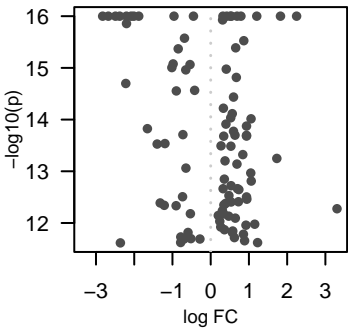
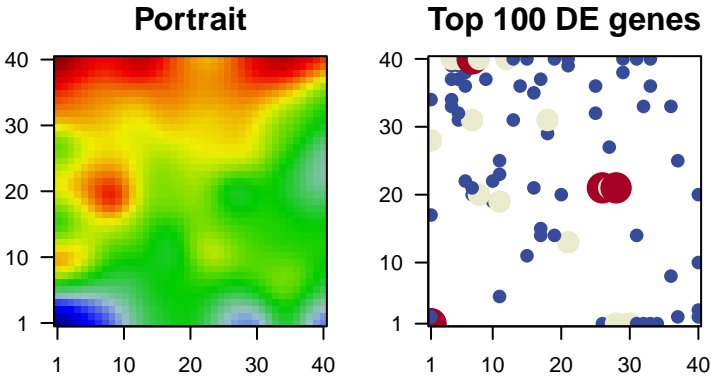


Sangio_acclim

Global Summary

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

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



Differentially expressed genes

Rank		log(FC)	fdr	Description		
ID		p-value		Metagene		
Overexpressed						
1	Vitv05g0146E	1.21	1e-16	2e-13	12 x 40	The part of the cytoplasm that does not contain organelles bu
2	Vitv06g000464	0.69	1e-16	2e-13	4 x 37	A semiautonomous, self replicating organelle that occurs in vi
3	Vitv08g0128E	0.32	1e-16	2e-13	11 x 23	The contents of a cell excluding the plasma membrane and n
4	Vitv09g00502	1.83	1e-16	2e-13	8 x 20	Binding to ADP, adenosine 5'-diphosphate.
5	Vitv10g0113E	2.25	1e-16	2e-13	33 x 40	Binding to a heme, a compound composed of iron complexed
6	Vitv12g0027E	0.42	1e-16	2e-13	6 x 31	A lipid bilayer along with all the proteins and protein complex
7	Vitv13g01952	0.79	1e-16	2e-13	5 x 40	
8	Vitv15g0106E	0.51	1e-16	2e-13	8 x 40	The directed movement of proteins in a cell, including the mo
9	Vitv16g0000E	0.54	1e-16	2e-13	5 x 32	Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, (
10	Vitv01g0012C	0.31	1e-16	2e-13	11 x 25	Binding to ATP, adenosine 5'-triphosphate, a universally impac
11	Vitv07g0186E	0.87	3e-16	6e-13	32 x 33	
12	Vitv05g0154E	0.65	4e-16	6e-13	5 x 39	
13	Vitv13g000594	0.41	1e-15	1e-12	10 x 22	The chemical reactions and pathways resulting in the formati
14	Vitv12g0238E	0.67	2e-15	4e-12	4 x 34	
15	Vitv03g0150E	0.6	4e-15	1e-11	25 x 36	The component of a membrane consisting of the gene produc
16	Vitv03g00041	0.33	6e-15	1e-11	6 x 22	
17	Vitv01g0077E	0.56	8e-15	1e-11	7 x 40	A membrane-bounded organelle of eukaryotic cells in which
18	Vitv05g0033C	0.52	9e-15	1e-11	7 x 40	The synthesis of an RNA transcript from a DNA template.
19	Vitv16g00284	1.06	1e-14	1e-11	4 x 40	Binding to ATP, adenosine 5'-triphosphate, a universally impac
20	Vitv05g0146E	0.4	1e-14	1e-11	18 x 31	Binding to ATP, adenosine 5'-triphosphate, a universally impac
Underexpressed						
1	Vitv10g0174E	-2.49	1e-16	2e-13	1 x 1	
2	Vitv02g0095E	-0.45	1e-16	2e-13	16 x 21	Binding to a nucleic acid.
3	Vitv05g0225C	-2.68	1e-16	2e-13	37 x 25	
4	Vitv07g0239C	-2.08	1e-16	2e-13	17 x 15	
5	Vitv10g0161E	-2.38	1e-16	2e-13	27 x 21	Binding to ATP, adenosine 5'-triphosphate, a universally impac
6	Vitv12g0217E	-1.88	1e-16	2e-13	29 x 40	The component of a membrane consisting of the gene produc
7	Vitv12g0254E	-0.96	1e-16	2e-13	28 x 21	Binding to ATP, adenosine 5'-triphosphate, a universally impac
8	Vitv14g00297	-2.83	1e-16	2e-13	30 x 1	
9	Vitv15g0113E	-2.01	1e-16	2e-13	28 x 21	Binding to ADP, adenosine 5'-diphosphate.
10	Vitv16g0144E	-2.2	1e-16	2e-13	1 x 28	
11	Vitv04g0192C	-2.2	1e-16	6e-13	1 x 1	
12	Vitv07g00097	-0.69	3e-16	6e-13	26 x 1	Binding to monomeric or multimeric forms of actin, including a
13	Vitv07g0046E	-0.85	4e-16	1e-12	40 x 20	Binding to ATP, adenosine 5'-triphosphate, a universally impac
14	Vitv12g0238E	-0.98	8e-16	1e-12	26 x 21	Catalysis of the transfer of a methyl group to the oxygen atom
15	Vitv04g0128E	-0.54	9e-16	1e-12	31 x 14	
16	Vitv14g02594	-1.02	1e-15	1e-12	1 x 17	
17	Vitv14g02627	-0.65	1e-15	4e-12	26 x 21	
18	Vitv12g00274	-2.22	2e-15	4e-12	1 x 1	A membrane-bounded organelle of eukaryotic cells in which
19	Vitv03g0069C	-0.42	3e-15	4e-12	27 x 21	A lipid bilayer along with all the proteins and protein complex
20	Vitv00g0217E	-0.9	3e-15	7e-12	30 x 1	

Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
Overexpressed				
1	3.86	0e+00	51	Plant specific signaling signaling pathway
2	3.71	2e-04	110	Ubiquitin system ubiquitin system
3	3.6	4e-04	62	Ribosome ribosome
4	3.48	6e-04	32	Circadian rhythm circadian rhythm - plant
5	3.42	1e-03	13	Cofactors cofactors in metabolism
6	3.23	2e-03	11	Transcription factors - GRF
7	3.2	2e-03	129	Enzyme - Glycosylases
8	3.17	2e-03	12	Channel - CNG
9	3.16	2e-03	18	Transcription factors - ARF
10	3.13	3e-03	21	Thiamine metabolism
11	3.03	3e-03	100	Plant specific signaling signaling pathway
12	2.9	5e-03	67	Replication and repair
13	2.84	6e-03	151	RNA polymerase II system
14	2.82	6e-03	75	Mitochondrial transcription and translation factors
15	2.77	7e-03	116	Ribosome ribosome
16	2.64	9e-03	111	Transporter - ABC
17	2.61	1e-02	10	Transcription factors - C2C2-CO
18	2.61	1e-02	31	Autophagy - other
19	2.6	1e-02	28	Transcription factors - MTERF
20	2.55	1e-02	34	Transcription factors - PCG
Underexpressed				
1	-7	0.000	73	Transcription factors - EREBP
2	-5.34	0.000	211	Ribosome ribosome
3	-5.2	0.000	140	Hormone signaling signaling
4	-5.12	0.000	144	Ribosome ribosome
5	-4.93	0.000	247	Translation
6	-4.74	0.000	45	Galactose metabolism
7	-4.53	0.000	49	Transcription factors - NAC
8	-4.3	0.000	48	Transcription factors - WRKY
9	-4.29	0.000	64	Transcription factors - GRF
10	-3.33	0.001	44	Energy metabolism
11	-3.23	0.002	97	Ribosome ribosome
12	-3.19	0.002	77	Cysteine metabolism
13	-3.02	0.004	15	Stilbenoid metabolism
14	-2.76	0.007	51	Other metabolism
15	-2.75	0.007	26	Glycosyltransferase
16	-2.59	0.011	81	Enzyme - Glycosylases
17	-2.42	0.018	22	Fatty acid elongation
18	-2.41	0.018	153	Plant-pathogen interaction
19	-2.41	0.019	18	Chaperone - HSP20
20	-2.39	0.019	29	Transcription factors - GRAS

