

Additional file 1

Fig. S1

Schematic highlighting the main steps in the *Malaria-Profiler* pipeline. The first step entails finding k-mers that are species specific using *kmc* software. The second step maps the reads to the reference genome using either *BWA-mem* software for Illumina or the *minimap2* tool for ONT and stores the alignments in a bam file. Additionally, Illumina reads are first trimmed using *trimmomatic* software. The third step calls variants from the bam alignment file using *freebayes* software. These are then compared to known resistance variants to predict drug resistance. Orange icons indicate files, blue icons indicate software processes and green icons indicate databases.

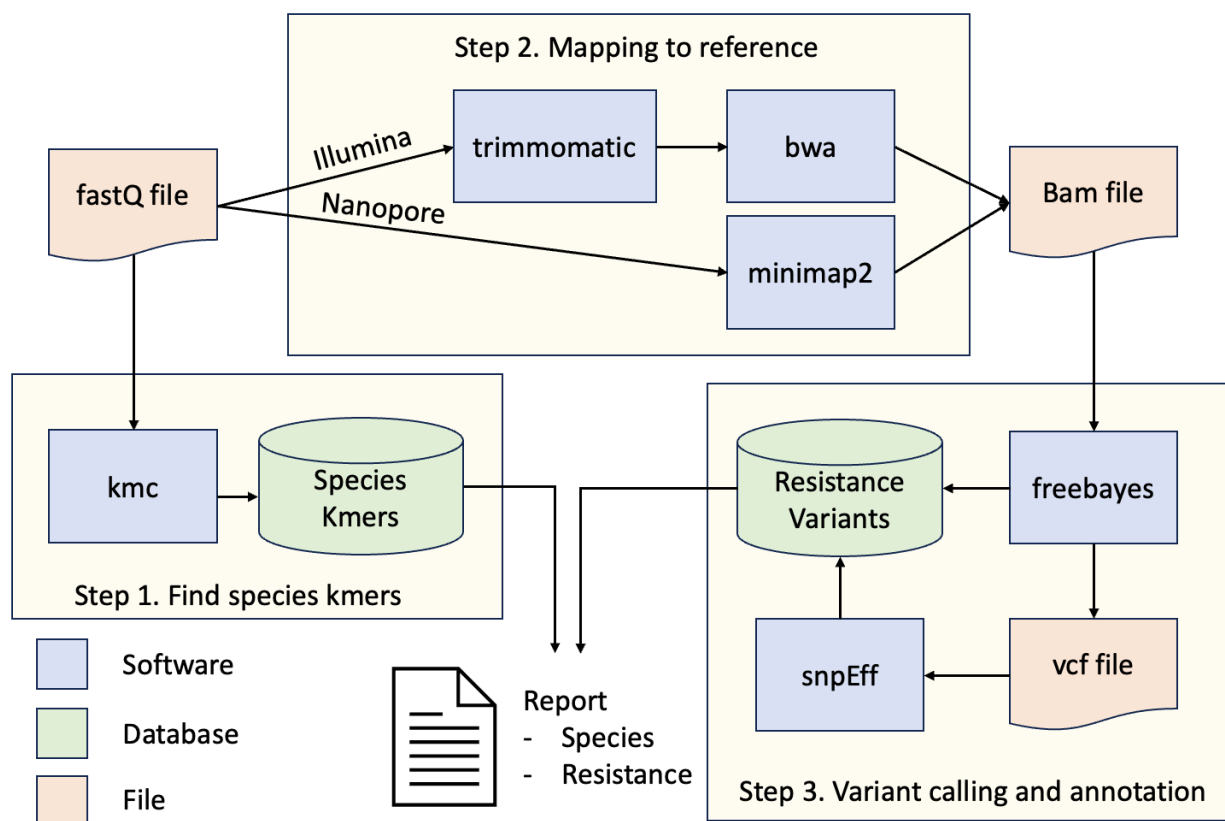


Fig. S2

Malaria-Profiler tool

(a) The website for data input (bioinformatics.lshtm.ac.uk/malaria-profiler)

bioinformatics.lshtm.ac.uk/malaria-
bioinformatics.lshtm.ac.uk/malaria-profiler/analysis

Malaria-Profiler Analysis Results

IMPORT DATA FILE

FOR THE ANALYSIS YOU CAN UPLOAD MULTIPLE FASTQ OR BAM FILES BELOW. IN THE SINGLE RUN ALL UPLOADED DATA SHOULD BE FROM THE SAME PLATFORM - ILLUMINA OR NANOPORE. DURING UPLOAD, EACH SAMPLE WILL BE ASSIGNED A UNIQUE RESULT ID THAT IS REQUIRED TO RETRIEVE THE CORRESPONDING RESULT. AFTER SUBMITTING, LOGFILE WITH ALL RESULT IDS AND SAMPLE NAME PAIRS WILL BE AUTOMATICALLY DOWNLOADED.

PLEASE DROP YOUR FILES IN HERE AND CLICK SUBMIT WHEN DONE.

☒ Illumina ☐ Nanopore

Plasmodium falciparum

SUBMIT

(b) Example of an isolate from a traveller diagnosed and treated with malaria in Europe, sequenced on Oxford Nanopore Technology (ONT), and determined to be from Africa and resistant to Sulfadoxine and Pyrimethamine (SP) (accession no. ERR11254083).

bioinformatics.lshtm.ac.uk/malaria-
bioinformatics.lshtm.ac.uk/malaria-profiler/result/ce99b2c8-228a-43e0-be65-1f0e693f15de

Malaria-Profiler Analysis Results

Species

Plasmodium falciparum

Mean kmer coverage	Standard dev
371	53.99

Genomic variants

Resistance report

Drug	Mutations
Chloroquine	
Mefloquine	
Pyrimethamine	DHFR-TS p.Asn511le (0.92), DHFR-TS p.Ser108Asn (0.99)
Sulfadoxine	PPPK-DHPS p.Ala437Gly (0.99), PPPK-DHPS p.Lys540Glu (0.98)
Artemisinin	

RESISTANCE REPORT OTHER VARIANTS MISSING POSITIONS

SHOW MORE INFO

Estimated Region of Origin

Africa

Analysis

Analysis	Program
Kmer counting	kmc
Mapping	minimap2
Variant calling	freebayes

Coverage report

Gene	Locus Tag	Cutoff	Fraction
MDR1	PF3D7_052300	0	0.0

SEE ALL