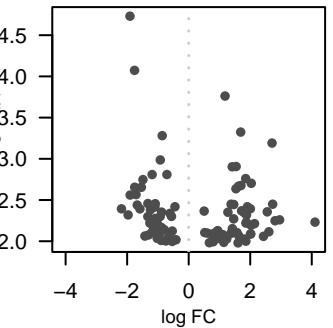
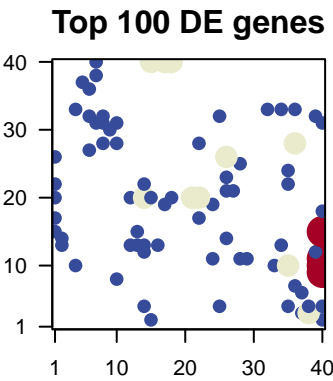
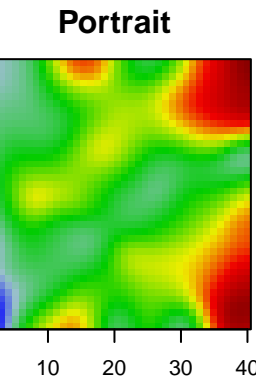


Sangio_warm_r1

Global Summary

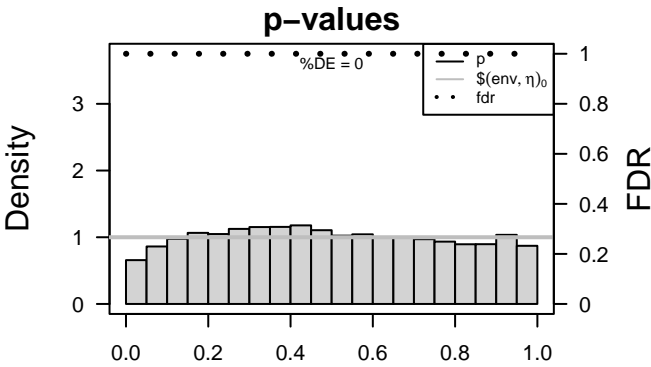
%DE = 0
genes with $\text{fdr} < 0.2 = 0$ (0 + / 0 -)
genes with $\text{fdr} < 0.1 = 0$ (0 + / 0 -)
genes with $\text{fdr} < 0.05 = 0$ (0 + / 0 -)
genes with $\text{fdr} < 0.01 = 0$ (0 + / 0 -)

<FC> = 0
<p-value> = 0.39
<fdr> = 1



Differentially expressed genes

Rank	ID	log(FC)	fdr	Description
		p-value		Metagene
Overexpressed				
1	Vitv01g00313	1.18	2e-04	14 x 22 A membrane-bound organelle of eukaryotic cells in which
2	Vitv01g0098E	1.69	5e-04	24 x 11 The component of a membrane consisting of the gene produ
3	Vitv05g0056E	2.71	6e-04	15 x 40
4	Vitv10g0188C	1.54	1e-03	15 x 20 The component of a membrane consisting of the gene produ
5	Vitv05g0048E	1.41	1e-03	35 x 10 Binding to a copper (Cu) ion.
6	Vitv16g0128E	1.85	2e-03	34 x 13 A membrane-bound organelle of eukaryotic cells in which
7	Vitv09g0029C	2.03	2e-03	35 x 4 A membrane-bound organelle of eukaryotic cells in which
8	Vitv06g00674	1.7	2e-03	40 x 9 A process that is carried out at the cellular level which results
9	Vitv08g01024	1.62	2e-03	39 x 10 Binding to a lipid.
10	Vitv14g0025C	1.54	2e-03	14 x 20 Binding to a protein kinase, any enzyme that catalyzes the tra
11	Vitv14g0133E	2.73	4e-03	40 x 4
12	Vitv12g0231E	1.38	4e-03	12 x 20
13	Vitv10g00631	1.46	4e-03	14 x 20
14	Vitv10g01814	1.91	4e-03	40 x 10 Catalysis of the hydrolysis of internal, alpha-peptide bonds in
15	Vitv14g0164E	2	4e-03	40 x 11
16	Vitv08g0167E	1.72	4e-03	17 x 40 A lipid bilayer along with all the proteins and protein complex
17	Vitv19g02074	0.5	4e-03	33 x 10
18	Vitv09g0156E	2.55	4e-03	38 x 4 Functions in the storage of nutritious substrates.
19	Vitv08g0111C	1.27	4e-03	37 x 3
20	Vitv00g0203E	1.8	4e-03	40 x 9
Underexpressed				
1	Vitv05g0030E	-1.91	2e-05	1 x 22
2	Vitv18g0089E	-1.76	8e-05	35 x 22 The component of a membrane consisting of the gene produ
3	Vitv05g00397	-0.86	5e-04	10 x 28 The process in which a signal is passed on to downstream co
4	Vitv04g0189C	-0.92	1e-03	24 x 19 A membrane-bound organelle of eukaryotic cells in which
5	Vitv09g0013E	-0.71	2e-03	21 x 20 Binding to a protein.
6	Vitv08g0016C	-1.19	2e-03	28 x 25 A membrane-bound organelle of eukaryotic cells in which
7	Vitv17g00137	-1.49	2e-03	6 x 32 Binding to ATP, adenosine 5'-triphosphate, a universally imp
8	Vitv18g0187E	-1.76	2e-03	1 x 15 A membrane-bound organelle of eukaryotic cells in which
9	Vitv07g0056E	-1.54	2e-03	22 x 17 A transcription coregulator activity that activates or increas
10	Vitv17g0088C	-1.71	3e-03	7 x 40 A membrane-bound organelle of eukaryotic cells in which
11	Vitv16g0086E	-1.9	3e-03	26 x 14 Organized structure of distinctive morphology and function, b
12	Vitv17g00221	-1.33	3e-03	26 x 21
13	Vitv02g0072E	-1.09	4e-03	26 x 26 The part of the cytoplasm that does not contain organelles b
14	Vitv08g0165E	-1.67	4e-03	35 x 24 Binding to ATP, adenosine 5'-triphosphate, a universally imp
15	Vitv03g0009E	-0.45	4e-03	22 x 20 A membrane-bound organelle of eukaryotic cells in which
16	Vitv10g0156E	-1.1	4e-03	26 x 26 The contents of a cell excluding the plasma membrane and n
17	Vitv08g01217	-2.18	4e-03	2 x 13
18	Vitv13g0219C	-1.59	4e-03	2 x 14
19	Vitv17g0068C	-1.24	4e-03	10 x 8 The membrane surrounding a cell that separates the cell fro
20	Vitv11g0068C	-0.88	4e-03	18 x 20 The formation of a protein dimer, a macromolecular structur



Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	7.87	0e+00	47	Transporter Carrier Carrier Transporter carriers
2	7.71	0e+00	206	Cell growth Cell growth Cell wall Cell wall
3	6.89	0e+00	18	Energy metabolism Biosynthesis proteins
4	6.51	0e+00	39	Pentose and gluconate interconversions
5	6.41	0e+00	18	Photosynthesis proteins
6	6.32	0e+00	78	Energy metabolism Biosynthesis
7	5.73	0e+00	38	Photosynthesis
8	5.47	0e+00	134	Hormone signaling signaling signaling
9	4.55	0e+00	30	Glycan biosynthesis metabolism Glycan degradation
10	4.31	0e+00	19	Aquaporin transporters aquaporins
11	4.05	0e+00	44	Hormone signaling signaling signaling
12	4.05	0e+00	10	Photosynthesis Photosynthesis
13	3.87	8e-05	40	Transport transport transport pathway
14	3.82	1e-04	78	Glycosylation Glycosylation Glycosylation
15	3.74	1e-04	58	Carbohydrate metabolism Fructose metabolism
16	3.59	4e-04	197	Transporter Transporter Transporter
17	3.48	7e-04	168	Plant hormone signaling signaling
18	3.07	2e-03	51	Other metabolism signaling reactions
19	2.94	4e-03	44	Fructose metabolism metabolism
20	2.89	4e-03	41	Porphyrin metabolism
<i>Underexpressed</i>				
1	-7.53	0e+00	48	Transcription WRKY - WRKY
2	-6.59	0e+00	64	Transcription Transcription factors
3	-6.35	0e+00	73	Transcription Transcription factors
4	-5.32	0e+00	140	Hormone signaling signaling signaling
5	-5.18	0e+00	49	Transcription Transcription factors - NAC
6	-4.51	0e+00	116	Ribosome Ribosome Ribosome
7	-4.35	0e+00	64	Ribosome Ribosome Ribosome
8	-4.27	0e+00	75	Translation Translation Translation
9	-3.86	8e-05	36	DNA replication
10	-3.83	8e-05	219	Cell growth Cell growth Cell cycle
11	-3.58	4e-04	62	Ribosome Ribosome Ribosome
12	-3.57	4e-04	118	Transcription Transcription factors
13	-3.53	5e-04	162	Plant signaling signaling signaling
14	-3.41	9e-04	41	Replication Replication Replication
15	-3.35	1e-03	153	Plant-pathogen interaction
16	-3.32	1e-03	144	Ribosome Ribosome Ribosome
17	-3.31	1e-03	157	Protein processing processing processing
18	-3.29	1e-03	83	Transcription Transcription factors - MYB
19	-3.24	1e-03	24	Replication Replication Replication
20	-3.2	1e-03	27	Enzyme Enzyme Enzyme

