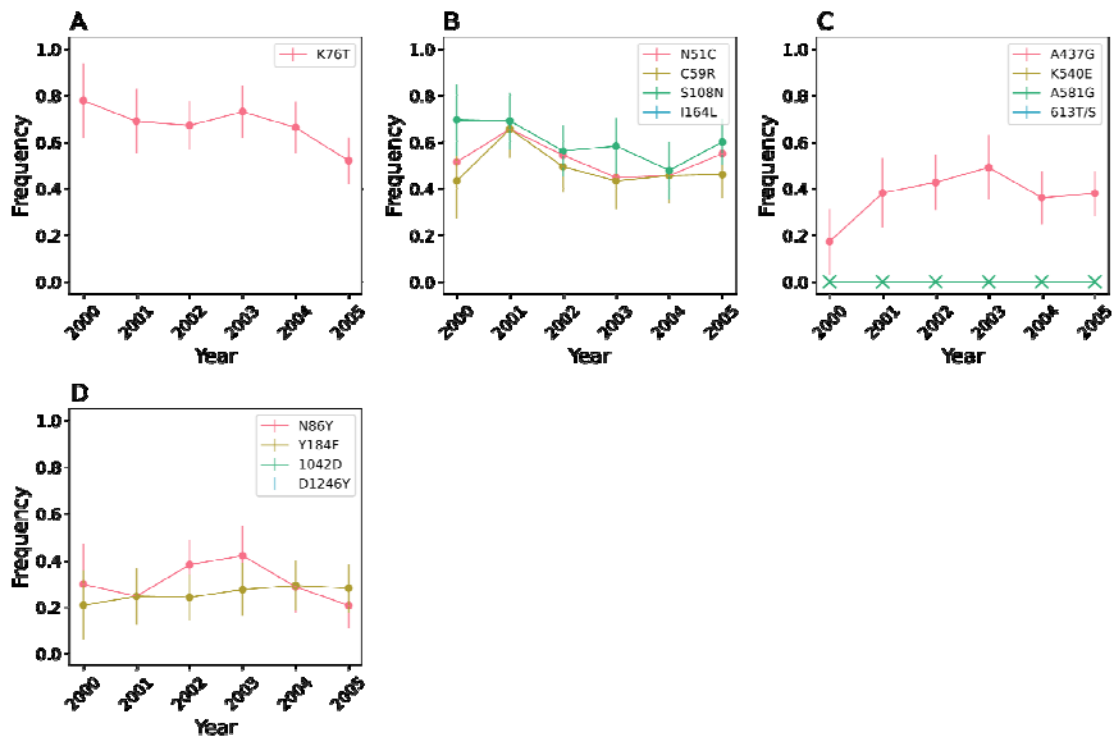527 **Supplemental Figures**

528

529 **Fig S1**. **Sample sizes for SNP-based molecular surveillance.** Sample size per year per

530 region for the SNP-based molecular surveillance.

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532

533 **Fig S2. SNP-based molecular surveillance in Pikine** for **A**) Pfcrt, **B**) *Pfdhfr*, **C**) *Pfdhps* and

534 **D**) Pfmdr1. The *Pfkelch13* SNPs were not examined in Pikine. Error bars indicate two

535 binomial standard deviations from the mean. X's denote years where samples were collected

536 but the mutation was not observed. Gaps in the data were because samples were not

