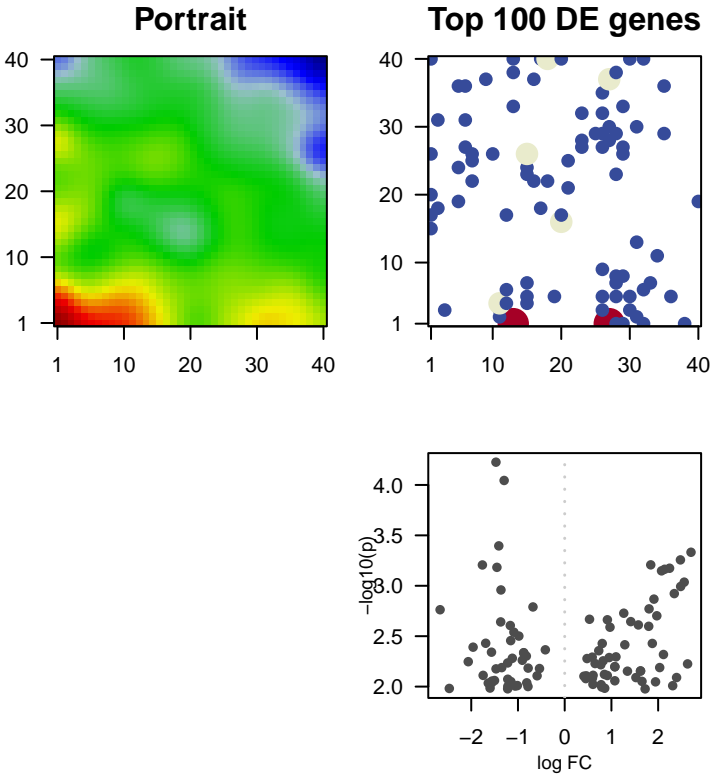


Riesl\_freeze\_r2

Global Summary

%DE = 0.11  
# genes with fdr < 0.2 = 0 ( 0 + / 0 - )  
# genes with fdr < 0.1 = 0 ( 0 + / 0 - )  
# genes with fdr < 0.05 = 0 ( 0 + / 0 - )  
# genes with fdr < 0.01 = 0 ( 0 + / 0 - )

<FC> = 0  
<p-value> = 0.36  
<fdr> = 0.89



Differentially expressed genes

Rank	ID	log(FC)	fdr	Description		
		p-value		Metagene		
Overexpressed						
1	Vitv02g0144E	2.7	5e-04	0.8	29 x 1	
2	Vitv16g0110C	2.48	6e-04	0.8	27 x 1	Binding to ATP, adenosine 5'-triphosphate, a universally impo
3	Vitv18g0143E	1.84	6e-04	0.8	7 x 22	
4	Vitv15g0011C	2.24	7e-04	0.8	30 x 3	A lipid bilayer along with all the proteins and protein complex
5	Vitv08g0218E	2.14	7e-04	0.8	38 x 1	The contents of a cell excluding the plasma membrane and n
6	Vitv10g0049E	2.07	7e-04	0.8	12 x 4	The process of assisting in the covalent and noncovalent assu
7	Vitv03g0037E	2.56	9e-04	0.8	12 x 6	Binding to a heme, a compound composed of iron complexed
8	Vitv16g0068I	2.48	1e-03	0.8	5 x 24	
9	Vitv11g0168C	2.35	1e-03	0.8	1 x 17	
10	Vitv08g0068E	1.91	1e-03	0.8	11 x 3	Catalysis of an oxidation-reduction (redox) reaction, a reversi
11	Vitv18g0259Z	1.81	2e-03	0.8	2 x 31	The space external to the outermost structure of a cell. For ce
12	Vitv10g0134E	1.26	2e-03	0.8	15 x 4	Binding to a nucleic acid.
13	Vitv17g0069E	1.97	2e-03	0.8	36 x 5	The contents of a cell excluding the plasma membrane and n
14	Vitv18g00577	0.53	2e-03	0.8	26 x 9	The component of a membrane consisting of the gene produc
15	Vitv04g0122Z	0.91	2e-03	0.8	5 x 19	The irregular network of unit membranes, visible only by elect
16	Vitv05g0191E	1.41	2e-03	0.8	30 x 5	A membrane-bounded organelle of eukaryotic cells in which
17	Vitv04g0179Z	1.58	2e-03	0.8	26 x 3	Any process that results in a change in state or activity of a c
18	Vitv03g0172Z	1.8	3e-03	0.8	28 x 1	A lipid bilayer along with all the proteins and protein complex
19	Vitv03g0084E	0.97	3e-03	0.8	15 x 7	The contents of a cell excluding the plasma membrane and n
20	Vitv02g00374	1.88	4e-03	0.8	11 x 2	Binding to a protein.
Underexpressed						
1	Vitv16g0105E	-1.47	6e-05	0.7	26 x 32	The chemical reactions and pathways involving lipids, compo
2	Vitv10g0196Z	-1.3	9e-05	0.8	23 x 28	The action of a molecule that contributes to the structural inte
3	Vitv14g0167E	-1.41	4e-04	0.8	20 x 17	The contents of a cell excluding the plasma membrane and n
4	Vitv17g00837	-1.76	6e-04	0.8	18 x 40	The component of a membrane consisting of the gene produc
5	Vitv12g0238Z	-1.45	7e-04	0.8	9 x 37	Catalysis of the hydrolysis of any ester bond.
6	Vitv09g0022E	-1.36	1e-03	0.8	13 x 33	Any process that modulates the frequency, rate or extent of pl
7	Vitv14g0159E	-0.68	2e-03	0.8	23 x 27	The component of a membrane consisting of the gene produc
8	Vitv18g0039E	-2.67	2e-03	0.8	32 x 40	Binding to a protein.
9	Vitv04g0014E	-1.37	2e-03	0.8	27 x 37	Catalysis of a biochemical reaction at physiological temperat
10	Vitv09g0149Z	-1.16	2e-03	0.8	27 x 28	
11	Vitv05g0062Z	-1.09	3e-03	0.8	23 x 32	Binding to ATP, adenosine 5'-triphosphate, a universally impo
12	Vitv14g0294E	-0.98	3e-03	0.8	26 x 35	Organized structure of distinctive morphology and function, bi
13	Vitv18g0090C	-1.16	4e-03	0.8	20 x 16	Binding to a protein.
14	Vitv15g0092E	-1.69	4e-03	0.8	35 x 29	Binding to a calcium ion (Ca2+).
15	Vitv12g0165E	-1.96	4e-03	0.8	5 x 36	Any molecular function by which a gene product interacts sele
16	Vitv09g0006E	-0.41	4e-03	0.8	21 x 21	Any process involved in the conversion of a primary mRNA tra
17	Vitv19g0154E	-1.57	5e-03	0.8	29 x 27	A chlorophyll-containing plastid with thylakoids organized into
18	Vitv08g0160E	-0.88	5e-03	0.8	28 x 23	The double lipid bilayer enclosing the chloroplast and separat
19	Vitv14g0041C	-0.88	5e-03	0.8	34 x 11	Binding to a metal ion.
20	Vitv16g0138Z	-0.82	5e-03	0.8	16 x 37	Binding to a metal ion.

Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
Overexpressed				
1	6.61	0e+00	17	Proteasome assembly factors
2	6.49	0e+00	15	Chaperone protein / DNAK
3	6.43	0e+00	157	Protein processing in endoplasmic reticulum
4	6.19	0e+00	12	Endoplasmic reticulum membrane and cytosol
5	5.9	0e+00	140	Hormone signaling pathway
6	5.75	0e+00	48	Transcription factor WIPK - WRKY
7	5.64	0e+00	18	Chaperone protein - HSP20
8	5.57	0e+00	73	Transcription factor EREBP2 EREBP
9	5.36	0e+00	64	Transcription factor GTR1 transcription factors
10	4.9	0e+00	71	Exosome protein - Exosome
11	4.86	0e+00	38	Protein - Chaperone protein (CMA)
12	4.74	0e+00	162	Plant specific signaling pathway
13	4.24	0e+00	49	Transcription factor NAC
14	3.9	4e-05	38	Protein - Clathrin - Clathrin-mediated endocytosis
15	3.88	8e-05	45	Galactose metabolism
16	3.57	4e-04	153	Plant-pathogen interaction
17	3.32	1e-03	116	Ribosome biogenesis
18	3.1	2e-03	35	Mitochondrial factors
19	2.87	5e-03	86	Signal transduction pathway
20	2.72	8e-03	39	Enzyme - Ethylating agent
Underexpressed				
1	-7.83	0e+00	80	Cytoskeleton
2	-7.82	0e+00	18	Energy metabolism
3	-7.56	0e+00	18	Photosynthesis
4	-7.33	0e+00	47	Transport
5	-7.28	0e+00	217	Cell motility
6	-6.39	0e+00	78	Energy metabolism
7	-6.24	0e+00	38	Photosynthesis
8	-6.24	0e+00	219	Cell growth
9	-5.44	0e+00	10	Photosynthesis
10	-5.12	0e+00	24	Replication
11	-4.32	0e+00	36	DNA replication
12	-4.24	0e+00	40	Transport
13	-4.22	0e+00	11	Transcription
14	-4.1	0e+00	41	Replication
15	-4.02	0e+00	34	Peptidase
16	-3.83	8e-05	129	Enzyme
17	-3.79	1e-04	39	Pentose
18	-3.46	8e-04	41	Porphyrin
19	-3.39	9e-04	30	Glycan
20	-3.21	1e-03	26	Flavonoid

