

Figure S2. Leave-one-out plot for screen time and astigmatism. The plot shows the estimated effect by sequentially dropping one single-nucleotide polymorphism (SNP) at a time. Each black dot in the forest plot represents the Mendelian randomization (MR) results (inverse variance-weighted method) excluding that particular SNP. The result including all SNPs is shown in red at the bottom of the plot.

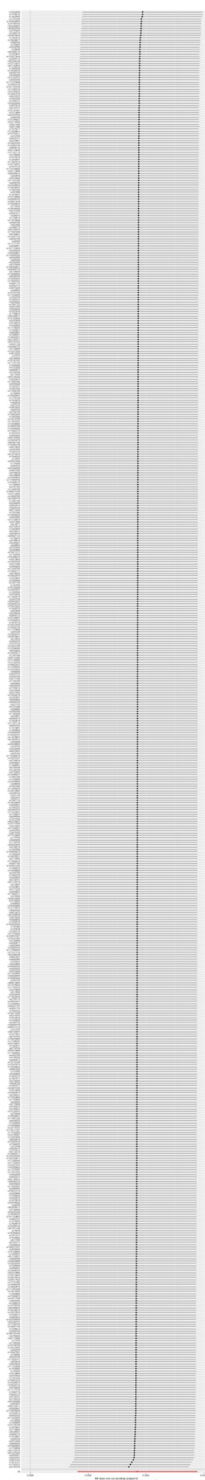


Figure S3. Leave-one-out plot for body height and astigmatism. The plot shows the estimated effect by sequentially dropping one single-nucleotide polymorphism (SNP) at a time. Each black dot in the forest plot represents the Mendelian randomization (MR) results (inverse variance-weighted method) excluding that particular SNP. The result including all SNPs is shown in red at the bottom of the plot.

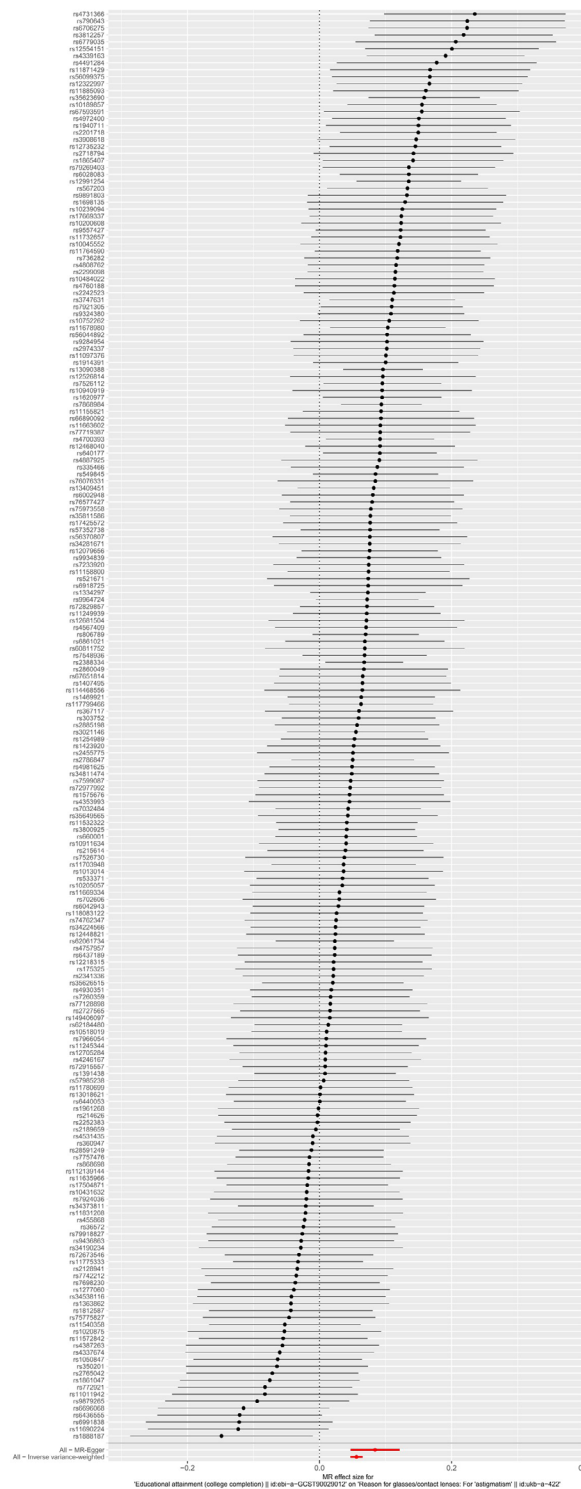


Figure S4. Forest plot for educational attainment and astigmatism. The horizontal coordinates indicate the magnitude of the effect of each genetic variant on the outcome variable (expressed as odds ratio), and the vertical coordinates indicate the individual genetic variants. Each point represents the estimated effect of a genetic variant and its 95% confidence interval. Abbreviation: MR: Mendelian randomization.