537 collected for that year.
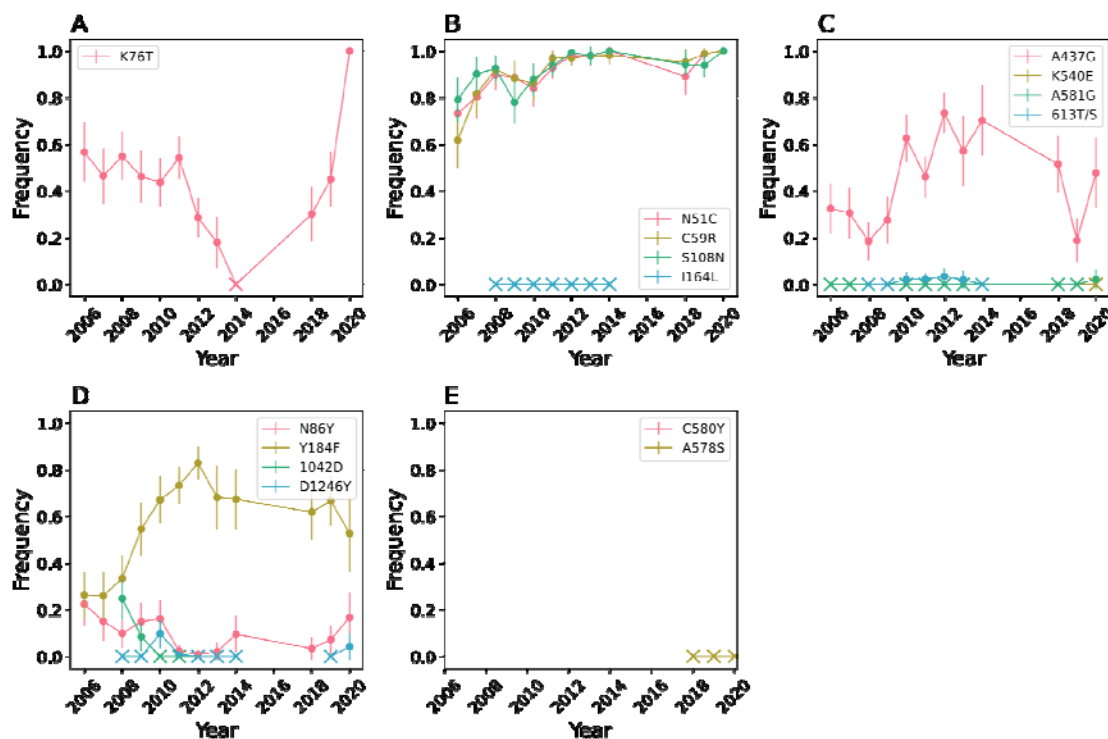
538

539 **Fig S3. SNP-based molecular surveillance in Thies** for **A**) Pfcrt, **B**) *Pfdhfr*, **C**) *Pfdhps* and

540 **D**) Pfmdr1, and **E**) *Pfkelch13*. Error bars indicate two binomial standard deviations from the

541 mean. X's denote years where samples were collected but the mutation was not observed.

542 Gaps in the data were because samples were not collected for that year.

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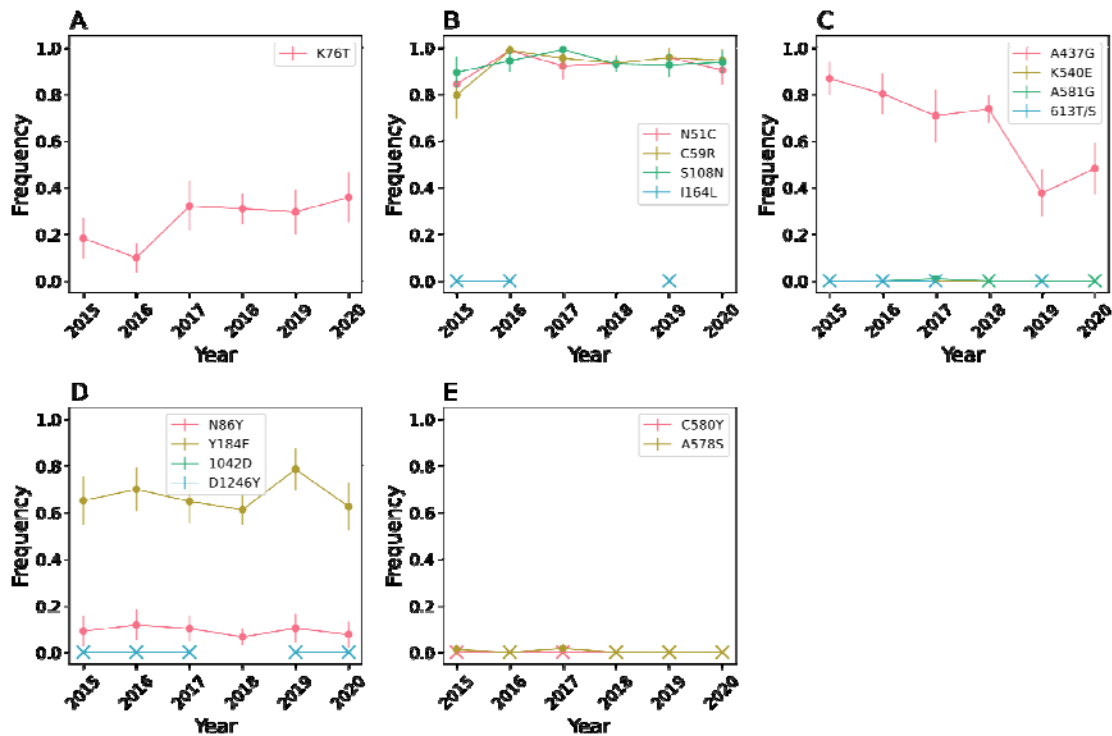
Fig S4. SNP-based molecular surveillance in Kedougou for **A**) Pfcrt, **B**) *Pfdhfr*, **C**)

