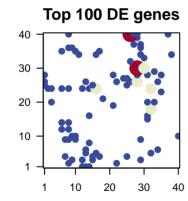
# Riesl\_freeze\_r3

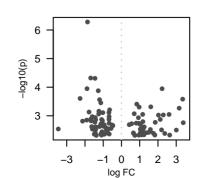
## **Global Summary**

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

# Portrait 40 30 20 10 1 10 20 30 40





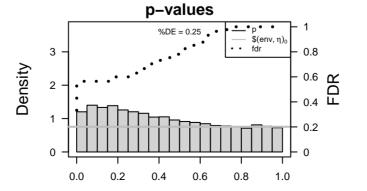
## Differentially expressed genes

log(FC)

Rank

| itai                       | ïD            | .09(.          | p-va           | lue | Meta               | gene   |             |
|----------------------------|---------------|----------------|----------------|-----|--------------------|--|-------------|
| Over                       | expressed     |                |                |     |                    |  | 0           |
| 1                          | Vitvi05g00139 | 2.23           | 1e-04          | 0.4 | 1 x 26             | The chemical reactions and pathways involving carbohydrate:      | 1           |
| 2                          | Vitvi18g03161 | 3.35           | 3e-04          | 0.6 | 8 x 2              |  | 2           |
| 3                          | Vitvi13g00497 | 0.84           | 4e-04          | 0.6 | 16 x 24            |  | 2<br>3      |
| 4                          | Vitvi04g00249 | 1.61           | 5e-04          | 0.6 | 9 x 10             | Binding to ATP, adenosine 5'-triphosphate, a universally impo    | 4           |
| 3<br>4<br>5                | Vitvi08g01164 | 0.97           | 5e-04          | 0.6 | 15 x 25            | Catalysis of the transfer of an acetyl group to an acceptor mol  | 5           |
| 6                          | Vitvi18g00993 | 3.16           | 5e-04          | 0.6 | 12 x 1             | The component of a membrane consisting of the gene produc        | 6           |
| 7                          | Vitvi04g01493 | 0.7            | 8e-04          | 0.6 | 21 x 28            | The chemical reactions and pathways resulting in the breakdo     | 7           |
| 8                          | Vitvi11g01318 | 1.16           | 9e-04          | 0.6 | 17 x 4             | Binding to ATP, adenosine 5'-triphosphate, a universally impo    | 8           |
| 9                          | Vitvi02g01349 | 2.61           | 9e-04          | 0.6 | 7 x 4              | A lipid bilayer along with all the proteins and protein complexe | 9           |
| 10                         | Vitvi01g00803 | 2.29           | 9e-04          | 0.6 | 14 x 1             | The component of a membrane consisting of the gene produc        | Ĭ           |
| 11                         | Vitvi12g00755 | 2.03           | 9e-04          | 0.6 | 34 x 6             | Binding to a zinc ion (Zn).                                      | 1           |
| 12                         | Vitvi01g00591 | 0.93           | 1e-03          | 0.6 | 8 x 14             |  | 1           |
| 13                         | Vitvi02g00096 | 2.13           | 1e-03          | 0.6 | 13 x 6             |  | 1           |
| 14                         | Vitvi19g01985 | 1.17           | 2e-03          | 0.6 | 6 x 14             | The cellular catabolic process in which cells digest parts of th | 1           |
| 15                         | Vitvi04g00527 | 1.85           | 2e-03          | 0.6 | 12 x 3             | Any process that stops, prevents, or reduces the frequency, ra   | 1           |
| 16                         | Vitvi17g01613 | 3.39           | 2e-03          | 0.6 | 8 x 9              | Binds to and stops, prevents or reduces the activity of an end   | 1           |
| 17                         | Vitvi01g01824 | 0.81           | 2e-03          | 0.6 | 14 x 8             | A transcription coregulator activity that activates or increases | 1           |
| 18                         | Vitvi07g01242 | 0.95           | 2e-03          | 0.6 | 8 x 24             | Catalysis of a biochemical reaction at physiological temperatu   | 1           |
