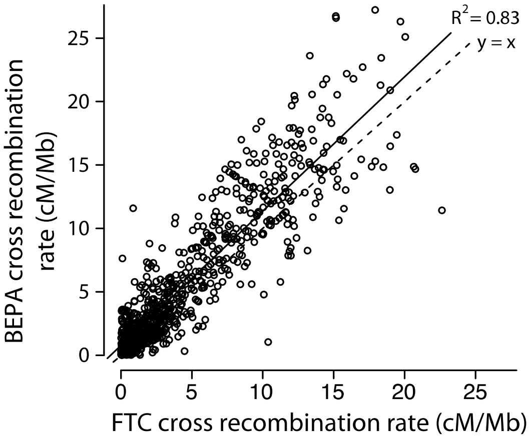

Figure S5 High correlation of recombination rates
Recombination rate in the FTC cross plotted against recombination rate in the BEPA cross. Each point is a marker. Recombination rates were calculated by taking the local slope of the loess-smoothed genetic vs. physical plots shown in Figure 3. Recombination rates are highly correlated ($R^2 = 0.83$). Solid line: best fit line from a linear regression; dotted line: y=x. Total genetic map size was smaller in the FTC cross (1569.9 cM) compared to the BEPA cross (1963.3 cM). Most points were displaced from the y=x line, indicating a higher recombination rate throughout the genome in the BEPA cross.