**Table 1. 3h UDA vs 0h**

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| --- | --- | --- | --- |
| **ID** | **Gene Product Name** | **log2FC** | **padj** |
| TERG\_01405 | glutathione S-transferase (T. equinum) | 5,791938243 | 8,83E-63 |
| TERG\_04960 | glutathione S-transferase Ure2-like, putative (A. benhamiae) | 5,786880906 | 4,07E-95 |
| TERG\_03078 | cytochrome P450 oxidoreductase OrdA-like, putative (T. verrucosum) | 5,325847532 | 1,48E-73 |
| TERG\_08077 | hypothetical protein | 4,897680892 | 8,92E-84 |
| TERG\_01937 | short chain dehydrogenase (T. tonsurans) | 4,783187046 | 8,10E-84 |
| TERG\_07830 | hypothetical protein | 4,51492024 | 6,64E-50 |
| TERG\_00254 | peroxisomal dehydratase (T. equinum) | 4,48055326 | 6,21E-85 |
| TERG\_00823 | rhamnolipids biosynthesis 3-oxoacyl-[acyl-carrier-protein] reductase (T. equinum) | 4,068203704 | 2,57E-97 |
| TERG\_12530 | 3-ketoacyl-CoA thiolase peroxisomal A (T. tonsurans) | 4,004012088 | 4,55E-70 |
| TERG\_05363 | hypothetical protein | 3,960319577 | 1,29E-45 |
| TERG\_05484 | acyl-CoA dehydrogenase (T. tonsurans) | 3,902028187 | 1,68E-78 |
| TERG\_05347 | epoxide hydrolase, putative (T. verrucosum) | 3,887973709 | 1,03E-32 |
| TERG\_05621 | short chain dehydrogenase/reductase family oxidoreductase, putative (A. benhamiae) | 3,856180068 | 4,58E-62 |
| TERG\_06509 | glutamate synthase (T. tonsurans) | 3,829309979 | 9,70E-49 |
| TERG\_04232 | 2-nitropropane dioxygenase (T. equinum) | 3,797700402 | 5,99E-78 |
| TERG\_07143 | potassium/sodium efflux P-type ATPase, fungal-type | 3,786235981 | 3,39E-65 |
| TERG\_00162 | MFS multidrug transporter, putative (A. benhamiae) | 3,731117013 | 5,12E-48 |
| TERG\_02909 | acyl-CoA oxidase, putative (T. verrucosum) | 3,666432983 | 5,41E-48 |
| TERG\_01512 | mitochondrial tricarboxylate transporter (Ctp), putative (T. verrucosum) | 3,574141341 | 3,83E-71 |
| TERG\_04038 | acyl-CoA dehydrogenase (T. tonsurans) | 3,553511753 | 2,31E-54 |
| TERG\_11928 | hypothetical protein | 3,507335449 | 1,45E-40 |
| TERG\_03008 | zinc-containing alcohol dehydrogenase, putative (A. benhamiae) | 3,485930268 | 1,81E-29 |
| TERG\_02814 | hypothetical protein | 3,449096237 | 3,21E-25 |
| TERG\_03154 | 2-nitropropane dioxygenase (M. gypseum) | 3,433890876 | 2,26E-51 |
| TERG\_03483 | carnitine acetyl transferase (T. tonsurans) | 3,431193821 | 2,05E-60 |
| TERG\_01233 | 3,2-trans-enoyl-CoA isomerase (T. equinum) | 3,266205943 | 2,31E-42 |
| TERG\_02747 | cytochrome P450 alkane hydroxylase (A. benhamiae) | 3,26275898 | 2,31E-54 |
| TERG\_01742 | hypothetical protein | 3,239449519 | 1,38E-50 |
| TERG\_07721 | isopenicillin N-CoA epimerase (T. equinum) | 3,237104527 | 3,93E-40 |
| TERG\_02423 | hypothetical protein | 3,211330857 | 9,10E-44 |
| TERG\_04714 | mitochondrial phosphate carrier protein (T. tonsurans) | 3,173915859 | 2,09E-38 |
| TERG\_04500 | peroxisomal membrane protein Pmp47 (T. tonsurans) | 3,165078315 | 3,43E-49 |
| TERG\_12351 | hypothetical protein | 3,126507564 | 5,58E-42 |
| TERG\_08102 | 3-isopropylmalate dehydrogenase A | 3,096864655 | 1,18E-21 |
| TERG\_02846 | conidial pigment biosynthesis oxidase Arb2/brown2 (T. equinum) | 3,089213197 | 5,79E-10 |
| TERG\_03881 | epoxide hydrolase (T. tonsurans) | 3,054912911 | 1,55E-31 |
| TERG\_01463 | cytochrome c peroxidase (T. tonsurans) | 3,047686922 | 3,72E-34 |
| TERG\_02041 | glutathione S-transferase (T. equinum) | 3,038560427 | 7,60E-22 |
| TERG\_02918 | alkaline phytoceramidase (T. equinum) | 3,013945927 | 1,77E-39 |
| TERG\_04131 | heat shock trehalose synthase, putative (T. verrucosum) | 3,012161791 | 1,17E-25 |
| TERG\_08360 | metallo-beta-lactamase superfamily protein (T. equinum) | 2,990248929 | 1,43E-07 |
| TERG\_07659 | peroxisomal 3-ketoacyl-coA thiolase (Kat1), putative (A. benhamiae) | 2,960021552 | 1,94E-48 |
| TERG\_01784 | oxidoreductase, short-chain dehydrogenase/reductase family, putative (T. verrucosum) | 2,916049499 | 6,64E-50 |
| TERG\_03390 | glutation S-transferase (T. equinum) | 2,912790731 | 9,07E-30 |
| TERG\_07919 | thioesterase family protein (T. verrucosum) | 2,850051748 | 4,62E-40 |
| TERG\_02822 | MFS multidrug transporter, putative (A. benhamiae) | 2,848917463 | 4,56E-19 |
| TERG\_03832 | enoyl-CoA hydratase/isomerase (T. equinum) | 2,846200192 | 1,85E-40 |
| TERG\_03329 | hypothetical protein | 2,812954266 | 1,53E-17 |
| TERG\_00216 | endochitinase (T. equinum) | 2,805840561 | 4,56E-23 |
| TERG\_11539 | 3-oxoacyl-(acyl-carrier-protein) reductase (T. tonsurans) | 2,779996277 | 2,49E-36 |
| TERG\_06155 | phosphotransferase (T. tonsurans) | 2,757507488 | 4,55E-32 |
| TERG\_04389 | carnitinyl-CoA dehydratase (T. tonsurans) | 2,731197979 | 1,14E-36 |
| TERG\_12032 | hypothetical protein | 2,724851094 | 2,09E-17 |
| TERG\_11538 | 3-oxoacyl-(acyl-carrier-protein) reductase (T. tonsurans) | 2,720573757 | 3,93E-40 |
| TERG\_07691 | sterol carrier protein (T. tonsurans) | 2,712861519 | 6,42E-39 |
| TERG\_03305 | C-4 methylsterol oxidase (T. tonsurans) | 2,691405292 | 1,07E-23 |
| TERG\_08050 | acetamidase (T. equinum) | 2,689444241 | 2,94E-23 |
| TERG\_02845 | cercosporin toxin biosynthesis protein (T. equinum) | 2,677371682 | 4,76E-11 |
| TERG\_04765 | MFS transporter, putative (A. benhamiae) | 2,6487544 | 2,22E-27 |
| TERG\_07544 | lipase (T. tonsurans) | 2,644537285 | 1,32E-12 |
| TERG\_01077 | metallo-beta-lactamase domain-containing protein (T. equinum) | 2,624270502 | 3,96E-22 |
| TERG\_02488 | hypothetical protein | 2,609348503 | 1,70E-18 |
| TERG\_00009 | peroxisomal biogenesis factor (T. tonsurans) | 2,608459528 | 1,54E-33 |
| TERG\_00013 | ThiJ/PfpI family protein (A. benhamiae) | 2,605312615 | 1,23E-15 |
| TERG\_02651 | NRPS-like enzyme, putative (A. benhamiae) | 2,599395051 | 1,94E-15 |
