

CabFra_warm_r3

Global Summary

$$\%DE = 0.31$$

genes with $\text{fdr} < 0.2 = 3$ (0 + / 3 -)

genes with $\text{fdr} < 0.1 = 3$ (0 + / 3 -)

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# genes with fdr < 0.05 = 0 ( 0 + / 0 -)
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# genes with fdr < 0.01 = 0 ( 0 + / 0 -)
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$$\langle FC \rangle = 0$$

$\langle p\text{-value} \rangle = 0.25$

$\langle \text{fdr} \rangle = 0.69$

Differentially expressed genes

Rank	ID	log(FC)	fdr	Description		
		p-value	Metagene			
Overexpressed						
1	Vitv05g0184E	1.68	2e-04	0.2	35 x 23	A membrane-bound organelle of eukaryotic cells in which
2	Vitv08g0115E	1.77	4e-04	0.2	36 x 23	Binding to ATP, adenosine 5'-triphosphate, a universally impo
3	Vitv01g0042A	2.01	5e-04	0.2	36 x 23	Binding to a metal ion.
4	Vitv01g0155E	2.42	5e-04	0.2	40 x 23	Any molecular function by which a gene product interacts sel
5	Vitv05g00407	0.98	5e-04	0.2	33 x 19	Catalysis of the reaction: ATP + GMP = ADP + GDP.
6	Vitv08g0069E	1.25	5e-04	0.2	35 x 20	
7	Vitv05g0189E	1.19	6e-04	0.2	24 x 16	A chlorophyll-containing plastid with thylakoids organized inte
8	Vitv08g01397	1.78	6e-04	0.2	34 x 23	The action of a molecule that contributes to the structural inte
9	Vitv06g0061A	2.68	8e-04	0.2	40 x 25	The process resulting in division and partitioning of componen
10	Vitv05g0125A	0.99	9e-04	0.2	32 x 21	The action of a molecule that contributes to the structural inte
11	Vitv18g0094E	1.54	1e-03	0.2	36 x 23	
12	Vitv04g0006A	1.39	1e-03	0.2	32 x 25	The action of a molecule that contributes to the structural inte
13	Vitv05g0057C	2.01	1e-03	0.2	38 x 24	A membrane-bound organelle of eukaryotic cells in which
14	Vitv13g0053E	1	1e-03	0.2	36 x 20	
15	Vitv08g0143E	1.2	1e-03	0.2	36 x 21	A membrane-bound organelle of eukaryotic cells in which
16	Vitv18g0083A	0.82	1e-03	0.2	35 x 19	The part of the cytoplasm that does not contain organelles bu
17	Vitv08g0144E	1.49	1e-03	0.2	38 x 20	
18	Vitv01g0067E	0.9	1e-03	0.2	26 x 15	A semiautonomous, self replicating organelle that occurs in vi
19	Vitv14g0024E	1.56	2e-03	0.2	37 x 22	Binding to ATP, adenosine 5'-triphosphate, a universally impo
20	Vitv14g00497	0.88	2e-03	0.2	28 x 17	Binding to a protein.
Underexpressed						
1	Vitv19g0196E	-2.69	1e-05	0.05	7 x 18	
2	Vitv09g0099A	-1.49	1e-05	0.05	13 x 18	The action of a molecule that contributes to the structural inte
3	Vitv18g0021E	-1.05	2e-05	0.05	7 x 32	The contents of a cell excluding the plasma membrane and n
4	Vitv07g0061A	-1.09	2e-05	0.24	6 x 25	Catalysis of the transfer of ubiquitin from one protein to anoth
5	Vitv07g0025E	-1.15	5e-05	0.24	10 x 15	A vesicle-mediated transport process in which transmembran
6	Vitv07g0258E	-1.57	1e-04	0.24	2 x 28	Any process that modulates the frequency, rate or extent of tr
7	Vitv00g0137A	-1.25	1e-04	0.24	1 x 24	
8	Vitv09g0181E	-1.53	2e-04	0.24	9 x 22	
9	Vitv08g0219A	-1.29	2e-04	0.24	1 x 22	
10	Vitv17g0090E	-1.99	2e-04	0.24	1 x 13	The component of a membrane consisting of the gene produc
11	Vitv15g0067E	-1.23	2e-04	0.24	4 x 32	Binding to a calcium ion (Ca2+).
12	Vitv07g0079E	-1.08	3e-04	0.24	4 x 25	The joining together of exons from one or more primary trans
13	Vitv02g0062C	-2.29	3e-04	0.24	1 x 28	Binding to a metal ion.
14	Vitv09g0185E	-0.78	3e-04	0.24	12 x 13	A semiautonomous, self replicating organelle that occurs in vi
15	Vitv11g0065E	-1.55	4e-04	0.24	1 x 32	Any molecular function by which a gene product interacts sel
16	Vitv01g0095A	-2	4e-04	0.24	1 x 16	Binding to ATP, adenosine 5'-triphosphate, a universally impo
17	Vitv18g0039E	-2.18	4e-04	0.24	1 x 35	The component of a membrane consisting of the gene produc
18	Vitv09g0066E	-1.44	4e-04	0.24	7 x 35	
19	Vitv03g0060C	-1.8	5e-04	0.24	16 x 39	Binding to a protein.
20	Vitv11g01507	-2.02	5e-04	0.24	1 x 35	The component of a membrane consisting of the gene produc

