To do list for estimation of L1 detection bias

1. Check MELT error message for simulated genomes
2. Check MELT Google group for explanation of error message for simulated genomes
3. Try whether using bwa mem gets rid of error
4. Run L1 simulation analysis for 11 genomes that produced an error
5. Check wgsim parameters to get similar sensitivity as Gardner et al. (2017)
6. Run L1 simulation analysis for 50 genomes with features as in Gardner et al. (2017) or variable difference from consensus L1 to get similar sensitivity as Gardner et al. (2017)
7. Run L1 simulation analysis for additional 50 genomes
8. Try MELT-SGE on simulated genomes
9. Re-run MELT Group on 1000 genome data
10. Run estimation of fitness effect of L1 width for resampled L1 width

Issues for estimation of L1 detection bias

1. Some bam files contain discordant read pairs with MAPQ ≠ 0 (see points I-III above)
2. Sensitivity in simulated genomes is higher than in to get similar sensitivity as Gardner et al. (2017) (see point V above). The length-dependent detection might therefore be underestimated.