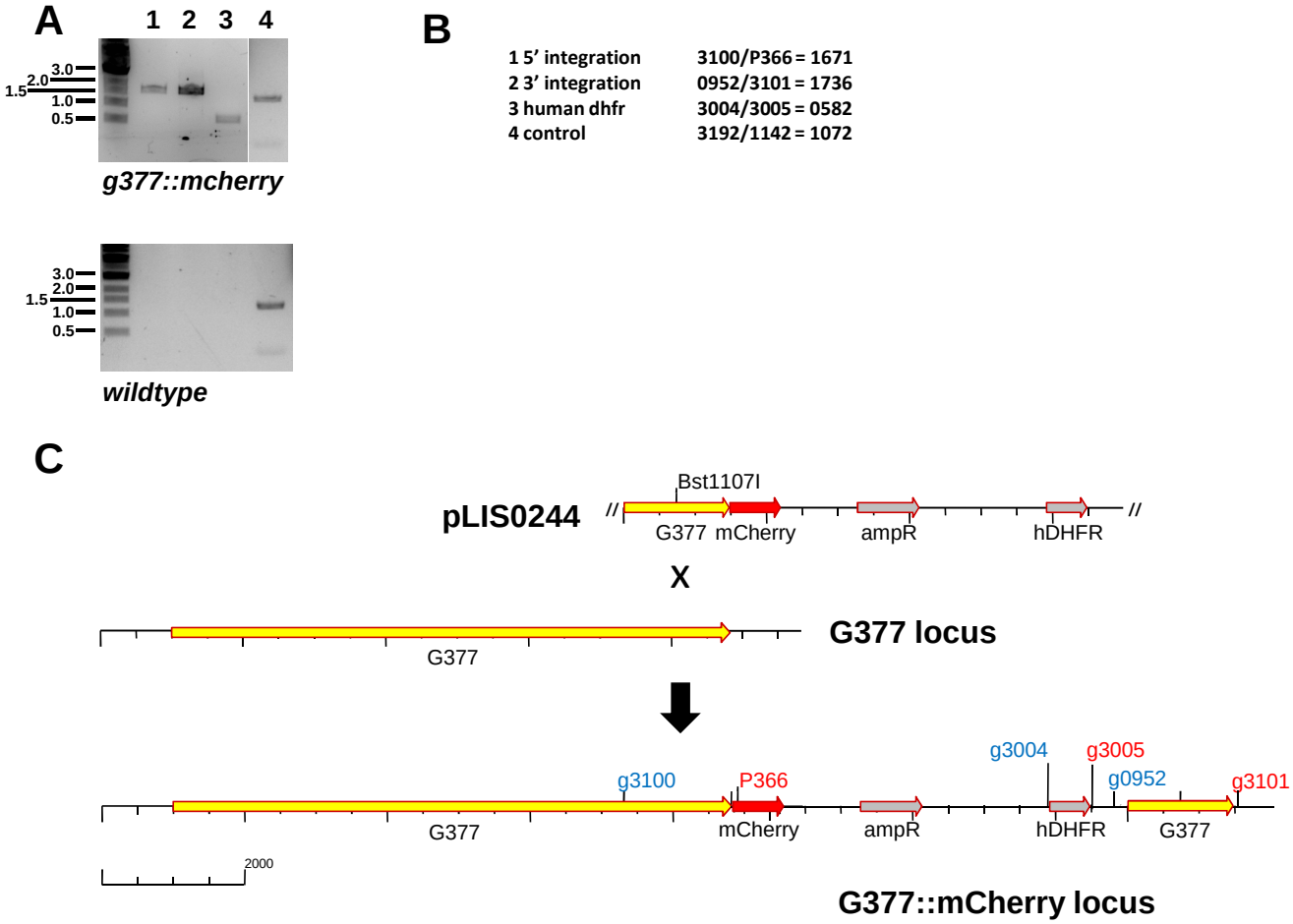

Figure S1. Genotyping of *g377::mcherry*. (A) Agarose gels of PCRs using wildtype and mutant parasite DNA. **(B)** Reactions as indicated on the top right. Primer/Primer = Size in base pairs. **(C)** Genomic loci and position of primers.

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PF3D7_1250100     1 MKLLLFFFISSIFLQLTSGKRILNFDNIIKHLKESKLLPEDIPHVLENDIIIVPPYLIYK
PKNH_1470100      1 MRFSLCATLLCLLCGLAKCRKGLNFDQIIKYLKETKVIPEHIPDTLEDAIQIVPPYIIYK
PVX_101400        1 MRISLCAALLGLLCGLANCRKGLNFDQIIKYLKETKVIAENIPDTLEDAIQIVPPYLIYK
PCHAS_1465300     1 MRILLYTLLLCICSGFTKGQKAHNFDNIIKYLKEIKIIPQYIPDQLEENIQIIPPYLAYK
PBANKA_1463000    1 MKILLYTFLFCICSGFAKCQKAYNFDNIIKYLKEIKVIPSYIPDKLEENIQLIPPYLVYK
PY17X_1465600     1 MKILLYTFLFCICSGFAKCQKAYNFDNIIKYLKEIKVIPSYIPDQLEDNIQLIPPYLAYK

PF3D7_1250100    61 YKGKIYHLHNNVDLTLINHPEEDSCDKEEIWESPFPPKVPEPERPHEPEMEPQVEPEPGP
PKNH_1470100     61 YKGKIYYLHNNVDITPVDERK------------------TDPVFPVHENELEAINP----
PVX_101400       61 YKGKVYYLHNNVDITPVEEKR------------------PDPVFPMPENELDAMSP----
PCHAS_1465300    61 YKNRIYYIHNNVDIYPVIDIK------------------PKPIFPIDPEDIA--------
PBANKA_1463000   61 YKNRIYYIHNNVDIYPVINKK------------------PKPVFPIDPDDTY--------
PY17X_1465600    61 YKNRIYYIHNNVDIYPVINKK------------------PKPVFPIDPDDTT--------

PF3D7_1250100   121 LPEEVREPEPEPE-AEPEKELEMEEQEEVIEADMVLDEETGIKIPKKTEQDVLEVSKFRE
PKNH_1470100     99 LECHPVVPGIDGAVSPVLPE-SVTSEEVADTIKMVLDEDTGIMVATNTNVIIEKEKHTVE
PVX_101400       99 LECHPMVPGSAAAGSGTPHQ-SASSGEAVDTIQMVMDEDTGIMVPTNTKEIIEKEKLTTE
PCHAS_1465300    95 -ECGHNNPKN-----PIDEELEEDDDDTVDTNTFVVDNETGMYVPNIQIDGIDGQTGISA
PBANKA_1463000   95 -ECTHNNIKN-----TVDDEVEE-DDDTVDINSFVPDNETGMFVPNI--NDIKEQAGTSD
PY17X_1465600    95 -ECTHNNVKN-----PVEDEVED-DDDTVDINSFVPDNETGMFVPNIKVNGIEEQTGISD

PF3D7_1250100   180 EYELPNVVELTPEEKEKNNIL-HFAGNKSTAFNLKEIINYKKDESLMNSLSSSFDHFYTP
PKNH_1470100    158 GFTIPQDAQWSSEDKEKNKNVYLFGGENSTVYKVKEIIQYKENKDMCKNIQIGYERFYSK
PVX_101400      158 VFSIPKDPQWSAEEKEKNANVYLFGKENSTVYKVTEIIKYIESKDMCKNIQMGYERFYSK
PCHAS_1465300   149 GFEIPKNNQVPTDQNGPNAIVNIFPGEGCTNFPIGEIVDIKENKEICKDIKTGFEIFYKD
PBANKA_1463000  146 EFEIPKNNQVLIDQNGSNAIVNIFETEGCTNYLIGELVEFRKNKEICENIKTEFEIFNKD
PY17X_1465600   148 GFEIPKNNQVPTEQNGPNAIVNIIGTEGCTNYSIGEIVEFKENKEICENIKTEFEIFNKD

PF3D7_1250100   239 NVE----------ERNLSNAYNVDINDYYDLLRALHILCKDED----NKLYTINRIPKDE
PKNH_1470100    218 PSSYGDDLGITSEEKSPKIVHNVDTKDYSSFLTALHILFRKDEEIGVEKIYKINNIPKTD
PVX_101400      218 APSYADELGGATDEKTPKVVHNVDMKDYSSFLTALHILFRKDEEIGGKKIYKINNVPKTD
PCHAS_1465300   209 NLY------EYDEQNEKAPSHNINISDFYTFLNAIHILFHEGE---YNKNYTINNIPVND
PBANKA_1463000  206 NIY------EYNEQDEKTPTHNIEISDFYTFLNAIHILFHEDE---YNKYYTINNVSVKD
PY17X_1465600   208 NIY------EP---TEKIPTHNIDISDFYTFLNAIHILFHEDE---YNKYYTINNISVKD

PF3D7_1250100   285 LLFFLKHAYVNIYNSLKKYILLNGYNFEDYIYTSENFTLDQIFKDYFFLSNDD-TNENGS
PKNH_1470100    278 LLLFIKQAYKNIHDTLKNYILVSGFSFYDYTYDVGSFSLDVFMNDFFFLSNNN-NKDRGT
PVX_101400      278 LQLFIKQAYKNIHDTLKNYIAVSGFSFYDYSYDVGSFSIDVFINDFFFLSSSN-NKDRGT
PCHAS_1465300   260 VKLFMKEVYINIHNSLKTYILFSGLNFSDYTYSPNEFSIDSLLNDFYHLTNDSNDNMSGS
PBANKA_1463000  257 IKLFIKEAYINIHNSLKTYILFSGLNFSDYTYSPKEFSIDALLNDFFHLTNDSNDNMNGS
PY17X_1465600   256 VKLFMKEVYINIHNSLKTYILFSGLNFSDYSYTPKEFSIDAILNDFYHLTNDSNDNMNGS

