Supplementary Information for

Mutations in Plasmodium falciparum Actin-binding Protein Coronin Confer Reduced Artemisinin Susceptibility

Allison R. Demas[1a], Aabha I. Sharma[1a] Wesley Wong[a], Angela M. Early[b], Seth Redmond[b], Selina Bopp[a], Daniel E. Neafsey[a,b], Sarah K. Volkman[a,b,c], Daniel L. Hartl[a,d], Dyann F. Wirth[a,b,2]

[a] Department of Immunology and Infectious Diseases, Harvard T.H. Chan School of Public Health, 665 Huntington Avenue, Boston, MA 02115, U.S.A.

[b] Infectious Disease and Microbiome Program, Broad Institute, 415 Main St, Cambridge, MA 02142, U.S.A.

[c] School of Nursing and Health Sciences, Simmons College, 300 The Fenway Boston, MA 02115, U.S.A.

[d] Department of Organismic and Evolutionary Biology, Harvard University, 16 Divinity Street, Cambridge, MA 02138, U.S.A.

[1]These two authors contributed equally to the work.

[2] Corresponding author. Mailing address: Department of Immunology and Infectious Diseases, Harvard T.H. Chan School of Public Health, 665 Huntington Avenue, Boston, MA 02115, U.S.A. telephone: (617) 432-2214, e-mail: dhartl@oeb.harvard.edu and dfwirth@hsph.harvard.edu

This PDF file includes:

Figs. S1 to S8

Tables S1 to S2

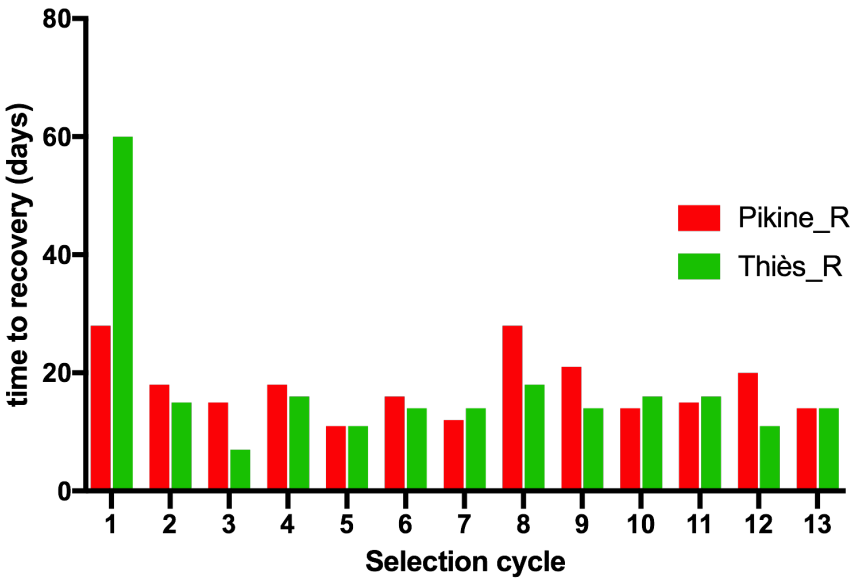

Fig. S1. Recovery period for selected lines Pikine_R and Thiès_R following each Dihydroartemisinin (DHA) pulse over 13 selection cycles with increasing drug concentration.

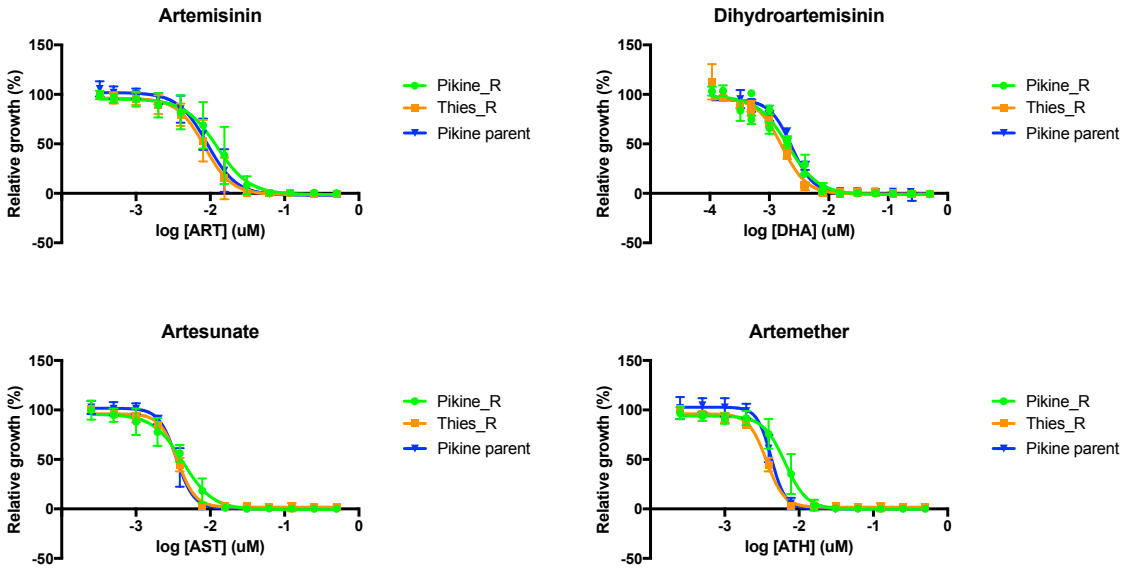

Fig. S2. Selected lines Pikine_R and Thiès_R after 13 selection cycles under increasing drug pressure show no change in EC_{50} in response to artemisinin or its derivatives. Parasite drug sensitivity was measured by 72-hour *in vitro* assays with SYBR Green. The Thiès parent response is not shown as it is virtually indistinguishable from that of the Pikine parent.

