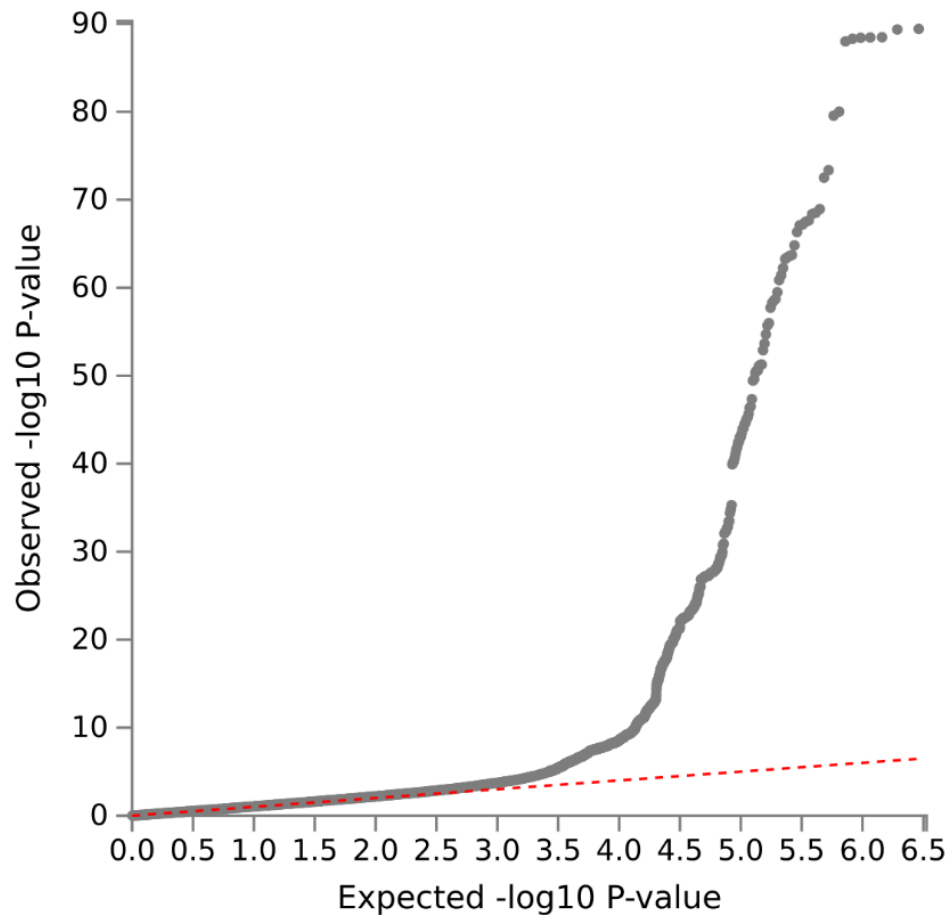
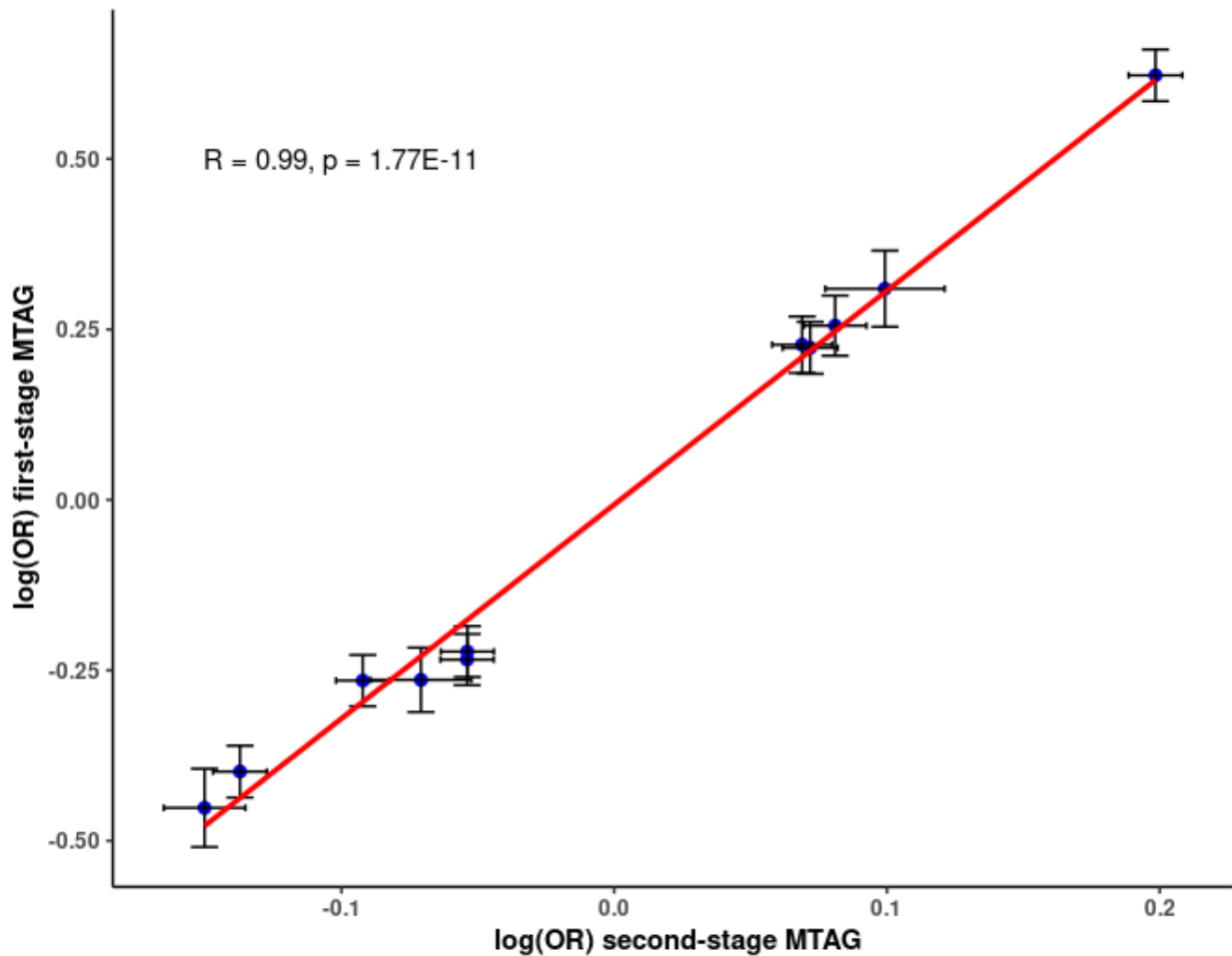


**Genome-wide meta-analysis identifies 22 loci for normal tension glaucoma
with significant overlap with high tension glaucoma**

