

Supplemental Figure 1:

Rev1 Alignment

Pf3D7_0910500 mdieyggardfekyvnckeekiplsynkkylaeieeshkkck-ndsllfmcncFYIDDFVSFFSICNTldnsntqtkciY
LF_Rev1 -----
PHC_Rev1 mdmeyggarsmglyfrnkekrtprrsykkkyveieesaknysltncriftnccnFYIDDLISLSTIGNNSstntplkewaY
PHT_Rev1 -----
HPC_Rev1 -----FYIDDFVSLFPLYSS-----Y

Pf3D7_0910500 RNekdsvedskelnnymnnsinkttlgkfnmenkmeynytsinehnnnyyinkihndsvfKYQMDKTPMKNIDNNS
LF_Rev1 -----
PHC_Rev1 PQ-----vKRERLSESENEKEKE---
PHT_Rev1 -----KRERLSESENEKEKEKEK
HPC_Rev1 EHv-----nntieqtp---fpyecktqikyp--neyneynkhlntstvtd-----MYRTPTKSNFYSFN

Pf3D7_0910500 NNNNNNDnnnNNGNTYLYDNYLEDQFNQT-----IKNRYSTPNDQISTCTKSFNTCIKTYEEQASSCK
LF_Rev1 -----ESPLK
PHC_Rev1 -----YCATEVFHNTCFEDPVFVSdgsseqngvlnttpIKSECRYDEANTMYTYPVSVKTYINTNEESAHTT-P
PHT_Rev1 ENENENENeeaYCATEVFQSNYFDDPLF-----tpIRNECRYDETNTIYTNPSASKTCYNTNGELTYTT-S
HPC_Rev1 STLYNNDG-----MYHEYKNKSNFMStqrsyksiidd---RNTNYIKDINGINNSYNKFDNFMNVHKNI--NSFE

Pf3D7_0910500 KNVYNSYINKKENLEILIVQNGGVIHNTLTskVTHIISNNMALGSKKYMDYKKAIKKSKVFIVIDQYIFDCVNMQCRLPE
LF_Rev1 SITHNSYINKKERLEILIGQYGGTIHNVLTskVTHIVSNMMSIGSKKYSDLKKIKKWSVCIVTDSYIFDSVKEKTRLSE
PHC_Rev1 TPVHNSYINKKENLEILIVQNGGRIHNI LTGEVTHIISNNMALGNKKYADFkrkvkrskvfiiedtyvfdcvkansrlce
PHT_Rev1 TPVHNSYINKKENLEILIVQNGGRIHNI LTGEVTHIISNNMALGNKKYADFkrkvkrskvfiiedtyvfdcvkansrlce
HPC_Rev1 KPvQATYINKKELEILIVQNGGILHNA LTNKVKNIISNNMALGSKKYMDYKksLkknkifivvdkyifdcvYRGKRLPE

Pf3D7_0910500 QSYLPSMLRYNCHQITEYFSLRKkdkeQNKKMQNKKIQDKINNDQNFLKEHKEGEQnvtildtskcdKQlNDYyVEKKL
LF_Rev1 QSYLPLSLRFNSHQITEYFKLHK-----RKNNRTHDFSEKQKSLPTNIRKETERIEEfkevsrss--LAHSTGLLQSFT
PHC_Rev1 QLylPKTLRYNSRQITEYFPLNK----QRKRSQTNSKSKD-----
PHT_Rev1 QLylPKTLRYNSRQITEYFPLNK----QRKRSQTNSKSKDKNSENKETIEKKSVD-----lnkdQTLNLEEDEV
HPC_Rev1 QSYL-----INNn**-----

P Pf3D7_0910500 STCHNKTSVNNNLNKTDMYGTK--edNNLLIHKDIgnnenlnyiNEQKVREENNNEEKENITNNDN--INKHLEILNMN
LF_Rev1 RVNQSGFSNFNNIVVDTRKGNVi---HVGVPERTItyqdknplsNDNSQIHNNNNNNNEECIENDKefIENKkkQLyLN

PHC_Rev1 -----EKEK-----EKEKETGMEQTEEKELNA-EENK--SSEKMKALLME
PHT_Rev1 KYCPSEGNNGNLKNQKEANEerneeQEEMEKEQ-----EQEKKK-KEQTEENDPSTTEEKE--SNEKMKTLLEME
HPC_Rev1 -----VNILNMN

Pf3D7_0910500 MDYEHVKKFIICNSNEYFKRLQEYYLEKELKENIYSNvSSNLYLNKNTFEDFCRKYRILNLYLSDEEIKWLKCKSELNINI
LF_Rev1 MSYEKLITLIKTPGDEYFKMLFQKCRFMELENPVFPI-KSEVYLNGTNFEFLKKNYININFDSEEIRWIREESRLNLKI
PHC_Rev1 MDYDELKKYIITDYSSYFSRLYKYYCDKERKETIFCT-TSDLYLNKNNFEFARKYRILNLYLTEEEIRWIKNKSKLNLKI
PHT_Rev1 MSYDELKKYIITNYSNYFSRLYKYYCDKERKETIFCT-TSDLYLNKNNFEFARKHRILNLYLTEEEISWIKNKSKLNLKI
HPC_Rev1 MSYINVKKYIILSNSSEYFKKLYKYIIDKELKQNSFPNiQSDLFINKDTCPEFLQKYKIRNYFNMNEIKWLKNSKINIHI

Pf3D7_0910500 KNLWENDIIHFFFDLVLRKKEHFKNNTVGNnignhgnnnnignnHNIGNNNNIGNnnntqsyTDINKsSSYICE
LF_Rev1 KNIWENDIMHFLFKMILRKYPRFSEETRk-----DKEKKKPSVTEEKtthny-----DSMSE
PHC_Rev1 RNIWENNfVHFFNMVLKKK-----FDVSKQNCsMTND-----TKKDeDEEMSD
PHT_Rev1 RNIWENDFIHFFNMVLKKK-----FDVSKQNCsMENND-----TKEDG-DEEMSD
HPC_Rev1 KNVWENDMVHFFFDTVLKSVMQNYDEKLks-----DRGKLSEEIKETS-----SN

Pf3D7_0910500 NLIESISAYLYNSRLYILGNWNYISKELFNFDIKEYEKgsKKFVYLYIDFDNYFLNASIR-----nkiemYEKKKSM
LF_Rev1 GLIQHISEYLYNSRLYILGNWNYIAKLFPPFRDLREKDK--RKHVYLYIDFDYFLNssVNKDSYH-----YKECNM
PHC_Rev1 KLIDSISGYFNNSRLYILGNWSYITKALFDNDIQLTAE--KKCVYLYIDYDYFLNASINKNNND-----NKNI
PHT_Rev1 KLIDSISGYFNNSRLYILGNWSYITKALFDNDIQLTTE--KKCAYLYIDFDYFLNASINKNNNDkvnspisYGDKNI
HPC_Rev1 ELIKTIKDYLYNSRLYVILGNWSYINKIFNFHDIKTSKs-pNKCVYLYIDFDYFLNASIKRGNNL-----FRSNDSF