| TERG\_04620 | peroxin 20 (T. equinum) | 2,587330083 | 4,55E-32 |
| TERG\_11946 | hypothetical protein | 2,584802402 | 4,23E-21 |
| TERG\_05435 | hypothetical protein | 2,579144672 | 3,73E-10 |
| TERG\_07060 | acyl-CoA thioesterase II | 2,548747487 | 1,38E-31 |
| TERG\_04010 | sporulation protein SPS19 (T. equinum) | 2,542979549 | 5,24E-26 |
| TERG\_05575 | MFS multidrug transporter (T. tonsurans) | 2,529184485 | 2,58E-17 |
| TERG\_11639 | isocitrate lyase | 2,522905484 | 1,01E-26 |
| TERG\_00950 | hypothetical protein | 2,522303854 | 1,89E-27 |
| TERG\_06686 | hypothetical protein | 2,479015325 | 3,93E-33 |
| TERG\_03330 | hypothetical protein | 2,464519447 | 1,89E-14 |
| TERG\_08336 | MFS multidrug transporter, putative (A. benhamiae) | 2,436666311 | 5,38E-22 |
| TERG\_01833 | peroxisomal membrane protein (T. tonsurans) | 2,424095745 | 1,43E-19 |
| TERG\_04837 | thioesterase (T. equinum) | 2,422076155 | 4,01E-22 |
| TERG\_04310 | alcohol dehydrogenase (T. tonsurans) | 2,413046658 | 4,42E-15 |
| TERG\_01270 | AMP dependent ligase (T. tonsurans) | 2,406932929 | 6,09E-21 |
| TERG\_08051 | 3-oxoacyl-(acyl-carrier-protein) reductase (T. tonsurans) | 2,400376876 | 4,09E-28 |
| TERG\_00284 | peroxin 14 (T. tonsurans) | 2,39670563 | 5,89E-31 |
| TERG\_08585 | ankyrin repeat protein (A. benhamiae) | 2,394087079 | 7,94E-06 |
| TERG\_04817 | hypothetical protein | 2,393951503 | 7,75E-17 |
| TERG\_11702 | hypothetical protein | 2,393080853 | 2,60E-23 |
| TERG\_04650 | iron sulfur cluster assembly protein 1, mitochondrial | 2,389298337 | 4,41E-24 |
| TERG\_11638 | isocitrate lyase | 2,378101599 | 3,47E-21 |
| TERG\_01281 | malate synthase, glyoxysomal | 2,377930055 | 1,45E-25 |
| TERG\_08074 | hypothetical protein | 2,370103357 | 1,83E-05 |
| TERG\_11637 | isocitrate lyase | 2,352587005 | 1,27E-19 |
| TERG\_04224 | ABC transporter | 2,33469057 | 1,23E-23 |
| TERG\_03907 | neutral amino acid permease (T. tonsurans) | 2,334318635 | 7,47E-18 |
| TERG\_00575 | F-box domain protein (T. verrucosum) | 2,316135321 | 5,85E-24 |
| TERG\_01986 | Fe-S protein assembly co-chaperone HscB | 2,314424536 | 5,20E-23 |
| TERG\_04753 | 3-isopropylmalate dehydratase, large subunit | 2,288080881 | 4,15E-14 |
| TERG\_01349 | glutathione peroxidase (T. tonsurans) | 2,285751346 | 1,00E-27 |
| TERG\_08321 | hypothetical protein | 2,273197741 | 5,44E-14 |
| TERG\_03231 | cytochrome P450 52A12 (T. tonsurans) | 2,252402227 | 7,72E-18 |
| TERG\_03464 | stress response protein (T. equinum) | 2,250962022 | 5,27E-23 |
| TERG\_06622 | hydrolase (T. tonsurans) | 2,244111752 | 6,18E-21 |
| TERG\_12131 | alcohol dehydrogenase (T. tonsurans) | 2,235327758 | 3,58E-12 |
| TERG\_04074 | hypothetical protein | 2,21354787 | 3,16E-05 |
| TERG\_00836 | QDE-2-interacting protein (M. gypseum) | 2,199078156 | 1,26E-14 |
| TERG\_03983 | HPP family protein (T. verrucosum) | 2,196982961 | 1,00E-17 |
| TERG\_08170 | fatty acid elongase gig30 (T. equinum) | 2,196513479 | 4,29E-14 |
| TERG\_01641 | FK506 suppressor Sfk1 (T. equinum) | 2,174248895 | 2,46E-14 |
| TERG\_03510 | peroxisomal membrane anchor protein, putative (A. benhamiae) | 2,16105967 | 5,89E-23 |
| TERG\_06064 | quinone oxidoreductase (T. equinum) | 2,151672773 | 7,40E-27 |
| TERG\_08781 | hypothetical protein | 2,150704532 | 2,91E-11 |
| TERG\_05562 | 2-hydroxychromene-2-carboxylate isomerase, putative (A. benhamiae) | 2,146721778 | 8,51E-15 |
| TERG\_05551 | hypothetical protein | 2,146471933 | 1,61E-18 |
| TERG\_00176 | hydroxyisourate hydrolase | 2,134979435 | 7,25E-15 |
| TERG\_12282 | glycosyl hydrolase (T. tonsurans) | 2,113073131 | 2,95E-14 |
| TERG\_02533 | aldose 1-epimerase (T. equinum) | 2,104924574 | 3,12E-14 |
| TERG\_12497 | hypothetical protein | 2,097731411 | 6,14E-11 |
| TERG\_06361 | ATP-dependent protease La | 2,076545052 | 8,04E-19 |
| TERG\_00163 | siderochrome-iron transporter, putative (A. benhamiae) | 2,075762557 | 1,55E-12 |
| TERG\_02283 | MFS transporter, putative (T. verrucosum) | 2,071741075 | 1,69E-23 |
| TERG\_04092 | peroxisomal matrix protein importer Pex3 (T. tonsurans) | 2,070958858 | 1,26E-20 |
| TERG\_06177 | mitochondrial carrier protein, putative (T. verrucosum) | 2,069884362 | 3,91E-18 |
| TERG\_03331 | F-box protein (T. equinum) | 2,0396262 | 1,24E-16 |
| TERG\_07331 | integral membrane protein (T. tonsurans) | 2,038661473 | 1,49E-15 |
| TERG\_06494 | hypothetical protein | 2,035962451 | 1,17E-16 |
| TERG\_11541 | hypothetical protein | 2,03028955 | 5,21E-09 |
| TERG\_01754 | oxidoreductase, 2-nitropropane dioxygenase family, putative (A. benhamiae) | 2,026711734 | 6,01E-13 |
| TERG\_05411 | hypothetical protein | 2,025762615 | 9,75E-12 |
| TERG\_08519 | mitochondrial enoyl reductase (T. equinum) | 2,020101426 | 5,43E-17 |
| TERG\_08182 | hypothetical protein | 2,019116942 | 0,005413359 |
| TERG\_07242 | di-trans,poly-cis-decaprenylcistransferase | 2,01648125 | 7,65E-19 |
| TERG\_05244 | hypothetical protein | 2,016107524 | 2,66E-16 |
| TERG\_04598 | NRPS-like enzyme, putative (A. benhamiae) | 2,004703232 | 7,60E-22 |
| TERG\_12098 | DUF1649 domain-containing protein (T. equinum) | 2,003828098 | 2,34E-11 |
| TERG\_08069 | glutathione-disulfide reductase | 2,002068627 | 2,70E-21 |
| TERG\_04422 | NmrA family transcriptional regulator, putative (T. verrucosum) | 1,996018921 | 3,05E-12 |
| TERG\_01936 | COP9 signalosome complex subunit 1 (T. equinum) | 1,97143969 | 2,25E-18 |
| TERG\_01759 | peroxisome assembly protein 10 (T. equinum) | 1,964257214 | 6,94E-16 |
| TERG\_05023 | calcium/proton exchanger | 1,963997531 | 5,06E-11 |
| TERG\_04951 | U-box domain-containing protein (T. equinum) | 1,962582254 | 1,48E-17 |
| TERG\_07224 | hypothetical protein | 1,950507981 | 6,62E-12 |
| TERG\_02842 | 6-hydroxy-D-nicotine oxidase (T. equinum) | 1,949319621 | 5,87E-11 |
