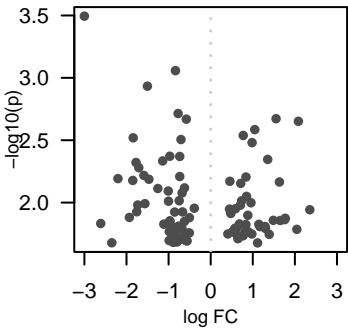
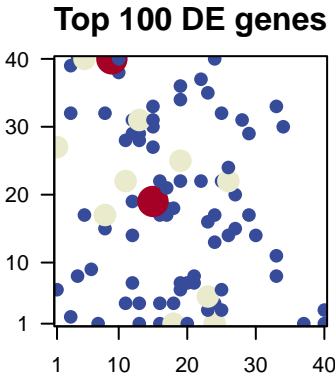
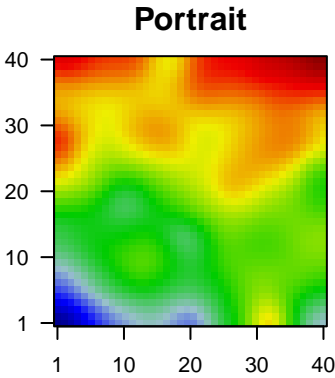


Riesl_acclim_r1

Global Summary

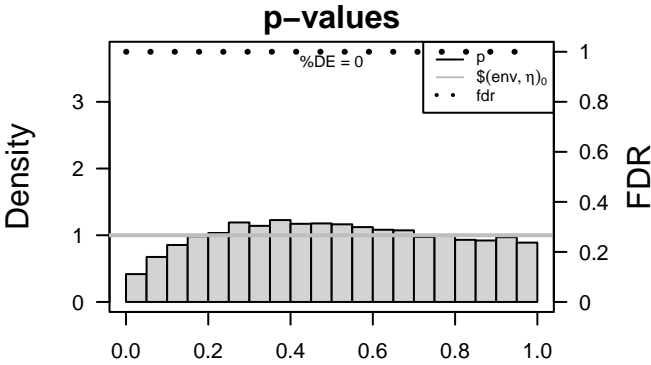
%DE = 0
genes with fdr < 0.2 = 0 (0 + / 0 -)
genes with fdr < 0.1 = 0 (0 + / 0 -)
genes with fdr < 0.05 = 0 (0 + / 0 -)
genes with fdr < 0.01 = 0 (0 + / 0 -)

