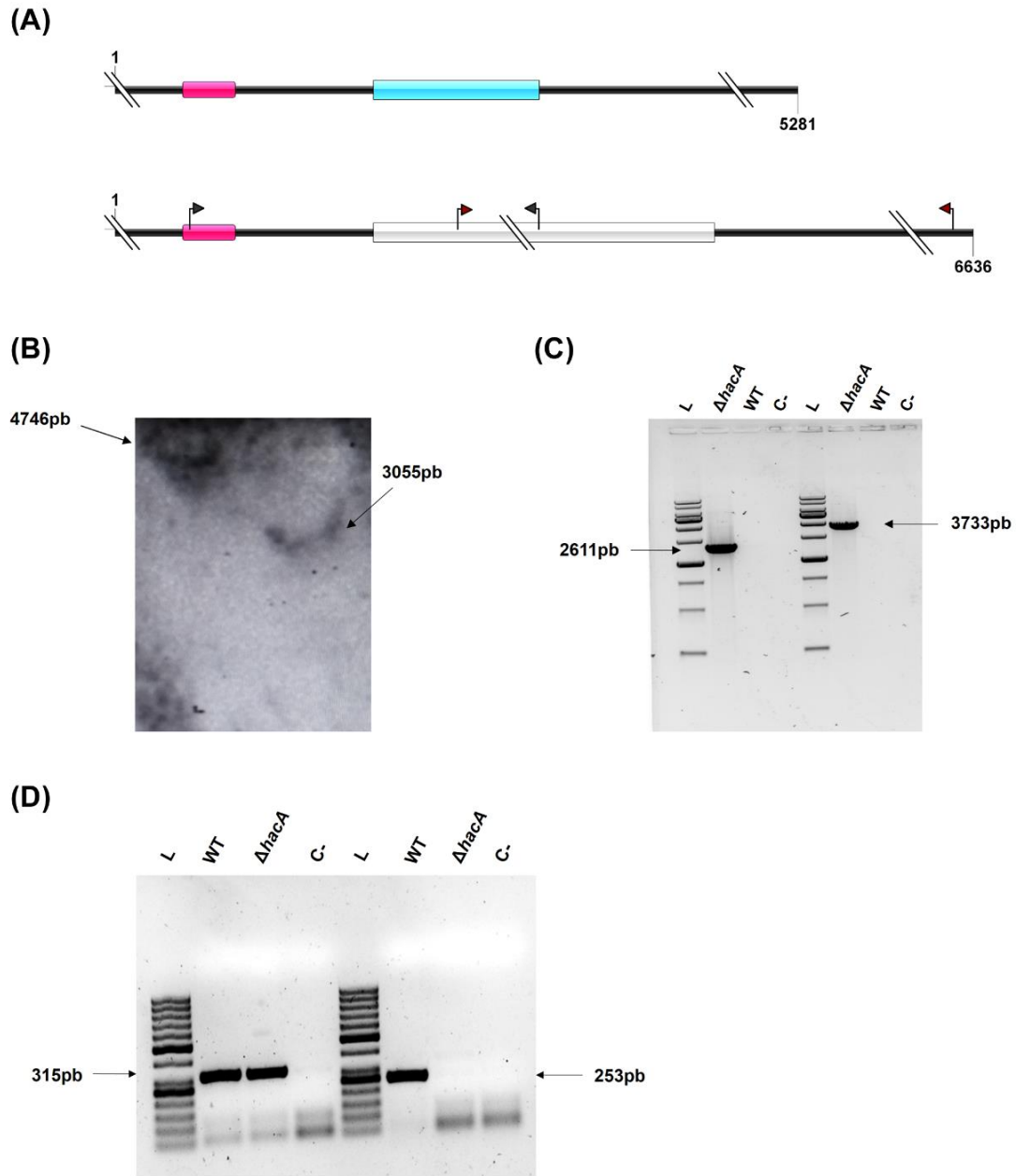
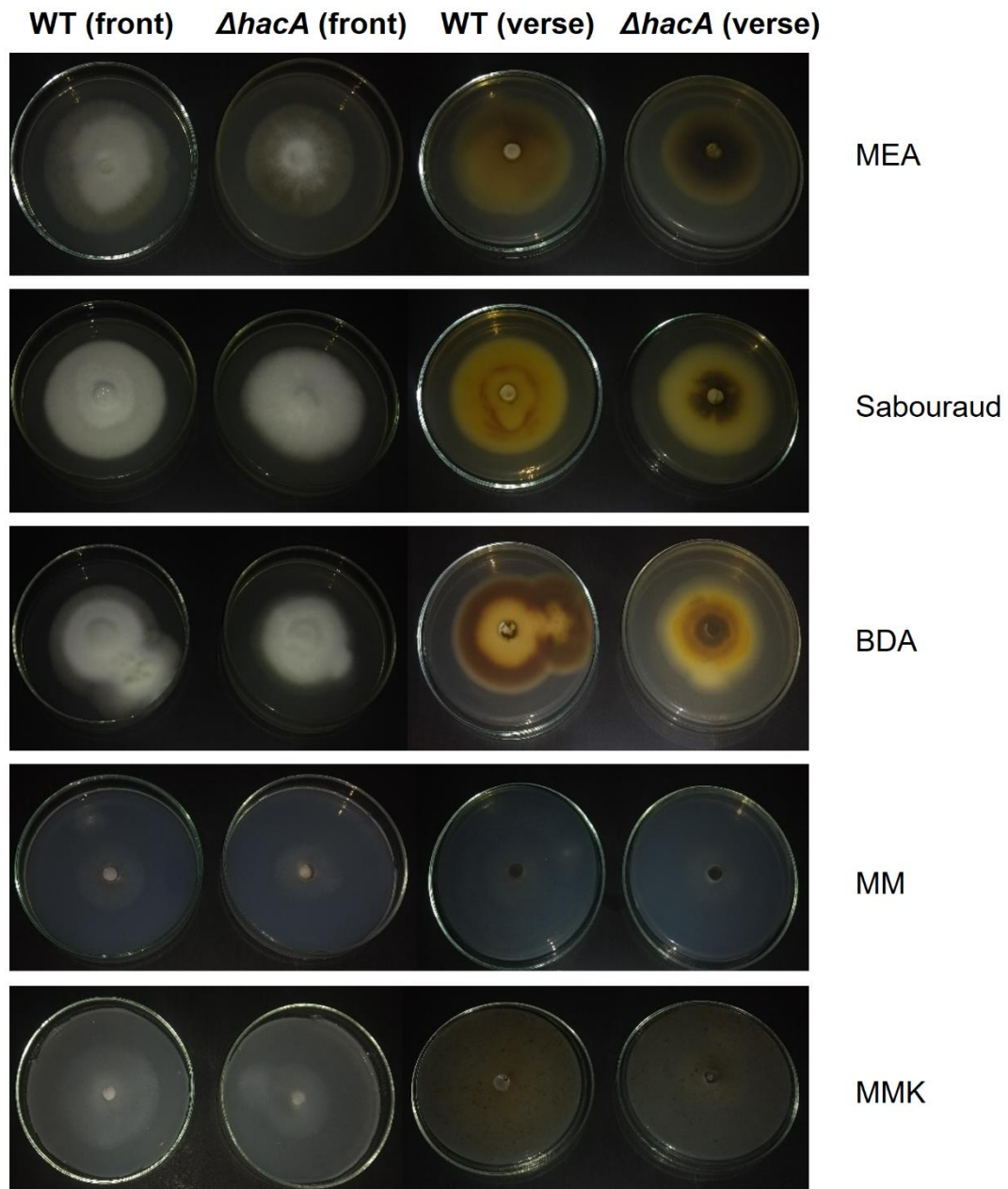


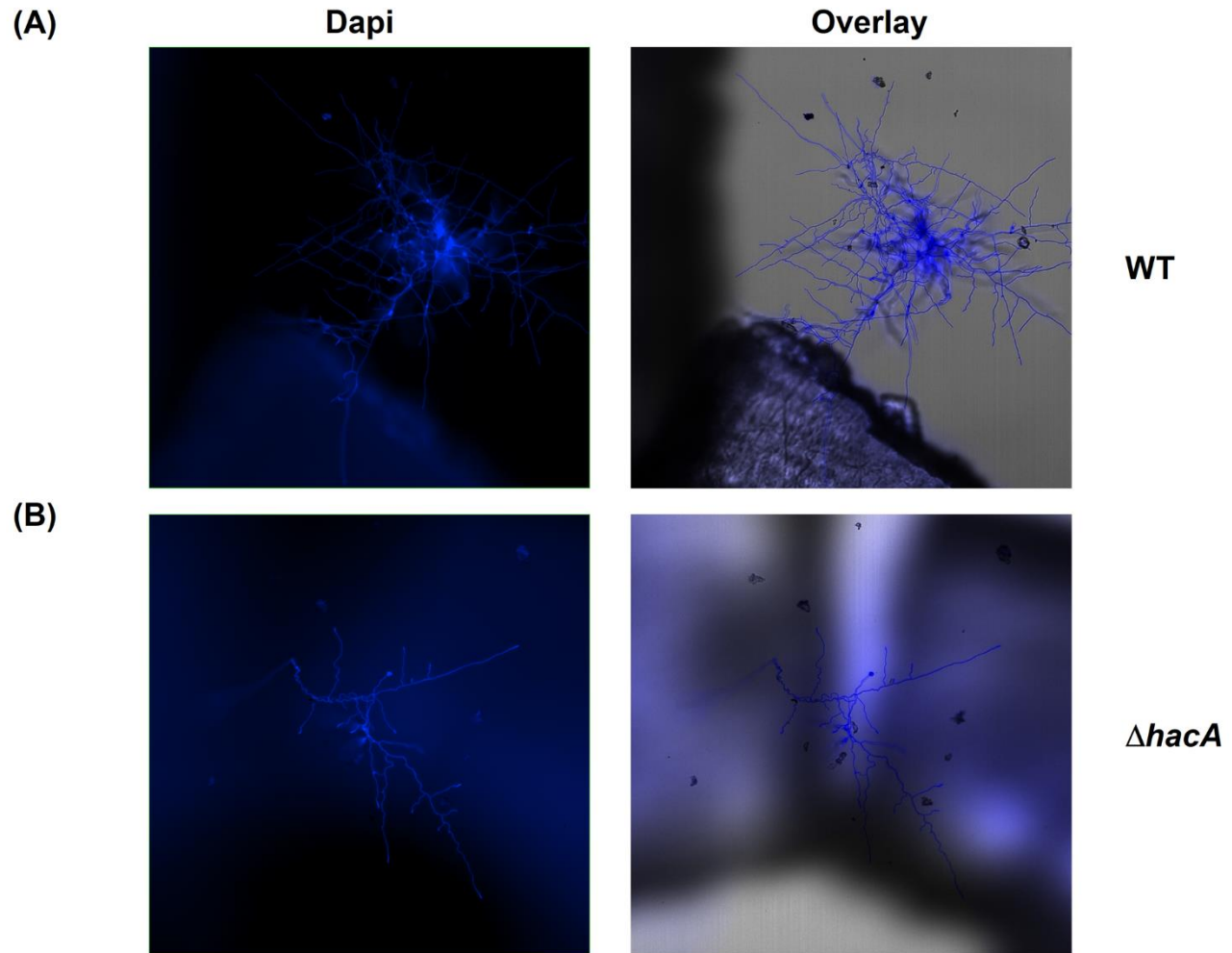
*Supplementary Material*



**Supplementary Figure S1.** Schematic representation of the Southern blot assay. (A) Overview of *hacA* gene: coding sequence indicated by a light blue rectangle, and 5' UTR and 3' UTR regions depicted with black rectangles. The deletion cassette is represented by the removal of the coding sequence and the insertion of a hygromycin resistance gene (light gray rectangle). Restriction sites for BtgZI are represented by cut lines, and the *hacA* fragment which was used as probe is indicated by a pink box. Arrows are used to represent primers used for PCR reactions carried out to gene deletion confirmation. (B) Southern blot of the digested DNAs with BTgZI was probed with a *hacA* fragment. The expected fragments are depicted in the figure as 4746 pb for WT and 3055 pb for mutant strain. (C) Amplification with primers flanking the region of 5'UTR*hacA* and *hph* or 3'UTR*hacA* and *hph* from  $\Delta$ *hacA* strain. (D) Amplification of a 253 bp internal region of the *hacA* gene from wild type strain. Amplification with primers for  $\beta$ -tubulin (315 pb) was used as a control.



**Supplementary Figure S2.** *hacA* is involved in *T. rubrum* pigmentation during growth in different cultures.



**Supplementary Figure S3.** Analysis of *hacA* gene deletion on the growth of *T. rubrum* on human nail fragments after staining with CFW 2  $\mu\text{g/ml}$  for 5 min. Conidia (approximately  $10^4$ ) from (A) wild type and (B) mutant strain were incubated on human nails for 72 h at 28 °C. Stained fungal cells was visualized under DAPI channel using ImageXpress Micro XLS system at magnification  $\times 100$ .

**Supplementary Table S1.** Set of primers used for the *hacA* deletion cassette.

| <b>ID</b>                      | <b>Sequence 5'-3'</b>   | <b>pb</b> |
|--------------------------------|---|-----------|
| <i>hacA</i> 5'UTR              | F: GACGACTTGGGTCTGCATAT<br>R: ACTGGCCGTCGTTTTACGGTGTGGCTGTCTTCTGTCAAA | 2012      |
| <i>hacA</i> 3'UTR              | F: GTCATAGCTGTTTCCTGGAGTGCAATGCTCGGATC<br>R: ATCACAAGCGGGTAACATCCAC   | 1994      |
| <i>hph</i> marker              | F: GTAAAACGACGGCCAGT<br>R: CAGGAAACAGCTATGAC                          | 2636      |
| 5' <i>hacA</i> split<br>marker | F: CGGCCTGGAAGTGGTATTATT<br><i>hph</i> R: GATGTTGGCGACCTCGTATT        | 2611      |
| 3' <i>hacA</i> split marker    | <i>hph</i> F: CTGCCTGAAACCGAACTGC<br>R: GGGAACACATCCACAGGTATTG        | 3733      |

**Supplementary Table S2.** *In silico* prediction of DNA-binding sites for the HacA consensus (UPRE-1 CAGNGTG, UPRE-2 TACGTG ,UPRE-3 AGGACAAC).

| ID         | Gene Product Name  | Consensus    | Position | Type   |
|------------|--|--------------|----------|--------|
| TERG_00004 | alanine aminotransferase ( <i>T. tonsurans</i> )   | CAGTGTG      | 710      | UPRE-1 |
| TERG_00014 | hypothetical protein   | CACCCTG (rc) | 190      | UPRE-1 |
| TERG_00015 | stromal membrane-associated protein ( <i>T. equinum</i> )                                | CACTCTG (rc) | 209      | UPRE-1 |
| TERG_00026 | flavin-binding monooxygenase, putative ( <i>T. verrucosum</i> )                          | CAGGGTG      | 330      | UPRE-1 |
| TERG_00033 | chromosomal organization and DNA repair protein Mms21, putative ( <i>T. verrucosum</i> ) | CACTCTG (rc) | 992      | UPRE-1 |
| TERG_00034 | mRNA cap guanine-N7 methyltransferase  | CACTCTG (rc) | 685      | UPRE-1 |
| TERG_00041 | hypothetical protein   | CAGGGTG      | 267      | UPRE-1 |
| TERG_00056 | IBR domain-containing protein ( <i>M. gypseum</i> )                                      | CACCCTG (rc) | 170      | UPRE-1 |
| TERG_00059 | hypothetical protein   | CACCCTG (rc) | 150      | UPRE-1 |
| TERG_00060 | GPI anchored cell wall protein, putative ( <i>A. benhamiae</i> )                         | CAGGGTG      | 647      | UPRE-1 |
| TERG_00061 | GDP-mannose pyrophosphorylase A ( <i>T. equinum</i> )                                    | CACCCTG (rc) | 392      | UPRE-1 |
| TERG_00062 | dynamain GTPase, putative ( <i>T. verrucosum</i> )                                       | CAGGGTG      | 623      | UPRE-1 |
| TERG_00078 | nicotinate (nicotinamide) nucleotide adenylyltransferase                                 | CACGCTG (rc) | 820      | UPRE-1 |
| TERG_00084 | chromosome segregation protein (Pcs1), putative ( <i>T. verrucosum</i> )                 | CACGCTG (rc) | 953      | UPRE-1 |
| TERG_00092 | ubiquinone biosynthesis methyltransferase coq5 ( <i>T. equinum</i> )                     | CACGCTG (rc) | 365      | UPRE-1 |
| TERG_00099 | cytochrome P450 family protein ( <i>T. equinum</i> )                                     | CAGTGTG      | 951      | UPRE-1 |
| TERG_00100 | flavin-containing monooxygenase ( <i>T. equinum</i> )                                    | CACACTG (rc) | 557      | UPRE-1 |
| TERG_00103 | hypothetical protein   | CAGAGTG      | 323      | UPRE-1 |
| TERG_00107 | ubiquitin-conjugating enzyme E2 N  | CACCCTG (rc) | 805      | UPRE-1 |
| TERG_00108 | WD repeat protein ( <i>T. equinum</i> )  | CAGGGTG      | 933      | UPRE-1 |
| TERG_00109 | thioesterase family protein ( <i>A. benhamiae</i> )                                      | CACTCTG (rc) | 526      | UPRE-1 |
| TERG_00110 | ubiquitin C-terminal hydrolase ( <i>T. tonsurans</i> )                                   | CACGCTG (rc) | 164      | UPRE-1 |
| TERG_00111 | ARP2/3 complex 20 kDa subunit ( <i>T. tonsurans</i> )                                    | CAGTGTG      | 411      | UPRE-1 |
| TERG_00112 | hypothetical protein   | CAGCGTG      | 167      | UPRE-1 |
| TERG_00114 | hypothetical protein   | CAGAGTG      | 849      | UPRE-1 |
| TERG_00119 | CAMK/CAMKL/GIN4 protein kinase   | CACCCTG (rc) | 930      | UPRE-1 |
| TERG_00132 | signal peptide peptidase ( <i>T. tonsurans</i> )   | CAGTGTG      | 194      | UPRE-1 |
| TERG_00151 | hypothetical protein   | CAGTGTG      | 277      | UPRE-1 |
| TERG_00153 | actin associated protein Wsp1 ( <i>T. equinum</i> )                                      | CACACTG (rc) | 209      | UPRE-1 |
| TERG_00160 | GNAT family acetyltransferase, putative ( <i>A. benhamiae</i> )                          | CACGCTG (rc) | 389      | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_00163 | siderochrome-iron transporter, putative ( <i>A. benhamiae</i> )      | CACACTG (rc) | 934 | UPRE-1 |
| TERG_00164 | FAD dependent sulfhydryl oxidase Erv2 ( <i>T. tonsurans</i> )        | CAGTGTG      | 281 | UPRE-1 |
| TERG_00172 | hypothetical protein   | CACGCTG (rc) | 737 | UPRE-1 |
| TERG_00176 | hydroxyisourate hydrolase  | CAGCGTG      | 208 | UPRE-1 |
| TERG_00184 | ribose-phosphate pyrophosphokinase ( <i>T. tonsurans</i> )           | CACCCTG (rc) | 277 | UPRE-1 |
| TERG_00190 | ribosomal protein S15  | CAGTGTG      | 311 | UPRE-1 |
| TERG_00191 | hypothetical protein   | CAGCGTG      | 57  | UPRE-1 |
| TERG_00191 | hypothetical protein   | CAGCGTG      | 470 | UPRE-1 |
| TERG_00194 | Rad2-like endonuclease, putative ( <i>T. verrucosum</i> )            | CACGCTG (rc) | 680 | UPRE-1 |
| TERG_00195 | hypothetical protein   | CAGCGTG      | 828 | UPRE-1 |
| TERG_00196 | hypothetical protein   | CAGAGTG      | 720 | UPRE-1 |
| TERG_00197 | aldose 1-epimerase family protein, putative ( <i>T. verrucosum</i> ) | CACACTG (rc) | 447 | UPRE-1 |
| TERG_00198 | AT DNA binding protein, putative ( <i>T. verrucosum</i> )            | CAGTGTG      | 339 | UPRE-1 |
| TERG_00211 | proteasome subunit alpha type 6 ( <i>T. equinum</i> )                | CACCCTG (rc) | 988 | UPRE-1 |
| TERG_00212 | proteasome subunit alpha type-6 ( <i>T. equinum</i> )                | CAGTGTG      | 453 | UPRE-1 |
| TERG_00212 | proteasome subunit alpha type-6 ( <i>T. equinum</i> )                | CAGGGTG      | 541 | UPRE-1 |
| TERG_00221 | hypothetical protein   | CACACTG (rc) | 127 | UPRE-1 |
| TERG_00228 | ThiJ/PfpI family protein ( <i>A. benhamiae</i> )                     | CACACTG (rc) | 439 | UPRE-1 |
| TERG_00230 | RINT-1 family protein ( <i>T. equinum</i> )                          | CAGTGTG      | 294 | UPRE-1 |
| TERG_00245 | PHD finger domain protein, putative ( <i>T. verrucosum</i> )         | CACACTG (rc) | 341 | UPRE-1 |
| TERG_00255 | trimethyllysine dioxygenase  | CAGCGTG      | 988 | UPRE-1 |
| TERG_00279 | pre-mRNA splicing factor ( <i>T. equinum</i> )                       | CAGGGTG      | 95  | UPRE-1 |
| TERG_00280 | dihydroneopterin aldolase domain protein ( <i>A. benhamiae</i> )     | CAGCGTG      | 396 | UPRE-1 |
| TERG_00285 | hypothetical protein   | CAGTGTG      | 934 | UPRE-1 |
| TERG_00289 | hypothetical protein   | CACACTG (rc) | 299 | UPRE-1 |
| TERG_00290 | Ccr4-Not transcription complex subunit NOT1 ( <i>T. tonsurans</i> )  | CACCCTG (rc) | 211 | UPRE-1 |
| TERG_00293 | DASH complex subunit Duo1, putative ( <i>T. verrucosum</i> )         | CACACTG (rc) | 655 | UPRE-1 |
| TERG_00296 | hypothetical protein   | CAGCGTG      | 164 | UPRE-1 |
| TERG_00297 | galactokinase  | CACGCTG (rc) | 171 | UPRE-1 |
| TERG_00299 | acetolactate synthase, large subunit, biosynthetic type              | CAGCGTG      | 684 | UPRE-1 |
| TERG_00310 | dolichol-phosphate mannosyltransferase ( <i>T. tonsurans</i> )       | CACACTG (rc) | 628 | UPRE-1 |
| TERG_00310 | dolichol-phosphate mannosyltransferase ( <i>T. tonsurans</i> )       | CACTCTG (rc) | 720 | UPRE-1 |
| TERG_00311 | hypothetical protein   | CAGAGTG      | 707 | UPRE-1 |
| TERG_00311 | hypothetical protein   | CAGTGTG      | 799 | UPRE-1 |
| TERG_00357 | SNARE-dependent exocytosis protein ( <i>T. tonsurans</i> )           | CAGAGTG      | 422 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_00362 | glutaminase ( <i>T. equinum</i> )   | CACTCTG (rc) | 954 | UPRE-1 |
| TERG_00366 | hypothetical protein  | CAGCGTG      | 129 | UPRE-1 |
| TERG_00377 | hypothetical protein  | CAGGGTG      | 480 | UPRE-1 |
| TERG_00392 | integral membrane protein ( <i>T. equinum</i> )                                     | CACACTG (rc) | 490 | UPRE-1 |
| TERG_00412 | CMGC/SRPK protein kinase ( <i>T. tonsurans</i> )                                    | CAGAGTG      | 619 | UPRE-1 |
| TERG_00416 | phenylacetaldoxime dehydratase family protein, putative ( <i>A. benhamiae</i> )     | CAGAGTG      | 174 | UPRE-1 |
| TERG_00421 | TBC domain protein, putative ( <i>T. verrucosum</i> )                               | CAGCGTG      | 544 | UPRE-1 |
| TERG_00447 | hypothetical protein  | CACGCTG (rc) | 130 | UPRE-1 |
| TERG_00449 | mandelate racemase/muconate lactonizing enzyme family protein ( <i>T. equinum</i> ) | CAGCGTG      | 221 | UPRE-1 |
| TERG_00460 | protein phosphatase PP2A regulatory subunit A ( <i>T. equinum</i> )                 | CACGCTG (rc) | 334 | UPRE-1 |
| TERG_00464 | respiratory complex assembly protein Rmp1, putative ( <i>T. verrucosum</i> )        | CACTCTG (rc) | 329 | UPRE-1 |
| TERG_00471 | hypothetical protein  | CAGAGTG      | 342 | UPRE-1 |
| TERG_00477 | fungal specific transcription factor, putative ( <i>T. verrucosum</i> )             | CACGCTG (rc) | 733 | UPRE-1 |
| TERG_00480 | class I alpha-mannosidase ( <i>T. tonsurans</i> )                                   | CAGCGTG      | 510 | UPRE-1 |
| TERG_00483 | hypothetical protein  | CACTCTG (rc) | 403 | UPRE-1 |
| TERG_00488 | inositol phospholipid biosynthesis protein Scs3, putative ( <i>A. benhamiae</i> )   | CAGCGTG      | 44  | UPRE-1 |
| TERG_00512 | hypothetical protein  | CAGTGTG      | 712 | UPRE-1 |
| TERG_00524 | trans-sialidase ( <i>M. canis</i> )   | CACTCTG (rc) | 586 | UPRE-1 |
| TERG_00525 | NAK protein kinase  | CAGAGTG      | 494 | UPRE-1 |
| TERG_00528 | hypothetical protein  | CAGAGTG      | 11  | UPRE-1 |
| TERG_00528 | hypothetical protein  | CAGCGTG      | 291 | UPRE-1 |
| TERG_00528 | hypothetical protein  | CAGGGTG      | 607 | UPRE-1 |
| TERG_00535 | calcium-translocating P-type ATPase, PMCA-type                                      | CACACTG (rc) | 970 | UPRE-1 |
| TERG_00539 | F-box and WD40 domain-containing protein ( <i>T. tonsurans</i> )                    | CAGAGTG      | 207 | UPRE-1 |
| TERG_00546 | glutaredoxin  | CAGTGTG      | 270 | UPRE-1 |
| TERG_00548 | elongation factor 1-alpha   | CACACTG (rc) | 64  | UPRE-1 |
| TERG_00548 | elongation factor 1-alpha   | CACCCTG (rc) | 632 | UPRE-1 |
| TERG_00553 | amino acid permease ( <i>T. equinum</i> )   | CACTCTG (rc) | 345 | UPRE-1 |
| TERG_00555 | hypothetical protein  | CAGAGTG      | 910 | UPRE-1 |
| TERG_00574 | MFS multidrug transporter, putative ( <i>T. verrucosum</i> )                        | CACCCTG (rc) | 822 | UPRE-1 |
| TERG_00604 | nucleolar protein ( <i>T. equinum</i> )   | CACTCTG (rc) | 702 | UPRE-1 |
| TERG_00605 | imidazoleglycerol-phosphate dehydratase ( <i>T. equinum</i> )                       | CAGAGTG      | 446 | UPRE-1 |



