

Description of Additional Supplementary Files

Supplementary Data 1: Description of participating studies: study design and phenotype distribution.

Supplementary Data 2: 5,790 Genome-wide significant SNPs in the meta-analysis of eGFR GWASs from BBJ and TWB-based discovery data sets.

Supplementary Data 3: 97 Genomic risk loci in the meta-analysis of eGFR GWASs from BBJ and TWB-based discovery data sets.

Supplementary Data 4: Replication of eGFR-associated SNPs in an independent TWB-based replication data set.

Supplementary Data 5: Association of 3,899 replicated eGFR-associated SNPs with BUN in the meta-analysis of BUN GWASs from BBJ and TWB-based discovery data sets.

Supplementary Data 6: CKD validation of replicated eGFR-associated SNPs in the CMUH-CRDR data set.

Supplementary Data 7: ESKD validation of replicated eGFR-associated SNPs in the CMUH-CRDR data set.

Supplementary Data 8: Genetic correlation between eGFR, BUN, and 119 phenotypes GWAS from the TWB-based discovery data set.

Supplementary Data 9: Tissue enrichment analysis of eGFR and BUN GWASs by MAGMA.

Supplementary Data 10: Gene set enrichment analysis of eGFR and BUN GWASs by MAGMA.

Supplementary Data 11: Cell-type-specific analysis of eGFR and BUN GWASs by using LD score regression.

Supplementary Data 12: Credible set size of independent significant SNPs by using GCTA-COJO.

Supplementary Data 13: Functional annotation of SNPs in small credible sets (5 SNPs) or credible sets containing at least one SNP with posterior probability >50%.

Supplementary Data 14: Co-localization of Asian-specific eGFR-associations with gene expression in two kidney tissues: variants with >0.80 probability of colocalization.

Supplementary Data 15: Summary of constantly highlighted genes across different validation analyses.