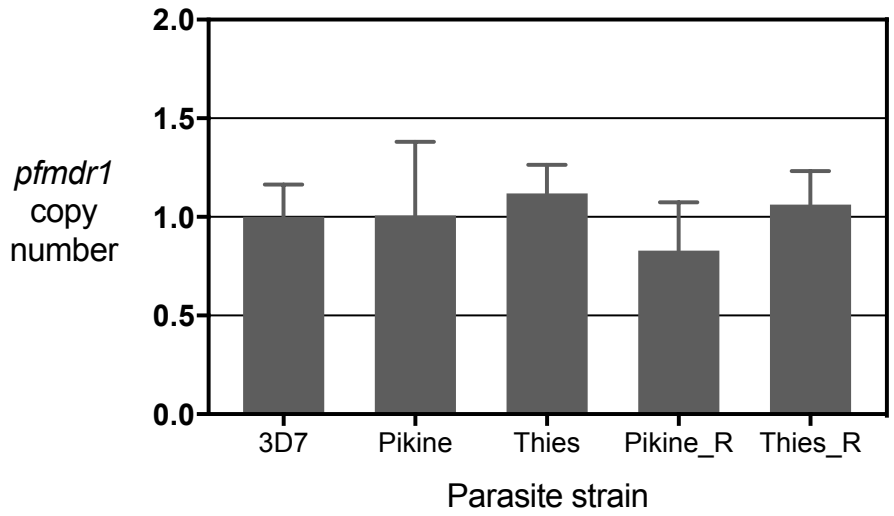

Fig. S3. Copy number of *pfmdr1* as estimated from quantitative real-time polymerase chain reaction assays in 3D7, a laboratory line, both parental lines, and selected lines Pikine_R and Thiès_R after 13 selection cycles under increasing drug pressure. The *pfmdr1* copy number was normalized to that of the gene for seryl tRNA.

Gene Name	Gene ID	Pikine_R	Thiès_R
conserved Plasmodium protein unknown function	PF3D7_1433800	S1054F	I575M
transporter putative	PF3D7_0209600	D1035N	
coronin	PF3D7_1251200	R100K, E107V	G50E
autophagy-related protein 7, putative (ATG7)	PF3D7_1126100	N1041S	

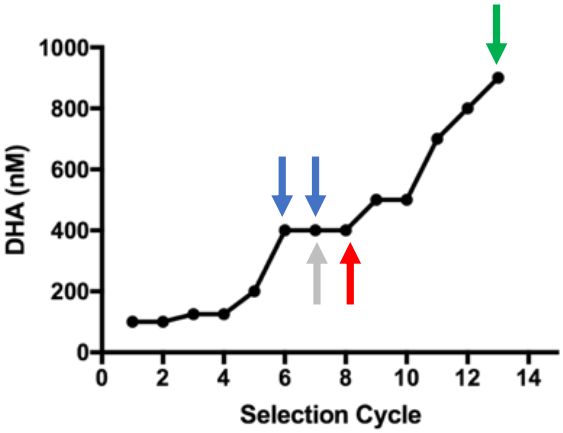

Fig. S4. Timeline of the appearance for some of the mutations after intermittent Dihydroartemisinin (DHA) pulse. The mutations were identified via Sanger sequencing after PCR amplification of the bulk gDNA. *PF3D7_1433800* I575M in Thiès_A was the first mutation to appear after six selection cycles followed by S1054F (*PF3D7_1433800*) and D1035N (*PF3D7_0209600*) in Pikine_R. All mutations in *pfcoronin* appeared after eight selection cycles.

A. Homology region for G50E replacement: 501bp

GTATAGCTTGTAGTGCTGGATATATTGCTgtaaggaaaaaaaaaaaaaataataataataaaaaattaaaa
tgtacaaatgatgcagtatatatgtatatgtatttatgtatatatttatgtatatatgtatgtacatattt
atgtatgtatatatttggtgcgctttaaagattaattcattattcatatatatcgttttatatgatttgtt
catattatagGTACCATGGCAAGTTGAGGGTGAAGGAATGATCGGAGTTATCAGATTAGAAAATCAAGTGA
GAAATCCCCCTGTAATAAAATTGAAGAGTCATACATCTCCCATCCTTGATTTGTCATTTAACCCGTGTTAT
AGTGAGATATTAGCTTCATGTTCAGAAGATATGTCTATAAGAATATGGGAGATACGTCATGAGGATGAGAA
TGTGAATGAGGTAAAGGATCCTTTATGTATATTAAATGGTCATAAGAAAAAAGTAAATATATTATCATGGA
ATCC

Guide RNA for Cas9 plasmid
Guide 1 5'CCATGGCAAGTTGAAGGGGG
Guide 2 5'ATCCTTGATTTGTCATTTAA

WT AA Sequence: VPWQVEGGGMIGVIRLEN
Modified AA Sequence: VPWQVEGEGMIGVIRLEN

B.

