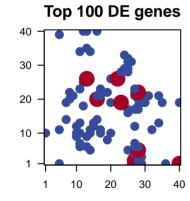
# Sangio\_acclim\_r1

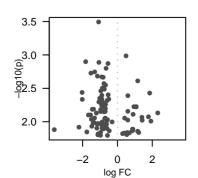
## **Global Summary**

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 > = 0.45< fdr > = 1

## **Portrait** 40 30 20 10 -10 20 30





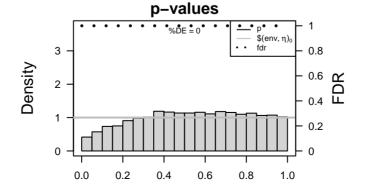
### Differentially expressed genes

log(FC) fdr

Rank

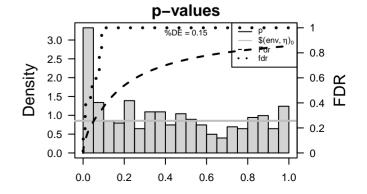
	ID	•	p-value		Metagene					
Ove	Overexpressed Overexpres									
1	Vitvi04g00582	0.49	0.001	1	11 x 23	Binding to a carbohydrate, which includes monosaccharides,	1	5.22	0e+00	
2	Vitvi04g00156	1.16	0.002	1	24 x 33	A membrane-bounded organelle of eukaryotic cells in which	2	5.07	0e+00	
3	Vitvi06g00547	1.85	0.004	1	12 x 40	Catalysis of the hydrolysis of internal, alpha-peptide bonds in	3	5.05	0e+00	
4	Vitvi18g00224	0.6	0.004	1	22 x 26	Catalysis of the geometric or structural changes within one m	4	3.89	8e-05	
5	Vitvi00g00736	1.08	0.006	1	13 x 26		5	3.83	8e-05	
6	Vitvi12g01971	0.94	0.006	1	22 x 26		6	3.56	5e-04	
7	Vitvi07g02801	1.07	0.006	1	13 x 26		7	3.25	1e-03	
8	Vitvi14q01003	0.6	0.007	1	14 x 34	The contents of a cell excluding the plasma membrane and n	8	3.01	3e-03	
9	Vitvi07g00130	2.31	0.007	1	1 x 10	Binding to a magnesium (Mg) ion.	9	2.97	3e-03	
10	Vitvi02g01559	0.9	0.008	1	26 x 31	5 5 , 5,	10	2.96	3e-03	
11	Vitvi15g01618	1.78	0.008	1	13 x 40	Catalysis of the transfer of a nucleotidyl group to a reactant.	11	2.94	4e-03	
12	Vitvi07g00188	1.4	0.009	1	16 x 40	Catalysis of the hydrolysis of any ester bond.	12	2.84	5e-03	
13	Vitvi03g00022	0.41	0.009	1	13 x 35	The component of a membrane consisting of the gene produc	13	2.83	5e-03	
14	Vitvi18g00337	0.59	0.009	1	25 x 31	A membrane-bounded organelle of eukaryotic cells in which	14	2.82	6e-03	
15	Vitvi07g02647	1.42	0.010	1	5 x 11	Binding to ATP, adenosine 5'-triphosphate, a universally impo	15	2.73	8e-03	
16	Vitvi15g01667	1.92	0.010	1	8 x 20	Binding to ADP, adenosine 5'-diphosphate.	16	2.71	8e-03	
17	Vitvi04g00489	0.88	0.013	1	24 x 29	A lipid bilayer along with all the proteins and protein complexe	17	2.69	8e-03	
18	Vitvi19g00151	0.86	0.013	1	8 x 22	The synthesis of RNA from a DNA template by RNA polymera	18	2.65	9e-03	
19	Vitvi02g00508	0.87	0.014	1	25 x 28	Any molecular function by which a gene product interacts sele	19	2.64	9e-03	
20	Vitvi01g01632	1.16	0.014	1	9 x 21	Binding to a protein.	20	2.64	9e-03	
Und	erexpressed						Undere	pressec	1	
1	Vitvi07g00300	-1.08	3e-04	1	17 x 10	Catalysis of an oxidation-reduction (redox) reaction, a reversi	1	-6.43	0e+00	
2	Vitvi13q00687	-1.83	1e-03	1	40 x 1	Binding to an amino acid, organic acids containing one or mo	2	-6.43 -6.22	0e+00	
3	Vitvi04g01785	-1.07	1e-03	1	28 x 18	briding to an armino acid, organic acids containing one or mo	3	-6.16	0e+00	
4	Vitvi19g01752	-0.54	1e-03	1	28 x 17		4	-5.06	0e+00	
5	Vitvi03g00560	-0.65	2e-03	1	16 x 20	A lipid bilayer along with all the proteins and protein complexe	5	-4.51	0e+00	
5 6	Vitvi01g01443	-1.31	2e-03	1	14 x 5	The component of a membrane consisting of the gene produc	ŏ	-4.36	0e+00	
7	Vitvi09g01027	-1.53	2e-03	1	7 x 19	Binding to a protein.	7	-3.98	0e+00	
8	Vitvi10g01885	-1.15	2e-03	1	13 x 9		8	-3.82	1e-04	
9	Vitvi07g02059	-0.9	2e-03	1	28 x 2		9	-3.54	5e-04	
10	Vitvi15g00692	-0.82	2e-03	1	28 x 22	Binding to a metal ion.	10	-3.16	2e-03	
11	Vitvi06g00568	-0.78	3e-03	1	25 x 16	A semiautonomous, self replicating organelle that occurs in va	11	-3.06	2e-03	
12	Vitvi01g00092	-0.69	3e-03	1	34 x 13	A membrane-bounded organelle of eukaryotic cells in which	12	-3.06	2e-03	
13	Vitvi08g01926	-0.87	3e-03	1	27 x 7	A membrane–bounded organelle of eukaryotic cells in which	13	-2.95	3e-03	
14	Vitvi05g00049	-0.75	3e-03	1	27 x 17	A semiautonomous, self replicating organelle that occurs in vi	14	-2.8	6e-03	
15	Vitvi11g00314	-0.96	3e-03	1	10 x 12	A membrane-bounded organelle of eukaryotic cells in which	15	-2.58	1e-02	
16	Vitvi08g01826	-2.03	4e-03	1	10 x 9	Catalysis of an oxidation–reduction (redox) reaction, a reversi	16	-2.52	1e-02	
17	Vitvi18g00752	-0.53	4e-03	1	17 x 22	Catalysis of the transfer of a group, e.g. a methyl group, glyco	17	-2.52	1e-02	
18	Vitvi09g00723 Vitvi01g02022	-0.9	4e-03	1	28 x 5	Any process involved in the conversion of a primary mRNA tra	18	-2.46	2e-02	
19 20	Vitvi11g02022	-1.02 -0.5	4e-03 5e-03	1 1	27 x 2 19 x 22	Any process involved in the conversion of a philitary mixina to	19	-2.43 -2.31	2e-02 2e-02	
20	vitvii igooos/	-0.5	JE-03	1	19 x 22		20	-2.31	26-02	

