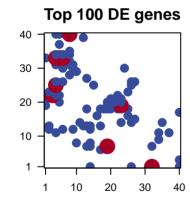
# Chard\_warm\_r3

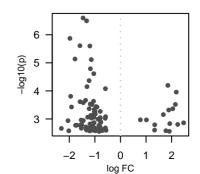
# **Global Summary**

%DE = 0.12 # genes with fdr < 0.2 = 8 (0 + /8 -) # genes with fdr < 0.1 = 6 (0 + /6 -) # genes with fdr < 0.05 = 6 (0 + /6 -) # genes with fdr < 0.01 = 1 (0 + /1 -)

<FC> = 0<p-value> = 0.34<fdr> = 0.88

# Portrait 40 30 20 10 1 10 20 30 40





### Differentially expressed genes

Rank ID		log(F	g(FC) fdr p-value		Meta	Description gene			
Overexpressed									
1	, Vitvi09g00022	1.85	6e-05	0.2	34 x 9				
2 3 4 5 6 7	Vitvi15g00523	2.18	1e-04	0.4	31 x 1	Binding to a heme, a compound composed of iron complexed			
	Vitvi03g01453	2.15	3e-04	0.4	40 x 3	Any process that results in a change in state or activity of a co			
	Vitvi05g00546	2.04	4e-04	0.4	40 x 17	The component of a membrane consisting of the gene produc			
	Vitvi10g01662	1.89	5e-04	0.4	37 x 11	The membrane surrounding a cell that separates the cell from			
	Vitvi01g00264	1.68	7e-04	0.5	13 x 18	Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, (			
	Vitvi10g00230	0.78	1e-03	0.5	15 x 25	A membrane-bounded organelle of eukaryotic cells in which			
8	Vitvi04g01359	1.01	1e-03	0.5	35 x 14	A lipid bilayer along with all the proteins and protein complexe			
9	Vitvi13g00143	2.47	1e-03	0.5	40 x 1	The space external to the outermost structure of a cell. For ce			
10	Vitvi05g00527	1.93	1e-03	0.5	26 x 1	The directed movement of lipids into, out of or within a cell, or			
11 12 13 14 15	Vitvi16g00309	2.24	2e-03	0.5	14 x 1	The component of a membrane consisting of the gene produc			
	Vitvi04g00158	1.34	2e-03	0.5	34 x 11	A membrane-bounded organelle of eukaryotic cells in which			
	Vitvi19g01284	1.33	3e-03	0.5	17 x 6	The component of a membrane consisting of the gene produc			
	Vitvi13g01638	1.78	3e-03	0.5	32 x 1	Binding to ADP, adenosine 5'-diphosphate.			
	Vitvi05g02197	1.91	3e-03	0.5	32 x 1	A lipid bilayer along with all the proteins and protein complexe			
16	Vitvi15g00877	8.0	3e-03	0.5	15 x 18	The component of a membrane consisting of the gene produc			
17	Vitvi16g01285	1.77	3e-03	0.5	34 x 13	A membrane-bounded organelle of eukaryotic cells in which			
18	Vitvi07g01396	1.36	3e-03	0.5	40 x 16	Catalysis of the transfer of a glycosyl group from a UDP-suga			
19	Vitvi13g01736	1.5	3e-03	0.5	35 x 30				
20	Vitvi09g00339	0.7	3e-03	0.5	20 x 26	The formation of a protein dimer, a macromolecular structure			
Underexpressed									
1	Vitvi12g01915	-1.46	3e-07	0.003	14 x 13	The contents of a cell excluding the plasma membrane and n			
ż	Vitvi06g00237	-1.32	3e-07	0.012	27 x 15	Binding to a specific sequence of DNA that is part of a regula			
2	Vitvi09g01011	-1.98	1e-06	0.012	5 x 33	Binding to a metal ion.			
4	Vitvi16g02077	-1.58	2e-06	0.012	8 x 35	Binding to a nucleic acid.			
5	Vitvi13g00174	-1.2	3e-06	0.041	17 x 18				
4 5 6 7	Vitvi05g00274	-1.78	7e-06	0.041	32 x 7	Any process that activates or increases the frequency, rate or			
	Vitvi08g00955	-1.14	8e-06	0.133	19 x 18	A membrane–bounded organelle of eukaryotic cells in which			
8	Vitvi18g01219	-1.18	2e-05	0.133	18 x 18	The network of interconnected tubular and cisternal structure:			
9 10 11	Vitvi17g00120	-1.04	2e-05	0.235	21 x 20	A membrane-bounded organelle of eukaryotic cells in which			
	Vitvi06g00702	-1.23	4e-05	0.235	3 x 22	The process in which relatively unspecialized cells, e.g. embr			
	Vitvi12g02033	-1.31	7e-05	0.235	8 x 31	Binding to an RNA molecule or a portion thereof.			
12	Vitvi16g01076	-0.59	8e-05	0.387	21 x 21	The process in which a methyl group is covalently attached to			
13	Vitvi04g00362 Vitvi11g00445	-1.95 -1.36	2e-04 2e-04	0.387	10 x 8 3 x 22	The component of a membrane consisting of the gene produc			
14 15 16 17 18	Vitvi06g00384	-1.05	2e-04 2e-04	0.387	3 X 22	The process whose specific outcome is the progression of a p			
	Vitvi02g00365	-1.58	2e-04 2e-04	0.387	8 x 40	Binding to ATP, adenosine 5'-triphosphate, a universally impo			
	Vitvi07g00220	-1.45	3e-04	0.387	17 x 13	A membrane–bounded organelle of eukaryotic cells in which			
	Vitvi18g00646	-1.18	3e-04	0.387	13 x 27	Binding to a protein.			
19	Vitvi19g00196	-1.12	3e-04	0.387	9 x 31	A lipid bilayer along with all the proteins and protein complexe			
~~	10.110.00010								