| 19                         | Vitvi15g00558 | 0.56           | 2e-03          | 0.6 | 12 x 24            |  | 1           |
| 20                         | Vitvi13g00792 | 1.03           | 2e-03          | 0.6 | 16 x 5             | The chemical reactions and pathways involving carbohydrates      | 2           |
| Unde                       | erexpressed   |                |                |     |                    |  | U           |
|                            | Vitvi14g01279 | 4.00           | F- 07          | 0.0 | 4440               | Organized structure of distinctive morphology and function, by   |             |
| 1                          | Vitvi13g01837 | -1.86<br>-1.69 | 5e-07<br>5e-05 | 0.3 | 14 x 16<br>27 x 30 | Binding to ATP, adenosine 5'–triphosphate, a universally impo    | 1           |
| 2                          | Vitvi13g01557 | -1.45          | 5e-05          | 0.3 | 10 x 35            | The chemical reactions and pathways resulting in the formatic    | 2<br>3      |
| 1                          | Vitvi07g01358 | -1.43          | 1e-04          | 0.4 | 26 x 40            | The component of a membrane consisting of the gene produc        | 4           |
| 5                          | Vitvi03q00324 | -1.27          | 1e-04          | 0.6 | 8 x 36             | The compensation a monitorane consisting of the gene product     | 5           |
| 2<br>3<br>4<br>5<br>6<br>7 | Vitvi15g00789 | -2.27          | 2e-04          | 0.6 | 30 x 30            | Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N, (   | 5<br>6<br>7 |
| 7                          | Vitvi10g00194 | -1.2           | 3e-04          | 0.6 | 29 x 30            | The contents of a cell excluding the plasma membrane and n       | 7           |
| 8                          | Vitvi08g00691 | -1.13          | 4e-04          | 0.6 | 17 x 35            | Binding to a metal ion.  | 8           |
| 9                          | Vitvi10g00326 | -0.65          | 6e-04          | 0.6 | 31 x 16            |  | 9           |
| 10                         | Vitvi16g00984 | -1.24          | 7e-04          | 0.6 | 28 x 26            | The component of a membrane consisting of the gene produc        | Ĭ           |
| 11                         | Vitvi08g02413 | -1.78          | 7e-04          | 0.6 | 28 x 39            | The component of a membrane consisting of the gene produc        | 1           |
| 12                         | Vitvi03g00647 | -0.69          | 8e-04          | 0.6 | 21 x 19            | A lipid bilayer along with all the proteins and protein complexe | 1           |
| 13                         | Vitvi13g00568 | -1.02          | 8e-04          | 0.6 | 28 x 26            | The action of a molecule that contributes to the structural inte | 1           |
| 14                         | Vitvi16g01055 | -1.25          | 9e-04          | 0.6 | 26 x 32            | The chemical reactions and pathways involving lipids, compo      | 1           |
| 15                         | Vitvi18g00060 | -0.68          | 1e-03          | 0.6 | 26 x 26            | The component of a membrane consisting of the gene produc        | 1           |
| 16                         | Vitvi03g00016 | -1.6           | 1e-03          | 0.6 | 22 x 2             | Binding to a metal ion.  | 1           |
| 17                         | Vitvi08g01786 | -1.44          | 1e-03          | 0.6 | 33 x 29            | Binding to a protein.  | 1           |
| 18                         | Vitvi14g00163 | -1.68          | 1e-03          | 0.6 | 29 x 37            | Binding to a metal ion.  | _1          |
| 19                         | Vitvi14g01031 | -0.68          | 1e-03          | 0.6 | 32 x 18            | Any process that stops or reduces the activity of an enzyme.     | 1           |
| 20                         | Vitvi12g01971 | -1.09          | 1e-03          | 0.6 | 22 x 26            |  | 2           |

