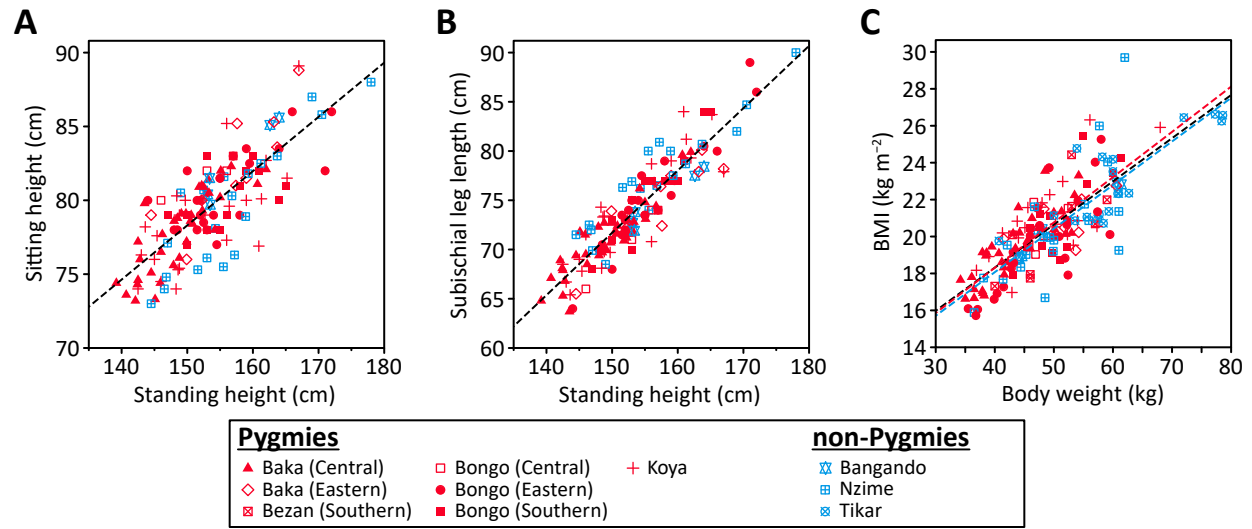Figure S1. Relationships between quantitative traits. Scatterplots are shown of (**A**) sitting height against standing height (R^2=0.620), (**B**) subischial leg length against standing height (R^2=0.829), and (**C**) BMI against body weight (R^2=0.631). The black, red, and blue dashed lines depict the regression lines for all individuals, Pygmies only, and non-Pygmies only, respectively. Only individuals with measurements for the trait being compared are included.
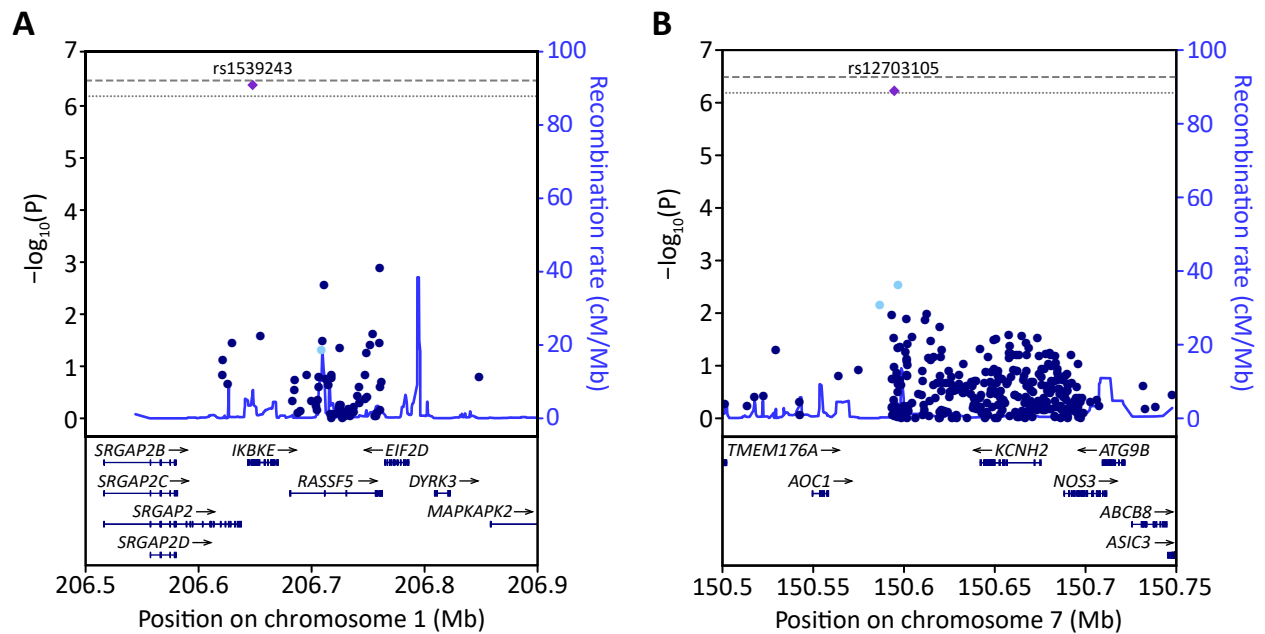
A

B

