SUPPLEMENTARY DATA

Genome-wide Association Studies Identify Genetic Loci Associated with Albuminuria in Diabetes

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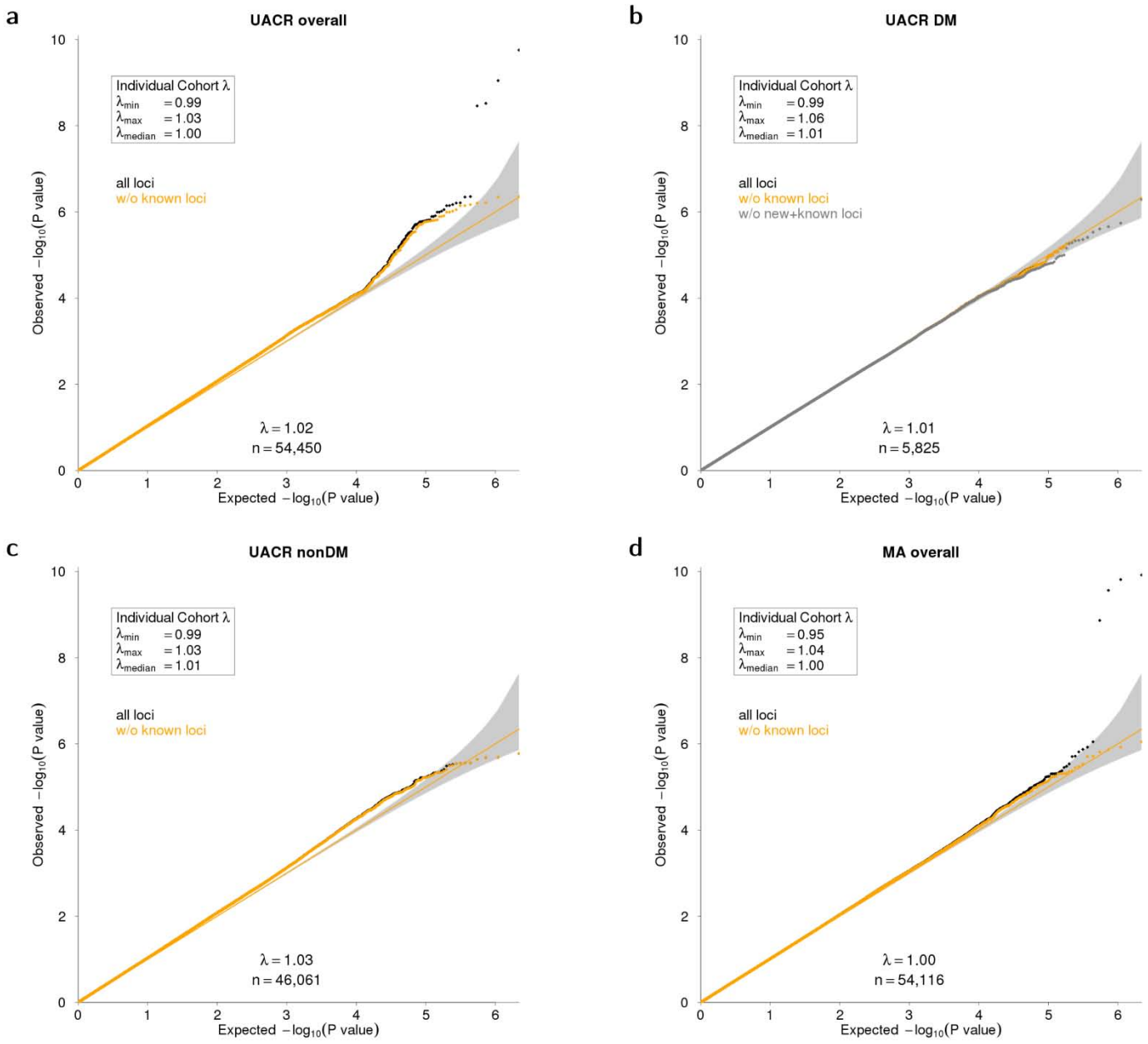
Supplementary Figure 1: QQ plots for all GWAS meta-analyses

Quantile-quantile (QQ) plots of the GWAS meta-analysis results for (**a**) the urinary albumin-to-creatinine ratio (UACR) in the overall sample, (**b**) UACR among those with diabetes (**c**) UACR among those without diabetes, and (**d**) microalbuminuria (MA) in the overall sample. The observed p-values are plotted on the y-axis against their expected distribution under the null hypothesis of no association on the x-axis.



Results for all SNPs are shown in black, and results after removal of loci previously known to contain trait-associated variants are shown in yellow. Gray bands represent 95% confidence intervals. λ: lambda, genomic control parameter; n: sample size.

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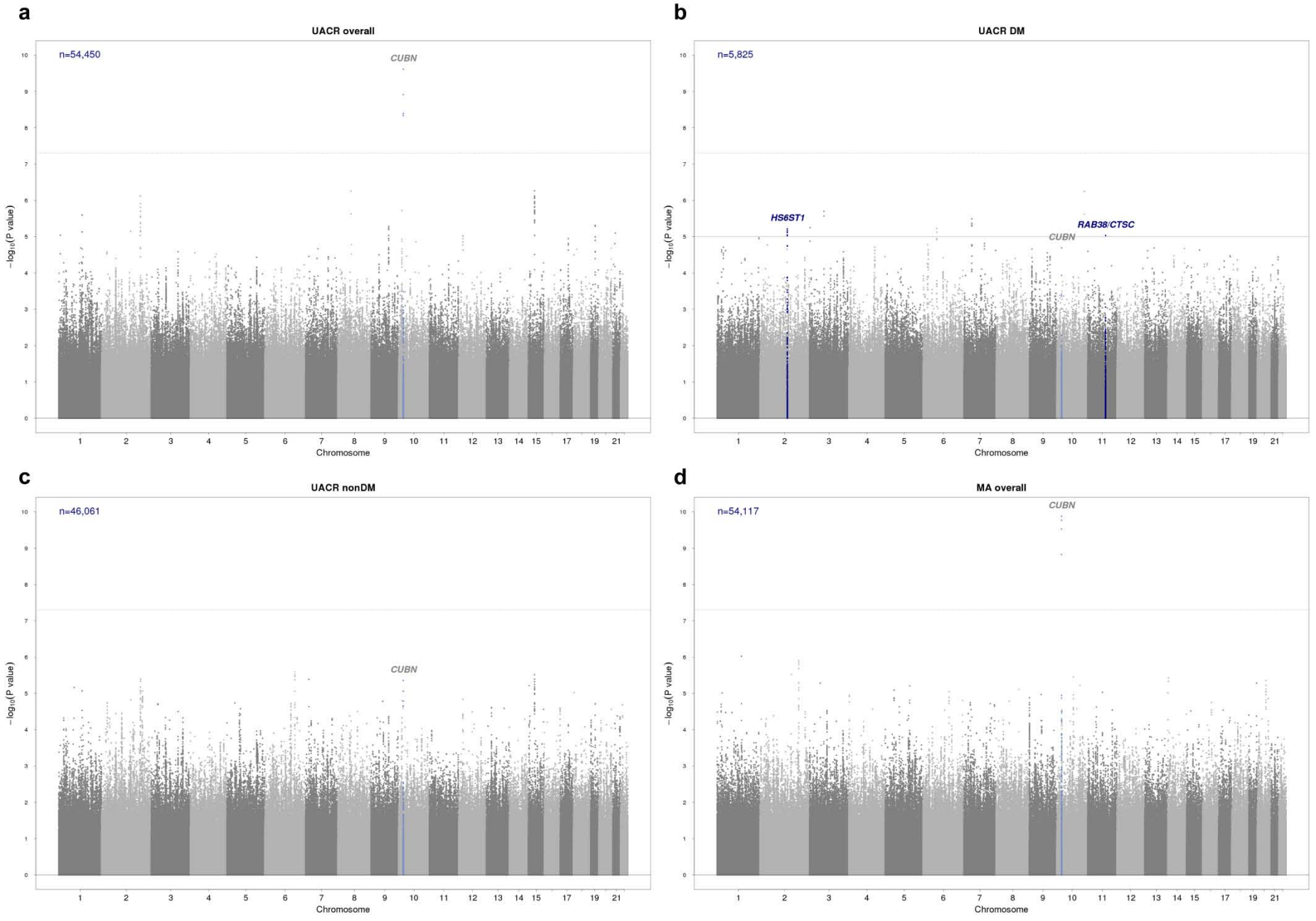
Supplementary Figure 2: Manhattan plots for all GWAS meta-analyses

Manhattan plots of the GWAS meta-analysis results for (**a**) UACR in the overall sample, (**b**) UACR among those with diabetes, (**c**) UACR among those without diabetes, and (**d**) microalbuminuria in the overall sample. SNPs are plotted on the x-axis according to their position on each chromosome with the -log10(p-value) on the y-axis. The upper solid horizontal line indicates the threshold for genome-wide significance, $5*10^{-8}$. The lower solid horizontal line for UACR among those with diabetes (**b**) represents the threshold of $1*10^{-5}$ applied to select SNPs for replication. Genomic loci previously known to contain trait-associated variants are colored in light blue, new findings in dark blue.



Supplementary Figure 3: Regional association plots

Regional association plots are shown for all loci that contained at least one index SNP associated with the trait at $p<10^{-5}$ after correction for genomic control. Correlation with the index SNP is estimated based on the HapMap r22 CEU samples. Plots were generated using the stand-alone version of LocusZoom (Pruim RJ *et al.*, Bioinformatics 2010). When association in a genomic region was observed with more than one trait, the regional association plot of the trait with the lowest p-value is shown. Genetic positions refer to NCBI build 36/hg18 coordinates.

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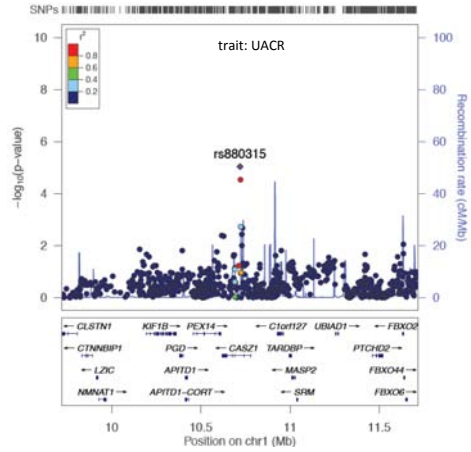

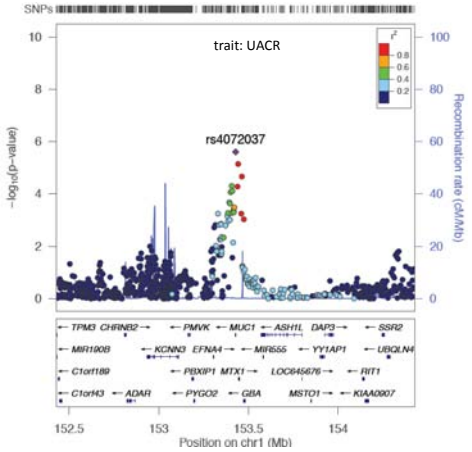

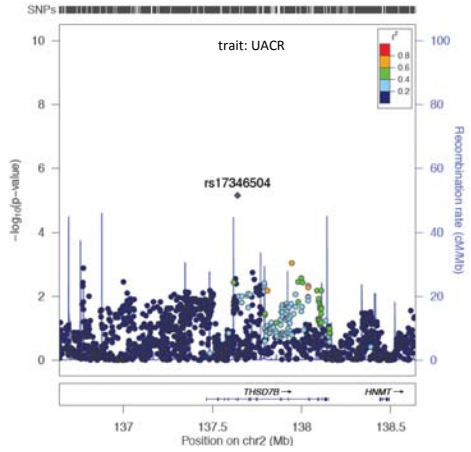

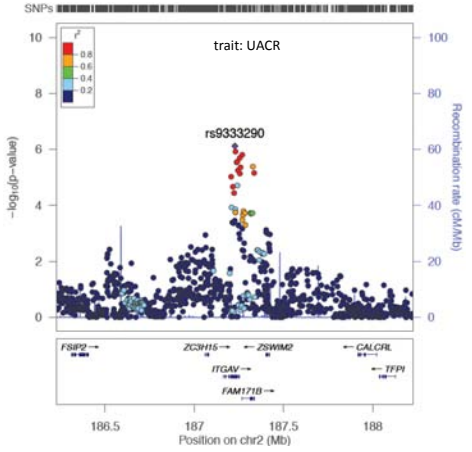

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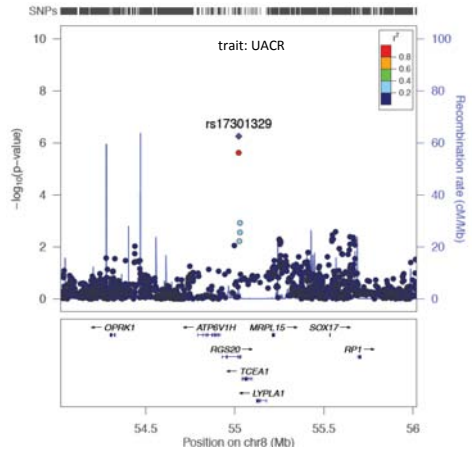

