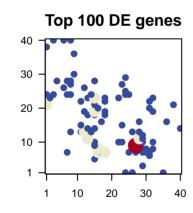
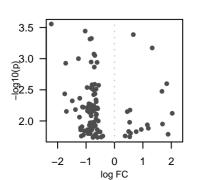
Tocai_accfreeze_r1

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> = 0.46 <fdr> = 1





Differentially expressed genes

fdr

log(FC)

Rank

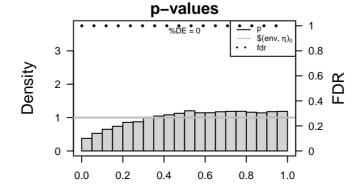
Nai	II.	109(1	Ο,	iui		Description	rank	GSZ	p-vai
	ID		p-va	lue	Meta	gene			
Over	expressed						Overexp	ressed	
1	Vitvi07g00449	0.66	4e-04	1	22 x 23	A semiautonomous, self replicating organelle that occurs in va	1	7.56	0e+00
ż	Vitvi13g01973	1.33	7e-04	1	8 x 40	The contents of a cell excluding the plasma membrane and n	ż	7.44	0e+00
3	Vitvi03q00932	1.84	3e-03	1	12 x 19	Binding to an RNA molecule or a portion thereof.	3	5.59	0e+00
4	Vitvi13g02017	1.67	3e-03	1	6 x 40	Any process that results in a change in state or activity of a co	4	5.18	0e+00
5 6 7 8 9 10 11 12 13 14 15	Vitvi14q01571		7e-03	1	9 x 30	Binding to a metal ion.	5	4.59	0e+00
	Vitvi17g00428	0.45	7e-03	1	24 x 29	The contents of a cell excluding the plasma membrane and n	6	3.71	1e-04
	Vitvi13g00409	2.03	8e-03	1	3 x 40	Any process that results in a change in state or activity of a co	7	3.65	3e-04
	Vitvi17g00767	0.53	1e-02	1	18 x 19	The component of a membrane consisting of the gene produc	8	2.93	4e-03
	Vitvi06g00155	1.69	1e-02	1	17 x 16	Binding to a metal ion.	9	2.9	4e-03
	-	1.16	1e-02	1	4 x 28	Catalysis of the transfer of a glycosyl group from one compou	10	2.85	5e-03
	Vitvi02g00097	1.19	1e-02	1	13 x 18	The contents of a cell excluding the plasma membrane and n	11	2.7	8e-03
	Vitvi10g00373	0.94	1e-02	1	15 x 28		12	2.58	1e-02
	Vitvi10g00492	0.5	1e-02	1	15 x 18		13	2.51	1e-02
	-	0.77	1e-02	1	9 x 36	Binding to GTP, guanosine triphosphate.	14	2.34	2e-02
	Vitvi04g01303	0.57	2e-02	1	11 x 22	Catalysis of a biochemical reaction at physiological temperatu	15	2.33	2e-02
16	Vitvi06g00024	1.89	2e-02	1	1 x 38	Any molecular function by which a gene product interacts sele	16	2.19	3e-02
17	Vitvi19g01557	0.38	2e-02	1	23 x 27	The chemical reactions and pathways resulting in the formation	17	2.16	3e-02
18	-	0.54	2e-02	1	18 x 18	A lipid bilayer along with all the proteins and protein complexe	18	2.14	3e-02
19	Vitvi10g00411	0.87	2e-02	1	12 x 28	7. Inpla bilayor along mar all the proteine and protein complexe	19	2.04	4e-02
