



Figure S1. A. Histogram of ratios of C4A read/k-mer counts to total C4 read/k-mer counts, scaled by total C4A and C4B copy, for the C4Investigator and GenomeSTRiP workflows for C4A/C4B discordant samples from the 1000 Genomes Project dataset. B. Histogram of quality scores reported by Genome STRiP for C4A and /C4B concordant (match) and discordant (mismatch) samples from the 1000 Genomes Project dataset.