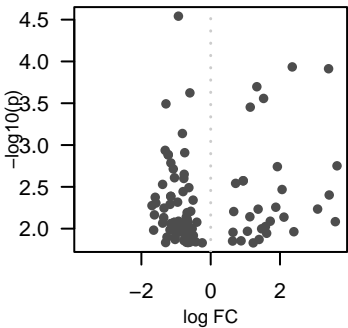
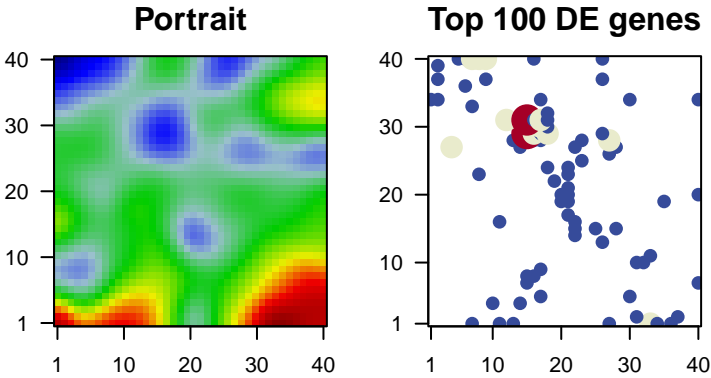


Chard_freeze_r1

Global Summary

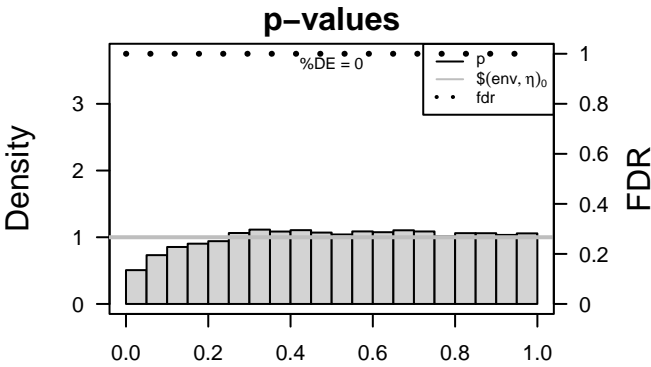
%DE = 0
genes with $\text{fdr} < 0.2 = 0$ (0 + / 0 -)
genes with $\text{fdr} < 0.1 = 0$ (0 + / 0 -)
genes with $\text{fdr} < 0.05 = 0$ (0 + / 0 -)
genes with $\text{fdr} < 0.01 = 0$ (0 + / 0 -)