|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_00606 | alpha-1,6 mannosyltransferase subunit Mnn9 ( <i>T. tonsurans</i> )          | CACGCTG (rc) | 229 | UPRE-1 |
| TERG_00606 | alpha-1,6 mannosyltransferase subunit Mnn9 ( <i>T. tonsurans</i> )          | CACTCTG (rc) | 879 | UPRE-1 |
| TERG_00613 | hypothetical protein  | CAGTGTG      | 774 | UPRE-1 |
| TERG_00615 | HLH transcription factor, putative ( <i>A. benhamiae</i> )                  | CAGGGTG      | 798 | UPRE-1 |
| TERG_00625 | glycolipid anchored surface protein (GAS1) ( <i>T. equinum</i> )            | CAGGGTG      | 872 | UPRE-1 |
| TERG_00631 | urate oxidase   | CAGCGTG      | 108 | UPRE-1 |
| TERG_00632 | ribosomal protein L13   | CACGCTG (rc) | 608 | UPRE-1 |
| TERG_00639 | hypothetical protein  | CACCCTG (rc) | 726 | UPRE-1 |
| TERG_00639 | hypothetical protein  | CACACTG (rc) | 856 | UPRE-1 |
| TERG_00649 | DUF408 domain protein ( <i>A. benhamiae</i> )                               | CAGCGTG      | 402 | UPRE-1 |
| TERG_00658 | hypothetical protein  | CACGCTG (rc) | 684 | UPRE-1 |
| TERG_00669 | C-5 sterol desaturase ( <i>T. tonsurans</i> )                               | CACGCTG (rc) | 614 | UPRE-1 |
| TERG_00674 | actin ( <i>T. tonsurans</i> )   | CAGAGTG      | 286 | UPRE-1 |
| TERG_00683 | hypothetical protein  | CACTCTG (rc) | 218 | UPRE-1 |
| TERG_00684 | ubiquinol-cytochrome C chaperone ( <i>T. equinum</i> )                      | CAGAGTG      | 670 | UPRE-1 |
| TERG_00694 | glutamate 5-kinase  | CACTCTG (rc) | 765 | UPRE-1 |
| TERG_00696 | WEE/WEE-UNCLASSIFIED protein kinase   | CACGCTG (rc) | 77  | UPRE-1 |
| TERG_00701 | cytochrome b5, putative ( <i>T. verrucosum</i> )                            | CAGCGTG      | 354 | UPRE-1 |
| TERG_00703 | nuclear migration protein, putative ( <i>A. benhamiae</i> )                 | CACACTG (rc) | 503 | UPRE-1 |
| TERG_00707 | GPI anchored serine-threonine rich protein ( <i>T. verrucosum</i> )         | CACGCTG (rc) | 520 | UPRE-1 |
| TERG_00730 | phospholipid metabolism enzyme regulator, putative ( <i>T. verrucosum</i> ) | CACCCTG (rc) | 885 | UPRE-1 |
| TERG_00734 | dipeptidase ( <i>T. tonsurans</i> )   | CACTCTG (rc) | 375 | UPRE-1 |
| TERG_00734 | dipeptidase ( <i>T. tonsurans</i> )   | CACTCTG (rc) | 515 | UPRE-1 |
| TERG_00741 | V-ATPase in vacuolar membrane protein 1 regulator ( <i>T. equinum</i> )     | CAGCGTG      | 581 | UPRE-1 |
| TERG_00754 | hypothetical protein  | CAGCGTG      | 649 | UPRE-1 |
| TERG_00763 | hypothetical protein  | CAGAGTG      | 327 | UPRE-1 |
| TERG_00776 | MFS transporter ( <i>T. tonsurans</i> )                                     | CAGGGTG      | 136 | UPRE-1 |
| TERG_00783 | guanine nucleotide-binding protein subunit beta-like protein                | CACACTG (rc) | 820 | UPRE-1 |
| TERG_00793 | calponin domain-containing protein ( <i>T. tonsurans</i> )                  | CAGTGTG      | 462 | UPRE-1 |
| TERG_00796 | ORM1 ( <i>M. gypseum</i> )  | CACGCTG (rc) | 946 | UPRE-1 |
| TERG_00798 | zinc knuckle domain protein ( <i>T. verrucosum</i> )                        | CAGCGTG      | 627 | UPRE-1 |
| TERG_00818 | aldehyde dehydrogenase 3B1 ( <i>T. equinum</i> )                            | CACACTG (rc) | 728 | UPRE-1 |
| TERG_00828 | hypothetical protein  | CAGTGTG      | 414 | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_00857 | polyketide synthase ( <i>T. equinum</i> )                                | CAGTGTG      | 762 | UPRE-1 |
| TERG_00875 | glutamate-cysteine ligase  | CAGTGTG      | 690 | UPRE-1 |
| TERG_00881 | zinc-containing alcohol dehydrogenase, putative ( <i>T. verrucosum</i> ) | CAGAGTG      | 127 | UPRE-1 |
| TERG_00892 | hypothetical protein   | CAGAGTG      | 167 | UPRE-1 |
| TERG_00896 | hypothetical protein   | CACTCTG (rc) | 238 | UPRE-1 |
| TERG_00897 | hypothetical protein   | CAGAGTG      | 827 | UPRE-1 |
| TERG_00898 | hypothetical protein   | CACCCTG (rc) | 326 | UPRE-1 |
| TERG_00906 | cAMP-dependent protein kinase regulatory subunit                         | CACTCTG (rc) | 268 | UPRE-1 |
| TERG_00908 | extensin ( <i>M. canis</i> )   | CAGAGTG      | 691 | UPRE-1 |
| TERG_00914 | hypothetical protein   | CAGGGTG      | 92  | UPRE-1 |
| TERG_00916 | MFS sugar permease, putative ( <i>A. benhamiae</i> )                     | CAGCGTG      | 728 | UPRE-1 |
| TERG_00929 | N-acetylglucosaminyl transferase component Gpi1 ( <i>T. tonsurans</i> )  | CACGCTG (rc) | 335 | UPRE-1 |
| TERG_00936 | integral membrane protein ( <i>T. equinum</i> )                          | CACCCTG (rc) | 214 | UPRE-1 |
| TERG_00938 | RNA-binding protein (Nab3), putative ( <i>A. benhamiae</i> )             | CACTCTG (rc) | 553 | UPRE-1 |
| TERG_00939 | peptidyl-tRNA hydrolase domain protein ( <i>T. verrucosum</i> )          | CAGAGTG      | 916 | UPRE-1 |
| TERG_00949 | extracellular proline rich protein ( <i>T. verrucosum</i> )              | CAGAGTG      | 682 | UPRE-1 |
| TERG_00958 | amino acid permease ( <i>T. tonsurans</i> )                              | CACCCTG (rc) | 110 | UPRE-1 |
| TERG_00959 | RNA binding protein, putative ( <i>A. benhamiae</i> )                    | CACACTG (rc) | 100 | UPRE-1 |
| TERG_00959 | RNA binding protein, putative ( <i>A. benhamiae</i> )                    | CACCCTG (rc) | 378 | UPRE-1 |
| TERG_00960 | histone acetyltransferase ( <i>T. equinum</i> )                          | CAGGGTG      | 988 | UPRE-1 |
| TERG_00981 | hypothetical protein   | CAGAGTG      | 924 | UPRE-1 |
| TERG_00983 | eukaryotic translation initiation factor 3 subunit K                     | CAGGGTG      | 233 | UPRE-1 |
| TERG_00999 | hypothetical protein   | CACCCTG (rc) | 331 | UPRE-1 |
| TERG_01000 | hypothetical protein   | CACCCTG (rc) | 985 | UPRE-1 |
| TERG_01001 | GDP-mannose transporter  | CAGGGTG      | 698 | UPRE-1 |
| TERG_01004 | extracellular sialidase/neuraminidase ( <i>T. equinum</i> )              | CAGAGTG      | 15  | UPRE-1 |
| TERG_01016 | hypothetical protein   | CACACTG (rc) | 120 | UPRE-1 |
| TERG_01016 | hypothetical protein   | CACCCTG (rc) | 751 | UPRE-1 |
| TERG_01017 | cytoplasm to vacuole targeting Vps64 ( <i>T. equinum</i> )               | CAGGGTG      | 754 | UPRE-1 |
| TERG_01050 | metal homeostatis protein bsd2 ( <i>T. tonsurans</i> )                   | CACCCTG (rc) | 315 | UPRE-1 |
| TERG_01051 | hypothetical protein   | CAGTGTG      | 259 | UPRE-1 |
| TERG_01053 | MFS monocarboxylate transporter, putative ( <i>T. verrucosum</i> )       | CAGAGTG      | 95  | UPRE-1 |
| TERG_01053 | MFS monocarboxylate transporter, putative ( <i>T. verrucosum</i> )       | CAGTGTG      | 201 | UPRE-1 |
| TERG_01056 | PH domain-containing protein ( <i>T. equinum</i> )                       | CAGCGTG      | 702 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_01081 | hypothetical protein  | CAGAGTG      | 411 | UPRE-1 |
| TERG_01095 | hypothetical protein  | CACGCTG (rc) | 892 | UPRE-1 |
| TERG_01101 | hypothetical protein  | CAGAGTG      | 186 | UPRE-1 |
| TERG_01107 | anthranilate synthase component I ( <i>T. equinum</i> )               | CACCCTG (rc) | 590 | UPRE-1 |
| TERG_01107 | anthranilate synthase component I ( <i>T. equinum</i> )               | CACCCTG (rc) | 895 | UPRE-1 |
| TERG_01108 | hypothetical protein  | CAGGGTG      | 730 | UPRE-1 |
| TERG_01119 | BolA domain-containing protein ( <i>T. tonsurans</i> )                | CACACTG (rc) | 101 | UPRE-1 |
| TERG_01125 | SprT family metalloproteinase, putative ( <i>T. verrucosum</i> )      | CACACTG (rc) | 635 | UPRE-1 |
| TERG_01126 | 1,3-beta-glucanosyltransferase, putative ( <i>T. verrucosum</i> )     | CACGCTG (rc) | 31  | UPRE-1 |
| TERG_01130 | hypothetical protein  | CACTCTG (rc) | 277 | UPRE-1 |
| TERG_01134 | metalloprotease MEP1 ( <i>A. benhamiae</i> )                          | CAGAGTG      | 116 | UPRE-1 |
| TERG_01134 | metalloprotease MEP1 ( <i>A. benhamiae</i> )                          | CAGAGTG      | 845 | UPRE-1 |
| TERG_01150 | hypothetical protein  | CACACTG (rc) | 639 | UPRE-1 |
| TERG_01151 | 26S proteasome non-ATPase regulatory subunit 13 ( <i>T. equinum</i> ) | CAGTGTG      | 604 | UPRE-1 |
| TERG_01156 | integral membrane protein ( <i>T. equinum</i> )                       | CAGTGTG      | 326 | UPRE-1 |
| TERG_01159 | hypothetical protein  | CACGCTG (rc) | 654 | UPRE-1 |
| TERG_01160 | ubiquitin C-terminal hydrolase Ubp8, putative ( <i>A. benhamiae</i> ) | CAGCGTG      | 293 | UPRE-1 |
| TERG_01164 | beta-alanine synthase, putative ( <i>T. verrucosum</i> )              | CAGAGTG      | 219 | UPRE-1 |
| TERG_01175 | LovB-like polyketide synthase, putative ( <i>A. benhamiae</i> )       | CACTCTG (rc) | 705 | UPRE-1 |
| TERG_01183 | RNase3 domain-containing protein ( <i>T. equinum</i> )                | CACGCTG (rc) | 253 | UPRE-1 |
| TERG_01183 | RNase3 domain-containing protein ( <i>T. equinum</i> )                | CACCCTG (rc) | 283 | UPRE-1 |
| TERG_01183 | RNase3 domain-containing protein ( <i>T. equinum</i> )                | CACCCTG (rc) | 782 | UPRE-1 |
| TERG_01186 | SWI/SNF family DNA-dependent ATPase                                   | CAGTGTG      | 443 | UPRE-1 |
| TERG_01191 | NADPH oxidase ( <i>T. equinum</i> )                                   | CACTCTG (rc) | 553 | UPRE-1 |
| TERG_01193 | PRO41 protein ( <i>T. equinum</i> )                                   | CAGAGTG      | 784 | UPRE-1 |
| TERG_01197 | nitrilase ( <i>T. tonsurans</i> )                                     | CACTCTG (rc) | 968 | UPRE-1 |
| TERG_01198 | pre-mRNA-splicing factor rse1   | CACGCTG (rc) | 251 | UPRE-1 |
| TERG_01203 | 75k gamma secalin ( <i>M. canis</i> )                                 | CACTCTG (rc) | 868 | UPRE-1 |
| TERG_01204 | acetyl-CoA acetyltransferase ( <i>T. tonsurans</i> )                  | CACCCTG (rc) | 684 | UPRE-1 |
| TERG_01208 | phosphoethanolamine transferase class O ( <i>T. equinum</i> )         | CACGCTG (rc) | 683 | UPRE-1 |
| TERG_01226 | GAS2 domain-containing protein ( <i>T. equinum</i> )                  | CACCCTG (rc) | 239 | UPRE-1 |
| TERG_01227 | cell cycle checkpoint protein ( <i>T. tonsurans</i> )                 | CAGGGTG      | 869 | UPRE-1 |
| TERG_01228 | COPII vesicle coat protein Sec16, putative ( <i>A. benhamiae</i> )    | CACACTG (rc) | 564 | UPRE-1 |
| TERG_01240 | secreted protein ( <i>T. equinum</i> )                                | CACCCTG (rc) | 833 | UPRE-1 |
| TERG_01249 | hypothetical protein  | CACTCTG (rc) | 572 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_01265 | HhH-GPD family base excision DNA repair protein ( <i>T. tonsurans</i> )       | CACTCTG (rc) | 388 | UPRE-1 |
| TERG_01269 | 2-methylcitrate dehydratase   | CAGTGTG      | 26  | UPRE-1 |
| TERG_01273 | alpha-1,2-mannosidase, putative subfamily ( <i>T. verrucosum</i> )            | CACTCTG (rc) | 928 | UPRE-1 |
| TERG_01275 | hypothetical protein  | CACTCTG (rc) | 758 | UPRE-1 |
| TERG_01290 | N-acetyl-gamma-glutamyl-phosphate reductase                                   | CAGGGTG      | 627 | UPRE-1 |
| TERG_01310 | nascent polypeptide-associated complex subunit beta                           | CACCCTG (rc) | 453 | UPRE-1 |
| TERG_01318 | hypothetical protein  | CACCCTG (rc) | 315 | UPRE-1 |
| TERG_01323 | WW domain binding protein ( <i>T. equinum</i> )                               | CACACTG (rc) | 250 | UPRE-1 |
| TERG_01325 | hypothetical protein  | CAGCGTG      | 913 | UPRE-1 |
| TERG_01326 | hypothetical protein  | CAGAGTG      | 603 | UPRE-1 |
| TERG_01328 | metalloreductase transmembrane component, putative ( <i>A. benhamiae</i> )    | CACTCTG (rc) | 457 | UPRE-1 |
| TERG_01340 | hypothetical protein  | CAGTGTG      | 110 | UPRE-1 |
| TERG_01347 | TIGR01456 family HAD hydrolase  | CAGTGTG      | 282 | UPRE-1 |
| TERG_01355 | DUF1713 domain-containing protein ( <i>T. equinum</i> )                       | CACACTG (rc) | 182 | UPRE-1 |
| TERG_01359 | transketolase   | CACGCTG (rc) | 372 | UPRE-1 |
| TERG_01363 | SET domain-containing protein ( <i>T. equinum</i> )                           | CACACTG (rc) | 236 | UPRE-1 |
| TERG_01364 | hypothetical protein  | CAGTGTG      | 573 | UPRE-1 |
| TERG_01369 | ubiquinol-cytochrome C reductase complex subunit UcrQ ( <i>T. tonsurans</i> ) | CACTCTG (rc) | 517 | UPRE-1 |
| TERG_01377 | hypothetical protein  | CACCCTG (rc) | 169 | UPRE-1 |
| TERG_01379 | serine/threonine-protein phosphatase 2A activator 2 ( <i>T. equinum</i> )     | CAGGGTG      | 182 | UPRE-1 |
| TERG_01383 | dienelactone hydrolase ( <i>T. tonsurans</i> )                                | CACCCTG (rc) | 737 | UPRE-1 |
| TERG_01408 | hypothetical protein  | CACTCTG (rc) | 516 | UPRE-1 |
| TERG_01409 | F-box and WD domain-containing protein ( <i>T. equinum</i> )                  | CAGAGTG      | 602 | UPRE-1 |
| TERG_01447 | bcp1 ( <i>T. equinum</i> )  | CAGAGTG      | 529 | UPRE-1 |
| TERG_01448 | chorismate mutase   | CACGCTG (rc) | 284 | UPRE-1 |
| TERG_01448 | chorismate mutase   | CACTCTG (rc) | 894 | UPRE-1 |
| TERG_01449 | mitochondrial division protein 1  | CAGAGTG      | 248 | UPRE-1 |
| TERG_01449 | mitochondrial division protein 1  | CAGCGTG      | 858 | UPRE-1 |
| TERG_01473 | Pro-apoptotic serine protease NMA111  | CAGAGTG      | 183 | UPRE-1 |
| TERG_01473 | Pro-apoptotic serine protease NMA111  | CAGTGTG      | 452 | UPRE-1 |
| TERG_01473 | Pro-apoptotic serine protease NMA111  | CAGAGTG      | 589 | UPRE-1 |
| TERG_01481 | MFS multidrug transporter, putative ( <i>A. benhamiae</i> )                   | CACCCTG (rc) | 432 | UPRE-1 |
| TERG_01488 | hypothetical protein  | CACCCTG (rc) | 560 | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_01502 | U3 small nucleolar ribonucleoprotein Lcp5 ( <i>T. equinum</i> )              | CACTCTG (rc) | 443 | UPRE-1 |
| TERG_01503 | DUF895 domain membrane protein ( <i>T. verrucosum</i> )                      | CACTCTG (rc) | 484 | UPRE-1 |
| TERG_01509 | hypothetical protein   | CACGCTG (rc) | 752 | UPRE-1 |
| TERG_01514 | beta-1,4-mannosyltransferase ( <i>T. tonsurans</i> )                         | CACGCTG (rc) | 47  | UPRE-1 |
| TERG_01515 | CDF zinc transporter (Msc2), putative ( <i>T. verrucosum</i> )               | CAGCGTG      | 853 | UPRE-1 |
| TERG_01519 | hypothetical protein   | CAGTGTG      | 393 | UPRE-1 |
| TERG_01543 | s-adenosylmethionine (SAM)-dependent methyltransferase ( <i>M. gypseum</i> ) | CAGCGTG      | 508 | UPRE-1 |
| TERG_01549 | N-acetyltransferase 9 ( <i>T. tonsurans</i> )                                | CAGGGTG      | 379 | UPRE-1 |
| TERG_01565 | clathrin heavy chain 1 ( <i>T. equinum</i> )                                 | CACTCTG (rc) | 488 | UPRE-1 |
| TERG_01569 | hypothetical protein   | CACCCTG (rc) | 75  | UPRE-1 |
| TERG_01588 | MAK11 ( <i>T. equinum</i> )  | CACTCTG (rc) | 606 | UPRE-1 |
| TERG_01589 | MYB and HSA domain protein ( <i>T. verrucosum</i> )                          | CAGAGTG      | 909 | UPRE-1 |
| TERG_01590 | pre-mRNA-splicing factor spp2 ( <i>T. equinum</i> )                          | CAGTGTG      | 697 | UPRE-1 |
| TERG_01602 | proteasome component PUP3  | CACCCTG (rc) | 83  | UPRE-1 |
| TERG_01606 | peptidase, putative ( <i>A. benhamiae</i> )                                  | CAGAGTG      | 966 | UPRE-1 |
| TERG_01627 | hypothetical protein   | CAGTGTG      | 50  | UPRE-1 |
| TERG_01645 | mitochondrial carrier protein ( <i>T. tonsurans</i> )                        | CACTCTG (rc) | 895 | UPRE-1 |
| TERG_01646 | proteasome component (Ecm29), putative ( <i>A. benhamiae</i> )               | CAGAGTG      | 847 | UPRE-1 |
| TERG_01649 | lipase, putative ( <i>A. benhamiae</i> )                                     | CACGCTG (rc) | 897 | UPRE-1 |
| TERG_01650 | Arp2/3 complex chain sop2 ( <i>T. equinum</i> )                              | CACCCTG (rc) | 24  | UPRE-1 |
| TERG_01651 | U1 small nuclear ribonucleoprotein A ( <i>T. equinum</i> )                   | CAGTGTG      | 81  | UPRE-1 |
| TERG_01652 | Atg10p ( <i>M. gypseum</i> )   | CACCCTG (rc) | 365 | UPRE-1 |
| TERG_01665 | pre-rRNA-processing protein PNO1   | CACCCTG (rc) | 593 | UPRE-1 |
| TERG_01677 | glutamine-fructose-6-phosphate transaminase (isomerizing)                    | CACTCTG (rc) | 305 | UPRE-1 |
| TERG_01694 | ankyrin repeat-containing protein ( <i>T. equinum</i> )                      | CACACTG (rc) | 559 | UPRE-1 |
| TERG_01708 | ARF GTPase activator ( <i>T. tonsurans</i> )                                 | CACCCTG (rc) | 188 | UPRE-1 |
| TERG_01709 | hypothetical protein   | CAGAGTG      | 236 | UPRE-1 |
| TERG_01734 | hypothetical protein   | CACCCTG (rc) | 969 | UPRE-1 |
| TERG_01737 | NSDC ( <i>T. equinum</i> )   | CAGCGTG      | 79  | UPRE-1 |
| TERG_01738 | hypothetical protein   | CACCCTG (rc) | 402 | UPRE-1 |
| TERG_01755 | hypothetical protein   | CACCCTG (rc) | 724 | UPRE-1 |
| TERG_01781 | endo-1,3(4)-beta-glucanase, putative ( <i>A. benhamiae</i> )                 | CAGAGTG      | 467 | UPRE-1 |
| TERG_01801 | hypothetical protein   | CAGCGTG      | 662 | UPRE-1 |
| TERG_01815 | origin recognition complex subunit 3, putative ( <i>A. benhamiae</i> )       | CAGTGTG      | 643 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_01816 | translocation protein ( <i>T. tonsurans</i> )   | CACGCTG (rc) | 855 | UPRE-1 |
| TERG_01817 | AAA family ATPase ( <i>T. tonsurans</i> )   | CACCCTG (rc) | 421 | UPRE-1 |
| TERG_01824 | DNA-binding protein SMUBP-2 ( <i>T. equinum</i> )                                     | CACGCTG (rc) | 25  | UPRE-1 |
| TERG_01824 | DNA-binding protein SMUBP-2 ( <i>T. equinum</i> )                                     | CACGCTG (rc) | 172 | UPRE-1 |
| TERG_01826 | ubiquitin-conjugating enzyme ( <i>T. tonsurans</i> )                                  | CAGCGTG      | 226 | UPRE-1 |
| TERG_01826 | ubiquitin-conjugating enzyme ( <i>T. tonsurans</i> )                                  | CAGCGTG      | 373 | UPRE-1 |
| TERG_01833 | peroxisomal membrane protein ( <i>T. tonsurans</i> )                                  | CAGTGTG      | 564 | UPRE-1 |
| TERG_01837 | glycosyl hydrolase ( <i>T. equinum</i> )  | CACCCTG (rc) | 11  | UPRE-1 |
| TERG_01838 | LIM domain protein ( <i>A. benhamiae</i> )  | CACACTG (rc) | 515 | UPRE-1 |
| TERG_01844 | hypothetical protein  | CAGCGTG      | 511 | UPRE-1 |
| TERG_01845 | amidase family protein, putative ( <i>T. verrucosum</i> )                             | CACCCTG (rc) | 290 | UPRE-1 |
| TERG_01848 | integral membrane protein ( <i>M. gypseum</i> )                                       | CACACTG (rc) | 380 | UPRE-1 |
| TERG_01867 | hypothetical protein  | CACTCTG (rc) | 207 | UPRE-1 |
| TERG_01867 | hypothetical protein  | CACGCTG (rc) | 527 | UPRE-1 |
| TERG_01867 | hypothetical protein  | CACTCTG (rc) | 649 | UPRE-1 |
| TERG_01872 | polyketide synthase, putative ( <i>T. verrucosum</i> )                                | CACTCTG (rc) | 499 | UPRE-1 |
| TERG_01889 | RING finger domain-containing protein ( <i>T. tonsurans</i> )                         | CACGCTG (rc) | 24  | UPRE-1 |
| TERG_01892 | alanyl-tRNA synthetase  | CACCCTG (rc) | 866 | UPRE-1 |
| TERG_01893 | hypothetical protein  | CAGGGTG      | 554 | UPRE-1 |
| TERG_01894 | hypothetical protein  | CACTCTG (rc) | 804 | UPRE-1 |
| TERG_01896 | hypothetical protein  | CACACTG (rc) | 3   | UPRE-1 |
| TERG_01897 | oryzin ( <i>T. equinum</i> )  | CAGTGTG      | 412 | UPRE-1 |
| TERG_01905 | AMP deaminase   | CAGTGTG      | 527 | UPRE-1 |
| TERG_01912 | MFS transporter ( <i>T. equinum</i> )   | CAGCGTG      | 74  | UPRE-1 |
| TERG_01915 | O-methyltransferase ( <i>A. benhamiae</i> )   | CACACTG (rc) | 283 | UPRE-1 |
| TERG_01915 | O-methyltransferase ( <i>A. benhamiae</i> )   | CACACTG (rc) | 597 | UPRE-1 |
| TERG_01916 | TdiA protein ( <i>T. equinum</i> )  | CACTCTG (rc) | 993 | UPRE-1 |
| TERG_01917 | O-methyltransferase, putative ( <i>A. benhamiae</i> )                                 | CAGAGTG      | 457 | UPRE-1 |
| TERG_01925 | hypothetical protein  | CACTCTG (rc) | 674 | UPRE-1 |
| TERG_01937 | short chain dehydrogenase ( <i>T. tonsurans</i> )                                     | CAGGGTG      | 386 | UPRE-1 |
| TERG_01950 | serine/threonine protein kinase ( <i>T. tonsurans</i> )                               | CACTCTG (rc) | 18  | UPRE-1 |
| TERG_01950 | serine/threonine protein kinase ( <i>T. tonsurans</i> )                               | CACTCTG (rc) | 689 | UPRE-1 |
| TERG_01951 | SET and MYND domain protein, putative ( <i>A. benhamiae</i> )                         | CAGAGTG      | 211 | UPRE-1 |
| TERG_01951 | SET and MYND domain protein, putative ( <i>A. benhamiae</i> )                         | CAGAGTG      | 882 | UPRE-1 |
| TERG_01959 | RNA polymerase Rpb1 C-terminal repeat domain-containing protein ( <i>T. equinum</i> ) | CACGCTG (rc) | 45  | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_01967 | GPI anchored protein, putative ( <i>T. verrucosum</i> )   | CAGGGTG      | 267 | UPRE-1 |
| TERG_01973 | mRNA cleavage and polyadenylation specificity factor complex subunit (Pta1), putative ( <i>A. benhamiae</i> ) | CAGTGTG      | 185 | UPRE-1 |
| TERG_01980 | hypothetical protein  | CAGCGTG      | 724 | UPRE-1 |
| TERG_01980 | hypothetical protein  | CAGCGTG      | 775 | UPRE-1 |
| TERG_01981 | hypothetical protein  | CACGCTG (rc) | 125 | UPRE-1 |
| TERG_02004 | ureidoglycolate hydrolase, putative ( <i>T. verrucosum</i> )  | CACTCTG (rc) | 780 | UPRE-1 |
| TERG_02005 | catalase ( <i>T. tonsurans</i> )  | CAGAGTG      | 574 | UPRE-1 |
| TERG_02008 | hypothetical protein  | CACTCTG (rc) | 8   | UPRE-1 |
| TERG_02009 | short chain oxidoreductase (CsgA), putative ( <i>T. verrucosum</i> )  | CAGAGTG      | 746 | UPRE-1 |
| TERG_02055 | hypothetical protein  | CACCCTG (rc) | 279 | UPRE-1 |
| TERG_02058 | ribosome biogenesis protein RPF2 ( <i>T. equinum</i> )  | CACTCTG (rc) | 827 | UPRE-1 |
| TERG_02074 | 26S protease regulatory subunit 7   | CACGCTG (rc) | 230 | UPRE-1 |
| TERG_02077 | hypothetical protein  | CAGGGTG      | 412 | UPRE-1 |
| TERG_02085 | hypothetical protein  | CAGGGTG      | 232 | UPRE-1 |
| TERG_02086 | exocyst complex component Sec10 ( <i>T. tonsurans</i> )   | CACGCTG (rc) | 146 | UPRE-1 |
| TERG_02092 | hypothetical protein  | CAGGGTG      | 950 | UPRE-1 |
| TERG_02099 | uracil permease ( <i>T. equinum</i> )   | CAGCGTG      | 103 | UPRE-1 |
| TERG_02132 | 5-histidylcysteine sulfoxide synthase   | CACGCTG (rc) | 486 | UPRE-1 |
| TERG_02133 | fluG protein ( <i>T. equinum</i> )  | CAGCGTG      | 205 | UPRE-1 |
| TERG_02139 | eukaryotic translation initiation factor 3 subunit D  | CACCCTG (rc) | 859 | UPRE-1 |
| TERG_02140 | bZIP transcription factor ( <i>T. tonsurans</i> )   | CACTCTG (rc) | 57  | UPRE-1 |
| TERG_02140 | bZIP transcription factor ( <i>T. tonsurans</i> )   | CACGCTG (rc) | 789 | UPRE-1 |
| TERG_02147 | 3-demethylubiquinone-9 3-methyltransferase, putative ( <i>T. verrucosum</i> )                                 | CACACTG (rc) | 451 | UPRE-1 |
| TERG_02151 | hypothetical protein  | CACGCTG (rc) | 559 | UPRE-1 |
| TERG_02152 | hypothetical protein  | CAGCGTG      | 966 | UPRE-1 |
| TERG_02155 | type I phosphodiesterase/nucleotide pyrophosphatase ( <i>T. tonsurans</i> )                                   | CACGCTG (rc) | 221 | UPRE-1 |
| TERG_02164 | indoleamine 2,3-dioxygenase ( <i>T. equinum</i> )   | CACTCTG (rc) | 96  | UPRE-1 |
| TERG_02167 | phosphotransferase enzyme family protein ( <i>T. equinum</i> )  | CACTCTG (rc) | 209 | UPRE-1 |
| TERG_02168 | hypothetical protein  | CACCCTG (rc) | 139 | UPRE-1 |
| TERG_02169 | carboxylesterase, putative ( <i>A. benhamiae</i> )  | CACTCTG (rc) | 465 | UPRE-1 |
| TERG_02172 | cytochrome P450 monooxygenase ( <i>T. equinum</i> )   | CACGCTG (rc) | 277 | UPRE-1 |
| TERG_02172 | cytochrome P450 monooxygenase ( <i>T. equinum</i> )   | CACCCTG (rc) | 322 | UPRE-1 |
| TERG_02185 | hypothetical protein  | CAGTGTG      | 318 | UPRE-1 |
| TERG_02188 | mechanosensitive ion channel family protein ( <i>T. tonsurans</i> )   | CACACTG (rc) | 543 | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_02194 | exonuclease ( <i>T. tonsurans</i> )  | CAGGGTG      | 305 | UPRE-1 |
| TERG_02202 | NADH-ubiquinone oxidoreductase 12 kDa subunit, mitochondrial                             | CAGTGTG      | 453 | UPRE-1 |
| TERG_02212 | short chain dehydrogenase/reductase family protein ( <i>T. verrucosum</i> )              | CAGGGTG      | 757 | UPRE-1 |
| TERG_02214 | carboxypeptidase 2   | CAGCGTG      | 362 | UPRE-1 |
| TERG_02226 | DUF453 domain-containing protein ( <i>T. equinum</i> )                                   | CAGAGTG      | 216 | UPRE-1 |
| TERG_02243 | hypothetical protein   | CACACTG (rc) | 522 | UPRE-1 |
| TERG_02244 | MFS transporter, putative ( <i>A. benhamiae</i> )  | CAGTGTG      | 285 | UPRE-1 |
| TERG_02250 | cyclopropane-fatty-acyl-phospholipid synthase ( <i>T. tonsurans</i> )                    | CACTCTG (rc) | 41  | UPRE-1 |
| TERG_02250 | cyclopropane-fatty-acyl-phospholipid synthase ( <i>T. tonsurans</i> )                    | CACCCTG (rc) | 564 | UPRE-1 |
| TERG_02275 | hypothetical protein   | CACACTG (rc) | 633 | UPRE-1 |
| TERG_02282 | hypothetical protein   | CAGAGTG      | 419 | UPRE-1 |
| TERG_02287 | calcium dependent mitochondrial carrier protein ( <i>T. tonsurans</i> )                  | CACACTG (rc) | 173 | UPRE-1 |
| TERG_02297 | TRAF-like signal transducer, putative ( <i>A. benhamiae</i> )                            | CAGCGTG      | 886 | UPRE-1 |
| TERG_02299 | HET-C domain-containing protein ( <i>T. tonsurans</i> )                                  | CACGCTG (rc) | 685 | UPRE-1 |
| TERG_02300 | hypothetical protein   | CAGCGTG      | 116 | UPRE-1 |
| TERG_02314 | cofactor for methionyl- and glutamyl-tRNA synthetases, putative ( <i>T. verrucosum</i> ) | CACGCTG (rc) | 47  | UPRE-1 |
| TERG_02326 | WD domain-containing protein ( <i>T. tonsurans</i> )                                     | CACGCTG (rc) | 97  | UPRE-1 |
| TERG_02336 | hypothetical protein   | CACCCTG (rc) | 143 | UPRE-1 |
| TERG_02336 | hypothetical protein   | CACTCTG (rc) | 178 | UPRE-1 |
| TERG_02337 | multidomain presynaptic cytomatrix related protein ( <i>T. verrucosum</i> )              | CAGAGTG      | 908 | UPRE-1 |
| TERG_02337 | multidomain presynaptic cytomatrix related protein ( <i>T. verrucosum</i> )              | CAGGGTG      | 943 | UPRE-1 |
| TERG_02341 | DEAD box helicase ( <i>T. tonsurans</i> )  | CACCCTG (rc) | 800 | UPRE-1 |
| TERG_02357 | amino acid permease ( <i>T. equinum</i> )  | CACCCTG (rc) | 913 | UPRE-1 |
| TERG_02361 | 5'-nucleotidase, putative ( <i>A. benhamiae</i> )  | CACGCTG (rc) | 96  | UPRE-1 |
| TERG_02362 | hypothetical protein   | CACGCTG (rc) | 536 | UPRE-1 |
| TERG_02362 | hypothetical protein   | CACGCTG (rc) | 992 | UPRE-1 |
| TERG_02363 | succinate-semialdehyde dehydrogenase ( <i>T. tonsurans</i> )                             | CAGCGTG      | 45  | UPRE-1 |
| TERG_02367 | hypothetical protein   | CAGGGTG      | 94  | UPRE-1 |
| TERG_02367 | hypothetical protein   | CAGAGTG      | 762 | UPRE-1 |
| TERG_02368 | extracellular developmental signal biosynthesis protein FluG ( <i>A. benhamiae</i> )     | CAGCGTG      | 315 | UPRE-1 |
| TERG_02380 | hypothetical protein   | CACCCTG (rc) | 656 | UPRE-1 |



|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_02384 | hypothetical protein  | CAGCGTG      | 523 | UPRE-1 |
| TERG_02404 | 40S ribosomal protein S4  | CAGCGTG      | 578 | UPRE-1 |
| TERG_02405 | mating locus protein, putative ( <i>T. verrucosum</i> )                     | CACTCTG (rc) | 160 | UPRE-1 |
| TERG_02408 | DNA lyase ( <i>T. tonsurans</i> )   | CACACTG (rc) | 459 | UPRE-1 |
| TERG_02409 | ABcox13, cytochrome c oxidase subunit VIa, putative ( <i>A. benhamiae</i> ) | CAGAGTG      | 238 | UPRE-1 |
| TERG_02413 | hypothetical protein  | CACCCTG (rc) | 293 | UPRE-1 |
| TERG_02417 | anaphase-promoting complex protein ( <i>T. tonsurans</i> )                  | CAGCGTG      | 577 | UPRE-1 |
| TERG_02418 | translation initiation factor SUI1  | CAGTGTG      | 376 | UPRE-1 |
| TERG_02424 | rho2 ( <i>T. equinum</i> )  | CAGCGTG      | 822 | UPRE-1 |
| TERG_02438 | hypothetical protein  | CACTCTG (rc) | 77  | UPRE-1 |
| TERG_02438 | hypothetical protein  | CACGCTG (rc) | 134 | UPRE-1 |
| TERG_02444 | hypothetical protein  | CACCCTG (rc) | 190 | UPRE-1 |
| TERG_02451 | lipoyl synthase, mitochondrial  | CACGCTG (rc) | 3   | UPRE-1 |
| TERG_02456 | siroheme synthase ( <i>T. tonsurans</i> )                                   | CACCCTG (rc) | 377 | UPRE-1 |
| TERG_02467 | pyridoxamine phosphate oxidase ( <i>T. tonsurans</i> )                      | CAGGGTG      | 414 | UPRE-1 |
| TERG_02468 | ubiquitin thiolesterase (OtuB1), putative ( <i>T. verrucosum</i> )          | CACTCTG (rc) | 219 | UPRE-1 |
| TERG_02492 | ubiquitin-conjugating enzyme E2-16 kDa                                      | CAGAGTG      | 233 | UPRE-1 |
| TERG_02498 | CMGC/SRPK protein kinase  | CAGGGTG      | 45  | UPRE-1 |
| TERG_02500 | phosphatidylinositol-4-phosphate 5-kinase ( <i>T. tonsurans</i> )           | CAGCGTG      | 322 | UPRE-1 |
| TERG_02505 | MFS transporter, putative ( <i>A. benhamiae</i> )                           | CAGTGTG      | 194 | UPRE-1 |
| TERG_02507 | transcription factor Rba50 ( <i>T. tonsurans</i> )                          | CAGTGTG      | 684 | UPRE-1 |
| TERG_02512 | hypothetical protein  | CAGTGTG      | 659 | UPRE-1 |
| TERG_02513 | TAM domain methyltransferase ( <i>T. equinum</i> )                          | CACACTG (rc) | 601 | UPRE-1 |
| TERG_02515 | STE/STE7/MEK1 protein kinase  | CACGCTG (rc) | 989 | UPRE-1 |
| TERG_02526 | hypothetical protein  | CAGCGTG      | 756 | UPRE-1 |
| TERG_02527 | WD40 repeat protein ( <i>A. benhamiae</i> )                                 | CAGAGTG      | 754 | UPRE-1 |
| TERG_02527 | WD40 repeat protein ( <i>A. benhamiae</i> )                                 | CAGTGTG      | 858 | UPRE-1 |
| TERG_02535 | nicotinate-nucleotide diphosphorylase (carboxylating)                       | CAGCGTG      | 178 | UPRE-1 |
| TERG_02541 | FAD-dependent monooxygenase, putative ( <i>T. verrucosum</i> )              | CACTCTG (rc) | 469 | UPRE-1 |
| TERG_02541 | FAD-dependent monooxygenase, putative ( <i>T. verrucosum</i> )              | CACGCTG (rc) | 734 | UPRE-1 |
| TERG_02550 | ZZ type zinc finger domain protein ( <i>T. verrucosum</i> )                 | CACCCTG (rc) | 689 | UPRE-1 |
| TERG_02563 | esterase family protein ( <i>A. benhamiae</i> )                             | CAGTGTG      | 821 | UPRE-1 |
| TERG_02566 | hypothetical protein  | CAGTGTG      | 172 | UPRE-1 |
| TERG_02567 | phytanoyl-CoA dioxygenase ( <i>T. tonsurans</i> )                           | CAGCGTG      | 114 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_02567 | phytanoyl-CoA dioxygenase ( <i>T. tonsurans</i> )                             | CAGGGTG      | 980 | UPRE-1 |
| TERG_02578 | nuclear protein ( <i>T. tonsurans</i> )                                       | CACCCTG (rc) | 611 | UPRE-1 |
| TERG_02584 | hypothetical protein  | CACCCTG (rc) | 264 | UPRE-1 |
| TERG_02584 | hypothetical protein  | CACACTG (rc) | 475 | UPRE-1 |
| TERG_02588 | hypothetical protein  | CAGAGTG      | 194 | UPRE-1 |
| TERG_02590 | peptidyl-prolyl cis-trans isomerase D   | CACCCTG (rc) | 435 | UPRE-1 |
| TERG_02593 | C2H2 finger domain protein, putative ( <i>T. verrucosum</i> )                 | CAGTGTG      | 60  | UPRE-1 |
| TERG_02601 | Phosphoglucomutase ( <i>T. tonsurans</i> )                                    | CACCCTG (rc) | 470 | UPRE-1 |
| TERG_02605 | CCCH zinc finger domain-containing protein ( <i>T. equinum</i> )              | CACCCTG (rc) | 875 | UPRE-1 |
| TERG_02609 | actin patches distal protein 1 ( <i>T. equinum</i> )                          | CAGCGTG      | 379 | UPRE-1 |
| TERG_02615 | oxidoreductase, 2OG-Fe(II) oxygenase family, putative ( <i>A. benhamiae</i> ) | CAGTGTG      | 510 | UPRE-1 |
| TERG_02625 | hypothetical protein  | CACCCTG (rc) | 228 | UPRE-1 |
| TERG_02626 | RING finger domain protein ( <i>A. benhamiae</i> )                            | CAGGGTG      | 357 | UPRE-1 |
| TERG_02626 | RING finger domain protein ( <i>A. benhamiae</i> )                            | CAGTGTG      | 707 | UPRE-1 |
| TERG_02634 | C2H2 finger domain protein, putative ( <i>A. benhamiae</i> )                  | CACCCTG (rc) | 512 | UPRE-1 |
| TERG_02635 | hypothetical protein  | CAGGGTG      | 682 | UPRE-1 |
| TERG_02636 | F-box protein ( <i>T. tonsurans</i> )   | CACCCTG (rc) | 544 | UPRE-1 |
| TERG_02657 | phosphoglycerate mutase ( <i>T. equinum</i> )                                 | CACACTG (rc) | 26  | UPRE-1 |
| TERG_02658 | CAMK/CAMKL/AMPK protein kinase  | CAGTGTG      | 935 | UPRE-1 |
| TERG_02659 | non-classical export protein Nce102, putative ( <i>A. benhamiae</i> )         | CAGCGTG      | 585 | UPRE-1 |
| TERG_02659 | non-classical export protein Nce102, putative ( <i>A. benhamiae</i> )         | CAGCGTG      | 668 | UPRE-1 |
| TERG_02665 | FunK1 protein kinase ( <i>M. gypseum</i> )                                    | CAGCGTG      | 312 | UPRE-1 |
| TERG_02669 | pre-mRNA splicing factor ( <i>T. equinum</i> )                                | CACCCTG (rc) | 379 | UPRE-1 |
| TERG_02688 | hypothetical protein  | CAGTGTG      | 992 | UPRE-1 |
| TERG_02696 | hypothetical protein  | CAGCGTG      | 387 | UPRE-1 |
| TERG_02699 | protein kinase, putative ( <i>T. verrucosum</i> )                             | CAGGGTG      | 797 | UPRE-1 |
| TERG_02750 | protoporphyrinogen oxidase  | CAGGGTG      | 515 | UPRE-1 |
| TERG_02753 | E3 ubiquitin-protein ligase ubr1 ( <i>T. equinum</i> )                        | CAGCGTG      | 429 | UPRE-1 |
| TERG_02772 | DNA polymerase V ( <i>T. tonsurans</i> )                                      | CACGCTG (rc) | 192 | UPRE-1 |
| TERG_02773 | tartrate dehydrogenase  | CAGCGTG      | 105 | UPRE-1 |
| TERG_02778 | SCF ubiquitin ligase subunit CulC ( <i>T. tonsurans</i> )                     | CACGCTG (rc) | 200 | UPRE-1 |
| TERG_02780 | HEAT repeat protein ( <i>T. tonsurans</i> )                                   | CACACTG (rc) | 92  | UPRE-1 |
| TERG_02798 | DUF895 domain membrane protein ( <i>T. equinum</i> )                          | CACGCTG (rc) | 949 | UPRE-1 |
| TERG_02801 | hypothetical protein  | CACGCTG (rc) | 22  | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_02803 | 3-oxoacyl-(acyl-carrier-protein) reductase ( <i>T. verrucosum</i> )    | CAGGGTG      | 578 | UPRE-1 |
| TERG_02816 | dienelactone hydrolase ( <i>T. equinum</i> )                           | CACACTG (rc) | 238 | UPRE-1 |
| TERG_02817 | hypothetical protein   | CAGGGTG      | 443 | UPRE-1 |
| TERG_02854 | dynein light chain ( <i>T. tonsurans</i> )                             | CACCCTG (rc) | 172 | UPRE-1 |
| TERG_02863 | protein kinase activator ( <i>T. tonsurans</i> )                       | CACACTG (rc) | 572 | UPRE-1 |
| TERG_02863 | protein kinase activator ( <i>T. tonsurans</i> )                       | CACCCTG (rc) | 764 | UPRE-1 |
| TERG_02864 | hypothetical protein   | CAGGGTG      | 782 | UPRE-1 |
| TERG_02864 | hypothetical protein   | CAGTGTG      | 974 | UPRE-1 |
| TERG_02867 | ribosome biogenesis ATPase RIX7 ( <i>T. tonsurans</i> )                | CACTCTG (rc) | 28  | UPRE-1 |
| TERG_02869 | DUF1000 domain-containing protein ( <i>T. equinum</i> )                | CACGCTG (rc) | 97  | UPRE-1 |
| TERG_02878 | eukaryotic translation initiation factor 3 subunit F                   | CAGAGTG      | 516 | UPRE-1 |
| TERG_02879 | transcription initiation factor TFIID subunit 13 ( <i>T. equinum</i> ) | CACCCTG (rc) | 399 | UPRE-1 |
| TERG_02887 | aminotransferase ( <i>T. tonsurans</i> )                               | CAGAGTG      | 247 | UPRE-1 |
| TERG_02901 | N-acetyltransferase complex ARD1 subunit ( <i>T. tonsurans</i> )       | CAGGGTG      | 19  | UPRE-1 |
| TERG_02906 | PAB1 binding protein ( <i>T. tonsurans</i> )                           | CACCCTG (rc) | 581 | UPRE-1 |
| TERG_02907 | actin-interacting protein ( <i>T. tonsurans</i> )                      | CAGGGTG      | 567 | UPRE-1 |
| TERG_02915 | ESCRT-II complex component ( <i>T. tonsurans</i> )                     | CAGGGTG      | 373 | UPRE-1 |
| TERG_02922 | phosphoserine phosphatase ( <i>T. tonsurans</i> )                      | CACACTG (rc) | 99  | UPRE-1 |
| TERG_02923 | protein kinase subdomain-containing protein ( <i>T. equinum</i> )      | CAGCGTG      | 989 | UPRE-1 |
| TERG_02927 | hypothetical protein   | CACTCTG (rc) | 86  | UPRE-1 |
| TERG_02938 | vacuolar membrane protein ( <i>T. equinum</i> )                        | CACGCTG (rc) | 933 | UPRE-1 |
| TERG_02939 | Ser/Thr protein phosphatase ( <i>T. tonsurans</i> )                    | CAGCGTG      | 178 | UPRE-1 |
| TERG_02941 | hypothetical protein   | CAGGGTG      | 19  | UPRE-1 |
| TERG_02949 | 54S ribosomal protein L6 ( <i>T. equinum</i> )                         | CAGAGTG      | 161 | UPRE-1 |
| TERG_02951 | VHS domain protein ( <i>A. benhamiae</i> )                             | CAGAGTG      | 543 | UPRE-1 |
| TERG_02953 | hypothetical protein   | CACGCTG (rc) | 172 | UPRE-1 |
| TERG_02959 | hypothetical protein   | CAGGGTG      | 779 | UPRE-1 |
| TERG_02966 | PHD finger domain protein, putative ( <i>A. benhamiae</i> )            | CAGAGTG      | 694 | UPRE-1 |
| TERG_02966 | PHD finger domain protein, putative ( <i>A. benhamiae</i> )            | CAGAGTG      | 992 | UPRE-1 |
| TERG_02973 | morphogenesis protein (Msb1), putative ( <i>T. verrucosum</i> )        | CAGTGTG      | 994 | UPRE-1 |
| TERG_02987 | mitochondrial import inner membrane translocase subunit tim-17         | CAGCGTG      | 278 | UPRE-1 |
| TERG_02988 | asparaginase ( <i>T. tonsurans</i> )                                   | CAGGGTG      | 527 | UPRE-1 |
| TERG_02996 | hypothetical protein   | CAGGGTG      | 106 | UPRE-1 |
| TERG_03003 | autophagy protein Apg12 ( <i>T. equinum</i> )                          | CAGTGTG      | 160 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_03011 | MFS transporter, putative ( <i>A. benhamiae</i> )                           | CACACTG (rc) | 172 | UPRE-1 |
| TERG_03013 | pyridoxal-5'-phosphate-dependent enzyme ( <i>T. equinum</i> )               | CACTCTG (rc) | 546 | UPRE-1 |
| TERG_03014 | ER membrane protein Wsc4 ( <i>T. equinum</i> )                              | CACCCTG (rc) | 985 | UPRE-1 |
| TERG_03024 | hypothetical protein  | CAGTGTG      | 195 | UPRE-1 |
| TERG_03026 | WD repeat protein ( <i>T. tonsurans</i> )                                   | CAGGGTG      | 690 | UPRE-1 |
| TERG_03027 | hypothetical protein  | CACTCTG (rc) | 683 | UPRE-1 |
| TERG_03028 | hypothetical protein  | CAGAGTG      | 250 | UPRE-1 |
| TERG_03028 | hypothetical protein  | CAGAGTG      | 662 | UPRE-1 |
| TERG_03033 | BTB domain and ankyrin repeat protein ( <i>A. benhamiae</i> )               | CAGCGTG      | 185 | UPRE-1 |
| TERG_03048 | adenylate cyclase ( <i>T. tonsurans</i> )                                   | CACGCTG (rc) | 928 | UPRE-1 |
| TERG_03053 | serine/threonine protein kinase ( <i>T. tonsurans</i> )                     | CAGTGTG      | 151 | UPRE-1 |
| TERG_03066 | MFS peptide transporter, putative ( <i>T. verrucosum</i> )                  | CACCCTG (rc) | 789 | UPRE-1 |
| TERG_03078 | cytochrome P450 oxidoreductase OrdA-like, putative ( <i>T. verrucosum</i> ) | CACTCTG (rc) | 649 | UPRE-1 |
| TERG_03081 | intracellular protein transporter ( <i>T. equinum</i> )                     | CACGCTG (rc) | 96  | UPRE-1 |
| TERG_03081 | intracellular protein transporter ( <i>T. equinum</i> )                     | CACCCTG (rc) | 727 | UPRE-1 |
| TERG_03090 | hypothetical protein  | CAGCGTG      | 355 | UPRE-1 |
| TERG_03102 | sterol 24-C-methyltransferase ( <i>T. equinum</i> )                         | CAGAGTG      | 409 | UPRE-1 |
| TERG_03105 | hypothetical protein  | CAGGGTG      | 654 | UPRE-1 |
| TERG_03120 | conserved glutamic acid-rich protein ( <i>A. benhamiae</i> )                | CACGCTG (rc) | 842 | UPRE-1 |
| TERG_03131 | alpha-1,2-mannosyltransferase ( <i>T. equinum</i> )                         | CACTCTG (rc) | 368 | UPRE-1 |
| TERG_03132 | hypothetical protein  | CAGCGTG      | 398 | UPRE-1 |
| TERG_03139 | hypothetical protein  | CACTCTG (rc) | 108 | UPRE-1 |
| TERG_03151 | import inner membrane translocase subunit tim-21 ( <i>T. equinum</i> )      | CACTCTG (rc) | 988 | UPRE-1 |
| TERG_03152 | arf GTPase-activating protein ( <i>T. equinum</i> )                         | CAGAGTG      | 854 | UPRE-1 |
| TERG_03153 | dihydropteroate synthase  | CACGCTG (rc) | 826 | UPRE-1 |
| TERG_03154 | 2-nitropropane dioxygenase ( <i>M. gypseum</i> )                            | CAGCGTG      | 202 | UPRE-1 |
| TERG_03160 | hypothetical protein  | CAGCGTG      | 871 | UPRE-1 |
| TERG_03179 | NlpC/P60-like cell-wall peptidase, putative ( <i>A. benhamiae</i> )         | CAGCGTG      | 372 | UPRE-1 |
| TERG_03201 | CMGC/DYRK/YAK protein kinase ( <i>T. tonsurans</i> )                        | CAGCGTG      | 193 | UPRE-1 |
| TERG_03205 | DNA polymerase alpha catalytic subunit ( <i>T. equinum</i> )                | CAGAGTG      | 184 | UPRE-1 |
| TERG_03206 | hsp7-like protein   | CACACTG (rc) | 56  | UPRE-1 |
| TERG_03214 | hypothetical protein  | CAGCGTG      | 927 | UPRE-1 |
| TERG_03225 | betaine aldehyde dehydrogenase, putative ( <i>A. benhamiae</i> )            | CAGAGTG      | 880 | UPRE-1 |
| TERG_03230 | hypothetical protein  | CACACTG (rc) | 575 | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_03231 | cytochrome P450 52A12 ( <i>T. tonsurans</i> )  | CAGTGTG      | 947 | UPRE-1 |
| TERG_03240 | transmembrane efflux protein ( <i>T. tonsurans</i> )                                 | CACTCTG (rc) | 206 | UPRE-1 |
| TERG_03241 | hypothetical protein   | CAGGGTG      | 211 | UPRE-1 |
| TERG_03248 | extracellular metalloproteinase 3  | CAGAGTG      | 631 | UPRE-1 |
| TERG_03254 | hypothetical protein   | CAGTGTG      | 25  | UPRE-1 |
| TERG_03256 | carbonate dehydratase ( <i>T. equinum</i> )  | CAGAGTG      | 169 | UPRE-1 |
| TERG_03256 | carbonate dehydratase ( <i>T. equinum</i> )  | CAGTGTG      | 187 | UPRE-1 |
| TERG_03261 | pre-mRNA splicing factor prp1 ( <i>T. tonsurans</i> )                                | CACGCTG (rc) | 84  | UPRE-1 |
| TERG_03267 | oligomeric Golgi complex component 4 ( <i>T. equinum</i> )                           | CACGCTG (rc) | 18  | UPRE-1 |
| TERG_03269 | hexokinase   | CAGCGTG      | 5   | UPRE-1 |
| TERG_03292 | NADH-ubiquinone dehydrogenase 24 kDa subunit ( <i>T. tonsurans</i> )                 | CACTCTG (rc) | 512 | UPRE-1 |
| TERG_03313 | fucose-specific lectin FleA ( <i>A. benhamiae</i> )                                  | CAGTGTG      | 740 | UPRE-1 |
| TERG_03314 | TfdA family oxidoreductase, putative ( <i>T. verrucosum</i> )                        | CACCCTG (rc) | 79  | UPRE-1 |
| TERG_03316 | hypothetical protein   | CACGCTG (rc) | 903 | UPRE-1 |
| TERG_03318 | N(5)-glutamine methyltransferase MTQ2 ( <i>T. equinum</i> )                          | CAGCGTG      | 53  | UPRE-1 |
| TERG_03319 | small nuclear ribonucleoprotein Sm D1 ( <i>T. tonsurans</i> )                        | CACACTG (rc) | 713 | UPRE-1 |
| TERG_03320 | hypothetical protein   | CAGTGTG      | 212 | UPRE-1 |
| TERG_03327 | ER membrane protein (Pkr1), putative ( <i>T. verrucosum</i> )                        | CAGCGTG      | 987 | UPRE-1 |
| TERG_03331 | F-box protein ( <i>T. equinum</i> )  | CACTCTG (rc) | 307 | UPRE-1 |
| TERG_03352 | tyrosine decarboxylase ( <i>T. equinum</i> )   | CACTCTG (rc) | 371 | UPRE-1 |
| TERG_03369 | fungal specific transcription factor domain-containing protein ( <i>T. equinum</i> ) | CACCCTG (rc) | 514 | UPRE-1 |
| TERG_03389 | orotidine 5'-phosphate decarboxylase   | CAGAGTG      | 664 | UPRE-1 |
| TERG_03397 | hypothetical protein   | CACTCTG (rc) | 480 | UPRE-1 |
| TERG_03398 | chitinase ( <i>M. canis</i> )  | CAGGGTG      | 570 | UPRE-1 |
| TERG_03401 | high affinity nickel transporter ( <i>T. tonsurans</i> )                             | CACACTG (rc) | 581 | UPRE-1 |
| TERG_03402 | zinc carboxypeptidase, putative ( <i>A. benhamiae</i> )                              | CACGCTG (rc) | 786 | UPRE-1 |
| TERG_03414 | acetyl-CoA carboxylase ( <i>T. equinum</i> )   | CAGTGTG      | 460 | UPRE-1 |
| TERG_03426 | hypothetical protein   | CACTCTG (rc) | 64  | UPRE-1 |
| TERG_03428 | peptidyl-prolyl cis-trans isomerase ( <i>T. tonsurans</i> )                          | CAGAGTG      | 297 | UPRE-1 |
| TERG_03438 | MFS monocarboxylate transporter ( <i>T. equinum</i> )                                | CACACTG (rc) | 947 | UPRE-1 |
| TERG_03441 | hypothetical protein   | CAGAGTG      | 428 | UPRE-1 |
| TERG_03452 | HEAT repeat protein ( <i>T. equinum</i> )  | CAGAGTG      | 510 | UPRE-1 |
| TERG_03458 | hypothetical protein   | CACACTG (rc) | 577 | UPRE-1 |
| TERG_03458 | hypothetical protein   | CACTCTG (rc) | 739 | UPRE-1 |
| TERG_03458 | hypothetical protein   | CACTCTG (rc) | 887 | UPRE-1 |
| TERG_03464 | stress response protein ( <i>T. equinum</i> )  | CACCCTG (rc) | 547 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_03465 | pre-mRNA-splicing factor cwc15  | CACCCTG (rc) | 269 | UPRE-1 |
| TERG_03477 | DUF1674 domain-containing protein ( <i>T. equinum</i> )               | CACACTG (rc) | 955 | UPRE-1 |
| TERG_03478 | class III aminotransferase, putative ( <i>A. benhamiae</i> )          | CAGTGTG      | 744 | UPRE-1 |
| TERG_03481 | hypothetical protein  | CAGCGTG      | 663 | UPRE-1 |
| TERG_03485 | NADPH-adrenodoxin reductase ( <i>T. tonsurans</i> )                   | CAGAGTG      | 864 | UPRE-1 |
| TERG_03493 | hypothetical protein  | CACGCTG (rc) | 36  | UPRE-1 |
| TERG_03493 | hypothetical protein  | CACTCTG (rc) | 191 | UPRE-1 |
| TERG_03509 | hypothetical protein  | CACGCTG (rc) | 599 | UPRE-1 |
| TERG_03510 | peroxisomal membrane anchor protein, putative ( <i>A. benhamiae</i> ) | CAGCGTG      | 94  | UPRE-1 |
| TERG_03511 | calcineurin binding protein ( <i>T. equinum</i> )                     | CACTCTG (rc) | 315 | UPRE-1 |
| TERG_03511 | calcineurin binding protein ( <i>T. equinum</i> )                     | CACTCTG (rc) | 645 | UPRE-1 |
| TERG_03512 | hypothetical protein  | CAGGGTG      | 887 | UPRE-1 |
| TERG_03526 | hypothetical protein  | CACCCTG (rc) | 735 | UPRE-1 |
| TERG_03528 | cytochrome c  | CACCCTG (rc) | 345 | UPRE-1 |
| TERG_03530 | 3' exoribonuclease ( <i>T. tonsurans</i> )                            | CACCCTG (rc) | 79  | UPRE-1 |
| TERG_03530 | 3' exoribonuclease ( <i>T. tonsurans</i> )                            | CACGCTG (rc) | 478 | UPRE-1 |
| TERG_03556 | transcriptional regulator Medusa ( <i>A. benhamiae</i> )              | CACGCTG (rc) | 178 | UPRE-1 |
| TERG_03562 | hypothetical protein  | CAGCGTG      | 503 | UPRE-1 |
| TERG_03569 | RING finger domain-containing protein ( <i>T. equinum</i> )           | CACGCTG (rc) | 678 | UPRE-1 |
| TERG_03571 | kinetochore protein spc24 ( <i>M. canis</i> )                         | CAGGGTG      | 200 | UPRE-1 |
| TERG_03571 | kinetochore protein spc24 ( <i>M. canis</i> )                         | CAGCGTG      | 623 | UPRE-1 |
| TERG_03577 | GATA transcription factor ( <i>T. tonsurans</i> )                     | CAGAGTG      | 300 | UPRE-1 |
| TERG_03578 | nitrogen regulatory protein DAL80                                     | CAGAGTG      | 764 | UPRE-1 |
| TERG_03582 | hypothetical protein  | CACTCTG (rc) | 192 | UPRE-1 |
| TERG_03582 | hypothetical protein  | CACTCTG (rc) | 432 | UPRE-1 |
| TERG_03604 | replication factor C subunit 5  | CAGTGTG      | 179 | UPRE-1 |
| TERG_03605 | ribosomal protein L16   | CACACTG (rc) | 733 | UPRE-1 |
| TERG_03606 | replication factor C protein ( <i>T. tonsurans</i> )                  | CAGTGTG      | 236 | UPRE-1 |
| TERG_03609 | endoplasmic reticulum protein ( <i>M. canis</i> )                     | CAGCGTG      | 692 | UPRE-1 |
| TERG_03631 | sister chromatid cohesion factor ( <i>T. equinum</i> )                | CACACTG (rc) | 657 | UPRE-1 |
| TERG_03632 | hypothetical protein  | CAGTGTG      | 519 | UPRE-1 |
| TERG_03636 | ankyrin repeat protein ( <i>T. equinum</i> )                          | CACACTG (rc) | 678 | UPRE-1 |
| TERG_03636 | ankyrin repeat protein ( <i>T. equinum</i> )                          | CACGCTG (rc) | 691 | UPRE-1 |
| TERG_03640 | peptidase M28 ( <i>T. tonsurans</i> )                                 | CAGAGTG      | 9   | UPRE-1 |
| TERG_03647 | hypothetical protein  | CACCCTG (rc) | 232 | UPRE-1 |
| TERG_03652 | chromosome segregation protein sudA                                   | CAGCGTG      | 133 | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_03661 | hypothetical protein   | CACGCTG (rc) | 320 | UPRE-1 |
| TERG_03661 | hypothetical protein   | CACTCTG (rc) | 701 | UPRE-1 |
| TERG_03661 | hypothetical protein   | CACTCTG (rc) | 943 | UPRE-1 |
| TERG_03663 | hypothetical protein   | CACCCTG (rc) | 36  | UPRE-1 |
| TERG_03672 | hypothetical protein   | CAGCGTG      | 254 | UPRE-1 |
| TERG_03674 | EBP domain-containing protein ( <i>T. tonsurans</i> )                    | CACACTG (rc) | 131 | UPRE-1 |
| TERG_03674 | EBP domain-containing protein ( <i>T. tonsurans</i> )                    | CACTCTG (rc) | 471 | UPRE-1 |
| TERG_03695 | pyrroline-5-carboxylate reductase  | CACGCTG (rc) | 737 | UPRE-1 |
| TERG_03696 | CTD kinase subunit gamma ( <i>T. equinum</i> )                           | CAGCGTG      | 817 | UPRE-1 |
| TERG_03704 | integral membrane protein Pth11-like, putative ( <i>T. verrucosum</i> )  | CACGCTG (rc) | 292 | UPRE-1 |
| TERG_03706 | trichodiene oxygenase ( <i>T. equinum</i> )                              | CACGCTG (rc) | 734 | UPRE-1 |
| TERG_03707 | geranylgeranyl diphosphate synthase, putative ( <i>A. benhamiae</i> )    | CAGGGTG      | 3   | UPRE-1 |
| TERG_03707 | geranylgeranyl diphosphate synthase, putative ( <i>A. benhamiae</i> )    | CAGCGTG      | 299 | UPRE-1 |
| TERG_03709 | hypothetical protein   | CACGCTG (rc) | 696 | UPRE-1 |
| TERG_03710 | hypothetical protein   | CAGGGTG      | 393 | UPRE-1 |
| TERG_03710 | hypothetical protein   | CAGCGTG      | 972 | UPRE-1 |
| TERG_03711 | histone acetyltransferase type B catalytic subunit ( <i>T. equinum</i> ) | CACTCTG (rc) | 485 | UPRE-1 |
| TERG_03711 | histone acetyltransferase type B catalytic subunit ( <i>T. equinum</i> ) | CACGCTG (rc) | 958 | UPRE-1 |
| TERG_03715 | zinc transporter SLC39A9 ( <i>T. equinum</i> )                           | CAGCGTG      | 211 | UPRE-1 |
| TERG_03719 | MFS sugar transporter ( <i>T. tonsurans</i> )                            | CACACTG (rc) | 727 | UPRE-1 |
| TERG_03724 | RING finger domain-containing protein ( <i>T. equinum</i> )              | CACCCTG (rc) | 272 | UPRE-1 |
| TERG_03739 | hypothetical protein   | CAGCGTG      | 128 | UPRE-1 |
| TERG_03740 | beta-1,6 glucan synthetase ( <i>T. tonsurans</i> )                       | CAGAGTG      | 587 | UPRE-1 |
| TERG_03744 | hypothetical protein   | CAGCGTG      | 367 | UPRE-1 |
| TERG_03750 | small nuclear ribonucleoprotein ( <i>T. tonsurans</i> )                  | CACCCTG (rc) | 498 | UPRE-1 |
| TERG_03775 | fructose-2,6-bisphosphatase ( <i>T. tonsurans</i> )                      | CACGCTG (rc) | 198 | UPRE-1 |
| TERG_03789 | glutamine-serine rich protein MS8, putative ( <i>A. benhamiae</i> )      | CAGGGTG      | 221 | UPRE-1 |
| TERG_03790 | DUF1275 domain-containing protein ( <i>T. equinum</i> )                  | CAGCGTG      | 136 | UPRE-1 |
| TERG_03796 | sorting nexin 41 ( <i>T. tonsurans</i> )                                 | CACCCTG (rc) | 708 | UPRE-1 |
| TERG_03800 | hypothetical protein   | CAGCGTG      | 139 | UPRE-1 |
| TERG_03801 | CAMK protein kinase  | CAGAGTG      | 654 | UPRE-1 |
| TERG_03807 | hypothetical protein   | CACCCTG (rc) | 187 | UPRE-1 |
| TERG_03811 | actin-binding protein ( <i>T. equinum</i> )                              | CACTCTG (rc) | 57  | UPRE-1 |
| TERG_03812 | kinesin motor domain-containing protein ( <i>T. tonsurans</i> )          | CAGAGTG      | 80  | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_03833 | isochorismatase family protein ( <i>A. benhamiae</i> )                   | CACCCTG (rc) | 921 | UPRE-1 |
| TERG_03834 | ketol-acid reductoisomerase, mitochondrial                               | CAGGGTG      | 179 | UPRE-1 |
| TERG_03840 | bromodomain associated domain protein ( <i>A. benhamiae</i> )            | CACGCTG (rc) | 199 | UPRE-1 |
| TERG_03850 | hypothetical protein   | CAGAGTG      | 733 | UPRE-1 |
| TERG_03854 | laccase ( <i>T. tonsurans</i> )  | CAGGGTG      | 299 | UPRE-1 |
| TERG_03865 | actin cytoskeleton-regulatory complex protein END3                       | CACCCTG (rc) | 741 | UPRE-1 |
| TERG_03879 | cell wall biogenesis protein Mhp1, putative ( <i>T. verrucosum</i> )     | CACGCTG (rc) | 126 | UPRE-1 |
| TERG_03879 | cell wall biogenesis protein Mhp1, putative ( <i>T. verrucosum</i> )     | CACCCTG (rc) | 322 | UPRE-1 |
| TERG_03892 | CAMK/CAMKL protein kinase ( <i>T. tonsurans</i> )                        | CAGAGTG      | 508 | UPRE-1 |
| TERG_03895 | lipase/thioesterase family protein ( <i>A. benhamiae</i> )               | CACGCTG (rc) | 984 | UPRE-1 |
| TERG_03899 | hypothetical protein   | CACGCTG (rc) | 166 | UPRE-1 |
| TERG_03903 | DUF6 domain-containing protein ( <i>T. equinum</i> )                     | CACACTG (rc) | 796 | UPRE-1 |
| TERG_03905 | tubulin gamma chain  | CAGAGTG      | 634 | UPRE-1 |
| TERG_03907 | neutral amino acid permease ( <i>T. tonsurans</i> )                      | CAGAGTG      | 754 | UPRE-1 |
| TERG_03916 | geranylgeranyl pyrophosphate synthetase ( <i>T. tonsurans</i> )          | CACTCTG (rc) | 196 | UPRE-1 |
| TERG_03917 | carotene cyclase ( <i>T. equinum</i> )                                   | CAGAGTG      | 984 | UPRE-1 |
| TERG_03919 | phytoene dehydrogenase ( <i>T. equinum</i> )                             | CAGAGTG      | 991 | UPRE-1 |
| TERG_03933 | ABC metal ion transporter ( <i>T. equinum</i> )                          | CACCCTG (rc) | 166 | UPRE-1 |
| TERG_03935 | hypothetical protein   | CACACTG (rc) | 811 | UPRE-1 |
| TERG_03936 | CAMK protein kinase  | CAGTGTG      | 567 | UPRE-1 |
| TERG_03938 | hypothetical protein   | CAGGGTG      | 567 | UPRE-1 |
| TERG_03938 | hypothetical protein   | CAGGGTG      | 852 | UPRE-1 |
| TERG_03944 | hypothetical protein   | CACCCTG (rc) | 34  | UPRE-1 |
| TERG_03949 | equisetin synthetase ( <i>T. equinum</i> )                               | CAGCGTG      | 630 | UPRE-1 |
| TERG_03959 | myo-inositol oxygenase ( <i>T. tonsurans</i> )                           | CACACTG (rc) | 381 | UPRE-1 |
| TERG_03963 | mannosyl phosphorylinositol ceramide synthase SUR1 ( <i>T. equinum</i> ) | CAGGGTG      | 631 | UPRE-1 |
| TERG_03973 | zinc finger protein gcs1 ( <i>T. equinum</i> )                           | CACGCTG (rc) | 475 | UPRE-1 |
| TERG_03977 | hypothetical protein   | CACGCTG (rc) | 474 | UPRE-1 |
| TERG_03985 | hypothetical protein   | CACGCTG (rc) | 818 | UPRE-1 |
| TERG_03989 | cyclin ( <i>T. tonsurans</i> )   | CACACTG (rc) | 951 | UPRE-1 |
| TERG_03991 | phosphotransferase enzyme family protein ( <i>T. verrucosum</i> )        | CACCCTG (rc) | 216 | UPRE-1 |
| TERG_03992 | 26S protease regulatory subunit 4 ( <i>M. gypseum</i> )                  | CAGAGTG      | 77  | UPRE-1 |
| TERG_04001 | NADH-ubiquinone oxidoreductase B12 subunit ( <i>T. tonsurans</i> )       | CAGCGTG      | 307 | UPRE-1 |



