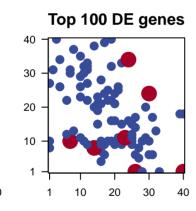
# Chard\_acclim\_r3

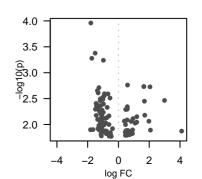
## **Global Summary**

%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> = 0.45 <fdr> = 1

## 



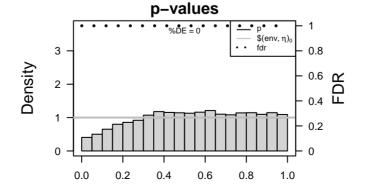


### Differentially expressed genes

Rank

	ID		p-value		Metagene			
Overexpressed							Overex	pressed
1	Vitvi03g00307	0.59	0.002	1	10 x 26	The component of a membrane consisting of the gene produc	1	6.59
2	Vitvi07g03061	1.65	0.002	1	30 x 24	The component of a membrane consisting of the gene produc	2	6.47
3	Vitvi00g00589	1.65	0.002	1	30 x 24		3	5.05
4	Vitvi09g00172	2.05	0.002	1	4 x 34	The component of a membrane consisting of the gene produc	4	4.61
5	Vitvi05g01760	2.99	0.003	1	1 x 8	A membrane-bounded organelle of eukaryotic cells in which	5	4.36
6	Vitvi18g02592	1.69	0.004	1	2 x 31	The space external to the outermost structure of a cell. For $c\varepsilon$	6	4.35
7	Vitvi09g01020	0.58	0.005	1	15 x 19		7	3.8
8	Vitvi04g01434	0.58	0.005	1	7 x 30		8	3.71
9	Vitvi17g01553	0.56	0.005	1	31 x 17	A semiautonomous, self replicating organelle that occurs in va	9	3.54
10	Vitvi02g00737	0.47	0.005	1	12 x 31	A lipid bilayer along with all the proteins and protein complexe	10	3.48
11	Vitvi14g02885	1.71	0.007	1	24 x 34		11	3.34
12	Vitvi19g01375	1.19	0.007	1	24 x 34	Binding to a protein.	12	3.22
13	Vitvi15g01052	0.94	0.008	1	29 x 20	A macromolecular complex that contains both RNA and prote	13	3.15
14	Vitvi08g01512	0.56	0.008	1	26 x 17	A small, dense body one or more of which are present in the	14	2.98
15	Vitvi01g00669	0.38	0.009	1	21 x 25	Organized structure of distinctive morphology and function, be	15	2.93
16	Vitvi10g01886	1.98	0.009	1	3 x 40		16	2.81
17	Vitvi07g02014	0.83	0.009	1	8 x 37	The directed movement of substances to, from or across the	17	2.72
18	Vitvi04g00346	1.19	0.009	1	12 x 27	Binding to a nucleic acid.	18	2.67
19	Vitvi16g00784	1.08	0.009	1	7 x 31		19	2.67
20	Vitvi11g00057	0.46	0.010	1	19 x 22		20	2.63
Unde	erexpressed						Undere	xpressed
1	Vitvi06q01418	-1.8	1e-04	1	26 x 1	The contents of a cell excluding the plasma membrane and n	1	-5.09
2	Vitvi06q00366	-1.52	4e-04	1	19 x 10	A semiautonomous, self replicating organelle that occurs in va	2	-5.08
3	Vitvi19g00532	-1.73	5e-04	1	27 x 5		3	-4.01
4	Vitvi18g00176	-0.98	6e-04	1	23 x 11	Binding to ATP, adenosine 5'-triphosphate, a universally impo	4	-3.85
	Vitvi14g02465	-1.27	2e-03	1	17 x 9	The component of a membrane consisting of the gene produc	5	-3.84
5 6	Vitvi11g00435	-1.37	2e-03	1	27 x 8	A membrane-bounded organelle of eukaryotic cells in which	6	-3.79
7	Vitvi18g00515	-1.32	2e-03	1	24 x 16		7	-3.46
8	Vitvi08g01120	-0.91	3e-03	1	32 x 13	A multisubunit protein complex that contains the Ino80p ATPa	8	-3.35
9	Vitvi12g00656	-0.68	3e-03	1	29 x 11	Binding to a nucleic acid.	9	-3.02
10	Vitvi11g01656	-0.93	3e-03	1	25 x 15	A membrane-bounded organelle of eukaryotic cells in which	10	-2.85
11	Vitvi04g01787	-1.03	3e-03	1	26 x 6	The component of a membrane consisting of the gene produc	11	-2.82
12	Vitvi06g00167	-0.55	3e-03	1	20 x 24	Catalysis of the transfer of a methyl group to an acceptor mol	12	-2.81
13	Vitvi06g01505	-1.18	3e-03	1	15 x 21	Any process that results in a change in state or activity of a co	13	-2.79
14	Vitvi18g00637	-1.01	3e-03	1	10 x 11	A lipid bilayer along with all the proteins and protein complexe	14	-2.78
15	Vitvi07g00824	-1.19	3e-03	1	26 x 14	Binding to ATP, adenosine 5'-triphosphate, a universally impo	15	-2.76
16 17	Vitvi13g01817 Vitvi03g00279	-1.45 -0.98	4e-03 4e-03	1	6 x 12 22 x 9	Binding to the oxidized form, FAD, of flavin–adenine dinucleot	16 17	-2.73 -2.61
18	Vitvi03g00278 Vitvi08g02251	-0.98	4e-03	1	19 x 16	A lipid bilayer along with all the proteins and protein complexe	18	-2.51 -2.58
19	Vitvi04g00081	-1.15	4e-03	1	8 x 13	The component of a membrane consisting of the gene produc	19	-2.56
20	Vitvi13g02287	-1.42	4e-03	1	40 x 18	The desirponent of a membrane deficiently of the gene product	20	-2.51
20		1.72	.0 00		.0 1 10		20	2.0.

