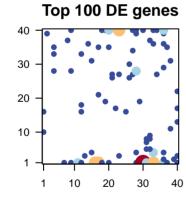
# Chard\_freeze\_r3

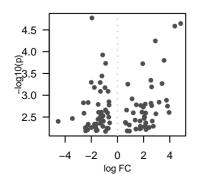
#### **Global Summary**

%DE = 0.17 # genes with fdr < 0.2 = 2 (1 + /1 -) # 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> = 0.35<fdr> = 0.83

## 





### Differentially expressed genes

Rank		log(FC)		fdr		Description
	ID	•	p-va	lue	Meta	gene
Overexpressed						
1	Vitvi12g02565	4.83	2e-05	0.1	36 x 1	The space external to the outermost structure of a cell. For ce
2	Vitvi09g02008	4.38	3e-05	0.5	31 x 1	An intracellular non-membrane-bounded organelle comprisir
3	Vitvi07g01624	2.89	6e-05	0.5	36 x 1	The irregular network of unit membranes, visible only by elect
4	Vitvi07g00259	3.56	2e-04	0.5	9 x 1	The contents of a cell excluding the plasma membrane and n
5	Vitvi07g01823	1.93	2e-04	0.7	33 x 4	A membrane-bounded organelle of eukaryotic cells in which
6	Vitvi14g01840	2.55	5e-04	0.7	28 x 1	Binding to ATP, adenosine 5'-triphosphate, a universally impo
7	Vitvi19g01028	3.4	5e-04	0.7	7 x 1	Binding to a heme, a compound composed of iron complexed
8	Vitvi11g00055	0.79	6e-04	0.7	32 x 9	The inner, i.e. lumen-facing, lipid bilayer of the mitochondrial
9	Vitvi02g01167	2.61	6e-04	0.7	17 x 1	A lipid bilayer along with all the proteins and protein complexe
10	Vitvi04g01336	1.11	1e-03	0.7	31 x 5	The component of a membrane consisting of the gene produc
11	Vitvi05g01353	3.75	1e-03	0.7	1 x 16	The space external to the outermost structure of a cell. For ce
12	Vitvi09g00258	3.18	1e-03	0.7	17 x 1	Binding to ATP, adenosine 5'-triphosphate, a universally impo
13	Vitvi02g00673	2.56	2e-03	0.7	12 x 1	Any molecular function by which a gene product interacts sele
14	Vitvi11g00165	2.12	2e-03	0.7	1 x 10	The formation of a protein dimer, a macromolecular structure
15	Vitvi12g00154	1.44	2e-03	0.7	32 x 5	The component of a membrane consisting of the gene produc
16	Vitvi18g03220	1.79	2e-03	0.7	12 x 18	
17	Vitvi18g00290	2.61	2e-03	0.7	36 x 2	The component of a membrane consisting of the gene produc
18	Vitvi13g00369	3.82	2e-03	0.7	40 x 3	Catalysis of the hydrolysis of internal, alpha-peptide bonds in
19	Vitvi02g00683	1.98	2e-03	0.7	16 x 1	A lipid bilayer along with all the proteins and protein complexe
20	Vitvi06g00973	0.7	2e-03	0.7	31 x 8	An thiol-dependent isopeptidase activity that cleaves ubiquiting
Unde	erexpressed					
1	Vitvi13g00538	-1.95	2e-05	0.1	8 x 37	Binding to a microtubule, a filament composed of tubulin mon
2	Vitvi11g00153	-1.13	1e-04	0.5	22 x 17	The component of a membrane consisting of the gene produc
3	Vitvi08g01356	-0.91	2e-04	0.5	9 x 28	Binding to ATP, adenosine 5'-triphosphate, a universally impo

Vitvi04g01578 -1.19 4e-04 0.7 29 x 19 Any molecular function by which a gene product interacts sele 5e-04 32 x 37 Binding to an amino acid, organic acids containing one or mo Vitvi08g01378 -1.32 27 x 34 Vitvi07g00903 -1.77 36 x 29 The component of a membrane consisting of the gene produc Vitvi01g00043 -0.95 28 x 28 Binding to a polysaccharide, a polymer of many (typically mor Vitvi12g02042 -0.72 26 x 30 Reactions, triggered in response to the presence of a foreign Vitvi18g01535 -1.3 27 x 27 Binding to GTP, guanosine triphosphate. Vitvi09g00116 -0.65 23 x 27 Any molecular function by which a gene product interacts sele Vitvi13g01744 -2.24 1e-03 30 x 40 Catalysis of the transfer of ubiquitin from one protein to anoth Vitvi17g00963 -2.6 19 x 40 The formation of the principal food-conducting tissue of a vas Vitvi06g00230 -1.47 34 x 27 Binding to a heme, a compound composed of iron complexed Vitvi03g00371 15 x 31 Binding to a protein. Vitvi04g00067 -0.91 Vitvi06g01073 -0.88

21 x 27 Any process that modulates the frequency, rate or extent of or 23 x 40 The component of a membrane consisting of the gene produc 40 x 17 A membrane—bound cytoplasmic organelle of the endomemb 28 x 28 The process in which one or more ubiquitin groups are added

### Differentially expressed gene sets

Rank	GSZ	p-value	#all	Genese
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-3.37

