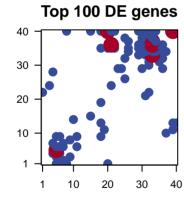
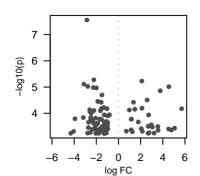
CabFra_freeze_r3

Global Summary

%DE = 0.43 # genes with fdr < 0.2 = 1955 (886 + / 1069 -) # genes with fdr < 0.1 = 248 (89 + / 159 -) # genes with fdr < 0.05 = 23 (9 + / 14 -) # genes with fdr < 0.01 = 0 (0 + / 0 -)

<FC> = 0 <p-value> = 0.19 <fdr> = 0.57





Differentially expressed genes

Rank ID		log(F	log(FC) fdr p-value		Description Metagene		F		
Overexpressed									
1	Vitvi09g00444	2.1	6e-06	0.02	5 x 9	Catalysis of a biochemical reaction at physiological temperatu	1		
2	Vitvi19g02038	4.55	1e-05	0.02	6 x 4	,			
3	Vitvi06g01714	3.77	1e-05	0.05	19 x 11		7		
4	Vitvi19g02040	2.58	3e-05	0.05	11 x 6		3		
5	Vitvi04g00566	1.36	4e-05	0.05	15 x 15		5		
6	Vitvi05g00696	2.12	6e-05	0.05	18 x 13		6		
7	Vitvi06g01713	5.7	7e-05	0.05	5 x 1		7		
8	Vitvi02g00128	1.48	7e-05	0.05	9 x 8	The chemical reactions and pathways involving fatty acids, ali	8		
9	Vitvi11g00303	0.98	8e-05	0.05	21 x 24		9		
10	Vitvi02g01344	2.72	1e-04	0.06	6 x 6	The component of a membrane consisting of the gene produc	1		
11	Vitvi04g01695	1.17	2e-04	0.06	10 x 14		i		
12	Vitvi04g01032 Vitvi08g00027	1.17	2e-04 2e-04	0.06	18 x 9	The component of a membrane consisting of the gene produc	1		
13	Vitvi19g00143	1.79	2e-04 2e-04	0.00	11 x 9	The component of a membrane consisting of the gene produc			
	Vitvi13g02077					The component of a membrane consisting of the gene produc	1		
14	_	2.97	3e-04	0.07	8 x 1	The part of the autoplasm that does not contain argonallas by	1		
15	Vitvi18g01223	2.69	3e-04	0.07	9 x 3	The part of the cytoplasm that does not contain organelles bu	1		
16	Vitvi11g01522	2.68	3e-04	0.07	7 x 6	A lipid bilayer along with all the proteins and protein complexe	1		
17	Vitvi08g01580	3.56	3e-04	0.07	6 x 2	Catalysis of the transfer of a glycosyl group from a UDP-suga	1		
18	Vitvi06g00772	3.06	3e-04	0.07	5 x 5	Out of the first o	1		
19	Vitvi18g00353	5.07	4e-04	0.07	5 x 6	Catalysis of a biochemical reaction at physiological temperatu	1		
20	Vitvi05g00822	2.06	4e-04	0.07	6 x 9		2		
Underexpressed									
1	Vitvi14g00321	-2.85	3e-08	0.02	31 x 34	The action of a molecule that contributes to the structural inte	1		
	Vitvi18g01866	-2.23	5e-06	0.02	31 x 36	Catalysis of the transfer of a group, e.g. a methyl group, glyco			
3	Vitvi17g00809	-3.12	8e-06	0.02	33 x 38	A membrane-bounded organelle of eukaryotic cells in which	3		
2 3 4 5 6 7	Vitvi06g00360	-2.77	9e-06	0.02	32 x 39	A membrane-bounded organelle of eukaryotic cells in which	4		
5	Vitvi02g00706	-2.27	1e-05	0.02	32 x 35	Binding to a nucleic acid.	5		
6	Vitvi01g01295	-2	1e-05	0.03	29 x 36	Binding to DNA of a specific nucleotide composition, e.g. GC-	5		
	Vitvi14g00337	-1.49	2e-05	0.05	40 x 13		7		
8	Vitvi06g01343	-1.87	4e-05	0.05	32 x 33	Any process that modulates the frequency, rate or extent of the	8		
9	Vitvi01g01757	-1.56	4e-05	0.05	29 x 35	The formation of a protein dimer, a macromolecular structure	9		
10	Vitvi04g00485	-1.34	6e-05	0.05	21 x 36	The component of a membrane consisting of the gene produc	1		
11	Vitvi11g00206	-1.54	7e-05	0.05	25 x 38		1		
12	Vitvi12g00428	-1.04	7e-05	0.05	32 x 22	A semiautonomous, self replicating organelle that occurs in vi	1		
13	Vitvi07g02249	-2.59	7e-05	0.05	33 x 34	Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, (1		
14	Vitvi14g00020	-2.21	8e-05	0.05	30 x 40		1		
15	Vitvi05g00838	-1.63	8e-05	0.06	31 x 21	A membrane-bounded organelle of eukaryotic cells in which	1		
16	Vitvi09g01471	-2.57	9e-05	0.06	32 x 36	Die Frank ATD automiter Elektrich automater im 1	1		
17	Vitvi07g00719	-2.45	1e-04	0.06	34 x 37		1		
18	Vitvi03g00287	-0.81	1e-04	0.06	24 x 29	Binding to a metal ion.	1		
19 20	Vitvi17g00957 Vitvi18g00641	-1.28	1e-04	0.06	18 x 35	Catalysis of the transfer of a group, e.g. a methyl group, glyco The contents of a cell excluding the plasma membrane and n	1		
20	vitvi 10900041	-0.97	1e-04	0.06	4 x 28	The contents of a cell excluding the plasma membrane and n			

