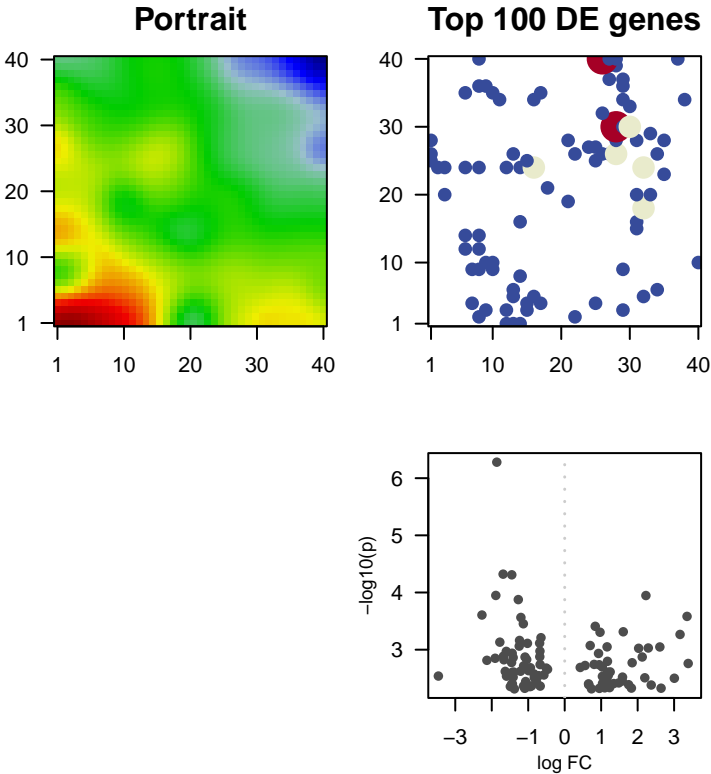


# Riesl\_freeze\_r3

## Global Summary

%DE = 0.25  
# 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> = 0.31  
<fdr> = 0.75