Figure S2. Genomic regions associated with Pygmy/non-Pygmy categorization. LocusZoom plots [147] of the genomic regions surrounding SNPs (**A**) rs1539243 and (**B**) rs12703105 that are marginally associated with Pygmy/non-Pygmy categorization. The figure follows the same format as **Figure 6C**.
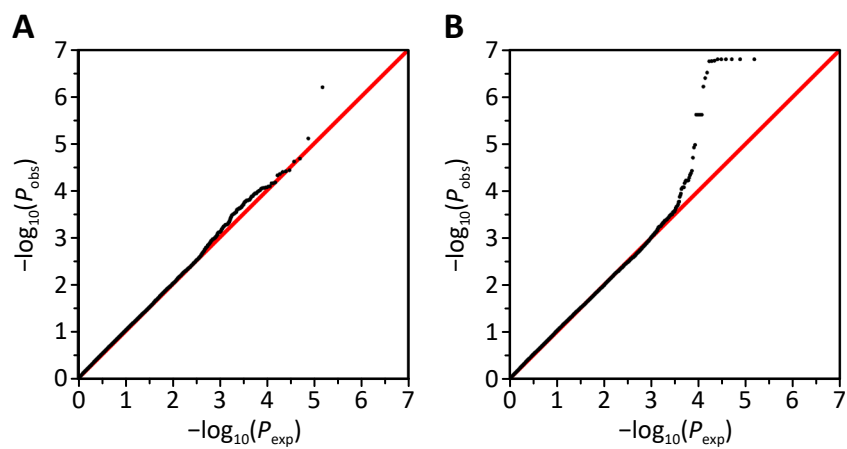
A

B

Figure S3. Effect of village covariate on Pygmy/non-Pygmy association signals. Quantile-quantile plots are shown for the 153,798 autosomal SNPs in the genetic dataset in association analyses of Pygmy/non-Pygmy categorization considering either (**A**) no or (**B**) village affiliation as covariates. The identity line is shown in red.
