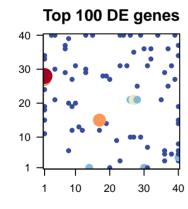
Sangio_warm

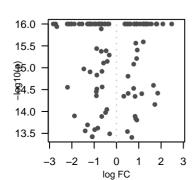
Global Summary

%DE = NA # genes with fdr < 0.2 = 8256 (3948 + /4308 -)# genes with fdr < 0.1 = 5479 (2712 + /2767 -)# genes with fdr < 0.05 = 3655 (1793 + /1862 -)# genes with fdr < 0.01 = 2104 (996 + /1108 -)

<FC> = 0< p-value > = 0.03< fdr > = 0.37

Portrait 40 30 20 10 10 20 30





Differentially expressed genes

Rank

	ID	p-value		Metagene					
Overexpressed									
1	, Vitvi10g00299	1.22	1e-16	1e-13	32 x 36				
ż	Vitvi01g00080	0.55	1e-16	1e-13	25 x 31	•			
3	Vitvi01g00157	0.8	1e-16	1e-13	40 x 19	The contents of a cell excluding the plasma membrane and n			
	Vitvi01g00161	0.42	1e-16	1e-13	29 x 10	Any process involved in the conversion of a primary mRNA tra			
5	Vitvi01g00277	0.9	1e-16	1e-13	36 x 5	A lipid bilayer along with all the proteins and protein complexe			
6 7 8 9	Vitvi01g01969	0.82	1e-16	1e-13	31 x 31				
	Vitvi02g00144	0.49	1e-16	1e-13	40 x 14	A lipid bilayer along with all the proteins and protein complexe			
	Vitvi04g00907	0.37	1e-16	1e-13	20 x 27	Binding to a metal ion.			
	Vitvi06q00153	1.56	1e-16	1e-13	20 x 1	Binding to a metal ion.			
	Vitvi08q01454	1.33	1e-16	1e-13	40 x 6	Binding to a zinc ion (Zn).			
11	Vitvi08g00115	0.63	1e-16	1e-13	23 x 31	The component of a membrane consisting of the gene produc			
12 13 14 15	Vitvi09g00502	1.78	1e-16	1e-13	8 x 20	Binding to ADP, adenosine 5'-diphosphate.			
	Vitvi12g00327	2.08	1e-16	1e-13	40 x 37	A lipid bilayer along with all the proteins and protein complexe			
	Vitvi12g02041	1.19	1e-16	1e-13	38 x 31	The component of a membrane consisting of the gene produc			
	Vitvi13g01200	1.33	1e-16	1e-13	13 x 40	Catalysis of an oxidation-reduction (redox) reaction in which			
16	Vitvi13g00137	0.93	1e-16	1e-13	40 x 15	Organized structure of distinctive morphology and function, by			
17 18	Vitvi14g02707	1.81	1e-16	1e-13	9 x 19	Binding to ADP, adenosine 5'-diphosphate.			
	Vitvi14g01272	1.06	1e-16	1e-13	38 x 5	Catalysis of the transfer of a group, e.g. a methyl group, glyco			
19	Vitvi17g00366	1.32	1e-16	1e-13	40 x 5	Any molecular function by which a gene product interacts sele			
20	Vitvi17g00648	0.92	1e-16	1e-13	40 x 4	A membrane-bounded organelle of eukaryotic cells in which			
_	-								
	erexpressed					•			
1	Vitvi10g00361	-1.27	1e-16	1e-13	27 x 21				
2	Vitvi00g01887	-1.17	1e-16	1e-13	1 x 27				
3	Vitvi07g02998	-1.17	1e-16	1e-13	1 x 27 1 x 28	•			
3 4 5 6 7	Vitvi00g02197 Vitvi07g03139	-0.79 -0.79	1e-16 1e-16	1e-13 1e-13	1 x 28				
5	Vitvi01g00114	-1.21	1e-16	1e-13	27 x 21	The action of a molecule that contributes to the structural inte			
7	Vitvi02g00942	-0.75	1e-16	1e-13	1 x 18	A lipid bilayer along with all the proteins and protein complexe			
8	Vitvi03g01092	-0.75	1e-16	1e-13	1 x 10	The chemical reactions and pathways resulting in the formatic			
9	Vitvi03q00633	-0.79	1e-16	1e-13	35 x 21	Fibrous structure (light microscope view) that arises between			
Ĭ0	Vitvi04g00244	-0.51	1e-16	1e-13	7 x 29	A lipid bilayer along with all the proteins and protein complexe			
11	Vitvi04g01904	-1.3	1e-16	1e-13	17 x 12	· · · · · · · · · · · · · · · · · · ·			
12	Vitvi05g00032	-1.12	1e-16	1e-13	1 x 34	Catalysis of the transfer of an acyl group from one compound			
13	Vitvi05g02250	-2.73	1e-16	1e-13	37 x 25	•			
14	Vitvi05g01636	-0.39	1e-16	1e-13	12 x 12				
15	Vitvi06g00493	-0.64	1e-16	1e-13	7 x 36	Any process involved in the maturation of a precursor 5.8S rit			
16	Vitvi07g01798	-0.92	1e-16	1e-13	1 x 33	The contents of a cell excluding the plasma membrane and n			
17	Vitvi07g02390	-2.14	1e-16	1e-13	17 x 15				
18	Vitvi08g01722	-0.34	1e-16	1e-13	13 x 30	Binding to a nucleic acid.			
19	Vitvi09g01925	-1	1e-16	1e-13	17 x 15				
20	Vitvi10g01789	-0.67	1e-16	1e-13	28 x 25	3			

