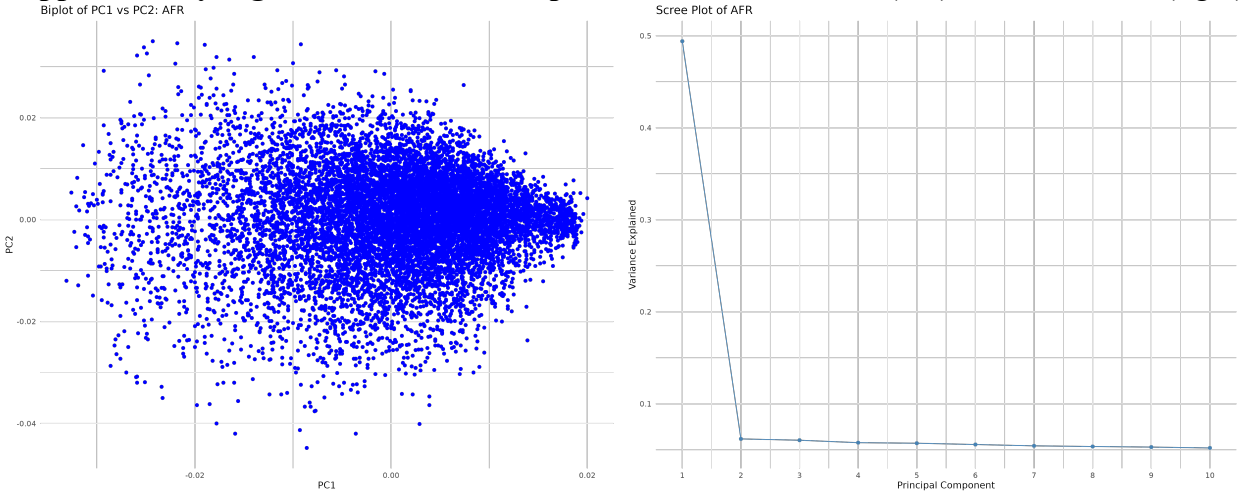
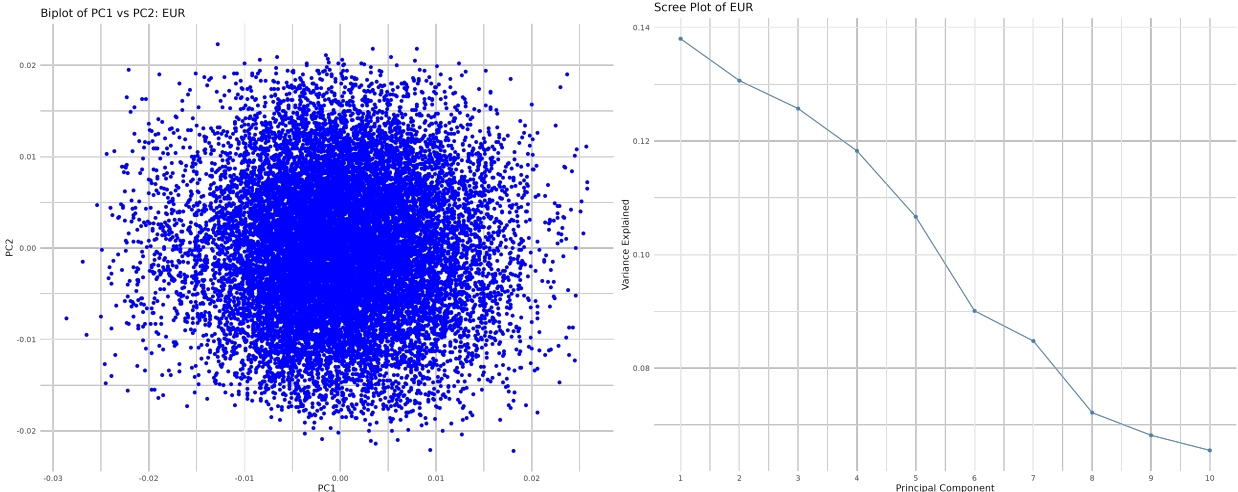