PF3D7_1250100   344 FNNIIESIKYIKKAIEKLNVKRIEEKIKYFFQIYEVHAFDFKLLHYIFSRNQLLNYSEDD
PKNH_1470100    337 FKNVTSSIKYASTAKDKLSVYKIEKAIKDFLAESNLRVLDLKLIHHLFSRNFILNCTEND
PVX_101400      337 FKNVTSSIKYASTAKDKLSVYKIEKAIKDFLAESNLRVLDLKLIHHLFSRNFILNCTEND
PCHAS_1465300   320 FENIERLLKYVATSKSKLTIKLVENAIKSFLDEHNLMVLDIKLIAHIFSTNRVLNYNEND
PBANKA_1463000  317 FENIERIIKYVATSKSRLTIKLVENAIINFLDEQNLMVLDIKLISHIFSTNRILNYNEND
PY17X_1465600   316 FENIERIIKYVATSKSRLRIKLIEKAIINFLEEENLMVLDIKLISHIFSSNRMLNYNESD

PF3D7_1250100   404 LIHHAVDIMNITRIDISPRVISALFMYFLNKVNIFLVPQYVTRNRNDFTLLLEHNDLLLR
PKNH_1470100    397 IVDFVTNLVNITGVDISPRIGATIFAYLLQKVNIYLMPSYPTKTRNSYLLFMENNDLLFF
PVX_101400      397 MIDFVTNLVNITGVDISPRIGATIFAYLLQKVNIFLMPSYPTKTRSGYLLFRENNDLLFI
PCHAS_1465300   380 IIKYAADLVNISEIDISPRIISTVFIYFAQKINIFPMPNYPTLFEYGNVLFLENNDLLET
PBANKA_1463000  377 IIKYAADLVNISEIDISPRIISTIFIYFAQKVNIFPMPNYPTSIDYDSLLFLENNDLLAN
PY17X_1465600   376 IIKYASDLVNISEIDISPRVVSTIFIYFAQKINIFPMPNYPTSFDYDSLLFLENNDLLET

PF3D7_1250100   464 TEIIYRDFLKHFFKHKTPHVHLKK-NNHDNAYQLVPWSQVLFSEFNSTYDFLNFKYMIIL
PKNH_1470100    457 VESIYRDIFKNFYRISNSHGDLPNAQNLDQVLALTPWVQKIYPNFGSTYDFLTMKYGLSL
PVX_101400      457 VESIYRDIFKNFYRIGSSHGDLPNAQNMDKVLATTPWVQKIYPHFASTYDFLSMKYGIAL
PCHAS_1465300   440 VDKIYNKFFKHFYRHGNNTNKGKSNMSHEEILDTIPWAEQIYSKFKSTYDLLAFKYGAIL
PBANKA_1463000  437 IENIYNNFFKHFYRHSNSTNKGKKGKSHEQILQTIPWAEQIYSKFKTTHDLLSFKYGVIL
PY17X_1465600   436 IDNIYNKFFKNFYRHSNSTNKGKKGKSHEQILQTIPWAEQIYSKFKTTYDLLSFKYGVVL

PF3D7_1250100   523 FHDSYHAFVDYFEGDDKLNQVLNDNKENKTIDNLDKFFNELLNLFLIENVGILSTLEEY-
PKNH_1470100    517 FYNTYHMIINFFQGDIKMKQILLEHKESKKVDTLDKFLNEVLALFPQGSSSSVWPSSLLS
PVX_101400      517 FYNIYHMAVNFFQGDTQMKQILLEHKDSKKVDTLDKFLNEVVALFPLGSGGSAWPASLLS
PCHAS_1465300   500 FYNSYVNIINYLSKNKNIKDIIEKNKGNHQIKTLDQFINELIKLLQIAPPESNTVKG---
PBANKA_1463000  497 FYNSYVNIMEYLSRNKSIKDIIEKHKENKQIGNLDQFINELIKLLQIAPPESNIVKETQD
PY17X_1465600   496 FYNSYVNIMDYLRRNKNIKDIIEKHKENKQIATLDQFINELIKLLQIAPPESNTVKEVQE

PF3D7_1250100   582 ----------FVSTVKQVGRVLSDDHDIDSKEYTENYFTPEEEEQALKDFKEDEASVHHL
PKNH_1470100    577 ---------MAQVEEKPRGRVLSEDKISGM-----------------------------
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PVX_101400      577 ---------MAQVEEKPRGRLLSGETGDDG------------------------------
PCHAS_1465300   557 TKESLPIFISLKDTNRHNSRVLSEDF----------------------------------
PBANKA_1463000  557 AKETLPIFISLKDANRHNRRVLSDDL----------------------------------
PY17X_1465600   556 KKETLPIFISLKDANKHNSRVLSEDI----------------------------------

PF3D7_1250100   632 DHYDNNMDPYYEYQGEFGSYEEEEDELRKFKEDEPEPWPLDESPHIEHGTLHDDELNPFQ
PKNH_1470100    598 --------------GE--------------------------------------------
PVX_101400      598 --------------GD--------------------------------------------
PCHAS_1465300   583 ------------------------------------------------------------
PBANKA_1463000  583 ------------------------------------------------------------
PY17X_1465600   582 ------------------------------------------------------------

PF3D7_1250100   692 EEKKDDESFYTSEDEDTLDHSHEKEDDVSHPEHEDHNEGYIPHTYDDDSFFTDEEDDEGD
PKNH_1470100    600 -------------------------------------E--------SN------EDDDEDD
PVX_101400      600 -------------------------------------YGGYYDSVYGG------DYDSDDD
PCHAS_1465300   583 ------------------------------------------------------DEDDI
PBANKA_1463000  583 ------------------------------------------------------YDSDI
PY17X_1465600   582 ------------------------------------------------------SDSDL

PF3D7_1250100   752 EV-NEENVPLNHEEENVPLNHEEDNFPLNHEEDNFPLNHEEENVPLNHEEENVPLNHEEE
PKNH_1470100    610 DVPDDEDD-----------------------EESKEAKEA-----------------QEE
PVX_101400      618 DVPDDEDD-----------------------EESKEAKEA-----------------QEE
PCHAS_1465300   588 DIH----------------------------ET--L--------------------EE-
PBANKA_1463000  588 DEI----------------------------DSHEM--------------------SE-
PY17X_1465600   587 DEI----------------------------DSYEL--------------------SE-

PF3D7_1250100   811 NVPLNHEEENYNSFLSYQKYDERDISPHNVNQHKKEIFHHRNITPYHVNHHNQHMDQHDH
PKNH_1470100    630 AT----ADENHA-------------------------------------------------
PVX_101400      638 NT----ADENHA-------------------------------------------------
PCHAS_1465300   596 ----------YN-------------------------------------------------
PBANKA_1463000  598 ----------DN-------------------------------------------------
PY17X_1465600   597 ----------DN-------------------------------------------------

PF3D7_1250100   871 HIDHHNHHIDHHNHHIDHHNHHIDHHNHHIDHQDHHIDHHNHHIDHHNHHIDHHDHHIDH
PKNH_1470100    638 ------------------------------------------------------------
PVX_101400      646 ------------------------------------------------------------
PCHAS_1465300   598 ------------------------------------------------------------
PBANKA_1463000  600 ------------------------------------------------------------
PY17X_1465600   599 ------------------------------------------------------------

PF3D7_1250100   931 HDHHIDHHNHHIDHKSNNQFLQKHQNYVRGHSSFITISEGEENHDNRELRKKIEANLKEE
PKNH_1470100    638 -------------------------------------DVYAREKNKYNELRQIVETELIKE
PVX_101400      646 -------------------------------------DVYAREKNKYNELRQIVEAELIKE
PCHAS_1465300   598 -------------------------------------DTSDQENKYFKELKITVENELIDE
PBANKA_1463000  600 -------------------------------------DTPDENNKYLKELKITVENELIEE
PY17X_1465600   599 -------------------------------------DVSDENNKYFKELKITVENELIEE

PF3D7_1250100   991 WKKRFNEQQEQRERKKKAEEDEMNETIQKHDMETSKLEKKEEVDEVTQDEEFDKQYAIDD
PKNH_1470100    662 RKEYAQKKHDEEERIKKEEQEKIAETDKKHELETQALEAEEAKTEPDDDAKFEKDYQASR
PVX_101400      670 RKAYAQQRNEEEARKKKEEEDNIAETDKKHELETQKLEAEEEKSEPDDDQKFEREYQAGL
PCHAS_1465300   622 RKKFVLAKNKAIKEEEERIQKEIDELDAKHELETQNLEKEEPQKEIIQDQEIDRQYEEGL
PBANKA_1463000  624 RKKYVLERNQEKQKKEQFIKKEIEEIDKKHELETQKLEKEEPQKEILQDEQIDREYENGL
PY17X_1465600   623 RKKYVLERNQEKQKNDEIIKKEIKEIDTKHELETQKLEKEEPEKEKLQDEQIDRDYENGL

