

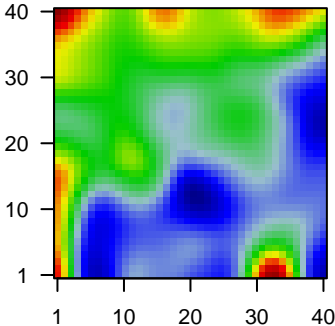
Chard_accfreeze_r2

Global Summary

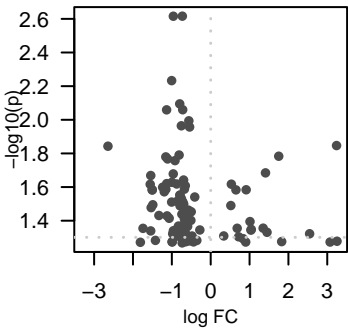
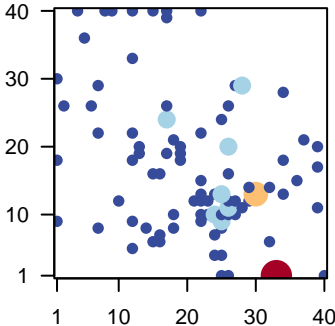
%DE = 0
genes with fdr < 0.2 = 0 (0 + / 0 -)
genes with fdr < 0.1 = 0 (0 + / 0 -)
genes with fdr < 0.05 = 0 (0 + / 0 -)
genes with fdr < 0.01 = 0 (0 + / 0 -)

<FC> = 0
<p-value> = 0.54
<fdr> = 1

Portrait

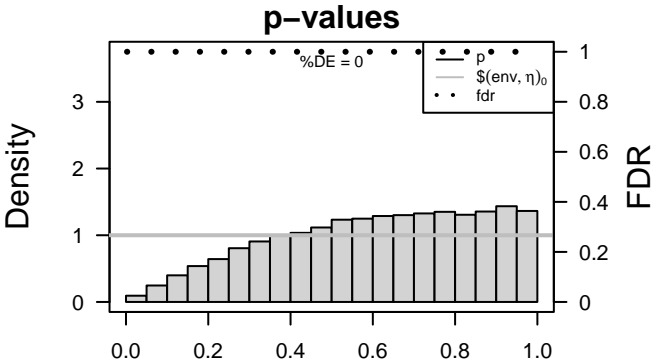


Top 100 DE genes



Differentially expressed genes

Rank	ID	log(FC)	fdr	Description
		p-value		Metagene
Overexpressed				
1	Vitv10g01863	3.24	0.01	1
2	Vitv12g0071C	1.75	0.02	1
3	Vitv08g0063E	1.41	0.02	1
4	Vitv04g00614	0.53	0.02	1
5	Vitv17g0051E	0.91	0.03	1
6	Vitv10g00662	0.65	0.03	1
7	Vitv15g0056E	0.52	0.03	1
8	Vitv01g0166E	1.01	0.04	1
9	Vitv06g0158E	1.35	0.04	1
10	Vitv07g00687	0.68	0.04	1
11	Vitv13g00667	1.04	0.04	1
12	Vitv04g01532	1.04	0.05	1
13	Vitv14g0185E	1.45	0.05	1
14	Vitv12g02324	2.55	0.05	1
15	Vitv11g00224	0.34	0.05	1
16	Vitv08g01143	0.72	0.05	1
17	Vitv13g00134	0.83	0.05	1
18	Vitv04g01863	3.25	0.05	1
19	Vitv13g0135E	1.83	0.05	1
20	Vitv15g0024E	0.9	0.05	1
Underexpressed				
1	Vitv05g00301	-0.73	0.002	1
2	Vitv07g00233	-0.96	0.002	1
3	Vitv07g01172	-1	0.006	1
4	Vitv13g00001	-0.8	0.008	1
5	Vitv09g0097E	-0.72	0.009	1
6	Vitv12g02404	-1.13	0.009	1
7	Vitv07g0001E	-0.56	0.010	1
8	Vitv16g0137C	-0.76	0.011	1
9	Vitv13g0024E	-0.54	0.011	1
10	Vitv04g01103	-2.64	0.014	1
11	Vitv15g01063	-0.81	0.016	1
12	Vitv05g0070E	-1.15	0.017	1
13	Vitv03g0048C	-1.11	0.017	1
14	Vitv07g01222	-0.92	0.017	1
15	Vitv08g0164C	-0.96	0.021	1
16	Vitv19g0025E	-1.54	0.021	1
17	Vitv14g02644	-0.7	0.023	1
18	Vitv09g00297	-1	0.024	1
19	Vitv18g02772	-1.13	0.024	1
20	Vitv06g0185E	-0.87	0.024	1



Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
Overexpressed				
1	10.42	0e+00	73	Transcription factor binding site (TFBS) - EREBP
2	9.66	0e+00	64	Transcription factor binding site (TFBS) - EREBP
3	7.07	0e+00	140	Hormone signaling pathway - EREBP
4	5.5	0e+00	11	Biosynthesis of amino acids - EREBP
5	5.23	0e+00	18	Photosynthesis - EREBP
6	5.06	0e+00	18	Energy metabolism - EREBP
7	5.02	0e+00	48	Transcription factor binding site (TFBS) - WRKY
8	4.78	0e+00	238	Enzyme - EREBP
9	4.64	0e+00	47	Transporter - EREBP
10	4.16	0e+00	49	Transcription factor binding site (TFBS) - NAC
11	3.86	8e-05	10	Photosynthesis - EREBP
12	3.67	3e-04	40	Transporter - EREBP
13	3.64	3e-04	29	Carotenoid biosynthesis - EREBP
14	3.14	2e-03	44	Hormone signaling pathway - EREBP
15	3.12	2e-03	66	Exosome - EREBP
16	3.01	3e-03	75	Translation - EREBP
17	2.94	4e-03	101	Starch and carbohydrate metabolism - EREBP
18	2.88	5e-03	223	Enzyme - EREBP
19	2.85	5e-03	64	Ribosome - EREBP
20	2.83	6e-03	195	Carbohydrate metabolism - EREBP
Underexpressed				
1	-3.52	6e-04	41	Transporter - EREBP
2	-3.36	1e-03	247	Translation - EREBP
3	-3.25	1e-03	22	Transcription factor binding site (TFBS) - D-DOF
4	-3.17	2e-03	105	Energy metabolism - EREBP
5	-3.03	3e-03	211	Ribosome - EREBP
6	-3.02	3e-03	67	Ribosome - EREBP
7	-2.89	4e-03	72	Ribosome - EREBP
8	-2.73	8e-03	44	Energy metabolism - EREBP
9	-2.69	8e-03	33	Carbohydrate metabolism - EREBP
10	-2.41	2e-02	48	Lipid metabolism - EREBP
11	-2.39	2e-02	50	Transcription factor binding site (TFBS) - MYB
12	-2.33	2e-02	19	Cofactors - EREBP
13	-2.23	3e-02	24	Folate biosynthesis - EREBP
14	-2.21	3e-02	97	Ribosome - EREBP
15	-2.18	3e-02	71	Amino acid metabolism - EREBP
16	-2.17	3e-02	33	alpha-Linolenic acid metabolism - EREBP
17	-2.14	3e-02	18	Chaperone - EREBP
18	-2.14	3e-02	25	Transcription factor binding site (TFBS) - GNAT
19	-2.09	4e-02	38	Lipid metabolism - EREBP
20	-2.05	4e-02	29	Transcription factor binding site (TFBS) - Trihelix