<FC> = 0
<p-value> = 0.42
<fdr> = 1



Differentially expressed genes

| Rank | ID | log(FC) | fdr | Description | | |
|----------------|--------------|---------|-------|-------------|---------|--|
| | | p-value | | Metagene | | |
| Overexpressed | | | | | | |
| 1 | Vitv02g00242 | 1.55 | 0.002 | 1 | 28 x 31 | A membrane-bounded organelle of eukaryotic cells in which |
| 2 | Vitv08g0199E | 2.08 | 0.002 | 1 | 5 x 40 | The component of a membrane consisting of the gene produc |
| 3 | Vitv11g01117 | 1.05 | 0.003 | 1 | 19 x 25 | A small RNA-based gene silencing process in which small in |
| 4 | Vitv14g0178E | 0.77 | 0.003 | 1 | 25 x 32 | |
| 5 | Vitv04g0016E | 0.98 | 0.003 | 1 | 13 x 31 | A lipid bilayer along with all the proteins and protein comple |
| 6 | Vitv16g0135E | 1.35 | 0.005 | 1 | 29 x 29 | Binding to ATP, adenosine 5-triphosphate, a universally impc |
| 7 | Vitv07g0003E | 0.84 | 0.006 | 1 | 13 x 29 | Any process involved in the conversion of a primary ribosoma |
| 8 | Vitv07g0043E | 0.46 | 0.007 | 1 | 13 x 31 | Binding to a zinc ion (Zn). |
| 9 | Vitv18g0247E | 1.63 | 0.007 | 1 | 33 x 33 | Catalysis of an oxidation-reduction (redox) reaction in which |
| 10 | Vitv15g0005C | 0.71 | 0.007 | 1 | 15 x 30 | The contents of a cell excluding the plasma membrane and n |
| 11 | Vitv15g0121E | 0.85 | 0.009 | 1 | 10 x 38 | Binding to a protein. |
| 12 | Vitv04g0155E | 0.73 | 0.010 | 1 | 15 x 33 | The network of interconnected tubular and cisternal structure: |
| 13 | Vitv05g0186C | 0.96 | 0.010 | 1 | 15 x 27 | |
| 14 | Vitv18g0095C | 0.71 | 0.010 | 1 | 26 x 22 | The chemical reactions and pathways resulting in the breakd |
| 15 | Vitv08g00112 | 0.59 | 0.011 | 1 | 12 x 31 | A membrane-bounded organelle of eukaryotic cells in which |
| 16 | Vitv17g00032 | 0.45 | 0.011 | 1 | 25 x 22 | Binding to an RNA molecule or a portion thereof. |
| 17 | Vitv12g0223E | 2.35 | 0.011 | 1 | 1 x 27 | |
| 18 | Vitv08g0176E | 0.48 | 0.012 | 1 | 11 x 28 | Any process that modulates the frequency, rate or extent of ai |
| 19 | Vitv07g0141C | 0.88 | 0.013 | 1 | 22 x 22 | Binding to a zinc ion (Zn). |
| 20 | Vitv13g0208E | 1.77 | 0.013 | 1 | 1 x 27 | A lipid bilayer along with all the proteins and protein comple |
| Underexpressed | | | | | | |
| 1 | Vitv04g00031 | -3 | 3e-04 | 1 | 20 x 1 | Binding to ATP, adenosine 5-triphosphate, a universally impc |
| 2 | Vitv07g0204E | -0.84 | 9e-04 | 1 | 12 x 19 | The contents of a cell excluding the plasma membrane and n |
| 3 | Vitv04g00227 | -1.5 | 1e-03 | 1 | 18 x 4 | |
| 4 | Vitv04g0052C | -0.77 | 2e-03 | 1 | 15 x 19 | Binding to a nucleic acid. |
| 5 | Vitv16g0045E | -0.58 | 2e-03 | 1 | 30 x 14 | The contents of a cell excluding the plasma membrane and n |
| 6 | Vitv00g02111 | -1.84 | 3e-03 | 1 | 18 x 1 | |
| 7 | Vitv01g00301 | -0.71 | 3e-03 | 1 | 21 x 7 | |
| 8 | Vitv11g0148C | -0.97 | 4e-03 | 1 | 5 x 17 | |
| 9 | Vitv18g0238C | -0.74 | 4e-03 | 1 | 16 x 17 | A lipid bilayer along with all the proteins and protein comple |
| 10 | Vitv14g03047 | -1.14 | 5e-03 | 1 | 23 x 3 | The irregular network of unit membranes, visible only by elect |
| 11 | Vitv01g00842 | -1.77 | 5e-03 | 1 | 37 x 1 | The component of a membrane consisting of the gene produc |
| 12 | Vitv14g0170C | -1.71 | 5e-03 | 1 | 11 x 4 | Binding to a protein. |
| 13 | Vitv13g0244E | -1.59 | 6e-03 | 1 | 6 x 9 | |
| 14 | Vitv16g00111 | -0.74 | 6e-03 | 1 | 25 x 6 | Catalysis of the reaction: acetyl-CoA + peptide = CoA + N-al |
| 15 | Vitv19g0232A | -2.2 | 6e-03 | 1 | 40 x 3 | The component of a membrane consisting of the gene produc |
| 16 | Vitv14g0152E | -1.47 | 7e-03 | 1 | 8 x 17 | |
| 17 | Vitv13g0160E | -1.85 | 7e-03 | 1 | 13 x 1 | Any process that modulates the frequency, rate or extent of ai |
| 18 | Vitv04g0130C | -0.62 | 8e-03 | 1 | 11 x 22 | Catalysis of a biochemical reaction at physiological temperat |
| 19 | Vitv10g00944 | -1.26 | 8e-03 | 1 | 24 x 1 | Catalysis of the reaction: N-acetyl-D-glucosamine + ATP = f |
| 20 | Vitv00g0104E | -1.01 | 8e-03 | 1 | 18 x 18 | |



