

| # | FUNCTIONAL CLASSIFICATION | PLASMODB ID | OLIGO | ANNOTATION | GO ID | FUNCTIONAL ANNOTATION | FOLD CHANGE TO RELATIVE I0 WITH P-VALUES ADJUSTED FOR MDR DATA WITH P<0.05 ARE PRESENTED | | | | | | | | |
|------------------------|---------------------------|-------------|-----------------|---|------------|--|--|--------------------|--------------|-------------------------------------|--------------------|--------------|-------------------------------------|--------------------|--------------|
| | | | | | | | T ₁₁ log ₂ FC | T ₁₁ FC | adj. p value | T ₁₂ log ₂ FC | T ₁₂ FC | adj. p value | T ₁₃ log ₂ FC | T ₁₃ FC | adj. p value |
| | | | | | | | | | | | | | | | |
| CYTOKINESIS/CELL CYCLE | | | | | | | | | | | | | | | |
| 1 | | PF10_0084 | J73_4 | tubulin beta chain, putative:PF10_0084::(J73_4) | GO:000226 | microtubule cytoskeleton organization and biogenesis | -0.877117856 | 0.544454029 | 1.73E-06 | -0.685815503 | 0.621654329 | 1.51E-06 | -0.386724309 | 0.764864286 | 0.000464246 |
| 2 | | PF11_0066 | KS79_2 | putative:PF11_0066::(KS79_2) | GO:0007067 | mitosis | -0.615929357 | 0.652509424 | 4.00E-05 | -0.803545517 | 0.57293941 | 1.79E-06 | | | |
| 3 | | PF13_0328 | M36754_1 | proliferating cell nuclear antigen:PF13_0328::(M36754_1) | GO:006275 | regulation of DNA replication (cyclin signature) | -1.706908296 | 0.306315803 | 7.54E-07 | -1.241921596 | 0.422809121 | 1.19E-06 | -0.89604367 | 0.53735832 | 3.01E-05 |
| 4 | | PF14_0443 | N151_64 | centrin, putative:PF14_0443::(N151_64) | GO:008150 | biological_process | -0.846822885 | 0.556007834 | 0.000417307 | -0.686334045 | 0.62143093 | 0.002198874 | | | |
| 5 | | PF14_0604 | N134_76 | hypothetical protein:PF14_0604::(N134_76) | DAVID | cyclin-related protein | -0.430957268 | 0.741760183 | 0.002597857 | -0.791235564 | 0.577848994 | 7.11E-06 | | | |
| 6 | | PFA0190c | A8010_16 | actin:PF0190c::(A8010_16) | GO:0015629 | actin cytoskeleton | -0.996994918 | 0.501042567 | 0.012324662 | -0.797480159 | 0.575353224 | 0.021713375 | | | |
| 7 | | PFA0520c | A13725_9 | chromatin assembly factor 1 protein WD40 domain, putative:PFA0520c::(A13725_9) | GO:0006334 | nucleosome assembly | -1.049414161 | 0.483164324 | 2.63E-06 | -0.877686062 | 0.544239637 | 1.39E-06 | -0.684803092 | 0.622090728 | 1.70E-05 |
| 8 | | PFC0860w | C569 | kinesin, putative:PFC0860w::(C569) | GO:0007018 | microtubule-based movement | -0.558239134 | 0.679130564 | 0.009316004 | -0.774708401 | 0.584506753 | 0.000121797 | -0.38676511 | 0.764842655 | 0.020245942 |
| 9 | | PFE0165w | E13013_1 | actin depolymerizing factor, putative:PFE0165w::(E13013_1) | GO:0030042 | actin filament depolymerization | -0.832352633 | 0.561612662 | 2.15E-06 | -1.186394342 | 0.43939966 | 2.13E-09 | -0.987152039 | 0.50447265 | 8.31E-09 |
| 10 | | PFE0175c | OPFBLOB0060 | unconventional myosin pfm-b::PFE0175c::(OPFBLOB0060) | GO:0016459 | myosin complex | | | | -0.826336897 | 0.563959358 | 4.34E-05 | -0.810398212 | 0.570224443 | 4.30E-05 |
| | | PFE0175c | E15509_5 | unconventional myosin pfm-b::PFE0175c::(E15509_5) | GO:0016459 | myosin complex | | | | -1.188434644 | 0.438778687 | 7.94E-06 | -1.074370306 | 0.474878286 | 1.45E-05 |
| 11 | | PF1320c | PMAL6P1.156_432 | troponin c-like protein, putative:PF1320c::(PMAL6P1.156_432) | GO:0005509 | calcium ion binding | | | | -0.752079108 | 0.593747275 | 0.038816605 | | | |
| 12 | | PF10180w | OPF17633 | alpha tubulin:PF10180w::(OPF17633) | GO:0007017 | microtubule-based process | -0.924538667 | 0.526848962 | 1.48E-06 | -0.785617967 | 0.580103421 | 4.45E-07 | -0.598991642 | 0.660215245 | 6.93E-06 |
| 13 | | PF10180w | I16837_2 | alpha tubulin:PF10180w::(I16837_2) | GO:0007017 | microtubule-based process | -1.142794503 | 0.452881495 | 2.19E-05 | -0.958007559 | 0.515481459 | 1.04E-05 | -0.72099311 | 0.606721731 | 0.000157754 |
| | | PF10260c | I16684_1 | hypothetical protein:PF10260c::(I16684_1) | GO:0007018 | microtubule-based movement | | | | -1.19492245 | 0.436809927 | 0.012748816 | | | |
| 14 | | PF10975c | F37487_1 | hypothetical protein:PF10975c::(F37487_1) | DAVID | cell division and chromosome partitioning, regulator of chromosome condensation (RCC1) | | | | 0.530780447 | 1.444710521 | 0.027698267 | 0.798175725 | 1.738900911 | 0.00196178 |
| 15 | | PF11565w | OPF117675 | conserved protein:PF11565w::(OPF117675) | GO:0007010 | cytoskeleton organization and biogenesis | | | | -1.115877302 | 0.461410487 | 3.45E-07 | -1.01026044 | 0.456456618 | 7.99E-07 |
| 16 | | PFL0660w | OPFL0028 | dynein light chain 1, putative:PFL0660w::(OPFL0028) | GO:0007017 | microtubule-based process | -1.065368845 | 0.477850474 | 6.56E-05 | -0.650029683 | 0.637267202 | 0.000558758 | -0.440854859 | 0.736697954 | 0.008723241 |
| | | PFL0660w | L2_212 | dynein light chain 1, putative:PFL0660w::(L2_212) | GO:0007017 | microtubule-based process | -1.003640427 | 0.498739915 | 3.92E-06 | -0.635862498 | 0.643555957 | 4.08E-05 | -0.59186888 | 0.663482869 | 6.94E-05 |
| 17 | | PFL0850w | KN5578_1 | anaphase promoting complex subunit 10::PFL0850w::(KN5578_1) | GO:0030071 | regulation of mitotic metaphase/anaphase transition | | | | -0.871494662 | 0.546580289 | 0.004300339 | -1.13726983 | 0.45461909 | 0.000217803 |
| 18 | | PFL0925w | PPFL0925W_8630 | Formin 2, putative:PFL0925w::(PPFL0925W_8630) | GO:0009910 | cytokinesis | 0.51801918 | 1.431987779 | 0.000367799 | 0.797994453 | 1.738682435 | 3.45E-07 | 0.924070347 | 1.89746115 | 3.29E-08 |
| 19 | | PFL1330c | KN479_3 | hypothetical protein:PF1330c::(KN479_3) | DAVID | cell division and chromosome partitioning, cyclin-like domain | | | | 0.846244271 | 1.797814626 | 0.001959374 | | | |
| 20 | | PFL2460w | OPFL0022 | coronin::PFL2460w::(OPFL0022) | GO:0009910 | cytokinesis | | | | -0.51835663 | 0.69816666 | 0.033245288 | -0.98397441 | 0.505585008 | 0.000347047 |
| | | PFL2460w | OPFL0013 | coronin::PFL2460w::(OPFL0013) | GO:0009910 | cytokinesis | 1.043654849 | 2.061443398 | 6.99E-05 | | | | -0.520532069 | 0.697114688 | 0.000446852 |
| DNA METABOLISM | | | | | | | | | | | | | | | |
| 21 | | MAL13P1.177 | KN1069_1 | hypothetical protein, conserved in P. falciparum::MAL13P1.177::(KN1069_1) | GO:0006260 | DNA replication | 0.829881518 | 1.777539375 | 0.029707356 | | | | | | |
| 22 | | PF10_0154 | J53_46 | ribonucleotide reductase small subunit, putative:PF10_0154::(J53_46) | GO:0006260 | DNA replication | -0.837943234 | 0.559440563 | 0.014931732 | | | | -0.545125292 | 0.68531882 | 0.041128105 |
| 23 | | PF11_0087 | KS42_6 | Rad51 homolog, putative:PF11_0087::(KS42_6) | GO:0006259 | DNA metabolic process | -1.018402605 | 0.493662648 | 0.000112849 | -0.755948916 | 0.592156773 | 0.000188157 | -0.710660516 | 0.611040319 | 0.000292201 |
| 24 | | PF11_0117 | KS26_11 | replication factor C subunit 5, putative:PF11_0117::(KS26_11) | GO:0006260 | DNA replication | -0.972025383 | 0.509789872 | 1.82E-05 | -1.053120575 | 0.481924625 | 4.84E-07 | -0.831121611 | 0.562092079 | 5.14E-06 |
| 25 | | PF11_0131 | KS17_15 | hypothetical protein:PF11_0131::(KS17_15) | DAVID | DNA metabolism, DNA replication (Replication factor C conserved region) | 0.777047053 | 1.713619798 | 0.017863119 | | | | | | |
| 26 | | PF11_0249 | KS168_5 | hypothetical protein:PF11_0249::(KS168_5) | GO:0006259 | DNA metabolic process | -0.887715905 | 0.54046912 | 0.000480366 | | | | | | |
| 27 | | PF11_0282 | KS3180_1 | deoxyuridine 5'-triphosphate nucleotidohydrolase, putative:PF11_0282::(KS3180_1) | GO:0006260 | DNA replication | -1.14384802 | 0.452550903 | 1.86E-06 | -1.693641805 | 0.309145561 | 1.13E-09 | -1.515078237 | 0.349877492 | 1.67E-09 |
| 28 | | PF13_0095 | M4927_3 | DNA replication licensing factor mcm4-related:PF13_0095::(M4927_3) | GO:0006268 | DNA unwinding during replication | -1.122298742 | 0.459361311 | 8.05E-06 | -0.708200211 | 0.612083248 | 7.77E-05 | -0.443165088 | 0.735519202 | 0.004032128 |
| 29 | | PF13_0291 | M446_3 | replication licensing factor, putative:PF13_0291::(M446_3) | GO:0006270 | DNA replication initiation | -0.888574793 | 0.547687632 | 1.19E-05 | -0.540696123 | 0.687439129 | 0.000117409 | -0.239704134 | 0.84691898 | 0.038195398 |
| 30 | | PF13_0349 | M38941_10 | nucleoside diphosphate kinase b, putative:PF13_0349::(M38941_10) | GO:0006183 | GTP biosynthetic process | -1.282871591 | 0.410976672 | 8.79E-08 | -1.105227034 | 0.464829316 | 2.13E-08 | -0.933195182 | 0.523697208 | 9.53E-08 |