Pf3D7_0910500 NNEIFCVCHSLKKEDSYGIISSTNYWGKKNKILKGMVKGEATK-MNKNINfVKYDFSNILKCSYLFLLLVLINYSKNVRVL
LF_Rev1 NNSVLCVCHSVKKEESYANISSVNYWAQKNKIYKGLMKKEATN-LHKDIHFVKYNfSNILRNSFLFLLLVLLNFsYVVKVS
PHC_Rev1 NNSIFCVCHSTKKEDSFGMISSINYWAAKNKIYKGLMKMDATRILHKTIFIRYDFSNILKCSFLMLLLVLMNYSSTNVKVS
PHT_Rev1 NNSIFCVCHSTKKEDSFGMISSINYWAAKNKIYKGLMKMDATRILHKTIFIRYDFSNILKCSFLMLLLVLMNYSKNIKVS
HPC_Rev1 NNRIVCVCHSLKKENSYGIISATNYWGKKNKI KGMVKSDVTKVHKNNEfVKYDFSNILKCSYLFLLLILINYSKYVRVI

Pf3D7_0910500 SVDESILQLFYEKKEEDIFIISKKISDDIYRLTNLSVSIIGISHDLSTSRKALKFCKKRfMFFDFYHHFNIFIK-KYISLKN
LF_Rev1 SIDECVLQLFYEKKEEVIQIAKRISNHISYLTDLNVTIGIAKDLASARVAAKFCKKRYMFFDFYHHFCIFLR-KYIDQKN
PHC_Rev1 SVDESVVQLFYEKKEEIFTIAKKISNDIYNLTRLNVTIGISDNLEVARHAAKfCKKRFLFFDFYHHFCIFLR-KYIDWKR
PHT_Rev1 SVDESVVQLFYTKKEEIFTIAKQISNDIYNLTRLNVTIGISDKLEVARHAVKfCKKRFLFFDFYHHFCIFLR-KYIDWKK
HPC_Rev1 SIDECILQLFYEKETDINIANKICDDIYSLTNLVVSIGISDDLILAKHALKYCKKRYIFFDFYHHFKIFIRrKCVRGSG

Pf3D7_0910500 KES-----NITPEASNDNINKSNTISDDKIINGKCLKHMIEQKNVNGTNTDDYRTNWMSDDKLDLFKEYL
LF_Rev1 ESKM-----NSMKEDFKKDLTT-----TMTTTTTTTTTTTTTITNSSEPPDPCILFNAYL
PHC_Rev1 EGEFvdfniyylnhykNRRNKINNNNNNNHNNKNDNRNDKNAFFMNGENK-----

PHT_Rev1 ER-----mqqkrKKRNEKQKQKNEVTDETKNETKNETKDITKD-ETKNETKNETKDE--TTNETKNETTDLFDVYV
HPC_Rev1 ESTS-----SNSCNGNSCNSNIYELNSSEIN-VEQLFNEYM

Pf3D7_0910500 SFEKKRKSELKYNENNKEKYNMNI DNIYFMNLIK-GKREkeVEEYIYNKFLEMNKEN--IEQMNTYFEEVI-HPVSTYFF
LF_Rev1 S---EMNEETKWNTCTNEDRDRD-----FLNHVK-RIDP-EVQTLFASFMTKHKNE--LESILNTFFEKVV-HPISKHFF
PHC_Rev1 -----
PHT_Rev1 KFEEKKRKR-DFGEDEKEETQA EYIDVAFLKHVK-QKDE-EVENVFEKFMNLHQNN--LETILNTFFDKIV-HPVSKYFF
HPC_Rev1 LFEEKRGHSSINPNGT PNNMPNNTPNKYFLNGIE dKKEEkeIEIILFDKFIKIHKEKkkMENILNTYYEDVtpQQVSKYFY

Pf3D7_0910500 FYKPNE-YYFNILKNMNYLNG-YFISFNMYLPHIENDSNNNNNNNNHHHSNNNLHSNNNFHSNNNWLN--nkMDRNINK
LF_Rev1 FFKKDDaFYFKILQQFNMYMHG-KFISFNIRMFDDIEIMNEKKNKTSKVP AQHSN-----
PHC_Rev1 -----MEVGTNP
PHT_Rev1 FYLKNN-FYFDILKKYNYMKG-KFVDFNIYYLNNE SYINNGSNNGSNNNNNNNRKNKKNKNTIFLNgenkMESNQNT
HPC_Rev1 FYKKNY-YHLNILNKLNYMDGgTFINLNIYY-----NNQDNQDDNIYANTYVDKDKTKVTM-----

Pf3D7_0910500 KELENNDEKKS INISVNYGVRFNKINDFYFLIYFMTKQLYLRLKIKNLKAKLLHVNF FIKAEENVNPMKYLGGRVIRI
LF_Rev1 -----DLSKS INIRVNYGVRFTKINDFYFLIYFMCQQLFLRLKIKKLKARSLHISFFIKLEEAPVNP IKFLGRGKVSRA
PHC_Rev1 NISENLNETKSMS IRANYGIRFNKINDFYFLIYFMTKQLYLRLKIKNSKAKNLT MNFFLREENENVDPAKYLGGRKVINL
PHT_Rev1 GINENLNETKSMS IRANYGIRFNKINDFYFLIYFMTKQLYLRLKIKNSKAKNLSMNFFLREENENVDPAKYLGGRKVINL
HPC_Rev1 RTQNEGNEKKS INISVNYGVRFSNINDFYFLIYFMTKQLYIRLKI KKWTKCLSVFFFIREKNENINPTKFLGRGKVYRV

Pf3D7_0910500 SSKIKLNQHTNCFVYFFKVIHTFDFLANNLSDLRGVQIICS DTINENKTHV-NKKSILYFyVNteknknknckya
LF_Rev1 YDKVQLNHYTDSMEVFFFKTISTFRI IEDKLHEL RGVELSISDIISGEINYS-NKKNILYF-----
PHC_Rev1 KSQIKLNNHTNFFVYFFKVI FKFQYIMHKLEDLRGVQLTCFDI IKE-VSRP-NNKSILHYF-QN-----
PHT_Rev1 KSQIKLNNHTNFFVYFFKVI FKFQYIMHKLEDLRGVQLTCFDI IKE-VSHP-NNKTILHYF-ANtvkrkntstii tmsk
HPC_Rev1 GSKIKLNSYTNCFFIYFFKI IYEF SALSSKLEDLRGVQIVCSDMIHDETYYPvGKKSILHYF-----

