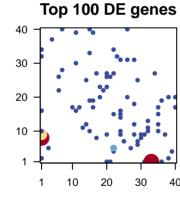
Chard_accfreeze_r1

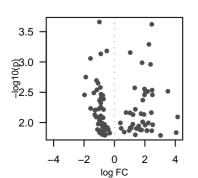
Global Summary

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 > = 0.46< fdr > = 1

Portrait 40 30 20 10 10 20 30



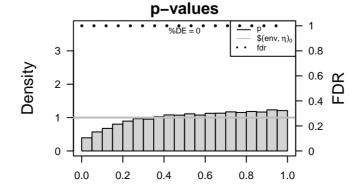


Differentially expressed genes

Rank

	ID		p-va	lue	Meta	gene	
Over	expressed						
1	Vitvi02g01440	2.45	2e-04	1	22 x 34	The space external to the outermost structure of a cell. For $c\varepsilon$	
2	Vitvi13g00189	2.27	5e-04	1	1 x 8	A membrane-bounded organelle of eukaryotic cells in which	
2	Vitvi03g00249	1.03	7e-04	1	22 x 5	Binding to a calcium ion (Ca2+).	
4	Vitvi01g00608	1.81	1e-03	1	4 x 37	Binding to a protein.	
5	Vitvi18g00967	2.37	1e-03	1	26 x 40	A membrane-bounded organelle of eukaryotic cells in which	
6	Vitvi02g00410	1.33	3e-03	1	1 x 32	The process in which a solute is transported across a lipid bili	
	Vitvi09g01398	1.97	3e-03	1	1 x 8	Binding to ATP, adenosine 5'-triphosphate, a universally impo	
8	Vitvi18g01937	2.47	3e-03	1	20 x 1	Binding to a calcium ion (Ca2+).	
9	Vitvi12g02565	3.51	3e-03	1	36 x 1	The space external to the outermost structure of a cell. For ce	
10	Vitvi02g01488	2.18	3e-03	1	1 x 7	A lipid bilayer along with all the proteins and protein complexe	
11	Vitvi01g00784	2.04	3e-03	1	22 x 4	The chemical reactions and pathways involving carbohydrate:	
12	Vitvi19g01850	1.98	3e-03	1	1 x 9	The component of a membrane consisting of the gene produc	
13	Vitvi16g00988	2.49	3e-03	1	1 x 9		
14	Vitvi04g01160	1.86	4e-03	1	1 x 34	The contents of a cell excluding the plasma membrane and n	
15	Vitvi12g02644	1.37	6e-03	1	11 x 16		
16	Vitvi04g02185	0.76	7e-03	1	11 x 30	The irregular network of unit membranes, visible only by elect	
17	Vitvi16g01459	2.42	7e-03	1	1 x 8		
18	Vitvi08g01816	1.02	7e-03	1	22 x 5	Binding to a metal ion.	
19	Vitvi01g00849	1.75	7e-03	1	31 x 1	Binding to a protein.	
20	Vitvi18g02011	1.94	7e-03	1	1 x 9	Any molecular function by which a gene product interacts sele	
Unde	erexpressed						
1	Vitvi17g00285	-0.99	2e-04	1	30 x 9		
	Vitvi08q00198	-0.51	7e-04	1	19 x 22	The component of a membrane consisting of the gene produc	
2 3 4 5 6 7	Vitvi18g00080	-0.9	7e-04	1	18 x 23	The chemical reactions and pathways resulting in the formatic	
4	Vitvi04g00069	-1.58	9e-04	1	36 x 19	A lipid bilayer along with all the proteins and protein complexe	
5	Vitvi01g00619	-1.89	2e-03	1	39 x 4	Binding to a heme, a compound composed of iron complexed	
6	Vitvi13g00315	-1.18	2e-03	1	35 x 12	The process in which a methyl group is covalently attached to	
	Vitvi07g00069	-1.08	2e-03	1	20 x 26	Any member of a family of organelles found in the cytoplasm	
8	Vitvi07g00427	-0.93	3e-03	1	24 x 15	A semiautonomous, self replicating organelle that occurs in va	
9	Vitvi06g00254	-1.16	3e-03	1	17 x 27		
10	Vitvi17g00921	-1.35	3e-03	1	29 x 25	The process of removing sections of the primary RNA transcr	
11	Vitvi05g00939	-0.88	3e-03	1	20 x 27	Binding to ATP, adenosine 5'-triphosphate, a universally impo	
12 13 14	Vitvi06g00763 Vitvi07g00168	-1.97 -0.76	3e-03 4e-03	1	40 x 20	The formation of a protein dimer, a macromolecular structure The process whose specific outcome is the progression of the	
	Vitvi07g0016c	-0.76	4e-03	1	35 x 15 32 x 13	A multisubunit protein complex that contains the Ino80p ATPa	
15	Vitvi03g01066	-0.72	4e-03 4e-03	1	32 X 13	Catalysis of the reaction: an orthophosphoric monoester + H2	
16	Vitvi03g01060 Vitvi08g01963	-0.72	4e-03 4e-03	1	7 X 28 29 x 7	Catalysis of the reaction: All of thophospholic monoester + H2 Catalysis of the reaction: hydroxymethylbilane = H(2)O + uror	
17	Vitvi06g01363	-0.99	5e-03	1	29 x 7	Catalysis of the reaction. Hydroxymethylbilane = 11(2)0 + drop.	
18	Vitvi14g00190	-0.9	6e-03	1	17 x 8	Catalysis of the hydrolysis of internal, alpha-peptide bonds in	
19							
1.9	Vitvi04g00118	-1.57	6e-03	1	6 x 22	Binding to ATP, adenosine 5'-triphosphate, a universally impo	
20	Vitvi04g00118 Vitvi17g00363	-1.57 -1.03	6e-03 6e-03	1	6 x 22 27 x 5	Binding to AIP, adenosine 5 – triphosphate, a universally impo	