| TERG\_05556 | hypothetical protein | 1,93922027 | 1,58E-10 |
| TERG\_08757 | hypothetical protein | 1,936555538 | 3,51E-07 |
| TERG\_00818 | aldehyde dehydrogenase 3B1 (T. equinum) | 1,926580619 | 2,10E-19 |
| TERG\_05622 | uridine/cytidine kinase (T. equinum) | 1,924766077 | 1,98E-14 |
| TERG\_05199 | MFS gliotoxin efflux transporter GliA (T. verrucosum) | 1,923412512 | 6,20E-12 |
| TERG\_06106 | sulfate permease 2 (T. tonsurans) | 1,920467398 | 0,004618244 |
| TERG\_01625 | FMP32 (M. gypseum) | 1,915327678 | 1,78E-19 |
| TERG\_12135 | hypothetical protein | 1,908415119 | 1,46E-09 |
| TERG\_07533 | hypothetical protein | 1,902816869 | 9,26E-14 |
| TERG\_07957 | hypothetical protein | 1,900410053 | 7,76E-13 |
| TERG\_08825 | bZIP transcription factor JlbA/IDI-4 (T. verrucosum) | 1,898968436 | 2,91E-10 |
| TERG\_05044 | epoxide hydrolase, putative (A. benhamiae) | 1,885873274 | 4,90E-09 |
| TERG\_04766 | calcium/proton exchanger | 1,880608207 | 1,92E-18 |
| TERG\_02767 | pyroglutamyl peptidase type I (T. equinum) | 1,879652346 | 7,92E-19 |
| TERG\_01053 | MFS monocarboxylate transporter, putative (T. verrucosum) | 1,878011034 | 1,52E-06 |
| TERG\_08908 | hypothetical protein | 1,877905293 | 8,24E-09 |
| TERG\_02403 | glycolate oxidase, subunit GlcD | 1,872364521 | 1,42E-10 |
| TERG\_07501 | nitrate reductase (T. tonsurans) | 1,86695113 | 8,87E-08 |
| TERG\_01122 | heat shock protein Awh11, putative (A. benhamiae) | 1,859336165 | 0,008237896 |
| TERG\_00616 | potassium/sodium efflux P-type ATPase, fungal-type | 1,85864822 | 6,54E-20 |
| TERG\_00631 | urate oxidase | 1,856791863 | 5,56E-10 |
| TERG\_08066 | STE/STE7 protein kinase | 1,855936137 | 1,05E-16 |
| TERG\_02510 | hypothetical protein | 1,854439266 | 2,00E-07 |
| TERG\_08245 | branched-chain amino acid aminotransferase (T. tonsurans) | 1,85426683 | 4,65E-10 |
| TERG\_08909 | hypothetical protein | 1,852787645 | 2,68E-15 |
| TERG\_05918 | glutamyl-tRNA(Gln) amidotransferase subunit A (T. equinum) | 1,85270498 | 2,24E-13 |
| TERG\_05769 | NAD(P)H-dependent D-xylose reductase (T. equinum) | 1,845868496 | 7,76E-13 |
| TERG\_02848 | short chain dehydrogenase/reductase family protein (A. benhamiae) | 1,840762048 | 7,28E-05 |
| TERG\_11757 | hypothetical protein | 1,834524676 | 8,61E-15 |
| TERG\_02508 | ABC multidrug transporter, putative (A. benhamiae) | 1,82707795 | 7,78E-11 |
| TERG\_05281 | thioesterase (T. tonsurans) | 1,825546052 | 1,18E-07 |
| TERG\_11897 | hypothetical protein | 1,824117636 | 1,30E-05 |
| TERG\_12491 | carboxylesterase, putative (A. benhamiae) | 1,81891425 | 8,25E-08 |
| TERG\_08339 | F-box domain-containing protein (T. equinum) | 1,816325748 | 2,01E-05 |
| TERG\_08116 | hypothetical protein | 1,816226856 | 3,73E-09 |
| TERG\_01190 | RNA binding protein (T. equinum) | 1,815617509 | 4,26E-08 |
| TERG\_07334 | HIT domain-containing protein (T. equinum) | 1,812917304 | 1,32E-09 |
| TERG\_00701 | cytochrome b5, putative (T. verrucosum) | 1,794249186 | 2,92E-11 |
| TERG\_01733 | alcohol dehydrogenase, putative (T. verrucosum) | 1,78709341 | 5,22E-07 |
| TERG\_12281 | glycosyl hydrolase (T. tonsurans) | 1,78601836 | 4,11E-12 |
| TERG\_06507 | oxidoreductase, 2OG-Fe(II) oxygenase family (T. verrucosum) | 1,767744433 | 3,04E-06 |
| TERG\_03278 | hypothetical protein | 1,763146631 | 1,17E-05 |
| TERG\_03177 | RING finger domain protein, putative (A. benhamiae) | 1,757059401 | 9,49E-10 |
| TERG\_06016 | glycosyl hydrolase (T. tonsurans) | 1,755175506 | 8,96E-19 |
| TERG\_02841 | AURR1 aurofusarin regulatory protein (T. equinum) | 1,755069872 | 3,17E-06 |
| TERG\_06234 | 2,5-diketo-D-gluconic acid reductase A (T. equinum) | 1,747064813 | 1,25E-10 |
| TERG\_05372 | hypothetical protein | 1,744527317 | 0,000455415 |
| TERG\_07872 | homoserine O-acetyltransferase | 1,735989614 | 9,24E-15 |
| TERG\_08100 | CDP-diacylglycerol-inositol 3-phosphatidyltransferase PIS (T. equinum) | 1,734075237 | 1,43E-12 |
| TERG\_01621 | DnaJ chaperone (Caj1), putative (T. verrucosum) | 1,730769858 | 7,27E-07 |
| TERG\_08686 | hypothetical protein | 1,721050282 | 6,36E-05 |
| TERG\_08297 | hypothetical protein | 1,717785255 | 0,003406494 |
| TERG\_01632 | hypothetical protein | 1,716489032 | 3,23E-06 |
| TERG\_02059 | AbpA protein (T. equinum) | 1,7009453 | 2,44E-16 |
| TERG\_07479 | hypothetical protein | 1,700897701 | 6,14E-11 |
| TERG\_07991 | proline-rich protein (T. tonsurans) | 1,697468895 | 9,10E-10 |
| TERG\_06354 | SVP1-like protein (T. tonsurans) | 1,697398676 | 2,70E-16 |
| TERG\_03301 | hypothetical protein | 1,695486536 | 1,72E-07 |
| TERG\_01225 | GTPase-activating protein GYP7 (T. equinum) | 1,683553365 | 4,66E-10 |
| TERG\_00439 | hypothetical protein | 1,683516503 | 1,34E-08 |
| TERG\_12599 | hypothetical protein | 1,678023399 | 7,18E-05 |
| TERG\_01825 | DNA repair protein Ntg1 (T. tonsurans) | 1,666975169 | 2,00E-13 |
| TERG\_08104 | potassium/sodium efflux P-type ATPase, fungal-type | 1,664141346 | 1,93E-09 |
| TERG\_00577 | BAR domain-containing protein (T. tonsurans) | 1,664044153 | 5,28E-16 |
| TERG\_01546 | oxidoreductase (T. tonsurans) | 1,664030839 | 1,80E-06 |
| TERG\_04332 | phosphatidylinositol transporter (T. tonsurans) | 1,658056353 | 1,74E-13 |
| TERG\_02039 | 2-hydroxyphytanoyl-CoA lyase (T. tonsurans) | 1,655982366 | 7,86E-10 |
| TERG\_08070 | enoyl-CoA hydratase/isomerase (T. tonsurans) | 1,65579981 | 3,40E-10 |
| TERG\_11780 | pre-mRNA splicing factor (T. tonsurans) | 1,655712041 | 2,52E-07 |
| TERG\_02038 | peroxisomal targeting signal receptor (T. equinum) | 1,653438748 | 7,94E-13 |
| TERG\_12290 | mitochondrial cytochrome b2 (T. tonsurans) | 1,653054175 | 3,68E-10 |
| TERG\_05747 | alcohol dehydrogenase (T. tonsurans) | 1,650359978 | 7,95E-10 |
| TERG\_02243 | hypothetical protein | 1,649177492 | 2,21E-05 |
