



Figure S5: Comparison of the h-trans interaction probabilities $\tau(I)$ estimated by HapCUT2 (for chromosomes 1 and 19 of NA12878 using $90\times$ Hi-C data) against probabilities estimated using knowledge of ground truth haplotypes on the same dataset. Raw HapCUT2 probabilities are smoothed with a Savitzky-Golay filter for visualization, and ground truth probabilities are created using 1 Mb bins.