|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_04002 | ribosome assembly protein SQT1 ( <i>T. equinum</i> )                                   | CACCCTG (rc) | 389 | UPRE-1 |
| TERG_04006 | Rho1 guanine nucleotide exchange factor 3 ( <i>T. equinum</i> )                        | CAGAGTG      | 69  | UPRE-1 |
| TERG_04023 | hypothetical protein   | CACACTG (rc) | 290 | UPRE-1 |
| TERG_04031 | BAR domain protein ( <i>A. benhamiae</i> )   | CACACTG (rc) | 487 | UPRE-1 |
| TERG_04036 | adenosine kinase ( <i>T. tonsurans</i> )   | CAGTGTG      | 389 | UPRE-1 |
| TERG_04044 | vacuolar protein sorting protein DigA ( <i>T. tonsurans</i> )                          | CACTCTG (rc) | 540 | UPRE-1 |
| TERG_04045 | SNF2 family helicase/ATPase ( <i>T. tonsurans</i> )                                    | CAGAGTG      | 207 | UPRE-1 |
| TERG_04065 | filamentation protein (Rhfl), putative ( <i>T. verrucosum</i> )                        | CACACTG (rc) | 394 | UPRE-1 |
| TERG_04069 | hypothetical protein   | CAGTGTG      | 792 | UPRE-1 |
| TERG_04072 | SNF2 family helicase/ATPase, putative ( <i>T. verrucosum</i> )                         | CACTCTG (rc) | 212 | UPRE-1 |
| TERG_04073 | glutathione synthetase   | CAGAGTG      | 507 | UPRE-1 |
| TERG_04080 | transcription elongation factor spt4   | CACTCTG (rc) | 68  | UPRE-1 |
| TERG_04096 | SUMO activating enzyme ( <i>T. tonsurans</i> )   | CAGCGTG      | 396 | UPRE-1 |
| TERG_04098 | Swi5 domain-containing protein ( <i>T. equinum</i> )                                   | CAGTGTG      | 458 | UPRE-1 |
| TERG_04101 | G-protein coupled receptor ( <i>T. equinum</i> )                                       | CACCCTG (rc) | 201 | UPRE-1 |
| TERG_04102 | hypothetical protein   | CAGGGTG      | 740 | UPRE-1 |
| TERG_04104 | autophagocytosis protein ( <i>T. tonsurans</i> )                                       | CACCCTG (rc) | 828 | UPRE-1 |
| TERG_04115 | aldo-keto reductase, putative ( <i>T. verrucosum</i> )                                 | CACGCTG (rc) | 329 | UPRE-1 |
| TERG_04115 | aldo-keto reductase, putative ( <i>T. verrucosum</i> )                                 | CACGCTG (rc) | 655 | UPRE-1 |
| TERG_04116 | hypothetical protein   | CAGCGTG      | 386 | UPRE-1 |
| TERG_04116 | hypothetical protein   | CAGCGTG      | 712 | UPRE-1 |
| TERG_04123 | hypothetical protein   | CAGAGTG      | 158 | UPRE-1 |
| TERG_04124 | hypothetical protein   | CAGAGTG      | 228 | UPRE-1 |
| TERG_04126 | dual specificity phosphatase ( <i>T. equinum</i> )                                     | CACCCTG (rc) | 524 | UPRE-1 |
| TERG_04127 | hypothetical protein   | CAGGGTG      | 766 | UPRE-1 |
| TERG_04132 | hypothetical protein   | CAGAGTG      | 320 | UPRE-1 |
| TERG_04133 | major allergen and cytotoxin AspF1 ( <i>A. benhamiae</i> )                             | CACACTG (rc) | 947 | UPRE-1 |
| TERG_04143 | Cytochrome c oxidase polypeptide V ( <i>T. tonsurans</i> )                             | CAGCGTG      | 529 | UPRE-1 |
| TERG_04146 | FAD/FMN-containing isoamyl alcohol oxidase MreA-like, putative ( <i>A. benhamiae</i> ) | CAGTGTG      | 697 | UPRE-1 |
| TERG_04151 | GTP-binding protein ypt3 ( <i>T. tonsurans</i> )                                       | CAGCGTG      | 390 | UPRE-1 |
| TERG_04154 | hypothetical protein   | CACACTG (rc) | 37  | UPRE-1 |
| TERG_04156 | hypothetical protein   | CAGGGTG      | 754 | UPRE-1 |
| TERG_04178 | 1,3-beta-glucan biosynthesis protein ( <i>T. tonsurans</i> )                           | CACCCTG (rc) | 417 | UPRE-1 |
| TERG_04184 | CorA family metal ion transporter, putative ( <i>A. benhamiae</i> )                    | CAGAGTG      | 841 | UPRE-1 |
| TERG_04200 | hypothetical protein   | CAGCGTG      | 440 | UPRE-1 |

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|------------|--|--------------|-----|--------|
| TERG_04201 | histone-lysine N-methyltransferase, H3 lysine-36 specific                          | CACCCTG (rc) | 705 | UPRE-1 |
| TERG_04208 | HAL protein kinase   | CACGCTG (rc) | 143 | UPRE-1 |
| TERG_04221 | H/ACA ribonucleoprotein complex subunit 3  | CAGCGTG      | 543 | UPRE-1 |
| TERG_04222 | art-4 protein ( <i>M. canis</i> )  | CACGCTG (rc) | 253 | UPRE-1 |
| TERG_04233 | hypothetical protein   | CAGCGTG      | 643 | UPRE-1 |
| TERG_04234 | hydrophobin, putative ( <i>T. verrucosum</i> )                                     | CACACTG (rc) | 712 | UPRE-1 |
| TERG_04235 | WW domain-containing protein ( <i>T. tonsurans</i> )                               | CAGTGTG      | 534 | UPRE-1 |
| TERG_04258 | histone acetylase complex subunit Paf400 ( <i>T. equinum</i> )                     | CAGGGTG      | 263 | UPRE-1 |
| TERG_04259 | mRNA splicing protein ( <i>T. tonsurans</i> )                                      | CACTCTG (rc) | 173 | UPRE-1 |
| TERG_04263 | hypothetical protein   | CAGCGTG      | 714 | UPRE-1 |
| TERG_04281 | woronin body major protein   | CAGTGTG      | 581 | UPRE-1 |
| TERG_04291 | urea amidolyase, putative ( <i>A. benhamiae</i> )                                  | CACCCTG (rc) | 895 | UPRE-1 |
| TERG_04292 | hypothetical protein   | CAGGGTG      | 787 | UPRE-1 |
| TERG_04294 | methylcrotonoyl-CoA carboxylase subunit beta ( <i>T. tonsurans</i> )               | CAGTGTG      | 94  | UPRE-1 |
| TERG_04294 | methylcrotonoyl-CoA carboxylase subunit beta ( <i>T. tonsurans</i> )               | CAGTGTG      | 201 | UPRE-1 |
| TERG_04294 | methylcrotonoyl-CoA carboxylase subunit beta ( <i>T. tonsurans</i> )               | CAGGGTG      | 491 | UPRE-1 |
| TERG_04297 | ab-hydrolase associated lipase, putative ( <i>A. benhamiae</i> )                   | CACCCTG (rc) | 232 | UPRE-1 |
| TERG_04297 | ab-hydrolase associated lipase, putative ( <i>A. benhamiae</i> )                   | CACCCTG (rc) | 359 | UPRE-1 |
| TERG_04299 | dolichyl-diphosphooligosaccharide-protein glycotransferase ( <i>T. tonsurans</i> ) | CACGCTG (rc) | 814 | UPRE-1 |
| TERG_04300 | NADH-ubiquinone oxidoreductase 9.5 kDa subunit ( <i>T. tonsurans</i> )             | CAGCGTG      | 732 | UPRE-1 |
| TERG_04301 | transcription factor RfeG ( <i>T. tonsurans</i> )                                  | CACCCTG (rc) | 90  | UPRE-1 |
| TERG_04303 | hypothetical protein   | CACTCTG (rc) | 613 | UPRE-1 |
| TERG_04309 | multidrug resistance protein ( <i>T. equinum</i> )                                 | CACACTG (rc) | 904 | UPRE-1 |
| TERG_04311 | mitochondrial phosphate carrier protein ( <i>T. tonsurans</i> )                    | CAGGGTG      | 833 | UPRE-1 |
| TERG_04318 | hypothetical protein   | CACTCTG (rc) | 853 | UPRE-1 |
| TERG_04325 | ubiquitin conjugating enzyme, putative ( <i>T. verrucosum</i> )                    | CAGCGTG      | 649 | UPRE-1 |
| TERG_04330 | DUF1620 domain-containing protein ( <i>T. equinum</i> )                            | CAGTGTG      | 934 | UPRE-1 |
| TERG_04332 | phosphatidylinositol transporter ( <i>T. tonsurans</i> )                           | CACTCTG (rc) | 116 | UPRE-1 |
| TERG_04334 | fungal specific transcription factor, putative ( <i>A. benhamiae</i> )             | CACTCTG (rc) | 597 | UPRE-1 |
| TERG_04346 | HSP70 family protein ( <i>A. benhamiae</i> )                                       | CACCCTG (rc) | 981 | UPRE-1 |
| TERG_04350 | hypothetical protein   | CACTCTG (rc) | 978 | UPRE-1 |
| TERG_04360 | RNA binding protein ( <i>T. equinum</i> )  | CAGCGTG      | 190 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_04362 | condensin complex component cnd3 ( <i>T. equinum</i> )                  | CACCCTG (rc) | 118 | UPRE-1 |
| TERG_04364 | sulfite oxidase ( <i>T. equinum</i> )                                   | CACTCTG (rc) | 480 | UPRE-1 |
| TERG_04367 | hypothetical protein  | CACCCTG (rc) | 976 | UPRE-1 |
| TERG_04369 | hypothetical protein  | CAGGGTG      | 105 | UPRE-1 |
| TERG_04375 | D-lactate dehydrogenase ( <i>T. tonsurans</i> )                         | CACACTG (rc) | 400 | UPRE-1 |
| TERG_04386 | hypothetical protein  | CACTCTG (rc) | 498 | UPRE-1 |
| TERG_04396 | a-pheromone processing metallopeptidase Ste23 ( <i>T. equinum</i> )     | CACCCTG (rc) | 198 | UPRE-1 |
| TERG_04406 | heat shock transcription factor Hsf1, putative ( <i>T. verrucosum</i> ) | CACCCTG (rc) | 195 | UPRE-1 |
| TERG_04415 | CMGC/SRPK protein kinase  | CAGCGTG      | 47  | UPRE-1 |
| TERG_04418 | tRNA (adenine-N(1)-)-methyltransferase non-catalytic subunit trm6       | CAGTGTG      | 4   | UPRE-1 |
| TERG_04424 | MYB DNA-binding domain protein ( <i>A. benhamiae</i> )                  | CAGGGTG      | 845 | UPRE-1 |
| TERG_04438 | GDP-mannose transporter 1   | CAGGGTG      | 648 | UPRE-1 |
| TERG_04446 | eukaryotic peptide chain release factor subunit 1                       | CACTCTG (rc) | 683 | UPRE-1 |
| TERG_04446 | eukaryotic peptide chain release factor subunit 1                       | CACGCTG (rc) | 830 | UPRE-1 |
| TERG_04447 | protein kinase subdomain-containing protein ( <i>T. equinum</i> )       | CAGCGTG      | 670 | UPRE-1 |
| TERG_04447 | protein kinase subdomain-containing protein ( <i>T. equinum</i> )       | CAGAGTG      | 817 | UPRE-1 |
| TERG_04448 | CMGC/DYRK protein kinase ( <i>M. gypseum</i> )                          | CAGCGTG      | 14  | UPRE-1 |
| TERG_04448 | CMGC/DYRK protein kinase ( <i>M. gypseum</i> )                          | CAGAGTG      | 161 | UPRE-1 |
| TERG_04456 | DUF1671 domain-containing protein ( <i>T. equinum</i> )                 | CAGGGTG      | 832 | UPRE-1 |
| TERG_04457 | POS9-activating factor FAP7 ( <i>T. tonsurans</i> )                     | CAGGGTG      | 706 | UPRE-1 |
| TERG_04461 | P-type ATPase ( <i>T. equinum</i> )                                     | CAGCGTG      | 975 | UPRE-1 |
| TERG_04469 | D-lactate dehydrogenase, putative ( <i>T. verrucosum</i> )              | CACGCTG (rc) | 157 | UPRE-1 |
| TERG_04480 | C6 transcription factor, putative ( <i>A. benhamiae</i> )               | CAGCGTG      | 417 | UPRE-1 |
| TERG_04483 | Mitochondrial ribosomal subunit S27 ( <i>T. tonsurans</i> )             | CAGTGTG      | 250 | UPRE-1 |
| TERG_04487 | hypothetical protein  | CACGCTG (rc) | 284 | UPRE-1 |
| TERG_04490 | NADH-ubiquinone oxidoreductase 78 kDa subunit, mitochondrial            | CACACTG (rc) | 593 | UPRE-1 |
| TERG_04494 | hypothetical protein  | CACTCTG (rc) | 992 | UPRE-1 |
| TERG_04501 | WD repeat protein ( <i>T. equinum</i> )                                 | CAGAGTG      | 528 | UPRE-1 |
| TERG_04506 | 60S ribosomal protein L4-A ( <i>T. tonsurans</i> )                      | CAGAGTG      | 458 | UPRE-1 |
| TERG_04518 | histone acetyltransferase type B subunit 2                              | CAGTGTG      | 785 | UPRE-1 |
| TERG_04538 | pyruvate dehydrogenase kinase ( <i>T. tonsurans</i> )                   | CAGCGTG      | 289 | UPRE-1 |
| TERG_04541 | Ulp1 protease family protein ( <i>T. verrucosum</i> )                   | CACCCTG (rc) | 737 | UPRE-1 |
| TERG_04551 | hypothetical protein  | CAGAGTG      | 738 | UPRE-1 |
| TERG_04558 | nucleoside diphosphate kinase   | CACGCTG (rc) | 696 | UPRE-1 |

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|------------|--|--------------|-----|--------|
| TERG_04570 | NSFL1 cofactor p47 ( <i>T. equinum</i> )   | CACCCTG (rc) | 277 | UPRE-1 |
| TERG_04572 | mitochondrial export translocase Oxa1, putative ( <i>T. verrucosum</i> )         | CAGGGTG      | 205 | UPRE-1 |
| TERG_04580 | NADP-specific glutamate dehydrogenase  | CAGAGTG      | 777 | UPRE-1 |
| TERG_04596 | SUMO-conjugating enzyme ubc9   | CACTCTG (rc) | 934 | UPRE-1 |
| TERG_04601 | hypothetical protein   | CACGCTG (rc) | 810 | UPRE-1 |
| TERG_04608 | C6 transcription factor, putative ( <i>A. benhamiae</i> )                        | CAGCGTG      | 681 | UPRE-1 |
| TERG_04612 | branched-chain amino acid aminotransferase                                       | CACGCTG (rc) | 413 | UPRE-1 |
| TERG_04622 | ankyrin repeat protein nuc-2 ( <i>T. equinum</i> )                               | CACGCTG (rc) | 117 | UPRE-1 |
| TERG_04635 | JmjC domain-containing protein ( <i>T. equinum</i> )                             | CACGCTG (rc) | 937 | UPRE-1 |
| TERG_04636 | 4-hydroxybenzoate polyprenyl transferase   | CAGCGTG      | 458 | UPRE-1 |
| TERG_04650 | iron sulfur cluster assembly protein 1, mitochondrial                            | CACCCTG (rc) | 614 | UPRE-1 |
| TERG_04652 | uracil-DNA glycosylase   | CACGCTG (rc) | 252 | UPRE-1 |
| TERG_04653 | hypothetical protein   | CAGCGTG      | 123 | UPRE-1 |
| TERG_04661 | yippee family protein ( <i>T. tonsurans</i> )                                    | CACGCTG (rc) | 106 | UPRE-1 |
| TERG_04662 | protein disulfide-isomerase domain-containing protein                            | CAGTGTG      | 296 | UPRE-1 |
| TERG_04666 | hypothetical protein   | CAGAGTG      | 269 | UPRE-1 |
| TERG_04666 | hypothetical protein   | CAGCGTG      | 519 | UPRE-1 |
| TERG_04669 | hypothetical protein   | CAGAGTG      | 597 | UPRE-1 |
| TERG_04670 | CHY and RING finger domain protein, putative ( <i>A. benhamiae</i> )             | CAGCGTG      | 741 | UPRE-1 |
| TERG_04677 | guanylate kinase   | CACGCTG (rc) | 319 | UPRE-1 |
| TERG_04682 | shugoshin family protein ( <i>T. verrucosum</i> )                                | CAGTGTG      | 496 | UPRE-1 |
| TERG_04691 | nuclear division Rft1 protein, putative ( <i>T. verrucosum</i> )                 | CACGCTG (rc) | 971 | UPRE-1 |
| TERG_04692 | replication protein A DNA-binding subunit ( <i>T. tonsurans</i> )                | CAGCGTG      | 596 | UPRE-1 |
| TERG_04703 | DUF1715 domain-containing protein ( <i>T. equinum</i> )                          | CAGCGTG      | 139 | UPRE-1 |
| TERG_04703 | DUF1715 domain-containing protein ( <i>T. equinum</i> )                          | CAGTGTG      | 353 | UPRE-1 |
| TERG_04709 | glucose-6-phosphate 1-dehydrogenase  | CACGCTG (rc) | 701 | UPRE-1 |
| TERG_04713 | cystathionine beta-synthase ( <i>T. tonsurans</i> )                              | CACCCTG (rc) | 382 | UPRE-1 |
| TERG_04746 | nucleolar GTP-binding protein ( <i>T. tonsurans</i> )                            | CAGAGTG      | 473 | UPRE-1 |
| TERG_04747 | phosphatidylglycerol/phosphatidylinositol transfer protein ( <i>T. equinum</i> ) | CAGGGTG      | 219 | UPRE-1 |
| TERG_04758 | SAGA complex subunit Ada2 ( <i>T. tonsurans</i> )                                | CACTCTG (rc) | 467 | UPRE-1 |
| TERG_04759 | AGC/AKT protein kinase   | CAGAGTG      | 121 | UPRE-1 |
| TERG_04765 | MFS transporter, putative ( <i>A. benhamiae</i> )                                | CAGGGTG      | 431 | UPRE-1 |
| TERG_04771 | ribonuclease T2 family, putative ( <i>A. benhamiae</i> )                         | CAGGGTG      | 749 | UPRE-1 |
| TERG_04782 | 37S ribosomal protein Mrp10 ( <i>T. equinum</i> )                                | CACCCTG (rc) | 445 | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_04784 | hypothetical protein   | CACACTG (rc) | 441 | UPRE-1 |
| TERG_04785 | hypothetical protein   | CAGTGTG      | 737 | UPRE-1 |
| TERG_04795 | HIT finger domain-containing protein ( <i>T. equinum</i> )                 | CAGGGTG      | 110 | UPRE-1 |
| TERG_04806 | ABC transporter ( <i>T. tonsurans</i> )                                    | CAGTGTG      | 862 | UPRE-1 |
| TERG_04819 | Fe superoxide dismutase ( <i>T. tonsurans</i> )                            | CACCCTG (rc) | 233 | UPRE-1 |
| TERG_04820 | hypothetical protein   | CAGGGTG      | 978 | UPRE-1 |
| TERG_04825 | hypothetical protein   | CACTCTG (rc) | 433 | UPRE-1 |
| TERG_04826 | actin binding protein ( <i>T. equinum</i> )                                | CAGGGTG      | 297 | UPRE-1 |
| TERG_04826 | actin binding protein ( <i>T. equinum</i> )                                | CAGAGTG      | 982 | UPRE-1 |
| TERG_04847 | hypothetical protein   | CACCCTG (rc) | 35  | UPRE-1 |
| TERG_04848 | ABC transporter, putative ( <i>T. verrucosum</i> )                         | CAGGGTG      | 935 | UPRE-1 |
| TERG_04851 | Acyl CoA binding protein family protein ( <i>A. benhamiae</i> )            | CACCCTG (rc) | 602 | UPRE-1 |
| TERG_04856 | triosephosphate isomerase ( <i>T. tonsurans</i> )                          | CACCCTG (rc) | 408 | UPRE-1 |
| TERG_04857 | ribose 5-phosphate isomerase   | CAGGGTG      | 717 | UPRE-1 |
| TERG_04894 | alcohol dehydrogenase IV ( <i>T. equinum</i> )                             | CAGTGTG      | 394 | UPRE-1 |
| TERG_04920 | KH domain-containing protein ( <i>T. tonsurans</i> )                       | CACCCTG (rc) | 982 | UPRE-1 |
| TERG_04927 | fermentation associated protein (Csf1), putative ( <i>A. benhamiae</i> )   | CAGCGTG      | 137 | UPRE-1 |
| TERG_04936 | meiotic chromosome segregation protein ( <i>T. equinum</i> )               | CAGCGTG      | 198 | UPRE-1 |
| TERG_04948 | hypothetical protein   | CAGAGTG      | 117 | UPRE-1 |
| TERG_04950 | cytochrome P450 monooxygenase ( <i>T. equinum</i> )                        | CACTCTG (rc) | 304 | UPRE-1 |
| TERG_04979 | RNA exonuclease 4 ( <i>T. tonsurans</i> )                                  | CACGCTG (rc) | 212 | UPRE-1 |
| TERG_04990 | deoxyhypusine hydroxylase  | CACGCTG (rc) | 621 | UPRE-1 |
| TERG_04991 | NADH-ubiquinone oxidoreductase 64 kDa subunit ( <i>T. tonsurans</i> )      | CAGCGTG      | 185 | UPRE-1 |
| TERG_04998 | mitochondrial ATP-dependent RNA helicase ( <i>T. tonsurans</i> )           | CACCCTG (rc) | 477 | UPRE-1 |
| TERG_04999 | Sec1 family protein ( <i>T. tonsurans</i> )                                | CAGGGTG      | 641 | UPRE-1 |
| TERG_05002 | UDP-glucose 4-epimerase GalE   | CACCCTG (rc) | 408 | UPRE-1 |
| TERG_05003 | NmrA family protein ( <i>T. equinum</i> )                                  | CAGGGTG      | 223 | UPRE-1 |
| TERG_05008 | hypothetical protein   | CACTCTG (rc) | 951 | UPRE-1 |
| TERG_05009 | Dishevelled, Egl-10, and Pleckstrin domain protein ( <i>A. benhamiae</i> ) | CAGAGTG      | 529 | UPRE-1 |
| TERG_05037 | hypothetical protein   | CACCCTG (rc) | 100 | UPRE-1 |
| TERG_05057 | DUF775 domain-containing protein ( <i>T. equinum</i> )                     | CACGCTG (rc) | 213 | UPRE-1 |
| TERG_05058 | thiamine pyrophosphokinase ( <i>T. tonsurans</i> )                         | CAGCGTG      | 946 | UPRE-1 |
| TERG_05067 | hypothetical protein   | CACCCTG (rc) | 942 | UPRE-1 |
| TERG_05077 | D-amino-acid oxidase ( <i>T. equinum</i> )                                 | CACACTG (rc) | 628 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_05083 | adaptin ear-binding coat-associated protein 1 ( <i>M. canis</i> )                     | CACTCTG (rc) | 564 | UPRE-1 |
| TERG_05084 | translation initiation factor eIF-2B alpha subunit ( <i>T. tonsurans</i> )            | CACACTG (rc) | 209 | UPRE-1 |
| TERG_05104 | MFS transporter of unknown specificity ( <i>T. verrucosum</i> )                       | CAGAGTG      | 870 | UPRE-1 |
| TERG_05105 | hypothetical protein  | CACTCTG (rc) | 364 | UPRE-1 |
| TERG_05106 | integral membrane protein ( <i>T. equinum</i> )                                       | CAGAGTG      | 815 | UPRE-1 |
| TERG_05118 | actin cytoskeleton organization protein ( <i>T. tonsurans</i> )                       | CAGTGTG      | 52  | UPRE-1 |
| TERG_05124 | gliotoxin biosynthesis protein GliK ( <i>T. verrucosum</i> )                          | CACGCTG (rc) | 802 | UPRE-1 |
| TERG_05127 | aminotransferase GliI ( <i>A. benhamiae</i> )   | CAGGGTG      | 170 | UPRE-1 |
| TERG_05146 | protein methyltransferase ( <i>T. tonsurans</i> )                                     | CACACTG (rc) | 261 | UPRE-1 |
| TERG_05147 | pre-mRNA-splicing factor ATP-dependent RNA helicase PRP43                             | CAGTGTG      | 686 | UPRE-1 |
| TERG_05150 | tRNA wybutosine-synthesizing protein 2 ( <i>T. equinum</i> )                          | CACTCTG (rc) | 61  | UPRE-1 |
| TERG_05154 | protein-vacuolar targeting protein Atg18 ( <i>T. tonsurans</i> )                      | CACTCTG (rc) | 351 | UPRE-1 |
| TERG_05154 | protein-vacuolar targeting protein Atg18 ( <i>T. tonsurans</i> )                      | CACCCTG (rc) | 567 | UPRE-1 |
| TERG_05155 | Leucine carboxyl methyltransferase family ( <i>A. benhamiae</i> )                     | CAGGGTG      | 745 | UPRE-1 |
| TERG_05155 | Leucine carboxyl methyltransferase family ( <i>A. benhamiae</i> )                     | CAGAGTG      | 961 | UPRE-1 |
| TERG_05178 | nuclear and cytoplasmic polyadenylated RNA-binding protein pub1 ( <i>T. equinum</i> ) | CAGTGTG      | 652 | UPRE-1 |
| TERG_05180 | glucosamine 6-phosphate synthetase ( <i>T. equinum</i> )                              | CACTCTG (rc) | 283 | UPRE-1 |
| TERG_05182 | msp1 ( <i>T. equinum</i> )  | CAGAGTG      | 312 | UPRE-1 |
| TERG_05185 | RING finger ubiquitin ligase ( <i>T. tonsurans</i> )                                  | CACACTG (rc) | 156 | UPRE-1 |
| TERG_05191 | hypothetical protein  | CAGAGTG      | 202 | UPRE-1 |
| TERG_05195 | radical SAM domain-containing protein ( <i>T. tonsurans</i> )                         | CACTCTG (rc) | 252 | UPRE-1 |
| TERG_05225 | nuclear localization protein ( <i>T. equinum</i> )                                    | CAGAGTG      | 42  | UPRE-1 |
| TERG_05236 | 60S ribosomal protein L35   | CACACTG (rc) | 746 | UPRE-1 |
| TERG_05241 | hypothetical protein  | CACGCTG (rc) | 418 | UPRE-1 |
| TERG_05253 | chromodomain helicase ( <i>T. tonsurans</i> )   | CACGCTG (rc) | 587 | UPRE-1 |
| TERG_05270 | C6 and C2H2 transcription factor RegA-like, putative ( <i>A. benhamiae</i> )          | CAGAGTG      | 346 | UPRE-1 |
| TERG_05278 | microtubule associated protein ( <i>T. tonsurans</i> )                                | CAGCGTG      | 906 | UPRE-1 |
| TERG_05285 | translation initiation factor 4B ( <i>T. equinum</i> )                                | CACGCTG (rc) | 711 | UPRE-1 |
| TERG_05303 | phospholipase PldA, putative ( <i>T. verrucosum</i> )                                 | CACTCTG (rc) | 40  | UPRE-1 |
| TERG_05303 | phospholipase PldA, putative ( <i>T. verrucosum</i> )                                 | CACGCTG (rc) | 949 | UPRE-1 |
| TERG_05304 | cyanate hydratase   | CAGAGTG      | 659 | UPRE-1 |
| TERG_05305 | glutathione-dependent formaldehyde-activating enzyme ( <i>T. tonsurans</i> )          | CACTCTG (rc) | 739 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_05307 | hypothetical protein  | CAGTGTG      | 392 | UPRE-1 |
| TERG_05313 | PEK protein kinase  | CACTCTG (rc) | 589 | UPRE-1 |
| TERG_05318 | polyphosphoinositide phosphatase ( <i>T. tonsurans</i> )                      | CAGAGTG      | 502 | UPRE-1 |
| TERG_05323 | hypothetical protein  | CACACTG (rc) | 139 | UPRE-1 |
| TERG_05327 | DUF1237 domain-containing protein ( <i>T. equinum</i> )                       | CAGTGTG      | 71  | UPRE-1 |
| TERG_05348 | nuclear protein SDK3, putative ( <i>A. benhamiae</i> )                        | CACCCTG (rc) | 145 | UPRE-1 |
| TERG_05349 | oxidoreductase, 2OG-Fe(II) oxygenase family, putative ( <i>A. benhamiae</i> ) | CACCCTG (rc) | 480 | UPRE-1 |
| TERG_05352 | benzoate 4-monooxygenase cytochrome P450 ( <i>T. equinum</i> )                | CACACTG (rc) | 627 | UPRE-1 |
| TERG_05357 | succinate:fumarate antiporter ( <i>T. tonsurans</i> )                         | CACGCTG (rc) | 246 | UPRE-1 |
| TERG_05358 | CAF1 family ribonuclease, putative ( <i>A. benhamiae</i> )                    | CACCCTG (rc) | 673 | UPRE-1 |
| TERG_05360 | 50S ribosomal subunit L30 ( <i>T. equinum</i> )                               | CAGAGTG      | 311 | UPRE-1 |
| TERG_05363 | hypothetical protein  | CAGTGTG      | 176 | UPRE-1 |
| TERG_05381 | sodium/hydrogen antiporter  | CACCCTG (rc) | 564 | UPRE-1 |
| TERG_05389 | septum-promoting GTP-binding protein 1  | CAGGGTG      | 18  | UPRE-1 |
| TERG_05391 | MFS glucose transporter, putative ( <i>T. verrucosum</i> )                    | CAGTGTG      | 539 | UPRE-1 |
| TERG_05395 | serine/threonine protein kinase ( <i>T. tonsurans</i> )                       | CACGCTG (rc) | 153 | UPRE-1 |
| TERG_05397 | beta-lactamase ( <i>T. equinum</i> )  | CACTCTG (rc) | 120 | UPRE-1 |
| TERG_05407 | phosphotransferase enzyme family protein ( <i>T. equinum</i> )                | CACGCTG (rc) | 269 | UPRE-1 |
| TERG_05408 | ThiJ/PfpI family protein ( <i>T. tonsurans</i> )                              | CAGCGTG      | 741 | UPRE-1 |
| TERG_05415 | TRI7-like toxin biosynthesis protein, putative ( <i>A. benhamiae</i> )        | CAGAGTG      | 174 | UPRE-1 |
| TERG_05416 | hypothetical protein  | CAGCGTG      | 43  | UPRE-1 |
| TERG_05416 | hypothetical protein  | CAGGGTG      | 239 | UPRE-1 |
| TERG_05421 | alpha-galactosidase A ( <i>M. canis</i> )                                     | CACACTG (rc) | 162 | UPRE-1 |
| TERG_05422 | hypothetical protein  | CAGTGTG      | 818 | UPRE-1 |
| TERG_05424 | hypothetical protein  | CAGTGTG      | 191 | UPRE-1 |
| TERG_05430 | hypothetical protein  | CACTCTG (rc) | 406 | UPRE-1 |
| TERG_05430 | hypothetical protein  | CACCCTG (rc) | 857 | UPRE-1 |
| TERG_05431 | sterol 24-C-methyltransferase ( <i>T. tonsurans</i> )                         | CACACTG (rc) | 966 | UPRE-1 |
| TERG_05432 | pre-mRNA-splicing factor slt11  | CAGTGTG      | 579 | UPRE-1 |
| TERG_05434 | ribosome associated DnaJ chaperone Zuotin ( <i>T. equinum</i> )               | CAGCGTG      | 521 | UPRE-1 |
| TERG_05443 | hypothetical protein  | CACTCTG (rc) | 604 | UPRE-1 |
| TERG_05446 | sarcosine oxidase ( <i>T. equinum</i> )                                       | CACACTG (rc) | 330 | UPRE-1 |
| TERG_05447 | lysophospholipase NTE1  | CAGTGTG      | 291 | UPRE-1 |
| TERG_05448 | hypothetical protein  | CACGCTG (rc) | 423 | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_05449 | viral A-type inclusion protein repeat protein ( <i>T. tonsurans</i> )              | CAGCGTG      | 486 | UPRE-1 |
| TERG_05458 | MGMT family protein ( <i>T. tonsurans</i> )  | CACCCTG (rc) | 924 | UPRE-1 |
| TERG_05459 | hypothetical protein   | CAGGGTG      | 449 | UPRE-1 |
| TERG_05462 | CMGC/SRPK protein kinase   | CACTCTG (rc) | 129 | UPRE-1 |
| TERG_05463 | phosphoric ester hydrolase ( <i>T. equinum</i> )                                   | CAGGGTG      | 316 | UPRE-1 |
| TERG_05467 | hypothetical protein   | CACTCTG (rc) | 480 | UPRE-1 |
| TERG_05468 | serine/threonine protein kinase  | CAGAGTG      | 438 | UPRE-1 |
| TERG_05472 | hypothetical protein   | CACACTG (rc) | 601 | UPRE-1 |
| TERG_05474 | profilin-A ( <i>T. equinum</i> )   | CAGTGTG      | 89  | UPRE-1 |
| TERG_05479 | bZIP transcription factor, putative ( <i>T. verrucosum</i> )                       | CACCCTG (rc) | 402 | UPRE-1 |
| TERG_05488 | hypothetical protein   | CACTCTG (rc) | 68  | UPRE-1 |
| TERG_05492 | hypothetical protein   | CAGAGTG      | 167 | UPRE-1 |
| TERG_05493 | hypothetical protein   | CAGAGTG      | 591 | UPRE-1 |
| TERG_05511 | AT DNA binding protein ( <i>T. equinum</i> )                                       | CACGCTG (rc) | 850 | UPRE-1 |
| TERG_05518 | oxidoreductase, short chain dehydrogenase/reductase family ( <i>A. benhamiae</i> ) | CACACTG (rc) | 83  | UPRE-1 |
| TERG_05526 | MFS multidrug transporter ( <i>T. tonsurans</i> )                                  | CACTCTG (rc) | 859 | UPRE-1 |
| TERG_05528 | hypothetical protein   | CACGCTG (rc) | 510 | UPRE-1 |
| TERG_05529 | telomere length regulator protein (Rif1), putative ( <i>A. benhamiae</i> )         | CACCCTG (rc) | 65  | UPRE-1 |
| TERG_05537 | MFS multidrug transporter ( <i>T. equinum</i> )                                    | CACGCTG (rc) | 121 | UPRE-1 |
| TERG_05537 | MFS multidrug transporter ( <i>T. equinum</i> )                                    | CACCCTG (rc) | 578 | UPRE-1 |
| TERG_05538 | ABC a-pheromone efflux pump AtrD ( <i>T. verrucosum</i> )                          | CAGCGTG      | 108 | UPRE-1 |
| TERG_05546 | palmitoyltransferase pfa4 ( <i>M. gypseum</i> )                                    | CACTCTG (rc) | 235 | UPRE-1 |
| TERG_05560 | histone acetyltransferase GCN5 ( <i>T. tonsurans</i> )                             | CAGTGTG      | 427 | UPRE-1 |
| TERG_05561 | histone acetyltransferase GCN5 ( <i>T. tonsurans</i> )                             | CACCCTG (rc) | 308 | UPRE-1 |
| TERG_05562 | 2-hydroxychromene-2-carboxylate isomerase, putative ( <i>A. benhamiae</i> )        | CACGCTG (rc) | 715 | UPRE-1 |
| TERG_05563 | hypothetical protein   | CAGCGTG      | 523 | UPRE-1 |
| TERG_05565 | hypothetical protein   | CACGCTG (rc) | 55  | UPRE-1 |
| TERG_05583 | polyketide synthase, putative ( <i>A. benhamiae</i> )                              | CACTCTG (rc) | 417 | UPRE-1 |
| TERG_05583 | polyketide synthase, putative ( <i>A. benhamiae</i> )                              | CACCCTG (rc) | 933 | UPRE-1 |
| TERG_05620 | RING finger protein ( <i>T. tonsurans</i> )  | CACCCTG (rc) | 894 | UPRE-1 |
| TERG_05645 | vacuolar protein sorting protein Vps36 ( <i>T. tonsurans</i> )                     | CACTCTG (rc) | 925 | UPRE-1 |
| TERG_05646 | GANP domain-containing protein ( <i>M. canis</i> )                                 | CAGAGTG      | 856 | UPRE-1 |
| TERG_05656 | thymidylate synthase   | CACACTG (rc) | 574 | UPRE-1 |
| TERG_05659 | hypothetical protein   | CACGCTG (rc) | 412 | UPRE-1 |



