e-16	1e-14	37 x 31	The chemical reactions and pathways involving lipids, compounds
7	Vitvi07g02535	1.38	1e-16	1e-14	38 x 22	The contents of a cell excluding the plasma membrane and nucleus
8	Vitvi07g01342	1.38	1e-16	1e-14	40 x 4	
9	Vitvi00g00723	3.07	1e-16	1e-14	40 x 27	
10	Vitvi07g02983	3.07	1e-16	1e-14	40 x 27	The component of a membrane consisting of the gene product
11	Vitvi00g00784	1.23	1e-16	1e-14	37 x 21	
12	Vitvi02g01712	1.22	1e-16	1e-14	37 x 21	The action of a molecule that contributes to the structural integrity
13	Vitvi10g00477	0.77	1e-16	1e-14	37 x 18	
14	Vitvi10g01652	1.91	1e-16	1e-14	40 x 25	
15	Vitvi01g01376	1.96	1e-16	1e-14	40 x 38	Binding to the oxidized form, FAD, of flavin-adenine dinucleotide
16	Vitvi01g0153C	0.67	1e-16	1e-14	35 x 18	An RNA polymerase complex containing polypeptides encoded by
17	Vitvi01g0225E	0.99	1e-16	1e-14	33 x 25	The action of a molecule that contributes to the structural integrity
18	Vitvi01g00055	1.41	1e-16	1e-14	40 x 22	The membrane surrounding a cell that separates the cell from the
19	Vitvi01g00142	0.75	1e-16	1e-14	34 x 21	The action of a molecule that contributes to the structural integrity
20	Vitvi01g0016E	0.72	1e-16	1e-14	33 x 23	
<i>Underexpressed</i>						
1	Vitvi10g000184	-2.07	1e-16	1e-14	1 x 29	
2	Vitvi07g0124E	-0.46	1e-16	1e-14	8 x 24	The cell cycle process in which the sister chromatids of a replicated
3	Vitvi10g00029E	-2.08	1e-16	1e-14	1 x 15	
4	Vitvi10g0176Z	-0.87	1e-16	1e-14	1 x 34	A lipid bilayer along with all the proteins and protein complexes
5	Vitvi00g0215Z	-1.26	1e-16	1e-14	1 x 10	
6	Vitvi10g0238E	-1.26	1e-16	1e-14	1 x 10	A lipid bilayer along with all the proteins and protein complexes
7	Vitvi00g02197	-0.95	1e-16	1e-14	1 x 28	
8	Vitvi07g0313C	-0.95	1e-16	1e-14	1 x 28	
9	Vitvi01g0025E	-0.76	1e-16	1e-14	3 x 33	The component of a membrane consisting of the gene product
10	Vitvi01g0040E	-1.62	1e-16	1e-14	1 x 40	A lipid bilayer along with all the proteins and protein complexes
11	Vitvi01g01981	-2.52	1e-16	1e-14	37 x 3	Reactions, triggered in response to the presence of a foreign
12	Vitvi03g00047	-2.25	1e-16	1e-14	1 x 40	Any process that results in a change in state or activity of a cell
13	Vitvi04g00012	-1.65	1e-16	1e-14	17 x 40	A membrane-bounded organelle of eukaryotic cells in which
14	Vitvi04g0189E	-0.9	1e-16	1e-14	8 x 20	A lipid bilayer along with all the proteins and protein complexes
15	Vitvi04g02197	-1.69	1e-16	1e-14	1 x 29	
16	Vitvi05g0190C	-1.09	1e-16	1e-14	1 x 29	
17	Vitvi05g0134Z	-0.43	1e-16	1e-14	6 x 31	Binding to a protein.
18	Vitvi05g0176Z	-0.49	1e-16	1e-14	6 x 28	
19	Vitvi06g0047C	-0.5	1e-16	1e-14	4 x 31	Binding to ATP, adenosine 5'-triphosphate, a universally important
20	Vitvi06g0048E	-0.55	1e-16	1e-14	3 x 33	A membrane-bounded organelle of eukaryotic cells in which

## Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	16.03	0	247	Translation Translation Ribosome
2	15.85	0	211	Ribosome Ribosome
3	14.31	0	144	Ribosome Ribosome Eukaryotes
4	12.14	0	24	Replication DNA Replication DNA Replication Factors
5	12.05	0	219	Cell growth Cell cycle Cell cycle
6	11.66	0	80	Cytoskeleton Microtubule Microtubules
7	10.8	0	97	Ribosome Ribosome Archaea
8	10.56	0	36	DNA replication DNA replication
9	9.38	0	217	Cell motility Cell motility Regulation of cytoskeleton
10	8.73	0	41	Replication DNA Replication DNA replication
11	7.36	0	67	Ribosome Ribosome Bacteria
12	7.02	0	72	Ribosome Ribosome Mitochondrion Chloroplast
13	6.06	0	44	Replication DNA Replication DNA Replication Factors
14	5.85	0	34	Peptidase Serine protease Family S10
15	5.82	0	18	Energy metabolism Photosynthesis proteins
16	5.59	0	78	Energy metabolism Photosynthesis
17	5.34	0	18	Photosynthesis proteins
18	5.26	0	27	Mismatch repair Mismatch repair
19	5.25	0	113	Exosome Exosome protein cancer cells
20	4.91	0	38	Photosynthesis Photosynthesis
<i>Underexpressed</i>				
1	-7.85	0e+00	140	Hormone signaling Signaling
2	-7.43	0e+00	73	Transcription P2-EREBP
3	-6.49	0e+00	64	Transcription Transcription factors
4	-5.85	0e+00	49	Transcription Transcription factors - NAC
5	-5.84	0e+00	48	Transcription Transcription factors - WRKY
6	-4.52	0e+00	170	Transcription Transcription factors - C3HC4
7	-4.19	0e+00	111	Hormone signaling Signaling
8	-4.05	0e+00	35	Mitophagy Mitophagy factors
9	-3.89	0e+00	96	Transport Transporters - Rf1 to 6
10	-3.83	0e+00	162	Plant specific signaling signaling interaction
11	-3.52	5e-04	128	Ubiquitin Ubiquitin Signaling type E3
12	-3.46	7e-04	80	Transport Transport factors
13	-3.43	1e-03	51	Plant specific signaling signaling
14	-3.42	1e-03	31	Autophagy Autophagy - other
15	-3.4	1e-03	20	Protein - Putative degradation/protein
16	-3.19	2e-03	92	Lipid metabolism Lipid metabolism
17	-2.98	4e-03	11	Biosynthesis Biosynthesis
18	-2.97	4e-03	20	Transport and signaling signaling
19	-2.97	4e-03	86	Signal transduction Signaling pathway
20	-2.85	5e-03	26	Transcription Transcription - G2-like

