# Riesl_freeze

## Global Summary

%DE = NA

# genes with fdr < 0.2 = 8114 ( 4300 + / 3814 −)

# genes with fdr < 0.1 = 5861 ( 3124 + / 2737 −)

# genes with fdr < 0.05 = 4032 ( 2136 + / 1896 −)

# genes with fdr < 0.01 = 2587 ( 1357 + / 1230 −)

<FC> = 0

<p−value> = 0.02

<fdr> = 0.38

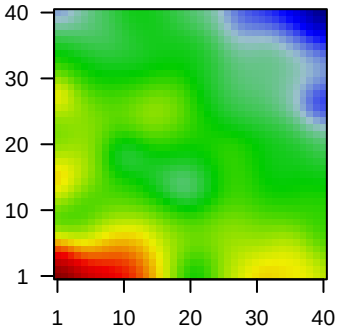
## Differentially expressed genes

| Rank | ID | log(FC) | p−value | fdr | Description Metagene |
|---|---|---|---|---|---|
| *Overexpressed* | | | | | |
| 1 | Vitvi04g01095 | 1.64 | 1e−16 | 7e−14 | 8 x 1 Binding to a protein. |
| 2 | Vitvi00g01866 | 1.67 | 1e−16 | 7e−14 | 1 x 28 |
| 3 | Vitvi10g02284 | 1.67 | 1e−16 | 7e−14 | 1 x 28 A lipid bilayer along with all the proteins and protein complexe |
| 4 | Vitvi01g00053 | 0.91 | 1e−16 | 7e−14 | 34 x 5 The component of a membrane consisting of the gene produc |
| 5 | Vitvi01g00330 | 0.78 | 1e−16 | 7e−14 | 1 x 18 The component of a membrane consisting of the gene produc |
| 6 | Vitvi01g00472 | 0.66 | 1e−16 | 7e−14 | 27 x 8 |
| 7 | Vitvi01g00812 | 1.15 | 1e−16 | 7e−14 | 33 x 3 The component of a membrane consisting of the gene produc |
| 8 | Vitvi01g00918 | 1.77 | 1e−16 | 7e−14 | 3 x 1 A membrane−bounded organelle of eukaryotic cells in which |
| 9 | Vitvi02g00696 | 0.92 | 1e−16 | 7e−14 | 1 x 13 The process whose specific outcome is the progression of the |
| 10 | Vitvi02g01268 | 0.37 | 1e−16 | 7e−14 | 29 x 12 The part of the cytoplasm that does not contain organelles bu |
| 11 | Vitvi03g01397 | 1.19 | 1e−16 | 7e−14 | 39 x 1 |
| 12 | Vitvi03g00133 | 0.76 | 1e−16 | 7e−14 | 12 x 4 The membrane surrounding a cell that separates the cell from |
| 13 | Vitvi03g00397 | 2.45 | 1e−16 | 7e−14 | 1 x 1 Binding to a protein. |
| 14 | Vitvi04g01854 | 0.88 | 1e−16 | 7e−14 | 36 x 5 The component of a membrane consisting of the gene produc |
| 15 | Vitvi04g02091 | 0.76 | 1e−16 | 7e−14 | 16 x 1 Binding to ADP, adenosine 5'−diphosphate. |
| 16 | Vitvi05g00376 | 0.73 | 1e−16 | 7e−14 | 5 x 19 The component of a membrane consisting of the gene produc |
| 17 | Vitvi06g00646 | 1.07 | 1e−16 | 7e−14 | 12 x 1 Catalysis of a biochemical reaction at physiological temperat |
| 18 | Vitvi06g01215 | 0.56 | 1e−16 | 7e−14 | 3 x 27 Binding to a protein. |