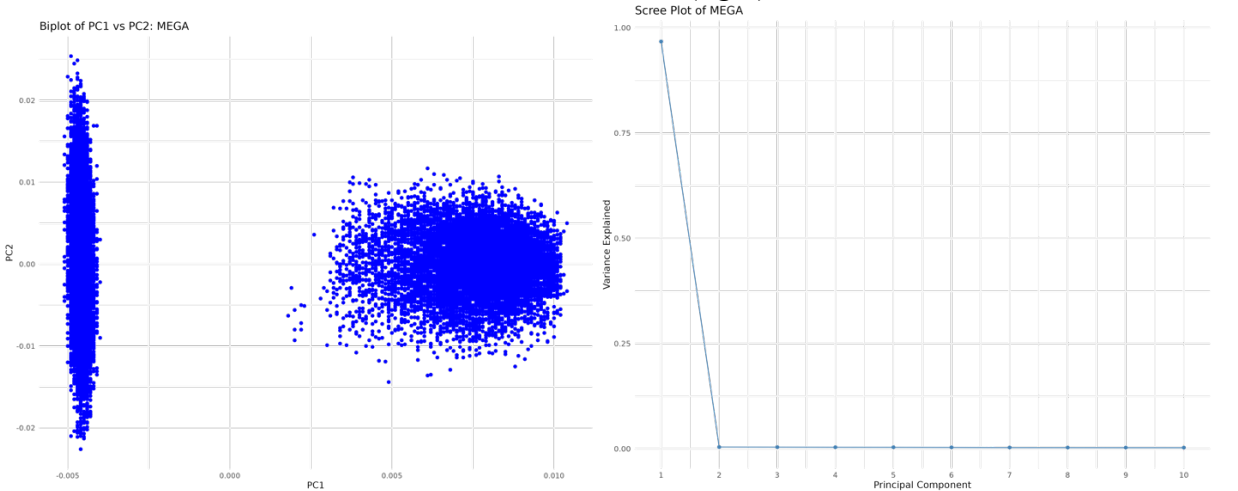
Supplementary Figure 1: PMBB AFR-Specific PC1 vs. PC2 Plot (left) and Scree Plot (right)