| TERG\_07804 | PBSP domain-containing protein (T. tonsurans) | 1,646816173 | 2,62E-09 |
| TERG\_08107 | phosphoglycerate mutase (T. tonsurans) | 1,646778511 | 2,14E-10 |
| TERG\_02249 | phenylacetyl-CoA ligase (T. tonsurans) | 1,631515499 | 2,88E-12 |
| TERG\_05624 | C6 transcription factor, putative (T. verrucosum) | 1,630123425 | 4,24E-13 |
| TERG\_06594 | DUF1183 domain-containing protein (T. equinum) | 1,627134523 | 6,04E-07 |
| TERG\_01676 | 6,7-dimethyl-8-ribityllumazine synthase | 1,626693679 | 3,45E-14 |
| TERG\_08300 | branched-chain amino acid aminotransferase | 1,619209578 | 4,97E-07 |
| TERG\_02744 | NAD-dependent methanol dehydrogenase (T. equinum) | 1,617913415 | 2,15E-12 |
| TERG\_08952 | long-chain-fatty-acid-CoA ligase (T. equinum) | 1,611976869 | 1,07E-12 |
| TERG\_02815 | extracellular dihydrogeodin oxidase/laccase, putative (A. benhamiae) | 1,597645504 | 2,76E-05 |
| TERG\_05037 | hypothetical protein | 1,595663245 | 2,00E-09 |
| TERG\_02087 | hypothetical protein | 1,594042318 | 2,44E-12 |
| TERG\_00865 | hypothetical protein | 1,594010662 | 2,54E-10 |
| TERG\_12602 | 4-coumarate-CoA ligase (T. equinum) | 1,591949198 | 9,51E-05 |
| TERG\_12601 | 4-coumarate-CoA ligase (T. tonsurans) | 1,588060964 | 0,00176612 |
| TERG\_02558 | oxysterol binding protein (T. tonsurans) | 1,582134451 | 5,79E-10 |
| TERG\_03141 | hypothetical protein | 1,581747789 | 1,04E-08 |
| TERG\_04392 | dephospho-CoA kinase | 1,577476099 | 1,01E-10 |
| TERG\_02340 | polysaccharide deacetylase (T. equinum) | 1,571227728 | 2,08E-07 |
| TERG\_06235 | hypothetical protein | 1,567862676 | 0,0003077 |
| TERG\_01184 | fatty acid-binding protein (T. equinum) | 1,565551129 | 9,42E-09 |
| TERG\_08347 | cytochrome P450 monooxygenase, putative (A. benhamiae) | 1,564618103 | 2,22E-06 |
| TERG\_04721 | glutamate carboxypeptidase (T. equinum) | 1,563597487 | 5,89E-12 |
| TERG\_07923 | neutral amino acid permease (T. equinum) | 1,563304219 | 5,55E-05 |
| TERG\_00382 | luciferin 4-monooxygenase (M. gypseum) | 1,560670387 | 3,07E-10 |
| TERG\_05331 | peroxisome biosynthesis protein (T. tonsurans) | 1,552945456 | 3,75E-08 |
| TERG\_00471 | hypothetical protein | 1,550479398 | 4,16E-10 |
| TERG\_00959 | RNA binding protein, putative (A. benhamiae) | 1,549893218 | 1,28E-06 |
| TERG\_00919 | Phospholipid:diacylglycerol acyltransferase (T. equinum) | 1,548755605 | 2,77E-09 |
| TERG\_02042 | peroxisomal membrane protein PEX13 (T. equinum) | 1,543111598 | 1,78E-10 |
| TERG\_01636 | ADP-ribosylglycohydrolase (M. gypseum) | 1,542271998 | 6,38E-08 |
| TERG\_06240 | peroxisomal biogenesis factor 2 (T. tonsurans) | 1,536580222 | 1,45E-10 |
| TERG\_08322 | short chain dehydrogenase, putative (T. verrucosum) | 1,536181633 | 2,20E-07 |
| TERG\_00117 | SNF2 family helicase, putative (T. verrucosum) | 1,533580636 | 0,037062853 |
| TERG\_08355 | zinc alcohol dehydrogenase, putative (T. verrucosum) | 1,531864967 | 7,46E-09 |
| TERG\_04363 | cysteine synthase | 1,530939601 | 1,37E-13 |
| TERG\_05373 | peroxin 11C (T. equinum) | 1,528593835 | 3,38E-08 |
| TERG\_05359 | peroxin-26 (T. tonsurans) | 1,526518076 | 3,81E-09 |
| TERG\_03780 | pyruvate dehydrogenase dihydrolipoamide acetyltransferase component (M. gypseum) | 1,522191189 | 0,014142682 |
| TERG\_04810 | bifunctional fatty acid transporter/acyl-CoA synthetase (FAT1), putative (A. benhamiae) | 1,519425826 | 8,59E-10 |
| TERG\_01162 | CRAL/TRIO domain protein (A. benhamiae) | 1,516497519 | 1,15E-08 |
| TERG\_00645 | sterigmatocystin 8-O-methyltransferase (M. gypseum) | 1,51593921 | 0,028484772 |
| TERG\_03293 | hypothetical protein | 1,513274798 | 8,25E-06 |
| TERG\_02265 | MFS multidrug transporter (T. equinum) | 1,51154686 | 6,51E-06 |
| TERG\_01056 | PH domain-containing protein (T. equinum) | 1,503887213 | 1,95E-09 |
| TERG\_12230 | peptidase S41 family protein (A. benhamiae) | 1,50196425 | 0,001764534 |
| TERG\_01902 | phosphotransferase (M. canis) | -1,50003138 | 2,74E-07 |
| TERG\_01328 | metalloreductase transmembrane component, putative (A. benhamiae) | -1,504313709 | 2,77E-09 |
| TERG\_03708 | short-chain dehydrogenase, putative (A. benhamiae) | -1,504926778 | 1,71E-08 |
| TERG\_05090 | rho-gdp dissociation inhibitor (T. equinum) | -1,506916619 | 2,25E-11 |
| TERG\_00899 | Neutral/alkaline non-lysosomal ceramidase (T. equinum) | -1,507565141 | 1,49E-11 |
| TERG\_02973 | morphogenesis protein (Msb1), putative (T. verrucosum) | -1,510452582 | 3,95E-09 |
| TERG\_02353 | UbiD family decarboxylase, putative (T. verrucosum) | -1,514181028 | 6,48E-06 |
| TERG\_06267 | hypothetical protein | -1,515955923 | 2,16E-10 |
| TERG\_00529 | acetate kinase | -1,518531457 | 0,000359361 |
| TERG\_02664 | hypothetical protein | -1,519114079 | 7,57E-08 |
| TERG\_04478 | 40S ribosomal protein S1 | -1,51957232 | 3,96E-11 |
| TERG\_11814 | FAD dependent oxidoreductase, putative (A. benhamiae) | -1,519842178 | 3,66E-05 |
| TERG\_00783 | guanine nucleotide-binding protein subunit beta-like protein | -1,520967515 | 9,25E-09 |
| TERG\_05599 | null (T. verrucosum) | -1,522397209 | 0,01108272 |
| TERG\_02076 | hypothetical protein | -1,523844266 | 2,25E-09 |
| TERG\_05528 | hypothetical protein | -1,528689531 | 6,96E-08 |
| TERG\_08190 | Mrsp1 (T. equinum) | -1,530248574 | 0,041949619 |
| TERG\_00583 | hypothetical protein | -1,53290597 | 6,33E-09 |
| TERG\_02521 | 60S ribosomal protein L27a | -1,536240885 | 2,70E-12 |
| TERG\_08961 | hypothetical protein | -1,537553471 | 5,84E-06 |
| TERG\_07285 | hypothetical protein | -1,539504075 | 1,72E-10 |
| TERG\_04323 | ATP-dependent bile acid permease (T. equinum) | -1,540722802 | 8,01E-06 |
| TERG\_08195 | peptidase S41 family protein (M. gypseum) | -1,542420804 | 3,78E-07 |
| TERG\_07641 | GPI-anchored cell wall protein Pst1, putative (A. benhamiae) | -1,551102519 | 2,38E-10 |