## Differentially expressed genes

| Rank                  | ID           | log(FC) | p-value | fdr | Description  |
|-----------------------|--------------|---------|---------|-----|--|
| <i>Overexpressed</i>  |              |         |         |     |  |
| 1                     | Vitv05g0013E | 2.23    | 1e-04   | 0.4 | The chemical reactions and pathways involving carbohydrate:              |
| 2                     | Vitv18g03161 | 3.35    | 3e-04   | 0.6 | 8 x 2  |
| 3                     | Vitv13g00497 | 0.84    | 4e-04   | 0.6 | 16 x 24  |
| 4                     | Vitv04g0024E | 1.61    | 5e-04   | 0.6 | 9 x 10 Binding to ATP, adenosine 5'-triphosphate, a universally impc     |
| 5                     | Vitv08g01164 | 0.97    | 5e-04   | 0.6 | 15 x 25 Catalysis of the transfer of an acetyl group to an acceptor mo   |
| 6                     | Vitv18g0099E | 3.16    | 5e-04   | 0.6 | 12 x 1 The component of a membrane consisting of the gene produc         |
| 7                     | Vitv04g0149E | 0.7     | 8e-04   | 0.6 | 21 x 28 The chemical reactions and pathways resulting in the breakd      |
| 8                     | Vitv11g0131E | 1.16    | 9e-04   | 0.6 | 17 x 4 Binding to ATP, adenosine 5'-triphosphate, a universally impc     |
| 9                     | Vitv02g0134E | 2.61    | 9e-04   | 0.6 | 7 x 4 A lipid bilayer along with all the proteins and protein comple     |
| 10                    | Vitv01g0080E | 2.29    | 9e-04   | 0.6 | 14 x 1 The component of a membrane consisting of the gene produc         |
| 11                    | Vitv12g0075E | 2.03    | 9e-04   | 0.6 | 34 x 6 Binding to a zinc ion (Zn).                                       |
| 12                    | Vitv01g00591 | 0.93    | 1e-03   | 0.6 | 8 x 14   |
| 13                    | Vitv02g0009E | 2.13    | 1e-03   | 0.6 | 13 x 6   |
| 14                    | Vitv19g0198E | 1.17    | 2e-03   | 0.6 | 6 x 14 The cellular catabolic process in which cells digest parts of th  |
| 15                    | Vitv04g00527 | 1.85    | 2e-03   | 0.6 | 12 x 3 Any process that stops, prevents, or reduces the frequency, r     |
| 16                    | Vitv17g0161E | 3.39    | 2e-03   | 0.6 | 8 x 9 Binds to and stops, prevents or reduces the activity of an end     |
| 17                    | Vitv01g01824 | 0.81    | 2e-03   | 0.6 | 14 x 8 A transcription coregulator activity that activates or increases  |
| 18                    | Vitv07g0124E | 0.95    | 2e-03   | 0.6 | 8 x 24 Catalysis of a biochemical reaction at physiological temperat     |
| 19                    | Vitv15g0055E | 0.56    | 2e-03   | 0.6 | 12 x 24  |
| 20                    | Vitv13g0079E | 1.03    | 2e-03   | 0.6 | 16 x 5 The chemical reactions and pathways involving carbohydrate:       |
| <i>Underexpressed</i> |              |         |         |     |  |
| 1                     | Vitv14g0127E | -1.86   | 5e-07   | 0.3 | 14 x 16 Organized structure of distinctive morphology and function, bi   |
| 2                     | Vitv13g01837 | -1.69   | 5e-05   | 0.3 | 27 x 30 Binding to ATP, adenosine 5'-triphosphate, a universally impc    |
| 3                     | Vitv13g01557 | -1.45   | 5e-05   | 0.4 | 10 x 35 The chemical reactions and pathways resulting in the formati     |
| 4                     | Vitv07g0135E | -1.89   | 1e-04   | 0.4 | 26 x 40 The component of a membrane consisting of the gene produc        |
| 5                     | Vitv03g00324 | -1.27   | 1e-04   | 0.6 | 8 x 36   |
| 6                     | Vitv15g0078E | -2.27   | 2e-04   | 0.6 | 30 x 30 Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, (   |
| 7                     | Vitv10g00194 | -1.2    | 3e-04   | 0.6 | 29 x 30 The contents of a cell excluding the plasma membrane and n       |
| 8                     | Vitv08g00691 | -1.13   | 4e-04   | 0.6 | 17 x 35 Binding to a metal ion.  |
| 9                     | Vitv10g0032E | -0.65   | 6e-04   | 0.6 | 31 x 16  |
| 10                    | Vitv16g00984 | -1.24   | 7e-04   | 0.6 | 28 x 26 The component of a membrane consisting of the gene produc        |
| 11                    | Vitv08g0241E | -1.78   | 7e-04   | 0.6 | 28 x 39 The component of a membrane consisting of the gene produc        |
| 12                    | Vitv03g00647 | -0.69   | 8e-04   | 0.6 | 21 x 19 A lipid bilayer along with all the proteins and protein comple   |
| 13                    | Vitv13g0056E | -1.02   | 8e-04   | 0.6 | 28 x 26 The action of a molecule that contributes to the structural inte |
| 14                    | Vitv16g0105E | -1.25   | 9e-04   | 0.6 | 26 x 32 The chemical reactions and pathways involving lipids, compo      |
| 15                    | Vitv18g0006E | -0.68   | 1e-03   | 0.6 | 26 x 26 The component of a membrane consisting of the gene produc        |
| 16                    | Vitv03g0001E | -1.6    | 1e-03   | 0.6 | 22 x 2 Binding to a metal ion.   |
| 17                    | Vitv08g0178E | -1.44   | 1e-03   | 0.6 | 33 x 29 Binding to a protein.  |
| 18                    | Vitv14g0016E | -1.68   | 1e-03   | 0.6 | 29 x 37 Binding to a metal ion.  |
| 19                    | Vitv14g01031 | -0.68   | 1e-03   | 0.6 | 32 x 18 Any process that stops or reduces the activity of an enzyme.     |
| 20                    | Vitv12g01971 | -1.09   | 1e-03   | 0.6 | 22 x 26  |

