



Figure S3: Comparison of the performance of HapCUT2 with other tools on NA12878 44x coverage PacBio SMRT data across all chromosomes: (A) Switch error rate, (B) Mismatch rate, (C) Fraction of covered variants pruned, and (D) Runtime in CPU-minutes. Switch and mismatch errors were calculated using the set of phased variants specific to each tool. ProbHap exceeded 20 CPU-hours for some chromosomes.