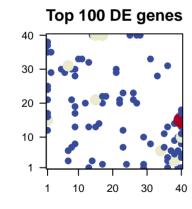
Sangio_warm_r3

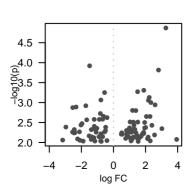
Global Summary

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

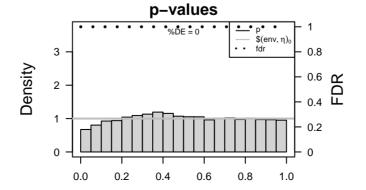
Portrait 40 30 20 10 -30 10 20





Differentially expressed genes

Rank ID		log(FC) fdr p-value		Meta	Description Metagene		GSZ	p-value	#a	
Overexpressed						Overexpressed				
1	Vitvi02g01118	3.27	1e-05	1	39 x 1	Catalysis of the transfer of an acyl group, other than amino-a	1 .	7.73	0e+00	26
ż	Vitvi11g01303	2.81	2e-04	1	40 x 1	Catalysis of a biochemical reaction at physiological temperatu	ż	5	0e+00	206
3	-	1.89	5e-04	1	35 x 7	The component of a membrane consisting of the gene produc	3	4.68	0e+00	47
4	Vitvi07g01927	1.5	5e-04	1	40 x 11	The chemical reactions and pathways involving carbohydrate:	4	4.51	0e+00	78
5 6 7 8 9 10 11 12	Vitvi19g00505	2.23	7e-04	1	40 x 17		5	4.43	0e+00	78
	Vitvi02g01473	2.18	9e-04	1	17 x 2	Catalysis of an oxidation-reduction (redox) reaction, a reversi	6	4.04	0e+00	38
	Vitvi18g02763	2.33	1e-03	1	40 x 10	Binding to a metal ion.	7	4.04	0e+00	39
	Vitvi05g00566	2.59	1e-03	1	15 x 40		8	3.99	0e+00	30
	Vitvi04g01155	1.19	2e-03	1	17 x 40	A lipid bilayer along with all the proteins and protein complexe	9	3.89	8e-05	58
	Vitvi18g00086	1.39	2e-03	1	40 x 14	Binding to a protein.	10	3.88	8e-05	18
	Vitvi12g02718	2.05	2e-03	1	17 x 40	A membrane-bounded organelle of eukaryotic cells in which	11	3.52	6e-04	217
	Vitvi02g01126	2.28	2e-03	1	13 x 1	Catalysis of the transfer of an acyl group, other than amino-a	12	3.52	6e-04	197
13	Vitvi09g00049	1.04	3e-03	1	29 x 10		13	3.43	8e-04	18
14	Vitvi14g01780	1.51	3e-03	1	40 x 8	A membrane-bounded organelle of eukaryotic cells in which	14	3.28	1e-03	81
15	Vitvi08g00913	1.24	3e-03	1	35 x 11	Enables the transfer of a substance, usually a specific substa	15	3.28	1e-03	25
16	Vitvi10g01814	1.95	3e-03	1	40 x 10	Catalysis of the hydrolysis of internal, alpha-peptide bonds in	16	3.27	1e-03	44
17	Vitvi12g02046	1.28	4e-03	1	38 x 3	Catalysis of an oxidation-reduction (redox) reaction, a reversi	17	3.14	2e-03	195
18	Vitvi03g01432	2.4	4e-03	1	14 x 3		18	3.13	2e-03	101
19	Vitvi17g00331	2	4e-03	1	40 x 13		19	3.02	3e-03	19
20	Vitvi04g00726	1.94	4e-03	1	14 x 40		20	2.99	3e-03	10
l local							I In do so		,	
	erexpressed					The control of the co	Underex	•		
1	Vitvi18g00958	-1.49	1e-04	1	5 x 30	The component of a membrane consisting of the gene produc	1	-7.69	0e+00	64
2	Vitvi04g00591		6e-04	1	18 x 22	Binding to a ribosome.	2	-6.73	0e+00	73
	Vitvi18g02600 Vitvi18g03049	-0.78 -1.72	9e-04 1e-03	1 1	9 x 28 2 x 29	The contents of a cell excluding the plasma membrane and n A membrane–bounded organelle of eukaryotic cells in which	3 4	-6.38 -5.31	0e+00 0e+00	140 48
4 5	Vitvi04g02017		1e-03	1	2 x 29 29 x 2	A membrane-bounded organiene or edikaryonic cens in which	5	-5.31 -4.02	0e+00 0e+00	46 144
6	Vitvi04g02017 Vitvi09g00275	-2.54	1e-03	1	1 x 25		6	-4.02 -3.81	1e-04	27
7	Vitvi18g01507	-0.82	2e-03	1	8 x 30	Binding to a nucleotide, any compound consisting of a nucleo	7	-3.79	1e-04	49
8	Vitvi10g00025	-0.62	2e-03	1	10 x 33	The contents of a cell excluding the plasma membrane and n	8	-3.78	1e-04	153
9	Vitvi11g00072		2e-03	1	23 x 23	A membrane-bounded organelle of eukaryotic cells in which	9	-3.74	1e-04	247
10	Vitvi02g00663	-0.67	3e-03	1	9 x 30	•	Ĭ0	-3.31	1e-03	89
11	Vitvi06g00776	-0.88	3e-03	1	26 x 23	The error-free repair of a double-strand break in DNA in which	11	-3.2	1e-03	211
12	Vitvi00g01289	-1.2	3e-03	1	15 x 13		12	-2.92	4e-03	36
13	Vitvi09g00050	-1.67	3e-03	1	9 x 17		13	-2.9	4e-03	42
14	Vitvi10g00191	-1.96	3e-03	1	25 x 40	A membrane-bounded organelle of eukaryotic cells in which	14	-2.89	4e-03	24
15	Vitvi17g00256	-2.03	4e-03	1	1 x 16		15	-2.85	5e-03	170
16	Vitvi05g00297	-1.19	4e-03	1	29 x 1		16	-2.8	6e-03	162
17	Vitvi05g01756	-2.97	4e-03	1	1 x 12		17	-2.79	6e-03	80
18	Vitvi12g00828	-0.49	4e-03	1	22 x 21	Catalysis of the transfer of a group, e.g. a methyl group, glyco	18	-2.79	6e-03	17
19	Vitvi02g01429	-1.04	4e-03	1	1 x 24	The formation of a protein dimer, a macromolecular structure	19	-2.74	7e-03	41
20	Vitvi04g00512	-1.25	5e-03	1	16 x 14	Binding to ATP, adenosine 5'-triphosphate, a universally impo	20	-2.67	8e-03	128