PF3D7_1250100  1051 QEELEFLRTRDSEGSESDVPKDKVKPFPDGRSPDSFYYNTAISSFHEKMEELYNTSISSS
PKNH_1470100    722 EQERESARRRIEASIKDGT---YNAHAEITKPPDSFYYSTSLNALYDQMKKEYEKGVDSG
PVX_101400      730 AEEKEYERKRKEEDLRNGV---VRKPDRENETPESYYYTNSINILHDQMKRVYEKGVDSG
PCHAS_1465300   682 EEEKEIDRQRLIALG-KDV---VKSPATRDSRNDQSYYEIAFNSLTRDPNETYTRIVKAG
PBANKA_1463000  684 EDETIIERDRLIALG-KEN---IRSTVDKSKRYDKMYYELALKTLTDDPDEVYGRIVKAG
PY17X_1465600   683 EDERIIERDRLLALG-KEN---ANLPIERSKRYHKMYYEAALNALTIDTADIYDKIVKTG

PF3D7_1250100  1111 LNYVKEINRKFDDVYKELKSKTYPKFDDLTSQTKTNCNKLFQKLNETIKDKEY---QKNI
PKNH_1470100    779 FQVVAEIEAKLNQVYKTLARKGVPDYAELKDEVIEANQKLFEELSTKVKNEES--RKKNI
PVX_101400      787 FQVVAEIEAKLRQVYKSLKKKGVPDYEKLKEQVVKENEKLFEDLSAKVKNQES--KKKNI
PCHAS_1465300   738 YDFITKAEEQFEQTVYRLKQTTAPIYPELKFEVLRSINKSFTTLMKKITNKENITKSDNL
PBANKA_1463000  740 YGFASKSEQQFQQIVYTLNDTTAPKYDELKADVFRSLDKSFNTLLKKIKNQKNITKSDNL
PY17X_1465600   739 YGMSSKCGEQFQQIVYILKDTTAPKYNELKVEVIRAINKNFNILLKKIKSKKNINKSDNL

PF3D7_1250100  1168 QSYKNKVIDILDDIQKK-ANGKYII-IQNLIIEKIDIYKGDVVRLSDRKFYKNFRKVLGK
PKNH_1470100    837 LEYKSELDTCLEKIMAKNEDGQYNITA-GLIMQNFKKYQNDLMEQCEKGFYGKFRKSLGS
PVX_101400      845 LEYKADIDTQLDKVMAKGEDGMYTITA-GLIMQNFKKYQKDLMEECGKRFYGKFRISLGT
PCHAS_1465300   798 SSYKNDIISYLNEIAKKSPDGKYYMCIEDIMATQYKEYRDELMKLCDKKFYANFRKSLSK
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PBANKA_1463000  800 NSYKKDVESYLNTITKKNPDGKYYMCIEDLMVTKFNAYKKELMNLCDKKFYGNFRKSLSK
PY17X_1465600   799 NSYKKDVESYINTIAKKSPDGKYYICMEELMITKFNDYKKELMKLCDKKFYGNFRKSLSK

PF3D7_1250100  1226 RKMKMLEDFRAQFKGAIRFIKDLTTTYMEEEYTKVLEDIYMEKKKYYKEEYSKMRRIISS
PKNH_1470100    896 RKKIMLKKLREALKYSIRIMQDLAPSYDEAAYTKTFTDIYMTKKESYKKDYITARRVISK
PVX_101400      904 RKKTILNQFREALMYSIRVMQDLAPSYDEAEYTKTFTKIYKTKKDSYKVEYAKARRIISK
PCHAS_1465300   858 HYLKMMREFRITLKNAIKLAQDLAPSYDQKEYIPKFTSVYTERKNFYKNKYAEDRRKISK
PBANKA_1463000  860 HYLKMMREFRITLKNAIRLAQDLAASYDQNVYIPKFTNIYTEKKNLYKTKYAEDRRKISK
PY17X_1465600   859 QYLKMMREFRIILKNSIRLAQDLAPSYDQNEYIPKFTNIYTEQKNLHKTKYSEDRRKISK

PF3D7_1250100  1286 NLDYEVNKQIKEHYHKVDTISEHKFQEIRQHMRDKIENTIHELYKEMYVQIQIDLTNYYH
PKNH_1470100    956 NMDIAFRKHIKLHYEEIDVEIRKELQIIRQEALKKIDEIYAELFNIAHVEVQIDLESIKN
PVX_101400      964 NMDIAFRKHIKLHYEEKDAIIRNELQIIRQQVINKLDEIFPELYKDLHVEVLIDLESIKN
PCHAS_1465300   918 YLDGSYRNLLNKDHKLKQRAINKELQRIKLYTIDHINDASTKLYKVAYTELQIDKVYLFK
PBANKA_1463000  920 HLDKSYRNMLNKHYKKKQRTINKELQKIKKYVINHINGAIKVLYNTVYTELQIDKVYIFK
PY17X_1465600   919 YLDKSYRNMLNKHYKQKQRTINNELQKIKKHVIKHINSAIKELYVTVYTELQIDKLHLSK

PF3D7_1250100  1346 QLENIHSELLQALQQNKNIPRHLNVLEKKLEITKRKKKNKPDISTSSHATDEQQVSDTLI
PKNH_1470100   1016 EKLKVKKKVFQIVRQNTNYPNDLKLLESTLAKYNADE-------TAEGK-----------
PVX_101400     1024 EKLKVKKKVFQIVRQNVNYPNDLKLLEGSLASYKTDE-------TPEGK-----------
PCHAS_1465300   978 QISEINTTVTELYKENESLNITLTNLEADLKNIPNFN-------SKNFS-----------
PBANKA_1463000  980 QINEININVSELSKENESLNIKLANLEADLQNIPNFD-------SKNFT-----------
PY17X_1465600   979 QINEINIIVSELSKENESLNITLTNLEIDLKNIPNFD-------SKNFT-----------

PF3D7_1250100  1406 RGAHNHGDIIKGEDNDEVLLIEQIQSLKTKMGDNQNQVGSILEKLNNLSDQYQLLQDKLN
PKNH_1470100   1058 --------------SKKDQLNADITKLKATIEKNKTDAASLITHFQSISEKYEQVLIKMD
PVX_101400     1066 --------------KKKEALNAEIATLKQRIEKNKADTANLRTHFESISEKYQQVLIKMD
PCHAS_1465300  1020 --------------GKKETITKGITSAKENIKNNTNKINEFKDKFNSLCSQHDTVVKKMN
PBANKA_1463000 1022 --------------AKKETINKGITNVKENIKQNIKKINDFKDQFNSLSTQHDIVVKKIN
PY17X_1465600  1021 --------------EKKETINKGITNAKEKIKQNIQKINDFKDQFNSLSTQYDIVIKKID

PF3D7_1250100  1466 VVEDIYKNLRNFKHYIEKLHKESKINREKFITKVDVLSNVYSTLEYMVKFLLHDFQEWSF
PKNH_1470100   1104 AIDYLEKRFRLFRFEVAKEYKDSNLHTDALVPLSNKDAGEYIRIESITKDLLNDLDQINY
PVX_101400     1112 AIDHLEKRFRLFRFEIVKEHKDCKLHIDALVPLSDKDAGEYRRMEDLTKELLNDVDQINY
PCHAS_1465300  1066 TVHEIEKQFRLFKYEIEKSYKKELIKKEKIVDDFTHLRRVYKVIQETILDLFNELYDIEN
PBANKA_1463000 1068 TIHEIEKKLRLFKYDIEKSYKNEVLNKEIIVDQFTHLRMVYKIIQDTILDLFNELYDIEN
PY17X_1465600  1067 IIHGIDKKLRLFKYDIEKSYKNEVLSREIIVDQFTHLRMVYKIIQNTILDLFNELYNMEI

PF3D7_1250100  1526 EKDELEKHLYELEERKKYITLEIQIRDTLSTNIQNGEGDHINNNNNNNNVRNNLKKQVLK
PKNH_1470100   1164 DIHETRILLHSLKTKKKHIELDIQIGEKLYKMEEKADINTMND----------KNKEKLK
PVX_101400     1172 DIDEARLLLHALKIKKKHVELDIQIGEKLHKMEKNEQISSKND----------AKREELK
PCHAS_1465300  1126 HHNELKIDLEILTENYNDKKIQVDVLEKLYQNQANTKEINMEP--------LVSQKAELL
PBANKA_1463000 1128 QHIELKIDLEILTDNYNDKKVQVSVLEKLYQSQLNTKESNIEN--------LVLQKTQLT
PY17X_1465600  1127 QDKELKIELQILTDNYNDKKIQVSILEKLYQNQLNKQELNIES--------LVSQKTQLT

PF3D7_1250100  1586 DLDLEISKLKGHILEVDIKKNIALEQINYLTNNTNETVPDVIRDLMPAPRIV--PVSEDI
PKNH_1470100   1214 EVVTDIENEEHKLEKLYIRRDIFMKDLNFIVSDSEKDPPETIKFLLPELIQK--TDKKNL
PVX_101400     1222 EIVTNIENEEHKREKLYIRRDVFMKDLNFVISDSEKDPPETVKFLLPQLVKK--TDKKNL
PCHAS_1465300  1178 KLEAQMKVIQTNIDKLKIKRGIISNEVNFITSDSARNPPHTLNYLQKFPLDPYLRTNTVF
PBANKA_1463000 1180 KLENQIKILKTNIDKLKIKREIILNEVNYITSDSARNPPHTINYLKKFPLEPIIRTNTTF
PY17X_1465600  1179 KLENQIKIIKTNIDKLKFKREIIINEVNYMTSDSARKPPHTINYLKKFPLEPVIRTNNTF