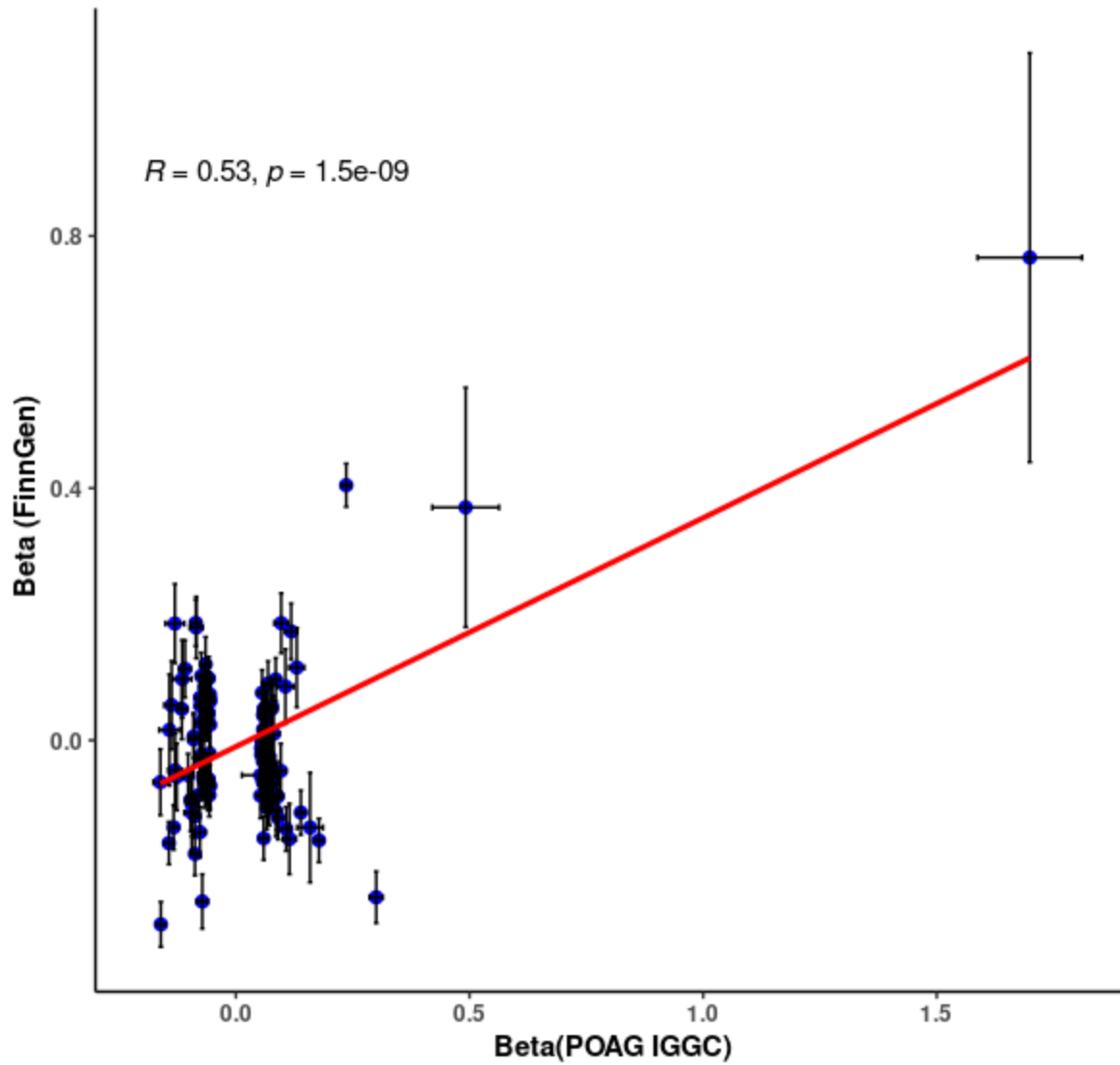
Diaz-Torres *et al.*



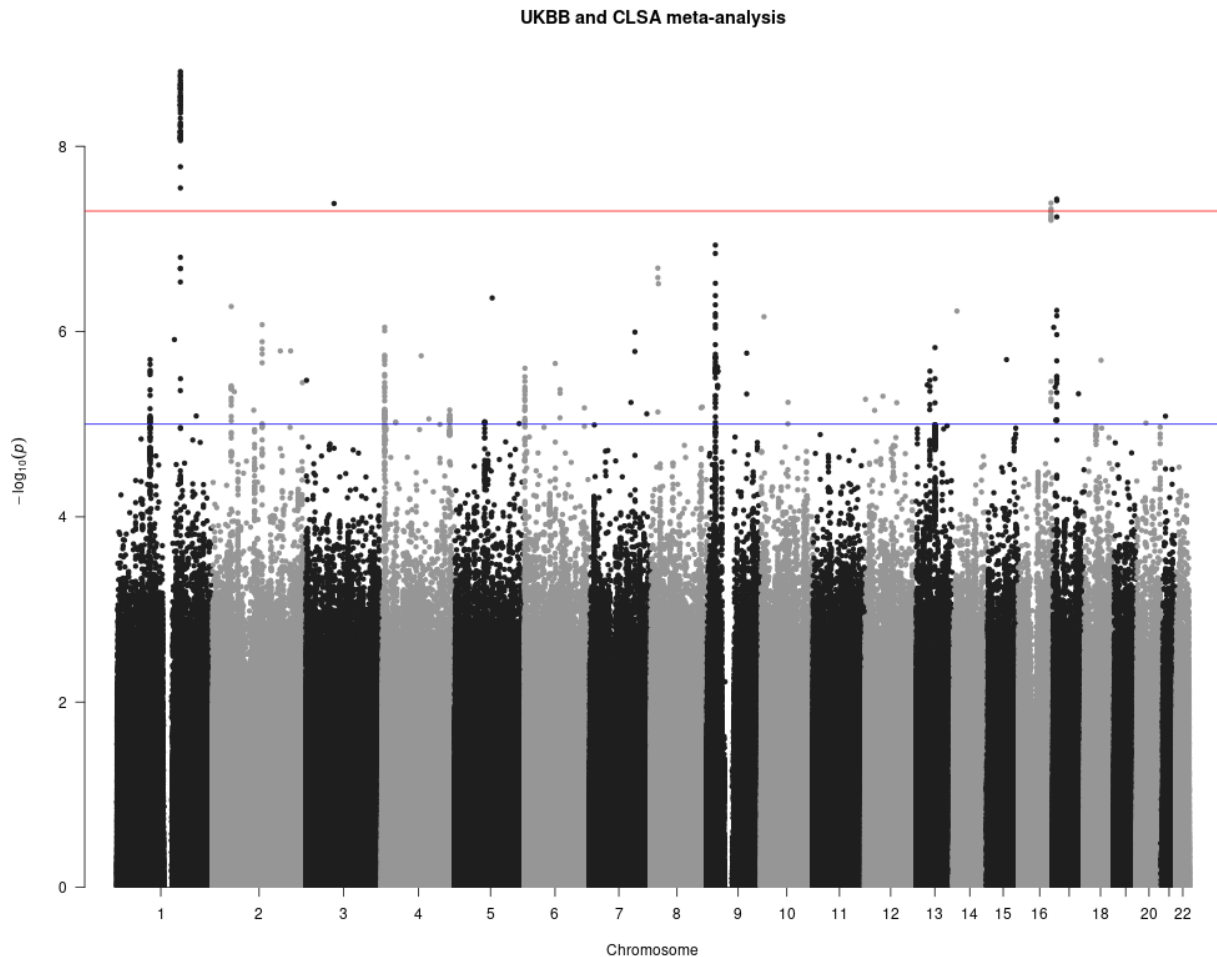
Supplementary Figure 1. QQ Plot based on the stage-two meta-analysis of normal tension glaucoma (NTG) with an estimated genetic inflation factor (λ) of 1.08.



