Figure S4: Efficacy of HapCUT2, ProbHap, and RefHaps' post-processing strategies on 11× coverage PacBio SMRT data. (A) Reduction in mismatch error rate by pruning individual low-confidence variants and (B) Reduction in switch error rate by splitting haplotype blocks at possible switch errors (block size represented by the AN50 metric). RefHap is presented as a single point since it does not support variant confidence thresholding or block-splitting.