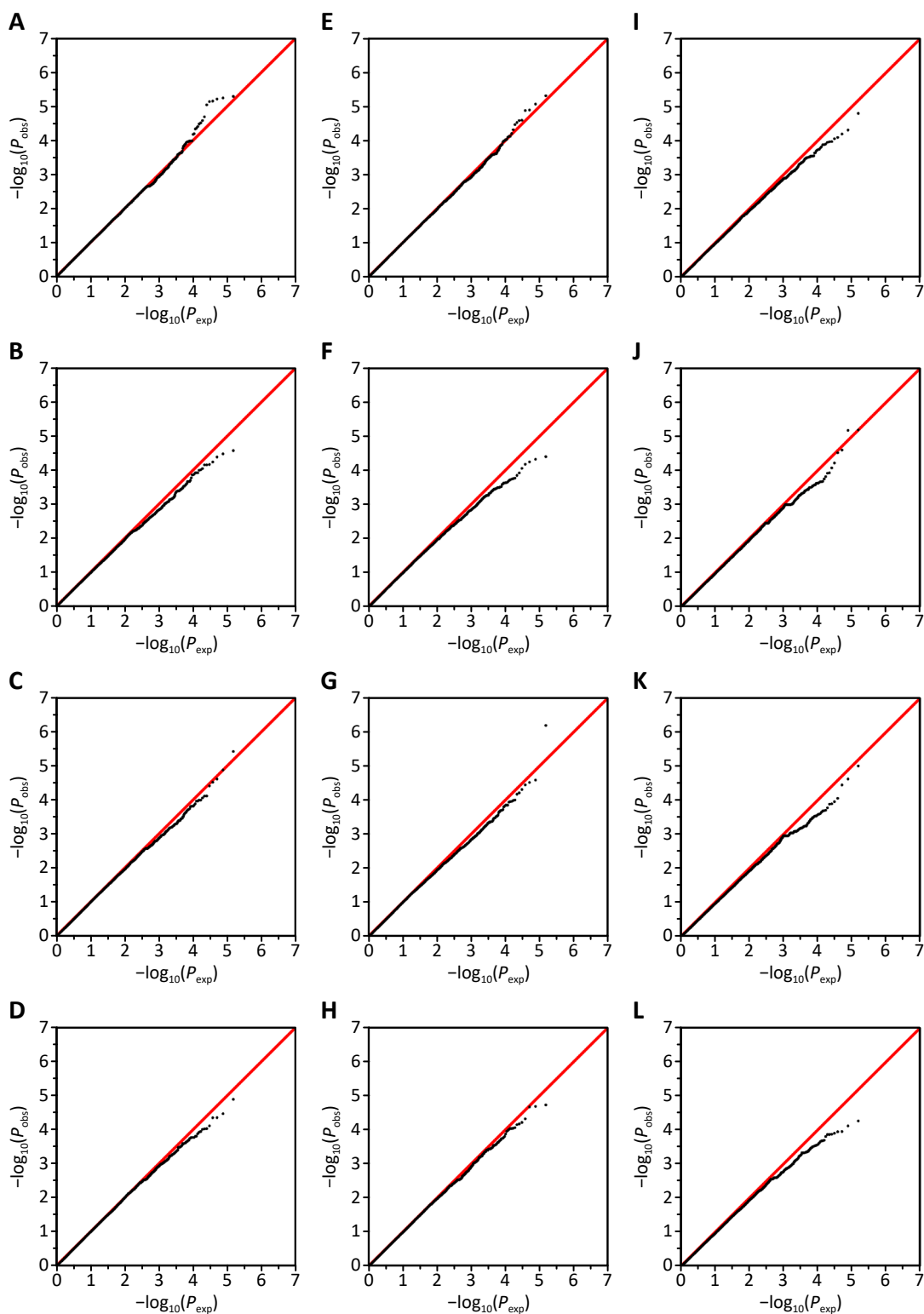
Figure S4. Effect of categorization covariates on quantitative trait association signals. Quantile-quantile plots are shown for the 153,798 autosomal SNPs in the genetic dataset in association analyses considering standing height (**A**, **E**, and **I**), sitting height (**B**, **F**, and **J**), sitting/standing height ratio (**C**, **G**, and **K**), and subischial leg length (**D**, **H**, and **L**) with either no (**A-D**), Pygmy/non-Pygmy categorization (**E-H**), or village affiliation (**I-L**) as covariates. The identity line is shown in red.