PF3D7_1250100  1644 YDYITWVRDNTAVINNTLRHFVMTFDQKIYDYDDHLIFVYNIKELIYKENLADEKYNANY
PKNH_1470100   1272 ENFLIEIMMETEIENNALTNLIKTFNKDVLFYKYHIINPYDYLQLPTDEKNIDEKFSAQV
PVX_101400     1280 ETFMIEIMIETDIENNALTKMIKTFNEDVLFYKYHIINTQDYLRLPNDEKNIDEKFSAQL
PCHAS_1465300  1238 EDFMEDLIINFEIDNQIYQKFIKIIKGYIRRVPKNAIFSFKFLENHNRKKIINEKYYQVY
PBANKA_1463000 1240 EKFMEDLIINLEIDNQIYQKFIKIVKGYIRRVPKNAIFSFKYLENQNKKKIINEKYYQIY
PY17X_1465600  1239 EDFMEDLIINIEIDNQIYQKFIKIVRGYIRRVPKNAIFSFKFLENQNKKKIINEKYYQIY

PF3D7_1250100  1704 YYEMNRFYLHLEEFFYILKHYVELRKIQDLGEVAIPSFEENIKTKGSLIDVHQKDKDGTQ
PKNH_1470100   1332 HKNSEMFAQKLESFRVELKKYRKLVKNQG------------------------GLKQIE
PVX_101400     1340 DRNEKMFAEKLESFRKELKSYKQLVKKQG------------------------GGKQPG
PCHAS_1465300  1298 KKGLNTYIKHLYAFYTNFQKYVEAKKKRVTPNLLSENAG-----K------TNLLSPQPT
PBANKA_1463000 1300 RKGLNIFVERLYIFHSNLKNYIDAKKKKNIPNILPESGK-----K------TNIASTQSN
PY17X_1465600  1299 RKGLNMFVQKLYIFHSNLKNYIDLLKKKSIPNILSESSK-----K------TNVELTPSN

PF3D7_1250100  1764 IIEYLERNVLHIYSILRNIKNNNIHLYHYLVPDLSNILIDPEEFKK-MSNGEQPELNKLH
PKNH_1470100   1367 ALTYLKRNIAHLKNMIHSLRNG------IHIEDFSYILTSPDFFQNKGIKNEDMQSEQAH
PVX_101400     1375 ALTYLKRNIAHLKNMIHSLRNG------VHIVDFSYILTNPDFFQSGGIKNEDRESELAH
PCHAS_1465300  1347 LISYLERNLIHMEDVLNKLKTD------VYIPDVSYVITQPDYFLK-EIKNDDPQNATLY
PBANKA_1463000 1349 EISYLERNIIHIENILNTLKAN------VYIPDISYIITKPEYFLN-EIKNEDPENARRY
PY17X_1465600  1348 DVLYLERNIIHIENILNMIKEN------VYIPDVSYIITQPEYFLK-EIKNENPENEKLY
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PF3D7_1250100   1823 KYLLDAYTNLKKEGQVVDQIYVEYINFHNHFEHTYDKLLWYKTILKRYIERSKKIYEKSY
PKNH_1470100    1421 TSLVKSYLSLNSLGKVLTDTQNKALHFGIHYKYTSDKVLWYLAILKKYIERTEMVYNNSY
PVX_101400      1429 TALLKRYFALNSLGKVLTDTQNKAIHFGIHYRYTSDKVLWYLAILKKYIERAEMVYNNSY
PCHAS_1465300   1400 KNLVSHYTQLVDMAYNINIVHENMTKYNKYYNHASDRILRYRASLKFFHEVSDKIYYLSF
PBANKA_1463000  1402 KDLLNSYTQLKDIANNINIVYEKMSAYNSYYKHASERILRYRASLKFYHEVSDKIYYFSF
PY17X_1465600   1401 KDLLNSYTQLKDIGSNINVVYEKMSAYNSHYKHASERILRYRASLKFYHEVSDKIYYFSF

PF3D7_1250100   1883 GTYTVSHIQLYDNKKDGHDNHHDQHHDNHHDQHHDHHHDQHHDHHHDHDQHHNNNYNYNN
PKNH_1470100    1481 DGQKKSSLLLPEFIK-------------------------------------------
PVX_101400      1489 DAAKKSRLKLAEFID-------------------------------------------
PCHAS_1465300   1460 KEEKIRTAIVDGQVVQV------------------------------------------
PBANKA_1463000  1462 RNEQIRTAVIDGKVVTV------------------------------------------
PY17X_1465600   1461 KNEKIRTALINGEVVPV------------------------------------------

PF3D7_1250100   1943 ISFLRSFVQLNYHNTLHERSDHIFLKSPILLQYDPEK---------IVESNEKRHIRVIR
PKNH_1470100    1496 ------------------NKADLALEHPVLLQYGGDIWDGSWGFAWGEAADKKKYLRVVK
PVX_101400      1504 ------------------SRANAALDEPVLLQYGGDIWGGSWGFSWGEAADKQKYLRVMK
PCHAS_1465300   1477 ------------------DKYGRHIMPFSMLQYVDNV--------VEDVYDKDKYLNVIK
PBANKA_1463000  1479 ------------------DKYGKHIKPFSMLQYINNV--------IEDVYDKDKYLSVIK
PY17X_1465600   1478 ------------------NKYGTQIKPFSMLQYIDNV--------VEDAYDKDKYLNVIK

PF3D7_1250100   1994 DQNNFPYKLGEVKETYVLNKSIHDKFVKSKKLDEYKKYMNNKLYDIVHEFKRGKGKLYLF
PKNH_1470100    1538 KEQTYPYKLKEIKDVYVVDKIVKEKLVRTGKLDSLKEYMHVKVYNIVEVKD---SPITLF
PVX_101400      1546 KEQTFPYKLKEIKDVYVVDKIVKDKLVRTGKLDSLKDYMHVKVYNIVEVKG---PPLTLF
PCHAS_1465300   1511 EESIYPFPLKPLKDVYILGKSLKYNLLRNNQLSEFKTFVKAKMYTIIENHD---INPYIF
PBANKA_1463000  1513 EETMYPFPLKPLKDIYILGKTLKYNLLRNNQLSEFKTFVKSKMYTIIEKND---NNPYIF
PY17X_1465600   1512 EETMYPFPLKPLKDIYILSKTLKYNLLRNNQLSEFKTFVKSKMYTIIEKDD---INSYIF

PF3D7_1250100   2054 EKEELEKYQLIFG------GKTLIKGSLLNFLSHININLNK----------NLLINQIND
PKNH_1470100    1595 DKEELKQLKLLTP------DGHITQGSVKNYLTHLGFWSKGGANVEGGTSAEEHLPAILQ
PVX_101400      1603 DKEELTSLKLLTP------EGHIAPGSVKNYLTHLGFTMKGGEPNIEATNWEAHLPAILQ
PCHAS_1465300   1568 TKEELAKLNIIKDIDATNNNINLIEGSLHNFFSHYPNILQGTDNKIPN--------LVEN
PBANKA_1463000  1570 DKDELDKLKIIKNMDETNNNTNLIEGSLKNFFSHYSDIFQGIDNNIHN--------LVEN
PY17X_1465600   1569 NKDELDKLKIIKNIDDTNNNTNLIEGNLTNFFSHYSHIFQDTNNNIPN--------LVEN

PF3D7_1250100   2098 TINEYLKKRNLSYNSIIELIKYLQKNPSVIHFIDLIKLGKNILERSNVLYIKKEWFTLYL
PKNH_1470100    1649 TAAEYLKQSNISYDAILEVLKYLKATPNAINVRDIITLSEIILDNSNVFFVKEDTLSIYI
PVX_101400      1657 TAADYLKQSSLSYDAILEVLKYLKATPNAINVRDIITLSEIILDNSNVFFVKQDTLSIYI
PCHAS_1465300   1620 TINDLLKKHGITYNALLEIIKYLKTKPNILRVKEIILLCEKIINKSNLYFINPDQLAFFI
PBANKA_1463000  1622 TINELLKKNGLSYNALLEIIKYLKEKPNILRIKEIILLCERILNKSNLHFINPDKLAFFF
PY17X_1465600   1621 TINDLLKKNGLTYNALLEIIKYLKTKPNILRIKEIILLSEQILNKSNLHFITPDKLAFFF

PF3D7_1250100   2158 YTLLELLGIEVNMEHVDVHEERGLKNEHNNYISEKSYALHYLYVLRNYNK-RIEIKNQIQ
PKNH_1470100    1709 ITFLDLLGVQVNMDDIQRKD-------------KKSRVMTYLSILKSYYKKV-EIKEEIK
PVX_101400      1717 LTLLELLGVQVKMDDIQKRD-------------RKSRVMTYLSILKSHYKRA-TIRDEVK
PCHAS_1465300   1680 ISTLDAFNIKVLMTNVKRND-------------NKSTIISYLNLLKMDHKKCFVLSNYVK
PBANKA_1463000  1682 VSILEAFDIKVLMTNVKRND-------------NKSTIISYLNLLKMDHKKCLVLSNYVK
PY17X_1465600   1681 VSILDAFDIKVLMTNVKRND-------------NKSTIISYLKLLKMDHKKCIILSNYVK