# Differentially expressed gene sets

neset

	Overex	xpressed			
	1	6.94	0e+00	78	Energy m Etadorglysmmetal Bholistons yn Phacosia synthesis
xed	2	6.7	0e+00	134	Hormonelskigmating sighalingsign/alining signaling
a ce	3	6.39	0e+00	19	AquaporirAsquapicarinas llametus ratablo fuetet itala so pudet era n (\$ i @ rite Ass)[TC:1.A
duc	4	6.32	0e+00	47	Transport@iracaspatutger-datedsgo-rt@eecspoortoelecieron carriers
ron	5	6.3	0e+00	38	Photosyn Pleasis synthesis
Ν, (	6	6.28	0e+00	206	Cell grow@catingtroutertithandOdddauthall Cell wall
ch	7	5.87	0e+00	18	Energy mētadogljisimetal@blistors.ym@lecsiosajimtderesais.paroteimaa proteins
ехє	8	5.35	0e+00	40	Transport Transtepport Stylastenkoid Tlaybettinig berthetiang pathway
r ce	9	5.07	0e+00	18	Photosyn Plecis synathlesis a-proteins proteins
, or	10	4.55	0e+00	39	Pentose a Pethylise unoday kuinterroateven seiros nversions
duc	11	4.53	0e+00	19	Transcription factions and Ald Miles A. AUXIAA
ch	12	4.44	0e+00	34	PeptidaseSeantidaseisbiators in Hibitohs S1Family S10
duc	13	4.19	0e+00	80	Cytoskeletonoskeletonubulleisrotubules
	14	4.1	0e+00	10	Photosyn <b>Pleasis-symutleissis-Photeinsys-Rehnoto(sP/50e</b> noth( <b>(P70)0)</b> ytth <b>ai</b> )rophy
exe	15	3.87	8e-05	63	Phenylpro?hamojibbiopsynotidelsissynthesis
duc	16	3.84	8e-05	168	Plant hormalizame is signabitimens is sphedition and duction
ch	17	3.8	1e-04	129	Enzyme -E8x2/n024ye03s2/la6s4xcosylases
uga	18	3.54	5e-04	219	Cell grow@ethnandOuttlandOutladincleCell cycle
	19	3.43	8e-04	217	Cell motilitigell finetjiilfatioRedialatiioncytfoskelletonoskeleton
ıre	20	3.25	1e-03	24	Replication Republication Political Republic Advantage Fractors
	Under	expressed	d		
d n	1	-5.29	0e+00	116	RibosomeRitiosemesisieo@rees660S PaetidleS particles
ula	2	-4.69	0e+00	49	Transcription faction factorists - NAC
	ริ	-4.52	0e+00	64	Transcription factors (atterstran@threptionnfactiontion factors
	3 4 5	-4.38	0e+00	62	RibosomeRibiosenesIsiec@@@sparti@@s particles
	5	-3.69	3e-04	73	Transcription factions ARCOEREBP2 EREBP
or	Ğ	-3.66	3e-04	64	RibosomeRitiogenesisiogenesisjotesukaryotes
ch	7	-3.58	4e-04	165	TranscriptToans@ipiticerosc@pdiceosome
ure:	8	-3.46	8e-04	140	Hormonelskigmating sigital/jregne sittnyteing signaling
ch	9	-3.32	1e-03	115	Enzyme -E8z6ynAvetin 6.6n Avodiid gandnyalcidean hydrides
nbr	10	-3.19	2e-03	34	Tyrosine ritigetassiolismmetabolism
	11	-3.17	2e-03	83	RNA deg Markide gradation
d tc	12	-3.15	2e-03	75	Translatio Translatiosome Ribiogenes Isiong Endos isyotes ukaryotes
	13	-2.99	3e-03	13	Peptidase Seputidas leisiators in Hibitohys G 1F. apraipai G 1fa praigain family
duc	14	-2.85	5e-03	67	Replication
аţ	15	-2.85	5e-03	39	Carbohyd Cateborle, talbat lisme ta Citilistra ey Clierate cycle
npc	16	-2.81	6e-03	40	Citrate cyClien(aTeCeyclec)(aT)CA cycle)
ch	17	-2.77	6e-03	151	RNA polyRNA Aspellyrayestesen II system
	18	-2.75	7e-03	86	Signal tra6sghadttoansdCadtionm-sQalailing sightaliang pathway
exe	19	-2.62	1e-02	36	RibosomeRibiogenesisiogenesisiS PaetidleS particles
ch	20	-2.58	1e-02	27	Regulator Refgaltatohon dnital dhiogelnieshisiogenesis

