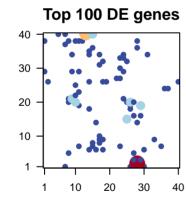
Sangio_acclim_r3

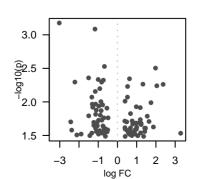
Global Summary

%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> = 0.48 <fdr> = 1

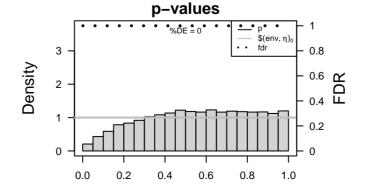
Portrait 40 30 20 10 1 10 20 30 40





Differentially expressed genes

| Rank ID | | log(FC) fdr p-value | | Meta | Description gene | Rar | | | |
|----------------------------|--------------------------------|------------------------|----------------|------|---------------------|--|----------------------------|--|--|
| Overexpressed Ove | | | | | | | | | |
| 1 | Vitvi15g01618 | 1.98 | 0.003 | 1 | 13 x 40 | Catalysis of the transfer of a nucleotidyl group to a reactant. | 1 | | |
| ż | Vitvi14q01003 | 0.62 | 0.005 | 1 | 14 x 34 | The contents of a cell excluding the plasma membrane and n | ż | | |
| 3 | Vitvi18g00711 | 1.32 | 0.005 | 1 | 7 x 40 | A transcription coregulator activity that represses or decrease | 3 | | |
| 4 | Vitvi11g01513 | 2.37 | 0.005 | 1 | 1 x 38 | Binding to ATP, adenosine 5'-triphosphate, a universally impo | 4 | | |
| 5 | Vitvi15q01667 | 2.05 | 0.006 | 1 | 8 x 20 | Binding to ADP, adenosine 5'-diphosphate. | 5 | | |
| 6 | Vitvi17g00240 | 0.53 | 0.006 | 1 | 9 x 29 | The component of the peroxisomal membrane consisting of the | 5 6 | | |
| 7 | Vitvi16g00898 | 0.52 | 0.008 | 1 | 23 x 27 | The formation of a protein dimer, a macromolecular structure | 7 | | |
| 8 | Vitvi04g00582 | 0.39 | 0.010 | 1 | 11 x 23 | Binding to a carbohydrate, which includes monosaccharides, | 8 | | |
| 9 | Vitvi10g00986 | 1.74 | 0.010 | 1 | 10 x 20 | , | 9 | | |
| 10 | Vitvi04g00156 | 0.98 | 0.012 | 1 | | A membrane-bounded organelle of eukaryotic cells in which | 10 | | |
| 11 | Vitvi18g02361 | 1.19 | 0.012 | 1 | 12 x 38 | Growth of pollen via tip extension of the intine wall. | 11 | | |
| 12 | Vitvi09q01320 | 0.68 | 0.015 | 1 | 18 x 32 | The component of a membrane consisting of the gene produc | 12 | | |
| 13 | Vitvi06g00547 | 1.55 | 0.016 | 1 | 12 x 40 | Catalysis of the hydrolysis of internal, alpha–peptide bonds in | 13 | | |
| 14 | Vitvi12g00766 | 1.19 | 0.018 | 1 | 28 x 38 | Catalysis of the hydrolysis of internal, alpha–peptide bonds in | 14 | | |
| 15 | Vitvi19g00549 | 0.76 | 0.019 | 1 | 25 x 32 | The contents of a cell excluding the plasma membrane and n | 15 | | |
| 16 | Vitvi02g00425 | 0.38 | 0.019 | 1 | 22 x 27 | A membrane-bounded organelle of eukaryotic cells in which | 16 | | |
| 17 | Vitvi01g00088 | 1.64 | 0.020 | 1 | 13 x 40 | Binding to ADP, adenosine 5'-diphosphate. | 17 | | |
| 18 | Vitvi16g01510 | 0.48 | 0.020 | 1 | 14 x 35 | The component of a membrane consisting of the gene produc | 18 | | |
