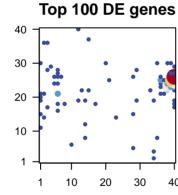
Tocai_warm_r3

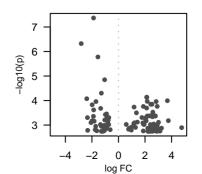
Global Summary

%DE = 0.22 # genes with fdr < 0.2 = 19 (11 + /8 -)# genes with fdr < 0.1 = 2 (0 + /2 -)# genes with fdr < 0.05 = 2 (0 + /2 -)# genes with fdr < 0.01 = 1 (0 + / 1 -)

<FC> = 0< p-value > = 0.27< fdr > = 0.78

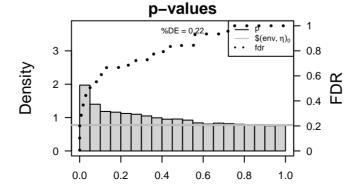
Portrait 40 30 -20 · 10 -10 20 30





Differentially expressed genes

Rank ID		log(F	og(FC) fdr p–value		Meta	Description gene		
Overexpressed								
1	Vitvi00g00967	2.13	7e-05	0.2	38 x 23			
2 3 4 5 6 7	Vitvi10g02198	2.13	7e-05	0.2	38 x 23			
	Vitvi10g01388	3.68	1e-04	0.2	40 x 26			
	Vitvi03g00692	2.17	1e-04	0.2	40 x 19	Catalysis of the transfer of an acyl group, other than amino-a		
	Vitvi07g01298	2.84	1e-04	0.2	40 x 23	A membrane-bounded organelle of eukaryotic cells in which		
	Vitvi05g01478	2.52	1e-04	0.2	35 x 30	A lipid bilayer along with all the proteins and protein complexe		
	Vitvi15g00710	2.43	1e-04	0.2	37 x 25	Binding to a zinc ion (Zn).		
8	Vitvi16g02059	2.92	2e-04	0.2	40 x 22	Binding to a metal ion.		
9	Vitvi01g01028	1.88	2e-04	0.2	38 x 22	A membrane-bounded organelle of eukaryotic cells in which		
10 11 12 13	Vitvi14g00052	1.18	2e-04	0.2	23 x 14	Binding to a metal ion.		
	Vitvi02g00051	2.12	2e-04	0.2	36 x 25	A lipid bilayer along with all the proteins and protein complexe		
	Vitvi05g00084	2.59	3e-04	0.2	39 x 23	A membrane-bounded organelle of eukaryotic cells in which		
	Vitvi07g00542	1.35	3e-04	0.2	29 x 28			
14	Vitvi10g01894	2.58	4e-04	0.2	40 x 24	Any process that results in a change in state or activity of a ce		
15	Vitvi14g01926	2.36	4e-04	0.2	39 x 30	The formation of a protein dimer, a macromolecular structure		
16	Vitvi07g02613	2.18	4e-04	0.2	36 x 25	The formation of a protein dimer, a macromolecular structure		
17	Vitvi10g00131	2.49	4e-04	0.2	39 x 24	Binding to a protein.		
18	Vitvi00g00761	2.78	4e-04	0.2	39 x 25			
19	Vitvi10g02256	2.78	4e-04	0.2	39 x 25	The part of a cell encompassing the cell cortex, the plasma m		
20	Vitvi11g00028	2.56	5e-04	0.2	39 x 24	Binding to ATP, adenosine 5'-triphosphate, a universally impo		
Underexpressed								
1	Vitvi13g01251	-1.88	4e-08	0.006	28 x 5	Any process that modulates the frequency, rate or extent of $\boldsymbol{\alpha}$		
2	Vitvi14g00291	-2.81	5e-07	0.017	2 x 36	Binding to ATP, adenosine 5'-triphosphate, a universally impo		
3	Vitvi17g01240	-1.55	2e-06	0.170	1 x 20			
4 5 6 7	Vitvi13g01840	-1.04	1e-05	0.170	6 x 26	The component of a membrane consisting of the gene produc		
5	Vitvi11g01445	-1.29	5e-05	0.170	12 x 19	The component of a membrane consisting of the gene produc		
6	Vitvi05g00675	-2.39	8e-05	0.170	1 x 11	A lipid bilayer along with all the proteins and protein complexe		
7 8 9 10 11 12 13 14	Vitvi05g01687	-1.7	1e-04	0.170	8 x 18	The part of the cytoplasm that does not contain organelles bu		
	Vitvi03g01524	-1.98	1e-04	0.174	12 x 40	The component of a membrane consisting of the gene produc		
	Vitvi10g00756	-1.34	2e-04	0.225	1 x 21	A membrane-bounded organelle of eukaryotic cells in which		
	Vitvi13g02565	-1.87	2e-04	0.225	3 x 28 6 x 27	A linid bilayer along with all the proteins and protein complays		
	Vitvi04g01577 Vitvi04g00585	-0.9 -0.99	4e-04 4e-04	0.225 0.225	6 X 27 20 X 30	A lipid bilayer along with all the proteins and protein complexe Binding to a metal ion.		
	Vitvi04g00303	-1.89	4e-04 4e-04	0.225	34 x 4	briding to a motal ion.		
	Vitvi09g00056	-0.86	5e-04	0.225	15 x 37	A membrane-bounded organelle of eukaryotic cells in which		
13	Vitvi11g00720	-2.34	5e-04	0.225	2 x 14	Catalysis of the transfer of an acyl group, other than amino-a		