Differentially expressed gene sets

| Rank | GSZ | p-value | #all | Geneset |
|-----------------------|-------|---------|------|--|
| <i>Overexpressed</i> | | | | |
| 1 | 6.97 | 0e+00 | 18 | Energy mEtragsynBiosynPheosynthesisproteins proteins |
| 2 | 6.69 | 0e+00 | 18 | PhotosynPheosynthesisproteins proteins |
| 3 | 5.4 | 0e+00 | 47 | TransportCaraportCatalportTransportation carriers |
| 4 | 4.92 | 0e+00 | 38 | PhotosynPheosynthesis |
| 5 | 4.68 | 0e+00 | 217 | Cell motileCell RegulationRegulation of cytoskeleton |
| 6 | 4.35 | 0e+00 | 211 | RibosomeRibosome |
| 7 | 4.17 | 0e+00 | 134 | HormoneHormone signaling signaling |
| 8 | 4.16 | 0e+00 | 247 | TranslationTranslationRibosomeRibosome |
| 9 | 4.14 | 0e+00 | 11 | Transcriptiontranscription GRFs - GRF |
| 10 | 3.68 | 3e-04 | 78 | Energy mEtragsynBiosynPheosynthesis |
| 11 | 3.48 | 7e-04 | 144 | RibosomeRibosomeEukaryotes |
| 12 | 3.46 | 8e-04 | 10 | PhotosynPheosynthesis PhotosynPhotosynPhotosynPhotosyn |
| 13 | 3.41 | 9e-04 | 75 | Mitochondrialtranscription and translation factors |
| 14 | 3.36 | 1e-03 | 80 | CytoskeletonMicrotubules |
| 15 | 3.21 | 1e-03 | 66 | ExosomeExosomeExosomeExosomeExosomeExosome |
| 16 | 3.13 | 2e-03 | 62 | RibosomeRibosomeRibosomeRibosomeRibosomeRibosome |
| 17 | 3.12 | 2e-03 | 75 | TranslationTranslationRibosomeRibosomeRibosomeRibosome |
| 18 | 2.94 | 4e-03 | 97 | RibosomeRibosomeArchaea |
| 19 | 2.88 | 5e-03 | 41 | Porphyrimetabolism |
| 20 | 2.86 | 5e-03 | 31 | ChromosomeChromosomeChromosomeChromosomeChromosome |
| <i>Underexpressed</i> | | | | |
| 1 | -7.58 | 0e+00 | 48 | Transcriptiontranscription WRKY - WRKY |
| 2 | -6.84 | 0e+00 | 162 | Plant spePlant signaling signalingPlant signalingPlant signaling |
| 3 | -5.91 | 0e+00 | 153 | Plant-pathogenpathogeninteraction |
| 4 | -5.45 | 0e+00 | 49 | Transcriptiontranscription NACs - NAC |
| 5 | -5.01 | 0e+00 | 26 | FlavonoidFlavonoidbiosynthesis |
| 6 | -4.8 | 0e+00 | 11 | BiosynthesisBiosynthesisBiosynthesisBiosynthesisBiosynthesis |
| 7 | -4.58 | 0e+00 | 45 | GalactoseGalactosemetabolism |
| 8 | -4.38 | 0e+00 | 73 | Transcriptiontranscription EREBP2 EREBP |
| 9 | -4.28 | 0e+00 | 56 | HormoneHormone signaling signaling signaling |
| 10 | -4.16 | 0e+00 | 92 | Lipid metabolismmetabolismmetabolismmetabolismmetabolism |
| 11 | -4.13 | 0e+00 | 140 | HormoneHormone signaling signaling signaling |
| 12 | -3.65 | 3e-04 | 77 | CarbohydrateCarbohydrateGalactoseGalactosemetabolism |
| 13 | -3.6 | 4e-04 | 58 | Other amOther ammetabolismmetabolismmetabolismmetabolism |
| 14 | -3.56 | 5e-04 | 77 | Pores ionPores ionPores ionPores ionPores ion |
| 15 | -3.4 | 9e-04 | 29 | CarotenoidCarotenoidbiosynthesis |
| 16 | -3.26 | 1e-03 | 96 | TransportTransportTransportTransportTransport |
| 17 | -3.18 | 2e-03 | 64 | Transcriptiontranscription Othertranscription factors |
| 18 | -3.03 | 2e-03 | 10 | Linoleic acidmetabolism |
| 19 | -3 | 3e-03 | 28 | Transcriptiontranscription Basictranscription factors |
| 20 | -2.92 | 4e-03 | 111 | HormoneHormone signaling signaling signaling |

