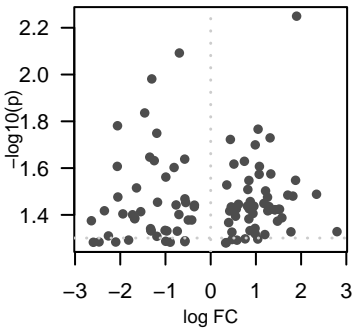
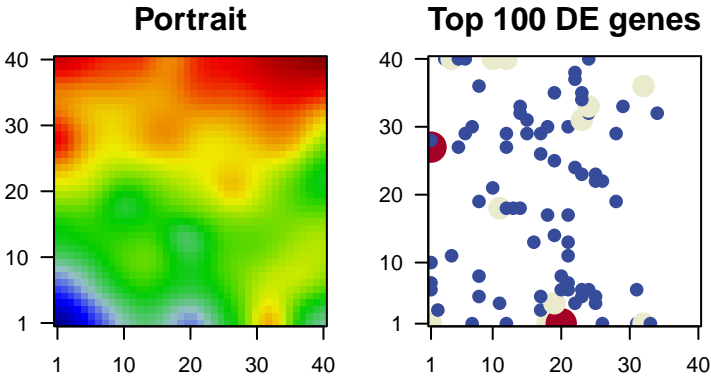


Riesl_acclim_r2

Global Summary

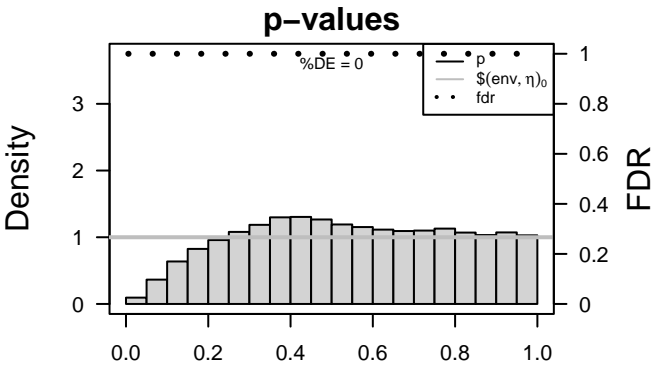
%DE = 0
genes with $\text{fdr} < 0.2 = 0$ (0 + / 0 -)
genes with $\text{fdr} < 0.1 = 0$ (0 + / 0 -)
genes with $\text{fdr} < 0.05 = 0$ (0 + / 0 -)
genes with $\text{fdr} < 0.01 = 0$ (0 + / 0 -)

<FC> = 0
<p-value> = 0.47
<fdr> = 1



Differentially expressed genes

Rank	ID	log(FC)	p-value	fdr	Description
Overexpressed					
1	Vitv08g0199E	1.9	0.006	1	5 x 40 The component of a membrane consisting of the gene product
2	Vitv01g0229E	1.05	0.017	1	17 x 29 The component of a membrane consisting of the gene product
3	Vitv13g0137E	1.31	0.019	1	22 x 38 The contents of a cell excluding the plasma membrane and nucleus
4	Vitv06g0112Z	0.44	0.019	1	23 x 23 Catalysis of a biochemical reaction at physiological temperature
5	Vitv09g0059C	0.99	0.020	1	24 x 32 Binding to a protein.
6	Vitv04g0155E	0.75	0.023	1	24 x 33 The contents of a cell excluding the plasma membrane and nucleus
7	Vitv07g01757	0.51	0.024	1	25 x 22 A small, dense body one or more of which are present in the nucleus
8	Vitv09g0145E	1.08	0.025	1	10 x 40 Binding to ATP, adenosine 5'-triphosphate, a universally important
9	Vitv13g0188A	1.33	0.027	1	12 x 40 Binding to ATP, adenosine 5'-triphosphate, a universally important
10	Vitv07g0133E	1.07	0.027	1	23 x 35
11	Vitv05g0009C	1.88	0.028	1	4 x 40
12	Vitv05g0188E	0.85	0.028	1	21 x 30
13	Vitv08g0214C	0.36	0.030	1	23 x 31 A membrane-bound organelle of eukaryotic cells in which
14	Vitv07g0131E	0.82	0.031	1	5 x 27
15	Vitv14g0036E	1.21	0.031	1	1 x 27 The component of a membrane consisting of the gene product
16	Vitv07g0209Z	2.34	0.032	1	12 x 40 The initial step of transcription, consisting of the assembly of
17	Vitv02g0017Z	1.71	0.033	1	1 x 28
18	Vitv08g0211A	1.82	0.033	1	32 x 1
19	Vitv05g0140C	1.26	0.033	1	28 x 29 Catalysis of the reaction: a very long chain fatty acyl-CoA + H
20	Vitv10g01131	0.88	0.035	1	8 x 36
Underexpressed					
1	Vitv04g0122E	-0.69	0.008	1	20 x 6 A lipid bilayer along with all the proteins and protein complexes
2	Vitv14g0136E	-1.3	0.010	1	8 x 19 Binding to ATP, adenosine 5'-triphosphate, a universally important
3	Vitv10g0031Z	-1.46	0.015	1	16 x 13
4	Vitv04g00031	-2.06	0.017	1	20 x 1 Binding to ATP, adenosine 5'-triphosphate, a universally important
5	Vitv15g0167A	-1.19	0.018	1	21 x 11
6	Vitv10g01361	-1.35	0.023	1	11 x 4 The space external to the outermost structure of a cell. For example
7	Vitv13g0093Z	-0.57	0.023	1	23 x 6
8	Vitv04g00531	-1.25	0.023	1	17 x 3
9	Vitv12g0272E	-2.07	0.025	1	21 x 13
10	Vitv06g0045C	-0.81	0.025	1	19 x 4 Catalysis of the transfer of ubiquitin from one protein to another
11	Vitv02g00467	-0.99	0.027	1	22 x 4 Binding to an amino acid, organic acids containing one or more
12	Vitv13g00161	-1.64	0.031	1	12 x 1
13	Vitv04g0188E	-2.05	0.033	1	20 x 1 A lipid bilayer along with all the proteins and protein complexes
14	Vitv08g0026Z	-0.57	0.034	1	25 x 5
15	Vitv03g0160E	-1.18	0.035	1	8 x 8 The component of a membrane consisting of the gene product
16	Vitv12g0202C	-0.55	0.035	1	21 x 6 The component of a membrane consisting of the gene product
17	Vitv10g0063E	-0.77	0.036	1	26 x 1 A transcription regulator activity that modulates transcription of
18	Vitv18g0168Z	-0.36	0.036	1	22 x 24 A lipid bilayer along with all the proteins and protein complexes
19	Vitv08g0139A	-0.36	0.037	1	24 x 6 A membrane-bound organelle of eukaryotic cells in which
20	Vitv00g0071C	-2.35	0.038	1	1 x 10



Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
Overexpressed				
1	7.52	0.000	18	Energy metabolism, Biosynthesis, Protein synthesis, Proteins
2	7.36	0.000	47	Transport, Carbohydrate metabolism, Ion transporters, Carriers
3	7.26	0.000	18	Photosynthesis, Protein synthesis, Proteins
4	5.77	0.000	38	Photosynthesis
5	5.09	0.000	78	Energy metabolism, Biosynthesis, Protein synthesis
6	4.6	0.000	217	Cell motility, Cell regulation, Regulation of cytoskeleton
7	4.38	0.000	10	Photosynthesis, Protein synthesis, Photosynthesis, Photosynthesis (Prothyl)
8	3.16	0.002	11	Transcription, Transcription, GRF
9	3.16	0.002	26	Steroid biosynthesis, Steroid biosynthesis
10	2.92	0.004	41	Porphyria, Porphyrin metabolism
11	2.87	0.005	21	Thiamine metabolism, Thiamine metabolism
12	2.8	0.006	80	Cytoskeleton, Cytoskeleton, Microtubules
13	2.77	0.007	101	Starch and starch metabolism, Starch metabolism
14	2.68	0.008	40	Transport, Transport, Glycolysis, Glycolysis pathway
15	2.62	0.010	12	ABCB (MRCA) family, ABC family
16	2.47	0.015	41	Transcription, Transcription, RNA polymerase
17	2.47	0.015	31	Chromosome, Chromosome, Chromosome, Chromosome silencing
18	2.43	0.016	66	Exosome, Exosome, Exosome, Exosome, Exosome
19	2.41	0.018	28	Transcription, Transcription, MTERF - MTERF
20	2.37	0.019	90	Lipid metabolism, Lipid metabolism, Lipid metabolism
Underexpressed				
1	-10.13	0e+00	48	Transcription, Transcription, WRKY - WRKY
2	-7.6	0e+00	162	Plant species, Plant species, Plant species, Plant species
3	-7.26	0e+00	73	Transcription, Transcription, AP2, EREBP2, EREBP
4	-7.16	0e+00	153	Plant-pathogen interaction, Plant-pathogen interaction
5	-6.55	0e+00	49	Transcription, Transcription, NACs - NAC
6	-6.29	0e+00	140	Hormone signaling, Hormone signaling, Signaling
7	-5.66	0e+00	64	Transcription, Transcription, Other transcription factors
8	-4.52	0e+00	77	Pores ion channels, Pores ion channels [TC:1]
9	-4.46	0e+00	45	Galactose metabolism, Galactose metabolism
10	-4.21	0e+00	11	Biosynthesis, Biosynthesis, Biosynthesis, Biosynthesis
11	-4.09	0e+00	56	Hormone signaling, Hormone signaling, Signaling
12	-3.9	4e-05	58	Other amino acid metabolism, Other amino acid metabolism
13	-3.82	1e-04	26	Flavonoid biosynthesis, Flavonoid biosynthesis
14	-3.52	6e-04	83	Transcription, Transcription, MYB - MYB
15	-3.5	6e-04	111	Hormone signaling, Hormone signaling, Signaling
16	-3.45	8e-04	38	Protein - Chaperone, Protein - Chaperone, Chaperone (CMA)
17	-3.34	1e-03	71	Exosome, Exosome, Exosome, Exosome, Exosome
18	-3.24	1e-03	118	Transcription, Transcription, Helix-turn-helix
19	-3.13	2e-03	17	Protease, Protease, Protease, Protease, Protease
20	-2.97	3e-03	15	Chaperone, Chaperone, Chaperone, Chaperone, Chaperone

