

Description of Additional Supplementary Files

File: Supplementary Data 1

Description: Within-sibship and population (Backman et al.) GWAS model results for 1939 quantitative trait associated rare variants (MAF <1%, MAC >20 in siblings, $P < 1 \times 10^{-5}$ in Backman et al.). CHR = chromosome, BP = base pair position, EA = effect allele, OA = other allele, EAF = effect allele frequency, SE = standard error, CI = 95% confidence interval, P = p-value, Q = Cochran's Q statistic, Adj. P = (FDR adjusted p-value). Population (pop) data is taken from Backman et al. Supplementary Data Table SD2.

File: Supplementary Data 2

Description: Genetic instruments used for rare variants Mendelian Randomization analysis of height (exposure) on years in education (outcome) with population (Backman et al.) or within-sibship GWAS derived effect estimates.
CHR = chromosome, BP = base pair position, EA = effect allele, OA = other allele, EAF = effect allele frequency, SE = standard error, P = p-value. Population data is taken from Backman et al. Supplementary Data Table SD2.