Description



## Differentially expressed gene sets

| Rank GSZ p-val | ue #all Geneset |
|----------------|-----------------|
|----------------|-----------------|

| 1  |           | Overex   | pressed   |       |     |  |
|--|-----------|----------|-----------|-------|-----|--|
| 2 5.27 0e+00 140 Hormonelskymating sigftbijfrep Eithytkling signaling 3 4.84 0e+00 73 Transcriptfoar facipitos AB20EREBP2 EREBP 2 EREBP 64 4.74 0e+00 77 CarbohytklarbohytklarisbijestbilismenteGolaciosos-Galetatoelismetabolism 65 3.94 4e-05 49 Transcriptfoar facipitos NAt0rs – NAC 65 3.74 1e-04 28 Transcriptfoar facipitos Nat0rs – NAC 66 3.74 1e-04 28 Transcriptfoar facipitos Restarts-eu-Besicitipazirip Eziliper (bZIP) 65 8 3.66 3e-04 11 BiosyntheBiosyntheosiscity protestartiyismetabilismic Signaturi (bZIP) 65 8 9 3.57 4e-04 35 Mitophagly/Resphere (bZIP) 75 8 8 3.66 3e-04 11 BiosyntheBiosyntheosiscity protestartiyismetabilismic factors 11 3.4 9e-04 92 Lipid metahpitismetabilismetabilismic factorismic factors 11 3.4 9e-04 92 Lipid metahpitismetabilismetabilismic factorismic factors 11 3.4 9e-04 92 Lipid metahpitismetabilismic factorismic factors 11 3.4 1e-03 13 Peptidas-Resphidasibilismic infiliations of Expanylario fareignain family 13 3.17 2e-03 43 Transcriptfoar factorismic BZIPs – BZIP 14 3.11 2e-03 25 Lysine delyvaidatidogradation 14 Energy mEtahpijsmetabilismetabolism 16 3.02 3e-03 20 Transport Tadopton BZIPs – BZIP 14 3.11 2e-03 25 Lysine delyvaidatidogradation 16 3.02 3e-03 20 Protein – Pattistpidismetabilismetabolisme 17 3.01 3e-03 20 Protein – Pattistpidismetabilismetabolism 18 2.99 3e-03 309 Enzyme - EBZIPshiphiaghaghatosynatrismiproteitra proteins 19 2.9 4e-03 29 Other am@theciatsimetabilismetabolismetabolisme 19 2.9 4e-03 29 Other am@theciatsimetabilismetabilismetabolismetabolisme 20 2.84 5e-03 79 TransportTarastproper-Rationger- | <b>B!</b> | 1        | 6.42      | 0e+00 | 45  | Galactos@alatatbo@smetabolism  |
| 3  |           |          | 5.27      | 0e+00 | 140 | Hormonel signating signating signaling   |
| Carbohyc@athofheathalesmetaGollactoos@anletatbollsm   S  |           |          | 4.84      | 0e+00 | 73  | Transcription faction ARCIDESREBP2 EREBP   |
| S  | OC        |          |           |       | 77  |  |
| 1  | 0         |          |           |       |     | Transcriptionniaction hactors - NAC  |
|  |           |          |           |       |     | · · · · · ·  |
| Sec.      |           |          |           |       |     |  |
|  |           |          |           |       |     | ÿ ÿ  |
| 10   3.52   6e-04   64   Transcriptomactipation Catherstractitrispation factors   11   3.4   9e-04   92   Lipid metalpitismestabilismost inflibitions of Expression factors   12   3.24   1e-03   13   Peptidas-designatidashibitions inflibitions of Expression factors   13   3.17   2e-03   43   Transcription Biziditism   |           |          |           |       |     |  |
| 1  |           |          |           |       |     |  |
| 12   3.24   1e-03   13   Peptidasdesemidaslabis tands in lift britohys C Figuralspaid Tapraligrain family   13   3.17   2e-03   43   Transcript@rartactpiscon BicIdens - BZIP   Lysine delgravitation gradation   15   3.1   2e-03   25   Lysine delgravitation gradation   15   3.1   2e-03   24   Energy mitrataglysmetabiditagen histotyeinsmetabolism   16   3.02   3e-03   20   Transport landspatiation/stractaßelgratation/egulatophagy   17   3.01   3e-03   20   Protein - Pautaphagobstophagoreadrom/proteinsm proteins   19   2.9   4e-03   29   Other am/litheociatis inne tabidismentabolism   19   2.9   4e-03   29   Other am/litheociatis inne tabidismentabolism elevation   19   2.9   4e-03   29   Other am/litheociatis inne tabidismentabolism   10   2.9   Transport@rarastatus.es   20   2.84   5e-03   79   Transport@rarastatus.es   20   2.84   20   247   Translationamentabloscome   20   2.84   20   247   Translationamentabloscome   20   2.84   2.94   2.95   2   |           |          |           |       |     |  |
| 13   3.17   2e-03   43   Transcripfloerfactiption BizitiPrs - BZIP   Lysine deltyradiatidegradation     14   3.11   2e-03   25   Lysine deltyradiatidegradation     15   3.1   2e-03   24   Energy mētatplysmetabidistagen histobjerismetabolism     16   3.02   3e-03   20   Transport Bandsputatradistrateabelistatien Regulatituphofguutophagy     17   3.01   3e-03   20   Protein - Pkuttaphaghstuphaggosatium/proteitum proteins     18   2.99   3e-03   309   Enzyme - Eazymheting, ankatiegtumdester bonds     19   2.9   4e-03   29   Other am@thecialsimetabelismetabelismetabolismetab   |           |          |           |       |     |  |