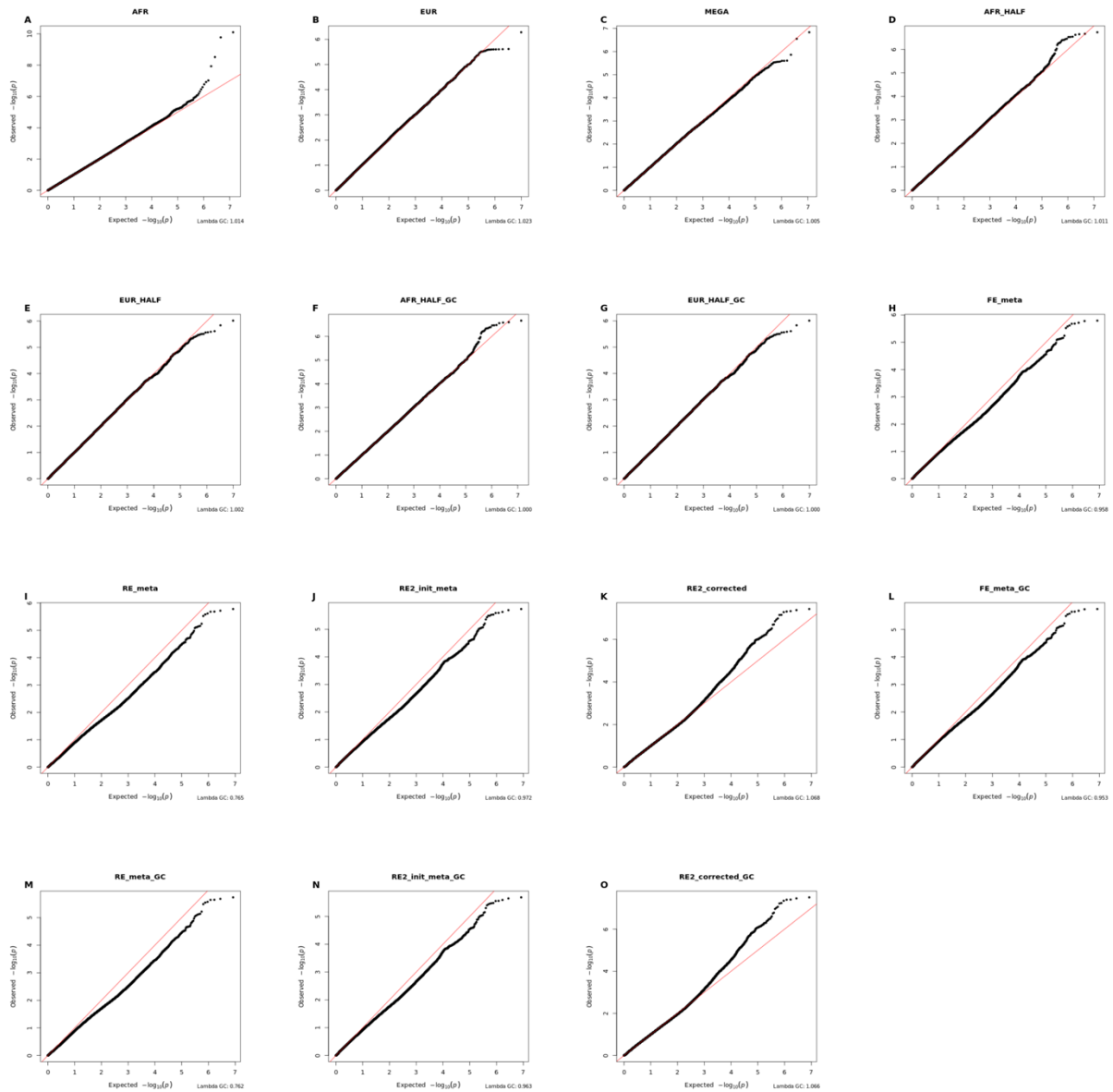
Supplementary Figure 2: PMBB EUR-Specific PC1 vs. PC2 Plot (left) and Scree Plot (right)