| TERG\_07777 | O-acetylhomoserine (thiol)-lyase | -1,551494857 | 2,45E-11 |
| TERG\_05353 | PKS-like enzyme, putative (A. benhamiae) | -1,552075382 | 7,19E-06 |
| TERG\_07385 | 60S acidic ribosomal protein P1 | -1,554259844 | 9,64E-14 |
| TERG\_00738 | 60S ribosomal protein L44 | -1,560045341 | 1,37E-12 |
| TERG\_00756 | TBC domain protein, putative (T. verrucosum) | -1,560578108 | 4,32E-10 |
| TERG\_07673 | hypothetical protein | -1,562272091 | 1,71E-07 |
| TERG\_06246 | extracellular serine-threonine rich protein (A. benhamiae) | -1,562572447 | 1,29E-09 |
| TERG\_03095 | methyltransferase, putative (A. benhamiae) | -1,562799286 | 2,06E-05 |
| TERG\_06553 | hypothetical protein | -1,570079225 | 6,89E-11 |
| TERG\_04834 | rab GDP-dissociation inhibitor (T. tonsurans) | -1,57496318 | 7,10E-09 |
| TERG\_00501 | GPI anchored serine-rich protein (T. verrucosum) | -1,577742026 | 5,20E-12 |
| TERG\_02356 | hypothetical protein | -1,577894353 | 3,92E-05 |
| TERG\_08459 | cell wall glucanase, putative (T. verrucosum) | -1,578420788 | 1,06E-14 |
| TERG\_01329 | Ctr copper transporter, putative (T. verrucosum) | -1,579321581 | 6,00E-08 |
| TERG\_00359 | MeaB protein (T. equinum) | -1,58006086 | 1,32E-11 |
| TERG\_00217 | ubiquitin-40S ribosomal protein S27a | -1,580155738 | 2,06E-13 |
| TERG\_01550 | 60S ribosomal protein L38 (T. tonsurans) | -1,583440797 | 3,68E-12 |
| TERG\_02215 | NADP-dependent glycerol-2-dehydrogenase (T. tonsurans) | -1,584376355 | 2,01E-05 |
| TERG\_04169 | DUF829 domain protein (PaxU), putative (A. benhamiae) | -1,584739436 | 1,92E-05 |
| TERG\_01994 | OPT family oligopeptide transporter | -1,587210811 | 7,35E-06 |
| TERG\_06481 | cell polarity protein (T. tonsurans) | -1,587709074 | 1,69E-06 |
| TERG\_00402 | ABC multidrug transporter, putative (T. verrucosum) | -1,597230176 | 3,16E-05 |
| TERG\_07065 | UMTA (T. equinum) | -1,597473693 | 4,82E-10 |
| TERG\_00511 | hypothetical protein | -1,598911072 | 1,28E-11 |
| TERG\_07865 | septin-1 (T. equinum) | -1,599567268 | 1,24E-13 |
| TERG\_11551 | telomere and ribosome associated protein Stm1 (T. tonsurans) | -1,602583319 | 7,92E-10 |
| TERG\_01181 | protein kinase subdomain-containing protein (T. tonsurans) | -1,60558841 | 9,76E-05 |
| TERG\_06118 | hypothetical protein | -1,605674535 | 2,52E-06 |
| TERG\_05780 | hypothetical protein | -1,606316717 | 9,73E-06 |
| TERG\_01957 | proteinase T (M. gypseum) | -1,607127244 | 4,08E-06 |
| TERG\_04925 | hypothetical protein | -1,608873278 | 4,79E-12 |
| TERG\_00066 | 4-hydroxyphenylpyruvate dioxygenase | -1,61008106 | 1,39E-06 |
| TERG\_02604 | 40S ribosomal protein S20 | -1,611942075 | 4,65E-15 |
| TERG\_01749 | hypothetical protein | -1,616092675 | 7,63E-12 |
| TERG\_01330 | GPI anchored protein, putative (A. benhamiae) | -1,62015139 | 4,06E-08 |
| TERG\_12231 | DUF221 domain-containing protein (T. equinum) | -1,620291328 | 3,07E-11 |
| TERG\_05615 | hsp70-like protein (T. equinum) | -1,622444585 | 2,06E-05 |
| TERG\_06646 | arrestin (T. equinum) | -1,623450361 | 6,80E-13 |
| TERG\_12682 | hypothetical protein | -1,626254537 | 6,26E-10 |
| TERG\_08047 | hypothetical protein | -1,628700995 | 7,21E-07 |
| TERG\_01953 | 60S acidic ribosomal protein P2 | -1,630584747 | 1,74E-14 |
| TERG\_01731 | hypothetical protein | -1,631988951 | 0,02975954 |
| TERG\_11968 | hypothetical protein | -1,633021175 | 3,58E-07 |
| TERG\_08267 | oxidoreductase (T. equinum) | -1,639927046 | 8,18E-05 |
| TERG\_12294 | histidine acid phosphatase, putative (T. verrucosum) | -1,640964114 | 2,46E-06 |
| TERG\_02263 | hypothetical protein | -1,641151452 | 2,98E-10 |
| TERG\_06936 | hypothetical protein | -1,643145243 | 2,65E-11 |
| TERG\_12232 | DUF221 domain-containing protein (T. equinum) | -1,64327476 | 7,18E-07 |
| TERG\_01202 | histone H3-like centromeric protein cnp1 | -1,643290234 | 8,05E-07 |
| TERG\_01179 | polyketide synthase, putative (A. benhamiae) | -1,64468485 | 0,00012115 |
| TERG\_06584 | hypothetical protein | -1,645765462 | 1,07E-12 |
| TERG\_12313 | hypothetical protein | -1,6460448 | 1,71E-06 |
| TERG\_05971 | ribonucleoside-diphosphate reductase small chain | -1,650946678 | 2,53E-13 |
| TERG\_00159 | hypothetical protein | -1,652438804 | 5,54E-06 |
| TERG\_12083 | hypothetical protein | -1,654781969 | 6,09E-07 |
| TERG\_11667 | hypothetical protein | -1,657781545 | 6,10E-05 |
| TERG\_07269 | mannose-1-phosphate guanyltransferase | -1,659150803 | 1,37E-08 |
| TERG\_08405 | leucine aminopeptidase 2 | -1,659515959 | 1,28E-14 |
| TERG\_07598 | serine carboxypeptidase (T. equinum) | -1,664626181 | 0,001328216 |
| TERG\_01838 | LIM domain protein (A. benhamiae) | -1,667558321 | 1,39E-09 |
| TERG\_02153 | RdgB/HAM1 family non-canonical purine NTP pyrophosphatase | -1,669199476 | 4,07E-07 |
| TERG\_07796 | oxidoreductase, short-chain dehydrogenase/reductase family (A. benhamiae) | -1,672407219 | 9,59E-09 |
| TERG\_02197 | nitrilase, putative (T. verrucosum) | -1,676088287 | 4,31E-09 |
| TERG\_11782 | hypothetical protein | -1,676928762 | 0,000112988 |
| TERG\_02630 | histone H2A | -1,683150756 | 1,06E-12 |
| TERG\_02183 | C2H2 finger domain-containing protein (T. equinum) | -1,688035481 | 4,51E-07 |
| TERG\_11550 | telomere and ribosome associated protein Stm1, putative (T. verrucosum) | -1,688592357 | 1,27E-08 |
| TERG\_01397 | C2H2 finger domain-containing protein (T. equinum) | -1,694869602 | 9,12E-15 |
| TERG\_08191 | glucooligosaccharide oxidase (T. equinum) | -1,699171662 | 2,12E-06 |
| TERG\_01165 | 40S ribosomal protein S10b (T. equinum) | -1,700628584 | 3,76E-14 |
| TERG\_03352 | tyrosine decarboxylase (T. equinum) | -1,701025416 | 1,77E-06 |
| TERG\_00707 | GPI anchored serine-threonine rich protein (T. verrucosum) | -1,703421644 | 7,73E-08 |
