

# Chard\_warm\_r2

## Global Summary

%DE = 0.12  
# genes with  $\text{fdr} < 0.2 = 0$  (0 + / 0 -)  
# genes with  $\text{fdr} < 0.1 = 0$  (0 + / 0 -)  
# genes with  $\text{fdr} < 0.05 = 0$  (0 + / 0 -)  
# genes with  $\text{fdr} < 0.01 = 0$  (0 + / 0 -)

<FC> = 0  
<p-value> = 0.36  
<fdr> = 0.88

## Differentially expressed genes

Rank	ID	log(FC)	p-value	fdr	Description
Overexpressed					
1	Vitv06g00094	0.76	0.002	0.8	23 x 29 The chemical reactions and pathways resulting in the formati
2	Vitv07g0139E	1.38	0.003	0.8	40 x 16 Catalysis of the transfer of a glycosyl group from a UDP-sug
3	Vitv06g0067E	2.05	0.003	0.8	40 x 21 Catalysis of the transfer of an acetyl group to a nitrogen atom
4	Vitv11g0130C	2.2	0.004	0.8	40 x 1 Catalysis of a biochemical reaction at physiological temperat
5	Vitv02g0183Z	2.24	0.005	0.8	40 x 23
6	Vitv00g0121E	2.24	0.005	0.8	40 x 23
7	Vitv07g0230C	1.75	0.006	0.8	36 x 29 Catalysis of the hydrolysis of internal, alpha-peptide bonds in
8	Vitv19g0140E	0.74	0.006	0.8	28 x 13 Binding to a nucleic acid.
9	Vitv10g0063E	1.19	0.006	0.8	21 x 30 A lipid bilayer along with all the proteins and protein complex
10	Vitv04g0210E	1.27	0.006	0.8	30 x 1
11	Vitv18g0250E	1.15	0.006	0.8	31 x 32
12	Vitv06g0036Z	0.96	0.007	0.8	40 x 15 Binding to ATP, adenosine 5'-triphosphate, a universally impc
13	Vitv07g0141E	1.45	0.007	0.8	40 x 19 Catalysis of the transfer of a glycosyl group from a UDP-sug
14	Vitv14g0159E	0.58	0.007	0.8	23 x 27 The component of a membrane consisting of the gene produc
15	Vitv11g01114	1.79	0.008	0.8	40 x 1
16	Vitv10g0087C	1.88	0.008	0.8	40 x 30 Catalysis of a biochemical reaction at physiological temperat
17	Vitv02g00971	0.77	0.008	0.8	28 x 14
18	Vitv04g00437	0.88	0.009	0.8	30 x 12 Binding to a protein.
19	Vitv17g00171	1.24	0.009	0.8	34 x 25 Binding to ATP, adenosine 5'-triphosphate, a universally impc
20	Vitv19g02024	3.08	0.009	0.8	40 x 34
Underexpressed					
1	Vitv18g0253E	-1.23	2e-05	0.5	18 x 19
2	Vitv06g0079E	-0.62	1e-04	0.5	18 x 20 A membrane-bounded organelle of eukaryotic cells in which
3	Vitv14g0113E	-1.32	1e-04	0.5	4 x 20
4	Vitv07g0150Z	-1.59	1e-04	0.5	4 x 34 The space external to the outermost structure of a cell. For ce
5	Vitv18g01531	-1.12	2e-04	0.5	6 x 29 The directed movement of proteins in a cell, including the mo
6	Vitv06g0175E	-0.72	3e-04	0.5	7 x 30 Catalysis of an oxidation-reduction (redox) reaction in which
7	Vitv13g0155E	-2.34	3e-04	0.5	1 x 15 A membrane-bounded organelle of eukaryotic cells in which
8	Vitv07g02984	-0.89	3e-04	0.5	12 x 29 Binding to a nucleic acid.
9	Vitv00g0071E	-0.89	3e-04	0.5	12 x 29
10	Vitv05g0079E	-0.73	3e-04	0.5	11 x 30 Binding to a nucleic acid.
11	Vitv04g00897	-0.97	3e-04	0.5	5 x 30
12	Vitv07g00697	-0.99	4e-04	0.5	13 x 11 Binding to a protein.
13	Vitv00g01057	-1.11	4e-04	0.5	1 x 24
14	Vitv07g03117	-1.11	4e-04	0.5	1 x 24
15	Vitv13g00213	-0.87	5e-04	0.5	11 x 11 Binding to a metal ion.
16	Vitv10g0019C	-1.27	5e-04	0.5	21 x 18
17	Vitv15g0108E	-1.69	5e-04	0.5	24 x 40 Catalysis of the hydrolysis of a peptide bond. A peptide bond
18	Vitv04g0188C	-1.28	5e-04	0.5	17 x 12 The component of a membrane consisting of the gene produc
19	Vitv15g0095E	-2.26	6e-04	0.5	4 x 11 A lipid bilayer along with all the proteins and protein complex
20	Vitv19g0055E	-0.94	6e-04	0.5	14 x 11 A membrane-bounded organelle of eukaryotic cells in which

