



Figure 5-figure supplement 5 Comparison of inferred crossover recombination map to published deCODE male-specific recombination map. By binning the deCODE recombination map within each 1 Mbp bin for each chromosome, a weighted average recombination rate was calculated and compared to the number of Sperm-seq inferred crossovers for each corresponding bin. (A) A high correlation of 0.9 was observed overall. (B) Sample specific correlations ranged from 0.69 to 0.9. Information from each sample is shown with its Donor ID (FF3, NC1, etc.), following the conventions from the papers in which they were initially published [1,2] and throughout our manuscript.