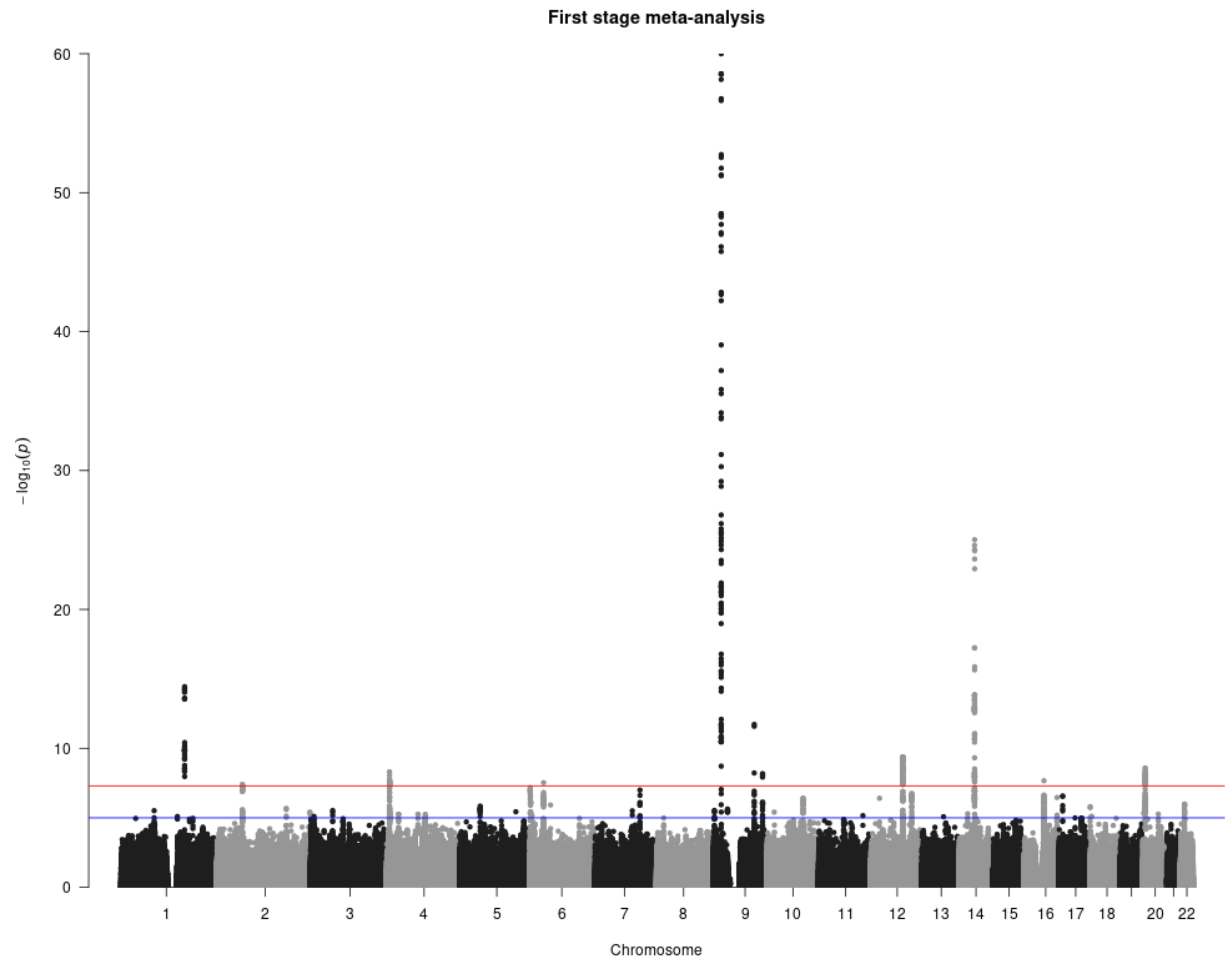
Supplementary Figure 2. Inverse weighted variance correlation between the effect sizes of the first and second stages of the meta-analysis (N=11). Estimated in log(OR) and based on the stage-one genome-wide independent loci. Effects estimates are presented as centre points and black crosses represent 95% confidence intervals.



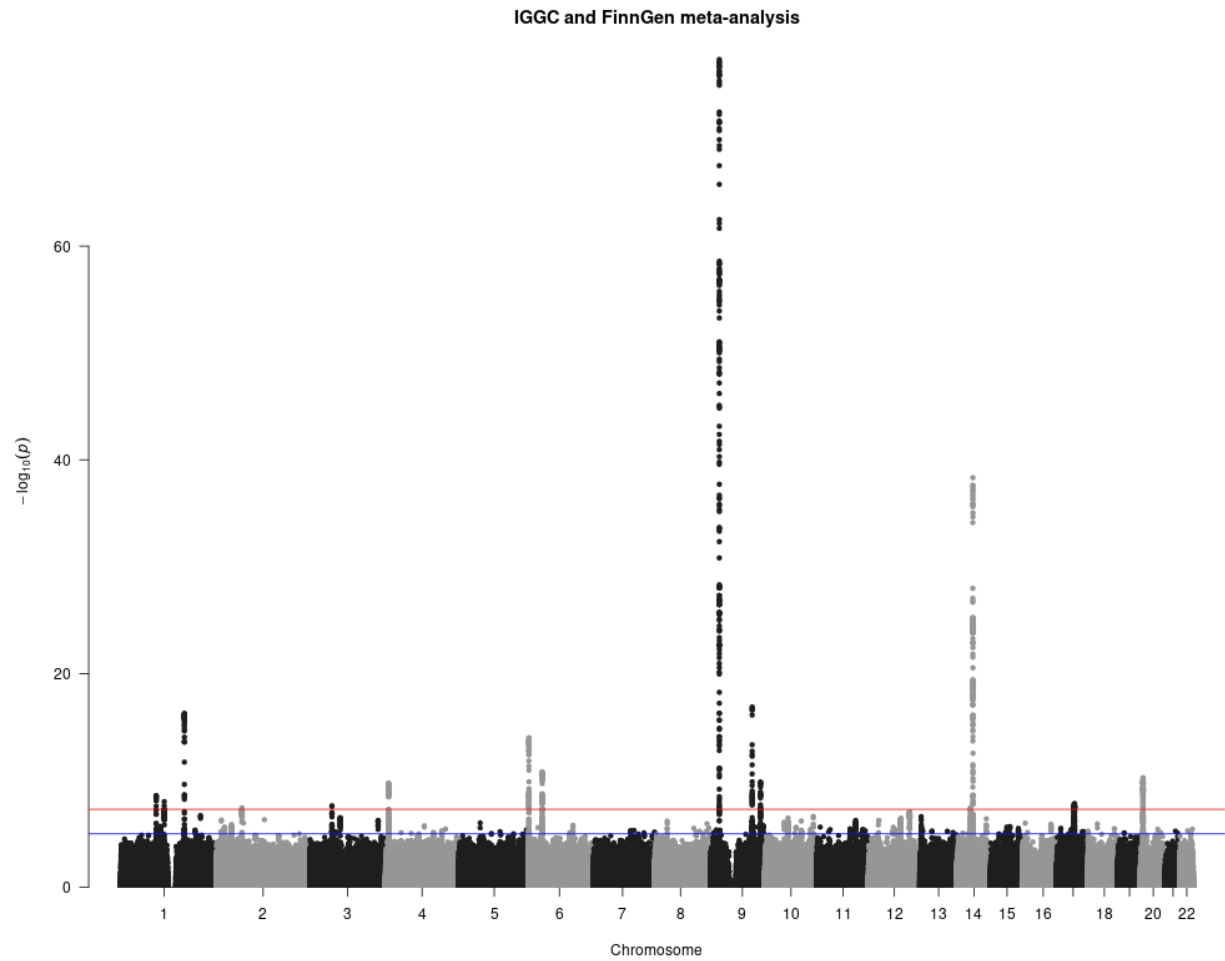
Supplementary Figure 3. Inverse weighted variance correlation of the allele effect estimates (N=127) between POAG risk loci and FinnGen NTG. Effects estimate (Beta) are presented as blue centre points and black crosses represent 95% confidence intervals