| 31 | | PF14_0053 | N159_20 | ribonucleotide reductase small subunit:PF14_0053::(N159_20) | GO:0006260 | DNA replication | -1.430870813 | 0.370906945 | 1.73E-06 | -0.661099179 | 0.632396295 | 0.000346597 | -0.437891003 | 0.738212973 | 0.008014905 |
| 32 | | PF14_0081 | N150_87 | DNA repair helicase, putative:PF14_0081::(N150_87) | GO:0008150 | biological_process | -0.757931123 | 0.591343731 | 0.000609044 | -0.529370752 | 0.692856866 | 0.001713566 | -0.389138464 | 0.76358546 | 0.013626664 |
| 33 | | PF14_0112 | N150_19 | POM1, putative:PF14_0112::(N150_19) | GO:0006260 | DNA replication | -1.023330001 | 0.491979463 | 0.000104238 | -1.007372412 | 0.497451434 | 9.80E-06 | -0.81838976 | 0.56707452 | 7.18E-05 |
| 34 | | PF14_0254 | N157_4 | DNA mismatch repair protein Msh2p, putative:PF14_0254::(N157_4) | GO:0006259 | DNA metabolic process | -0.809762699 | 0.570475685 | 1.92E-05 | -0.714729783 | 0.609319247 | 4.76E-06 | -0.44510263 | 0.734532062 | 0.000497067 |
| 35 | | PF14_0297 | N138_52 | ecto-nucleoside triphosphate diphosphohydrolase 1, putative:PF14_0297::(N138_52) | GO:0017110 | nucleoside-diphosphatase activity | -0.71398854 | 0.60963239 | 0.011134483 | -0.811369742 | 0.569840576 | 0.000896613 | -0.604747879 | 0.657586288 | 0.011033731 |
| 36 | | PF14_0314 | N138_104 | chromatin assembly factor 1 p55 subunit, putative:PF14_0314::(N138_104) | GO:0006334 | nucleosome assembly | 0.568993502 | 1.483488252 | 0.000100582 | 1.059987295 | 2.084913161 | 7.61E-09 | 1.289922841 | 2.445149779 | 2.95E-10 |
| | | PF14_0314 | N138_102 | chromatin assembly factor 1 p55 subunit, putative:PF14_0314::(N138_102) | GO:0006334 | nucleosome assembly | 0.546474599 | 1.460512392 | 0.000301129 | 0.970597037 | 1.959851399 | 5.04E-08 | 1.042223742 | 2.059399526 | 1.01E-08 |
| 37 | | PF14_0316 | N172_3 | DNA topoisomerase II, putative:PF14_0316::(N172_3) | GO:0006259 | DNA metabolic process | 0.417676789 | 1.335774788 | 0.01382464 | -0.389732315 | 0.763271213 | 0.005329606 | -0.791796588 | 0.577624328 | 6.85E-06 |
| 38 | | PF14_0374 | F66030_3 | hypothetical protein:PF14_0374::(F66030_3) | GO:0043565 | sequence-specific DNA binding | 0.103950292 | 2.056156807 | 0.008761815 | | | | | | |
| 39 | | PF14_0601 | N134_82 | replication factor C3::PF14_0601::(N134_82) | GO:0006260 | DNA replication | -1.001830333 | 0.499366057 | 0.004479688 | -1.071448001 | 0.609424751 | 0.001797888 | -0.695477609 | 0.617504858 | 0.002065487 |
| 40 | | PFA0290w | A8109_12 | DNA binding protein, putative:PFA0290w::(A8109_12) | GO:0005622 | intracellular | -0.599598663 | 0.659937515 | 0.048384782 | -0.845758547 | 0.556418176 | 0.00022722 | -0.558886924 | 0.678825693 | 0.005602482 |
| 41 | | PFB0180w | B110 | 5'-3' exonuclease, N-terminal resolvase-like domain, putative:PFB0180w::(B110) | GO:0003677 | DNA binding (DNA metabolism and repair) | -0.887206158 | 0.540660117 | 0.006119884 | | | | | | |
| 42 | | PFB0895c | B564 | replication factor C subunit 1, putative:PFB0895c::(B564) | GO:0006260 | DNA replication | -1.00693513 | 0.497602235 | 1.45E-05 | -0.443931223 | 0.735128713 | 0.000342272 | -0.274115734 | 0.826957027 | 0.011613976 |
| 43 | | PFD0470c | D17715_49 | replication factor a protein, putative:PFD0470c::(D17715_49) | GO:0006260 | DNA replication | -0.907256396 | 0.533198122 | 0.00011655 | -1.301480875 | 0.405709538 | 1.67E-07 | -1.266662046 | 0.415620279 | 1.48E-07 |
| 44 | | PFD0685c | F30473_2 | chromosome associated protein, putative:PFD0685c::(F30473_2) | GO:0006259 | DNA metabolic process | -1.000906541 | 0.499685916 | 2.71E-05 | -0.372379337 | 0.772507403 | 0.013347851 | | | |
| | | PFD0685c | D23156_40 | chromosome associated protein, putative:PFD0685c::(D23156_40) | GO:0006259 | DNA metabolic process | -0.984317838 | 0.50546467 | 4.41E-07 | -0.728331587 | 0.603601549 | 5.20E-07 | -0.497555912 | 0.708305715 | 2.75E-05 |
| 45 | | PFD0830w | Z_6_100 | Control oligonucleotide to bifunctional dihydrofolate reductase-thymidylate synthase(PFD0830w)::PFD0830w::(Z_6_100) | GO:0006231 | dTMP biosynthetic process | -1.08952596 | 0.469915754 | 2.57E-05 | -0.645414784 | 0.639308959 | 0.000383275 | -0.638314751 | 0.642462988 | 0.000377977 |

| # | FUNCTIONAL CLASSIFICATION | PLASMODB ID | OLIGO | ANNOTATION | GO ID | FUNCTIONAL ANNOTATION | FOLD CHANGE TO RELATIVE I0 WITH P-VALUES ADJUSTED FOR MDR DATA WITH P<0.05 ARE PRESENTED | | | | | | | | |
|----|-----------------------------------|-------------|-------------|---|------------|---|---|-------------|--------------|--------------|-------------|--------------|--------------|-------------|--------------|
| | | | | | | | T11 log2FC | T11 FC | adj. p value | T12 log2FC | T12 FC | adj. p value | T13 log2FC | T13 FC | adj. p value |
| | | PFD0830w | OPFD66954 | bifunctional dihydrofolate reductase-thymidylate synthase::PFD0830w::(OPFD66954) | GO:006231 | dTMP biosynthetic process | -0.905177863 | 0.53396687 | 0.00024105 | -0.77419848 | 0.584713384 | 0.000110918 | -0.722171625 | 0.606184293 | 0.000184442 |
| 46 | | PFD0950w | D12635_36 | ran binding protein 1::PFD0950w::(D12635_36) | GO:006260 | DNA replication | 1.001557896 | 2.002160869 | 0.011627335 | 0.881820095 | 1.842698572 | 0.00647603 | | | |
| 47 | | PFE0675c | OPFG0052 | deoxyribodipyrimidine photolyase (photoreactivating enzyme, DNA photolyase), putative::PFE0675c::(OPFG0052) | GO:006281 | DNA repair | -0.846048988 | 0.55630617 | 2.73E-05 | -0.72350935 | 0.605622475 | 1.08E-05 | -0.626807406 | 0.647607947 | 4.14E-05 |
| | | PFE0675c | F17495_1 | deoxyribodipyrimidine photolyase (photoreactivating enzyme, DNA photolyase), putative::PFE0675c::(F17495_1) | GO:006281 | DNA repair | -1.507194144 | 0.351794749 | 4.81E-06 | -0.809414946 | 0.570613211 | 0.000367807 | | | |
| 48 | | PF11470c | F57777_1 | DNA polymerase epsilon, catalytic subunit a, putative::PF11470c::(F57777_1) | GO:006260 | DNA replication | | | | -0.771951596 | 0.585624739 | 0.000615153 | -0.572688907 | 0.672362465 | 0.005678353 |
| 49 | | PFI0235w | OPFI17721 | replication factor A-related protein, putative::PFI0235w::(OPFI17721) | GO:0003676 | nucleic acid binding | -0.858636286 | 0.551473595 | 2.63E-06 | -0.382144525 | 0.767296179 | 0.000780851 | | | |
| | | PFI0235w | F18417_1 | replication factor A-related protein, putative::PFI0235w::(F18417_1) | GO:0003676 | nucleic acid binding | -1.201009797 | 0.434970723 | 1.13E-06 | -0.531571996 | 0.69180052 | 0.000320647 | -0.27166648 | 0.828362139 | 0.032239814 |
| 50 | | PFI0530c | I11401_2 | DNA primase, large subunit, putative::PFI0530c::(I11401_2) | GO:0005658 | alpha DNA polymerase:primase complex | -0.832838283 | 0.56142364 | 0.000252301 | -0.652996762 | 0.635957931 | 2.81E-05 | -0.285255569 | 0.82059623 | 0.018289905 |
| 51 | HOST PARASITE INTERACTION | PFL1655c | KN973_2 | hypothetical protein::PFL1655c::(KN973_2) | GO:006260 | DNA replication | -1.110795088 | 0.463038774 | 0.031468896 | | | | | | |
| 52 | | MAL13P1.176 | I8058_1 | Plasmodium falciparum reticulocyte binding protein 2 homolog b::MAL13P1.176::(I8058_1) | GO:0030260 | entry into host cell | 1.05451678 | 2.077022407 | 0.000358752 | | | | | | |
| 53 | | MAL7P1.176 | I14975_1 | erythrocyte binding antigen::MAL7P1.176::(I14975_1) | GO:009405 | pathogenesis | 0.598854488 | 1.514513552 | 0.000180764 | -0.819937014 | 0.566466673 | 4.97E-07 | -0.874507825 | 0.545439911 | 1.53E-07 |
| | | MAL7P1.176 | F739_1 | erythrocyte binding antigen::MAL7P1.176::(F739_1) | GO:009405 | pathogenesis | 0.645728884 | 1.564529524 | 0.000189871 | -1.041773487 | 0.485730005 | 7.80E-08 | -1.186475396 | 0.439374974 | 8.31E-09 |
| 54 | | MAL7P1.61 | OPFG0014 | erythrocyte membrane protein 1 (PIEMP1) pseudogene::MAL7P1.61::(OPFG0014) | GO:009405 | pathogenesis | 0.768472128 | 1.70346479 | 0.01209336 | | | | -0.821077202 | 0.566019161 | 0.001612568 |
| | | MAL7P1.61 | F17545_3 | erythrocyte membrane protein 1 (PIEMP1) pseudogene::MAL7P1.61::(F17545_3) | GO:009405 | pathogenesis | | | | -0.49918905 | 0.707504363 | 0.028177476 | -1.210686355 | 0.432063015 | 2.11E-05 |
| 55 | | PF07_0049 | F52444_1 | erythrocyte membrane protein 1 (PIEMP1)::PF07_0049::(F52444_1) | GO:009405 | pathogenesis | 0.836793372 | 1.786075878 | 0.028969674 | | | | | | |
| 56 | | PF10_0019 | J33_16 | early transcribed membrane protein::PF10_0019::(J33_16) | GO:008150 | biological_process | 0.493593215 | 1.407947184 | 0.024164421 | | | | -1.145480077 | 0.452039241 | 2.29E-06 |
