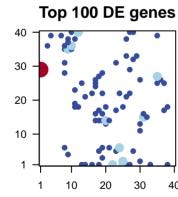
CabFra_acclim_r3

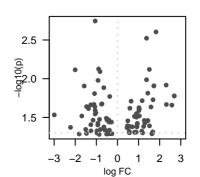
Global Summary

%DE = 0 # genes with fdr < 0.2 = 0 (0+/0 -) # 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> = 0.49 <fdr> = 1

Portrait T 40 30 20 10 1 10 20 30 40 1





Differentially expressed genes

fdr

Description

log(FC)

Vitvi07g0147€ -1.06

Vitvi14g01657 -2.99

0.029

0.029

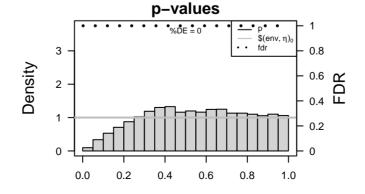
Rank

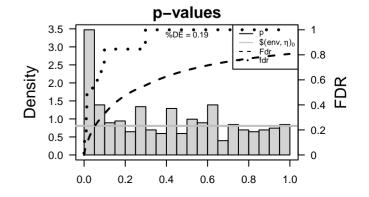
	 ID	9(p-va	lue	Meta	igene	rtanit	002	p	"an	
Overexpressed							Overexpressed				
1	Vitvi01g01907	1.83	0.002	1	38 x 18	The membrane surrounding a cell that separates the cell from	1	8.49	0.000	18	Energy mētæbrgljsmmetalBbbistors.ynfPlessiossymttéressispanoteimsa proteins
2	Vitvi03g00392	1.38	0.003	1	27 x 22	Binding to a heme, a compound composed of iron complexed	2	8.47	0.000	18	Photosyn Pleasies y rathies is a proteins a proteins
3	Vitvi05g00733	1.51	0.008	1	7 x 39	The component of a membrane consisting of the gene produc	3	8.1	0.000	47	Transporterarestatorige-rotatenisgo-riteterospoortoelerideron carriers
4	Vitvi15g01216	1.38	0.010	1	19 x 16		4	5.79	0.000	38	Photosyn Pleasis synthesis
5	Vitvi08g02147	2.31	0.012	1	35 x 27	The membrane surrounding a cell that separates the cell from	5	5.64	0.000	217	Cell motilitiell inetiliulation edulation cytoskelleton
6	Vitvi10g02111	1.72	0.012	1	20 x 14		6	5.58	0.000	78	Energy metæbrgljsmetalBblittosyntPlessissynthesis
7	Vitvi00g01858	1.72	0.012	1	20 x 14		7	5.12	0.000	10	Photosyn (Phecetos spyroutheies is fortouteins ys felmouto(spysocenochil (1276/00) y dhato) rophyll a)
8	Vitvi08g01470	1.44	0.015	1	10 x 35	A membrane-bounded organelle of eukaryotic cells in which	8	4.78	0.000	80	Cytoskele@ntoskeletotubulkeisrotubules
9	Vitvi00g01655	2.69	0.017	1	12 x 40		9	4.67	0.000	11	Transcriptioanfactipition (albifors - GRF
10	Vitvi10g02094	2.69	0.017	1	12 x 40		10	3.08	0.002	28	Transcriptioanfactipition Motions - MTERF
11	Vitvi16g01740	1.68	0.019	1	20 x 13		11	2.72	0.008	18	Transcriptioanfactipition faitfors - ARF
12	Vitvi07g00439	1.17	0.019	1	18 x 14	The component of a membrane consisting of the gene produc	12	2.71	0.008	10	PeptidaseRepridaseisiaons inhiibirohs A1FapreipsiA fapreipsin family
13	Vitvi18g01696	0.65	0.020	1	26 x 33		13	2.68	0.008	17	Kinase – KRAdséamiliyAK family
14	Vitvi17g00609	2.32	0.022	1	19 x 14	Catalysis of the hydrolysis of any ester bond.	14	2.63	0.009	219	Cell grow (Bealing fooler tithan o Cottellant lincle Cell cycle
15	Vitvi15g00396	2.58	0.022	1	37 x 25	Catalysis of the transfer of a methyl group to the oxygen atom	15	2.63	0.010	31	Fatty acidFaithsyntthdelsicsynthesis
16	Vitvi19g02316	1.59	0.023	1	21 x 14		16	2.63	0.010	101	Starch and tauchosetarbelismetabolism
17	Vitvi06g00650	1.02	0.024	1	28 x 32	The component of a membrane consisting of the gene produc	17	2.61	0.010	100	Plant spellitansignædifig sigfilaling delvizivpmdætelopment
18	Vitvi17g01204	0.59	0.024	1	25 x 18	Binding to a protein.	18	2.6	0.010	41	Porphyrin Poephalyoitismetabolism
19	Vitvi12g00211	1.03	0.025	1	8 x 31	The component of a membrane consisting of the gene produc	19	2.6	0.010	75	Mitochon delite de de mandi i pat locana acci pita mas la tieb trá anastantis on factors