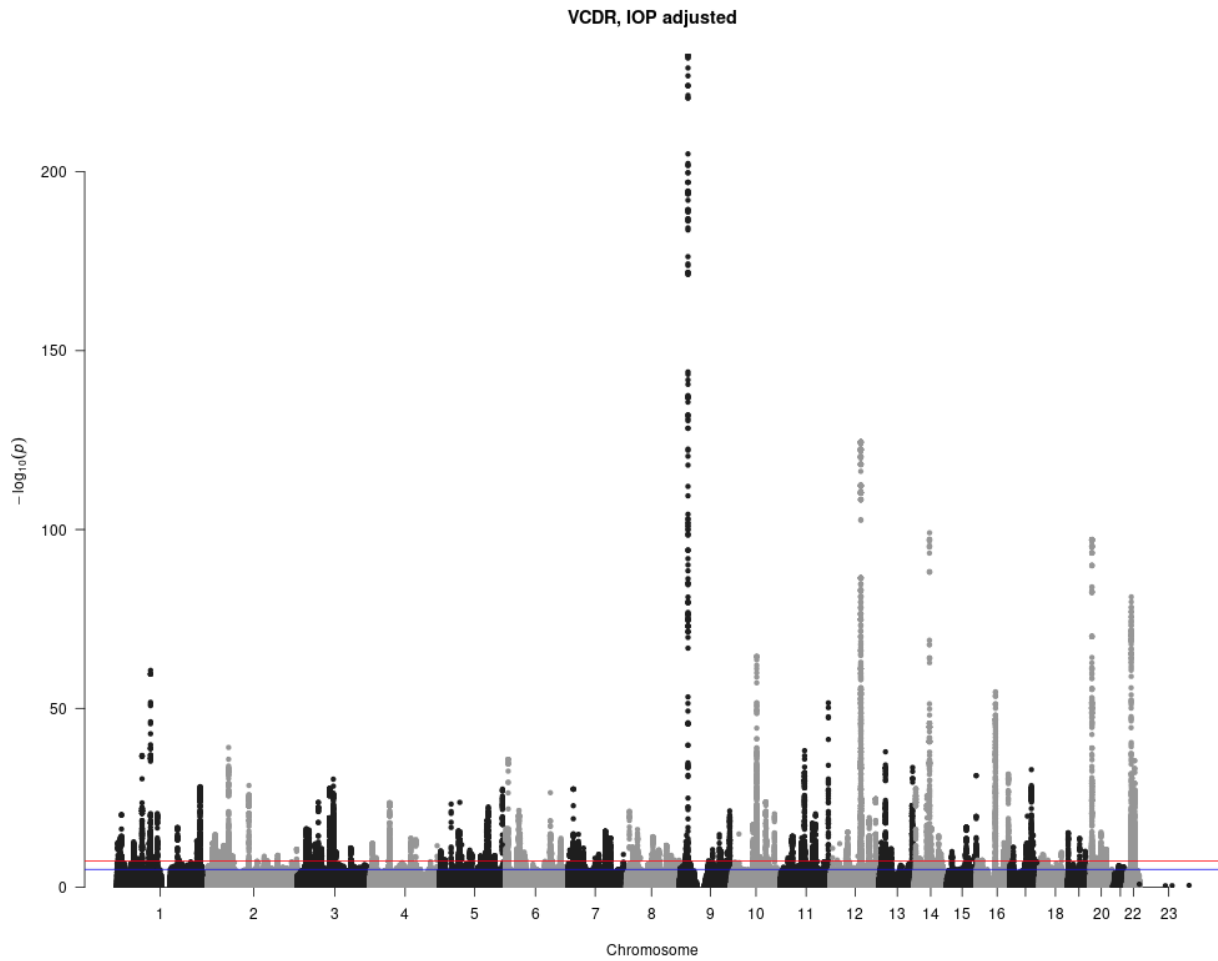
Supplementary Figure 4. Manhattan plot based on the GWAS meta-analysis of UKBB and CLSA (N Cases = 2,939, N Controls = 10,000). The red line represents the threshold for multiple testing correction ($p < 5 \times 10^{-8}$) and the blue line $p < 5 \times 10^{-6}$; p-values derived from logistic regression models are two-sided.



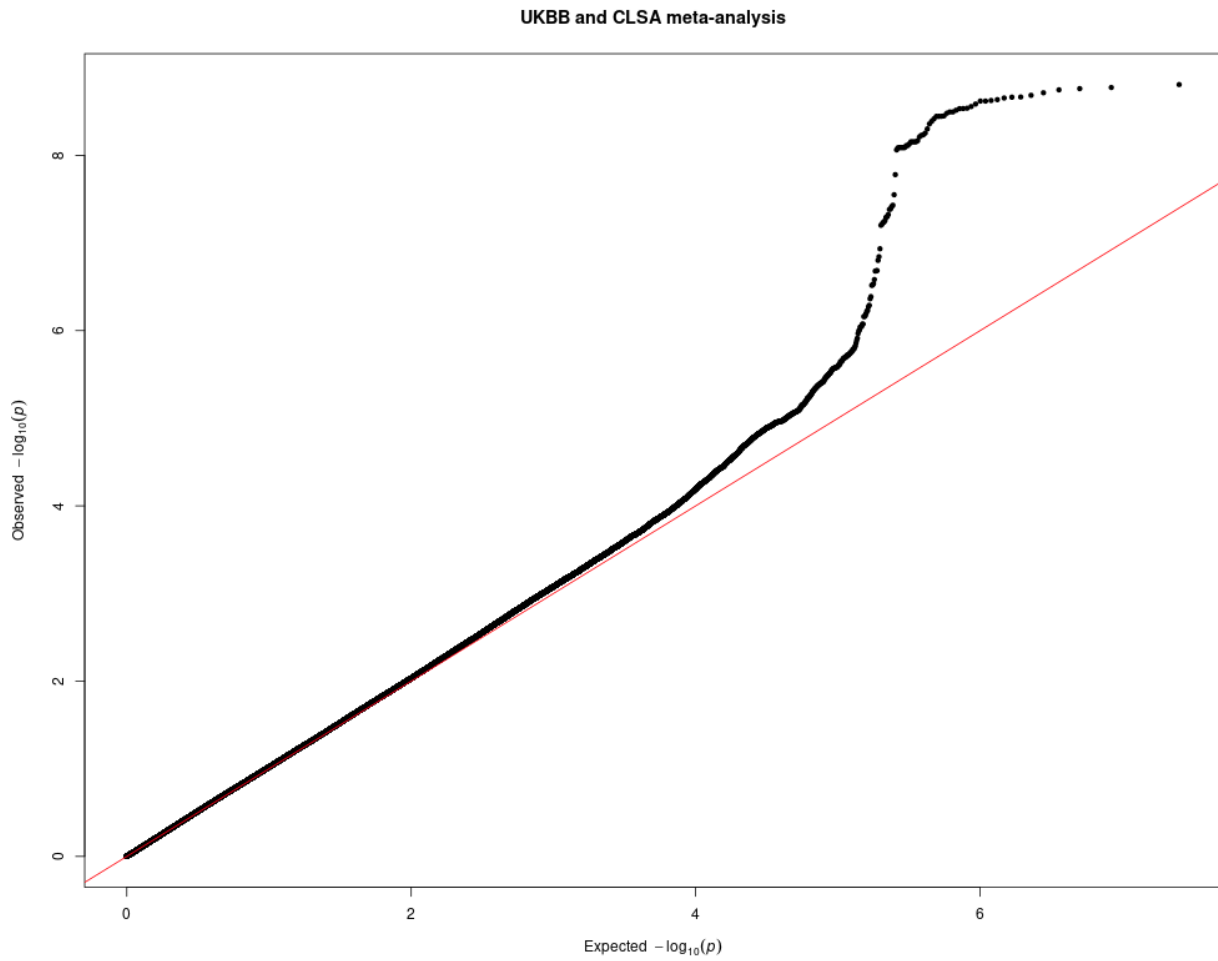
Supplementary Figure 5. Manhattan plot based on the first stage of the GWAS meta-analysis (N Cases = 6,186; N Controls = 57,997; N VCDR = 97,939). The red line represents the threshold for multiple testing correction ($p < 5 \times 10^{-8}$) and the blue line $p < 5 \times 10^{-6}$; p-values derived from logistic regression models are two-sided.



