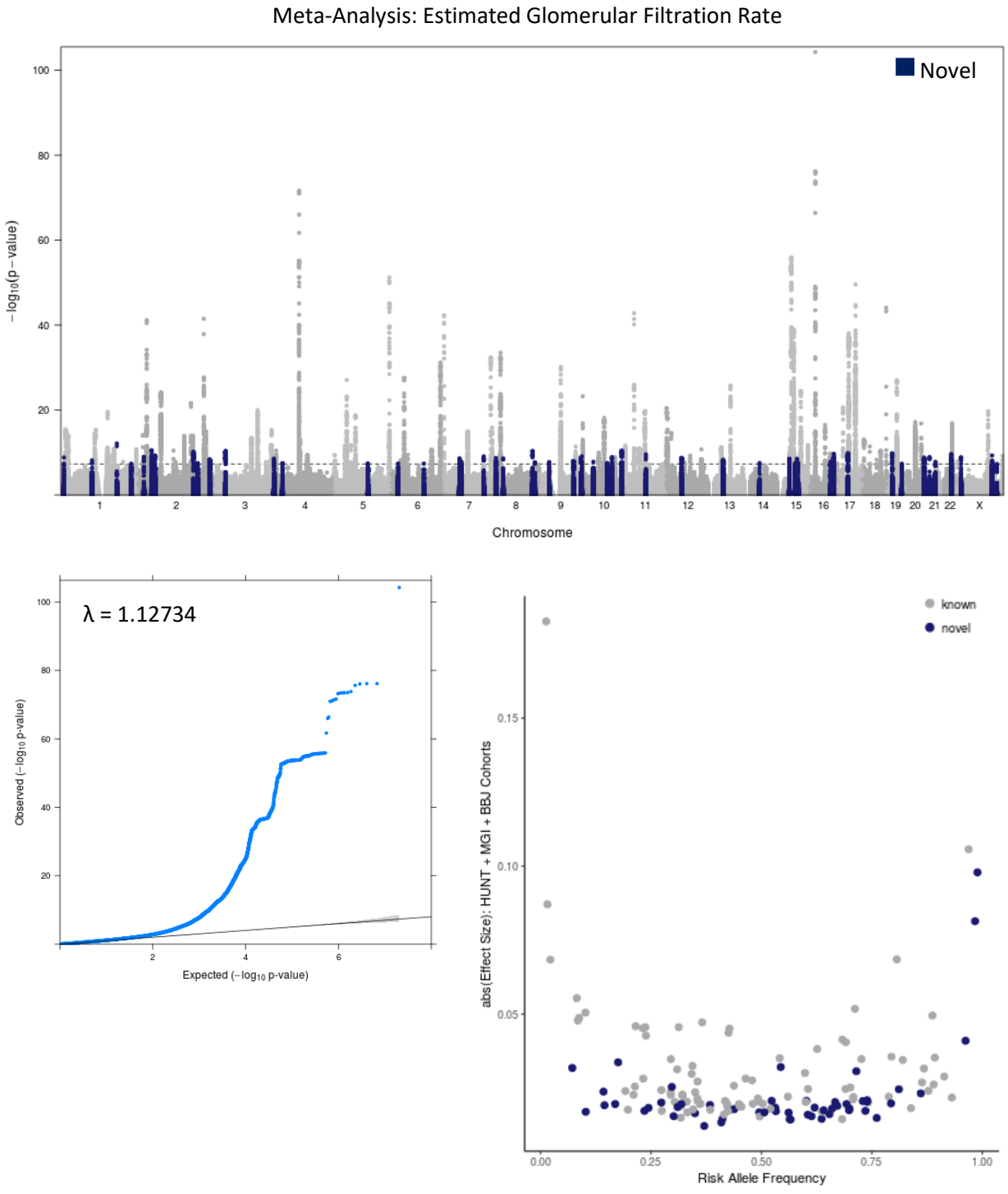
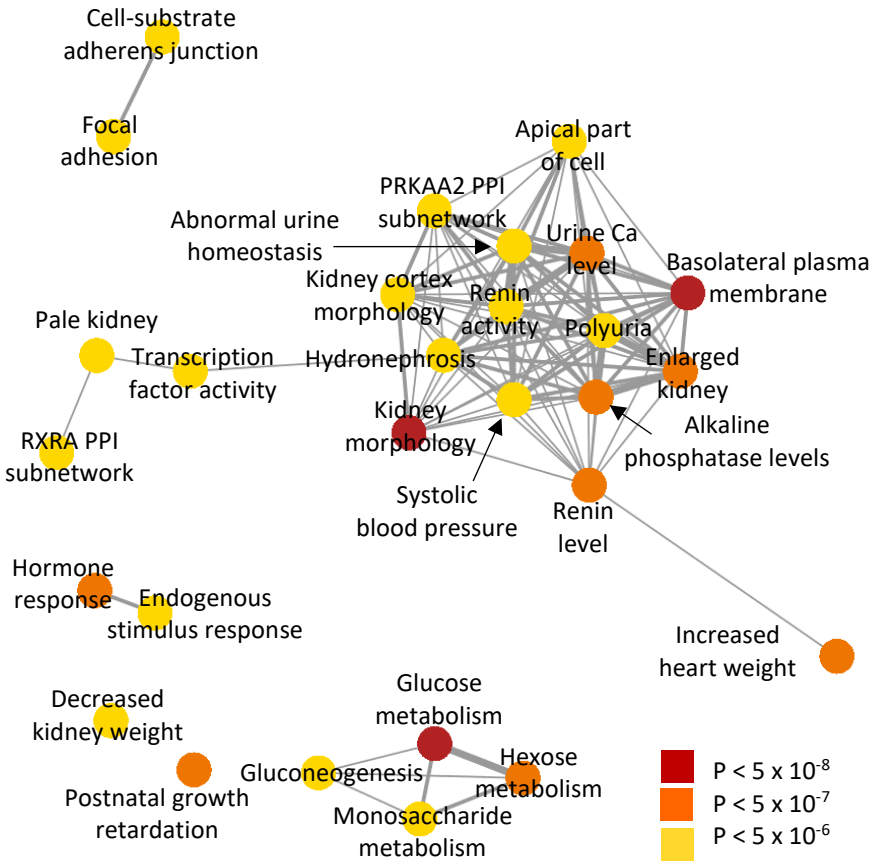
Supplementary information for Graham et al. manuscript

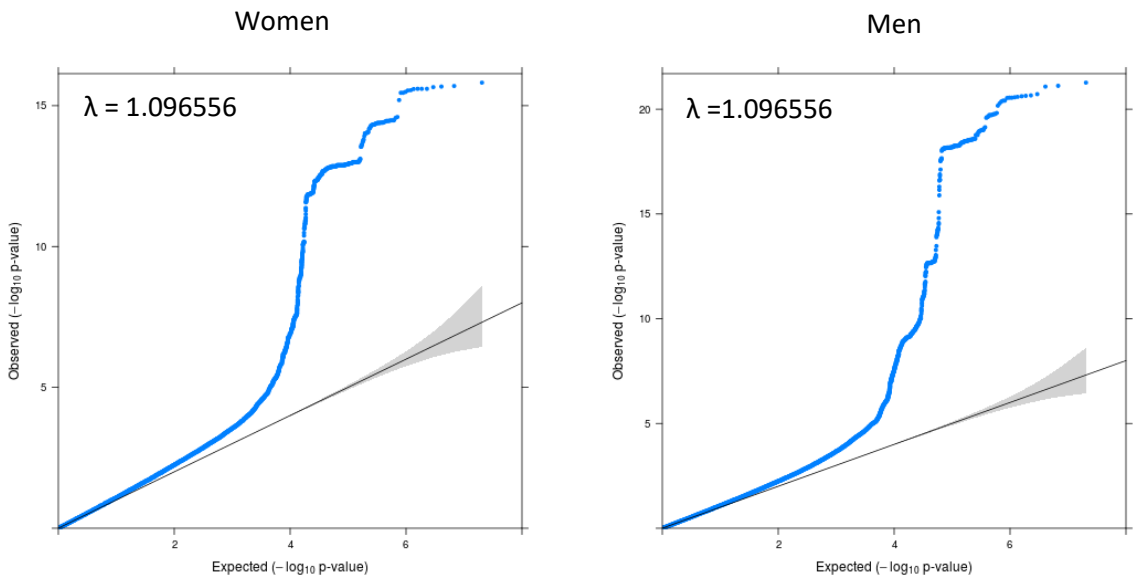
Supplementary Figure 1: Manhattan and QQ Plot (MAF > 0.5%) from Meta-analysis of eGFR. The effect sizes (from meta-analysis of HUNT, MGI, and BBJ cohorts due to differing units of CKDGen consortium) are plotted against the risk allele frequencies for the index variants from the overall meta-analysis.



