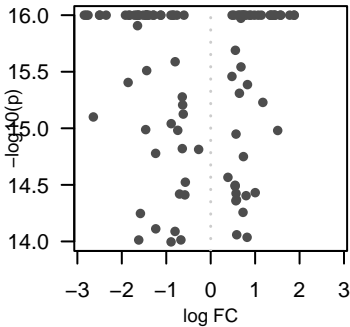
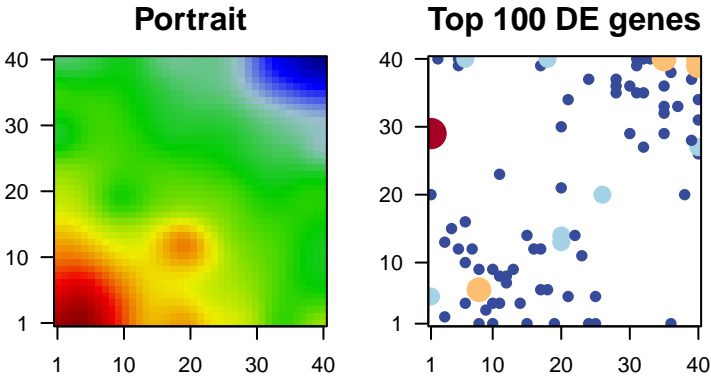


# CabFra\_freeze

## Global Summary

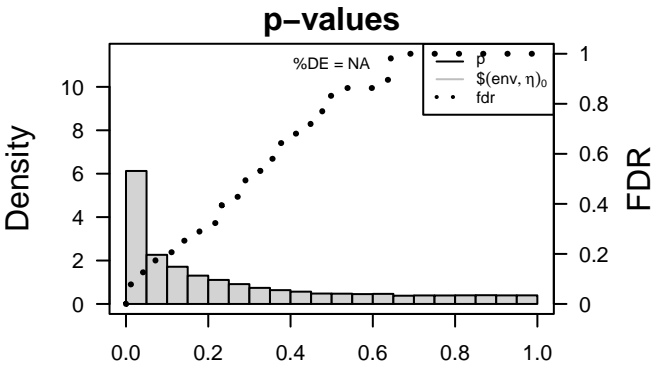
%DE = NA  
# genes with  $\text{fdr} < 0.2$  = 7391 ( 3847 + / 3544 - )  
# genes with  $\text{fdr} < 0.1$  = 3994 ( 2106 + / 1888 - )  
# genes with  $\text{fdr} < 0.05$  = 2249 ( 1180 + / 1069 - )  
# genes with  $\text{fdr} < 0.01$  = 1311 ( 663 + / 648 - )

