**Table 2. 12h UDA vs 0h**

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| --- | --- | --- | --- |
| **ID** | **Gene Product Name** | **log2FC** | **padj** |
| TERG\_08102 | 3-isopropylmalate dehydrogenase A | 4,148839195 | 8,34E-38 |
| TERG\_07143 | potassium/sodium efflux P-type ATPase, fungal-type | 3,441626485 | 1,23E-52 |
| TERG\_00508 | hypothetical protein | 3,437365305 | 7,23E-31 |
| TERG\_04753 | 3-isopropylmalate dehydratase, large subunit | 3,422685101 | 2,23E-30 |
| TERG\_04765 | MFS transporter, putative (A. benhamiae) | 3,361877424 | 9,46E-43 |
| TERG\_00507 | hypothetical protein | 2,787241893 | 1,74E-11 |
| TERG\_12233 | hypothetical protein | 2,677849272 | 3,93E-11 |
| TERG\_06727 | homoserine dehydrogenase | 2,442307946 | 2,83E-17 |
| TERG\_00865 | hypothetical protein | 2,409239105 | 2,91E-22 |
| TERG\_00504 | hypothetical protein | 2,378046492 | 2,17E-08 |
| TERG\_00059 | hypothetical protein | 2,354877561 | 9,70E-13 |
| TERG\_07071 | 2-isopropylmalate synthase | 2,347710017 | 1,11E-28 |
| TERG\_03278 | hypothetical protein | 2,335023981 | 8,26E-09 |
| TERG\_00175 | ferric-chelate reductase (Fre2), putative (T. verrucosum) | 2,307601832 | 1,22E-05 |
| TERG\_11963 | hypothetical protein | 2,294379806 | 8,60E-10 |
| TERG\_08339 | F-box domain-containing protein (T. equinum) | 2,266247635 | 2,53E-07 |
| TERG\_07802 | siderophore biosynthesis acetylase AceI, putative (T. verrucosum) | 2,265559559 | 5,41E-25 |
| TERG\_08969 | cytosolic Cu/Zn superoxide dismutase, putative (A. benhamiae) | 2,249125116 | 3,66E-11 |
| TERG\_01252 | catalase A | 2,247280756 | 3,08E-12 |
| TERG\_07721 | isopenicillin N-CoA epimerase (T. equinum) | 2,235410438 | 3,38E-18 |
| TERG\_07923 | neutral amino acid permease (T. equinum) | 2,199383047 | 2,82E-08 |
| TERG\_08059 | sugar transporter (T. equinum) | 2,169817549 | 1,79E-10 |
| TERG\_00852 | Phytanoyl-CoA dioxygenase PhyH (T. equinum) | 2,152819996 | 0,000244348 |
| TERG\_00176 | hydroxyisourate hydrolase | 2,12605548 | 1,65E-13 |
| TERG\_08436 | hypothetical protein | 2,117318928 | 2,42E-11 |
| TERG\_03826 | hypothetical protein | 2,097523421 | 4,71E-14 |
| TERG\_02990 | subtilisin-like protease 6 | 2,093375801 | 3,23E-06 |
| TERG\_00823 | rhamnolipids biosynthesis 3-oxoacyl-[acyl-carrier-protein] reductase (T. equinum) | 2,09296374 | 5,84E-25 |
| TERG\_01347 | TIGR01456 family HAD hydrolase | 2,092784866 | 1,41E-19 |
| TERG\_08261 | glutamate decarboxylase | 2,088092392 | 1,17E-13 |
| TERG\_01463 | cytochrome c peroxidase (T. tonsurans) | 2,083866095 | 1,96E-15 |
| TERG\_00506 | hypothetical protein | 2,054037709 | 7,36E-08 |
| TERG\_00855 | aromatic amino acid aminotransferase, putative (A. benhamiae) | 2,041001776 | 7,80E-06 |
| TERG\_04038 | acyl-CoA dehydrogenase (T. tonsurans) | 2,001291483 | 1,17E-16 |
| TERG\_05769 | NAD(P)H-dependent D-xylose reductase (T. equinum) | 1,998254657 | 3,70E-14 |
| TERG\_08264 | L-xylulose reductase | 1,948048055 | 0,002044789 |
| TERG\_00854 | hypothetical protein | 1,942327409 | 4,40E-09 |