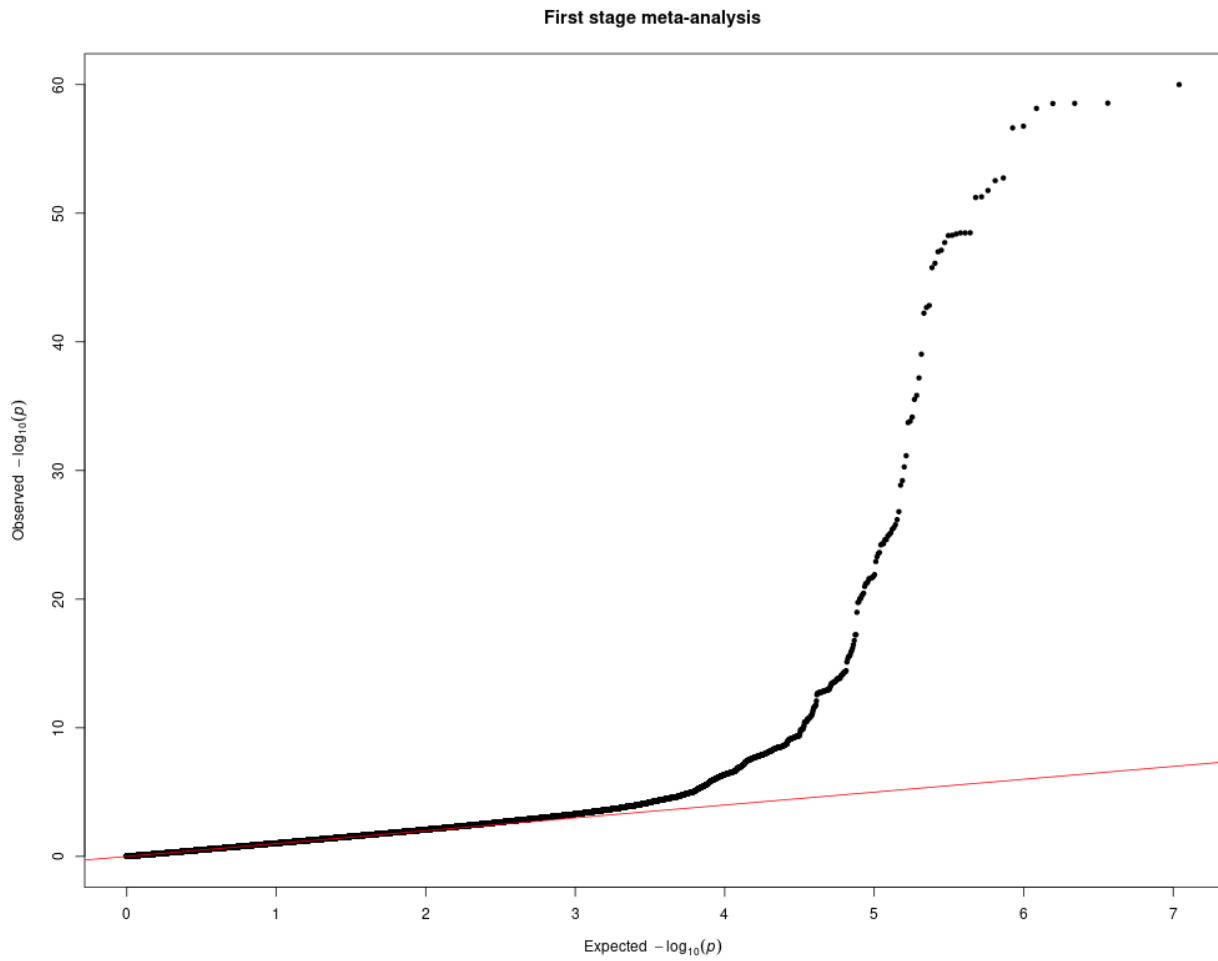
Supplementary Figure 6. Manhattan plot based on the GWAS meta-analysis of IGGC and FinnGen, as part of the second meta-analysis stage (N Cases = 7,942; N Controls = 384,431; N VCDR = 97,939). The red line represents the threshold for multiple testing correction ($p < 5 \times 10^{-8}$) and the blue line $p < 5 \times 10^{-6}$; p-values derived from logistic regression models are two-sided.



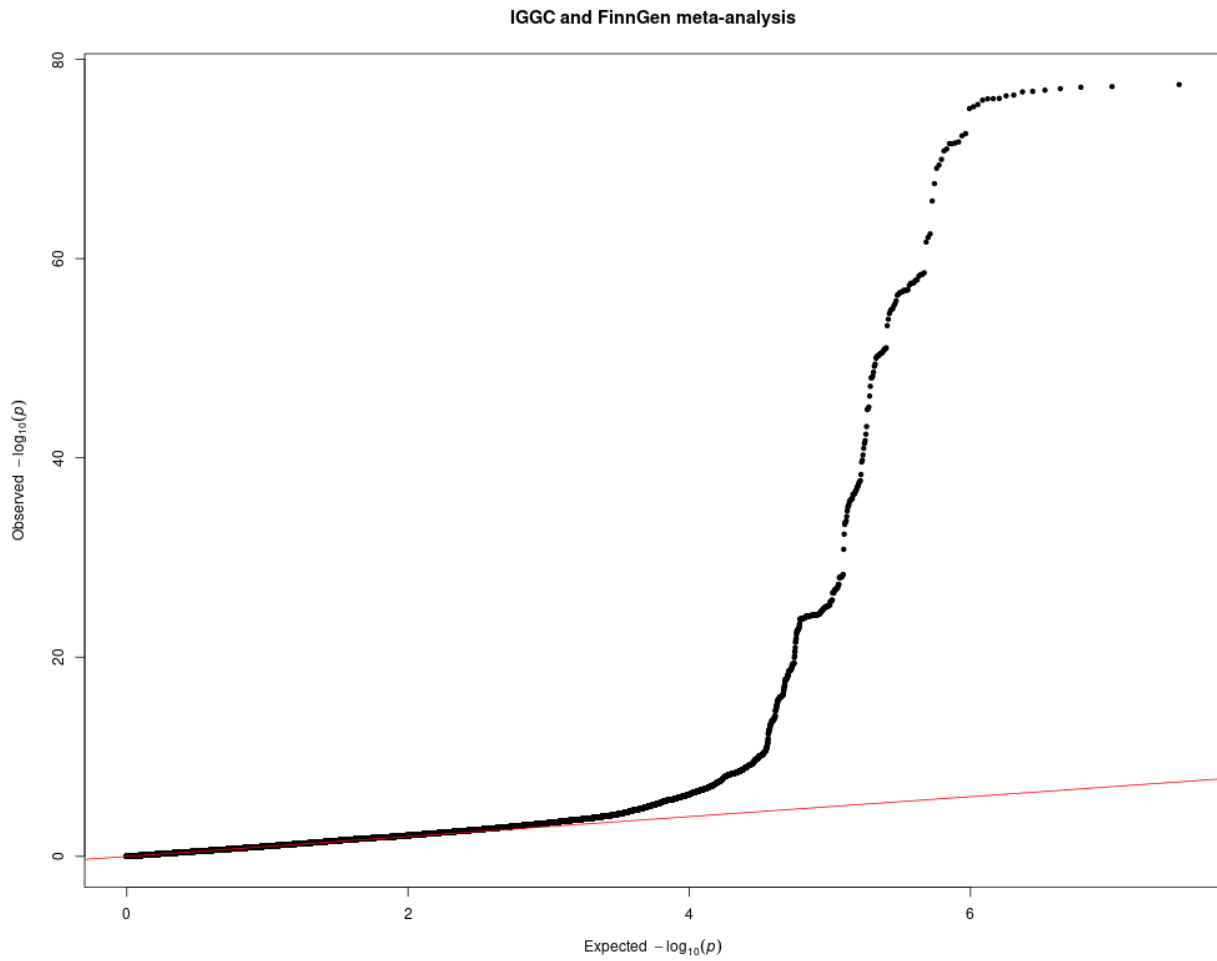
Supplementary Figure 7. Manhattan plot based on the association of VCDR loci adjusted by intra-ocular pressure using the mtCOJO method ($N = 97,939$). The red line represents the threshold for multiple testing correction ($p < 5 \times 10^{-8}$) and the blue line $p < 5 \times 10^{-6}$; p-values derived from logistic regression models are two-sided.