## Differentially expressed gene sets

| Rank                  | GSZ   | p-value | #all | Geneset   |
|-----------------------|-------|---------|------|---|
| <i>Overexpressed</i>  |       |         |      |   |
| 1                     | 6.42  | 0e+00   | 45   | GalactoseGalactosemetabolism                          |
| 2                     | 5.27  | 0e+00   | 140  | HormoneSignaling signaling                            |
| 3                     | 4.84  | 0e+00   | 73   | Transcription factor AP2-EREBP2 EREBP                 |
| 4                     | 4.74  | 0e+00   | 77   | Carbohydrate metabolismGalactoseGalactosemetabolism   |
| 5                     | 3.94  | 4e-05   | 49   | Transcription factor NACs - NAC                       |
| 6                     | 3.74  | 1e-04   | 28   | Transcription factor Basic leucine zipper (bZIP)      |
| 7                     | 3.73  | 1e-04   | 45   | Valine leucine isoleucine degradation                 |
| 8                     | 3.66  | 3e-04   | 11   | Biosynthesis of proteinMetabolismBiosynthesis         |
| 9                     | 3.57  | 4e-04   | 35   | MitochondriaMitochondria                              |
| 10                    | 3.52  | 6e-04   | 64   | Transcription factor Other transcription factors      |
| 11                    | 3.4   | 9e-04   | 92   | Lipid metabolismLipid metabolism                      |
| 12                    | 3.24  | 1e-03   | 13   | PeptidasePeptidase and inhibitors of peptidase family |
| 13                    | 3.17  | 2e-03   | 43   | Transcription factor BZIPs - BZIP                     |
| 14                    | 3.11  | 2e-03   | 25   | Lysine degradation                                    |
| 15                    | 3.1   | 2e-03   | 44   | Energy metabolismMetabolism                           |
| 16                    | 3.02  | 3e-03   | 20   | Transport and metabolismRegulation of autophagy       |
| 17                    | 3.01  | 3e-03   | 20   | Protein - Autophagosome degradation proteins          |
| 18                    | 2.99  | 3e-03   | 309  | Enzyme - Enzyme in the glycolysis pathway             |
| 19                    | 2.9   | 4e-03   | 29   | Other amino acid metabolismMetabolism                 |
| 20                    | 2.84  | 5e-03   | 79   | TransporterTransporter                                |
| <i>Underexpressed</i> |       |         |      |   |
| 1                     | -9.73 | 0       | 247  | TranslationTranslation                                |
| 2                     | -9.67 | 0       | 211  | RibosomeRibosome                                      |
| 3                     | -9.04 | 0       | 144  | RibosomeRibosome                                      |
| 4                     | -8.79 | 0       | 18   | Energy metabolismBiosynthesis of proteins             |
| 5                     | -8.65 | 0       | 18   | PhotosynthesisPhotosynthesis                          |
| 6                     | -7.7  | 0       | 80   | CytoskeletonCytoskeleton                              |
| 7                     | -7.05 | 0       | 47   | TransporterTransporter                                |
| 8                     | -6.91 | 0       | 97   | RibosomeRibosome                                      |
| 9                     | -6.41 | 0       | 217  | Cell motilityRegulation of cytoskeleton               |
| 10                    | -5.47 | 0       | 113  | ExosomeExosome  |
| 11                    | -5.35 | 0       | 66   | ExosomeExosome  |
| 12                    | -5.29 | 0       | 11   | Transcription factor GRFs - GRF                       |
| 13                    | -5.28 | 0       | 24   | ReplicationReplication                                |
| 14                    | -4.57 | 0       | 38   | PhotosynthesisPhotosynthesis                          |
| 15                    | -4.48 | 0       | 36   | DNA replicationDNA replication                        |
| 16                    | -4.48 | 0       | 41   | Porphyrin metabolism                                  |
| 17                    | -4.47 | 0       | 219  | Cell growth and divisionCell cycle                    |
| 18                    | -4.27 | 0       | 10   | PhotosynthesisPhotosynthesis                          |
| 19                    | -4.22 | 0       | 40   | TransporterTransporter                                |
| 20                    | -4.05 | 0       | 206  | Cell growth and divisionCell cycle                    |

