

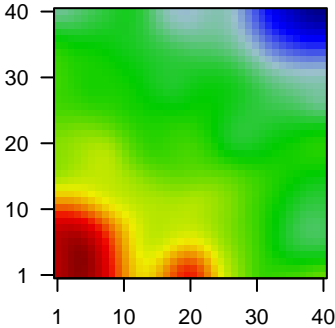
Sangio_freeze_r1

Global Summary

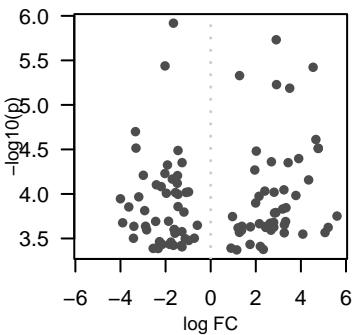
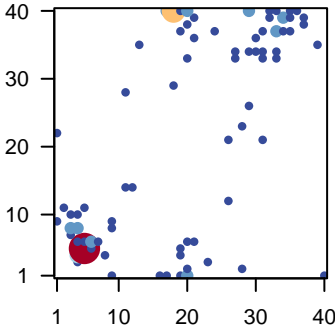
%DE = 0.41
genes with $\text{fdr} < 0.2 = 2422$ (1163 + / 1259 -)
genes with $\text{fdr} < 0.1 = 448$ (194 + / 254 -)
genes with $\text{fdr} < 0.05 = 79$ (44 + / 35 -)
genes with $\text{fdr} < 0.01 = 6$ (4 + / 2 -)

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

Portrait



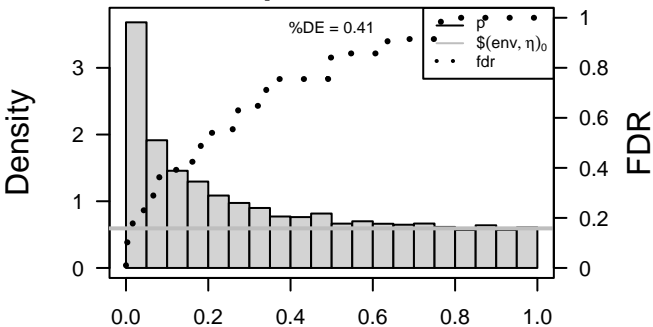
Top 100 DE genes



Differentially expressed genes

Rank	ID	log(FC)	fdr	Description		
		p-value		Metagene		
Overexpressed						
1	Vitv19g0006E	2.91	2e-06	0.01	3 x 10	Binding to ATP, adenosine 5'-triphosphate, a universally impc
2	Vitv05g0064E	4.54	4e-06	0.01	5 x 5	Catalysis of the hydrolysis of any ester bond.
3	Vitv14g0250C	1.28	5e-06	0.01	26 x 12	A lipid bilayer along with all the proteins and protein complex
4	Vitv14g0200E	2.92	6e-06	0.01	23 x 3	Binding to ATP, adenosine 5'-triphosphate, a universally impc
5	Vitv10g00877	3.5	6e-06	0.03	8 x 4	
6	Vitv16g01321	4.66	2e-05	0.03	6 x 5	
7	Vitv00g00932	4.77	3e-05	0.03	4 x 4	
8	Vitv02g01747	4.77	3e-05	0.03	4 x 4	
9	Vitv14g0200E	2.02	3e-05	0.03	17 x 1	
10	Vitv14g0048E	3.9	4e-05	0.03	6 x 6	
11	Vitv08g01794	2.69	4e-05	0.03	20 x 1	A membrane-bounded organelle of eukaryotic cells in which
12	Vitv10g0028E	3.43	4e-05	0.03	9 x 1	The component of a membrane consisting of the gene produc
13	Vitv17g00747	1.96	5e-05	0.03	20 x 6	The space external to the outermost structure of a cell. For ce
14	Vitv18g0126E	4.34	7e-05	0.03	5 x 4	
15	Vitv05g0052E	3.25	9e-05	0.03	5 x 5	Catalysis of the transfer of an acetyl group to an acceptor moi
16	Vitv03g0029E	2.4	9e-05	0.03	4 x 10	
17	Vitv00g0131E	2.81	1e-04	0.03	5 x 5	
18	Vitv18g0284C	3.78	1e-04	0.03	3 x 8	
19	Vitv01g0157E	2.14	1e-04	0.03	16 x 1	Binding to ATP, adenosine 5'-triphosphate, a universally impc
20	Vitv17g0153E	1.99	1e-04	0.04	28 x 2	
Underexpressed						
1	Vitv06g00107	-1.65	1e-06	0.01	28 x 23	Any process that modulates the frequency, rate or extent of c
2	Vitv04g0132E	-2.02	4e-06	0.01	31 x 33	A chlorophyll-containing plastid with thylakoids organized int
3	Vitv08g01831	-3.34	2e-05	0.03	34 x 39	A membrane-bounded organelle of eukaryotic cells in which
4	Vitv07g01627	-3.31	3e-05	0.03	34 x 39	Catalysis of the hydrolysis of internal, alpha-peptide bonds in
5	Vitv06g0134E	-1.45	3e-05	0.03	19 x 37	The nonsense-mediated decay pathway for nuclear-transcrit
6	Vitv02g00617	-1.27	4e-05	0.03	20 x 38	Binding to ATP, adenosine 5'-triphosphate, a universally impc
7	Vitv03g0026E	-1.92	5e-05	0.03	30 x 36	Any process that modulates the frequency, rate or extent of c
8	Vitv17g00837	-2.03	6e-05	0.03	18 x 40	The component of a membrane consisting of the gene produc
9	Vitv09g0028E	-2.99	6e-05	0.03	33 x 40	The component of a membrane consisting of the gene produc
10	Vitv05g0020E	-1.47	6e-05	0.03	29 x 34	The component of a membrane consisting of the gene produc
11	Vitv19g0205E	-1.7	7e-05	0.03	31 x 34	A lipid bilayer along with all the proteins and protein complex
12	Vitv11g0147E	-1.48	8e-05	0.03	19 x 40	The component of a membrane consisting of the gene produc
13	Vitv19g0067E	-2.41	8e-05	0.03	29 x 40	A membrane-bounded organelle of eukaryotic cells in which
14	Vitv13g01764	-2.19	8e-05	0.03	18 x 40	The formation of a protein dimer, a macromolecular structure
15	Vitv11g0123C	-0.98	9e-05	0.03	27 x 33	A membrane-bounded organelle of eukaryotic cells in which
16	Vitv05g00771	-1.09	1e-04	0.03	21 x 39	The membrane surrounding a cell that separates the cell from
17	Vitv12g00287	-1.56	1e-04	0.03	21 x 36	A ribonucleoprotein complex that contains an RNA molecule
18	Vitv03g0007E	-1.97	1e-04	0.03	33 x 34	The component of a membrane consisting of the gene produc
19	Vitv17g0136E	-1.45	1e-04	0.03	18 x 40	The component of a membrane consisting of the gene produc
20	Vitv15g01024	-3.19	1e-04	0.04	18 x 40	A lipid bilayer along with all the proteins and protein complex