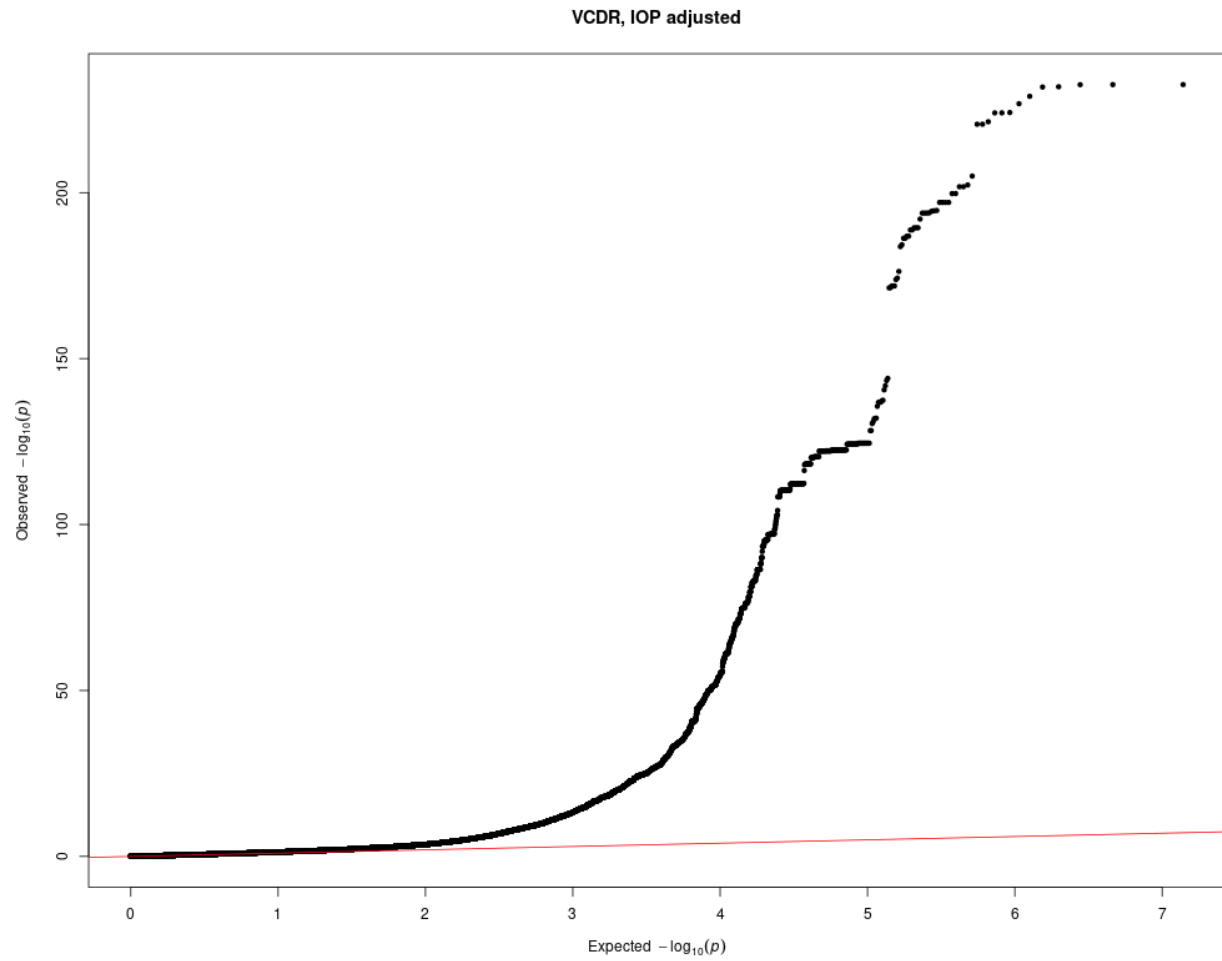
Supplementary Figure 8. QQ Plot based on the UKBB and CLSA meta-analysis of normal tension glaucoma (NTG) with an estimated genetic inflation factor (λ) of 1.02.



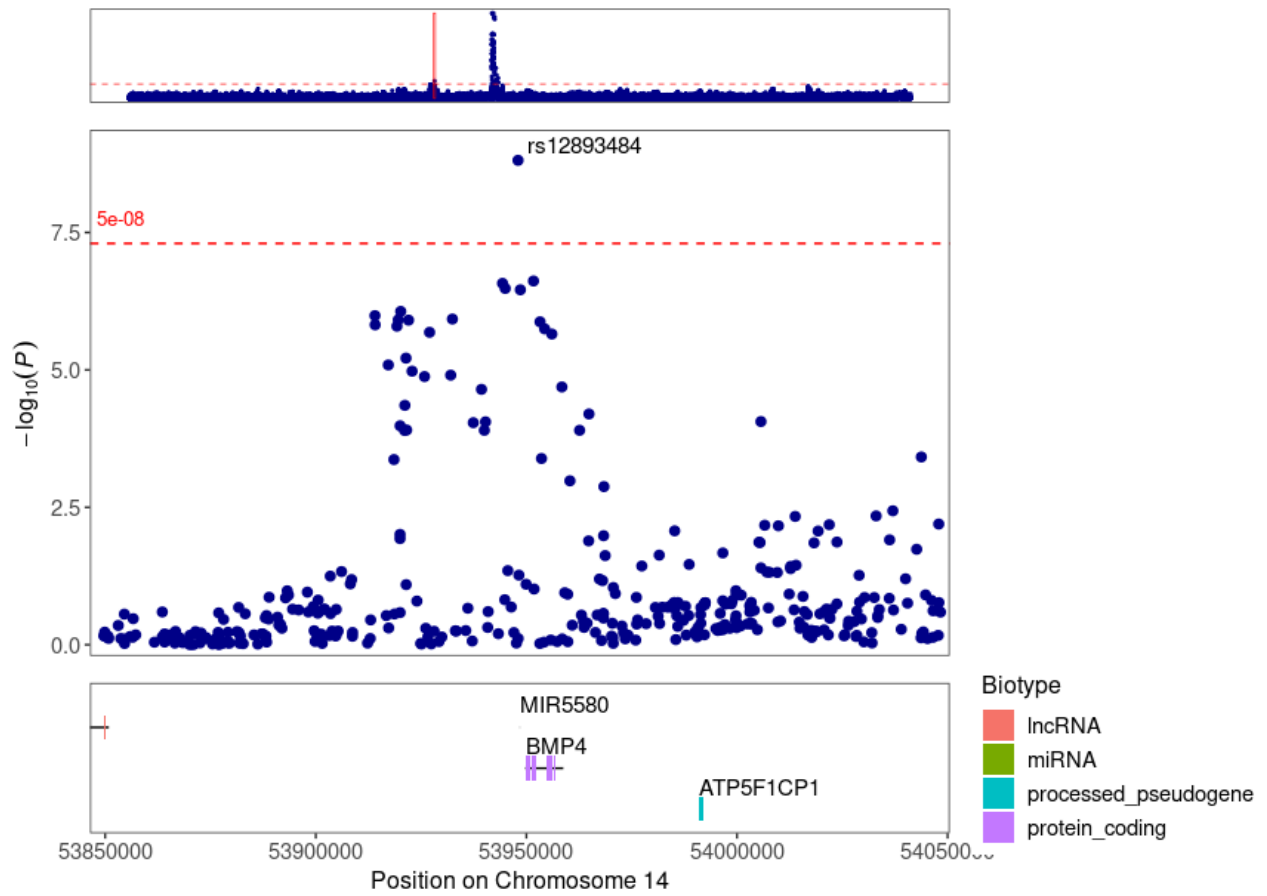
Supplementary Figure 9. QQ Plot based on the IGGC and FinnGen meta-analysis of normal tension glaucoma (NTG) with an estimated genetic inflation factor (λ) of 1.02



