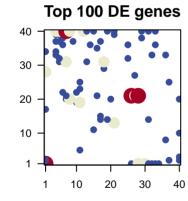
# Sangio\_acclim

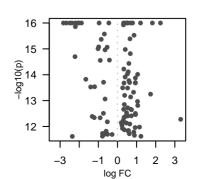
#### **Global Summary**

%DE = NA # genes with fdr < 0.2 = 5639 (3342 + /2297 -)# genes with fdr < 0.1 = 3950 (2362 + /1588 -)# genes with fdr < 0.05 = 2773 (1657 + /1116 -)# genes with fdr < 0.01 = 1744 (1037 + /707 -)

<FC> = 0< p-value > = 0.04< fdr > = 0.47

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





#### Differentially expressed genes

log(FC)

Rank

ID		9(	p-value		Meta	rtaint		
Over	rexpressed					Overexpress		
1	Vitvi05q01469	1.21	1e-16	2e-13	12 x 40	The part of the cytoplasm that does not contain organelles bu	1 .	3.8
ż	Vitvi06q00464	0.69	1e-16	2e-13	4 x 37	A semiautonomous, self replicating organelle that occurs in va	ż	3.7
3	Vitvi08g01288	0.32	1e-16	2e-13	11 x 23	The contents of a cell excluding the plasma membrane and n	3	3.6
4	Vitvi09g00502	1.83	1e-16	2e-13	8 x 20	Binding to ADP, adenosine 5'-diphosphate.	4	3.4
5	Vitvi10g01138	2.25	· · · · · · · · · · · · · · · · · · ·		Binding to a heme, a compound composed of iron complexed	5	3.4	
6	Vitvi12g00279	0.42	1e-16	2e-13	6 x 31	A lipid bilayer along with all the proteins and protein complexe	6	3.2
7	Vitvi13g01952	0.79	1e-16	2e-13	5 x 40	. ,	7	3.2
8	Vitvi15g01068	0.51	1e-16	2e-13	8 x 40	The directed movement of proteins in a cell, including the mo	8	3.1
9	Vitvi16g00005	0.54	1e-16	2e-13	5 x 32	Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, (	9	3.1
10	Vitvi01g00120	0.31	1e-16	2e-13	11 x 25	Binding to ATP, adenosine 5'-triphosphate, a universally impo	Ĭ0	3.1
11	Vitvi07g01868	0.87	3e-16	6e-13	32 x 33		11	3.0
12	Vitvi05g01549	0.65	4e-16	6e-13	5 x 39		12	2.9
13	Vitvi13g00594	0.41	1e-15	1e-12	10 x 22	The chemical reactions and pathways resulting in the formatic	13	2.8
14	Vitvi12g02383	0.67	2e-15	4e-12	4 x 34		14	2.8
15	Vitvi03g01505	0.6	4e-15	1e-11	25 x 36	The component of a membrane consisting of the gene produc	15	2.7
16	Vitvi03g00041	0.33	6e-15	1e-11	6 x 22		16	2.6
17	Vitvi01g00779	0.56	8e-15	1e-11	7 x 40	A membrane-bounded organelle of eukaryotic cells in which	17	2.6
18	Vitvi05g00330	0.52	9e-15	1e-11	7 x 40	The synthesis of an RNA transcript from a DNA template.	18	2.6
19	Vitvi16g00284	1.06	1e-14	1e-11	4 x 40	Binding to ATP, adenosine 5'-triphosphate, a universally impo	19	2.6
20	Vitvi05g01468	0.4	1e-14	1e-11	18 x 31	Binding to ATP, adenosine 5'-triphosphate, a universally impo	20	2.5
Unde	erexpressed						Underex	pres
1	Vitvi10g01743	-2.49	1e-16	2e-13	1 x 1		1	-7
2	Vitvi02g00953	-0.45	1e-16	2e-13	16 x 21	Binding to a nucleic acid.	2	-5.
3	Vitvi05g02250	-2.68	1e-16	2e-13	37 x 25		2	-5.
4	Vitvi07g02390	-2.08	1e-16	2e-13	17 x 15		4	-5.
5	Vitvi10g01613	-2.38	1e-16	2e-13	27 x 21	Binding to ATP, adenosine 5'-triphosphate, a universally impo	5	-4.
6	Vitvi12g02179	-1.88	1e-16	2e-13	29 x 40	The component of a membrane consisting of the gene produc	<u>6</u>	-4.
7	Vitvi12g02545	-0.96	1e-16	2e-13	28 x 21	Binding to ATP, adenosine 5'-triphosphate, a universally impo	7	-4.
8	Vitvi14g00297	-2.83	1e-16	2e-13	30 x 1	District ADD allowed of Palaceter	8	-4.
9	Vitvi15g01136	-2.01	1e-16	2e-13	28 x 21	Binding to ADP, adenosine 5'-diphosphate.	9	-4.
10	Vitvi16g01449	-2.2	1e-16	2e-13	1 x 28		10	-3.