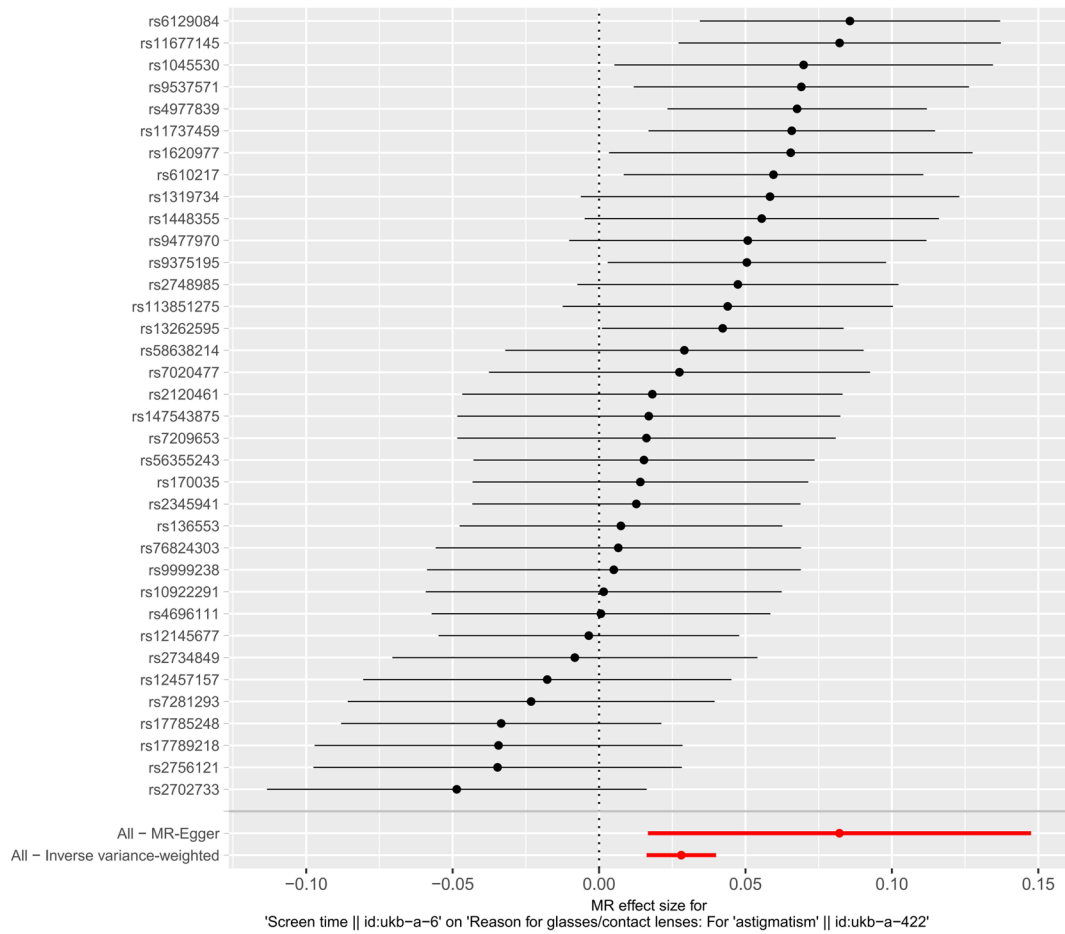


Figure S5. Forest plot for screen time and astigmatism. The horizontal coordinates indicate the magnitude of the effect of each genetic variant on the outcome variable (expressed as odds ratio), and the vertical coordinates indicate the individual genetic variants. Each point represents the estimated effect of a genetic variant and its 95% confidence interval. Abbreviation: MR: Mendelian randomization.

