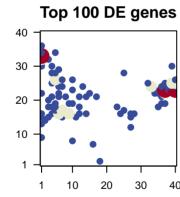
# CabFra\_warm\_r2

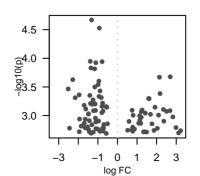
#### **Global Summary**

%DE = 0.28 # genes with fdr < 0.2 = 1 (0+/1 -) # 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> = 0.25<fdr> = 0.72

## 





#### Differentially expressed genes

log(FC) fdr

Rank

Vitvi01q00486

Vitvi12g00360

Vitvi16g01066 -1.16

Vitvi13q00351 -2.52

Vitvi06g00541 -1.95

Vitvi19g00907 -1.41

Vitvi16g00115 -0.94 Vitvi08g00671 -0.83

Vitvi07g02656 -2.16

Vitvi17g00614 -1.25

Vitvi04g01422 -0.76

-0.99

3e-04 0.2

3e-04 0.2

3e-04

4e-04

5e-04

5e-04 0.2

		ID		p-va	lue	Meta	gene	
Overexpressed								
1	1	Vitvi12g00022	2.69	2e-04	0.2	39 x 25	A membrane-bounded organelle of eukaryotic cells in which	1
2345678910	2	Vitvi01g00014	2.14	2e-04	0.2	37 x 23	A membrane-bounded organelle of eukaryotic cells in which	2
	3	Vitvi05g00570	2.18	4e-04	0.2	38 x 24	A membrane-bounded organelle of eukaryotic cells in which	3
	1	Vitvi00g00969	1.59	5e-04	0.2	37 x 22		4
	5	Vitvi10g02201	1.59	5e-04	0.2	37 x 22	A membrane-bounded organelle of eukaryotic cells in which	4 5
	3	Vitvi18g00942	1.62	5e-04	0.2	36 x 23		6
		Vitvi08g00739	1.92	7e-04	0.2	37 x 23	A membrane-bounded organelle of eukaryotic cells in which	7
	3	Vitvi01g01559	2.35	8e-04	0.2	40 x 23	Any molecular function by which a gene product interacts sele	8
	)	Vitvi10g01068	1.26	8e-04	0.2	33 x 24	A process that is carried out at the cellular level which results	9
	10	Vitvi01g00178	0.75	8e-04	0.2	27 x 15	The component of a membrane consisting of the gene produc	10
1	11	Vitvi06g00614	2.68	8e-04	0.2	40 x 25	The process resulting in division and partitioning of componer	11
1	12	Vitvi15g00545	2.51	8e-04	0.2	39 x 25	Binding to ATP, adenosine 5'-triphosphate, a universally impo	12
1	13	Vitvi09g01927	1.22	9e-04	0.2	35 x 22	The action of a molecule that contributes to the structural inte	13
14	14	Vitvi14g01870	1.42	9e-04	0.2	37 x 19	Any process that modulates the frequency, rate or extent of co	14
1	15	Vitvi01g01547	1.69	9e-04	0.2	37 x 23	A membrane-bounded organelle of eukaryotic cells in which	15
1	16	Vitvi13g01778	2.1	1e-03	0.2	37 x 25	The cell cycle process in which the sister chromatids of a repl	16
1	17	Vitvi13g01819	8.0	1e-03	0.2	27 x 16	Binding to a metal ion.	17
1	18	Vitvi02g00508	1.13	1e-03	0.2	25 x 28	Any molecular function by which a gene product interacts sele	18
1	19	Vitvi08g01478	2.83	1e-03	0.2	40 x 23	The component of a membrane consisting of the gene produc	19
2	20	Vitvi14g01674	1.21	1e-03	0.2	34 x 23		20
ι	Jnde	erexpressed						Un
1	1	Vitvi14g01604	-1.32	2e-05	0.2	5 x 18	The contents of a cell excluding the plasma membrane and n	1
	2	Vitvi16g00094	-0.93	3e-05	0.2	16 x 7		2
3	3	Vitvi18g00561	-1.39	1e-04	0.2	1 x 32	A membrane-bounded organelle of eukaryotic cells in which	2
4	1	Vitvi06g00586	-0.79	1e-04	0.2	14 x 21	Catalysis of the reaction: acyl-CoA + H2O = CoA + a carboxy	4
	5	Vitvi02g00378	-1.11	1e-04	0.2	10 x 23	Any process that modulates the frequency, rate or extent of co	5
6		Vitvi07g01258	-1.36	1e-04	0.2	5 x 34		4 5 6 7
7		Vitvi15g00718	-1.16	2e-04	0.2	7 x 17	A lipid bilayer along with all the proteins and protein complexe	
8		Vitvi15g01540	-2.29	2e-04	0.2	9 x 19	The component of a membrane consisting of the gene produc	8
ć	<sub>j</sub>	Vitvi08g01475	-0.95	3e-04	0.2	11 x 15	A lipid bilayer along with all the proteins and protein complexe	9