| 19 | Vitvi07g00595 | 1.72 | 1e−16 | 7e−14 | 5 x 1 The component of a membrane consisting of the gene produc |
| 20 | Vitvi07g01610 | 1.5 | 1e−16 | 7e−14 | 7 x 3 Any process that modulates the frequency, rate or extent of g |
| *Underexpressed* | | | | | |
| 1 | Vitvi10g00245 | −2.44 | 1e−16 | 7e−14 | 12 x 18 Binding to a metal ion. |
| 2 | Vitvi10g00159 | −0.71 | 1e−16 | 7e−14 | 7 x 37 |
| 3 | Vitvi01g00241 | −1.51 | 1e−16 | 7e−14 | 35 x 40 A membrane−bound cytoplasmic organelle of the endomemb |
| 4 | Vitvi01g00394 | −2.96 | 1e−16 | 7e−14 | 40 x 40 Binding to a metal ion. |
| 5 | Vitvi05g01596 | −1.93 | 1e−16 | 7e−14 | 34 x 40 The component of a membrane consisting of the gene produc |
| 6 | Vitvi06g01226 | −2.04 | 1e−16 | 7e−14 | 40 x 38 The process whose specific outcome is the progression of the |
| 7 | Vitvi06g01513 | −3.58 | 1e−16 | 7e−14 | 40 x 40 |
| 8 | Vitvi07g00708 | −0.61 | 1e−16 | 7e−14 | 23 x 40 |
| 9 | Vitvi07g02666 | −1.17 | 1e−16 | 7e−14 | 32 x 40 A process that is carried out at the cellular level which results |
| 10 | Vitvi08g01423 | −2.02 | 1e−16 | 7e−14 | 39 x 38 Binding to a protein. |
| 11 | Vitvi08g01664 | −1.15 | 1e−16 | 7e−14 | 29 x 40 Catalysis of a biochemical reaction at physiological temperat |
| 12 | Vitvi10g00523 | −1.98 | 1e−16 | 7e−14 | 40 x 39 Catalysis of the hydrolysis of any ester bond. |
| 13 | Vitvi12g00330 | −2.15 | 1e−16 | 7e−14 | 19 x 14 |
| 14 | Vitvi12g01873 | −0.77 | 1e−16 | 7e−14 | 29 x 38 Catalysis of an oxidation−reduction (redox) reaction, a reversi |
| 15 | Vitvi12g00353 | −0.67 | 1e−16 | 7e−14 | 29 x 37 Any molecular function by which a gene product interacts sele |
| 16 | Vitvi13g01882 | −1.34 | 1e−16 | 7e−14 | 29 x 40 Catalysis of the reaction: S−adenosyl−L−methionine + histon |
| 17 | Vitvi13g01001 | −1.67 | 1e−16 | 7e−14 | 36 x 38 A membrane−bounded organelle of eukaryotic cells in which |
| 18 | Vitvi14g00242 | −1.48 | 1e−16 | 7e−14 | 27 x 40 Binding to ATP, adenosine 5'−triphosphate, a universally impo |
| 19 | Vitvi15g00998 | −1.09 | 1e−16 | 7e−14 | 29 x 37 Binding to a zinc ion (Zn). |
| 20 | Vitvi15g00754 | −0.98 | 1e−16 | 7e−14 | 29 x 38 The component of the endoplasmic reticulum membrane cons |