<FC> = 0  
<p-value> = 0.04  
<fdr> = 0.39



## Differentially expressed genes

| Rank           | ID           | log(FC) | fdr   | Description |         |  |
|----------------|--------------|---------|-------|-------------|---------|--|
|                |              | p-value |       | Metagene    |         |  |
| Overexpressed  |              |         |       |             |         |  |
| 1              | Vitv00g0024E | 1.88    | 1e-16 | 5e-14       | 20 x 14 |  |
| 2              | Vitv18g0337E | 1.88    | 1e-16 | 5e-14       | 20 x 14 |  |
| 3              | Vitv01g0152I | 0.64    | 1e-16 | 5e-14       | 10 x 9  | The cellular process in which a signal is conveyed to trigger a  |
| 4              | Vitv01g00227 | 0.48    | 1e-16 | 5e-14       | 17 x 6  | The joining together of exons from one or more primary trans     |
| 5              | Vitv01g0196E | 1.58    | 1e-16 | 5e-14       | 6 x 4   |  |
| 6              | Vitv01g00392 | 0.72    | 1e-16 | 5e-14       | 23 x 11 | Binding to a protein.  |
| 7              | Vitv01g01993 | 1.34    | 1e-16 | 5e-14       | 8 x 6   |  |
| 8              | Vitv01g0070E | 1.57    | 1e-16 | 5e-14       | 19 x 1  | Binding to a metal ion.  |
| 9              | Vitv03g0028E | 0.75    | 1e-16 | 5e-14       | 3 x 13  |  |
| 10             | Vitv03g0029E | 0.75    | 1e-16 | 5e-14       | 24 x 1  | Binding to ATP, adenosine 5'-triphosphate, a universally impo    |
| 11             | Vitv03g01704 | 1.07    | 1e-16 | 5e-14       | 10 x 4  | The component of a membrane consisting of the gene produc        |
| 12             | Vitv04g0183E | 0.61    | 1e-16 | 5e-14       | 7 x 12  | The series of molecular signals initiated by a ligand binding to |
| 13             | Vitv05g0140I | 0.79    | 1e-16 | 5e-14       | 1 x 20  | The aggregation, arrangement and bonding together of one or      |
| 14             | Vitv06g0094E | 1.45    | 1e-16 | 5e-14       | 1 x 5   | The contents of a cell excluding the plasma membrane and n       |
| 15             | Vitv07g02204 | 1.78    | 1e-16 | 5e-14       | 20 x 13 | Catalysis of an oxidation-reduction (redox) reaction, a reversi  |
| 16             | Vitv07g0043E | 0.87    | 1e-16 | 5e-14       | 5 x 12  | Binding to a nucleic acid.                                       |
| 17             | Vitv09g0122C | 0.52    | 1e-16 | 5e-14       | 25 x 5  | Catalysis of the reaction: protein serine phosphate + H2O = p    |
| 18             | Vitv10g0048E | 0.98    | 1e-16 | 5e-14       | 8 x 6   | The membrane surrounding a cell that separates the cell from     |
| 19             | Vitv10g00107 | 1.41    | 1e-16 | 5e-14       | 8 x 1   | The component of a membrane consisting of the gene produc        |
| 20             | Vitv11g0014I | 0.67    | 1e-16 | 5e-14       | 14 x 4  |  |
| Underexpressed |              |         |       |             |         |  |
| 1              | Vitv10g0174C | -0.84   | 1e-16 | 5e-14       | 28 x 37 | A ubiquitin ligase complex in which a cullin from the Cul1 sub   |
| 2              | Vitv10g0034E | -1.39   | 1e-16 | 5e-14       | 31 x 40 |  |
| 3              | Vitv10g0029C | -1.44   | 1e-16 | 5e-14       | 36 x 38 |  |
| 4              | Vitv03g00677 | -1.45   | 1e-16 | 5e-14       | 39 x 37 | The chemical reactions and pathways involving cytokinins, a      |
| 5              | Vitv03g0085I | -1.82   | 1e-16 | 5e-14       | 32 x 40 | The irregular network of unit membranes, visible only by elect   |
| 6              | Vitv06g0122E | -1.72   | 1e-16 | 5e-14       | 40 x 38 | The process whose specific outcome is the progression of the     |
| 7              | Vitv07g0037E | -1.67   | 1e-16 | 5e-14       | 40 x 26 | The component of a membrane consisting of the gene produc        |
| 8              | Vitv07g00654 | -1.12   | 1e-16 | 5e-14       | 18 x 40 | Binding to a protein.  |
| 9              | Vitv07g0211E | -1.46   | 1e-16 | 5e-14       | 35 x 36 | Catalysis of the hydrolysis of a carboxylic ester bond.          |
| 10             | Vitv08g0129C | -1.45   | 1e-16 | 5e-14       | 35 x 40 |  |
| 11             | Vitv08g0003C | -1.52   | 1e-16 | 5e-14       | 33 x 40 | Binding to a protein.  |
| 12             | Vitv09g0019C | -0.76   | 1e-16 | 5e-14       | 24 x 37 | The component of a membrane consisting of the gene produc        |
| 13             | Vitv09g01272 | -1.92   | 1e-16 | 5e-14       | 40 x 40 | Catalysis of the hydrolysis of internal, alpha-peptide bonds i   |
| 14             | Vitv10g00494 | -0.6    | 1e-16 | 5e-14       | 20 x 30 | The contents of a cell excluding the plasma membrane and n       |
| 15             | Vitv11g0001E | -2.5    | 1e-16 | 5e-14       | 35 x 40 | Binds to and stops, prevents or reduces the activity of an enz   |
| 16             | Vitv14g0162I | -1.85   | 1e-16 | 5e-14       | 40 x 27 | The contents of a cell excluding the plasma membrane and n       |
| 17             | Vitv15g0050C | -1.28   | 1e-16 | 5e-14       | 39 x 28 | A lipid bilayer along with all the proteins and protein comple   |
| 18             | Vitv15g01067 | -1.29   | 1e-16 | 5e-14       | 35 x 29 | The component of a membrane consisting of the gene produc        |
| 19             | Vitv16g0031C | -0.89   | 1e-16 | 5e-14       | 30 x 29 | Binding to a protein kinase, any enzyme that catalyzes the tra   |
| 20             | Vitv16g0078E | -2.8    | 1e-16 | 5e-14       | 1 x 29  | Binding to a heme, a compound composed of iron complexed w       |



