

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

Differentially expressed genes

| Rank | ID | log(FC) | fdr | Description | |
|----------------|--------------|---------|-------|-------------|---|
| | | p-value | | Metagene | |
| Overexpressed | | | | | |
| 1 | Vitv02g0144C | 2.45 | 2e-04 | 1 | 22 x 34 The space external to the outermost structure of a cell. For ce |
| 2 | Vitv13g0018E | 2.27 | 5e-04 | 1 | 1 x 8 A membrane-bounded organelle of eukaryotic cells in which |
| 3 | Vitv03g0024E | 1.03 | 7e-04 | 1 | 22 x 5 Binding to a calcium ion (Ca2+). |
| 4 | Vitv01g0060E | 1.81 | 1e-03 | 1 | 4 x 37 Binding to a protein. |
| 5 | Vitv18g00967 | 2.37 | 1e-03 | 1 | 26 x 40 A membrane-bounded organelle of eukaryotic cells in which |
| 6 | Vitv02g0041C | 1.33 | 3e-03 | 1 | 1 x 32 The process in which a solute is transported across a lipid bil |
| 7 | Vitv09g0139E | 1.97 | 3e-03 | 1 | 1 x 8 Binding to ATP, adenosine 5-triphosphate, a universally impo |
| 8 | Vitv18g01937 | 2.47 | 3e-03 | 1 | 20 x 1 Binding to a calcium ion (Ca2+). |
| 9 | Vitv12g0256E | 3.51 | 3e-03 | 1 | 36 x 1 The space external to the outermost structure of a cell. For ce |
| 10 | Vitv02g0148E | 2.18 | 3e-03 | 1 | 1 x 7 A lipid bilayer along with all the proteins and protein comple |
| 11 | Vitv01g00784 | 2.04 | 3e-03 | 1 | 22 x 4 The chemical reactions and pathways involving carbohydrate: |
| 12 | Vitv19g0185C | 1.98 | 3e-03 | 1 | 1 x 9 The component of a membrane consisting of the gene produ |
| 13 | Vitv16g0098E | 2.49 | 3e-03 | 1 | 1 x 9 |
| 14 | Vitv04g0116C | 1.86 | 4e-03 | 1 | 1 x 34 The contents of a cell excluding the plasma membrane and n |
| 15 | Vitv12g02644 | 1.37 | 6e-03 | 1 | 11 x 16 |
| 16 | Vitv04g0218E | 0.76 | 7e-03 | 1 | 11 x 30 The irregular network of unit membranes, visible only by elect |
| 17 | Vitv16g0145E | 2.42 | 7e-03 | 1 | 1 x 8 |
| 18 | Vitv08g0181E | 1.02 | 7e-03 | 1 | 22 x 5 Binding to a metal ion. |
| 19 | Vitv01g0084E | 1.75 | 7e-03 | 1 | 31 x 1 Binding to a protein. |
| 20 | Vitv18g02011 | 1.94 | 7e-03 | 1 | 1 x 9 Any molecular function by which a gene product interacts sele |
| Underexpressed | | | | | |
| 1 | Vitv17g0028E | -0.99 | 2e-04 | 1 | 30 x 9 |
| 2 | Vitv08g0019E | -0.51 | 7e-04 | 1 | 19 x 22 The component of a membrane consisting of the gene produ |
| 3 | Vitv18g0008C | -0.9 | 7e-04 | 1 | 18 x 23 The chemical reactions and pathways resulting in the formati |
| 4 | Vitv04g0006E | -1.58 | 9e-04 | 1 | 36 x 19 A lipid bilayer along with all the proteins and protein comple |
| 5 | Vitv01g0061E | -1.89 | 2e-03 | 1 | 39 x 4 Binding to a heme, a compound composed of iron complexed |
| 6 | Vitv13g0031E | -1.18 | 2e-03 | 1 | 35 x 12 The process in which a methyl group is covalently attached to |
| 7 | Vitv07g0006E | -1.08 | 2e-03 | 1 | 20 x 26 Any member of a family of organelles found in the cytoplasm |
| 8 | Vitv07g00427 | -0.93 | 3e-03 | 1 | 24 x 15 A semiautonomous, self replicating organelle that occurs in vi |
| 9 | Vitv06g00254 | -1.16 | 3e-03 | 1 | 17 x 27 |
| 10 | Vitv17g00921 | -1.35 | 3e-03 | 1 | 29 x 25 The process of removing sections of the primary RNA transcr |
| 11 | Vitv05g0093E | -0.88 | 3e-03 | 1 | 20 x 27 Binding to ATP, adenosine 5-triphosphate, a universally impo |
| 12 | Vitv06g0076E | -1.97 | 3e-03 | 1 | 40 x 20 The formation of a protein dimer, a macromolecular structure |
| 13 | Vitv07g0016E | -0.76 | 4e-03 | 1 | 35 x 15 The process whose specific outcome is the progression of the |
| 14 | Vitv08g0112C | -0.88 | 4e-03 | 1 | 32 x 13 A multisubunit protein complex that contains the Ino80p ATPa |
| 15 | Vitv03g0106E | -0.72 | 4e-03 | 1 | 7 x 28 Catalysis of the reaction: an orthophosphoric monoester + H2 |
| 16 | Vitv08g0196E | -0.99 | 4e-03 | 1 | 29 x 7 Catalysis of the reaction: hydroxymethylbilane = H(2)O + urop |
| 17 | Vitv06g0116E | -0.9 | 5e-03 | 1 | 35 x 17 Catalysis of the endonucleolytic cleavage at a junction such a |
| 18 | Vitv14g0019C | -0.9 | 6e-03 | 1 | 17 x 8 Catalysis of the hydrolysis of internal, alpha-peptide bonds in |
| 19 | Vitv04g0011E | -1.57 | 6e-03 | 1 | 6 x 22 Binding to ATP, adenosine 5-triphosphate, a universally impo |
| 20 | Vitv17g0036E | -1.03 | 6e-03 | 1 | 27 x 5 |

