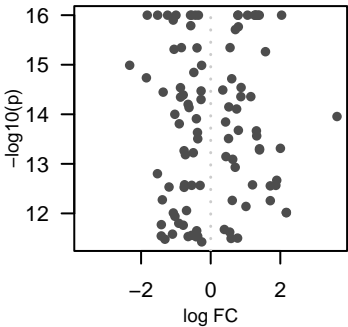
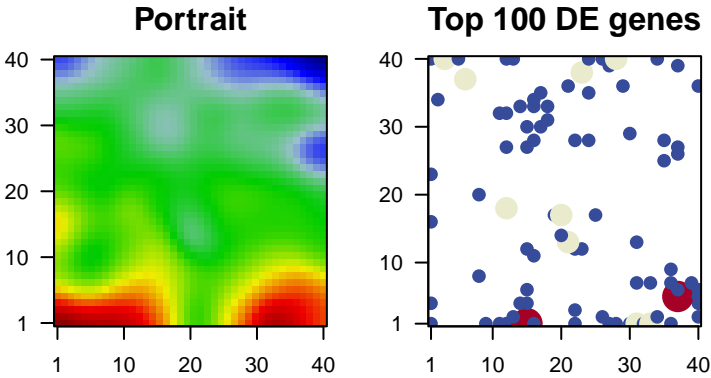


Chard_freeze

Global Summary

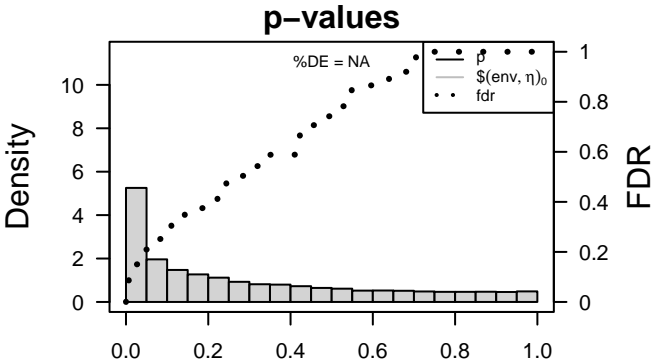
%DE = NA
genes with $\text{fdr} < 0.2 = 4717$ (2517 + / 2200 -)
genes with $\text{fdr} < 0.1 = 2567$ (1365 + / 1202 -)
genes with $\text{fdr} < 0.05 = 1789$ (957 + / 832 -)
genes with $\text{fdr} < 0.01 = 1128$ (574 + / 554 -)

<FC> = 0
<p-value> = 0.06
<fdr> = 0.47



Differentially expressed genes

Rank	ID	log(FC)	fdr	Description
		p-value		Metagene
Overexpressed				
1	Vitv00g01051	0.78	1e-16	2e-13 37 x 5
2	Vitv02g0174E	0.78	1e-16	2e-13 37 x 5
3	Vitv02g0016C	1.26	1e-16	2e-13 12 x 1
4	Vitv03g01094	2.04	1e-16	2e-13 11 x 1
5	Vitv03g00292	1.29	1e-16	2e-13 13 x 1
6	Vitv04g0024C	1.4	1e-16	2e-13 9 x 1
7	Vitv06g01503	1.36	1e-16	2e-13 37 x 6
8	Vitv09g01773	1.3	1e-16	2e-13 30 x 1
9	Vitv18g00962	1.06	1e-16	2e-13 36 x 7
10	Vitv03g0016E	0.79	2e-16	2e-13 15 x 1
11	Vitv03g0004E	0.71	2e-16	6e-13 14 x 4
12	Vitv18g0231C	0.56	5e-16	6e-13 33 x 7
13	Vitv04g01097	1.57	5e-16	2e-12 32 x 1
14	Vitv09g01391	0.6	2e-15	2e-12 31 x 7
15	Vitv01g01882	0.87	3e-15	2e-12 16 x 1
16	Vitv01g0208C	0.35	3e-15	2e-12 31 x 13
17	Vitv15g00931	1.15	4e-15	2e-12 15 x 1
18	Vitv13g0049C	0.87	4e-15	2e-12 15 x 6
19	Vitv08g0106E	0.52	7e-15	6e-12 27 x 1
20	Vitv10g0189E	0.75	8e-15	1e-11 28 x 1
Underexpressed				
1	Vitv03g00012	-0.44	1e-16	2e-13 22 x 28
2	Vitv04g00302	-0.58	1e-16	2e-13 23 x 38
3	Vitv05g0029E	-0.35	1e-16	2e-13 21 x 36
4	Vitv09g0052E	-1	1e-16	2e-13 17 x 30
5	Vitv12g0214C	-1.82	1e-16	2e-13 8 x 8
6	Vitv14g0061E	-0.55	1e-16	2e-13 16 x 28
7	Vitv16g0105C	-1.24	1e-16	2e-13 27 x 39
8	Vitv17g01417	-1.52	1e-16	2e-13 20 x 17
9	Vitv18g0210E	-1.08	1e-16	2e-13 8 x 20
10	Vitv05g01863	-0.57	2e-16	2e-13 15 x 27
11	Vitv13g00242	-0.84	5e-16	6e-13 24 x 40
12	Vitv13g00013	-0.39	5e-16	6e-13 12 x 32
13	Vitv16g01494	-1.05	5e-16	6e-13 1 x 23
14	Vitv18g0184E	-2.33	1e-15	2e-12 37 x 26
15	Vitv16g0052E	-0.26	1e-15	2e-12 24 x 28
16	Vitv11g0012E	-0.48	1e-15	2e-12 20 x 17
17	Vitv05g01751	-1.85	2e-15	2e-12 21 x 13
18	Vitv14g0148E	-0.87	3e-15	2e-12 28 x 40
19	Vitv12g0066E	-0.28	3e-15	2e-12 15 x 30
20	Vitv08g01291	-1.37	4e-15	2e-12 37 x 39



Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	6.29	0.000	73	Transcription factor binding site (TFBS) - EREBP
2	6.08	0.000	64	Transcription factor binding site (TFBS) - EREBP
3	4.77	0.000	140	Hormone signaling pathway - EREBP
4	4.61	0.000	26	Flavonoid biosynthesis
5	3.88	0.000	45	Galactose metabolism
6	3.84	0.000	92	Lipid metabolism
7	3.76	0.000	51	Carbon fixation in photosynthetic organisms
8	3.43	0.001	15	Chaperone binding site (CBS) - DNAK
9	3.32	0.001	44	Energy metabolism
10	3.27	0.002	11	Biosynthesis of secondary metabolites
11	3.24	0.002	48	Transcription factor binding site (TFBS) - WRKY
12	3.23	0.002	15	Stilbenoid, diarylheptanoid, and lignan biosynthesis
13	3.2	0.002	38	Protein - Chaperone binding site (CBS) - DNAK
14	3.14	0.003	12	SLC15: SLC15A1, SLC15A2, SLC15A3, SLC15A4, SLC15A5, SLC15A6, SLC15A7, SLC15A8, SLC15A9, SLC15A10, SLC15A11, SLC15A12, SLC15A13, SLC15A14, SLC15A15, SLC15A16, SLC15A17, SLC15A18, SLC15A19, SLC15A20, SLC15A21, SLC15A22, SLC15A23, SLC15A24, SLC15A25, SLC15A26, SLC15A27, SLC15A28, SLC15A29, SLC15A30, SLC15A31, SLC15A32, SLC15A33, SLC15A34, SLC15A35, SLC15A36, SLC15A37, SLC15A38, SLC15A39, SLC15A40, SLC15A41, SLC15A42, SLC15A43, SLC15A44, SLC15A45, SLC15A46, SLC15A47, SLC15A48, SLC15A49, SLC15A50, SLC15A51, SLC15A52, SLC15A53, SLC15A54, SLC15A55, SLC15A56, SLC15A57, SLC15A58, SLC15A59, SLC15A60, SLC15A61, SLC15A62, SLC15A63, SLC15A64, SLC15A65, SLC15A66, SLC15A67, SLC15A68, SLC15A69, SLC15A70, SLC15A71, SLC15A72, SLC15A73, SLC15A74, SLC15A75, SLC15A76, SLC15A77, SLC15A78, SLC15A79, SLC15A80, SLC15A81, SLC15A82, SLC15A83, SLC15A84, SLC15A85, SLC15A86, SLC15A87, SLC15A88, SLC15A89, SLC15A90, SLC15A91, SLC15A92, SLC15A93, SLC15A94, SLC15A95, SLC15A96, SLC15A97, SLC15A98, SLC15A99, SLC15A100
15	3.12	0.003	26	Glycosyltransferase activity
16	3.1	0.003	49	Transcription factor binding site (TFBS) - NAC
17	3.01	0.004	17	Proteasome assembly
18	2.97	0.004	78	Energy metabolism
19	2.91	0.005	108	Carbohydrate metabolism
20	2.85	0.005	29	Carotenoid biosynthesis
<i>Underexpressed</i>				
1	-7.83	0e+00	217	Cell motility
2	-6.99	0e+00	206	Cell growth
3	-6.89	0e+00	80	Cytoskeleton
4	-6.83	0e+00	219	Cell growth
5	-5.74	0e+00	24	Replication
6	-5.54	0e+00	10	Peptidase
7	-5.09	0e+00	41	Replication
8	-4.75	0e+00	78	Glycosyltransferase activity
9	-4.69	0e+00	36	DNA replication
10	-4.67	0e+00	66	Exosome
11	-4.34	0e+00	11	Transcription factor binding site (TFBS) - GRF
12	-4.34	0e+00	19	Aquaporin
13	-3.6	4e-04	113	Exosome
14	-3.57	4e-04	19	Hormone signaling pathway
15	-3.51	5e-04	30	Glycan biosynthesis
16	-3.46	7e-04	65	Phagosome
17	-3.45	7e-04	168	Plant hormone signaling pathway
18	-3.43	1e-03	34	Peptidase
19	-3.2	2e-03	134	Hormone signaling pathway
20	-3.17	2e-03	129	Enzyme