## Differentially expressed gene sets

| Rank           | GSZ   | p-value | #all | Geneset  |
|----------------|-------|---------|------|--|
| Overexpressed  |       |         |      |  |
| 1              | 6.38  | 0e+00   | 48   | Transcription factor WRKY                        |
| 2              | 5.07  | 0e+00   | 45   | Galactose metabolism                             |
| 3              | 4.85  | 0e+00   | 162  | Plant species-specific signaling pathway         |
| 4              | 4.69  | 0e+00   | 49   | Transcription factor NAC                         |
| 5              | 4.27  | 0e+00   | 58   | Other amino acid metabolism                      |
| 6              | 3.77  | 0e+00   | 77   | Pores ion channels (TC:1)                        |
| 7              | 3.66  | 2e-04   | 42   | Tryptophan metabolism                            |
| 8              | 3.49  | 6e-04   | 153  | Plant-pathogen interaction                       |
| 9              | 3.33  | 1e-03   | 51   | Biosynthesis of secondary metabolites            |
| 10             | 3.14  | 3e-03   | 24   | Tropine alkaloid biosynthesis                    |
| 11             | 3.05  | 3e-03   | 80   | Transport system                                 |
| 12             | 2.98  | 4e-03   | 28   | Transcription factor Basic leucine zipper (bZIP) |
| 13             | 2.93  | 4e-03   | 140  | Hormone signaling pathway                        |
| 14             | 2.8   | 6e-03   | 39   | beta-Alanine metabolism                          |
| 15             | 2.76  | 7e-03   | 17   | Isoquinoline alkaloid biosynthesis               |
| 16             | 2.74  | 8e-03   | 96   | Transport system                                 |
| 17             | 2.73  | 8e-03   | 34   | Tyrosine metabolism                              |
| 18             | 2.71  | 8e-03   | 45   | Valine leucine isoleucine degradation            |
| 19             | 2.69  | 8e-03   | 12   | Enzyme Class - Class I                           |
| 20             | 2.59  | 1e-02   | 29   | Other amino acid metabolism                      |
| Underexpressed |       |         |      |  |
| 1              | -9.78 | 0       | 80   | Cytoskeleton                                     |
| 2              | -9.45 | 0       | 18   | Photosynthesis                                   |
| 3              | -9.35 | 0       | 18   | Energy metabolism                                |
| 4              | -9.04 | 0       | 217  | Cell motility                                    |
| 5              | -8.81 | 0       | 206  | Cell growth and division                         |
| 6              | -7.94 | 0       | 47   | Transport system                                 |
| 7              | -6.82 | 0       | 38   | Photosynthesis                                   |
| 8              | -6.77 | 0       | 78   | Energy metabolism                                |
| 9              | -5.99 | 0       | 10   | Photosynthesis                                   |
| 10             | -5.81 | 0       | 219  | Cell growth and division                         |
| 11             | -5.1  | 0       | 113  | Exosome  |
| 12             | -5.09 | 0       | 66   | Exosome  |
| 13             | -5.03 | 0       | 40   | Transport system                                 |
| 14             | -4.95 | 0       | 134  | Hormone signaling pathway                        |
| 15             | -4.7  | 0       | 211  | Ribosome   |
| 16             | -4.64 | 0       | 10   | Peptidase  |
| 17             | -4.4  | 0       | 30   | Glycan   |
| 18             | -4.22 | 0       | 11   | Transcription factor GRF                         |
| 19             | -4.13 | 0       | 19   | Aquaporin  |
| 20             | -4.12 | 0       | 78   | Glycosyltransferase                              |

