

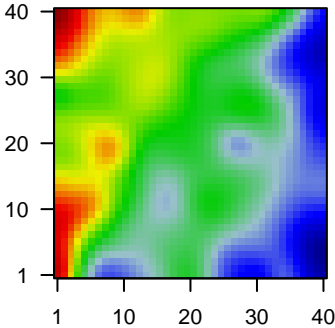
# Sangio\_accfreeze

## Global Summary

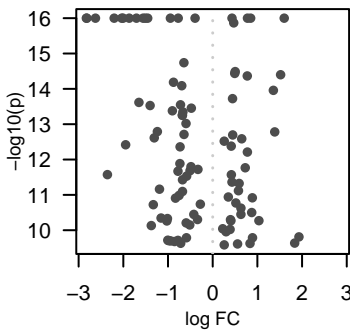
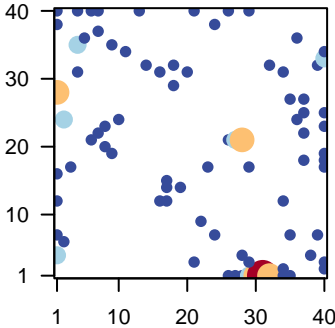
%DE = NA  
# genes with  $\text{fdr} < 0.2 = 1940$  ( 1085 + / 855 -)  
# genes with  $\text{fdr} < 0.1 = 1181$  ( 625 + / 556 -)  
# genes with  $\text{fdr} < 0.05 = 962$  ( 490 + / 472 -)  
# genes with  $\text{fdr} < 0.01 = 598$  ( 273 + / 325 -)