| 57 | | PF10_0268 | J170_10 | merozoite capping protein 1::PF10_0268::(J170_10) | GO:0030260 | entry into host cell | 1.013523961 | 2.01883634 | 6.54E-05 | | | | -0.402285325 | 0.756658736 | 0.013890695 |
| 58 | | PF10_0323 | D32606_3 | hypothetical protein::PF10_0323::(D32606_3) | DAVID | early transcribed membrane protein (ETRAMP) | | | | 0.509592046 | 1.423647571 | 0.000243113 | 0.824914759 | 1.771430371 | 1.32E-06 |
| 59 | | PF10_0345 | J116_9 | merozoite Surface Protein 3, MSP3::PF10_0345::(J116_9) | GO:0030260 | entry into host cell | 0.852102723 | 1.805129979 | 0.000579299 | -0.425993598 | 0.744325931 | 0.018666216 | -0.416790498 | 0.749089239 | 0.019685748 |
| 60 | | PF10_0346 | J116_7 | merozoite Surface protein 6, MSP6::PF10_0346::(J116_7) | GO:0030260 | entry into host cell | 0.787051392 | 1.725544156 | 0.000104238 | | | | -0.276296653 | 0.825707862 | 0.034026116 |
| 61 | | PF11_0010 | KS4_10 | rifin::PF11_0010::(KS4_10) | GO:0020033 | antigenic variation | | | | 0.887724335 | 1.850255282 | 0.007040394 | | | |
| 62 | | PF11_0039 | OPFK12894 | early transcribed membrane protein 11.1::PF11_0039::(OPFK12894) | GO:008150 | biological_process | 0.79968064 | 1.740715753 | 0.001319797 | -0.773416034 | 0.58503059 | 0.000238034 | -1.644003413 | 0.319967347 | 3.86E-08 |
| | | PF11_0039 | KS75_16 | early transcribed membrane protein 11.1::PF11_0039::(KS75_16) | GO:008150 | biological_process | | | | | | | -1.227893146 | 0.426940478 | 3.50E-05 |
| 63 | | PF11_0040 | KS75_15 | early transcribed membrane protein 11.2::PF11_0040::(KS75_15) | GO:008150 | biological_process | 0.544237952 | 1.458249877 | 0.013134384 | -0.755296605 | 0.592424576 | 0.000188157 | -1.466997932 | 0.36173424 | 9.52E-08 |
| 64 | | PF13_0193 | M23550_1 | MSP7-like protein::PF13_0193::(M23550_1) | GO:0030260 | entry into host cell | 0.963646773 | 1.950233373 | 0.001128213 | | | | | | |
| 65 | | PF13_0197 | M36656_1 | merozoite Surface Protein 7 precursor, MSP7::PF13_0197::(M36656_1) | GO:0030260 | entry into host cell | 0.805492076 | 1.747741812 | 0.001736515 | | | | 0.290706293 | 1.223238986 | 0.044901451 |
| 66 | | PF14_0102 | N150_50 | rhoptry-associated protein 1, RAPI::PF14_0102::(N150_50) | GO:0020008 | rhoptry | | | | -0.834906549 | 0.560619352 | 4.84E-05 | -0.786189068 | 0.579873829 | 7.39E-05 |
| 67 | | PFB0010w | B11 | erythrocyte membrane protein 1 (PIEMP1)::PFB0010w::(B11) | GO:009405 | pathogenesis | 1.580284538 | 2.990288204 | 5.73E-05 | 0.524032537 | 1.437968963 | 0.035324852 | | | |
| 68 | | PFB0095c | OPFB0677 | erythrocyte membrane protein 3::PFB0095c::(OPFB0677) | GO:008150 | biological_process | | | | | | | 0.751915401 | 1.684027154 | 0.003081374 |
| 69 | | PFB0120w | B70 | early transcribed membrane protein, putative::PFB0120w::(B70) | GO:008150 | biological_process | 0.52268038 | 1.436621867 | 0.005928674 | -0.402170524 | 0.756718948 | 0.007832264 | -1.016353551 | 0.494364293 | 1.16E-06 |
| 70 | | PFB0300c | B188 | merozoite surface protein 2 precursor::PFB0300c::(B188) | GO:007155 | cell adhesion | 0.776234231 | 1.712654607 | 9.38E-05 | -0.563300007 | 0.676752395 | 0.00018887 | -0.569785654 | 0.673716877 | 0.000147262 |
| 71 | | PFC0110w | OPFC0769 | Cytoadherence linked asexual protein, CLAG::PFC0110w::(OPFC0769) | GO:0020035 | by parasite protein | 0.973635302 | 1.963782704 | 0.002508239 | | | | | | |
| 72 | | PFC0115c | C74 | erythrocyte membrane protein 1 (PIEMP1) pseudogene::PFC0115c::(C74) | GO:009405 | pathogenesis | 0.346418272 | 1.271400245 | 0.014653412 | -0.319031553 | 0.801607797 | 0.006299858 | -0.764133462 | 0.588806922 | 1.47E-06 |
| 73 | | PF11580c | D63903_1 | erythrocyte membrane protein 1 (PIEMP1)::PF11580c::(D63903_1) | GO:009405 | pathogenesis | 1.035342496 | 2.049600164 | 0.002802739 | | | | | | |
| 74 | | PF11595c | OPFF72421 | erythrocyte membrane protein 1 (PIEMP1)::PF11595c::(OPFF72421) | GO:009405 | pathogenesis | 0.822253125 | 1.768165265 | 0.009154954 | | | | | | |
| 75 | | PF10015c | OPFBL0B0064 | rifin::PF10015c::(OPFBL0B0064) | GO:0020033 | antigenic variation | 0.683741535 | 1.845154388 | 0.039886144 | | | | 0.431097954 | 1.348259271 | 0.029484362 |
| 76 | | PF10035c | KN1802_2 | rifin::PF10035c::(KN1802_2) | GO:0020033 | antigenic variation | 0.664651646 | 1.820999939 | 0.009225093 | | | | | | |
| 77 | | PFI0265c | I11448_5 | rhoptry protein, putative::PFI0265c::(I11448_5) | GO:0020008 | rhoptry | | | | -0.871576003 | 0.546549473 | 7.13E-05 | -0.386857906 | 0.764793461 | 0.029356344 |
| 78 | | PF11475w | Z_4_60 | Control oligonucleotide to merozoite surface protein 1, precursor(PF11475w)::PF11475w::(Z_4_60) | GO:009405 | pathogenesis | 0.365725333 | 1.288529291 | 0.049862602 | -0.677497301 | 0.625248978 | 0.000174216 | -0.786794159 | 0.579630671 | 3.44E-05 |
| | | PF11475w | Z_4_100 | Control oligonucleotide to merozoite surface protein 1, precursor(PF11475w)::PF11475w::(Z_4_100) | GO:009405 | pathogenesis | | | | -0.896988969 | 0.537006342 | 2.43E-07 | -0.792520771 | 0.577334454 | 7.07E-07 |
| | | PF11475w | I6653_2 | merozoite surface protein 1, precursor::PF11475w::(I6653_2) | GO:009405 | pathogenesis | 0.709655062 | 1.635413055 | 0.00042841 | -0.809634163 | 0.570526513 | 1.11E-05 | -0.610498382 | 0.654970402 | 0.000170388 |
| | | PF11475w | F8511_1 | merozoite surface protein 1, precursor::PF11475w::(F8511_1) | GO:009405 | pathogenesis | | | | -0.93086267 | 0.524544593 | 0.022411773 | | | |
| 79 | | PFL0940c | OPFL0012 | erythrocyte membrane protein 1 (PIEMP-1) pseudogene::PFL0940c::(OPFL0012) | GO:009405 | pathogenesis | 0.352034945 | 1.276359684 | 0.05021075 | -0.385798216 | 0.765355425 | 0.010048694 | -0.754678452 | 0.592678467 | 2.96E-05 |
| | | PFL0940c | J1058_2 | erythrocyte membrane protein 1 (PIEMP-1) pseudogene::PFL0940c::(J1058_2) | GO:009405 | pathogenesis | | | | -0.628780003 | 0.646723077 | 0.001069654 | -0.975988737 | 0.508391306 | 1.55E-05 |
| | | PFL0940c | J1058_1 | erythrocyte membrane protein 1 (PIEMP-1) pseudogene::PFL0940c::(J1058_1) | GO:009405 | pathogenesis | | | | | | | -0.860701889 | 0.550684578 | 0.024838807 |
| 80 | POLYAMINE & METHIONINE METABOLISM | PFL1420w | OPFL0099 | macrophage migration inhibitory factor homolog, putative::PFL1420w::(OPFL0099) | GO:0020012 | evasion of host immune response | -0.745255085 | 0.596562383 | 5.37E-05 | -0.953479995 | 0.51638536 | 2.43E-07 | -0.9989933 | 0.500349017 | 8.92E-08 |

| # | FUNCTIONAL CLASSIFICATION | PLASMODB ID | OLIGO | ANNOTATION | GO ID | FUNCTIONAL ANNOTATION | FOLD CHANGE TO RELATIVE I0 WITH P-VALUES ADJUSTED FOR MDR DATA WITH P<0.05 ARE PRESENTED | | | | | | | | |
|-----|---------------------------|-------------|----------------|--|------------|--|--|--------------------|--------------|-------------------------------------|--------------------|--------------|-------------------------------------|--------------------|--------------|
| | | | | | | | T ₁₁ log ₂ FC | T ₁₁ FC | adj. p value | T ₁₂ log ₂ FC | T ₁₂ FC | adj. p value | T ₁₃ log ₂ FC | T ₁₃ FC | adj. p value |
| | | | | | | | | | | | | | | | |
| 81 | | MAL13P1.214 | OPFM60499 | phosphoethanolamine N-methyltransferase, putative: MAL13P1.214::(OPFM60499) | GO:0006656 | phosphatidylcholine biosynthetic process | -1.432709505 | 0.370434531 | 2.86E-07 | -1.484325333 | 0.357415639 | 7.61E-09 | -1.4380441 | 0.36906732 | 3.97E-09 |
| 82 | | PF10_0289 | J151_11 | adenosine deaminase, putative: PF10_0289::(J151_11) | GO:0009168 | purine ribonucleoside monophosphate biosynthetic process | -1.385676843 | 0.382709908 | 1.93E-06 | -1.294198873 | 0.407762533 | 2.43E-07 | -1.244965777 | 0.421917907 | 2.67E-07 |
| 83 | | PF10_0322 | J50_1 | S-adenosylmethionine decarboxylase-ornithine decarboxylase: PF10_0322::(J50_1) | GO:0006596 | polyamine biosynthetic process | -0.711910585 | 0.610511093 | 0.000498845 | -0.907991033 | 0.53292668 | 4.02E-06 | -0.6859555 | 0.621594007 | 6.79E-05 |
| 84 | | PF14_0309 | N138_92 | protein-L-isospartate O-methyltransferase beta-aspartate methyltransferase, putative: PF14_0309::(N138_92) | GO:0006464 | protein modification | | | | -0.883566438 | 0.54202585 | 0.020214628 | | | |
| 85 | | PF14_0526 | N168_17 | hypothetical protein, conserved: PF14_0526::(N168_17) | DAVID | generic methyltransferase (SAM dep meth domain) | -1.508415047 | 0.351497164 | 0.000686953 | -1.179433704 | 0.441524774 | 9.61E-05 | -1.075204933 | 0.474603639 | 0.000193923 |
