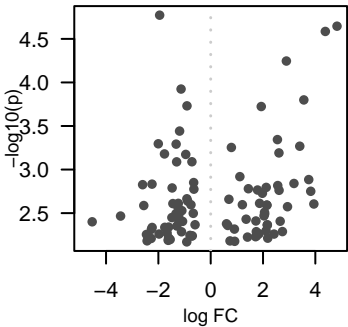
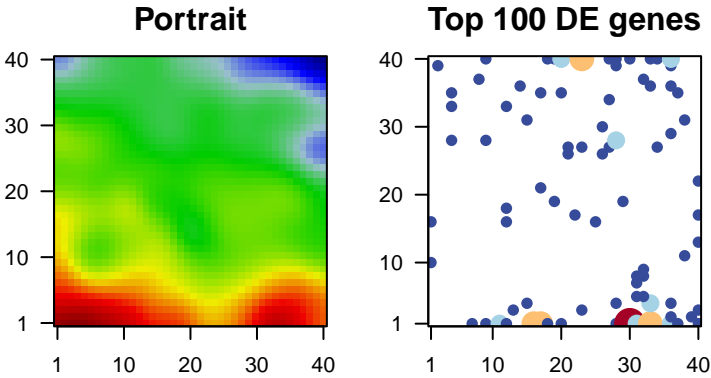


# Chard\_freeze\_r3

## Global Summary

%DE = 0.17  
# genes with  $\text{fdr} < 0.2 = 2 \ (1 + 1 \rightarrow)$   
# genes with  $\text{fdr} < 0.1 = 0 \ (0 + 0 \rightarrow)$   
# genes with  $\text{fdr} < 0.05 = 0 \ (0 + 0 \rightarrow)$   
# genes with  $\text{fdr} < 0.01 = 0 \ (0 + 0 \rightarrow)$

<FC> = 0  
<p-value> = 0.35  
<fdr> = 0.83



## Differentially expressed genes

Rank	ID	log(FC)	fdr	Description		
		p-value		Metagene		
Overexpressed						
1	Vitv112g0256E	4.83	2e-05	0.1	36 x 1	The space external to the outermost structure of a cell. For ce
2	Vitv109g0200E	4.38	3e-05	0.5	31 x 1	An intracellular non-membrane-bounded organelle compris
3	Vitv107g0162A	2.89	6e-05	0.5	36 x 1	The irregular network of unit membranes, visible only by elect
4	Vitv107g0025E	3.56	2e-04	0.5	9 x 1	The contents of a cell excluding the plasma membrane and n
5	Vitv107g0182C	1.93	2e-04	0.7	33 x 4	A membrane-bounded organelle of eukaryotic cells in which
6	Vitv114g0184C	2.55	5e-04	0.7	28 x 1	Binding to ATP, adenosine 5-triphosphate, a universally impo
7	Vitv119g0102E	3.4	5e-04	0.7	7 x 1	Binding to a heme, a compound composed of iron complexed
8	Vitv111g0005E	0.79	6e-04	0.7	32 x 9	The inner, i.e. lumen-facing, lipid bilayer of the mitochondrial
9	Vitv102g01167	2.61	6e-04	0.7	17 x 1	A lipid bilayer along with all the proteins and protein complex
10	Vitv104g0133E	1.11	1e-03	0.7	31 x 5	The component of a membrane consisting of the gene produc
11	Vitv105g0135C	3.75	1e-03	0.7	1 x 16	The space external to the outermost structure of a cell. For ce
12	Vitv109g0025E	3.18	1e-03	0.7	17 x 1	Binding to ATP, adenosine 5-triphosphate, a universally impo
13	Vitv102g0067C	2.56	2e-03	0.7	12 x 1	Any molecular function by which a gene product interacts sel
14	Vitv11g0016E	2.12	2e-03	0.7	1 x 10	The formation of a protein dimer, a macromolecular structure
15	Vitv112g0015A	1.44	2e-03	0.7	32 x 5	The component of a membrane consisting of the gene produc
16	Vitv118g0322C	1.79	2e-03	0.7	12 x 18	
17	Vitv118g0029C	2.61	2e-03	0.7	36 x 2	The component of a membrane consisting of the gene produc
18	Vitv113g0036E	3.82	2e-03	0.7	40 x 3	Catalysis of the hydrolysis of internal, alpha-peptide bonds in
19	Vitv102g0068C	1.98	2e-03	0.7	16 x 1	A lipid bilayer along with all the proteins and protein complex
20	Vitv106g0097C	0.7	2e-03	0.7	31 x 8	An thiol-dependent isopeptidase activity that cleaves ubiquiti
Underexpressed						
1	Vitv113g0053E	-1.95	2e-05	0.1	8 x 37	Binding to a microtubule, a filament composed of tubulin mon
2	Vitv111g0015C	-1.13	1e-04	0.5	22 x 17	The component of a membrane consisting of the gene produc
3	Vitv108g0135E	-0.91	2e-04	0.5	9 x 28	Binding to ATP, adenosine 5-triphosphate, a universally impo
4	Vitv104g0157E	-1.19	4e-04	0.7	29 x 19	Any molecular function by which a gene product interacts sel
5	Vitv117g0008E	-2	5e-04	0.7	32 x 37	Binding to an amino acid, organic acids containing one or mo
6	Vitv108g0137E	-1.32	5e-04	0.7	27 x 34	
7	Vitv107g0090C	-1.77	7e-04	0.7	36 x 29	The component of a membrane consisting of the gene produc
8	Vitv101g0004C	-0.95	7e-04	0.7	28 x 28	Binding to a polysaccharide, a polymer of many (typically mor
9	Vitv112g0204C	-0.72	8e-04	0.7	26 x 30	Reactions, triggered in response to the presence of a foreign
10	Vitv118g0153E	-1.3	8e-04	0.7	27 x 27	Binding to GTP, guanosine triphosphate.
11	Vitv109g0011E	-0.65	1e-03	0.7	23 x 27	Any molecular function by which a gene product interacts sel
12	Vitv113g0174A	-2.24	1e-03	0.7	30 x 40	Catalysis of the transfer of ubiquitin from one protein to anoth
13	Vitv117g0096C	-2.6	1e-03	0.7	19 x 40	The formation of the principal food-conducting tissue of a vas
14	Vitv106g0023C	-1.47	2e-03	0.7	34 x 27	Binding to a heme, a compound composed of iron complexed
15	Vitv103g0037I	-0.64	2e-03	0.7	15 x 31	Binding to a protein.
16	Vitv104g00067	-0.91	2e-03	0.7	25 x 16	Binding to a metal ion.
17	Vitv106g0107C	-0.88	2e-03	0.7	21 x 27	Any process that modulates the frequency, rate or extent of c
18	Vitv111g00977	-1.24	2e-03	0.7	23 x 40	The component of a membrane consisting of the gene produc
19	Vitv113g00777	-1.45	2e-03	0.7	40 x 17	A membrane-bound cytoplasmic organelle of the endomemb
20	Vitv106g0037E	-0.75	3e-03	0.7	28 x 28	The process in which one or more ubiquitin groups are addc

## Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
Overexpressed				
1	4.19	0e+00	45	Galactose metabolism
2	4.12	0e+00	51	Carbon fixation in photosynthetic organisms
3	4.12	0e+00	48	Transcription factor activity, RNA polymerase
4	4.1	0e+00	64	Transcription factor activity, RNA polymerase
5	3.93	4e-05	10	SLC39: Metal ion transporter
6	3.75	1e-04	73	Transcription factor activity, RNA polymerase
7	3.51	6e-04	49	Transcription factor activity, RNA polymerase
8	3.49	7e-04	77	Pores ion channels (TC:1)
9	3.49	7e-04	15	Chaperone binding
10	3.42	9e-04	44	Energy metabolism
11	3.26	1e-03	41	Arginine metabolism
12	3.24	1e-03	157	Protein processing in endoplasmic reticulum
13	3.23	1e-03	11	Biosynthesis of amino acids
14	3.14	2e-03	24	Tropene biosynthesis
15	3.14	2e-03	15	Stilbenoid biosynthesis
16	3.13	2e-03	140	Hormone signaling
17	3.12	2e-03	71	Exosome biogenesis
18	3.11	2e-03	38	Amino acid metabolism
19	3.07	2e-03	38	Protein biogenesis
20	2.96	3e-03	42	Tryptophan metabolism
Underexpressed				
1	-7.59	0e+00	206	Cell growth
2	-7.41	0e+00	217	Cell motility
3	-6.8	0e+00	219	Cell growth
4	-6.59	0e+00	80	Cytoskeleton
5	-6.21	0e+00	10	Peptidase
6	-5.05	0e+00	11	Transcription factor activity
7	-4.92	0e+00	78	Glycosyltransferase
8	-4.87	0e+00	24	Replication
9	-4.54	0e+00	41	Replication
10	-4.33	0e+00	36	DNA replication
11	-4.05	0e+00	39	Pentose
12	-3.99	0e+00	19	Aquaporin
13	-3.9	4e-05	19	Hormone signaling
14	-3.69	3e-04	13	Cutin subunit
15	-3.68	3e-04	66	Exosome
16	-3.56	5e-04	195	Carbohydrate
17	-3.37	9e-04	34	Peptidase
18	-3.1	2e-03	30	Glycan
19	-2.85	5e-03	37	Homologous recombination
20	-2.67	8e-03	31	Chromosome

