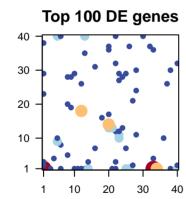
# Chard\_acclim

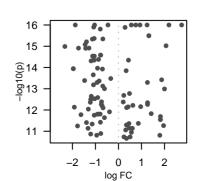
## **Global Summary**

%DE = NA # genes with fdr < 0.2 = 3869 ( 2137 + /1732 -) # genes with fdr < 0.1 = 2449 ( 1320 + /1129 -) # genes with fdr < 0.05 = 1864 ( 976 + /888 -) # genes with fdr < 0.01 = 1121 ( 556 + /565 -)

<FC> = 0<p-value> = 0.07<fdr> = 0.52

# Portrait 40 30 20 10 1 10 20 30 40





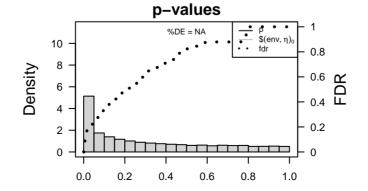
## Differentially expressed genes

log(FC) fdr

Rank

ID		•	p-value		Metagene			
Overexpressed Overe								
1	Vitvi12g02324	2.75	1e-16	1e-13	33 x 1	Binding to a protein.	1	
2	Vitvi13g01759	0.75	1e-16	1e-13	28 x 24	Binding to single-stranded DNA.	2	
3	Vitvi13g01298	2.19	1e-16	1e-13	12 x 18	Catalysis of an oxidation-reduction (redox) reaction in which:	3	
4	Vitvi16g01495	0.93	1e-16	1e-13	36 x 10	A lipid bilayer along with all the proteins and protein complexe	4	
5	Vitvi17g00148	1.24	1e-16	1e-13	1 x 38	A small organelle enclosed by a single membrane, and found	5	
6	Vitvi19g00105	0.56	1e-16	1e-13	13 x 35	Any process that modulates the rate of GTP hydrolysis by a G	6	
7	Vitvi07g02036	0.29	1e-16	2e-13	24 x 28	The modification of histones by removal of acetyl groups.	7	
8	Vitvi10g02163	1.32	3e-16	6e-13	13 x 40		8	
9	Vitvi00g00358	1.32	3e-16	6e-13	13 x 40		9	
10	Vitvi12g02454	2.07	1e-15	1e-12	34 x 1	Catalysis of the transfer of an acyl group, other than amino-a	10	
11	Vitvi03g00690	0.43	5e-15	5e-12	27 x 21	A lipid bilayer along with all the proteins and protein complexe	11	
12	Vitvi07g01674	0.33	1e-14	5e-11	23 x 29	The component of a membrane consisting of the gene produc	12	
13	Vitvi01g00350	1.88	4e-14	5e-11	33 x 1		13	
14	Vitvi12g02316	1.26	5e-14	5e-11	32 x 37	Binding to a protein.	14	
15	Vitvi11g01446	2	1e-13	3e-10	33 x 1	Any molecular entity that serves as an electron acceptor and	15	
16	Vitvi07g01449	0.48	2e-13	3e-10	22 x 40	An thiol-dependent isopeptidase activity that cleaves ubiquitii	16	
17	Vitvi09g00722	0.23	2e-13	3e-10	8 x 28	Binding to ATP, adenosine 5'-triphosphate, a universally impo	17	
18	Vitvi16g00153	0.21	4e-13	3e-10	23 x 27	The component of a membrane consisting of the gene produc	18	
19	Vitvi00g01489	1.26	5e-13	4e-10	34 x 1		19	
20	Vitvi07g02812	1.26	5e-13	4e-10	34 x 1	Reactions, triggered in response to the presence of a foreign	20	
Underexpressed Under								
1	Vitvi04g00415	-0.46	1e-16	1e-13	16 x 7	Binding to the oxidized form, FAD, of flavin-adenine dinucleot	1	
2	Vitvi05g01751	-1.88	1e-16	1e-13	21 x 13			
3	Vitvi08g01057	-1.04	1e-16	1e-13	13 x 1		2 3 4 5 6 7	
4	Vitvi18g02109	-1.08	1e-16	1e-13	8 x 20		4	
5	Vitvi13g01917	-0.79	2e-16	6e-13	25 x 1		5	
6	Vitvi16g01494	-1.06	4e-16	6e-13	1 x 23		<u>6</u>	
7	Vitvi17g00094	-0.68	5e-16	6e-13	24 x 13	A protein complex that interacts with the carboxy–terminal do		
8	Vitvi06g00216	-1.13	5e-16	1e-12	10 x 1	The component of a membrane consisting of the gene produc	8	
9	Vitvi14g01367	-1.39	6e-16	1e-12	1 x 1	Binding to ATP, adenosine 5'-triphosphate, a universally impo	9	
10	Vitvi05g00062	-1.45	8e-16	1e-12	22 x 1	Reactions, triggered in response to the presence of a foreign	10	
11	Vitvi18g01849	-2.33	1e-15	1e-12	37 x 26	Binding to ADP, adenosine 5'-diphosphate.	11	
12	Vitvi13g00161	-1.28	1e-15	1e-12	12 x 1	Pinding to ADD adapasing 5' diphosphoto	12	
13	Vitvi12g02011 Vitvi10g00227	-1.74	1e-15	1e-12	23 x 11	Binding to ADP, adenosine 5'–diphosphate.  The component of a membrane consisting of the gene produce.	13	
14 15	Vitvi04g01470	-1.43 -0.78	1e-15 3e-15	4e-12 4e-12	28 x 30 14 x 1	The space external to the outermost structure of a cell. For ce	14 15	
16	Vitvi07g01831	-0.78 -0.77	3e-15	4e-12 4e-12	14 x 1	Binding to ATP, adenosine 5'–triphosphate, a universally impo	16	
17	Vitvi07g01031 Vitvi05g02001	-1.12	3e-15	4e-12	20 x 13	The contents of a cell excluding the plasma membrane and n	17	
18	Vitvi12g02701		3e-15	5e-12		Binding to ADP, adenosine 5'–diphosphate.	18	
10	VIII 140 04000		30 .0	50 .2	_0 x 12	District ATD a least of the lea	10	