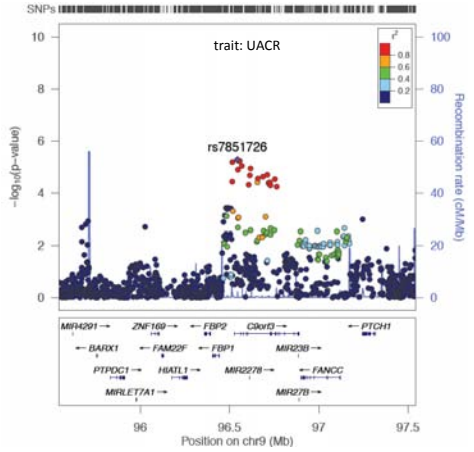

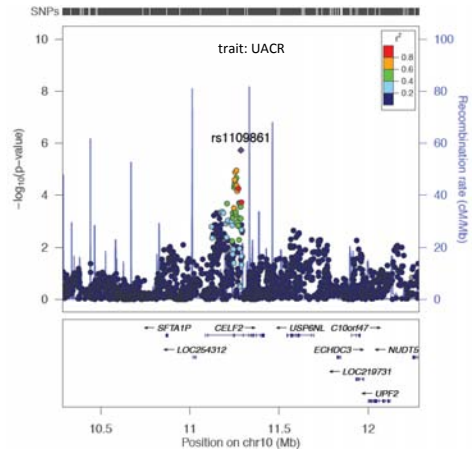

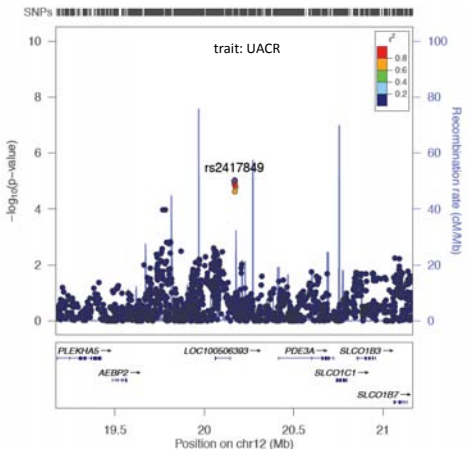

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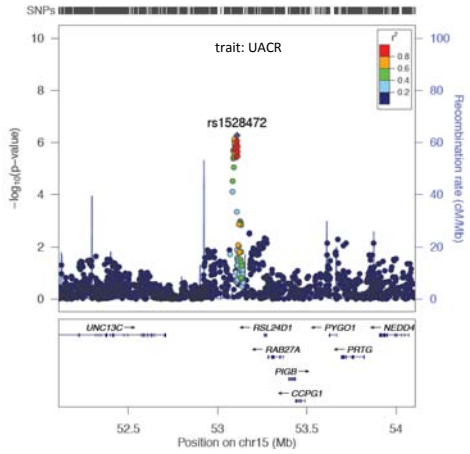

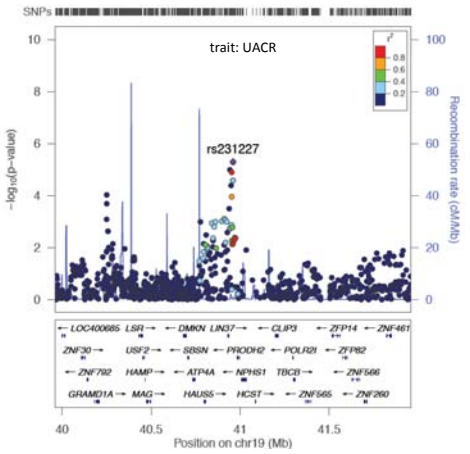

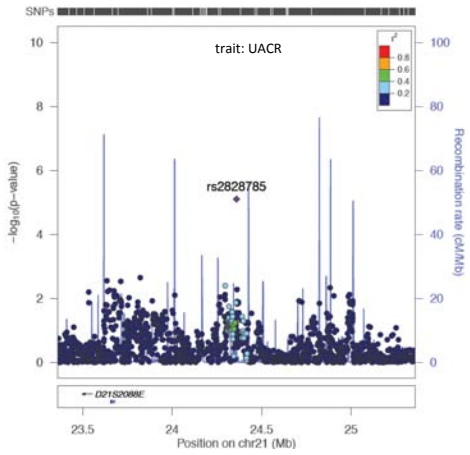

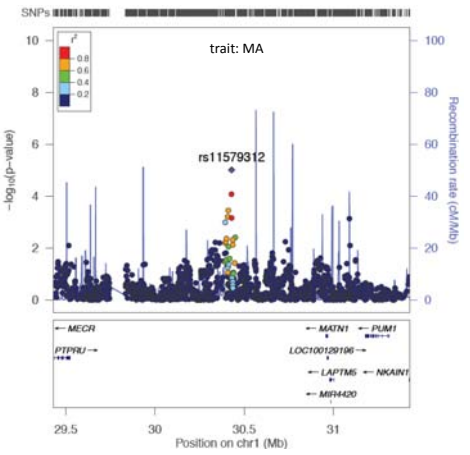

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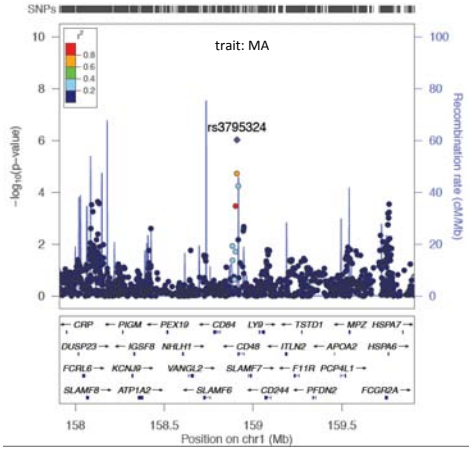

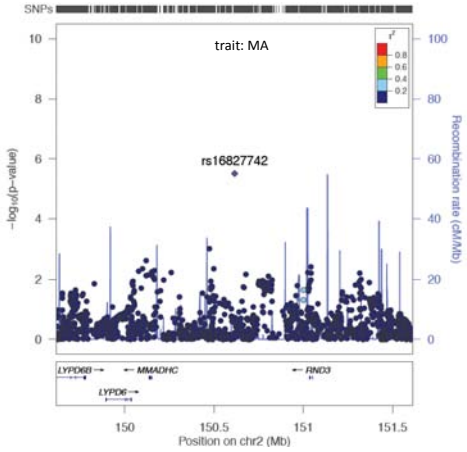

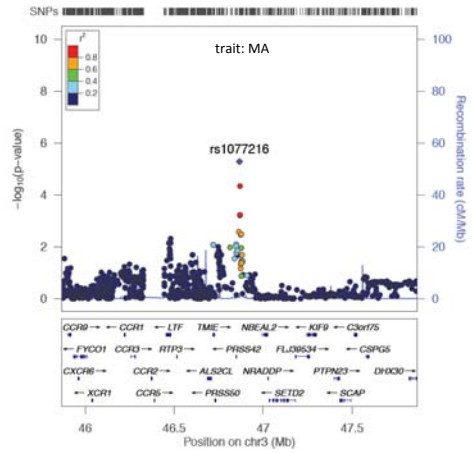

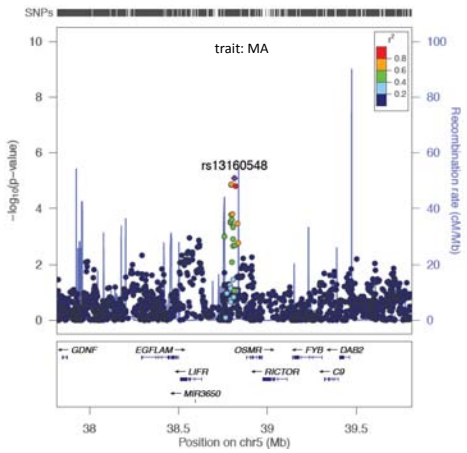

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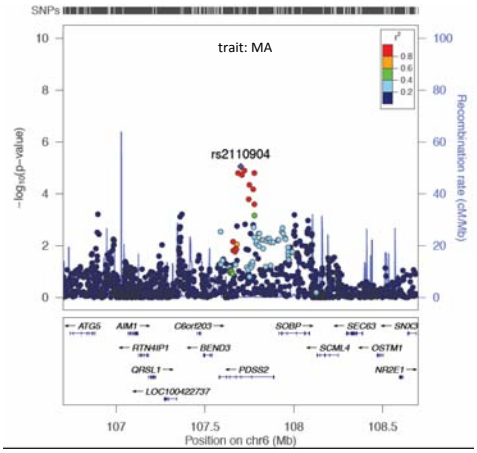

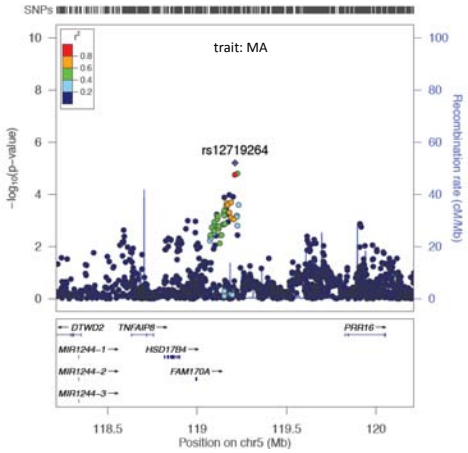

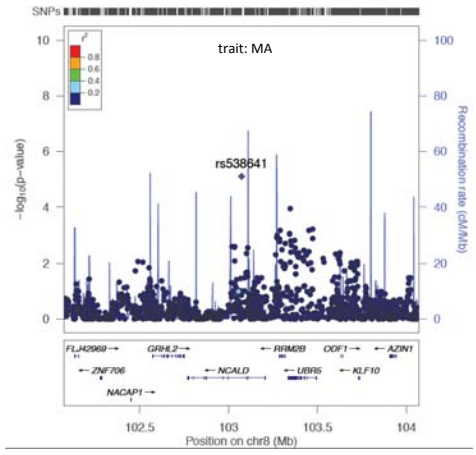

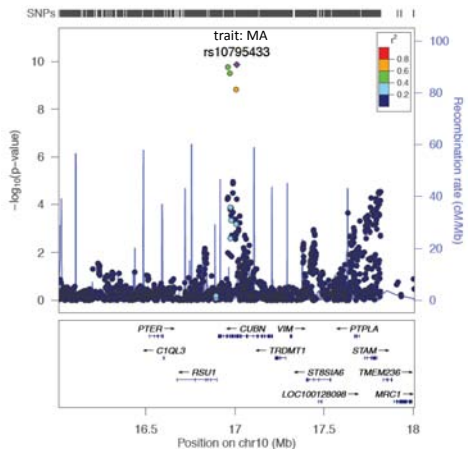

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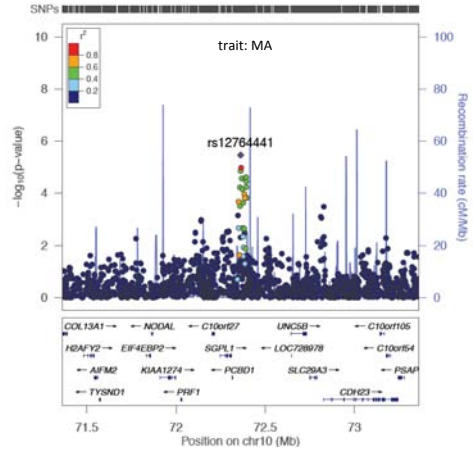

