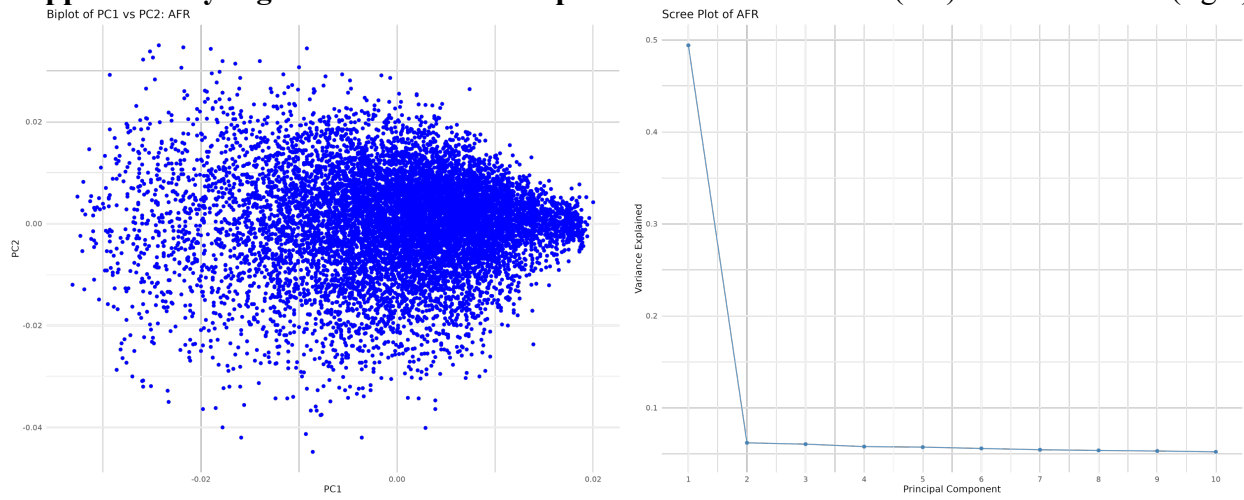
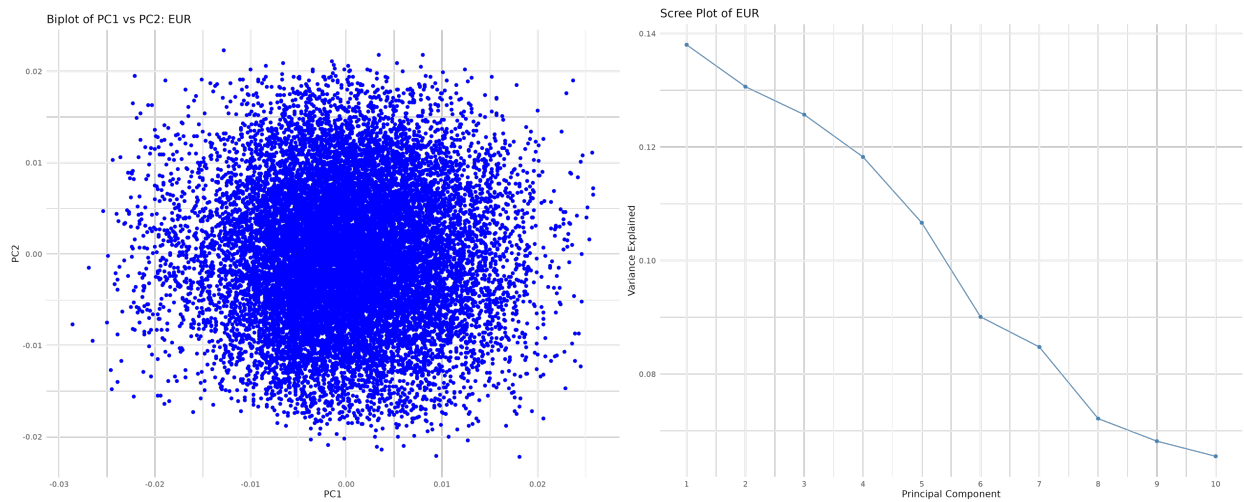