<FC> = 0
<p-value> = 0.42
<fdr> = 1



Differentially expressed genes

Rank	ID	log(FC)	fdr	Description
		p-value		Metagene
<i>Overexpressed</i>				
1	Vitv14g02502	2.35	1e-04	31 x 2 Binding to a protein.
2	Vitv108g01434	3.4	1e-04	33 x 1 The chemical reactions and pathways involving carbohydrate
3	Vitv119g0235E	1.33	2e-04	15 x 7
4	Vitv108g0099E	1.53	3e-04	27 x 1 A complex composed of TATA binding protein (TBP) and TBP
5	Vitv104g01304	1.14	4e-04	26 x 29 A membrane-bounded organelle of eukaryotic cells in which
6	Vitv119g02024	3.65	2e-03	40 x 34
7	Vitv115g0157E	1.92	2e-03	35 x 19
8	Vitv104g0229C	0.94	3e-03	4 x 27
9	Vitv100g0173E	0.94	3e-03	4 x 27
10	Vitv101g0164E	0.72	3e-03	31 x 10 Catalysis of the hydrolysis of phosphoric monoesters, releasir
11	Vitv119g01854	2.06	3e-03	30 x 34 Catalysis of the transfer of a glycosyl group from a UDP-sug
12	Vitv112g0256E	3.42	4e-03	36 x 1 The space external to the outermost structure of a cell. For α
13	Vitv118g0143C	1.88	6e-03	40 x 20 Innate immune responses are defense responses mediated b
14	Vitv11g0028E	3.09	6e-03	11 x 1 A membrane-bounded organelle of eukaryotic cells in which
15	Vitv101g0062C	1.37	6e-03	40 x 7 Binding to a heme, a compound composed of iron complexed
16	Vitv115g0088C	0.66	6e-03	33 x 11 A lipid bilayer along with all the proteins and protein comple
17	Vitv110g00544	1.13	7e-03	16 x 8 Catalysis of the transfer of an acyl group, other than amino-a
18	Vitv119g0017C	2.11	7e-03	34 x 1
19	Vitv102g0005C	1.72	8e-03	13 x 1 The space external to the outermost structure of a cell. For α
20	Vitv108g01547	3.6	8e-03	7 x 1
<i>Underexpressed</i>				
1	Vitv106g0176E	-0.93	3e-05	15 x 30 The action of a molecule that contributes to the structural inte
2	Vitv102g00737	-0.6	2e-04	12 x 31 A lipid bilayer along with all the proteins and protein comple
3	Vitv102g0001E	-1.29	3e-04	15 x 29 Binding to a protein.
4	Vitv114g0144E	-0.82	7e-04	23 x 28 The component of a membrane consisting of the gene produ
5	Vitv104g0044E	-1.31	1e-03	7 x 40 The process in which a methyl group is covalently attached to
6	Vitv103g0016C	-0.75	1e-03	21 x 19 A cellular transport process in which transported substances
7	Vitv107g0309C	-1.23	1e-03	16 x 29
8	Vitv100g00751	-1.23	1e-03	16 x 29
9	Vitv107g0123E	-1.15	2e-03	16 x 31
10	Vitv108g0179C	-1.08	2e-03	17 x 31 A membrane-bounded organelle of eukaryotic cells in which
11	Vitv102g00274	-0.77	2e-03	27 x 26 The inner, i.e. lumen-facing, lipid bilayer of the mitochondrial
12	Vitv101g01704	-1.04	2e-03	27 x 28 Binding to an amino acid, organic acids containing one or mo
13	Vitv113g0001E	-0.77	3e-03	18 x 24 The component of a membrane consisting of the gene produ
14	Vitv100g00997	-1.39	3e-03	16 x 28
15	Vitv101g01667	-0.63	3e-03	28 x 15
16	Vitv100g0116E	-0.8	4e-03	21 x 17
17	Vitv100g00857	-1.15	4e-03	21 x 30
18	Vitv107g0295E	-1.15	4e-03	17 x 30
19	Vitv117g00037C	-1.6	4e-03	26 x 40 Binding to ATP, adenosine 5'-triphosphate, a universally impc
20	Vitv112g00837	-0.51	5e-03	20 x 20 Binding to ATP, adenosine 5'-triphosphate, a universally impc



Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	8.4	0e+00	26	Flavonoid biosynthesis
2	7.08	0e+00	73	Transcription factor binding site (TFBS) binding
3	6.46	0e+00	78	Energy metabolism
4	5.26	0e+00	64	Transcription factor binding site (TFBS) binding
5	4.65	0e+00	38	Photosynthesis
6	4.29	0e+00	92	Lipid metabolism
7	4.22	0e+00	140	Hormone signaling
8	4.16	0e+00	26	Glycosyltransferase activity
9	3.85	8e-05	15	Stilbenoid, chalcone and flavonoid biosynthesis
10	3.81	1e-04	63	Phenylpropanoid biosynthesis
11	3.78	1e-04	206	Cell growth
12	3.19	2e-03	57	Transcription factor binding site (TFBS) binding
13	3.11	2e-03	10	Linoleic acid metabolism
14	2.92	4e-03	40	Transport
15	2.91	4e-03	118	Transcription factor binding site (TFBS) binding
16	2.77	7e-03	44	Energy metabolism
17	2.6	1e-02	83	Transcription factor binding site (TFBS) binding
18	2.56	1e-02	50	Transcription factor binding site (TFBS) binding
19	2.55	1e-02	17	Proteasome
20	2.52	1e-02	12	SLC15: PAT1
<i>Underexpressed</i>				
1	-6.4	0e+00	41	Replication
2	-6.07	0e+00	36	DNA replication
3	-5.43	0e+00	24	Replication
4	-4.83	0e+00	219	Cell growth
5	-4.61	0e+00	409	Enzyme
6	-4.14	0e+00	37	Homologous recombination
7	-3.95	4e-05	142	Transport
8	-3.71	1e-04	27	Mismatch repair
9	-3.55	5e-04	62	Ribosome
10	-3.37	9e-04	22	Replication
11	-3.36	1e-03	21	Replication
12	-3.33	1e-03	66	Exosome
13	-3.24	1e-03	110	Ubiquitin
14	-3.02	3e-03	75	Translation
15	-3	3e-03	64	Ribosome
16	-2.96	3e-03	37	Repair
17	-2.88	5e-03	44	Replication
18	-2.85	5e-03	73	Nucleotide
19	-2.81	6e-03	144	Ribosome
20	-2.73	8e-03	65	Phagosome