Description



#### Differentially expressed gene sets

	Rank	GSZ	p-value	#all	Geneset
	Overexp	ressed			
les,	1	5.22	0e+00	18	Photosyn Priecusios syrathhesios a-paroteims a proteins
ich	ż	5.07	0e+00	18	Energy m Etæbrglýsmmetal Blobistors yn Priecolos symtheres às pero teims a proteins
ds in	3	5.05	0e+00	129	Enzyme -E8z2/rf0dyec0sQla@excosylases
e m	4	3.89	8e-05	10	PeptidaseReputidasteits items in Hibitoits A1F. apreitys iA familys in family
	5	3.83	8e-05	47	Transport@rareatatorter-Caterlogo-tTeteratportoelerideron carriers
	6	3.56	5e-04	217	Cell motilitigell finetjilitjatioRedjulationcydfoskteletoytoskeleton
	7	3.25	1e-03	11	TranscriptToanfactipttion (aBtions - GRF
nd n	8	3.01	3e-03	38	Photosyn Pleases synthesis
	9	2.97	3e-03	18	TranscriptToanfactipition ARTors - ARF
	10	2.96	3e-03	197	Transport@iranatalonger-@ihailongels@imahpneriesand pores
nt.	11	2.94	4e-03	101	Starch an Standinos edna etabolism
	12	2.84	5e-03	31	Chromos@heoarrosasseciatedsscotteited-p@eeiasile@eing silencing
oduc	13	2.83	5e-03	66	Exosome Ex Excusorem a Epocoxie in a lop roble bituse o Calmodal contractor cells
ich	14	2.82	6e-03	10	Photosyn Priecolos symutreis is Princitous ys Pelnotos Problem (Prophytha) rophyll a)
mpc	15	2.73	8e-03	13	Cofactors Confections ram direct abrilisme ta bolismine The tablo is metabolism
	16	2.71	8e-03	30	Glycan bi@dycatmelsics:symdhessitsaboblismetalsle@dycanNele@dyadantide.gradatio
lexe	17	2.69	8e-03	100	Plant spellfamsigmadifig signalineg dellengemelentelopment
nera	18	2.65	9e-03	32	Circadian@frydadinan phythtm - plant
sele	19	2.64	9e-03	219	Cell growthetingtobethandbattacleCell cycle
	20	2.64	9e-03	21	Thiamine Theatatioesmetabolism
	Underex	pressed	,		
ersi	1	-6.43	0e+00	211	RibosomeRibosome
mo	ż	-6.22	0e+00	247	Translatio Translatiosome Ribosome
	3	-6.16	0e+00	144	RibosomeRib EstkaneyoteSukaryotes
	3 4	-5.06	0e+00	73	TranscriptToanfactiontion AR20ESREBP2 EREBP
lexe	5	-4.51	0e+00	49	TranscriptToanfactipition Na&Cors - NAC
oduc	6	-4.36	0e+00	140	Hormone Hongmating signaling signaling
	7	-3.98	0e+00	45	Galactos Galatatos Esimetabolism
	8	-3.82	1e-04	97	RibosomeRib Aschaea Archaea
	9	-3.54	5e-04	64	TranscriptToanfactipition (attlersran@theptiloanfactipition factors
	10	-3.16	2e-03	58	Other am 10 the cials nime tacidis smeta 6 bilitanthie not untettaibolis metabolism
in v	11	-3.06	2e-03	77	Cysteine @ysteriethiamdneenteitarbiolism
ich	12	-3.06	2e-03	11	Biosynthe Biosynthesis dafra en etabarlysmeta Ablastrios Arbinos Arbin
ich	13	-2.95	3e-03	44	Energy metabolismetablidhisgen Matabelismetabolism
in va	14	-2.8	6e-03	48	Transcriptioantactipition taleters - WRKY
ich	15	-2.58	1e-02	51	Other me@athodisameta&iolidenrea&itionhas reactions



Chaperor@halbt86029 - HSP20

Tryptopha**Trypttabelism**etabolism

Arginine aArdipiroërændhetabioësmetabolism

PantotherPatetathue CattA birus @dAclsissynthesis