

Figure S3 Recombination rates are very similar in both parental maps. Each point represents a ~1Mb genomic region. Points are jittered (random noise added) for ease of visualization, rounded up so that all rates are nonzero, and plotted on a log scale. Recombination rates across the genome in both parents were highly correlated ($r_s = 0.48$; P < 10^{-13}). Most (60%) genomic regions showed no recombination in either parent, and those showing recombination often showed it in both parents.