Pf3D7_0910500 swkddnflevpqkvndkdqvgenvkdphqinenkiHLHNIMLSSQKKNETNKKETNGKISKNNinsssilsyikdknkg t
LF_Rev1 -----HSMNKRSIISKSKEGKEVSDPKEKMNRvet-----
PHC_Rev1 -----
PHT_Rev1 nskndtllslylndstqqkmennyiketntneelvHWEGKEKEKEKGKEEGKKEGKENEKER-----kkkll
HPC_Rev1 -----

Pf3D7_0910500 niltsqinwthSNNNNNNNNNTYSRKEIRKTVRKGTSTSIKRKIKNKINthiryDK-----NIRNNKLYH--yeYKQ
LF_Rev1 -----HEEETTSNNKQEEEEERQITS TNKGSKDKTFKNRMTEK-----KQSNT--knVKKRKNEVi---KCK
PHC_Rev1 -----
PHT_Rev1 nkkpknsnrkHNSSCNSNEGESKIKRKRKTGI IKNEETYEKKITDYIEgfvtlKSSSTynstNVRKKKNTNdicdNTK

HPC_Rev1 -----RASADKSINKSINKSINTSINKSINKSIN-----KSINT-----NTS

Pf3D7_0910500 NILNYFVHNNHNSNRTQNLIHKKENNFQNNQNVSLCSskTINKGFKRKCNIILRSNANfLNIRKKIKITKNYKISDFFPS
LF_Rev1 NILSYFVKN-PDIKNNNSILQISNKLIRKNNHNSVLQG---YIRISSKQNMPLKKKSS-----SRIHVYRNYRIYDFFPL
PHC_Rev1 -----
PHT_Rev1 DILSYFIKNINEVQTKNQLINRRTTKI IKGTKKTQNRNncfHPLLSTQNIKFIRSRSMhIEKYNQRKETVELEHINMFDS
HPC_Rev1 NIKKVYKKREKKQSTNSNKL SVNKKMYVNN-----LKKIAKINVTQNYKILHFFPN

Pf3D7_0910500 ILKKKIY---IRNNKNIYDDEIKTYGNGNI IMHTNIFDSI INKKIKKENdeendeene-eneqnekneknelcdknyHMK
LF_Rev1 FCKNKINretTNNESRSMDDDEDNDSSCTSDHKKNIFDSISNVKIKKEQ-----RIK
PHC_Rev1 -----
PHT_Rev1 IINMKVN---VKTELDAYIEAEVSKEKEKGGKGGTEKEIEVKVQVKTEAgsgteaeteteieaaetei keeaeteiEKN
HPC_Rev1 ILIKRQT-----NDPKNGTKNGTKNGTKNNKVKTNMYDSIFNLKIKNEK-----EML

Pf3D7_0910500 KQFTCCYFRYKEITQYL-----VHKEKLFEEENHK-----CNDLCRNDIFCFTYICNNLFLFNHTND-KLN
LF_Rev1 EEPTCCYLSYQRHHHI-----QVLITLE---K-----WEDDDTKNLFYCNSLNCNELLLMNQHNVNQMH
PHC_Rev1 --MTCCYKFCIKIYSDV-----KEKQNAHTHNVN-----YFVECAHHSICYICICNRLYVISQKNEEKFH
PHT_Rev1 QKMTCCYKFCITIYSDV-----KEKQNAHTQNVN-----YFMECAHHSICYICICNRLYTINQKNEEHFH
HPC_Rev1 EEVNNCYLCYQQICNSAtgtgtgcccndigivsKIDSNATTEKISdstsvCKQNNNSGLFCYACICKDLHQFNKKND-ILS

Pf3D7_0910500 LYLYIKKIINSYRSYFHNTFEEHDCVCNNTlkkdqeNIYYLNKFMVKVIDDICEMLHKKRYIDVLQNF LKNFKYVWSLNN
LF_Rev1 LYLHIKRMILSYISYFNHLYEKHDCENTNK-----DTKFVYKFVLDHINNISNTLHNYKQIDMLFTFLIHFKRVWEIYK
PHC_Rev1 FYLYVKKIFNSYISHFINILKNHKCDTND-----DNEYLYKFLLYILNDLCEILHKKRFIDVLQKLLINFKCFWKLQK
PHT_Rev1 FYLYVKKIFNCYISHFMNILESHKCDTNDissddvnKDKYLYKFLLYILNDLCEILHKKRFIDVLQKLLINFKCFWKLQK
HPC_Rev1 LYIYIKKIYAYINYFNIFCDNKCNNNCD-----SQYYLQKFICYILDNICNELHDKRLIDILHIFLTNFKHVWCLDK

Pf3D7_0910500 -ELFPEIFQRIILIKYninhmtt
LF_Rev1 -FPYSQILQKILIK-----
PHC_Rev1 kDLFSNLLQNILNKY-----
PHT_Rev1 kDLFSNLLQNILNKY-----
HPC_Rev1 -KPFPSIFQTIIFIKYnv-----

DNA Polymerase ζ Alignment

Pf3D7_1037000 MNLAEKPKAFFICKFLFFYYIYKKPILPFDSLKCKISGKEIPYVCI IQILGLSLLGQRVCLYIHDFYPPFFYLLIPPEEKQ
LF_PolZ -----YGQQVCLYVHQFFPPFFYVLIPEEKE
PHC_PolZ MNSLEKANVFFICKFLFFDYLMTKPKYPLDPSKCTISNRELPFVSVIRILGVTPYGQTVCLYVHDFPPFFYVLIPEEEN
PHT_PolZ -----EKY-----
HPC_PolZ MNIIDNPEAFFVCKFLFFYYIYKKPTLPFDSWVCKISNKKIPYVCVIQILGLTLYGQSVCMYIHGFYPPFFYVLIPEEKG

Pf3D7_1037000 NDKLEIELCSFLEEEY GKARKDPSNNV-CVYNI ERVKRKG IYGYNEECDD FLKISFLYPNTINYFASLLKKKLFKKRIWD
LF_PolZ NYDLEKELCFFLDNEYHKL GTDKNKNV-CVYNI KRVKRKC IYGYTEDYED FLKISLLNPDVVKYVASLLKKKLFKERSWD
PHC_PolZ NPHLERELCDFLETQSKNNKKQEGRVS-CIYKI ERVKKKC IYGYTEKLDT FLKVYVLPDVIKYLATLLKRKLFKSKSWN
PHT_PolZ -----EKHEEVVS-CVYKI ERVKKRC IYGYTEKWDT FLKVYVLPNPNWIKYFATLLKRKLFKNKSWN
HPC_PolZ NKNLEIEICKFLEDEY GKLKKN TNENS vCIYNI ERVKRRC IYGYKECHDD FLKIYCLYPDTIYYLASYL SKPLFKNRI--

