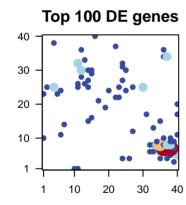
Sangio_accfreeze_r1

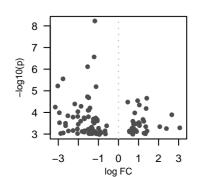
Global Summary

%DE = 0.27# genes with fdr < 0.2 = 196 (82 + /114 -)# genes with fdr < 0.1 = 19 (5 + /14 -)# genes with fdr < 0.05 = 5 (0 + / 5 -)# genes with fdr < 0.01 = 2 (0 + /2 -)

<FC> = 0< p-value > = 0.26< fdr > = 0.73

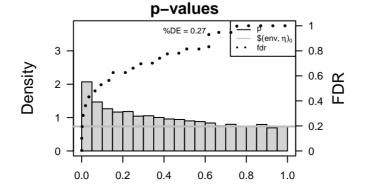
Portrait 40 30 20 10 -10 20 30





Differentially expressed genes

| Rank ID | | log(F | FC) p–va | fdr llue | Meta | Description gene | Rank | GSZ | p-value | #all | Geneset | | |
|---------------|---------------|-------|-------------|-------------|---------|--|--------|---------------|---------|------|--|--|--|
| Overexpressed | | | | | | | | Overexpressed | | | | | |
| 1 | Vitvi09g00149 | 1.41 | 2e-05 | 0.07 | 15 x 30 | Binding to ATP, adenosine 5'-triphosphate, a universally impo | 1 | 6.16 | 0e+00 | 62 | RibosomeRitiosemesIsiog@008spartisIeS particles | | |
| 2 | Vitvi10g01122 | 0.95 | 3e-05 | 0.07 | 11 x 32 | | 2 | 5.84 | 0e+00 | 116 | RibosomeRitiogenesisieg@nes660S Pasticl@S particles | | |
| 3 | Vitvi13g00010 | 0.46 | 3e-05 | 0.07 | 17 x 21 | Binding to a metal ion. | 3 | 5.56 | 0e+00 | 140 | Hormonelstigmating sigitalijitegne stigmating signaling | | |
| 4 | Vitvi02g00954 | 1.04 | 5e-05 | 0.07 | 12 x 30 | Binding to ATP, adenosine 5'-triphosphate, a universally impo | 4 | 5.25 | 0e+00 | 75 | Translatio Tranklibiosom Ribiosom Enission Enissis yot Esukaryotes | | |
| 5 | Vitvi17g00319 | 1.38 | 7e-05 | 0.09 | 2 x 25 | | 5 | 5.07 | 0e+00 | 64 | RibosomeRittiogenessIsiongenessisyonessukaryotes | | |
| 6 | Vitvi12g02175 | 0.81 | 1e-04 | 0.13 | 15 x 29 | A membrane-bounded organelle of eukaryotic cells in which | 6 | 5.03 | 0e+00 | 73 | Transcription faction fall to EREBP | | |
| 7 | Vitvi08g02220 | 2.66 | 1e-04 | 0.13 | 1 x 10 | The component of a membrane consisting of the gene produc | 7 | 4.75 | 0e+00 | 144 | RibosomeRib EsukaneyoteEsukaryotes | | |
| 8 | Vitvi10g00937 | 1.22 | 2e-04 | 0.13 | 19 x 19 | Binds to and increases the activity of a GTPase, an enzyme t | 8 | 4.69 | 0e+00 | 64 | TranscriptToanfactipition CattlerstranCathieptioanfactipition factors | | |
| 9 | Vitvi01g01055 | 0.72 | 3e-04 | 0.13 | 27 x 12 | Binding to ATP, adenosine 5'-triphosphate, a universally impo | 9 | 4.57 | 0e+00 | 151 | RNA polyRini Aupellyrayestesen II system | | |
| 10 | Vitvi18g01090 | 1.26 | 3e-04 | 0.13 | 12 x 28 | The initial step of transcription, consisting of the assembly of | 10 | 4.35 | 0e+00 | 49 | TranscriptToanfactipttion MACOrs - NAC | | |