|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_05665 | protein kinase, putative ( <i>A. benhamiae</i> )  | CAGCGTG      | 819 | UPRE-1 |
| TERG_05666 | YggS family pyridoxal phosphate enzyme  | CAGCGTG      | 510 | UPRE-1 |
| TERG_05671 | THO complex subunit 1 ( <i>T. equinum</i> )   | CACACTG (rc) | 923 | UPRE-1 |
| TERG_05672 | intron-binding protein aquarius ( <i>T. equinum</i> )                                       | CAGTGTG      | 420 | UPRE-1 |
| TERG_05673 | PaaI-thioesterase ( <i>T. equinum</i> )   | CACCCTG (rc) | 806 | UPRE-1 |
| TERG_05679 | 3-hydroxyacyl-CoA dehydrogenase, putative ( <i>A. benhamiae</i> )                           | CAGGGTG      | 625 | UPRE-1 |
| TERG_05680 | IBR domain containing protein ( <i>T. equinum</i> )   | CACACTG (rc) | 195 | UPRE-1 |
| TERG_05688 | GTP binding protein ( <i>T. equinum</i> )   | CACCCTG (rc) | 602 | UPRE-1 |
| TERG_05692 | HSF-type DNA-binding domain-containing protein ( <i>M. canis</i> )                          | CAGCGTG      | 721 | UPRE-1 |
| TERG_05697 | short chain dehydrogenase/reductase ( <i>T. tonsurans</i> )                                 | CACCCTG (rc) | 135 | UPRE-1 |
| TERG_05702 | Atypical/ABC1/ABC1-C protein kinase   | CACACTG (rc) | 506 | UPRE-1 |
| TERG_05705 | a-pheromone receptor PreA ( <i>A. benhamiae</i> )   | CACGCTG (rc) | 496 | UPRE-1 |
| TERG_05707 | phosphatase family protein ( <i>T. verrucosum</i> )   | CACGCTG (rc) | 118 | UPRE-1 |
| TERG_05734 | ubiquitin fusion degradation protein ( <i>T. tonsurans</i> )                                | CACCCTG (rc) | 327 | UPRE-1 |
| TERG_05741 | DNA-directed RNA polymerase II ( <i>T. tonsurans</i> )                                      | CAGTGTG      | 178 | UPRE-1 |
| TERG_05744 | GTP-binding protein EsdC ( <i>T. equinum</i> )  | CAGTGTG      | 781 | UPRE-1 |
| TERG_05752 | serine/threonine-protein phosphatase PP1  | CAGCGTG      | 217 | UPRE-1 |
| TERG_05754 | hypothetical protein  | CACTCTG (rc) | 249 | UPRE-1 |
| TERG_05754 | hypothetical protein  | CACCCTG (rc) | 838 | UPRE-1 |
| TERG_05761 | hypothetical protein  | CAGCGTG      | 191 | UPRE-1 |
| TERG_05766 | hypothetical protein  | CAGAGTG      | 560 | UPRE-1 |
| TERG_05774 | general stress response phosphoprotein phosphatase Psr1/2, putative ( <i>A. benhamiae</i> ) | CAGAGTG      | 29  | UPRE-1 |
| TERG_05780 | hypothetical protein  | CACACTG (rc) | 147 | UPRE-1 |
| TERG_05783 | Sin3 complex subunit (Stb2), putative ( <i>T. verrucosum</i> )                              | CACCCTG (rc) | 888 | UPRE-1 |
| TERG_05784 | macrophage erythroblast attacher ( <i>M. gypseum</i> )                                      | CAGGGTG      | 291 | UPRE-1 |
| TERG_05788 | 60S ribosomal protein L18A ( <i>T. tonsurans</i> )  | CAGAGTG      | 294 | UPRE-1 |
| TERG_05788 | 60S ribosomal protein L18A ( <i>T. tonsurans</i> )  | CAGGGTG      | 381 | UPRE-1 |
| TERG_05796 | transcriptional regulator Ngg1 ( <i>T. equinum</i> )  | CACGCTG (rc) | 833 | UPRE-1 |
| TERG_05805 | multidrug resistance protein fnx1 ( <i>T. equinum</i> )                                     | CACGCTG (rc) | 711 | UPRE-1 |
| TERG_05811 | 40S ribosomal protein S8 ( <i>T. tonsurans</i> )  | CACCCTG (rc) | 39  | UPRE-1 |
| TERG_05813 | 1-phosphatidylinositol-3-phosphate 5-kinase ( <i>T. equinum</i> )                           | CACACTG (rc) | 7   | UPRE-1 |
| TERG_05813 | 1-phosphatidylinositol-3-phosphate 5-kinase ( <i>T. equinum</i> )                           | CACTCTG (rc) | 343 | UPRE-1 |
| TERG_05830 | hypothetical protein  | CAGGGTG      | 682 | UPRE-1 |
| TERG_05831 | hypothetical protein  | CAGGGTG      | 123 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_05837 | plasma membrane ammonium transporter (Ato3), putative ( <i>A. benhamiae</i> ) | CAGAGTG      | 98  | UPRE-1 |
| TERG_05844 | U3 small nucleolar RNA-associated protein 4 ( <i>T. equinum</i> )             | CACTCTG (rc) | 184 | UPRE-1 |
| TERG_05859 | hypothetical protein  | CACCCTG (rc) | 829 | UPRE-1 |
| TERG_05860 | nicotinate phosphoribosyltransferase  | CAGGGTG      | 722 | UPRE-1 |
| TERG_05872 | thiosulfate sulfurtransferase, putative ( <i>T. verrucosum</i> )              | CAGGGTG      | 583 | UPRE-1 |
| TERG_05873 | hypothetical protein  | CAGAGTG      | 902 | UPRE-1 |
| TERG_05875 | Ser/Thr protein phosphatase ( <i>T. equinum</i> )                             | CAGGGTG      | 919 | UPRE-1 |
| TERG_05886 | hypothetical protein  | CACACTG (rc) | 518 | UPRE-1 |
| TERG_05896 | hypothetical protein  | CAGTGTG      | 6   | UPRE-1 |
| TERG_05897 | CoA-binding protein ( <i>T. equinum</i> )                                     | CACGCTG (rc) | 261 | UPRE-1 |
| TERG_05922 | acyl-CoA desaturase   | CAGAGTG      | 775 | UPRE-1 |
| TERG_05924 | transcription factor TFIIIB complex subunit brf1 ( <i>M. gypseum</i> )        | CAGCGTG      | 338 | UPRE-1 |
| TERG_05951 | alpha/beta hydrolase ( <i>T. tonsurans</i> )                                  | CAGGGTG      | 50  | UPRE-1 |
| TERG_05963 | WD repeat protein ( <i>T. tonsurans</i> )                                     | CAGTGTG      | 717 | UPRE-1 |
| TERG_05973 | WD repeat protein ( <i>T. tonsurans</i> )                                     | CAGGGTG      | 396 | UPRE-1 |
| TERG_05992 | translational initiation factor 2 beta ( <i>T. tonsurans</i> )                | CAGAGTG      | 104 | UPRE-1 |
| TERG_05993 | DUF124 domain-containing protein ( <i>T. equinum</i> )                        | CACTCTG (rc) | 803 | UPRE-1 |
| TERG_05995 | conserved serine-rich protein ( <i>A. benhamiae</i> )                         | CAGCGTG      | 848 | UPRE-1 |
| TERG_05996 | AT DNA binding protein ( <i>T. equinum</i> )                                  | CACCCTG (rc) | 870 | UPRE-1 |
| TERG_06002 | NIMA-interacting protein TinC ( <i>T. equinum</i> )                           | CACCCTG (rc) | 164 | UPRE-1 |
| TERG_06008 | FAD-linked sulfhydryl oxidase ALR ( <i>T. equinum</i> )                       | CACCCTG (rc) | 313 | UPRE-1 |
| TERG_06021 | proteasome regulatory particle subunit ( <i>T. equinum</i> )                  | CACGCTG (rc) | 195 | UPRE-1 |
| TERG_06022 | hypothetical protein  | CAGTGTG      | 48  | UPRE-1 |
| TERG_06029 | UDP-N-acetylglucosamine pyrophosphorylase ( <i>T. equinum</i> )               | CAGCGTG      | 138 | UPRE-1 |
| TERG_06032 | ribosomal small subunit assembly protein, putative ( <i>A. benhamiae</i> )    | CAGAGTG      | 911 | UPRE-1 |
| TERG_06036 | hypothetical protein  | CAGAGTG      | 202 | UPRE-1 |
| TERG_06036 | hypothetical protein  | CAGAGTG      | 561 | UPRE-1 |
| TERG_06037 | OefA protein ( <i>M. gypseum</i> )  | CACTCTG (rc) | 523 | UPRE-1 |
| TERG_06051 | 4-dimethylallyltryptophan methyltransferase ( <i>T. tonsurans</i> )           | CACCCTG (rc) | 452 | UPRE-1 |
| TERG_06054 | hypothetical protein  | CACTCTG (rc) | 17  | UPRE-1 |
| TERG_06055 | NmrA-like family protein ( <i>A. benhamiae</i> )                              | CAGAGTG      | 190 | UPRE-1 |
| TERG_06058 | NADH:ubiquinone oxidoreductase 20.1kD subunit ( <i>T. tonsurans</i> )         | CACTCTG (rc) | 190 | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_06065 | conserved glycine-rich protein ( <i>T. verrucosum</i> )                                | CAGGGTG      | 607 | UPRE-1 |
| TERG_06066 | Mss51p ( <i>M. gypseum</i> )   | CACACTG (rc) | 249 | UPRE-1 |
| TERG_06066 | Mss51p ( <i>M. gypseum</i> )   | CACGCTG (rc) | 427 | UPRE-1 |
| TERG_06081 | hypothetical protein   | CAGAGTG      | 281 | UPRE-1 |
| TERG_06087 | mRNA export factor mex67 ( <i>T. equinum</i> )   | CACTCTG (rc) | 451 | UPRE-1 |
| TERG_06087 | mRNA export factor mex67 ( <i>T. equinum</i> )   | CACTCTG (rc) | 687 | UPRE-1 |
| TERG_06088 | PH domain-containing protein ( <i>T. equinum</i> )                                     | CAGAGTG      | 46  | UPRE-1 |
| TERG_06091 | DNA-directed RNA polymerase I ( <i>T. tonsurans</i> )                                  | CAGAGTG      | 94  | UPRE-1 |
| TERG_06093 | MFS monocarboxylate transporter, putative ( <i>T. verrucosum</i> )                     | CAGGGTG      | 607 | UPRE-1 |
| TERG_06116 | indoleamine 2,3-dioxygenase ( <i>T. equinum</i> )                                      | CAGGGTG      | 263 | UPRE-1 |
| TERG_06121 | wd and tetratricopeptide repeat protein ( <i>T. tonsurans</i> )                        | CAGGGTG      | 655 | UPRE-1 |
| TERG_06125 | cell division control protein 16 ( <i>T. equinum</i> )                                 | CACACTG (rc) | 487 | UPRE-1 |
| TERG_06131 | hypothetical protein   | CAGGGTG      | 919 | UPRE-1 |
| TERG_06148 | protein vts1   | CACGCTG (rc) | 338 | UPRE-1 |
| TERG_06157 | ATP synthase F1 epsilon subunit ( <i>T. equinum</i> )                                  | CACTCTG (rc) | 309 | UPRE-1 |
| TERG_06166 | hypothetical protein   | CACGCTG (rc) | 626 | UPRE-1 |
| TERG_06196 | hypothetical protein   | CACTCTG (rc) | 270 | UPRE-1 |
| TERG_06197 | cytochrome c oxidase assembly protein ( <i>T. tonsurans</i> )                          | CACTCTG (rc) | 412 | UPRE-1 |
| TERG_06199 | lipase ( <i>T. tonsurans</i> )   | CAGAGTG      | 39  | UPRE-1 |
| TERG_06209 | UTR2 protein ( <i>M. gypseum</i> )   | CAGTGTG      | 786 | UPRE-1 |
| TERG_06212 | vacuolar ABC heavy metal transporter (Hmt1) ( <i>T. tonsurans</i> )                    | CACGCTG (rc) | 266 | UPRE-1 |
| TERG_06220 | hypothetical protein   | CAGTGTG      | 224 | UPRE-1 |
| TERG_06222 | MYB DNA-binding domain-containing protein ( <i>T. equinum</i> )                        | CAGGGTG      | 602 | UPRE-1 |
| TERG_06225 | hypothetical protein   | CACTCTG (rc) | 495 | UPRE-1 |
| TERG_06235 | hypothetical protein   | CAGGGTG      | 857 | UPRE-1 |
| TERG_06237 | dual specificity phosphatase catalytic domain-containing protein ( <i>T. equinum</i> ) | CACTCTG (rc) | 744 | UPRE-1 |
| TERG_06242 | glucanase, putative ( <i>T. verrucosum</i> )   | CACGCTG (rc) | 692 | UPRE-1 |
| TERG_06247 | DUF821 domain-containing protein ( <i>T. equinum</i> )                                 | CAGGGTG      | 728 | UPRE-1 |
| TERG_06249 | hypothetical protein   | CACTCTG (rc) | 498 | UPRE-1 |
| TERG_06249 | hypothetical protein   | CACTCTG (rc) | 531 | UPRE-1 |
| TERG_06254 | pre-mRNA splicing factor ATP-dependent RNA helicase prp16 ( <i>T. equinum</i> )        | CAGAGTG      | 375 | UPRE-1 |
| TERG_06264 | steroid monooxygenase, putative ( <i>T. verrucosum</i> )                               | CAGCGTG      | 314 | UPRE-1 |
| TERG_06267 | hypothetical protein   | CAGCGTG      | 241 | UPRE-1 |
| TERG_06269 | hypothetical protein   | CACCCTG (rc) | 447 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_06270 | hypothetical protein  | CACTCTG (rc) | 134 | UPRE-1 |
| TERG_06283 | cyclohexanone 1,2-monooxygenase ( <i>T. tonsurans</i> )                     | CACGCTG (rc) | 776 | UPRE-1 |
| TERG_06287 | cellular morphogenesis protein ( <i>T. equinum</i> )                        | CACTCTG (rc) | 698 | UPRE-1 |
| TERG_06288 | FACT complex subunit pob3   | CAGAGTG      | 699 | UPRE-1 |
| TERG_06325 | autophagy protein 16 ( <i>T. equinum</i> )                                  | CACTCTG (rc) | 31  | UPRE-1 |
| TERG_06327 | integral membrane protein ( <i>T. equinum</i> )                             | CAGAGTG      | 522 | UPRE-1 |
| TERG_06337 | hypothetical protein  | CAGAGTG      | 923 | UPRE-1 |
| TERG_06339 | hypothetical protein  | CACCCTG (rc) | 279 | UPRE-1 |
| TERG_06340 | AGC/PKC protein kinase  | CAGGGTG      | 988 | UPRE-1 |
| TERG_06342 | beta-tubulin cofactor d ( <i>T. tonsurans</i> )                             | CAGTGTG      | 353 | UPRE-1 |
| TERG_06351 | WD repeat protein ( <i>T. tonsurans</i> )                                   | CAGGGTG      | 26  | UPRE-1 |
| TERG_06377 | metalloproteinase, putative ( <i>A. benhamiae</i> )                         | CACGCTG (rc) | 414 | UPRE-1 |
| TERG_06379 | transcription factor RfeF ( <i>T. tonsurans</i> )                           | CAGAGTG      | 874 | UPRE-1 |
| TERG_06399 | ATP-dependent permease MDL2 ( <i>T. equinum</i> )                           | CAGTGTG      | 10  | UPRE-1 |
| TERG_06420 | RNA polymerase II Elongator subunit ( <i>T. tonsurans</i> )                 | CACACTG (rc) | 661 | UPRE-1 |
| TERG_06421 | hypothetical protein  | CAGTGTG      | 482 | UPRE-1 |
| TERG_06429 | sterol delta 5,6-desaturase, putative ( <i>T. verrucosum</i> )              | CACGCTG (rc) | 582 | UPRE-1 |
| TERG_06457 | hypothetical protein  | CACTCTG (rc) | 152 | UPRE-1 |
| TERG_06459 | SWIRM domain-containing protein ( <i>T. tonsurans</i> )                     | CAGCGTG      | 591 | UPRE-1 |
| TERG_06465 | O-mannosyl transferase pmtA- <i>Aspergillus niger</i> ( <i>T. equinum</i> ) | CAGTGTG      | 91  | UPRE-1 |
| TERG_06470 | hypothetical protein  | CACACTG (rc) | 610 | UPRE-1 |
| TERG_06474 | hypothetical protein  | CAGCGTG      | 520 | UPRE-1 |
| TERG_06478 | peroxisomal membrane protein pex16 ( <i>T. equinum</i> )                    | CAGAGTG      | 228 | UPRE-1 |
| TERG_06481 | cell polarity protein ( <i>T. tonsurans</i> )                               | CACTCTG (rc) | 530 | UPRE-1 |
| TERG_06489 | hypothetical protein  | CAGGGTG      | 65  | UPRE-1 |
| TERG_06493 | mRNA cleavage factor complex component Pcf11 ( <i>T. equinum</i> )          | CACCCTG (rc) | 268 | UPRE-1 |
| TERG_06493 | mRNA cleavage factor complex component Pcf11 ( <i>T. equinum</i> )          | CACTCTG (rc) | 481 | UPRE-1 |
| TERG_06494 | hypothetical protein  | CAGGGTG      | 38  | UPRE-1 |
| TERG_06494 | hypothetical protein  | CAGTGTG      | 968 | UPRE-1 |
| TERG_06524 | hypothetical protein  | CACGCTG (rc) | 625 | UPRE-1 |
| TERG_06525 | plasma membrane antiporter, putative ( <i>T. verrucosum</i> )               | CAGCGTG      | 620 | UPRE-1 |
| TERG_06526 | NAD binding Rossmann fold oxidoreductase ( <i>T. tonsurans</i> )            | CACACTG (rc) | 593 | UPRE-1 |
| TERG_06542 | cyclin ( <i>T. tonsurans</i> )  | CAGTGTG      | 353 | UPRE-1 |
| TERG_06542 | cyclin ( <i>T. tonsurans</i> )  | CAGAGTG      | 593 | UPRE-1 |

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|------------|---|--------------|-----|--------|
| TERG_06543 | phosphatidate cytidyltransferase ( <i>T. tonsurans</i> )                  | CACTCTG (rc) | 472 | UPRE-1 |
| TERG_06544 | DNA repair protein Rad26 ( <i>T. equinum</i> )                            | CAGAGTG      | 742 | UPRE-1 |
| TERG_06548 | hypothetical protein  | CAGCGTG      | 217 | UPRE-1 |
| TERG_06552 | aspartic-type endopeptidase (OpsB), putative ( <i>T. verrucosum</i> )     | CACGCTG (rc) | 639 | UPRE-1 |
| TERG_06560 | pyruvate dehydrogenase (acetyl-transferring) E1 component, alpha subunit  | CAGGGTG      | 518 | UPRE-1 |
| TERG_06561 | sex determining protein ( <i>M. canis</i> )                               | CACTCTG (rc) | 458 | UPRE-1 |
| TERG_06563 | 30S ribosomal subunit S4 ( <i>T. tonsurans</i> )                          | CACTCTG (rc) | 642 | UPRE-1 |
| TERG_06563 | 30S ribosomal subunit S4 ( <i>T. tonsurans</i> )                          | CACGCTG (rc) | 917 | UPRE-1 |
| TERG_06564 | alpha/beta hydrolase, putative ( <i>T. verrucosum</i> )                   | CAGCGTG      | 312 | UPRE-1 |
| TERG_06564 | alpha/beta hydrolase, putative ( <i>T. verrucosum</i> )                   | CAGAGTG      | 587 | UPRE-1 |
| TERG_06576 | hypothetical protein  | CAGAGTG      | 794 | UPRE-1 |
| TERG_06592 | E3 ubiquitin-protein ligase bre1 ( <i>T. tonsurans</i> )                  | CACTCTG (rc) | 792 | UPRE-1 |
| TERG_06593 | transcription factor TFIIB component ( <i>T. equinum</i> )                | CAGAGTG      | 533 | UPRE-1 |
| TERG_06615 | hypothetical protein  | CACGCTG (rc) | 34  | UPRE-1 |
| TERG_06624 | HATPase-c domain-containing protein ( <i>T. equinum</i> )                 | CAGAGTG      | 967 | UPRE-1 |
| TERG_06631 | vacuolar protein sorting-associated protein 55 ( <i>T. tonsurans</i> )    | CAGCGTG      | 341 | UPRE-1 |
| TERG_06634 | hsp70-like protein ( <i>T. equinum</i> )                                  | CACGCTG (rc) | 251 | UPRE-1 |
| TERG_06638 | endochitinase ( <i>T. equinum</i> )                                       | CACACTG (rc) | 167 | UPRE-1 |
| TERG_06645 | alpha/beta hydrolase ( <i>T. equinum</i> )                                | CACACTG (rc) | 378 | UPRE-1 |
| TERG_06646 | arrestin ( <i>T. equinum</i> )  | CAGTGTG      | 57  | UPRE-1 |
| TERG_06647 | alpha/beta superfamily hydrolase, putative ( <i>A. benhamiae</i> )        | CACGCTG (rc) | 369 | UPRE-1 |
| TERG_06652 | Amt4 ( <i>T. equinum</i> )  | CACCCTG (rc) | 504 | UPRE-1 |
| TERG_06653 | conserved serine-rich protein ( <i>T. verrucosum</i> )                    | CACACTG (rc) | 899 | UPRE-1 |
| TERG_06665 | serine carboxypeptidase ( <i>T. tonsurans</i> )                           | CACGCTG (rc) | 422 | UPRE-1 |
| TERG_06665 | serine carboxypeptidase ( <i>T. tonsurans</i> )                           | CACCCTG (rc) | 430 | UPRE-1 |
| TERG_06673 | pachytene checkpoint component Pch2 ( <i>T. tonsurans</i> )               | CAGGGTG      | 348 | UPRE-1 |
| TERG_06680 | DUF221 domain-containing protein ( <i>T. equinum</i> )                    | CACACTG (rc) | 87  | UPRE-1 |
| TERG_06684 | molybdenum cofactor biosynthetic protein ( <i>T. equinum</i> )            | CAGAGTG      | 417 | UPRE-1 |
| TERG_06686 | hypothetical protein  | CACGCTG (rc) | 735 | UPRE-1 |
| TERG_06689 | succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial   | CACGCTG (rc) | 731 | UPRE-1 |
| TERG_06695 | hypothetical protein  | CACGCTG (rc) | 675 | UPRE-1 |
| TERG_06698 | hypothetical protein  | CAGTGTG      | 21  | UPRE-1 |
| TERG_06720 | lipase/esterase, putative ( <i>A. benhamiae</i> )                         | CAGAGTG      | 541 | UPRE-1 |
| TERG_06726 | O-methylsterigmatocystin oxidoreductase, putative ( <i>A. benhamiae</i> ) | CAGAGTG      | 675 | UPRE-1 |

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|------------|---|--------------|-----|--------|
| TERG_06732 | peroxisomal membrane protein receptor Pex19, putative ( <i>A. benhamiae</i> ) | CACGCTG (rc) | 747 | UPRE-1 |
| TERG_06748 | hypothetical protein  | CAGCGTG      | 556 | UPRE-1 |
| TERG_06759 | C2H2 transcription factor (Seb1), putative ( <i>A. benhamiae</i> )            | CAGGGTG      | 135 | UPRE-1 |
| TERG_06765 | ULK/ULK protein kinase  | CAGTGTG      | 6   | UPRE-1 |
| TERG_06771 | FAD binding domain protein ( <i>A. benhamiae</i> )                            | CAGAGTG      | 377 | UPRE-1 |
| TERG_06777 | hypothetical protein  | CACCCTG (rc) | 267 | UPRE-1 |
| TERG_06780 | hypothetical protein  | CACTCTG (rc) | 724 | UPRE-1 |
| TERG_06785 | cytochrome P450 monooxygenase ( <i>T. equinum</i> )                           | CAGGGTG      | 91  | UPRE-1 |
| TERG_06787 | hypothetical protein  | CACACTG (rc) | 38  | UPRE-1 |
| TERG_06789 | CDK-activating kinase assembly factor MAT1                                    | CAGAGTG      | 307 | UPRE-1 |
| TERG_06790 | hypothetical protein  | CACTCTG (rc) | 212 | UPRE-1 |
| TERG_06790 | hypothetical protein  | CACACTG (rc) | 369 | UPRE-1 |
| TERG_06790 | hypothetical protein  | CACGCTG (rc) | 630 | UPRE-1 |
| TERG_06791 | short chain dehydrogenase/reductase, putative ( <i>T. verrucosum</i> )        | CAGGGTG      | 742 | UPRE-1 |
| TERG_06793 | PEX11 domain protein ( <i>A. benhamiae</i> )                                  | CACACTG (rc) | 768 | UPRE-1 |
| TERG_06794 | minor allergen Alt a 7  | CAGTGTG      | 492 | UPRE-1 |
| TERG_06795 | nuclear protein localization protein 4  | CAGAGTG      | 763 | UPRE-1 |
| TERG_06806 | hypothetical protein  | CACCCTG (rc) | 33  | UPRE-1 |
| TERG_06806 | hypothetical protein  | CACTCTG (rc) | 91  | UPRE-1 |
| TERG_06806 | hypothetical protein  | CACCCTG (rc) | 881 | UPRE-1 |
| TERG_06808 | RNA-binding protein 8A ( <i>T. tonsurans</i> )                                | CAGTGTG      | 578 | UPRE-1 |
| TERG_06816 | 14-3-3 family protein ( <i>T. tonsurans</i> )                                 | CACCCTG (rc) | 26  | UPRE-1 |
| TERG_06817 | hypothetical protein  | CAGGGTG      | 612 | UPRE-1 |
| TERG_06824 | 60S ribosomal protein L23   | CACACTG (rc) | 506 | UPRE-1 |
| TERG_06829 | hypothetical protein  | CACTCTG (rc) | 346 | UPRE-1 |
| TERG_06831 | F-box domain protein ( <i>A. benhamiae</i> )                                  | CAGGGTG      | 498 | UPRE-1 |
| TERG_06837 | membrane transporter ( <i>T. tonsurans</i> )                                  | CACCCTG (rc) | 157 | UPRE-1 |
| TERG_06849 | SH3 domain-containing protein ( <i>T. tonsurans</i> )                         | CACCCTG (rc) | 416 | UPRE-1 |
| TERG_06850 | monocarboxylate permease ( <i>T. equinum</i> )                                | CAGGGTG      | 273 | UPRE-1 |
| TERG_06851 | hypothetical protein  | CACGCTG (rc) | 828 | UPRE-1 |
| TERG_06865 | hypothetical protein  | CACGCTG (rc) | 779 | UPRE-1 |
| TERG_06866 | isochorismatase family hydrolase ( <i>T. equinum</i> )                        | CAGCGTG      | 887 | UPRE-1 |
| TERG_06880 | MFS transporter Fmp42, putative ( <i>T. verrucosum</i> )                      | CACCCTG (rc) | 810 | UPRE-1 |
| TERG_06882 | hypothetical protein  | CACCCTG (rc) | 790 | UPRE-1 |
| TERG_06918 | hypothetical protein  | CACGCTG (rc) | 871 | UPRE-1 |

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|------------|---|--------------|-----|--------|
| TERG_06919 | hypothetical protein  | CAGCGTG      | 768 | UPRE-1 |
| TERG_06920 | hypothetical protein  | CACCCTG (rc) | 40  | UPRE-1 |
| TERG_06925 | class V chitinase ( <i>T. tonsurans</i> )   | CAGTGTG      | 183 | UPRE-1 |
| TERG_06929 | chitinase ( <i>T. equinum</i> )   | CACACTG (rc) | 28  | UPRE-1 |
| TERG_06929 | chitinase ( <i>T. equinum</i> )   | CACCCTG (rc) | 552 | UPRE-1 |
| TERG_06932 | serine/threonine protein kinase   | CAGGGTG      | 145 | UPRE-1 |
| TERG_06932 | serine/threonine protein kinase   | CAGTGTG      | 669 | UPRE-1 |
| TERG_06937 | hypothetical protein  | CACCCTG (rc) | 703 | UPRE-1 |
| TERG_06938 | zinc metalloproteinase ( <i>T. tonsurans</i> )  | CAGGGTG      | 169 | UPRE-1 |
| TERG_06945 | WD domain-containing protein ( <i>T. equinum</i> )  | CACCCTG (rc) | 744 | UPRE-1 |
| TERG_06946 | ARP2/3 complex 34 kDa subunit ( <i>T. tonsurans</i> )                                       | CAGTGTG      | 102 | UPRE-1 |
| TERG_06946 | ARP2/3 complex 34 kDa subunit ( <i>T. tonsurans</i> )                                       | CAGGGTG      | 956 | UPRE-1 |
| TERG_06955 | hypothetical protein  | CACTCTG (rc) | 475 | UPRE-1 |
| TERG_06956 | RNA polymerase I-specific transcription initiation factor <i>rrn3</i> ( <i>M. gypseum</i> ) | CAGAGTG      | 318 | UPRE-1 |
| TERG_06958 | aspartate-tRNA(Asn) ligase  | CAGCGTG      | 293 | UPRE-1 |
| TERG_06964 | NTF2 domain-containing protein ( <i>T. tonsurans</i> )                                      | CACGCTG (rc) | 895 | UPRE-1 |
| TERG_06967 | rnapii degradation factor <i>def1</i> ( <i>T. tonsurans</i> )                               | CAGTGTG      | 351 | UPRE-1 |
| TERG_06969 | CMGC/CDK/CDK5 protein kinase  | CACCCTG (rc) | 789 | UPRE-1 |
| TERG_06989 | C6 finger domain protein, putative ( <i>T. verrucosum</i> )                                 | CACGCTG (rc) | 551 | UPRE-1 |
| TERG_06989 | C6 finger domain protein, putative ( <i>T. verrucosum</i> )                                 | CACTCTG (rc) | 795 | UPRE-1 |
| TERG_07001 | hydroxysocaproate dehydrogenase ( <i>T. tonsurans</i> )                                     | CAGCGTG      | 214 | UPRE-1 |
| TERG_07005 | PAB-dependent poly(A)-specific ribonuclease subunit PAN3 ( <i>T. tonsurans</i> )            | CAGGGTG      | 199 | UPRE-1 |
| TERG_07008 | diaminopropionate ammonia-lyase ( <i>T. equinum</i> )                                       | CACCCTG (rc) | 562 | UPRE-1 |
| TERG_07011 | conserved fungal protein ( <i>A. benhamiae</i> )  | CAGCGTG      | 96  | UPRE-1 |
| TERG_07021 | helix-loop-helix DNA-binding domain-containing protein ( <i>T. tonsurans</i> )              | CACACTG (rc) | 370 | UPRE-1 |
| TERG_07038 | glutamine-tRNA ligase   | CACTCTG (rc) | 528 | UPRE-1 |
| TERG_07045 | hypothetical protein  | CAGTGTG      | 175 | UPRE-1 |
| TERG_07047 | cholesterol delta-isomerase, putative ( <i>T. verrucosum</i> )                              | CAGCGTG      | 182 | UPRE-1 |
| TERG_07059 | hypothetical protein  | CAGGGTG      | 28  | UPRE-1 |
| TERG_07061 | CMGC/SRPK protein kinase  | CAGCGTG      | 128 | UPRE-1 |
| TERG_07079 | C6 transcription factor, putative ( <i>T. verrucosum</i> )                                  | CAGTGTG      | 80  | UPRE-1 |
| TERG_07085 | peptidase ( <i>T. tonsurans</i> )   | CACTCTG (rc) | 167 | UPRE-1 |
| TERG_07089 | GPI-anchored wall transfer protein 1 ( <i>T. tonsurans</i> )                                | CACTCTG (rc) | 569 | UPRE-1 |
| TERG_07094 | hypothetical protein  | CACCCTG (rc) | 386 | UPRE-1 |
| TERG_07105 | transcription factor TFIIA complex subunit <i>Toa1</i> , putative ( <i>T. verrucosum</i> )  | CACCCTG (rc) | 243 | UPRE-1 |

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|------------|--|--------------|-----|--------|
| TERG_07108 | WD-repeat containing protein slp1 ( <i>T. tonsurans</i> )                    | CACTCTG (rc) | 162 | UPRE-1 |
| TERG_07114 | ubiquitin-protein ligase Sell/Ubx2 ( <i>T. equinum</i> )                     | CACTCTG (rc) | 416 | UPRE-1 |
| TERG_07118 | phosphotransferase enzyme family protein ( <i>T. equinum</i> )               | CACGCTG (rc) | 189 | UPRE-1 |
| TERG_07132 | hypothetical protein   | CACTCTG (rc) | 801 | UPRE-1 |
| TERG_07140 | serine/threonine protein kinase ( <i>T. tonsurans</i> )                      | CACCCTG (rc) | 165 | UPRE-1 |
| TERG_07140 | serine/threonine protein kinase ( <i>T. tonsurans</i> )                      | CACTCTG (rc) | 724 | UPRE-1 |
| TERG_07141 | RING and UBP finger domain-containing protein ( <i>T. tonsurans</i> )        | CAGGGTG      | 520 | UPRE-1 |
| TERG_07146 | 3-demethylubiquinone-9 3-O-methyltransferase                                 | CAGCGTG      | 983 | UPRE-1 |
| TERG_07154 | iron donor protein CyaY  | CAGCGTG      | 273 | UPRE-1 |
| TERG_07161 | hypothetical protein   | CAGAGTG      | 491 | UPRE-1 |
| TERG_07178 | synaptic glycoprotein SC2 ( <i>T. equinum</i> )                              | CACTCTG (rc) | 689 | UPRE-1 |
| TERG_07188 | xanthine dehydrogenase ( <i>T. tonsurans</i> )                               | CAGTGTG      | 524 | UPRE-1 |
| TERG_07189 | plasma membrane fusion protein PRM1 ( <i>T. equinum</i> )                    | CACCCTG (rc) | 77  | UPRE-1 |
| TERG_07190 | hypothetical protein   | CACACTG (rc) | 217 | UPRE-1 |
| TERG_07202 | acetyl-coenzyme A synthetase   | CAGAGTG      | 206 | UPRE-1 |
| TERG_07207 | Sit4-associated protein ( <i>T. tonsurans</i> )                              | CACTCTG (rc) | 694 | UPRE-1 |
| TERG_07222 | carbonic anhydrase family protein ( <i>T. verrucosum</i> )                   | CAGCGTG      | 228 | UPRE-1 |
| TERG_07228 | MOSC domain-containing protein ( <i>T. equinum</i> )                         | CACGCTG (rc) | 62  | UPRE-1 |
| TERG_07229 | vacuolar ATP synthase 116kDa subunit ( <i>T. tonsurans</i> )                 | CAGAGTG      | 436 | UPRE-1 |
| TERG_07233 | acriflavine sensitivity control protein acr-2 ( <i>T. equinum</i> )          | CACACTG (rc) | 486 | UPRE-1 |
| TERG_07234 | hypothetical protein   | CAGTGTG      | 467 | UPRE-1 |
| TERG_07241 | saccharopine dehydrogenase [NADP+, L-glutamate-forming]                      | CACGCTG (rc) | 591 | UPRE-1 |
| TERG_07242 | di-trans,poly-cis-decaprenylcistransferase                                   | CACCCTG (rc) | 122 | UPRE-1 |
| TERG_07242 | di-trans,poly-cis-decaprenylcistransferase                                   | CACGCTG (rc) | 461 | UPRE-1 |
| TERG_07260 | hypothetical protein   | CAGAGTG      | 349 | UPRE-1 |
| TERG_07264 | thermatolerance membrane protein Dlt1, putative ( <i>A. benhamiae</i> )      | CAGAGTG      | 528 | UPRE-1 |
| TERG_07265 | sucrase/ferredoxin domain-containing protein ( <i>T. equinum</i> )           | CAGTGTG      | 302 | UPRE-1 |
| TERG_07269 | mannose-1-phosphate guanyltransferase  | CACTCTG (rc) | 237 | UPRE-1 |
| TERG_07281 | protein kinase subdomain-containing protein ( <i>T. tonsurans</i> )          | CACACTG (rc) | 53  | UPRE-1 |
| TERG_07294 | glyoxylate reductase ( <i>T. tonsurans</i> )                                 | CAGAGTG      | 661 | UPRE-1 |
| TERG_07308 | iron-sulfur cluster assembly associated protein Nar1 ( <i>T. tonsurans</i> ) | CAGCGTG      | 931 | UPRE-1 |
| TERG_07312 | metallothionein-I transcription activator ( <i>T. equinum</i> )              | CAGAGTG      | 543 | UPRE-1 |