| TERG\_08139 | NAD dependent epimerase/dehydratase (M. gypseum) | 1,935457899 | 4,90E-13 |
| TERG\_08074 | hypothetical protein | 1,917453053 | 0,001681746 |
| TERG\_01741 | hypothetical protein | 1,908708219 | 2,20E-08 |
| TERG\_07291 | hypothetical protein | 1,886881428 | 5,22E-13 |
| TERG\_08170 | fatty acid elongase gig30 (T. equinum) | 1,881354145 | 6,15E-10 |
| TERG\_05466 | MFS transporter, putative (T. verrucosum) | 1,867331669 | 2,25E-13 |
| TERG\_05868 | opsin, putative (A. benhamiae) | 1,866169949 | 1,06E-06 |
| TERG\_04240 | cupin 2 domain-containing protein (T. equinum) | 1,859434531 | 6,17E-16 |
| TERG\_07631 | hypothetical protein | 1,85470941 | 1,68E-07 |
| TERG\_04504 | extracellular protein (T. equinum) | 1,836364821 | 1,31E-07 |
| TERG\_04894 | alcohol dehydrogenase IV (T. equinum) | 1,797439485 | 1,14E-08 |
| TERG\_03257 | hypothetical protein | 1,783324298 | 0,00194199 |
| TERG\_06839 | extracellular proline-rich protein (T. verrucosum) | 1,758880899 | 0,000373051 |
| TERG\_06735 | oxysterol binding protein (T. tonsurans) | 1,746672456 | 1,15E-11 |
| TERG\_03464 | stress response protein (T. equinum) | 1,739911204 | 2,45E-13 |
| TERG\_01979 | pirin domain protein, putative (A. benhamiae) | 1,734727253 | 3,41E-06 |
| TERG\_08771 | extracellular serine-threonine rich protein (T. tonsurans) | 1,726246956 | 1,59E-10 |
| TERG\_03193 | hypothetical protein | 1,71285339 | 1,46E-05 |
| TERG\_04131 | heat shock trehalose synthase, putative (T. verrucosum) | 1,710787189 | 1,75E-07 |
| TERG\_05003 | NmrA family protein (T. equinum) | 1,707545179 | 2,37E-11 |
| TERG\_08245 | branched-chain amino acid aminotransferase (T. tonsurans) | 1,707069704 | 3,37E-08 |
| TERG\_03212 | hypothetical protein | 1,695657015 | 3,52E-07 |
| TERG\_08186 | hypothetical protein | 1,684025751 | 2,29E-05 |
| TERG\_12135 | hypothetical protein | 1,667650063 | 1,08E-06 |
| TERG\_07352 | aldehyde reductase (AKR1), putative (T. verrucosum) | 1,65820416 | 0,000368439 |
| TERG\_08533 | poly(A) polymerase Cid1 (T. equinum) | 1,649611963 | 0,000555875 |
| TERG\_02641 | cystathionine gamma-synthase (T. equinum) | 1,646197583 | 6,72E-13 |
| TERG\_03896 | mannose-6-phosphate isomerase | 1,634784485 | 1,68E-07 |
| TERG\_05363 | hypothetical protein | 1,612231876 | 1,83E-07 |
| TERG\_01937 | short chain dehydrogenase (T. tonsurans) | 1,606058322 | 2,36E-08 |
| TERG\_00223 | hypothetical protein | 1,586376227 | 0,000204071 |
| TERG\_05841 | AmmeMemoRadiSam system protein B | 1,577562812 | 1,44E-08 |
| TERG\_12156 | hypothetical protein | 1,571464438 | 6,11E-05 |
| TERG\_03881 | epoxide hydrolase (T. tonsurans) | 1,570020125 | 5,10E-08 |
| TERG\_02777 | DNA replication complex GINS protein SLD5 (T. equinum) | 1,5517651 | 6,07E-06 |
| TERG\_02767 | pyroglutamyl peptidase type I (T. equinum) | 1,549232096 | 2,14E-12 |
| TERG\_01784 | oxidoreductase, short-chain dehydrogenase/reductase family, putative (T. verrucosum) | 1,54855288 | 1,70E-13 |
| TERG\_03283 | dienelactone hydrolase (M. gypseum) | 1,542145258 | 0,000169834 |
| TERG\_06927 | hypothetical protein | 1,54173386 | 1,13E-08 |
