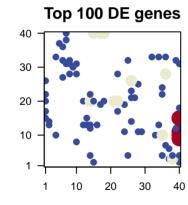
# Sangio\_warm\_r1

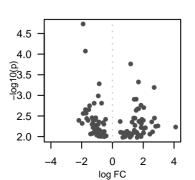
## **Global Summary**

%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> = 0.39 <fdr> = 1

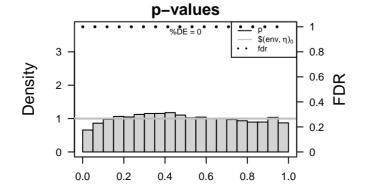
## 





### Differentially expressed genes

Rank ID		log(FC) fdr p-value		Description Metagene			
	Over	Overexpressed					
	1	Vitvi01g00313	1.18	2e-04	1	14 x 22	A membrane-bounded organelle of eukaryotic cells in which
		Vitvi01g00989	1.69	5e-04	1	24 x 11	The component of a membrane consisting of the gene produc
	วิ	Vitvi05q00566	2.71	6e-04	1	15 x 40	3
	4	Vitvi10g01880	1.54	1e-03	1	15 x 20	The component of a membrane consisting of the gene produc
	5	Vitvi05q00485	1.41	1e-03	1	35 x 10	Binding to a copper (Cu) ion.
	2 3 4 5 6 7	Vitvi16g01285	1.85	2e-03	1	34 x 13	A membrane-bounded organelle of eukaryotic cells in which
	7	Vitvi09g00290	2.03	2e-03	1	35 x 4	A membrane-bounded organelle of eukaryotic cells in which
	8	Vitvi06q00674	1.7	2e-03	1	40 x 9	A process that is carried out at the cellular level which results
	9	Vitvi08q01024	1.62	2e-03	1	39 x 10	Binding to a lipid.
	10	Vitvi14g00250	1.54	2e-03	1	14 x 20	Binding to a protein kinase, any enzyme that catalyzes the tra
	11	Vitvi14g01336	2.73	4e-03	1	40 x 4	
	12	Vitvi12g02315	1.38	4e-03	1	12 x 20	
	13	Vitvi10g00631	1.46	4e-03	1	14 x 20	
	14	Vitvi10g01814	1.91	4e-03	1	40 x 10	Catalysis of the hydrolysis of internal, alpha-peptide bonds in
	15	Vitvi14g01645	2	4e-03	1	40 x 11	
	16	Vitvi08g01673	1.72	4e-03	1	17 x 40	A lipid bilayer along with all the proteins and protein complexe
	17	Vitvi19g02074	0.5	4e-03	1	33 x 10	
	18	Vitvi09g01562	2.55	4e-03	1	38 x 4	Functions in the storage of nutritious substrates.
	19	Vitvi08g01110	1.27	4e-03	1	37 x 3	-
	20	Vitvi00g02033	1.8	4e-03	1	40 x 9	
	_						
		erexpressed					
	1	Vitvi05g00302	-1.91	2e-05	1	1 x 22	
	2	Vitvi18g00899	-1.76	8e-05	1	35 x 22	The component of a membrane consisting of the gene produc
	3	Vitvi05g00397 Vitvi04g01893	-0.86 -0.92	5e-04	1	10 x 28	The process in which a signal is passed on to downstream co
	4	Vitvi04g01693 Vitvi09g00132	-0.92	1e-03 2e-03	1	24 x 19 21 x 20	A membrane–bounded organelle of eukaryotic cells in which Binding to a protein.
	2 3 4 5 6 7	Vitvi08g00160	-1.19	2e-03	1	28 x 25	A membrane–bounded organelle of eukaryotic cells in which
	7	Vitvi17g00137	-1.49	2e-03	1	6 x 32	Binding to ATP, adenosine 5'-triphosphate, a universally impo
	8	Vitvi18g01875	-1.76	2e-03	1	1 x 15	A membrane–bounded organelle of eukaryotic cells in which
	9	Vitvi07g00563	-1.54	2e-03	1	22 x 17	A transcription coregulator activity that activates or increases
	Ĭ0	Vitvi17g00880	-1.71	3e-03	1	7 x 40	A membrane-bounded organelle of eukaryotic cells in which
	1ĭ	Vitvi16g00863	-1.9	3e-03	1	26 x 14	Organized structure of distinctive morphology and function, b
	12	Vitvi17g00221	-1.33	3e-03	1	26 x 21	
	13	Vitvi02g00729	-1.09	4e-03	1	26 x 26	The part of the cytoplasm that does not contain organelles bu
	14	Vitvi08g01653	-1.67	4e-03	1	35 x 24	Binding to ATP, adenosine 5'-triphosphate, a universally impo
	15	Vitvi03g00099	-0.45	4e-03	1	22 x 20	A membrane-bounded organelle of eukaryotic cells in which
	16	Vitvi10g01568	-1.1	4e-03	1	26 x 26	The contents of a cell excluding the plasma membrane and n
	17	Vitvi08g01217	-2.18	4e-03	1	2 x 13	
	18	Vitvi13g02190	-1.59	4e-03	1	2 x 14	
	19	Vitvi17g00680	-1.24	4e-03	1	10 x 8	The membrane surrounding a cell that separates the cell from
	20	Vitvi11g00680	-0.88	4e-03	1	18 x 20	The formation of a protein dimer, a macromolecular structure