Differentially expressed gene sets

Rank GSZ	p-value	#all (Geneset
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	rtanit	002	p	<i>n</i> an	Geneset
	Overexp	ressed			
nino-a	1	7.73	0e+00	26	Flavonoid Flavosyntildelsie synthesis
nperatu	2	5	0e+00	206	Cell grow@etingtrodertithandOutellatinall- Cell wall
produc	3	4.68	0e+00	47	Transport@iranataloute-catalogo-tl@eteratpoortoelerideron carriers
ydrate:	4	4.51	0e+00	78	Energy metaboglismmetalBobitsonsyntPlacofesynthesis
	5	4.43	0e+00	78	Glycosyltr@ivsfessylteens@erasterra@inulestarcethcorle/seaccharide
reversi	6	4.04	0e+00	38	Photosyn Places synthesis
	7	4.04	0e+00	39	Pentose a Pentulse undate internate ensinos nversions
	8	3.99	0e+00	30	Glycan bi GslycatnetsiossyndhæsitsaboblsmetalbletGslycarNdeQslycatartide grad
mplexe	9	3.89	8e-05	58	Carbohydateborie/talbatismetalbalistose Enulotoseravaelmætabsismeta
	10	3.88	8e-05	18	Energy mētadorglijsmetalēbolistors yn Priecsios samtilerers as peroteimsa proteins
which	11	3.52	6e-04	217	Cell motilibell metilibation exiberation control contr
nino-a	12	3.52	6e-04	197	Transport@razatatorte= @ltaionels@mahpelssand pores
illio-a	13	3.43		18	Photosyn Priessios syrathitesisa-paroteimsa proteins
which			8e-04		Enzyme -E4:2/n0arb4n2-o0apdaonlyasegen lyases
	14	3.28	1e-03	81	
substa	15	3.28	1e-03	25	Nitrogen Mittagelismetabolism
onds in	16	3.27	1e-03	44	Fructose Enubtroseramademmentaloseismetabolism
reversi	17	3.14	2e-03	195	CarbohydCateborte,talbatiësmmeta8talissmm an 8t soudnoased nse tarboëssmmet aboli
	18	3.13	2e-03	101	Starch an 8 tandhoæednsetarbeësmetabolism
	19	3.02	3e-03	19	AquaporinAsqaaplosninasllametutsraalstoluetetutaalsopudeteran(\$1000rfteAss)[TC:1.A
	20	2.99	3e-03	10	Linoleic alcidoreidatocitismetabolism
	Underex	pressed	1		
produc	1	-7.69	0e+00	64	Transcriptionniscotipation Catherstran Othreptionniscotipation factors
	2	-6.73	0e+00	73	Transcription factipation factorist EREBP
and n	2 3	-6.38	0e+00	140	Hormone Hogmating signating signaling
which	4	-5.31	0e+00	48	Transcriptioanisctipition taletois – WRKY
	4 5 6 7	-4.02	0e+00	144	RibosomeRib EsakaneyoteEsukaryotes
	6	-3.81	1e-04	27	Enzyme -E2ix5ymTeens2le8rinTegnistfergiengouistreggeungsus groups
nucleo		-3.79	1e-04	49	TranscriptToanfactipition Nations – NAC
and n	8	-3.78	1e-04	153	Plant-pathtagetepateogetointeraction
which	9	-3.74	1e-04	247	Translatio Tran Blatiso meRibosome
	10	-3.31	1e-03	89	MAPK sig viálPký sightaviang-patlanvi ay – plant
in whic	11	-3.2	1e-03	211	Ribosome Ribosome
	12	-2.92	4e-03	36	DNA replication
	13	-2.9	4e-03	42	Tryptopha Tryptetpbelism etabolism
which	14	-2.89	4e-03	24	Replication Reproductation Polisia iRepublish depolitication Factors
	15	-2.85	5e-03	170	TranscriptToanfactipition Catherszf-O8heCef-C3HC4
	16	-2.8	6e-03	162	Plant spellfansignadifig signalingpathlagetepathcagetionnteraction
	17	-2.79	6e-03	80	Transport Torgasteprort Styesteering Tethering factors
, glyco	18	-2.79	6e-03	17	Kinase – KRrAds camilityAK family
ucture	19	-2.74	7e-03	41	Arginine altrogiprio ei rændn e tabio eismetabolism
ly impc	20	-2.67	8e-03	128	Ubiquitin Ыжінрітін-Sindelen Rin Sijangilen Birtigp ér fig@er type E3