| 86 | | PFD0285c | D49176_36 | lysine decarboxylase, putative: PFD0285c::(D49176_36) | GO:0006554 | lysine catabolic process | 0.873703237 | 1.832360333 | 0.00058695 | 1.314213943 | 2.486668068 | 1.79E-06 | 1.475983656 | 2.78173243 | 3.97E-07 |
| 87 | | PFE0660c | E29567_11 | uridine phosphorylase, putative: PFE0660c::(E29567_11) | GO:0009116 | nucleoside metabolic process | -1.691320588 | 0.30964336 | 8.43E-09 | -1.542718629 | 0.343238044 | 6.77E-10 | -1.431794173 | 0.370669632 | 3.58E-10 |
| 88 | | PFE1050w | E18031_6 | adenosylhomocysteinase(S-adenosyl-L-homocysteine hydrolase)::PFE1050w::(E18031_6) | GO:0006730 | one-carbon compound metabolic process | -0.892241125 | 0.538776517 | 6.49E-06 | -0.629207711 | 0.646531375 | 2.22E-05 | -0.561930236 | 0.677395245 | 5.70E-05 |
| 89 | | PFF0435w | OPFF72412 | ornithine aminotransferase: PFF0435w::(OPFF72412) | GO:0006591 | ornithine metabolic process | 0.544477675 | 1.458492204 | 0.038058218 | 0.910328551 | 1.87947347 | 0.000219986 | 0.841535489 | 1.791956342 | 0.000397735 |
| 90 | PRIMARY METABOLISM | PF11090w | I14812_1 | S-adenosylmethionine synthase, putative: PF11090w::(I14812_1) | GO:0006730 | one-carbon compound metabolic process | -1.252185962 | 0.41981163 | 2.63E-06 | -0.850355936 | 0.554647879 | 1.38E-05 | -0.572899469 | 0.672264341 | 0.000573384 |
| 91 | | Col | F40451_2 | putative cytochrome oxidase I::Col::(F40451_2) | | oxidative phosphorylation | -0.491915853 | 0.711080179 | 0.039921615 | -0.971709374 | 0.509901549 | 4.84E-05 | -0.852154118 | 0.553956994 | 0.000151481 |
| 92 | | CoxI | E23986_4 | putative cytochrome oxidase I::CoxI::(E23986_4) | | oxidative phosphorylation | | | | -0.784088843 | 0.580718603 | 0.000203228 | -0.628317431 | 0.64693047 | 0.001273794 |
| 93 | | coxIII_2 | OPFBLOB0002 | mitochondrial encoded cytochrome oxidase subunit 3::coxIII_2::(OPFBLOB0002) | | oxidative phosphorylation | -0.479948061 | 0.717003437 | 0.000895863 | -0.984766639 | 0.505307452 | 4.40E-08 | -0.697001197 | 0.616853073 | 1.71E-06 |
| 94 | | MAL13P1.210 | M19188_9 | hypothetical protein: MAL13P1.210::(M19188_9) | DAVID | mannosyltransferase_III | | | | -0.810046412 | 0.570363509 | 0.0002597 | -0.423875931 | 0.745419295 | 0.02415755 |
| 95 | | MAL7P1.75 | PMAL7P1.75_101 | mitochondrial ATP synthase F1, epsilon subunit, putative: MAL7P1.75::(PMAL7P1.75_101) | GO:0015986 | ATP synthesis coupled proton transport | -0.866700349 | 0.548399686 | 0.001986385 | -0.698501451 | 0.616211943 | 0.001736089 | -0.783480723 | 0.580963438 | 0.000613282 |
| 96 | | PF07_0005 | F45524_1 | lysophospholipases-like protein, putative: PF07_0005::(F45524_1) | GO:0006644 | phospholipid metabolic process | | | | -0.451550804 | 0.731256372 | 0.006188211 | -1.016176402 | 0.494425 | 2.91E-06 |
| 97 | | PF07_0129 | F8921_1 | ATP-dept. acyl-coa synthetase: PF07_0129::(F8921_1) | GO:0006631 | fatty acid metabolic process | -1.068807109 | 0.476713006 | 2.19E-05 | -0.839612218 | 0.558793747 | 2.14E-05 | -0.674271664 | 0.626648499 | 0.00015848 |
| 98 | | PF10_0015 | OPFJ12802 | acyl CoA binding protein, putative: PF10_0015::(OPFJ12802) | GO:0006631 | fatty acid metabolic process | | | | -1.50975904 | 0.351169867 | 2.82E-08 | -1.869490158 | 0.273670122 | 2.57E-09 |
| 99 | | PF10_0016 | J33_21 | acyl CoA binding protein, putative: PF10_0016::(J33_21) | GO:0006631 | fatty acid metabolic process | -1.428265234 | 0.371577427 | 5.46E-08 | -0.807690635 | 0.571295616 | 1.51E-06 | -0.623303691 | 0.649182632 | 2.12E-05 |
| 100 | | PF10_0155 | J53_48 | enolase: PF10_0155::(J53_48) | GO:0006094 | gluconeogenesis | -0.852972944 | 0.553642675 | 6.76E-07 | -0.867178808 | 0.548217844 | 2.13E-08 | -0.969970796 | 0.510516397 | 2.56E-09 |
| 101 | | PF10_0221 | J183_4 | GcpE protein: PF10_0221::(J183_4) | GO:0016114 | terpenoid biosynthetic process | -0.875721173 | 0.544981373 | 0.046766261 | | | | | | |
| 102 | | PF10_0275 | J504_4 | protoporphyrinogen oxidase, putative: PF10_0275::(J504_4) | GO:0006118 | electron transport | | | | | | | -0.908000762 | 0.532923087 | 0.002214689 |
| 103 | | PF10_0407 | J587_6 | dihydroipoamide acetyltransferase, putative: PF10_0407::(J587_6) | GO:0008415 | acyltransferase activity | | | | -0.854856319 | 0.55292039 | 8.07E-05 | -1.041890099 | 0.485690745 | 8.88E-06 |
| 104 | | PF11_0257 | KS497_2 | ethanolamine kinase, putative: PF11_0257::(KS497_2) | GO:0006629 | lipid metabolic process | -1.37243457 | 0.386238914 | 3.56E-07 | -0.803972697 | 0.572769789 | 9.56E-06 | -0.462458167 | 0.725748622 | 0.000848283 |
| 105 | | PF11_0276 | KS266_16 | hypothetical protein: PF11_0276::(KS266_16) | GO:0006629 | lipid metabolic process | | | | 0.750665594 | 1.682568912 | 1.08E-05 | 0.6534751 | 1.572952495 | 3.72E-05 |
| 106 | | PF11_0412 | KS667_1 | Vacuolar ATP synthase subunit F, putative: PF11_0412::(KS667_1) | GO:0007035 | vacuolar acidification | -0.825629636 | 0.564235899 | 0.035814245 | | | | | | |
| 107 | | PF13_0066 | M46791_2 | malonyl coa-acyl carrier protein transacylase precursor: PF13_0066::(M46791_2) | GO:0006633 | fatty acid biosynthetic process | | | | -1.453220606 | 0.365205246 | 0.004191929 | -2.219039069 | 0.214784372 | 0.000245083 |
| 108 | | PF13_0121 | OPFBLOB0100 | dihydroipoamide succinyltransferase, putative: PF13_0121::(OPFBLOB0100) | GO:0006099 | tricarboxylic acid cycle | -0.798561917 | 0.574921976 | 0.000315913 | -0.554654702 | 0.680819988 | 0.001519681 | | | |
| 109 | | PF13_0128 | M44397_17 | beta-hydroxyacyl-ACP dehydratase precursor: PF13_0128::(M44397_17) | GO:0006633 | fatty acid biosynthetic process | -1.117594796 | 0.460861515 | 7.80E-08 | -1.094936811 | 0.468156628 | 6.00E-08 | | | |
| 110 | | PF13_0141 | Z_5_90 | Control oligonucleotide to L-lactate dehydrogenase(PF13_0141)::PF13_0141::(Z_5_90) | GO:0006096 | glycolysis | -0.820166023 | 0.566376761 | 0.000167308 | -0.631478197 | 0.645514677 | 0.000712771 | -0.607328279 | 0.656411182 | 0.000286236 |
| | | PF13_0141 | Z_5_80 | Control oligonucleotide to L-lactate dehydrogenase(PF13_0141)::PF13_0141::(Z_5_80) | GO:0006096 | glycolysis | -0.84342902 | 0.557317353 | 6.01E-06 | -0.421398249 | 0.746700577 | 0.000545488 | -0.555037151 | 0.680639531 | 3.34E-05 |
| | | PF13_0141 | Z_5_70 | Control oligonucleotide to L-lactate dehydrogenase(PF13_0141)::PF13_0141::(Z_5_70) | GO:0006096 | glycolysis | -0.782004753 | 0.581558105 | 6.54E-05 | -0.267164004 | 0.830951395 | 0.032942141 | -0.329569655 | 0.795773822 | 0.009633679 |
| | | PF13_0141 | Z_5_60 | Control oligonucleotide to L-lactate dehydrogenase(PF13_0141)::PF13_0141::(Z_5_60) | GO:0006096 | glycolysis | -0.856708199 | 0.552211103 | 2.38E-06 | -0.570019454 | 0.673607705 | 1.44E-05 | -0.554117243 | 0.681073666 | 1.57E-05 |
| | | PF13_0141 | Z_5_100 | Control oligonucleotide to L-lactate dehydrogenase(PF13_0141)::PF13_0141::(Z_5_100) | GO:0006096 | glycolysis | -0.878298222 | 0.544008756 | 2.53E-06 | -0.576379547 | 0.670644655 | 1.87E-05 | -0.594087576 | 0.662463294 | 1.07E-05 |
| 111 | | PF13_0227 | M8686_1 | vacuolar ATP synthase subunit D, putative: PF13_0227::(M8686_1) | GO:0006818 | hydrogen transport | | | | 0.913377452 | 1.883449631 | 4.83E-05 | 0.785085487 | 1.723194424 | 0.000180613 |
| 112 | | PF13_0269 | OPFM60500 | glycerol kinase, putative: PF13_0269::(OPFM60500) | GO:0005975 | carbohydrate metabolic process | 0.570643619 | 1.485185998 | 0.049375847 | -0.85096756 | 0.554412788 | 0.000991593 | -0.891497368 | 0.539054345 | 0.000607899 |
| 113 | | PF14_0378 | OPFN0252 | triose-phosphate isomerase: PF14_0378::(OPFN0252) | GO:0006094 | gluconeogenesis | -0.920774469 | 0.528225382 | 1.50E-06 | -0.356149255 | 0.781247052 | 0.001330664 | -0.195744625 | 0.873122131 | 0.050407438 |
| | | PF14_0378 | N132_40 | triose-phosphate isomerase: PF14_0378::(N132_40) | GO:0006094 | gluconeogenesis | -0.760840826 | 0.59015228 | 2.71E-05 | -0.540901313 | 0.687341363 | 7.32E-05 | -0.310436658 | 0.806397651 | 0.006939839 |
| 114 | | PF14_0415 | N128_60 | dephospho-CoA kinase, putative: PF14_0415::(N128_60) | GO:0015937 | coenzyme A biosynthetic process | 0.887090579 | 1.849442669 | 0.007438143 | -0.718270757 | 0.607825558 | 0.00214032 | -0.505644624 | 0.704345592 | 0.013188037 |
| 115 | | PF14_0484 | N149_9 | acetyl-CoA acetyltransferase, putative: PF14_0484::(N149_9) | GO:0006631 | fatty acid metabolic process | -0.876333597 | 0.544750078 | 0.000243926 | -0.799223296 | 0.574658473 | 1.21E-05 | -0.408050307 | 0.753641175 | 0.002225213 |