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|------------|--|--------------|-----|--------|
| TERG_07313 | anthranilate phosphoribosyltransferase   | CACCCTG (rc) | 164 | UPRE-1 |
| TERG_07313 | anthranilate phosphoribosyltransferase   | CACTCTG (rc) | 728 | UPRE-1 |
| TERG_07314 | hypothetical protein   | CAGGGTG      | 70  | UPRE-1 |
| TERG_07324 | ubiquitin-conjugating enzyme ( <i>T. equinum</i> )                                     | CAGAGTG      | 478 | UPRE-1 |
| TERG_07326 | glutathione S-transferase PARB ( <i>T. equinum</i> )                                   | CACTCTG (rc) | 584 | UPRE-1 |
| TERG_07327 | pyridoxamine phosphate oxidase ( <i>T. tonsurans</i> )                                 | CACTCTG (rc) | 651 | UPRE-1 |
| TERG_07327 | pyridoxamine phosphate oxidase ( <i>T. tonsurans</i> )                                 | CACTCTG (rc) | 911 | UPRE-1 |
| TERG_07330 | chromatin regulatory protein sir2 ( <i>T. tonsurans</i> )                              | CAGAGTG      | 202 | UPRE-1 |
| TERG_07335 | G2/M-specific cyclin NimE ( <i>T. tonsurans</i> )                                      | CACGCTG (rc) | 160 | UPRE-1 |
| TERG_07337 | 54S ribosomal protein RML2 ( <i>T. equinum</i> )                                       | CAGCGTG      | 264 | UPRE-1 |
| TERG_07338 | C6 transcription factor Prf, putative ( <i>A. benhamiae</i> )                          | CAGAGTG      | 17  | UPRE-1 |
| TERG_07343 | HLH transcription factor ( <i>T. tonsurans</i> )                                       | CACGCTG (rc) | 132 | UPRE-1 |
| TERG_07355 | PAP2 domain protein ( <i>A. benhamiae</i> )  | CAGCGTG      | 413 | UPRE-1 |
| TERG_07361 | hybrid PKS-NRPS enzyme, putative ( <i>A. benhamiae</i> )                               | CACCCTG (rc) | 531 | UPRE-1 |
| TERG_07363 | hypothetical protein   | CAGGGTG      | 380 | UPRE-1 |
| TERG_07364 | oxidoreductase, zinc-binding dehydrogenase family superfamily ( <i>T. verrucosum</i> ) | CAGGGTG      | 811 | UPRE-1 |
| TERG_07379 | leucine rich repeat protein ( <i>T. equinum</i> )                                      | CAGTGTG      | 605 | UPRE-1 |
| TERG_07382 | importin beta-3 subunit ( <i>T. tonsurans</i> )  | CAGTGTG      | 706 | UPRE-1 |
| TERG_07406 | alpha-mannosidase ( <i>T. tonsurans</i> )  | CAGAGTG      | 349 | UPRE-1 |
| TERG_07409 | amino acid permease ( <i>T. equinum</i> )  | CACCCTG (rc) | 99  | UPRE-1 |
| TERG_07417 | hypothetical protein   | CACTCTG (rc) | 211 | UPRE-1 |
| TERG_07418 | MFS multidrug transporter ( <i>T. equinum</i> )  | CACCCTG (rc) | 509 | UPRE-1 |
| TERG_07425 | JmjC domain-containing protein ( <i>T. equinum</i> )                                   | CAGAGTG      | 99  | UPRE-1 |
| TERG_07442 | hypothetical protein   | CAGCGTG      | 742 | UPRE-1 |
| TERG_07455 | mitochondrial import protein mmp37 ( <i>T. tonsurans</i> )                             | CAGTGTG      | 920 | UPRE-1 |
| TERG_07466 | hypothetical protein   | CAGGGTG      | 496 | UPRE-1 |
| TERG_07475 | C6 transcription factor ( <i>T. equinum</i> )  | CACCCTG (rc) | 87  | UPRE-1 |
| TERG_07477 | copper-sulfate regulated protein 1 ( <i>T. equinum</i> )                               | CACGCTG (rc) | 935 | UPRE-1 |
| TERG_07482 | ribonuclease H1, putative ( <i>A. benhamiae</i> )                                      | CACGCTG (rc) | 286 | UPRE-1 |
| TERG_07489 | hypothetical protein   | CACCCTG (rc) | 50  | UPRE-1 |
| TERG_07494 | golgi apparatus membrane protein TVP23   | CAGTGTG      | 43  | UPRE-1 |
| TERG_07495 | acyl-CoA dehydrogenase family member 9 ( <i>T. equinum</i> )                           | CACGCTG (rc) | 113 | UPRE-1 |
| TERG_07495 | acyl-CoA dehydrogenase family member 9 ( <i>T. equinum</i> )                           | CACCCTG (rc) | 232 | UPRE-1 |
| TERG_07503 | phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase           | CACCCTG (rc) | 352 | UPRE-1 |
| TERG_07510 | hypothetical protein   | CACTCTG (rc) | 744 | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_07532 | ubiquitination network signaling protein ( <i>T. tonsurans</i> )                 | CAGGGTG      | 206 | UPRE-1 |
| TERG_07532 | ubiquitination network signaling protein ( <i>T. tonsurans</i> )                 | CAGGGTG      | 409 | UPRE-1 |
| TERG_07535 | methyltransferase domain-containing protein ( <i>T. tonsurans</i> )              | CACCCTG (rc) | 169 | UPRE-1 |
| TERG_07541 | phosphoesterase ( <i>T. tonsurans</i> )  | CAGGGTG      | 341 | UPRE-1 |
| TERG_07553 | C2H2 transcription factor Crz1, putative ( <i>T. verrucosum</i> )                | CACCCTG (rc) | 606 | UPRE-1 |
| TERG_07553 | C2H2 transcription factor Crz1, putative ( <i>T. verrucosum</i> )                | CACACTG (rc) | 931 | UPRE-1 |
| TERG_07558 | lipoyltransferase and lipoate-protein ligase ( <i>T. equinum</i> )               | CACTCTG (rc) | 76  | UPRE-1 |
| TERG_07578 | GTP-binding protein rhoA   | CAGAGTG      | 191 | UPRE-1 |
| TERG_07582 | hypothetical protein   | CACCCTG (rc) | 295 | UPRE-1 |
| TERG_07586 | DNA methyltransferase 1-associated protein DMAP1 ( <i>T. tonsurans</i> )         | CAGCGTG      | 725 | UPRE-1 |
| TERG_07589 | 3-oxo-5-alpha-steroid 4-dehydrogenase family protein ( <i>T. verrucosum</i> )    | CACCCTG (rc) | 758 | UPRE-1 |
| TERG_07597 | SOK1 ( <i>T. equinum</i> )   | CACACTG (rc) | 318 | UPRE-1 |
| TERG_07603 | DNA helicase ( <i>T. tonsurans</i> )   | CAGCGTG      | 216 | UPRE-1 |
| TERG_07622 | UBX domain-containing protein ( <i>T. equinum</i> )                              | CAGGGTG      | 260 | UPRE-1 |
| TERG_07640 | mannan polymerase II complex ANP1 subunit ( <i>T. equinum</i> )                  | CACACTG (rc) | 168 | UPRE-1 |
| TERG_07643 | ubiquinol-cytochrome c reductase complex protein ( <i>T. equinum</i> )           | CACACTG (rc) | 809 | UPRE-1 |
| TERG_07644 | mitochondrial carrier protein ( <i>T. tonsurans</i> )                            | CAGTGTG      | 549 | UPRE-1 |
| TERG_07647 | hypothetical protein   | CAGAGTG      | 372 | UPRE-1 |
| TERG_07650 | membrane-tethered transcription factor (SPT23), putative ( <i>A. benhamiae</i> ) | CAGCGTG      | 757 | UPRE-1 |
| TERG_07652 | Delta(12) fatty acid desaturase ( <i>T. equinum</i> )                            | CAGGGTG      | 316 | UPRE-1 |
| TERG_07652 | Delta(12) fatty acid desaturase ( <i>T. equinum</i> )                            | CAGAGTG      | 885 | UPRE-1 |
| TERG_07664 | rho GTPase activator Rga ( <i>T. equinum</i> )                                   | CACACTG (rc) | 832 | UPRE-1 |
| TERG_07672 | GABA permease ( <i>T. equinum</i> )  | CAGTGTG      | 191 | UPRE-1 |
| TERG_07683 | hypothetical protein   | CAGAGTG      | 272 | UPRE-1 |
| TERG_07692 | hypothetical protein   | CACACTG (rc) | 160 | UPRE-1 |
| TERG_07692 | hypothetical protein   | CACACTG (rc) | 204 | UPRE-1 |
| TERG_07693 | mitochondrial carrier protein ( <i>T. tonsurans</i> )                            | CAGTGTG      | 667 | UPRE-1 |
| TERG_07693 | mitochondrial carrier protein ( <i>T. tonsurans</i> )                            | CAGTGTG      | 711 | UPRE-1 |
| TERG_07698 | CHL4 family chromosome segregation protein, putative ( <i>T. verrucosum</i> )    | CAGGGTG      | 475 | UPRE-1 |
| TERG_07706 | hypothetical protein   | CACCCTG (rc) | 704 | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_07708 | hypothetical protein   | CACGCTG (rc) | 567 | UPRE-1 |
| TERG_07708 | hypothetical protein   | CACGCTG (rc) | 992 | UPRE-1 |
| TERG_07716 | hypothetical protein   | CACGCTG (rc) | 351 | UPRE-1 |
| TERG_07719 | hypothetical protein   | CACTCTG (rc) | 545 | UPRE-1 |
| TERG_07721 | isopenicillin N-CoA epimerase ( <i>T. equinum</i> )                                  | CACTCTG (rc) | 89  | UPRE-1 |
| TERG_07721 | isopenicillin N-CoA epimerase ( <i>T. equinum</i> )                                  | CACCCTG (rc) | 601 | UPRE-1 |
| TERG_07731 | 2Fe-2S iron-sulfur cluster binding domain-containing protein ( <i>T. tonsurans</i> ) | CACTCTG (rc) | 42  | UPRE-1 |
| TERG_07731 | 2Fe-2S iron-sulfur cluster binding domain-containing protein ( <i>T. tonsurans</i> ) | CACGCTG (rc) | 75  | UPRE-1 |
| TERG_07737 | hypothetical protein   | CACCCTG (rc) | 98  | UPRE-1 |
| TERG_07737 | hypothetical protein   | CACTCTG (rc) | 113 | UPRE-1 |
| TERG_07737 | hypothetical protein   | CACACTG (rc) | 805 | UPRE-1 |
| TERG_07738 | hypothetical protein   | CAGTGTG      | 555 | UPRE-1 |
| TERG_07753 | hypothetical protein   | CAGCGTG      | 206 | UPRE-1 |
| TERG_07758 | hypothetical protein   | CAGGGTG      | 533 | UPRE-1 |
| TERG_07760 | integral membrane protein ( <i>T. verrucosum</i> )                                   | CACTCTG (rc) | 637 | UPRE-1 |
| TERG_07761 | hypothetical protein   | CAGAGTG      | 269 | UPRE-1 |
| TERG_07763 | hypothetical protein   | CACTCTG (rc) | 94  | UPRE-1 |
| TERG_07764 | protein transporter SEC61 subunit alpha  | CAGAGTG      | 771 | UPRE-1 |
| TERG_07769 | hypothetical protein   | CACTCTG (rc) | 367 | UPRE-1 |
| TERG_07773 | tubulin alpha chain  | CAGAGTG      | 551 | UPRE-1 |
| TERG_07775 | hypothetical protein   | CACCCTG (rc) | 237 | UPRE-1 |
| TERG_07781 | hypothetical protein   | CAGAGTG      | 540 | UPRE-1 |
| TERG_07781 | hypothetical protein   | CAGGGTG      | 856 | UPRE-1 |
| TERG_07783 | MFS peptide transporter, putative ( <i>T. verrucosum</i> )                           | CACACTG (rc) | 44  | UPRE-1 |
| TERG_07797 | amino acid permease ( <i>T. equinum</i> )  | CACGCTG (rc) | 499 | UPRE-1 |
| TERG_07803 | HEAT repeat protein ( <i>T. equinum</i> )  | CACGCTG (rc) | 706 | UPRE-1 |
| TERG_07803 | HEAT repeat protein ( <i>T. equinum</i> )  | CACGCTG (rc) | 730 | UPRE-1 |
| TERG_07804 | PBSP domain-containing protein ( <i>T. tonsurans</i> )                               | CAGCGTG      | 853 | UPRE-1 |
| TERG_07804 | PBSP domain-containing protein ( <i>T. tonsurans</i> )                               | CAGCGTG      | 877 | UPRE-1 |
| TERG_07806 | 54S ribosomal protein L3 ( <i>T. equinum</i> )                                       | CACACTG (rc) | 555 | UPRE-1 |
| TERG_07823 | ATP-dependent DNA helicase ( <i>T. tonsurans</i> )                                   | CAGTGTG      | 991 | UPRE-1 |
| TERG_07838 | YjeF family domain-containing protein  | CAGAGTG      | 154 | UPRE-1 |
| TERG_07839 | ubiquitin homeostasis protein lub1 ( <i>T. equinum</i> )                             | CACTCTG (rc) | 658 | UPRE-1 |
| TERG_07839 | ubiquitin homeostasis protein lub1 ( <i>T. equinum</i> )                             | CACTCTG (rc) | 666 | UPRE-1 |
| TERG_07847 | hypothetical protein   | CACCCTG (rc) | 411 | UPRE-1 |
| TERG_07847 | hypothetical protein   | CACTCTG (rc) | 874 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_07856 | hypothetical protein  | CACGCTG (rc) | 414 | UPRE-1 |
| TERG_07862 | dynein light intermediate chain ( <i>T. tonsurans</i> )                     | CACTCTG (rc) | 40  | UPRE-1 |
| TERG_07862 | dynein light intermediate chain ( <i>T. tonsurans</i> )                     | CACTCTG (rc) | 49  | UPRE-1 |
| TERG_07863 | U2 snRNP component IST3 ( <i>T. equinum</i> )                               | CAGCGTG      | 104 | UPRE-1 |
| TERG_07875 | integral membrane protein ( <i>T. equinum</i> )                             | CACTCTG (rc) | 661 | UPRE-1 |
| TERG_07876 | hypothetical protein  | CACTCTG (rc) | 814 | UPRE-1 |
| TERG_07891 | DUF255 domain-containing protein ( <i>T. equinum</i> )                      | CAGGGTG      | 987 | UPRE-1 |
| TERG_07899 | hypothetical protein  | CAGAGTG      | 927 | UPRE-1 |
| TERG_07902 | STE/STE11/SSK protein kinase  | CACTCTG (rc) | 732 | UPRE-1 |
| TERG_07903 | nuclear mRNA splicing factor-associated protein ( <i>T. tonsurans</i> )     | CAGAGTG      | 211 | UPRE-1 |
| TERG_07905 | 1-pyrroline-5-carboxylate dehydrogenase                                     | CACACTG (rc) | 228 | UPRE-1 |
| TERG_07907 | hypothetical protein  | CACTCTG (rc) | 263 | UPRE-1 |
| TERG_07922 | glycine cleavage system T protein   | CACTCTG (rc) | 176 | UPRE-1 |
| TERG_07932 | vesicle-mediated transport protein Vid24, putative ( <i>T. verrucosum</i> ) | CACTCTG (rc) | 848 | UPRE-1 |
| TERG_07940 | histone-lysine n-methyltransferase ( <i>T. equinum</i> )                    | CAGGGTG      | 842 | UPRE-1 |
| TERG_07943 | hypothetical protein  | CACCCTG (rc) | 93  | UPRE-1 |
| TERG_07944 | 60S ribosomal protein L6 ( <i>T. equinum</i> )                              | CAGGGTG      | 91  | UPRE-1 |
| TERG_07959 | GPI-anchored cell wall beta-1,3-endoglucanase EglC ( <i>A. benhamiae</i> )  | CACTCTG (rc) | 666 | UPRE-1 |
| TERG_07963 | hypothetical protein  | CACCCTG (rc) | 240 | UPRE-1 |
| TERG_07969 | acyl-CoA dehydrogenase ( <i>T. tonsurans</i> )                              | CAGCGTG      | 282 | UPRE-1 |
| TERG_07971 | macrophomate synthase, putative ( <i>A. benhamiae</i> )                     | CAGGGTG      | 834 | UPRE-1 |
| TERG_07997 | acetamidase ( <i>T. tonsurans</i> )   | CACTCTG (rc) | 470 | UPRE-1 |
| TERG_07998 | hypothetical protein  | CACGCTG (rc) | 780 | UPRE-1 |
| TERG_08001 | nucleoside hydrolase, putative ( <i>T. verrucosum</i> )                     | CACCCTG (rc) | 721 | UPRE-1 |
| TERG_08002 | hypothetical protein  | CAGGGTG      | 618 | UPRE-1 |
| TERG_08002 | hypothetical protein  | CAGGGTG      | 977 | UPRE-1 |
| TERG_08011 | metallocarboxypeptidase A-like protein                                      | CAGGGTG      | 75  | UPRE-1 |
| TERG_08016 | calcium transporter ( <i>T. tonsurans</i> )                                 | CACGCTG (rc) | 432 | UPRE-1 |
| TERG_08031 | PHD finger domain-containing protein ( <i>T. equinum</i> )                  | CACACTG (rc) | 14  | UPRE-1 |
| TERG_08038 | polysaccharide deacetylase family protein ( <i>T. equinum</i> )             | CACGCTG (rc) | 312 | UPRE-1 |
| TERG_08042 | hypothetical protein  | CAGGGTG      | 416 | UPRE-1 |
| TERG_08062 | alpha-glucosidase AgdA, putative ( <i>A. benhamiae</i> )                    | CACGCTG (rc) | 484 | UPRE-1 |
| TERG_08064 | choline kinase, putative ( <i>A. benhamiae</i> )                            | CACCCTG (rc) | 17  | UPRE-1 |
| TERG_08065 | auxin Efflux Carrier superfamily protein ( <i>T. equinum</i> )              | CACCCTG (rc) | 634 | UPRE-1 |
| TERG_08078 | ubiquitin carboxyl-terminal hydrolase ( <i>T. equinum</i> )                 | CAGTGTG      | 558 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_08080 | hypothetical protein  | CAGGGTG      | 911 | UPRE-1 |
| TERG_08085 | DUF803 domain membrane protein ( <i>T. equinum</i> )                            | CACGCTG (rc) | 772 | UPRE-1 |
| TERG_08090 | plasma membrane iron permease ( <i>T. tonsurans</i> )                           | CACCCTG (rc) | 127 | UPRE-1 |
| TERG_08090 | plasma membrane iron permease ( <i>T. tonsurans</i> )                           | CACTCTG (rc) | 958 | UPRE-1 |
| TERG_08091 | conidial pigment biosynthesis oxidase Abr1/brown ( <i>T. verrucosum</i> )       | CAGGGTG      | 498 | UPRE-1 |
| TERG_08092 | orotidine 5'-phosphate decarboxylase ( <i>M. canis</i> )                        | CACCCTG (rc) | 52  | UPRE-1 |
| TERG_08092 | orotidine 5'-phosphate decarboxylase ( <i>M. canis</i> )                        | CACTCTG (rc) | 130 | UPRE-1 |
| TERG_08101 | TAM domain methyltransferase ( <i>T. equinum</i> )                              | CACACTG (rc) | 367 | UPRE-1 |
| TERG_08103 | anaphase promoting complex subunit 10 (APC10), putative ( <i>A. benhamiae</i> ) | CACCCTG (rc) | 596 | UPRE-1 |
| TERG_08115 | hypothetical protein  | CACGCTG (rc) | 720 | UPRE-1 |
| TERG_08115 | hypothetical protein  | CACTCTG (rc) | 765 | UPRE-1 |
| TERG_08117 | feruloyl esterase, putative ( <i>A. benhamiae</i> )                             | CACCCTG (rc) | 896 | UPRE-1 |
| TERG_08118 | hypothetical protein  | CACACTG (rc) | 768 | UPRE-1 |
| TERG_08123 | C6 finger domain protein, putative ( <i>A. benhamiae</i> )                      | CAGAGTG      | 191 | UPRE-1 |
| TERG_08128 | hypothetical protein  | CACCCTG (rc) | 184 | UPRE-1 |
| TERG_08141 | bZIP transcription factor (LziP), putative ( <i>A. benhamiae</i> )              | CAGAGTG      | 901 | UPRE-1 |
| TERG_08150 | Swr1p complex component ( <i>T. equinum</i> )                                   | CAGGGTG      | 375 | UPRE-1 |
| TERG_08161 | hypothetical protein  | CACCCTG (rc) | 912 | UPRE-1 |
| TERG_08163 | hypothetical protein  | CAGGGTG      | 324 | UPRE-1 |
| TERG_08164 | hypothetical protein  | CAGAGTG      | 566 | UPRE-1 |
| TERG_08169 | hypothetical protein  | CACGCTG (rc) | 65  | UPRE-1 |
| TERG_08171 | C6 finger domain protein, putative ( <i>A. benhamiae</i> )                      | CAGCGTG      | 172 | UPRE-1 |
| TERG_08172 | hypothetical protein  | CACTCTG (rc) | 911 | UPRE-1 |
| TERG_08173 | C6 finger domain protein, putative ( <i>A. benhamiae</i> )                      | CAGAGTG      | 37  | UPRE-1 |
| TERG_08197 | hypothetical protein  | CACCCTG (rc) | 816 | UPRE-1 |
| TERG_08199 | hypothetical protein  | CAGGGTG      | 6   | UPRE-1 |
| TERG_08200 | hypothetical protein  | CACTCTG (rc) | 745 | UPRE-1 |
| TERG_08201 | subtilisin-like protease 5  | CAGCGTG      | 363 | UPRE-1 |
| TERG_08203 | isopenicillin N synthase  | CACTCTG (rc) | 897 | UPRE-1 |
| TERG_08204 | alpha-aminoadypil-cysteinyI-valine synthetase ( <i>T. equinum</i> )             | CAGAGTG      | 388 | UPRE-1 |
| TERG_08218 | ADP-ribosylation factor family protein ( <i>T. verrucosum</i> )                 | CACGCTG (rc) | 17  | UPRE-1 |
| TERG_08222 | hypothetical protein  | CAGCGTG      | 890 | UPRE-1 |
| TERG_08228 | sphinganine hydroxylase ( <i>T. tonsurans</i> )                                 | CAGTGTG      | 43  | UPRE-1 |
| TERG_08229 | hypothetical protein  | CACGCTG (rc) | 137 | UPRE-1 |
| TERG_08235 | long chain fatty alcohol oxidase ( <i>T. tonsurans</i> )                        | CAGCGTG      | 889 | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_08236 | hypothetical protein   | CACACTG (rc) | 133 | UPRE-1 |
| TERG_08237 | DUF543 domain-containing protein ( <i>T. equinum</i> )                                       | CAGTGTG      | 279 | UPRE-1 |
| TERG_08240 | methyltransferase, putative ( <i>T. verrucosum</i> )   | CACTCTG (rc) | 93  | UPRE-1 |
| TERG_08250 | cation diffusion facilitator family metal ion transporter, putative ( <i>T. verrucosum</i> ) | CACTCTG (rc) | 992 | UPRE-1 |
| TERG_08264 | L-xylulose reductase   | CAGCGTG      | 720 | UPRE-1 |
| TERG_08271 | RNA lariat debranching enzyme, putative ( <i>A. benhamiae</i> )                              | CACACTG (rc) | 945 | UPRE-1 |
| TERG_08272 | hypothetical protein   | CAGTGTG      | 594 | UPRE-1 |
| TERG_08282 | hypothetical protein   | CACTCTG (rc) | 749 | UPRE-1 |
| TERG_08283 | acetamidase ( <i>T. tonsurans</i> )  | CAGAGTG      | 932 | UPRE-1 |
| TERG_08284 | DNA polymerase delta subunit 4, putative ( <i>A. benhamiae</i> )                             | CAGAGTG      | 935 | UPRE-1 |
| TERG_08288 | ATP-citrate synthase subunit 1   | CAGAGTG      | 638 | UPRE-1 |
| TERG_08291 | nuclear pore complex subunit ( <i>T. equinum</i> )   | CAGGGTG      | 510 | UPRE-1 |
| TERG_08310 | XAP5 domain-containing protein ( <i>T. equinum</i> )   | CACTCTG (rc) | 315 | UPRE-1 |
| TERG_08318 | HAD superfamily hydrolase ( <i>T. tonsurans</i> )  | CACCCTG (rc) | 675 | UPRE-1 |
| TERG_08319 | CMGC/SRPK protein kinase   | CACCCTG (rc) | 59  | UPRE-1 |
| TERG_08323 | serine/threonine-protein phosphatase PP2A catalytic subunit                                  | CACTCTG (rc) | 478 | UPRE-1 |
| TERG_08324 | hypothetical protein   | CACTCTG (rc) | 308 | UPRE-1 |
| TERG_08327 | Ser/Thr protein phosphatase ( <i>T. tonsurans</i> )  | CACTCTG (rc) | 163 | UPRE-1 |
| TERG_08328 | basic proline-rich protein ( <i>M. canis</i> )   | CAGAGTG      | 807 | UPRE-1 |
| TERG_08329 | flavin containing amine oxidase ( <i>T. tonsurans</i> )                                      | CACACTG (rc) | 649 | UPRE-1 |
| TERG_08333 | 1-pyrroline-5-carboxylate dehydrogenase  | CAGAGTG      | 509 | UPRE-1 |
| TERG_08333 | 1-pyrroline-5-carboxylate dehydrogenase  | CAGAGTG      | 666 | UPRE-1 |
| TERG_08343 | hypothetical protein   | CACTCTG (rc) | 240 | UPRE-1 |
| TERG_08344 | hypothetical protein   | CAGCGTG      | 336 | UPRE-1 |
| TERG_08348 | terpene synthase family protein ( <i>A. benhamiae</i> )                                      | CACACTG (rc) | 105 | UPRE-1 |
| TERG_08348 | terpene synthase family protein ( <i>A. benhamiae</i> )                                      | CACGCTG (rc) | 579 | UPRE-1 |
| TERG_08351 | hypothetical protein   | CACCCTG (rc) | 708 | UPRE-1 |
| TERG_08352 | hypothetical protein   | CAGGGTG      | 975 | UPRE-1 |
| TERG_08355 | zinc alcohol dehydrogenase, putative ( <i>T. verrucosum</i> )                                | CACACTG (rc) | 326 | UPRE-1 |
| TERG_08355 | zinc alcohol dehydrogenase, putative ( <i>T. verrucosum</i> )                                | CACGCTG (rc) | 959 | UPRE-1 |
| TERG_08356 | oxidoreductase, 2OG-Fe(II) oxygenase family, putative ( <i>A. benhamiae</i> )                | CAGCGTG      | 934 | UPRE-1 |
| TERG_08377 | copper transporter Ctr ( <i>T. tonsurans</i> )   | CACCCTG (rc) | 219 | UPRE-1 |
| TERG_08381 | NUDIX domain-containing protein ( <i>T. equinum</i> )  | CACCCTG (rc) | 640 | UPRE-1 |
| TERG_08390 | hypothetical protein   | CAGAGTG      | 456 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_08394 | sugar transporter family protein ( <i>T. verrucosum</i> )                       | CACCCTG (rc) | 595 | UPRE-1 |
| TERG_08395 | 4-nitrophenylphosphatase ( <i>T. tonsurans</i> )                                | CAGGGTG      | 359 | UPRE-1 |
| TERG_08402 | protein transport membrane glycoprotein Sec20, putative ( <i>A. benhamiae</i> ) | CAGAGTG      | 402 | UPRE-1 |
| TERG_08403 | inorganic pyrophosphatase   | CACTCTG (rc) | 67  | UPRE-1 |
| TERG_08412 | TLC domain-containing protein ( <i>T. tonsurans</i> )                           | CAGCGTG      | 362 | UPRE-1 |
| TERG_08418 | mitochondrial inner membrane translocase subunit TIM44 ( <i>T. tonsurans</i> )  | CACTCTG (rc) | 121 | UPRE-1 |
| TERG_08433 | hypothetical protein  | CACTCTG (rc) | 116 | UPRE-1 |
| TERG_08435 | 3-oxoacyl-(acyl-carrier-protein) reductase ( <i>M. canis</i> )                  | CACTCTG (rc) | 119 | UPRE-1 |
| TERG_08436 | hypothetical protein  | CACACTG (rc) | 124 | UPRE-1 |
| TERG_08466 | hypothetical protein  | CAGCGTG      | 153 | UPRE-1 |
| TERG_08469 | signal peptidase I  | CAGTGTG      | 754 | UPRE-1 |
| TERG_08471 | 50S ribosomal protein L4  | CAGTGTG      | 735 | UPRE-1 |
| TERG_08497 | mRNA turnover protein 4 ( <i>T. equinum</i> )                                   | CACTCTG (rc) | 261 | UPRE-1 |
| TERG_08498 | triosephosphate isomerase   | CAGAGTG      | 136 | UPRE-1 |
| TERG_08498 | triosephosphate isomerase   | CAGGGTG      | 766 | UPRE-1 |
| TERG_08501 | serine/threonine protein kinase   | CAGGGTG      | 351 | UPRE-1 |
| TERG_08504 | helicase ( <i>T. equinum</i> )  | CACCCTG (rc) | 100 | UPRE-1 |
| TERG_08508 | hypothetical protein  | CAGCGTG      | 737 | UPRE-1 |
| TERG_08511 | hypothetical protein  | CACTCTG (rc) | 286 | UPRE-1 |
| TERG_08525 | hypothetical protein  | CAGAGTG      | 460 | UPRE-1 |
| TERG_08528 | fatty acid synthase beta subunit dehydratase ( <i>T. tonsurans</i> )            | CAGGGTG      | 48  | UPRE-1 |
| TERG_08542 | GTP-binding protein ypt2  | CACCCTG (rc) | 771 | UPRE-1 |
| TERG_08545 | C-4 methyl sterol oxidase Erg25 ( <i>T. equinum</i> )                           | CAGCGTG      | 294 | UPRE-1 |
| TERG_08550 | tRNA-specific adenosine deaminase subunit Tad2p/ADAT2 ( <i>T. tonsurans</i> )   | CAGGGTG      | 781 | UPRE-1 |
| TERG_08561 | FGGY-family carbohydrate kinase ( <i>T. tonsurans</i> )                         | CACGCTG (rc) | 13  | UPRE-1 |
| TERG_08563 | hypothetical protein  | CACGCTG (rc) | 542 | UPRE-1 |
| TERG_08589 | cysteine-tRNA ligase  | CACGCTG (rc) | 154 | UPRE-1 |
| TERG_08591 | multidrug resistance protein ( <i>T. tonsurans</i> )                            | CAGTGTG      | 260 | UPRE-1 |
| TERG_08591 | multidrug resistance protein ( <i>T. tonsurans</i> )                            | CAGTGTG      | 871 | UPRE-1 |
| TERG_08592 | short-chain oxidoreductase, putative ( <i>A. benhamiae</i> )                    | CAGCGTG      | 8   | UPRE-1 |
| TERG_08598 | eukaryotic translation initiation factor 6                                      | CACTCTG (rc) | 425 | UPRE-1 |
| TERG_08627 | C6 transcription factor GliZ2 ( <i>T. equinum</i> )                             | CACACTG (rc) | 315 | UPRE-1 |
| TERG_08648 | cell division control protein (Cdc15), putative ( <i>A. benhamiae</i> )         | CAGGGTG      | 226 | UPRE-1 |
| TERG_08655 | ADP,ATP carrier protein   | CACGCTG (rc) | 203 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_08662 | hypothetical protein  | CACACTG (rc) | 840 | UPRE-1 |
| TERG_08666 | hypothetical protein  | CACACTG (rc) | 537 | UPRE-1 |
| TERG_08672 | HFR-3 ( <i>M. canis</i> )   | CACACTG (rc) | 811 | UPRE-1 |
| TERG_08680 | amino acid permease ( <i>T. tonsurans</i> )                           | CACTCTG (rc) | 49  | UPRE-1 |
| TERG_08692 | GATA transcriptional activator AreA ( <i>A. benhamiae</i> )           | CAGAGTG      | 632 | UPRE-1 |
| TERG_08711 | hypothetical protein  | CAGCGTG      | 475 | UPRE-1 |
| TERG_08717 | tRNA methyltransferase ( <i>T. tonsurans</i> )                        | CAGGGTG      | 151 | UPRE-1 |
| TERG_08724 | hypothetical protein  | CAGAGTG      | 672 | UPRE-1 |
| TERG_08742 | hypothetical protein  | CACGCTG (rc) | 958 | UPRE-1 |
| TERG_08744 | hypothetical protein  | CAGAGTG      | 160 | UPRE-1 |
| TERG_08749 | pH signal transduction protein PaII, putative ( <i>A. benhamiae</i> ) | CACACTG (rc) | 933 | UPRE-1 |
| TERG_08751 | ABC multidrug transporter, putative ( <i>A. benhamiae</i> )           | CACACTG (rc) | 705 | UPRE-1 |
| TERG_08756 | cercosporin toxin biosynthesis protein ( <i>T. equinum</i> )          | CACACTG (rc) | 476 | UPRE-1 |
| TERG_08771 | extracellular serine-threonine rich protein ( <i>T. tonsurans</i> )   | CACCCTG (rc) | 418 | UPRE-1 |
| TERG_08794 | pyruvate dehydrogenase kinase ( <i>T. equinum</i> )                   | CACACTG (rc) | 941 | UPRE-1 |
| TERG_08831 | acetyltransferase ( <i>T. tonsurans</i> )                             | CAGAGTG      | 845 | UPRE-1 |
| TERG_08839 | hypothetical protein  | CACCCTG (rc) | 609 | UPRE-1 |
| TERG_08843 | hypothetical protein  | CAGTGTG      | 64  | UPRE-1 |
| TERG_08845 | pyridoxamine phosphate oxidase ( <i>T. tonsurans</i> )                | CACCCTG (rc) | 272 | UPRE-1 |
| TERG_08878 | hypothetical protein  | CACCCTG (rc) | 618 | UPRE-1 |
| TERG_08883 | hypothetical protein  | CACTCTG (rc) | 299 | UPRE-1 |
| TERG_08909 | hypothetical protein  | CACACTG (rc) | 376 | UPRE-1 |
| TERG_08919 | hypothetical protein  | CACCCTG (rc) | 15  | UPRE-1 |
| TERG_08952 | long-chain-fatty-acid-CoA ligase ( <i>T. equinum</i> )                | CAGGGTG      | 340 | UPRE-1 |
| TERG_08954 | hypothetical protein  | CACCCTG (rc) | 699 | UPRE-1 |
| TERG_08960 | SET domain protein ( <i>T. verrucosum</i> )                           | CACGCTG (rc) | 367 | UPRE-1 |
| TERG_08961 | hypothetical protein  | CAGCGTG      | 132 | UPRE-1 |
| TERG_08964 | hypothetical protein  | CAGGGTG      | 265 | UPRE-1 |
| TERG_08975 | importin beta-1 subunit ( <i>T. tonsurans</i> )                       | CACCCTG (rc) | 385 | UPRE-1 |
| TERG_08987 | hypothetical protein  | CACCCTG (rc) | 613 | UPRE-1 |
| TERG_08992 | hypothetical protein  | CAGAGTG      | 467 | UPRE-1 |
| TERG_11504 | hypothetical protein  | CAGGGTG      | 70  | UPRE-1 |
| TERG_11504 | hypothetical protein  | CAGGGTG      | 96  | UPRE-1 |
| TERG_11504 | hypothetical protein  | CAGAGTG      | 825 | UPRE-1 |
| TERG_11505 | phosphoenolpyruvate carboxykinase [ATP]                               | CAGAGTG      | 68  | UPRE-1 |
| TERG_11508 | C6 finger domain protein, putative ( <i>A. benhamiae</i> )            | CACGCTG (rc) | 4   | UPRE-1 |



|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_11509 | hypothetical protein  | CAGCGTG      | 297 | UPRE-1 |
| TERG_11511 | hypothetical protein  | CAGAGTG      | 870 | UPRE-1 |
| TERG_11514 | lipase/esterase, putative ( <i>T. verrucosum</i> )                          | CAGTGTG      | 412 | UPRE-1 |
| TERG_11517 | hypothetical protein  | CAGGGTG      | 458 | UPRE-1 |
| TERG_11524 | hypothetical protein  | CAGCGTG      | 657 | UPRE-1 |
| TERG_11527 | tenascin C ( <i>T. equinum</i> )  | CAGTGTG      | 694 | UPRE-1 |
| TERG_11528 | tenascin C ( <i>T. equinum</i> )  | CAGTGTG      | 307 | UPRE-1 |
| TERG_11528 | tenascin C ( <i>T. equinum</i> )  | CAGTGTG      | 650 | UPRE-1 |
| TERG_11528 | tenascin C ( <i>T. equinum</i> )  | CAGTGTG      | 781 | UPRE-1 |
| TERG_11528 | tenascin C ( <i>T. equinum</i> )  | CAGTGTG      | 856 | UPRE-1 |
| TERG_11528 | tenascin C ( <i>T. equinum</i> )  | CAGTGTG      | 931 | UPRE-1 |
| TERG_11533 | hypothetical protein  | CAGAGTG      | 719 | UPRE-1 |
| TERG_11535 | hypothetical protein  | CAGAGTG      | 933 | UPRE-1 |
| TERG_11536 | hypothetical protein  | CAGGGTG      | 918 | UPRE-1 |
| TERG_11538 | 3-oxoacyl-(acyl-carrier-protein) reductase ( <i>T. tonsurans</i> )          | CAGGGTG      | 348 | UPRE-1 |
| TERG_11552 | hypothetical protein  | CAGAGTG      | 608 | UPRE-1 |
| TERG_11556 | hypothetical protein  | CAGTGTG      | 726 | UPRE-1 |
| TERG_11557 | luciferin 4-monooxygenase ( <i>T. equinum</i> )                             | CAGCGTG      | 550 | UPRE-1 |
| TERG_11569 | uridine nucleosidase ( <i>T. tonsurans</i> )                                | CAGTGTG      | 504 | UPRE-1 |
| TERG_11575 | phosphotransferase enzyme family protein ( <i>T. equinum</i> )              | CAGAGTG      | 4   | UPRE-1 |
| TERG_11584 | hexose transporter protein ( <i>A. benhamiae</i> )                          | CAGGGTG      | 422 | UPRE-1 |
| TERG_11595 | LipA and NB-ARC domain-containing protein ( <i>M. canis</i> )               | CAGTGTG      | 29  | UPRE-1 |
| TERG_11619 | hypothetical protein  | CAGTGTG      | 454 | UPRE-1 |
| TERG_11622 | hypothetical protein  | CAGGGTG      | 613 | UPRE-1 |
| TERG_11656 | class V chitinase ( <i>T. tonsurans</i> )                                   | CAGTGTG      | 169 | UPRE-1 |
| TERG_11683 | NADH-ubiquinone oxidoreductase 40 kDa subunit, mitochondrial                | CACACTG (rc) | 558 | UPRE-1 |
| TERG_11686 | hypothetical protein  | CAGGGTG      | 40  | UPRE-1 |
| TERG_11697 | hypothetical protein  | CACGCTG (rc) | 100 | UPRE-1 |
| TERG_11701 | hypothetical protein  | CACTCTG (rc) | 51  | UPRE-1 |
| TERG_11706 | hypothetical protein  | CACCCTG (rc) | 278 | UPRE-1 |
| TERG_11708 | hypothetical protein  | CAGTGTG      | 513 | UPRE-1 |
| TERG_11725 | C6 transcription factor, putative ( <i>T. verrucosum</i> )                  | CAGTGTG      | 478 | UPRE-1 |
| TERG_11731 | zinc/cadmium resistance protein ( <i>T. tonsurans</i> )                     | CACTCTG (rc) | 683 | UPRE-1 |
| TERG_11738 | cytoskeleton organization protein (Dec1), putative ( <i>T. verrucosum</i> ) | CAGCGTG      | 451 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_11739 | cytoskeleton organization protein (Dec1), putative ( <i>T. verrucosum</i> ) | CAGCGTG      | 39  | UPRE-1 |
| TERG_11739 | cytoskeleton organization protein (Dec1), putative ( <i>T. verrucosum</i> ) | CAGCGTG      | 855 | UPRE-1 |
| TERG_11744 | arylsulfatase, putative ( <i>T. verrucosum</i> )                            | CAGGGTG      | 124 | UPRE-1 |
| TERG_11749 | hypothetical protein  | CAGAGTG      | 134 | UPRE-1 |
| TERG_11749 | hypothetical protein  | CAGTGTG      | 720 | UPRE-1 |
| TERG_11754 | hypothetical protein  | CAGGGTG      | 384 | UPRE-1 |
| TERG_11767 | amidase family protein, putative ( <i>T. verrucosum</i> )                   | CAGTGTG      | 331 | UPRE-1 |
| TERG_11772 | TKL protein kinase ( <i>T. tonsurans</i> )                                  | CAGAGTG      | 705 | UPRE-1 |
| TERG_11772 | TKL protein kinase ( <i>T. tonsurans</i> )                                  | CAGCGTG      | 827 | UPRE-1 |
| TERG_11775 | hypothetical protein  | CAGGGTG      | 353 | UPRE-1 |
| TERG_11781 | hypothetical protein  | CAGGGTG      | 454 | UPRE-1 |
| TERG_11782 | hypothetical protein  | CAGTGTG      | 98  | UPRE-1 |
| TERG_11784 | extracellular metalloproteinase 5   | CAGGGTG      | 685 | UPRE-1 |
| TERG_11786 | oligosaccharyl transferase stt3 subunit ( <i>T. equinum</i> )               | CAGCGTG      | 859 | UPRE-1 |
| TERG_11787 | oligosaccharyl transferase stt3 subunit ( <i>T. equinum</i> )               | CAGCGTG      | 378 | UPRE-1 |
| TERG_11789 | DNA mismatch repair protein Msh1 ( <i>T. equinum</i> )                      | CAGAGTG      | 550 | UPRE-1 |
| TERG_11796 | hypothetical protein  | CACGCTG (rc) | 34  | UPRE-1 |
| TERG_11797 | hypothetical protein  | CACGCTG (rc) | 673 | UPRE-1 |
| TERG_11814 | FAD dependent oxidoreductase, putative ( <i>A. benhamiae</i> )              | CAGCGTG      | 440 | UPRE-1 |
| TERG_11821 | hypothetical protein  | CAGGGTG      | 50  | UPRE-1 |
| TERG_11821 | hypothetical protein  | CAGAGTG      | 836 | UPRE-1 |
| TERG_11831 | hypothetical protein  | CACCCTG (rc) | 316 | UPRE-1 |
| TERG_11831 | hypothetical protein  | CACACTG (rc) | 466 | UPRE-1 |
| TERG_11844 | RNA polymerase II mediator complex component Srb8 ( <i>T. equinum</i> )     | CAGGGTG      | 75  | UPRE-1 |
| TERG_11851 | hypothetical protein  | CAGAGTG      | 704 | UPRE-1 |
| TERG_11865 | hypothetical protein  | CACGCTG (rc) | 49  | UPRE-1 |
| TERG_11865 | hypothetical protein  | CACGCTG (rc) | 181 | UPRE-1 |
| TERG_11868 | MFS monosaccharide transporter ( <i>T. tonsurans</i> )                      | CAGGGTG      | 195 | UPRE-1 |
| TERG_11880 | hypothetical protein  | CAGGGTG      | 40  | UPRE-1 |
| TERG_11885 | ABC bile acid transporter, putative ( <i>T. verrucosum</i> )                | CAGAGTG      | 12  | UPRE-1 |
| TERG_11890 | hypothetical protein  | CAGGGTG      | 182 | UPRE-1 |
| TERG_11897 | hypothetical protein  | CAGTGTG      | 585 | UPRE-1 |
| TERG_11904 | hypothetical protein  | CACTCTG (rc) | 916 | UPRE-1 |
| TERG_11905 | hypothetical protein  | CAGAGTG      | 435 | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_11914 | Protein phosphatase 2C, putative ( <i>T. verrucosum</i> )              | CAGAGTG      | 431 | UPRE-1 |
| TERG_11924 | ankyrin repeat protein ( <i>T. tonsurans</i> )                         | CAGGGTG      | 687 | UPRE-1 |
| TERG_11925 | tRNA methyltransferase ( <i>T. tonsurans</i> )                         | CAGGGTG      | 173 | UPRE-1 |
| TERG_11933 | Cytochrome b5 ( <i>T. tonsurans</i> )                                  | CACCCTG (rc) | 662 | UPRE-1 |
| TERG_11934 | PAB-dependent poly(A)-specific ribonuclease subunit PAN2               | CAGAGTG      | 377 | UPRE-1 |
| TERG_11943 | MFS maltose permease ( <i>T. tonsurans</i> )                           | CACGCTG (rc) | 757 | UPRE-1 |
| TERG_11945 | hypothetical protein   | CACTCTG (rc) | 126 | UPRE-1 |
| TERG_11946 | hypothetical protein   | CAGAGTG      | 774 | UPRE-1 |
| TERG_11948 | hypothetical protein   | CAGAGTG      | 979 | UPRE-1 |
| TERG_11949 | hypothetical protein   | CAGGGTG      | 65  | UPRE-1 |
| TERG_11952 | mandelate racemase/muconate lactonizing enzyme ( <i>T. tonsurans</i> ) | CAGAGTG      | 95  | UPRE-1 |
| TERG_11954 | hypothetical protein   | CAGCGTG      | 23  | UPRE-1 |
| TERG_11960 | CMGC/CDK/PITSLRE protein kinase  | CAGCGTG      | 985 | UPRE-1 |
| TERG_11962 | DEAD/DEAH box RNA helicase ( <i>T. tonsurans</i> )                     | CAGCGTG      | 310 | UPRE-1 |
| TERG_11968 | hypothetical protein   | CAGGGTG      | 650 | UPRE-1 |
| TERG_11975 | integral membrane protein ( <i>T. verrucosum</i> )                     | CACTCTG (rc) | 468 | UPRE-1 |
| TERG_11976 | integral membrane protein ( <i>T. tonsurans</i> )                      | CACCCTG (rc) | 480 | UPRE-1 |
| TERG_11982 | ankyrin repeat protein ( <i>T. verrucosum</i> )                        | CACGCTG (rc) | 223 | UPRE-1 |
| TERG_11985 | vacuolar fusion protein mon1   | CAGAGTG      | 408 | UPRE-1 |
| TERG_11994 | hypothetical protein   | CAGGGTG      | 499 | UPRE-1 |
| TERG_11996 | chitinase ( <i>M. canis</i> )  | CAGGGTG      | 830 | UPRE-1 |
| TERG_12004 | lipase ( <i>T. tonsurans</i> )   | CACGCTG (rc) | 985 | UPRE-1 |
| TERG_12011 | hypothetical protein   | CAGGGTG      | 8   | UPRE-1 |
| TERG_12016 | hypothetical protein   | CAGCGTG      | 929 | UPRE-1 |
| TERG_12021 | Zn cluster transcription factor Rds2 ( <i>T. tonsurans</i> )           | CACGCTG (rc) | 636 | UPRE-1 |
| TERG_12022 | hypothetical protein   | CAGCGTG      | 238 | UPRE-1 |
| TERG_12032 | hypothetical protein   | CACCCTG (rc) | 450 | UPRE-1 |
| TERG_12034 | hypothetical protein   | CAGGGTG      | 230 | UPRE-1 |
| TERG_12039 | hypothetical protein   | CACGCTG (rc) | 700 | UPRE-1 |
| TERG_12041 | priB protein ( <i>M. gypseum</i> )                                     | CACCCTG (rc) | 707 | UPRE-1 |
| TERG_12042 | RNA helicase/RNase III, putative ( <i>A. benhamiae</i> )               | CACACTG (rc) | 853 | UPRE-1 |
| TERG_12042 | RNA helicase/RNase III, putative ( <i>A. benhamiae</i> )               | CACGCTG (rc) | 927 | UPRE-1 |
| TERG_12045 | hypothetical protein   | CAGAGTG      | 987 | UPRE-1 |
| TERG_12048 | guanyl-nucleotide exchange factor Sec7 ( <i>T. equinum</i> )           | CAGAGTG      | 366 | UPRE-1 |
| TERG_12048 | guanyl-nucleotide exchange factor Sec7 ( <i>T. equinum</i> )           | CAGGGTG      | 706 | UPRE-1 |
| TERG_12049 | DUF890 domain-containing protein ( <i>T. equinum</i> )                 | CAGCGTG      | 698 | UPRE-1 |

