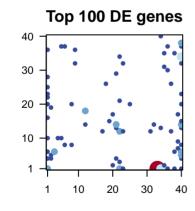
# Chard\_warm

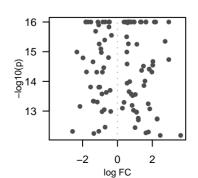
## **Global Summary**

%DE = NA # genes with fdr < 0.2 = 5418 (2889 + /2529 -)# genes with fdr < 0.1 = 3489 (1926 + /1563 -)# genes with fdr < 0.05 = 2446 (1363 + /1083 -)# genes with fdr < 0.01 = 1594 (886 + /708 -)

<FC> = 0< p-value > = 0.04< fdr > = 0.45

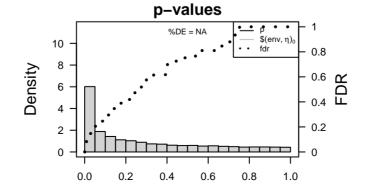
## **Portrait** 40 30 20 10 -30 10 20





### Differentially expressed genes

Rank ID		log(FC) for p-value		fdr lue	Description Metagene		Rank	
Ove	Overexpressed							
1	Vitvi00g00040	1.63	1e-16	5e-14	34 x 1		1	
2	Vitvi07g02832	1.63	1e-16	5e-14	34 x 1	Binding to a protein.	ż	
3	Vitvi10g00345	1.36	1e-16	5e-14	40 x 20	A membrane-bounded organelle of eukaryotic cells in which	3	
4 5	Vitvi03g00699	0.64	1e-16	5e-14	23 x 32	Catalysis of the transfer of an acyl group, other than amino-a	4	
	Vitvi05g00496	0.48	1e-16	5e-14	18 x 26	Binding to a metal ion.	5	
6	Vitvi05g01276	1.32	1e-16	5e-14	40 x 32	Catalysis of the transfer of a glycosyl group from a UDP-suga	6	
7	Vitvi08g01519	0.37	1e-16	5e-14	21 x 29	Binding to a metal ion.	7	
8	Vitvi08g01856	0.73	1e-16	5e-14	40 x 15	The formation of a protein dimer, a macromolecular structure	8	
9	Vitvi08g00151	0.96	1e-16	5e-14	40 x 5	The component of a membrane consisting of the gene produc	9	
10	Vitvi09g01670	0.65	1e-16	5e-14	40 x 8	The component of a membrane consisting of the gene produc	10	
11	Vitvi10g01554	0.67	1e-16	5e-14	40 x 14	The part of the cytoplasm that does not contain organelles bu	11	
12	Vitvi12g02328	2.19	1e-16	5e-14	32 x 1		12	
13	Vitvi13g00293	0.96	1e-16	5e-14	39 x 7		13	
14	Vitvi17g00188	0.57	1e-16	5e-14	40 x 14	The formation of a protein dimer, a macromolecular structure	14	
15	Vitvi17g00283	2.12	1e-16	5e-14	40 x 34	The directed movement of lipids into, out of or within a cell, or	15	
16	Vitvi18g00322	0.81	1e-16	5e-14	40 x 13	Binding to ATP, adenosine 5'-triphosphate, a universally impo	16	
17	Vitvi19g01990	2.94	1e-16	5e-14	33 x 1		17	
18	Vitvi18g00835	0.57	1e-16	2e-13	39 x 9	A chlorophyll-containing plastid with thylakoids organized into	18	
19	Vitvi06g00401	0.53	3e-16	4e-13	37 x 12	Binding to ATP, adenosine 5'-triphosphate, a universally impo	19	
20	Vitvi19g01988	2.73	4e-16	4e-13	33 x 1		20	
Underexpressed							Undere	
						The contests of a cell cook disc the closure acceptance and a		
2	Vitvi04g00113 Vitvi05g00858	-0.46	1e-16	5e-14	12 x 14 9 x 32	The contents of a cell excluding the plasma membrane and n  Any molecular function by which a gene product interacts sele	1	
	Vitvi05g0065c	-0.47 -1.82	1e-16 1e-16	5e-14 5e-14	9 x 32 21 x 13	Any molecular function by which a gene product interacts ser	2	
3 4	Vitvi05g01751	-1.12	1e-16	5e-14	20 x 2	The chemical reactions and pathways involving carbohydrate:	2 3 4 5 6 7	
5	Vitvi07g00182	-0.5	1e-16	5e-14	9 x 36	Binding to GTP, quanosine triphosphate.	5	
5	Vitvi12g02230	-0.84	1e-16	5e-14	21 x 4	Binding to ATP, adenosine 5'-triphosphate, a universally impo	6	
7	Vitvi12g02140	-1.81	1e-16	5e-14	8 x 8	The component of a membrane consisting of the gene produc	7	
8	Vitvi13g01937	-1.68	1e-16	5e-14	21 x 14		8	
9	Vitvi13g02263	-0.7	1e-16	5e-14	25 x 20	A membrane-bounded organelle of eukaryotic cells in which	9	
10	Vitvi17g01417	-1.53	1e-16	5e-14	20 x 17	-	Ĭ0	
11	Vitvi18g02109	-1.08	1e-16	2e-13	8 x 20		11	
12	Vitvi08g00665	-0.49	1e-16	4e-13	2 x 19	Catalysis of the reaction: $NADP(+) + thioredoxin = H(+) + NAI$	12	
13 14 15 16 17	Vitvi10g00887	-1.25	2e-16	4e-13	1 x 28		13	
	Vitvi05g00340	-0.34	3e-16	4e-13	22 x 21	The contents of a cell excluding the plasma membrane and n	14	
	Vitvi08g01683	-0.73	4e-16	4e-13	1 x 16	Binding to a calcium ion (Ca2+).	15	
	Vitvi16g01494	-1.05	6e-16	4e-13	1 x 23		<u> 16</u>	
	Vitvi04g00065	-0.95	8e-16	1e-12	1 x 6	The component of a membrane consisting of the gene produc	17	
18	Vitvi18g01849	-2.33	1e-15	1e-12	37 x 26	Binding to ADP, adenosine 5'-diphosphate.	18	
19	Vitvi14g02975	-0.93	1e-15	2e-12	19 x 15		19	