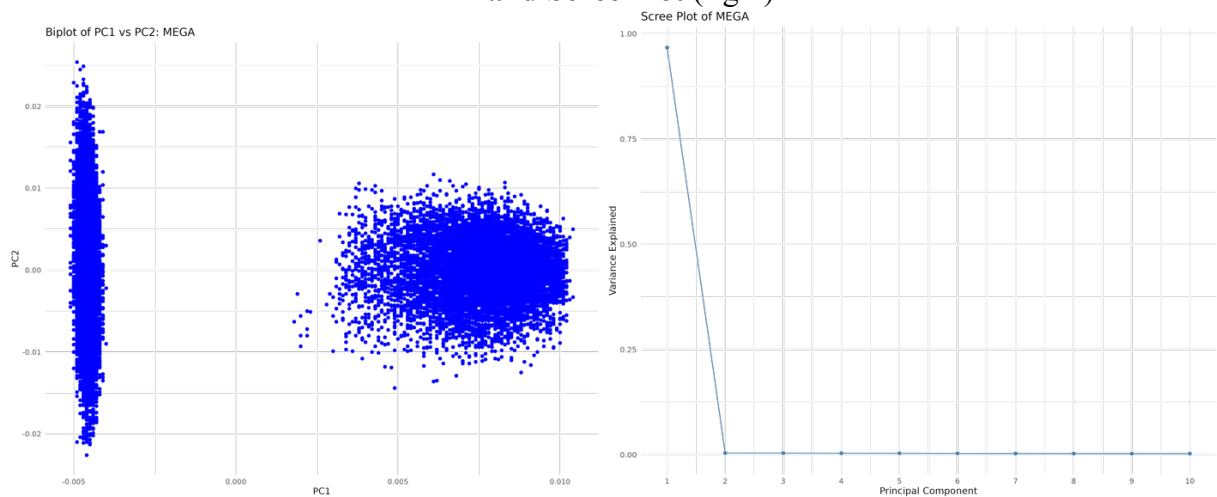
Supplementary Figure 1: PMBB AFR-Specific PC1 vs. PC2 Plot (left) and Scree Plot (right)



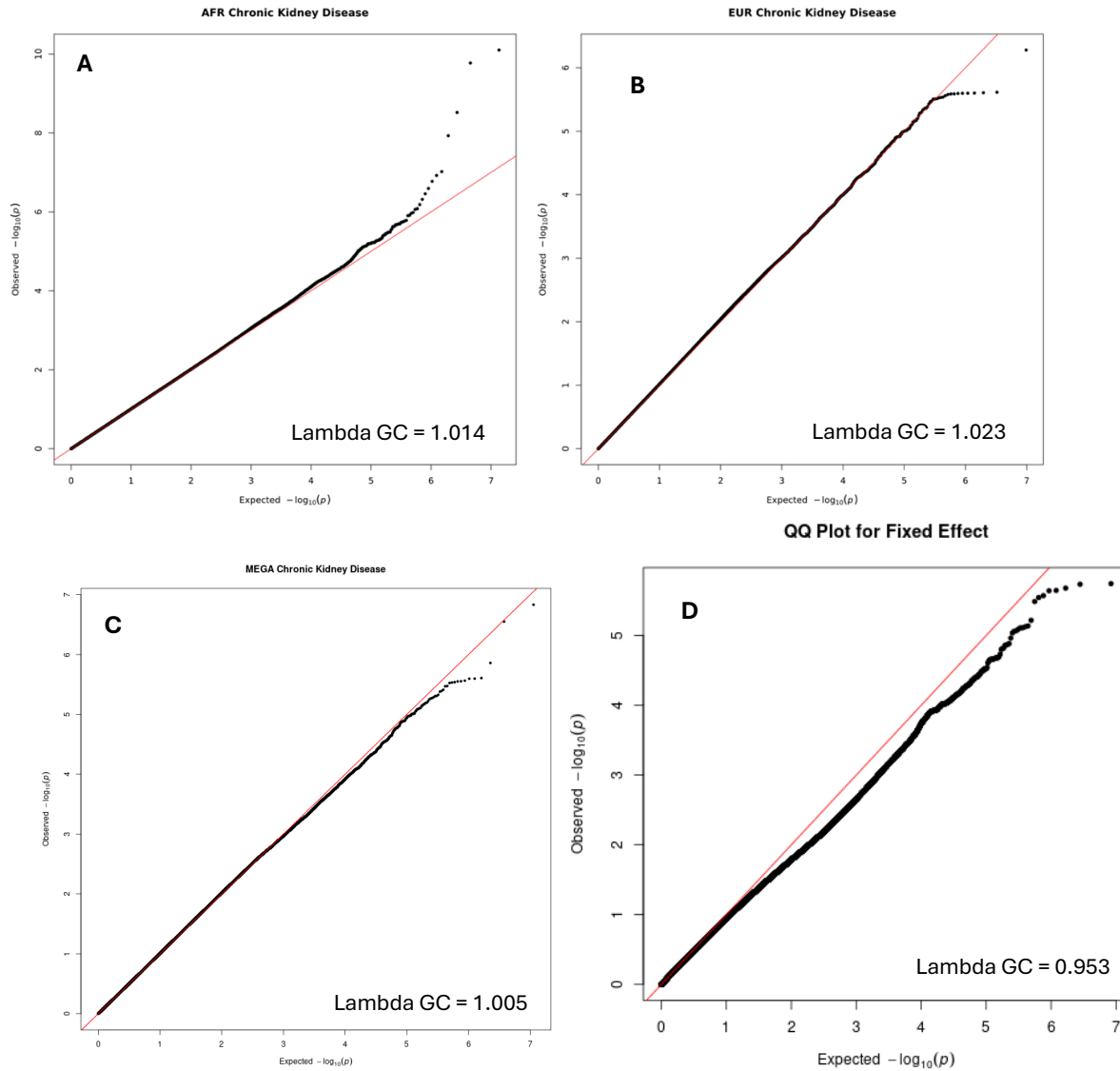
Supplementary Figure 2: PMBB EUR-Specific PC1 vs. PC2 Plot (left) and Scree Plot (right)