Pfdhps, **D**) Pfmdr1, and **E**) *Pfkelch13*. Error bars indicate two binomial standard deviations

from the mean. X's denote years where samples were collected but the mutation was not

observed. Gaps in the data were because samples were either not collected or not

genotyped for that year.

550
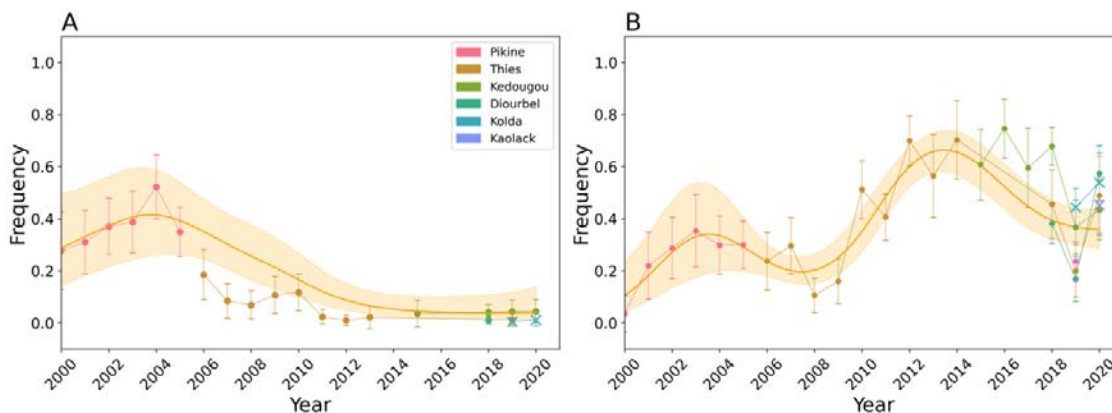
Fig S5. A) Frequency of *Pfdhfr* triple sensitive (N51, C59, S108) parasites. **B**) Frequency of

"quadruple" (*Pfdhfr* triple mutant + *Pfdhps* A437G) parasites. The scatterplots show the

observed frequencies and their 95% binomial confidence interval. Model predictions from a

calibrated generalized additive model and the 95% confidence intervals are shown in orange.

The model was calibrated with data from Pikine, Thiès, Diourbel, and Kedougou (denoted

