



Figure S1: An expanded version of Figure 1 with shaded areas added to represent the standard deviation of the 10 replicate experiments. Comparison of runtime (top) and switch+mismatch error rate (bottom) for HapCUT2 with leading methods for haplotype assembly (HapCUT, RefHap, ProbHap, and FastHare) on simulated read data as a function of (A): mean coverage per variant (variants per read fixed at 4), (B): mean variants per read (mean coverage per variant fixed at 5), (C): mean number of paired-end reads crossing a variant (mean coverage per variant fixed at 5, read length 150 base pairs, random insert size up to a variable maximum value). Lines represent the mean of 10 replicate simulations and shaded regions represent the standard deviation. FastHare is not visible on panel C (bottom) due to error rates 10 to 18 times higher than HapCUT2.