Deep sequencing of *Plasmodium falciparum* genetic crosses: a resource for the study of genome variation and meiotic recombination -  
supplementary information

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# Variant discovery and genotype calling

## Alignment method (BWA/GATK)

@@TODO details of variant discovery, genotyping, filtering etc.

## Assembly method (Cortex)

@@TODO details of variant discovery, genotyping, filtering etc.

# Recombination analyses

## Simulation of crossover recombination

Simple simulations of random crossover recombination were performed to determine the distribution of contiguous inheritance block sizes expected from crossover recombination alone. Inheritance blocks shorter than those expected to arise with any appreciable frequency under crossover recombination alone were then assumed to indicate conversion tracts.

@@TODO results of simulations

# References

Ranford-Cartwright, L. C., & Mwangi, J. M. (2012). Analysis of malaria parasite phenotypes using experimental genetic crosses of Plasmodium falciparum. *International Journal for Parasitology*, *42*(6), 529–34. doi:10.1016/j.ijpara.2012.03.004