

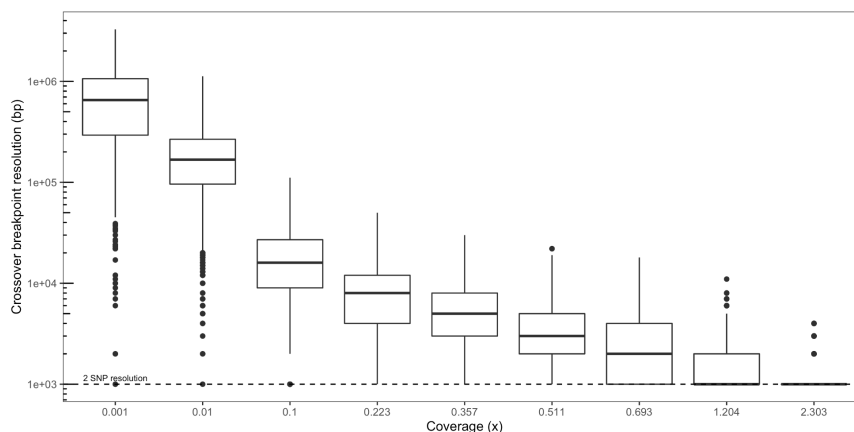
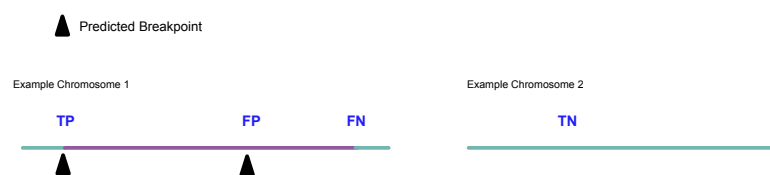
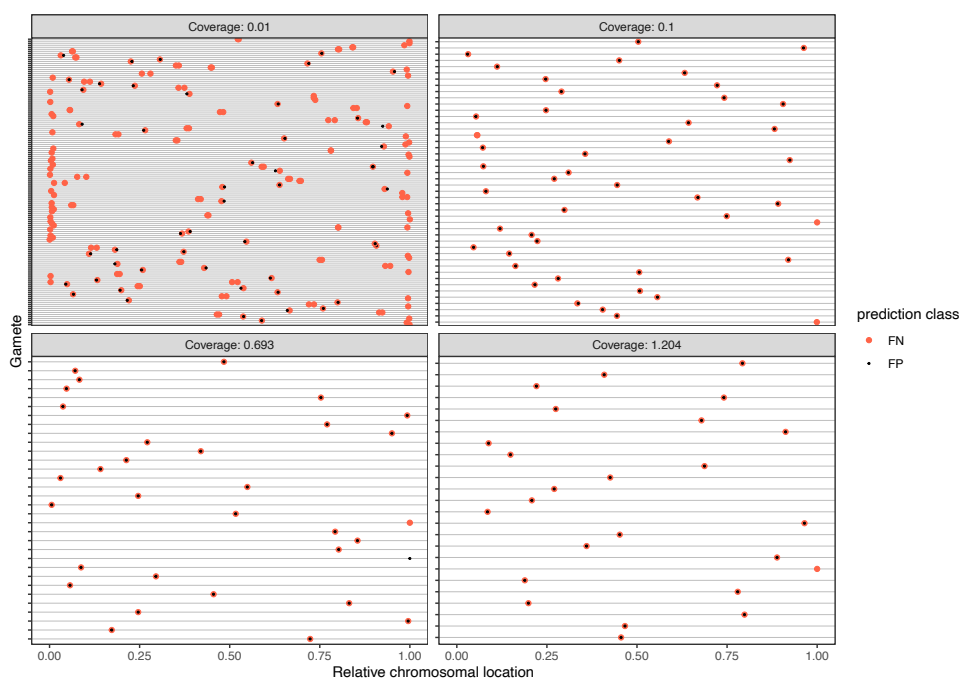
A: Breakpoint Resolution -- 1K gametes, 30K hetSNPs**B: Definition of Prediction Classes****C: Relative Location of False Negatives & False Positives -- 1K gametes, 30K hetSNPs**

Figure 2-figure supplement 5 Discovery of meiotic recombination events in simulated data reflecting characteristics of the Sperm-seq data. (A) Breakpoint resolution stratified by depth of coverage. Resolution is scaled to base pairs assuming pairwise nucleotide diversity of 0.001 (i.e., one hetSNP per 1000 bp). The minimum possible resolution of 2 hetSNPs is denoted with a dashed line. (B) Definition of prediction classes. True positive (TP); True negative (TN); False positive (FP); & False negative (FN). Colors reflect the donor haplotypes, and transitions between these colors indicate recombination events. (C) Relative locations of FN & FP breakpoints within gametes from selected, simulated coverages. Each row in each panel represents an individual gamete with at least one FN or FP. Pairs of FPs and FNs is owed to slight displacement of the inferred crossover breakpoint, which may arise by consequence of premature or delayed switching behaviors of the HMM.