



Figure S12: Estimates for the proportion of recombination occupying various proportions of the sequence differ between LD- and pedigree-based maps. For dogs (A), the LD data¹ (black line) appears to be more uniform than the pedigree-based estimates. In humans (B), the LD data⁴ (black line) appears to be less uniform than the thinned pedigree-based estimates.