

Supplemental Table 1

| GI    | Day 3 av Day 6 av | Final arch                                      | function                             | notes                   | pfam                          | runprofiles      | rps             | Pfam                | gene                                          | fa                                                 |
|-------|-------------------|-------------------------------------------------|--------------------------------------|-------------------------|-------------------------------|------------------|-----------------|---------------------|-----------------------------------------------|----------------------------------------------------|
| 1E+08 | 2.28              | SIG+G10 (ZnR?)                                  | Cell cycle                           |                         | G10                           | SIG              | -               | G10                 | PFE1140c                                      | 147 G10 protein                                    |
| 3E+08 | 8.324             | Histone Acetyltransferase (2 or 3 repeats)      | Chromatin                            |                         | Hat1_N+RNA_po                 | ACET+ACET+HMF    | ACET+MIP-T3+/-  | Hat1_N+RNA_pol_3    | PF00795w                                      | 1259 conserved, unknown function, Pf3D7            |
| 3E+08 | 6.747             | PHD+PHD+PHD+BROMO+PHD+SET+LRRNT                 | Chromatin                            |                         | Med3+Utp14+PH                 | PHD+PHD+BRON     | MIP-T3+Termin   | Med3+Utp14+PHD+     | PF1440w                                       | 6753 SET domain protein, putative Pf3D7            |
| 3E+08 | 2.485             | TM+TM+TM+ANK+DEACET+DEACET (histo               | Chromatin                            |                         | TM+TM+TM+Anl                  | TM+TM+TM+AN      | ANK+Tox-DDRG    | Ank_5+Med3+Hist_c   | PF14_069f                                     | 2251 histone deacetylase, putative Pf3D7           |
| 3E+08 | 6.381             | 6.568 BetaPropeller+BetaPropeller+BetaPropeller | Cytoskeleton                         |                         | WD40+Herpes_L                 | BetaPropeller+B  | BetaPropeller+I | WD40+Herpes_LMP     | PF14_026f                                     | 1990 probable protein, unknown function Pf3D7      |
| 1E+08 | 4.483             | 2.894 SIG+BetaPropeller+BetaPropeller+TM        | Cytoskeleton                         |                         | SIG+VCBS+VCBS+                | SIG+IG           | BetaPropeller   | VCBS+VCBS           | PFE1445c                                      | 719 conserved, unknown function, Pf3D7             |
| 1E+08 | 3.563             | Low comp (and fibrinogen-hhpred)                | Cytoskeleton                         |                         | SMC_N                         | -                | sigma           | SMC_N               | PF02035w                                      | 1139 conserved, unknown function, Pf3D7            |
| 1E+08 | 0.372             | MOZART1                                         | Cytoskeleton                         |                         | MOZART1                       | -                | -               | MOZART1             | PF13_021f                                     | 72 conserved, unknown function, Pf3D7              |
| 1E+08 | 0.44              | Rila(Regulatory subunit of type II PKA-R)       | Cytoskeleton                         | hhpred                  | -                             | -                | -               | -                   | PF14_023f                                     | 175 conserved, unknown function, Pf3D7             |
| 3E+08 | 0.426             | TTL+ATPgrasp+ATPgraspC (TTL6/13)                | Cytoskeleton                         |                         | TTL                           | TTL-ATPgrasp+A   | TTL-ATPgrasp+/- | TTL                 | PF10_009f                                     | 553 tubulin-tyrosine ligase, putative Pf3D7        |
| 1E+08 | 0.289             | ZnR                                             | DNA binding                          | Plasmodium i -          | -                             | TRANSLUTAM       | -               | -                   | PF14_040f                                     | 2511 conserved, unknown function, Pf3D7            |
| 1E+08 | -                 | 4.605 MutS_III+MutS_V                           | DNA repair                           |                         | MutS_III+MutS_V               | -                | SbcC+SbcC       | MutS_III+MutS_V     | PF14_025f                                     | 811 DNA mismatch repair protein Msh2p, Pf3D7       |
| 1E+08 | 6.364             | SRAP/BB1717-like (DUF159,12n6A)                 | DNA repair                           |                         | DUF159+Utp14+I                | SRAP+IMP+SRAP    | SRAP+MIP-T3+5   | DUF159+Utp14+DUF    | PF10105w                                      | 401 conserved, unknown function, Pf3D7             |
| 1E+08 | 0.469             | Pur_DNA_glyco                                   | DNA repair                           |                         | Pur_DNA_glyco                 | -                | -               | Pur_DNA_glyco       | PF14_063f                                     | 501 DNA-3-methyladenine glycosylase, Pf3D7         |
| 1E+08 | -                 | 15.32 SF-I-Helicase                             | DNA repair;RNA                       |                         | Viral_helicase1+/-            | IES1+RNA-Helica  | RNA-Helicase    | Viral_helicase1+AAA | PF13_018f                                     | 1328 conserved, unknown function, Pf3D7            |
| 1E+08 | 0.389             | MCM-AAA                                         | DNA replication                      |                         | MCM_N+MCM                     | MCM-AAA          | MCM-AAA         | MCM_N+MCM           | PF13_029f                                     | 929 replication licensing factor, putative Pf3D7   |
| 1E+08 | 2.959             | GCV_T+GCV_T_C (Aminomethyltransferase           | Metabolism                           |                         | GCV_T+GCV_T_C                 | -                | -               | GCV_T+GCV_T_C       | PF13_034f                                     | 406 aminomethyltransferase, mitochondrial Pf3D7    |
| 1E+08 | 0.399             | Flavokinase                                     | Metabolism                           |                         | Flavokinase                   | -                | -               | Flavokinase         | MAL13P1                                       | 707 riboflavin kinase / FAD synthase family, Pf3D7 |
| 1E+08 | 2.574             | Abhydrolase_6                                   | metabolism (Lipid)                   |                         | Abhydrolase_6                 | 7TMR-HDED+3H-    | -               | Abhydrolase_6       | PF14_073f                                     | 371 lysophospholipase, putative Pf3D7              |
| 1E+08 | 10.37             | SIG+OTCace_N+OTCace (Aspartate carbom           | Metabolism (Nucleotide)              |                         | SIG+OTCace_N+G                | -                | -               | OTCace_N+OTCace     | MAL13P1                                       | 375 aspartate carbamoyltransferase Pf3D7           |
| 3E+08 | 20.84             | 5.606 TM+TM+WD40                                | Misc                                 |                         | Mito_carr+Mito                | TM+TM+McR-B-A    | TRANSLUTAM      | Spore_YhcN_YlaJ+S   | PF11120c                                      | 4255 conserved, unknown function, Pf3D7            |
