



Figure S10: Theoretical mean squared error as a function of sample size for samples of outbred diploid full-siblings (A), outbred diploid avuncular pairs (B), inbred diploid full-siblings (C), inbred diploid avuncular pairs (D), male-female full siblings at an X-linked locus with the reduced set omitting males and retaining females (E), and male-female full siblings at an X-linked locus with the reduced set omitting females and retaining males (F). The samples were evaluated for a biallelic locus with minor allele frequency of 0.05 ( $H = 0.095$ ), and sample size was always twice the number of relative pairs included in the sample for samples containing 2 to 100 relative pairs. Each individual in the sample was related to exactly one other.