556   with circles). The data from Kolda and Kaolack (denoted with X) were not used for model
557   calibration.
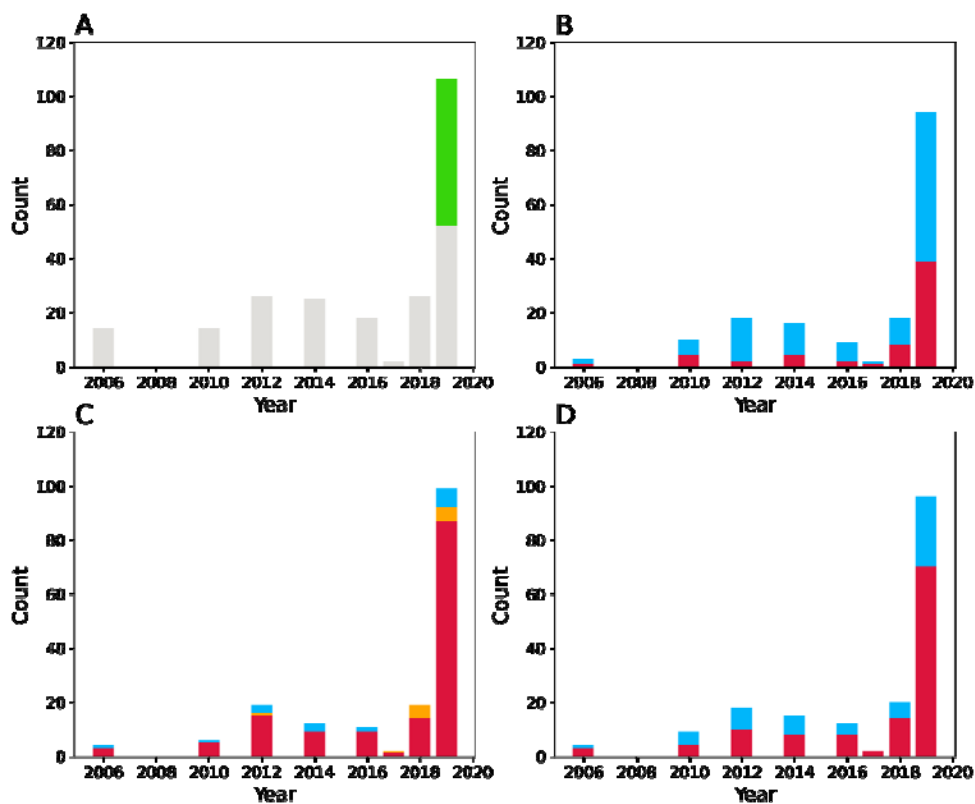
558
559   **Fig S6 Sampling distribution for our whole genome sequence collection** (**A**). Grey
560   indicates the sample came from Thiès. Green indicates the sample came from Kedougou.
561   Sampling distributions for **B**) the *Pfcrt* genomic region, **C**) the *Pfdhfr* genomic region, and **D**)
562   the *Pfdhps* genomic regions. For **B** and **D**, blue denotes samples with the sensitive allele and
563   red indicates those with the resistance allele. For **C**, red denotes samples that are *Pfdhfr*
564   triple mutant, blue indicates those that are *Pfdhfr* triple sensitive, and orange indicates those
565   with a mix of resistant and sensitive alleles at the three examined *Pfdhfr* loci.
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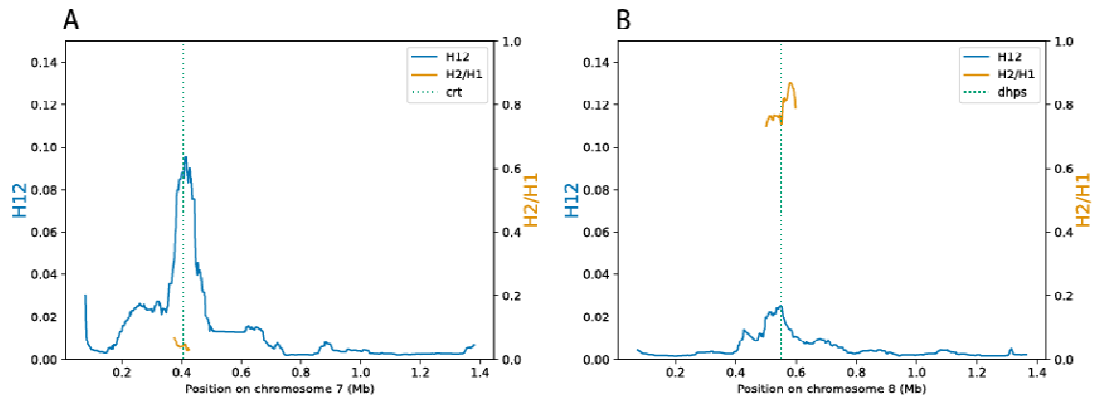
569 **Fig S7 Evidence of Hard and Soft Sweeps** H12 (*blue*, left y-axis) and H2/H1 (*orange*, right
570 y-axis) statistics for **A**) chromosome 7 and **B**) chromosome 8. The dotted green lines show
571 the location of *Pfcrt* or *Pfdhps*.