20	Vitvi02g00460	1.01	0.026	1	30 x 26		20	2.57	0.011	40	Transport Transport Stylastenkoid Tlaytetkinig partheniang pathway
Underexpressed Underexpressed											
1	Vitvi18g00339	-1.06	0.002	1	30 x 11	Binding to a zinc ion (Zn).	1	-8.39	0e+00	48	Transcriptioanfactipation taleton - WRKY
2	-		0.002	1	12 x 18		2	-7.75	0e+00	162	Plant spe@liansispedifig signalitepatRizgetapiatecogeiointeraction
3	Vitvi18g02077		0.008	1	18 x 1	Binding to ADP, adenosine 5'-diphosphate.	3	-5.73	0e+00	49	TranscriptToarnfactiontson MacCors - NAC
4	Vitvi17g00143		0.008	1	25 x 2	Binding to a zinc ion (Zn).	4	-5.19	0e+00	153	Plant-pathagenpiathagenionnteraction
5	Vitvi07g00362		0.011	1		A semiautonomous, self replicating organelle that occurs in va	5	-4.94	0e+00	26	Flavonoid Flavosynttitules is synthesis
6	Vitvi03g01727	-1.57	0.012	1	38 x 1	Binding to a zinc ion (Zn).	6	-4.82	0e+00	140	Hormonelstigmating signitalitene sittmating signaling
7	Vitvi19g02014		0.013	1	23 x 5	A membrane-bounded organelle of eukaryotic cells in which	7	-4.74	0e+00	73	TranscriptToanfactiontion AdetoEsREMP2 EREBP
8	Vitvi11g00953	-1.09	0.016	1	11 x 18	The chemical reactions and pathways resulting in the formatic	8	-4.72	0e+00	45	Galactos@alatatbs@smetabolism
9			0.017	1	19 x 22	The membrane surrounding a cell that separates the cell from	9	-4.2	0e+00	77	Pores ion Robrassriels (Ti@nth)els [TC:1]
10	Vitvi07g02170		0.021	1	18 x 27		10	-3.84	8e-05	58	Other am lithecials immetalcidlismetalciblismthie (clutættabolismetabolism
11	-		0.021	1	19 x 6	A lipid bilayer along with all the proteins and protein complexe	11	-3.8	1e-04	26	Glycosyltr@inysfessylteenstreyndrissepholblycolmople.obile molecule
12	Vitvi15g01106		0.022	1	19 x 28		12	-3.7	1e-04	15	StilbenoidSdillaeylloèghtaiaoytheptagiorigearothgiosgeatolelsissynthesis
13	Vitvi18g01254		0.022	1	28 x 5	A membrane-bounded organelle of eukaryotic cells in which	13	-3.67	3e-04	15	Chaperon@hapts@n7@ ≠ DNS.R7K0 / DNAK
14	Vitvi13g02359		0.023	1	1 x 29	A membrane-bounded organelle of eukaryotic cells in which	14	-3.56	5e-04	24	Tropane pilpæpiadneepiepæriplyniedianædadvanldidebiadsgitatidebiassynthesis
15	Vitvi18g00335		0.023	1	16 x 1	The component of a membrane consisting of the gene produc	15	-3.39	9e-04	71	Exosome Exosomes for the first
16	Vitvi01g00306 Vitvi05g00618		0.024	1	13 x 1	A membrane-bounded organelle of eukaryotic cells in which	16	-3.31	1e-03	64 11	Transcriptionarfactipition (atterstan@triptionarfactipition factors Biosynthe@iscoyintheesisclafrageoetataculismeta@blastriosy/htheesiscsynthesis
17	vitvioagoo618	-1.06	0.026	1	30 x 2	A membrane-bounded organelle of eukaryotic cells in which	17	-3.19	2e-03	17	DIOSYTH TEXNOSYN ISBESTISCAN SECURIALIAN I SITTLE CARBON SIDIOS SYNDRESIS SYNTHESIS

22 x 1 The contents of a cell excluding the plasma membrane and n

19 x 3 The component of a membrane consisting of the gene product

1 x 29 Binding to a heme, a compound composed of iron complexed





Hormone Hogmating sightaling nathasignoalang signaling

Protein - Poloagierer@hapedrateedraetbipteedgau(@bl/A)gy (CMA)

Differentially expressed gene sets

Rank GSZ p-value #all Geneset

-3.17 2e-03

-3.13 2e-03

2e-03

-3.08

56

38