Description



#### Differentially expressed gene sets

	Rank	GSZ	p-value	#all	Geneset				
	Overexp	ressed							
uc	1	6.59	0e+00	18	Photosyn@lessissyrathlessisa-paroteimsa proteins				
uc	2	6.47	0e+00	18	Energy mētæbrglijsmeta@bibbosyn@lecsiosaymteresasparoteimsa proteins				
	3	5.05	0e+00	47	Transport@iransapalootger-@intenlegort@ierospoort@ieros				
uc	4	4.61	0e+00	134	Hormone Higmating sightalingsign Auling signaling				
h	5	4.36	0e+00	66	ExosomeEx6sxosremaEproxeimalqrirbitæitdæochalradeterettancer cells				
CE	6	4.35	0e+00	206	Cell grow@edingfoolettthancOddlathall- Cell wall				
	7	3.8	1e-04	10	Photosyn Priecosio spyroutreeiss is Prirouteius ys Pelmouto (\$P750@nochli (\$P7600) ybthab) rophyll a)				
	8	3.71	1e-04	113	ExosomeEx <b>Exosœm</b> aEproxeinalqriroteinecotáloceloreentatetlancer cells				
Vi	9	3.54	5e-04	38	PhotosynfPiecsissynthesis				
xε	10	3.48	7e-04	26	Steroid bi6ssyndladsiesynthesis				
	11	3.34	1e-03	17	Kinase - KnakstamilityAK family				
	12	3.22	1e-03	78	Glycosyltr@inysfessyltreans@erasterralSptoulystracethpeolysteaccharide				
te	13	3.15	2e-03	78	Energy mētæbrglijsmetaBbbisosyntPlæssissynthesis				
9	14	2.98	3e-03	42	Folding softolidinglespratidagidegra?thatieaseifleoteasome				
bı	15	2.93	4e-03	44	Proteason Proteasome				
	16	2.81	6e-03	13	Cofactors Confectives named neitabrilis meta Trollamine Theatatio Estmetabolism				
9	17	2.72	8e-03	75	TranslatioTranklatissomeRitiogenesisiongEndsaisyoteEukaryotes				
	18	2.67	8e-03	62	RibosomeRitiogenessIsiog@00@spiantidleS particles				
	19	2.67	8e-03	40	Transport Topustaport Stylsytenkoid Ttaydpektinig pearthentiang pathway				
	20	2.63	1e-02	64	Ribosom <b>eRtbiogenesisiogenkaisyotes</b> ukaryotes				
	Underexpressed								
n	1	-5.09	0e+00	49	TranscriptTownfactiontion MacCors - NAC				
Vi		-5.08	0e+00	10	Linoleic abidorleitatacidismetabolism				
	2 3 4	-4.01	0e+00	73	Transcription faction fall 20 EREBP				
OC		-3.85	8e-05	29	TranscriptToenfactiontion Califacts - GRAS				
uc	5 6 7	-3.84	8e-05	140	Hormonel signating signating signating signaling				
h	<u>6</u>	-3.79	1e-04	48	Transcription taketints - WRKY				
		-3.46	8e-04	153	Plant-pathtagenpathagenionnteraction				
a	8	-3.35	1e-03	45	Galactos@aletatbs@smetabolism				

Other me@athodismetaSiorlisienreaSithorles reactions

alpha-Linadpehraic-baicidlemetratocidismmetabolism

Carotenoi@driptsynttluelsiesynthesis

Transcription faction (albiATs - GNAT

Chaperon@habt861269 - HSP20

Transcription factioniscon Catterszf-O8heC4f-C3HC4

Energy mEtæbrglijsmetalslithisgen inlittabelismetabolism

Hormone Higmating sightstingnatus signaling

Enzyme -Ethz8ynAestingt.8n/acstadguargeosphfadrograppsof donors

TranscriptTownfactiontion Basicriseu@aeizippoein(bZliP)per (bZIP)

Carbohyd@ateborle.tdbatesmeeta@aliasotos@alataboesmeetabolism

3e-03

5e-03

6e-03

6e-03

6e-03

6e-03

7e-03

8e-03

1e-02

1e-02

1e-02

1e-02

170

33

29

38

28

11

25

77