Description

## Differentially expressed gene sets Rank GSZ p-value #all Geneset

ar	ik ID	log(r	p–va	lue	Meta	gene	Rank	GSZ	p-value	#all	Geneset
erexpressed					Overexpressed						
	Vitvi05g01469	1.21	1e-16	2e-13	12 x 40	The part of the cytoplasm that does not contain organelles bu	1 .	3.86	0e+00	51	Plant spe <b>Elfantsignedifig</b> signiadiandian Chrytholian rhythm
	Vitvi06g00464		1e-16	2e-13	4 x 37	A semiautonomous, self replicating organelle that occurs in va	2	3.71	2e-04	110	Ubiquitin systemutin-systemsub-whith Removember integration in the control of the
	Vitvi08g01288		1e-16	2e-13	11 x 23		3	3.6	4e-04	62	RibosomeRitiosenesisieg@@@spartisles particles
	Vitvi09g00502		1e-16	2e-13	8 x 20	Binding to ADP, adenosine 5'-diphosphate.	4	3.48	6e-04	32	Circadian Cinyatadran plant
	Vitvi10g01138		1e-16	2e-13	33 x 40	• •	5	3.42	1e-03	13	CofactorsConfactionsnamed abolismeta biolismeta biolismine Theatatiolismeta bolism
	Vitvi12g00279		1e-16	2e-13	6 x 31	A lipid bilayer along with all the proteins and protein complexe	6	3.23	2e-03	11	Transcription (agription (agricultum)
	Vitvi13g01952		1e-16	2e-13	5 x 40	1	7	3.2	2e-03	129	Enzyme -E8z2/n024yeo3s9laGebcosylases
	Vitvi15g01068		1e-16	2e-13	8 x 40	The directed movement of proteins in a cell, including the mo	8	3.17	2e-03	12	Channel - Changine In-u Cayotid en-ugate etidah-agateb (CiNaGi)nel (CNG)
	Vitvi16g00005		1e-16	2e-13	5 x 32	Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, (	9	3.16	2e-03	18	Transcription faction factors - ARF
١	Vitvi01g00120		1e-16	2e-13		· · · · · · · · · · · · · · · · · · ·	10	3.13	3e-03	21	Thiamine Thiatatioësmetabolism
•	Vitvi07g01868		3e-16	6e-13	32 x 33	,,	11	3.03	3e-03	100	Plant spellfansispradifig signaling development
,	Vitvi05g01549		4e-16	6e-13	5 x 39		12	2.9	5e-03	67	Replication
	Vitvi13g00594		1e-15	1e-12		The chemical reactions and pathways resulting in the formation	13	2.84	6e-03	151	RNA polyRNAspellyraystase II system
,	Vitvi12g02383		2e-15	4e-12	4 x 34	The chemical reactions and parmays resulting in the formation	14	2.82	6e-03	75	Mitochon diffite dramsamigatta ansand phitams bertiab tránstaction factors
	Vitvi03g01505		4e-15	1e-11		The component of a membrane consisting of the gene produc	15	2.77	7e-03	116	RibosomeRibiogenessisieg@ressisS Paetioles particles
	Vitvi03g00041		6e-15	1e-11	6 x 22	The compensit of a monitorane consisting of the gene produc	16	2.64	9e-03	111	Transport@iranasjaluntger-@atallengs-caRdofterts @att 66 to 94
,	Vitvi01g00779		8e-15	1e-11	7 x 40	A membrane-bounded organelle of eukaryotic cells in which	17	2.61	1e-02	10	Transcription (activities GCC2C2-CO
2	Vitvi05g00330		9e-15	1e-11	7 x 40	The synthesis of an RNA transcript from a DNA template.	18	2.61	1e-02	31	AutophagAutophegy – other
,	Vitvi16g00284		1e-14	1e-11	4 x 40	Binding to ATP, adenosine 5'-triphosphate, a universally impo	19	2.6	1e-02	28	Transcription factoristico MTERF