| 1E+08 | -                 | 6.047 Conserved DxD with Fast_1                 | Misc                                 | Apicomplexa             | Vfa1                          | -                | CDC27           | Vfa1                | PF10_009f                                     | 779 conserved, unknown function, Pf3D7             |
| 1E+08 | -                 | 4.691 PF14_0074 conserved domain (PF14_0074     | Misc                                 | Apicomplexa             | -                             | -                | -               | -                   | PF14_007f                                     | 406 conserved, unknown function, Pf3D7             |
| 3E+08 | -                 | 2.133 SIG+Plasmodium-specific (PF0315c aln)     | Misc                                 | Plasmodium i            | SIG                           | SIG              | -               | -                   | PF0315c                                       | 116 conserved, unknown function, Pf3D7             |
| 3E+08 | -                 | 0.487 SIG+Lowcomplexity(Fast_1 LRR?)            | Misc                                 | Plasmodium i            | SIG                           | SIG              | -               | -                   | PF0855c                                       | 476 conserved, unknown function, Pf3D7             |
| 3E+08 | -                 | 0.418 PF10_0304, Pfa only. Conserved Ds (PF10_  | Misc                                 | Plasmodium i -          | FUNGAL-DEAM-i                 | -                | -               | -                   | PF10_030f                                     | 184 conserved, unknown function, Pf3D7             |
| 1E+08 | 9.366             | 3.703 Lowcomp+TM+Lowcomp+C.H...C                | Misc                                 | Plasmodium i            | TM+DUF2076                    | TM               | -               | DUF2076             | PF07_002f                                     | 954 conserved, unknown function, Pf3D7             |
| 1E+08 | 8.964             | 8.683 Low comp+Sugar-Transferase??(hhpred-PFL   | Misc                                 | Apicomplexa             | Innate_immun+/-               | -                | sigma+TRANS     | Innate_immun+TFIIF  | PF13175w                                      | 1401 conserved, unknown function, Pf3D7            |
| 1E+08 | 4.645             | Lowcomp                                         | Misc                                 | Plasmodium i            | Inca+Inca+TT_ORF1             | -                | -               | Inca+Inca+TT_ORF1   | PFE1485w                                      | 1906 conserved, unknown function, Pf3D7            |
| 1E+08 | 0.445             | Lowcomplexity                                   | Misc                                 | Plasmodium i            | SMC_N+SMC_N+DUF3300           | -                | sigma+EP1+sigr  | SMC_N+SMC_N+DU      | PF10350c                                      | 2612 conserved, unknown function, Pf3D7            |
| 3E+08 | 0.441             | Plasmodium only                                 | Misc                                 | Plasmodium i -          | -                             | -                | -               | -                   | MAL8P1.1                                      | 135 conserved, unknown function, Pf3D7             |
| 3E+08 | 0.429             | TM+TM+Plasmodium-specific                       | Misc                                 | Plasmodium i            | TM+TM                         | TM+TM            | -               | BioY                | PF14_062f                                     | 485 conserved, unknown function, Pf3D7             |
| 1E+08 | 0.389             | LowComp                                         | Misc                                 | -                       | -                             | -                | -               | -                   | PF10640c                                      | 789 conserved, unknown function, Pf3D7             |
| 3E+08 | 0.369             | Lowcomplexity                                   | Misc                                 | Plasmodium i            | YfhO+Med3                     | -                | -               | YfhO+Med3           | PF11_038f                                     | 656 conserved, unknown function, Pf3D7             |
| 1E+08 | 0.311             | (PF14_0130-aln)                                 | Misc                                 | Plasmodium only         | -                             | -                | -               | -                   | PF14_013f                                     | 573 conserved, unknown function, Pf3D7             |
| 1E+08 | 0.393             | Nucleoporin_FG-repeat                           | Nuclear envelop                      |                         | Nucleoporin_FG+Nucleoporin_FG | -                | SbcC+TRANSL     | Nucleoporin_FG+Nu   | PF14_044f                                     | 3001 conserved, unknown function, Pf3D7            |
| 1E+08 | 5.496             | HSP-like Iron Sulfur scaffold domain            | Protein folding                      | (FeS ase 2d2a_A ; PFD - | -                             | -                | -               | -                   | PF08320c                                      | 160 iron-sulfur assembly protein, putative Pf3D7   |
| 1E+08 | 8.359             | 9.408 TPR+DNAJ                                  | protein folding/Stress response      |                         | DnaJ                          | DNAJ             | DNAJ            | DnaJ                | PF11_027f                                     | 640 DNAJ protein, putative Pf3D7                   |
| 1E+08 | 3.58              | 7.557 SIG+ClpABN-AAA+ClpABC-AAA                 | protein folding/Stress response      |                         | SIG+Clp_N+AAA+                | SIG+ClpABN-AA    | SbcC+ClpABN-A   | Clp_N+AAA+OmpH+     | PF11_017f                                     | 906 heat shock protein 101, putative Pf3D7         |
| 3E+08 | 2.068             | DnaJ+DnaJ-X+DnaJ-X                              | protein folding/Stress response      |                         | DnaJ+DnaJ-X+Dn                | DNAJ             | -               | DnaJ+DnaJ-X+DnaJ    | PF14_001f                                     | 492 DNAJ protein, putative Pf3D7                   |
| 1E+08 | 0.42              | SIG+DNAJ-X                                      | protein folding/Stress response      |                         | SIG+DnaJ-X                    | SIG              | -               | DnaJ-X              | PF11_002f                                     | 282 hypothetical protein PF11_0026 Pf3D7           |
| 1E+08 | 0.402             | HSP-20-like chaperone(NudC)                     | protein folding/Stress re            | hhpred                  | -                             | -                | Nimm37          | -                   | PF14_046f                                     | 333 conserved, unknown function, Pf3D7             |
| 3E+08 | 2.448             | HSP70-C-like-IG+TM                              | protein folding/Stress re            | 1ud0_A                  | TM                            | TM               | -               | -                   | PF10_041f                                     | 182 conserved, unknown function, Pf3D7             |
| 3E+08 | 0.431             | SIG+Peptidase_M16+Peptidase_M16_C+Pe            | Protein processing                   |                         | SIG+Peptidase_M               | SIG              | -               | Peptidase_M16+Pep   | PF14_038f                                     | 1560 Stromal-processing peptidase, putative Pf3D7  |
| 1E+08 | 6.285             | SIG+SERAProtease                                | Protein processing                   |                         | SIG+Pneumo_att                | SIG+SERAProtea   | GT+SERAProtea   | Pneumo_att_G+Pep    | PF08350c                                      | 930 serine repeat antigen 3 (SERA-3) Pf3D7         |