| 11 | Vitvi14g01895 | 1.01 | 3e-04 | 0.13 | 27 x 25 | Catalysis of a biochemical reaction at physiological temperatu | 11 | 3.91 | 4e-05 | 48 | TranscriptToanfactipition Ya/RIS/S - WRKY | | |
| 12 | Vitvi00g00533 | 1.04 | 3e-04 | 0.13 | 4 x 25 | | 12 | 3.74 | 1e-04 | 165 | TranscriptToans@ipiticeoscopeiceosome | | |
| 13 | Vitvi10g02178 | 1.04 | 3e-04 | 0.13 | 4 x 25 | Functions in the initiation of ribosome-mediated translation of | 13 | 3.63 | 3e-04 | 126 | TranslatioTranStatiflotranSphiAt transport | | |
| 14 | Vitvi15g00772 | 0.85 | 3e-04 | 0.13 | 13 x 26 | Binding to an RNA molecule or a portion thereof. | 14 | 3.26 | 1e-03 | 115 | Enzyme -E8:26/nAe:tin@:6nAe:tidga.om/yalcideanhydrides | | |
| 15 | Vitvi04g00279 | 0.75 | 4e-04 | 0.13 | 11 x 26 | A membrane-bounded organelle of eukaryotic cells in which | 15 | 3.25 | 1e-03 | 99 | mRNA sumviRiNanserpeilhawaye pathway | | |
| 16 | Vitvi04g01201 | | 4e-04 | 0.17 | 12 x 36 | The contents of a cell excluding the plasma membrane and n | 16 | 3.2 | 1e-03 | 81 | Translatio Transl Billoh sum Rinanserpetihanaye pathway | | |
| 17 | Vitvi01g00216 | 1.36 | 5e-04 | 0.17 | 14 x 27 | | 17 | 3.15 | 2e-03 | 36 | RibosomeRitiogenesisieg@neesis0S Pastidl@S particles | | |
| 18 | Vitvi14g01530 | 2.06 | 5e-04 | 0.17 | 14 x 30 | The component of a membrane consisting of the gene produc | 18 | 3.15 | 2e-03 | 67 | Replication | | |
| 19 | Vitvi19g00111 | 3.06 | 5e-04 | 0.17 | 6 x 11 | | 19 | 3.05 | 2e-03 | 85 | Nucleocytolpideoroiytonalasproid transport | | |
| 20 | Vitvi08g00187 | 0.67 | 5e-04 | 0.17 | 12 x 30 | The component of a membrane consisting of the gene produc | 20 | 3.02 | 3e-03 | 128 | Ubiquitin bijostopintin-Spisopen Rinognofilosoftintge fürfoger type E3 | | |
| Und | erexpressed | | | | | | Undere | xpressed | 1 | | | | |
| 1 | Vitvi05g00420 | _1 18 | 6e-09 | 0.004 | 23 x 22 | Any process involved in the maintenance of an internal steady | 1 | • | | 47 | Transport@irarastatooter-datastego+tTeterospoortoelerideren carriers | | |
| 2 | Vitvi10g00844 | | 3e-07 | 0.007 | 14 x 15 | | 2 | -14.74 | | 18 | Energy metæbrglismetæBbtisonsyn@hexsiossymtleresæsparoteimsa protein: | | |
| 3 | Vitvi12g00905 | | 8e-07 | 0.025 | 24 x 4 | Catalysis of the oxidation of ubiquinol by diverting electrons fr | 3 | -14.49 | | 18 | Photosyn Priessies syrathlesis a-paroteims a proteins | | |
| 4 | Vitvi18g02574 | | 3e-06 | 0.025 | 40 x 5 | Catalysis of a biochemical reaction at physiological temperatu | 4 | -12.24 | 0 | 78 | Energy metæboglijsmmetælebblistonsyntPhecosiosynthesis | | |