Pf3D7_1037000 LYE VHI NYMLHFLC MKNIYGCSEIYIDKNIYFRKEFVNEINFECIEKEERWYLgEKKYNLD -NFKRNKYLEVDAPLV
LF_PolZ LYE VHT NYMLQFLC SKEICGCSDFIGRGIQFRPDLPKDITFHQFSKVEKWDL-TLKNDFE KKI KGSKYIEKDAPKY
PHC_PolZ LYE VHIT YMLHFLC SKNIYGGAEIYIDHNIYFRKEFPEDTLFDNFIKHEKWKV-QKRWEFD EHIQRSKYVDKEAPLF
PHT_PolZ LYE VHIT YMLHFLC SKNIYGGAEIYIDHNIYFRKEFPEDSLFDNFIKHEKWKV-QKRWEFD EHIQRSKYVDKRAPLF
HPC_PolZ LYE VHIN YV L HFLC SKHIYGC SKIYVNKNIYFRKDFVSSINFENFIKEDKWDV-KKKKTNT [5] ESVKKNYISADAPYV

Pf3D7_1037000 FTIKTINVNFSSLKRETTYDIECDIKHQHILNEKIYTYE FEKNKIKWKKEFNFDLPINHLDSFAKMWMKEKKRCKYMDMD
LF_PolZ WTYETRDVVSFTLQKETKYDIECDILHNEIMNEAICIHKFEKNKKKWKKEELGQEMPLQYIETFVDIWIKEKKRCKQKYPH
PHC_PolZ FTKKTKNVNFSSKWERETTYDIECDIKHQSI LNEQVYSYEF EKNKKEWKREMGFDLPVGYLDAFANLWIKEKDRCKNLNCK
PHT_PolZ FTKKTKNINFSKWERETTYDIECDIKHQSI LNEQVYSYEF EKNKKEWKREMGFDLPVNYLDAFANLWIKEKERCKEVNYK
HPC_PolZ FTQETRNVI FSNLKKETS YDIECDILHDN I LNQQIYTIKFNKYKKKWKKEELNFDLPINYIDSFAKMWMKEKKRCKNVNPE

Pf3D7_1037000 LKRELFYFKSYENDLCFDTFDVLTERTKKMFQGFLEFMKRM----QSEKDKVNYEQILEYDNIENVKKYNKVINDDMKLLK
LF_PolZ LAKELFHFD-----
PHC_PolZ QLKEIFHF DKYETEVDNFNTFDILTARTRMLDDFAKFLENR-rnEKREKGN SMEPQHEAKHEAKHEAKQGAENETKSEK
PHT_PolZ QLKEIFYFDKYETEVDNFNTFDVLTERTRMLDDFVNFLKERqrnENRQK----ESLKETKQKEKQEEENVTENKTETET
HPC_PolZ LMKTI FNFDFEKKLDFNSFDILTGRTKWLYNQLVTFIKSR---EQKNEPNIGNEKKNLSSNGKVDEKDIKTGDMLKKG

Pf3D7_1037000 EDHNFNSDMNIEVNIKQINNNDNINNCKNV-VDNEEENDMLS NMI SNKKKDHMGISP NLF---IQNKEQEKEKQDEREK
LF_PolZ -----
PHC_PolZ ENKTNNETE H KPGNETKTET-----KS IKKDETSPLSHANVI INDI ILLAGPMES---KQINNKEFQKDYQMEKEK
PHT_PolZ VNKTNNKTENKTENEIETETENKTNEIKQIETDNKSSLSDTDVIID-----YNPTDSIKKQIKNKKYHNDYKVEKEK
HPC_PolZ E IYDKKCSHSEINNNIKKSQNI EKEHN VGLNNTNNKLANTNNE LANTNKEI VVMTDYKKIR-NKVNNKVKGMASFEINK

Pf3D7_1037000 EKQDEREKEKQDEREKEKQDEREKEKQEEEREKEKQEEEREKEKQEEEREKEKQEEERECFIEYVNEKGCIASFEINKKRKDVV
LF_PolZ -----
PHC_PolZ IEKDYLKKAHTDVVENHVNSINEKKNSVEAPCHINTKGKITGTDVKTLTNINRKANEANNCYTTKVLQSEKEGEANL
PHT_PolZ NEKYSLSKKEHKNVVAIYSNDSENDRKENSVEVTTCHINTNGKITGTNVSTLTNINRRINEENNYCRSRLQSEKEGKSYL
HPC_PolZ KKKYVI-RYVYKKKMPIIKKGYAVSRFWRGAHNIVGSNDDAGINEDNVNGNVN-NSWNNVNSGNDNV---NNSGNDV

Pf3D7_1037000 RYS [6]RINKCYAVINNLVDHISGRDNKN- MKEKMKG---NIYNRIHDNIED ENKEDTSKFEYIgkeNHMENK
LF_PolZ --- -----YSK-----
PHC_PolZ KNS KNIRYTTVISKSITNEKRNNNRFI [4]LHNKLGivrYIYKKKPPRILN [9]RDKTKEKEAEAEadiDKQEKE
PHT_PolZ KNN KQIHNSIVINKSITDEKKNNRFI [4]LHNKLGivrYIYKKKPPRVLN [10]KNKTKEQKPERD---DKQEKK
HPC_PolZ NNS [1]-NDNINNSGNDNINNSGNDNRMV -HNQTKC----- -NKLEENKVR-----NKKENK

Pf3D7_1037000 ENIRKQYEQIKSDNMKKKINIKYGNIFFLEILTEIKDENCYSSDYNQDKIKAVFYIVREERLMNLYEDYNNCMGIIATKP
LF_PolZ -----
PHC_PolZ KCTTQKVEKTMEKILPRKINIKYGNLFFIDILTEIEGEEWYYPDALQDEIKAVFYVIEDERIKSYENYDVIIGIASKP
PHT_PolZ KYSTEEVEKTMKKIVPRKINIKYGNLLFIEILTEIEGEEWYYPDALQDEIKALFYIIEDERIKSYDNYDVIIGIASKP
HPC_PolZ K-----SIKYGNIFFCEILTAIKNENCYSSNYEDETKAIFYLIKDERILNSYEEYTNVCGIATKP