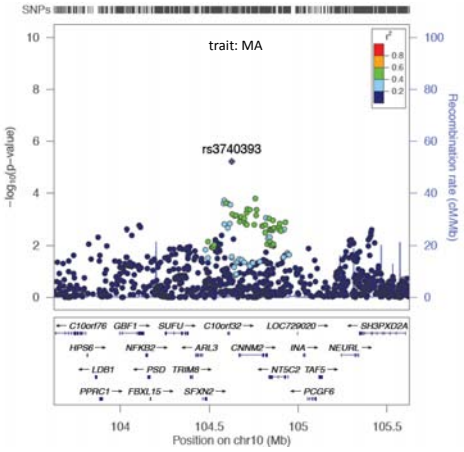

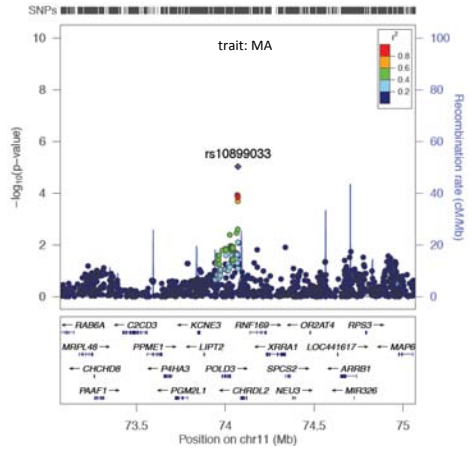

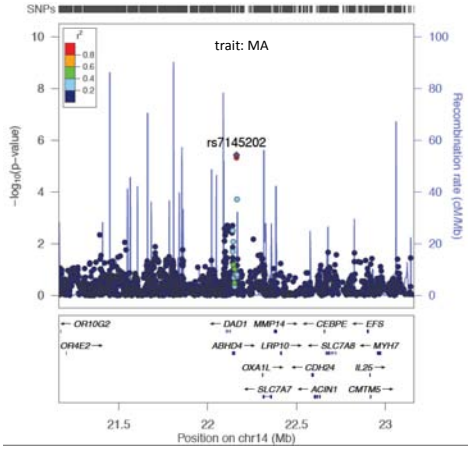

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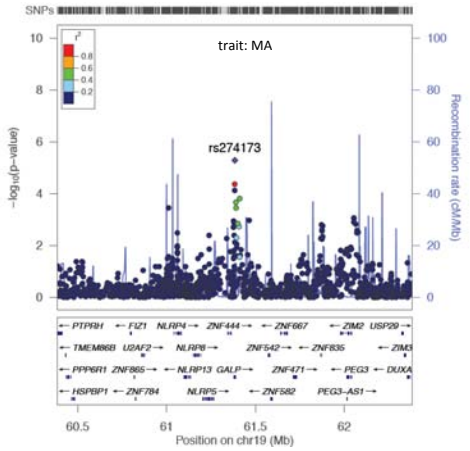

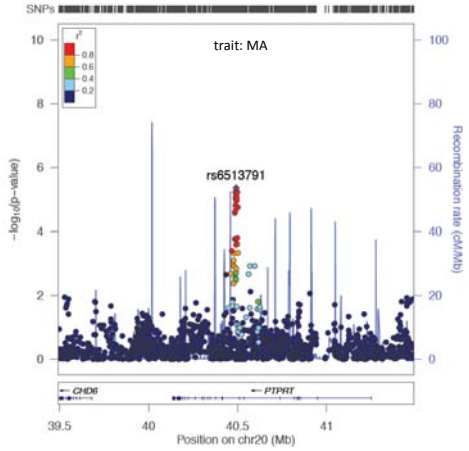

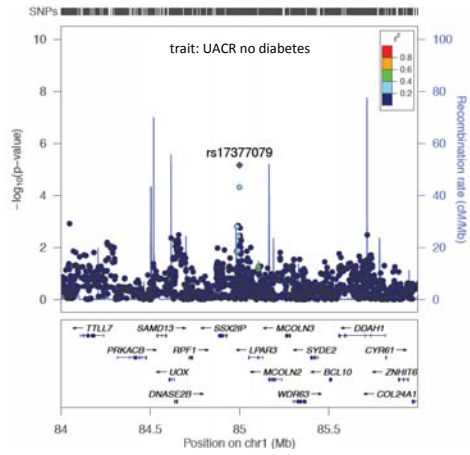

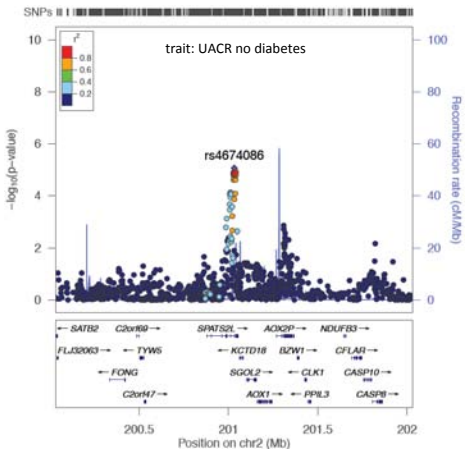

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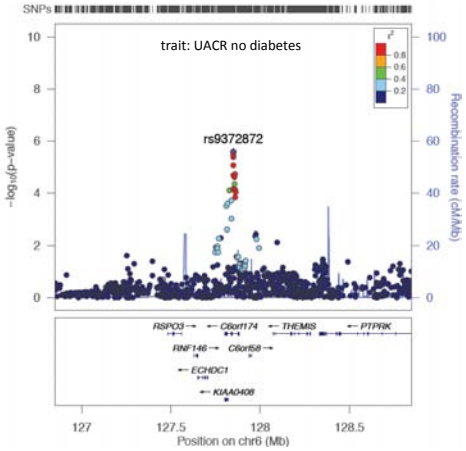

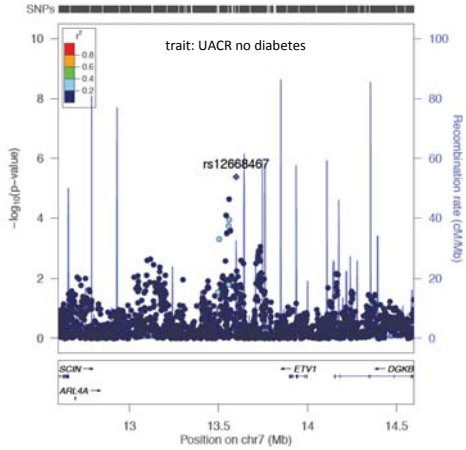

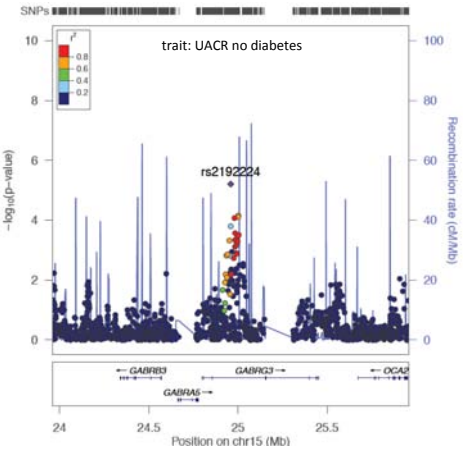

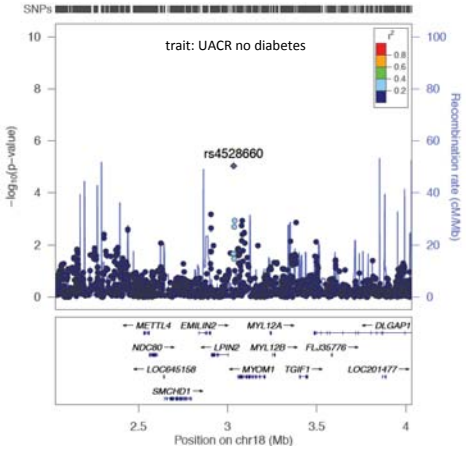

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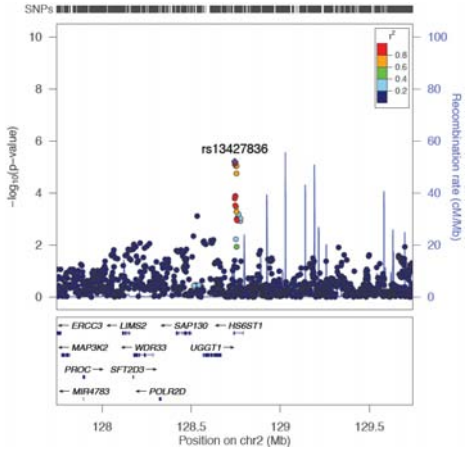

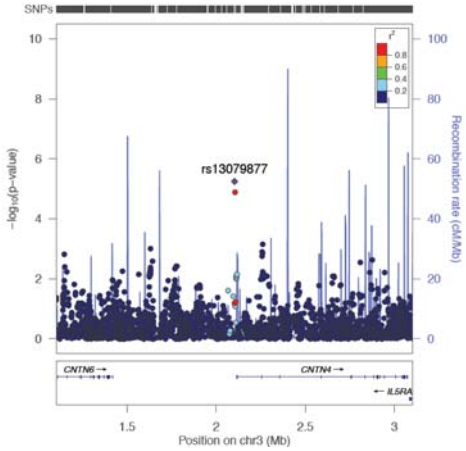

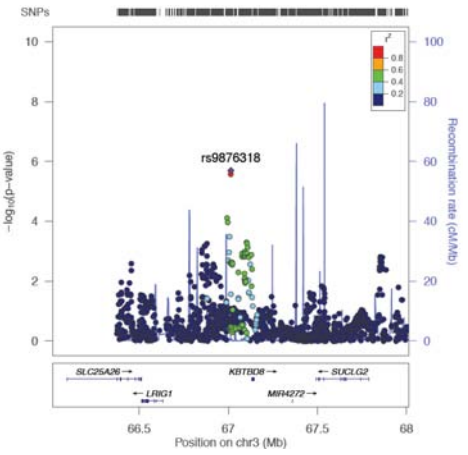

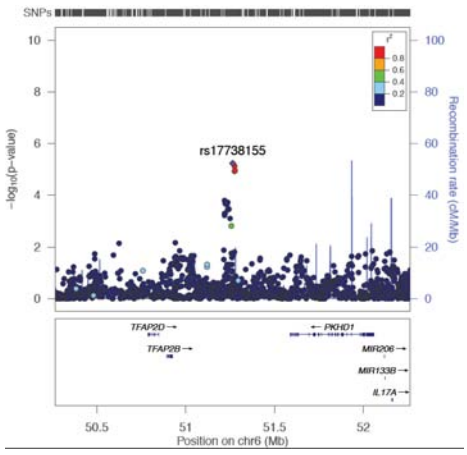

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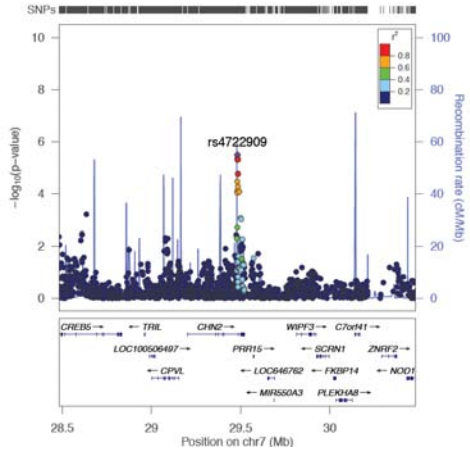

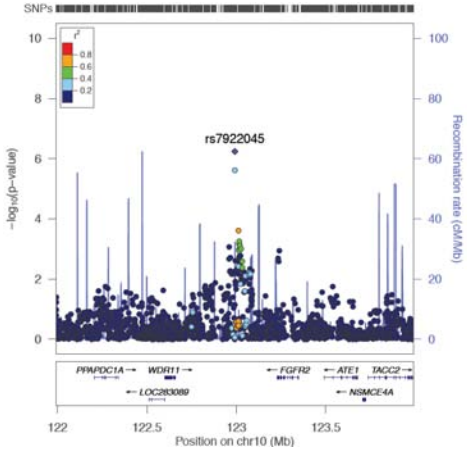

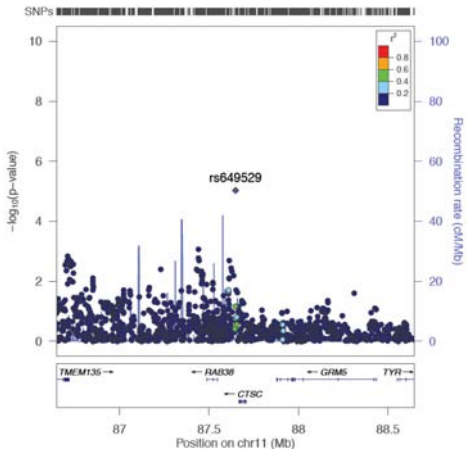

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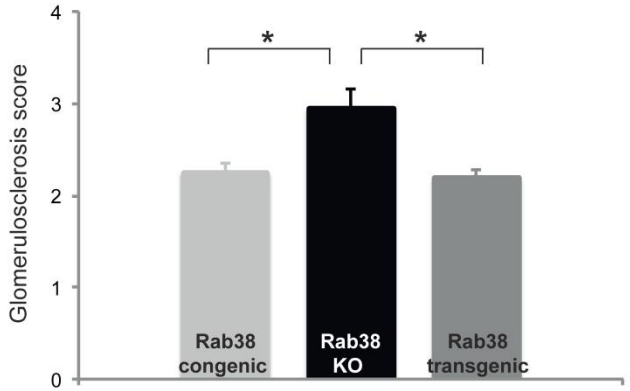
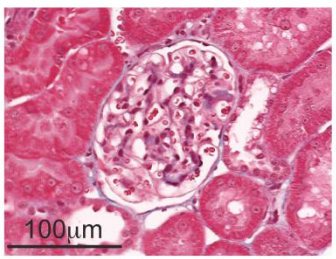
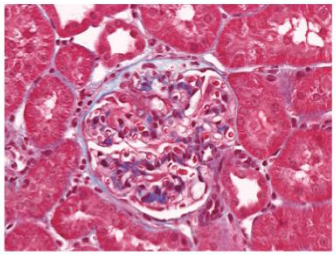
Supplementary Figure 4: Evaluation of glomerulosclerosis in Rab38 KO, congenic and transgenic rats.

