



Figure S8: Mean squared error for samples of (A) diploid individuals (parent-offspring, second-degree avuncular, and full-sibling, labeled as PO, AV, and FS), (B) male and female individuals observed at an X-linked locus (male-male, male-female, and female-female full-siblings, labeled as MM, MF, and FF), or (C) diploid individuals with inbreeding as previously defined (inbred full-sibling, second-degree, or outbred full-sibling, labeled as FSi, AV, and FSo), fixed at size 40 across changing sample composition, obtained from simulated values. The samples were modeled on the D3S2427 locus and contained 20 relative pairs such that each individual was related to exactly one other. Each point on the heat maps represents the mean of 10^4 simulations.