20	-	1.31		1	1 x 28	Binding to a calcium ion (Ca2+).	20	2.02	5e-02
_	-		20 02		20				
	erexpressed						Underex	•	
1	Vitvi18g00955	-2.22	3e-04	1	26 x 1	The chemical reactions and pathways involving carbohydrate:	1	-4.79	0e+00
2 3 4 5 6 7	Vitvi08g01177	-1.03	4e-04	1	12 x 26	The part of the cytoplasm that does not contain organelles bu	2	-3.51	6e-04
	Vitvi04g01257	-0.81	5e-04	1	15 x 22	A membrane-bounded organelle of eukaryotic cells in which	3	-3.38	9e-04
	Vitvi14g00137	-0.86	5e-04	1	29 x 11	Any process that modulates the frequency, rate or extent of co	4	-3.33	1e-03
	Vitvi14g00034	-0.72	8e-04	1	18 x 22	Binding to a metal ion.	5	-3.08	2e-03
	Vitvi19g01522	-0.69	9e-04	1	27 x 9	Cleavage of the 5'-cap of a nuclear mRNA triggered by short The import of proteins across the outer and inner mitochondri	6 7	-2.87	5e-03
8	Vitvi17g00024 Vitvi14g01255	-1.27 -0.82	1e-03	1	27 x 9 30 x 8	The chemical reactions and pathways by which individual cell	8	-2.78 -2.53	6e-03 1e-02
9	Vitvi11g00210	-0.61	1e-03 1e-03	1	13 x 23	A protein complex that has protein serine/threonine phosphat	9	-2.53 -2.46	2e-02
10	Vitvi18g01315	-1.72	1e-03	1	29 x 3	A lipid bilayer along with all the proteins and protein complexe	10	-2.46	2e-02 2e-02
11	Vitvi18g00277	-0.71	1e-03	1	28 x 11		11	-2.38	2e-02
12	Vitvi19q00118	-0.7	3e-03	1	8 x 27	Binding to a zinc ion (Zn).	12	-2.34	2e-02
13	Vitvi14q01422	-0.79	3e-03	1	18 x 7	A membrane–bounded organelle of eukaryotic cells in which	13	-2.26	3e-02
14	Vitvi19g00731	-0.56	3e-03	1	15 x 23	Binding to a calcium ion (Ca2+).	14	-2.26	3e-02
15	Vitvi11g00614	-0.8	3e-03	1	28 x 13	The action of a molecule that contributes to the structural inte	13	-2.2	3e-02
16	Vitvi08g01109	-0.96	3e-03	1	28 x 11	The component of a membrane consisting of the gene produc	16	-2.18	3e-02
17	Vitvi13g00674	-0.82	3e-03	1	32 x 10	Any process that modulates the frequency, rate or extent of co	17	-2.14	3e-02
18	Vitvi03g00001	-0.78	3e-03	1	14 x 13	Binding to ATP, adenosine 5'-triphosphate, a universally impo	18	-2.13	3e-02
19	Vitvi18g00223	-0.65	3e-03	1	8 x 28	A membrane-bounded organelle of eukaryotic cells in which	19	-2.12	4e-02
\sim	101 104 00 400					A contract of the contract of	00		