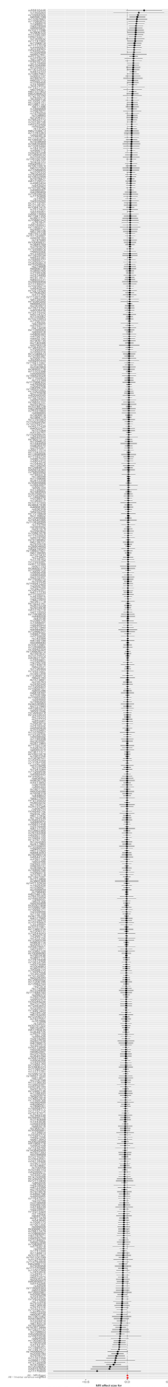


Figure S6. Forest plot for body height and astigmatism. The horizontal coordinates indicate the magnitude of the effect of each genetic variant on the outcome variable (expressed as odds ratio), and the vertical coordinates indicate the individual genetic variants. Each point represents the estimated effect of a genetic variant and its 95% confidence interval.

Abbreviation: MR: Mendelian randomization.

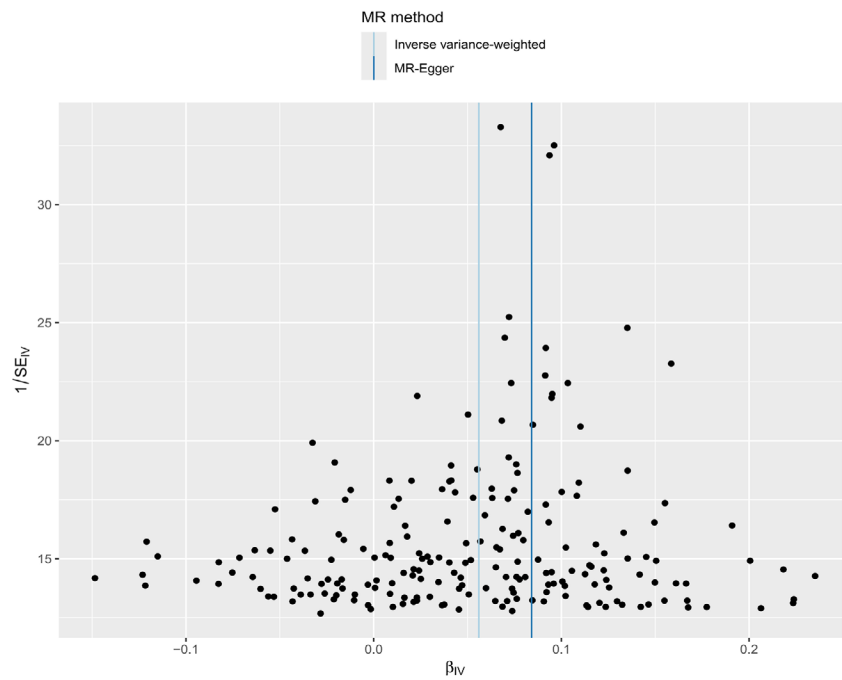


Figure S7. Funnel plot for educational attainment and astigmatism. The plot shows the effect estimate (β) of a particular single-nucleotide polymorphism (SNP) against the SNP expected precision (1/standard error [SE]). Asymmetry in the funnel plot is an indication of horizontal pleiotropy. The dark and light blue lines represent the Mendelian randomization-Egger and inverse variance-weighted slopes, respectively.

