

Figure 4 - Figure Supplements

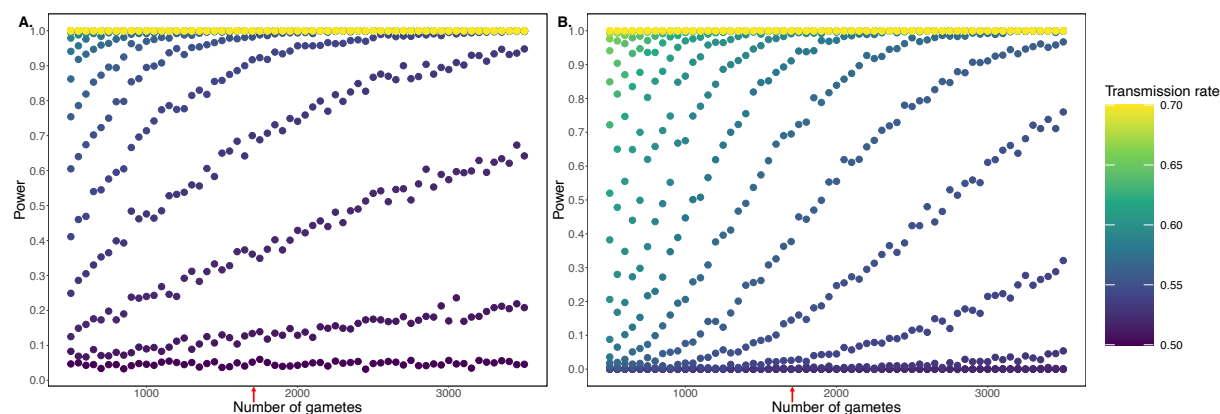


Figure 4-figure supplement 1 Simulation demonstrating power to detect deviations from binomial expectations across sample sizes of sperm cells, without (A) and with (B) multiple hypothesis testing correction. For each combination of transmission rate and number of gametes, power was calculated based on 1000 independent simulations and assuming full knowledge of gamete genotypes. Panel A uses the standard $\alpha = 0.05$, while panel B uses an adjusted p-value threshold of 1.78×10^{-7} as employed in our study. Note that this correction is conservative in that it adjusts for multiple testing across the genome as well as across donor individuals. Red arrows indicate gamete sample sizes roughly matching the Spermi-seq data (average $n = 1711$ sperm cells per donor).