|            |   |              |     |        |
|------------|---|--------------|-----|--------|
| TERG_12054 | HEAT repeat protein ( <i>A. benhamiae</i> )   | CACGCTG (rc) | 304 | UPRE-1 |
| TERG_12056 | hypothetical protein  | CAGGGTG      | 281 | UPRE-1 |
| TERG_12058 | transporter smf2 ( <i>T. tonsurans</i> )  | CAGGGTG      | 213 | UPRE-1 |
| TERG_12071 | AGC/DMPK protein kinase ( <i>T. equinum</i> )   | CACTCTG (rc) | 521 | UPRE-1 |
| TERG_12082 | hypothetical protein  | CAGAGTG      | 791 | UPRE-1 |
| TERG_12099 | hypothetical protein  | CAGTGTG      | 83  | UPRE-1 |
| TERG_12102 | hypothetical protein  | CACTCTG (rc) | 805 | UPRE-1 |
| TERG_12104 | hypothetical protein  | CAGGGTG      | 465 | UPRE-1 |
| TERG_12105 | amino-acid N-acetyltransferase subunit Mak10 ( <i>T. tonsurans</i> )                              | CACACTG (rc) | 99  | UPRE-1 |
| TERG_12107 | 1,4-alpha-glucan-branching enzyme   | CAGCGTG      | 555 | UPRE-1 |
| TERG_12112 | hypothetical protein  | CACACTG (rc) | 779 | UPRE-1 |
| TERG_12121 | DNA replication licensing factor mcm5 ( <i>T. tonsurans</i> )                                     | CAGCGTG      | 459 | UPRE-1 |
| TERG_12127 | phosphatidylinositol?glycan ( <i>T. equinum</i> )   | CAGTGTG      | 207 | UPRE-1 |
| TERG_12130 | hypothetical protein  | CAGGGTG      | 693 | UPRE-1 |
| TERG_12132 | hypothetical protein  | CAGAGTG      | 561 | UPRE-1 |
| TERG_12138 | hypothetical protein  | CAGGGTG      | 733 | UPRE-1 |
| TERG_12139 | hypothetical protein  | CAGGGTG      | 224 | UPRE-1 |
| TERG_12143 | hypothetical protein  | CAGCGTG      | 234 | UPRE-1 |
| TERG_12145 | histone deacetylase HdaA ( <i>T. tonsurans</i> )  | CACACTG (rc) | 645 | UPRE-1 |
| TERG_12160 | STE/STE11/CDC15 protein kinase ( <i>T. tonsurans</i> )  | CAGCGTG      | 572 | UPRE-1 |
| TERG_12163 | RSC complex subunit Sfh1 ( <i>T. tonsurans</i> )  | CAGGGTG      | 215 | UPRE-1 |
| TERG_12165 | PX domain protein ( <i>T. verrucosum</i> )  | CACTCTG (rc) | 701 | UPRE-1 |
| TERG_12170 | WD domain-containing protein ( <i>T. equinum</i> )  | CACTCTG (rc) | 639 | UPRE-1 |
| TERG_12172 | glycerol-3-phosphate dehydrogenase ( <i>T. equinum</i> )  | CACACTG (rc) | 110 | UPRE-1 |
| TERG_12175 | hypothetical protein  | CAGCGTG      | 320 | UPRE-1 |
| TERG_12176 | hypothetical protein  | CAGGGTG      | 18  | UPRE-1 |
| TERG_12192 | hypothetical protein  | CAGTGTG      | 671 | UPRE-1 |
| TERG_12198 | hypothetical protein  | CACCCTG (rc) | 190 | UPRE-1 |
| TERG_12200 | hypothetical protein  | CAGGGTG      | 214 | UPRE-1 |
| TERG_12201 | hypothetical protein  | CACTCTG (rc) | 963 | UPRE-1 |
| TERG_12204 | RNA polymerase I specific transcription initiation factor Rrn7, putative ( <i>T. verrucosum</i> ) | CAGAGTG      | 676 | UPRE-1 |
| TERG_12206 | translation regulator (Cya5), putative ( <i>T. verrucosum</i> )                                   | CAGCGTG      | 1   | UPRE-1 |
| TERG_12212 | hypothetical protein  | CAGAGTG      | 292 | UPRE-1 |
| TERG_12213 | hypothetical protein  | CAGGGTG      | 641 | UPRE-1 |
| TERG_12265 | glutathione-dependent formaldehyde-activating enzyme ( <i>T. tonsurans</i> )                      | CAGCGTG      | 333 | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_12285 | hypothetical protein   | CAGAGTG      | 310 | UPRE-1 |
| TERG_12290 | mitochondrial cytochrome b2 ( <i>T. tonsurans</i> )                        | CACGCTG (rc) | 328 | UPRE-1 |
| TERG_12290 | mitochondrial cytochrome b2 ( <i>T. tonsurans</i> )                        | CACCCTG (rc) | 837 | UPRE-1 |
| TERG_12292 | hypothetical protein   | CAGAGTG      | 931 | UPRE-1 |
| TERG_12293 | hypothetical protein   | CAGCGTG      | 580 | UPRE-1 |
| TERG_12298 | hypothetical protein   | CAGTGTG      | 877 | UPRE-1 |
| TERG_12302 | hypothetical protein   | CAGCGTG      | 619 | UPRE-1 |
| TERG_12310 | null ( <i>T. verrucosum</i> )  | CACACTG (rc) | 24  | UPRE-1 |
| TERG_12316 | phosphotransferase enzyme family protein ( <i>T. equinum</i> )             | CAGGGTG      | 828 | UPRE-1 |
| TERG_12317 | phosphotransferase enzyme family protein ( <i>T. equinum</i> )             | CAGGGTG      | 78  | UPRE-1 |
| TERG_12324 | hypothetical protein   | CAGGGTG      | 316 | UPRE-1 |
| TERG_12325 | hypothetical protein   | CAGGGTG      | 416 | UPRE-1 |
| TERG_12334 | hypothetical protein   | CAGAGTG      | 35  | UPRE-1 |
| TERG_12335 | proliferating cell nuclear antigen (pcna)                                  | CAGCGTG      | 127 | UPRE-1 |
| TERG_12342 | membrane zinc transporter ( <i>T. tonsurans</i> )                          | CAGCGTG      | 195 | UPRE-1 |
| TERG_12347 | Anaphase promoting complex subunit Apc11, putative ( <i>T. tonsurans</i> ) | CACCCTG (rc) | 193 | UPRE-1 |
| TERG_12348 | anaphase promoting complex subunit Apc11 ( <i>T. equinum</i> )             | CACGCTG (rc) | 489 | UPRE-1 |
| TERG_12348 | anaphase promoting complex subunit Apc11 ( <i>T. equinum</i> )             | CACCCTG (rc) | 943 | UPRE-1 |
| TERG_12362 | mitochondrial molecular chaperone ( <i>T. tonsurans</i> )                  | CACACTG (rc) | 828 | UPRE-1 |
| TERG_12372 | multidrug resistance protein ( <i>T. tonsurans</i> )                       | CAGGGTG      | 964 | UPRE-1 |
| TERG_12374 | UDP-N-acetylglucosaminyltransferase ( <i>T. equinum</i> )                  | CACCCTG (rc) | 140 | UPRE-1 |
| TERG_12412 | MFS sugar transporter, putative ( <i>T. verrucosum</i> )                   | CAGCGTG      | 211 | UPRE-1 |
| TERG_12412 | MFS sugar transporter, putative ( <i>T. verrucosum</i> )                   | CAGAGTG      | 263 | UPRE-1 |
| TERG_12419 | uracil permease ( <i>M. gypseum</i> )                                      | CAGGGTG      | 698 | UPRE-1 |
| TERG_12422 | SPX domain-containing protein ( <i>T. tonsurans</i> )                      | CAGCGTG      | 628 | UPRE-1 |
| TERG_12426 | T-complex protein 1 ( <i>T. tonsurans</i> )                                | CACCCTG (rc) | 159 | UPRE-1 |
| TERG_12442 | hypothetical protein   | CACGCTG (rc) | 936 | UPRE-1 |
| TERG_12443 | hypothetical protein   | CAGAGTG      | 31  | UPRE-1 |
| TERG_12454 | cutinase, putative ( <i>A. benhamiae</i> )                                 | CAGGGTG      | 102 | UPRE-1 |
| TERG_12454 | cutinase, putative ( <i>A. benhamiae</i> )                                 | CAGAGTG      | 892 | UPRE-1 |
| TERG_12454 | cutinase, putative ( <i>A. benhamiae</i> )                                 | CAGGGTG      | 950 | UPRE-1 |
| TERG_12456 | hypothetical protein   | CACTCTG (rc) | 422 | UPRE-1 |
| TERG_12460 | hypothetical protein   | CAGGGTG      | 894 | UPRE-1 |
| TERG_12461 | HMG-CoA reductase ( <i>A. benhamiae</i> )                                  | CAGGGTG      | 642 | UPRE-1 |
| TERG_12473 | FYVE zinc finger protein ( <i>T. equinum</i> )                             | CACGCTG (rc) | 726 | UPRE-1 |
| TERG_12488 | rRNA processing protein ( <i>T. tonsurans</i> )                            | CAGTGTG      | 6   | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_12491 | carboxylesterase, putative ( <i>A. benhamiae</i> )                           | CAGGGTG      | 415 | UPRE-1 |
| TERG_12500 | sorbitol dehydrogenase ( <i>T. equinum</i> )                                 | CAGCGTG      | 239 | UPRE-1 |
| TERG_12501 | catechol dioxygenase, putative ( <i>T. verrucosum</i> )                      | CAGCGTG      | 274 | UPRE-1 |
| TERG_12501 | catechol dioxygenase, putative ( <i>T. verrucosum</i> )                      | CAGGGTG      | 364 | UPRE-1 |
| TERG_12518 | phosphotransferase enzyme family protein ( <i>T. equinum</i> )               | CAGAGTG      | 576 | UPRE-1 |
| TERG_12522 | 4-hydroxyphenylpyruvate dioxygenase ( <i>T. tonsurans</i> )                  | CAGTGTG      | 264 | UPRE-1 |
| TERG_12534 | glycerol-3-phosphate O-acyltransferase ( <i>T. equinum</i> )                 | CACCCTG (rc) | 278 | UPRE-1 |
| TERG_12534 | glycerol-3-phosphate O-acyltransferase ( <i>T. equinum</i> )                 | CACTCTG (rc) | 680 | UPRE-1 |
| TERG_12541 | hypothetical protein   | CAGGGTG      | 93  | UPRE-1 |
| TERG_12543 | hypothetical protein   | CAGAGTG      | 549 | UPRE-1 |
| TERG_12544 | hypothetical protein   | CAGCGTG      | 259 | UPRE-1 |
| TERG_12544 | hypothetical protein   | CAGGGTG      | 921 | UPRE-1 |
| TERG_12546 | chromosome segregation protein BIR1 ( <i>T. equinum</i> )                    | CACACTG (rc) | 86  | UPRE-1 |
| TERG_12547 | chromosome segregation protein BIR1 ( <i>T. equinum</i> )                    | CACACTG (rc) | 610 | UPRE-1 |
| TERG_12555 | hypothetical protein   | CAGGGTG      | 585 | UPRE-1 |
| TERG_12556 | hypothetical protein   | CAGAGTG      | 561 | UPRE-1 |
| TERG_12562 | hypothetical protein   | CAGTGTG      | 446 | UPRE-1 |
| TERG_12566 | hypothetical protein   | CAGTGTG      | 707 | UPRE-1 |
| TERG_12571 | ATP-dependent RNA helicase DOB1 ( <i>T. equinum</i> )                        | CAGTGTG      | 661 | UPRE-1 |
| TERG_12571 | ATP-dependent RNA helicase DOB1 ( <i>T. equinum</i> )                        | CAGAGTG      | 943 | UPRE-1 |
| TERG_12579 | MFS transporter ( <i>T. tonsurans</i> )                                      | CAGTGTG      | 596 | UPRE-1 |
| TERG_12582 | hypothetical protein   | CAGCGTG      | 529 | UPRE-1 |
| TERG_12582 | hypothetical protein   | CAGCGTG      | 954 | UPRE-1 |
| TERG_12588 | spindle pole body associated protein Snad, putative ( <i>T. verrucosum</i> ) | CAGGGTG      | 937 | UPRE-1 |
| TERG_12595 | ABC multidrug transporter SitT ( <i>T. tonsurans</i> )                       | CAGCGTG      | 58  | UPRE-1 |
| TERG_12596 | hypothetical protein   | CAGGGTG      | 936 | UPRE-1 |
| TERG_12597 | hypothetical protein   | CAGGGTG      | 151 | UPRE-1 |
| TERG_12598 | hypothetical protein   | CAGAGTG      | 600 | UPRE-1 |
| TERG_12599 | hypothetical protein   | CAGGGTG      | 154 | UPRE-1 |
| TERG_12603 | hypothetical protein   | CACTCTG (rc) | 202 | UPRE-1 |
| TERG_12606 | protease DPPV, putative ( <i>A. benhamiae</i> )                              | CACACTG (rc) | 281 | UPRE-1 |
| TERG_12614 | succinyl-CoA synthetase beta subunit, putative ( <i>T. verrucosum</i> )      | CAGAGTG      | 890 | UPRE-1 |
| TERG_12620 | hypothetical protein   | CAGAGTG      | 513 | UPRE-1 |
| TERG_12630 | nicotinamide nucleotide transhydrogenase ( <i>T. tonsurans</i> )             | CAGGGTG      | 711 | UPRE-1 |
| TERG_12647 | hypothetical protein   | CAGGGTG      | 435 | UPRE-1 |

|            |  |              |     |        |
|------------|--|--------------|-----|--------|
| TERG_12656 | endoribonuclease ysh1 ( <i>T. tonsurans</i> )                                  | CACTCTG (rc) | 383 | UPRE-1 |
| TERG_12672 | hypothetical protein   | CAGAGTG      | 136 | UPRE-1 |
| TERG_12672 | hypothetical protein   | CAGAGTG      | 458 | UPRE-1 |
| TERG_12673 | hypothetical protein   | CAGGGTG      | 282 | UPRE-1 |
| TERG_12684 | hypothetical protein   | CACGCTG (rc) | 380 | UPRE-1 |
| TERG_12688 | Cullin family protein ( <i>T. equinum</i> )                                    | CAGAGTG      | 963 | UPRE-1 |
| TERG_12692 | hypothetical protein   | CAGCGTG      | 944 | UPRE-1 |
| TERG_12704 | hypothetical protein   | CACACTG (rc) | 167 | UPRE-1 |
| TERG_12712 | hypothetical protein   | CACTCTG (rc) | 197 | UPRE-1 |
| TERG_12712 | hypothetical protein   | CACGCTG (rc) | 366 | UPRE-1 |
| TERG_12721 | transferase ( <i>M. canis</i> )  | CAGTGTG      | 188 | UPRE-1 |
| TERG_12725 | MFS transporter ( <i>T. equinum</i> )  | CAGTGTG      | 219 | UPRE-1 |
| TERG_12727 | cytochrome P450 monooxygenase GliC2 ( <i>T. equinum</i> )                      | CAGAGTG      | 554 | UPRE-1 |
| TERG_00009 | peroxisomal biogenesis factor ( <i>T. tonsurans</i> )                          | TACGTG       | 310 | UPRE-2 |
| TERG_00019 | mitochondrial Rho GTPase 1   | CACGTA (rc)  | 174 | UPRE-2 |
| TERG_00055 | essential cytoplasmic protein Ctr86 ( <i>T. equinum</i> )                      | TACGTG       | 100 | UPRE-2 |
| TERG_00057 | hypothetical protein   | CACGTA (rc)  | 677 | UPRE-2 |
| TERG_00061 | GDP-mannose pyrophosphorylase A ( <i>T. equinum</i> )                          | CACGTA (rc)  | 648 | UPRE-2 |
| TERG_00062 | dynamain GTPase, putative ( <i>T. verrucosum</i> )                             | TACGTG       | 368 | UPRE-2 |
| TERG_00063 | lysine-tRNA ligase   | TACGTG       | 121 | UPRE-2 |
| TERG_00065 | cytochrome c oxidase assembly protein COX15 ( <i>T. equinum</i> )              | CACGTA (rc)  | 748 | UPRE-2 |
| TERG_00073 | NADH-dependent flavin oxidoreductase, putative ( <i>T. verrucosum</i> )        | TACGTG       | 131 | UPRE-2 |
| TERG_00117 | SNF2 family helicase, putative ( <i>T. verrucosum</i> )                        | CACGTA (rc)  | 868 | UPRE-2 |
| TERG_00141 | DUF803 domain-containing protein ( <i>T. equinum</i> )                         | CACGTA (rc)  | 533 | UPRE-2 |
| TERG_00159 | hypothetical protein   | TACGTG       | 596 | UPRE-2 |
| TERG_00227 | glutamine amidotransferase subunit pdxT ( <i>T. equinum</i> )                  | TACGTG       | 731 | UPRE-2 |
| TERG_00250 | phosphoacetylglucosamine mutase ( <i>T. equinum</i> )                          | CACGTA (rc)  | 111 | UPRE-2 |
| TERG_00256 | 26S protease regulatory subunit 6A   | TACGTG       | 799 | UPRE-2 |
| TERG_00266 | hypothetical protein   | CACGTA (rc)  | 327 | UPRE-2 |
| TERG_00274 | mitochondrial methyltransferase (predicted) ( <i>A. benhamiae</i> )            | CACGTA (rc)  | 349 | UPRE-2 |
| TERG_00276 | TATA-box-binding protein   | CACGTA (rc)  | 379 | UPRE-2 |
| TERG_00278 | electron transfer flavoprotein-ubiquinone oxidoreductase ( <i>T. equinum</i> ) | TACGTG       | 187 | UPRE-2 |
| TERG_00292 | hypothetical protein   | CACGTA (rc)  | 926 | UPRE-2 |
| TERG_00310 | dolichol-phosphate mannosyltransferase ( <i>T. tonsurans</i> )                 | CACGTA (rc)  | 800 | UPRE-2 |
| TERG_00311 | hypothetical protein   | TACGTG       | 628 | UPRE-2 |

|            |  |             |     |        |
|------------|--|-------------|-----|--------|
| TERG_00322 | hypothetical protein   | CACGTA (rc) | 401 | UPRE-2 |
| TERG_00323 | DNA damage response protein ( <i>T. tonsurans</i> )                    | TACGTG      | 493 | UPRE-2 |
| TERG_00331 | golgi apparatus membrane protein TVP18 ( <i>T. tonsurans</i> )         | CACGTA (rc) | 244 | UPRE-2 |
| TERG_00340 | hypothetical protein   | TACGTG      | 145 | UPRE-2 |
| TERG_00357 | SNARE-dependent exocytosis protein ( <i>T. tonsurans</i> )             | TACGTG      | 354 | UPRE-2 |
| TERG_00357 | SNARE-dependent exocytosis protein ( <i>T. tonsurans</i> )             | TACGTG      | 842 | UPRE-2 |
| TERG_00372 | hypothetical protein   | CACGTA (rc) | 615 | UPRE-2 |
| TERG_00390 | AP-1 complex subunit gamma-1 ( <i>T. tonsurans</i> )                   | CACGTA (rc) | 144 | UPRE-2 |
| TERG_00417 | zinc-binding oxidoreductase, putative ( <i>A. benhamiae</i> )          | CACGTA (rc) | 92  | UPRE-2 |
| TERG_00417 | zinc-binding oxidoreductase, putative ( <i>A. benhamiae</i> )          | CACGTA (rc) | 209 | UPRE-2 |
| TERG_00474 | tRNA-specific adenosine deaminase ( <i>T. equinum</i> )                | TACGTG      | 518 | UPRE-2 |
| TERG_00504 | hypothetical protein   | CACGTA (rc) | 15  | UPRE-2 |
| TERG_00524 | trans-sialidase ( <i>M. canis</i> )                                    | CACGTA (rc) | 988 | UPRE-2 |
| TERG_00525 | NAK protein kinase   | TACGTG      | 93  | UPRE-2 |
| TERG_00548 | elongation factor 1-alpha  | CACGTA (rc) | 338 | UPRE-2 |
| TERG_00570 | autophagy protein ( <i>T. equinum</i> )                                | CACGTA (rc) | 627 | UPRE-2 |
| TERG_00577 | BAR domain-containing protein ( <i>T. tonsurans</i> )                  | CACGTA (rc) | 102 | UPRE-2 |
| TERG_00579 | glutathione S-transferase ( <i>T. tonsurans</i> )                      | TACGTG      | 525 | UPRE-2 |
| TERG_00579 | glutathione S-transferase ( <i>T. tonsurans</i> )                      | TACGTG      | 945 | UPRE-2 |
| TERG_00587 | nuclear pore complex protein sonA ( <i>T. equinum</i> )                | CACGTA (rc) | 875 | UPRE-2 |
| TERG_00596 | M protein repeat-containing protein ( <i>T. equinum</i> )              | TACGTG      | 713 | UPRE-2 |
| TERG_00608 | hypothetical protein   | CACGTA (rc) | 239 | UPRE-2 |
| TERG_00609 | ankyrin repeat protein ( <i>T. equinum</i> )                           | TACGTG      | 685 | UPRE-2 |
| TERG_00644 | ER membrane DUF1077 domain-containing protein ( <i>T. equinum</i> )    | CACGTA (rc) | 394 | UPRE-2 |
| TERG_00646 | integral membrane protein ( <i>T. verrucosum</i> )                     | TACGTG      | 850 | UPRE-2 |
| TERG_00651 | phosphatidylinositol 3-kinase ( <i>T. tonsurans</i> )                  | CACGTA (rc) | 802 | UPRE-2 |
| TERG_00669 | C-5 sterol desaturase ( <i>T. tonsurans</i> )                          | CACGTA (rc) | 305 | UPRE-2 |
| TERG_00670 | hypothetical protein   | TACGTG      | 195 | UPRE-2 |
| TERG_00681 | 5-oxoprolinase ( <i>T. tonsurans</i> )                                 | TACGTG      | 602 | UPRE-2 |
| TERG_00697 | nonribosomal siderophore peptide synthase SidC ( <i>A. benhamiae</i> ) | CACGTA (rc) | 480 | UPRE-2 |
| TERG_00707 | GPI anchored serine-threonine rich protein ( <i>T. verrucosum</i> )    | CACGTA (rc) | 373 | UPRE-2 |
| TERG_00725 | hypothetical protein   | TACGTG      | 924 | UPRE-2 |
| TERG_00738 | 60S ribosomal protein L44  | CACGTA (rc) | 115 | UPRE-2 |
| TERG_00740 | rds1 ( <i>T. equinum</i> )   | TACGTG      | 33  | UPRE-2 |



|            |   |             |     |        |
|------------|---|-------------|-----|--------|
| TERG_00746 | vacuolar carboxypeptidase Cps1, putative ( <i>A. benhamiae</i> )        | TACGTG      | 347 | UPRE-2 |
| TERG_00761 | homocitrate synthase ( <i>T. equinum</i> )                              | CACGTA (rc) | 163 | UPRE-2 |
| TERG_00761 | homocitrate synthase ( <i>T. equinum</i> )                              | CACGTA (rc) | 498 | UPRE-2 |
| TERG_00762 | vesicular-fusion protein SEC18 ( <i>M. gypseum</i> )                    | TACGTG      | 771 | UPRE-2 |
| TERG_00799 | Haloacid dehalogenase ( <i>T. tonsurans</i> )                           | CACGTA (rc) | 973 | UPRE-2 |
| TERG_00800 | hypothetical protein  | TACGTG      | 708 | UPRE-2 |
| TERG_00804 | U1 small nuclear ribonucleoprotein C ( <i>T. tonsurans</i> )            | CACGTA (rc) | 378 | UPRE-2 |
| TERG_00805 | benzoate 4-monooxygenase cytochrome P450 ( <i>T. equinum</i> )          | CACGTA (rc) | 516 | UPRE-2 |
| TERG_00809 | glycosyltransferase family 28 protein, putative ( <i>A. benhamiae</i> ) | CACGTA (rc) | 820 | UPRE-2 |
| TERG_00824 | neutral trehalase   | TACGTG      | 534 | UPRE-2 |
| TERG_00883 | acyl carrier protein  | CACGTA (rc) | 412 | UPRE-2 |
| TERG_00888 | hypothetical protein  | CACGTA (rc) | 744 | UPRE-2 |
| TERG_00900 | BCAS2 domain containing protein ( <i>T. equinum</i> )                   | TACGTG      | 317 | UPRE-2 |
| TERG_00929 | N-acetylglucosaminyl transferase component Gpi1 ( <i>T. tonsurans</i> ) | CACGTA (rc) | 131 | UPRE-2 |
| TERG_00940 | rRNA processing protein Utp6 ( <i>T. tonsurans</i> )                    | CACGTA (rc) | 699 | UPRE-2 |
| TERG_00954 | hypothetical protein  | TACGTG      | 888 | UPRE-2 |
| TERG_00955 | ABC drug exporter AtrF ( <i>T. verrucosum</i> )                         | TACGTG      | 515 | UPRE-2 |
| TERG_00957 | transporter sec-24 ( <i>T. equinum</i> )                                | CACGTA (rc) | 296 | UPRE-2 |
| TERG_00957 | transporter sec-24 ( <i>T. equinum</i> )                                | CACGTA (rc) | 454 | UPRE-2 |
| TERG_00993 | allantoinase ( <i>T. tonsurans</i> )                                    | CACGTA (rc) | 560 | UPRE-2 |
| TERG_00995 | hypothetical protein  | CACGTA (rc) | 63  | UPRE-2 |
| TERG_01010 | Leucine Rich Repeat domain protein ( <i>A. benhamiae</i> )              | CACGTA (rc) | 870 | UPRE-2 |
| TERG_01019 | hypothetical protein  | TACGTG      | 19  | UPRE-2 |
| TERG_01038 | hypothetical protein  | TACGTG      | 29  | UPRE-2 |
| TERG_01039 | DNA topoisomerase III ( <i>T. tonsurans</i> )                           | CACGTA (rc) | 791 | UPRE-2 |
| TERG_01040 | DUF1295 domain-containing protein ( <i>T. equinum</i> )                 | TACGTG      | 926 | UPRE-2 |
| TERG_01079 | prenyltransferase ( <i>T. equinum</i> )                                 | CACGTA (rc) | 180 | UPRE-2 |
| TERG_01080 | di-trans,poly-cis-decaprenylcistransferase                              | TACGTG      | 871 | UPRE-2 |
| TERG_01134 | metalloprotease MEP1 ( <i>A. benhamiae</i> )                            | TACGTG      | 393 | UPRE-2 |
| TERG_01157 | rhomboid family protein ( <i>T. tonsurans</i> )                         | TACGTG      | 8   | UPRE-2 |
| TERG_01198 | pre-mRNA-splicing factor rse1   | CACGTA (rc) | 350 | UPRE-2 |
| TERG_01241 | ClpTM1 domain-containing protein ( <i>T. tonsurans</i> )                | CACGTA (rc) | 588 | UPRE-2 |
| TERG_01250 | hypothetical protein  | TACGTG      | 271 | UPRE-2 |
| TERG_01261 | serine/threonine protein kinase   | CACGTA (rc) | 231 | UPRE-2 |
| TERG_01274 | mRNA export factor elf1 ( <i>T. equinum</i> )                           | TACGTG      | 538 | UPRE-2 |

|            |   |             |     |        |
|------------|---|-------------|-----|--------|
| TERG_01276 | amino acid permease family protein, putative ( <i>A. benhamiae</i> )              | TACGTG      | 136 | UPRE-2 |
| TERG_01277 | nexin-1 ( <i>T. equinum</i> )   | TACGTG      | 36  | UPRE-2 |
| TERG_01302 | lipase, putative ( <i>T. verrucosum</i> )   | TACGTG      | 119 | UPRE-2 |
| TERG_01346 | lipase/serine esterase ( <i>T. tonsurans</i> )                                    | TACGTG      | 174 | UPRE-2 |
| TERG_01349 | glutathione peroxidase ( <i>T. tonsurans</i> )                                    | TACGTG      | 468 | UPRE-2 |
| TERG_01354 | V-type proton ATPase proteolipid subunit  | TACGTG      | 278 | UPRE-2 |
| TERG_01369 | ubiquinol-cytochrome C reductase complex subunit UcrQ ( <i>T. tonsurans</i> )     | CACGTA (rc) | 90  | UPRE-2 |
| TERG_01371 | hypothetical protein  | TACGTG      | 86  | UPRE-2 |
| TERG_01377 | hypothetical protein  | CACGTA (rc) | 18  | UPRE-2 |
| TERG_01379 | serine/threonine-protein phosphatase 2A activator 2 ( <i>T. equinum</i> )         | TACGTG      | 334 | UPRE-2 |
| TERG_01401 | high affinity copper transporter ( <i>T. tonsurans</i> )                          | TACGTG      | 563 | UPRE-2 |
| TERG_01403 | serine/threonine-protein phosphatase  | TACGTG      | 146 | UPRE-2 |
| TERG_01405 | glutathione S-transferase ( <i>T. equinum</i> )                                   | TACGTG      | 62  | UPRE-2 |
| TERG_01418 | integral membrane protein, putative ( <i>T. verrucosum</i> )                      | TACGTG      | 913 | UPRE-2 |
| TERG_01437 | MFS transporter, putative ( <i>T. verrucosum</i> )                                | CACGTA (rc) | 365 | UPRE-2 |
| TERG_01455 | hypothetical protein  | TACGTG      | 726 | UPRE-2 |
| TERG_01468 | hypothetical protein  | CACGTA (rc) | 217 | UPRE-2 |
| TERG_01470 | serine/threonine protein kinase ( <i>M. canis</i> )                               | TACGTG      | 947 | UPRE-2 |
| TERG_01477 | cwl1 ( <i>M. gypseum</i> )  | CACGTA (rc) | 703 | UPRE-2 |
| TERG_01505 | hypothetical protein  | TACGTG      | 758 | UPRE-2 |
| TERG_01512 | mitochondrial tricarboxylate transporter (Ctp), putative ( <i>T. verrucosum</i> ) | TACGTG      | 307 | UPRE-2 |
| TERG_01520 | hypothetical protein  | TACGTG      | 692 | UPRE-2 |
| TERG_01522 | kinesin heavy chain   | TACGTG      | 679 | UPRE-2 |
| TERG_01537 | hypothetical protein  | CACGTA (rc) | 276 | UPRE-2 |
| TERG_01546 | oxidoreductase ( <i>T. tonsurans</i> )  | CACGTA (rc) | 594 | UPRE-2 |
| TERG_01547 | hypothetical protein  | CACGTA (rc) | 115 | UPRE-2 |
| TERG_01548 | DNA polymerase subunit delta-2 ( <i>T. tonsurans</i> )                            | TACGTG      | 80  | UPRE-2 |
| TERG_01555 | L-serine dehydratase, putative ( <i>T. verrucosum</i> )                           | TACGTG      | 188 | UPRE-2 |
| TERG_01560 | conserved eukaryotic protein ( <i>A. benhamiae</i> )                              | CACGTA (rc) | 166 | UPRE-2 |
| TERG_01579 | hypothetical protein  | TACGTG      | 903 | UPRE-2 |
| TERG_01588 | MAK11 ( <i>T. equinum</i> )   | CACGTA (rc) | 237 | UPRE-2 |
| TERG_01634 | MFS multidrug transporter, putative ( <i>T. verrucosum</i> )                      | TACGTG      | 395 | UPRE-2 |
| TERG_01645 | mitochondrial carrier protein ( <i>T. tonsurans</i> )                             | CACGTA (rc) | 385 | UPRE-2 |
| TERG_01674 | hypothetical protein  | CACGTA (rc) | 628 | UPRE-2 |

|            |  |             |     |        |
|------------|--|-------------|-----|--------|
| TERG_01675 | proteasome subunit alpha type-3 ( <i>T. tonsurans</i> )                              | TACGTG      | 164 | UPRE-2 |
| TERG_01694 | ankyrin repeat-containing protein ( <i>T. equinum</i> )                              | CACGTA (rc) | 756 | UPRE-2 |
| TERG_01709 | hypothetical protein   | TACGTG      | 268 | UPRE-2 |
| TERG_01738 | hypothetical protein   | CACGTA (rc) | 383 | UPRE-2 |
| TERG_01764 | rab6 ( <i>T. equinum</i> )   | CACGTA (rc) | 147 | UPRE-2 |
| TERG_01765 | V-ATPase proteolipid subunit Ppa1 ( <i>T. tonsurans</i> )                            | TACGTG      | 472 | UPRE-2 |
| TERG_01782 | hypothetical protein   | CACGTA (rc) | 212 | UPRE-2 |
| TERG_01786 | DENN domain-containing protein ( <i>T. tonsurans</i> )                               | TACGTG      | 967 | UPRE-2 |
| TERG_01793 | ATP-dependent RNA helicase DBP10   | TACGTG      | 188 | UPRE-2 |
| TERG_01798 | MATE efflux family protein subfamily, putative ( <i>T. verrucosum</i> )              | CACGTA (rc) | 261 | UPRE-2 |
| TERG_01812 | nucleolar complex protein 14 ( <i>T. equinum</i> )                                   | CACGTA (rc) | 356 | UPRE-2 |
| TERG_01815 | origin recognition complex subunit 3, putative ( <i>A. benhamiae</i> )               | TACGTG      | 720 | UPRE-2 |
| TERG_01857 | mitochondrial import inner membrane translocase subunit Tim9 ( <i>T. tonsurans</i> ) | TACGTG      | 97  | UPRE-2 |
| TERG_01871 | acetyl-CoA acetyltransferase ( <i>T. tonsurans</i> )                                 | CACGTA (rc) | 467 | UPRE-2 |
| TERG_01872 | polyketide synthase, putative ( <i>T. verrucosum</i> )                               | CACGTA (rc) | 633 | UPRE-2 |
| TERG_01915 | O-methyltransferase ( <i>A. benhamiae</i> )  | CACGTA (rc) | 628 | UPRE-2 |
| TERG_01931 | bis(5'-nucleosyl)-tetrphosphatase ( <i>T. equinum</i> )                              | CACGTA (rc) | 947 | UPRE-2 |
| TERG_01936 | COP9 signalosome complex subunit 1 ( <i>T. equinum</i> )                             | CACGTA (rc) | 637 | UPRE-2 |
| TERG_01936 | COP9 signalosome complex subunit 1 ( <i>T. equinum</i> )                             | CACGTA (rc) | 860 | UPRE-2 |
| TERG_01985 | hypothetical protein   | CACGTA (rc) | 668 | UPRE-2 |
| TERG_01986 | Fe-S protein assembly co-chaperone HscB  | CACGTA (rc) | 430 | UPRE-2 |
| TERG_01996 | serine/threonine protein kinase  | CACGTA (rc) | 115 | UPRE-2 |
| TERG_02025 | hypothetical protein   | TACGTG      | 900 | UPRE-2 |
| TERG_02046 | cysteine synthase ( <i>T. tonsurans</i> )  | CACGTA (rc) | 231 | UPRE-2 |
| TERG_02063 | hypothetical protein   | TACGTG      | 295 | UPRE-2 |
| TERG_02086 | exocyst complex component Sec10 ( <i>T. tonsurans</i> )                              | CACGTA (rc) | 485 | UPRE-2 |
| TERG_02138 | AGC protein kinase   | TACGTG      | 104 | UPRE-2 |
| TERG_02221 | proteasome component PRE3  | CACGTA (rc) | 119 | UPRE-2 |
| TERG_02245 | hypothetical protein   | TACGTG      | 55  | UPRE-2 |
| TERG_02272 | DUF323 domain-containing protein ( <i>T. equinum</i> )                               | TACGTG      | 716 | UPRE-2 |
| TERG_02282 | hypothetical protein   | TACGTG      | 611 | UPRE-2 |
| TERG_02299 | HET-C domain-containing protein ( <i>T. tonsurans</i> )                              | CACGTA (rc) | 977 | UPRE-2 |
| TERG_02304 | importin subunit beta-5 ( <i>T. equinum</i> )  | CACGTA (rc) | 236 | UPRE-2 |
| TERG_02317 | phosphatidylethanolamine N-methyltransferase   | TACGTG      | 92  | UPRE-2 |
| TERG_02327 | rRNA biogenesis protein RRP5 ( <i>T. tonsurans</i> )                                 | TACGTG      | 9   | UPRE-2 |
| TERG_02353 | UbiD family decarboxylase, putative ( <i>T. verrucosum</i> )                         | CACGTA (rc) | 642 | UPRE-2 |

|            |   |             |     |        |
|------------|---|-------------|-----|--------|
| TERG_02355 | hypothetical protein  | TACGTG      | 989 | UPRE-2 |
| TERG_02356 | hypothetical protein  | TACGTG      | 127 | UPRE-2 |
| TERG_02368 | extracellular developmental signal biosynthesis protein<br>FluG ( <i>A. benhamiae</i> ) | TACGTG      | 134 | UPRE-2 |
| TERG_02371 | hypothetical protein  | TACGTG      | 842 | UPRE-2 |
| TERG_02376 | 60S ribosomal protein ( <i>T. equinum</i> )   | CACGTA (rc) | 81  | UPRE-2 |
| TERG_02392 | MYB DNA-binding domain protein ( <i>T. verrucosum</i> )                                 | CACGTA (rc) | 555 | UPRE-2 |
| TERG_02405 | mating locus protein, putative ( <i>T. verrucosum</i> )                                 | CACGTA (rc) | 904 | UPRE-2 |
| TERG_02408 | DNA lyase ( <i>T. tonsurans</i> )   | CACGTA (rc) | 198 | UPRE-2 |
| TERG_02408 | DNA lyase ( <i>T. tonsurans</i> )   | CACGTA (rc) | 288 | UPRE-2 |
| TERG_02481 | F-box domain-containing protein ( <i>M. canis</i> )                                     | CACGTA (rc) | 317 | UPRE-2 |
| TERG_02497 | serine/threonine protein kinase ( <i>T. tonsurans</i> )                                 | TACGTG      | 110 | UPRE-2 |
| TERG_02538 | carboxylesterase ( <i>T. equinum</i> )  | TACGTG      | 479 | UPRE-2 |
| TERG_02556 | dynammin GTPase, putative ( <i>T. verrucosum</i> )                                      | TACGTG      | 458 | UPRE-2 |
| TERG_02572 | hypothetical protein  | CACGTA (rc) | 168 | UPRE-2 |
| TERG_02575 | hypothetical protein  | TACGTG      | 87  | UPRE-2 |
| TERG_02575 | hypothetical protein  | TACGTG      | 811 | UPRE-2 |
| TERG_02599 | dihydrolipoyl dehydrogenase   | TACGTG      | 335 | UPRE-2 |
| TERG_02611 | WD repeat protein ( <i>A. benhamiae</i> )   | CACGTA (rc) | 888 | UPRE-2 |
| TERG_02612 | DNA-directed RNA polymerase I, II, and III subunit<br>RPABC5                            | TACGTG      | 170 | UPRE-2 |
| TERG_02645 | hypothetical protein  | CACGTA (rc) | 117 | UPRE-2 |
| TERG_02649 | benzoate 4-monooxygenase cytochrome P450 ( <i>T. equinum</i> )                          | CACGTA (rc) | 131 | UPRE-2 |
| TERG_02650 | NmrA family protein ( <i>T. equinum</i> )   | CACGTA (rc) | 443 | UPRE-2 |
| TERG_02651 | NRPS-like enzyme, putative ( <i>A. benhamiae</i> )                                      | TACGTG      | 815 | UPRE-2 |
| TERG_02653 | hypothetical protein  | CACGTA (rc) | 576 | UPRE-2 |
| TERG_02714 | proteinase, putative ( <i>A. benhamiae</i> )  | CACGTA (rc) | 49  | UPRE-2 |
| TERG_02715 | beta-lactamase ( <i>T. equinum</i> )  | TACGTG      | 736 | UPRE-2 |
| TERG_02728 | 3-hydroxyisobutyrate dehydrogenase  | TACGTG      | 11  | UPRE-2 |
| TERG_02732 | hypothetical protein  | TACGTG      | 889 | UPRE-2 |
| TERG_02753 | E3 ubiquitin-protein ligase ubr1 ( <i>T. equinum</i> )                                  | TACGTG      | 536 | UPRE-2 |
| TERG_02763 | ankyrin and HET domain containing protein ( <i>T. equinum</i> )                         | CACGTA (rc) | 221 | UPRE-2 |
| TERG_02769 | RNP domain protein ( <i>A. benhamiae</i> )  | TACGTG      | 879 | UPRE-2 |
| TERG_02770 | hypothetical protein  | TACGTG      | 88  | UPRE-2 |
| TERG_02788 | DNA-directed RNA polymerase I ( <i>T. tonsurans</i> )                                   | TACGTG      | 603 | UPRE-2 |
| TERG_02802 | amino acid permease, putative ( <i>T. verrucosum</i> )                                  | TACGTG      | 289 | UPRE-2 |