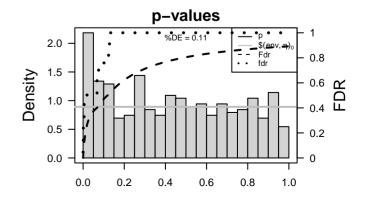
32 x 8 A vesicle with a coat formed of clathrin connected to the mem

Description

Differentially expressed gene sets

	IVALIK	GSZ	p-value	#all	Geneset
	Overexp	ressed			
n va	1	7.56	0e+00	18	Photosyn Pleasissy rathlessis a-paroteims a proteins
d n	2	7.44	0e+00	18	Energy mEtæbrglysmetalBblistorsynPleosissaymteresasparoteimsa proteins
	3	5.59	0e+00	47	Transport@rareatatotger-datedegort@etercapoortoedericten carriers
a Ct	4	5.18	0e+00	238	Enzyme -E2iztyrf3etye-02sylltr@inycfessylteansferases
	5	4.59	0e+00	41	Porphyrin Poetalyolismetabolism
d n	6	3.71	1e-04	10	Photosyn Priessis synotheissis Priodeins ys Remoto(\$750@nchl)(175000ythid) rophy
a CE	7	3.65	3e-04	206	Cell grow@catingtroutettthandOatellauthall- Cell wall
duc	8	2.93	4e-03	78	Glycosylt/Glycfesylteans/Berrasterral/Strolycsarcal/peolycsaccharide
	9	2.9	4e-03	73	TranscriptToanfactipition ARCOSREBP2 EREBP
oou	10	2.85	5e-03	18	Chaperon@haptsBn2e - HSP20
d n	11	2.7	8e-03	101	Starch an Standing and considerated setabolism
	12	2.58	1e-02	21	Thiamine Thiatatio is smetabolism
	13	2.51	1e-02	38	Photosyn Plessis synthesis
	14	2.34	2e-02	40	Transport Transtaport Stylistenkoid Tlaybaktoid parthetiang pathway
ratu	15	2.33	2e-02	44	Hormone Hogmating signation signation of the Hormone Hogmating signature is the Hormone Hogmating signature in the Hormone Hogmating signature is the Hormone Hogmating signature in the Hormone Hogmating signature is the Hormone Hogmating signature in the Hormone Hogmating signature is the Hormone Hogmating signature in the Hormone Hogmating signature is the Hormone Hogmating signature in the Hormone Hogmating signature is the Hormone Hogmating signature in the Hormone Hogmating signature is the Hormone Ho
sele	16	2.19	3e-02	34	CarbohydCateborle/talbatissmetalblutiserotidelsolepatisdenetaborlissmetabolis
atic	17	2.16	3e-02	66	Exosome Exessos com a Excession a logi ribitación de concentrancer cells
exe	18	2.14	3e-02	195	CarbohydCatdoorleytdbatleismetaStalissim an Staudincaednsetarbeleismetabol
	19	2.04	4e-02	12	Transcription factoristion (acoberns ØHdhlarus zf-b box
	20	2.02	5e-02	78	Energy metaboglismmetalebiolossynthesis
	Underex	nressen	,		
ate:		-4.79		144	RibosomeRibEsukannyeteEsukaryotes
bu	1 2	-4.79 -3.51	0e+00 6e-04	219	Cell growthethrandouthlandouth
ch	3	-3.38	9e-04	211	RibosomeRibosome
f CI	4	-3.33	1e-03	247	TranslatioTranslatiosomeRibosome
	5	-3.08	2e-03	139	Spliceosome
ort	6	-2.87	5e-03	51	Other me@uthodismeta@inlighenre@inlighes reactions
ndri	7	-2.78	6e-03	45	Galactos
cell	8	-2.53	1e-02	134	Hormone Higgmating sighalingsig Malking signaling
hat	9	-2.46	2e-02	10	Valine leut/artienenheusionle accidestoilessyoritheelsiesynthesis
ехє	Ĭ0	-2.46	2e-02	11	Lipid metalipoidismeta6@llsr6ter6@llh-@tercoid Incetabolismetabolism
epl	11	-2.38	2e-02	165	TranscriptToans@ipiticerosc@peticeosome
	12	-2.34	2e-02	27	Common Splinerus os palioeus sprinale at smponents
ch	13	-2.26	3e-02	26	PantotherRatetathde Cattle birds (Croth Aclasies synthesis
	14	-2.26	3e-02	24	Enzyme -Eñzlyn©aatalīyslin.© #thelynsin.glotona tiram slibbo;adioom sif hydrons
nte	15	-2.2	3e-02	42	Tryptopha Tryptxtpbelism etabolism
duc	16	-2.18	3e-02	57	TranscriptToanfactipition falBtors - HB
f CI	17	-2.14	3e-02	29	TranscriptToanfactipition Taidtelis - Trihelix
npc	18	-2.13	3e-02	126	Translatio Tran State otran SphiAt transport





-2.09

Transcription factorisco Bassion de Clasici particle (bZlip) per (bZlip)