| 3E+08 | 4.672             | Peptidase_M24/Creatinase/aminopeptidasi         | Protein processing                   |                         | Peptidase_M24                 | -                | -               | Peptidase_M24       | PFE1360c                                      | 327 methionine aminopeptidase, putative Pf3D7      |
| 1E+08 | -                 | 2.428 Peptidase_C54+Peptidase_C54 (Cysteine Pr  | Protein processing/Autophagy         |                         | Peptidase_C54+-               | -                | -               | Peptidase_C54+Secr  | PF14_017f                                     | 1124 conserved, unknown function, Pf3D7            |
| 3E+08 | 4.48              | TM+TM+Rhomboid+TM                               | Protein processing; Surface/exported |                         | TM+TM+Rhomboid                | TM+RHOMBOLD      | RHOMBOLD        | Rhomboid            | MAL8P1.1                                      | 267 rhomboid protease ROM3, putative Pf3D7         |
| 1E+08 | -                 | 5.327 X-term+TM+TM+RAP(VSR-Rease) relatec       | RNA                                  |                         | Atrophin-1+TM+TM              | TM+TM            | -               | Atrophin-1+RAP      | PFE1295c                                      | 806 RAP protein, putative Pf3D7                    |
| 1E+08 | -                 | 2.237 RAP(VSR-Rease)                            | RNA                                  |                         | RAP                           | RIFIN            | -               | RAP                 | PF14_067f                                     | 532 RAP protein, putative Pf3D7                    |
| 1E+08 | 10.51             | 4.228 Conserved Cs+RAP(VSR-Rease)               | RNA                                  |                         | RAF                           | MED7             | -               | RAP                 | PF14_050f                                     | 1725 RAP protein, putative Pf3D7                   |
| 3E+08 | -                 | 4.46 CCCH(zf-CDGSH)+CCCH(zf-CDGSH-degraded      | RNA                                  |                         | zf-CDGSH+TM                   | TM               | -               | zf-CDGSH            | PF10_022f                                     | 118 PfMNL-3 CSD1-like iron-sulfur protein, Pf3D7   |
| 1E+08 | -                 | 4.075 RRM+RRM                                   | RNA                                  |                         | RRM_1                         | RRM              | RRM             | RRM_1               | PF10_019f                                     | 322 NOP12-like protein Pf3D7                       |
| 1E+08 | 14.22             | 4.465 RRM                                       | RNA                                  |                         | RRM_1                         | RRM              | RRM             | RRM_1               | PF10_002f                                     | 248 RNA binding protein, putative Pf3D7            |
| 9E+07 | 3.368             | 3.721 RRM+RRM                                   | RNA                                  |                         | RRM_1+RRM_6+                  | RRM+RRM          | MIF             | RRM_1+RRM_6+Tra     | PF03000w                                      | 582 RNA binding protein, putative Pf3D7            |
| 1E+08 | 2.24              | CCCH+CCCH+CCCH                                  | RNA                                  |                         | -                             | ZNKNUCK+PLC      | -               | -                   | PF13_031f                                     | 1005 conserved, unknown function, Pf3D7            |
| 9E+07 | 0.458             | RNA Helicase (3rc3A ATP-dependent RNA h         | RNA                                  |                         | Innate_immun+I                | IES1             | -               | Innate_immun+Helic  | PF11140c                                      | 1137 ATP dependent DEAD-box helicase, Pf3D7        |
| 1E+08 | 0.391             | RRM7+LittleFinger+RRM+C2H2                      | RNA                                  |                         | zf-RanBP+DUF24                | LittleFinger+RRM | MIP-T3+LittleF  | zf-RanBP+DUF2457    | PF13_027f                                     | 1164 ran-binding protein, putative Pf3D7           |
| 1E+08 | 0.455             | NUDIX                                           | RNA                                  |                         | NUDIX_2                       | -                | -               | NUDIX_2             | PFA_0450f                                     | 232 mRNA cleavage factor-like protein, Pf3D7       |
| 1E+08 | -                 | 5.911 RNA-Helicase                              | RNA metabolism                       |                         | DEAD+Helicase_C               | (RNA-Helicase    | RNA-Helicase    | DEAD+Helicase_C     | PF13_003f                                     | 630 DEAD box helicase, putative Pf3D7              |
| 1E+08 | 12.43             | NIC+MA3(TPR)                                    | RNA metabolism                       |                         | Macolilin+MIF4G               | NIC              | -               | Macolilin+MIF4G+DU  | PF11855w                                      | 967 cell cycle control protein, putative Pf3D7     |
| 3E+08 | 6.246             | PIN+OB+OB+RNASEII+51-OB (exonuclease            | RNA metabolism                       | 4ifd_j                  | RNB                           | RNASEII          | SFII-RAD3+RNA   | RNB                 | MAL13P1                                       | 1073 mitotic control protein dis3 homologue, Pf3D7 |
| 3E+08 | 2.344             | 7.32 SIG+TM+Nop5(3id6)                          | RNA metabolism                       |                         | Plasmodium i                  | ETRAMP           | SIG+TM          | -                   | PF14_072f                                     | 177 early transcribed membrane protein 14.2, Pf    |
| 3E+08 | 0.466             | SIG+KOW(hhpred)+Fast_1??+ARL2_Bind_B            | RNA metabolism                       | all hhpred              | STRAMP                        | SIG              | -               | -                   | PF11468c                                      | 1150 leucine-rich repeat protein 8, LRR8 Pf3D7     |
| 3E+08 | 0.452             | DUF2418??+Sm (both hhpred)                      | RNA metabolism                       | Plasmodium i -          | -                             | -                | -               | -                   | PF10355w                                      | 218 conserved, unknown function, Pf3D7             |
| 1E+08 | 0.363             | RnasePH                                         | RNA metabolism                       |                         | -                             | RnasePH          | RnasePH         | -                   | PF06050c                                      | 332 conserved, unknown function, Pf3D7             |
| 3E+08 | 0.327             | NIC                                             | RNA metabolism                       |                         | Utp14                         | NIC              | NIC             | Utp14               | PF14_011f                                     | 947 conserved, unknown function, Pf3D7             |
| 1E+08 | 6.665             | Alba                                            | RNA metabolism;chromatin             |                         | Alba                          | Alba             | Alba            | Alba                | PF10_006f                                     | 107 DNA/RNA-binding protein, putative Pf3D7        |
| 1E+08 | -                 | 4.083 CCR4                                      | RNA; chromatin                       |                         | SIG+SMC_N                     | SIG+IPP          | CCR4            | SMC_N               | PF08500c                                      | 906 endonuclease/exonuclease/phosphatase           |