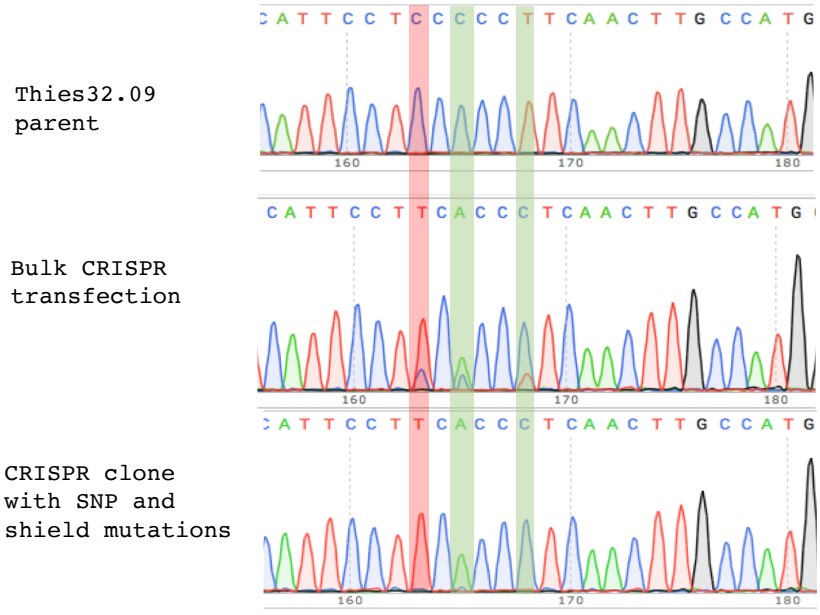

Fig. S5. A. CRISPR gene editing strategy for generating *pfcoronin* mutants in SenTh032.09 (Thiès) parental background. Homology region with primer sequences underlined, *pfcoronin* mutated site indicated in red, shield mutations in green, protospacer adjacent motif (PAM) sequences highlighted in yellow. Shield mutations were added for guide 1 but not guide 2. **B.** Sanger sequencing confirmation of CRISPR edited parasite gDNA from bulk transfection and an individual clone highlighting the target SNP in red and shield mutations in green.

A. Homology region for R100K E107V replacement: 500bp

ggtgcgctttaaagattaattcattattcatatatatcgttttatatgatttgttcatattatagGTACCA
TGGCAAGTTGAAGGGGGAGGAATGATCGGAGTTATCAGATTAGAAAATCAAGTGAGAAATCCCCCTGTAAT
AAAATTGAAGAGTCATACATCTCCCATCCTTGATTTGTCATTTAACCCGTGTTATAGTGAGATATTAGCTT
CATGTTCAGAAGATATGTCTATAAAAATATGGGAGATTCGACATGTGGATGAGAATGTGAATGAGGTAAAG
GATCCTTTATGTATATTAAATGGTCATAAGAAAAAAGTAAATATATTATCATGGAATCCTATGAATTATTT
TATATTATCATCTACCTCTTTTGATTCTTCTGTTAATATATGGGATATAGAAAATGAGAAGAAAGCCTTTG
AAATAAATATGCCAAAGAAATTAAGTTCTTTACAATGGGATATCGGTGGTAATTTATTAAGTGGAACTTGT
CAG

Guide RNA for Cas9 plasmid
Guide 1 5'GAATATGGGAGATACGTCATG
Guide 2 5'TGAGGATGAGAATGTGAATG

WT AA Sequence: SEDMSIRIWEIRHEDENVNEV
Modified AA Sequence: SEDMSIKIWEIRHVDENVNEV

B.