## Differentially expressed gene sets

Rank	GSZ	p-value	#all	Geneset
Overexpressed				
1	8.89	0e+00	211	RibosomeRibosome
2	8.22	0e+00	247	TranslationRibosomeRibosome
3	8.14	0e+00	144	RibosomeRibosomeEukaryotes
4	7.44	0e+00	26	Flavonoidbiosynthesis
5	6.33	0e+00	97	RibosomeRibosomeArchaea
6	5.77	0e+00	78	Energy metabolismPhotosynthesis
7	5.43	0e+00	38	Photosynthesis
8	4.91	0e+00	24	ReplicationDNAReplication Factors
9	4.65	0e+00	47	TransporterCarrierTransporter carriers
10	4.62	0e+00	134	Hormone signaling signaling signaling
11	4.58	0e+00	206	Cell growthCell wallCell wall
12	4.46	0e+00	18	Energy metabolismPhotosynthesisproteins
13	4.04	0e+00	80	CytoskeletonMicrotubules
14	4.03	0e+00	18	Photosynthesisproteins
15	4.03	0e+00	67	RibosomeRibosomeBacteria
16	4.01	0e+00	40	TransporterCarrierTransporter pathway
17	4	0e+00	39	Pentose phosphate cycleinterconversions
18	3.89	8e-05	34	PeptidaseinhibitorsFamily S10
19	3.74	1e-04	26	Glycosyltransferasehydrolase
20	3.63	3e-04	81	EnzymeEC2Carbohydrate lyases
Underexpressed				
1	-6.48	0e+00	64	Transcription factorsTranscription factors
2	-6.31	0e+00	49	Transcription factorsNACs - NAC
3	-5.06	0e+00	140	Hormone signaling signaling signaling
4	-4.9	0e+00	73	Transcription factorsAP2EREBP EREBP
5	-4.46	0e+00	153	Plant-pathogen interaction
6	-4.31	0e+00	48	Transcription factorsWRKYs - WRKY
7	-3.69	3e-04	35	Mitophagy factors
8	-3.43	8e-04	170	Transcription factorsChlorophyllase
9	-3.28	1e-03	13	PeptidaseinhibitorsFamily S10
10	-3.24	1e-03	20	Protein - Autophagosome formation
11	-3.12	2e-03	27	EnzymeEC2Carbohydrate lyases
12	-3.09	2e-03	86	Signal transductionCalcium signaling pathway
13	-2.86	5e-03	20	TransporterCarrierTransporter
14	-2.77	6e-03	31	Autophagy - other
15	-2.75	7e-03	80	TransporterCarrierTransporter factors
16	-2.73	8e-03	128	Ubiquitin ligaseRING type E3
17	-2.68	8e-03	119	Endocytosis
18	-2.64	9e-03	33	Carbohydrate metabolismsugarsmetabolism
19	-2.59	1e-02	45	Valine metabolismacid degradation
20	-2.54	1e-02	24	Ubiquitin ligaseRING type E3

