Supplemental Data

Genome-wide SNP analysis reveals no gain in power for association studies of common variants in the Finnish Saami

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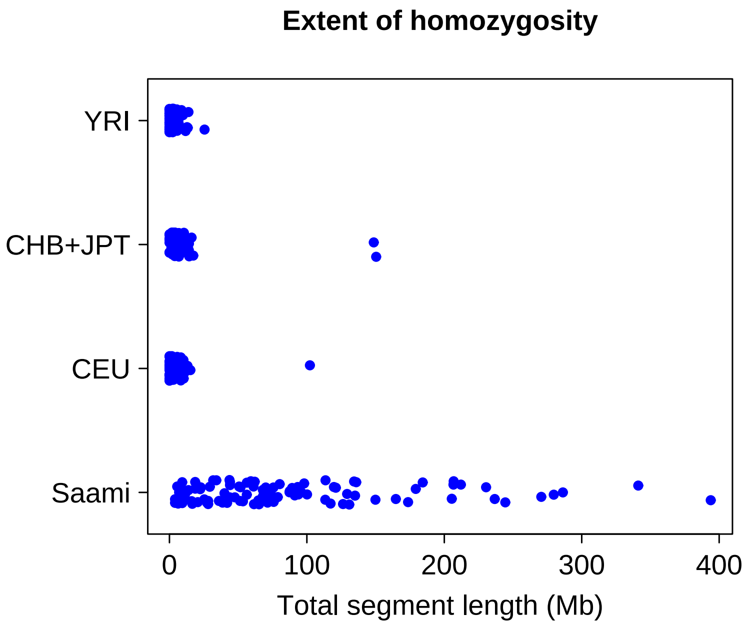
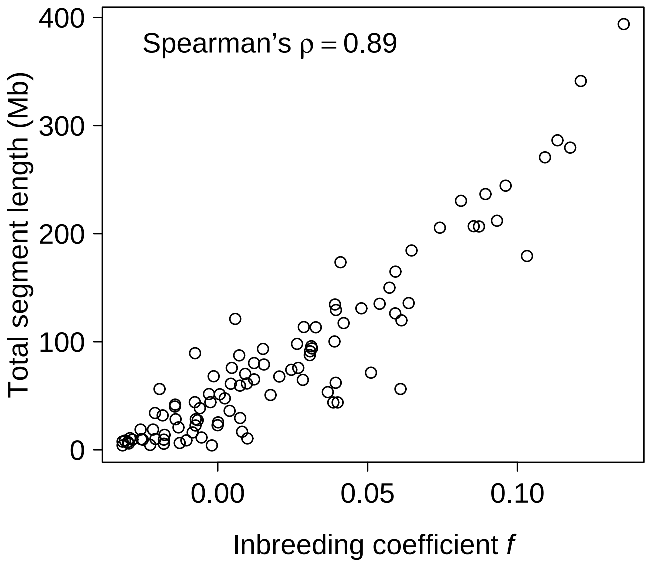


Supplementary Figure 1: Total length of genome composed of extended regions of homozygosity for Saami and HapMap samples



Supplementary Figure 2: Total length of genome composed of homozygous segments plotted against inbreeding coefficients for Saami sample

Note that inbreeding coefficient estimates were calculated using an estimator based on genome-wide data. Hence, these values are not estimates of the classically defined inbreeding coefficient, which is derived from pedigree information.