| 19 | Vitvi19g00587 | 1.14 | 0.020 | 1 | 9 x 21 | The component of a membrane consisting of the gene produc | 19 | | |
| 20 | Vitvi10g00316 | 0.96 | 0.021 | 1 | 8 x 21 | | 20 | | |
| | = | | | • | | | 20 | | |
| Underexpressed | | | | | | | Unde | | |
| 1 | Vitvi18g01129 | -3.03 | 7e-04 | 1 | 29 x 1 | Catalysis of the transfer of a group, e.g. a methyl group, glyco | 1 | | |
| 2 | Vitvi15g00696 | -1.17 | 8e-04 | 1 | 18 x 9 | A lipid bilayer along with all the proteins and protein complexe | 2 | | |
| 3 | Vitvi08g01730 | -0.68 | 3e-03 | 1 | 17 x 8 | A membrane-bounded organelle of eukaryotic cells in which | 3 | | |
| 2 3 4 5 6 7 | Vitvi03g00514 | -1.5 | 4e-03 | 1 | 26 x 1 | The contents of a cell excluding the plasma membrane and n | 2 3 4 5 6 7 | | |
| 5 | Vitvi04g00540 | -1 | 5e-03 | 1 | 15 x 8 | | 5 | | |
| 6 | Vitvi09g01491 | -0.73 | 5e-03 | 1 | 26 x 20 | The component of the mitochondrial inner membrane consisti | <u>6</u> | | |
| (| Vitvi19g00557 | -2.22 | 5e-03 | 1 | 37 x 24 | The chemical reactions and pathways involving carbohydrate: | (| | |
| 8 | Vitvi07g02059 | -0.83 | 5e-03 | 1 | 28 x 2 | C-4-1 | 8 | | |
| 9 | Vitvi12g00319 | -0.92 | 6e-03 | 1 | 29 x 19 | Catalysis of the reaction: a protein with reduced sulfide group | 9 | | |
| 10 11 | Vitvi09g01488 Vitvi14g00002 | -1.16 -1.33 | 7e-03 9e-03 | 1 | 16 x 6 28 x 1 | | 10 11 | | |
| 12 | Vitvi03g00454 | -0.86 | 1e-02 | 1 | 33 x 9 | A membrane-bounded organelle of eukaryotic cells in which | 12 | | |
| 13 | Vitvi14g02653 | -1.14 | 1e-02 | 1 | 28 x 2 | The chemical reactions and pathways involving carbohydrate: | 13 | | |
| 14 | Vitvi18g02741 | -1.31 | 1e-02 | 1 | 27 x 20 | Binding to a heme, a compound composed of iron complexed | 14 | | |
| 15 | Vitvi14g01696 | -0.77 | 1e-02 | 1 | 30 x 6 | The component of a membrane consisting of the gene produc | 15 | | |
| 16 | Vitvi05g01498 | -0.97 | 1e-02 | 1 | 18 x 6 | and gone productions are a second productions and gone productions are a second productions and gone productions are a second productions are a second productions and gone productions are a second production and a second production are a second production and a second production are a s | 16 | | |
| 17 | Vitvi08g00669 | -1.29 | 1e-02 | 1 | 11 x 7 | | 17 | | |
| 18 | Vitvi07g01114 | -0.55 | 1e-02 | 1 | 27 x 16 | Binding to a nucleic acid. | 18 | | |
| 19 | Vitvi01g00084 | -1.1 | 1e-02 | 1 | 28 x 2 | - | 19 | | |
| 20 | Vitvi14g01989 | -0.85 | 1e-02 | 1 | | The action of a molecule that contributes to the structural inte | 20 | | |
| _ | | | | | | | - | | |