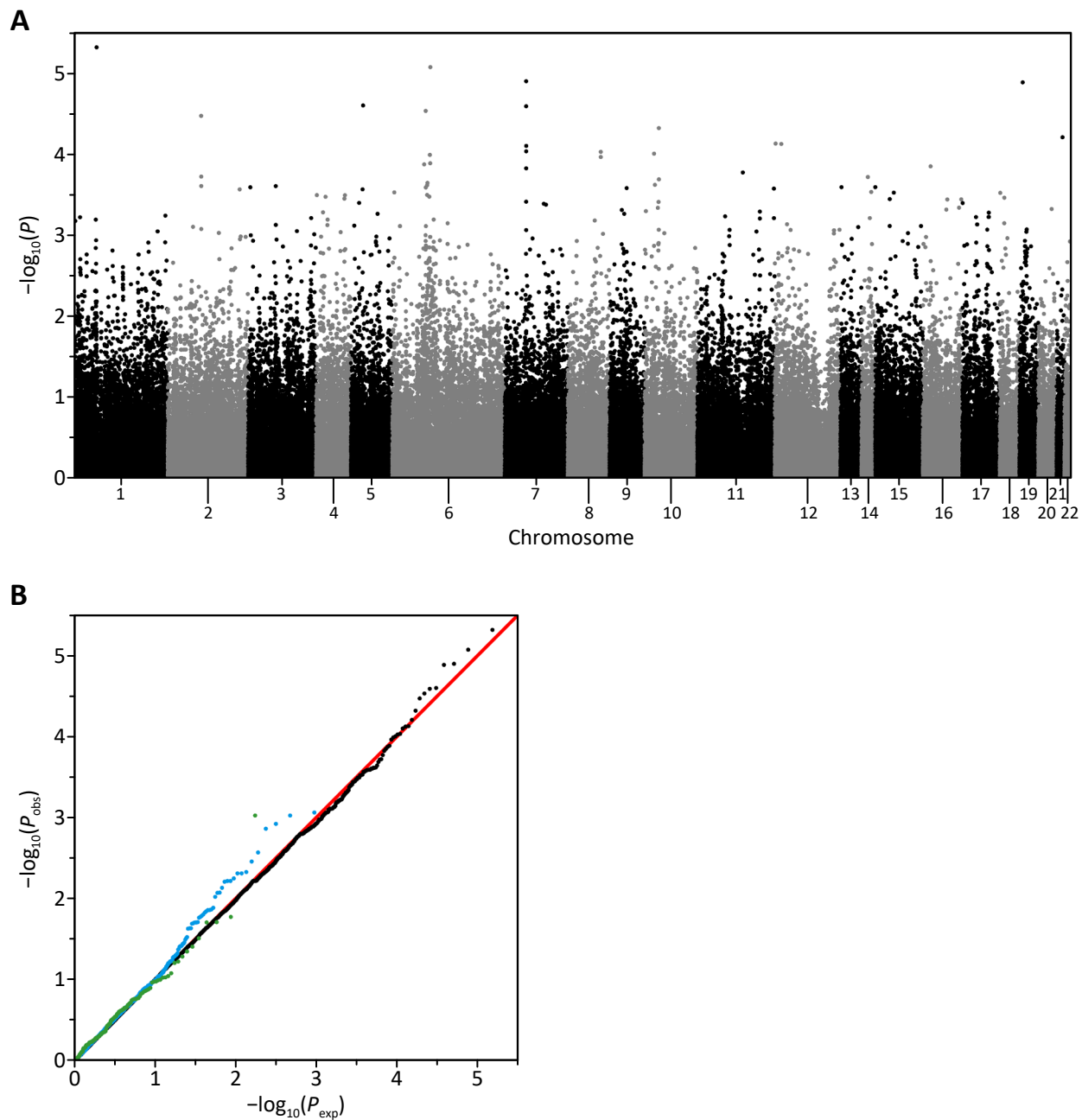
A

B

Figure S5. Association signals for standing height. Manhattan (**A**) and quantile–quantile (**B**) plots of the 153,798 autosomal SNPs in the genetic dataset restricted to the 159 individuals with standing height measurements available (Additional File 1: **Table S1**). Figure follows the same format as **Figure 6**.
