

Genome-wide association study of kidney function decline in individuals of European descent

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Genome-wide association studies (GWASs) have identified multiple loci associated with cross-sectional eGFR, but a systematic genetic analysis of kidney function decline over time is missing. Here we conducted a GWAS meta-analysis among 63,558 participants of European descent, initially from 16 cohorts with serial kidney function measurements within the CKDGen Consortium, followed by independent replication among additional participants from 13 cohorts.

In stage 1 GWAS meta-analysis, single-nucleotide polymorphisms (SNPs) at *MEOX2*, *GALNT11*, *IL1RAP*, *NPPA*, *HPCAL1*, and *CDH23* showed the strongest associations for at least one trait, in addition to the known *UMOD* locus, which showed genome-wide significance with an annual change in eGFR. In stage 2 meta-analysis, the significant association at *UMOD* was replicated. Associations at *GALNT11* with Rapid Decline (annual eGFR decline of 3 ml/min per 1.73 m² or

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