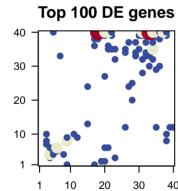
# Sangio\_freeze\_r3

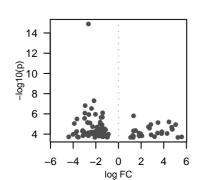
## **Global Summary**

%DE = 0.39# genes with fdr < 0.2 = 2160 ( 1038 + /1122 –) # genes with fdr < 0.1 = 585 ( 249 + /336 –) # genes with fdr < 0.05 = 129 ( 44 + /85 –) # genes with fdr < 0.01 = 23 ( 5 + /18 –)

<FC> = 0 <p-value> = 0.17 <fdr> = 0.61

## 



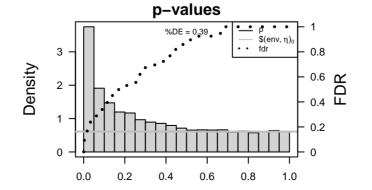


### Differentially expressed genes

Rank

	ID		p-value		Metagene			
Over	Overexpressed							
1	Vitvi14g02500	1.33	2e-06	0.004	26 x 12	A lipid bilayer along with all the proteins and protein complexe	1	
2	Vitvi05g00643	4.46	6e-06	0.009	5 x 5	Catalysis of the hydrolysis of any ester bond.		
3	Vitvi10g00877	3.49	7e-06	0.009	8 x 4		2	
4	Vitvi08g01794	2.86	1e-05	0.009	20 x 1	A membrane-bounded organelle of eukaryotic cells in which	4	
5	Vitvi02g01405	5.05	1e-05	0.009	4 x 6	Reactions, triggered in response to the presence of a foreign	5	
5 6	Vitvi19g00068	2.65	2e-05	0.021	3 x 10	Binding to ATP, adenosine 5'-triphosphate, a universally impo	6	
7	Vitvi16g01321	4.7	2e-05	0.021	6 x 5		7	
8	Vitvi14g02006	2.74	3e-05	0.022	23 x 3	Binding to ATP, adenosine 5'-triphosphate, a universally impo	8	
9	Vitvi00g00932	4.75	3e-05	0.022	4 x 4		9	
10	Vitvi02g01747	4.75	3e-05	0.022	4 x 4		Ĭ	
11	Vitvi02g00128	1.51	4e-05	0.022	9 x 8	The chemical reactions and pathways involving fatty acids, ali	1	
12	Vitvi14g01631	1.33	5e-05	0.022	21 x 6	The component of a membrane consisting of the gene produc	1	
13	Vitvi14g00485	3.83	6e-05	0.022	6 x 6		1	
14	Vitvi07g01784	3.45	8e-05	0.024	3 x 7	The space external to the outermost structure of a cell. For $c\varepsilon$	1	
15	Vitvi14g00423	1.82	8e-05	0.024	9 x 8		1	
16	Vitvi18g01263	4.29	9e-05	0.024	5 x 4		1	
17	Vitvi18g02840	3.81	9e-05	0.024	3 x 8		1	
18	Vitvi07g02289	1.98	1e-04	0.024	19 x 2	The component of a membrane consisting of the gene produc	1	
19	Vitvi14g02005	1.9	1e-04	0.035	17 x 1		1	
20	Vitvi05g01348	2.88	1e-04	0.035	6 x 6	The component of a membrane consisting of the gene produc	2	
Underexpressed						U		
1	Vitvi17g00986	-2.65	1e-15	6e-04	20 x 39	Binding to a protein.	1	
	Vitvi14g00314	-2.16	5e-08	1e-03	21 x 35	The component of a membrane consisting of the gene produc		
3	Vitvi17g00157	-2.94	2e-07	2e-03	31 x 39	Binding to a metal ion.	3	
4	Vitvi18g00755	-2.38	3e-07	2e-03	30 x 35		4	
2 3 4 5 6 7	Vitvi07g01685	-1.4	8e-07	2e-03	27 x 24	Binding to a nucleic acid.	2 3 4 5	
6	Vitvi14g01856	-2.97	8e-07	2e-03	34 x 35	Catalysis of a biochemical reaction at physiological temperatu	6 7	
7	Vitvi11g00787	-2.03	1e-06	2e-03	28 x 25	A subcomplex of the nuclear pore complex (NPC) that forms t		
8	Vitvi14g02987	-2.61	1e-06	4e-03	22 x 40	The cell cycle process in which the sister chromatids of a repl	8	
9	Vitvi18g00282	-1.42	2e-06	4e-03	23 x 35	Binding to ATP, adenosine 5'-triphosphate, a universally impo	9	
10	Vitvi19g00368	-1.54	2e-06	5e-03	20 x 27	Binding to a protein.	1	
11	Vitvi19g00469	-2.99	3e-06	5e-03	34 x 38	The biological process whose specific outcome is the progres	1	
12 13	Vitvi14g03000	-3.67	3e-06	9e-03	33 x 40 20 x 40		1	
	Vitvi19g02084 Vitvi19g01737	-1.61	7e-06	9e-03		Binding to an RNA molecule or a portion thereof.	1	
14 15	Vitvi01g00830	-2.73 -2.67	7e-06 8e-06	9e-03 9e-03	5 x 40 32 x 37	A membrane–bounded organelle of eukaryotic cells in which	1	
16	Vitvi19g00137	-2.52	8e-06	9e-03	35 x 29	The process in which a pre–tRNA molecule is converted to a	1	
17	Vitvi18g01109	-3.9	9e-06	9e-03	34 x 40	F	1	
18	Vitvi13g00315	-1.62	1e-05	9e-03	35 x 12	The process in which a methyl group is covalently attached to	1	
19	Vitvi13g01264	-1.45	1e-05	2e-02	22 x 35	The chemical reactions and pathways involving lipids, compo	i	
20	Vitvi15g00880	-2.29	2e-05	2e-02	18 x 40	Binding to a protein.	2	