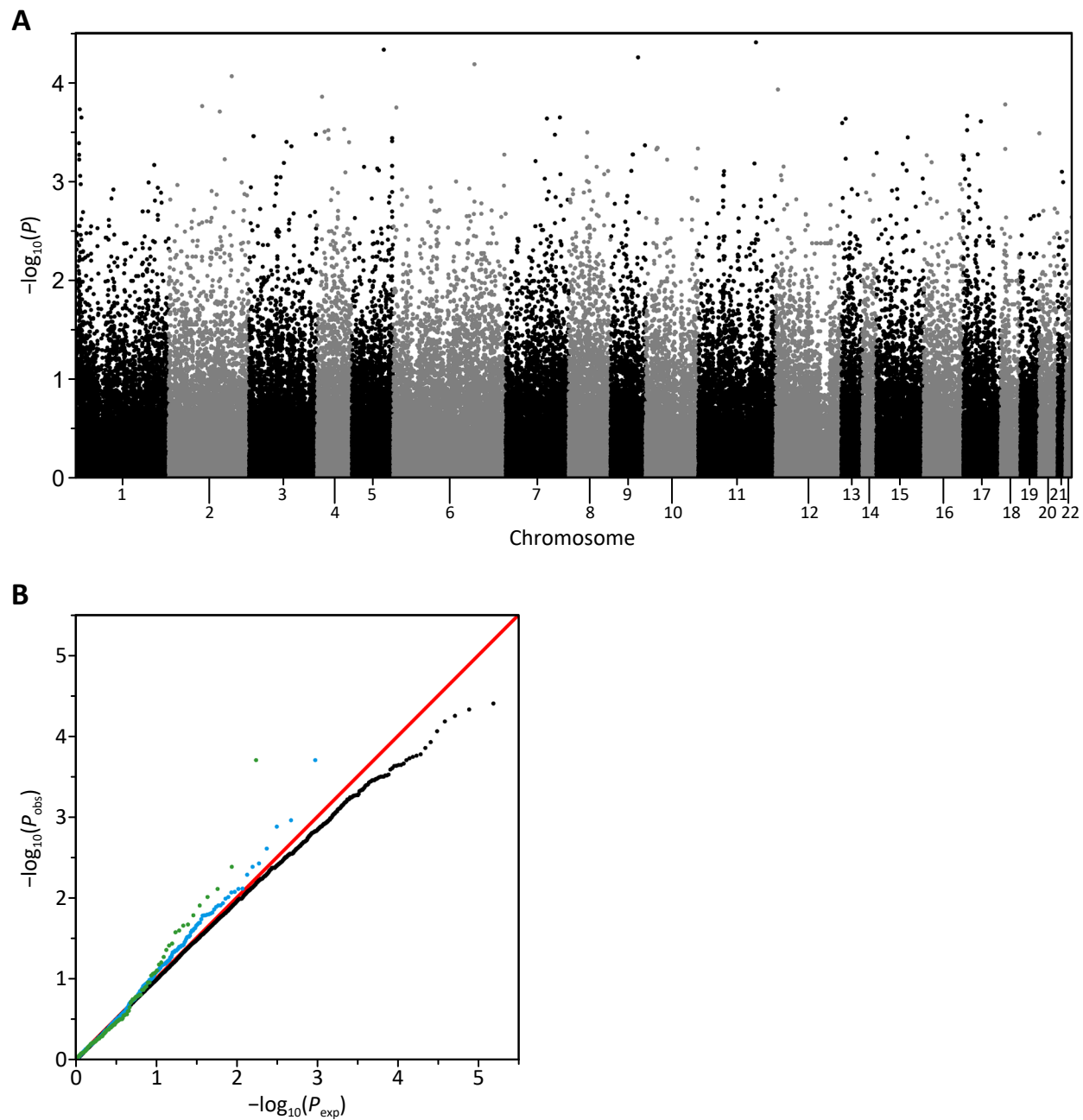
A

B

Figure S6. Association signals for sitting height. Manhattan (**A**) and quantile–quantile (**B**) plots of the 153,798 autosomal SNPs in the genetic dataset restricted to the 133 individuals with sitting height measurements available (Additional File 1: **Table S1**). Figure follows the same format as **Figure 6**.