6 x 28

7 x 26

6e-04 0.252 6 x 21 The chemical reactions and pathways involving carbohydrates

The membrane surrounding a cell that separates the cell from

The component of a membrane consisting of the gene produc

5e-04 0.252

7e-04

6e-04 0.252

7e-04 0.252 3 x 36

Vitvi05g01135 -1.03

Differentially expressed gene sets

	Rank	GSZ	p-value	#all	Geneset
	Overexp	ressed			
	1	13.13	0	211	Ribosome Ribosome
	2	13.01	0	247	Translatio Tran Rilatissome Ribosome
	3	12.98	0	219	Cell grow@catingtroutertithandOatellathjicleCell cycle
-a	4	12.48	0	144	RibosomeRib EsukannyoteEsukaryotes
ch	5	12.38	0	80	Cytoskele@ntoskeletotubulkisrotubules
exe	6	11.81	0	24	Replication application posite in epocha and polication fractors
	7	10.38	0	217	Cell motilible li metilityation egulation egubakti letonoskeleton
	8	10.16	0	36	DNA replication
ch	9	9.32	0	97	RibosomeRibAsolnaea- Archaea
	10	9.28	0	41	Replication
эхе	11	6.92	0	44	Replication and a physical republishment of the Rep
ch	12	6.2	0	34	Peptidaseseputidaseisbianus in Hibitohs S1Ramily S10
	13	5.52	0	27	MismatchMespaiatch repair
Cŧ	14	5.52	0	37	Homologo de la metagrobis naticombination
re	15	5.05	0	113	Exosome Ex Exosomema Exosoteima loprocoteima cotá locatorica tatella ncer cells
re	16	5.03	0	66	Exosome Ex Escos cema Epocoste in a lopino lacitote o character cretta ncer cells
	17	4.87	0	67	RibosomeRibBanteeia-Bacteria
	18	4.71	0	72	RibosomeRibbstoroleondMitodoDolodojalaShloroplast
n	19	4.46	0	29	Base exclision repair
рс	20	4.13	0	25	Replication Repulidational and Bassaiexe Biassere poission repair
	Underex	pressed	1		
CI	1	-6.89	0e+00	49	Transcription faction factors - NAC
рс	2	-6.61	0e+00	73	Transcription factions And to EREBP EREBP
	3 4	-6.6	0e+00	140	Hormonel signating signaling signaling
duc	4	-6.12	0e+00	48	TranscriptToenfactipitson taleters - WRKY
duc	5	-4.83	0e+00	64	TranscriptToanfactipition CatherstranOstrieptionnfactipition factors
exe	6	-4.28	0e+00	92	Lipid met alipiidismetaGolisenolipiidiyovenalipiidism etabolism
bu	7	-3.89	8e-05	29	Caroteno i dani utay muti dela io synthesis
duc	8	-3.82	1e-04	162	Plant spe Elfansigradifig sigNaling atRoagetnpiatecagetionnteraction
ch	9	-3.74	1e-04	170	Transcription/scutiputson Catherszf-Othec4f-C3HC4
	10	-3.51	6e-04	153	Plant-patRagenpaterageio interaction
exe	11	-3.46	8e-04	55	Glycerolip (http://www.matapoitismetabolism
	12	-3.26	1e-03	86	Signal tra6sghadtioanscCaltioum-sCalailing sigthaling pathway
sh	13	-3.19	2e-03	77	CarbohydCatebonetabatësmetaGalisatoseGalletatboësmetabolism
:h	14	-3.03	2e-03	35	Mitophag Wifa ophragy factors

-2.88 5e-03

-2.68

-2.67

-2.67

-2.65

-2.65

8e-03

8e-03

8e-03

9e-03

16

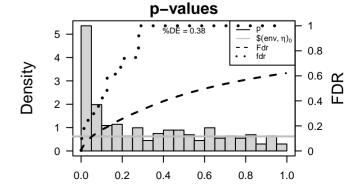
18

12

31

74

238



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Valine leuk/arlien en heluisionle varid ei subbeque idratide gradation

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Enzyme -E2izlyn@dyc@s4ltn@dysfessystessnsferases