Description



Vitvi16g01866 -0.87 4e-15 5e-12 22 x 12 Binding to ATP, adenosine 5'-triphosphate, a universally impo

Vitvi07g00403 -1.06 5e-15 5e-12 23 x 10 The action of a molecule that contributes to the structural inte

### Differentially expressed gene sets

Rank GSZ p-val	ue #all Geneset
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-2.75 7e-03

8e-03

9e-03

1e-02

-2.67

-2.64

-2.62

-2.58

-2.5

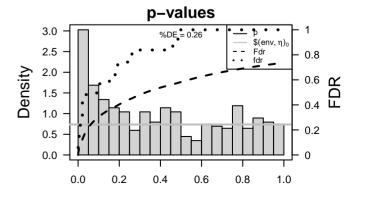
29

44

162

71

Overe	xpressed			
1	6.37	0e+00	18	Energy m <b>EtæbrglismmetalBhöldasynfPleasiasaymtlehesiaspanoteinns</b> a proteins
	6.25	0e+00	18	Photosyn <b>Placsissyrathlesis</b> a-paroteimsa proteins
3	5.23	0e+00	47	Transporteraratatorter-Catalogo-tTelevispoortoeleideron carriers
ă	4.44	0e+00	38	Photosyn <b>tPleasis</b> synthesis
2 3 4 5 6 7	4.2	0e+00	10	Photosyn Pleasis syrratteissis Planteins ys Pelnoto (1975) Denchl (1975) Dividina) rophyll
ñ	3.91	0e+00	78	Energy mētatoralismetal Bulistons yn Plansies synthesis
7	3.58	4e-04	217	Cell motilitiell metilitation exitation exitos seite to moskeleton
8	3.5	5e-04	26	Steroid bi <b>6teyrolidelsis</b> synthesis
á	3.4	1e-03	10	PeptidaseSepartidasesbitanas in Hibitaitaits A1FarreitsiA farmellysin family
10	3.25	2e-03	80	Cytoskele@ntosl\deletotubul\desrotubulles
11	3.24	2e-03	40	Transport Translamort Stylsytenkoid Thaybektorid perthediang pathway
12	3.17	2e-03	66	ExosomeExExosremaExosteinalqfibiteitidscocalerettancer cells
13	3.16	2e-03	31	Chromos@heoanosaosaociatedssoctaitesd-p@deiasile@aing silencing
14	3.04	3e-03	219	Cell growthethrandothathroleCell cycle
5	3.04	3e-03	17	Kinase – Krinakskamilika Kamily
6	3.02	4e-03	18	Transcription faction factor - ARF
7	2.99	4e-03	11	Transcription faction (aRtiors – GRF
8	2.94	4e-03	21	Thiamine Thiatetinesmetabolism
9	2.94	8e-03	32	Circadian@hyddian phythim – plant
20	2.65	9e-03	113	Exosome Exessors ama Exosoma logino obtains cotá locator acetal estas no cer cells
.0	2.00	36-03	113	EXOSOTTICE A CARBON BUTTAL PROGRAM SOCIAL COMMUNICATION OF COMMUNICATION O
Inder	expresse	d		
l	-6.06	0e+00	73	Transcription faction factors REBP2 EREBP
<u>'</u>	-5.98	0e+00	140	Hormonelskigmating signthijnene Sitynyating signaling
3	-4.8	0e+00	48	Transcriptioaniscription taletox - WRKY
1	-4.76	0e+00	49	TranscriptToarfactipitison Mattors - NAC
2 3 4 5 7 8	-4.24	0e+00	45	Galactos@alatatosesmetabolism
3	-3.86	0e+00	153	Plant-pathagenpathagenioninteraction
7	-3.46	7e-04	64	Transcription factors at Catherstran Cathe
3	-3.41	1e-03	51	Other me@utralismetaSionlightenreabitingthenreactions
)_	-3.13	3e-03	26	Transcription faction Gaztolike G2-like
10	-3.12	3e-03	77	Carbohydicateborteytalbadeismeeta@allisotos@allatatboeismetabolism
1	-2.87	5e-03	11	Cofactors@orfdotitesramdreitabrilismetall/idäsmin-Bl/itaetiabBl/ismetabolis
12	-2.87	5e-03	10	Linoleic alcidorleitatocitismetabolism
3	-2.83	6e-03	15	Chaperon@hapts@n7@ ≠ DNS.R7X0 / DNAK
14	-2.75	7e-03	58	Other am 10 th a cials nime talcidis meta 6 blitanthie roll utatta bolis metabolis m



Transcription faction (aRtAS) - GRAS

Proteason Prote Asseme blinks southfulling factors

Plant spellfantigradifig signatingpathlagenpathogetionnteraction