| 1E+08 | 3.229             | RING+RRM+CCCH(inserted?)                        | RNA; Ubiquitin                       |                         | zf-RING_4+TT_OI               | RING+RRM         | DHH+RING+RR1    | zf-RING_4+TT_ORF1   | PF11705w                                      | 1662 RNA binding protein, putative Pf3D7           |
| 1E+08 | 0.464             | MAL7P1.125-repeats aln (hhpred and PSlib)       | see aln                              | see aln                 | -                             | -                | -               | -                   | MAL7P1.1                                      | 880 conserved, unknown function, Pf3D7             |
| 1E+08 | -                 | 2.905 Adenylate kinase                          | Signaling                            |                         | ADK                           | -                | -               | ADK                 | PF10_008f                                     | 242 adenylate kinase Pf3D7                         |
| 1E+08 | -                 | 2.434 STYKIN                                    | Signaling                            |                         | Pkinase                       | DOC              | STYKIN+SPX      | Pkinase             | PF12280w                                      | 909 cyclin g-associated kinase, putative Pf3D7     |
| 3E+08 | -                 | 2.399 SIG+STYKIN                                | Signaling                            |                         | SIG+Pkinase                   | SIG+STYKIN       | STYKIN          | Pkinase             | PF10105c                                      | 633 Serine/Threonine protein kinase, FIKK Pf3D7    |
| 3E+08 | -                 | 2.378 TM+phosphodiesterase+TM+TM+TM+TM+         | alkaline - pho                       | TM+TM+TM+Acyl           | TM+TM+TM+TM                   | MADS+CCXcp+/-    | Acyl_transf_3   | PF10685w            | 1373 Phosphatidylinositol-glycan biosynthesis |                                                    |
| 1E+08 | -                 | 2.313 IPK                                       | Signaling                            |                         | IPK                           | -                | -               | IPK                 | PFE0740c                                      | 903 kinase, putative Pf3D7                         |
| 1E+08 | 15.11             | sGTPase+TM?                                     | Signaling                            |                         | MMR_HSR1+TM                   | TM               | -               | MMR_HSR1            | PF14_056f                                     | 797 conserved, unknown function, Pf3D7             |
| 1E+08 | 7.141             | C2+Lowcomp                                      | Signaling                            | Apicomplexa             | -                             | MED3             | Asp-B-Hydro_N   | -                   | PF13_017f                                     | 1001 conserved, unknown function, Pf3D7            |
| 3E+08 | 5.776             | STYKIN                                          | Signaling                            |                         | EDR1+Pkinase                  | TRANSLUTAM       | SbcC+CDC27+Ti   | EDR1+Pkinase        | PF11285w                                      | 1179 protein kinase, putative Pf3D7                |
| 3E+08 | 5.124             | STYKIN+TM+TM+B2IP+TM+xx+TM+TBC+TM               | Signaling                            |                         | Pkinase+TM+TM                 | STYKIN+TM+TM     | STYKIN+TRANS    | Pkinase+RabGAP-TB   | MAL7P1.1                                      | 1936 conserved, unknown function, Pf3D7            |
| 9E+07 | 2.043             | sGTP                                            | Signaling                            |                         | Ras                           | sGTP+sGTP-MgI    | sGTP-MgIa       | Ras                 | PFA_0125f                                     | 516 conserved, unknown function, Pf3D7             |
| 3E+08 | 0.441             | EF-hand                                         | Signaling                            |                         | -                             | -                | -               | -                   | PFA_0305f                                     | 215 conserved, unknown function, Pf3D7             |
| 9E+07 | 0.44              | EGF                                             | Signaling                            |                         | EF-hand_7                     | EFHAND           | EFHAND          | EF-hand_7           | PF0265c                                       | 160 calcium-binding protein, putative Pf3D7        |
| 1E+08 | 0.329             | 14-3-3                                          | Signaling                            |                         | 14-3-3                        | -                | -               | 14-3-3              | PF14_022f                                     | 425 conserved, unknown function, Pf3D7             |
| 3E+08 | 3.705             | STYKIN+Beta-lactamase+C-rich                    | Signaling                            | C-term 2/201            | ABCI+Beta-lacta               | STYKIN           | -               | STYKIN+Asp-B+I      | PF14_014f                                     | 2763 Atypical protein kinase, ABC-1 family, Pf3D7  |
| 3E+08 | 3.204             | TM+fragment of a kinase                         | Signaling                            |                         | ABCI+Beta-lacta               | STYKIN           | -               | -                   | PF14_073f                                     | 347 Serine/Threonine protein kinase, FIKK Pf3D7    |
| 3E+08 | -                 | 6.107 SIG                                       | Surface/exported protein             | Falcaparum o            | SIG                           | -                | -               | -                   | PFE1615c                                      | 161 Plasmodium exported protein, Pf3D7             |
| 1E+08 | -                 | 5.409 SIG+PF07_0087-C...CxxC...HxxRg...C (PF07  | Surface/exported protein             | Apicomplexa             | SIG                           | SIG              | -               | -                   | PF07_008f                                     | 244 conserved, unknown function, Pf3D7             |
| 1E+08 | -                 | 5.316 SIG+ACBP+ANK                              | Surface/exported protein             |                         | SIG+ACBP+Ank_2                | SIG+ANK          | ANK             | ACBP+Ank_2          | PF11_019f                                     | 371 conserved Pf3D7                                |
| 1E+08 | -                 | 5.14 TM+TM+DHHC-ZNF+TM+TM                       | Surface/exported protein             |                         | TM+zf-DHHC                    | TM+TM+DHHC-2     | DHHC-ZNF        | zf-DHHC             | MAL13P1                                       | 313 DHHC-type zinc finger protein, putative Pf3D7  |
| 1E+08 | -                 | 4.609 common+TM+TM+TM+TM+TM                     | Surface/exported protein             | Apicomplexa             | TM+TM+TM+TM                   | TM+TM+TM+TM      | TM+TM+TM+TM     | TM+TM+TM+TM         | PF10775w                                      | 293 conserved, unknown function, Pf3D7             |
| 3E+08 | -                 | 3.653 TM                                        | Surface/exported protein             | Apicomplexa             | TM                            | TM               | -               | -                   | PF141432w                                     | 82 conserved Pf3D7                                 |