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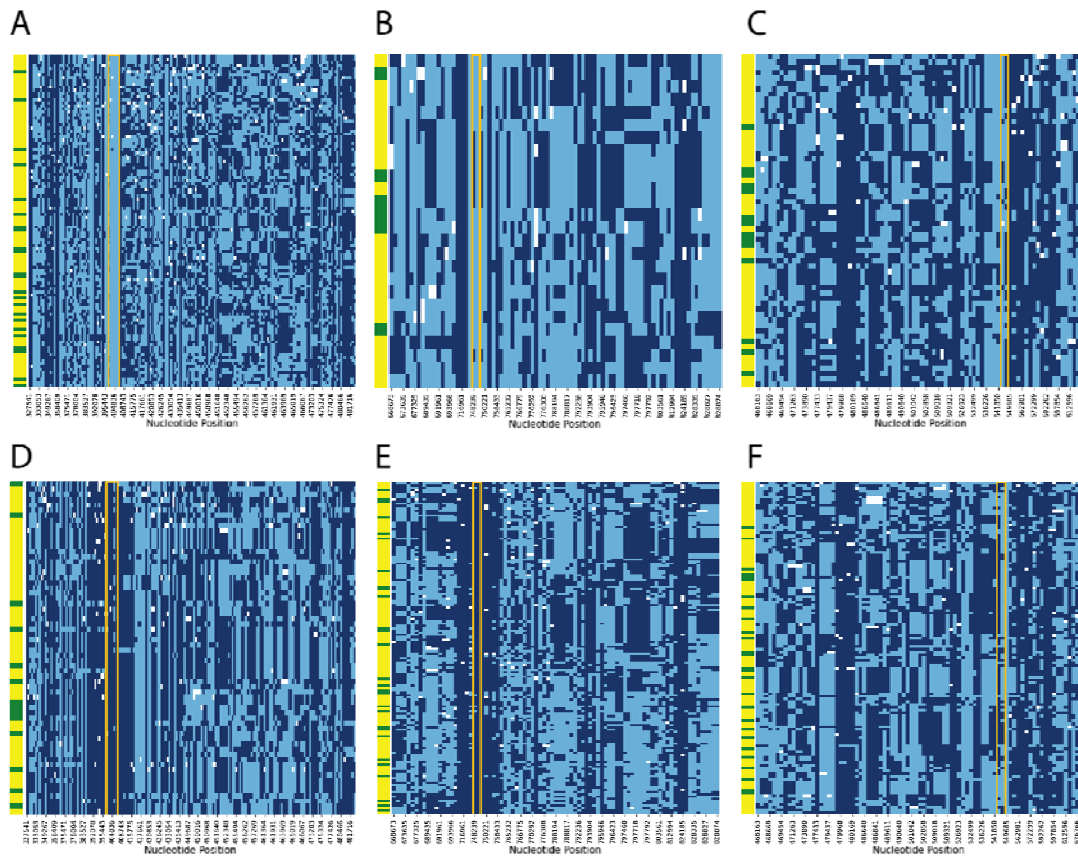
574 **Fig S8. SNPs used to define genomic haplotypes.** Genomic haplotypes surrounding the

575 wild-type mutations: **A**) *Pfcrt* K76, **B**) *Pfdhfr* C59, **C**) *Pfdhps* A437 and the drug resistance

576 mutations: **D**) *Pfcrt* K76T, **E**) *Pfdhfr* C59R, **F**) *Pfdhps* A437G. Each row represents a sample.

577 The left most column indicates whether the sample was collected before 2014 (*green*) or

578   after 2014 (*yellow*). Alleles corresponding to the 3D7 reference are indicated by *light blue*

579   and alleles corresponding to the alternative allele are indicated by *dark blue*. White

580   corresponds to missing data. The orange boxes highlight the boundaries of the *Pfcrt* (**A/D**),

581   *Pfdhfr* (**B/E**), and *Pfdhps* (**C/F**) genes,

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