| TERG\_05644 | mucin family signaling protein Msb2, putative (T. verrucosum) | -1,705378427 | 1,50E-09 |
| TERG\_02049 | hypothetical protein | -1,70567132 | 3,15E-05 |
| TERG\_04254 | oxidoreductase (T. equinum) | -1,706989715 | 0,002109304 |
| TERG\_04658 | imidazole glycerol phosphate synthase hisHF | -1,709064047 | 5,12E-15 |
| TERG\_04862 | C6 transcription factor RosA (A. benhamiae) | -1,713222654 | 2,15E-12 |
| TERG\_01268 | C-5 cytosine methyltransferase DmtA (T. verrucosum) | -1,713498921 | 1,06E-05 |
| TERG\_05576 | cell wall glucanase (Scw11), putative (A. benhamiae) | -1,714032013 | 7,90E-14 |
| TERG\_00619 | tripeptidyl-peptidase SED2 | -1,718875422 | 2,77E-05 |
| TERG\_05608 | hypothetical protein | -1,722789611 | 1,75E-08 |
| TERG\_01443 | ABC multidrug transporter (T. tonsurans) | -1,723652908 | 7,01E-12 |
| TERG\_06854 | glutamine-serine-proline rich protein, putative (A. benhamiae) | -1,726365998 | 1,08E-08 |
| TERG\_06055 | NmrA-like family protein (A. benhamiae) | -1,730236083 | 0,008110158 |
| TERG\_00657 | hypothetical protein | -1,730382261 | 1,17E-08 |
| TERG\_08200 | hypothetical protein | -1,731861224 | 0,020005956 |
| TERG\_04917 | thiamine pyrophosphate enzyme, putative (A. benhamiae) | -1,733353759 | 1,58E-05 |
| TERG\_06770 | cytochrome P450, putative (T. verrucosum) | -1,733693435 | 6,93E-09 |
| TERG\_07410 | hypothetical protein | -1,736112901 | 5,03E-07 |
| TERG\_02787 | polyketide synthase (T. tonsurans) | -1,738399296 | 4,33E-10 |
| TERG\_08234 | TCTP family protein (T. verrucosum) | -1,739213063 | 6,37E-09 |
| TERG\_07283 | GABA permease (T. equinum) | -1,756960523 | 3,98E-13 |
| TERG\_07211 | NAD binding Rossmann fold oxidoreductase, putative (A. benhamiae) | -1,758412684 | 1,46E-05 |
| TERG\_02529 | hypothetical protein | -1,762377637 | 7,88E-08 |
| TERG\_06829 | hypothetical protein | -1,762634528 | 0,000380791 |
| TERG\_08219 | hypothetical protein | -1,763953092 | 1,26E-06 |
| TERG\_02496 | histone H1 (T. tonsurans) | -1,765653419 | 8,53E-17 |
| TERG\_05374 | hypothetical protein | -1,775661538 | 5,96E-14 |
| TERG\_05612 | hypothetical protein | -1,775936839 | 3,37E-07 |
| TERG\_04879 | hypothetical protein | -1,779337966 | 0,000106856 |
| TERG\_00414 | 3-beta hydroxysteroid dehydrogenase/isomerase family protein (A. benhamiae) | -1,781669744 | 3,43E-15 |
| TERG\_04192 | lactonohydrolase, putative (A. benhamiae) | -1,78964572 | 2,07E-08 |
| TERG\_03621 | hypothetical protein | -1,790225431 | 5,98E-07 |
| TERG\_02424 | rho2 (T. equinum) | -1,790759187 | 6,70E-08 |
| TERG\_07907 | hypothetical protein | -1,791534176 | 9,38E-09 |
| TERG\_01444 | nonribosomal peptide synthase Pes1 (A. benhamiae) | -1,795852489 | 2,00E-09 |
| TERG\_01012 | hypothetical protein | -1,796208925 | 6,75E-13 |
| TERG\_03794 | hypothetical protein | -1,797737735 | 3,81E-09 |
| TERG\_08226 | hypothetical protein | -1,807508921 | 1,30E-17 |
| TERG\_04226 | MFS allantoate transporter (T. equinum) | -1,808189991 | 9,75E-05 |
| TERG\_04514 | cell division control protein 12 (T. tonsurans) | -1,809733754 | 2,90E-14 |
| TERG\_02795 | thiazole biosynthetic enzyme, mitochondrial | -1,81296883 | 4,37E-19 |
| TERG\_03382 | ThiJ/PfpI family protein (A. benhamiae) | -1,829342895 | 4,34E-07 |
| TERG\_07059 | hypothetical protein | -1,829576678 | 1,95E-13 |
| TERG\_06933 | hypothetical protein | -1,832230057 | 5,70E-11 |
| TERG\_02405 | mating locus protein, putative (T. verrucosum) | -1,837036692 | 4,00E-05 |
| TERG\_07543 | hypothetical protein | -1,837683674 | 3,84E-14 |
| TERG\_01277 | nexin-1 (T. equinum) | -1,84096605 | 0,00023009 |
| TERG\_07770 | importin 13, putative (T. verrucosum) | -1,841492593 | 7,14E-17 |
| TERG\_00069 | fumarylacetoacetase | -1,848985856 | 1,50E-11 |
| TERG\_06113 | NACHT and TPR domain-containing protein (T. equinum) | -1,853002231 | 9,03E-08 |
| TERG\_03956 | hypothetical protein | -1,853214788 | 2,43E-06 |
| TERG\_11863 | hypothetical protein | -1,857904477 | 0,000141007 |
| TERG\_02650 | NmrA family protein (T. equinum) | -1,859354766 | 0,000830061 |
| TERG\_03448 | hypothetical protein | -1,859375819 | 0,008166522 |
| TERG\_05626 | chitinase (T. equinum) | -1,860580411 | 4,81E-12 |
| TERG\_06022 | hypothetical protein | -1,863028883 | 4,00E-08 |
| TERG\_01623 | MFS transporter (T. equinum) | -1,863566851 | 1,11E-07 |
| TERG\_01802 | hypothetical protein | -1,865415893 | 0,000138183 |
| TERG\_05274 | hypothetical protein | -1,866383023 | 1,43E-07 |
| TERG\_07963 | hypothetical protein | -1,873392595 | 1,18E-11 |
| TERG\_00281 | AGC/RSK protein kinase | -1,87751152 | 4,29E-12 |
| TERG\_02350 | endochitinase (T. equinum) | -1,87964428 | 7,96E-10 |
| TERG\_03183 | hypothetical protein | -1,888383525 | 1,30E-08 |
| TERG\_11813 | FAD dependent oxidoreductase, putative (A. benhamiae) | -1,888656585 | 3,47E-05 |
| TERG\_02735 | fatty acid oxygenase PpoC, putative (A. benhamiae) | -1,890088176 | 9,34E-08 |
| TERG\_02588 | hypothetical protein | -1,894924575 | 4,65E-07 |
| TERG\_08130 | ABC ATPase (T. equinum) | -1,896921432 | 5,35E-13 |
| TERG\_03157 | NDT80 / PhoG like DNA-binding family protein (A. benhamiae) | -1,89783277 | 3,01E-13 |
| TERG\_00543 | A-agglutinin anchorage subunit (M. canis) | -1,898154745 | 6,42E-18 |
| TERG\_07408 | acetyltransferase, GNAT family (A. benhamiae) | -1,899014029 | 4,32E-10 |
| TERG\_06049 | dimethylallyl tryptophan synthase, putative (T. verrucosum) | -1,900489029 | 7,67E-05 |
| TERG\_08046 | beta-lactamase (M. gypseum) | -1,905638554 | 0,003026543 |
| TERG\_02081 | RNA binding protein | -1,91211553 | 7,23E-19 |
| TERG\_11998 | potassium uptake transporter (T. equinum) | -1,921855447 | 6,94E-07 |
| TERG\_06528 | Delta(24(24(1)))-sterol reductase (T. equinum) | -1,925982224 | 2,25E-12 |