<FC> = 0  
<p-value> = 0.12  
<fdr> = 0.59

Portrait



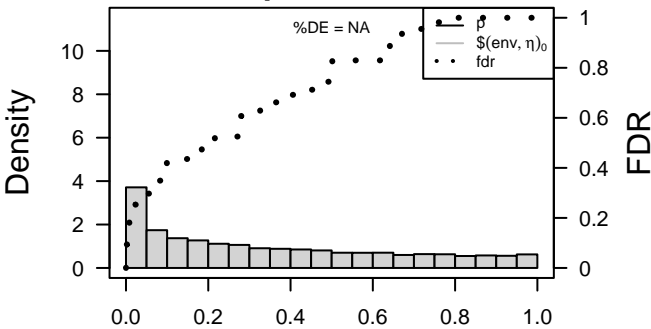
Top 100 DE genes



## Differentially expressed genes

Rank	ID	log(FC)	fdr	Description		
		p-value	Metagene			
Overexpressed						
1	Vitv07g01231	0.78	1e-16	4e-13	7 x 37	A process that is carried out at the cellular level which results
2	Vitv05g00464	0.43	1e-16	4e-13	8 x 23	A lipid bilayer along with all the proteins and protein complex
3	Vitv09g00546	0.85	1e-16	4e-13	34 x 2	Binding to ADP, adenosine 5'-diphosphate.
4	Vitv13g01200	1.6	1e-16	4e-13	13 x 40	Catalysis of an oxidation-reduction (redox) reaction in which
5	Vitv06g00472	0.47	1e-16	9e-12	4 x 31	Binding to ATP, adenosine 5'-triphosphate, a universally impc
6	Vitv10g01607	0.5	3e-15	9e-12	6 x 21	The contents of a cell excluding the plasma membrane and n
7	Vitv04g01234	0.49	4e-15	9e-12	14 x 32	A transcription regulator activity that modulates transcription c
8	Vitv04g00282	1.52	4e-15	9e-12	8 x 20	The membrane surrounding a cell that separates the cell from
9	Vitv08g01682	0.77	4e-15	2e-11	1 x 16	Binding to a calcium ion (Ca2+).
10	Vitv03g00017	1.36	1e-14	5e-11	9 x 19	Binding to a metal ion.
11	Vitv14g01820	0.44	2e-14	5e-11	18 x 32	The component of a membrane consisting of the gene produc
12	Vitv03g01260	1.39	2e-13	3e-10	1 x 7	
13	Vitv06g00681	0.45	2e-13	3e-10	5 x 36	A membrane-bound organelle of eukaryotic cells in which
14	Vitv08g01582	0.65	3e-13	5e-10	4 x 40	The contents of a cell excluding the plasma membrane and n
15	Vitv07g01806	0.26	3e-13	5e-10	20 x 31	The component of a membrane consisting of the gene produc
16	Vitv09g01346	0.41	4e-13	5e-10	23 x 17	The irregular network of unit membranes, visible only by elect
17	Vitv08g00950	0.78	6e-13	3e-09	1 x 12	The component of a membrane consisting of the gene produc
18	Vitv01g00511	0.73	2e-12	3e-09	1 x 38	A membrane-bound organelle of eukaryotic cells in which
19	Vitv05g01537	0.42	3e-12	3e-09	24 x 38	A membrane-bound organelle of eukaryotic cells in which
20	Vitv15g01062	0.43	4e-12	6e-09	7 x 22	The component of a membrane consisting of the gene produc
Underexpressed						
1	Vitv05g02250	-2.62	1e-16	4e-13	37 x 25	
2	Vitv07g02390	-2.04	1e-16	4e-13	17 x 15	
3	Vitv11g01385	-1.45	1e-16	4e-13	40 x 17	The component of a membrane consisting of the gene produc
4	Vitv12g02160	-1.71	1e-16	4e-13	27 x 21	A membrane-bound organelle of eukaryotic cells in which
5	Vitv12g02176	-1.87	1e-16	4e-13	29 x 40	The component of a membrane consisting of the gene produc
6	Vitv12g02545	-0.95	1e-16	4e-13	28 x 21	Binding to ATP, adenosine 5'-triphosphate, a universally impc
7	Vitv13g01997	-1.51	1e-16	4e-13	36 x 24	Catalysis of an oxidation-reduction (redox) reaction, a reversi
8	Vitv13g00521	-0.77	1e-16	4e-13	27 x 1	The component of a membrane consisting of the gene produc
9	Vitv14g00297	-2.82	1e-16	4e-13	30 x 1	
10	Vitv15g01136	-2.01	1e-16	4e-13	28 x 21	Binding to ADP, adenosine 5'-diphosphate.
11	Vitv16g01446	-2.2	1e-16	4e-13	1 x 28	
12	Vitv18g02715	-2.83	1e-16	4e-13	31 x 1	Binding to a heme, a compound composed of iron complexed
13	Vitv18g02371	-1.56	1e-16	4e-13	34 x 31	
14	Vitv19g00446	-0.39	1e-16	4e-13	34 x 12	The component of a membrane consisting of the gene produc
15	Vitv14g02627	-0.64	2e-15	9e-12	26 x 21	
16	Vitv15g01552	-0.88	7e-15	2e-11	16 x 12	
17	Vitv14g01474	-0.69	8e-15	3e-11	37 x 22	Catalysis of an oxidation-reduction (redox) reaction, a reversi
18	Vitv19g00422	-1.65	2e-14	5e-11	32 x 1	Binding to a protein.
19	Vitv14g01647	-0.72	3e-14	5e-11	28 x 21	
20	Vitv16g00160	-1.4	3e-14	5e-11	19 x 14	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	7.23	0e+00	48	Transcription factor WRKYs - WRKY
2	6.33	0e+00	49	Transcription factor NACs - NAC
3	5.75	0e+00	64	Transcription factor GATA1 - GATA1
4	5.66	0e+00	73	Transcription factor AP2/ERF2 EREBP
5	5.64	0e+00	162	Plant specific signaling pathway - Plant
6	5.22	0e+00	140	Hormone signaling pathway - Plant
7	5.05	0e+00	153	Plant-pathogen interaction
8	4.81	0e+00	62	Ribosome biogenesis - Ribosome
9	4.07	0e+00	116	Ribosome biogenesis - Ribosome
10	3.64	2e-04	89	MAPK signaling pathway - plant
11	3.49	6e-04	151	RNA polymerase II system
12	3.47	6e-04	86	Signal transduction - Calcium signaling pathway
13	3.42	1e-03	75	Translation - Ribosome biogenesis - Ribosome
14	3.39	1e-03	64	Ribosome biogenesis - Ribosome
15	3.26	2e-03	128	Ubiquitin-proteasome system - Ubiquitin
16	2.93	4e-03	67	Replication and DNA metabolism - DNA
17	2.76	7e-03	51	Plant specific signaling pathway - Plant
18	2.68	8e-03	110	Ubiquitin-proteasome system - Ubiquitin
19	2.64	9e-03	12	Channel - CNG channel (CNG)
20	2.55	1e-02	33	Carbohydrate metabolism - Carbohydrate
<i>Underexpressed</i>				
1	-8.87	0e+00	47	Transport - Transport - Transport
2	-8.42	0e+00	78	Energy metabolism - Energy metabolism
3	-8.38	0e+00	18	Energy metabolism - Energy metabolism
4	-7.73	0e+00	18	Photosynthesis - Photosynthesis
5	-7.58	0e+00	38	Photosynthesis - Photosynthesis
6	-5.45	0e+00	10	Photosynthesis - Photosynthesis
7	-4.85	0e+00	67	Ribosome biogenesis - Ribosome
8	-4.67	0e+00	26	Flavonoid biosynthesis - Flavonoid
9	-4.35	0e+00	40	Transport - Transport - Transport
10	-4.23	0e+00	24	Replication and DNA metabolism - DNA
11	-4.17	0e+00	41	Transport - Transport - Transport
12	-4.11	0e+00	72	Ribosome biogenesis - Ribosome
13	-4.01	0e+00	80	Cytoskeleton - Cytoskeleton
14	-3.87	0e+00	25	Nitrogen metabolism - Nitrogen
15	-3.87	0e+00	79	Transport - Transport - Transport
16	-3.79	0e+00	105	Energy metabolism - Energy metabolism
17	-3.5	5e-04	26	Glycosylation - Glycosylation
18	-3.38	1e-03	81	Enzyme - Enzyme
19	-3.38	1e-03	57	Glycolysis - Glycolysis
20	-3.33	1e-03	81	Oxidative phosphorylation - Oxidative

p-values

