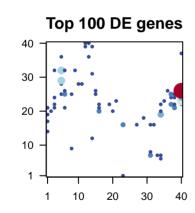
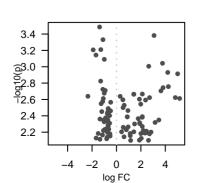
Tocai_warm_r2

Global Summary

%DE = 0.15 # 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> = 0.33<fdr> = 0.85





Differentially expressed genes

Rank

Vitvi17g00435 -0.47

Vitvi05g00559 -1.26

Vitvi17g00298 -0.68

Vitvi06g00973 -0.67

Vitvi13g01414 -1.2

3e-03 0.7

3e-03 0.7

4e-03 0.7

	ID			p-value		Metagene			
Overexpressed									
1	Vitvi08g01789	3.08	4e-04	0.7	40 x 22	The component of a membrane consisting of the gene produc			
2	Vitvi12g00722	3.77	9e-04	0.7	40 x 25	Binding to nicotinamide-adenine dinucleotide phosphate, a c			
3 4 5 6 7	Vitvi14g02932	2.64	1e-03	0.7	40 x 24				
	Vitvi11g01224	4.2	1e-03	0.7	40 x 26	Catalysis of the transfer of an acyl group, other than amino-a			
	Vitvi11g01227	5.01	1e-03	0.7	40 x 26	Catalysis of the transfer of an acyl group, other than amino-a			
	Vitvi18g01488	4.25	2e-03	0.7	40 x 26	The cell membranes and intracellular regions in a plant are co			
	Vitvi18g02928	3.82	2e-03	0.7	40 x 26	The cell membranes and intracellular regions in a plant are co			
8	Vitvi14g00338	3.64	2e-03	0.7	40 x 26	Catalysis of the reaction: 3-dehydroquinate = 3-dehydroshik			
9	Vitvi06g00928	2.12	2e-03	0.7	37 x 25	The directed movement of malate into, out of or within a cell,			
10	Vitvi00g00969	1.42	2e-03	0.7	37 x 22				
11	Vitvi10g02201	1.42	2e-03	0.7	37 x 22	A membrane-bounded organelle of eukaryotic cells in which			
12	Vitvi03g00348	0.3	2e-03	0.7	21 x 23	Binding to GTP, guanosine triphosphate.			
13	Vitvi11g01222	4.82	2e-03	0.7	40 x 26	Catalysis of the transfer of an acyl group, other than amino-a			
14	Vitvi09g01641	2.71	2e-03	0.7	40 x 23				
15	Vitvi18g02927	5.17	2e-03	0.7	40 x 26	The cell membranes and intracellular regions in a plant are co			
16	Vitvi08g02384	1.88	2e-03	0.7	38 x 21				
17	Vitvi13g02037	0.53	3e-03	0.7	27 x 16	The component of a membrane consisting of the gene produc			
18	Vitvi01g00095	2.38	3e-03	0.7	38 x 25	The component of a membrane consisting of the gene produc			
19	Vitvi04g01666	1.99	3e-03	0.7	37 x 25	Binds to and stops, prevents or reduces the activity of an enz			
20	Vitvi06g01731	0.63	3e-03	0.7	32 x 16				
Underexpressed									
1	Vitvi10g00457	-1.38	3e-04	0.7	5 x 29	Binding to ATP, adenosine 5'-triphosphate, a universally impo			
	Vitvi13g01536	-1.11	5e-04	0.7	12 x 39	Any process involved in the conversion of a primary small nuc			
2	Vitvi12g02441	-1.28	6e-04	0.7	34 x 6	Binding to a zinc ion (Zn).			
4	Vitvi00g01382	-1.91	6e-04	0.7	15 x 26				
5 6 7	Vitvi18g00534	-1.68	7e-04	0.7	6 x 21	Binding to ATP, adenosine 5'-triphosphate, a universally impo			
6	Vitvi09g01243	-1	8e-04	0.7	11 x 28	Any process that modulates the frequency, rate or extent of tr			
	Vitvi05g01379	-1.29	1e-03	0.7	12 x 40	A membrane-bound cytoplasmic organelle of the endomemb			
8 9 10 11 12 13	Vitvi06g01165	-1.12	2e-03	0.7	5 x 29	Binding to a protein.			
	Vitvi16g01556	-0.92	2e-03	0.7	6 x 25	A membrane-bounded organelle of eukaryotic cells in which			
	Vitvi07g02101	-1	2e-03	0.7	31 x 7				
	Vitvi02g00250	-2.34	2e-03	0.7	1 x 14	Catalysis of the transfer of a glycosyl group from one compou			
	Vitvi08g00862	-1.08	2e-03	0.7	2 x 20	The component of a membrane consisting of the gene produc			
	Vitvi05g01703	-1.13	3e-03	0.7	14 x 12	Binding to a protein.			