| TERG\_06507 | oxidoreductase, 2OG-Fe(II) oxygenase family (T. verrucosum) | 1,540359225 | 0,000159164 |
| TERG\_08174 | hypothetical protein | 1,538202902 | 6,55E-06 |
| TERG\_05435 | hypothetical protein | 1,534323645 | 0,000986293 |
| TERG\_01349 | glutathione peroxidase (T. tonsurans) | 1,526866484 | 5,52E-12 |
| TERG\_00573 | hypothetical protein | 1,519627754 | 1,10E-09 |
| TERG\_03834 | ketol-acid reductoisomerase, mitochondrial | 1,517503313 | 3,31E-12 |
| TERG\_00510 | hypothetical protein | 1,516589538 | 3,93E-05 |
| TERG\_06509 | glutamate synthase (T. tonsurans) | 1,509204488 | 1,55E-07 |
| TERG\_03598 | aspartate-semialdehyde dehydrogenase | 1,504878683 | 7,80E-10 |
| TERG\_04117 | tannase, putative (A. benhamiae) | -1,502540845 | 0,000253446 |
| TERG\_08195 | peptidase S41 family protein (M. gypseum) | -1,504039079 | 3,40E-06 |
| TERG\_06769 | hypothetical protein | -1,510312205 | 2,74E-05 |
| TERG\_07139 | hypothetical protein | -1,512314107 | 3,90E-05 |
| TERG\_12580 | dihydrodipicolinate synthetase family protein (T. verrucosum) | -1,512780415 | 2,13E-06 |
| TERG\_03935 | hypothetical protein | -1,513395731 | 2,46E-06 |
| TERG\_02303 | ankyrin repeat protein (A. benhamiae) | -1,513772725 | 0,000206894 |
| TERG\_08708 | SesA protein (T. equinum) | -1,514486968 | 0,002310172 |
| TERG\_08346 | hypothetical protein | -1,521544944 | 0,000753497 |
| TERG\_08363 | tyrosinase (T. verrucosum) | -1,52290396 | 9,94E-11 |
| TERG\_08587 | AtaP4 protein (T. equinum) | -1,53279882 | 0,001971153 |
| TERG\_06802 | hypothetical protein | -1,541070704 | 0,027220788 |
| TERG\_00967 | hypothetical protein | -1,547422689 | 5,94E-06 |
| TERG\_12085 | hypothetical protein | -1,548153807 | 1,29E-06 |
| TERG\_03157 | NDT80 / PhoG like DNA-binding family protein (A. benhamiae) | -1,559026358 | 5,64E-08 |
| TERG\_05604 | C6 finger domain-containing protein (T. equinum) | -1,561727378 | 4,35E-05 |
| TERG\_03132 | hypothetical protein | -1,574519781 | 1,15E-05 |
| TERG\_08924 | MIZ zinc finger domain protein (A. benhamiae) | -1,57948192 | 0,000244348 |
| TERG\_08029 | HMG box protein, putative (T. verrucosum) | -1,58219809 | 2,76E-07 |
| TERG\_07410 | hypothetical protein | -1,584201135 | 1,70E-05 |
| TERG\_05429 | MFS multidrug transporter, putative (T. verrucosum) | -1,595361403 | 2,28E-06 |
| TERG\_02837 | 3-beta hydroxysteroid dehydrogenase/isomerase family protein, putative (T. verrucosum) | -1,596134227 | 4,11E-08 |
| TERG\_01346 | lipase/serine esterase (T. tonsurans) | -1,605818841 | 0,00016842 |
| TERG\_03753 | hypothetical protein | -1,608028313 | 3,10E-05 |
| TERG\_05274 | hypothetical protein | -1,61413168 | 2,04E-05 |
| TERG\_05055 | MFS multidrug transporter (T. tonsurans) | -1,616374262 | 3,83E-08 |
| TERG\_04184 | CorA family metal ion transporter, putative (A. benhamiae) | -1,616908252 | 4,22E-08 |
| TERG\_05617 | hypothetical protein | -1,627450633 | 4,99E-05 |
| TERG\_01794 | C6 zinc finger domain-containing protein (M. canis) | -1,641383575 | 0,000247535 |
| TERG\_06358 | dicer (T. tonsurans) | -1,65923152 | 3,40E-09 |