| 14   3.11   2e-03   25   |           |          |           |       |     |  |
| 15   | h         |          |           |       |     | · · · · · ·  |
| 16   3.02   3e-03   20   Transport@adspatetzbidicates8eigutatioRegialettprhetigutophagy     17   3.01   3e-03   20   Protein - Pacitigina-goastuphagoasturin/proteitism proteins     18   2.99   3e-03   309   Enzyme-Eña2yn-keting_on-kastlegisumatisch proteins     19   2.9   4e-03   29   Other am/Otheraistsime tabidismetabelismetabelismetabolis   |           |          |           |       |     |  |
| 17   3.01   3e-03   20   Protein - Platitațina glastrupă gloreatium (proteinium proteinium ta la 2.99   3e-03   309   Enzyme - Eazynfacting), ûn katilegium dister bonds   19   2.9   4e-03   29   Other ami@the cials ime tabidis:metabel   |           |          |           |       |     | 0, 0,  |
| 18   |           |          |           |       |     |  |
| 19   2.9   4e-03   29   Other amf@thecialsimetabidismetaBidismetaBidismetaBidismetabidismet   |           |          |           |       |     |  |
| Processor  |           |          |           |       |     | , , , ,  |
| Underexpressed  Di 1   | ٠.        |          |           |       |     |  |
| 1  | 5.        |          |           |       | 79  | Transporteral appling - Galancia Catalog Catal |
| 2  |           | Undere   | expressed | d     |     |  |
| 8         -6.91         0         97         RibosomeRibAschrae a Archaea           9         -6.41         0         217         Cell molitigle/H Regitulption egitaction ryptobebile tryntos keleton           xx         10         -5.47         0         113         ExosomeEscRacorramaEporaterinal cytobalance (subtractal collaborater cells           xx         11         -5.35         0         66         ExosomeEscRacorrama Eporaterina cytobalance (subtractal certains cert  | bі        |          | -9.73     | 0     | 247 | Translatio <b>Translatisom</b> eRibosome   |
| 8         -6.91         0         97         RibosomeRibAschrae a Archaea           9         -6.41         0         217         Cell molitigle/H Regitulption egitaction ryptobebile tryntos keleton           xx         10         -5.47         0         113         ExosomeEscRacorramaEporaterinal cytobalance (subtractal collaborater cells           xx         11         -5.35         0         66         ExosomeEscRacorrama Eporaterina cytobalance (subtractal certains cert  |           | 2        | -9.67     | 0     | 211 |  |
| 8         -6.91         0         97         RibosomeRibAschrae a Archaea           9         -6.41         0         217         Cell molitigle/H Regitulption egitaction ryptobebile tryntos keleton           xx         10         -5.47         0         113         ExosomeEscRacorramaEporaterinal cytobalance (subtractal collaborater cells           xx         11         -5.35         0         66         ExosomeEscRacorrama Eporaterina cytobalance (subtractal certains cert  | tic       | 3        |           |       |     |  |
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| 8         -6.91         0         97         RibosomeRibAschrae a Archaea           9         -6.41         0         217         Cell molitigle/H Regitulption egitaction ryptobebile tryntos keleton           xx         10         -5.47         0         113         ExosomeEscRacorramaEporaterinal cytobalance (subtractal collaborater cells           xx         11         -5.35         0         66         ExosomeEscRacorrama Eporaterina cytobalance (subtractal certains cert  |           | 5        |           | -     |     |  |
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| e 1 3 -5.28 0 24 ReplicatioRegnitation   |           |          |           |       |     | · ·  |
| DNA repli@bakbimeplication 14 -4.57 0 38 PhotosynPhesicsynthesis 15 -4.48 0 36 DNA repli@bakbimeplication 16 -4.48 0 41 PorphyrinPorphybidismetabolism 17 -4.47 0 219 Cell grow@bakhgrelodetitlan-Obikhdspiel-Cell cycle 18 -4.27 0 10 PhotosynPhesicspunterisis PhotosynSpherich(Prophydria)rophyll a) 19 -4.22 0 40 TransportTispskapor+3TystankoidTlaydeking pathway  |           |          |           | -     |     | ·  |
| は 15 -4.48 0 36 DNA replication 16 -4.48 0 41 Porphyrin Propsiby Dismetabolism 17 -4.47 0 219 Cell grow Desting translation Holder Description H   |           |          |           |       |     |  |
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