16 x 20 The chemical reactions and pathways resulting in the breakdo

34 x 7 A membrane-bounded organelle of eukaryotic cells in which

31 x 8 An thiol-dependent isopeptidase activity that cleaves ubiquiting

16 x 20 A membrane-bounded organelle of eukaryotic cells in which

3 x 32 A lipid bilayer along with all the proteins and protein complexe

3 x 24 A membrane-bounded organelle of eukaryotic cells in which

The directed movement of proteins in a cell, including the movement

Description

Differentially expressed gene sets

	Rank	GSZ	p-value	#all	Geneset
	Overexp	ressed			
duc	1	12.17	0	211	RibosomeRibosome
a cı	2	11.43	0	247	Translatio Tran Ribitiso me Ribosome
	3	11.42	0	80	Cytoskele@moskeletotubulleisrotubules
-a	4	11.23	0	219	Cell grow@eatingtrodertithandOatellathicleCell cycle
-a	5	10.21	0	24	Replication application positive in epocha and initiation fractors
cc	6	10.2	0	144	RibosomeRib Esukanneyet eEsukaryotes
e cc	7	8.23	0	217	Cell motilitigell in netjiid ation network net
niki	8	8.23	0	97	RibosomeRib Aschaea Archaea
ell, c	9	8.2	0	36	DNA replication
	10	7.22	0	34	PeptidaseReputidassesbitanus in Hibitohys S1Ramily S10
ch	11	6.77	0	41	Replication Reprind artipaian CD hydrate plication
	12	6.7	0	67	RibosomeRibBanteeia-Bacteria
-a	13	6.04	0	72	RibosomeRibbstoroteon@lite/@bloodojalaShloroplast
	14	5.35	0	113	Exosome Ex Excusum a Epocuteina lopino de localo meent adelbancer cells
e cc	15	4.71	0	81	Enzyme -E4z2yn@arb4n2-oQqdeonlyoxyegen lyases
	16	4.68	0	31	Biosynthe Biosynthe is is sophamic ses ophalar percetada olites
duc	17	4.4	0	66	Exosome Ex Escos com a Epocoste in a log inblacitote o Calhaded ex edian cer cells
duc	18	4.39	0	44	Replication phytheiReplication Factors
nz	19	4.3	0	22	Fatty acidFelttyngastiobelongation
	20	4.26	0	65	Phagosor Rhagosome
	Underex	pressed	,		
прс	1	-5.6	0e+00	73	Transcriptionniscotipution And DEREBP2 EREBP
nuc		-4.9	0e+00	140	Hormone Hormaning sigirthlyingne Sittmahing signaling
	2 3 4 5 6 7	-3.86	8e-05	170	TranscriptToanfactipition Cathers:f-OtheC4f-C3HC4
	4	-3.85	8e-05	35	Mitophagl///famphragy factors
прс	5	-3.83	8e-05	12	TranscriptToanfactipttion Carphaens Offthaous zf-b box
f tr	6	-3.7	1e-04	64	TranscriptToanfactipttion CattlerstranCathripttioanfactipttion factors
mb		-3.62	3e-04	27	Regulator Refgorlato hon drital dhog en esis
	8	-3.51	6e-04	151	RNA poly RNA sellyrsystem II system
ch	9	-3.32	1e-03	116	RibosomeRitionsemesIsieg@nees660S Paeticl@S particles
	10	-3.27	1e-03	111	Hormonelstigmating sightalingignalibals signaling
oou	11	-3.26	1e-03	26	Transcription factipition factoritie- G2-like
duc	12	-3.21	1e-03	51	Signal traßighadtionnsdRindisphatRhytisphatidisplignostitud signtaling system
	13	-3.12	2e-03	62	RibosomeRibiogenessisieg@@@spartis@es particles

-2.99 3e-03

6e-03

7e-03

8e-03

18

100

29

-2.96 3e-03

-2.79

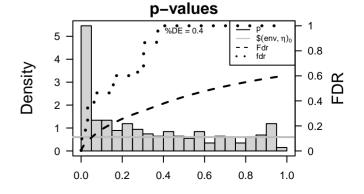
-2.78 6e-03

-2.75

-2.69

-2.65

15



Ubiquitin systemitin syntgen Ringen glingentypeniger type E3

Plant spellfantsignadifig signaling deliberatelopment

CarbohydCateborletdbatesmetalbodisitol plhospitralte hoetalbatesmetabolism

Plant spe Ellian signedifig signiadian direction rhythm

SLC15: PSht61 Sali@opteptiolegopteptisleoroteransporter

Chaperon@habbs@20 - HSP20