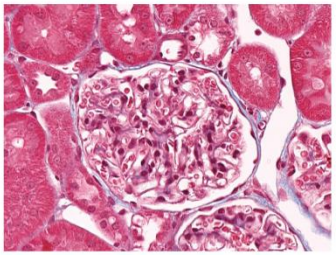
Representative images of trichrome-stained glomeruli from *Rab38* congenic, KO and transgenic animals. The glomerulosclerosis score was determined from left kidneys of 13-week-old rats (n=3 of each strain) as described previously (O'Meara CC *et al.* JASN, 2011). 50 to 60 40x magnified cortical glomeruli were imaged and scored, and scores were averaged for each animal. *p<0.05, **p<0.01 KO vs. transgenic, $^{\#\#}$p<0.01 KO vs. congenic. Glomerulosclerosis was analyzed using one-way ANOVA followed by Tukey's post hoc test.





Rab38 congenic


Rab38 KO


Rab38 transgenic

Supplementary Table 1: Characteristics of the study populations

Study	UACR sample size	Women, %	Age (years)	eGFR <60 (ml/min/1.73m^2)[1]	HTN, %	DM, %	UACR (mg/g) (median, 25th%, 75th%)	MA, %
Disovery cohorts								
3C	1072	63.6	77.8 (4.8)	19.9	74.4	12.3	5.3 (2.6, 10.7)	11.7
Advance	2203	32.8	66.7 (6.76)	14.7	47.6	100	15.6 (6.44, 54.8)	45
AGES	3196	58	76.4 (5.46)	24.2	80.6	11.5	2.66 (1.2, 7.0)	11.9
Amish**	727	48.9	49.5 (16.9)	3.1	18.9	1.7	7 (4.3, 13.5)	NA
ARIC	7243	53.1	61.8 (6.1)	8.7	40.7	14.2	5.3 (3.0, 9.5)	9.4
BLSA**	361	46.1	70.4 (15.2)	17.4	21.9	7.7	7 (4.4, 11.0)	NA
CHS	1865	61.3	71.9 (5.0)	9.5	51.4	11	9.3 (5.3, 19.9)	23
COLAUS	5311	53.2	53.4 (10.8)	3.8	36.1	9.6	5.1 (3.4, 9.1)	9.5
CROATIA-SPLIT**	472	59.8	49.3 (14.65)	5	39.4	5	2.5 (1.3, 5.8)	7.8
EPIC	2371	53.3	59.2 (9.00)	29.87	49.3	3	3.6 (1.5, 8.3)	8.1
Fenland**	1398	56.2	44.9 (7.3)	0.9	18.9	1.4	4.5 (3.2, 7.1)	5.5
FHS	6523	54.3	51.2 (14.0)	10.7	57.5	9.7	4.58 (2.62, 9.89)	9.69
INCIPE**	940	52.7	61.0 (11.0)	8.6	69.6	10.6	NA*	7.4
KORA-F3	1530	50.5	62.5 (10.1)	10.8	41.1	11.1	4.9 (2.1, 11.1)	12.5
KORA-F4	1804	51.3	60.9 (8.9)	7	20.9	9.2	6.1 (3.8, 11.9)	12.5
LIFELINES	8085	57.2	47.4 (11.2)	NA	31.5	2.2	3.12 (2.2, 4.7)	2.4
MESA	2511	52.3	62.67 (10.2)	9.72	38.6	5.99	4.60 (3.10, 8.50)	9.52
MICROS**	504	56.5	46.2 (16.1)	3.8	37.7	4.3	6.0 (4.0, 9.0)	5.4
PREVEND	3634	48.4	49.6 (12.5)	3.3	31.8	3.4	7.9 (5.0, 15.5)	10.2
SHIP	2655	51.7	54.5 (15.3)	7.7	51.1	11.2	8.95 (5.00, 20.59)	25.2
SHIP-TREND**	985	56.2	50.1 (13.7)	4.3	39.6	1.8	6 (3.9, 10.3)	8.5
Total	**55390**							

Replication cohorts								
ESTHER	2958	55.6	61.87	15.7	57.52	15.87	9.8 (6.2, 19.7)	23.06
GANI_MED	1674	44.0	60.0	36.1	71.2	24.9	11.8 (6.1, 43.9)	37.2
GENDIAN	450	47.1	65.05	32.3	53	100	7.54 (3.57,23.65)	27.6
KORAF4 non-GWAS	1195	52.4	49.2	5.8	13.3	4	5.7 (3.5, 11.4)	23.6
KORAF3 non-GWAS	1389	52.5	51.7	2.6	29.4	5.1	4.4 (1.87, 9.6)	11
SAPHIR	1690	37.1	51.4	6.9	55.7	3.3	3.8 (2.3, 8.3)	9.9
SKIPOGH**	807	52.3	47.1	5.7	22.9	4.5	4.2 (2.7, 7.7)	5.7
Vanderbilt Omni1	472	47.3	54.5	27.7	70.5	18	11.5 (6.0, 39.0)	36.7
Vanderbilt Omni5	144	46.9	50.5	21.7	58.2	33.3	14.5 (6.0, 42.2)	35.4
Vanderbilt 660W	365	56.5	56.5	20.6	57.2	17.9	9.0 (5.0, 26.0)	30.7
Total	**11144**							

*Because of the lower detection limit of the assay, the INCIPE Study only contributed to analyses of MA.
**Studies that did not contribute data for analyses of MA or UACR among those with diabetes because of low case numbers.
[1]Timepoint of serum creatinine measurement can differ from that of urinary albumin measurements in some of the studies.

Supplementary Table 2: Information about study design and UACR measurement

Study	Study Design	Total genotyped sample size	Study exclusions or disease enrichment, and data quality control	Urinary albumin measurements + QC	Key Study References
Discovery study					
3C	Prospective population-based	1072	**Study exclusions or disease enrichment**: none. **Exclusions**. none.	At 4-year follow-up, urinary albumin and creatinine were measured in a fresh morning urine sample in a single laboratory using an immunoturbidimetric assay for albumin and Jaffe method for creatinine.	1. The 3C Study Group. Vascular factors and risk of dementia. Design of the Three-City Study and baseline characteristics of the study population. Neuroepidemiology. 2003; 22:316-325. 2. Lambert J-C, Heath S, Even G, Campion D, Sleegers K, Hiltunen M, Combarros O, Zelenika D, Bullido MJ, Tavernier B, Letenneur L, Bettens K, Berr B, Pasquier F, Fiévet N, Barberger-Gateau P, Engelborghs S, De Deyn P, Mateo I, Franck F, Helisalmi S, Porcellini E, Hanon O, the European Alzheimer's Disease Investigators, De Pancorbo MM, Lendon C, Dufouil C, Jaillard C, Leveillard T, Alvarez V, Bosco P, Mancuso M, Panza F, Nacmias B, Bossù P, Piccardi P, Annoni G, Seripa D, Galimberti D, Hannequin D, Licastro F, Soininen H, Ritchie K, Galan P, Dartigues J-F, Tzourio C, Gut I, Van Broeckhoven C, Alpérovitch A, Lathrop M, Amouyel P. Genome-wide association study identifies variants at CLU and CR1 associated with Alzheimer's disease. Nat Genet. 2009;41:1094-9.

Advance	Randomized controlled trial	2203	**Study exclusions or disease enrichment**: multicenter trial done by 215 collaborating centres in 20 countries, including 11,140 type 2 diabetes subjects all of Caucasian origin. **Exclusions**: 8829 with no genotype; 10 samples excluded due to sex mismatch, high sample missingness or having <0.8 of Caucasian ethnicity (STRUCTURE 2.3). Of the 2301 remaining samples of good genotype quality, 98 did not have data for UACR.	Urinary albumin and creatinine were measured in the same morning fresh sample in local certified laboratoires using local regulations in 20 countries. Units were harmonized centrally by the George Insitute. Two samples were required for the determination of the stage of albuminuria. UACR were repeated every 6 months during a 5-year follow-up.	1. Ninomiya T et al. Albuminuria and kidney function independently predict cardiovascular and renal outcomes in diabetes. J Am Soc Nephrol. 2009 Aug;20(8):1813-21. 2. Patel A et al for the ADVANCE Collaborative Group. Effects of a fixed combination of perindopril and indapamide on macrovascular and microvascular outcomes in patients with type 2 diabetes mellitus (the ADVANCE trial). Lancet 2007; 370: 829-40.
AGES	Population-based	3196	**Study information or disease enrichment**: none. **Exclusions**: exclusion criteria included sample failure, genotype mismatch with reference panel, and sex mismatch, resulting in clean genotype data on 3,219 individuals.	Urinary albumin was measured in a morning urine sample using the Tina-quant immunoturbimetric assay (Roche Diagnostics, Mannheim). The intra-assay CV was 7.2%. Urinary creatinine in the same samples was measured using the HiCo Creatinine Jaffe method (Roche Diagnostics, Mannheim). The intra-assay CV was 4.2%.	Harris TB, Launer LJ, Eiriksdottir G, Kjartansson O, Jonsson PV, Sigurdsson G, Thorgeirsson G, Aspelund T, Garcia ME, Cotch MF, Hoffman HJ, Gudnason V.Age, Gene/Environment Susceptibility-Reykjavik Study: multidisciplinary applied phenomics. Am J Epidemiol. 2007 May 1;165(9):1076-87.
Amish	Population-based "founder" cohort	727	**Study information or disease enrichment**: none. **Exclusions**: age < 20, severe chronic disease, call rate < 95%.	Urinary albumin concentration was measured from stored samples using a quantitative immunoturbimetric assay (Roche Diagnostics, Indianapolis), and creatinine in urine was measured using a modified Jaffe method.	1. Mitchell BD et al. The genetic response to short-term interventions affecting cardiovascular function: rationale and design of the Heredity and Phenotype Intervention (HAPI) Heart Study. Am. Heart J. 155, 823-828 (2008). 2. Rampersaud E et al. The association of coronary artery calcification and carotid artery intima-media thickness with distinct, traditional coronary artery disease risk factors in asymptomatic adults. Am. J. Epidemiol. 168, 1016-1023 (2008).