| TERG\_03777 | hypothetical protein | -1,663121436 | 2,40E-05 |
| TERG\_08278 | serine/threonine protein kinase (T. tonsurans) | -1,674484405 | 5,56E-07 |
| TERG\_08503 | secalin (M. canis) | -1,675958946 | 2,09E-05 |
| TERG\_03343 | fatty acid desaturase (T. equinum) | -1,680964749 | 7,48E-15 |
| TERG\_03963 | mannosyl phosphorylinositol ceramide synthase SUR1 (T. equinum) | -1,682415076 | 4,97E-07 |
| TERG\_12093 | poly(ADP)-ribose polymerase PARP, putative (T. verrucosum) | -1,684899368 | 7,47E-09 |
| TERG\_12682 | hypothetical protein | -1,68693666 | 1,13E-09 |
| TERG\_01480 | MFS multidrug transporter, putative (A. benhamiae) | -1,687967447 | 2,88E-07 |
| TERG\_07892 | SCP-like extracellular protein, putative (A. benhamiae) | -1,690396737 | 1,62E-07 |
| TERG\_05746 | hypothetical protein | -1,690910792 | 1,16E-05 |
| TERG\_06228 | hypothetical protein | -1,698389083 | 4,42E-05 |
| TERG\_02787 | polyketide synthase (T. tonsurans) | -1,699126512 | 2,74E-08 |
| TERG\_03706 | trichodiene oxygenase (T. equinum) | -1,702118112 | 2,85E-08 |
| TERG\_03926 | hypothetical protein | -1,706246317 | 1,24E-05 |
| TERG\_05680 | IBR domain containing protein (T. equinum) | -1,706368455 | 5,78E-07 |
| TERG\_03459 | GDSL Lipase/Acylhydrolase family protein (A. benhamiae) | -1,707927779 | 7,04E-07 |
| TERG\_08597 | ankyrin repeat protein (T. equinum) | -1,708566915 | 1,25E-06 |
| TERG\_03095 | methyltransferase, putative (A. benhamiae) | -1,70951635 | 6,86E-06 |
| TERG\_06414 | DUF1338 domain-containing protein (T. equinum) | -1,711418844 | 4,31E-06 |
| TERG\_05492 | hypothetical protein | -1,712644136 | 0,000150143 |
| TERG\_00619 | tripeptidyl-peptidase SED2 | -1,71730447 | 0,0002293 |
| TERG\_07282 | cytochrome P450 monooxygenase, putative (T. verrucosum) | -1,71939136 | 2,31E-08 |
| TERG\_08045 | DUF455 domain-containing protein (T. equinum) | -1,722413502 | 3,22E-13 |
| TERG\_08046 | beta-lactamase (M. gypseum) | -1,732204637 | 0,011164404 |
| TERG\_03291 | SNF2 family helicase, putative (T. verrucosum) | -1,734575784 | 0,00186468 |
| TERG\_03681 | leucine aminopeptidase (T. equinum) | -1,737555643 | 4,49E-05 |
| TERG\_05876 | hypothetical protein | -1,742987972 | 2,99E-06 |
| TERG\_02350 | endochitinase (T. equinum) | -1,747531603 | 1,85E-07 |
| TERG\_11800 | serine/threonine protein kinase (T. equinum) | -1,753397349 | 0,000543772 |
| TERG\_00257 | conserved predicted protein (A. benhamiae) | -1,754154432 | 1,51E-08 |
| TERG\_01728 | hypothetical protein | -1,759599695 | 4,65E-07 |
| TERG\_02593 | C2H2 finger domain protein, putative (T. verrucosum) | -1,760859057 | 2,56E-10 |
| TERG\_07346 | tRNA ligase (M. gypseum) | -1,767907919 | 1,10E-09 |
| TERG\_00199 | serine/threonine protein kinase | -1,768985993 | 6,16E-06 |
| TERG\_00539 | F-box and WD40 domain-containing protein (T. tonsurans) | -1,773450828 | 5,09E-07 |
| TERG\_06022 | hypothetical protein | -1,774949755 | 4,59E-07 |
| TERG\_04263 | hypothetical protein | -1,778879926 | 0,000222174 |
| TERG\_05616 | hypothetical protein | -1,779865957 | 2,81E-08 |