| 116 | | PF14_0598 | M48835_1 | glyceraldehyde-3-phosphate dehydrogenase: PF14_0598::(M48835_1) | GO:0006006 | glucose metabolic process | -1.092721701 | 0.468875987 | 0.00011768 | -0.962855913 | 0.513040309 | 3.72E-05 | -0.939298971 | 0.521486218 | 3.93E-05 |
| 117 | | PF14_0751 | N139_20 | fatty acyl coenzyme A synthetase-1, putative: PF14_0751::(N139_20) | GO:0006631 | fatty acid metabolic process | | | | | | | 0.831982479 | 1.780129847 | 0.022920201 |
| 118 | | PFB0695c | B465 | acyl-CoA synthetase: PFB0695c::(B465) | GO:0006631 | fatty acid metabolic process | 0.771923177 | 1.7075445 | 0.002517525 | | | | -0.742812606 | 0.597573217 | 0.00048103 |
| 119 | | PFC0910w | C600 | hypothetical protein: PFC0910w::(C600) | GO:0008152 | metabolic process | | | | 0.84467223 | 1.795856694 | 2.43E-07 | 1.042742541 | 2.060140228 | 1.01E-08 |

| # | FUNCTIONAL CLASSIFICATION | PLASMODB ID | OLIGO | ANNOTATION | GO ID | FUNCTIONAL ANNOTATION | FOLD CHANGE TO RELATIVE I0 WITH P-VALUES ADJUSTED FOR MDR DATA WITH P<0.05 ARE PRESENTED | | | | | | | | | | | | |
|-----|---------------------------|-------------|------------------|---|------------|--|---|--------------------|--------------|-------------------------------------|--------------------|--------------|-------------------------------------|--------------------|--------------|--------------|-------------|-------------|--|
| | | | | | | | T ₁₁ log ₂ FC | T ₁₁ FC | adj. p value | T ₁₂ log ₂ FC | T ₁₂ FC | adj. p value | T ₁₃ log ₂ FC | T ₁₃ FC | adj. p value | | | | |
| 248 | | PF08_0064 | OPFH0022 | hypothetical protein, conserved::PF08_0064::(OPFH0022) | GO:0015031 | protein transport | 0.897956691 | 1.863424919 | 0.003821039 | | | | | | | | | | |
| 249 | | PF10_0331 | J141_1 | hypothetical protein, conserved::PF10_0331::(J141_1) | GO:0006904 | vesicle docking during exocytosis | | | | 0.797096106 | 1.737600118 | 9.02E-05 | 0.875011251 | 1.834022389 | 3.02E-05 | | | | |
| 250 | | PF10_0337 | J649_1 | ADP-ribosylation factor-like protein::PF10_0337::(J649_1) | GO:0006886 | intracellular protein transport | -1.101923132 | 0.465895037 | 0.003200759 | | | | | | | | | | |
| 251 | | PF11_0210 | KS12_6 | hypothetical protein::PF11_0210::(KS12_6) | GO:0030001 | metal ion transport | -0.714203291 | 0.60954165 | 0.00102597 | -0.819842094 | 0.566503944 | 7.03E-05 | -0.679663527 | 0.624310863 | 0.000184318 | | | | |
| 252 | | PFA0295c | A8109_9 | hypothetical protein::PFA0295c::(A8109_9) | | ABC transporter, putative::PFA0590w::(A14801_7) | -0.67500933 | 0.626328169 | 0.005853764 | -0.845866335 | 0.556376606 | 0.000145314 | -0.705993722 | 0.613020098 | 0.000663827 | | | | |
| 253 | | PFA0590w | A14801_7 | ABC transporter, putative::PFA0590w::(A14801_7) | GO:0006810 | transport | -0.801559272 | 0.573728753 | 0.000222072 | -0.379869144 | 0.768507293 | 0.011408311 | | | | | | | |
| 254 | | PFB0435c | B303 | hypothetical protein::PFB0435c::(B303) | GO:0006836 | neurotransmitter transport | | | | -0.80912746 | 0.570726928 | 3.99E-05 | -0.626406881 | 0.647787762 | 0.000374312 | | | | |
| 255 | | PFC0125w | C83 | ABC transporter, putative::PFC0125w::(C83) | GO:0006810 | transport | -0.905851687 | 0.533717534 | 0.002841553 | -0.451446376 | 0.731309305 | 0.020952463 | | | | | | | |
| 256 | | PFE0260w | F62610_5 | hypothetical protein::PFE0260w::(F62610_5) | GO:0008643 | carbohydrate transport | 1.004225947 | 2.005866995 | 0.002670728 | -0.472700479 | 0.720614467 | 0.017588753 | | | | | | | |
| 257 | | PFE0410w | E21208_1 | triose or hexose phosphate / phosphate translocator, putative::PFE0410w::(E21208_1) | GO:0016020 | membrane | -0.94202355 | 0.520502302 | 2.28E-06 | -0.343363204 | 0.788201716 | 0.003228217 | | | | | | | |
| 258 | | PFF0655c | OPFF72499 | adapter-related protein, putative::PFF0655c::(OPFF72499) | GO:0016192 | vesicle-mediated transport | | | | 0.711125353 | 1.6370806 | 0.005727646 | 0.91525692 | 1.88590489 | 0.000767629 | | | | |
| 259 | | PFI1560c | I17152_1 | hypothetical protein::PFI1560c::(I17152_1) | DAVID | Inorganic ion transport and metabolism (Cecropin, DUF21) | | | | | | | | | | | | | |
| 260 | UNKNOWN | PFL1875w | PPFL1875W_1297 | hypothetical protein::PFL1875w::(PPFL1875W_1297) | GO:0006813 | potassium ion transport | -0.803501652 | 0.57295683 | 0.010082836 | | | | 0.527773895 | 1.441702904 | 0.028415284 | | | | |
| 261 | | MAL13P1.107 | I10218_1 | hypothetical protein::MAL13P1.107::(I10218_1) | | | -0.980203594 | 0.5069082 | 0.001986385 | | | | | | | | | | |
| 262 | | MAL13P1.110 | OPFM60544 | hypothetical protein::MAL13P1.110::(OPFM60544) | | | -2.024560892 | 0.245779945 | 2.10E-05 | -2.196559877 | 0.21815722 | 5.66E-07 | -2.355520961 | 0.19539684 | 1.66E-07 | | | | |
| 263 | | MAL13P1.128 | PMAL13P1.128_122 | hypothetical protein::MAL13P1.128::(PMAL13P1.128_122) | | | | | | | | | -0.842723646 | 0.557589908 | 0.009706284 | | | | |
| 264 | | MAL13P1.168 | PMAL13P1.168_448 | hypothetical protein::MAL13P1.168::(PMAL13P1.168_448) | | | | | | -1.321485901 | 0.400122621 | 1.12E-06 | -1.225031033 | 0.427788311 | 2.01E-06 | | | | |
| 265 | | MAL13P1.183 | PMAL13P1.183_168 | hypothetical protein::MAL13P1.183::(PMAL13P1.183_168) | | | 0.409476912 | 1.328204151 | 0.021814129 | -0.372201253 | 0.772602786 | 0.010658985 | -0.906240883 | 0.533573572 | 3.10E-06 | | | | |
| 266 | | MAL13P1.193 | J1113_1 | hypothetical protein::MAL13P1.193::(J1113_1) | GO:0020011 | apicoplast | -1.001246431 | 0.499568206 | 0.000119997 | -0.747364017 | 0.595690965 | 0.000189869 | -0.492037207 | 0.711020368 | 0.00543659 | | | | |
| 267 | | MAL13P1.238 | M15752_2 | hypothetical protein::MAL13P1.238::(M15752_2) | GO:0005515 | protein binding | | | | -0.936316683 | 0.52256533 | 0.002463482 | -1.196891086 | 0.436214283 | 0.000185273 | | | | |
| 268 | | MAL13P1.24 | OPFM60531 | hypothetical protein::MAL13P1.24::(OPFM60531) | | | 0.534573448 | 1.448513819 | 0.045053803 | 0.886995655 | 1.849320987 | 0.000327845 | 0.573371634 | 1.487997017 | 0.008930087 | | | | |
| | | MAL13P1.24 | M29079_4 | hypothetical protein::MAL13P1.24::(M29079_4) | | | | | | 0.80626388 | 1.748677058 | 0.000336037 | 0.701839254 | 1.626577152 | 0.001032519 | | | | |
| 269 | | MAL13P1.254 | PMAL13P1.254_185 | hypothetical protein::MAL13P1.254::(PMAL13P1.254_185) | GO:0020011 | apicoplast | 0.725862829 | 1.653889478 | 0.000793728 | | | | -0.778608332 | 0.582928833 | 3.98E-05 | | | | |
| 270 | | MAL13P1.268 | M33579_4 | hypothetical protein::MAL13P1.268::(M33579_4) | | | -0.472199191 | 0.7208649 | 0.069320445 | -1.44458139 | 0.367398747 | 2.49E-06 | -1.795429798 | 0.288085749 | 3.61E-07 | | | | |
| 271 | | MAL13P1.30 | PMAL13P1.30_216 | hypothetical protein::MAL13P1.30::(PMAL13P1.30_216) | | | -0.860015366 | 0.55094669 | 0.023017541 | | | | | | | | | | |
| 272 | | MAL13P1.308 | M36754_2 | hypothetical protein, conserved::MAL13P1.308::(M36754_2) | | | 0.946669764 | 1.927418375 | 0.00019396 | | | | | | | | | | |
| 273 | | MAL13P1.354 | L1_21 | erythrocyte membrane protein 1 (PIEMP1), pseudogene::MAL13P1.354::(L1_21) | | | 0.530653325 | 1.444583227 | 0.000535218 | -0.597499103 | 0.660898624 | 1.83E-05 | -1.030047026 | 0.489694186 | 2.07E-08 | | | | |
| 274 | | MAL13P1.37 | PMAL13P1.37_1810 | hypothetical protein::MAL13P1.37::(PMAL13P1.37_1810) | GO:0005622 | intracellular | 1.036883384 | 2.051790434 | 0.027994409 | | | | | | | | | | |
| 275 | | MAL13P1.40 | OPFM60513 | hypothetical protein::MAL13P1.40::(OPFM60513) | | | -0.794791786 | 0.576426359 | 7.29E-05 | -0.861560995 | 0.55035675 | 2.32E-06 | -0.488263761 | 0.712882514 | 0.000631732 | | | | |
| 276 | | MAL13P1.480 | PHRP111_502 | Histidine Rich protein III (HRP111)::MAL13P1.480::(PHRP111_502) | | | | | | | | | -0.754268551 | 0.592846884 | 2.30E-06 | | | | |
| 277 | | MAL13P1.61 | M26214_1 | hypothetical protein::MAL13P1.61::(M26214_1) | GO:0020011 | apicoplast | | | | -0.92674019 | 0.526045615 | 1.31E-07 | -1.84777704 | 0.277820114 | 1.08E-11 | | | | |
| 278 | | MAL7P1.11 | PMAL7P1.11_107 | hypothetical protein::MAL7P1.11::(PMAL7P1.11_107) | | | | | | 0.900289563 | 1.866440558 | 4.19E-05 | 0.79734345 | 1.737898047 | 0.000113802 | | | | |
| 279 | | MAL7P1.119 | KN5587_2 | hypothetical protein::MAL7P1.119::(KN5587_2) | GO:0020011 | apicoplast | 0.865022206 | 1.821367702 | 0.022124734 | | | | | | | | | | |