ARIC	Prospective, population-based	7243	**Study information or disease enrichment**: none. **Exclusions**: of the 9713 genotyped individuals of European ancestry, we excluded 658 individuals based on discrepancies with previous genotypes, disagreement between reported and genotypic sex, one randomly selected member of a pair of first-degree relatives, or outlier based on measures of average DST or more than 8 SD away on any of the first 10 principal components. Additional samples were excluded for this analysis because of the unavailability of the phenotype.	Using stored specimen from samples collected at visit 4, urinary albumin was measured by a nephelometric method either on the Dade Behring BN100 or on the Beckman Image Nephelometer. Urinary creatinine was measured using the Jaffe method.	The Atherosclerosis Risk in Communities (ARIC) Study: design and objectives. The ARIC investigators. Am J Epidemiol. 1989 Apr;129(4):687-702.
BLSA	Population-based	361	**Study information or disease enrichment**: none. **Exclusions**: non-European descent or with missing UACR information.	Urinary measurements were conducted on 24-hour urine samples. Urinary albumin was determined with nephelometry (Beckman Array System). Urinary creatinine was measured using a Vitros enzymatic assay (Johnson & Johnson Co., Rochester, NY).	Shock NW et al. Normal Human Aging: The Baltimore Study of Aging. 1984.
CHS	Prospective population-based	1865	**Study information or disease enrichment**: A total of 1908 persons were excluded from the GWAS study sample due to the presence at study baseline of coronary heart disease, congestive heart failure, peripheral vascular disease, valvular heart disease, stroke or transient ischemic attack or lack of available DNA. **Exclusions**: The present report is based upon genotyping results from 3,329 CHS Caucasian participants, who were free of clinical cardiovascular disease at baseline, consented to genetic testing, and had DNA available for genotyping. Genotypes were called using the Illumina BeadStudio software. Genotyping was successful in 3,291 persons.	Urinary parameters were measured from a morning urine sample. The albumin was measured by rate nephelometry (Array 360 CE Protein Analyzer, Beckman Instruments, Fullerton, CA). The creatinine was measured using a Kodak Ektachem 700 Analyzer (Eastman Kodak company, Rochester, NY).	1. Fried LP, Borhani NO, Enright P, Furberg CD, Gardin JM, Kronmal RA, Kuller LH, Manolio TA, Mittelmark MB, Newman A, et al. The Cardiovascular Health Study: design and rationale. Ann Epidemiol. 1991;1(3):263-276. 2. Heard-Costa, NL et al. NRXN3 is a novel locus for waist circumference: a genome-wide association study from the CHARGE Consortium. 2009. Plos Genet. 5(6): e1000539.

COLAUS	Population-based	5311	**Study exclusions or disease enrichment**: none. **Exclusions**: samples with call rate < 90% and related individuals.	Urinary albumin was measured using a Bromocresol green assay (Roche Diagnostics, Basel, Switzerland). The inter- and intra-assay CVs were 2.5% and 0.4%. Urinary creatinine was measured using a Jaffe kinetic compensated method. The inter- and intra-assay CVs were 2.9% and 0.7%.	Firmann M, Mayor V, Vidal PM, Bochud M, Pécoud A, Hayoz D, Paccaud F, Preisig M, Song KS, Yuan X, Danoff TM, Stirnadel HA, Waterworth D, Mooser V, Waeber G, Vollenweider P. The CoLaus study: a population-based study to investigate the epidemiology and genetic determinants of cardiovascular risk factors and metabolic syndrome.BMC Cardiovasc Disord. 2008 Mar 17;8:6. doi: 10.1186/1471-2261-8-6.
CROATIA-SPLIT	Population-based	472	**Study exclusions or disease enrichment**: none. **Exclusions**: missing UACR levels.	Urinary albumin excretion was measured, in stored urine samples, by an automated assay based on a turbimetric method with automatic calibration and quality control (Synchron CX System, Beckman Coulter).	"10001 Dalmatiians" Croatia launches its national biobank Rudan I, Marusić A, Janković S, Rotim K, Boban M, Lauc G, Grković I, Dogas Z, Zemunik T, Vatavuk Z, Bencić G, Rudan D, Mulić R, Krzelj V, Terzić J, Stojanović D, Puntarić D, Bilić E, Ropac D, Vorko-Jović A, Znaor A, Stevanović R, Biloglav Z, Polasek O.Croat Med J. 2009 Feb;50(1):4-6.
EPIC	Population-based	2371	**Study exclusions or disease enrichment**: participants taking colchicine, probenecid or allopurinol at 1st, 2nd health checks or 3rd follow-up; gout from hospital discharge ICD10 M10, between 1997-2008. **Exclusions**: none.	Urinary albumin was measured in spot urine by immunonephelometry using the Nephelometer II analyzer (Dade Behring, Marburg, Germany). The intra-assay CV was 2.91%. Urinary creatinine was measured by means of colorimetry using the Dimension AR Analyzer (Dade Behring Marburg, Germany).	1. Day N et al. EPIC-Norfolk: study design and characteristics of the cohort. European Prospective Investigation of Cancer. Br J Cancer 80 Suppl 1, 95-103 (1999). 2. Lee CT et al. Cross-sectional association between fish consumption and albuminuria: the European Prospective Investigation of Cancer-Norfolk Study. Am J Kidney Dis 52, 876-86 (2008).
Fenland	Population-based	1398	**Study exclusions or disease enrichment**: exclusion criteria for the study were: age<30 or age>55, prevalent diabetes, pregnant and lactating women, inability to participate including terminal illness, psychotic illness, or inability to walk unaided. **Exclusions**: 102 exluded due to call rate < 95%, heterozygosity check (upper bound 0.2882, lower bound 0.2735), relatedness check and duplicate check.	Using stored samples, urinary albumin was measured by means of immunonephelometry using the Nephelometer II analyzer (Dade Behring, Marburg, Germany; intra-assay CV 2.91%). Urinary creatinine was measured through colorimetry using the Dimension AR Analyzer (Dade Behring Marburg, Germany).	Willer CJ, Speliotes EK, Loos RJ et al. (2009) Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nat Genet, 41(1): 25-34.

FHS	Prospective family-based	6523	**Study exclusions or disease enrichment**: none. **Exclusions**: Of the 9,274 participants who underwent genotyping, we made the following exclusions: sample call rate <97% (n=666), genotype heterozygosity > 5 standard deviations, and ambiguous family data (n=127). This resulted in a total of 8,481 genotyped individuals. Of them, 1958 did not have the phenotype available.	Urinary albumin was measured from stored samples using a Tina-quant immunoturbimetric assay (Roche Diagnostics, Indianapolis, Indiana). The intra-assay CV was 7.2% for the Offspring cohort and 2.1% for the Third Generation. Urinary creatinine was measured using a modified Jaffe method. Its intra-assay CV was 2.3% for the Offspring cohort and 1.0% for the Third Generation cohort.	1. Feinleib M, Kannel WB, Garrison RJ, McNamara PM, Castelli WP. The Framingham Offspring Study. Design and preliminary data. Prev Med. 1975;4:518-525. 2. Kannel WB, Feinleib M, McNamara PM, Garrison RJ, Castelli WP. An investigation of coronary heart disease in families. The Framingham offspring study. Am J Epidemiol. 1979;110:281-290. 3. Splansky GL, Corey D, Yang Q, Atwood LD, Cupples LA, Benjamin EJ, D'Agostino RB, Sr., Fox CS, Larson MG, Murabito JM, O'Donnell CJ, Vasan RS, Wolf PA, Levy D. The Third Generation Cohort of the National Heart, Lung, and Blood Institute's Framingham Heart Study: design, recruitment, and initial examination. Am J Epidemiol. 2007;165:1328-1335.
INCIPE	Cross-sectional, population based	940	**Study exclusions or disease enrichment:** individuals <40 year old. **Exclusions:** pregnant women	Using stored specimen, urinary albumin was measured by a nephelometric method. Urinary creatinine was measured using the Jaffé method.	Gambaro, G. et al. Prevalence of CKD in northeastern Italy: results of the INCIPE study and comparison with NHANES. Clin. J. Am. Soc. Nephrol. 5, 1946-1953 (2010).
KORA-F3	Prospective population-based	1530	**Study exclusions or disease enrichment:** none**. Exclusions:** none.	Using stored urine samples, urinary albumin concentration was measured with a latex enhanced nephelometric assay (Siemens Healthcare Diagnostics) on a Dade Behring BN2 apparatus. Urinary creatinine concentration was measured using an enzymatic method.	1. Baumeister SE, Böger CA, Krämer BK, Doring A, Eheberg D, Fischer B, John J, Koenig W & Meisinger C: Effect of chronic kidney disease and comorbid conditions on health care costs: A 10-year observational study in a general population. Am J Nephrol 31: 222-229, 2010. 2. Wichmann HE, Gieger C & Illig T: KORA-gen--resource for population genetics, controls and a broad spectrum of disease phenotypes. Gesundheitswesen 67 Suppl 1: S26-30, 2005.

KORA-F4	Prospective population-based	1804	**Study exclusions or disease enrichment**: none. **Exclusions**: none.	Using stored urine samples, urinary albumin concentration was measured with a latex enhanced nephelometric assay (Siemens Healthcare Diagnostics) on a Dade Behring BN2 apparatus. Urinary creatinine concentration was measured using a kinetic Jaffe method in KORA F4.	1. Baumeister SE, Böger CA, Krämer BK, Doring A, Eheberg D, Fischer B, John J, Koenig W & Meisinger C: Effect of chronic kidney disease and comorbid conditions on health care costs: A 10-year observational study in a general population. Am J Nephrol 31: 222-229. 2. Wichmann HE, Gieger C & Illig T: KORA-gen--resource for population genetics, controls and a broad spectrum of disease phenotypes. Gesundheitswesen 67 Suppl 1: S26-30, 2005.
LIFELINES	3-generations, population-based	8085	**Study exclusions or disease enrichment**: living outside the 3 Northern provinces of The Netherlands. **Exclusions**: none.	Urinary albumin and creatinine were measured using the Roche Modular.	Stolk RP, Rosmalen JGM, Postma DS, de Boer RA, Navis G, Slaets JPJ, Ormel J, and Wolffenbuttel BHR. Universal risk factors for multifactorial diseases: LifeLines: a three-generation population-based study. Eur. J. Epidemiol., vol. 23, no. 1, pp. 67–74, Jan. 2008.
MESA	Community-based cohort study	2511	**Study exclusions or disease enrichment**: none. **Exclusions**: none.	Urine albumin and creatinine were measured at the Clinical Chemistry Laboratory at Fletcher Allen Health Care (Burlington, Vt). Urine albumin and creatinine were measured by nephelometry and the rate Jaffe reaction, respectively.	Bild DE et al. Multi-ethnic study of atherosclerosis: objectives and design. Am J Epidemiol 156, 871-81 (2002).

MICROS	Cross-sectional, population-based study using extended pedigrees	504	**Study exclusions or disease enrichment**: <18 years of age. **Exclusions**: samples with overall SNP call rate < 95%, showing excess of heterozygosity, or being classified as outliers by IBS clustering analysis were excluded prior to further analyses.	The urinary albumin-to-creatinine ratio was measured on a point-of-care diabetes management platform (Bayer DCA 2000+ analyzer).	1. Pattaro C, Marroni F, Riegler A, Mascalzoni D, Pichler I, Volpato CB, Dal Cero U, De Grandi A, Egger C, Eisendle A, Fuchsberger C, Gögele M, Pedrotti S, Pinggera GK, Stefanov SA, Vogl FD, Wiedermann CJ, Meitinger T, Pramstaller PP. The genetic study of three population microisolates in South Tyrol (MICROS): study design and epidemiological perspectives. BMC Med Genet. 2007;8:29. 2. Marroni F, Grazio D, Pattaro C, Devoto M, Pramstaller P. Estimates of genetic and environmental contribution to 43 quantitative traits support sharing of a homogeneous environment in an isolated population from South Tyrol, Italy. Hum Hered. 2008;65(3):175-82.
PREVEND	Population-based	3634	**Study exclusions or disease enrichment**: aged between 28-75 yrs, enriched for microalbuminuria. **Exclusions**: none.	Urinary albumin was determined from fresh urine samples by nephelometry (BNII; Dade Behring Diagnostic, Marburg, Germany). Intra- and inter-assay coefficients of variation were 2.2 and 2.6%, respectively.	Hillege HL, Fidler V, Diercks GFH, van Gilst WH, de Zeeuw D, van Veldhuisen DJ, Gans ROB, Janssen WMT, Grobbee DE, and de Jong PE. Urinary albumin excretion predicts cardiovascular and noncardiovascular mortality in general population. Circulation, vol. 106, no. 14, pp. 1777–82, Oct. 2002.
SHIP	Prospective population-based	2655	**Study exclusions or disease enrichment**: none. **Exclusions**: sample call rate < 92%, duplicate samples (by IBS estimation), individuals with reported / genotyped gender mismatch.	Urinary albumin was measured from spot first morning void urine by nephelometry (BNII, Dade Behring Diagnostica, Marburg, Germany). Intra-assay and interassay coefficients of variation were 4.3% and 4.4%, respectively. Urinary creatinine concentration was measured using Kodak Ektachem dry chemistry (Eastman Kodak, Rochester, NY). Intra-assay and interassay coefficients of variation were 0.9% and 2.9%, respectively.	1. John U et al. Study of Health in Pomerania (SHIP). A health examination in an east German region: objectives and design. Soz Praventivmed 46:186-194, 2001. 2. Völzke H et al. Cohort Profile: The Study of Health in Pomerania. Int J Epidemiol, vol. 40, no. 2, pp. 294–307, Apr. 2011.

