



Figure S9: Comparison of haplotypes obtained using HapCUT2 on 40x coverage MboI Hi-C reads combined with 10X Genomics linked-reads (34x short-read coverage) to the haplotypes obtained using the two datasets separately: (A) Switch error rate, (B) Mismatch rate, (C) Fraction of covered variants pruned, and (D) Fraction of variants phased in largest block.