Pf3D7_1037000 FP [75]KNVINKKNDTYGSS [20]NNDIKKVK-RTFFDFNINYNVNICIVENERELIQKLINKILFYSPLSIVSYEND
LF_PolZ -- -----VNVCIVEDEIELIQKLVEKINFFCPLSISFENH
PHC_PolZ FN RNIMNGLKWSQLGTK GKDVKEKsACSSSFLPDVDTVNICIVENEKELIMKFIELIRLFCPLSISYEND
PHT_PolZ FN RNVLNVLKRSQLGTK GKDVKGKsRNSSSFLPDVDRVNICIVENEKELIMKFIELVRLFCPVSISYEND
HPC_PolZ FP [6]-----KELYKELINKINFYCPLSISYEND

Pf3D7_1037000 KYNINYNQRCLALDIGNFYKMIC---KLNDQKFLDLHNAYSRNIGKIIIESLYKLSNTYNTSFENLCKHYLNINIPSI
PF_PolZ KYGINYNERCILLDLGNFYKLIS---KVKDQCNFLQYNNNSYNKSIKGRVI---CRLADVSNSSFENICLEYLRVTIPSI
PHC_PolZ KFSLNYINKRCTILKIGNLYKLMS---SVNNQPVFTDMNNSYNKRIKGRVIESVYRLSDESNTSFENLCKVYLNVTIPSI
PHT_PolZ KFNLNYINKRCATLKIIGNLYKLMS---NVNNQTAFTDINNSYNKRIKGRVIESVYRMSDESNTSFENLCKVYLNVTIPSI
HPC_PolZ KYNISYNKRCFLNIGSFYMHIS tnnKLNDQYNFINLKNTHKTNIGKIIIESLYKLTNISNTSFENLCKHYLHINIPTI

Pf3D7_1037000 NKYTLYYWYNYNTRKRIKANGSSTVVNKD [7]NDMDEEHIYFPYRHITIKHYLRKVYFILLIYDKICFLKRMNFCKYIH
LF_PolZ SKYTLYYWYSYENKKKEDG-----LISRD SCSKESSTFFPYRYLTMKHILMRLNLIQLVYEKINFLKRMMSFAKYLH
PHC_PolZ SKHMLLYWYIYSSG-YKDNRHGTCIDS DN SCKDNNCIYFPYRYIVIKHMLMRVIFTKQIYEKINFKKKIGFAKYTH
PHT_PolZ SKHLLYWYIYKDKMYKDRCPVDFIDNDN NCGNNSCMYFPYRDIVIKHMLMRIIFTKQIYEKINFKKKIGFAKYTH
HPC_PolZ SKYTLYSWYMYNEQ-----DN -----

Pf3D7_1037000 VDLLSLINRGSQYIESFLLKMSIKYNYVLYSPSNKEIFDQRPILHTPLIILQPKSSINFFPLLVFDFQSLYPSILIAFNI

LF_PolZ VDFLSLINRGSQYIIIESFLLKLAMRNDYLLFSPSNKEIFHQRPIMYTPILIQPLSSINFFPLLVFDFQSLYASIAIAFNI
PHC_PolZ VDILSLITRGSQFIIESFLLKISLKRNFLLYSPSIQEISNQRPI LHTPVLVLPQSSSQFFPLLVFDFQSLYASILIAFNI
PHT_PolZ VDILSLITRGSQFIIESFLLKISLKRNFLLYSPSIQEISNQRPI LHTPVLVLPQSSSQFFPLLVFDFQSLYASILIAFNI
HPC_PolZ -----

Pf3D7_1037000 CYSTCLGTITLKR[13]KDENIEGSLMEKCETYKNGINDKNhiyDKNELSCSNKNDLPSDEYTDMMNISEDAKYLIDLLD
LF_PolZ CYTTCIGTLTKKR KTQVEKIHQEEEEKEEHTNINISN---DSKNMNPINMNNTTNTALQLNFEEKKNIEYEFNDLN
PHC_PolZ CYTTCIGTLCRKS[13]SSKNERIPLRESVEKTDKPLQTNQ---DKFQTNKSKTKWRVFDLEIYQIYENKQSSVRYVSSS
PHT_PolZ CYTTCIGTLCRK- --KNERIPLRESVEQTDKTIQTDH---DKFQTNKSKTKWRVFDLETFQMYENKQSSIHYVSTS
HPC_PolZ -----

Pf3D7_1037000 ENIND[21]GENIPSENMITED[4]KYKLDMMNKLEMGN[14]NIN[7]EEKSLESNFEFIKLGVMKNVPSISSRIKNLK
LF_PolZ EKHNE DEEEEEEEEEQEN[4]IHANHLNDDSQSKN NGE ETSEEEIYDFLKLGVKKKDPRI MRVVKQLN
PHC_PolZ EKKKE GEDIRREEYSGNE IFENEKNDKKKI-- ---SDEEIPFEFIKLGVKGKDETVMEKVKDFR
PHT_PolZ EKKKE GENTRREDYRNGG IFENEKNDKEMVL NEE[7]TKSDKNIPFEFIKLGVKEKDETVMEKVKYFQ
HPC_PolZ -----FEFIRLGVKKSAPDMRNTLKNIK

Pf3D7_1037000 SEDIITSNNTIYVKKHKRKGICPLFLEDILKTRIMLKRCMGMYEER-VNKKLNERMGKLLKILNVATGYIGANFSGRMP
LF_PolZ RNDLIITSNNTIYVTREKRKGLFSIFLEDILKSRIMLKRCIEKYNEPRIKKKLEKRVHLFKLVLNVAIGYIGASFSGRMP
PHC_PolZ KDDMVITSNNTIYVSRKIRKKGICAVFLEDILKTRIMLKRCMNIHSDKYIKKKLSDRTFIFKLIILNVAVGYIGASFSGRMP
PHT_PolZ KEDIITSNNTIYVSRKIRKKGICSVFLEDILKTRIMLKRCVNIHSDKYIKKKLSDRTFIFKLIILNVAVGYIGANFSGRMP
HPC_PolZ SDDFIISNNTIYVKKKHKRKGICVCFLEDILKTRIMLKNKIVICNGR--ETQLKEKIQLKMLLNTAAGYIGASFSGRMP

Pf3D7_1037000 CVDISESIIISIGNRFLFLIEYIKENYKFKVILYGD TDSLFLLNETtDDIQSSFKLAYEILNSINNILPLPMYLNFEKIY
LF_PolZ CLDISESVISLAKNSLMFIIQYIKNNYANTQILYGD TDSLFLLSKC-DDMLYSFCLAHHTTHINNI VPTPMCLIFEKIY
PHC_PolZ CVDISESVISIGNSLAFIIEYIKRKYINVDVLYGD TDSLFLLNKT-DNLHYSFQLAYNIINTINSILPPPMFLNFEKIY
PHT_PolZ CVDISESVISIGNSLAFIIEYIKRKYTNVDVLYGD TDSLFLLNKT-DNLHYSFQLAYNIINTINSILPPPMFLNFEKIY
HPC_PolZ CVDISESICTGKNFLFLIEYIRINYKYIKILYGD TDSLFLLNKI-DDLKYSFNIAYDILNKINNILPKPMFLNFEKIY