SHIP-TREND	Prospective population-based	985	**Study exclusions or disease enrichment**: this analysis concerns the subset of 988 individuals with genotype information. **Exclusions**: sample call rate < 94%, duplicate samples (by IBS estimation), individuals with reported/genotyped gender mismatch.	In a sample of spot urine, both the urinary albumin (intra-assay CV 4.5-7.6% for 1.0-24.5 mg/dl) and creatinine (Jaffe method, intra-assay CV 1.4-2.1% for 5.7-14.6 mmol/l) were measured on a Siemens Dimension Vista 1500 analyzer (Siemens Healthcare Diagnostics, Marburg, Germany), respectively.	1. John U et al. Study of Health in Pomerania (SHIP). A health examination in an east German region: objectives and design. Soz Praventivmed 46:186-194, 2001. 2. Völzke H et al. Cohort Profile: The Study of Health in Pomerania. Int J Epidemiol, vol. 40, no. 2, pp. 294–307, Apr. 2011.
Replication study					
ESTHER	Prospective study	2958	**Study exclusions or disease enrichment**: study participants were required to be ≥50 year old and having a good knowledge of the German language. **Exclusions**: samples with insufficient amount of DNA for genotyping.	Urinary albumin concentration was measured using nephelometric method (Siemens. Marburg, Germany). The urinary creatinine levels were photometrically measured using the modified kinetic Jaffe method (Greiner Diagnostic GmbH. Bahlingen, Germany).	1. Raum E, Rothenbacher D, Low M, Stegmaier C, Ziegler H, Brenner H. Changes of cardiovascular risk factors and their implications in subsequent birth cohorts of older adults in Germany: a life course approach. Eur J Cardiovasc Prev Rehabil 2007;14:809-814. 2. Schottker B, Haug U, Schomburg L, et al. Strong associations of 25-hydroxyvitamin D concentrations with all-cause, cardiovascular, cancer, and respiratory disease mortality in a large cohort study. Am J Clin Nutr 2013. 3. Weck MN, Stegmaier C, Rothenbacher D et al. Epidemiology of chronic atrophic gastritis: population-based study among 9444 older adults from Germany. Aliment Pharmacol Ther. 2007;26:879-887.
GANI_MED	Cohort study	1674	**Study exclusions or disease enrichment**: six main cohorts: heart failure, stroke, periodontal disease, renal insufficiency, metabolic syndrome, and fatty liver disease. **Exclusions:** sample call rate < 94%, heterozygosity rate > 6SD (MAF > 1%), PCA outliers (EV 1-4 > 8SD), duplicate samples (by IBS estimation), individuals with reported/genotyped gender mismatch..	In a sample of spot urine, the urinary albumin was measured on a Siemens Dimension Vista 1500 analyzer (Siemens Healthcare Diagnostics, Marburg, Germany). Urinary creatinine was measured either by an enzymatic or Jaffe method, whereas the analyses were adjusted accordingly for the method used.	Grabe HJ, Assel H, Bahls T et al. Cohort profile: Greifswald approach to individualized medicine (GANI_MED). J. Transl. Med. 2014; 12: 144.

GENDIAN	Cohort study	450	**Study exclusions or disease enrichment**: study on type 2 diabetes patients. **Exclusions**: of the 1,026 subjects undergoing genotyping, 53 were excluded due to call-rate < 95% (n=22), relatedness and duplicates (n=11), gender mismatch (n=16), ethnicity check (n=4); in addition, we excluded the following patients for the current analysis of cross-sectional UACR: patients with end-stage renal disease (n=438) or advanced, histologically proven diabetic nephropathy (n=84) or missing phenotype (n=1).	Urinary creatinine was measured using an enzymatic assay, urinary albumin was measured using the Roche Tina Quant assay.	1. Böger CA et al: effect of ACE and AT-2 inhibitors on mortality and progression to microalbuminuria in a nested case control study of diabetic nephropathy in diabetes mellitus type 2: results from the GENDIAN study. Int J Clin Pharmacol Ther 2006;44:364-74. 2. Böger CA et al. Association of eGFR-related loci identified by GWAS with incident CKD and ESRD. Plos Genet 2011;7:e1002292.
KORAF4 non-GWAS	Prospective population-based	1195	**Study exclusions or disease enrichment**: none. **Exclusions**: none.	Using stored urine samples, urinary albumin concentration was measured with a latex enhanced nephelometric assay (Siemens Healthcare Diagnostics) on a Dade Behring BN2 apparatus. Urinary creatinine concentration was measured using an enzymatic method.	1. Baumeister SE, Böger CA, Krämer BK, Doring A, Eheberg D, Fischer B, John J, Koenig W & Meisinger C: Effect of chronic kidney disease and comorbid conditions on health care costs: A 10-year observational study in a general population. Am J Nephrol 31: 222-229, 2010. 2. Wichmann HE, Gieger C & Illig T: KORA-gen--resource for population genetics, controls and a broad spectrum of disease phenotypes. Gesundheitswesen 67 Suppl 1: S26-30, 2005.
KORAF3 non-GWAS	Prospective population-based	1389	**Study exclusions or disease enrichment**: none. **Exclusions**: none.	Using stored urine samples, urinary albumin concentration was measured with a latex enhanced nephelometric assay (Siemens Healthcare Diagnostics) on a Dade Behring BN2 apparatus. Urinary creatinine concentration was measured using a kinetic Jaffe method in KORA F4.	1. Baumeister SE, Böger CA, Krämer BK, Doring A, Eheberg D, Fischer B, John J, Koenig W & Meisinger C: Effect of chronic kidney disease and comorbid conditions on health care costs: A 10-year observational study in a general population. Am J Nephrol 31: 222-229, 2010. 2. Wichmann HE, Gieger C & Illig T: KORA-gen--resource for population genetics, controls and a broad spectrum of disease phenotypes. Gesundheitswesen 67 Suppl 1: S26-30, 2005.

SAPHIR	Healthy working population	1690	**Study exclusions or disease enrichment**: none. **Exclusions**: none.	Urinary creatinine was measured using a modified kinetic Jaffe reaction (CREA, Roche Diagnostics GmbH, Mannheim, Germany). Urinary albumin concentration was determined using the Tinaquant assay (Roche Diagnostics GmbH, Mannheim, Germany).	1. Heid IM, Wagner SA, Gohlke H, Iglseder B, Mueller JC, Cip P, Ladurner G, Reiter R, Stadlmayr A, Mackevics V, Illig T, Kronenberg F, Paulweber B: Genetic architecture of the APM1 gene and its influence on adiponectin plasma levels and parameters of the metabolic syndrome in 1,727 healthy Caucasians. Diabetes 55:375-384, 2006. 2. Kollerits B, Coassin S, Kiechl S, Hunt SC, Paulweber B, Willeit J, Brandstätter A, Lamina C, Adams TD, Kronenberg F: A common variant in the adiponutrin gene influences liver enzyme levels. Journal of Medical Genetics 47:116-119, 2010.
SKIPOGH	Cross-sectional family-based population-based	807	**Study exclusions or disease enrichment**: none. **Exclusions**: of the 941 participants who underwent genotyping, we excluded 71 participants with call rate < 90%, resulting in a total of 870 genotyped individuals.	Urinary creatinine was measured using an IDMS-traceable Jaffe kinetic compensated method. Urinary albumin concentration was measured using a quantitative immuno-nephelometry.	Pruijm M, Ponte B, Ackermann D, Vuistiner P, Paccaud F, Guessous I, Ehret G, Eisenberger U, Mohaupt M, Burnier M, Martin PY, Bochud M. Eur Radiol. 2013 May 28. [Epub ahead of print].
Vanderbilt Omni1	Practice-based cohort	472	**Study exclusions or disease enrichment**: samples chosen based on being a case or control for one of 31 pharmacogenetic analyses. **Exclusions**: individuals of non-white ancestry in the electronic medical record. Also excluded any lab measurements of individuals after initiation of dialysis or a kidney transplant.	The urinary albumin concentration was measured using turbidimetric immunoassay with endpoint determination. Urinary creatinine levels were measured using the modified Jaffé method.	
Vanderbilt Omni5	Practice-based cohort	144	**Study exclusions or disease enrichment**: samples chosen based on being a case or control for one of 31 pharmacogenetic analyses. **Exclusions**: individuals of non-white ancestry in the electronic medical record. Also excluded any lab measurements of individuals after initiation of dialysis or a kidney transplant.	The urinary albumin concentration was measured using turbidimetric immunoassay with endpoint determination. Urinary creatinine levels were measured using the modified Jaffé method.	

Vanderbilt 660W	Practice-based cohort	365	**Study exclusions or disease enrichment**: samples chosen for normal cardiac conduction, meaning that at some point in time they had a normal electrocardiogram without the presence of heart disease, arrhythmias, or electrocardiographically-active medications. **Exclusions**: children (age <18) and individuals of non-white ancestry in the electronic medical record. Also excluded any lab measurements from individuals after initiation of dialysis or a kidney transplant. At some point in their electronic medical record, the patients were absent of heart disease, but could later develop it.	The urinary albumin concentration was measured using turbidimetric immunoassay with endpoint determination. Urinary creatinine levels were measured using the modified Jaffé method.	Denny JC, Ritchie MD, Crawford DC, Schildcrout JS, Ramirez AH, Pulley JM, Basford MA, Masys DR, Haines JL, Roden DM. Identification of genomic predictors of atrioventricular conduction: Using electronic medical records as a tool for genome science. Circulation 2010;122(20):2016-21.
Clinical characterization study					
DCCT/EDIC	Trial of patients with type I diabetes	1304	**Study exclusions or disease enrichment**: individuals with insulin-dependent type I diabetes mellitus between 1 and 15 years of duration, age 13-39 years at enrolment, free of advanced diabetes-related complications, absence of several comorbidities. **Exclusions**: Subjects meeting the criteria for persistent microalbuminuria at DCCT baseline and DCCT year 1 (n = 60) were excluded from the analyses of the time to incident albuminuria. Analyses were restricted to individuals of European ancestry.	The urinary albumin concentration was measured from times urine samples using a solid-phase fluoroimmunoassay. Urinary creatinine levels were measured using the Jaffé method.	1. The Diabetes Control and Complications (DCCT) Research Group. Effect of intensive therapy on the development and progression of diabetic nephropathy in the Diabetes Control and Complications Trial. Kidney Int 1995;47(6):1703–20. 2. de Boer IH et al. Long-term renal outcomes of patients with type 1 diabetes mellitus and microalbuminuria: an analysis of the Diabetes Control and Complications Trial/Epidemiology of Diabetes Interventions and Complications cohort. Arch Intern Med. 2011 Mar 14;171(5):412-20.

Supplementary Table 3: Study-specific information about genotyping, imputation and data management and analysis

Study Name	Genotyping Array type	Genotype calling algorithm	QC filters for genotyped SNPs used for imputation (listed are criteria for exclusion)	No of SNPs used for imputation	Imputation software, version	Imputation Backbone (NCBI build)	Filtering of imputed genotypes	Data management and statistical analysis
3C	Illumina Human610-Quad	BeadStudio	call rate < 98%, pHWE < 10E-6, MAF < 1%	492,897	MACH	1000 Genomes EUR, Dec 2010 (Build 37)	none	R and ProbABEL
Advance	Affymetrix 5.0 Affymetrix 6.0	Affymetrix	SNPs genotyped on Affymetrix 5.0: call rate < 96% (<99% if MAF < 5%); SNPs genotyped on Affymetrix 6.0: call rate < 97% (<99% if MAF < 5%)	876,688	IMPUTE2 2.1.2	1000 Genomes CEU Pilot, Jun 2010 plus HapMap 3 rel. 2 all available haplotypes, Feb 2009 (build 36)	imputation info < 0.5	SNPTEST
AGES	Illumina Hu370CNV	Illumina	call rate < 97%, pHWE < 1e-6, MAF < 0.01, mishap p < 1e-9, SNPs not in Hapmap or strandedness issues merging with Hapmap	329,804	MACH 1.0.16	HapMap rel. 22 (build 36)	none	R,ProbABEL, Linear and Logistic Regression
Amish	Affymetrix 500K	BRLMM	call rate < 95%, pHWE < 10E-6, MAF < 1%, non-HapMap	338,598	MACH 1.0.15	HapMap rel. 22 phased CEU haplotypes (build 36)	none	Measured genotype accounting for polygenic component
ARIC	Affymetrix 6.0	Birdseed	call rate < 95%, pHWE < 10E-5, MAF < 1%	669,450	MACH 1.0.16	HapMap rel. 22 (build 36)	none	ProbABEL, PLINK, R
BLSA	Illumina Infinium HumanHap 550K	Beadstudio	call rate < 99%, pHWE < 10E-4, MAF < 1%	501,764	MACH 1.0.15	HapMap rel. 21 phased CEU haplotypes (build 35)	MAF < 1%, r2hat < 0.3	SAS, Merlin, R
CHS	Illumina 370CNV	BeadStudio	call rate<97%, pHWE<10E-5, heterozygotes=0, SNP not in HapMap	306,655	BimBam 0.99	HapMap rel. 22 (build 36)	dosage variance<0.01	Linear and logistic regression using R, robust estimates of SE
COLAUS	Affymetrix 500K	BRLMM	call rate < 70%, pHWE < 10E-7	390,631	IMPUTE 0.2.0	HapMap rel. 21 (build 35)	none	Matlab
CROATIA-SPLIT	HAP370CNV	Illumina	call rate < 98%, pHWE < 10E-10	330,997	MACH 1.0.15	HapMap rel. 22 CEU haplotypes (build 36)	none	R(GenABEL, ProABEL)
EPIC	Affymetrix 500K	BRLMM	call rate < 90%, pHWE < 10e-6	382,037	IMPUTE 0.3.1	HapMap rel. 21 (Build 35)	none	SAS, Stata, Linux scripts
Fenland	Affymetrix 500K	BRLMM	call rate < 90%, pHWE < 10E-6, MAF < 1%	362,055	IMPUTE 0.4.2	HapMap rel. 22 (build 36)	proper_info<0.4	Linux, Stata 10.1, SNPTEST 1.1.5
FHS	Affymetrix 500K Affymetrix 50K	Affymetrix	call rate < 95%, pHWE < 10E-6	503,526	MACH 1.0.15	HapMap rel. 22 phased CEU haplotypes (build 36)	none	R

