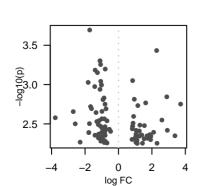
CabFra_warm_r1

Global Summary

%DE = 0.24# 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> = 0.3 < fdr > = 0.76

Portrait Top 100 DE genes 40 30 -30 20 · 20 10 -10 10 20 30



10

30

20

Differentially expressed genes

fdr

Description

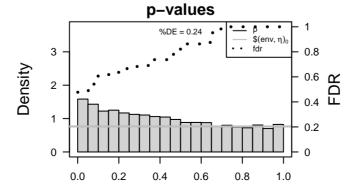
log(FC)

Vitvi10g01099 -0.74 2e-03 0.5

2e-03 0.5

Rank

	Itai		109(1		luc	Moto	ann	Italik	002	p value	#aii	Oene
		ID		p-va	iue	Meta	gene					
	Over	rexpressed						Overexp	ressed			
	1	Vitvi03g00432	2.28	4e-04	0.5	35 x 25		1	15.09	0	247	Translatio
	2	Vitvi18g00834	0.85	9e-04	0.5	35 x 19	The part of the cytoplasm that does not contain organelles bu	2	15.02	0	211	Ribosom
	3	Vitvi04g02120	2.89	1e-03	0.5	22 x 1		3	13.52	0	144	Ribosom
	4	Vitvi05g00098	0.95	2e-03	0.5	34 x 21	The action of a molecule that contributes to the structural inte	4	10.67	0	219	Cell grow
	5	Vitvi03g00380	1.63	2e-03	0.5	35 x 28		5	10.47	0	97	Ribosom
	6	Vitvi14g00940	3.72	2e-03	0.5	40 x 23		6	10.39	0	24	Replication
	7	Vitvi08g01432	1.16	2e-03	0.5	36 x 21	A membrane-bounded organelle of eukaryotic cells in which	7	10.29	0	80	Cytoskele
	8	Vitvi05g01254	0.91	3e-03	0.5	32 x 21	The action of a molecule that contributes to the structural inte	8	9.18	0	36	DNA repl
	9	Vitvi08g01478	2.6	3e-03	0.5	40 x 23	The component of a membrane consisting of the gene produc	9	7.99	0	217	Cell moti
	10	Vitvi07g00120	0.87	3e-03	0.5	34 x 21	A transcription coregulator activity that represses or decrease	10	7.28	0	41	Replication
	11	Vitvi08g01778	1.28	3e-03	0.5	36 x 22	The action of a molecule that contributes to the structural inte	11	7.02	0	67	Ribosom
	12	Vitvi08g01397	1.55	3e-03	0.5	34 x 23	The action of a molecule that contributes to the structural inte	12	6.77	0	72	Ribosom
	13	Vitvi04g01384	0.85	3e-03	0.5	33 x 20	Catalysis of a biochemical reaction at physiological temperatu	13	5.55	0	34	Peptidase
	14	Vitvi05g01594	0.84	3e-03	0.5	25 x 14	The action of a molecule that contributes to the structural inte	14	5.27	0	78	Energy m
	15	Vitvi08g01431	0.83	4e-03	0.5	34 x 23		15	5.19	0	18	Energy m
	16	Vitvi02g00174	2.92	4e-03	0.5	37 x 28		16	5.12	0	44	Replication
	17	Vitvi08g01256	1.06	4e-03	0.5	37 x 21	The contents of a cell excluding the plasma membrane and n	17	4.9	0	113	Exosome
	18	Vitvi09g00221	1.25	4e-03	0.5	37 x 22		18	4.82	0	18	Photosyn
	19	Vitvi05g00084	2.1	4e-03	0.5	39 x 23	A membrane-bounded organelle of eukaryotic cells in which	19	4.63	0	38	Photosyn
	20	Vitvi01g00166	1.05	4e-03	0.5	35 x 20	Catalysis of the hydrolysis of internal, alpha-peptide bonds in	20	4.39	0	47	Transpor
	Unde	Inderexpressed						Underex	pressed			
	1	Vitvi14g00025	1 72	2e-04	0.5	1 x 29		1	-6.61	0e+00	140	Hormone
	2	Vitvi00g01057		5e-04	0.5	1 x 24		2	-6.23	0e+00	73	Transcrip
	3	Vitvi07g03117		5e-04	0.5	1 x 24		3	-5.88	0e+00	49	Transcrip
	4	Vitvi01g00062		6e-04	0.5	6 x 16	A lipid bilayer along with all the proteins and protein complexe	4	-5.05	0e+00	64	Transcrip
	5	Vitvi08g00140		6e-04	0.5	15 x 21	The process of creating protein oligomers, compounds compounds	5	-4.16	0e+00	111	Hormone
	6	Vitvi05g01401	-1.39	7e-04	0.5	1 x 20	The aggregation, arrangement and bonding together of one o	Ğ	-4.09	0e+00	35	Mitophag
	7	Vitvi01g00478	-1.26	7e-04	0.5	4 x 29	The component of a membrane consisting of the gene produc	7	-4.09	0e+00	170	Transcrip
	8	Vitvi14g01718	-1.06	9e-04	0.5	4 x 19	A lipid bilayer along with all the proteins and protein complexe	8	-3.79	1e-04	45	Galactos
	9	Vitvi08g02210	-1.81	9e-04	0.5	11 x 19	Catalysis of an oxidation-reduction (redox) reaction, a reversi	9	-3.73	1e-04	77	Carbohyo
	10	Vitvi00g01739		1e-03	0.5	4 x 27		10	-3.49	7e-04	31	Autophag
	11	Vitvi04g02290		1e-03	0.5	4 x 27		11	-3.48	7e-04	48	Transcrip
	12	Vitvi16g01791		1e-03	0.5	4 x 33	The lipid bilayer surrounding the endoplasmic reticulum.	12	-3.44	8e-04	20	Protein –
	13	Vitvi14g00891		1e-03	0.5	7 x 36	A membrane-bounded organelle of eukaryotic cells in which	13	-3.43	8e-04	11	Biosynthe
	14	Vitvi14g01425	-0.86	1e-03	0.5	4 x 27	An thiol-dependent isopeptidase activity that cleaves ubiquitin	14	-3.35	1e-03	45	Valine le
	15		-0.93	2e-03	0.5	7 x 29	A chlorophyll–containing plastid with thylakoids organized into	15	-3.17	2e-03	51	Plant spe
	16	Vitvi15g00648	-0.8	2e-03	0.5		Any process involved in the conversion of a primary ribosoma	16	-3.17	2e-03	96	Transpor
	17 18	Vitvi11g00927 Vitvi11g00574		2e-03 2e-03	0.5	5 x 18 1 x 34	The contents of a cell excluding the plasma membrane and n	17 18	-3.14 -3.13	2e-03 2e-03	29 128	Caroteno