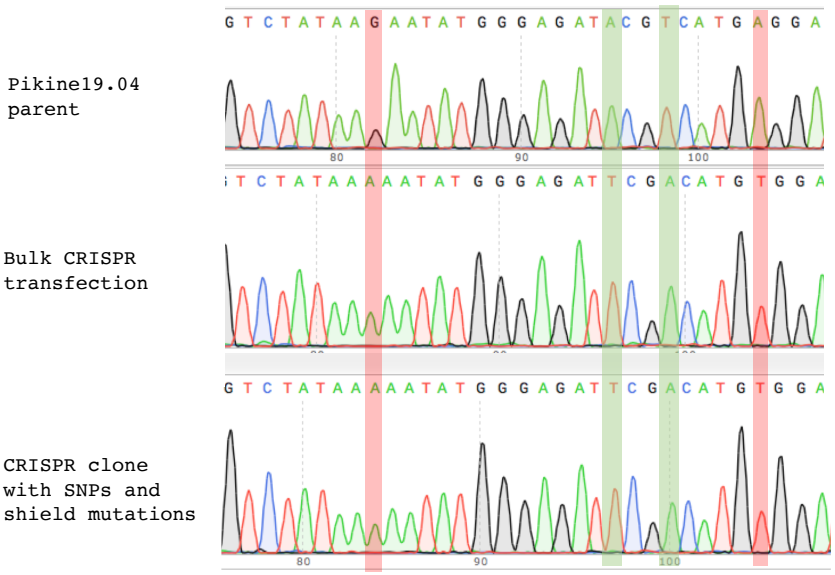

Fig. S6. A. CRISPR gene editing strategy for generating *pfcoronin* mutants in SenP019.04 (Pikine) parental background. Homology region with primer sequences underlined, *pfcoronin* mutated sites indicated in red, shield mutations in green, protospacer adjacent motif (PAM) sequences highlighted in yellow. Shield mutations were added for guide 1 but not guide 2. **B.** Sanger sequencing confirmation of CRISPR edited parasite gDNA highlighting the target SNPs in red and shield mutations in green. The bulk transfection and individual clone sequencing chromatograms were virtually indistinguishable.