Differentially expressed gene sets

	Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>					
1	15.4	0	247	Translation	Ribosome
2	15.11	0	211	Ribosome	Ribosome
3	13.86	0	144	Ribosome	Eukaryotes
4	11.72	0	24	Replication	Chromosome
5	11.67	0	219	Cell growth	Cell cycle
6	11.17	0	80	Cytoskeleton	Microtubules
7	10.36	0	36	DNA replication	DNA replication
8	10.1	0	97	Ribosome	Archaea
9	9.05	0	217	Cell motility	Regulation of cytoskeleton
10	8.73	0	41	Replication	DNA replication
11	6.77	0	67	Ribosome	Bacteria
12	6.48	0	72	Ribosome	Chloroplast
13	5.89	0	74	Replication	DNA replication
14	5.71	0	18	Energy metabolism	Photosynthesis proteins
15	5.49	0	34	Peptidase	Family S10
16	5.31	0	27	Mismatch	Repair
17	5.2	0	18	Photosynthesis	Photosynthesis proteins
18	5.17	0	37	Homologous	Recombination
19	5.16	0	78	Energy metabolism	Photosynthesis
20	5.01	0	113	Exosome	Exosome
<i>Underexpressed</i>					
1	-7.88	0e+00	140	Hormone	Signaling
2	-7.78	0e+00	73	Transcription	EREBP
3	-6.46	0e+00	64	Transcription	Transcription factors
4	-6.19	0e+00	48	Transcription	WRKY
5	-6	0e+00	49	Transcription	NAC
6	-4.6	0e+00	170	Transcription	C3HC4
7	-4.13	0e+00	111	Hormone	Signaling
8	-4.11	0e+00	35	Mitophagy	Mitophagy factors
9	-4.09	0e+00	162	Plant specific	Signaling
10	-3.83	8e-05	96	Transport	Protein
11	-3.63	3e-04	80	Transport	System
12	-3.48	7e-04	128	Ubiquitin	Protein
13	-3.42	9e-04	31	Autophagy	Autophagy
14	-3.4	9e-04	20	Protein	Protein
15	-3.34	1e-03	51	Plant specific	Signaling
16	-3.1	2e-03	153	Plant-pal	Signaling
17	-2.98	3e-03	12	Transport	Protein
18	-2.91	4e-03	20	Transcription	Protein
19	-2.86	5e-03	92	Lipid metabolism	Metabolism
20	-2.82	6e-03	86	Signal transduction	Signaling pathway