Differentially expressed gene sets

| Rank | GSZ | p-value | #all | Geneset |
|----------------|-------|---------|------|---|
| Overexpressed | | | | |
| 1 | 10.74 | 0.000 | 48 | Transcription factors - WRKY |
| 2 | 8.46 | 0.000 | 49 | Transcription factors - NAC |
| 3 | 7.77 | 0.000 | 162 | Plant species-specific signaling pathways |
| 4 | 5.81 | 0.000 | 238 | Enzyme - E2F family G1/S cyclin-dependent kinases |
| 5 | 5.68 | 0.000 | 64 | Transcription factors - Other transcription factors |
| 6 | 5.41 | 0.000 | 86 | Signal transduction - Calcium signaling pathway |
| 7 | 5.35 | 0.000 | 153 | Plant-pathogen interaction |
| 8 | 4.67 | 0.000 | 11 | Biosynthesis of proteinaceous metabolites |
| 9 | 4.52 | 0.000 | 73 | Transcription factors - AP2/ERF/WRKY/ERF |
| 10 | 4.13 | 0.000 | 140 | Hormone signaling - Ethylene signaling |
| 11 | 3.28 | 0.001 | 111 | Hormone signaling - Auxin signaling |
| 12 | 3.17 | 0.002 | 206 | Cell growth - Cell wall |
| 13 | 3 | 0.003 | 89 | MAPK signaling pathway - plant |
| 14 | 2.92 | 0.004 | 14 | Kinase - G-protein coupled receptor family |
| 15 | 2.9 | 0.004 | 17 | Kinase - Receptor tyrosine kinase family |
| 16 | 2.75 | 0.007 | 170 | Transcription factors - Other - C/EBP - C/EBP4 |
| 17 | 2.57 | 0.011 | 29 | Carotenoid biosynthesis |
| 18 | 2.5 | 0.013 | 78 | Glycosyltransferase - Glycosyltransferase |
| 19 | 2.47 | 0.014 | 16 | Transcription factors - HSF |
| 20 | 2.37 | 0.019 | 96 | Transporter - ABC transporter |
| Underexpressed | | | | |
| 1 | -3.76 | 1e-04 | 67 | Ribosome - Bacteria |
| 2 | -3.59 | 4e-04 | 26 | Flavonoid biosynthesis |
| 3 | -3.59 | 4e-04 | 28 | Transcription factors - MTF - MTERF |
| 4 | -3.43 | 8e-04 | 247 | Translation - Ribosome |
| 5 | -3.3 | 1e-03 | 72 | Ribosome - Mitochondrion |
| 6 | -3.14 | 2e-03 | 211 | Ribosome - Ribosome |
| 7 | -3.1 | 2e-03 | 39 | Pentose phosphate cycle intermediates |
| 8 | -3.02 | 3e-03 | 81 | Enzyme - E2F family G1/S cyclin-dependent kinases |
| 9 | -2.61 | 1e-02 | 44 | Energy metabolism - Nitrogen metabolism |
| 10 | -2.52 | 1e-02 | 48 | Lipid metabolism - Fatty acid metabolism |
| 11 | -2.49 | 1e-02 | 41 | Transporter - ABC transporter |
| 12 | -2.47 | 1e-02 | 75 | Mitochondrion - Mitochondrion |
| 13 | -2.46 | 2e-02 | 217 | Cell motility - Regulation of cytoskeleton |
| 14 | -2.42 | 2e-02 | 25 | Nitrogen metabolism |
| 15 | -2.4 | 2e-02 | 22 | Transcription factors - G2/M2 - DOF |
| 16 | -2.4 | 2e-02 | 97 | Ribosome - Archaea |
| 17 | -2.38 | 2e-02 | 18 | Chaperone - HSP20 |
| 18 | -2.35 | 2e-02 | 30 | Glycan biosynthesis - Glycan degradation |
| 19 | -2.29 | 2e-02 | 105 | Energy metabolism - Oxidative phosphorylation |
| 20 | -2.28 | 2e-02 | 12 | Enzyme - E2F family G1/S cyclin-dependent kinases |

