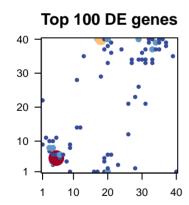
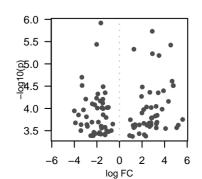
Sangio_freeze_r1

Global Summary

%DE = 0.41 # genes with fdr < 0.2 = 2422 (1163 + /1259 -) # genes with fdr < 0.1 = 448 (194 + /254 -) # genes with fdr < 0.05 = 79 (44 + /35 -) # genes with fdr < 0.01 = 6 (4 + /2 -)

<FC> = 0<p-value> = 0.18<fdr> = 0.59





Differentially expressed genes

log(FC)

Rank

ID		.09(.	p-value		Meta	Metagene			
Overexpressed									
1	Vitvi19g00068	2.91	2e-06	0.01	3 x 10	Binding to ATP, adenosine 5'-triphosphate, a universally impo			
2	Vitvi05g00643	4.54	4e-06	0.01	5 x 5	Catalysis of the hydrolysis of any ester bond.			
3	Vitvi14g02500	1.28	5e-06	0.01	26 x 12	A lipid bilayer along with all the proteins and protein complexe			
4	Vitvi14g02006	2.92	6e-06	0.01	23 x 3	Binding to ATP, adenosine 5'-triphosphate, a universally impo			
5	Vitvi10g00877	3.5	6e-06	0.03	8 x 4				
6	Vitvi16g01321	4.66	2e-05	0.03	6 x 5				
7	Vitvi00g00932	4.77	3e-05	0.03	4 x 4				
8	Vitvi02g01747	4.77	3e-05	0.03	4 x 4				
9	Vitvi14g02005	2.02	3e-05	0.03	17 x 1				
10	Vitvi14g00485	3.9	4e-05	0.03	6 x 6				
11 12 13 14	Vitvi08g01794	2.69	4e-05	0.03	20 x 1	A membrane-bounded organelle of eukaryotic cells in which			
	Vitvi10g00286	3.43	4e-05	0.03	9 x 1	The component of a membrane consisting of the gene produc			
	Vitvi17g00747	1.96	5e-05	0.03	20 x 6	The space external to the outermost structure of a cell. For $c\varepsilon$			
	Vitvi18g01263	4.34	7e-05	0.03	5 x 4				
15	Vitvi05g00523	3.25	9e-05	0.03	5 x 5	Catalysis of the transfer of an acetyl group to an acceptor mo			
16	Vitvi03g00295	2.4	9e-05	0.03	4 x 10				
17	Vitvi00g01319	2.81	1e-04	0.03	5 x 5				
18	Vitvi18g02840	3.78	1e-04	0.03	3 x 8				
19	Vitvi01g01573	2.14	1e-04	0.03	16 x 1	Binding to ATP, adenosine 5'-triphosphate, a universally impo			
20	Vitvi17g01538	1.99	1e-04	0.04	28 x 2				
Unde	erexpressed								
1	Vitvi06g00107	-1.65	1e-06	0.01	28 x 23	Any process that modulates the frequency, rate or extent of co			
2	Vitvi04g01322	-2.02	4e-06	0.01	31 x 33	A chlorophyll-containing plastid with thylakoids organized into			
3	Vitvi08g01831	-3.34	2e-05	0.03	34 x 39	A membrane-bounded organelle of eukaryotic cells in which			
4	Vitvi07g01627	-3.31	3e-05	0.03	34 x 39	Catalysis of the hydrolysis of internal, alpha-peptide bonds in			
5	Vitvi06g01348	-1.45	3e-05	0.03	19 x 37	The nonsense–mediated decay pathway for nuclear–transcrit			
2345678910	Vitvi02g00617	-1.27	4e-05	0.03	20 x 38	Binding to ATP, adenosine 5'-triphosphate, a universally impo			
	Vitvi03g00269	-1.92	5e-05	0.03	30 x 36	Any process that modulates the frequency, rate or extent of co			
	Vitvi17g00837 Vitvi09g00283	-2.03	6e-05	0.03	18 x 40	The component of a membrane consisting of the gene produc The component of a membrane consisting of the gene produc			
	Vitvi09g00283 Vitvi05g00209	-2.99 -1.47	6e-05 6e-05	0.03	33 x 40 29 x 34	The component of a membrane consisting of the gene produce. The component of a membrane consisting of the gene produce.			
11	Vitvi19g02059	-1.47	7e-05	0.03	29 x 34 31 x 34	A lipid bilayer along with all the proteins and protein complexe			
12	Vitvi11g01479	-1.48	8e-05	0.03	19 x 40	The component of a membrane consisting of the gene produc			
13	Vitvi19g00673	-2.41	8e-05	0.03	29 x 40	A membrane–bounded organelle of eukaryotic cells in which			
14	Vitvi13g01764	-2.19	8e-05	0.03	18 x 40	The formation of a protein dimer, a macromolecular structure			
15	Vitvi11g01230	-0.98	9e-05	0.03	27 x 33	A membrane-bounded organelle of eukaryotic cells in which			
16	Vitvi05g00771	-1.09	1e-04	0.03	21 x 39	The membrane surrounding a cell that separates the cell from			
iŏ	Vitvi12g00287	-1.56	1e-04	0.03	21 x 36	A ribonucleoprotein complex that contains an RNA molecule			
18	Vitvi03g00076	-1.97	1e-04	0.03	33 x 34	The component of a membrane consisting of the gene produc			
19	Vitvi17g01368	-1.45	1e-04	0.03	18 x 40	The component of a membrane consisting of the gene produc			
20	Vitvi15g01024	-3.19	1e-04	0.04	18 x 40	A lipid bilayer along with all the proteins and protein complexe			
20	Vitvi15g01024	-3.19	1e-04	0.04	18 x 40	A lipid bilayer along with all the proteins and protein compl			

