Figure S4  Recombination rates for each chromosome estimated by LDhat (red lines) and based on Cox et al. [51] genetic map (blue lines). Rates were smoothed over 10 Mb with a shift of 1 Mb. We scaled the the LDhat map according to the Cox et al. map and then recalculated recombination rates as \((4N_e^{scaled})/\text{Mb}\) (see also Materials and methods).