|            |   |             |     |        |
|------------|---|-------------|-----|--------|
| TERG_02803 | 3-oxoacyl-(acyl-carrier-protein) reductase ( <i>T. verrucosum</i> )                   | TACGTG      | 844 | UPRE-2 |
| TERG_02823 | hypothetical protein  | TACGTG      | 16  | UPRE-2 |
| TERG_02829 | hypothetical protein  | TACGTG      | 388 | UPRE-2 |
| TERG_02830 | hypothetical protein  | CACGTA (rc) | 645 | UPRE-2 |
| TERG_02831 | C2H2 finger domain protein, putative ( <i>A. benhamiae</i> )                          | CACGTA (rc) | 100 | UPRE-2 |
| TERG_02848 | short chain dehydrogenase/reductase family protein ( <i>A. benhamiae</i> )            | TACGTG      | 594 | UPRE-2 |
| TERG_02849 | flavin-containing monooxygenase ( <i>T. equinum</i> )                                 | CACGTA (rc) | 40  | UPRE-2 |
| TERG_02854 | dynein light chain ( <i>T. tonsurans</i> )  | CACGTA (rc) | 42  | UPRE-2 |
| TERG_02883 | R3H domain protein, putative ( <i>T. verrucosum</i> )                                 | TACGTG      | 579 | UPRE-2 |
| TERG_02892 | hypothetical protein  | CACGTA (rc) | 423 | UPRE-2 |
| TERG_02900 | hypothetical protein  | CACGTA (rc) | 628 | UPRE-2 |
| TERG_02901 | N-acetyltransferase complex ARD1 subunit ( <i>T. tonsurans</i> )                      | TACGTG      | 729 | UPRE-2 |
| TERG_02929 | carboxylesterase, putative ( <i>T. verrucosum</i> )                                   | TACGTG      | 573 | UPRE-2 |
| TERG_02929 | carboxylesterase, putative ( <i>T. verrucosum</i> )                                   | TACGTG      | 693 | UPRE-2 |
| TERG_02972 | SRF-type transcription factor rlmA ( <i>T. equinum</i> )                              | CACGTA (rc) | 73  | UPRE-2 |
| TERG_02973 | morphogenesis protein (Msb1), putative ( <i>T. verrucosum</i> )                       | TACGTG      | 886 | UPRE-2 |
| TERG_02974 | hypothetical protein  | CACGTA (rc) | 962 | UPRE-2 |
| TERG_02977 | hypothetical protein  | CACGTA (rc) | 617 | UPRE-2 |
| TERG_02978 | FAD-dependent oxygenase ( <i>T. tonsurans</i> )                                       | TACGTG      | 491 | UPRE-2 |
| TERG_02987 | mitochondrial import inner membrane translocase subunit tim-17                        | TACGTG      | 496 | UPRE-2 |
| TERG_03004 | 3-methyl-2-oxobutanoate hydroxymethyltransferase                                      | CACGTA (rc) | 714 | UPRE-2 |
| TERG_03009 | hypothetical protein  | TACGTG      | 137 | UPRE-2 |
| TERG_03010 | SIR2 family histone deacetylase ( <i>T. tonsurans</i> )                               | TACGTG      | 482 | UPRE-2 |
| TERG_03041 | class E vacuolar protein-sorting machinery protein HSE1 ( <i>T. equinum</i> )         | CACGTA (rc) | 590 | UPRE-2 |
| TERG_03076 | centrin-binding protein Sfi1, putative ( <i>T. verrucosum</i> )                       | TACGTG      | 180 | UPRE-2 |
| TERG_03078 | cytochrome P450 oxidoreductase OrdA-like, putative ( <i>T. verrucosum</i> )           | CACGTA (rc) | 448 | UPRE-2 |
| TERG_03084 | pentatricopeptide repeat protein ( <i>A. benhamiae</i> )                              | TACGTG      | 382 | UPRE-2 |
| TERG_03095 | methyltransferase, putative ( <i>A. benhamiae</i> )                                   | TACGTG      | 523 | UPRE-2 |
| TERG_03096 | hypothetical protein  | TACGTG      | 955 | UPRE-2 |
| TERG_03118 | transcriptional corepressor of histone genes (Hir3), putative ( <i>A. benhamiae</i> ) | CACGTA (rc) | 73  | UPRE-2 |
| TERG_03177 | RING finger domain protein, putative ( <i>A. benhamiae</i> )                          | CACGTA (rc) | 577 | UPRE-2 |
| TERG_03179 | NlpC/P60-like cell-wall peptidase, putative ( <i>A. benhamiae</i> )                   | TACGTG      | 661 | UPRE-2 |

|            |   |             |     |        |
|------------|---|-------------|-----|--------|
| TERG_03183 | hypothetical protein  | TACGTG      | 191 | UPRE-2 |
| TERG_03194 | nonribosomal peptide synthase, putative ( <i>A. benhamiae</i> )                         | CACGTA (rc) | 704 | UPRE-2 |
| TERG_03203 | ELL complex subunit Eap30 ( <i>T. tonsurans</i> )                                       | CACGTA (rc) | 135 | UPRE-2 |
| TERG_03206 | hsp7-like protein   | CACGTA (rc) | 88  | UPRE-2 |
| TERG_03226 | glucosamine-6-phosphate deaminase   | CACGTA (rc) | 10  | UPRE-2 |
| TERG_03234 | DUF907 domain-containing protein ( <i>T. equinum</i> )                                  | TACGTG      | 181 | UPRE-2 |
| TERG_03242 | mitochondrial respiratory complex I chaperone (Cia84), putative ( <i>A. benhamiae</i> ) | CACGTA (rc) | 250 | UPRE-2 |
| TERG_03244 | WD repeat containing protein 2 ( <i>T. tonsurans</i> )                                  | TACGTG      | 504 | UPRE-2 |
| TERG_03248 | extracellular metalloproteinase 3   | TACGTG      | 651 | UPRE-2 |
| TERG_03250 | MFS monocarboxylate transporter ( <i>T. equinum</i> )                                   | TACGTG      | 927 | UPRE-2 |
| TERG_03258 | alkaline phosphatase ( <i>T. tonsurans</i> )  | CACGTA (rc) | 605 | UPRE-2 |
| TERG_03279 | C6 finger domain-containing protein ( <i>T. tonsurans</i> )                             | TACGTG      | 29  | UPRE-2 |
| TERG_03296 | coatomer subunit zeta ( <i>T. equinum</i> )   | CACGTA (rc) | 773 | UPRE-2 |
| TERG_03313 | fucose-specific lectin FleA ( <i>A. benhamiae</i> )                                     | TACGTG      | 915 | UPRE-2 |
| TERG_03323 | hypothetical protein  | TACGTG      | 421 | UPRE-2 |
| TERG_03323 | hypothetical protein  | TACGTG      | 427 | UPRE-2 |
| TERG_03328 | anaphase-promoting complex subunit ApcB ( <i>T. equinum</i> )                           | TACGTG      | 12  | UPRE-2 |
| TERG_03328 | anaphase-promoting complex subunit ApcB ( <i>T. equinum</i> )                           | TACGTG      | 99  | UPRE-2 |
| TERG_03337 | hypothetical protein  | CACGTA (rc) | 165 | UPRE-2 |
| TERG_03339 | alternative oxidase, mitochondrial  | TACGTG      | 378 | UPRE-2 |
| TERG_03350 | RecQ family helicase MusN ( <i>T. verrucosum</i> )                                      | CACGTA (rc) | 625 | UPRE-2 |
| TERG_03351 | kelch repeats protein ( <i>T. equinum</i> )   | TACGTG      | 962 | UPRE-2 |
| TERG_03352 | tyrosine decarboxylase ( <i>T. equinum</i> )  | CACGTA (rc) | 671 | UPRE-2 |
| TERG_03362 | KH domain RNA binding protein ( <i>T. tonsurans</i> )                                   | TACGTG      | 668 | UPRE-2 |
| TERG_03365 | hypothetical protein  | TACGTG      | 180 | UPRE-2 |
| TERG_03379 | AGC/NDR/NDR protein kinase  | CACGTA (rc) | 892 | UPRE-2 |
| TERG_03382 | ThiJ/PfpI family protein ( <i>A. benhamiae</i> )  | TACGTG      | 507 | UPRE-2 |
| TERG_03388 | hypothetical protein  | TACGTG      | 767 | UPRE-2 |
| TERG_03389 | orotidine 5'-phosphate decarboxylase  | TACGTG      | 219 | UPRE-2 |
| TERG_03391 | diacylglycerol O-acyltransferase ( <i>T. equinum</i> )                                  | CACGTA (rc) | 906 | UPRE-2 |
| TERG_03406 | hypothetical protein  | CACGTA (rc) | 461 | UPRE-2 |
| TERG_03427 | peptidyl-prolyl cis-trans isomerase ( <i>T. tonsurans</i> )                             | CACGTA (rc) | 374 | UPRE-2 |
| TERG_03441 | hypothetical protein  | TACGTG      | 247 | UPRE-2 |
| TERG_03493 | hypothetical protein  | CACGTA (rc) | 444 | UPRE-2 |

|            |  |             |     |        |
|------------|--|-------------|-----|--------|
| TERG_03493 | hypothetical protein   | CACGTA (rc) | 596 | UPRE-2 |
| TERG_03495 | vesicular-fusion protein SEC17 ( <i>T. equinum</i> )                     | CACGTA (rc) | 469 | UPRE-2 |
| TERG_03501 | PtaB protein ( <i>T. tonsurans</i> )                                     | CACGTA (rc) | 771 | UPRE-2 |
| TERG_03502 | AAA-type ATPase ( <i>T. equinum</i> )                                    | TACGTG      | 162 | UPRE-2 |
| TERG_03554 | hypothetical protein   | TACGTG      | 972 | UPRE-2 |
| TERG_03561 | short chain dehydrogenase/reductase ( <i>M. canis</i> )                  | TACGTG      | 221 | UPRE-2 |
| TERG_03581 | DNA mismatch repair protein ( <i>T. tonsurans</i> )                      | TACGTG      | 95  | UPRE-2 |
| TERG_03587 | WD repeat protein ( <i>T. verrucosum</i> )                               | TACGTG      | 759 | UPRE-2 |
| TERG_03603 | cytochrome c oxidase assembly protein ( <i>T. tonsurans</i> )            | TACGTG      | 366 | UPRE-2 |
| TERG_03622 | hypothetical protein   | CACGTA (rc) | 64  | UPRE-2 |
| TERG_03628 | serine/threonine protein kinase ( <i>T. tonsurans</i> )                  | TACGTG      | 395 | UPRE-2 |
| TERG_03675 | hypothetical protein   | CACGTA (rc) | 967 | UPRE-2 |
| TERG_03690 | hypothetical protein   | TACGTG      | 229 | UPRE-2 |
| TERG_03704 | integral membrane protein Pth11-like, putative ( <i>T. verrucosum</i> )  | CACGTA (rc) | 845 | UPRE-2 |
| TERG_03711 | histone acetyltransferase type B catalytic subunit ( <i>T. equinum</i> ) | CACGTA (rc) | 325 | UPRE-2 |
| TERG_03729 | 6-phosphogluconate dehydrogenase (decarboxylating)                       | CACGTA (rc) | 73  | UPRE-2 |
| TERG_03731 | C6 transcription factor ( <i>T. equinum</i> )                            | TACGTG      | 122 | UPRE-2 |
| TERG_03738 | 60S ribosomal protein L3   | TACGTG      | 37  | UPRE-2 |
| TERG_03739 | hypothetical protein   | TACGTG      | 522 | UPRE-2 |
| TERG_03750 | small nuclear ribonucleoprotein ( <i>T. tonsurans</i> )                  | CACGTA (rc) | 225 | UPRE-2 |
| TERG_03752 | hypothetical protein   | TACGTG      | 240 | UPRE-2 |
| TERG_03772 | hypothetical protein   | CACGTA (rc) | 280 | UPRE-2 |
| TERG_03791 | NADH-ubiquinone oxidoreductase 20 kDa subunit ( <i>T. equinum</i> )      | TACGTG      | 896 | UPRE-2 |
| TERG_03813 | hexose transporter protein ( <i>A. benhamiae</i> )                       | TACGTG      | 233 | UPRE-2 |
| TERG_03815 | subtilisin-like protease 3   | TACGTG      | 745 | UPRE-2 |
| TERG_03850 | hypothetical protein   | TACGTG      | 45  | UPRE-2 |
| TERG_03877 | cytochrome P450 monooxygenase, putative ( <i>T. verrucosum</i> )         | TACGTG      | 894 | UPRE-2 |
| TERG_03879 | cell wall biogenesis protein Mhp1, putative ( <i>T. verrucosum</i> )     | CACGTA (rc) | 548 | UPRE-2 |
| TERG_03884 | hypothetical protein   | CACGTA (rc) | 402 | UPRE-2 |
| TERG_03885 | hypothetical protein   | TACGTG      | 298 | UPRE-2 |
| TERG_03903 | DUF6 domain-containing protein ( <i>T. equinum</i> )                     | CACGTA (rc) | 594 | UPRE-2 |
| TERG_03904 | aflatoxin B1 aldehyde reductase member 2 ( <i>T. tonsurans</i> )         | TACGTG      | 27  | UPRE-2 |
| TERG_03907 | neutral amino acid permease ( <i>T. tonsurans</i> )                      | TACGTG      | 42  | UPRE-2 |

|            |   |             |     |        |
|------------|---|-------------|-----|--------|
| TERG_03927 | leucine permease transcriptional regulator (SAC3), putative ( <i>A. benhamiae</i> )       | CACGTA (rc) | 531 | UPRE-2 |
| TERG_03967 | THO complex protein subunit 2 ( <i>T. equinum</i> )                                       | CACGTA (rc) | 114 | UPRE-2 |
| TERG_03970 | DUF636 domain-containing protein ( <i>T. equinum</i> )                                    | TACGTG      | 540 | UPRE-2 |
| TERG_04035 | hypothetical protein  | CACGTA (rc) | 705 | UPRE-2 |
| TERG_04052 | hypothetical protein  | TACGTG      | 173 | UPRE-2 |
| TERG_04054 | hypothetical protein  | TACGTG      | 268 | UPRE-2 |
| TERG_04061 | ribosome biogenesis GTPase Lsg1 ( <i>T. tonsurans</i> )                                   | TACGTG      | 257 | UPRE-2 |
| TERG_04063 | CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase ( <i>T. tonsurans</i> ) | CACGTA (rc) | 526 | UPRE-2 |
| TERG_04064 | NADH-ubiquinone oxidoreductase subunit ( <i>T. tonsurans</i> )                            | TACGTG      | 690 | UPRE-2 |
| TERG_04068 | cytochrome P450 monooxygenase, putative ( <i>A. benhamiae</i> )                           | TACGTG      | 542 | UPRE-2 |
| TERG_04072 | SNF2 family helicase/ATPase, putative ( <i>T. verrucosum</i> )                            | CACGTA (rc) | 465 | UPRE-2 |
| TERG_04073 | glutathione synthetase  | TACGTG      | 255 | UPRE-2 |
| TERG_04080 | transcription elongation factor spt4  | CACGTA (rc) | 871 | UPRE-2 |
| TERG_04081 | serine/threonine protein phosphatase PPT1 ( <i>T. tonsurans</i> )                         | TACGTG      | 726 | UPRE-2 |
| TERG_04087 | DnaJ domain-containing protein ( <i>T. tonsurans</i> )                                    | TACGTG      | 42  | UPRE-2 |
| TERG_04131 | heat shock trehalose synthase, putative ( <i>T. verrucosum</i> )                          | TACGTG      | 894 | UPRE-2 |
| TERG_04139 | hypothetical protein  | CACGTA (rc) | 729 | UPRE-2 |
| TERG_04142 | cofilin ( <i>T. equinum</i> )   | TACGTG      | 891 | UPRE-2 |
| TERG_04146 | FAD/FMN-containing isoamyl alcohol oxidase MreA-like, putative ( <i>A. benhamiae</i> )    | TACGTG      | 399 | UPRE-2 |
| TERG_04160 | hypothetical protein  | CACGTA (rc) | 608 | UPRE-2 |
| TERG_04160 | hypothetical protein  | CACGTA (rc) | 908 | UPRE-2 |
| TERG_04182 | MFS multidrug transporter ( <i>T. tonsurans</i> )   | CACGTA (rc) | 418 | UPRE-2 |
| TERG_04204 | hypothetical protein  | CACGTA (rc) | 801 | UPRE-2 |
| TERG_04235 | WW domain-containing protein ( <i>T. tonsurans</i> )                                      | TACGTG      | 64  | UPRE-2 |
| TERG_04236 | ankyrin repeat protein ( <i>T. tonsurans</i> )  | TACGTG      | 801 | UPRE-2 |
| TERG_04255 | hypothetical protein  | TACGTG      | 963 | UPRE-2 |
| TERG_04265 | palmitoyltransferase pfa5 ( <i>T. equinum</i> )   | TACGTG      | 365 | UPRE-2 |
| TERG_04283 | hypothetical protein  | TACGTG      | 760 | UPRE-2 |
| TERG_04324 | extracellular metalloproteinase 4   | CACGTA (rc) | 160 | UPRE-2 |
| TERG_04324 | extracellular metalloproteinase 4   | CACGTA (rc) | 583 | UPRE-2 |
| TERG_04370 | hypothetical protein  | CACGTA (rc) | 502 | UPRE-2 |
| TERG_04371 | hypothetical protein  | TACGTG      | 468 | UPRE-2 |



|            |  |             |     |        |
|------------|--|-------------|-----|--------|
| TERG_04374 | STE/STE20/YSK protein kinase   | CACGTA (rc) | 118 | UPRE-2 |
| TERG_04416 | penicillolysin/deuterolysin metalloprotease, putative ( <i>A. benhamiae</i> )                    | TACGTG      | 47  | UPRE-2 |
| TERG_04421 | hypothetical protein   | TACGTG      | 782 | UPRE-2 |
| TERG_04437 | nucleolar protein NOP2 ( <i>T. tonsurans</i> )   | TACGTG      | 627 | UPRE-2 |
| TERG_04438 | GDP-mannose transporter 1  | TACGTG      | 973 | UPRE-2 |
| TERG_04443 | lipase/esterase, putative ( <i>A. benhamiae</i> )  | CACGTA (rc) | 565 | UPRE-2 |
| TERG_04452 | cell cycle control protein ( <i>T. tonsurans</i> )   | CACGTA (rc) | 160 | UPRE-2 |
| TERG_04457 | POS9-activating factor FAP7 ( <i>T. tonsurans</i> )  | TACGTG      | 95  | UPRE-2 |
| TERG_04458 | RdgB/HAM1 family non-canonical purine NTP pyrophosphatase  | CACGTA (rc) | 470 | UPRE-2 |
| TERG_04459 | class V myosin ( <i>T. tonsurans</i> )   | CACGTA (rc) | 974 | UPRE-2 |
| TERG_04464 | hypothetical protein   | CACGTA (rc) | 491 | UPRE-2 |
| TERG_04502 | impact family protein ( <i>T. equinum</i> )  | TACGTG      | 690 | UPRE-2 |
| TERG_04506 | 60S ribosomal protein L4-A ( <i>T. tonsurans</i> )   | TACGTG      | 929 | UPRE-2 |
| TERG_04508 | AAA ATPase ( <i>T. equinum</i> )   | TACGTG      | 422 | UPRE-2 |
| TERG_04515 | WD domain-containing protein ( <i>T. tonsurans</i> )   | TACGTG      | 852 | UPRE-2 |
| TERG_04553 | thymidylate kinase   | CACGTA (rc) | 544 | UPRE-2 |
| TERG_04576 | CRAL/TRIO domain protein ( <i>T. verrucosum</i> )  | CACGTA (rc) | 859 | UPRE-2 |
| TERG_04616 | hypothetical protein   | TACGTG      | 432 | UPRE-2 |
| TERG_04666 | hypothetical protein   | TACGTG      | 682 | UPRE-2 |
| TERG_04713 | cystathionine beta-synthase ( <i>T. tonsurans</i> )  | CACGTA (rc) | 405 | UPRE-2 |
| TERG_04739 | 3-ketoacyl-CoA reductase   | CACGTA (rc) | 373 | UPRE-2 |
| TERG_04746 | nucleolar GTP-binding protein ( <i>T. tonsurans</i> )  | TACGTG      | 373 | UPRE-2 |
| TERG_04810 | bifunctional fatty acid transporter/acyl-CoA synthetase (FAT1), putative ( <i>A. benhamiae</i> ) | TACGTG      | 251 | UPRE-2 |
| TERG_04828 | IZH family channel protein ( <i>T. tonsurans</i> )   | CACGTA (rc) | 377 | UPRE-2 |
| TERG_04828 | IZH family channel protein ( <i>T. tonsurans</i> )   | CACGTA (rc) | 538 | UPRE-2 |
| TERG_04881 | hypothetical protein   | CACGTA (rc) | 773 | UPRE-2 |
| TERG_04891 | ubiquitin-protein ligase E3C ( <i>T. equinum</i> )   | TACGTG      | 828 | UPRE-2 |
| TERG_04896 | GARP complex subunit (Sac2), putative ( <i>T. verrucosum</i> )                                   | CACGTA (rc) | 352 | UPRE-2 |
| TERG_04923 | dynactin ( <i>T. equinum</i> )   | TACGTG      | 299 | UPRE-2 |
| TERG_04931 | allantoate permease ( <i>T. equinum</i> )  | CACGTA (rc) | 189 | UPRE-2 |
| TERG_04938 | hypothetical protein   | TACGTG      | 984 | UPRE-2 |
| TERG_04954 | hypothetical protein   | TACGTG      | 13  | UPRE-2 |
| TERG_04960 | glutathione S-transferase Ure2-like, putative ( <i>A. benhamiae</i> )                            | TACGTG      | 298 | UPRE-2 |
| TERG_04960 | glutathione S-transferase Ure2-like, putative ( <i>A. benhamiae</i> )                            | TACGTG      | 679 | UPRE-2 |

|            |  |             |     |        |
|------------|--|-------------|-----|--------|
| TERG_04980 | RNA exonuclease, putative ( <i>A. benhamiae</i> )  | CACGTA (rc) | 6   | UPRE-2 |
| TERG_04980 | RNA exonuclease, putative ( <i>A. benhamiae</i> )  | CACGTA (rc) | 392 | UPRE-2 |
| TERG_04985 | ATP synthase subunit F ( <i>T. tonsurans</i> )   | CACGTA (rc) | 889 | UPRE-2 |
| TERG_04986 | NADH-ubiquinone oxidoreductase 18 kDa subunit ( <i>T. tonsurans</i> )                          | TACGTG      | 941 | UPRE-2 |
| TERG_05024 | phosphomevalonate kinase ( <i>T. tonsurans</i> )   | TACGTG      | 500 | UPRE-2 |
| TERG_05026 | hypothetical protein   | TACGTG      | 276 | UPRE-2 |
| TERG_05057 | DUF775 domain-containing protein ( <i>T. equinum</i> )   | CACGTA (rc) | 14  | UPRE-2 |
| TERG_05077 | D-amino-acid oxidase ( <i>T. equinum</i> )   | CACGTA (rc) | 816 | UPRE-2 |
| TERG_05083 | adaptin ear-binding coat-associated protein 1 ( <i>M. canis</i> )                              | CACGTA (rc) | 120 | UPRE-2 |
| TERG_05174 | acetyltransferase, GNAT family ( <i>T. verrucosum</i> )  | CACGTA (rc) | 669 | UPRE-2 |
| TERG_05185 | RING finger ubiquitin ligase ( <i>T. tonsurans</i> )   | CACGTA (rc) | 617 | UPRE-2 |
| TERG_05208 | transcription factor iws1  | CACGTA (rc) | 208 | UPRE-2 |
| TERG_05263 | CCCH zinc finger DNA binding protein ( <i>A. benhamiae</i> )                                   | CACGTA (rc) | 873 | UPRE-2 |
| TERG_05264 | signal sequence receptor alpha chain ( <i>T. equinum</i> )                                     | TACGTG      | 852 | UPRE-2 |
| TERG_05265 | DEAD/DEAH box helicase ( <i>T. tonsurans</i> )   | CACGTA (rc) | 116 | UPRE-2 |
| TERG_05292 | hypothetical protein   | TACGTG      | 706 | UPRE-2 |
| TERG_05294 | hypothetical protein   | CACGTA (rc) | 825 | UPRE-2 |
| TERG_05295 | TFIIIC transcription initiation factor complex subunits Tfc3, putative ( <i>A. benhamiae</i> ) | TACGTG      | 689 | UPRE-2 |
| TERG_05318 | polyphosphoinositide phosphatase ( <i>T. tonsurans</i> )                                       | TACGTG      | 242 | UPRE-2 |
| TERG_05328 | pre-rRNA-processing protein ESF2 ( <i>T. tonsurans</i> )                                       | TACGTG      | 148 | UPRE-2 |
| TERG_05328 | pre-rRNA-processing protein ESF2 ( <i>T. tonsurans</i> )                                       | TACGTG      | 202 | UPRE-2 |
| TERG_05333 | DDT domain-containing protein ( <i>T. tonsurans</i> )  | CACGTA (rc) | 329 | UPRE-2 |
| TERG_05347 | epoxide hydrolase, putative ( <i>T. verrucosum</i> )   | CACGTA (rc) | 84  | UPRE-2 |
| TERG_05363 | hypothetical protein   | TACGTG      | 98  | UPRE-2 |
| TERG_05440 | hypothetical protein   | CACGTA (rc) | 289 | UPRE-2 |
| TERG_05441 | cytochrome P450 alkane hydroxylase, putative ( <i>T. verrucosum</i> )                          | TACGTG      | 908 | UPRE-2 |
| TERG_05483 | transcription elongation factor spt5 ( <i>M. gypseum</i> )                                     | CACGTA (rc) | 53  | UPRE-2 |
| TERG_05510 | DUF858 domain protein ( <i>T. verrucosum</i> )   | TACGTG      | 516 | UPRE-2 |
| TERG_05529 | telomere length regulator protein (Rif1), putative ( <i>A. benhamiae</i> )                     | CACGTA (rc) | 798 | UPRE-2 |
| TERG_05532 | monosaccharide transporter ( <i>T. tonsurans</i> )   | TACGTG      | 644 | UPRE-2 |
| TERG_05534 | hypothetical protein   | CACGTA (rc) | 190 | UPRE-2 |
| TERG_05537 | MFS multidrug transporter ( <i>T. equinum</i> )  | CACGTA (rc) | 801 | UPRE-2 |
| TERG_05554 | integral membrane protein ( <i>T. equinum</i> )  | CACGTA (rc) | 306 | UPRE-2 |
| TERG_05588 | NRPS-like enzyme, putative ( <i>A. benhamiae</i> )   | TACGTG      | 908 | UPRE-2 |

|            |  |             |     |        |
|------------|--|-------------|-----|--------|
| TERG_05605 | Hrq1p ( <i>M. gypseum</i> )  | CACGTA (rc) | 672 | UPRE-2 |
| TERG_05606 | hypothetical protein   | TACGTG      | 831 | UPRE-2 |
| TERG_05615 | hsp70-like protein ( <i>T. equinum</i> )                                       | CACGTA (rc) | 271 | UPRE-2 |
| TERG_05634 | mitochondrial protein ( <i>T. tonsurans</i> )                                  | CACGTA (rc) | 68  | UPRE-2 |
| TERG_05634 | mitochondrial protein ( <i>T. tonsurans</i> )                                  | CACGTA (rc) | 76  | UPRE-2 |
| TERG_05637 | 4'-phosphopantetheinyl transferase superfamily protein ( <i>T. tonsurans</i> ) | TACGTG      | 599 | UPRE-2 |
| TERG_05644 | mucin family signaling protein Msb2, putative ( <i>T. verrucosum</i> )         | CACGTA (rc) | 78  | UPRE-2 |
| TERG_05645 | vacuolar protein sorting protein Vps36 ( <i>T. tonsurans</i> )                 | CACGTA (rc) | 428 | UPRE-2 |
| TERG_05681 | actin ( <i>T. tonsurans</i> )  | CACGTA (rc) | 137 | UPRE-2 |
| TERG_05708 | decapping enzyme Dcp1 ( <i>T. tonsurans</i> )                                  | TACGTG      | 70  | UPRE-2 |
| TERG_05716 | PAP/25A associated domain-containing protein ( <i>T. equinum</i> )             | TACGTG      | 675 | UPRE-2 |
| TERG_05767 | dynein light chain ( <i>T. equinum</i> )                                       | CACGTA (rc) | 174 | UPRE-2 |
| TERG_05771 | hypothetical protein   | CACGTA (rc) | 358 | UPRE-2 |
| TERG_05799 | chlorophyll synthesis pathway protein BchC                                     | CACGTA (rc) | 687 | UPRE-2 |
| TERG_05800 | ubiquitin-protein ligase (Hul4), putative ( <i>A. benhamiae</i> )              | CACGTA (rc) | 425 | UPRE-2 |
| TERG_05806 | methionine aminopeptidase, type I  | CACGTA (rc) | 200 | UPRE-2 |
| TERG_05807 | kynurenine 3-monooxygenase ( <i>T. tonsurans</i> )                             | TACGTG      | 226 | UPRE-2 |
| TERG_05817 | hypothetical protein   | TACGTG      | 172 | UPRE-2 |
| TERG_05836 | hypothetical protein   | TACGTG      | 294 | UPRE-2 |
| TERG_05840 | hypothetical protein   | CACGTA (rc) | 740 | UPRE-2 |
| TERG_05841 | AmmeMemoRadiSam system protein B   | TACGTG      | 298 | UPRE-2 |
| TERG_05897 | CoA-binding protein ( <i>T. equinum</i> )                                      | CACGTA (rc) | 126 | UPRE-2 |
| TERG_05906 | serine/threonine protein kinase  | CACGTA (rc) | 167 | UPRE-2 |
| TERG_05917 | MOSC domain protein ( <i>A. benhamiae</i> )                                    | CACGTA (rc) | 18  | UPRE-2 |
| TERG_05924 | transcription factor TFIIIB complex subunit brf1 ( <i>M. gypseum</i> )         | TACGTG      | 217 | UPRE-2 |
| TERG_05938 | tetratricopeptide repeat domain-containing protein ( <i>T. equinum</i> )       | TACGTG      | 139 | UPRE-2 |
| TERG_05962 | phosphotransferase ( <i>M. canis</i> )   | TACGTG      | 58  | UPRE-2 |
| TERG_05964 | hypothetical protein   | TACGTG      | 449 | UPRE-2 |
| TERG_05991 | hypothetical protein   | CACGTA (rc) | 44  | UPRE-2 |
| TERG_06019 | hypothetical protein   | TACGTG      | 502 | UPRE-2 |
| TERG_06031 | meiotic recombination protein DLH1   | TACGTG      | 50  | UPRE-2 |
| TERG_06081 | hypothetical protein   | TACGTG      | 424 | UPRE-2 |
| TERG_06128 | phosphoribosylglycinamide formyltransferase                                    | CACGTA (rc) | 261 | UPRE-2 |
| TERG_06155 | phosphotransferase ( <i>T. tonsurans</i> )                                     | CACGTA (rc) | 851 | UPRE-2 |

|            |  |             |     |        |
|------------|--|-------------|-----|--------|
| TERG_06180 | endonuclease/exonuclease/phosphatase family protein ( <i>T. verrucosum</i> ) | TACGTG      | 700 | UPRE-2 |
| TERG_06249 | hypothetical protein   | CACGTA (rc) | 256 | UPRE-2 |
| TERG_06266 | hypothetical protein   | TACGTG      | 326 | UPRE-2 |
| TERG_06322 | alpha-1,2-mannosyltransferase ( <i>T. tonsurans</i> )                        | CACGTA (rc) | 181 | UPRE-2 |
| TERG_06367 | SH3 domain protein, putative ( <i>A. benhamiae</i> )                         | TACGTG      | 867 | UPRE-2 |
| TERG_06414 | DUF1338 domain-containing protein ( <i>T. equinum</i> )                      | TACGTG      | 422 | UPRE-2 |
| TERG_06449 | CCAAT-binding factor complex subunit HapE ( <i>T. tonsurans</i> )            | CACGTA (rc) | 984 | UPRE-2 |
| TERG_06465 | O-mannosyl transferase pmtA-Aspergillus niger ( <i>T. equinum</i> )          | TACGTG      | 594 | UPRE-2 |
| TERG_06492 | hypothetical protein   | TACGTG      | 285 | UPRE-2 |
| TERG_06500 | mitochondrial GTP/GDP carrier protein 1                                      | CACGTA (rc) | 613 | UPRE-2 |
| TERG_06501 | hypothetical protein   | TACGTG      | 605 | UPRE-2 |
| TERG_06510 | hypothetical protein   | CACGTA (rc) | 108 | UPRE-2 |
| TERG_06532 | chitin synthase export chaperone ( <i>M. gypseum</i> )                       | TACGTG      | 242 | UPRE-2 |
| TERG_06536 | tRNA-specific adenosine-34 deaminase subunit Tad3 ( <i>T. equinum</i> )      | CACGTA (rc) | 71  | UPRE-2 |
| TERG_06540 | glutathione transferase ( <i>T. tonsurans</i> )                              | CACGTA (rc) | 288 | UPRE-2 |
| TERG_06541 | hypothetical protein   | TACGTG      | 922 | UPRE-2 |
| TERG_06565 | protein kinase subdomain-containing protein ( <i>T. equinum</i> )            | CACGTA (rc) | 399 | UPRE-2 |
| TERG_06584 | hypothetical protein   | TACGTG      | 425 | UPRE-2 |
| TERG_06590 | ABC1 ( <i>T. equinum</i> )   | CACGTA (rc) | 81  | UPRE-2 |
| TERG_06591 | urease accessory protein UreF ( <i>T. tonsurans</i> )                        | TACGTG      | 650 | UPRE-2 |
| TERG_06607 | serine-rich protein, putative ( <i>T. verrucosum</i> )                       | CACGTA (rc) | 913 | UPRE-2 |
| TERG_06630 | proteasome component PRE5 ( <i>T. equinum</i> )                              | CACGTA (rc) | 210 | UPRE-2 |
| TERG_06653 | conserved serine-rich protein ( <i>T. verrucosum</i> )                       | CACGTA (rc) | 938 | UPRE-2 |
| TERG_06683 | hypothetical protein   | CACGTA (rc) | 490 | UPRE-2 |
| TERG_06684 | molybdenum cofactor biosynthetic protein ( <i>T. equinum</i> )               | TACGTG      | 964 | UPRE-2 |
| TERG_06714 | hypothetical protein   | CACGTA (rc) | 980 | UPRE-2 |
| TERG_06715 | LEA domain protein ( <i>A. benhamiae</i> )                                   | TACGTG      | 283 | UPRE-2 |
| TERG_06778 | PAP2 domain protein ( <i>T. verrucosum</i> )                                 | CACGTA (rc) | 573 | UPRE-2 |
| TERG_06785 | cytochrome P450 monooxygenase ( <i>T. equinum</i> )                          | TACGTG      | 489 | UPRE-2 |
| TERG_06798 | hypothetical protein   | TACGTG      | 649 | UPRE-2 |
| TERG_06801 | cyclic nucleotide-binding domain-containing protein ( <i>T. tonsurans</i> )  | TACGTG      | 778 | UPRE-2 |
| TERG_06833 | hypothetical protein   | TACGTG      | 294 | UPRE-2 |
| TERG_06844 | 40S ribosomal protein S21  | CACGTA (rc) | 47  | UPRE-2 |

|            |   |             |     |        |
|------------|---|-------------|-----|--------|
| TERG_06859 | exosome complex endonuclease 1/ribosomal RNA processing protein ( <i>T. equinum</i> ) | CACGTA (rc) | 395 | UPRE-2 |
| TERG_06872 | hypothetical protein  | CACGTA (rc) | 272 | UPRE-2 |
| TERG_06872 | hypothetical protein  | CACGTA (rc) | 437 | UPRE-2 |
| TERG_06884 | C6 transcription factor (War1), putative ( <i>T. verrucosum</i> )                     | CACGTA (rc) | 308 | UPRE-2 |
| TERG_06890 | DUF636 domain protein ( <i>T. verrucosum</i> )  | CACGTA (rc) | 474 | UPRE-2 |
| TERG_06891 | C6 transcription factor, putative ( <i>T. verrucosum</i> )                            | TACGTG      | 808 | UPRE-2 |
| TERG_06926 | chitosanase ( <i>T. equinum</i> )   | CACGTA (rc) | 531 | UPRE-2 |
| TERG_06929 | chitinase ( <i>T. equinum</i> )   | CACGTA (rc) | 822 | UPRE-2 |
| TERG_06955 | hypothetical protein  | CACGTA (rc) | 548 | UPRE-2 |
| TERG_06956 | RNA polymerase I-specific transcription initiation factor rrn3 ( <i>M. gypseum</i> )  | TACGTG      | 246 | UPRE-2 |
| TERG_06963 | hsp90-like protein  | TACGTG      | 804 | UPRE-2 |
| TERG_06971 | hypothetical protein  | CACGTA (rc) | 508 | UPRE-2 |
| TERG_06980 | hypothetical protein  | CACGTA (rc) | 291 | UPRE-2 |
| TERG_07012 | rRNA 2'-O-methyltransferase fibrillarin   | TACGTG      | 457 | UPRE-2 |
| TERG_07033 | glycerophosphodiesterase GDE1 ( <i>T. equinum</i> )                                   | TACGTG      | 17  | UPRE-2 |
| TERG_07035 | hypothetical protein  | TACGTG      | 690 | UPRE-2 |
| TERG_07057 | Hsp70 family chaperone, putative ( <i>A. benhamiae</i> )                              | TACGTG      | 619 | UPRE-2 |
| TERG_07060 | acyl-CoA thioesterase II  | CACGTA (rc) | 148 | UPRE-2 |
| TERG_07062 | Ser/Thr protein phosphatase family protein ( <i>T. verrucosum</i> )                   | TACGTG      | 839 | UPRE-2 |
| TERG_07062 | Ser/Thr protein phosphatase family protein ( <i>T. verrucosum</i> )                   | TACGTG      | 899 | UPRE-2 |
| TERG_07085 | peptidase ( <i>T. tonsurans</i> )   | CACGTA (rc) | 336 | UPRE-2 |
| TERG_07109 | phosphotransferase enzyme family protein ( <i>T. equinum</i> )                        | CACGTA (rc) | 416 | UPRE-2 |
| TERG_07110 | kelch domain-containing protein domain-containing protein ( <i>T. tonsurans</i> )     | TACGTG      | 949 | UPRE-2 |
| TERG_07158 | cell cycle regulatory protein, putative ( <i>T. verrucosum</i> )                      | CACGTA (rc) | 307 | UPRE-2 |
| TERG_07159 | geranylgeranyl transferase type II alpha subunit, putative ( <i>T. verrucosum</i> )   | CACGTA (rc) | 440 | UPRE-2 |
| TERG_07162 | geranylgeranyl transferase type II alpha subunit, putative ( <i>T. verrucosum</i> )   | TACGTG      | 640 | UPRE-2 |
| TERG_07170 | MFS transporter, putative ( <i>A. benhamiae</i> )                                     | CACGTA (rc) | 625 | UPRE-2 |
| TERG_07171 | hypothetical protein  | TACGTG      | 531 | UPRE-2 |
| TERG_07190 | hypothetical protein  | CACGTA (rc) | 714 | UPRE-2 |
| TERG_07201 | hypothetical protein  | TACGTG      | 579 | UPRE-2 |
| TERG_07216 | hypothetical protein  | CACGTA (rc) | 412 | UPRE-2 |
| TERG_07217 | histone acetyltransferase, putative ( <i>T. verrucosum</i> )                          | TACGTG      | 868 | UPRE-2 |
| TERG_07221 | hypothetical protein  | TACGTG      | 808 | UPRE-2 |

|            |   |             |     |        |
|------------|---|-------------|-----|--------|
| TERG_07227 | proteasome activator subunit 4 ( <i>T. tonsurans</i> )                            | TACGTG      | 626 | UPRE-2 |
| TERG_07229 | vacuolar ATP synthase 116kDa subunit ( <i>T. tonsurans</i> )                      | TACGTG      | 425 | UPRE-2 |
| TERG_07269 | mannose-1-phosphate guanylyltransferase   | CACGTA (rc) | 318 | UPRE-2 |
| TERG_07274 | hypothetical protein  | CACGTA (rc) | 935 | UPRE-2 |
| TERG_07284 | hypothetical protein  | TACGTG      | 283 | UPRE-2 |
| TERG_07290 | glutathione transferase ( <i>T. equinum</i> )                                     | CACGTA (rc) | 109 | UPRE-2 |
| TERG_07299 | O-methyltransferase ( <i>M. gypseum</i> )   | CACGTA (rc) | 327 | UPRE-2 |
| TERG_07323 | endosomal peripheral membrane protein ( <i>T. equinum</i> )                       | CACGTA (rc) | 971 | UPRE-2 |
| TERG_07324 | ubiquitin-conjugating enzyme ( <i>T. equinum</i> )                                | TACGTG      | 569 | UPRE-2 |
| TERG_07339 | WD repeat-containing protein ( <i>T. tonsurans</i> )                              | CACGTA (rc) | 324 | UPRE-2 |
| TERG_07351 | hypothetical protein  | CACGTA (rc) | 765 | UPRE-2 |
| TERG_07395 | WD repeat protein ( <i>T. tonsurans</i> )   | CACGTA (rc) | 114 | UPRE-2 |
| TERG_07396 | DNA-directed RNA polymerase II subunit RPB1 ( <i>M. gypseum</i> )                 | TACGTG      | 509 | UPRE-2 |
| TERG_07398 | tRNA(His) guanylyltransferase ( <i>T. tonsurans</i> )                             | CACGTA (rc) | 889 | UPRE-2 |
| TERG_07399 | fibronectin type III domain-containing protein ( <i>M. gypseum</i> )              | CACGTA (rc) | 194 | UPRE-2 |
| TERG_07399 | fibronectin type III domain-containing protein ( <i>M. gypseum</i> )              | CACGTA (rc) | 804 | UPRE-2 |
| TERG_07400 | nuclear elongation and deformation protein 1 ( <i>T. equinum</i> )                | TACGTG      | 149 | UPRE-2 |
| TERG_07416 | peroxisome targeting signal receptor Pex7 ( <i>T. tonsurans</i> )                 | CACGTA (rc) | 479 | UPRE-2 |
| TERG_07437 | class II aldolase/adducin domain-containing protein ( <i>T. tonsurans</i> )       | CACGTA (rc) | 762 | UPRE-2 |
| TERG_07441 | methyltransferase ( <i>T. tonsurans</i> )   | TACGTG      | 869 | UPRE-2 |
| TERG_07443 | hypothetical protein  | TACGTG      | 267 | UPRE-2 |
| TERG_07443 | hypothetical protein  | TACGTG      | 820 | UPRE-2 |
| TERG_07468 | hypothetical protein  | CACGTA (rc) | 593 | UPRE-2 |
| TERG_07482 | ribonuclease H1, putative ( <i>A. benhamiae</i> )                                 | CACGTA (rc) | 972 | UPRE-2 |
| TERG_07499 | CCCH zinc finger and SMR domain-containing protein ( <i>M. gypseum</i> )          | CACGTA (rc) | 286 | UPRE-2 |
| TERG_07501 | nitrate reductase ( <i>T. tonsurans</i> )   | TACGTG      | 617 | UPRE-2 |
| TERG_07509 | serine/threonine protein kinase ( <i>M. canis</i> )                               | CACGTA (rc) | 596 | UPRE-2 |
| TERG_07510 | hypothetical protein  | CACGTA (rc) | 28  | UPRE-2 |
| TERG_07530 | 50S ribosomal protein L36 ( <i>T. tonsurans</i> )                                 | CACGTA (rc) | 538 | UPRE-2 |
| TERG_07533 | hypothetical protein  | CACGTA (rc) | 724 | UPRE-2 |
| TERG_07534 | NADH-ubiquinone oxidoreductase complex 1/LYR family protein ( <i>M. gypseum</i> ) | TACGTG      | 148 | UPRE-2 |
| TERG_07596 | hypothetical protein  | CACGTA (rc) | 909 | UPRE-2 |