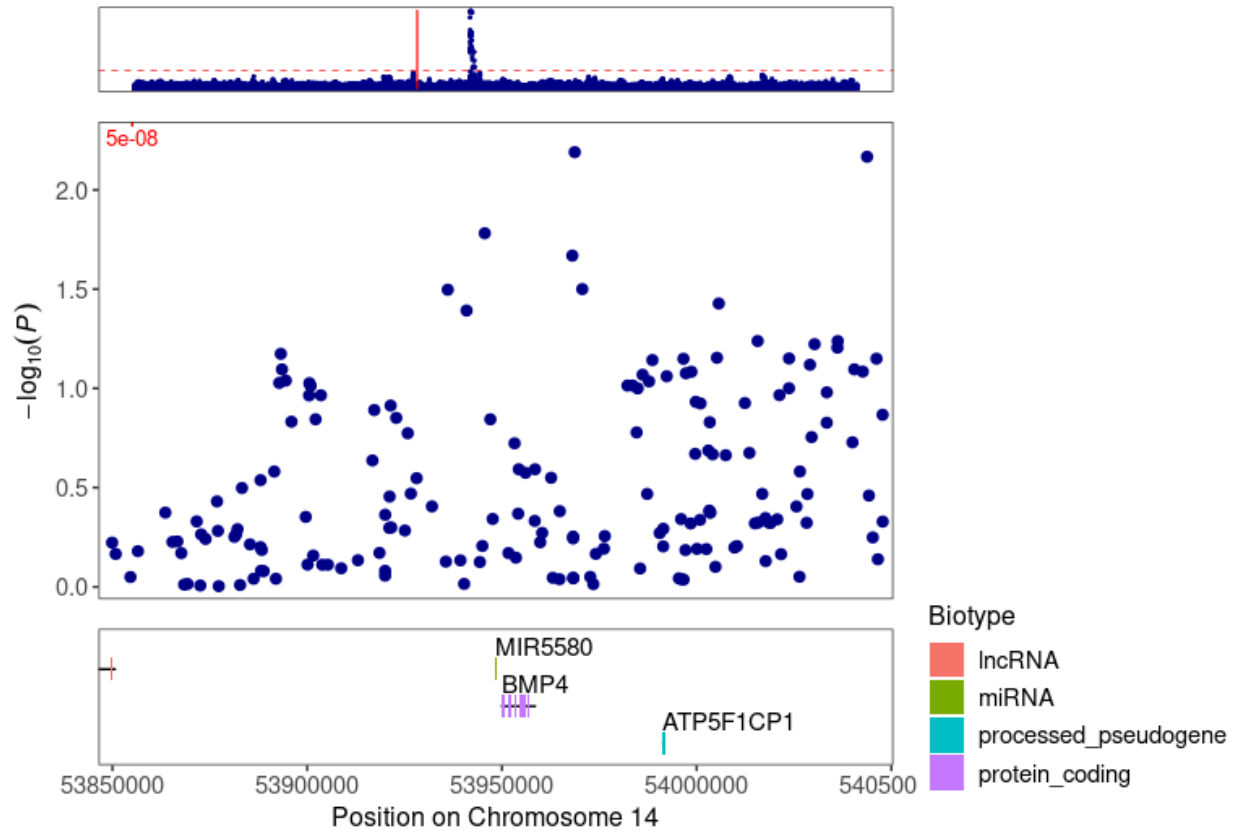
Supplementary Figure 10. QQ Plot based on the IGGC and FinnGen meta-analysis of normal tension glaucoma (NTG) with an estimated genetic inflation factor (λ) of 0.97



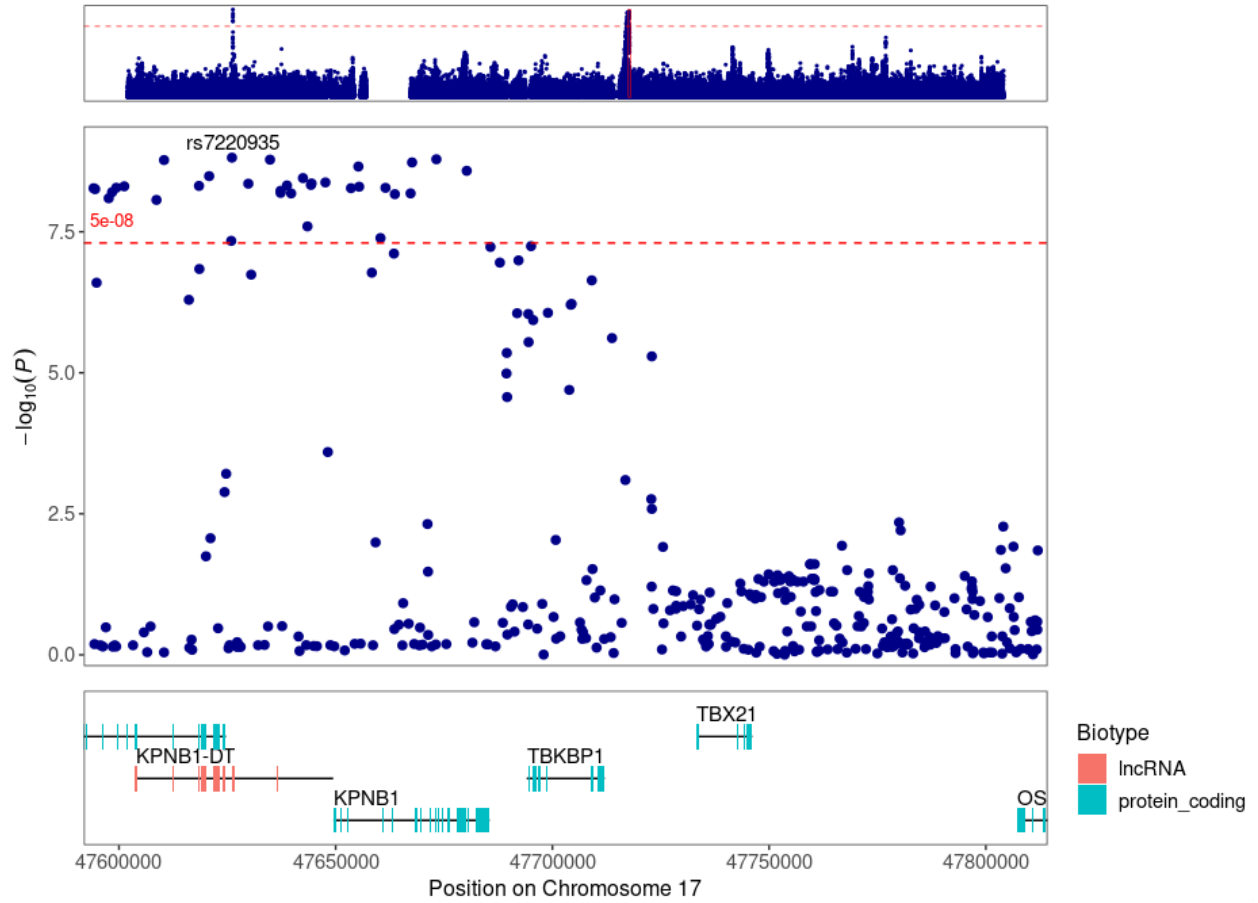
Supplementary Figure 11. QQ Plot based on the VCDR analysis adjusted for intra-ocular pressure with an estimated genetic inflation factor (λ) of 1.01.



