

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

Supplementary information

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1. Genome accessibility

@@TODO

2. Variant discovery and genotype calling

2.1. Alignment-based calling method (BWA/GATK)

@@TODO (Li & Durbin, 2009)

2.2. Assembly-based calling method (Cortex)

@@TODO

3. References

Li, H., & Durbin, R. (2009). Fast and accurate short read alignment with Burrows-Wheeler transform. *Bioinformatics (Oxford, England)*, 25(14), 1754–60.
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