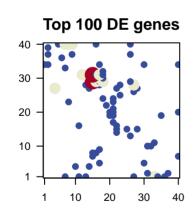
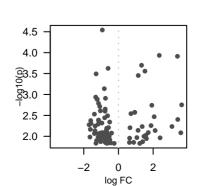
Chard_freeze_r1

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 -)

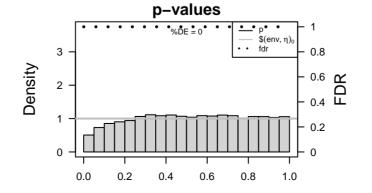
<FC> = 0 <p-value> = 0.42 <fdr> = 1





Differentially expressed genes

Rank ID		log(FC) fdr p-value		Meta	Description Metagene				
Overexpressed Over									
1	Vitvi14g02502	2.35	1e-04	1	31 x 2	Binding to a protein.	1		
ż	Vitvi08g01434	3.4	1e-04	1	33 x 1	The chemical reactions and pathways involving carbohydrate:	2		
3	Vitvi19g02355	1.33	2e-04	1	15 x 7		3		
4	Vitvi08g00998	1.53	3e-04	1	27 x 1	A complex composed of TATA binding protein (TBP) and TBP	4		
5	Vitvi04g01304	1.14	4e-04	1	26 x 29	A membrane-bounded organelle of eukaryotic cells in which	5		
6	Vitvi19g02024	3.65	2e-03	1	40 x 34	•	6		
7	Vitvi15g01579	1.92	2e-03	1	35 x 19		7		
8	Vitvi04g02290	0.94	3e-03	1	4 x 27		8		
9	Vitvi00g01739	0.94	3e-03	1	4 x 27		9		
10	Vitvi01g01645	0.72	3e-03	1	31 x 10	Catalysis of the hydrolysis of phosphoric monoesters, releasir	10		
11	Vitvi19g01854	2.06	3e-03	1	30 x 34	Catalysis of the transfer of a glycosyl group from a UDP-suga	11		
12	Vitvi12g02565	3.42	4e-03	1	36 x 1	The space external to the outermost structure of a cell. For ce	12		
13	Vitvi18g01433	1.88	6e-03	1	40 x 20	Innate immune responses are defense responses mediated b	13		
14	Vitvi11g00285	3.09	6e-03	1	11 x 1	A membrane-bounded organelle of eukaryotic cells in which	14		
15	Vitvi01g00620	1.37	6e-03	1	40 x 7	Binding to a heme, a compound composed of iron complexed	15		
16	Vitvi15g00882	0.66	6e-03	1	33 x 11	A lipid bilayer along with all the proteins and protein complexe	16		
17	Vitvi10g00544	1.13	7e-03	1	16 x 8	Catalysis of the transfer of an acyl group, other than amino-a	17		
18	Vitvi19g00173	2.11	7e-03	1	34 x 1		18		
19	Vitvi02g00052	1.72	8e-03	1	13 x 1	The space external to the outermost structure of a cell. For $c\varepsilon$	19		
20	Vitvi08g01547	3.6	8e-03	1	7 x 1		20		
Und	erexpressed						Unde		
	Vitvi06g01769	0.00	2- 05		45 20	The action of a molecule that contributes to the structural inte			
1	Vitvi02g00737	-0.93 -0.6	3e-05 2e-04	1	15 x 30 12 x 31	A lipid bilayer along with all the proteins and protein complexe	1		
2	Vitvi02g00737 Vitvi02g00018	-1.29	3e-04	1	15 x 29	Binding to a protein.	2 3		
4	Vitvi14q01445	-0.82	7e-04	1	23 x 28	The component of a membrane consisting of the gene produc	4		
5	Vitvi04g00446	-1.31	1e-03	1	7 x 40	The process in which a methyl group is covalently attached to	5		
4 5 6 7	Vitvi03g00160	-0.75	1e-03	1	21 x 19	A cellular transport process in which transported substances	6		
Ž	Vitvi07g03092	-1.23	1e-03	1	16 x 29		5 6 7		
8	Vitvi00g00751	-1.23	1e-03	1	16 x 29		8		
9	Vitvi07g01235	-1.15	2e-03	1	16 x 31		9		
10	Vitvi08g01790	-1.08	2e-03	1	17 x 31	A membrane-bounded organelle of eukaryotic cells in which	10		
11	Vitvi02g00274	-0.77	2e-03	1	27 x 26	The inner, i.e. lumen–facing, lipid bilayer of the mitochondrial	11		
12	Vitvi01g01704	-1.04	2e-03	1	27 x 28	Binding to an amino acid, organic acids containing one or mo	12		
13	Vitvi13g00018	-0.77	3e-03	1	18 x 24	The component of a membrane consisting of the gene produc	13		
14	Vitvi00g00997	-1.39	3e-03	1	16 x 28		14		
15	Vitvi01g01667	-0.63	3e-03	1	28 x 15		15		
16	Vitvi00g01168 Vitvi00g00857	-0.8	4e-03	1	21 x 17		16		
17 18	Vitvi07g02958	-1.15 -1.15	4e-03 4e-03	1	17 x 30 17 x 30		17 18		
19	Vitvi17g00373	-1.13	4e-03	1	26 x 40	Binding to ATP, adenosine 5'-triphosphate, a universally impo	19		
20	Vitvi12g00837	-0.51	5e-03	1	20 x 20	Binding to ATP, adenosine 5'-triphosphate, a universally impo	20		
20	3			•		5	20		