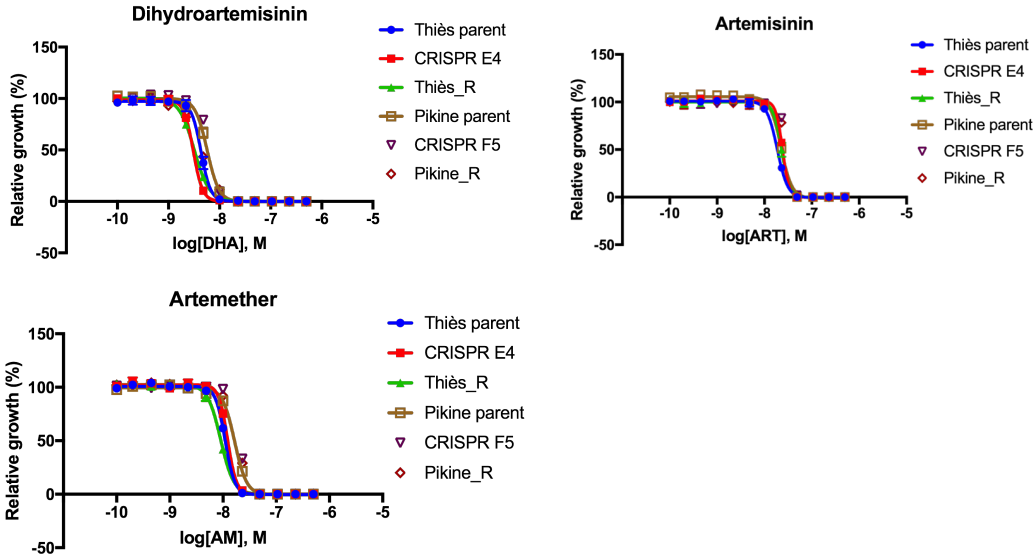

Fig. S7. Pikine and Thiès CRISPR *pfcoronin* mutants show no change in EC_{50} in response to artemisinin (ART) and its derivatives. *Pfcoronin* mutations identified in Pikine_R (R100K, E107V) and Thiès_R (G50E) were knocked into their respective parents to obtain independent clones in each background Thiès (CRISPR E4) and Pikine (CRISPR F5). Parasite drug sensitivity was measured by 96-hour *in vitro* assays with SYBR Green. Only results for one CRISPR clone per background are shown as the results were virtually indistinguishable from other clones.

```
TgondiiTGME49_216970              MADAVDVPLIKNLYAEAWKQQYSDLRLSTKQTESCGLAANTEYIAAPWDVGGGGVLGILR   60
PfalciparumPF3D7_1251200          ---MYNVPLIKNLYPDPSNNLYGDLRICSRATETCGIACSAGYIAVPWQVEGGGMIGVIR   57
PgaboniPGSY75_1251200             ----------------------------------GIACSAGYIAVPWQVEGGGMIGVVR   25
PvivaxPVP01_1468300               ---MSSVPYIKNLYPDPSNNLFDDLRICSRVIDSCGLACSSGFVAVPWEVEGGGLIGAIR   57
PcoatneyiPCOAH_00051520           ---MSSIPYLKNLYPDPSNNLFDDLRICSRVIDSCGIACSSGFVAVPWEVEGGGVIGAIR   57
PknowlesiPKNH_1471200             ---MSSIPYLKNLYPDPSNKLFDDLRICSRVIDSCGIACSSGFVAVPWEVEGGGLIGAIR   57
PyoeliiPY01337                    ---------------DPWNTAFDDLQICTKITESCGIACSSEYIATPWQVQGGGVIGVIK   45
PbergheiPBANKA_1464100.           --MVNDVPCIKNLYSDPWNSGFDDLRICTRITESCGIACSSEYIATPWQVQGGGVIGVIK   58
PchabaudiPCHAS_1466400            --MVNDIPCIKNLYSDQWNTAFDDLQICTRITESCGIACSSEYIATPWQVQGGGVIGVIK   58
                                                                  *:*..: ::*.**:* ***::* ::

TgondiiTGME49_216970              LADIGRNPAVAKIKGHTASIQDTNFSPFHRDILATACEDTIVRIWQLPEEVTGTTELKEP   120
PfalciparumPF3D7_1251200          LENQVRNPPVIKLKSHTSPILDLSFNPCYSEILASCSEDMSIRIWEIRHEDENVNEVKDP   117
PgaboniPGSY75_1251200             LENQVRNPPVIKLKSHTSPILDLSFNPCYSEILASCSEDMSIRIWEIRHEDENVNEVKDP   85
PvivaxPVP01_1468300               LENQMRKPPVIKLKGHTSSILDLQFNPCFSEILASGSEDLTIRVWEIPHNDESVKEIKDP   117
PcoatneyiPCOAH_00051520           LENQMRKPPVIKLKGHTSSIQDLQFNPCFSEILASGSEDLTVRVWEIPHNDESVKEIKDP   117
PknowlesiPKNH_1471200             LENQMRKPPVIKLKGHTSSILDLQFNPCFSEILASGSEDLTVRVWEIPHNDESVKEIKDP   117
PyoeliiPY01337                    LENMCRNPPVYKLKGHTSTILDIQFNPCYSEVIASSSEDMSIRIWEVCNKEDISEEIKNS   105
PbergheiPBANKA_1464100            LENMYRNPPVYKLKGHTSNILDIQFNPCYSEVIASSSEDMSIRIWEVCNKEDKSEEIKNS   118
PchabaudiPCHAS_1466400            LENMYRNPPVYKLKGHTSNILDIQFNPCYNEVIASSSEDMSIRIWEVCNKEDKSEEIKKS   118
                                  * :  *:* * *:*.**: * * .*.* . :::*: .**  :*:*:: .:     *:*.

TgondiiTGME49_216970              IATLTGALKKVLSAEWNPAVSGILASGCFDGTVAFWNVEKNENFASVKFQESLLSAKWSW   180
PfalciparumPF3D7_1251200          LCILNGHKKKVNILSWNPMNYFILSSTSFDSSVNIWDIENEKKAFEINMPKKLSSLQWDI   177
PgaboniPGSY75_1251200             LCILNGHKKKVNIISWNPMNYFILSSTSFDSSVNIWDIENEKKAFEINMPKKLSSLQWDI   145
PvivaxPVP01_1468300               QCILKGHKKKISIIDWNPMNYYIMCSSGFDSFVNIWDIENEKRAFQIIMPKKLSSLKWNV   177
PcoatneyiPCOAH_00051520           QCILKGHKKKISIIDWNPMNYYIMCSSGFDSFVNIWDIENEKRAFQIIMPKKLSSLKWNV   177
PknowlesiPKNH_1471200             QCILKGHKKKISIIDWNPMNYYIMCSSGFDSFVNIWDIENEKRAFQIVMPKKLSSLKWNI   177
PyoeliiPY01337                    LCVLKGHKKKVTIIDWNPLNYYILSSSGFDSNVNIWDIENEKKAFNINMPQKLTSLKWNS   165
PbergheiPBANKA_1464100            LCILKGHKKKVTIIDWNPLSYYILCSSSFDSTVNIWDIENEKKAFSINMPQKLTSLKWNS   178
PchabaudiPCHAS_1466400            LCILNGHKKKVTIIDWNPLNYYILSSSSFDSTVNIWDIENEKKAFNISMPQKLTSLKWNN   178
                                   . *.*  **:   .***    *:.*  **. * :*::*:::.  .: : :.* * :*.

TgondiiTGME49_216970              KGDLLACTTKDKALNIVDPRAAQVVGSVACHDGSKACKCTWIDGLAGRDGHVFTTGFGKM   240
PfalciparumPF3D7_1251200          GGNLLSGTCQNKQIHIIDPRKQEICNSFLIHDGGKSTKCIWIDGFGGEDKCILTTGFSKN   237
