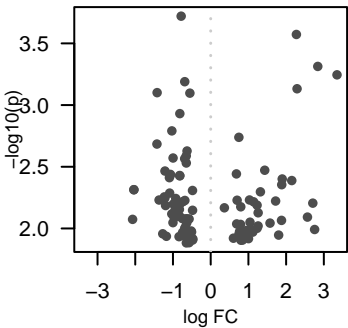
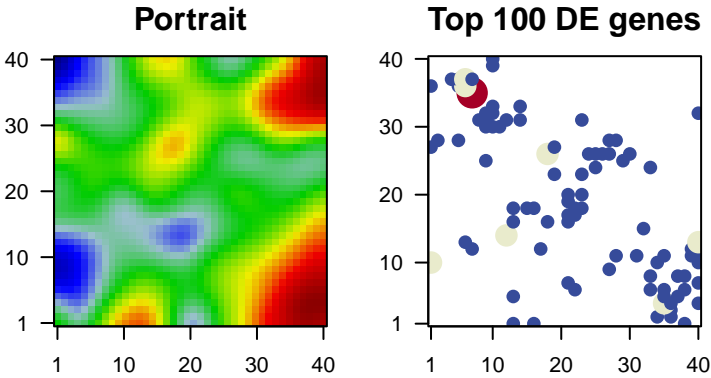


Riesl_warm_r1

Global Summary

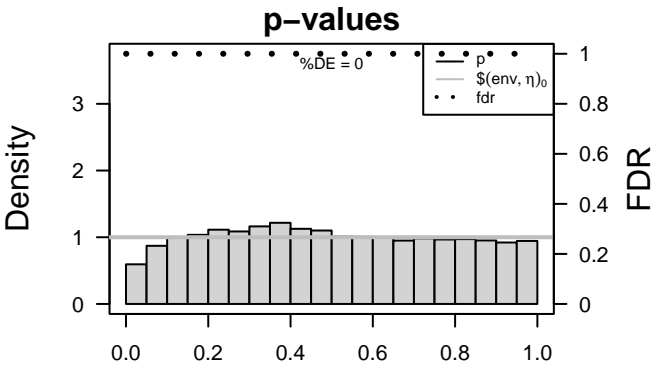
%DE = 0
genes with $\text{fdr} < 0.2 = 0$ (0 + / 0 -)
genes with $\text{fdr} < 0.1 = 0$ (0 + / 0 -)
genes with $\text{fdr} < 0.05 = 0$ (0 + / 0 -)
genes with $\text{fdr} < 0.01 = 0$ (0 + / 0 -)

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



Differentially expressed genes

Rank	ID	log(FC)	fdr	Description
		p-value		Metagene
<i>Overexpressed</i>				
1	Vitvi12g0245C	2.27	3e-04	40 x 11 Catalysis of the transfer of a group, e.g. a methyl group, glyco
2	Vitvi12g0245I	2.84	5e-04	40 x 4 Catalysis of the transfer of a group, e.g. a methyl group, glyco
3	Vitvi12g0036E	3.35	6e-04	1 x 27 The component of a membrane consisting of the gene produc
4	Vitvi07g01737	2.29	7e-04	16 x 1 Binding to ATP, adenosine 5'-triphosphate, a universally impc
5	Vitvi01g01317	0.75	2e-03	35 x 11 A lipid bilayer along with all the proteins and protein comple
6	Vitvi01g01404	1.43	3e-03	34 x 10 Binding to a protein.
7	Vitvi06g0035E	0.68	4e-03	19 x 27 Binding to a nucleic acid.
8	Vitvi09g0149E	1.9	4e-03	40 x 7
9	Vitvi02g0112E	2.15	4e-03	13 x 1 Catalysis of the transfer of an acyl group, other than amino-a
10	Vitvi09g0029C	1.88	4e-03	35 x 4 A membrane-bounded organelle of eukaryotic cells in which
11	Vitvi02g0001E	1.32	5e-03	37 x 5 Catalysis of a biochemical reaction at physiological temperat
12	Vitvi18g0032Z	1.03	6e-03	40 x 13 Binding to ATP, adenosine 5'-triphosphate, a universally impc
13	Vitvi19g00297	0.7	6e-03	39 x 12 Binding to ATP, adenosine 5'-triphosphate, a universally impc
14	Vitvi11g0023E	1.72	6e-03	35 x 4 Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, (
15	Vitvi17g0043C	1.14	6e-03	35 x 5 Catalysis of the hydrolysis of a peptide bond. A peptide bond
16	Vitvi02g0111C	2.71	6e-03	36 x 2
17	Vitvi17g0087Z	1.23	6e-03	38 x 8 A lipid bilayer along with all the proteins and protein comple
18	Vitvi14g01387	0.8	7e-03	33 x 8 A membrane-bounded organelle of eukaryotic cells in which
19	Vitvi04g00514	0.36	7e-03	19 x 23 The cell cycle process in which the sister chromatids of a repl
20	Vitvi18g0048E	1.26	7e-03	13 x 5 A membrane-bounded organelle of eukaryotic cells in which
<i>Underexpressed</i>				
1	Vitvi12g0062C	-0.78	2e-04	16 x 18
2	Vitvi10g0002E	-0.69	6e-04	10 x 33 The contents of a cell excluding the plasma membrane and n
3	Vitvi05g00624	-1.42	8e-04	5 x 36 The formation of a protein dimer, a macromolecular structure
4	Vitvi17g0062E	-0.55	8e-04	21 x 20
5	Vitvi12g0026E	-0.82	1e-03	13 x 16 A lipid bilayer along with all the proteins and protein comple
6	Vitvi19g00131	-1.03	2e-03	7 x 35 A membrane-bounded organelle of eukaryotic cells in which
7	Vitvi03g00327	-1.42	2e-03	4 x 37 A membrane-bounded organelle of eukaryotic cells in which
8	Vitvi03g00647	-0.63	2e-03	21 x 19 A lipid bilayer along with all the proteins and protein comple
9	Vitvi07g0268Z	-0.65	3e-03	23 x 20 Binding to a nucleic acid.
10	Vitvi03g00314	-1	3e-03	7 x 12 The membrane surrounding a cell that separates the cell from
11	Vitvi10g00177	-0.69	3e-03	12 x 14 Binding to a metal ion.
12	Vitvi16g0004E	-0.65	3e-03	15 x 18 Any process that activates or increases the frequency, rate or
13	Vitvi06g0105Z	-1.21	3e-03	7 x 35 A conserved complex that contains a heterodimer of SMC pr
14	Vitvi09g0096E	-1.07	4e-03	28 x 28
15	Vitvi08g0195E	-1.07	4e-03	6 x 37 Binding to a calcium ion (Ca2+).
16	Vitvi08g0185E	-0.82	4e-03	22 x 17
17	Vitvi10g0006E	-0.82	4e-03	9 x 25
18	Vitvi04g01161	-1.09	4e-03	18 x 16 A membrane-bounded organelle of eukaryotic cells in which
19	Vitvi10g0224E	-2.04	5e-03	1 x 10
20	Vitvi00g0032E	-2.04	5e-03	1 x 10



Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	5.92	0e+00	47	TransporterCarrierTransporterTransporter carriers
2	5.84	0e+00	206	Cell growthCell growthCell growthCell wall
3	5.69	0e+00	18	Energy metabolismPhotosynthesisPhotosynthesis proteins
4	5.25	0e+00	18	PhotosynthesisPhotosynthesis proteins
5	5.19	0e+00	134	Hormone signaling signaling signaling signaling
6	4.76	0e+00	38	PhotosynthesisPhotosynthesis
7	4.4	0e+00	39	Pentose phosphate and gluinterconvertions
8	3.61	4e-04	78	GlycosyltransferaseStratagolysaccharide
9	3.51	6e-04	78	Energy metabolismPhotosynthesisPhotosynthesis
10	3.41	9e-04	10	PhotosynthesisPhotosynthesisPhotosynthesisPhotosynthesis
11	3.2	1e-03	19	Transcription transcription AUXIAA-AUXIAA
12	3.01	3e-03	73	Transcription transcription A22-EREBP2 EREBP
13	2.86	5e-03	19	Aquaporin aquaporin aquaporin aquaporin
14	2.82	6e-03	90	Lipid metabolismGlycophospholipid metabolism
15	2.79	6e-03	12	Transcription transcription Bacteriophage (bph) (bHLH)
16	2.77	6e-03	217	Cell motilityRegulation of cytoskeleton
17	2.68	8e-03	44	Hormone signaling signaling signaling signaling
18	2.67	8e-03	10	Linoleic acid metabolism
19	2.51	1e-02	72	Glycerophospholipid metabolism
20	2.44	2e-02	50	Transcription transcription Mitochondrial Related
<i>Underexpressed</i>				
1	-6.72	0e+00	144	RibosomeRibosomeEukaryotes
2	-5.54	0e+00	247	TranslationTranslationRibosome
3	-5.11	0e+00	211	RibosomeRibosome
4	-4.92	0e+00	36	DNA replication
5	-3.95	4e-05	116	RibosomeRibosomeRibosomeRibosome particles
6	-3.78	1e-04	58	Other amino acid metabolismGlutathione metabolism
7	-3.75	1e-04	48	Transcription transcription WRKY - WRKY
8	-3.74	1e-04	64	RibosomeRibosomeRibosomeEukaryotes
9	-3.69	2e-04	33	Carbohydrate metabolismCarbohydrate metabolism
10	-3.59	4e-04	41	Replication replication DNA replication
11	-3.42	9e-04	44	Proteasome
12	-3.41	9e-04	34	Tyrosine metabolism
13	-3.38	9e-04	97	RibosomeRibosomeArchaea
14	-3.22	1e-03	24	Primary active transporters
15	-3.12	2e-03	71	Glutathione metabolism
16	-3.11	2e-03	75	TranslationTranslationRibosomeEukaryotes
17	-3.1	2e-03	62	RibosomeRibosomeRibosome particles
18	-3.05	2e-03	128	Ubiquitin-protein systemRings type E3
19	-2.95	3e-03	42	Folding folding degradationProteasome
20	-2.92	4e-03	24	Replication replication DNA replication factors