Vitvi00g02270 -0.51 2e-15 2e-12 1 x 25

#### Differentially expressed gene sets

Rank GSZ p-val	ue #all Geneset
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	Overex	pressed			
	1	7.37	0e+00	78	Energy metæbrglijsmetæleblötsosyntPlæsiosynthesis
	ż	6.83	0e+00	38	Photosyn Pleasies yn the sis
h	3	6.29	0e+00	206	Cell grow Dealing troube thin and Catalla trail. Cell wall
a	4	6.07	0e+00	134	Hormone Histograating signating signaling
	5	5.95	0e+00	47	Transport@iransatatotoper-Catanisport @etercapoort celerideron carriers
ga	6	5.6	0e+00	18	Energy mētadoglijsmetalēbibitors yn Placifesaiesamtidnes asparoteimsa proteins
•	7	5.52	0e+00	26	Flavonoid Flavos yn utildelsies synthesis
е	8	5.31	0e+00	19	Aquaporin/squadosimallamelusralaslothetet tala sobutet eran [3] Our texts [TC:1.A.
uc	9	5.04	0e+00	40	Transport Transport Stylestenort Stylestenkord Titaytektonid beathevising pathway
uc	10	4.99	0e+00	18	Photosyn Phessissy rathless is a paroteins a proteins
ou	11	4.62	0e+00	39	Pentose a Prehtdiseuro dateuro terro a teventeiro as niversions
	12	4.36	0e+00	10	Photosyn (Pleasis synatheis is followeis ys (Plnoto(s) 750 fine hill (1776) by their phyll
	13	4.23	0e+00	63	Phenylpro Planno ito bio pownosti del si es synthesis
е	14	4.12	0e+00	34	Peptidasel Segutidas leits its ords in Hijaritoins S1Ramily S10
or	15	3.75	0e+00	44	Hormone Hormadine si@hattinkinin Sidokalining signaling
o. oc	16	3.7	2e-04	211	RibosomeRibosome
-	17	3.65	2e-04	19	Transcriptioanisactipition falditinsA- AUXIAA
itc	18	3.49	6e-04	26	Glycosyltr@lysfesylteenstfeydrsspholbiyclmolleobile molecule
00	19	3.44	9e-04	168	Plant horificant signatures signatures and the signature signatures and the signatures are signatures are signatures and the signatures are signatures are signatures and the signatures are signatures and the signatures are signatures as signatures are signatures are signatures and the signatures are signatures are signatures are signatures and the signatures are signatures are signatures and the signatures are signatures are signatures and the signatures are signatures ar
-	20	3.43	1e-03	47	ABC transporters
	_			47	, as a damped and open of o
		expressed			
n	1	-6.43	0e+00	49	TranscriptToanfactipition NacCors - NAC
el€	2 3 4 5 6	-6.03	0e+00	64	Transcription/scutipution Catherstrar@threptican/scutipution factors
	3	-4.94	0e+00	73	Transcription factions Adeloes REBP
e:	4	-4.8	0e+00	140	Hormone Higmating signaling
	5	-4.39	0e+00	48	TranscriptToamfacutipition taleRtd16 - WRKY
OC	6	-4	0e+00	116	RibosomeRitiogenesisieg@reesis0S Paetid@S particles
u(	7	-3.75	0e+00	62	RibosomeRibiogenesisiog@@@spartides particles
xe h	8	-3.66	2e-04	153	Plant-pathtagenpathagetioninteraction
1	9	-3.26	2e-03	27	Enzyme -E2:26ymTeens2te6rinTigantifegerropoistrggeurpsus groups Tyrosine mTertastiotismetabolism
	10 11	-3.23 -3.14	2e-03 3e-03	34 86	Signal tra <b>6sophadtioansoCoatioinm-sCoatailing signiailing p</b> athway
AI	12	-3.14	4e-03	80	Transport Systeming Tethering factors
Α.	13	-3.02	6e-03	43	Mitochon Mital despitation respiration on the state of th
n	14	-2.78	6e-03	12	Enzyme -E6zassel - Class I
	15	-2.78	7e-03	35	Mitophagt///facebbrasqy factors
	16	-2.69	8e-03	151	RNA polyRNAasellyrsysteme II system
uc	17	-2.56	1e-02	20	Protein - ProteinhagAstorpeagosationforotelion proteins
	18	-2.56	1e-02	17	Isoquinolil <b>isequikialdidebidisqitatidebis</b> synthesis
	19	-2.5	1e-02	64	Ribosome Ribiosenes isione eukais voites ukaryotes
	20	-2.5	1e-02	119	Endocyto Sis docytosis
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