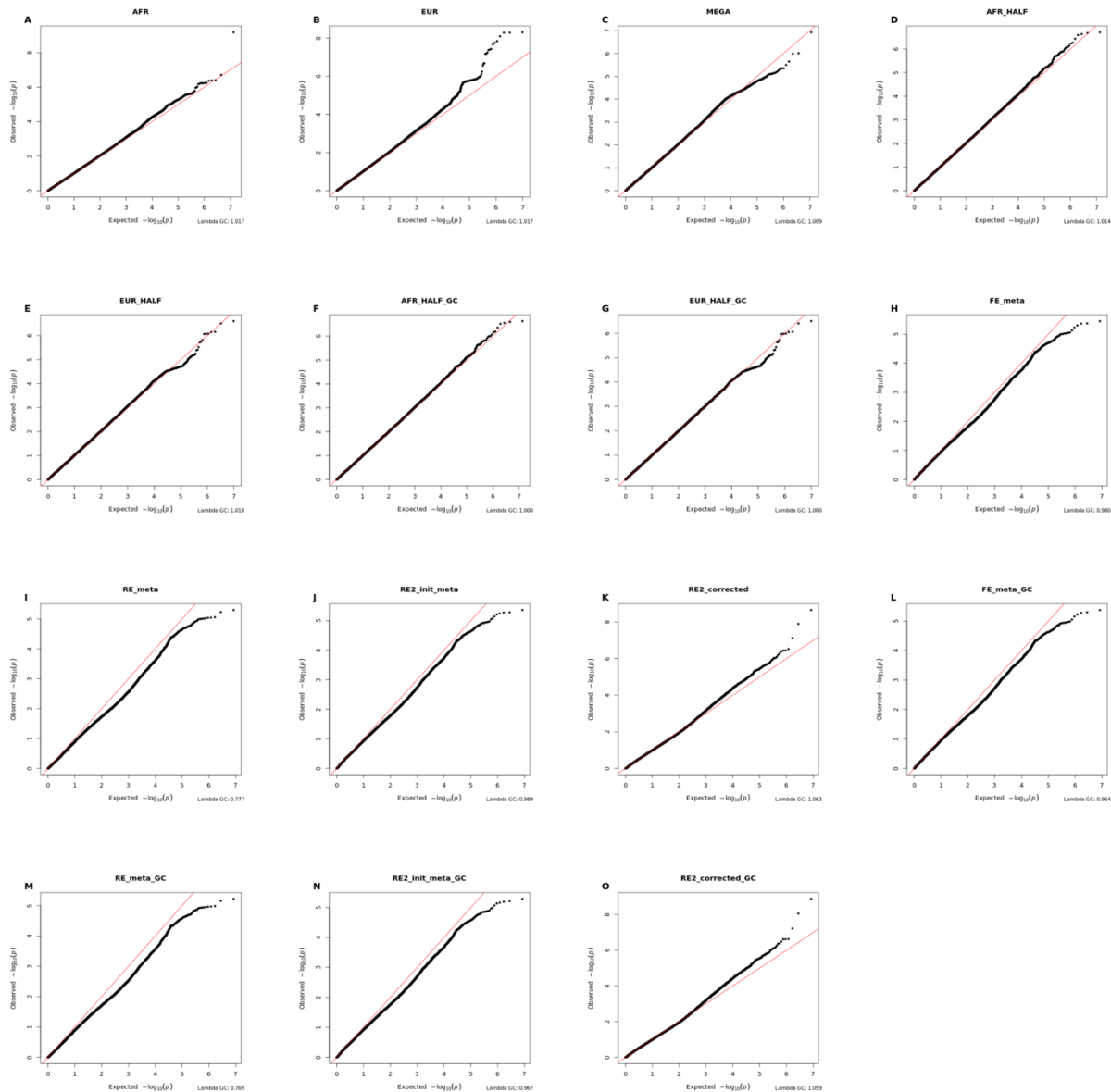
Supplementary Figure 3: PMBB Multi-Ancestry MEGA Analysis PC1 vs. PC2 Plot (left) and Scree Plot (right)



Supplementary Figure 4: CKD QQ Plots. A) AFR-specific, B) EUR-specific, C) Multi-Ancestry MEGA analysis, D) down-sampled AFR-specific (no genomic control) E) down-sampled EUR-specific (no genomic control), F) down-sampled AFR-specific (genomic control), G) down-sampled EUR-specific (genomic control), H) fixed effect meta-analysis (no genomic control), I) random-effect meta-analysis (no genomic control), J) modified random effect meta-analysis (no genomic control), K) modified random effect meta-analysis with adjustment for mean effect size and heterozygosity (no genomic control), L) fixed effect meta-analysis (genomic control), M) random-effect meta-analysis (genomic control), N) modified random effect meta-analysis (genomic control), and O) modified random effect meta-analysis with adjustment for mean effect and heterozygosity (genomic control).



Supplementary Figure 5: T2D QQ Plots. A) AFR-specific, B) EUR-specific, C) Multi-Ancestry MEGA analysis, D) down-sampled AFR-specific (no genomic control) E) down-sampled EUR-specific (no genomic control), F) down-sampled AFR-specific (genomic control), G) down-sampled EUR-specific (genomic control), H) fixed effect meta-analysis (no genomic control), I) random-effect meta-analysis (no genomic control), J) modified random effect meta-analysis (no genomic control), K) modified random effect meta-analysis with adjustment for mean effect size and heterozygosity (no genomic control), L) fixed effect meta-analysis (genomic control), M) random-effect meta-analysis (genomic control), N) modified random effect meta-analysis (genomic control), and O) modified random effect meta-analysis with adjustment for mean effect and heterozygosity (genomic control).



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, 75 variants were included in the T2D calculation, and 66 variants were included in the CKD calculation.

| Analysis Group | CKD | | T2D | |
|------------------------------|------------------------------------|---|------------------------------------|---|
| | 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% |