| TERG\_12708 | inositol kinase kinase (UvsB), putative (A. benhamiae) | -1,781678483 | 0,002683465 |
| TERG\_03984 | major facilitator superfamily transporter MFS-1 (M. canis) | -1,782224216 | 1,42E-06 |
| TERG\_01511 | hypothetical protein | -1,79558765 | 4,05E-08 |
| TERG\_02958 | sulfite reductase flavoprotein component (T. equinum) | -1,816943235 | 3,06E-10 |
| TERG\_12372 | multidrug resistance protein (T. tonsurans) | -1,818055472 | 3,01E-06 |
| TERG\_06552 | aspartic-type endopeptidase (OpsB), putative (T. verrucosum) | -1,819999488 | 2,97E-14 |
| TERG\_08614 | hypothetical protein | -1,823703634 | 1,62E-05 |
| TERG\_04234 | hydrophobin, putative (T. verrucosum) | -1,844892572 | 1,83E-16 |
| TERG\_07409 | amino acid permease (T. equinum) | -1,848905376 | 1,79E-09 |
| TERG\_07037 | hypothetical protein | -1,854941797 | 1,20E-07 |
| TERG\_03707 | geranylgeranyl diphosphate synthase, putative (A. benhamiae) | -1,857975355 | 3,54E-06 |
| TERG\_02664 | hypothetical protein | -1,859287911 | 1,28E-10 |
| TERG\_04359 | hypothetical protein | -1,862092907 | 3,57E-05 |
| TERG\_05987 | GTP-binding protein 1 (T. equinum) | -1,863417471 | 5,99E-12 |
| TERG\_03929 | hypothetical protein | -1,887302943 | 2,08E-08 |
| TERG\_02405 | mating locus protein, putative (T. verrucosum) | -1,889831611 | 0,000207967 |
| TERG\_04543 | aminotransferase GliI (T. equinum) | -1,890010154 | 3,85E-11 |
| TERG\_00281 | AGC/RSK protein kinase | -1,90332388 | 1,17E-11 |
| TERG\_00736 | alpha/beta hydrolase, putative (A. benhamiae) | -1,906012509 | 0,008382817 |
| TERG\_02214 | carboxypeptidase 2 | -1,911872661 | 1,61E-09 |
| TERG\_08613 | ABC multidrug transporter, putative (A. benhamiae) | -1,935841886 | 1,97E-12 |
| TERG\_08267 | oxidoreductase (T. equinum) | -1,93651766 | 4,31E-05 |
| TERG\_00213 | hypothetical protein | -1,943310532 | 2,24E-05 |
| TERG\_06625 | serine protease, putative (A. benhamiae) | -1,946736171 | 9,16E-13 |
| TERG\_08190 | Mrsp1 (T. equinum) | -1,947727253 | 0,010205542 |
| TERG\_05469 | hypothetical protein | -1,950078611 | 4,72E-12 |
| TERG\_03384 | aspartate aminotransferase, putative (A. benhamiae) | -1,952069065 | 3,87E-08 |
| TERG\_12092 | poly(ADP)-ribose polymerase PARP, putative (T. verrucosum) | -1,952224234 | 6,64E-07 |
| TERG\_07597 | SOK1 (T. equinum) | -1,968615377 | 2,14E-12 |
| TERG\_03552 | serine carboxypeptidase (T. tonsurans) | -1,970112177 | 4,15E-07 |
| TERG\_08961 | hypothetical protein | -1,977002289 | 4,56E-08 |
| TERG\_00487 | hypothetical protein | -1,981182882 | 4,46E-09 |
| TERG\_01802 | hypothetical protein | -1,985947202 | 0,000393216 |
| TERG\_05456 | hypothetical protein | -1,993286067 | 6,00E-09 |
| TERG\_03851 | serine/threonine protein kinase | -1,996142371 | 6,10E-11 |
| TERG\_06679 | MFS transporter, putative (A. benhamiae) | -2,003706234 | 9,29E-13 |
| TERG\_08130 | ABC ATPase (T. equinum) | -2,025307168 | 6,72E-13 |
| TERG\_03955 | RNA 3'-terminal phosphate cyclase, putative (T. verrucosum) | -2,052098304 | 1,83E-07 |
