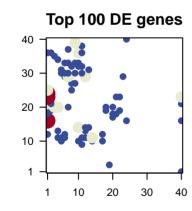
## Chard\_warm\_r2

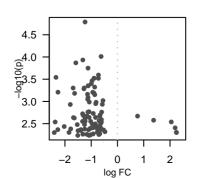
## **Global Summary**

%DE = 0.12 # 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> = 0.36 <fdr> = 0.88

## Portrait 40 30 20 10 1 10 20 30 40





## Differentially expressed genes

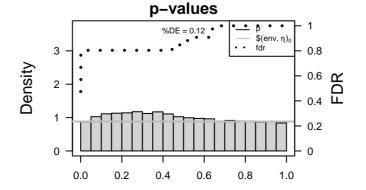
fdr

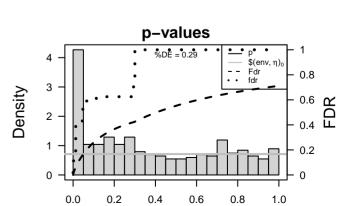
Description

log(FC)

Rank

| ıvaı    | ÏD            | .09(. | p-va  | lue | Meta               | gene  | rank           | 002    | p     | "an |
|---------|---------------|-------|-------|-----|--------------------|---|----------------|--------|-------|-----|
| Ovei    | verexpressed  |       |       |     |                    |   | Overexp        | ressed |       |     |
| 1       | Vitvi06g00094 | 0.76  | 0.002 | 0.8 | 23 x 29            | The chemical reactions and pathways resulting in the formatic       | 1              | 8.89   | 0e+00 | 211 |
| ż       | Vitvi07g01396 | 1.38  | 0.003 | 0.8 | 40 x 16            | Catalysis of the transfer of a glycosyl group from a UDP-suga       | 2              | 8.22   | 0e+00 | 247 |
| 3       | Vitvi06g00679 |       | 0.003 | 0.8 | 40 x 21            | Catalysis of the transfer of an acetyl group to a nitrogen atom     | 3              | 8.14   | 0e+00 | 144 |
| 4       | Vitvi11g01303 |       | 0.004 | 0.8 | 40 x 1             | Catalysis of a biochemical reaction at physiological temperatu      | 4              | 7.44   | 0e+00 | 26  |
| 5       | Vitvi02g01832 |       | 0.005 | 0.8 | 40 x 23            | ,   | 5              | 6.33   | 0e+00 | 97  |
| 6       | Vitvi00g01215 |       | 0.005 | 0.8 | 40 x 23            |   | 6              | 5.77   | 0e+00 | 78  |
| 7       | Vitvi07g02300 |       | 0.006 | 0.8 | 36 x 29            | Catalysis of the hydrolysis of internal, alpha-peptide bonds in     | 7              | 5.43   | 0e+00 | 38  |
| 8       | Vitvi19q01408 |       | 0.006 | 0.8 | 28 x 13            | Binding to a nucleic acid.  | 8              | 4.91   | 0e+00 | 24  |
| 9       |               | 1.19  | 0.006 | 0.8 | 21 x 30            | A lipid bilayer along with all the proteins and protein complexe    | 9              | 4.65   | 0e+00 | 47  |
| ย<br>10 | Vitvi04g02105 | 1.19  | 0.006 | 0.8 | 30 x 1             | A lipid bilayer along with all the proteins and protein complexe    | 10             | 4.62   | 0e+00 | 134 |
|         |               |       |       |     |                    |   | 11             | 4.58   |       | 206 |
| 11      | -             | 1.15  | 0.006 | 0.8 | 31 x 32<br>40 x 15 | Pinding to ATD adapasing 5' triphosphoto a universally impa         |                |        | 0e+00 |     |
| 12      | Vitvi06g00362 |       | 0.007 | 0.8 |                    |   | 12             | 4.46   | 0e+00 | 18  |
| 13      | Vitvi07g01415 |       | 0.007 | 0.8 | 40 x 19            | Catalysis of the transfer of a glycosyl group from a UDP-suga       | 13             | 4.04   | 0e+00 | 80  |
| 14      | Vitvi14g01595 |       | 0.007 | 0.8 | 23 x 27            | The component of a membrane consisting of the gene produc           | 14             | 4.03   | 0e+00 | 18  |
| 15      | Vitvi11g01114 |       | 0.008 | 0.8 | 40 x 1             |   | 15             | 4.03   | 0e+00 | 67  |
| 16      | Vitvi10g00870 |       | 0.008 | 8.0 | 40 x 30            | Catalysis of a biochemical reaction at physiological temperatu      | 16             | 4.01   | 0e+00 | 40  |
| 17      | Vitvi02g00971 |       | 0.008 | 8.0 | 28 x 14            |   | 17             | 4      | 0e+00 | 39  |