### Differentially expressed gene sets

R	lank	GSZ	p-value	#all	Geneset

	Overes	xpressed			
h .	1	7.87	0e+00	47	Transport@iranatabuter-catalogo-toetensportoetenan carriers
uc	2	7.71	0e+00	206	Cell growthethropethrandOddlauball Cell wall
u	3	6.89	0e+00	18	Energy metaebrgliysmmeta@blobsonsyn@lecsiossymmetaesaspanoteimsa proteins
uc	4		0e+00	39	Pentose afterholdseurondatevinternateventeinosnversions
ut		6.51			Photosyn Phasissy rathlesisa-paroteimsa proteins
	5	6.41	0e+00	18	
h	6	6.32	0e+00	78	Energy metaetroplysmetalebolotousynthesis
h	7	5.73	0e+00	38	Photosyn <b>Priessies</b> synthesis
ts	8	5.47	0e+00	134	Hormone Hatigmading signaling signaling signaling
	9	4.55	0e+00	30	Glycan biolisyotimetsiissaymithensiitalabolismetalliseliskyrcan Nakaliyadanti degrada
ra	10	4.31	0e+00	19	Aquaporin Aquaposimas ilametus ratas ioni et et trata soputet et ar (3 pontensa) (TC:1.A.)
	11	4.05	0e+00	44	Hormonelskigmading sigDyattinkignin Gigtokalining signaling
	12	4.05	0e+00	10	Photosyn Pleasis symutteiss is Plauteias ys Pelnotio(\$9750@nothi (1776) Bydhab) rophyll
	13	3.87	8e-05	40	Transport Transport Stylsytenkoid Ttaytyektinig perthetiang pathway
in	14	3.82	1e-04	78	Glycosyltr@ilysdessylteens@errasterralSptrollystarcathpeorlyseaccharide
	15	3.74	1e-04	58	CarbohydCateborte,tdbatësmetaBolistorse Enabtoseraoxemærtabsësmetab
хe	16	3.59	4e-04	197	Transporterarestatoriger-calitationgelsCalmathpoetesand pores
	17	3.48	7e-04	168	Plant hormalizate is beginnabitive assign additionans duction
	18	3.07	2e-03	51	Other me@athredismmeta.Bioligiten rea@intightes reactions
	19	2.94	4e-03	44	Fructose Enulotosenavalemaetalosiismetaloolism
	20	2.89	4e-03	41	Porphyrin Poeplalpoilismetabolism
	Under	expressed	d		
	1	-7.53	0e+00	48	Transcriptioanfactiontion taletons - WRKY
uc	ż	-6.59	0e+00	64	TranscriptToenfactipition CatherstranGthreptionnfactipition factors
CC	3	-6.35	0e+00	73	Transcription faction factors REBP2 EREBP
h ·	4	-5.32	0e+00	140	Hormonelskigmating sighthlijtegne Sittmatting signaling
	5	-5.18	0e+00	49	TranscriptToenfactipitison Na&Cors - NAC
h ·	Ğ	-4.51	0e+00	116	RibosomeRitiogenesisieg@nesis0S Paetidi@S particles
OC	Ž	-4.35	0e+00	64	RibosomeRibiogenesisiongeneaisyotesukaryotes
h	8	-4.27	0e+00	75	Translatio Tranklibitissom eRitiogenes isi ong Endesisy ot eSukaryotes
s	9	-3.86	8e-05	36	DNA replication
h -	Ĭ0	-3.83	8e-05	219	Cell growtDetlingtrollertithandDatellathroleCell cycle
bı	11	-3.58	4e-04	62	RibosomeRibiogenesilsieg@@@spartisleS particles
	12	-3.57	4e-04	118	TranscriptToanfactipitison faletiorsturil-letiali-turn-helix
ou	13	-3.53	5e-04	162	Plant spe@lfansignedifig.sigPlahingpatPlagrenplathaggetioninteraction
OC	14	-3.41	9e-04	41	Replication
h	15	-3.35	1e-03	153	Plant-pathtagenpiathcagetionnteraction
n	16	-3.32	1e-03	144	RibosomeRib EsakannyoteEsukaryotes
	17	-3.31	1e-03	157	Protein priocessingriocessinglas enicloetias inico reticulum
	18	-3.29	1e-03	83	TranscriptToanfactipttion faltfors - MYB
n	19	-3.24	1e-03	24	Replication Republication Political Republication Factors
е	20	-3.2	1e-03	27	Enzyme -E2iz6ymTeans2le6rinTiganisfergiengouisrgggampaus groups

