



Figure 2-figure supplement 2 Benchmarking performance across a range of study designs - Additional Metrics. Input data were created from the generative model and analyzed with rhapsodi. For all data in this figure, the genotyping error and recombination rates were matched between models. Each value is the average of three independent trials. LHS: Largest Haplotype Segment (as ratio of segment length / total hetSNPs); SER: Switch Error Rate; FPR: False Positive Rate; TNR: True Negative Rate.