Pf3D7_1037000 CPSLLLLTKKRYFGFSFKNENQDNPI DLKGVESIRSDQCILVKNILIQIYFIFLYFKNNCYFSYCCCCYLCKNFFSNLI
LF_PolZ SPSFLLTKKRYFGFAYKNEKIKKPILEIKGVESIRSDQCELVKKILKQVYFIFYYFKNHSYISRCCCCYLCSRFFNFI
PHC_PolZ TPSLLLLTKKRYFGFCYKNEFQKKPVLEIKGIESMRSDQCDLVKKILIQIYFVFFYFKNSYISSCCCCSLCSNFFSNLF
PHT_PolZ TPSLLLLTKKRYFGFCYKNEFQKKPVLEIKGIESMRSDQCDLVKKILIQIYFVFFYFKNSYISSCCCCFLCSNFFSNLF
HPC_PolZ CPSVLLTKKRYFGFAYKTENVKKGQIEIKGLESIRSDQCELVKNILKQIYFIFYYFKNTCYFSYCCSCCYMCVNFNTFV

Pf3D7_1037000 CSC--KELNVHKTDCFLFTLLKIVLSicKVRRYINQNE DKYInNNNNNN[31]DKVKLYKEVMNWVEYDNE NLLLK
LF_PolZ CNC--EKTGIHQKDHCFELSELLSTI-----LEIPLNDKLDKTElpKEGNTEK ERRYYYDELLHLLNF-DTHNRLQ

PHC_PolZ CSCtcKESKTPPNRPCFLSKLVKVVYP--ELQEFENNSLQKTT--KENWTKE TTKQFFDKCLQLLTKKEGNNIILK
PHT_PolZ CSCtcKKSKTFPNRPCLLSKLLKVLFP--ELBEFTNNKLQKMT--KTNETNE TTKQFFEKCLQLLTKKEGNNDILK
HPC_PolZ LYC--NVSYIHRKEPCDKLKLYKDI IK-----LIKMD-----K -----NNTVLK

Pf3D7_1037000 TLNFLYREKYSFLIYLFNLFDEATLHKEIEKIIQTNFEKIQNQKNN-KCCFINPSNVFKSCLCVKNI--NENIKCDQIRCY
LF_PolZ MLHYLYNEKYSYLMYTYTYHGPGILKEKVKKIIKDFDKLCSFAHN-NCLVDPNNHFNICLCVKEE--NRNLKCSKNTCY
PHC_PolZ TLNFLYKEKYNHLFYIFTHFDSVTFKREVGNLIKHKDEIVLDRYDyDCCFNSEGNVFNLCFCINEK-DRKYKCDNTKCY
PHT_PolZ ILNFLYKEKYNHLFYIFSHFDNITFKREVQNLIIKHKDEVIMDRQDyDCCFNLEGNVFNLCFCINEN-DKKYKCDNTRCY
HPC_PolZ TLNLYLYRNKHYYLLYILSNCNELVLKKKIQFIETDYEKIKEEQNE--CCLTNPNNILKICLCVKHTgDGNERCDSNNCY

Pf3D7_1037000 CNVKQAMFFFYNP-TYNkvdYVFNTKLFYSHLLSHIRQTLSEYFNKIYDNQISCDNFIIYRKVKLGTYKGEMQGIRRKVS
LF_PolZ CNIKQSMVfy-HA-EMN---YVFHTRPFYEHLSQVQVLLSIFIDVYENKIPLDNFIIYKQVKLGTYKGE LPNQKRKVP
PHC_PolZ CNFRQNYFFYVEN-NES---YVFESKLFYKQLSMKIENVLHFI FNKIYKNEISIDNFLIFKKVKLGTYVGELENLKRKVP
PHT_PolZ CNFRQNYFFYVEN-NKG---YVFESKLFYKHLSMKIENVLHFI FNKIYKNEISLDNFLIFKKVKLGTYVGELENLKRKVP
HPC_PolZ CNVKQATFLHYSGgNNNttYFIFNKKFFYSYLSLTIENVLSTYFNKIYNNTI PYNEFIYKVKRLGTYKSELKNNKRKTP

Pf3D7_1037000 LPPQAI VARKIMRDFPNSIITYKEKVPYIFTKKLKDDKIYSSVSHPHFIRGIYRSFRFDGCGSTEQLE--ISEDNCNNDSE
LF_PolZ LPHQAI AAKRMYQLFENCLILYKDKIPYVVSTKLKKEKIYESVSHPFYIKGLYKSCCKYFENYSALEksTEEDEDEDESE
PHC_PolZ LPPQAI VAKKLQHFKNMTMISYKERIPFVVVKKLKEEKMYTAVCSPFFLKGMFKSC-----
PHT_PolZ LPPQAI VAKKMQHFKNMTMISYKERIPFVVVKKLKEEKMYTAVCSPFFLKGMFKSCSNVFKNYHQIFqhLLEIKNNNQIQ
HPC_PolZ LPLQAI VAKKLLKTYSNVIISHKEKIPFIITQKLKGDLYDSVSHPFYIKGIHKTKKEELKN-----

Pf3D7_1037000 KNGDiEKNDNIEKND -NIEKIGDIEKIGDIKKIGDIEKNENIEKNENIEKNDN [125] KFNWNK-AKLEMFSKYYKN
LF_PolZ KEKEfnKKNRKKNK [6] LNYEYYIENLVLPLKRMLDLLPFSTLNLEKIAHMARR KYNS----NYYQMSFFRNL
PHC_PolZ -----
PHT_PolZ IQNQ-NQEKKEKKNE [6] INYEYYISNATIPPLKRMLDLLPFYPLDLEKIFYNTRR GGNDLktQSIEETSNIINK
HPC_PolZ ----- INFNYYIENLI IQPVKRMLDLLPMCSINLEKIFFKTKK QYNLNK-GKIDIFSAYYGS

Pf3D7_1037000 MDNKLK--NNNVTNKGINLMNILNEDKINNK [49] KIMNSYVEINKSQNMLKLNKICLMCANSEMEALACNYSVHCKI
LF_PolZ QNEHSLNkeSNKEIRQEKYVTELLEEEENQQT CIIKSYIKINELQNKMKVNRKCLECTNSEVKALACQYSIHCP
PHC_PolZ -----
PHT_PolZ RKKIYINmeGNNEYEKRKEK----EKEKERDK EIINSYILLSKYQNEMKLNHICFSCAHSEIKALGCSYAIHCPV
HPC_PolZ NTKKLLN--NNAKYNKKIKIKITNNSKIENK KIINNYIELNKSQNMLKRLNKLACANTEMEAMACNYALHCKI