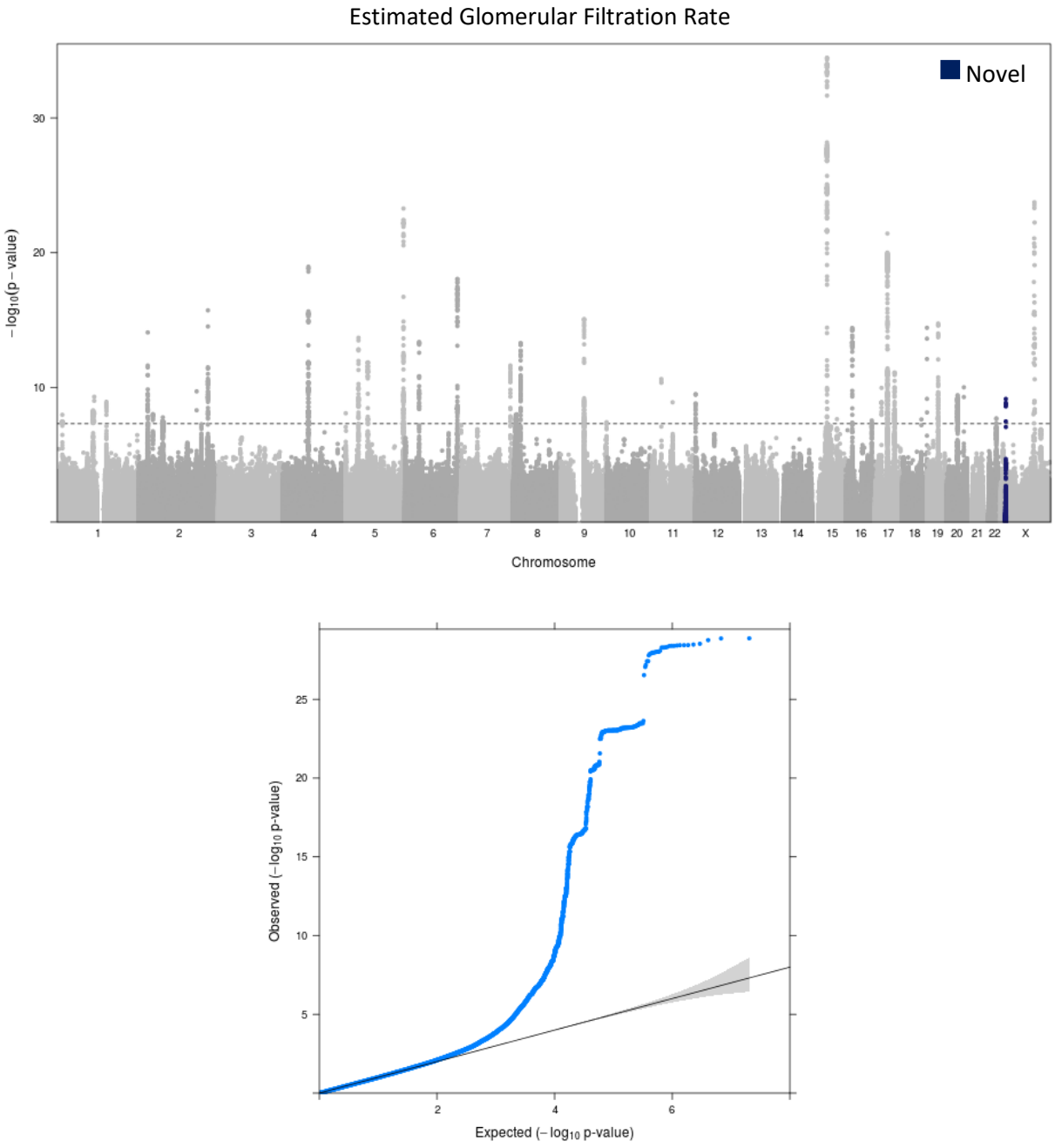
Supplementary Figure 2: DEPICT network graph prior to collapsing overlapping gene sets. Overlap between gene sets is depicted by the width of connecting lines.



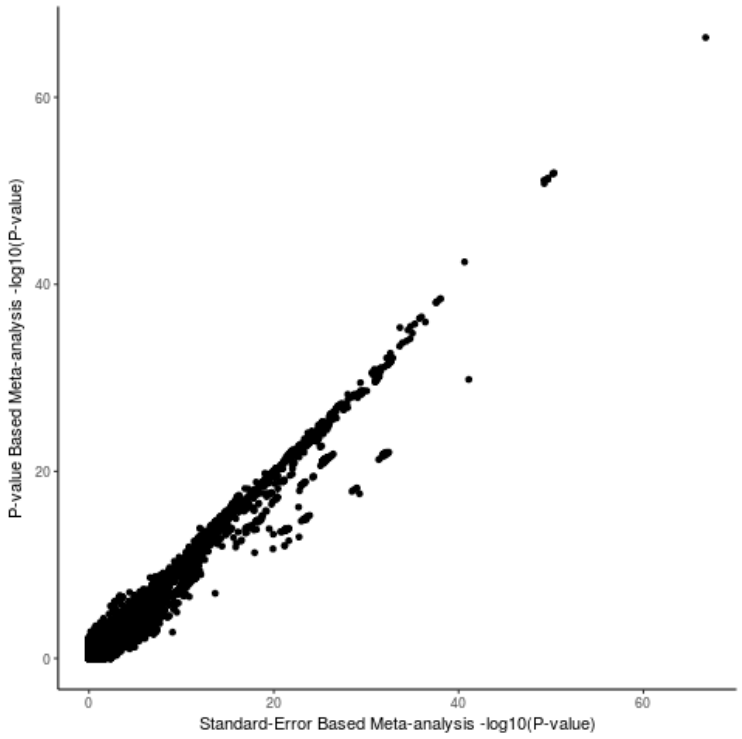
Supplemental Figure 3: QQ Plots from Sex-Specific Analysis



Supplementary Figure 4: Manhattan and QQ Plot from HUNT analysis of eGFR



Supplementary Figure 5: Meta-analysis of the HUNT, BBJ, and MGI cohorts was performed using both p-value and standard-error –based approaches. The overall correlation in p-values for individual variants between methods was extremely high (Pearson r = 0.9662302). P-values obtained using the standard-error-based approach trended towards increased significance for a subset of variants. Variants reaching genome-wide significance were overwhelmingly similar between methods.



Supplementary Figure 6: Genes from meta-analysis results were prioritized based on the consensus between the nearest gene, DEPICT prioritized gene, significantly colocalized eQTLs, and missense variants in LD with the index variant. In cases where there was not consensus, the gene was prioritized as the nearest gene.