PF3D7_1250100   2217 NYVLQFLLPEHKFDMEDYQPILYEFLKAINDSMDGDSITYNEFKKKNPEVYTTLVSVIKK
PKNH_1470100    1755 KHVLRFLRPSDAFPTLSYNPKLHEFLLGVQQSLDGNKILYEAFKKENTNFSTELLSGIKK
PVX_101400      1763 KHVLQFLRPSDAFPTLQYNPKLHEFLLSVQQSLDGNPTLYEAFKKENPQFATELLGGIKK
PCHAS_1465300   1727 DFILKFLKPKKSHTPLKYNPKLFEFLQSLNNSLDGNGKMYEAFKKKNPEFNTQLLSSIKN
PBANKA_1463000  1729 DFILRFLKPKENNTQLKYNPKLFEFLESINHSLDGNGKMYELFKNKNPEFNTQLLSSIKN
PY17X_1465600   1728 DIIFKFLKPKENNIQLKYNPKLFEFLESLNHSLDGNDKMYQIFKKKNPKFNSQLLSSVKN

PF3D7_1250100   2277 GIEDFFYTMFNKIIEEHPEL-KEEIYFDDNYNDEEKDRFRYANYTWERANLNEILTLYFY
PKNH_1470100    1815 GISDFMNYILAKVATYSPEHFKSKYYHEHKYNQQEMEVLRITSYSTQRINFGTLMTLFFY
PVX_101400      1823 GLDEFVDYFFAKVATSSPDHFMSPYYHVQDYTEEERKKLSISSYNYRYIDLNQMLTLFFY
PCHAS_1465300   1787 GLDAFLKYFIPTILSTH--NIQGDFFAYEEYNKKETEAFLFDKVDDT-KDLKKLLSTFLF
PBANKA_1463000  1789 SLDAFLKYFIPNIINTH--NIHGNFLSYYEYNKKETETFLFNKNDDHVSDFNRLLSFFLF
PY17X_1465600   1788 GIDGFLKYFMKTVIDTH--GIYGNFLTYYEYTKKEAEIFRFNKEEDHLNNFDIFLSFFIF

PF3D7_1250100   2336 VLNPGLRNVIYKHFIKVNIKCLKDYKNFDFKEIFSFLNYDDIGATFLNYLKEHELFEIPP
PKNH_1470100    1875 FVNPDLRNMLHEHVIKADLSCLDKFSTFDFKDIFSITSDTQLIKLFHEKIGHFQYGRTHS
PVX_101400      1883 FVNPDLRNMLNEYSIKASLTCLEKFPSFDFKDLFSITSDVQLNDLFLQKIGKFQYERVQS
PCHAS_1465300   1844 SINSEVRKLHNNHINSVSFKCLKDHPHFNFVNMIPYIDKNKLNEKFQNYMKTTKTHNIQP
PBANKA_1463000  1847 SINSEVRKLHKDHINNADIKCLKEHPHFNFADLIPNIDDDKINYNFNKYMSTTKTNNIQP
PY17X_1465600   1846 SINTEIRKLHKDHVSDVDLKCLKDHPHFNFVDLIPHIDYEHINDVFFRFMNTTKTHNILP
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PVX_101400     1943 LVYMWRYLLHPDNKDFFTYEKVSSVVERYFSGALFDDNTRAMLSKLVYSFLARISYHTVS
PCHAS_1465300  1904 IMVLFRLFFHPKNKDLFTYSNVISVVEKFFTSELFDNDTKHMIGKLVYSLMARLSFIVVS
PBANKA_1463000 1907 IMVLFRLFFHPKNKDLFTYSNVINVVEKFFTSNIFDNDTKKMIGKLAYSLMARLSFIVVS
PY17X_1465600  1906 LMILFRLFFHPKNKDLFTYSNVINAVEKYFTSEIFDSDTKKMIGKLAYSLMARLSFITVS

PF3D7_1250100  2456 YFDHDIFKIINKSDLNIIILFHTIINKINYLLYCGTEKLFIERYAPTNLFVQNRIFKIDA
PKNH_1470100   1995 YFDIQIEHLIEKSDIELISLFHNILNKLNFLLYCTNSKPYLERYAPANLLSYTRPFKLDA
PVX_101400     2003 YFDIQMEPLLNNSDIKLISLFHNILNKLNFILYCTNEKLYLERYSPANLLSYGRPFKLDA
PCHAS_1465300  1964 YLEPKIEDVVNGIDINLMNLFHTVINKMIYTLYCKNDKEHLEPFVPTSMIKNDKVFKLDA
PBANKA_1463000 1967 YLEPKIEDVIDGIDINLMNLFHSVINKIVYTLYCKNNKEHLEPFIPTSMIKNDKVFKLDA
PY17X_1465600  1966 YLEPKIDDVIDGIDIDLMNLFHNVINKMVYTLYCKEDKKLIEPFVPISMVKNRKMFKLDA

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PKNH_1470100   2055 LKIFHQFVNSLPHYLRSYIVNFFET-DFSEITENLIVDLFHHIQSFLENDS---SS---F
PVX_101400     2063 VKIFHQFVHSLPHYLRSHIVNFFET-DFAEVTENLLVDLFHQLESLLDSNS---SS---F
PCHAS_1465300  2024 LKIYNEFLMTLPDQDKRSAINFFQT-DFPNVATTIISDALTFVNHHMKKEP---GV---Y
PBANKA_1463000 2027 LKIYNEFLMSLPEQDKRSAINFFQT-DFPEVVTTIISDALGFVNHHLEKGP---GV---Y
PY17X_1465600  2026 LKIYNEFITSLPDQDKRSAINFLQT-DFPKVVTTLISDALDFVNRHLEKGP---DT---Y

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PKNH_1470100   2108 ESEKENKIESFFKLNYFFTKNKNVTDGNYQSMIQEDPKFKDA-KIIFNRRVKYDHVNKKS
PVX_101400     2116 ETEEENKLETFFKLNHLFTKSKNVTDGNYQSMLQDNPHFKDA-KIILSRRVKYDHVHKKS
PCHAS_1465300  2077 HSDEYVTLETLFKINYKLSSNPNLYYDNFDEFIQKKPEYTKAPNLLFIKRAEYDNSNNNI
PBANKA_1463000 2080 HSDEYIKLETLFKINYKLSSNNNLYYDNFDEFIQKNPEFTQSPNLLFMKKAEYDNTNKKI
PY17X_1465600  2079 HSDEYVKLETLFKINYQISSNQNLYYDNFDEFIKKNPEYTQAPNLLFIKKAEYDNINKQI

PF3D7_1250100  2635 QYKEELDLHDMIDNESFHQLLDLLNKESITLEQLSFLFSRYITEHANIKDFPKLFMFKKY
PKNH_1470100   2167 NYQENLHLADLIDEQSFKMLLQTLIKEQISFDEVNEKFKNFMNTKK--LVFPKFDILKTK
PVX_101400     2175 LFQENLHLKDLFDEQSFKMLLQTLTKEEITFDELNQKFKDFMTRKK--LLFPKFDIMKEK
PCHAS_1465300  2137 IYKNEINLEDIIDEKSFGLLTEELFKEHLTIKQVNNRFTDIMKKLK--VLMPKLHVFKDK
PBANKA_1463000 2140 IYKNELNLEDIIDEKSFGLLTEELFKEHLTIKQVNDRFTNIMKKLK--FLMPKMHVFKDR
PY17X_1465600  2139 KYKNDLNLEDIFDETSFGILTEEIFKEHLTIKQVNDKFTDTMKKLK--FLMPKMYVFKDK

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PKNH_1470100   2225 ITKTADDLYYLKIYKYLYDTF-QKMHVTQPIHDLYFLFIKVLLDYYVAPFKFKNEH-VQE
PVX_101400     2233 ITTSVDDLFYMKVYKHLYDFF-QNIHVTQPIHDLYFLFVKVLLDYSVLPFKFANDH-VQE
PCHAS_1465300  2195 LEKSGNTEIEKDIYEYIYRRF-KNINMSYSVQGLVYTPIKKLIDFILFPNVLVQNV-DAD
PBANKA_1463000 2198 LDKSGNQEIEKDIYEYIYKRF-KHLNLSYSIQGLVYIPIKKIIDFILFPSVLVQNV-DAD
PY17X_1465600  2197 LNKTGNKEVEKDIYEYIYKRF-KDLELSYSTQGLVYIPIKKVIDFILFPNVLVQNV-DAD

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PKNH_1470100   2283 DLHTELARKYQKYIEFLSQLFPCLFNFYYYDDTVLCQNFGNYS-EEEFSPEQKMLNILQT
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PCHAS_1465300  2253 YMTMQLGYKYNLYIKFLDQLSKCLIDIYYYNKNDSCMRFGNYTQ-NDTRIEQKVLNIMQT
PBANKA_1463000 2256 YMTMQLDYRYNRYIKYIDELTKCLIDIYYYNKNDSCLRFGNYTK-NEISIEQKVVNLMQT
PY17X_1465600  2255 YMTMQLDYRYNRYIKFIDELTTCLIDMYYYNKNDNCLRFGSYAK-EEMNVEQKVLNLMQT

PF3D7_1250100  2814 PFINISPII--KHNYIHDDYYMYEKDLNGNYLSSNINNNNNNNNINNIDSNYVNRRDKNG
PKNH_1470100   2342 PFVQLPQTV--QNNQINLDYH----------------------------------------
PVX_101400     2351 PFVQHPEKV--QNNQINFDYH----------------------------------------
PCHAS_1465300  2312 PFIETIEVN--KNNYIYNKYI----------------------------------------
PBANKA_1463000 2315 PFIETLEEN--KNNFVYNKYI----------------------------------------
PY17X_1465600  2314 PFIETIEEYKHKNNYIYNKYI----------------------------------------