| 1E+08 | -                 | 3.366 TM+TM+X+TM+TM+TM+TM                       | Surface/exported protein             | Plasmodium i            | TM+TM+TM+TM                   | TM+TM+TM+TM      | TM+TM+TM+TM     | TM+TM+TM+TM         | PF14_059f                                     | 523 conserved, unknown function, Pf3D7             |
| 1E+08 | -                 | 2.646 SIG+Rifin_STEVOR                          | Surface/exported protein             |                         | Rifin_STEVOR                  | RIFIN            | RIFIN           | Rifin_STEVOR        | PFL2645c                                      | 317 rifin Pf3D7                                    |
| 1E+08 | -                 | 2.375 HEAT repeats+TM+TPR(Vac14_Fab1_bdd        | Surface/exported protein             |                         | DUF2076+Vac14                 | TM               | UBC+SPX+8TMI    | DUF2076+Vac14_Fal   | PF11240c                                      | 1501 conserved Pf3D7                               |
| 1E+08 | -                 | 2.327 SIG+Duffy_binding+Duffy_binding+EBA-175   | Surface/exported protein             |                         | SIG+Duffy_bindin              | SIG+VAR+TM       | MIP-T3          | Duffy_binding+Duffy | PFA_0125f                                     | 1567 erythrocyte binding antigen-181 Pf3D7         |
| 1E+08 | -                 | 2.26 SIG+Rifin_STEVOR                           | Surface/exported protein             |                         | SIG+Rifin_STEVO               | RIFIN            | RIFIN           | Rifin_STEVOR        | PF14_000f                                     | 339 rifin Pf3D7                                    |
| 3E+08 | -                 | 2.123 Lowcomp+TM+TM+TM+TM+TM+TM+TM              | Surface/exported protein             |                         | HlyIII                        | TM+TM+TM+TM      | TM+TM+TM+TM     | -                   | PF14_052f                                     | 282 hemolysin, putative Pf3D7                      |
| 1E+08 | -                 | 2.111 TM                                        | Surface/exported protein             | Falcaparum o            | TM                            | TM               | -               | -                   | PF12525c                                      | 378 Plasmodium exported protein Pf3D7              |
| 1E+08 | 11.95             | SIG+TM+TM+TM+Tox-SUFU-associated                | Surface/exported protein             |                         | SIG+TM+TM+TM                  | SIG+TM+TM+TM     | Tox-SUFU-assoc  | -                   | MAL8P1.5                                      | 455 conserved, unknown function, Pf3D7             |
| 1E+08 | 11.12             | TM+TM+TM+TM+TM+TM+TM                            | Surface/exported protein             | Apicomplexa             | RP1-2+TM+TM                   | TM+TM+TM+TM      | TM+TM+TM+TM     | PUA+EP1             | PF11_043f                                     | 1828 conserved Pf3D7                               |
| 1E+08 | 10.25             | SIG+Rifin_STEVOR                                | Surface/exported protein             |                         | SIG+Rifin_STEVO               | RIFIN            | RIFIN           | Rifin_STEVOR        | PF11810w                                      | 359 rifin Pf3D7                                    |
| 3E+08 | 9.851             | SIG+TM+TM+EGF+TM                                | Surface/exported protein             |                         | SIG+TM+TM+TM                  | SIG+TM+TM+EGF    | EGF+PrsW        | -                   | PF10900w                                      | 1720 conserved, unknown function, Pf3D7            |
| 3E+08 | 8.787             | SIG+TM+TM+TM+TM+TM+TM+TM                        | Surface/exported protein             |                         | SIG+PSS+TM                    | TM               | -               | PSS                 | MAL13P1                                       | 357 phosphatidylser                                |

|       |       |                                            |                                          |                         |                            |                |                      |                    |                                    |                                                    |                                                    |                                    |
|-------|-------|--------------------------------------------|------------------------------------------|-------------------------|----------------------------|----------------|----------------------|--------------------|------------------------------------|----------------------------------------------------|----------------------------------------------------|------------------------------------|
| 1E+08 | 3.071 | SIG+Tox-ALFMPase[Zincin-Metalloprotease]   | Surface/exported protein                 | SIG                     | SIG                        | Tox-ALFMPase - | PFD0425w             | 984                | conserved, unknown function, Pf3D7 |                                                    |                                                    |                                    |
| 1E+08 | 3.06  | TM+TM+TM+TM+LowComp+TM+TM                  | Surface/exported protein                 | Falciparum or           | TM+TM+TM+TM                | TM+TM+TM+TM    | FIH                  | Secretin_N_2       | MAL7P1.1                           | 779                                                | conserved, unknown function, Pf3D7                 |                                    |
| 3E+08 | 2.94  | SIG+Rifin_STEVOR                           | Surface/exported protein                 | SIG+Rifin_STEVO         | RIFIN                      | RIFIN          | Rifin_STEVOR         |                    | PFB1035w                           | 330                                                | rifin Pf3D7                                        |                                    |
| 1E+08 | 2.841 | SIG+TM+(conserved WDY)                     | Surface/exported protein                 | Plasmodium              | SIG+TM                     | SIG+TM         | -                    | -                  | PFB0930w                           | 225                                                | Plasmodium exported protein (hyp9) Pf3D7           |                                    |
| 3E+08 | 2.72  | SIG+Methylase                              | Surface/exported protein                 | SIG+Cons_hypot          | SIG+DNAMETHY               | SPX+METHYLAS   | Cons_hypot95         |                    | MAL13P1.                           | 561                                                | N6-adenine-specific methylase, putative Pf3D7      |                                    |
| 1E+08 | 2.643 | SIG+Rifin_STEVOR                           | Surface/exported protein                 | SIG+Rifin_STEVO         | RIFIN                      | RIFIN          | Rifin_STEVOR         |                    | PF11_051i                          | 308                                                | stevor, putative [Plasmodium falciparum 3D7]       |                                    |
| 3E+08 | 2.631 | SIG+Rifin_STEVOR                           | Surface/exported protein                 | SIG+Rifin_STEVO         | RIFIN+TM                   | RIFIN          | Rifin_STEVOR         |                    | PFB0035c                           | 375                                                | rifin Pf3D7                                        |                                    |
| 1E+08 | 2.509 | SIG+PRESAN+PRESAN                          | Surface/exported protein                 | Plasmodium              | SIG+PRESAN+Noj             | SWC3+MIP-T3    | PRESAN+Nop14+PRI     |                    | PFL0050c                           | 653                                                | Plasmodium exported protein (PHISTb) Pf3D7         |                                    |