-3.1

-2.85

-2.67

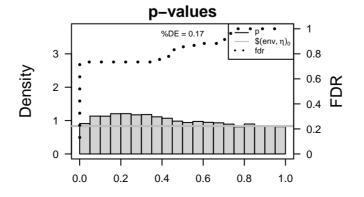
9e-04

5e-03

34

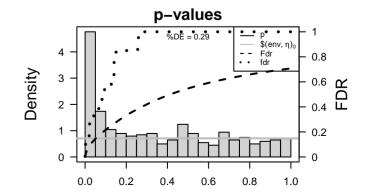
37

			•		
	Overexp	ressed			
E	1	4.19	0e+00	45	GalactoseΩ <b>ralatatbsi</b> ismetabolism
ir	2	4.19	0e+00	45 51	Carbon fixatistro infiplacitos vim the discover the construction of the construction o
ıı ct		4.12	0e+00 0e+00	48	Transcriptioaniscription taletor - WRKY
וו	3				·
	4	4.1	0e+00	64	Transcriptionanfactipation (AttherstranOthreptionanfactipation factors
11	5	3.93	4e-05	10	SLC39: Mattal 34n Manasporter
C .	6	3.75	1e-04	73	Transcription factipition fall 20 EREBP
d	7	3.51	6e-04	49	TranscriptToanfactiontson Mattors - NAC
I	8	3.49	7e-04	77	Pores ion Robrassriels (TiGath)els [TC:1]
Œ	9	3.49	7e-04	15	Chaperor@hapts@n7@ ≠ DNS.RR0 / DNAK
IC.	10	3.42	9e-04	44	Energy mētadogljsmetalsliditisgen ilkletalgelismetabolism
Œ	11	3.26	1e-03	41	Arginine aAmdipinoënændhetabioësmetabolism
С	12	3.24	1e-03	157	Protein processingrio cessing las eniclo plias anoiro reticulum
l€	13	3.23	1e-03	11	BiosyntheBiosylnsteesisdafraeoetadarlysmetaAbBlAstriosylnBlActsiosynthesis
9	14	3.14	2e-03	24	Tropane pTpopriatinecpipretiplymizilizmedaplyalldidebidlsgltdldebisssynthesis
ıc	15	3.14	2e-03	15	StilbenoidStillahentloieth taliacythepthagitriglearodthojorsgreatbletsisssynthesis
	16	3.13	2e-03	140	Hormonelstigmating signating signating signaling
ıc	17	3.12	2e-03	71	Exosome Ex Psotreias - f Provide instrumento de insponse se xosomes
n	18	3.11	2e-03	38	Amino aci <del>Ahninetaatoolitsmetaatoolismeeataatoolism</del>
Œ	19	3.07	2e-03	38	Protein – Płowięcieren Ghapedratecha etobetech pu (120 MA)
ii	20	2.96	3e-03	42	Tryptopha <b>Tryptxtpbelism</b> etabolism
	_0				
	Underex	pressec	1		
n	1	-7.59	0e+00	206	Cell grow@eatingtrodertithandCatalathall-Cell wall
IC.	2	-7.41	0e+00	217	Cell motilificell integration controls and motilification of the control of the c
С	3	-6.8	0e+00	219	Cell grow@eatingtrodertithandCatalactricleCell cycle
l€	4	-6.59	0e+00	80	Cytoskele@ytoskeletotubulkeisrotubules
О	5	-6.21	0e+00	10	Peptidase Reputidas leistiatoris in Hilartoins A1F. apreilysi A. farpeilysin family
	6	-5.05	0e+00	11	Transcriptionniscription Califors - GRF
IC.	7	-4.92	0e+00	78	Glycosyltr@inysfersyltecens@terracsterralSptrollycstarcathpartiysteaccharide
10	8	-4.87	0e+00	24	Replication Repriodation phylike in epochalic Republication Fractors
ì	9	-4.54	0e+00	41	Replication
	10	-4.33	0e+00	36	DNA repliDatiAmeplication
l€	11	-4.05	0e+00	39	Pentose a Pethydiseuronda gleuintermeteviensia inconversions
h	12	-3.99	0e+00	19	Aquaporin/Aquaposimal/amel.israbs/solvetetitabsolputetéran(\$1000/fte/ks8[TC:1.A.8]
E	13	-3.9	4e-05	19	Hormonelsignating si@hiblingelli@itsigeatlling signaling
d	14	-3.69	3e-04	13	Cutin sub@rintie anderiane laindymathelsiesynthesis
	15	-3.68	3e-04	66	Exosome Ex Escos cema Epocos e in a lopír foltació de o calecte de cella neces cella



Vitvi13q00777 -1.45

2e-03



CarbohydCateboriestalbateismeetaStalissim an Etauchoasedraetarbeeismeetabolism

Glycan bi@dycatmetsicsaymothrensitaabolilsmetallsle/l@lycarNde@lyacdartide.gradation

Chromos@heoarrasasseoiatedssectiaitesd-p@eeiasile@eing silencing

PeptidaseRegatidaskishistorus in Hibitoihs S1Ramily S10

Homologo de la completa del la completa de la completa de la completa del la completa de la completa del la completa de la completa del la compl