PF3D7_1250100  2872 DYIHGTNINSDILYHFIKQYIPLVEPSDEEHLQIEVFKFKYFTLEITKFVLRHILKKLPF
PKNH_1470100   2361 ------INEEDLFFDFIKEFIPESGKMDQNQLKVESFKIRYFITEISKFVMRKVMSKMPS
PVX_101400     2370 ------INEEDLFLDFIKEFIPESEKMDQKQLQVESFKIRYFVTEISKFVMRTVMSKMPP
PCHAS_1465300  2331 ------SDNDDIFYYFINKLLSNKDNTDKEKLSIQIFKVKYFFLEITKFVIKKVLSTMPP
PBANKA_1463000 2334 ------SDNDDIFYYFINKLLPINHNIEKNKLSIQIFKIKYFVLEITKFVIKKALSTMPS
PY17X_1465600  2335 ------SDNDDIIYYFINKLLPINKNIEKNQLIIQIFKIKYFVLEITKFVIKKVLSTMPS

PF3D7_1250100  2932 NYLIHMNWNDTYIHIDHIINNLFLHFFKKNKAHLLQQNQL-----QGLT----HKINFEN
PKNH_1470100   2415 SYIFNMGYKDFYINVDDIVNNLQPLFEQVRKVKEPS-----DSVNSSYGVISGTIANFMD
PVX_101400     2424 SYIFNMGYKDFYINVDDVVNNLQPFFEQVRKAKAPS-----DQVNSPYAVISGTIANFMD
PCHAS_1465300  2385 SYLTKMTHQHIQINIDTIINSLYSLYKKNNKGKVSK-----DQHTSTYLYTVGSIIHFMH
PBANKA_1463000 2388 SYLTKMTHRHININIDHIINSLYSLYAKANKTKTNEQQ---HQNTGTYAHTIGSIINFMY
PY17X_1465600  2389 SYLTKMTYHHTNINIDHIINSLYSLYTKANKAKTIEQEKGEQQITDGYTHTIGSIINFMY

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PVX_101400      2479 ANNEEAAS-----------------------------------------------------
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PY17X_1465600   2449 NANDELCDFEITGEFTPEELIHDPKEYETEDDYDEYDEDSDESVVKKTDESEEEKNENRS

PF3D7_1250100   3020 --DPNNLPPTYRHIKYYMDHYILQYSLHNHMLFKYLHNIFQHIDQYKTYFPTLAELYLYI
PKNH_1470100    2478 --------FRFQNIKFYLNSHVTQLFLQNNMSFKYFMDFIKNIDKFKTYFPSLSELYVFV
PVX_101400      2487 --------FRFQNIKFYLNSHVTQLFLQNNMSFKYFLEFIKNIDKFKTFFPSLSELYVFV
PCHAS_1465300   2500 VFMGLDGKQKVKNIKYYLNNYISEFLLNNNISFKHLYQFIQNMDSFKAYLPTLTELYIFV
PBANKA_1463000  2505 IMIGLGGKQKVKNIKLYLNNYISEFLLNNNISFKYLYQFIQNMDKFKAYLPTLSELYIFI
PY17X_1465600   2509 VMIGLGGKQKVKNIKIYLSNYISEFLLNNNISFKYLYQFIQNMDKFKAYLPTLSELYIFI

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PVX_101400      2539 DRHVNIINAITHPNFTERVTTQRVIQLFVDTLKNFGLDLYGV
PCHAS_1465300   2560 DKHVNIINSIYSSQYIPYTQTDDIISIFVDTFKALGLEIYSV
PBANKA_1463000  2565 DKHVNIINSIYSSYYIPYTQTDTIINIFVDTFKALGLDIYSV
PY17X_1465600   2569 DKHVNIINSIYSSSYIPYIQTDTIINIYVDTFKTLGLDIYSV
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Figure S2. Multiple sequence alignment of G377 from P. falciparum 3D7, P. knowlesi, P vivax, P. chabaudi, P. berghei ANKA and P. yoelii. Identical and conserved amino acid positions are indicated by black and grey shading.

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PCHAS_1434200      1 MKRINIPTSAIGCLLLFLLSSQNAQYECMNIKGSSNNGSENKANLNAQNGKLNTKWSETG
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PY17X_1434500      1 MKRINIPTSTIGCLLLFFLSSQNAQYECMNIKGSSNNASGDKTNFSVQDGKLNTKWSDSG
PF3D7_1216500      1 MKYPNFFILKVFYFLFFYLSFEDIYYHCINIGKPQVNTNGKNVNSNEKANNLSTEWSNRG
PKNH_1436100       1 MKNVAFSILHISSLFILYLSSQSGLYSCKNTGKTASKGNHSNPNSAVNSNSLSTEWSEKG
PVX_123505         1 MKNFAFPILNISSLFILYLSSQSGLYNCMNTGKTASSAKRSNENSGVNDNSLSTEWSEKG

PCHAS_1434200     61 YNFMDLIKNGYVKNK-DLDDIKDDLASELATKIQNTVSNYIKEDHD---EDEINDDDIKK
PBANKA_1432200    61 YSFMDLIKNGYVKNK-DLDDIKDDLASELATKIQNSISKYIKEDND---EDELNDDDIKN
PY17X_1434500     61 YSFMDLIKNGYVKNK-DLDDIKDDLASELATKIQNTVKNYIKEDND---EDELNDEDIKN
PF3D7_1216500     61 FNFMDLLKNGYLQSHGNLEEVKDELANELANKIQNKIGEYLKDEKNLSVLQHLQLEDLDD
PKNH_1436100      61 YNFMDLVKNGYLKNKGDLDEVKDYLADELAGKIKDKLNGILKDENIFYDLENMDEEDISD
PVX_123505        61 YNFMDLVKNGYLKNEGDLDEVKDYLADELASKIKDKLSDFLKDEKIFYDLENMDDQDKKD

PCHAS_1434200    117 LKIYVKDISEYVGLKAADLLDKNLENALKPIIENKGSDKPESKLSNEGTSSFRFNNE---
PBANKA_1432200   117 LKIYVKEISGYVGLKAADLLDKNLESALKPLIENKSFDKSESKLSNEGTSSFRFNNE---
PY17X_1434500    117 LKIYVKEISGYVGLKAADLLDKNLENALKPLIENK----SESKLSNEGTSSFRFNNE---
PF3D7_1216500    121 LKHYVKDVSEYIGAKAGDLLDENLESTLKPLLERKSFETFEQALHNKSTDNFVPFEE---
PKNH_1436100     121 FKNYLKDMSEYIGLKAADILNSNLEDSLKSFLPKGSFANLKEAMGSSSPVNLNFDDEDGE
PVX_123505       121 LKNYLKDMSEYIGLKAADILNSNIEESLKPLLSNSSFASLKEAMGSTSAVDLKIDDEDDE

PCHAS_1434200    174 ------------------------------------------------------------
PBANKA_1432200   174 ------------------------------------------------------------
PY17X_1434500    170 ------------------------------------------------------------
PF3D7_1216500    178 ------------------------------------------------------------
PKNH_1436100     181 TKKGKSKKGK---------------YKKG-------------------------YSNDEN
PVX_123505       181 TKEEKAKEEKAKEVKAKKAKAKKAKAKKGDSKKEDSKKEGSKDENAKDENAKDDNSSDGN

PCHAS_1434200    174 ----IIDDEDPEQEIDHFADDLTDEYEVKQIENLEHY------------------DQEIN
PBANKA_1432200   174 ----IIDDEDPEEEIDHFADDLTDKYEVKQNENLEQY------------------EKDIN
PY17X_1434500    170 ----IIDDEDPEEEIDHFADELADEYEVKQNENLEQYENLDQYENLDQYGNFDQYEKDIN
PF3D7_1216500    178 ----NNKSGNANEETENFVDELVEDYEKTKNPDLDEQT------------------KDIK
PKNH_1436100     201 ANDENANDEDVDETTEDFINELVDAYEEKHHKDLENYA------------------QEIK
PVX_123505       241 SSDDNADDMDVDEATEDFINELVDVYEENQQKDLEEYA------------------QEIK