PgaboniPGSY75_1251200             TGNLLSGTCQNKQIHIIDPRKQEICNSFLIHDGGKSTKCIWIDGFGGEDKCILTTGFSKN   205
PvivaxPVP01_1468300               KGSLLSGTCVGKHMHIIDPRKKEIASSFHIHNGGKNTKNIWVDGLGGDENYILSTGFSKN   237
PcoatneyiPCOAH_00051520           KGNLLSGTCVGKHMHIIDPRKKEIASSFHIHSGGKNTKNIWIDGLGGDDNYILSTGFSKN   237
PknowlesiPKNH_1471200             KGNLLSGTCVGKHMHIIDPRKREIASSFHIHSGGKNTKNIWIDGLGGDDNYILSTGFSKN   237
PyoeliiPY01337                    IGTLLSATCLNKKLHIIDPRQEKICTTFNGHSGGKCAKNIWIDGYSGNENYILSTGFSKN   225
PbergheiPBANKA_1464100            SGALLSATCLNKKLHIIDPRQEKICTTFNAHSGSKCAKNIWIDGYSGNENYILSTGFSKN   238
PchabaudiPCHAS_1466400            TGTLLTATCLNKKLHIIDPRQEKICTSFVGHTGGKCAKNIWIDGYSGNENYILSTGFSKN   238
                                   * **: *  .* ::*:***  ::  :.  * *.*  *  *:** .* :  :::***.*

TgondiiTGME49_216970              QEREMAIWDTRKFDKPVYHAEIDRGSSPLYPIFDETTGMLYVCGKGDSSCRYYQYHGGTL   300
PfalciparumPF3D7_1251200          NMRELKLWSLKNTTSPLTTITLDNAASPLLPHYDESVGMIYLIGKGDGNCRYYQYSQGSI   297
PgaboniPGSY75_1251200             NMRELKLWSLKNTTSPLTTITLDNAAAPLLPHYDESVGMIYLIGKGDGNCRYYQYSHGSM   265
PvivaxPVP01_1468300               NLREMKLWDLKNTSSALVTMSIDNASAPLIPHYDESTGLIYVIGKGDGNCRYYQHSLGSI   297
PcoatneyiPCOAH_00051520           NLREMKLWDLKNTTSALVTMSIDNASAPLIPHYDESTGLIYIIGKGDGNCRYYQHSLGSL   297
PknowlesiPKNH_1471200             NFREMKLWDLRNTTSALVTMSIDNASAPLIPHYDESTGLIYIIGKGDGNCRYYQHSLGSI   297
PyoeliiPY01337                    YMREMKLWDLKNISEPIYTISIDNASAPLLPHYDESIGIIYIIGKGDGNCRYYQHSEGVL   285
PbergheiPBANKA_1464100            YMREMKLWDLKNISDPLCTISIDNASAPLLPHYDESIGIIYIIGKGDGNCRYYQNSEGVL   298
PchabaudiPCHAS_1466400            YMREIKLWDLKNISDPISTISIDNASAPLLPHYDESIGIIYVIGKGDGNCRYYQHSEGVL   298
                                    **: :*. ::  . :    :*..::** * :**: *::*: ****..*****   * :

TgondiiTGME49_216970              RSVDAYRSSVPIKNFCFIPKLAVDQMRAEIGRMLKQENGNVLQPISFIVPRKNQDVFQAD   360
PfalciparumPF3D7_1251200          RKVDEYKSCLPFRSFGFLPKRMCDVYKCEIGRVYKNENNTDIRPISFYVPRKNSSIFQED   357
PgaboniPGSY75_1251200             RKVDEYKSCLPFRSFGFLPKRMCDVYKCEIGRVYKNENNTNIRPISFYVPRKNSSIFQED   325
PvivaxPVP01_1468300               RKVNEYKSCSPFRSFGFLPKQICDVYKCEIGRVYKNENNSSIRPISFYVPRKNPTKFQED   357
PcoatneyiPCOAH_00051520           RKVNEYKSCSPFRSFGFLPKQICDVYKCEIGRVYKNENNSSIRPISFYVPRKNPTKFQED   357
PknowlesiPKNH_1471200             RKVNEYKSCSPFRSFGFLPKQICDVYKCEIGRVYKNENNSSIRPISFYVPRKNPTKFQED   357
PyoeliiPY01337                    RKINEYKSCLPFKSFGFIPKQACNIYKCEIGRIYKNENDKNIKPISFYVPRKNPNIFQKD   345
PbergheiPBANKA_1464100            RKINEYKSCLPFKSFGFLPKQVCNIYKCEIGRIYKNENDKSIKPISFYVPRKNPNIFQED   358
PchabaudiPCHAS_1466400            RKINEYKSCLPFKSFGFLPKQVCNIYKCEIGRIYKNENNKSIKPISFYVPRKNPNIFQED   358
                                  *.:: *:*. *::.* *:**   :  :.****: *:**.. ::**** *****   ** *

TgondiiTGME49_216970              LYPPAPDVEPSMTAEEWFKGENKAIRRRSVKPGDVVSAQPRRMTVDTACVAAVAQAHGAA   420
PfalciparumPF3D7_1251200          LYPPIIMRDPERSTNKWIDGINLDIKRVSIKDLTEDDLL---ITKKFKQ---LPK----E   407
PgaboniPGSY75_1251200             LYPPIIMRDPEYNTNKWTDGINLDIKRVSIKDLTEDDLL---ITRKFKQ---VPK----S   375
PvivaxPVP01_1468300               LYPPILMHDPDSSSRNWINGKDNKMERINVKDLTQDDLR---ITKKYKF---VPQ----S   407
PcoatneyiPCOAH_00051520           LYPPILLHDPDNSSKNWINGKDNKMDRINIKDLTQDDLR---ITKKYKY---VPQ----S   407
PknowlesiPKNH_1471200             LYPPILLHDPENSSRNWIKGKDNKMSRINIKDLTEDDLR---ITKKYKF---VPQ----S   407
PyoeliiPY01337                    LYPPIIMHDPNYSSKSWINGNNLEIKRININELTDDDIK---IKKKFKS---VPK----S   395
PbergheiPBANKA_1464100            LYPPIIMHDPNYSSKSWINGNNLEIKRIYIKELTDDNIK---IKKKFKS---VPK----S   408
PchabaudiPCHAS_1466400            LYPPIIKHDPNYSSKSWINGNNLEITRINIKDLTDADIK---IYKKFKT---VPK----S   408
                                  ****    :*. .:..* .* :  : *  ::     .     :  .      : :
```