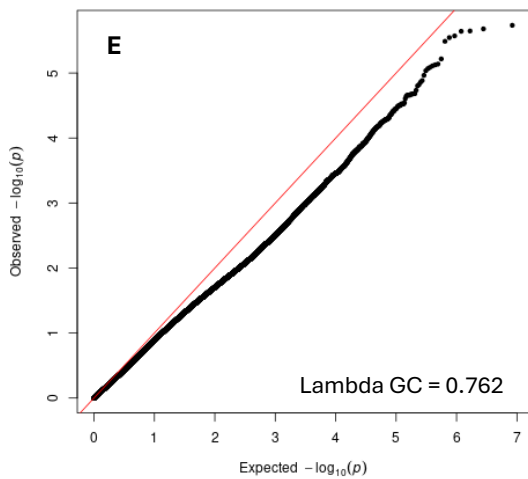
Supplementary Figure 3: PMBB Multi-Ancestry MEGA Analysis PC1 vs. PC2 Plot (left) and Scree Plot (right)



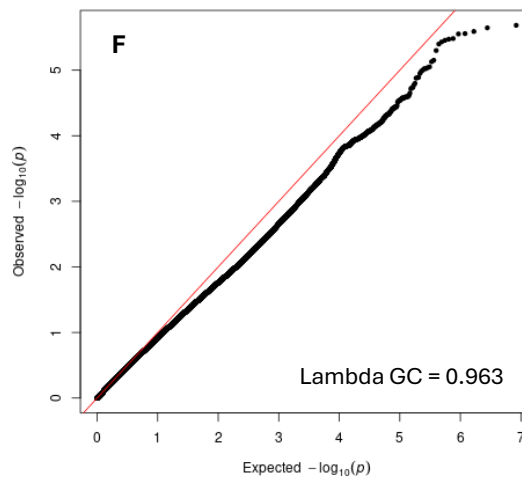
Supplementary Figure 4: CKD QQ Plots. A) AFR-specific, B) EUR-specific, C) Multi-Ancestry MEGA analysis, D) fixed effect meta-analysis E) random effect meta-analysis, F) modified random effect meta-analysis, and G) modified random effect meta-analysis with adjustment for mean effect size and heterozygosity.