| 1E+08 | 2.484 | SIG+Rifin_STEVOR                           | Surface/exported protein                 | SIG+Rifin_STEVO         | RIFIN                      | RIFIN          | Rifin_STEVOR         |                    | PF13_000i                          | 331                                                | rifin Pf3D7                                        |                                    |
| 3E+08 | 2.466 | SIG+LowComp+TM+TM                          | Surface/exported protein                 | Plasmodium              | SIG+TM+TM                  | SIG+TM+TM      | 7TMR-HD              | -                  | PF11_001i                          | 231                                                | Maurer's Cleft 2 transmembrane domain 11.1         |                                    |
| 1E+08 | 2.294 | LowComp+TM+TM                              | Surface/exported protein                 | Apicomplexa             | TM+TM                      | TM+TM          | -                    | -                  | MAL7P1.9                           | 179                                                | conserved, unknown function, Pf3D7                 |                                    |
| 1E+08 | 2.124 | SIG+TM+TM                                  | Surface/exported protein                 | Plasmodium              | SIG+TM+TM                  | SIG+TM+TM      | -                    | -                  | PFD1205w                           | 230                                                | Plasmodium exported protein (hyp15), Pf3D7         |                                    |
| 1E+08 | 2.051 | SIG+Rifin_STEVOR                           | Surface/exported protein                 | SIG+Rifin_STEVO         | RIFIN+TM                   | RIFIN          | Rifin_STEVOR         |                    | PF11_001i                          | 259                                                | stevor, putative, degenerate Pf3D7                 |                                    |
| 3E+08 | 0.464 | TM+TM+TM+TM+TM+TM+TM                       | Surface/exported protein                 | TM+TM+TM+TM             | TM+TM+TM+TM                | -              | -                    | -                  | PF14_077i                          | 373                                                | conserved, unknown function, Pf3D7                 |                                    |
| 1E+08 | 0.461 | SIG+Rifin_STEVOR                           | Surface/exported protein                 | SIG+Rifin_STEVO         | RIFIN                      | RIFIN          | Rifin_STEVOR         |                    | PFD0645w                           | 346                                                | rifin Pf3D7                                        |                                    |
| 3E+08 | 0.445 | SIG+Apicomplexa-specific                   | Surface/exported protein                 | Apicomplexa             | SIG                        | SIG            | Eukglutathione       | -                  | PF11_006i                          | 266                                                | conserved, unknown function, Pf3D7                 |                                    |
| 1E+08 | 0.436 | SIG+(conserved DxxD.... HDIN)              | Surface/exported protein                 | Plasmodium              | SIG                        | SIG            | -                    | -                  | PFC0795w                           | 202                                                | conserved, unknown function, Pf3D7                 |                                    |
| 1E+08 | 0.418 | TM+LowComp                                 | Surface/exported protein                 | Plasmodium              | TM                         | TM             | -                    | -                  | PF11055w                           | 421                                                | conserved, unknown function, Pf3D7                 |                                    |
| 1E+08 | 0.382 | TM+TM+TM+TM                                | Surface/exported protein                 | Plasmodium              | TM+TM+TM+TM                | TM+TM+TM+TM    | SbcC                 | -                  | PFE1180c                           | 1482                                               | conserved, unknown function, Pf3D7                 |                                    |
| 1E+08 | 0.37  | LowComp+TM+TM+TM+TM                        | Surface/exported protein                 | Plasmodium              | Rib_rec                    | KP_reg         | TM+TM+TM+TM          | MIP-T3+7TMR-I      | Rib_rec_KP_reg                     | MAL13P1.                                           | 324                                                | conserved, unknown function, Pf3D7 |
| 1E+08 | 0.333 | SIG+Lowcomp                                | Surface/exported protein                 | Plasmodium              | SIG                        | SIG            | -                    | -                  | PF10_003i                          | 553                                                | conserved, Pf3D7                                   |                                    |
| 1E+08 | 0.305 | SIG+LowComp                                | Surface/exported protein                 | Plasmodium              | SIG                        | SIG+IES4       | SPX                  | -                  | PF13_036i                          | 897                                                | conserved, unknown function, Pf3D7                 |                                    |
| 3E+08 | 4.004 | SIG+PF07422-s48_45/2ymo                    | Surface/exported protein                 | Plasmodium              | SIG+Secretin_N_1           | SIG            | Secretin_N_2         |                    | PFC0750w                           | 969                                                | conserved, unknown function Pf3D7                  |                                    |
| 3E+08 | 0.412 | Adaptin_N+Adaptin_N (TPR repeats)          | Trafficking                              | Adaptin_N+Adap          | IBD-HTH                    | Asp-B-Hydro_N  | Adaptin_N+Adaptin_N  |                    | PFI0200c                           | 1388                                               | conserved, unknown function, Pf3D7                 |                                    |
| 3E+08 | 2.424 | ZnR/zf-Tim10_DDP                           | Trafficking (mitochondrial)              | zf-Tim10_DDP            | -                          | -              | zf-Tim10_DDP         |                    | PFL2065c                           | 95                                                 | mitochondrial inner membrane translocase           |                                    |
| 1E+08 | 0.467 | ZnR/zf-Tim10_DDP                           | Trafficking (mitochondrial)              | zf-Tim10_DDP            | -                          | -              | zf-Tim10_DDP         |                    | PFE0140c                           | 82                                                 | zinc binding protein, putative Pf3D7               |                                    |
| 1E+08 | -     | 6.182                                      | SIG+Lowcomp+GOLD+TM                      | Trafficking (vesicular) | SIG+EMP24_GP2              | SIG+GOLD+TM    | GOLD                 | EMP24_GP25L        | PFD1037w                           | 385                                                | conserved, unknown function, Pf3D7                 |                                    |
| 1E+08 | 3.18  | Sig+TM+TM(Got1)                            | Trafficking (Vesicular)                  | Got1                    | SIG+TM                     | -              | -                    | Got1               | PFD0930w                           | 136                                                | CGI-141 protein homolog, putative Pf3D7            |                                    |