Pf3D7_1037000 FFKRINLQENILKNKDSINrls
LF_PolZ YLKKLQLEEQILIQQEIVE---
PHC_PolZ -----

PHT_Po1Z
HPC_Po1Z

YLKKNLEEKISKCKEITSr--
YFEKNLLVENISKQKV-----

SNF2 Helicase Alignment

Pf3D7_0604600 [438] FLYNKKFINFIE-SIKNRKG-IyKKVLNKYLSAYLKNDDFFNEINYLPLTWKPRKDYIKAGIFPFNLSKNNRKIES
LF_SNF2 -----FFNEMNYLPLTWKPRKDYINSGVFPFYLLKTKKIES
PHC_SNF2 FLYNWKFFQQFIEyQIKVRKDeKiKKRTRILSKCMDNDDFFKKINYLPI TWKPRKDNIESAIFPFYLSKKVKKKKT
PHT_SNF2 -----
HPC_SNF2 [332] FLYNEKIVHMLE-MEWSKKY-L-KCLMNKYLSTYLKNDDFFQEMNYFPLTWKPRKDYIKSGIFPFYFAKNVKKINS

Pf3D7_0604600 FGRLSVNNNNYLCGCVFPLCTYQLIVRYFYIKLFHTCFIYQIPNFIFYFFRYYYRinNNINKHKMYNYFLKNKYINIFIN
LF_SNF2 FRKLSYNNNNYLSGSVFLSSYPLIIRYFVSKFSHSFFIYQIPQTVLHFFSYFYP--TYNNKYRLHRYFLRDQYSSLLEK
PHC_SNF2 FRKWSIYNNEYLSGCVFNLCSYRLIFRYFISKFMDIYFIYEIPQTIIFYFRHFYK--KKYRKLNCYQYFLKDQYTNVLKD
PHT_SNF2 -----
HPC_SNF2 FKRLYVNNNNYLAGCVFNLCTYHLILHYFIYKNFETCFLY-----NLN-----

Pf3D7_0604600 IYhSKYQILDTIKEE [15] QKE [7] IKNLVLFQDLSNNTYIFSKQKIEKKI INHYHKKIQKIKRQMNQEIKNICLNEI
LF_SNF2 EL-TNWEREEIQIQER [16] EKE ILDQYHYEELCMNTYIFEKTELKKEI INHYFMKKECKIRKRSHKKIKEMCLDQI
PHC_SNF2 IM-AYKSPIITLKEK ELE VLKSYDFDELCSNSTFFLDKEQIRMEI IENYMKQKNKIQKKIQKELKMKCLKQI
PHT_SNF2 -----
HPC_SNF2 -----ELCNNNYIVSRKKLTKEIYKNYFEKEKHKLTCKFHKQMKELCLNEI

Pf3D7_0604600 KKKLPIRIQKVIILTYQLQAIYFFFKKRGRILIADEMGLGKTLQAISIFYFYHLYPVLIITPASLKINWFSEIEKYLPAFD
LF_SNF2 KRKLPRRIRNVILPYQLETIYFFKKKGGRILVGDDEMGLGKTLQASISIFSFFKLYPVLIIVCPASLKTNWLCEIKKFVPFLD
PHC_SNF2 KKQLPLAIQKIIILPYQLETIYFFKKRGRILLGDDEMGLGKTLQAISVFSFFQLFPVLIICPASLKINWLEIEKFVESLD
PHT_SNF2 -----
HPC_SNF2 KNKLPCKIKNVILPYQIETIYFFLKKGRILIGDEMGLGKTLQASISIFSFYHLYPTLIVVPTSLKIHWLSEIEKYLPQFC

Pf3D7_0604600 PQNVLIINSSNDMPKCASSYKIIIVSFNIYKKLYNLLKEIQFHLLIVDESHFIRTVHYGNQSQLTRLLKKKIRKTKHVLV
LF_SNF2 PSKILRISSNDVPNDLKKYKIIILSFHMFRRHTFHFIRFIQFQLLVDESHHIRSVHSGKESQLTNMMGLLTKQIKRVVF
PHC_SNF2 LSFILLVNSSNDLPKLHAHYKVIITSYEMFKRLYDVLKERTFRLIVDESHYIRTVYCGKESKFTETIKELAKRIKNVLF
PHT_SNF2 -----MFKRLYDILKERTFRLIVDESHHIRTVYCGKESKFTETIKELTKKIKNVLF
HPC_SNF2 ITQILVIHSSNDPCPRLDARYKIIIVSFDIYKRLYNVLKQIEFKLVIVDETHHIRTVYQYKQSQLSKKLKNKIINSKYVIL

Pf3D7_0604600 LSGTPSINRPINIFHQIKYLINNNKNIIFPKNKIIFGEDYCKKYFYRGEKIYEENLRSWEFHYFLNKIVMIRRTINQVFQN-
LF_SNF2 LSGTPSVNRPINLFHQIYLLIQNDSIFCNTKFI FGEEFCKRSMRGERKYEENLRAWESLFLKKTVLIRRHISVLDL
PHC_SNF2 LSGTPSVNRPINIFHQLKILINNNKNIIFPKNKYIFGEEFCKKICRRGEKIYEQNLRSEFFMFLKKTVLIRRLQQIFKE-
PHT_SNF2 LSGTPSVNRPINIFHQLKFLNNKNIIFPKNKYIFGEEFCKKICRRGEKIYEQNLRSEFFMFLKKTVLIRRLQQMFKK-
HPC_SNF2 LSGTASVNRPINIFHQIKYLINNNKLFKKNKYVFGEECCKKYIHRGEKIYEENLRSWEFSLFLKIVMIRRNKIIFKN-

Pf3D7_0604600 NFP^{SLKR}RFVYLKNDICDN [11]HEN SFINNSE [10]KCGYK^{MD}EMYKMNNLDKNNN [11]DDQNEYKH [12]SKKP
 LF_SNF2 QFLQLK^{RR}FFVFLPQEVKNE --- -----
 PHC_SNF2 NFPNLR^{RR}FFVPLSDP^SMDT --- -----
 PHT_SNF2 NFPNLR^{RR}FFIPLSDP^FMDK [11]TDE [6]ETLHTNL [10]NNNHLNNH^LLN^NHLENNHL [10]TEIGTEIG [5]CKCI
 HPC_SNF2 NFINLKRYFI^FFLPKD⁻⁻⁻ HDK SSIHSSR KILDKNESIEKNDNTDKHNT DKYNTDKY [1]TDKY