Description



#### Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
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	Overex	pressed			
olexe	1	7.54	0e+00	48	Transcriptioanfactipition taleton - WRKY
	2	6.29	0e+00	162	Plant spellfansignedifig signathtgpathlagetepathogetionnteraction
	3	6.14	0e+00	45	Galactos@alatabsesmetabolism
nich	4	5.36	0e+00	49	Transcripticanisactipition MacCors - NAC
eign	5	4.25	0e+00	58	Other am 10 th acials nime tabiolisme tabiolisme tabiolism
impc	6	3.95	4e-05	77	Carbohyd@ateborleytdbattësmeta@alisotos@aletabotësmetabolism
	7	3.85	8e-05	12	Enzyme -E6zayssel - Class I
impc	8	3.83	8e-05	153	Plant-pathagenpathagenointeraction
	9	3.77	1e-04	80	Transport Transport Stjetterring Tettlering factors
	10	3.6	4e-04	24	Tropane pTpopradicepeperiptymetiamedatkyaldidebadksyltdidebiosynthesis
s, ali	11	3.48	7e-04	51	BiosyntheBiosofnsbesisdafrsenoetabal/ismetaBal/ismbioskundmelsiosynthesis
oduc	12	3.46	8e-04	33	alpha-Lin <b>edphrée-biridlemétabolism</b> etabolism
	13	3.34	1e-03	18	Receptor Receptor - Others
or ce	14	3.31	1e-03	77	Pores ion Robrassriels (Fi@nth)els [TC:1]
	15	3.31	1e-03	92	Lipid metaloodismetaGolisenolipOdyweetaloodismetabolism
	16	3.28	1e-03	17	Isoquinolih se qulkia taliade biad sakut talesia synthesis
	17	3.2	1e-03	33	CarbohydCatebohetelbatesmetaBolisossugansimostatbatissmetabolism
oduc	18	3.06	2e-03	42	Tryptophaliryptabalismetabolism
ouut	19	3.06	2e-03	15	Stilbenoic Stillandio eta taian julian julia
oduc	20	3.04	2e-03	34	Tyrosine riteratioesmetabolism
ouut	20	0.04	20-00	04	Tyrosino Hybradolainotabolioni
	Under	expressed	'		
	1	-12.57	0e+00	18	Energy mētæbrgljsmmetalBbbbsosynfPleosiosaymtheresasparoteimsa proteins
oduc	2	-11.79	0e+00	18	Photosyn Pleasissy rathites is a paroteins a proteins
	3	-10.8	0e+00	47	Transporterareaalouge-rotaterlogo-rtTetercatpoortoealerideron carriers
	2 3 4 5 6	-8.59	0e+00	38	Photosyn Plassissynthesis
	5	-7.61	0e+00	78	Energy metabolismetaBbitosynthesis
eratu		-7.24	0e+00	217	Cell motilibell RegililatioRegialationcytoskeleton
rms 1	7	-7.1	0e+00	10	Photosyn Priessis symutreiss is Privateis ys Pelmoto (\$750@noth) (\$750@noth) (\$750@noth) (\$750@noth) (\$750@noth)
repl	8	-7.06	0e+00	80	Cytoskeletanoskeletotubulkisrotubules
impc	9	-5.94	0e+00	206	Cell growthetingroutethinan-challed with all Cell wall
	10	-5.6	0e+00	40	Transport Transport Stylatenkoid Titaytekinid parthetiang pathway
gres	11	-4.16	0e+00	41	Porphyrin <b>Poeplalyolism</b> etabolism  Postidosofilomidishibitumb in Kihitriba A 45 continua formilusia formilusia.
	12 13	-4.05	0e+00	10 219	Peptidase@emidaisleibitoms inlfibitoins A1FameilysiA familysin family  Cell growtbetingroutetthandoutelathreleCell cycle
		-3.91	4e-05		Transcriptionanfaction table ABtors - GRF
nich	14 15	-3.83	8e-05 1e-04	11 44	Hormonelskigmating sigthatinkinin Sighatining signaling
to a	16	-3.75			Hormonelsignating signating signating signating
.o a	17	-3.75 -3.72	1e-04 1e-04	134 18	Transcriptionarisactipation Author - ARF
ed to	18	-3.72 -3.61	1e-04 4e-04	19	Transcriptioanisaciontison Additions - AKF
mpoi	19	-3.61	4e-04 4e-04	19	AquaporirAsquaposimaslametusrabslohetetrahasoputeterarisioonftekss[TC:1.A.8]
	20	-3.46	8e-04	211	RibosomeRibosome

