Figure S9

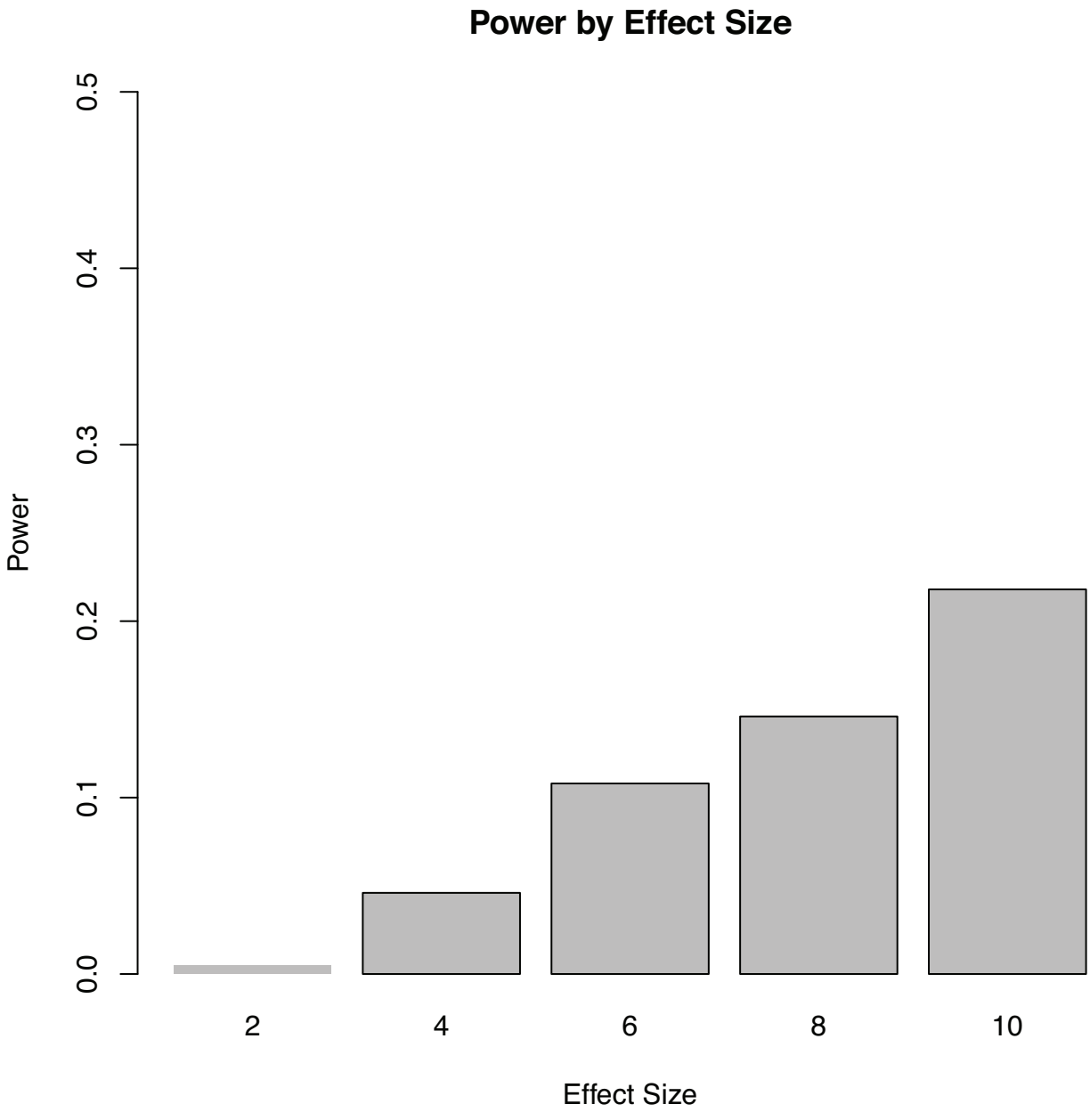

***Figure S9*.** Lack of power to detect a significant locus in the presence of strong polygenic effect. Simulation corresponds to a loop of size 60 (i.e., 60 parental strains) with 6 mice per cross. This setting was chosen for visualization because it most closely resembles the sample size of our own data. The numbers on the x-axis indicate multiples of the σ_poly.