Description



	Rank	GSZ	p-value	#all	Geneset
	Overexpi	ressed			
npc	1	8.04	0e+00	48	Transcriptioan/sacription tales - WRKY
	2	6.27	0e+00	45	Galactos@alatabsesmetabolism
ехє	3	5.81	0e+00	162	Plant spe@lfansigmedifig signalingpatPlagetepiatecognioniteraction
npc	4	5.63	0e+00	49	Transcriptioanisacitiption NAC
	5	4.64	0e+00	58	Other am 10 the cials nime tabidismeta 6 bulkarthie @utattaibolismetabolism
	6	4.31	0e+00	153	Plant-pathagenpathagenointeraction
	7	3.69	2e-04	77	Pores ion Robrassriels (TiGant)els [TC:1]
	8	3.57	5e-04	80	Transport Transport Stystherring Tethering factors
	9	3.56	5e-04	51	BiosyntheBiosynthesisdafraenoetadarljsmetaAokismbiosAuntimeIsiosynthesis
	10	3.55	5e-04	12	Enzyme -E6zayssel - Class I
ch	11	3.52	6e-04	24	Tropane pilpæpiadineepapætiplyniedianedaptyalldidebadksyltotlolelsiossynthesis
duc	12	3.5	6e-04	77	Carbohyd@atebofe,tdbatlësmeta@allasotose@alletatbslësmetabolism
r ce	13	3.49	7e-04	15	Stilbenoic Stillang rillo èto taia o y tha ptagiri gero blogio syvent blesio synthesis
	14	3.41	9e-04	92	Lipid metalipoidismetalGolyissenolipüdymsetalipoidismetabolism
mo	15	3.39	9e-04	33	alpha-Linad petrale-bizid le métadocidisme tabolism
	16	3.38	9e-04	26	Flavonoid Flavosynttldelsics synthesis
	17	3.37	1e-03	17	Isoquinolils@qulkindridebidlsqltdldebisssynthesis
	18	3.25	1e-03	42	Tryptopha Tryptetphalism etabolism
npc	19	3.23	1e-03	34	Tyrosine ritiertatiolismetabolism
	20	3.23	1e-03	18	Receptor Recorptors - Others
	Underex	oressed			
of Ct	1	-12.37	0e+00	18	Energy mētadogljsmetalBbitsosynPleosissaymiteresasproteimsa proteins
intc	2	-11.51	0e+00	18	Photosyn Pleasins syrathless is a paroteins a proteins
ch	3	-10.73	0e+00	47	Transporterareatatorter-datensporteeterareatatoriceron carriers
s in	4	-8.03	0e+00	38	Photosyn (Pleasies synthesis
crit	5	-7.4	0e+00	78	Energy metatrglijsmetalbbiistrusyntPlassiesynthesis
npc	6	-7.18	0e+00	80	Cytoskeletonioskeletotubulkisrotubules
of Ct	7	-7.17	0e+00	217	Cell motilitigell integlialization englatation regatos interpretos kelleton
duc	8	-6.99	0e+00	10	Photosyn Phesios synutreis is Photeins ys Pelmoto (\$750 enchl (\$750 by that) rophylla)
duc	9	-6.79	0e+00	206	Cell growthethrand Cathlathall Cell wall
duc	10	-6.04	0e+00	40	Transport Transport Stylstenkoid Titaytaktorid partitentiang pathway
exe	11	-4.49	0e+00	41	Porphyrin Roestalycitism etabolism
duc ch	12	-4.37	0e+00	10 19	Peptidase@equidaisleibiatorus inhfibirtoins A1F.qurejinsiA faquelipsin family Transcriptforumfacutipution AdditionsA- AUXIAA
ıre	13 14	-4.14	0e+00	134	Hormonelskigmating signatingsign/alining signaling
ch	15	-4.08 -4.07	0e+00 0e+00	18	Transcription faction to ARF
rom	16	-3.73	1e-04	30	Glycan bi Gsycatnelsiosayndhessitabolilsmetable/GslycarNet@lyadartide gradation
ıle (17	-3.64	3e-04	11	Transcription factorisation of the control of the c
duc	18	-3.6	4e-04	51	Plant spe Elfansispredifig sig Ciadiandian Cfryddidian rhythm
duc	19	-3.6	4e-04	219	Cell growtDetIngtroutetthandOutslathadeCell cycle
ехє	20	-3.54	5e-04	19	AquaporinAsquapicninas amelusrae storienentataspudeterar[3]@rfteAs3[TC:1.A.8]
	-				

