



Figure 4-figure supplement 3 Simulated signature of strong ($k = 0.99$) transmission distortion. We simulated data with 974 gametes, 79,630 SNPs, and $0.0075\times$ coverage, corresponding to the data profile of donor NC26 chromosome 8. Zooming in to region surrounding the causal SNP (denoted with the black, vertical line), we observe that the causal SNP and several flanking SNPs were filtered out due to apparent homozygosity across the sample of sperm cells. However, the imputed gamete genotypes still exhibit signal of the strong TD on either side of this region, far below the p-value threshold of genome-wide significance.