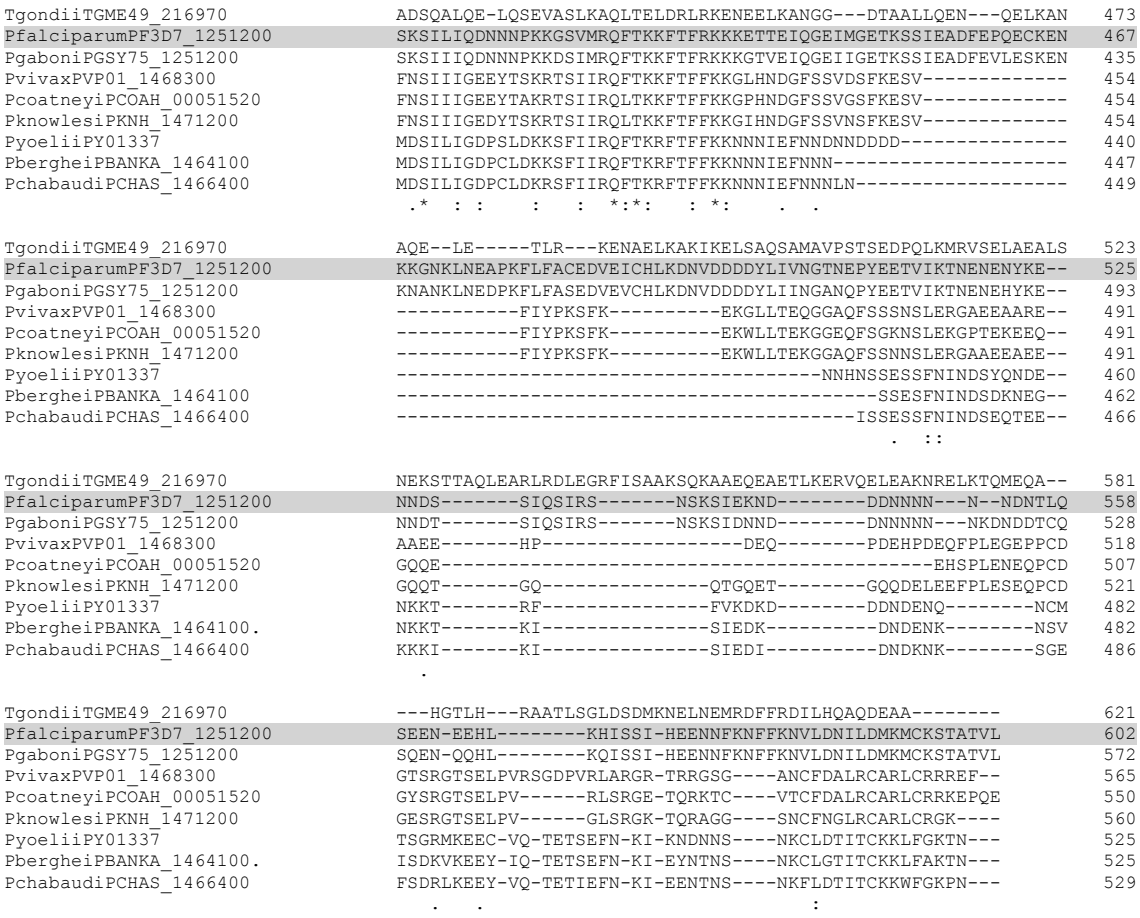

Fig. S8. Multiple sequence alignment of Coronin protein sequences from several *Plasmodium* species and *Toxoplasma gondii*. Highlighted in grey is the *Plasmodium falciparum* Coronin full amino acid sequence and highlighted in yellow are G50, R100 and E107 residues, which were found to be mutated in the DHA selected Senegalese parasites Thiès_R and Pikine_R. Analyses were done using the Clustal Omega multiple sequence alignment tool through EMBL.

Table S1. Summary of RSA values for all parasite lines

Parasite line	**RSA survival (%)**	**Standard error of measurement (SEM)**
Pikine19.04 (parent)	0.99	0.26
Pikine_R (8 cycles)	7.18	0.80
Pikine_R (13 cycles)	7.83	0.98
Pikine19.04 (parent)	0.55	0.08
Pikine CRISPR F4 (R100K, E107V)	6.75	0.91
Pikine CRISPR F5 (R100K, E107V)	9.35	1.09
Thiès32.09 (parent)	0.78	0.16
Thiès_R (8 cycles)	8.16	0.76
Thiès_R (13 cycles)	7.62	1.46
Thiès32.09 (parent)	0.48	0.09
Thiès CRISPR D4 (G50E)	5.22	1.38
Thiès CRISPR E4 (G50E)	5.30	0.72

Table S2. PCR resequencing primers to amplify candidate genes and *Pfkelch13* (PF3D7_1343700). For mutagenesis primers, shield mutations are highlighted in green and targeted mutation(s) are highlighted in red.