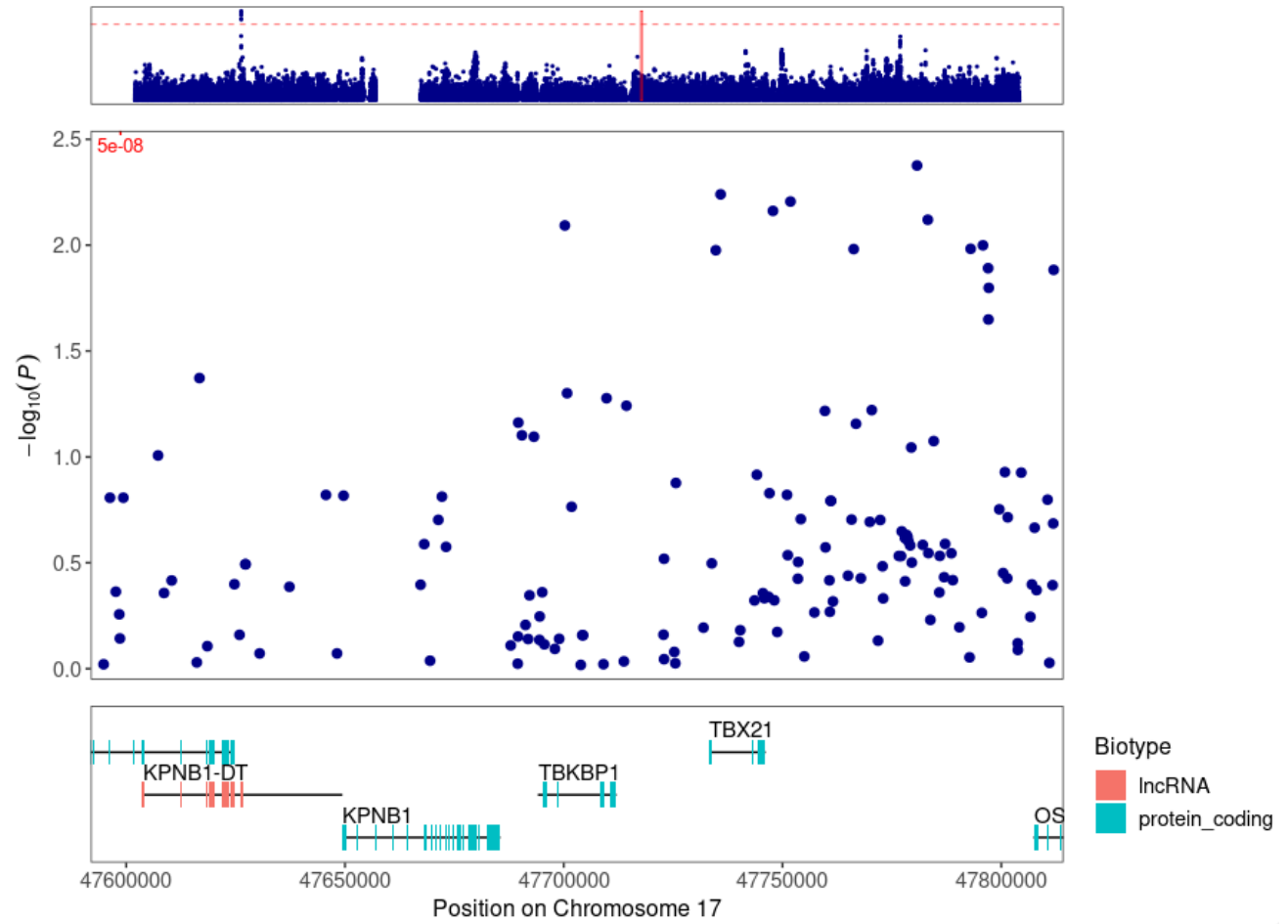
Supplementary Figure 12. Zoom plot of the *BMP4* region before conditional analysis of the rs12893484 locus using GCTA-COJO.



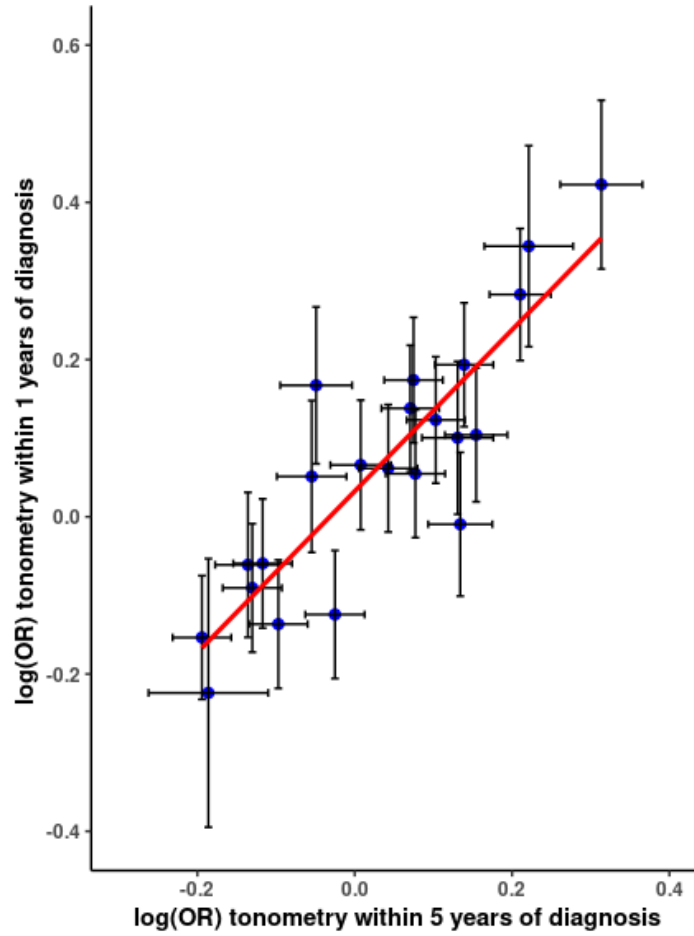
Supplementary Figure 13. Zoom plot of the BMP4 region after conditional analysis of the rs12893484 locus using GCTA-COJO.



Supplementary Figure 14. Zoom plot of the *TBKBP1* region before conditional analysis of the rs7220935 locus using GCTA-COJO.



Supplementary Figure 15. Zoom plot of the *TBKBP1* region after conditional analysis of the rs7220935 locus using GCTA-COJO.



Supplementary Figure 16. Inverse weighted variance correlation of the effect size between the 22 identified loci in two MTAG outputs (N=22): one including participants who had tonometry performed within 1 year of diagnosis, and the other within 5 years of diagnosis.