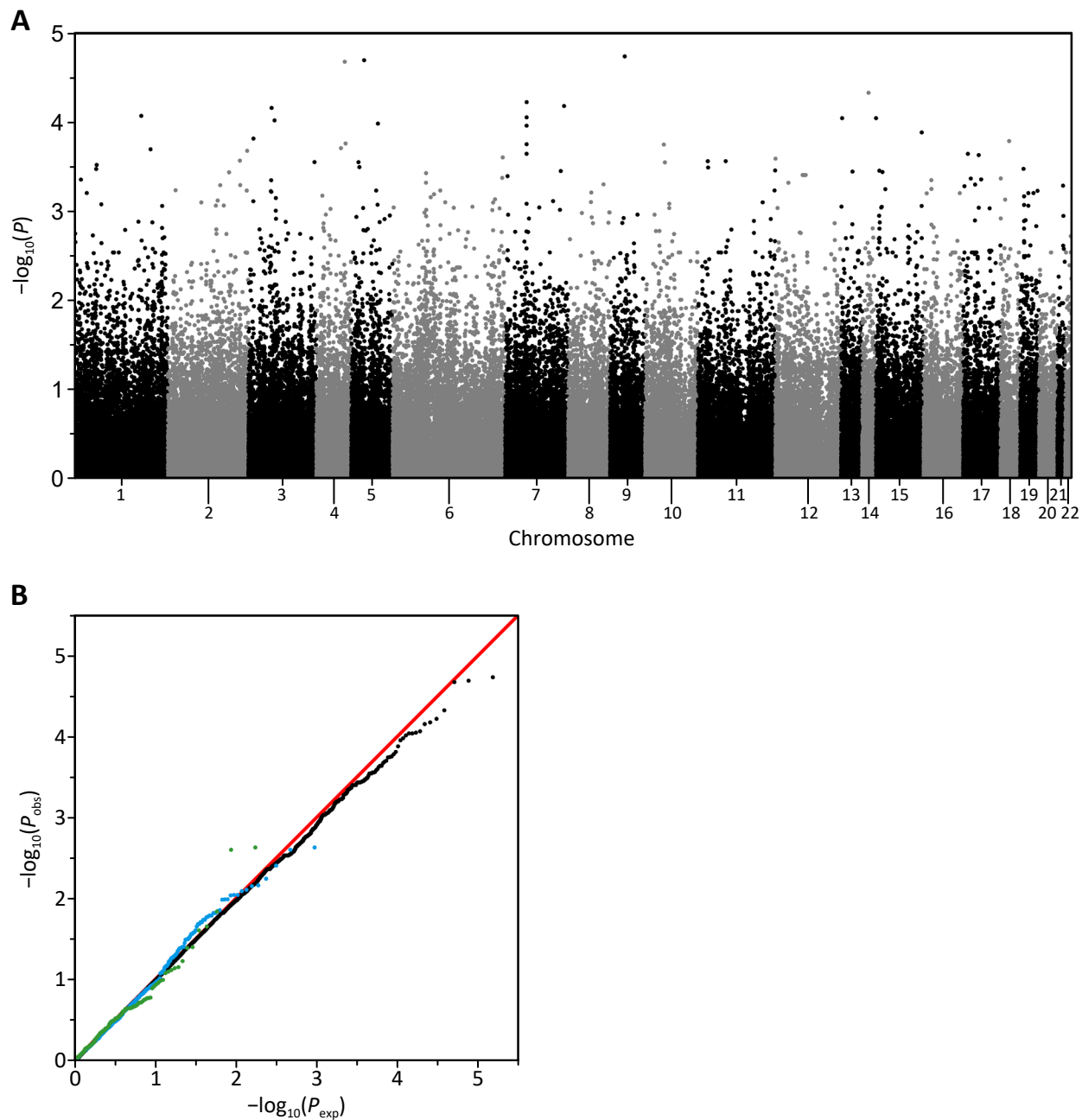
A

B

Figure S7. Association signals for subischial leg length. Manhattan (**A**) and quantile–quantile (**B**) plots of the 153,798 autosomal SNPs in the genetic dataset restricted to the 133 individuals with subischial leg length measurements available (Additional File 1: **Table S1**). Figure follows the same format as **Figure 6**.
