



Figure 4-figure supplement 4 Simulation demonstrating power to detect deviations from expectations using the transmission disequilibrium test (TDT), as applied to human pedigree studies, without (A) and with (B) multiple testing correction (alpha = 0.05 and 10^{-7} , respectively). The latter threshold is the standard for genome-wide significance (10^{-7}) used in past studies [26]. The sample size refers to the number of informative transmissions, where each trio with a parent heterozygous for the SNP of interest has one informative transmission of the given SNP. Power was calculated based on 1000 independent simulations. Panels C and D show the distributions of the number of informative transmissions per SNP from the two pedigrees in Meyer et al. [26] for which data were publicly available: AGRE (C) and HUTT (D). Meyer et al. [26] removed SNPs with fewer than 200 informative transmissions in AGRE and fewer than 50 informative transmissions in HUTT prior to their analysis. Note that the number of informative transmissions is typically substantially less than the total number of offspring in each pedigree (after quality control and sample size cutoffs, 1518 for AGRE and 848 for HUTT).