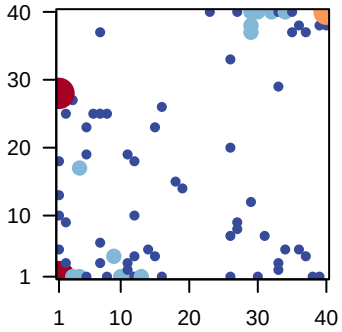
## Differentially expressed gene sets

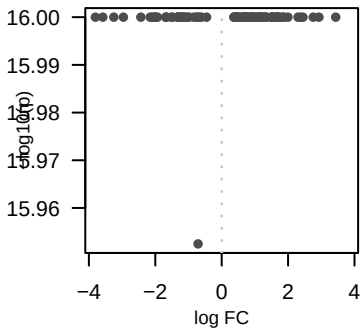
| Rank | GSZ | p−value | #all | Geneset |
|---|---|---|---|---|
| *Overexpressed* | | | | |
| 1 | 6.35 | 0e+00 | 140 | Hormone signaling − Ethylene signaling |
| 2 | 6.08 | 0e+00 | 73 | Transcription factors − AP2/EREBP |
| 3 | 5.59 | 0e+00 | 64 | Transcription factors − Other transcription factors |
| 4 | 5.49 | 0e+00 | 45 | Galactose metabolism |
| 5 | 5.48 | 0e+00 | 15 | Chaperones − HSP70 / DNAK |
| 6 | 5.35 | 0e+00 | 17 | Proteasome − Assembly factors |
| 7 | 5.16 | 0e+00 | 12 | Endoplasmic reticulum and cytosol |
| 8 | 4.98 | 0e+00 | 157 | Protein processing in endoplasmic reticulum |
| 9 | 4.92 | 0e+00 | 48 | Transcription factors − WRKY |
| 10 | 4.89 | 0e+00 | 18 | Chaperones − HSP20 |
| 11 | 4.42 | 0e+00 | 38 | Protein − Chaperone mediated autophagy (CMA) |
| 12 | 4.23 | 0e+00 | 49 | Transcription factors − NAC |
| 13 | 4.12 | 0e+00 | 71 | Exosome − Proteins found in exosomes |
| 14 | 3.59 | 4e−04 | 35 | Mitophagy − Yeast |
| 15 | 3.37 | 1e−03 | 38 | Protein − Clathrin mediated endocytosis |
| 16 | 3.13 | 3e−03 | 77 | Carbohydrate metabolism − Galactose metabolism |
| 17 | 2.97 | 4e−03 | 11 | Biosynthesis of secondary metabolites − ABA biosynthesis |
| 18 | 2.87 | 5e−03 | 28 | Transcription factors − Basic leucine zipper (bZIP) |
| 19 | 2.76 | 7e−03 | 29 | Other amino acid metabolism − Beta−Alanine metabolism |
| 20 | 2.75 | 7e−03 | 45 | Valine leucine and isoleucine degradation |
| *Underexpressed* | | | | |
| 1 | −8.79 | 0 | 18 | Energy metabolism − Photosynthesis − proteins |
| 2 | −8.61 | 0 | 80 | Cytoskeleton − Microtubules |
| 3 | −8.48 | 0 | 18 | Photosynthesis − proteins |
| 4 | −7.94 | 0 | 217 | Cell motility − Regulation of cytoskeleton |
| 5 | −7.78 | 0 | 47 | Transporters − Transporter catalog − Electron carriers |
| 6 | −6.2 | 0 | 78 | Energy metabolism − Photosynthesis |
| 7 | −6.19 | 0 | 38 | Photosynthesis |
| 8 | −6.1 | 0 | 219 | Cell growth and death − Cell cycle |
| 9 | −5.44 | 0 | 10 | Photosynthesis − Photosystem II (P700 chlorophyll a) |
| 10 | −5.31 | 0 | 24 | Replication − DNA Replication Factors |
| 11 | −5.13 | 0 | 11 | Transcription factors − GRF |
| 12 | −4.8 | 0 | 36 | DNA replication |
| 13 | −4.67 | 0 | 40 | Transporters − Tyrosine Tryptophan pathway |
| 14 | −4.33 | 0 | 41 | Replication and Repair − DNA replication |
| 15 | −4.28 | 0 | 41 | Porphyrin metabolism |
| 16 | −4.25 | 0 | 66 | Exosome − Exosome components of bladder cancer cells |
| 17 | −4.02 | 0 | 34 | Peptidases − Peptidases in Family S10 |
| 18 | −4 | 0 | 247 | Translation − Ribosome |
| 19 | −3.8 | 0 | 129 | Enzyme − Glycosylases |
| 20 | −3.76 | 0 | 211 | Ribosome |

**Portrait**

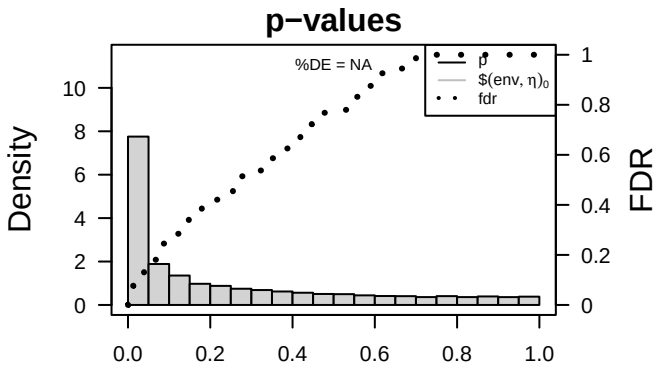



**Top 100 DE genes**




**p−values**




**p−values**