Description



Differentially expressed gene sets

	Rank	GSZ	p-value	#all	Geneset					
	Overexpressed									
CE	1	10.74	0.000	48	Transcription taketion taketis - WRKY					
h	2	8.46	0.000	49	TranscriptToanfactipition MacOrs - NAC					
	3	7.77	0.000	162	Plant spelllämsigmadifig signalingpathlagenpathagetiointeraction					
	4	5.81	0.000	238	Enzyme -E2izlyn@elye@sylltn@iysriesgritesnsferases					
h	5	5.68	0.000	64	Transcription factors (atterstran@trieptionnfscription factors					
ili	6	5.41	0.000	86	Signal tra SsphadtioansoCadioium-sQatailimg signitaliang pathway					
OC	7	5.35	0.000	153	Plant-patRizgrenpiathrzgeiointeraction					
	8	4.67	0.000	11	BiosyntheBiosynthesisdafryenetatarlysmetalbBlAstriosyNBIAelsiosynthesis					
CE	9	4.52	0.000	73	Transcription factipition factorische REBP2 EREBP					
ΧE	10	4.13	0.000	140	Hormone Hormating sidertal/iteme Sittmating signaling					
e:	11	3.28	0.001	111	Hormone Hormating sight Bulling					
uc	12	3.17	0.002	206	Cell grow@edingtrodestithandOeddautrall- Cell wall					
	13	3	0.003	89	MAPK sig htalipký sightaliang -p atlant ay – plant					
n	14	2.92	0.004	14	Kinase – Kilib & Kefar (10) PK family					
	15	2.9	0.004	17	Kinase – KRAdseamiRAK family					
ct	16	2.75	0.007	170	Transcription factorists on fatterszf-O8heC4f-C3HC4					
	17	2.57	0.011	29	Carotenoi@driggsyntdigelsiesynthesis					
	18	2.5	0.011	78	Glycosyltr@hysfessylteens@ernasterralSphollyssaradhpoligisaccharide					
	19	2.47	0.014	16	Transcription Montage Habitors - HSF					
ele	20	2.37	0.019	96	Transport eraratatorter-detailers-ca Roftters6cat 1 to 6					
	Underex	nressed								
	1	-3.76	1e-04	67	RibosomeRibBauteeia- Bacteria					
uc	2	-3.59	4e-04	26	Flavonoid Pharasyntilo Esiasynthesis					
tic	3	-3.59	4e-04 4e-04	28	Transcription factorisc MTERF					
XΕ	4	-3.43	8e-04	247	TranslatioTranslatiosomeRibosome					
ed	5	-3.3	1e-03	72	RibosomeRibleStoroleonellite/cDiblodoial/aShloroplast					
tc	5 6	-3.14	2e-03	211	Ribosom@ibosome					
n	7	-3.1	2e-03	39	Pentose aPentyliseurodayikuinuteroatevensenversions					
٧ŧ	8	-3.02	3e-03	81	Enzyme -E4z2/r0ærb4r2-d0ædæmlyaxesen lyases					
	9	-2.61	1e-02	44	Energy metabolismetabidhisgen Mittabelismetabolism					
cr	Ĭ0	-2.52	1e-02	48	Lipid metalipoidismmetalibatismacidFlaitinsyantilulelsissynthesis					
OC	11	-2.49	1e-02	41	Transporterarestatoriger-dentalagy-aletiveatryanaspioveterarestatolofter cat D1					
е	12	-2.47	1e-02	75	Mitochon d'Mital chromadniquitionna and ptionna bertiol tránslatis on factors					
h€	13	-2.46	2e-02	217	Cell motilitiell filetjulgation englalation cydfosktile taytoskeleton					
a	14	-2.42	2e-02	25	Nitrogen inliatabelismetabolism					
H2	15	-2.4	2e-02	22	Transcription factorism factors DOEC2-DOF					
or	16	-2.4	2e-02	97	RibosomeRib Aschaea Archaea					
а	17	-2.38	2e-02	18	Chaperor@hapt88020 - HSP20					
in	18	-2.35	2e-02	30	Glycan bi@sycamelsiosaymdnessitabobismetalsle@sycanNde@sycatetide.gradation					
OC	19	-2.29	2e-02	105	Energy mētadoglijsmeta Okalidsanti ve Okaidsaptive rpladiscriptorylation					
	20	-2.28	2e-02	12	Enzyme -Efiziyīm Aetifilgi on Achtrog 63H2Ighrouph12 groups					

