

Figure S1: Flow chart describing the bioinformatic pipeline of analysis from raw sequencing reads to variant calling.

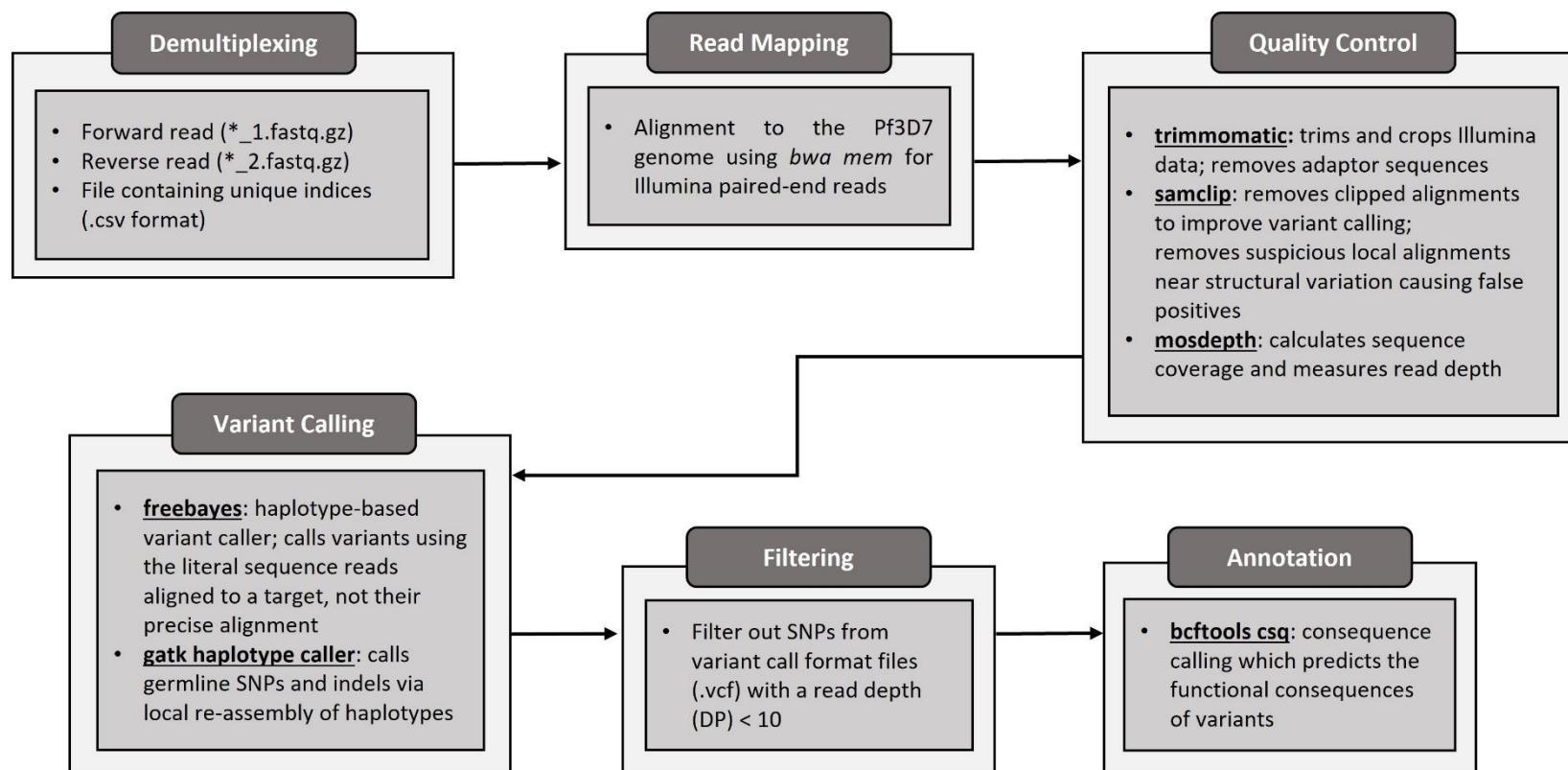


Table S1: Read depth of sequencing reads across the 5 sequenced resistance genes ($n = 70$).

Gene	Median	Max
<i>Pfcrt</i>	155	471
<i>Pfmdr1</i>	69	3962
<i>Pfdhps</i>	103	2793
<i>Pfdhfr</i>	126	2604
<i>Pfk13</i>	1760	31280

Table S2: Primers used for the amplification of amplicons on *Pfcrt*, *Pfmdr1*, *Pfdhps*, *Pfdhfr*, and *Pfk13*. (PCR reaction; S = simplex reaction, M = Multiplex reaction).

Amplicon name	Gene ID	Primer Sequence	PCR reaction
<i>Pfcrt</i>	PF3D7_0709000	Forward: TCTTGTCTTGGTAAATGTGCTCA	S1
		Reverse: AGGCCAAAATGACTGAACAGG	
<i>Pfmdr1.1</i>	PF3D7_0523000	Forward: CGTTTAAATGTTTACCTGCACAAC	M1
		Reverse: TGACACCACAAACATAAATTAACGG	
<i>Pfmdr1.7</i>	PF3D7_0523000	Forward: TTTGTCCAATTGTTGCAGCTGTATTAAC TTT	M4
		Reverse: TGCATTTTCTGAATCTCCTTTTAAGGACATT	
<i>Pfmdr1.8</i>	PF3D7_0523000	Forward: GGTAAGTTGATATTAAGATGTAAATTTCC	M3
		Reverse: TGGTCCAACATTTGTATCATATTTATTTGG	
<i>Pfdhfr</i>	PF3D7_0417200	Forward: ATGATGGAACAAGTCTGCGACGTTTTTCGA	M2
		Reverse: CTAAAAATTCTTGATAAACAACGGAACCTCC	
<i>Pfdhps.3</i>	PF3D7_0810800	Forward: ACCATCAGATGTTTATATAACAAATATGTG	M3
		Reverse: CTGGATTATTTGTACAAGCACTAATATCA	
<i>Pfdhps.4</i>	PF3D7_0810800	Forward: AGAATGTGTTGATAATGATTTAGTTGATAT	M4
		Reverse: GATATAAAAGTTGATCCTTGTCTTTCT	
<i>PfK13.4</i>	PF3D7_1343700	Forward: TAAGTGGAAGACATCATGTAACCAGAGA	M2
		Reverse: CTTCTACATTCGGTATAATAGAAGAGCC	
<i>PfK13.5</i>	PF3D7_1343700	Forward: ATGATGGCTCTTCTATTATACCGAATG	M1
		Reverse: GCTATTAACCGGAGTGACCAAATCTG	