Primer target	Primer name	Sequence 5'-3'
PF3D7_1343700	kelch13 Fwd1	ATGGAAGGAGAAAAAGTAAAAACAAAAGC
PF3D7_1343700	kelch13 Rev1	ACGGTTTTCTAATTCTTTGTACAATCGTAC
PF3D7_1343700	kelch13 Fwd2	GAAACGGAATTAAGTGATGCTAGTGA
PF3D7_1343700	kelch13 Rev2	CCAGCATTGTTGACTAATATCTAATAATTCCA
PF3D7_1343700	kelch13 Fwd3	CATTCCCATTAGTATTTTGTATAGGTGGAT
PF3D7_1343700	kelch13 Rev3	TTATATATTTGCTATTAAAACGGAGTGACCAA
PF3D7_1251200	coronin fwd1	ATGTATAATGTTCCTTTAATCAAGA
PF3D7_1251200	coronin rev1	CTTTGGCATATTTATTTCAAAGG
PF3D7_1251200	coronin fwd2	GTGGTATAGCTTGTAGTGCT
PF3D7_1251200	coronin rev2	CTTTAAACTCCATAATTTCAATTCTC
PF3D7_1251200	coronin fwd3	AAGTTCTTTACAATGGGATATCG
PF3D7_1251200	coronin rev3	CTGTCTCATGACAGAACCCT
PF3D7_1251200	coronin fwd4	GATTTATATCCTCCTATTATTATGAG
PF3D7_1251200	coronin rev4	TACCGTTGCTGTACTTTTACAC
PF3D7_1251200	coronin fwd5	GAGCTCAAGCTTGTATAGCTTGTAGTGCTGGATATATTG
PF3D7_1251200	coronin rev5	GAGCTCAAGCTTGGATTCCATGATAATATATTTACTTTTTTCTTATG
PF3D7_1251200	coronin mutfw1	gGTACCATGGCAAGTTGAGGGTGAAGGAATGATCGGAGTTATC
PF3D7_1251200	coronin mutrv1	CTGATAACTCCGATCATTCCTTCACCCTCAACTTGCCATGGTAC
PF3D7_1251200	coronin fwd6	GGTGCGCTTTAAAGATTAATTC
PF3D7_1251200	coronin rev6	CAGAAGAATCAAAAGAGGTAGATG
PF3D7_1251200	coronin seq1	CCTCATTCACATTCTCATCCTCATG
PF3D7_1251200	coronin fwd7	GAGCTGCTAGCGGTGCGCTTTAAAGATTAATTC
PF3D7_1251200	coronin rev7	GAGCTCAAGCTTCTGACAAGTTCCACTTAATAAATTAC
PF3D7_1251200	coronin mutfw2	GTCTATAAAAATATGGGAGATTCGACATGTGGATGAGAATGTG

PF3D7_1251200	coronin mutrv2	CTCATTCACATTCTCATCCACATGTCGAATCTC CCATATTTTTATAG
PF3D7_1251200	coronin fwd8	GAAATCCCCCTGTAATAAAATTG
PF3D7_1251200	coronin rev8	CTTGTTTTCTAGGATCTATTATATGTATCTG
PF3D7_1251200	coronin seq2	CCACCGATATCCCATTGTAAAGAAC
PF3D7_0209600	PF3D7_0209600 fwd	GTACTATATATTGGAAATATAGAAACC
PF3D7_0209600	PF3D7_0209600 rev	ATGGGAAAAGAAACAATAGGAGC
PF3D7_1126100	ATG7 fwd	CAAAGGTAATGGATATACCTATGC
PF3D7_1126100	ATG7 rev	TGCTACCGTAATACCTAAAGGAG
PF3D7_1433800	PF3D7_1433800 SNP1 fwd	CCATACAAATGTCAAAATATAACAAACC
PF3D7_1433800	PF3D7_1433800 SNP1 rev	CTAGTTGCACGATTTTGATAATTTCC
PF3D7_1433800	PF3D7_1433800 SNP2 fwd	GATGAATAATAATATGTTTTATGATAATGG
PF3D7_1433800	PF3D7_1433800 SNP2 rev	AACTGATAATAATTTAAATGATGTTGG
PF3D7_1121900	PF3D7_1121900 fwd	GATCAAAATTCAAACAAATGCGTTCTAG
PF3D7_1121900	PF3D7_1121900 rev	CTGTTGAACCATCAAATGGAACGG
PF3D7_1324300	PF3D7_1324300 fwd	AGTTCAGTTGTTATCATGTTC
PF3D7_1324300	PF3D7_1324300 rev	TGGCACATTCTTCGTTTTCC
PF3D7_1422400	PF3D7_1422400 fwd	CGTTTACCATGAGTTATGTACATCAAG
PF3D7_1422400	PF3D7_1422400 rev	ACACGGAACAATAAATATTTCTGTACTC