1 x 22 The component of a membrane consisting of the gene production

12 x 16 The contents of a cell excluding the plasma membrane and n

10 x 19 The component of a membrane consisting of the gene produc

1 x 33 Any molecular function by which a gene product interacts sele

5 x 28 Catalysis of the hydrolysis of peptide bonds in a polypeptide of

Binding to ATP, adenosine 5'-triphosphate, a universally impo

The component of a membrane consisting of the gene produc

A membrane-bounded organelle of eukaryotic cells in which

Catalysis of the hydrolysis of phosphoric monoesters, releasing

A ubiquitin ligase complex in which a cullin from the Cul1 sub

Description

#### 

### Differentially expressed gene sets

Rank GSZ p-value #all Geneset

34

78

27

37

5.67

5.42 5.08

-3.03

-2.91

2e-03

4e-03

4e-03

20

	Overex	pressed			
ich	1	15.03	0	247	Translatio TranslatissomeRibosome
ich	2	14.88	0	211	RibosomeRibosome
ich	3	13.22	0	144	RibosomeRib EsakarreyeteEsukaryotes
	4	12.42	0	24	Replication phytoletica phytoletical Republication Factors
ich	5	11.97	0	219	Cell growtDetlingtrollertithandDatellathicleCell cycle
	6	11.9	0	80	Cytoskele@ynoskleletotubulleisrotubules
ich	7	10.43	0	36	DNA replication
sele	8	10.15	0	97	RibosomeRib Aschaea Archaea
ults	9	9.8	0	217	Cell motilibell metilitration entration vitos kelleton
oduc	10	8.76	0	41	Replication
onei	11	7.21	0	67	RibosomeRibBanteeia-Bacteria
mpc	12	6.78	0	72	Ribosom Rib last wole on dulited collaborational a Shloroplast
inte	13	6.18	0	44	Replication phyteiReputation phyteiReputatione phyteiration Fac
	4 4		_		

-0	0.02	Ü					
Inderexpressed							
	-7.73	0e+00	140	Hormonelskigmating signitalithene signaling			
2	-6.96	0e+00	48	Transcription taketon taketon - WRKY			
3	-6.96	0e+00	73	Transcription faction factors Report EREBP			
ļ	-6.86	0e+00	64	Transcriptionnfactipition (althorstran@threptionnfactipition factors			
5	-5.51	0e+00	162	Plant spelllämsignedifig signalingpathlagenpathagetionteraction			
3	-4.86	0e+00	49	TranscriptToanfactipition MacCors - NAC			
7	-4.19	0e+00	170	Transcription factions at Transcription at Transcription (at the rest - Other 4 - C3HC4			
3	-4.13	0e+00	96	Transport <b>ēranaspalunt</b> ger-d <b>ētuallen</b> gs-caRofttensScat 1 to 6			
)	-3.81	1e-04	80	Transport Transport Systeming Tethering factors			
0	-3.8	1e-04	86	Signal traßisghadtionanso Caditionm-s Cantailing pightaviang pathway			
1	-3.71	1e-04	153	Plant-pathagenpathageiointeraction			
2	-3.69	3e-04	111	Hormonelsligmating sightallinggnallang signaling			
3	-3.49	7e-04	128	Ubiquitin <b>systemit</b> in <b>syintele</b> n Rin <b>syntyleg Birtyp tin</b> tgær type E3			
4	-3.4	9e-04	35	Mitophagly/litam/blrasgy factors			
5	-3.27	1e-03	51	Plant spe <b>ēlfām signedifig</b> sig <b>riadian din palmin</b> an rhythm			
6	-3.14	2e-03	18	Receptor Real epitor - Others			
7	2.4	20 02	02	Linid mathimiliametaBhimmolipBhimmotahaliamatahaliam			

Energy metabolismsynthesis

Exosome Ex Exos rema Exos teina loui root bina cotá localor reset adeblancer cells

Homologo de la complia de la c

TranscriptTomrfsactipation @2tdilse- G2-like

AutophagAutophagy - other

Protein - ProteinagAstorphagosationfprotetion proteins