p-values



Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	8.04	0e+00	48	Transcription factor WRKY - WRKY
2	6.27	0e+00	45	Galactose metabolism
3	5.81	0e+00	162	Plant species predicting signaling pathway
4	5.63	0e+00	49	Transcription factor NAC - NAC
5	4.64	0e+00	58	Other amino acid metabolism
6	4.31	0e+00	153	Plant-pathogen interaction
7	3.69	2e-04	77	Pores ion channels [TC:1]
8	3.57	5e-04	80	Transport system
9	3.56	5e-04	51	Biosynthesis of secondary metabolites
10	3.55	5e-04	12	Enzyme - Class I
11	3.52	6e-04	24	Tropene biosynthesis
12	3.5	6e-04	77	Carbohydrate metabolism
13	3.49	7e-04	15	Stilbenoid biosynthesis
14	3.41	9e-04	92	Lipid metabolism
15	3.39	9e-04	33	alpha-Linolenic acid metabolism
16	3.38	9e-04	26	Flavonoid biosynthesis
17	3.37	1e-03	17	Isoquinoline alkaloid biosynthesis
18	3.25	1e-03	42	Tryptophan metabolism
19	3.23	1e-03	34	Tyrosine metabolism
20	3.23	1e-03	18	Receptor - Others
<i>Underexpressed</i>				
1	-12.37	0e+00	18	Energy metabolism
2	-11.51	0e+00	18	Photosynthesis - proteins
3	-10.73	0e+00	47	Transport carrier
4	-8.03	0e+00	38	Photosynthesis
5	-7.4	0e+00	78	Energy metabolism
6	-7.18	0e+00	80	Cytoskeleton
7	-7.17	0e+00	217	Cell motility
8	-6.99	0e+00	10	Photosynthesis
9	-6.79	0e+00	206	Cell growth and division
10	-6.04	0e+00	40	Transport system
11	-4.49	0e+00	41	Porphyria
12	-4.37	0e+00	10	Peptidase
13	-4.14	0e+00	19	Transcription factor AUXIA - AUXIA
14	-4.08	0e+00	134	Hormone signaling
15	-4.07	0e+00	18	Transcription factor ARF - ARF
16	-3.73	1e-04	30	Glycan biosynthesis
17	-3.64	3e-04	11	Transcription factor GRF - GRF
18	-3.6	4e-04	51	Plant species predicting signaling pathway
19	-3.6	4e-04	219	Cell growth and division
20	-3.54	5e-04	19	Aquaporin

p-values