| TERG\_05142 | dimeric dihydrodiol dehydrogenase, putative (T. verrucosum) | -2,058117238 | 1,29E-07 |
| TERG\_00638 | cellobiose dehydrogenase, putative (A. benhamiae) | -2,061700324 | 5,25E-15 |
| TERG\_03790 | DUF1275 domain-containing protein (T. equinum) | -2,062335021 | 1,45E-08 |
| TERG\_06347 | hypothetical protein | -2,072790761 | 2,04E-10 |
| TERG\_08022 | bZIP transcription factor CpcA (T. verrucosum) | -2,072986329 | 4,99E-12 |
| TERG\_05408 | ThiJ/PfpI family protein (T. tonsurans) | -2,081529259 | 6,57E-05 |
| TERG\_01116 | hypothetical protein | -2,092454711 | 2,50E-11 |
| TERG\_00791 | developmental regulatory protein WetA (T. verrucosum) | -2,096437133 | 5,72E-15 |
| TERG\_05615 | hsp70-like protein (T. equinum) | -2,105350667 | 1,31E-07 |
| TERG\_07795 | WSC domain protein, putative (A. benhamiae) | -2,110234558 | 6,52E-15 |
| TERG\_12606 | protease DPPV, putative (A. benhamiae) | -2,113442129 | 1,79E-10 |
| TERG\_07665 | hypothetical protein | -2,137010783 | 7,95E-12 |
| TERG\_00734 | dipeptidase (T. tonsurans) | -2,150608143 | 1,02E-09 |
| TERG\_00709 | MOSC domain-containing protein (T. equinum) | -2,152532953 | 1,97E-12 |
| TERG\_11968 | hypothetical protein | -2,169039889 | 2,37E-11 |
| TERG\_11814 | FAD dependent oxidoreductase, putative (A. benhamiae) | -2,176538234 | 1,33E-08 |
| TERG\_11813 | FAD dependent oxidoreductase, putative (A. benhamiae) | -2,220187029 | 1,15E-05 |
| TERG\_02400 | amino acid transporter, putative (A. benhamiae) | -2,226191109 | 6,46E-10 |
| TERG\_00523 | hypothetical protein | -2,257724287 | 1,81E-09 |
| TERG\_04615 | hypothetical protein | -2,272670859 | 2,31E-07 |
| TERG\_02517 | N-acetyltransferase, GNAT family, putative (A. benhamiae) | -2,283133078 | 3,24E-17 |
| TERG\_12438 | gamma-glutamyltranspeptidase (T. tonsurans) | -2,314926857 | 4,58E-10 |
| TERG\_12238 | integral membrane protein (M. gypseum) | -2,324823244 | 0,000256516 |
| TERG\_07008 | diaminopropionate ammonia-lyase (T. equinum) | -2,325768579 | 5,42E-28 |
| TERG\_08298 | RTA1 domain-containing protein (T. equinum) | -2,334004504 | 1,43E-11 |
| TERG\_00066 | 4-hydroxyphenylpyruvate dioxygenase | -2,334568697 | 1,79E-12 |
| TERG\_11998 | potassium uptake transporter (T. equinum) | -2,344505021 | 7,49E-09 |
| TERG\_02406 | alpha-box mating type protein (T. tonsurans) | -2,34733509 | 7,48E-15 |
| TERG\_00068 | homogentisate 1,2-dioxygenase | -2,357002608 | 2,59E-12 |
| TERG\_02183 | C2H2 finger domain-containing protein (T. equinum) | -2,380988186 | 2,20E-12 |
| TERG\_07673 | hypothetical protein | -2,424286936 | 9,92E-16 |
| TERG\_05141 | NCS1 nucleoside transporter (T. equinum) | -2,477538208 | 4,01E-10 |
| TERG\_08191 | glucooligosaccharide oxidase (T. equinum) | -2,484680724 | 1,63E-09 |
| TERG\_02534 | hypothetical protein | -2,487194211 | 1,59E-11 |
| TERG\_05650 | blasticidin-resistance protein (T. tonsurans) | -2,487494242 | 5,95E-08 |
| TERG\_05625 | class V chitinase, putative (T. verrucosum) | -2,488833697 | 1,03E-25 |
| TERG\_01782 | hypothetical protein | -2,545075978 | 5,77E-19 |
| TERG\_06701 | gamma-glutamyltransferase | -2,551168496 | 5,23E-13 |