p-values %DE = 0.43... \$(env, η)₀ 0.8 0.6 4 0.4 0.2

0.6

0.8

1.0

0.0

0.2

Differentially expressed gene sets

neset

	Overex	pressed			
eratu	1	6.46	0e+00	45	Galactose Gralatat bolism
	2	5.24	0e+00	48	Transcriptioaniscription talibrais - WRKY
	3	4.81	0e+00	49	TranscriptToanfactipitson NAC
	4	3.97	4e-05	162	Plant spellfansignedifig signalingpathlagenpathogotioninteraction
	5	3.84	8e-05	77	CarbohydCateborleytdbateismetaGalisatossGallatatbseismetabolism
	6	3.7	1e-04	88	Electroch Erleictab plotenitiall-publicenti alfadisipent éran [3] 2021 prs [TC:2]
	7	3.66	3e-04	58	Other am 10 the cials innetabilismeta 6 blitathio 6 Jutatta bolismeta bolism
ls, ali	8	3.4	9e-04	77	Pores ion Robrassriels (Ti@nt)els [TC:1]
cture	9	3.39	9e-04	51	BiosyntheBiosyfnsbesisdafrs@oetabarljsmetaBokismbiosynthesiosynthesi
roduc	10	3.32	1e-03	42	Tryptopha Tryptetabalism etabolism
of a n	11	3.24	1e-03	45	Valine leulvánlim anhaluisionle varidésoblegurainhatide gradation
roduc	12	3.13	2e-03	12	Enzyme -E6zayssel - Class I
roduc	13	3.09	2e-03	80	Transport Issustanort Systeming Tethering factors
	14	3.07	2e-03	24	Tropane pTpepietinepipretiplynielæredaptyaldidebædsaltutelesissynthesis
es bu	15	3.01	3e-03	39	beta-Alarbieta-mAlterbiotismetabolism
plexe	16	2.87	5e-03	27	Enzyme -E2:26/mie:ens:2e6rinigenstfegengonistrggenasus groups
-suga	17	2.84	5e-03	33	alpha-Linadhamae-biridlemetaboridismetabolism
	18	2.84	5e-03	34	Tyrosine rhetatiolismetabolism
eratu	19	2.83	6e-03	33	Carbohyd Catebote tabatës meta Brotis or sugarri most atjantis metabolis m
	20	2.82	6e-03	29	Other am 10 the cials ime tabidismetaBetis nala Betamaltatio is metabolism
	_			20	Ottor armodiabasining anadasining casotasina anadasining casotasining and anadasining casotasining and anadasining casotasining and anadasining casotasining and anadasining and anadasining and anadasining anada
	Under	expressed	d		
I inte	1	-10.04	0	18	Energy mētadogljsmetalBblistors yn Pleasis saymtheresias paroteimsa proteins
glyco	2	-9.95	0	18	Photosyn Pleasissy rathites is a paroteims proteins
hich	3	-8.93	0	47	Transportēramatatorige-catalogo-tīeterospoortoelerieron carriers
hich	4	-8.76	0	38	Photosyn Pleasesynthesis
	5 6	-8.24	0	78	Energy m EtadogljsmetaBblistosynPlessis synthesis
. GC-		-8.09	0	80	Cytoskelettynoskeletorubulleisrotubules
	7	-7.42	0	217	Cell motilißell MetjilitjatioRedjulationcydosktiletrynoskeleton
t of th	8	-7.1	0	211	Ribosom&Ribosome
cture	9	-7.09	0	10	Photosyn Priessies symutreissis (Photeissys Pelmoto(SP)750@ncthl (Pr76/00ydhab) rophyll
roduc	10	-6.58	0	247	TranslatiofranRibitisomeRibosome
	11	-6.33	0	206	Cell grow@beatingtrodestathandOddetathall-Cell wall
s in va ≔N, (12	-5.5 -5.15	0	144 40	RibosomeRib EsukamyoteEsukaryotes Transport Esukakaryote Siyaytenkoid Thaybektoid bartheviang pathway
-IN, (13				
hich	14 15	-5.08	0	97	RibosomeRibAschaeea Archaea
HIGH	16	-4.92 -4.74	0	113 134	ExosomeExEsossemaEpoosteinalqrirodeinectálocalmeetaletlancer cells Hormonelstamating signalingsignaling signaling
impo	17	-4.74 -4.57	0	67	RibosomeRibBanteeia-Bacteria
mpc	18	-4.57 -4.56	0	41	Porphyrin Roestalycitism etabolism
glyco	19	-4.54	0	11	Transcription factions ablier - GRF
5.,00	19		5		Out and the best of the second

