Exploring the potential of adaptive sampling for *Plasmodium* WGS from blood samples

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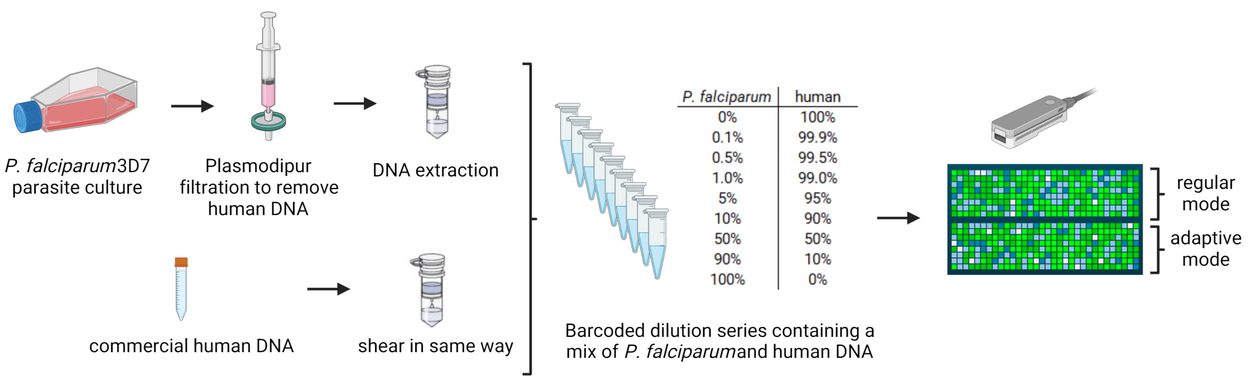
Adaptive sampling has the potential to replace more time-consuming protocols for *Plasmodium* WGS

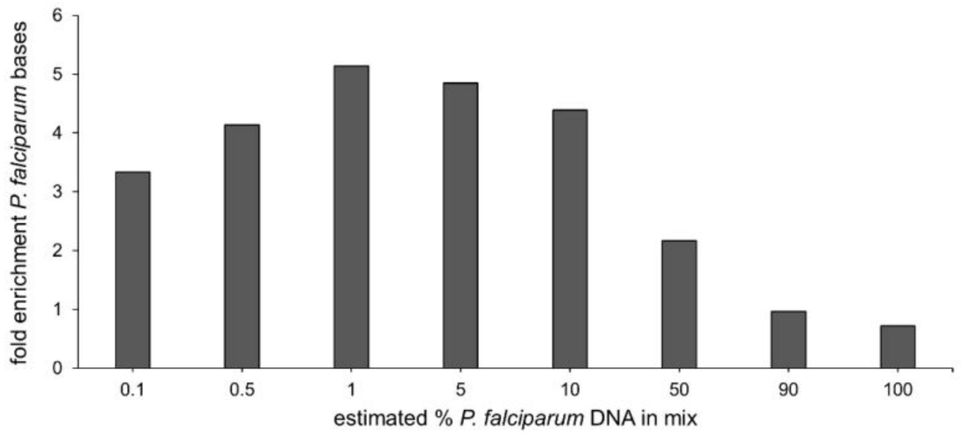
Whole-genome sequencing (WGS) of *Plasmodium* parasites from human blood currently requires **time-consuming lab procedures** to filter out human DNA or enrich *Plasmodium* DNA. We investigated the potential of adaptive sampling to enrich for *Plasmodium* DNA while sequencing unenriched blood samples on a minION device.

Pilot experiment on a dilution series (Kit 12)