|            |  |             |     |        |
|------------|--|-------------|-----|--------|
| TERG_07607 | hypothetical protein   | TACGTG      | 412 | UPRE-2 |
| TERG_07612 | hypothetical protein   | TACGTG      | 232 | UPRE-2 |
| TERG_07628 | tyrosine phosphatase family protein ( <i>A. benhamiae</i> )                          | CACGTA (rc) | 211 | UPRE-2 |
| TERG_07653 | DNA repair protein (Rad57), putative ( <i>T. verrucosum</i> )                        | TACGTG      | 306 | UPRE-2 |
| TERG_07656 | lupus La protein ( <i>T. equinum</i> )   | CACGTA (rc) | 529 | UPRE-2 |
| TERG_07657 | chitin synthase class VI ( <i>T. equinum</i> )                                       | TACGTG      | 568 | UPRE-2 |
| TERG_07672 | GABA permease ( <i>T. equinum</i> )  | TACGTG      | 377 | UPRE-2 |
| TERG_07689 | ribosomal biogenesis protein Gar2 ( <i>T. tonsurans</i> )                            | CACGTA (rc) | 639 | UPRE-2 |
| TERG_07706 | hypothetical protein   | CACGTA (rc) | 827 | UPRE-2 |
| TERG_07708 | hypothetical protein   | CACGTA (rc) | 404 | UPRE-2 |
| TERG_07720 | copper-transporting ATPase ( <i>T. equinum</i> )                                     | TACGTG      | 789 | UPRE-2 |
| TERG_07731 | 2Fe-2S iron-sulfur cluster binding domain-containing protein ( <i>T. tonsurans</i> ) | CACGTA (rc) | 221 | UPRE-2 |
| TERG_07731 | 2Fe-2S iron-sulfur cluster binding domain-containing protein ( <i>T. tonsurans</i> ) | CACGTA (rc) | 580 | UPRE-2 |
| TERG_07740 | farnesyl pyrophosphate synthetase ( <i>T. equinum</i> )                              | CACGTA (rc) | 690 | UPRE-2 |
| TERG_07755 | ergot alkaloid biosynthetic protein A ( <i>T. verrucosum</i> )                       | TACGTG      | 642 | UPRE-2 |
| TERG_07774 | EF hand domain-containing protein ( <i>T. tonsurans</i> )                            | TACGTG      | 426 | UPRE-2 |
| TERG_07794 | hypothetical protein   | TACGTG      | 509 | UPRE-2 |
| TERG_07831 | GNAT family acetyltransferase, putative ( <i>T. verrucosum</i> )                     | TACGTG      | 490 | UPRE-2 |
| TERG_07844 | HAL protein kinase   | CACGTA (rc) | 30  | UPRE-2 |
| TERG_07858 | aldo/keto reductase ( <i>T. equinum</i> )  | CACGTA (rc) | 823 | UPRE-2 |
| TERG_07859 | ubiquitin C-terminal hydrolase L3 ( <i>T. tonsurans</i> )                            | TACGTG      | 163 | UPRE-2 |
| TERG_07864 | SVP1-like protein ( <i>T. tonsurans</i> )  | CACGTA (rc) | 105 | UPRE-2 |
| TERG_07881 | pre-mRNA-splicing factor isyl  | CACGTA (rc) | 922 | UPRE-2 |
| TERG_07906 | hypothetical protein   | CACGTA (rc) | 769 | UPRE-2 |
| TERG_07962 | hypothetical protein   | TACGTG      | 321 | UPRE-2 |
| TERG_07993 | hypothetical protein   | TACGTG      | 243 | UPRE-2 |
| TERG_07998 | hypothetical protein   | CACGTA (rc) | 12  | UPRE-2 |
| TERG_08003 | fungal specific transcription factor domain-containing protein ( <i>T. equinum</i> ) | CACGTA (rc) | 307 | UPRE-2 |
| TERG_08013 | Rox3 mediator complex subunit ( <i>T. equinum</i> )                                  | CACGTA (rc) | 238 | UPRE-2 |
| TERG_08036 | mitochondrial carrier protein ( <i>T. equinum</i> )                                  | CACGTA (rc) | 105 | UPRE-2 |
| TERG_08064 | choline kinase, putative ( <i>A. benhamiae</i> )                                     | CACGTA (rc) | 673 | UPRE-2 |
| TERG_08097 | hypothetical protein   | TACGTG      | 123 | UPRE-2 |
| TERG_08102 | 3-isopropylmalate dehydrogenase A  | TACGTG      | 554 | UPRE-2 |
| TERG_08107 | phosphoglycerate mutase ( <i>T. tonsurans</i> )                                      | TACGTG      | 238 | UPRE-2 |
| TERG_08148 | hypothetical protein   | TACGTG      | 10  | UPRE-2 |

|            |  |             |     |        |
|------------|--|-------------|-----|--------|
| TERG_08182 | hypothetical protein   | CACGTA (rc) | 766 | UPRE-2 |
| TERG_08184 | dioxygenase, putative ( <i>T. verrucosum</i> )                                   | TACGTG      | 464 | UPRE-2 |
| TERG_08191 | glucosyltransferase ( <i>T. equinum</i> )  | CACGTA (rc) | 75  | UPRE-2 |
| TERG_08194 | serine/threonine protein kinase ( <i>M. canis</i> )                              | TACGTG      | 887 | UPRE-2 |
| TERG_08245 | branched-chain amino acid aminotransferase ( <i>T. tonsurans</i> )               | TACGTG      | 767 | UPRE-2 |
| TERG_08260 | subtilisin-like protease 2   | TACGTG      | 311 | UPRE-2 |
| TERG_08264 | L-xylulose reductase   | TACGTG      | 711 | UPRE-2 |
| TERG_08266 | hypothetical protein   | TACGTG      | 40  | UPRE-2 |
| TERG_08277 | transcriptional elongation regulator Elc1/Elongin C ( <i>T. tonsurans</i> )      | CACGTA (rc) | 369 | UPRE-2 |
| TERG_08289 | Rpp14 family protein ( <i>T. equinum</i> )                                       | TACGTG      | 267 | UPRE-2 |
| TERG_08295 | benzoate 4-monooxygenase cytochrome P450 ( <i>M. canis</i> )                     | CACGTA (rc) | 149 | UPRE-2 |
| TERG_08298 | RTA1 domain-containing protein ( <i>T. equinum</i> )                             | CACGTA (rc) | 549 | UPRE-2 |
| TERG_08306 | hypothetical protein   | CACGTA (rc) | 658 | UPRE-2 |
| TERG_08307 | ubiquitin-protein ligase ( <i>T. tonsurans</i> )                                 | TACGTG      | 828 | UPRE-2 |
| TERG_08316 | aflatoxin efflux pump ( <i>M. gypseum</i> )                                      | TACGTG      | 820 | UPRE-2 |
| TERG_08324 | hypothetical protein   | CACGTA (rc) | 526 | UPRE-2 |
| TERG_08368 | TTK protein kinase   | CACGTA (rc) | 474 | UPRE-2 |
| TERG_08401 | protein transport membrane glycoprotein Sec20, putative ( <i>T. verrucosum</i> ) | CACGTA (rc) | 719 | UPRE-2 |
| TERG_08417 | Hsc70 cochaperone ( <i>T. tonsurans</i> )  | TACGTG      | 156 | UPRE-2 |
| TERG_08444 | CipC protein ( <i>M. canis</i> )   | CACGTA (rc) | 154 | UPRE-2 |
| TERG_08460 | microfibril-associated protein ( <i>T. equinum</i> )                             | TACGTG      | 858 | UPRE-2 |
| TERG_08462 | NAD kinase/ATP NAD kinase ( <i>T. tonsurans</i> )                                | CACGTA (rc) | 308 | UPRE-2 |
| TERG_08462 | NAD kinase/ATP NAD kinase ( <i>T. tonsurans</i> )                                | CACGTA (rc) | 648 | UPRE-2 |
| TERG_08463 | hypothetical protein   | TACGTG      | 230 | UPRE-2 |
| TERG_08463 | hypothetical protein   | TACGTG      | 570 | UPRE-2 |
| TERG_08468 | hydroxyacylglutathione hydrolase   | TACGTG      | 654 | UPRE-2 |
| TERG_08474 | nuclear protein SNF4 ( <i>T. tonsurans</i> )                                     | CACGTA (rc) | 149 | UPRE-2 |
| TERG_08478 | translation initiation factor eif-2b delta subunit ( <i>T. tonsurans</i> )       | CACGTA (rc) | 892 | UPRE-2 |
| TERG_08479 | kinesin family protein ( <i>T. verrucosum</i> )                                  | CACGTA (rc) | 569 | UPRE-2 |
| TERG_08508 | hypothetical protein   | TACGTG      | 137 | UPRE-2 |
| TERG_08524 | C2H2 finger domain-containing protein ( <i>T. tonsurans</i> )                    | CACGTA (rc) | 26  | UPRE-2 |
| TERG_08526 | N2,N2-dimethylguanosine tRNA methyltransferase                                   | TACGTG      | 217 | UPRE-2 |
| TERG_08539 | Diacylglycerol kinase domain-containing protein ( <i>T. equinum</i> )            | TACGTG      | 142 | UPRE-2 |



|            |   |             |     |        |
|------------|---|-------------|-----|--------|
| TERG_08539 | Diacylglycerol kinase domain-containing protein ( <i>T. equinum</i> )         | TACGTG      | 433 | UPRE-2 |
| TERG_08539 | Diacylglycerol kinase domain-containing protein ( <i>T. equinum</i> )         | TACGTG      | 851 | UPRE-2 |
| TERG_08550 | tRNA-specific adenosine deaminase subunit Tad2p/ADAT2 ( <i>T. tonsurans</i> ) | TACGTG      | 977 | UPRE-2 |
| TERG_08593 | seven transmembrane protein 1 ( <i>T. equinum</i> )                           | TACGTG      | 744 | UPRE-2 |
| TERG_08601 | hypothetical protein  | TACGTG      | 865 | UPRE-2 |
| TERG_08602 | alpha-ketoglutarate-dependent taurine dioxygenase ( <i>T. verrucosum</i> )    | TACGTG      | 519 | UPRE-2 |
| TERG_08620 | siderophore iron transporter ( <i>T. equinum</i> )                            | CACGTA (rc) | 895 | UPRE-2 |
| TERG_08622 | transferase ( <i>M. canis</i> )   | TACGTG      | 371 | UPRE-2 |
| TERG_08697 | serine/threonine protein kinase   | CACGTA (rc) | 829 | UPRE-2 |
| TERG_08724 | hypothetical protein  | TACGTG      | 343 | UPRE-2 |
| TERG_08803 | hypothetical protein  | TACGTG      | 308 | UPRE-2 |
| TERG_08823 | hypothetical protein  | CACGTA (rc) | 678 | UPRE-2 |
| TERG_08869 | hypothetical protein  | TACGTG      | 711 | UPRE-2 |
| TERG_08924 | MIZ zinc finger domain protein ( <i>A. benhamiae</i> )                        | CACGTA (rc) | 346 | UPRE-2 |
| TERG_08979 | CMGC/SRPK protein kinase  | TACGTG      | 577 | UPRE-2 |
| TERG_08990 | hypothetical protein  | CACGTA (rc) | 33  | UPRE-2 |
| TERG_08990 | hypothetical protein  | CACGTA (rc) | 41  | UPRE-2 |
| TERG_11513 | esterase ( <i>T. equinum</i> )  | TACGTG      | 46  | UPRE-2 |
| TERG_11516 | hypothetical protein  | TACGTG      | 571 | UPRE-2 |
| TERG_11560 | sterol O-acyltransferase ( <i>T. tonsurans</i> )                              | TACGTG      | 479 | UPRE-2 |
| TERG_11573 | hypothetical protein  | TACGTG      | 484 | UPRE-2 |
| TERG_11574 | hypothetical protein  | CACGTA (rc) | 749 | UPRE-2 |
| TERG_11589 | hypothetical protein  | CACGTA (rc) | 727 | UPRE-2 |
| TERG_11593 | carboxypeptidase Y, putative ( <i>A. benhamiae</i> )                          | TACGTG      | 695 | UPRE-2 |
| TERG_11614 | hypothetical protein  | TACGTG      | 765 | UPRE-2 |
| TERG_11615 | hypothetical protein  | TACGTG      | 620 | UPRE-2 |
| TERG_11625 | allantoicase ( <i>T. equinum</i> )  | TACGTG      | 904 | UPRE-2 |
| TERG_11649 | hypothetical protein  | TACGTG      | 537 | UPRE-2 |
| TERG_11653 | calcofluor white hypersensitive protein ( <i>T. equinum</i> )                 | TACGTG      | 446 | UPRE-2 |
| TERG_11676 | hypothetical protein  | TACGTG      | 682 | UPRE-2 |
| TERG_11694 | hypothetical protein  | TACGTG      | 83  | UPRE-2 |
| TERG_11701 | hypothetical protein  | CACGTA (rc) | 123 | UPRE-2 |
| TERG_11713 | vesicle-associated membrane protein 712 ( <i>T. tonsurans</i> )               | TACGTG      | 411 | UPRE-2 |
| TERG_11719 | hypothetical protein  | TACGTG      | 232 | UPRE-2 |
| TERG_11729 | hypothetical protein  | TACGTG      | 709 | UPRE-2 |

|            |  |             |     |        |
|------------|--|-------------|-----|--------|
| TERG_11748 | hypothetical protein   | TACGTG      | 816 | UPRE-2 |
| TERG_11749 | hypothetical protein   | TACGTG      | 524 | UPRE-2 |
| TERG_11751 | PCI domain-containing protein ( <i>T. tonsurans</i> )                            | TACGTG      | 463 | UPRE-2 |
| TERG_11752 | hypothetical protein   | TACGTG      | 63  | UPRE-2 |
| TERG_11759 | hypothetical protein   | CACGTA (rc) | 570 | UPRE-2 |
| TERG_11795 | hypothetical protein   | TACGTG      | 21  | UPRE-2 |
| TERG_11804 | hypothetical protein   | CACGTA (rc) | 285 | UPRE-2 |
| TERG_11809 | hydroxymethylglutaryl-CoA synthase   | CACGTA (rc) | 427 | UPRE-2 |
| TERG_11813 | FAD dependent oxidoreductase, putative ( <i>A. benhamiae</i> )                   | TACGTG      | 84  | UPRE-2 |
| TERG_11855 | hypothetical protein   | TACGTG      | 27  | UPRE-2 |
| TERG_11880 | hypothetical protein   | TACGTG      | 649 | UPRE-2 |
| TERG_11898 | hypothetical protein   | CACGTA (rc) | 833 | UPRE-2 |
| TERG_11919 | extracellular lipase ( <i>T. tonsurans</i> )                                     | CACGTA (rc) | 448 | UPRE-2 |
| TERG_11919 | extracellular lipase ( <i>T. tonsurans</i> )                                     | CACGTA (rc) | 568 | UPRE-2 |
| TERG_11920 | vesicle-mediated transport protein Bfr2/Che-1, putative ( <i>T. verrucosum</i> ) | TACGTG      | 909 | UPRE-2 |
| TERG_11922 | myo-inositol-1(or 4)-monophosphatase ( <i>T. verrucosum</i> )                    | TACGTG      | 593 | UPRE-2 |
| TERG_11936 | sister chromatid separation protein ( <i>T. tonsurans</i> )                      | CACGTA (rc) | 948 | UPRE-2 |
| TERG_11938 | carboxylesterase, putative ( <i>A. benhamiae</i> )                               | TACGTG      | 429 | UPRE-2 |
| TERG_11939 | hypothetical protein   | TACGTG      | 11  | UPRE-2 |
| TERG_11942 | MFS maltose permease ( <i>T. tonsurans</i> )                                     | CACGTA (rc) | 621 | UPRE-2 |
| TERG_11943 | MFS maltose permease ( <i>T. tonsurans</i> )                                     | CACGTA (rc) | 567 | UPRE-2 |
| TERG_11946 | hypothetical protein   | TACGTG      | 976 | UPRE-2 |
| TERG_11963 | hypothetical protein   | TACGTG      | 740 | UPRE-2 |
| TERG_11986 | GABA permease, putative ( <i>A. benhamiae</i> )                                  | CACGTA (rc) | 867 | UPRE-2 |
| TERG_11992 | hypothetical protein   | TACGTG      | 682 | UPRE-2 |
| TERG_11993 | hypothetical protein   | TACGTG      | 387 | UPRE-2 |
| TERG_11994 | hypothetical protein   | TACGTG      | 9   | UPRE-2 |
| TERG_11998 | potassium uptake transporter ( <i>T. equinum</i> )                               | TACGTG      | 518 | UPRE-2 |
| TERG_11999 | ubiquitin carboxyl-terminal hydrolase ( <i>T. tonsurans</i> )                    | TACGTG      | 846 | UPRE-2 |
| TERG_12000 | ubiquitin C-terminal hydrolase, putative ( <i>T. verrucosum</i> )                | TACGTG      | 113 | UPRE-2 |
| TERG_12007 | DUF726 domain protein ( <i>T. verrucosum</i> )                                   | TACGTG      | 692 | UPRE-2 |
| TERG_12026 | nonsense-mediated mRNA decay protein 2 ( <i>T. tonsurans</i> )                   | CACGTA (rc) | 925 | UPRE-2 |
| TERG_12030 | DUF821 domain protein ( <i>T. verrucosum</i> )                                   | CACGTA (rc) | 784 | UPRE-2 |
| TERG_12060 | C-x8-C-x5-C-x3-H type zinc finger protein ( <i>T. equinum</i> )                  | TACGTG      | 793 | UPRE-2 |

|            |   |             |     |        |
|------------|---|-------------|-----|--------|
| TERG_12077 | hypothetical protein  | CACGTA (rc) | 717 | UPRE-2 |
| TERG_12079 | protein N-terminal asparagine amidohydrolase, putative ( <i>T. verrucosum</i> )                   | TACGTG      | 891 | UPRE-2 |
| TERG_12121 | DNA replication licensing factor mcm5 ( <i>T. tonsurans</i> )                                     | TACGTG      | 316 | UPRE-2 |
| TERG_12138 | hypothetical protein  | TACGTG      | 474 | UPRE-2 |
| TERG_12150 | serine/threonine-protein kinase bur1  | TACGTG      | 53  | UPRE-2 |
| TERG_12153 | pumilio-family RNA binding protein ( <i>T. tonsurans</i> )  | CACGTA (rc) | 353 | UPRE-2 |
| TERG_12157 | PQ-loop repeat-containing protein 1 ( <i>T. equinum</i> )   | TACGTG      | 189 | UPRE-2 |
| TERG_12160 | STE/STE11/CDC15 protein kinase ( <i>T. tonsurans</i> )  | TACGTG      | 52  | UPRE-2 |
| TERG_12181 | C6 finger domain protein, putative ( <i>T. verrucosum</i> )                                       | CACGTA (rc) | 920 | UPRE-2 |
| TERG_12198 | hypothetical protein  | CACGTA (rc) | 16  | UPRE-2 |
| TERG_12203 | GARP complex subunit (Sac2), putative ( <i>T. verrucosum</i> )                                    | TACGTG      | 382 | UPRE-2 |
| TERG_12204 | RNA polymerase I specific transcription initiation factor Rrn7, putative ( <i>T. verrucosum</i> ) | TACGTG      | 526 | UPRE-2 |
| TERG_12238 | integral membrane protein ( <i>M. gypseum</i> )   | TACGTG      | 264 | UPRE-2 |
| TERG_12293 | hypothetical protein  | TACGTG      | 985 | UPRE-2 |
| TERG_12301 | hypothetical protein  | TACGTG      | 873 | UPRE-2 |
| TERG_12310 | null ( <i>T. verrucosum</i> )   | CACGTA (rc) | 186 | UPRE-2 |
| TERG_12342 | membrane zinc transporter ( <i>T. tonsurans</i> )   | TACGTG      | 620 | UPRE-2 |
| TERG_12365 | secreted protein ( <i>T. equinum</i> )  | TACGTG      | 187 | UPRE-2 |
| TERG_12405 | cap binding protein ( <i>T. equinum</i> )   | TACGTG      | 965 | UPRE-2 |
| TERG_12417 | hypothetical protein  | TACGTG      | 992 | UPRE-2 |
| TERG_12419 | uracil permease ( <i>M. gypseum</i> )   | TACGTG      | 333 | UPRE-2 |
| TERG_12425 | von Willebrand RING finger domain-containing protein ( <i>T. tonsurans</i> )                      | TACGTG      | 811 | UPRE-2 |
| TERG_12432 | hypothetical protein  | TACGTG      | 754 | UPRE-2 |
| TERG_12441 | hypothetical protein  | CACGTA (rc) | 515 | UPRE-2 |
| TERG_12442 | hypothetical protein  | CACGTA (rc) | 599 | UPRE-2 |
| TERG_12459 | hypothetical protein  | TACGTG      | 409 | UPRE-2 |
| TERG_12480 | ribosome biogenesis protein Pescadillo ( <i>T. tonsurans</i> )                                    | TACGTG      | 385 | UPRE-2 |
| TERG_12483 | nonribosomal brevianamide peptide synthase FtmA ( <i>T. verrucosum</i> )                          | TACGTG      | 370 | UPRE-2 |
| TERG_12485 | nonribosomal brevianamide peptide synthase FtmA ( <i>T. verrucosum</i> )                          | TACGTG      | 756 | UPRE-2 |
| TERG_12486 | nonribosomal brevianamide peptide synthase FtmA ( <i>A. benhamiae</i> )                           | TACGTG      | 204 | UPRE-2 |
| TERG_12493 | averantin oxidoreductase ( <i>T. equinum</i> )  | TACGTG      | 45  | UPRE-2 |
| TERG_12513 | hypothetical protein  | CACGTA (rc) | 667 | UPRE-2 |
| TERG_12518 | phosphotransferase enzyme family protein ( <i>T. equinum</i> )                                    | TACGTG      | 568 | UPRE-2 |

|            |  |               |     |        |
|------------|--|---------------|-----|--------|
| TERG_12579 | MFS transporter ( <i>T. tonsurans</i> )                                  | TACGTG        | 124 | UPRE-2 |
| TERG_12590 | hypothetical protein   | CACGTA (rc)   | 889 | UPRE-2 |
| TERG_12592 | hypothetical protein   | TACGTG        | 874 | UPRE-2 |
| TERG_12593 | hypothetical protein   | TACGTG        | 451 | UPRE-2 |
| TERG_12628 | hypothetical protein   | CACGTA (rc)   | 199 | UPRE-2 |
| TERG_12633 | conserved lysine-rich protein, putative ( <i>A. benhamiae</i> )          | CACGTA (rc)   | 365 | UPRE-2 |
| TERG_12635 | sulfate transporter ( <i>T. equinum</i> )                                | CACGTA (rc)   | 26  | UPRE-2 |
| TERG_12644 | MFS transporter, putative ( <i>A. benhamiae</i> )                        | TACGTG        | 825 | UPRE-2 |
| TERG_12655 | hypothetical protein   | TACGTG        | 242 | UPRE-2 |
| TERG_12687 | ubiquitin ligase subunit CulD ( <i>T. tonsurans</i> )                    | TACGTG        | 545 | UPRE-2 |
| TERG_12697 | serine/threonine protein kinase ( <i>T. tonsurans</i> )                  | TACGTG        | 113 | UPRE-2 |
| TERG_12698 | serine/threonine protein kinase ( <i>T. equinum</i> )                    | TACGTG        | 397 | UPRE-2 |
| TERG_00327 | hypothetical protein   | GTTGTCCT (rc) | 985 | UPRE-3 |
| TERG_00331 | golgi apparatus membrane protein TVP18 ( <i>T. tonsurans</i> )           | GTTGTCCT (rc) | 445 | UPRE-3 |
| TERG_00377 | hypothetical protein   | AGGACAAC      | 907 | UPRE-3 |
| TERG_00568 | elongator associated protein ( <i>T. equinum</i> )                       | AGGACAAC      | 885 | UPRE-3 |
| TERG_00726 | short-chain dehydrogenase/reductase 2, putative ( <i>T. verrucosum</i> ) | AGGACAAC      | 431 | UPRE-3 |
| TERG_00815 | hypothetical protein   | AGGACAAC      | 399 | UPRE-3 |
| TERG_00841 | C6 transcription factor, putative ( <i>T. verrucosum</i> )               | GTTGTCCT (rc) | 810 | UPRE-3 |
| TERG_00851 | ankyrin repeat-containing protein ( <i>T. equinum</i> )                  | GTTGTCCT (rc) | 79  | UPRE-3 |
| TERG_00861 | hypothetical protein   | GTTGTCCT (rc) | 897 | UPRE-3 |
| TERG_00888 | hypothetical protein   | GTTGTCCT (rc) | 222 | UPRE-3 |
| TERG_00915 | CAMK protein kinase  | AGGACAAC      | 87  | UPRE-3 |
| TERG_01139 | kinesin family protein ( <i>T. tonsurans</i> )                           | AGGACAAC      | 841 | UPRE-3 |
| TERG_01280 | IgE-binding protein ( <i>A. benhamiae</i> )                              | AGGACAAC      | 503 | UPRE-3 |
| TERG_01329 | Ctr copper transporter, putative ( <i>T. verrucosum</i> )                | AGGACAAC      | 431 | UPRE-3 |
| TERG_01447 | bcp1 ( <i>T. equinum</i> )   | AGGACAAC      | 376 | UPRE-3 |
| TERG_01470 | serine/threonine protein kinase ( <i>M. canis</i> )                      | AGGACAAC      | 272 | UPRE-3 |
| TERG_01475 | DNA topoisomerase 2  | AGGACAAC      | 204 | UPRE-3 |
| TERG_01558 | cation chloride cotransporter ( <i>T. tonsurans</i> )                    | GTTGTCCT (rc) | 185 | UPRE-3 |
| TERG_01782 | hypothetical protein   | GTTGTCCT (rc) | 818 | UPRE-3 |
| TERG_01783 | hypothetical protein   | AGGACAAC      | 431 | UPRE-3 |
| TERG_01786 | DENN domain-containing protein ( <i>T. tonsurans</i> )                   | AGGACAAC      | 889 | UPRE-3 |
| TERG_01831 | adenylate-forming enzyme AfeA ( <i>A. benhamiae</i> )                    | GTTGTCCT (rc) | 301 | UPRE-3 |
| TERG_01851 | Pfs, NACHT and WD domain protein ( <i>A. benhamiae</i> )                 | AGGACAAC      | 96  | UPRE-3 |

|            |   |               |     |        |
|------------|---|---------------|-----|--------|
| TERG_02232 | Rho GTPase activator (Bem2), putative ( <i>T. verrucosum</i> )                  | GTTGTCCT (rc) | 384 | UPRE-3 |
| TERG_02363 | succinate-semialdehyde dehydrogenase ( <i>T. tonsurans</i> )                    | AGGACAAC      | 982 | UPRE-3 |
| TERG_02383 | mitochondrial carrier protein ( <i>T. tonsurans</i> )                           | AGGACAAC      | 72  | UPRE-3 |
| TERG_02421 | urea transporter ( <i>M. canis</i> )  | GTTGTCCT (rc) | 468 | UPRE-3 |
| TERG_02438 | hypothetical protein  | GTTGTCCT (rc) | 737 | UPRE-3 |
| TERG_02439 | palmitoyltransferase ( <i>T. tonsurans</i> )                                    | AGGACAAC      | 715 | UPRE-3 |
| TERG_02624 | hypothetical protein  | GTTGTCCT (rc) | 371 | UPRE-3 |
| TERG_02772 | DNA polymerase V ( <i>T. tonsurans</i> )  | GTTGTCCT (rc) | 920 | UPRE-3 |
| TERG_02785 | hypothetical protein  | GTTGTCCT (rc) | 581 | UPRE-3 |
| TERG_02870 | pre-mRNA-splicing factor ATP-dependent RNA helicase prp22 ( <i>T. equinum</i> ) | GTTGTCCT (rc) | 637 | UPRE-3 |
| TERG_02871 | CUE domain-containing protein ( <i>T. tonsurans</i> )                           | AGGACAAC      | 907 | UPRE-3 |
| TERG_03063 | hypothetical protein  | GTTGTCCT (rc) | 322 | UPRE-3 |
| TERG_03064 | MCAK-like kinesin ( <i>T. equinum</i> )   | AGGACAAC      | 363 | UPRE-3 |
| TERG_03114 | T-complex protein 1 subunit gamma   | AGGACAAC      | 336 | UPRE-3 |
| TERG_03222 | DUF895 domain membrane protein ( <i>T. verrucosum</i> )                         | GTTGTCCT (rc) | 488 | UPRE-3 |
| TERG_03388 | hypothetical protein  | AGGACAAC      | 160 | UPRE-3 |
| TERG_03481 | hypothetical protein  | AGGACAAC      | 895 | UPRE-3 |
| TERG_03486 | Lectin C-type domain protein ( <i>T. verrucosum</i> )                           | GTTGTCCT (rc) | 397 | UPRE-3 |
| TERG_03503 | ULK protein kinase ( <i>T. tonsurans</i> )                                      | GTTGTCCT (rc) | 31  | UPRE-3 |
| TERG_03587 | WD repeat protein ( <i>T. verrucosum</i> )                                      | AGGACAAC      | 531 | UPRE-3 |
| TERG_03636 | ankyrin repeat protein ( <i>T. equinum</i> )                                    | GTTGTCCT (rc) | 66  | UPRE-3 |
| TERG_03650 | hypothetical protein  | AGGACAAC      | 267 | UPRE-3 |
| TERG_03682 | hypothetical protein  | AGGACAAC      | 470 | UPRE-3 |
| TERG_03745 | ankyrin repeat-containing protein ( <i>T. equinum</i> )                         | GTTGTCCT (rc) | 427 | UPRE-3 |
| TERG_03797 | hypothetical protein  | GTTGTCCT (rc) | 215 | UPRE-3 |
| TERG_03854 | laccase ( <i>T. tonsurans</i> )   | AGGACAAC      | 387 | UPRE-3 |
| TERG_03898 | GTP cyclohydrolase II   | AGGACAAC      | 562 | UPRE-3 |
| TERG_04185 | calcium channel subunit Mid1 ( <i>T. verrucosum</i> )                           | AGGACAAC      | 767 | UPRE-3 |
| TERG_04339 | signal transduction protein Syg1, putative ( <i>A. benhamiae</i> )              | GTTGTCCT (rc) | 121 | UPRE-3 |
| TERG_04444 | hypothetical protein  | GTTGTCCT (rc) | 36  | UPRE-3 |
| TERG_04486 | ER lumen protein retaining receptor ( <i>T. tonsurans</i> )                     | AGGACAAC      | 495 | UPRE-3 |
| TERG_04686 | porphobilinogen synthase ( <i>T. tonsurans</i> )                                | AGGACAAC      | 443 | UPRE-3 |
| TERG_04724 | hypothetical protein  | AGGACAAC      | 661 | UPRE-3 |
| TERG_04873 | autophagy protein Apg5, putative ( <i>A. benhamiae</i> )                        | AGGACAAC      | 308 | UPRE-3 |
| TERG_04946 | rho GTPase ModA ( <i>T. tonsurans</i> )   | GTTGTCCT (rc) | 127 | UPRE-3 |
| TERG_05047 | hypothetical protein  | GTTGTCCT (rc) | 344 | UPRE-3 |

|            |   |               |     |        |
|------------|---|---------------|-----|--------|
| TERG_05048 | U2 small nuclear ribonucleoprotein A'   | AGGACAAC      | 700 | UPRE-3 |
| TERG_05062 | ribonuclease P complex subunit Pop4 ( <i>T. tonsurans</i> )                         | GTTGTCCT (rc) | 94  | UPRE-3 |
| TERG_05257 | integral membrane protein ( <i>T. tonsurans</i> )                                   | AGGACAAC      | 601 | UPRE-3 |
| TERG_05363 | hypothetical protein  | AGGACAAC      | 902 | UPRE-3 |
| TERG_05366 | hypothetical protein  | AGGACAAC      | 772 | UPRE-3 |
| TERG_05628 | GPI ethanolamine phosphate transferase ( <i>T. tonsurans</i> )                      | GTTGTCCT (rc) | 826 | UPRE-3 |
| TERG_05700 | hypothetical protein  | AGGACAAC      | 38  | UPRE-3 |
| TERG_05776 | peroxisomal ABC transporter ( <i>T. tonsurans</i> )                                 | AGGACAAC      | 807 | UPRE-3 |
| TERG_05908 | hypothetical protein  | GTTGTCCT (rc) | 147 | UPRE-3 |
| TERG_05956 | rRNA processing protein Ebp2p ( <i>T. equinum</i> )                                 | AGGACAAC      | 709 | UPRE-3 |
| TERG_06026 | ribosomal protein S24 ( <i>T. tonsurans</i> )                                       | AGGACAAC      | 118 | UPRE-3 |
| TERG_06057 | C2 domain-containing protein ( <i>T. equinum</i> )                                  | GTTGTCCT (rc) | 408 | UPRE-3 |
| TERG_06118 | hypothetical protein  | GTTGTCCT (rc) | 759 | UPRE-3 |
| TERG_06250 | alpha 1,6 mannosyltransferase ( <i>M. canis</i> )                                   | GTTGTCCT (rc) | 849 | UPRE-3 |
| TERG_06251 | hypothetical protein  | AGGACAAC      | 276 | UPRE-3 |
| TERG_06269 | hypothetical protein  | GTTGTCCT (rc) | 534 | UPRE-3 |
| TERG_06368 | hypothetical protein  | GTTGTCCT (rc) | 249 | UPRE-3 |
| TERG_06369 | PQ loop repeat protein ( <i>A. benhamiae</i> )                                      | AGGACAAC      | 292 | UPRE-3 |
| TERG_06379 | transcription factor RfeF ( <i>T. tonsurans</i> )                                   | AGGACAAC      | 858 | UPRE-3 |
| TERG_06506 | hypothetical protein  | GTTGTCCT (rc) | 615 | UPRE-3 |
| TERG_06507 | oxidoreductase, 2OG-Fe(II) oxygenase family ( <i>T. verrucosum</i> )                | AGGACAAC      | 61  | UPRE-3 |
| TERG_06507 | oxidoreductase, 2OG-Fe(II) oxygenase family ( <i>T. verrucosum</i> )                | AGGACAAC      | 649 | UPRE-3 |
| TERG_06577 | 37S ribosomal protein S9 ( <i>T. verrucosum</i> )                                   | GTTGTCCT (rc) | 747 | UPRE-3 |
| TERG_06658 | hypothetical protein  | AGGACAAC      | 340 | UPRE-3 |
| TERG_06685 | riboflavin aldehyde-forming enzyme ( <i>T. tonsurans</i> )                          | GTTGTCCT (rc) | 265 | UPRE-3 |
| TERG_06728 | hypothetical protein  | AGGACAAC      | 670 | UPRE-3 |
| TERG_06768 | pre-mRNA-splicing ATP-dependent RNA helicase PRP28                                  | GTTGTCCT (rc) | 86  | UPRE-3 |
| TERG_06769 | hypothetical protein  | GTTGTCCT (rc) | 798 | UPRE-3 |
| TERG_07077 | C6 transcription factor ( <i>T. equinum</i> )                                       | AGGACAAC      | 315 | UPRE-3 |
| TERG_07085 | peptidase ( <i>T. tonsurans</i> )   | GTTGTCCT (rc) | 819 | UPRE-3 |
| TERG_07159 | geranylgeranyl transferase type II alpha subunit, putative ( <i>T. verrucosum</i> ) | GTTGTCCT (rc) | 547 | UPRE-3 |
| TERG_07163 | GTPase activating protein ( <i>T. tonsurans</i> )                                   | AGGACAAC      | 938 | UPRE-3 |
| TERG_07168 | histone acetylase complex subunit ( <i>T. tonsurans</i> )                           | AGGACAAC      | 813 | UPRE-3 |
| TERG_07195 | AAA family ATPase ( <i>T. tonsurans</i> )   | AGGACAAC      | 982 | UPRE-3 |

|            |   |               |     |        |
|------------|---|---------------|-----|--------|
| TERG_07233 | acriflavine sensitivity control protein acr-2 ( <i>T. equinum</i> )           | GTTGTCCT (rc) | 559 | UPRE-3 |
| TERG_07234 | hypothetical protein  | AGGACAAC      | 393 | UPRE-3 |
| TERG_07253 | F-box and WD repeat-containing protein ( <i>T. tonsurans</i> )                | GTTGTCCT (rc) | 112 | UPRE-3 |
| TERG_07331 | integral membrane protein ( <i>T. tonsurans</i> )                             | GTTGTCCT (rc) | 143 | UPRE-3 |
| TERG_07433 | hypothetical protein  | AGGACAAC      | 668 | UPRE-3 |
| TERG_07435 | hypothetical protein  | AGGACAAC      | 397 | UPRE-3 |
| TERG_07446 | hypothetical protein  | AGGACAAC      | 685 | UPRE-3 |
| TERG_07469 | SUN domain-containing protein ( <i>T. equinum</i> )                           | GTTGTCCT (rc) | 270 | UPRE-3 |
| TERG_07472 | DNA repair helicase rad15   | AGGACAAC      | 671 | UPRE-3 |
| TERG_07479 | hypothetical protein  | GTTGTCCT (rc) | 793 | UPRE-3 |
| TERG_07485 | UDP-galactopyranose mutase ( <i>T. equinum</i> )                              | AGGACAAC      | 279 | UPRE-3 |
| TERG_07636 | dual specificity phosphatase ( <i>T. tonsurans</i> )                          | GTTGTCCT (rc) | 361 | UPRE-3 |
| TERG_07698 | CHL4 family chromosome segregation protein, putative ( <i>T. verrucosum</i> ) | AGGACAAC      | 235 | UPRE-3 |
| TERG_07844 | HAL protein kinase  | GTTGTCCT (rc) | 584 | UPRE-3 |
| TERG_07932 | vesicle-mediated transport protein Vid24, putative ( <i>T. verrucosum</i> )   | GTTGTCCT (rc) | 524 | UPRE-3 |
| TERG_07983 | hypothetical protein  | GTTGTCCT (rc) | 236 | UPRE-3 |
| TERG_08013 | Rox3 mediator complex subunit ( <i>T. equinum</i> )                           | GTTGTCCT (rc) | 519 | UPRE-3 |
| TERG_08017 | glutamyl-tRNA synthetase ( <i>T. tonsurans</i> )                              | AGGACAAC      | 505 | UPRE-3 |
| TERG_08031 | PHD finger domain-containing protein ( <i>T. equinum</i> )                    | GTTGTCCT (rc) | 210 | UPRE-3 |
| TERG_08153 | hypothetical protein  | GTTGTCCT (rc) | 547 | UPRE-3 |
| TERG_08191 | glucooligosaccharide oxidase ( <i>T. equinum</i> )                            | GTTGTCCT (rc) | 969 | UPRE-3 |
| TERG_08208 | glutathione S-transferase ( <i>T. verrucosum</i> )                            | AGGACAAC      | 832 | UPRE-3 |
| TERG_08282 | hypothetical protein  | GTTGTCCT (rc) | 222 | UPRE-3 |
| TERG_08289 | Rpp14 family protein ( <i>T. equinum</i> )                                    | AGGACAAC      | 343 | UPRE-3 |
| TERG_08316 | aflatoxin efflux pump ( <i>M. gypseum</i> )                                   | AGGACAAC      | 509 | UPRE-3 |
| TERG_08319 | CMGC/SRPK protein kinase  | GTTGTCCT (rc) | 738 | UPRE-3 |
| TERG_08320 | tetratricopeptide repeat protein 1 ( <i>T. equinum</i> )                      | AGGACAAC      | 940 | UPRE-3 |
| TERG_08421 | pH signal transduction protein Pall, putative ( <i>T. verrucosum</i> )        | GTTGTCCT (rc) | 548 | UPRE-3 |
| TERG_08422 | hypothetical protein  | AGGACAAC      | 224 | UPRE-3 |
| TERG_08503 | secalin ( <i>M. canis</i> )   | AGGACAAC      | 384 | UPRE-3 |
| TERG_08508 | hypothetical protein  | AGGACAAC      | 956 | UPRE-3 |
| TERG_08521 | Ser/Thr protein phosphatase ( <i>T. equinum</i> )                             | AGGACAAC      | 885 | UPRE-3 |
| TERG_08532 | DNA-binding protein HGH1, putative ( <i>T. verrucosum</i> )                   | AGGACAAC      | 968 | UPRE-3 |
| TERG_08708 | SesA protein ( <i>T. equinum</i> )  | GTTGTCCT (rc) | 246 | UPRE-3 |
| TERG_11527 | tenascin C ( <i>T. equinum</i> )  | AGGACAAC      | 116 | UPRE-3 |

# Supplementary Material

|            |  |               |     |        |
|------------|--|---------------|-----|--------|
| TERG_11614 | hypothetical protein   | AGGACAAC      | 301 | UPRE-3 |
| TERG_11646 | hypothetical protein   | AGGACAAC      | 506 | UPRE-3 |
| TERG_11827 | DUF323 domain-containing protein ( <i>T. equinum</i> )       | AGGACAAC      | 930 | UPRE-3 |
| TERG_11831 | hypothetical protein   | GTTGTCCT (rc) | 428 | UPRE-3 |
| TERG_11834 | hypothetical protein   | GTTGTCCT (rc) | 808 | UPRE-3 |
| TERG_11962 | DEAD/DEAH box RNA helicase ( <i>T. tonsurans</i> )           | AGGACAAC      | 369 | UPRE-3 |
| TERG_12004 | lipase ( <i>T. tonsurans</i> )                               | GTTGTCCT (rc) | 752 | UPRE-3 |
| TERG_12152 | hypothetical protein   | AGGACAAC      | 827 | UPRE-3 |
| TERG_12211 | ribosome biogenesis protein ( <i>T. tonsurans</i> )          | AGGACAAC      | 340 | UPRE-3 |
| TERG_12239 | integral membrane protein ( <i>M. gypseum</i> )              | AGGACAAC      | 972 | UPRE-3 |
| TERG_12342 | membrane zinc transporter ( <i>T. tonsurans</i> )            | AGGACAAC      | 871 | UPRE-3 |
| TERG_12432 | hypothetical protein   | AGGACAAC      | 423 | UPRE-3 |
| TERG_12477 | ABC bile acid transporter, putative ( <i>T. verrucosum</i> ) | GTTGTCCT (rc) | 592 | UPRE-3 |
| TERG_12622 | hypothetical protein   | GTTGTCCT (rc) | 140 | UPRE-3 |
| TERG_12663 | hypothetical protein   | AGGACAAC      | 969 | UPRE-3 |

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DNA sequences upstream (1,000-bp)

Number of unique genes (UPRE-1=1,518; UPRE-2=678; UPRE-3=142)

Overall number of unique genes=2,178

rc: reverse complement