PCHAS_1434200    212 PHH---
PBANKA_1432200   212 PHH---
PY17X_1434500    226 PHH---
PF3D7_1216500    216 THSDSD
PKNH_1436100     243 NHNNLD
PVX_123505       283 THNNLD
```

Figure S3. Multiple sequence alignment of MDV1/PEG3 from P. falciparum 3D7, P. knowlesi, P vivax, P. chabaudi, P. berghei ANKA and P. yoelii. Identical and conserved amino acid postiosn are indicated by black and grey shading.

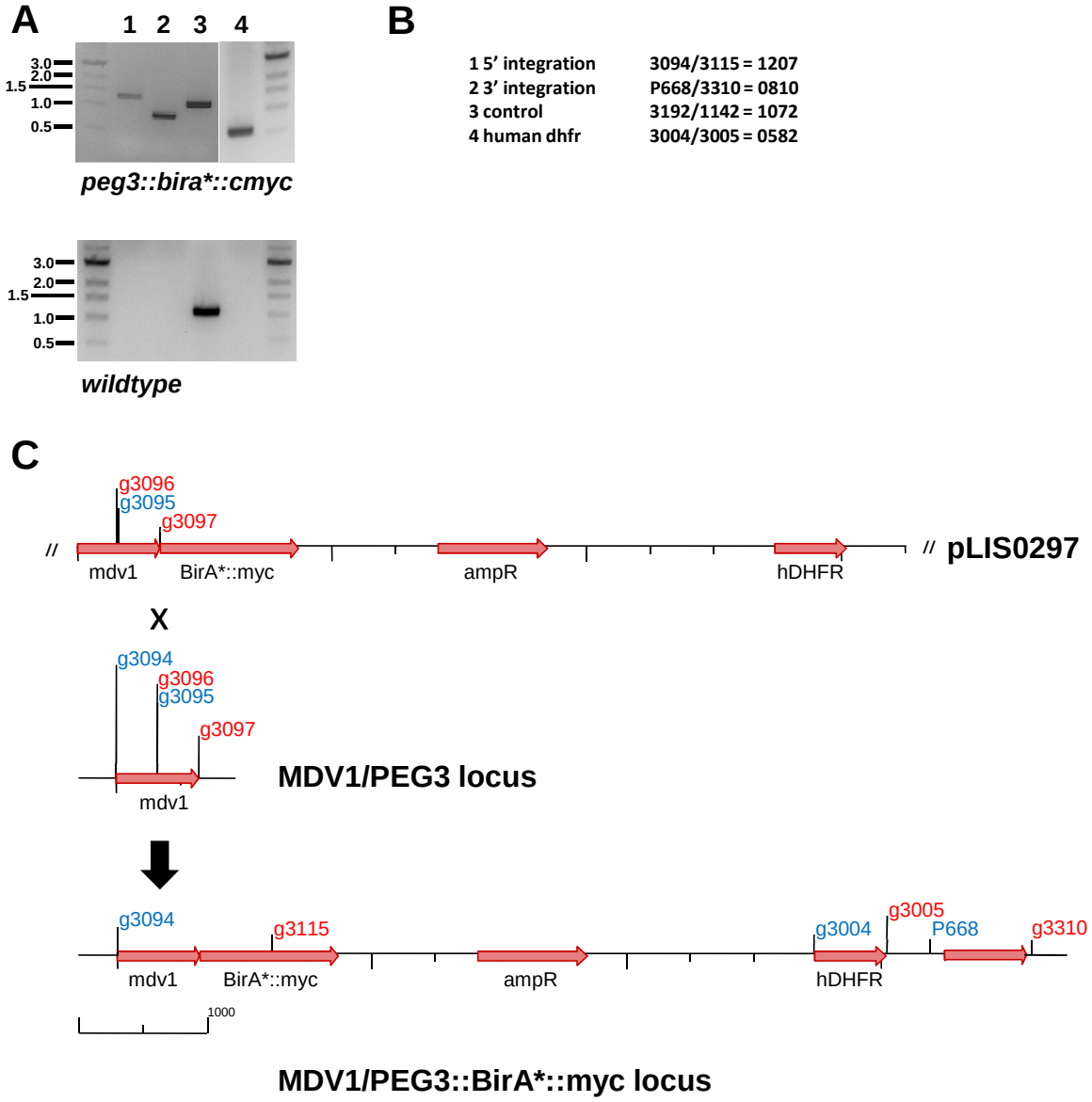

Figure S4. Genotyping of *mdv1/peg3::bira*::cmyc*. (A) Agarose gels of PCRs using wildtype and mutant parasite DNA. **(B)** Reactions as indicated on the top right. Primer/Primer = Size in base pairs. **(C)** Genomic loci and position of primers.

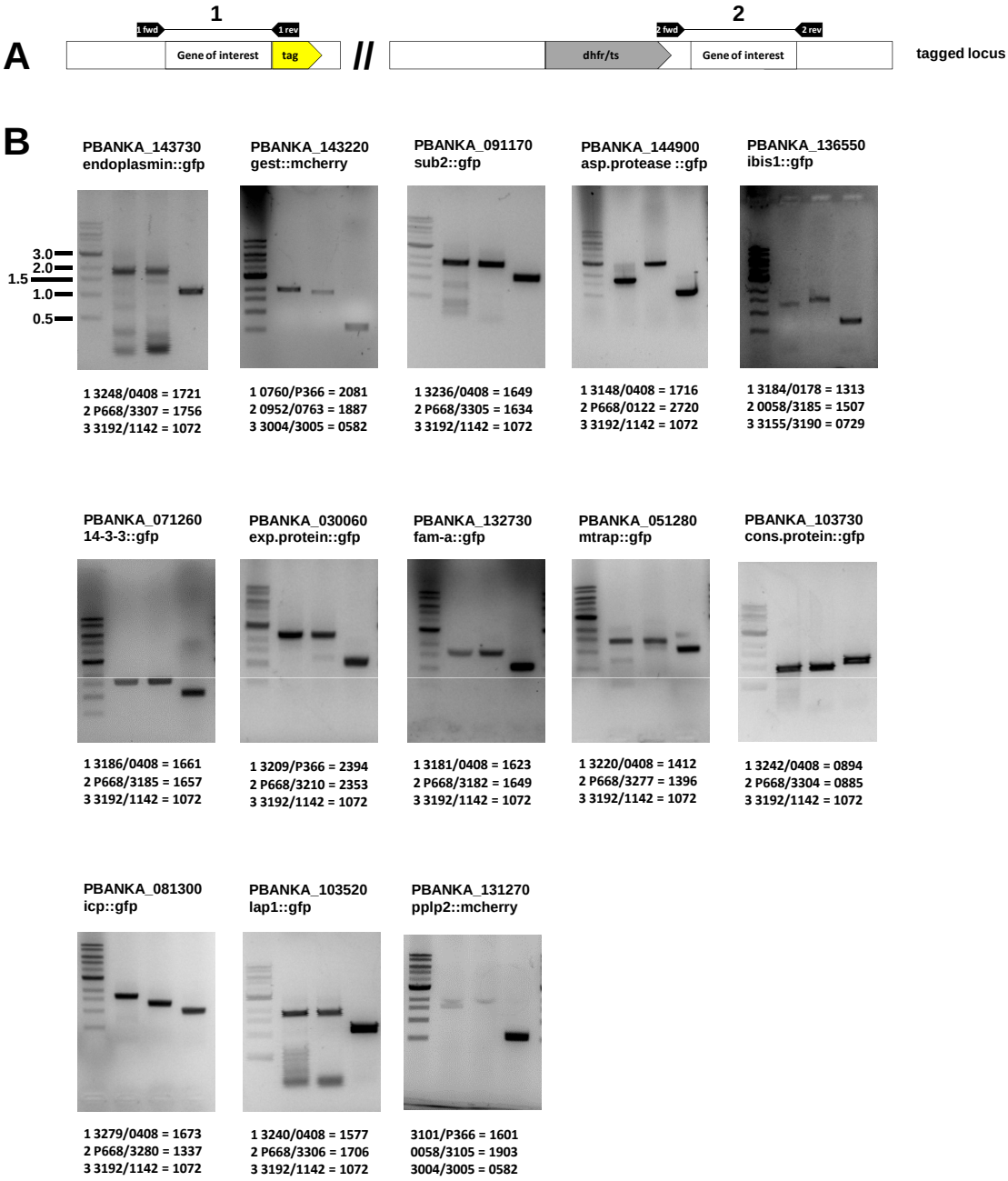

Figure S5. Genotyping of known and candidate egress vesicle components. **(A)** Schematic of primer pair locations for reactions 1 and 2 in transgenic parasites. **(B)** Agarose gels of PCRs using mutant parasite DNA. Reactions 1-3 amplify 5' integration, 3' integration and a control PCR, respectively. Below each gel picture: Primer/Primer = Size in base pairs. Size marker throughout: 1 kb ladder from New England Biolabs