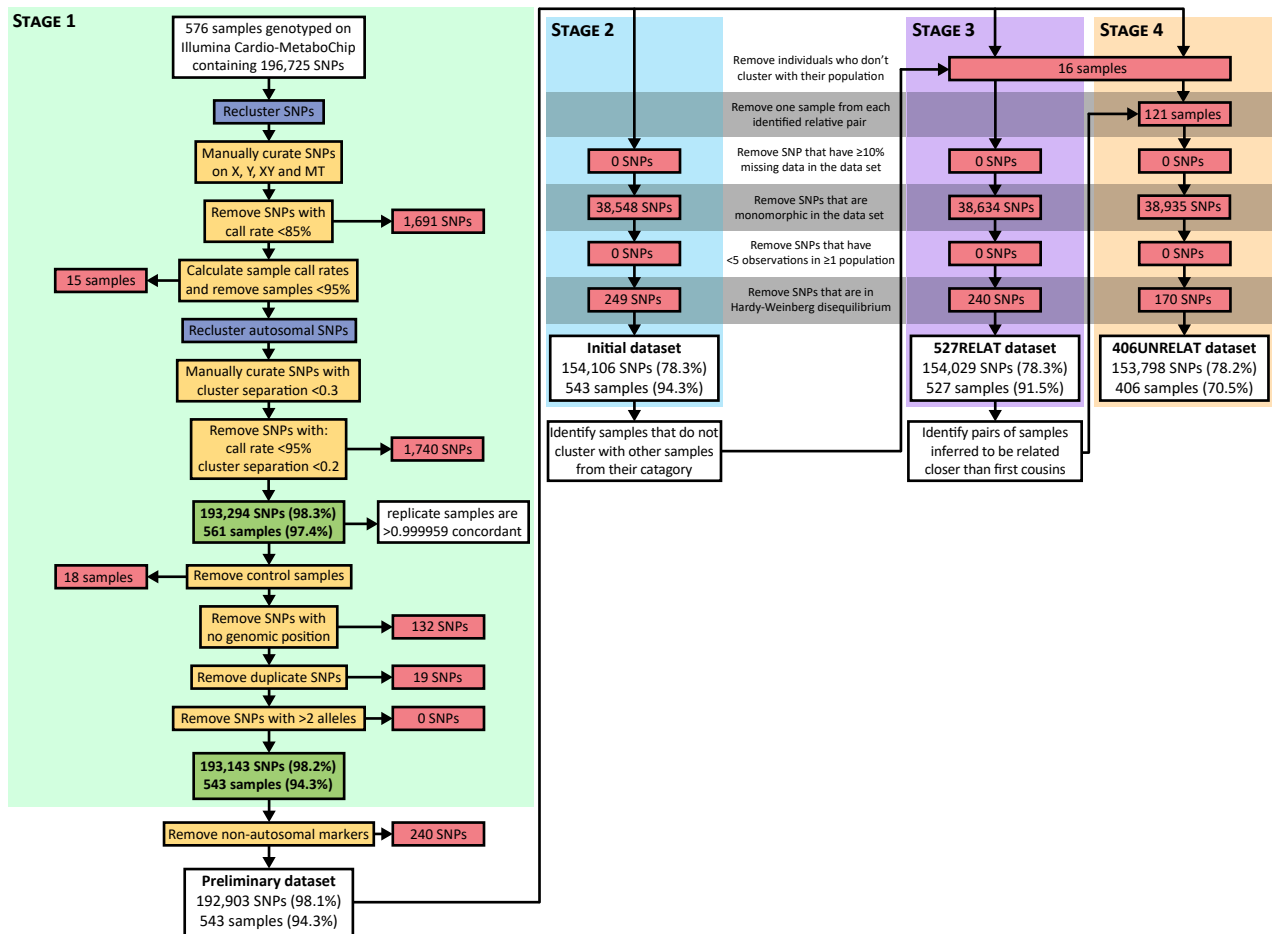
Figure S8. Data filtering steps used to prepare the combined datasets. Data filtering steps used to prepare the combined datasets are shown in the order in which they were applied. The numbers of SNPs or samples removed are shown in red shaded boxes. SNPs and samples removed in one step were not subsequently considered.