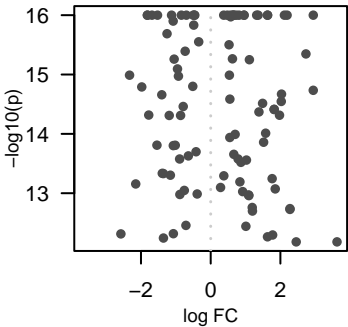
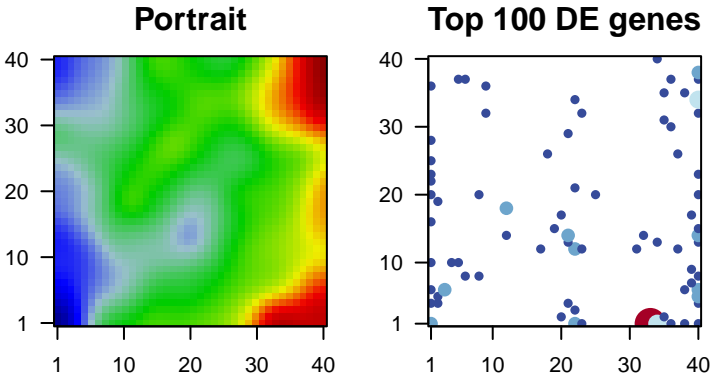


Chard_warm

Global Summary

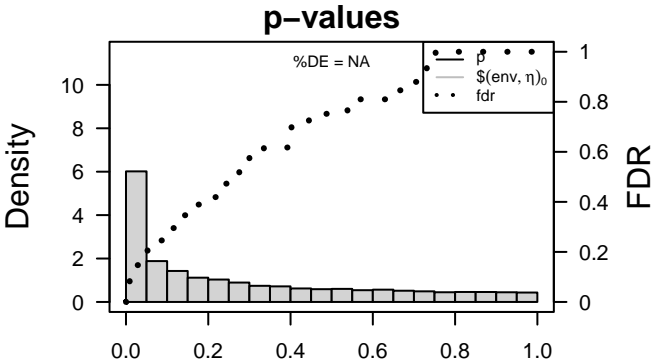
%DE = NA
genes with $\text{fdr} < 0.2$ = 5418 (2889 + / 2529 -)
genes with $\text{fdr} < 0.1$ = 3489 (1926 + / 1563 -)
genes with $\text{fdr} < 0.05$ = 2446 (1363 + / 1083 -)
genes with $\text{fdr} < 0.01$ = 1594 (886 + / 708 -)

<FC> = 0
<p-value> = 0.04
<fdr> = 0.45



Differentially expressed genes

Rank	ID	log(FC)	fdr	Description
		p-value		Metagene
Overexpressed				
1	Vitv00g0004C	1.63	1e-16	34 x 1
2	Vitv07g02832	1.63	1e-16	34 x 1
3	Vitv10g0034E	1.36	1e-16	40 x 20
4	Vitv03g0069E	0.64	1e-16	23 x 32
5	Vitv05g0049E	0.48	1e-16	18 x 26
6	Vitv05g0127E	1.32	1e-16	40 x 32
7	Vitv08g0151E	0.37	1e-16	21 x 29
8	Vitv08g0185E	0.73	1e-16	40 x 15
9	Vitv08g00151	0.96	1e-16	40 x 5
10	Vitv09g0167C	0.65	1e-16	40 x 8
11	Vitv10g0155A	0.67	1e-16	40 x 14
12	Vitv12g0232E	2.19	1e-16	32 x 1
13	Vitv13g0029C	0.96	1e-16	39 x 7
14	Vitv17g0018E	0.57	1e-16	40 x 14
15	Vitv17g0028C	2.12	1e-16	40 x 34
16	Vitv18g00322	0.81	1e-16	40 x 13
17	Vitv19g0199C	2.94	1e-16	33 x 1
18	Vitv18g0083E	0.57	1e-16	2e-13
19	Vitv06g0040I	0.53	3e-16	4e-13
20	Vitv19g0198E	2.73	4e-16	4e-13
Underexpressed				
1	Vitv04g0011C	-0.46	1e-16	12 x 14
2	Vitv05g0085E	-0.47	1e-16	9 x 32
3	Vitv05g0175I	-1.82	1e-16	5e-14
4	Vitv05g0157E	-1.12	1e-16	5e-14
5	Vitv07g0018Z	-0.5	1e-16	5e-14
6	Vitv12g0223C	-0.84	1e-16	5e-14
7	Vitv12g0214C	-1.81	1e-16	5e-14
8	Vitv13g01937	-1.68	1e-16	5e-14
9	Vitv13g0226C	-0.7	1e-16	5e-14
10	Vitv17g01417	-1.53	1e-16	5e-14
11	Vitv18g0210E	-1.08	1e-16	2e-13
12	Vitv08g0066E	-0.49	1e-16	4e-13
13	Vitv10g00887	-1.25	2e-16	4e-13
14	Vitv05g0034C	-0.34	3e-16	4e-13
15	Vitv08g0168C	-0.73	4e-16	4e-13
16	Vitv16g0149A	-1.05	6e-16	4e-13
17	Vitv04g0006E	-0.95	8e-16	1e-12
18	Vitv18g0184E	-2.33	1e-15	1e-12
19	Vitv14g0297E	-0.93	1e-15	2e-12
20	Vitv00g0227C	-0.51	2e-15	2e-12



Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
Overexpressed				
1	7.37	0e+00	78	Energy metabolism, Biosynthesis
2	6.83	0e+00	38	Photosynthesis
3	6.29	0e+00	206	Cell growth, Cell wall
4	6.07	0e+00	134	Hormone signaling
5	5.95	0e+00	47	Transport
6	5.6	0e+00	18	Energy metabolism, Biosynthesis
7	5.52	0e+00	26	Flavonoid biosynthesis
8	5.31	0e+00	19	Aquaporin
9	5.04	0e+00	40	Transport
10	4.99	0e+00	18	Photosynthesis
11	4.62	0e+00	39	Pentose phosphate cycle
12	4.36	0e+00	10	Photosynthesis
13	4.23	0e+00	63	Photosynthesis
14	4.12	0e+00	34	Peptidase
15	3.75	0e+00	44	Hormone signaling
16	3.7	2e-04	211	Ribosome
17	3.65	2e-04	19	Transcription
18	3.49	6e-04	26	Glycosyltransferase
19	3.44	9e-04	168	Plant hormone signaling
20	3.43	1e-03	47	ABC transporters
Underexpressed				
1	-6.43	0e+00	49	Transcription factors
2	-6.03	0e+00	64	Transcription factors
3	-4.94	0e+00	73	Transcription factors
4	-4.8	0e+00	140	Hormone signaling
5	-4.39	0e+00	48	Transcription factors
6	-4	0e+00	116	Ribosome
7	-3.75	0e+00	62	Ribosome
8	-3.66	2e-04	153	Plant-pathogen interaction
9	-3.26	2e-03	27	Enzyme
10	-3.23	2e-03	34	Tyrosine metabolism
11	-3.14	3e-03	86	Signal transduction
12	-3.02	4e-03	80	Transport
13	-2.82	6e-03	43	Mitochondrion
14	-2.78	6e-03	12	Enzyme
15	-2.78	7e-03	35	Mitochondrion
16	-2.69	8e-03	151	RNA polymerase
17	-2.56	1e-02	20	Protein
18	-2.56	1e-02	17	Isoquinoline alkaloid biosynthesis
19	-2.5	1e-02	64	Ribosome
20	-2.5	1e-02	119	Endocytosis