| 5 | Vitvi07g02608 | | 6e-06 | 0.025 | 38 x 7 | Catalysis of a biochemical reaction at physiological temperatu | 5 | -11.84 | 0 | 38 | Photosyn tPleasis synthesis | | |
| 6 | Vitvi05g01091 | -1.12 | 6e-06 | 0.052 | 35 x 15 | The contents of a cell excluding the plasma membrane and n | 6 | -9.2 | 0 | 10 | Photosyn Phesiosprotheis is Photeins ys Pelnoto(\$750@ncthl(P7500)vthalo) rop | | |
| 7 | Vitvi00g00770 | -1.54 | 2e-05 | 0.052 | 36 x 7 | | 7 | -8.33 | 0 | 26 | Flavonoid Flavosynttituelsies synthesis | | |
| 8 | Vitvi10g02218 | -1.54 | 2e-05 | 0.052 | 36 x 7 | The formation of a protein dimer, a macromolecular structure | 8 | -6.78 | 0 | 40 | Transport Tsastaport Systatkoid Ttaybatkoid parthetiang pathway | | |
| 9 | Vitvi14g01339 | -1.48 | 2e-05 | 0.052 | 34 x 8 | Catalysis of an oxidation-reduction (redox) reaction, a reversi | 9 | -6.21 | 0 | 80 | Cytoskele@ytoskAeletotubul\eisrotubulles | | |
| 10 | Vitvi04g01902 | -2.18 | 4e-05 | 0.073 | 37 x 8 | Binding to a protein or a protein-containing complex to assist | 10 | -6.18 | 0 | 57 | Glyoxylat . € byroxlydiataer broxlytbitea mbnextaybatilës mn etabolism | | |
| 11 | Vitvi00g00610 | | 5e-05 | 0.073 | 33 x 8 | A lipid bilayer along with all the proteins and protein complexe | 11 | -5.26 | 0 | 206 | Cell growtDealingtroolerHithandDatellanthall+ Cell wall | | |
| 12 | Vitvi13g02504 | | 6e-05 | 0.073 | 38 x 7 | | 12 | -5.24 | 0 | 25 | Nitrogen Mittagelismetabolism | | |
| 13 | Vitvi12g00084 | | 6e-05 | 0.073 | 35 x 8 | Catalysis of the transfer of an alkyl or aryl (but not methyl) grc | 13 | -4.93 | 0 | 217 | Cell motilitigell in a citility at ion Resolution regularition regularities regular | | |
| 14 | Vitvi17g00927 | | 8e-05 | 0.094 | 35 x 6 | | 14 | -4.47 | 0 | 13 | Cutin sub Crutine and enriane lained ynathelsis synthesis | | |
| 15 | Vitvi18g01674 | | 8e-05 | 0.111 | 37 x 8 | Catalysis of the hydrolysis of internal, alpha–peptide bonds in | 15 | -4.46 | 0 | 31 | Biosynthe Biosyntheisiosophataricses ophalatry enetadarilytes etabolites | | |
| 16 | Vitvi18g01218 | | 9e-05 | 0.111 | 37 x 7 | Binding to a calcium ion (Ca2+). | 16 | -4.43 | 0 | 51 | Carbon fixation inforacions impleditors y the sinon organisms | | |
| 17 | Vitvi11g00686 | | 1e-04 | 0.111 | 37 x 34 | | 17 | -4.21 | 0 | 24 | CarbohydCateboleyddbateismetaAstiorbateAsodrabateratedraledabateism | | |
| 18 | Vitvi18g00272 | -2.52 | 1e-04 | 0.131 | 39 x 6 | The component of a membrane consisting of the gene produc | 18 | -4.09 | 0 | 72 | Energy mEtadorgliysmmetal6alilsom-fix2atirboon fixation | | |