Differentially expressed gene sets

Rank GSZ p-val	ue #all Geneset
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	Overexpressed							
	1	8.4	0e+00	26	Flavonoid Flavosynttidelsics synthesis			
11	2	7.08	0e+00	73	Transcription factipation fall 20 EREBP EREBP			
	3	6.46	0e+00	78	Energy metabolismsynPhasissynthesis			
•	4	5.26	0e+00	64	Transcriptionniscotipation (attherstran@threptionniscotipation factors			
	4 5	4.65	0e+00	38	Photosyn Pleasis synthesis			
	6	4.29	0e+00	92	Lipid metalipoidismeta@byisenolip@dyvoentalipoidismetabolism			
	6 7	4.22	0e+00	140	Hormonel signating signating signating signaling			
	8	4.16	0e+00	26	Glycosylt/@hysfessylteans/flyrans.epholblychropleabile molecule			
	9	3.85	8e-05	15	Stilbenoic Stillan, nloco taino ithe ptaginigeno blojos gentolesies ynthesis			
r	10	3.81	1e-04	63	Phenylpro/pharrouithbiopaynotitelsissynthesis			
έ	11	3.78	1e-04	206	Cell growtDettingtroutettthandOutdlatthall Cell wall			
E	12	3.19	2e-03	57	Transcriptioanfactipition fallitors - HB			
b	13	3.11	2e-03	10	Linoleic alcidorieidatocidismetabolism			
	14	2.92	4e-03	40	Transport Tsranstepnor+ stylastenko-id Ttaytpetriorig pearthreviang pathway			
t	15	2.91	4e-03	118	Transcriptioanfactipition factionsturin-telled-inturn-helix			
E	16	2.77	7e-03	44	Energy mētæbrgljsmetalsidhisgen ilvietalgehismetabolism			
a	17	2.6	1e-02	83	Transcriptioanfactipition Motions - MYB			
	18	2.56	1e-02	50	Transcriptioanfactipition faitibre lated/Brelated			
E	19	2.55	1e-02	17	ProteasonProteAsserreblinAssertubring factors			
	20	2.52	1e-02	12	SLC15: P8ht6nf falli@opteptiolegopteptisleoroteransporter			
	l la de ses		_					
	Underex	•			Design Design of a DAIA to JDAPA and Post of			
9	1	-6.4	0e+00	41	Replication Replication			
E	2	-6.07	0e+00	36	DNA replication			
	3	-5.43	0e+00	24	Replication publication publication publication Factors			
0	4	-4.83 -4.61	0e+00	219 409	Cell growtheilnightaleththan-ChellathicleCell cycle Enzyme -E2/zi/mienstle7riniapslesspiharpslessp			
	5		0e+00	409 37	Homologottemetagrobination			
	2 3 4 5 6 7	-4.14	0e+00 4e-05	142	Transport system coat			
	8	-3.95 -3.71	4e-05 1e-04	27	Mismatch Mispaiatch repair			
	9	-3.55	5e-04	62	RibosomeRitiogenessisieo@06sigarti@6\$ particles			
	10	-3.37	9e-04	22	Replication			
	11	-3.36	1e-03	21	Replication Republication and Mispraiate Mispraiatch repair			
)	12	-3.33	1e-03	66	Exosome Exosoma Exosoma Exosoma logi folia dide pobalitate de retilancer cells			
	13	-3.24	1e-03	110	Ubiquitin systemin-systemub wild Raugh-imig Birtypeir Eger type E3			
	14	-3.02	3e-03	75	Translatio Translatiosome Ribiosemes ision Endesis/ortesukaryotes			
	13	-3	3e-03	64	RibosomeRibiogenesilsiongenikaisyonesukaryotes			
	16	-2.96	3e-03	37	Repair proteinair Orbenda po Orbenda po Orbenda po Repair proteinair Orbenda po Orbenda			
	17	-2.88	5e-03	44	Replication philiteine			
	18	-2.85	5e-03	73	Nucleotid Bluoteta bid Esmeta Bydismidin Pyrietatio Esm eta bolism			
0	19	-2.81	6e-03	144	RibosomeRib EsakarreyoteEsukaryotes			
0	20	-2.73	8e-03	65	Phagosome Phagosome			
	-							