Pf3D7_0604600 EQSKLNNSIIYKQERKHK^NREILN^QYFHIDIK SKKEE EGVSKIV -NALQFIEKNFPNKKKIIFCY-HIM
 LF_SNF2 -----MKEKENEVETNRREKLNKIYQVKL- [1]SKKEE EGILKI- KEGIEWIESHFPNEKKILLCY-HLV
 PHC_SNF2 ----- [4]KKEMKQIKIENKNVKKIILCNeHDL
 PHT_SNF2 EEELLLKLIKKEQE^QEQE^QEQKQ^QVHSPCIN [4]DKKKE [49]EKVQKIK [90]KKEIKQIKIENKNVKKIILCNeHDL
 HPC_SNF2 NTDKHDNTDKHDNTDNTTNRQKLNDF^FHVNIK SKKEE EGLSKIV -NALEYMETYFPTKKKIIFCY-HLI

Pf3D7_0604600 VSK--CTEDEL^LLKI^IKQKK EKENISIDYVSLNGCIPEKEK-IEKILYFQNNINCYYGIFTICSVSHGLD^FSFCNL^CF
 LF_SNF2 ICK--CIEDEL^LLKRIAKKK EEDTSLLDYVINGKVSEKHK-VERINYFKTNQTCTYAICTIGSVSHGFDF^TFSNL^CF
 PHC_SNF2 FCDgdCRKVYFLK^KSSNSL [5]ERDQGICN--VCNLD^CSDLLKqIRRMKYFSMEEKINYFI-----KYNPL--
 PHT_SNF2 FCDgdCRKFYFLK^KSSNSL [5]ERDQGICN--ICNLD^CSDLLKqIKRMKYFSMEEKINYFI-----KYNPL--
 HPC_SNF2 VCK--CIEE-----SIDYVVLNGSLNEKEK-LEKINYFKNTSNCYYGILTICSVTHGLD^FSFCNL^CF

Pf3D7_0604600 FMEFPVNFFHLQQCESRLFRKNQKHNTYVFYF--LLQKGLGSDHKTWNRFILCSNSTRSII^DGTNFINKDLIYDNI [467]
 LF_SNF2 FFELPVNFFHLQQCESRI^FRRNQT^KDTYVFYF--LLRKGLGSDYNTWNRFLKCANATHSVVDGVNFDHSDL-----
 PHC_SNF2 FLE-----NINQLKKII---DSPKEGYIWQVdhIIPVYKGGGQASFENLQTLCTFCHQKKTCDLQNKKEIKTRK [3]
 PHT_SNF2 FLE-----NINQLKKII---NSPKEGHIWQ-----
 HPC_SNF2 FIEFPIDFFHLQQCEARLFRRNQLYDTFVFYF--LLKNGLGSD^EKTWKRFVLC^AHSTRSTVDGT^CYEGN^DLFYEKF [410]

RING Finger Ligase Alignment

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Pf3D7_0415800      [8]VQNNLNRRARHSLTNTLSDMRLDE-SYLKSIRMNIKKRFDKLMNKIIPFET---IDENKRFVVIIEKKKN-YENFRCP
LF_Ligase          -----ESLKQSLLSQYEEQSEDP-DFIYNFRKHVKRTFELWIDRVVPLNR-----LVDRRFIVLVENRKN-YDNVRCP
PHC_Ligase         IIEKTNEARNILVKQVNELKAED-ITLSVCRSYIQEKMKNFIDVCIPA----KIIKERRYIVIKDKHKKH-YETFQCA
PHT_Ligase         -----LVNQVNELKEED-ITLEVCRSYIQEKMKSFIDVCIPA----KVIKEKRYIVIKDKYKH-YEAFQCA
HPC_Ligase         [8]INNNMENIRNNVIKAFENLRQIDnIYVNVNRTEIQKKVNSLLYKCLPLSEdkKIINERRFIVIEKDKNkYDNFRCP

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Pf3D7_0415800      ICMLILFKPVKTCGHIFCRECIEKVLLKFDYCPLCRNFIK-DKKLENVENSTLGSEYENIKIRCYKCKEITNIKNYEKH
LF_Ligase          ICMLVFYKPVITNCGHTFCHECLKRSVDKYACCPMCREPIApDSSLSEINAEVLGSEYSSIKIRCSVCRDVMTIKDYDPH
PHC_Ligase         ICTFLFYKPVLTPCGHIFCGDCLKRSLKNFNKNCPMCRNDIT-EETIKDIPAEYLGEIYTQLVVRCPICRYKTTVGEYKGH
PHT_Ligase         ICTFLFYKPVLTPCGHIFCEDCLKRSLKTFRSCPMCRHEIR-EETVKKIPAEYLGEIYTQLVVRCPICRFKTTVGDYKRH
HPC_Ligase         ICMLILFQPVQTQCKHIYCKECIEATLKKYNHCPLCREVTS-NQTLTDLPISYFGREYTNIKIRCYKCKQITTIEKYEQH

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Pf3D7_0415800      IINHI [26] IQKKKKNSN [4] ISNNNYIHNIYHHINPYNFDSYFNKKFQIIYMKEFFNLLKEhNINTHIDNFYLLYAQQNV
LF_Ligase          LVNKC      YSNRMKYRE [4] SIDNDITNKTKTNAHLKLKLNVFGKQFDINQMKELKRLLKK-STFDHIRHFSLVYAKSM
PHC_Ligase         L-----
PHT_Ligase         L-----
HPC_Ligase         LKNHI [ 1] YYGNKNYKN      NYSNYNSYLERTVKNLKNIKTLFNKKIRINEMNTFLLYIENiSIITDIYSIQLVYGRKV

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Pf3D7_0415800      LYDFKH [607]
LF_Ligase          KEEHIV [389]
PHC_Ligase         -----
PHT_Ligase         -----
HPC_Ligase         FNEAIY

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Supplemental Figure 1: Amino acid sequence alignments for orthologues of the four components of the translesion polymerases described in the text.

Sequences for *P. falciparum* were obtained from the EuPathDB database while the additional orthologous sequences were obtained from the fragmented genome assembly of *Parahaemoproteus tartakovskyi* (Bensch *et al.*, 2016), the transcriptome datasets of *Parahaemoproteus coatneyi* and *L. fringillinarum* (Galen *et al.*, 2019) and sequence data of a *Hepaticystis* parasite that was mined from the transcriptome of a Ugandan red colobus monkey (Simons *et al.*, 2019) using the ContamFinder pipeline (Borner *et al.*,

2017). Alignments were generated using the Constraint-based Multiple Alignment Tool (COBALT; Papadopoulos and Agarwala, 2007) available through the National Library of Medicine, National Center for Biotechnology Information website.

Alignments are displayed in the “compact” format to reduce space. Unaligned regions are displayed as [X] where X denotes the number of residues for a sequence in the unaligned range.

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