| 3E+08 | 0.264 | DUF1712/Mon1/CCZ1                          | Trafficking (Vesicular)                  | related to (Sf          | DUF1712                    | -              | -                    | DUF1712            | PF11_008i                          | 713                                                | conserved Pf3D7                                    |                                    |
| 3E+08 | 3.792 | Rab7 sGTP                                  |                                          | Ras                     | sGTP                       | sGTP           | Ras                  |                    | PFI0155c                           | 206                                                | PfRab7, GTPase Pf3D7                               |                                    |
| 1E+08 | 4.271 | RPB10-HTH                                  | Transcription                            | RNA_pol_N               | RPB10-HTH                  | RPB10-HTH      | RNA_pol_N            |                    | PF07_002i                          | 69                                                 | DNA-directed RNA polymerase, Pf3D7                 |                                    |
| 3E+08 | -     | 2.187                                      | (wHTH+C-rich)/RNA_pol_Rpc34+TM           | Transcription           | RNA_pol_Rpc34              | TM             | SbcC                 | RNA_pol_Rpc34      | PF14_020i                          | 311                                                | RNA polymerase subunit, putative Pf3D7             |                                    |
| 1E+08 | 2.643 | HTH (Apicomplexa 3 iteration)              | Transcription                            | HTH_3                   | CHTH                       | CHTH           | HTH_3                |                    | PFC0506w                           | 136                                                | conserved, unknown function, Pf3D7                 |                                    |
| 1E+08 | -     | 3.39                                       | Sin_N+HTH?+Sin_N_2(2/2015 Job-ID: 187667 | Transcription           | Sin_N - DNA+Sin_N+TT_ORF1- | -              | -                    | Sin_N+TT_ORF1+Sin  | PF14_056i                          | 865                                                | conserved, unknown function, Pf3D7                 |                                    |
| 1E+08 | -     | 4.251                                      | SIG+eIF-1 (S1)                           | Translation             | SIG+eIF-1a                 | SIG            | S1                   | elf-1a             | PF14_065i                          | 182                                                | translation initiation factor EF-1, putative Pf3D7 |                                    |
| 1E+08 | -     | 2.765                                      | TM+TM+PINT-HTH                           | Translation             | TM+TM+PCI                  | TM+TM+PINT     | PINT                 | PCI                | PFE1405c                           | 517                                                | eukaryotic translation initiation factor 3         |                                    |
| 1E+08 | -     | 2.516                                      | TetQ GTPase                              | Translation             | GTP_EFTU+Yae1              | sGTP           | -                    | GTP_EFTU+Yae1_N+   | PFL1710c                           | 1161                                               | tetQ family GTPase, putative Pf3D7                 |                                    |
| 1E+08 | 23.31 | Ribosomal_S11 (OB-S17)                     | Translation                              | Ribosomal_S17           | -                          | -              | Ribosomal_S17        |                    | PFC0775w                           | 161                                                | 40S ribosomal protein S11, putative Pf3D7          |                                    |
| 1E+08 | 21.36 | 6.695                                      | GTP_EFTU+GTP_EFTU_D2+GTP_EFTU_D3         | Translation             | GTP_EFTU+GTP               | sGTP-MglA      | SbcC                 | GTP_EFTU+GTP_EFT   | PF11_024i                          | 555                                                | translation elongation factor EF-1, Pf3D7          |                                    |
| 9E+07 | 14.34 | sGTP (IF2)                                 | Translation                              | SMC_N+GTP_EFT           | SIG+GTP                    | MIP-T3+GTP     | SMC_N+GTP_EFTU+      | PFF0345w           | 977                                | translation initiation factor IF-2, putative Pf3D7 |                                                    |                                    |
| 1E+08 | 13.15 | 4.087                                      | Ribosomal_L44                            | Translation             | Ribosomal_L44              | -              | -                    | Ribosomal_L44      | PFC0200w                           | 104                                                | 60S Ribosomal protein L44, putative Pf3D7          |                                    |
| 1E+08 | 6.815 | Ribosomal_L24e                             | Translation                              | Ribosomal_L24e          | -                          | -              | Ribosomal_L24e       |                    | PF13_004i                          | 162                                                | 60S ribosomal protein L24, putative Pf3D7          |                                    |
| 3E+08 | 4.817 | 3.104                                      | trnA_Synthetase+DALR-anticodon-binding   | Translation             | SIG+trnA-synt_1            | SIG            | -                    | trnA-synt_1e       | PF10_014i                          | 677                                                | cysteinyI-trNA synthetase, putative Pf3D7          |                                    |
| 1E+08 | 4.759 | tRNA_anti-codon-OB-fold+wHTH(hhpred)       | Translation                              | tRNA_anti-codon         | -                          | -              | tRNA_anti-codon      |                    | PF11_033i                          | 273                                                | conserved Pf3D7                                    |                                    |
| 1E+08 | 4.616 | PCRF+RF-1                                  | Translation                              | PCRF+RF-1               | -                          | SbcC           | -                    | PCRF+RF-1          | MAL7P1.2                           | 352                                                | peptide chain release factor, putative Pf3D7       |                                    |
| 1E+08 | 0.354 | Ribosomal_L28                              | Translation                              | Ribosomal_L28           | -                          | -              | Ribosomal_L28        |                    | PF14_053i                          | 281                                                | mitochondrial ribosomal protein L28, Pf3D7         |                                    |
| 1E+08 | 8.01  | SAM-Methylase                              | translation; RNA                         | Methyltransf_8          | SAM-methylase              | SAM-methylase  | Methyltransf_8       |                    | PF11235w                           | 413                                                | methyltransferase, putative Pf3D7                  |                                    |