| TERG\_05451 | integral membrane protein (T. equinum) | -2,559138889 | 1,64E-13 |
| TERG\_02704 | short-chain dehydrogenase/reductase, putative (A. benhamiae) | -2,583320908 | 1,28E-10 |
| TERG\_07796 | oxidoreductase, short-chain dehydrogenase/reductase family (A. benhamiae) | -2,587924649 | 3,37E-16 |
| TERG\_12239 | integral membrane protein (M. gypseum) | -2,60517591 | 7,54E-08 |
| TERG\_05627 | LysM domain-containing protein (M. canis) | -2,653018797 | 1,36E-05 |
| TERG\_01338 | hydantoinase (T. equinum) | -2,653464683 | 1,63E-12 |
| TERG\_07734 | O-methyltransferase, putative (T. verrucosum) | -2,659811733 | 3,04E-06 |
| TERG\_01454 | dipeptidyl aminopeptidase (T. equinum) | -2,660129624 | 2,06E-12 |
| TERG\_08709 | SesA protein (T. equinum) | -2,662731082 | 7,76E-09 |
| TERG\_03719 | MFS sugar transporter (T. tonsurans) | -2,683139015 | 1,86E-14 |
| TERG\_11997 | potassium uptake transporter (T. equinum) | -2,741941704 | 2,33E-10 |
| TERG\_00119 | CAMK/CAMKL/GIN4 protein kinase | -2,745418796 | 1,59E-11 |
| TERG\_05799 | chlorophyll synthesis pathway protein BchC | -2,812158111 | 5,97E-21 |
| TERG\_05537 | MFS multidrug transporter (T. equinum) | -2,82750897 | 3,10E-10 |
| TERG\_03998 | aspartic proteinase II-1 (T. equinum) | -2,837526091 | 2,54E-07 |
| TERG\_07184 | HMG box transcriptional regulator, putative (A. benhamiae) | -2,870010179 | 1,60E-15 |
| TERG\_12578 | PEP phosphonomutase (T. equinum) | -2,895554693 | 2,70E-15 |
| TERG\_01783 | hypothetical protein | -2,971859843 | 1,58E-19 |
| TERG\_11747 | hypothetical protein | -3,043553103 | 8,64E-30 |
| TERG\_12029 | hypothetical protein | -3,088108237 | 1,19E-32 |
| TERG\_03981 | hypothetical protein | -3,119617529 | 6,88E-29 |
| TERG\_01599 | hypothetical protein | -3,254366618 | 1,64E-45 |
| TERG\_04547 | aquaporin (T. tonsurans) | -3,292204861 | 5,17E-19 |
| TERG\_07280 | hypothetical protein | -3,395350477 | 1,46E-15 |
| TERG\_05854 | beta-lactamase (T. tonsurans) | -3,463687951 | 2,72E-36 |
| TERG\_08980 | hypothetical protein | -3,470683729 | 8,82E-21 |
| TERG\_06883 | NAD dependent epimerase/dehydratase family protein (T. verrucosum) | -3,509593585 | 3,86E-48 |
| TERG\_12626 | C-5 sterol desaturase (T. equinum) | -3,592118691 | 2,01E-27 |
| TERG\_12627 | C-5 sterol desaturase (T. equinum) | -3,644110845 | 7,98E-30 |
| TERG\_00806 | hypothetical protein | -3,645672359 | 2,31E-28 |
| TERG\_08004 | hypothetical protein | -3,717474519 | 7,51E-36 |
| TERG\_00911 | hypothetical protein | -3,766204012 | 8,44E-48 |
| TERG\_01981 | hypothetical protein | -4,126003823 | 7,00E-61 |
| TERG\_02746 | hypothetical protein | -4,181367463 | 1,19E-33 |
| TERG\_05266 | integral membrane protein (T. equinum) | -4,304476086 | 9,51E-13 |
| TERG\_06291 | malate dehydrogenase (T. verrucosum) | -4,429662622 | 6,47E-37 |
| TERG\_07769 | hypothetical protein | -4,900443108 | 2,85E-49 |
| TERG\_04728 | nuclear transcription factor Y subunit B-7 (T. equinum) | -5,743756524 | 2,15E-33 |
| TERG\_07516 | hypothetical protein | -5,761609782 | 2,02E-35 |