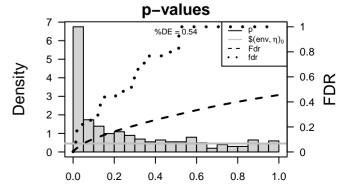


Vitvi04g00112 -2.03 2e-04 0.131 36 x 7 Catalysis of a biochemical reaction at physiological temperature

2e-04 0.131 37 x 6 Catalysis of the reaction:a 2'-deoxyribonucleoside 5'-monopl

Differentially expressed gene sets

| | Overexpi | ressed | | | |
|----------------|-------------|---------|-------|-----|--|
| OC | 1 | 6.16 | 0e+00 | 62 | RibosomeRitiogenessIsieg@008sparti@108 particles |
| | | 5.84 | 0e+00 | 116 | RibosomeRibiogenesisiog@reesis0S PaeticleS particles |
| | 2 | 5.56 | 0e+00 | 140 | Hormonel signating signating signating signaling |
| OC | 4 | 5.25 | 0e+00 | 75 | Translatio Translatiosome Ritiogenes ision Ends is jot Esukaryotes |
| | 5 | 5.07 | 0e+00 | 64 | Ribosom Ribiosen resision en kaisyotesukaryotes |
| h | 6 | 5.03 | 0e+00 | 73 | Transcription faction factors REBP2 EREBP |
| uc | Ž | 4.75 | 0e+00 | 144 | RibosomeRib EsakaneyoteEsukaryotes |
| t | 8 | 4.69 | 0e+00 | 64 | Transcription factors attended to the contraction of the contraction o |
| OC | 9 | 4.57 | 0e+00 | 151 | RNA polyRNAAspellyrsystems II system |
| f t | 10 | 4.35 | 0e+00 | 49 | Transcription factoristion falk ors - NAC |
| itu | 11 | 3.91 | 4e-05 | 48 | TranscriptToenfactipttson ta/Rts/s - WRKY |
| | 12 | 3.74 | 1e-04 | 165 | Transcripticans SiphicerosoSpeticeosome |
| O | 13 | 3.63 | 3e-04 | 126 | Translatio Translati Autran SphiAt transport |
| | 14 | 3.26 | 1e-03 | 115 | Enzyme -E8:26ynAvetin@.6nAactiid.ga.olnyalcideanhydrides |
| h | 15 | 3.25 | 1e-03 | 99 | mRNA summental manage pathway |
| n | 16 | 3.2 | 1e-03 | 81 | Translatio Translatil No A sum VRIMAn serpatilla waye pathway |
| | 17 | 3.15 | 2e-03 | 36 | RibosomeRitiogenessIsieg@reeslk0S Paetidl@S particles |
| uc | 18 | 3.15 | 2e-03 | 67 | Replication |
| | 19 | 3.05 | 2e-03 | 85 | Nucleocythiptaleonigetopalasspoint transport |
| uc | 20 | 3.02 | 3e-03 | 128 | Ubiquitin Ызітелі тін Sjistele n Rist ijn fileg Birtgp firtige r type E3 |
| | Underex | oressed | | | |
| d _i | 1 | -14.86 | 0 | 47 | Transporteransplutger-datarisgort Teteratportocierieron carriers |
| uc | 2 | -14.74 | 0 | 18 | Energy mētæbrglýsmetalBbötossynfPlessissaymtteressasparoteimsa proteins |
| fr | 3 | -14.49 | 0 | 18 | Photosyn@Nexsiossyrathtesrisa-paroteimsa proteins |
| itu | 4 | -12.24 | 0 | 78 | Energy metatorglijsmetalebiotousynthesis |
| itu | 5 6 7 | -11.84 | 0 | 38 | Photosyn (Pleasies synthesis |
| n | 6 | -9.2 | 0 | 10 | Photosyn Phessis sproutleeis is Photoeius ys Pelmoto(\$7)750@nothl (1777/010) dhab) rophyll a) |
| | | -8.33 | 0 | 26 | Flavonoid Flavor syntholesis synthesis |
| e | 8 | -6.78 | 0 | 40 | Transport Transport Stylestenkoid Ttaytgettinid partitentiang pathway |
| si | 9 | -6.21 | 0 | 80 | Cytoskele@ynoskleletotubulkisrotubules |
| st | 10 | -6.18 | 0 | 57 | Glyoxylat |
| XE | 11 | -5.26 | 0 | 206 | Cell grow@calingtrookeatthandOatellanthall+ Cell wall |



Phenylpro/phenojtobiopaynotitolelsis synthesis

-4.08 0

-4.06

63