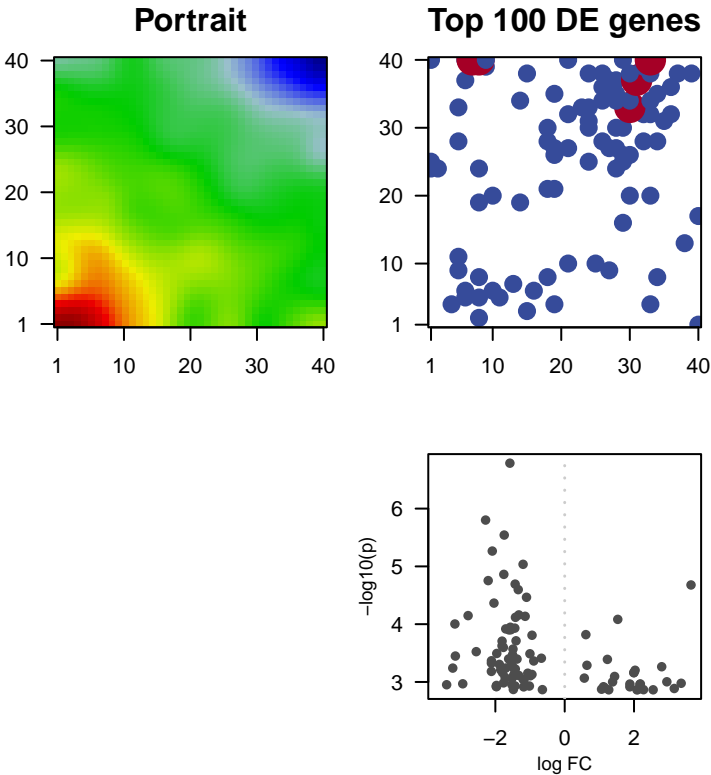


Sangio_freeze_r2

Global Summary

%DE = 0.29
genes with $\text{fdr} < 0.2 = 65$ (9 + / 56 -)
genes with $\text{fdr} < 0.1 = 22$ (2 + / 20 -)
genes with $\text{fdr} < 0.05 = 8$ (0 + / 8 -)
genes with $\text{fdr} < 0.01 = 0$ (0 + / 0 -)

<FC> = 0
<p-value> = 0.27
<fdr> = 0.71



Differentially expressed genes

Rank	ID	log(FC)	p-value	fdr	Description
Overexpressed					
1	Vitv01g0158E	3.64	2e-05	0.06	4 x 4 Binding to a calcium ion (Ca2+).
2	Vitv11g0130C	1.53	8e-05	0.10	2 x 24 The chemical reactions and pathways involving carbohydrate:
3	Vitv11g0134E	0.61	2e-04	0.19	18 x 21 Binding to a nucleic acid.
4	Vitv05g0009E	1.23	4e-04	0.20	16 x 6 Any molecular function by which a gene product interacts sel
5	Vitv04g0140I	0.64	5e-04	0.20	19 x 21 The contents of a cell excluding the plasma membrane and n
6	Vitv13g00517	2.8	5e-04	0.20	21 x 10 Catalysis of the transfer of an acyl group, other than amino-a
7	Vitv05g0060C	2.03	6e-04	0.20	19 x 4 The component of a membrane consisting of the gene produc
8	Vitv08g01112	1.99	7e-04	0.20	15 x 3 The component of a membrane consisting of the gene produc
9	Vitv07g0167Z	2	7e-04	0.20	5 x 11 Catalysis of an oxidation-reduction (redox) reaction, a reversi
10	Vitv07g0010I	1.44	8e-04	0.20	1 x 24
11	Vitv14g0141Z	0.57	9e-04	0.20	8 x 24 Binding to a protein.
12	Vitv05g0193Z	2.95	1e-03	0.20	6 x 5
13	Vitv10g0058A	1.38	1e-03	0.20	13 x 7 A membrane-bounded organelle of eukaryotic cells in which
14	Vitv17g0162I	3.36	1e-03	0.20	6 x 6
15	Vitv11g0013E	2.18	1e-03	0.20	10 x 6 Binding to ATP, adenosine 5'-triphosphate, a universally impc
16	Vitv15g00547	1.88	1e-03	0.20	8 x 8 Any molecular entity that serves as an electron acceptor and
17	Vitv03g0119E	2.17	1e-03	0.20	5 x 9 The component of a membrane consisting of the gene produc
18	Vitv14g0084I	1.12	1e-03	0.20	18 x 8 A membrane-bounded organelle of eukaryotic cells in which
19	Vitv03g0049E	1.88	1e-03	0.20	11 x 5 A membrane-bounded organelle of eukaryotic cells in which
20	Vitv08g0104Z	1.15	1e-03	0.20	25 x 10 Binding to a zinc ion (Zn).
Underexpressed					
1	Vitv06g0104A	-1.58	2e-07	0.02	29 x 30 Catalysis of an oxidation-reduction (redox) reaction, a reversi
2	Vitv19g0070E	-2.28	2e-06	0.02	7 x 40 The formation of a protein dimer, a macromolecular structure
3	Vitv05g0155E	-1.74	3e-06	0.03	19 x 35 Binds to and increases the activity of a GTPase, an enzyme t
4	Vitv14g0021E	-2.09	5e-06	0.04	5 x 33 Catalysis of the transfer of a methyl group to an acceptor mol
5	Vitv04g00847	-1.2	9e-06	0.04	14 x 34 The component of a membrane consisting of the gene produc
6	Vitv07g0090E	-1.76	1e-05	0.04	21 x 40 A lipid bilayer along with all the proteins and protein comple
7	Vitv06g00577	-2.21	2e-05	0.04	36 x 32 Either of the lipid bilayers that surround the mitochondrion an
8	Vitv14g0132E	-1.43	2e-05	0.04	30 x 33 The contents of a cell excluding the plasma membrane and n
9	Vitv14g0023E	-1.34	3e-05	0.10	9 x 39 The network of interconnected tubular and cisternal structure:
10	Vitv10g0085C	-1.1	3e-05	0.10	19 x 26 Binding to a protein.
11	Vitv13g0005E	-2.04	4e-05	0.10	7 x 40 The chemical reactions and pathways resulting in the formati
12	Vitv15g0072Z	-1.32	7e-05	0.10	28 x 27 A closed structure, found only in eukaryotic cells, that is comp
13	Vitv10g0116A	-2.79	7e-05	0.10	30 x 38 The component of a membrane consisting of the gene produc
14	Vitv15g0108E	-1.14	7e-05	0.10	14 x 19 Binding to a zinc ion (Zn).
15	Vitv02g0068A	-1.42	8e-05	0.10	15 x 38 The contents of a cell excluding the plasma membrane and n
16	Vitv17g0056C	-3.17	1e-04	0.10	37 x 38 Binding to a protein.
17	Vitv02g0041E	-1.57	1e-04	0.10	24 x 31 Catalysis of a biochemical reaction at physiological temperat
18	Vitv19g0183C	-1.44	1e-04	0.10	33 x 20 Any process that results in a change in state or activity of a c
19	Vitv19g0076Z	-1.7	1e-04	0.10	32 x 28 The component of a membrane consisting of the gene produc
20	Vitv01g0102Z	-1.55	1e-04	0.10	30 x 34 The component of a membrane consisting of the gene produc

Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
Overexpressed				
1	5.98	0e+00	140	Hormone signaling signaling signaling signaling
2	5.67	0e+00	45	Galactose metabolism
3	5.61	0e+00	73	Transcription factor AP2-EREBP2 EREBP
4	4.8	0e+00	92	Lipid metabolism Glycine metabolism
5	4.73	0e+00	49	Transcription factor NACs - NAC
6	4.72	0e+00	77	Carbohydrate metabolism Galactose metabolism
7	3.89	8e-05	64	Transcription factor Gatterstrat transcription factors
8	3.73	1e-04	42	Tryptophan metabolism
9	3.6	4e-04	58	Other amino acid metabolism Glutathione metabolism
10	3.37	1e-03	48	Transcription factor WRKY - WRKY
11	3.35	1e-03	153	Plant-pathogen interaction
12	3.29	1e-03	28	Transcription factor Basic leucine zipper (bZIP)
13	3.28	1e-03	45	Valine leucine acid degradation
14	3.18	2e-03	34	Tyrosine metabolism
15	2.99	3e-03	55	Glycerol metabolism
16	2.95	3e-03	26	Pantoic acid metabolism
17	2.94	4e-03	11	Lipid metabolism Steroid metabolism
18	2.84	5e-03	51	Biosynthesis of secondary metabolites
19	2.82	6e-03	43	Transcription factor BZIPs - BZIP
20	2.8	6e-03	35	Mitochondrial factors
Underexpressed				
1	-9.78	0e+00	47	Transporter transporters carriers
2	-9.67	0e+00	18	Energy metabolism Biosynthesis proteins
3	-9.35	0e+00	18	Photosynthesis proteins
4	-8.78	0e+00	80	Cytoskeleton Microtubules
5	-8.51	0e+00	217	Cell motility Regulation of cytoskeleton
6	-6.84	0e+00	206	Cell growth and division Cell wall
7	-5.95	0e+00	10	Photosynthesis Photosynthesis
8	-5.79	0e+00	38	Photosynthesis
9	-5.75	0e+00	78	Energy metabolism Biosynthesis
10	-5.3	0e+00	40	Transporter transporters carriers
11	-5.16	0e+00	66	Exosome Exosome Exosome
12	-5.13	0e+00	113	Exosome Exosome Exosome
13	-4.5	0e+00	24	Replication DNA Replication
14	-4.49	0e+00	219	Cell growth and division Cell cycle
15	-3.83	8e-05	65	Phagosome Phagosome
16	-3.52	6e-04	26	Steroid biosynthesis
17	-3.47	8e-04	78	Glycosylation Glycosylation
18	-3.32	1e-03	34	Peptidase Peptidase
19	-3.16	2e-03	21	Thiamine metabolism
20	-3.16	2e-03	10	Peptidase Peptidase