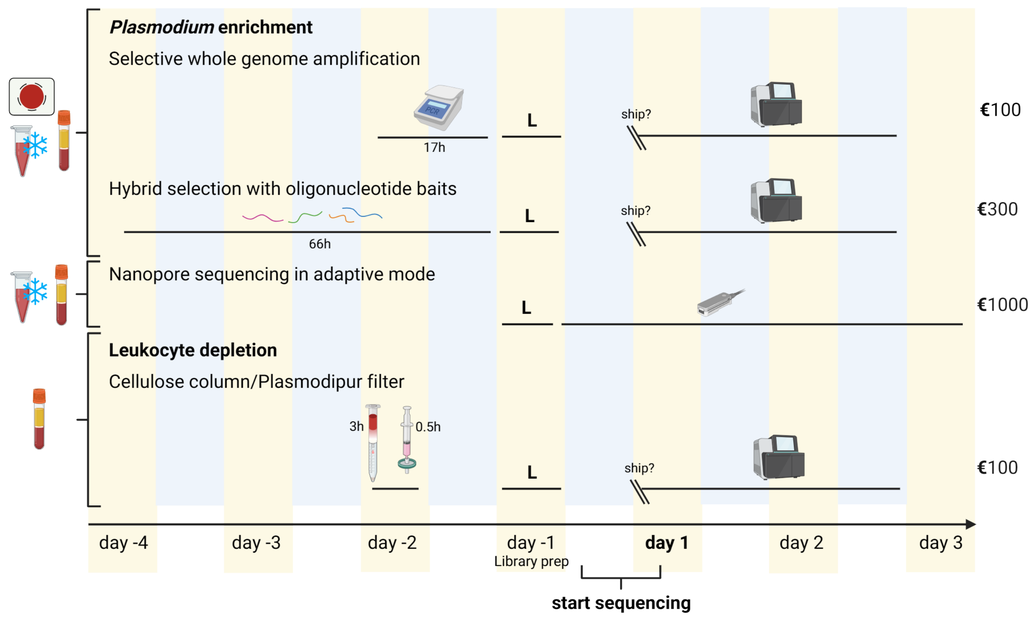


P. falciparum	human
0%	100%
0.1%	99.9%
0.5%	99.5%
1.0%	99.0%
5%	95%
10%	90%
50%	50%
90%	10%
100%	0%

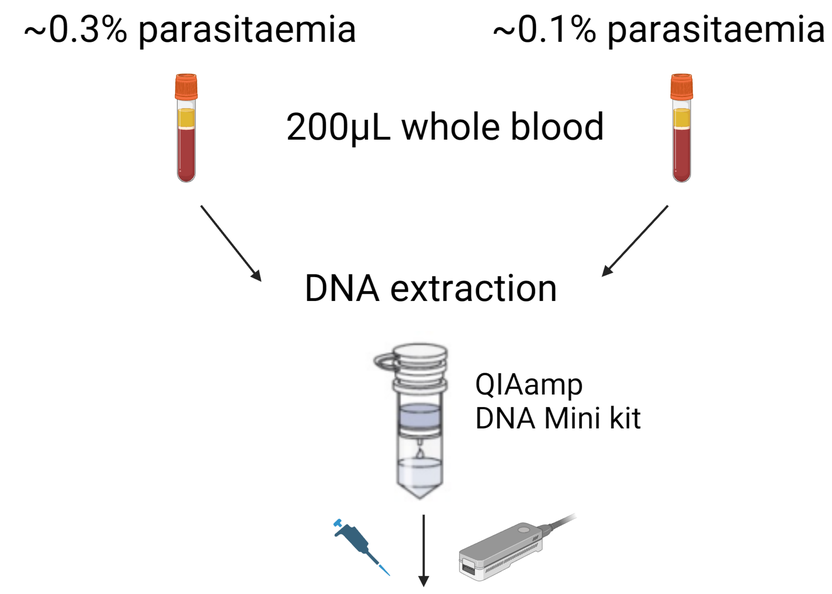
Mean 2.7 fold enrichment of *P. falciparum* bases



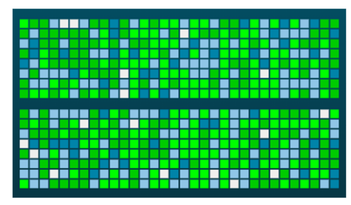
Faster compared to existing but cheaper methods



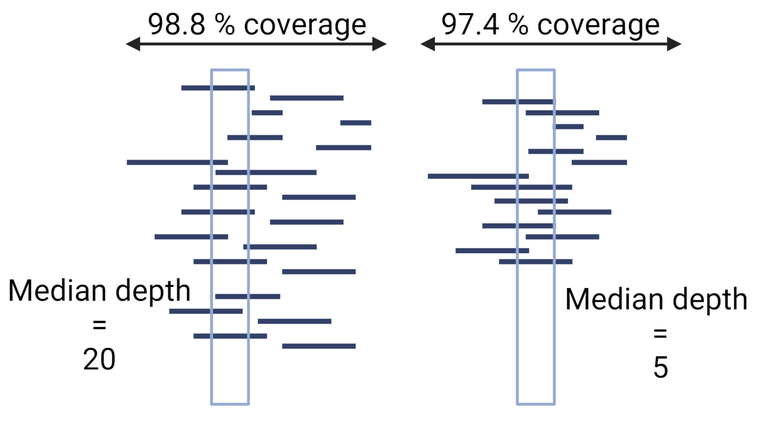
Direct sequencing of two blood samples (Kit 14)



Sequencing in adaptive sampling mode



Competitive read mapping



Resistance SNPs
-> high concordance with Sanger seq

Draft assembly

Complete assembly
-> 138 & 198 contigs were obtained

Conclusion

Nanopore sequencing in adaptive sampling mode has the potential to replace more time-consuming *Plasmodium*-enrichment protocols and to enable sequencing directly from patient blood, as improvements emerge to increase cost-efficiency.

Disclaimer