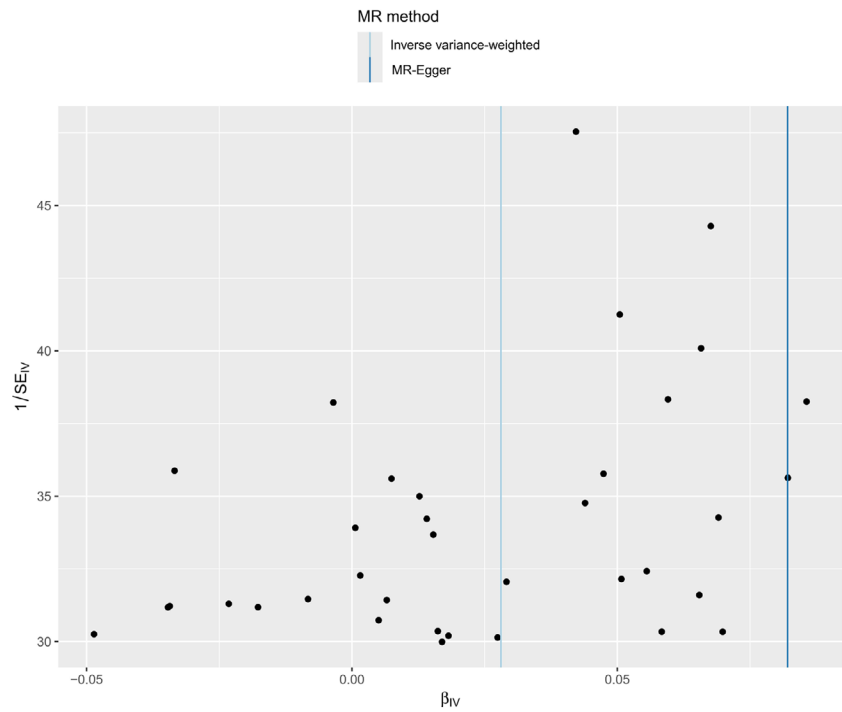


Figure S8. Funnel plot for screen time and astigmatism. The plot shows the effect estimate (β) of a particular single-nucleotide polymorphism (SNP) against the SNP expected precision (1/standard error [SE]). Asymmetry in the funnel plot is an indication of horizontal pleiotropy. The dark and light blue lines represent the Mendelian randomization-Egger and inverse variance-weighted slopes, respectively.

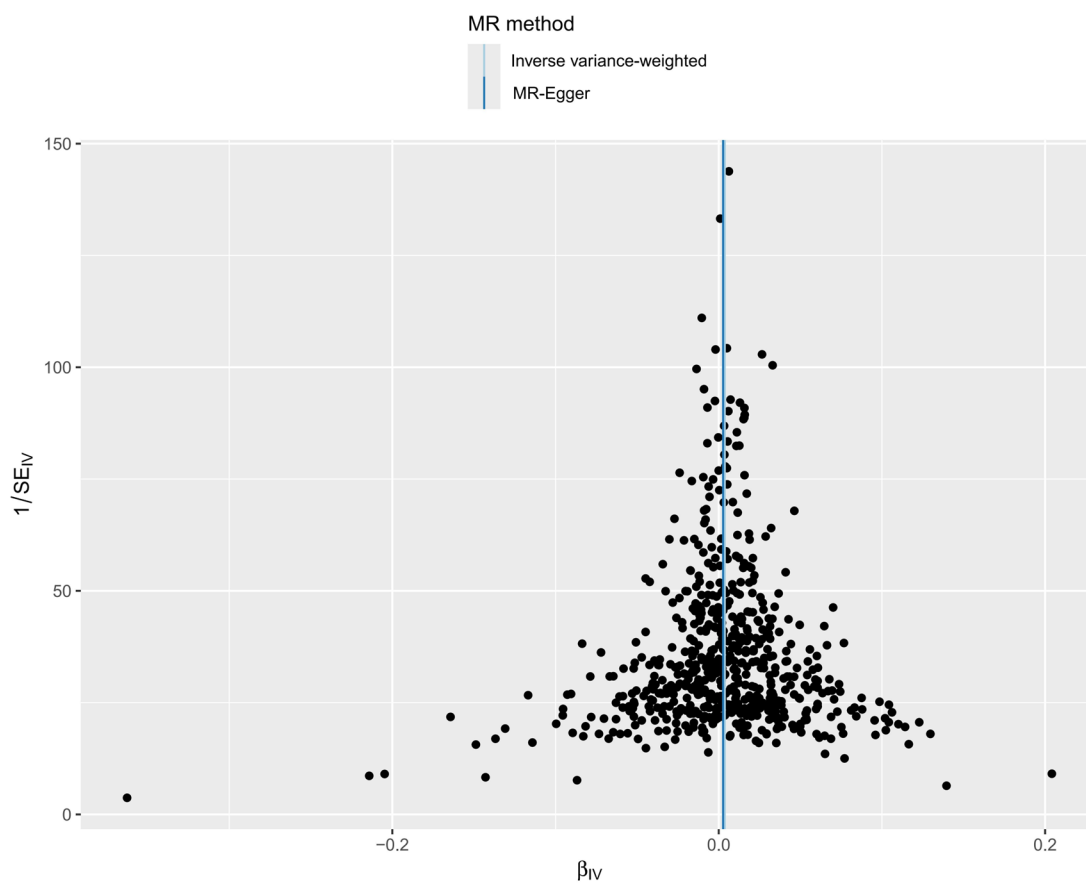


Figure S9. Funnel plot for body height and astigmatism. The plot shows the effect estimate (β) of a particular single-nucleotide polymorphism (SNP) against the SNP expected precision (1/standard error [SE]). Asymmetry in the funnel plot is an indication of horizontal pleiotropy. The dark and light blue lines represent the Mendelian randomization (MR)-Egger and inverse variance-weighted slopes, respectively.