	supplemental							
INCIPE	Illumina	Illumina	call rate < 95%, pHWE < 10E-6	635,646	IMPUTE 0.2.0	HapMap rel. 22 phased CEU haplotypes (build 36)	none	R
KORA-F3	Affymetrix 500K	BRLMM	per-chip call rate < 93%, MAF < 5%,discrepancy for one of the 50 SNPs common on both chips, gender checks	380,407	MACH	HapMap rel. 22 (build 35)	none	MACH2QTL, ProbABEL, R, Visual Basic
KORA-F4	Affymetrix 6.0	BRLMM	per-chip call rate < 93%, per SNP call rate < 93%, MAF < 1%, gender checks	629,893	MACH	HapMap rel. 22 (build 36)	none	MACH2QTL, ProbABEL, R, Visual Basic
LIFELINES	Illumina CytoSNP12 v2	GenomeStudio	call rate < 95%, pHWE < 1E-05	257,581		HapMap rel. 22 phased CEU haplotypes (build 36)	none	NO
MESA	Affymetrix Genome-Wide Human SNP Array 6.0	Birdseed v2	call rate < 95%, MAF ≤ 1%	897,979	IMPUTE 2.1.0	HapMap rel. 22 phased CEU haplotypes (build 36)	none	PLINK
MICROS	Illumina Infinium HumanHap300 v2 SNP bead microarrays	Beadstudio	call rate < 98%, pHWE < 10E-6, MAF < 1%	292,917	MACH 1.0.16	HapMap rel. 22 (build 36)	none	R, GenABEL, ProbABEL;
PREVEND	Illumina CytoSNP12 v2	GenomeStudio	call rate < 95%, pHWE < 1E-05	232,571		HapMap rel. 22 phased CEU haplotypes (build 36)	none	NO
SHIP	Affymetrix 6.0	Birdseed2	none	869,224	IMPUTE 0.5.0	HapMap rel. 22 (build 36)	none	SNPTEST 1.1.5, QUICKTEST 0.94, R, InforSense, InterSystems Caché
SHIP-TREND	Illumina Human Omni 2.5	GenomeStudio	call rate ≤ 0.9, pHWE ≤ 1E-04, monomorphic SNPs	1,782,967	IMPUTE 2.1.2.3	HapMap rel. 22 phased CEU haplotypes (build 36)	duplicate RSID but different positions	QUICKTEST 0.95, R, InforSense, InterSystems Caché
***in silico* replication**								
GANI_MED	Illumina Infinium PsychArray	GenomeStudio	call rate ≤ 0.95, pHWE ≤ 1E-04, MAF ≤ 0.005	305,145	IMPUTE 2.3.1	1000 Genomes Phase I v3 ALL (macGT1) (build 37)	duplicate IDs (via positions)	R, PLINK, gtool, InterSystems Caché
GENDIAN	Genome-Wide Human SNP Array 6.0	Birdseed (BRLMM)	n=126,259 SNPs (chr 1-chr22, chr X) were excluded from imputation by SNP QC due to one of the following: HWE-p < 10-6; monomorphic SNPs; MAF>.1 & call rate<.9 MAF>.09 & MAF <=.1 & call rate<.91 MAF>.08 & MAF <=.09 & call rate<.92	747,402	MACH 1.0.18.c MiniMac 2012-10-09	GIANT ALL 1000G v3 ref panel GRCh (build 37)	none	R

			MAF>.07 & MAF <=.08 & call rate<.93 MAF>.06 & MAF <=.07 & call rate<.94 MAF>.05 & MAF <=.06 & call rate<.95 MAF>.04 & MAF <=.05 & call rate<.96 MAF>.03 & MAF <=.04 & callr ate<.97 MAF>.02 & MAF <=.03 & call rate<.98 MAF>.01 & MAF <=.02 & call rate<.99 MAF <=.01 & call rate<.99					
Vanderbilt Omni1	Illumina HumanOmni1-Quad	BeadStudio	call rate < 98%, IBD (Z0<0.8), Mendel errors > 0, Duplicate concordance < 100%	946,523	IMPUTE 2.3.0	1000 Genomes Phase 1 integrated v3	Genotype Likelihood <0.9	Plink and R
Vanderbilt Omni5	Illumina HumanOmni5-Quad	BeadStudio	call rate < 98%, IBD (Z0<0.8), Mendel errors > 0, Duplicate concordance < 100%	3,819,154	IMPUTE 2.3.0	1000 Genomes Phase 1 integrated v3	Genotype Likelihood <0.9	Plink and R
Vanderbilt 660W	Illumina Human660W-Quad	BeadStudio	call rate < 98%, IBD (Z0<0.8), Mendel errors > 0, Duplicate concordance < 100%	530,014	IMPUTE 2.3.0	1000 Genomes Phase 1 integrated v3	Genotype Likelihood <0.9	Plink and R
***de novo* replication**								
	genotyping platform	**amount of DNA used per SNP (in ng)**	**genotyping method**	**n duplicates and concordance per SNP (provide per individual SNP)**	**number attempted /number genotyped (per individual SNP)**	**Other QC indices that your lab uses**		
ESTHER	LGC genomics SNP-line, using KASP Chemistry and 1536-well plates	3.75	De novo genotyping using KASPar v4.0 after whole genome amplification by primer extension preamplification (PEP) using thermostable DNA polymerases	LGC Genomics does not add duplicates. The data for each SNP represents one reaction per sample.	call rate range 0.98 - 1	none indicated by the lab		
SKIPOGH	LGC genomics SNP-line, using KASP Chemistry and 1536-well plates	5 -7.5	De novo genotyping using KASPar v4.0 after whole genome amplification by primer extension preamplification (PEP) using thermostable DNA polymerases	29 participants were genotyped in duplicate. SNP concordance	SNP call rates varied from 94.5% to 99.5% (median 97.2)	All assays have been validated on an in-house DNA panel (44 random Caucasian DNA samples). All sample plates genotyped include at least two negative controls. ie.		

				varied between 86% and 100%.		blank/water controls. All genotyping data are initially generated by an automated algorithm (genotype calling based upon recorded fluorescence values). All genotyping data is manually checked and verified by no less than two experienced scientists at LGC genomics.		
KORAF4 non-GWAS	Mass ARRAY Analyzer 4 system	15	iPlex Gold	At least 15% duplicate genotyping per SNP. Concordance≥95%, median = 100%	NA	NA		
KORAF3 non-GWAS	Mass ARRAY Analyzer 4 system	15	iPlex Gold	At least 15% duplicate genotyping per SNP. Concordance≥95%, median = 100%	NA	NA		
SAPHIR	Mass ARRAY Analyzer 4 system	15	iPlex Gold	70 duplicates; 46 SNPs were genotyped; 44 SNPs had a concordance of 100%; 2 SNPs had each 1 discordant sample	46 SNPs were genotyped and had an aerage callrate of 99,3% (between 98.15% and 99.65%)	automatic calculation of the HWE, comparison of the obtained genotypes with HapMap Data		

Supplementary Table 4: SNPs associated with UACR among all individuals with a p-value of <1E-05.

SNPID	chr	position (hg18)	Allele1	Allele2	Frequency Allele1	Effect	SE	p-value	I^2 %	Sample Size	In Gene	Genes Within 100kb
rs880315	1	10719453	t	c	0.65	-0.042	0.009	9.1E-06	0	41333	*CASZ1*	
rs4072037	1	153428691	t	c	0.54	0.029	0.006	2.5E-06	0	54450	*MUC1*	MIR92B(dist=2901),THBS3(dist=3312),TRIM46(dist=4620),KRTCAP2(dist=16263),MTX1(dist=16423),GBAP1(dist=21549),GBA(dist=42172),DPM3(dist=49071),SLC50A1(dist=50733),EFNA1(dist=54681),FAM189B(dist=54929),SCAMP3(dist=63703),CLK2(dist=70592),HCN3(dist=85151),PKLR(dist=97017)
rs914615	1	153442516	a	g	0.47	-0.030	0.007	7.4E-06	0	44877	*THBS3*	MTX1(dist=2598),GBAP1(dist=7724),MIR92B(dist=10829),MUC1(dist=13186),TRIM46(dist=18445),GBA(dist=28347),KRTCAP2(dist=30088),FAM189B(dist=41104),SCAMP3(dist=49878),CLK2(dist=56767),DPM3(dist=62896),SLC50A1(dist=64558),EFNA1(dist=68506),HCN3(dist=71326),PKLR(dist=83192)
rs17346504	2	137640231	t	c	0.12	0.050	0.011	7.2E-06	27	53401	*THSD7B*	
rs9333289	2	187206352	t	c	0.70	-0.030	0.007	9.3E-06	24	54441	*ITGAV*	FAM171B(dist=60682)
rs9333290	2	187227583	t	g	0.30	0.038	0.008	7.5E-07	15	54441	*ITGAV*	FAM171B(dist=39451)
rs13006483	2	187230995	t	g	0.30	0.037	0.008	1.2E-06	15	54441	*ITGAV*	FAM171B(dist=36039)
rs3816386	2	187236880	a	g	0.69	-0.035	0.007	2.9E-06	0	54441	*ITGAV*	FAM171B(dist=30154)
rs11685758	2	187241613	t	c	0.31	0.039	0.008	2.7E-06	0	44877	*ITGAV*	FAM171B(dist=25421)
rs12151442	2	187246092	t	c	0.70	-0.030	0.007	5.5E-06	1	54441	*ITGAV*	FAM171B(dist=20942)
rs13001028	2	187255140	a	g	0.69	-0.035	0.007	2.0E-06	0	54440		ITGAV(dist=1266),FAM171B(dist=11894)
rs13028817	2	187255744	t	g	0.70	-0.029	0.007	7.3E-06	0	54439		ITGAV(dist=1870),FAM171B(dist=11290)
rs12615659	2	187259552	a	t	0.30	0.030	0.007	4.3E-06	2	54439		ITGAV(dist=5678),FAM171B(dist=7482)
rs11678190	2	187268553	a	c	0.69	-0.036	0.007	1.5E-06	0	54441	*FAM171B*	ITGAV(dist=14679)
rs17750683	2	187328542	a	t	0.68	-0.033	0.007	4.1E-06	22	54439	*FAM171B*	ZSWIM2(dist=71910),ITGAV(dist=74668)
rs13026081	2	187334583	t	c	0.32	0.032	0.007	6.8E-06	21	54434	*FAM171B*	ZSWIM2(dist=65869),ITGAV(dist=80709)
rs11783652	8	55021047	a	g	0.32	0.037	0.008	2.4E-06	0	54450	*RGS20*	TCEA1(dist=20620)
rs17301329	8	55021534	a	t	0.29	0.042	0.008	5.6E-07	0	54450	*RGS20*	TCEA1(dist=20133),LYPLA1(dist=99946)
rs16919699	8	55021582	t	c	0.66	-0.037	0.008	2.3E-06	0	54450	*RGS20*	TCEA1(dist=20085),LYPLA1(dist=99898)
rs1016013	9	96516305	a	g	0.42	0.028	0.006	6.4E-06	5	54450		C9orf3(dist=12467),FBP1(dist=73953),MIR2278(dist=95760)
rs7851726	9	96543806	t	c	0.42	0.027	0.006	5.2E-06	3	54450	*C9orf3*	MIR2278(dist=68259)
rs446540	9	96549020	a	g	0.43	0.028	0.006	5.8E-06	10	54304	*C9orf3*	MIR2278(dist=63045)
rs183066	9	96557253	t	c	0.57	-0.028	0.006	5.8E-06	9	54448	*C9orf3*	MIR2278(dist=54812)
rs2584806	9	96569099	a	c	0.58	-0.027	0.006	9.3E-06	9	54449	*C9orf3*	MIR2278(dist=42966)
rs1109861	10	11286275	a	c	0.55	-0.030	0.006	1.9E-06	5	54442	*CELF2*	CELF2-AS2(dist=98818)
rs1801239	10	16959058	t	c	0.90	-0.066	0.011	4.6E-09	31	54450	*CUBN*	RSU1(dist=59599)

