

Figure 1: Coverage distribution for different mappers, before (top) and after (bottom) quality filtering (proper pairs and a mapping quality  $\geq 20$ ). Uniformly distributed paired end reads (2x100bp) with an insert size of  $100 \pm 0$ bp and an error rate of 0% were simulated from sequences with SNPs every 100bp, aligned, mpileup files were created and the coverage for each site was obtained from mpileup files.