| 1E+08 | -     | 3.554                                      | V_ATPase_I+V_ATPase_I+TM+TM+TM+TM        | Transport               | V_ATPase_I+PBP             | TM+TM+TM+TM    | -                    | V_ATPase_I+PBP1_T  | PF08_011i                          | 1053                                               | vacuolar proton translocating ATPase subunit A     |                                    |
| 1E+08 | 11.43 | 5.254                                      | TM+CDC50+TM                              | Transport               | TM+CDC50                   | TM+TM          | -                    | CDC50              | PF07_007i                          | 462                                                | transmembrane protein, putative Pf3D7              |                                    |
| 1E+08 | 7.554 | TM+TM+TM+TM+TM+ABC-ATPase+TM+TM            | Transport                                | TM+TM+TM+TM             | TM+TM+TM+TM                | TM+TM+TM+TM    | sigma+PTSEIIc        | ABC_tran+Herpes_L  | PFL1410c                           | 2108                                               | ABC transporter, (CT family) Pf3D7                 |                                    |
| 3E+08 | 6.016 | TM+TM (CorA)                               | Transport                                | CorA                    | TM+TM                      | -              | -                    | CorA               | MAL13P1.                           | 468                                                | unnamed protein product Pf3D7                      |                                    |
| 3E+08 | 0.393 | TM+TM+TM+TM+Mito_carr+TM                   | Transport                                | Mito_carr+Mito          | TM+TM+TM+TM                | -              | -                    | Mito_carr+Mito_car | PFA_0415i                          | 330                                                | mitochondrial carrier protein, putative Pf3D7      |                                    |
| 3E+08 | 4.453 | Ulp1. Cysteine Protease/Ulp1 protease/Pep  | Ubiquitin                                | Peptidase_C48           | Ulp1                       | SbcC+Ulp1      | -                    | Peptidase_C48      | PFL1635w                           | 1026                                               | Ulp1 protease, putative Pf3D7                      |                                    |
| 1E+08 | -     | 0.443                                      | SIG+UBA+EF-Ts-domain                     | Ubiquitin               | hhpred                     | SIG            | -                    | -                  | PF14_040i                          | 402                                                | conserved, unknown function, Pf3D7                 |                                    |
| 3E+08 | 14.79 | SIG+UFD(Double-psi-beta-barrel)            | Ubiquitin                                | SIG+UFD1                | SIG+UFD                    | -              | -                    | UFD1               | PF10810c                           | 296                                                | apicoplast Ufd1 precursor Pf3D7                    |                                    |
| 3E+08 | 3.958 | Cysteine Protease/UBP12/Peptidase_C12      | Ubiquitin                                | Peptidase_C12           | UBP12                      | UBP12          | Peptidase_C12        |                    | PF14_057i                          | 232                                                | ubiquitin carboxyl-terminal hydrolase, Pf3D7       |                                    |
| 3E+08 | 2.943 | SIG+RING                                   | Ubiquitin                                | SPX+zf-C3HC4            | 4 SIG+RING                 | SPX+RING       | -                    | SPX+zf-C3HC4       | PFB0440c                           | 568                                                | conserved Pf3D7                                    |                                    |
| 3E+08 | 0.429 | SIG+ubiquitin(beta-grasp)+alpha-helical+TM | Ubiquitin                                | SIG+ubiquitin+TM        | SIG+TM+TM+TM               | TM+TM+TM+TM    | UBI                  | ubiquitin          | PF08_006i                          | 373                                                | conserved, unknown function, Pf3D7                 |                                    |
| 1E+08 | 0.323 | UBHYD(with insert)                         | Ubiquitin                                | SART-1+UCH+UCH          | UBHYD                      | UBHYD          | -                    | SART-1+UCH+UCH     | PF14_014i                          | 1384                                               | ubiquitin C-terminal hydrolase, putative Pf3D7     |                                    |
| 9E+07 | 0.423 | Cullin+Cullin+Cullin                       | Ubiquitin                                | Cullin+Cullin+Cull      | CULLIN                     | CULLIN         | Cullin+Cullin+Cullin |                    | PFF1445c                           | 1129                                               | cullin-like protein, putative Pf3D7                |                                    |
| 3E+08 | -     | 3.701                                      | Baculo_Helicase/PF04735??(hhpred only)   | Plasmodium only         | Plasmodium                 | -              | -                    | ISOFLAVOMETH       | MAL13P1.                           | 2183                                               | conserved, unknown function, Pf3D7                 |                                    |
| 1E+08 | -     | 2.416                                      | HEAT repeats                             |                         | HEAT_2+HEAT_2              | ImmHEAT        | -                    | HEAT_2+HEAT_2      | PF13_001i                          | 411                                                | PBS lyase HEAT-like protein, putative Pf3D7        |                                    |
| 1E+08 | 18.98 | (camp-regulatory-sbubunit? -4f9k)          |                                          | Plasmodium only         | web-hhpred-2               | helix hit      | -                    | -                  | PF10_017i                          | 282                                                | conserved Pf3D7                                    |                                    |
| 1E+08 | 8.617 | 11.13                                      | HEAT Rpt(200...416)                      |                         | -                          | -              | -                    | -                  | PFE1060c                           | 1526                                               | conserved, unknown function, Pf3D7                 |                                    |
| 1E+08 | 4.993 | (HTH?)+ZnR                                 |                                          | -                       | -                          | -              | -                    | -                  | PFC0600w                           | 249                                                | conserved, unknown function, Pf3D7                 |                                    |
| 1E+08 | 3.696 | GAS (coiled-coil)                          |                                          | GAS                     | -                          | -              | -                    | GAS                | PFL2040w                           | 450                                                | conserved, unknown function, Pf3D7                 |                                    |
| 1E+08 | 0.491 | Thioredoxin                                |                                          | -                       | -                          | -              | -                    | -                  | PFI0245c                           | 281                                                | conserved, unknown function, Pf3D7                 |                                    |