Differentially expressed gene sets

| | Rank | GSZ | p-value | #all | Geneset |
|-----|----------|---------|---------|------|--|
| | Overexp | ressed | | | |
| | 1 | 3.77 | 1e-04 | 32 | Circadian@nytholinan phythtm - plant |
| n | ż | 3.35 | 1e-03 | 51 | Plant spe@lfansispredifig signiedardian@hydrolian rhythm |
| se | 3 | 3.27 | 1e-03 | 12 | Channel - Channie Inu Clayotiden ugate otidah agratebi (Clinta) inel (CNG) |
| oc | 4 | 3.22 | 1e-03 | 129 | Enzyme -E8:22/n0elyeo3s2/la@elycosylases |
| | 5 | 3.12 | 2e-03 | 111 | Transporterarastaturger-d?otalegs-ca?tottets 94t 66 to 94 |
| tł | 6 | 2.91 | 4e-03 | 18 | Photosyn Plecules y rathlesis a proteins a proteins |
| е | 7 | 2.9 | 4e-03 | 100 | Plant spellfantsgrædifig sigfilaling defilelingemelentelopment |
| 6, | 8 | 2.81 | 6e-03 | 110 | Ubiquitin sylvatentin-sylvatenau-buhith Raudo-dining Birtge Engler type E3 |
| | 9 | 2.75 | 7e-03 | 26 | Flavonoid Flavos y rotinesis |
| h | Ĭ0 | 2.69 | 8e-03 | 18 | Transcription factipition factoris - ARF |
| | 11 | 2.69 | 8e-03 | 18 | Energy m Etæbrglýsm eta Blotistors yn Plecsios symtheres às paroteims a proteins |
| uc | 12 | 2.68 | 8e-03 | 31 | Chromos@heoarrossassaciatedssacrtisited-p@eeiassile@eing silencing |
| in | 13 | 2.63 | 1e-02 | 10 | PeptidaseRepridaseksians in Hibitohs A1F are psi A family |
| in | 14 | 2.59 | 1e-02 | 62 | RibosomeRitiogenessIsiog@@@spiartidleS particles |
| n | 15 | 2.58 | 1e-02 | 223 | Enzyme -E8zlynAetin 3.4n Austiptigdenb pedside duptindas (ssèptidases) |
| h | 16 | 2.53 | 1e-02 | 13 | Cofactors Confections named about some tabolism et a Bolism in e Thick a biolism et a bolism |
| | 17 | 2.38 | 2e-02 | 11 | Transcription faction factoris - GRF |
| uc | 18 | 2.37 | 2e-02 | 26 | Sphingoli Siphine dalipoid smetabolism |
| uc | 19 | 2.37 | 2e-02 | 217 | Cell motilitigell in et julyation regulation regutos kelleton |
| | 20 | 2.3 | 2e-02 | 10 | Transcription factoristion factors GC 2C2-CO |
| | Underex | pressed | | | |
| 00 | 1 | -5.77 | 0e+00 | 73 | Transcription factions and Transcription factors |
| xε | ż | -5.71 | 0e+00 | 45 | Galactos@aletatbsesmetabolism |
| h | 3 | -5.7 | 0e+00 | 211 | RibosomeRibosome |
| n | 4 | -5.34 | 0e+00 | 247 | Translatio Tran Ribtiso me Ribosome |
| | 5 | -5.28 | 0e+00 | 144 | RibosomeRib EsukannyoteEsukaryotes |
| sti | 6 | -4.96 | 0e+00 | 140 | Hormonelskingmanding signitalijhene sitynyading signaling |
| e: | 7 | -4.58 | 0e+00 | 49 | TranscriptToanfactipition MacCors - NAC |
| | 8 | -3.83 | 8e-05 | 64 | TranscriptToanfactipition CatherstranCathreptionanfactipition factors |
| ıp | 9_ | -3.52 | 6e-04 | 97 | RibosomeRib Aschaea Archaea |
| | 10 | -3.42 | 9e-04 | 77 | Cysteine and Cysterieth and magnification is metabolism |
| | 11 | -3.35 | 1e-03 | 77 | CarbohydCateborleytdbateismmetaGaliasotoseGraletatboeismmetabolism |
| h · | 12 | -3.17 | 2e-03 | 26 | Transcription faction (a)2tdite G2-like |
| e: | 13 | -3.08 | 2e-03 | 11 | BiosynthetsiessylnateesisdalingenetataartysmetalabBl/astriosylnatesiesynthesis |

3e-03

3e-03

7e-03

1e-02

1e-02

37

-2.97

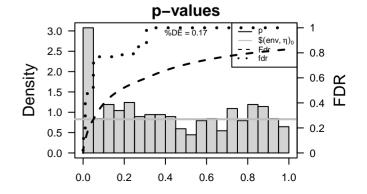
-2.74

-2.62

-2.59

-2.59

-2.47



Chaperor@haperoteim diPutffeimidismidismidiscissomerase

Energy mētadogljsmetalsidisgen inlietalgerismetabolism

Other me@athodisameta&ioligienrea&itiogles reactions

TranscriptToanfactipition #252ors - AS2

TranscriptToenfactiontion (aRtAS) - GRAS

Chaperon@hapts@@ae HSP20