

Figure 5 - Figure Supplements

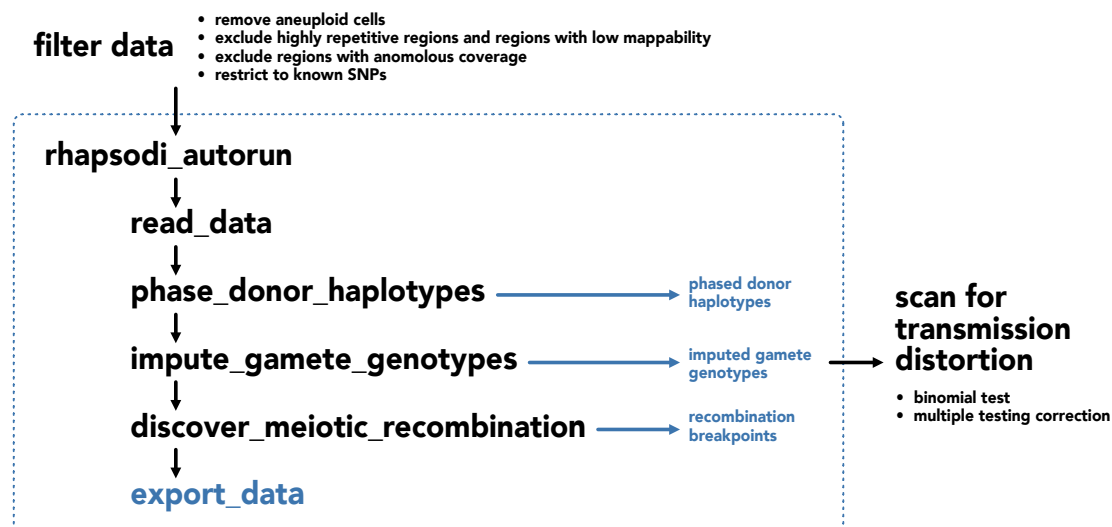


Figure 5-figure supplement 1 Workflow for application of rhapsodi to data from human sperm and downstream investigation of transmission distortion. Raw data containing hetSNPs from each chromosome are filtered to limit spurious signal caused by sequencing error. The autorun function from rhapsodi is applied, which generates and exports data from phased donor haplotypes, imputed gamete genotypes, and meiotic recombination breakpoints. Using the imputed gamete genotypes (generated with the unsmoothed option in rhapsodi), we conduct a binomial test for transmission distortion. We compare our results with our genome-wide threshold for statistical significance, which takes into account multiple hypothesis testing and the extreme linkage disequilibrium in these data.