Description

Differentially expressed gene sets

Rank GSZ p-val	ue #all Geneset
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	Nank	GSZ	p-value	#all	Genesei
	Overexp	ressed			
	1	6.99	0e+00	206	Cell growtDedingtrodettthandOddlauball- Cell wall
	ż	6.74	0e+00	47	Transport@iransalutter-dataloport@eexsportoeleideron carriers
nd n	3	6.12	0e+00	39	Pentose afrechtplseurondaţie.imterroateventeirocsnversions
NA tra	4	5.85	0e+00	78	Energy mētæbrglijsmeta@bbistors.yn@hecsiosynthesis
plexe	5	5.81	0e+00	18	Energy mētæboglismmeta@blötsons.yn@hecsiosaymthbressispanoteimsa proteins
	6	5.44	0e+00	38	Photosynthesis
plexe	7	5.29	0e+00	18	Photosyn Phasissyrathlesisa-proteins a proteins
	8	4.8	0e+00	26	FlavonoidFlavsynthdelsissynthesis
	9	4.67	0e+00	30	Glycan bi Gdycanelsissamthesitabolismetalsle/GlycarNd-Glyadatide gradation
	10	4.5	0e+00	19	Aquaporin/Aquaposimallamelusralasionietettalasoputet erar [3] 60 ntte/ks8[TC:1.A.8]
roduc	11	4.5	0e+00	197	Transporterarestatorer-calitatorels@mahperssand pores
ouut	12	4.34	0e+00	134	Hormone Hognating signating signaling signaling
plexe	13	4.29	0e+00	78	Glycosyltr@hysfessylteens@emasterral@houlestarcethaniletsaccharide
roduc	14	4.14	0e+00	58	CarbohydCatebotetdtatësmetaBolistorse Endctoaeravaemærtabeësmetabolis
hich :	15		2e-04	10	Photosyn Pleasies symuteissis Plauteissys Photosymuteissis Photosymuteissis Plauteissys Photosymuteissis Photosymuteissi Photosymuteissis Photosymuteissi Photosymuteissi Photosymuteissi Photosymuteissi Photosymuteissi
on, b	16	3.73 3.6	4e-04	44	Hormonelsignating signatishining signaling
JII, DI	: =				Fructose Enucltose raosate materialos esmetabolism
	17	3.41	1e-03	44	
glyco	18	3.33	1e-03	81	Enzyme -E4:22/n0ærb4n2-d0ærdæmlyaxægen lyases
s sele hich	19	3.32	1e-03	47	ABC transpilicteransporters
nich	20	3.2	2e-03	25	Nitrogen Mittagelismmetabolism
	Underex	pressea	1		
	1	-7.82	0e+00	64	Transcriptionniscotipition (attherstran@trieptionniscotipition factors
	2	-7.44	0e+00	73	Transcriptionniscotipition ARCOEREBP2 EREBP
	3	-6.04	0e+00	140	Hormonelskigmating sigfitalyitegne Sithmydding signaling
	1 2 3 4 5 6	-4.59	0e+00	48	TranscriptToanfactipition Ya/R/K/Y - WRKY
	5	-4.39	0e+00	36	DNA replication
I inte	<u>6</u>	-4.15	0e+00	116	RibosomeRibiogenessIsieg@reesisiS Paetid@S particles
plexe	7	-4.07	0e+00	41	Replication
matic	8	-3.9	0e+00	49	Transcriptionniscotipition MacCors – NAC
veen	9	-3.6	4e-04	64	Ribosome Ribiogenes isi ingentes is ingentes ukaryotes
plexe	10	-3.55	5e-04	247	Translatio T ran slatissome Ribosome
-N, (11	-3.53	5e-04	75	TranslatioTranSlatiosomeRitiogenesisiogEnesisjotesukaryotes
ound	12	-3.42	1e-03	27	Enzyme -E026/miens2e6/miganisfegergouisrggerpous groups
	13	-3.39	1e-03	144	RibosomeRibEstkarryoteSukarryotes
S rit	14 15	-3.38	1e-03	24	Replication publication publication publication Factors
nd n		-3.33	1e-03	219 17	Cell growtheilngtoulethhandaddathaleCell cycle Kinase – KrandsteamiRaK family
nu n	16 17	-3.02 -3	4e-03	11	Transcriptioanfactipition (albifors – GRF
	17	-3 -2.94	4e-03 4e-03	11 44	Replication publication publication publication publication factors
	19	-2.94 -2.88	4e-03 5e-03	211	RibosomeRibosome
	20	-2.87	5e-03	22	Replicationsome Replicationsome Repaired temperation and the second and the sec
	20	-2.01	55-05		