í	Vitvi05g01468		1e-14	1e-11	18 x 31	Binding to ATP, adenosine 5'-triphosphate, a universally impo	20	2.55	1e-02	34	Transcription factipation & Etilo & GOSET PCG
•		0.1	10-14	10-11	10 % 01	,,,,,,,	20	2.00	10 02	0.	
de	erexpressed						Underex	pressea	1		
	Vitvi10g01743	-2.49	1e-16	2e-13	1 x 1		1	-7	0.000	73	Transcription faction factors Reports EREBP
	Vitvi02g00953		1e-16	2e-13		Binding to a nucleic acid.	2	-5.34	0.000	211	Ribosome Ribosome
	Vitvi05g02250		1e-16	2e-13	37 x 25		3	-5.2	0.000	140	Hormonelskigmating sighttalijtegne stighnateting signaling
	Vitvi07g02390		1e-16	2e-13	17 x 15		4	-5.12	0.000	144	RibosomeRib EstkaneyeteEsukaryotes
	Vitvi10g01613		1e-16	2e-13	27 x 21	Binding to ATP, adenosine 5'-triphosphate, a universally impo	5	-4.93	0.000	247	Translatio Translatissome Ribosome
	Vitvi12g02179		1e-16	2e-13	29 x 40	The component of a membrane consisting of the gene produc	6	-4.74	0.000	45	Galactos@alatatosesmetabolism
	Vitvi12g02545		1e-16	2e-13	28 x 21	Binding to ATP, adenosine 5'-triphosphate, a universally impo	7	-4.53	0.000	49	TranscriptToanfactipition MacOrs - NAC
	Vitvi14g00297		1e-16	2e-13	30 x 1	Diadian to ADD adappairs 51 diabandate	8	-4.3	0.000	48	Transcription taketor WRKY
	Vitvi15g01136 Vitvi16g01449		1e-16	2e-13	28 x 21 1 x 28	Binding to ADP, adenosine 5'-diphosphate.	9	-4.29 -3.33	0.000 0.001	64	Transcription factors Energy metabolismetabidisgen Nietabelismetabolism
,	Vitvi04g01920		1e-16 1e-16	2e-13 6e-13	1 x 28		10 11	-3.33 -3.23	0.001	44 97	RibosomeRib <b>Ascina</b> ea- Archaea
,	Vitvi07g00097		3e-16	6e-13	26 x 1	Binding to monomeric or multimeric forms of actin, including a	12	-3.23 -3.19	0.002	97 77	Cysteine Onstreiethomine ethitatioës metabolism
	Vitvi07g00465		4e-16	1e-12	40 x 20	Binding to ATP, adenosine 5'-triphosphate, a universally impo	13	-3.19	0.002	15	Stilbenoic&tillaentoeptaionojtheptagorigenotbojorsgentblesissynthesis
i	Vitvi12g02389		8e-16	1e-12	26 x 21	Catalysis of the transfer of a methyl group to the oxygen atom	14	-2.76	0.007	51	Other me@athredismetaSirrighenre@bitighens reactions
:	Vitvi04g01288		9e-16	1e-12	31 x 14	,, g	15	-2.75	0.007	26	Glycosyltr@hysfesayteens/flavdrs:@holbirdmolleobile molecule
	Vitvi14g02594		1e-15		1 x 17		16	-2.59	0.011	81	Enzyme -E4:2/r0ærber2-o0ærdæonlyaxesen lyases
,	Vitvi14g02627		1e-15	4e-12	26 x 21		17	-2.42	0.018	22	Fatty acidFattyngaationelongation
3	Vitvi12g00274		2e-15	4e-12	1 x 1	A membrane-bounded organelle of eukaryotic cells in which	18	-2.41	0.018	153	Plant-pathagetepiathageteointeraction
)	Vitvi03g00690	-0.42	3e-15	4e-12	27 x 21	A lipid bilayer along with all the proteins and protein complexe	19	-2.41	0.019	18	Chaperon@hapt86020 - HSP20
)	Vitvi00g02175	-0.9	3e-15	7e-12	30 x 1		20	-2.39	0.019	29	Transcription factipition faltities - GRAS