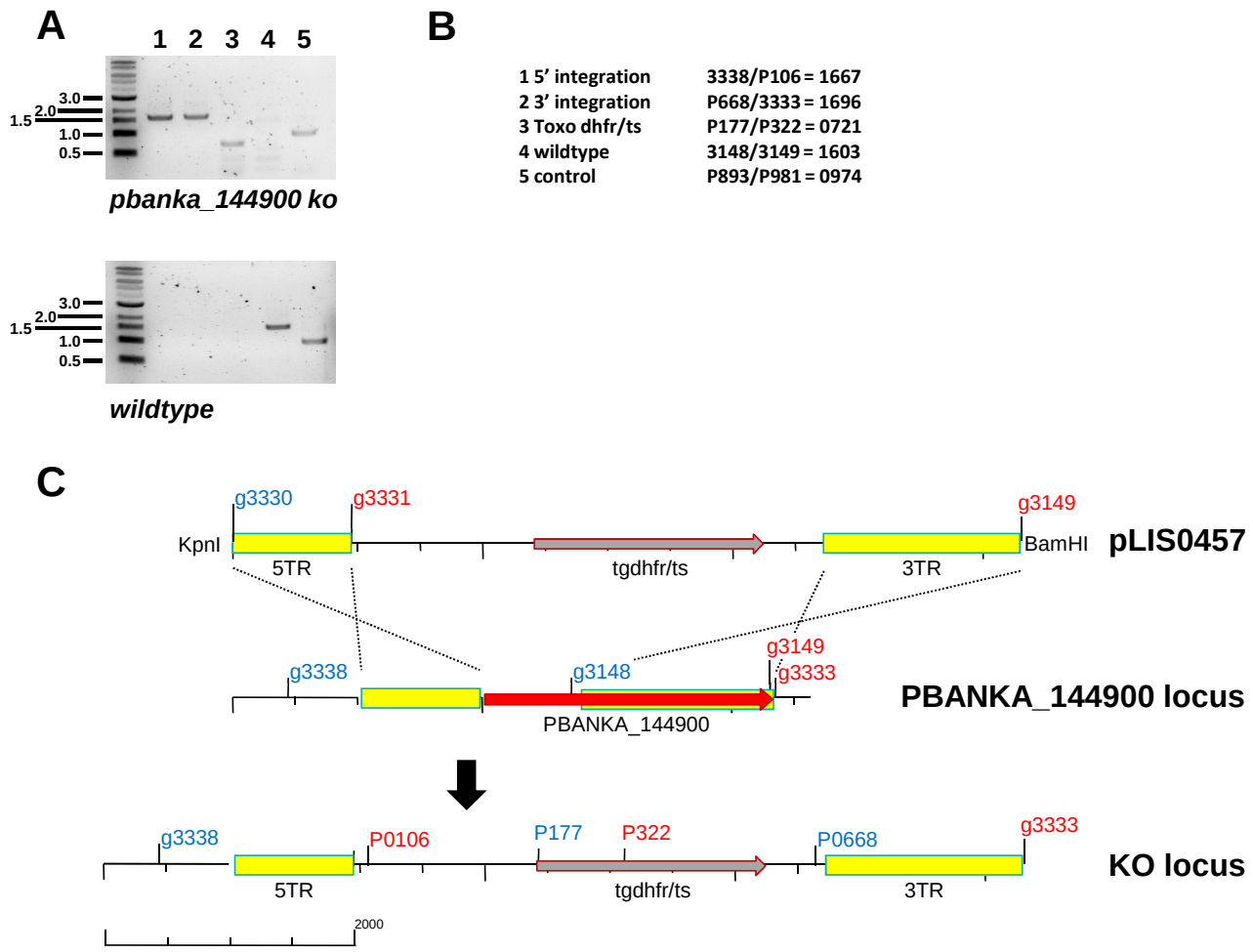

Figure S6. Genotyping of *pbanka_144900 knockout*. (A) Agarose gels of PCRs using wildtype and mutant parasite DNA. **(B)** Reactions as indicated on the top right. Primer/Primer = Size in base pairs. **(C)** Genomic loci and position of primers.

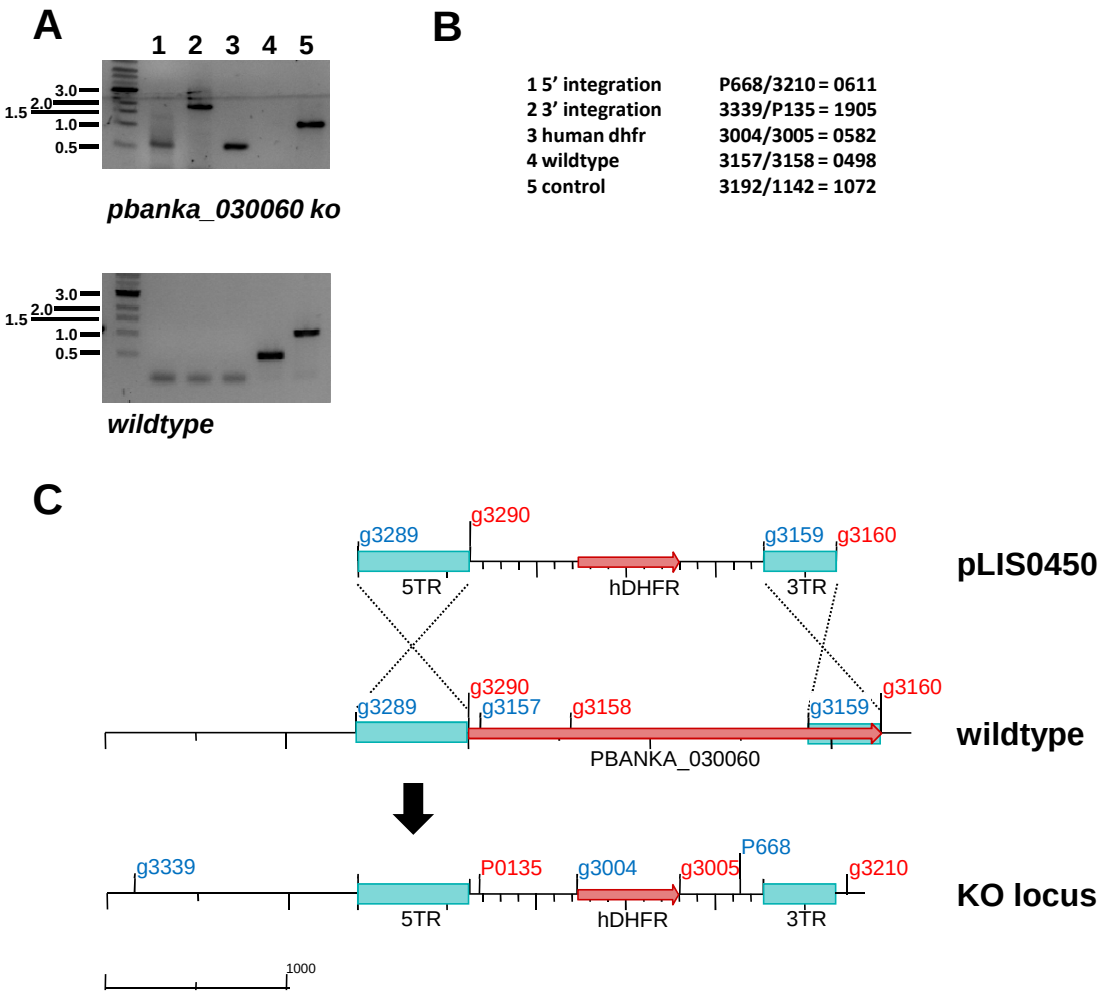

Figure S7. Genotyping of *pbanka_030060 knockout*. (A) Agarose gels of PCRs using wildtype and mutant parasite DNA. **(B)** Reactions as indicated on the top right. Primer/Primer = Size in base pairs. **(C)** Genomic loci and position of primers.

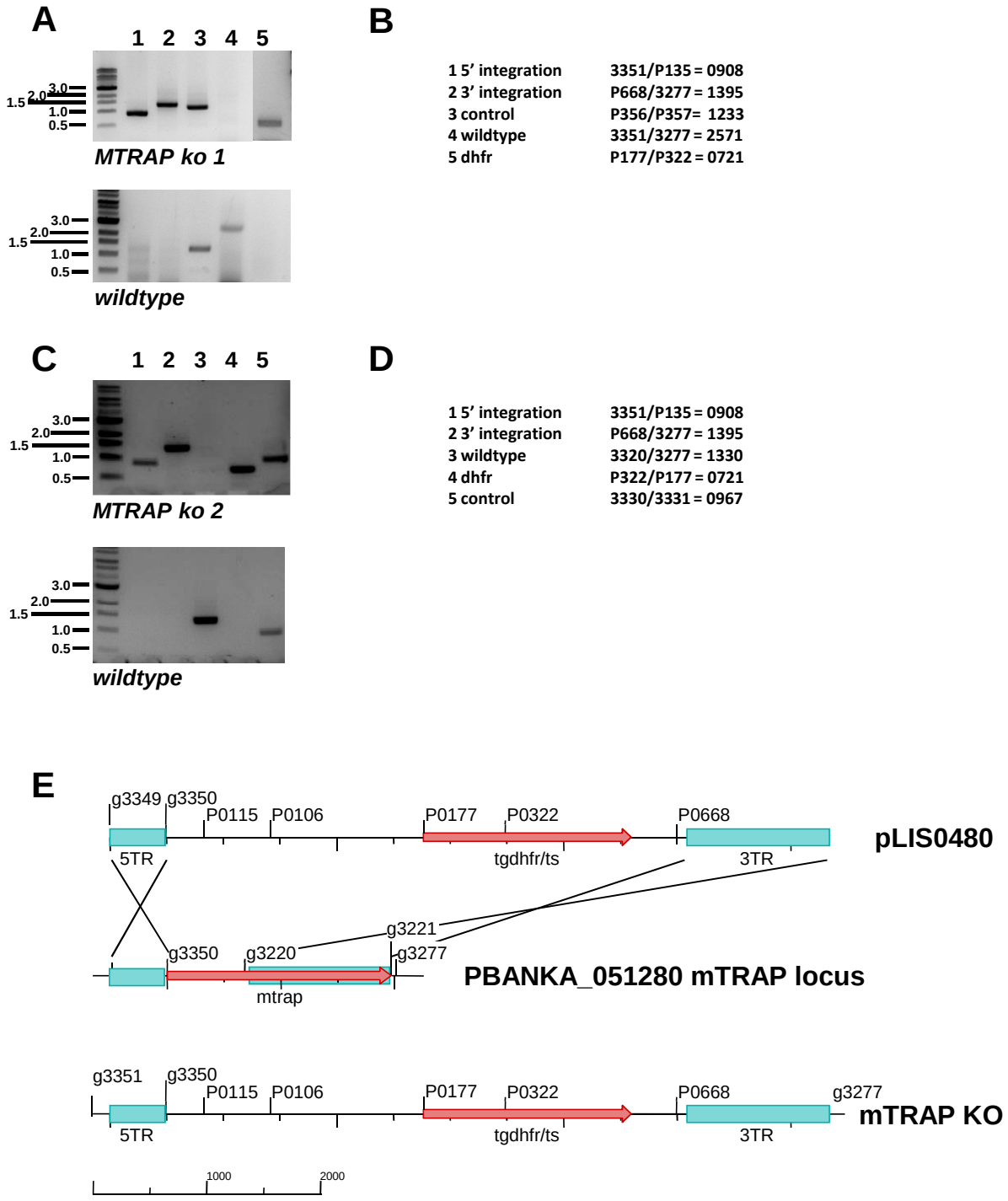

Figure S8. Genotyping of *mTRAP knockout*. (A) Agarose gels of PCRs using wildtype and mutant parasite DNA. **(B)** Reactions as indicated on the top right. Primer/Primer = Size in base pairs. **(C)** Genomic loci and position of primers.