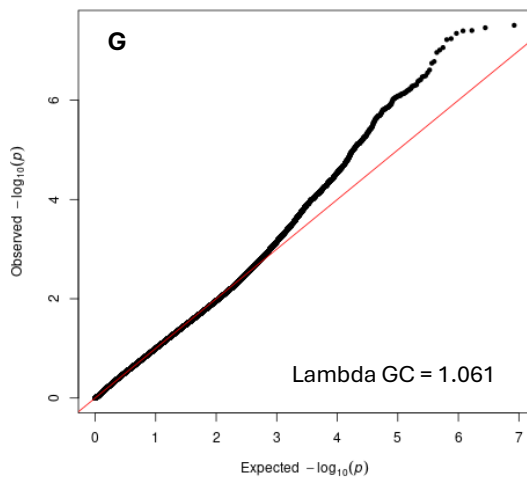
QQ Plot for Random Effect



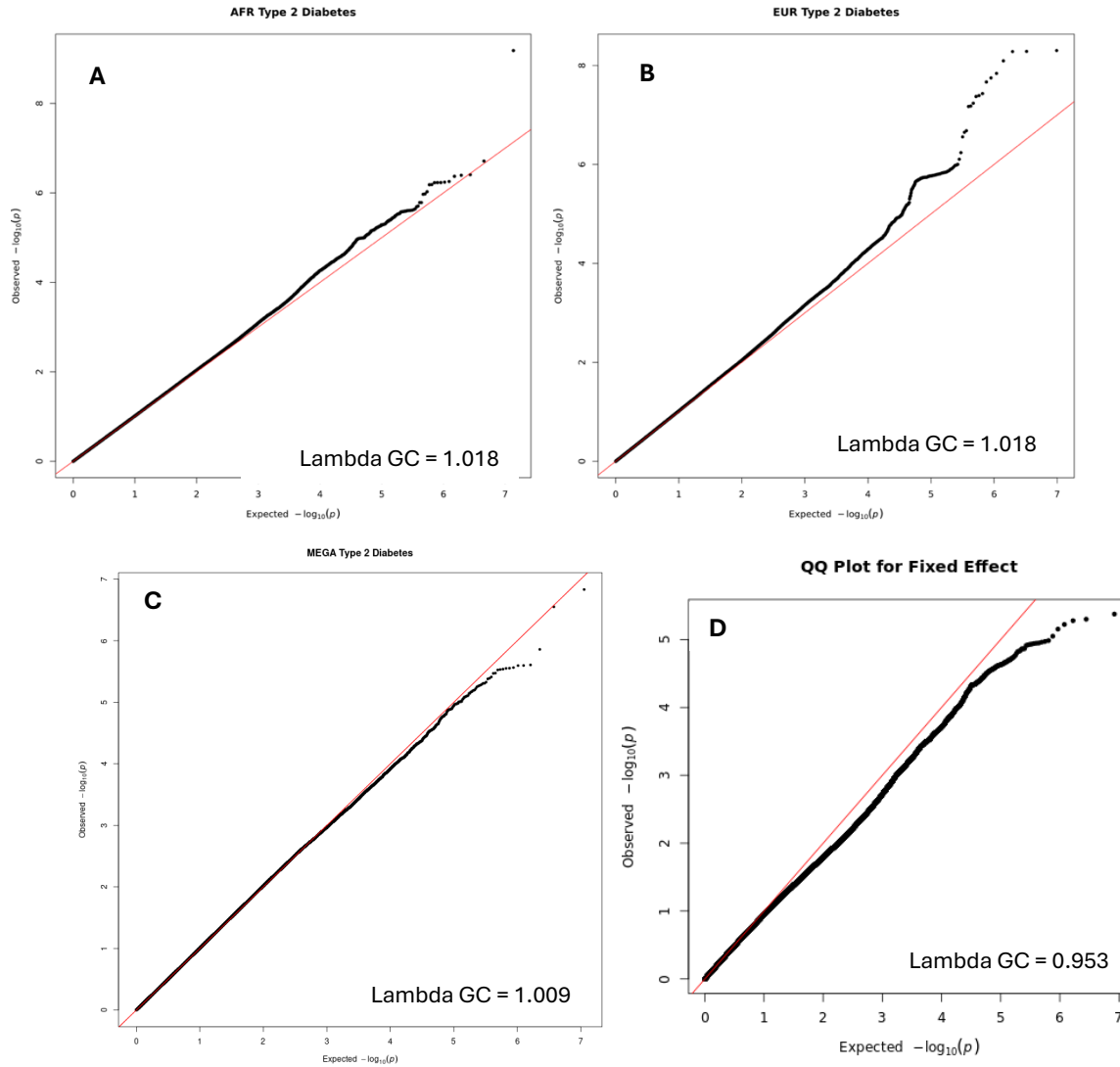
QQ Plot for RE2

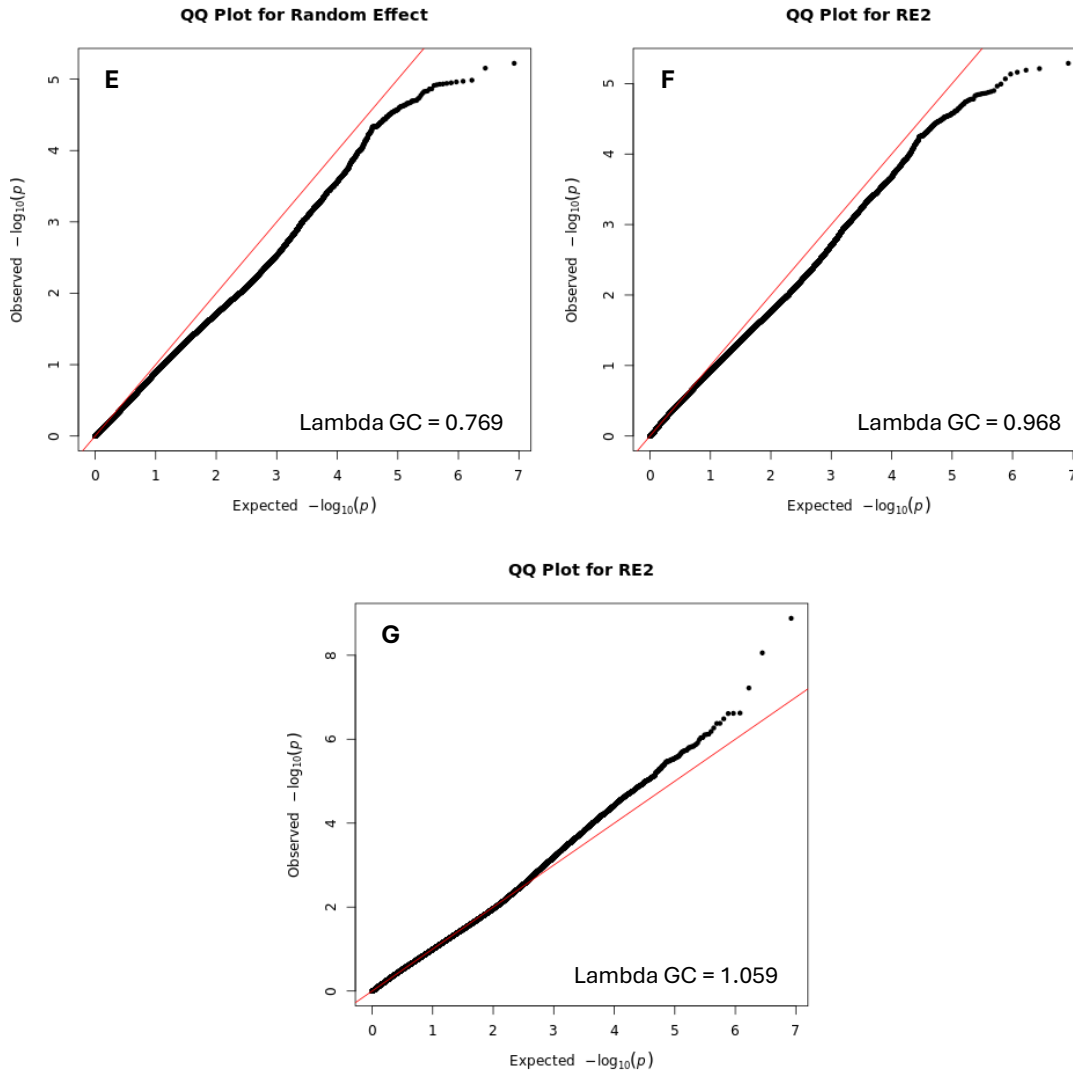


QQ Plot for RE2



Supplementary Figure 5: T2D QQ Plots. A) AFR-specific, B) EUR-specific, C) Multi-Ancestry MEGA analysis, D) fixed effect meta-analysis E) random effect meta-analysis, F) modified random effect meta-analysis, and G) modified random effect meta-analysis with adjustment for mean effect size and heterozygosity.





Supplementary Table 1: Percentage of Variants Genome-Wide with Direction of Effect Changes. 4,184,455 variants were included in the calculations.

Phenotype	All Analyses	AFR vs. Multi-Ancestry Analyses	EUR vs. Multi-Ancestry Analyses	MEGA vs. Meta Analyses	Fixed Effect vs. Random Effect Meta Analyses
Percentage of CKD Variants	67.78%	53.07%	54.14%	36.47%	2.26%
Percentage of T2D Variants	67.80%	53.89%	53.82%	36.70%	2.45%

Supplementary Table 2: Percentage of Variants in Multi-Ancestry Analyses with Effect Sizes within the Range of Ancestry-Specific Effect Sizes. 4,184,455 variants were included in the genome-wide calculations. Among the most significant variants, 74 variants were included in the T2D calculation, and 66 variants were included in the CKD calculation.

	CKD		T2D	
Analysis Group	Percentage of Genome-Wide Variants	Percentage of Most Significant Variants	Percentage of Genome-Wide Variants	Percentage of Most Significant Variants
Multi-Ancestry MEGA Analysis	47.73%	98.48%	46.23%	83.78%
Fixed Effect Meta Analysis	48.20%	84.85%	49.25%	86.49%
Random Effect Meta Analysis	48.15%	86.36%	49.24%	86.49%