| TERG\_02406 | alpha-box mating type protein (T. tonsurans) | -1,926780277 | 2,76E-11 |
| TERG\_03702 | hypothetical protein | -1,936467896 | 4,90E-09 |
| TERG\_01904 | hypothetical protein | -1,944137933 | 2,57E-11 |
| TERG\_04615 | hypothetical protein | -1,944618793 | 2,14E-06 |
| TERG\_11846 | hypothetical protein | -1,945606779 | 1,23E-07 |
| TERG\_00520 | hypothetical protein | -1,950637447 | 5,56E-08 |
| TERG\_01744 | hypothetical protein | -1,954017322 | 4,14E-11 |
| TERG\_01859 | general amidase GmdA, putative (T. verrucosum) | -1,968604616 | 3,73E-10 |
| TERG\_08225 | hypothetical protein | -1,97000531 | 4,20E-21 |
| TERG\_05636 | acyl-CoA:6-aminopenicillanic-acid- acyltransferase, putative (A. benhamiae) | -1,971010969 | 1,61E-10 |
| TERG\_05055 | MFS multidrug transporter (T. tonsurans) | -1,984836923 | 2,48E-13 |
| TERG\_03984 | major facilitator superfamily transporter MFS-1 (M. canis) | -1,985834591 | 4,95E-09 |
| TERG\_03459 | GDSL Lipase/Acylhydrolase family protein (A. benhamiae) | -1,988930087 | 1,05E-10 |
| TERG\_01786 | DENN domain-containing protein (T. tonsurans) | -2,00695275 | 1,25E-13 |
| TERG\_05771 | hypothetical protein | -2,010092677 | 2,56E-09 |
| TERG\_02134 | indoleamine 2,3-dioxygenase (T. equinum) | -2,014572521 | 1,66E-06 |
| TERG\_01820 | MFS transporter, putative (T. verrucosum) | -2,014825906 | 1,99E-14 |
| TERG\_03929 | hypothetical protein | -2,01860095 | 3,84E-11 |
| TERG\_08987 | hypothetical protein | -2,019993201 | 1,11E-12 |
| TERG\_03758 | hypothetical protein | -2,035057668 | 7,99E-09 |
| TERG\_08029 | HMG box protein, putative (T. verrucosum) | -2,036154146 | 3,01E-13 |
| TERG\_07892 | SCP-like extracellular protein, putative (A. benhamiae) | -2,039561036 | 6,63E-12 |
| TERG\_05545 | GNAT family acetyltransferase, putative (A. benhamiae) | -2,039999165 | 0,00200465 |
| TERG\_05651 | hypothetical protein | -2,04631615 | 5,83E-15 |
| TERG\_05409 | FAD dependent oxidoreductase (T. equinum) | -2,05020321 | 8,22E-09 |
| TERG\_04564 | mixed-linked glucanase (T. equinum) | -2,06058606 | 2,09E-08 |
| TERG\_05746 | hypothetical protein | -2,067499783 | 6,36E-09 |
| TERG\_02367 | hypothetical protein | -2,072370835 | 5,57E-20 |
| TERG\_07409 | amino acid permease (T. equinum) | -2,073815374 | 2,73E-13 |
| TERG\_05735 | dipeptidyl peptidase 4 | -2,08055626 | 3,57E-16 |
| TERG\_04558 | nucleoside diphosphate kinase | -2,085797001 | 5,89E-16 |
| TERG\_02100 | cytidine deaminase | -2,092747175 | 3,68E-14 |
| TERG\_04240 | cupin 2 domain-containing protein (T. equinum) | -2,093416756 | 7,53E-20 |
| TERG\_08620 | siderophore iron transporter (T. equinum) | -2,096094687 | 3,40E-10 |
| TERG\_05408 | ThiJ/PfpI family protein (T. tonsurans) | -2,109052229 | 9,99E-06 |
| TERG\_01638 | hypothetical protein | -2,11239501 | 3,94E-16 |
| TERG\_00553 | amino acid permease (T. equinum) | -2,125014083 | 3,61E-15 |
| TERG\_12298 | hypothetical protein | -2,146482145 | 6,95E-19 |
| TERG\_06228 | hypothetical protein | -2,148796846 | 8,72E-09 |
| TERG\_08466 | hypothetical protein | -2,156719041 | 1,83E-08 |
| TERG\_02393 | hypothetical protein | -2,159045247 | 4,91E-09 |
| TERG\_04543 | aminotransferase GliI (T. equinum) | -2,159073955 | 6,22E-16 |
| TERG\_00507 | hypothetical protein | -2,16034561 | 1,70E-06 |
| TERG\_00830 | cytochrome P450 monooxygenase, putative (A. benhamiae) | -2,162967707 | 1,18E-14 |
| TERG\_01148 | hypothetical protein | -2,167038959 | 6,67E-14 |
| TERG\_07795 | WSC domain protein, putative (A. benhamiae) | -2,170745927 | 7,26E-17 |
| TERG\_08622 | transferase (M. canis) | -2,180391534 | 1,89E-13 |
| TERG\_11997 | potassium uptake transporter (T. equinum) | -2,18620157 | 9,42E-08 |
| TERG\_03998 | aspartic proteinase II-1 (T. equinum) | -2,18629365 | 4,91E-06 |
| TERG\_08633 | hypothetical protein | -2,194256826 | 7,77E-14 |
| TERG\_08557 | carboxypeptidase S1, putative (A. benhamiae) | -2,210224149 | 7,36E-20 |
| TERG\_08709 | SesA protein (T. equinum) | -2,211483349 | 5,44E-08 |
| TERG\_06625 | serine protease, putative (A. benhamiae) | -2,212735842 | 1,76E-18 |
| TERG\_02189 | tubulin alpha-2 chain | -2,21733121 | 1,82E-25 |
| TERG\_08129 | general amino-acid permease GAP1 (T. equinum) | -2,222999837 | 1,70E-11 |
| TERG\_06512 | hypothetical protein | -2,230970504 | 1,66E-15 |
| TERG\_06358 | dicer (T. tonsurans) | -2,231081114 | 4,61E-18 |
| TERG\_05816 | hypothetical protein | -2,236448424 | 9,22E-05 |
| TERG\_02214 | carboxypeptidase 2 | -2,253584494 | 8,99E-14 |
| TERG\_07280 | hypothetical protein | -2,263517126 | 2,70E-09 |
| TERG\_03851 | serine/threonine protein kinase | -2,26706329 | 1,89E-15 |
| TERG\_02024 | hypothetical protein | -2,27933033 | 0,000218611 |
| TERG\_01915 | O-methyltransferase (A. benhamiae) | -2,282151691 | 0,000440046 |
| TERG\_02278 | hypothetical protein | -2,283374032 | 0,001050246 |
| TERG\_04616 | hypothetical protein | -2,287208249 | 6,73E-08 |
| TERG\_08614 | hypothetical protein | -2,291074362 | 6,11E-09 |
| TERG\_05625 | class V chitinase, putative (T. verrucosum) | -2,301154753 | 3,14E-23 |
| TERG\_06047 | hypothetical protein | -2,312870737 | 1,15E-26 |
| TERG\_02746 | hypothetical protein | -2,317074746 | 6,78E-18 |
| TERG\_02132 | 5-histidylcysteine sulfoxide synthase | -2,329660808 | 5,87E-12 |
| TERG\_01116 | hypothetical protein | -2,343070582 | 4,42E-15 |
| TERG\_05650 | blasticidin-resistance protein (T. tonsurans) | -2,350186753 | 4,26E-08 |
| TERG\_08240 | methyltransferase, putative (T. verrucosum) | -2,388616938 | 3,70E-21 |
| TERG\_03623 | hypothetical protein | -2,388875369 | 0,000297532 |
| TERG\_07665 | hypothetical protein | -2,392653052 | 2,59E-15 |
| TERG\_02958 | sulfite reductase flavoprotein component (T. equinum) | -2,404131022 | 6,42E-20 |
| TERG\_02368 | extracellular developmental signal biosynthesis protein FluG (A. benhamiae) | -2,414614922 | 1,65E-23 |
