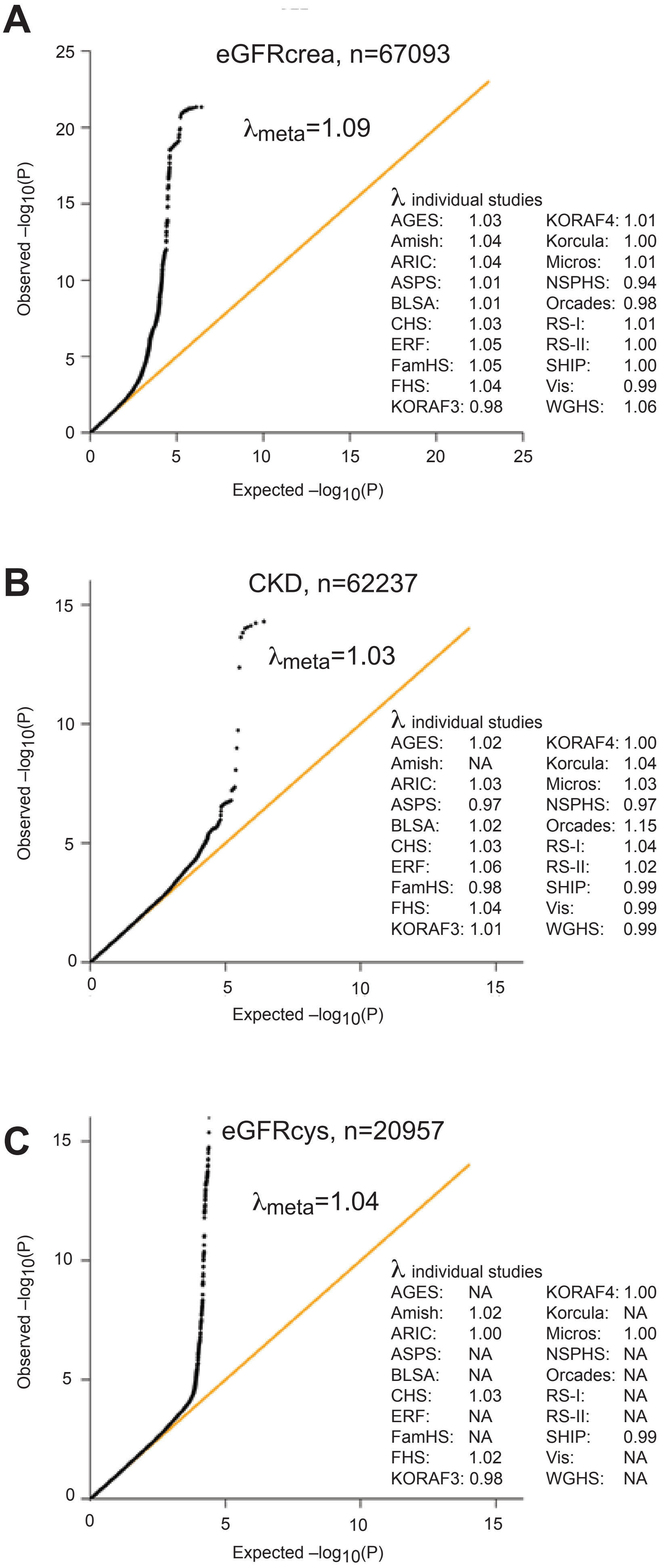
Suppl. Figure 1



λ_{meta} represents the genomic control parameters after discovery meta-analysis, and the λ for the individuals studies is reported next to each trait. The graphs present p-values corrected for inflation at the study-specific level before meta-analysis as well as after meta-analysis for the meta-analysis genomic control parameter. No correction was applied to data from studies with λ<1.The graph for eGFRcys is cut off; all SNPs with lower p-values are located at the *CST* locus on chromosome 20. NA denotes phenotype unavailability. Black: results from meta-analysis, orange: null hypothesis.