| | | MAL7P1.119 | F53897_2 | hypothetical protein::MAL7P1.119::(F53897_2) | GO:0020011 | apicoplast | 0.798507652 | 1.739301034 | 0.000579299 | | | | | | | | | | |
| 280 | | MAL7P1.141 | PMAL7P1.141_100 | hypothetical protein::MAL7P1.141::(PMAL7P1.141_100) | GO:0020011 | apicoplast | 0.992954745 | 1.990257012 | 0.007005983 | | | | -0.693428305 | 0.618382628 | 0.003311143 | | | | |
| 281 | | MAL7P1.17 | F30663_2 | hypothetical protein::MAL7P1.17::(F30663_2) | | | 0.789855899 | 1.728901766 | 0.000307894 | | | | | | | | | | |
| | | MAL7P1.17 | F17473_1 | hypothetical protein::MAL7P1.17::(F17473_1) | | | 0.885933582 | 1.847960068 | 0.035814245 | | | | | | | | | | |
| 282 | | MAL7P1.170 | OPFBLOB0026 | protein::MAL7P1.170::(OPFBLOB0026) | | | | | | -0.750796425 | 0.594275403 | 2.58E-06 | -1.227435832 | 0.427075833 | 3.97E-09 | | | | |
| 283 | | MAL7P1.173 | PMAL7P1.173_798 | hypothetical protein::MAL7P1.173::(PMAL7P1.173_798) | | | | | | -1.024856173 | 0.491459292 | 2.37E-05 | -1.578089695 | 0.334925077 | 1.22E-07 | | | | |
| 284 | | MAL7P1.177 | F47160_1 | predicted integral membrane protein, conserved in P. falciparum::MAL7P1.177::(F47160_1) | | | -0.575255884 | 0.671167199 | 0.002296157 | -0.812617719 | 0.569347859 | 1.08E-05 | -0.583810896 | 0.667199033 | 0.000262339 | | | | |
| 285 | | MAL7P1.321 | PHRP_180 | Histidine Rich protein I (HRP1)::MAL7P1.321::(PHRP_180) | | | 0.890791692 | 1.85419335 | 0.010772075 | | | | | | | | | | |
| 286 | | MAL7P1.33 | F53320_1 | hypothetical protein::MAL7P1.33::(F53320_1) | GO:0020011 | apicoplast | -0.866420669 | 0.548506009 | 2.55E-05 | -0.719340433 | 0.607375057 | 1.13E-06 | -0.716320334 | 0.608647851 | 8.96E-07 | | | | |
| 287 | | MAL7P1.6 | PMAL7P1.6_11 | hypothetical protein::MAL7P1.6::(PMAL7P1.6_11) | GO:0020011 | apicoplast | | | | -0.712595794 | 0.610221199 | 0.000534221 | -1.408822406 | 0.376618975 | 3.34E-07 | | | | |
| 288 | | MAL7P1.7 | F65043_4 | RESA-like protein::MAL7P1.7::(F65043_4) | | | 1.356918115 | 2.561374339 | 0.007826479 | | | | -1.304303194 | 0.404916631 | 0.006023378 | -1.342576963 | 0.394315694 | 0.005004476 | |
| | | MAL7P1.7 | F65043_1 | RESA-like protein::MAL7P1.7::(F65043_1) | | | | | | -1.304303194 | 0.404916631 | 0.006023378 | -1.342576963 | 0.394315694 | 0.005004476 | | | | |
| 289 | | MAL7P1.77 | F25543_1 | hypothetical protein::MAL7P1.77::(F25543_1) | | | -1.134592575 | 0.455463524 | 1.48E-06 | -0.47449724 | 0.719717558 | 0.000689893 | | | | | | | |
| 290 | | MAL7P1.82 | PMAL7P1.82_15 | hypothetical protein::MAL7P1.82::(PMAL7P1.82_15) | | | | | | -1.242675433 | 0.422588252 | 0.000128942 | -0.976342126 | 0.50826679 | 0.000522294 | | | | |

| # | FUNCTIONAL CLASSIFICATION | PLASMOID ID | OLIGO | ANNOTATION | GO ID | FUNCTIONAL ANNOTATION | FOLD CHANGE TO RELATIVE I0 WITH P-VALUES ADJUSTED FOR MDR DATA WITH P<0.05 ARE PRESENTED | | | | | | | | |
|-----|---------------------------|-------------|----------------|--|------------|----------------------------|--|-------------|--------------|--------------|-------------|--------------|--------------|-------------|--------------|
| | | | | | | | T1 | | | T2 | | | T3 | | |
| | | | | | | | log2 FC | T1 FC | adj. p value | log2 FC | T2 FC | adj. p value | log2 FC | T3 FC | adj. p value |
| 414 | | PF14_0570 | N130_6 | hypothetical protein, conserved::PF14_0570::(N130_6) | GO:0008150 | biological_process | -1.132399647 | 0.456156365 | 0.001815255 | -0.755047895 | 0.592526714 | 0.001091389 | | | |
| 415 | | PF14_0582 | OPFN0287 | hypothetical protein::PF14_0582::(OPFN0287) | | | -0.627117904 | 0.647468583 | 0.008514401 | -0.734136505 | 0.601177739 | 0.000493361 | -0.76299404 | 0.589272138 | 0.000317596 |
| 416 | | PF14_0582 | N134_126 | hypothetical protein::PF14_0582::(N134_126) | | | -0.772086809 | 0.585569855 | 0.000330823 | -0.629211506 | 0.646529675 | 0.000225633 | -0.468433545 | 0.722748921 | 0.002328233 |
| 417 | | PF14_0624 | N134_34 | hypothetical protein::PF14_0624::(N134_34) | | | -0.765100458 | 0.588412395 | 0.002012706 | | | | | | |
| 418 | | PF14_0624 | N134_22 | hypothetical protein::PF14_0624::(N134_22) | | | | | | -1.092760178 | 0.468863482 | 0.036388281 | | | |
| 419 | | PF14_0650 | N158_7 | hypothetical protein::PF14_0650::(N158_7) | | | | | | -0.428723038 | 0.742919069 | 0.029745287 | | | |
| 420 | | PF14_0662 | N137_14 | hypothetical protein::PF14_0662::(N137_14) | GO:0008150 | biological_process | | | | -0.725601292 | 0.604744944 | 0.000120079 | -1.011434402 | 0.496052801 | 3.07E-06 |
| 421 | | PF14_0666 | N137_23 | hypothetical protein::PF14_0666::(N137_23) | | | | | | 0.755476822 | 1.68818946 | 3.81E-07 | 0.885694821 | 1.847654262 | 3.27E-08 |
| 422 | | PF14_0666 | N137_21 | hypothetical protein::PF14_0666::(N137_21) | | | | | | -1.063028381 | 0.478626313 | 5.90E-06 | -0.721139194 | 0.606628879 | 2.35E-05 |
| 423 | | PF14_0666 | N137_23 | hypothetical protein::PF14_0666::(N137_23) | | | | | | -0.805400737 | 0.572203118 | 3.94E-06 | -0.634151661 | 0.644319579 | 3.27E-06 |
| 424 | | PF14_0666 | N137_21 | hypothetical protein::PF14_0666::(N137_21) | | | | | | | | | | | |
| 421 | | PF14_0680 | PPF14_0680_16 | hypothetical protein::PF14_0680::(PPF14_0680_16) | GO:0008150 | biological_process | -1.007553319 | 0.49738906 | 2.36E-06 | -0.608519595 | 0.65586937 | 3.99E-05 | -0.389823451 | 0.763222998 | 0.001998923 |
| 422 | | PF14_0730 | PPF14_0730_170 | hypothetical protein::PF14_0730::(PPF14_0730_170) | GO:0008150 | biological_process | | | | -0.69702962 | 0.61684092 | 3.20E-05 | -1.044573414 | 0.484788233 | 2.67E-07 |
| 423 | | PF14_0731 | N129_36 | hypothetical protein::PF14_0731::(N129_36) | | | 0.474898767 | 1.389820694 | 0.003009858 | -0.218981814 | 0.859171585 | 0.066506174 | -0.832080397 | 0.561718648 | 1.24E-06 |
| 424 | | PF14_0732 | N129_33 | hypothetical protein::PF14_0732::(N129_33) | GO:0008150 | biological_process | | | | -1.213701742 | 0.430086353 | 0.032015137 | | | |
| 425 | | PF14_0758 | N139_4 | hypothetical protein::PF14_0758::(N139_4) | GO:0008150 | biological_process | 0.878404145 | 1.838340673 | 1.73E-06 | 0.49517823 | 1.409494873 | 4.96E-05 | 0.282829386 | 1.216578477 | 0.005565319 |
| 426 | | PFA0115W | PPFA0115W_278 | hypothetical protein::PFA0115W::(PPFA0115W_278) | GO:0020011 | apicoplast | -1.718953652 | 0.303768957 | 7.46E-07 | -1.515169967 | 0.349855247 | 1.06E-08 | -1.452159858 | 0.365473863 | 2.00E-08 |
| 427 | | PFA0245W | A6420_1 | hypothetical protein::PFA0245W::(A6420_1) | | | -0.752017904 | 0.593772464 | 0.0031601 | -0.509230213 | 0.409597227 | 0.009788612 | -0.413341895 | 0.750881996 | 0.028837199 |
| 428 | | PFA0255c | A24704_11 | hypothetical protein::PFA0255c::(A24704_11) | | | | | | -0.930274853 | 0.524758359 | 0.000621281 | 0.359754382 | 1.283207414 | 0.017226235 |
| 429 | | PFA0285c | A8109_21 | hypothetical protein::PFA0285c::(A8109_21) | | | | | | -0.531636614 | 0.691769535 | 0.01129057 | -0.79339373 | 0.576985221 | 7.32E-05 |
| 430 | | PFA0425c | A21885_9 | hypothetical protein::PFA0425c::(A21885_9) | GO:0031072 | heat shock protein binding | | | | -0.829298422 | 0.562802865 | 0.000538559 | -0.663360442 | 0.631405861 | 0.002909124 |
| 431 | | PFA0440w | A31914_2 | hypothetical protein::PFA0440w::(A31914_2) | | | | | | -0.701660006 | 0.614864319 | 0.006587924 | -1.126229527 | 0.458111433 | 0.00011389 |
| 432 | | PFA0620c | A14801_13 | glutamic acid-rich protein (garp)::PFA0620c::(A14801_13) | | | | | | -0.81602612 | 0.568004349 | 0.002180424 | -0.917926145 | 0.529269291 | 0.000106212 |
| 433 | | PFA0635c | A14801_24 | hypothetical protein::PFA0635c::(A14801_24) | | | | | | | | | -1.114513335 | 0.461846924 | 1.18E-05 |
| 434 | | PFA0670c | PPFA0670C_135 | hypothetical protein::PFA0670c::(PPFA0670C_135) | | | | | | -0.451329396 | 0.731368605 | 0.048842038 | -0.882804158 | 0.542312317 | 0.001466208 |
| 435 | | PFB0105c | B60 | hypothetical protein::PFB0105c::(B60) | GO:0008150 | biological_process | | | | -0.434494546 | 0.739952955 | 0.011307194 | -1.091242229 | 0.469357062 | 6.45E-06 |
| 436 | | PFB0106c | B64 | hypothetical protein::PFB0106c::(B64) | GO:0008150 | biological_process | | | | -0.562848652 | 0.676964154 | 0.002770688 | -0.81156784 | 0.569762336 | 0.000100742 |
| 437 | | PFB0115w | B69 | hypothetical protein::PFB0115w::(B69) | | | | | | -0.730126772 | 0.602850938 | 0.001037013 | -1.371933111 | 0.386373188 | 1.61E-06 |