| 18      | Vitvi04g00437 | 0.88  | 0.009 | 8.0 | 30 x 12            | Binding to a protein.   | 18             | 3.89   | 8e-05 | 34  |
| 19      |               | 1.24  | 0.009 | 8.0 | 34 x 25            | Binding to ATP, adenosine 5'-triphosphate, a universally impo       | 19             | 3.74   | 1e-04 | 26  |
| 20      | Vitvi19g02024 | 3.08  | 0.009 | 8.0 | 40 x 34            |   | 20             | 3.63   | 3e-04 | 81  |
| Unde    | nderexpressed |       |       |     |                    |   | Underexpressed |        |       |     |
| 1       | Vitvi18g02535 | -1.23 | 2e-05 | 0.5 | 18 x 19            |   | 1              | -6.48  | 0e+00 | 64  |
| 2       | Vitvi06g00798 | -0.62 | 1e-04 | 0.5 | 18 x 20            | A membrane-bounded organelle of eukaryotic cells in which           | 2              | -6.31  | 0e+00 | 49  |
| 3       | Vitvi14g01138 | -1.32 | 1e-04 | 0.5 | 4 x 20             |   | 3              | -5.06  | 0e+00 | 140 |
| 4       | Vitvi07g01502 | -1.59 | 1e-04 | 0.5 | 4 x 34             | The space external to the outermost structure of a cell. For ce     | 4              | -4.9   | 0e+00 | 73  |
| 5       | Vitvi18g01531 | -1.12 | 2e-04 | 0.5 | 6 x 29             | The directed movement of proteins in a cell, including the movement | 5              | -4.46  | 0e+00 | 153 |
| 6       | Vitvi06g01759 | -0.72 | 3e-04 | 0.5 | 7 x 30             | Catalysis of an oxidation-reduction (redox) reaction in which:      | 6              | -4.31  | 0e+00 | 48  |
| 7       | Vitvi13g01556 | -2.34 | 3e-04 | 0.5 | 1 x 15             | A membrane-bounded organelle of eukaryotic cells in which           | 7              | -3.69  | 3e-04 | 35  |
| 8       | Vitvi07g02984 | -0.89 | 3e-04 | 0.5 | 12 x 29            | Binding to a nucleic acid.  | 8              | -3.43  | 8e-04 | 170 |
| 9       | Vitvi00g00719 | -0.89 | 3e-04 | 0.5 | 12 x 29            |   | 9              | -3.28  | 1e-03 | 13  |
| 10      | Vitvi05g00796 | -0.73 | 3e-04 | 0.5 | 11 x 30            | Binding to a nucleic acid.  | 10             | -3.24  | 1e-03 | 20  |
| 11      | Vitvi04g00897 | -0.97 | 3e-04 | 0.5 | 5 x 30             |   | 11             | -3.12  | 2e-03 | 27  |
| 12      | Vitvi07g00697 | -0.99 | 4e-04 | 0.5 | 13 x 11            | Binding to a protein.   | 12             | -3.09  | 2e-03 | 86  |
| 13      | Vitvi00g01057 | -1.11 | 4e-04 | 0.5 | 1 x 24             |   | 13             | -2.86  | 5e-03 | 20  |
| 14      | Vitvi07g03117 | -1.11 | 4e-04 | 0.5 | 1 x 24             |   | 14             | -2.77  | 6e-03 | 31  |
| 15      | Vitvi13g00213 | -0.87 | 5e-04 | 0.5 | 11 x 11            | Binding to a metal ion.   | 15             | -2.75  | 7e-03 | 80  |
| 16      | Vitvi10g00193 | -1.27 | 5e-04 | 0.5 | 21 x 18            |   | 16             | -2.73  | 8e-03 | 128 |
| 17      | Vitvi15g01088 | -1.69 | 5e-04 | 0.5 | 24 x 40            | Catalysis of the hydrolysis of a peptide bond. A peptide bond       | 17             | -2.68  | 8e-03 | 119 |
| 18      | Vitvi04g01880 | -1.28 | 5e-04 | 0.5 | 17 x 12            | The component of a membrane consisting of the gene produc           | 18             | -2.64  | 9e-03 | 33  |
| 19      | Vitvi15g00958 | -2.26 | 6e-04 | 0.5 | 4 x 11             | A lipid bilayer along with all the proteins and protein complexe    | 19             | -2.59  | 1e-02 | 45  |
| 20      | Vitvi19g00558 | -0.94 | 6e-04 | 0.5 | 14 x 11            | A membrane-bounded organelle of eukaryotic cells in which           | 20             | -2.54  | 1e-02 | 24  |
|         |               |       |       |     |                    |   |                |        |       |     |