| TERG\_04227 | ABC transporter (T. tonsurans) | -2,425678888 | 2,36E-14 |
| TERG\_04308 | MFS sugar transporter (T. tonsurans) | -2,427107636 | 2,16E-14 |
| TERG\_06230 | hypothetical protein | -2,433402473 | 2,88E-25 |
| TERG\_04213 | TAM domain methyltransferase (T. equinum) | -2,433520658 | 1,25E-14 |
| TERG\_05524 | 3-deoxy-7-phosphoheptulonate synthase | -2,443392273 | 8,46E-28 |
| TERG\_02610 | WD repeat protein (T. verrucosum) | -2,481957029 | 1,85E-17 |
| TERG\_02118 | GPI anchored protein, putative (A. benhamiae) | -2,499284772 | 2,34E-24 |
| TERG\_07904 | tubulin beta chain | -2,49937404 | 1,89E-27 |
| TERG\_03985 | hypothetical protein | -2,514964362 | 1,98E-18 |
| TERG\_04964 | RNA-binding protein (A. benhamiae) | -2,523531848 | 1,03E-23 |
| TERG\_00481 | beta-glucosidase, putative (T. verrucosum) | -2,554331962 | 4,11E-34 |
| TERG\_12722 | transferase (M. canis) | -2,565668415 | 2,76E-21 |
| TERG\_12578 | PEP phosphonomutase (T. equinum) | -2,570424138 | 2,59E-14 |
| TERG\_03719 | MFS sugar transporter (T. tonsurans) | -2,570530191 | 3,42E-14 |
| TERG\_12238 | integral membrane protein (M. gypseum) | -2,572106909 | 5,15E-06 |
| TERG\_11951 | prp 6 CRoW domain-containing protein (M. canis) | -2,572727991 | 6,06E-17 |
| TERG\_00791 | developmental regulatory protein WetA (T. verrucosum) | -2,574943889 | 7,25E-24 |
| TERG\_01685 | glutathione S-transferase, putative (A. benhamiae) | -2,577774918 | 1,30E-26 |
| TERG\_00967 | hypothetical protein | -2,596239549 | 2,02E-16 |
| TERG\_01401 | high affinity copper transporter (T. tonsurans) | -2,607465997 | 2,27E-15 |
| TERG\_05627 | LysM domain-containing protein (M. canis) | -2,620968335 | 8,23E-06 |
| TERG\_03955 | RNA 3'-terminal phosphate cyclase, putative (T. verrucosum) | -2,646366093 | 4,63E-13 |
| TERG\_07734 | O-methyltransferase, putative (T. verrucosum) | -2,691776753 | 9,72E-07 |
| TERG\_08980 | hypothetical protein | -2,714438383 | 1,13E-16 |
| TERG\_07282 | cytochrome P450 monooxygenase, putative (T. verrucosum) | -2,752736231 | 9,18E-23 |
| TERG\_08985 | hypothetical protein | -2,754570355 | 3,15E-11 |
| TERG\_03624 | SUN domain protein (Uth1), putative (T. verrucosum) | -2,756434351 | 1,09E-28 |
| TERG\_07456 | cell wall protein PhiA (T. equinum) | -2,77060311 | 6,13E-16 |
| TERG\_05799 | chlorophyll synthesis pathway protein BchC | -2,793715783 | 4,73E-23 |
| TERG\_03490 | hypothetical protein | -2,80401115 | 3,27E-06 |
| TERG\_00119 | CAMK/CAMKL/GIN4 protein kinase | -2,821366009 | 2,69E-15 |
| TERG\_03489 | hypothetical protein | -2,826731159 | 1,03E-06 |
| TERG\_07469 | SUN domain-containing protein (T. equinum) | -2,843135092 | 3,26E-27 |
| TERG\_12721 | transferase (M. canis) | -2,845622657 | 3,28E-21 |
| TERG\_04855 | hypothetical protein | -2,861972236 | 8,95E-15 |
| TERG\_12239 | integral membrane protein (M. gypseum) | -2,877297429 | 7,20E-12 |
| TERG\_08363 | tyrosinase (T. verrucosum) | -2,885585808 | 1,83E-39 |
| TERG\_07184 | HMG box transcriptional regulator, putative (A. benhamiae) | -2,894788808 | 5,43E-17 |
| TERG\_01869 | TOS1 (T. equinum) | -2,916005697 | 3,45E-24 |
| TERG\_03707 | geranylgeranyl diphosphate synthase, putative (A. benhamiae) | -2,924218606 | 1,89E-15 |
| TERG\_05854 | beta-lactamase (T. tonsurans) | -2,938752555 | 9,49E-33 |
| TERG\_01599 | hypothetical protein | -2,953701822 | 4,40E-42 |
| TERG\_00257 | conserved predicted protein (A. benhamiae) | -2,968231082 | 1,40E-25 |
| TERG\_00504 | hypothetical protein | -2,977753283 | 3,28E-11 |
| TERG\_06934 | hypothetical protein | -2,978195418 | 3,34E-26 |
| TERG\_05266 | integral membrane protein (T. equinum) | -3,017881046 | 5,52E-09 |
| TERG\_00598 | hypothetical protein | -3,039356216 | 1,20E-24 |
| TERG\_06291 | malate dehydrogenase (T. verrucosum) | -3,047032897 | 2,69E-23 |
| TERG\_06315 | integral membrane protein (A. benhamiae) | -3,111468204 | 1,20E-27 |
| TERG\_05537 | MFS multidrug transporter (T. equinum) | -3,112018506 | 6,13E-15 |
| TERG\_03706 | trichodiene oxygenase (T. equinum) | -3,123843108 | 3,47E-28 |
| TERG\_01981 | hypothetical protein | -3,128821672 | 5,16E-37 |
| TERG\_06883 | NAD dependent epimerase/dehydratase family protein (T. verrucosum) | -3,152759173 | 1,34E-41 |
| TERG\_00806 | hypothetical protein | -3,222336057 | 1,60E-29 |
| TERG\_11747 | hypothetical protein | -3,233293132 | 2,80E-35 |
| TERG\_05424 | hypothetical protein | -3,243906051 | 9,43E-31 |
| TERG\_03343 | fatty acid desaturase (T. equinum) | -3,262864342 | 3,44E-57 |
| TERG\_00911 | hypothetical protein | -3,296325033 | 2,82E-41 |
| TERG\_08619 | siderophore iron transporter mirB (T. equinum) | -3,318527285 | 7,90E-24 |
| TERG\_00487 | hypothetical protein | -3,403330905 | 2,22E-27 |
| TERG\_02057 | hypothetical protein | -3,409815705 | 5,35E-31 |
| TERG\_06144 | cell wall serine-threonine-rich galactomannoprotein Mp1 (A. benhamiae) | -3,443102213 | 1,83E-31 |
| TERG\_03981 | hypothetical protein | -3,463889407 | 1,51E-37 |
| TERG\_12627 | C-5 sterol desaturase (T. equinum) | -3,524471105 | 3,80E-33 |
| TERG\_07769 | hypothetical protein | -3,615377165 | 3,19E-28 |
| TERG\_01338 | hydantoinase (T. equinum) | -3,616601856 | 2,98E-24 |
| TERG\_12626 | C-5 sterol desaturase (T. equinum) | -3,645635617 | 2,60E-35 |
| TERG\_01480 | MFS multidrug transporter, putative (A. benhamiae) | -3,723311349 | 1,37E-34 |
| TERG\_02023 | extracellular matrix protein, putative (T. verrucosum) | -3,799881593 | 6,60E-54 |
| TERG\_08004 | hypothetical protein | -4,089045279 | 2,61E-46 |
| TERG\_04547 | aquaporin (T. tonsurans) | -4,154637047 | 1,72E-31 |
| TERG\_04234 | hydrophobin, putative (T. verrucosum) | -4,967146431 | 2,68E-121 |
| TERG\_07516 | hypothetical protein | -5,665769898 | 3,93E-50 |