| 438 | | PFB0256w | B161 | hypothetical protein::PFB0256w::(B161) | | | 0.751990209 | 1.684114478 | 0.030042123 | 1.343387567 | 2.537464374 | 7.32E-05 | 1.72953097 | 3.316136969 | 4.00E-06 |
| 439 | | PFB0440c | B310 | hypothetical protein::PFB0440c::(B310) | GO:0005515 | protein binding | | | | 1.001431301 | 2.001985189 | 0.000320647 | 0.645110598 | 1.563859385 | 0.004863071 |
| 440 | | PFB0535w | B371 | hypothetical protein::PFB0535w::(B371) | | | 0.808800829 | 1.751754775 | 0.001934286 | 0.466554106 | 1.381805066 | 0.016707457 | | | |
| 441 | | PFB0535w | B370 | hypothetical protein::PFB0535w::(B370) | | | -0.546104579 | 0.684868643 | 0.002156029 | -1.135523518 | 0.455169717 | 1.31E-07 | -1.041196004 | 0.485924472 | 2.53E-07 |
| 442 | | PFB0570w | B387 | hypothetical protein::PFB0570w::(B387) | GO:0008150 | biological_process | -0.784647298 | 0.580493856 | 0.001702729 | -0.944348252 | 0.519664261 | 4.42E-06 | -1.019444749 | 0.493306175 | 3.43E-06 |
| 443 | | PFB0580w | B389 | hypothetical protein::PFB0580w::(B389) | | | | | | -0.67021939 | 0.628411118 | 0.042641881 | -0.954156999 | 0.516145096 | 0.006711061 |
| 444 | | PFB0590w | B392 | hypothetical protein::PFB0590w::(B392) | GO:0008150 | biological_process | | | | -0.797528246 | 0.575334047 | 0.005607656 | | | |
| 445 | | PFB0680w | B455 | hypothetical protein::PFB0680w::(B455) | GO:0008150 | biological_process | -1.5493798 | 0.341656907 | 0.012197027 | -1.097752626 | 0.467243783 | 0.026545093 | -1.08808103 | 0.470386633 | 0.025116748 |
| 446 | | PFB0835c | B536 | hypothetical protein::PFB0835c::(B536) | GO:0008150 | biological_process | | | | 0.792494435 | 1.732066637 | 0.001765963 | | | |
| 447 | | PFB0900c | B565 | hypothetical protein::PFB0900c::(B565) | GO:0008150 | biological_process | -0.498991161 | 0.707601415 | 0.026746568 | -0.751452876 | 0.594005059 | 0.000295333 | -0.666409874 | 0.630072665 | 0.000767629 |
| 448 | | PFB0915w | B572 | liver stage antigen 3::PFB0915w::(B572) | GO:0008150 | biological_process | | | | -1.045070795 | 0.484621127 | 1.67E-07 | -1.653408945 | 0.317888131 | 3.26E-10 |
| 449 | | PFB0923c | B577 | hypothetical protein::PFB0923c::(B577) | GO:0008150 | biological_process | | | | -0.77145997 | 0.585824335 | 7.72E-06 | -1.07349071 | 0.475167902 | 1.22E-07 |
| 450 | | PFB0953w | OPFB0689 | hypothetical protein::PFB0953w::(OPFB0689) | GO:0008150 | biological_process | 0.50159197 | 1.415774965 | 0.006584194 | 0.924874509 | 1.898519094 | 2.93E-06 | 1.039929354 | 2.056126966 | 6.51E-07 |
| 451 | | PFB0953w | B603 | hypothetical protein::PFB0953w::(B603) | GO:0008150 | biological_process | | | | -0.931044874 | 0.52447835 | 0.000172202 | -0.629613251 | 0.466349662 | 0.000635033 |
| 452 | | PFC0085c | C49 | hypothetical protein, conserved::PFC0085c::(C49) | GO:0008150 | biological_process | | | | -1.06022294 | 0.479557948 | 7.46E-07 | -0.649863629 | 0.637340556 | 7.95E-06 |
| 453 | | PFC0090w | C54 | hypothetical protein, conserved::PFC0090w::(C54) | | | | | | 0.369280293 | 1.291708285 | 0.048465691 | 0.783664578 | 1.721498087 | 0.0002634 |
| 454 | | PFC0215c | C138 | hypothetical protein::PFC0215c::(C138) | GO:0020011 | apicoplast | | | | -0.932416622 | 0.523979901 | 0.000101328 | -1.067716718 | 0.477073442 | 2.11E-05 |
| 455 | | PFC0345w | C233 | hypothetical protein::PFC0345w::(C233) | GO:0005622 | intracellular | 0.759165964 | 1.692511884 | 0.033517154 | 1.174980507 | 2.257898302 | 0.004134871 | | | |
| 456 | | PFC0450w | C289 | hypothetical protein::PFC0450w::(C289) | GO:0020011 | apicoplast | | | | 0.891909489 | 1.855630532 | 0.000942142 | 0.708030859 | 1.633572924 | 0.004866696 |
| 457 | | PFC0506w | OPFC0768 | hypothetical protein::PFC0506w::(OPFC0768) | | | | | | -0.812154953 | 0.569530515 | 0.004270802 | -0.762776911 | 0.589360832 | 0.000170722 |
| 458 | | PFC0540w | F63999_1 | hypothetical protein::PFC0540w::(F63999_1) | | | | | | -1.346879585 | 0.393141458 | 6.51E-08 | -1.318278447 | 0.504103178 | 1.06E-07 |
| 459 | | PFC0540w | C365 | hypothetical protein::PFC0540w::(C365) | | | | | | -0.656545451 | 0.634395547 | 0.029545417 | -1.015591033 | 0.494625652 | 0.002514155 |
| 460 | | PFC0590c | OPFC0773 | hypothetical protein::PFC0590c::(OPFC0773) | GO:0020011 | apicoplast | | | | -0.514495659 | 0.700037611 | 0.007114114 | -0.81476515 | 0.568501023 | 1.92E-05 |
| 461 | | PFC0590c | C419 | hypothetical protein::PFC0590c::(C419) | GO:0020011 | apicoplast | | | | -0.659859592 | 0.632939894 | 0.001925886 | -0.772337516 | 0.585468105 | 0.004027294 |
| 462 | | PFC0730w | D47995_1 | putative::PFC0730w::(D47995_1) | GO:0008150 | biological_process | | | | -0.602164468 | 0.658764872 | 9.78E-05 | -0.804391849 | 0.572603404 | 4.20E-06 |
| 463 | | PFC0730w | C488 | conserved protein, putative::PFC0730w::(C488) | GO:0008150 | biological_process | | | | -0.662329801 | 0.63185709 | 2.45E-05 | -0.825284801 | 0.56437078 | 1.77E-06 |
| 464 | | PFC0830w | C541 | trophozoite stage antigen::PFC0830w::(C541) | | | | | | -0.738645324 | 0.599301827 | 0.001142964 | -1.290574029 | 0.408788346 | 4.83E-06 |
| 465 | | PFC0911c | C602 | hypothetical protein::PFC0911c::(C602) | | | | | | -0.786761297 | 0.579643874 | 0.0469994 | | | |
| 466 | | PFC0912w | OPFC0775 | hypothetical protein::PFC0912w::(OPFC0775) | | | | | | -1.080709238 | 0.472796107 | 4.92E-05 | -0.715538229 | 0.608977897 | 0.000242234 |
| 467 | | PFC0912w | C604 | hypothetical protein::PFC0912w::(C604) | | | | | | -0.92703166 | 0.525939348 | 0.003179198 | -0.481603719 | 0.711234041 | 0.009876529 |
| 468 | | PFC1035w | C686 | hypothetical protein::PFC1035w::(C686) | | | | | | -0.744417302 | 0.596808912 | 0.000615153 | -0.858686171 | 0.551454526 | 0.000297782 |
| 469 | | PFD0080c | D42243_42 | hypothetical protein::PFD0080c::(D42243_ | | | | | | | | | | | |

| # | FUNCTIONAL CLASSIFICATION | PLASMOID ID | OLIGO | ANNOTATION | GO ID | FUNCTIONAL ANNOTATION | FOLD CHANGE TO RELATIVE I0 WITH P-VALUES ADJUSTED FOR MDR | | | | | | | | | | | |
|-----|---------------------------|-------------|------------------|---|------------|-----------------------|---|--------------------|--------------|-------------------------------------|--------------------|--------------|-------------------------------------|--------------------|--------------|-------------|-------------|-----------|
| | | | | | | | DATA WITH P<0.05 ARE PRESENTED | | | | | | | | | | | |
| | | | | | | | T ₁₁ log ₂ FC | T ₁₁ FC | adj. p value | T ₁₂ log ₂ FC | T ₁₂ FC | adj. p value | T ₁₃ log ₂ FC | T ₁₃ FC | adj. p value | | | |
| 475 | | PFE0440w | OPFBLOB0182 | hypothetical protein::PFE0440w::(OPFBLOB0182) | | | 0.894566527 | 1.85905123 | 0.00384304 | | | | | | | | | |
| 476 | | PFE0600c | E20313_1 | hypothetical protein::PFE0600c::(E20313_1) | | | | | | | | | | | | | | |
| 477 | | PFE0650c | D8125_1 | hypothetical protein::PFE0650c::(D8125_1) | | | | | | | | | | | | | | |
| 478 | | PFE0685w | E8314_2 | hypothetical protein::PFE0685w::(E8314_2) | | | | | | | | | | | | | | |
| 479 | | PFE0785c | E3215_10 | hypothetical protein::PFE0785c::(E3215_10) | | | | | | | | | | | | | | |
| 480 | | PFE0855c | OPFBLOB0186 | hypothetical protein::PFE0855c::(OPFBLOB0186) | | | | | | | | | | | | | | |
| 481 | | PFE1190c | PPFE1190c_105 | hypothetical protein::PFE1190c::(PPFE1190c_105) | GO:0020011 | apicoplast | 0.302771263 | 1.233511583 | 0.020459589 | -0.363260768 | 0.777405507 | 0.001276356 | -0.7897616 | 0.578439669 | 3.72E-07 | | | |
| 482 | | PFE1205c | E16790_7 | hypothetical protein::PFE1205c::(E16790_7) | | | | | | | | | | | | | | |
| 483 | | PFE1215c | E16790_2 | developmentally regulated GTP-binding protein 1, putative::PFE1215c::(E16790_2) | GO:0005622 | intracellular | 0.500773859 | 1.414972347 | 0.013262472 | 1.203837459 | 2.303515745 | 0.000580142 | 0.773683022 | 1.709628688 | 0.008737014 | | | |
| 484 | | PFE1285w | E17645_8 | hypothetical protein::PFE1285w::(E17645_8) | | | | | | | | | | | | | | |
| 485 | | PFE1500c | E29307_2 | hypothetical protein::PFE1500c::(E29307_2) | | | | | | | | | | | | | | |
| 486 | | PFE1525w | E18606_1 | hypothetical protein::PFE1525w::(E18606_1) | GO:0020011 | apicoplast | -0.713496526 | 0.609840333 | 0.040119081 | -0.550317704 | 0.682869733 | 0.001424184 | -0.761722967 | 0.589791564 | 6.71E-05 | | | |
| 487 | | PFE1610w | PPFE1610w_21 | hypothetical protein::PFE1610w::(PPFE1610w_21) | GO:0020011 | apicoplast | 0.927512882 | 1.901994246 | 0.005490569 | 0.27512882 | 1.901994246 | 0.005490569 | | | | | | |