Differentially expressed gene sets

	Rank	GSZ	p-value	#all	Geneset
	Overexpi	ressed			
	1	15.09	0	247	Translatio T ran slatiso meRibosome
es bu	2	15.02	0	211	RibosomeRibosome
	3	13.52	0	144	RibosomeRib EstkameyeteEsukaryotes
I inte	4	10.67	0	219	Cell grow@catingtroutertithandCatellactricleCell cycle
	5	10.47	0	97	RibosomeRibAschaea Archaea
	6	10.39	0	24	Replication politication political republication Factors
hich	7	10.29	0	80	Cytoskele@anoskeletotubulkisrotubules
l inte	8	9.18	0	36	DNA replication
roduc	9	7.99	0	217	Cell motilithell intettilitetion englation mydfoskelleton
ease	Ĭ0	7.28	0	41	Replication Replication Replication
l inte	11	7.02	0	67	RibosomeRibBauteeia- Bacteria
l inte	12	6.77	0	72	RibosomeRiblesteroleoned/lite/d2lblesterolast
eratu	13	5.55	0	34	PeptidaseSeantidasseisbianors in Hibitoins S1Ramily S10
l inte	14	5.27	0	78	Energy metæbrglijsmetæBbüsosyntPleasiesynthesis
	15	5.19	0	18	Energy m EtæbrglismetaBbötsosyntPlecsiosaymteresa sp aroteims a proteins
	16	5.12	0	44	Replication phytheir epublishing religion Fact
nd n	17	4.9	0	113	ExosomeExExosremaEproxeinalquirodeinactálocarrecatalettancer cell
	18	4.82	0	18	Photosyn Pleasies synathlesis a-paroteins proteins
hich	19	4.63	0	38	Photosyn tPleasis synthesis
ds in	20	4.39	0	47	Transport@rarestaturter-datedoport@etercspoortoelerieron carriers
	Underex	nraeead			
	1	-6.61	0e+00	140	Hormone Hogynating signthlytegne Sittyndeling signaling
		-6.23	0e+00	73	Transcription faction faction factors REBP2
	3	-5.88	0e+00	49	Transcription MACOrs - NAC
plexe	2 3 4	-5.05	0e+00	64	TranscriptTownfactipation CatherstranCathrighttownfactipation factors
omp:	5	-4.16	0e+00	111	Hormonelskingmatting sightalAnsignallang signaling
ne o	Ğ	-4.09	0e+00	35	Mitophagly/liamphrasgy factors
roduc	7	-4.09	0e+00	170	TranscriptToanfactipition Catherszf-OtheCaf-C3HC4
plexe	8	-3.79	1e-04	45	Galactos@alatatbs@smetabolism
versi	9	-3.73	1e-04	77	CarbohydCateborteytalbattësmmetaGallisottoseGralletatbosësmmetabolism
	10	-3.49	7e-04	31	AutophagAutopthegy – other
	11	-3.48	7e-04	48	TranscriptToenfsactipation Yal@KKYS - WRKY
	12	-3.44	8e-04	20	Protein - ProteinagAstorpeagosatroenfprotetros proteins
hich	13	-3.43	8e-04	11	BiosyntheBiosoyInsteesiosdafrogenetadamljometa@BlAstriessynthe
quitii	14	-3.35	1e-03	45	Valine leul/datieneuthetuisionleuaridesobeguraithetidegradation
d intc	15	-3.17	2e-03	51	Plant speellian signedifig signiatian dian Chrystotian rhythm
soma	16	-3.17	2e-03	96	Transporterarate/outree-obtailers-caftoftters6cat 1 to 6
	17	-3.14	2e-03	29	Carotenoi@dxintsyntilulesissynthesis
nd n	18	-3.13	2e-03	128	Ubiquitin sylpitemitin sylpitem Ringingheng Birtype friger type E3
e mo	19	-3.13	2e-03	92	Lipid metalipsidismetaGb/issenolipiddyosenalipsidismetabolism
	20	-3.11	2e-03	20	Transport and spatial books of the light at the Regulation of the Company of the