Rank GSZ p-value #all Geneset

Differentially expressed gene sets

RibosomeRibosome
TranslatioTranslatioTranslatioTranslatioTranslatioTranslatioTranslatioNormeRibosome

RibosomeRib EsukaneyoteSukaryotes

FlavonoidPhavsunthelsissynthesis

RibosomeRibAschaeea Archaea Energy mEtæbralismetalBbitsosyntPleosiosynthesis

Cell grow@calingtrodestithandCatalautrall Cell wall

Photosyn Pleasios y rathinesis a-paroteims a proteins Ribosom Prib Bacuteeia-Bacteria

Cytoskele@moskeletotubulkisrotubules

TranscriptToamfactipition NatCors – NAC
Hormonelstigmating signital/itege Sitynating signaling
TranscriptToamfactiontoon AnCODERFEP2 EREBP

Plant-pathtaget-piathcagetioninteraction
Transcriptionanfacutionison Valentine

Transcriptioanfactipition Cathers: — OSHeC4f-C3HC4
PeptidaseReantidaseBabitions in Inflibitority G. Francipal Chaptalyain family
Protein — Protein

Transport Tispateport Systeming Tethering factors
Ubiquitin systemine Spiatem Ristingheing Eirtger type E3

Enzyme - E2ziymienszletriniganisfegengonisrgganpaus groups Signal traßighatitioansolvetrionn-signiciting piethwing pathway Transport in adspatationistroataßelijaniatio Regialatiophelijautophagy

CarbohydCatebotetalbatësmetahotisorsegaminoetajavismetabolism Valine leukätienetteuksiolevaridesteguaidatidegradation Ubiquitin klysteritie kylsteritie-kylsteritien-korigiografites enzymes

Mitophag Wifacutors

AutophagAutophagy - other

Endocyto Eisdocytosis

ReplicatioReptiotetion Dithite iRepDbtAGReptitization Factors
Transport@rareatetorger-Caterlegort@etersportcelerieren carriers
Hormonelstopnating sightetingsignhalking signaling

Energy mētaboglismeta@bibbosyn@lexxiosaymbleresaspanoteimsa proteins

Transport Transport Stylatakoid flaytaktoid tratteoliag pathway Pentose afterhyliseurandiajakutteroatevieteiroanversions Peptidaselteantidaseksi atansi hilibiitah sa fitamily S10 Glycosyltifahysiosylteansihyatasphahtijatropaleobile molecule Enzyme - Entalphahd-collaptismiyasegen lyases

TranscriptToanfactipition CattlerstrarCitrienttoanfactipition factors

Photosyn Pleasis synthesis