| 488 | | PFE1615c | D57574_1 | hypothetical protein::PFE1615c::(D57574_1) | GO:0020011 | apicoplast | 1.548501221 | 2.925130969 | 0.005071577 | 1.36152304 | 2.569563028 | 0.001828821 | 0.884104004 | 1.845618031 | 0.020337468 | | | |
| 489 | | PF0210w | PMAL6P1.46_2093 | hypothetical protein::PF0210w::(PMAL6P1.46_2093) | GO:0020011 | apicoplast | | | | 0.823203963 | 1.769330995 | 0.000446283 | 0.644574726 | 1.563278399 | 0.002490929 | | | |
| 490 | | PF0235c | PMAL6P1.51_1594 | hypothetical protein::PF0235c::(PMAL6P1.51_1594) | | | -1.088484256 | 0.470255181 | 0.001799928 | | | | | | | | | |
| 491 | | PF0440w | PMAL6P1.92_2916 | hypothetical protein::PF0440w::(PMAL6P1.92_2916) | | | | | | | | | | | | | | |
| 492 | | PF0490w | PMAL6P1.102_2416 | hypothetical protein::PF0490w::(PMAL6P1.102_2416) | | | | | | | | | | | | | | |
| 493 | | PF0595c | PMAL6P1.303_4968 | hypothetical protein::PF0595c::(PMAL6P1.303_4968) | GO:0020011 | apicoplast | 0.681065958 | 1.603323959 | 0.002852636 | | | | | | | | | |
| 494 | | PF0630c | PMAL6P1.295_219 | conserved::PF0630c::(PMAL6P1.295_219) | | | -1.519963929 | 0.348694635 | 1.82E-05 | -1.108784868 | 0.463684412 | 3.65E-05 | -1.052082826 | 0.482271404 | 5.08E-05 | | | |
| 495 | | PF0670w | F1021_3 | hypothetical protein::PF0670w::(F1021_3) | | | 0.905079503 | 1.872647689 | 8.35E-05 | 0.486300043 | 1.40084763 | 0.002323072 | 0.524934531 | 1.43868283 | 0.001173636 | | | |
| 496 | | PF0810c | F48270_1 | hypothetical protein::PF0810c::(F48270_1) | | | | | | 0.819268475 | 1.764511062 | 0.000942142 | 0.685147283 | 1.607866118 | 0.005388772 | | | |
| 497 | | PF1260c | E18445_1 | hypothetical protein::PF1260c::(E18445_1) | | | | | | 0.756174499 | 1.689006054 | 0.002527313 | 0.72185652 | 1.649303061 | 0.003324396 | | | |
| 498 | | PF10085c | D5782_1 | hypothetical protein::PF10085c::(D5782_1) | | | | | | 0.881683925 | 1.842524656 | 2.55E-05 | 0.88413907 | 1.845662891 | 1.99E-05 | | | |
| 499 | | PF10130c | I3470_1 | hypothetical protein::PF10130c::(I3470_1) | | | | | | | | | | | | | | |
| 500 | | PF10210c | I2689_1 | hypothetical protein::PF10210c::(I2689_1) | GO:0020011 | apicoplast | -1.085456227 | 0.471243222 | 1.89E-06 | 0.400432351 | 1.319903404 | 0.007878618 | 0.767393054 | 1.702191148 | 2.41E-05 | | | |
| 501 | | PF10335w | OPI117990 | hypothetical protein::PF10335w::(OPI117990) | | | 0.385603407 | 1.288420398 | 0.014653412 | -0.809461635 | 0.570990388 | 0.019012417 | -0.895345326 | 0.537616495 | 0.002656568 | | | |
| 502 | | PF10400c | I3854_2 | hypothetical protein::PF10400c::(I3854_2) | | | -0.868455834 | 0.547732794 | 0.011576611 | -0.534093822 | 0.690592312 | 0.046314493 | -0.564048042 | 0.676401591 | 0.03610441 | | | |
| 503 | | PF10490c | I13674_3 | hypothetical protein::PF10490c::(I13674_3) | GO:0020011 | apicoplast | -0.838080588 | 0.559387303 | 0.001019412 | | | | | | | | | |
| 504 | | PF10575c | KN1713_1 | hypothetical protein::PF10575c::(KN1713_1) | | | | | | | | | | | | | | |
| 505 | | PF10655c | I13369_2 | hypothetical protein::PF10655c::(I13369_2) | | | -0.974214638 | 0.509016865 | 0.012005023 | -0.897941856 | 0.536651771 | 5.03E-05 | -0.741672961 | 0.598045452 | 0.000280619 | | | |
| 506 | | PF10675w | F67796_1 | hypothetical protein::PF10675w::(F67796_1) | | | -0.766309992 | 1.700913756 | 0.010475052 | -0.586782186 | 0.665826324 | 0.002891113 | -0.844309657 | 0.556977264 | 0.000119261 | | | |
| 507 | | PF10725c | I4179_1 | hypothetical protein::PF10725c::(I4179_1) | | | -0.846565937 | 0.556108689 | 1.41E-05 | -0.385292381 | 0.765623819 | 0.002041769 | | | | | | |
| 508 | | PF10805w | KN2445_1 | hypothetical protein::PF10805w::(KN2445_1) | | | 0.662135224 | 1.582422916 | 0.026410476 | 1.071151698 | 2.101110006 | 4.16E-05 | 1.191134309 | 2.283321972 | 6.04E-06 | | | |
| 509 | | PF10880c | I11182_1 | putative::PF10880c::(I11182_1) | | | -0.546415498 | 0.684719262 | 0.013930248 | -0.769492828 | 0.586623663 | 0.000181655 | -0.394691246 | 0.760652148 | 0.023314946 | | | |
| 510 | | PF10915w | I17310_3 | hypothetical protein::PF10915w::(I17310_3) | | | | | | -0.71116523 | 0.61082659 | 0.016134582 | -1.228266123 | 0.628301116 | 0.001470648 | | | |
| 511 | | PF11035w | PPF11035W_245 | hypothetical protein::PF11035w::(PPF11035W_245) | | | | | | | | | | | | | | |
| 512 | | PF11165c | OPFBLOB0128 | hypothetical protein::PF11165c::(OPFBLOB0128) | | | | | | | | | | | | | | |
| 513 | | PF11190w | PPF11190W_3069 | hypothetical protein::PF11190w::(PPF11190W_3069) | | | 0.871794821 | 1.829938065 | 0.000496582 | | | | | | | | | |
| 514 | | PF11405c | KN5081_1 | hypothetical protein::PF11405c::(KN5081_1) | | | 0.462425582 | 1.377856442 | 0.000676279 | 1.047184811 | 2.066493479 | 8.01E-09 | 1.288185633 | 2.442207246 | 3.28E-10 | | | |
| 515 | | PF11430w | OPI117718 | hypothetical protein::PF11430w::(OPI117718) | | | | | | -1.001273812 | 0.499587725 | 2.82E-06 | -0.849307102 | 0.555051251 | 1.45E-05 | | | |
| 516 | | PF11720w | I7196_2 | hypothetical protein::PF11720w::(I7196_2) | | | | | | -1.070233483 | 0.476241919 | 7.80E-08 | -1.546740232 | 0.342282578 | 3.58E-10 | | | |
| 517 | | PF11720w | F68282_1 | hypothetical protein::PF11720w::(F68282_1) | | | | | | -0.955830146 | 0.515544853 | 2.50E-08 | -1.375884982 | 0.385316272 | 1.34E-10 | | | |
| 518 | | PF11735c | F37100_2 | hypothetical protein::PF11735c::(F37100_2) | | | 0.484351701 | 1.39895708 | 0.00042841 | -0.792571904 | 0.577313992 | 2.11E-07 | -1.667613966 | 0.314773531 | 1.08E-11 | | | |
| 519 | | PF11740c | OPI117638 | hypothetical protein::PF11740c::(OPI117638) | | | | | | -0.757956825 | 0.591333196 | 3.15E-07 | -1.616709332 | 0.326078374 | 1.08E-11 | | | |
| 520 | | PF11755c | I12552_2 | hypothetical protein::PF11755c::(I12552_2) | | | | | | -0.900562769 | 0.535677732 | 4.75E-08 | -1.629933443 | 0.323103113 | 1.08E-11 | | | |
| 521 | | PF11770w | PPF11770W_38 | hypothetical protein::PF11770w::(PPF11770W_38) | | | | | | | | | | | | | | |
| 522 | | PF11785w | F24156_1 | hypothetical protein::PF11785w::(F24156_1) | GO:0008150 | biological_process | | | | -0.566858235 | 0.675085326 | 3.30E-06 | -0.828185571 | 0.563237162 | 2.45E-08 | | | |
| 523 | | PFL0060w | L1_42 | hypothetical protein::PFL0060w::(L1_42) | | | | | | -1.046303972 | 0.484207063 | 1.06E-06 | -1.604944801 | 0.328748268 | 3.07E-09 | | | |
| 524 | | PFL0280c | L2_35 | hypothetical protein::PFL0280c::(L2_35) | | | -0.933030675 | 0.523756927 | 3.58E-05 | -0.700852532 | 0.615208554 | 5.36E-05 | -0.487506255 | 0.713256921 | 0.00131796 | | | |
| 525 | | PFL0610w | L2_195 | hypothetical protein::PFL0610w::(L2_195) | GO:0008150 | biological_process | -0.843363253 | 0.55734276 | 0.002063194 | -0.31857074 | 0.801863881 | 0.04348917 | | | | | | |
| 526 | | PFL0680c | L2_218 | hypothetical protein::PFL0680c::(L2_218) | GO:0008150 | biological_process | -0.571951053 | 0.672706427 | 0.010791077 | -0.918174224 | 0.529178288 | 1.09E-05 | -0.948265878 | 0.518255031 | 6.62E-06 | | | |
| 527 | | PFL0685w | L2_224 | hypothetical protein::PFL0685w::(L2_224) | GO:0008150 | biological_process | | | | -0.77818261 | 0.583126883 | 0.008936573 | -0.605460924 | 0.657261359 | 0.03260459 | | | |
| 528 | | PFL1020w | J2541_1 | hypothetical protein::PFL1020w::(J2541_1) | GO:0008150 | biological_process | 0.866791969 | 1.823603356 | 0.023162844 | 1.138663497 | 2.201769582 | 0.000101328 | 0.957099531 | 1.94402872 | 0.000433178 | | | |
| 529 | | PFL1075w | KN2497_2 | hypothetical protein::PFL1075w::(KN2497_2) | | | -0.751751967 | 0.593881926 | 0.002841553 | | | | | | | | | |
| 530 | | PFL1300c | KN302_1 | hypothetical protein::PFL1300c::(KN302_1) | | | | | | 0.54190622 | 1.455894908 | 0.007141306 | 0.836409308 | 1.785600465 | 0.000230169 | | | |
| 531 | | PFL1415w | PPFL1415W_1260 | hypothetical protein::PFL1415w::(PPFL1415W_1260) | GO:0008150 | biological_process | | | | -0.442174381 | 0.736024461 | 0.008856212 | -0.852705517 | 0.553745311 | 2.74E-05 | | | |
| 532 | | PFL1600c | KN2173_1 | hypothetical protein::PFL1600c::(KN2173_1) | | | 0.763594114 | 1.697714793 | 0.01382464 | 0.856287901 | 1.810374164 | 0.016463993 | 0.679032474 | 1.60106566 | 0.017680291 | 0.696281231 | 1.620322773 | 0.0143538 |
| 533 | | PFL1645w | KN2880_1 | hypothetical protein::PFL1645w::(KN2880_1) | | | | | | | | | | | | | | |
| 534 | | PFL1825w | PPFL1825W_23 | hypothetical protein::PFL1825w::(PPFL1825 | | | | | | | | | | | | | | |