rs17343073	10	16972202	a	t	0.90	-0.071	0.012	4.0E-09	22	54449	*CUBN*	RSU1(dist=72743)
rs6602163	10	17006772	a	g	0.84	-0.056	0.009	1.2E-09	5	54450	*CUBN*	
rs10795433*	10	17009929	a	c	0.86	-0.061	0.010	2.4E-10	6	54450	*CUBN*	
rs2417849	12	20167780	t	c	0.37	0.028	0.006	9.5E-06	39	54441		LOC100506393(dist=24711)
rs2303658	12	20169697	a	g	0.34	0.030	0.007	9.5E-06	31	54442		LOC100506393(dist=26628)
rs11609944	12	20170557	a	g	0.38	0.028	0.006	9.6E-06	42	54449		LOC100506393(dist=27488)
rs1728897	15	53088662	t	c	0.54	-0.028	0.006	4.1E-06	0	54433		
rs12594729	15	53088684	a	g	0.50	0.029	0.006	2.0E-06	0	54450		
rs7167661	15	53090751	t	c	0.54	-0.028	0.006	3.5E-06	0	54450		
rs11071163	15	53091242	a	g	0.50	-0.029	0.006	9.2E-06	0	54449		
rs7173577	15	53092295	a	g	0.45	-0.029	0.006	2.3E-06	0	54450		
rs1728867	15	53094106	a	g	0.45	-0.030	0.006	8.3E-07	0	54449		
rs951048	15	53094503	a	t	0.44	-0.030	0.006	8.7E-07	0	54449		
rs2414396	15	53094680	a	g	0.46	-0.031	0.006	7.6E-07	0	54449		
rs12907410	15	53095223	t	c	0.56	0.028	0.006	3.7E-06	0	54449		
rs1728886	15	53095714	t	c	0.56	0.030	0.006	1.2E-06	0	54449		
rs17818939	15	53096140	a	g	0.44	-0.030	0.006	1.1E-06	0	54450		
rs1728878	15	53097144	t	c	0.57	0.028	0.006	1.9E-06	0	54450		
rs8042768	15	53097375	a	g	0.43	-0.028	0.006	2.1E-06	0	54448		
rs1690363	15	53098119	a	g	0.43	-0.028	0.006	2.0E-06	0	54448		
rs1690365	15	53098549	t	c	0.56	0.028	0.006	1.9E-06	0	54450		
rs1614271	15	53098677	t	c	0.57	0.029	0.006	1.6E-06	0	54448		
rs1690366	15	53098855	t	g	0.44	-0.030	0.006	2.0E-06	0	54448		
rs1690367	15	53099066	a	g	0.43	-0.028	0.006	1.8E-06	0	54406		
rs7180127	15	53103432	t	c	0.51	0.029	0.006	3.7E-06	0	54449		
rs10083619	15	53106962	a	g	0.51	0.029	0.006	3.5E-06	0	54448		
rs2899576	15	53107909	t	c	0.48	-0.030	0.006	1.2E-06	0	54424		
rs1528472	15	53108420	a	c	0.48	-0.032	0.006	5.4E-07	0	54445		
rs17238122	15	53109188	a	g	0.48	-0.031	0.006	8.8E-07	0	54443		
rs1528477	15	53111680	a	g	0.48	-0.031	0.006	1.5E-06	0	54449		
rs1830324	15	53112207	a	g	0.51	-0.030	0.006	3.4E-06	0	54449		
rs11858741	15	53112699	a	g	0.51	0.030	0.006	2.2E-06	0	54450		
rs231226	19	40959617	t	c	0.62	-0.033	0.007	5.1E-06	22	44877	*ARHGAP33*	PROSER3(dist=7700),LINC01529(dist=12001),HSPB6(dist=19847),LIN37(dist=22357),PRODH2(dist=23115),PSENEN(dist=29721),U2AF1L4(dist=31434),IGFLR1(dist=34426),KMT2B(dist=37996),NPHS1(dist=48497),ZBTB32(dist=59837),KIRREL2(dist=80033),APLP1(dist=91624),UPK1A(dist=98390)
rs231227	19	40959907	a	g	0.38	0.033	0.007	4.9E-06	22	44877	*ARHGAP33*	PROSER3(dist=7990),LINC01529(dist=11711),HSPB6(dist=20137),LIN37(dist=22647),PRODH2(dist=22825),PSENEN(dist=30011),U2AF1L4(dist=31724),IGFLR1(dist=34716),KMT2B(dist=38286),NPHS1(dist=48207),ZBTB32(dist=60127),KIRREL2(dist=79743),APLP1(dist=91334),UPK1A(dist=98680)

rs2828785	21	24359376	t	c	0.27	-0.038	0.008	7.9E-06	0	54450

Standard error (SE) and p-values are corrected for genomic control. A1 is the coded allele.

*The previously identified missense variant rs18012399 in *CUBN* is correlated with the index variant rs10795433 in this study (r^2=0.54 and D'=1, based on HapMap r22 CEU data)

Supplementary Table 5: SNPs associated with MA among all individuals with a p-value of <1E-05.

SNPID	chr	position (hg18)	Allele 1	Allele 2	Fre-quency Allele1	Effect	SE	p-value	I^2 %	Sample Size	In Gene	Genes Within 100kb
rs11579312	1	30429159	t	c	0.69	0.11	0.025	9.7E-06	0	54116		
rs3795324	1	158909735	a	c	0.82	-0.15	0.031	9.4E-07	22	52716		CD48(dist=5425),SLAMF1(dist=26010),SLAMF7(dist=65736),CD84(dist=93805)
rs16827742	2	150615405	a	g	0.06	0.30	0.063	3.1E-06	12	35962		
rs9333289	2	187206352	t	c	0.71	-0.10	0.022	5.2E-06	0	54107	*ITGAV*	FAM171B(dist=60682)
rs9333290	2	187227583	t	g	0.29	0.11	0.023	5.0E-06	0	54107	*ITGAV*	FAM171B(dist=39451)
rs13006483	2	187230995	t	g	0.29	0.10	0.023	7.0E-06	0	54107	*ITGAV*	FAM171B(dist=36039)
rs12151442	2	187246092	t	c	0.70	-0.10	0.022	2.0E-06	0	54107	*ITGAV*	FAM171B(dist=20942)
rs13001028	2	187255140	a	g	0.70	-0.10	0.023	8.3E-06	0	54106		ITGAV(dist=1266),FAM171B(dist=11894)
rs13028817	2	187255744	t	g	0.70	-0.10	0.022	2.1E-06	0	54105		ITGAV(dist=1870),FAM171B(dist=11290)
rs12615659	2	187259552	a	t	0.30	0.11	0.022	1.3E-06	0	54105		ITGAV(dist=5678),FAM171B(dist=7482)
rs11678190	2	187268553	a	c	0.70	-0.10	0.023	5.1E-06	0	54107	*FAM171B*	ITGAV(dist=14679)
rs17750683	2	187328542	a	t	0.68	-0.11	0.022	1.4E-06	0	54105	*FAM171B*	ZSWIM2(dist=71910),ITGAV(dist=74668)
rs13026081	2	187334583	t	c	0.32	0.11	0.022	1.6E-06	0	54093	*FAM171B*	ZSWIM2(dist=65869),ITGAV(dist=80709)
rs1077216	3	46867165	t	c	0.07	0.20	0.044	5.2E-06	5	45096		MYL3(dist=7196),PRSS42(dist=16576),PTH1R(dist=27075),CCDC12(dist=71059)
rs13160548	5	38814607	t	c	0.69	-0.10	0.023	8.2E-06	14	53130	*OSMR-AS1*	LINC01265(dist=58475),OSMR(dist=67110)
rs12719264	5	119211839	a	g	0.30	-0.11	0.025	6.2E-06	29	54115		
rs2110904	6	107701464	t	c	0.65	0.10	0.022	8.9E-06	0	54116	*PDSS2*	
rs538641	8	103072879	a	g	0.05	0.28	0.062	7.8E-06	0	50048	*NCALD*	
rs1801239	10	16959058	t	c	0.90	-0.23	0.035	1.7E-10	18	54115	*CUBN*	RSU1(dist=59599)
rs17343073	10	16972202	a	t	0.90	-0.23	0.036	3.0E-10	0	54115	*CUBN*	RSU1(dist=72743)
rs6602163	10	17006772	a	g	0.83	-0.17	0.029	1.5E-09	5	54116	*CUBN*	
rs10795433	10	17009929	a	c	0.85	-0.20	0.031	1.3E-10	4	54116	*CUBN*	
rs12764441	10	72361657	t	c	0.48	-0.10	0.021	3.5E-06	0	54116		PCBD1(dist=43108),SGPL1(dist=50719)
rs3740393	10	104626645	c	g	0.21	0.13	0.028	6.1E-06	19	54048	*C10orf32-ASMT*	C10orf32(dist=11937),CYP17A1(dist=39365),CNNM2(dist=41420),WBP1L(dist=60634)
rs10899033	11	74070819	c	g	0.72	0.11	0.025	9.3E-06	0	54116		CHRDL2(dist=14303),MIR4696(dist=38142),POLD3(dist=39066),RNF169(dist=66742)
rs10498273	14	20214639	c	g	0.94	-0.21	0.047	9.6E-06	36	53131		ANG(dist=7537),RNASE4(dist=7573),OR6S1(dist=34949),EDDM3A(dist=69300),LOC254028(dist=69419),RNASE12(dist=85817),RNASE11(dist=86382),EDDM3B(dist=91787)
rs7145202	14	22161945	t	c	0.62	0.10	0.022	3.7E-06	0	54106		ABHD4(dist=10840),DAD1(dist=33962)
rs6572602	14	22163380	a	g	0.62	0.11	0.024	4.6E-06	0	41412		ABHD4(dist=12275),DAD1(dist=35397)
rs274173	19	61384255	c	g	0.17	-0.23	0.051	5.2E-06	12	38796	*GALP*	ZSCAN5B(dist=8615),ZNF444(dist=20181),ZSCAN5A(dist=40236),ZNF787(dist=59701)

rs6030216	20	40486448	t	c	0.17	0.12	0.027	6.0E-06	0	54115	*PTPRT*
rs4812598	20	40487956	c	g	0.83	-0.12	0.027	9.1E-06	0	54115	*PTPRT*
rs6513791	20	40491536	t	c	0.18	0.12	0.026	4.4E-06	12	54115	*PTPRT*
rs4810356	20	40491604	t	c	0.82	-0.13	0.028	7.6E-06	11	54115	*PTPRT*
rs6030232	20	40496297	a	t	0.82	-0.12	0.027	8.7E-06	0	54115	*PTPRT*
rs6030238	20	40498930	a	g	0.81	-0.12	0.026	6.0E-06	12	54115	*PTPRT*

Odds rations can be obtained by exponentiating the effect to the basis *e*.

Supplementary Table 6: SNPs associated with UACR among individuals without diabetes with a p-value of <1E-05.

SNPID	chr	position (hg18)	Allele 1	Allele 2	Fre-quency Allele1	Effect	SE	p-value	I^2%	Sample Size	In Gene	Genes Within 100kb
rs17377079	1	84999401	a	g	0.15	0.060	0.013	6.9E-06	9	46061		LPAR3(dist=52273),SSX2IP(dist=70573)
rs4072037	1	153428691	t	c	0.54	0.028	0.006	8.5E-06	0	46061	*MUC1*	MIR92B(dist=2901),THBS3(dist=3312),TRIM46(dist=4620),KRTCAP2(dist=16263),MTX1(dist=16423),GBAP1(dist=21549),GBA(dist=42172),DPM3(dist=49071),SLC50A1(dist=50733),EFNA1(dist=54681),FAM189B(dist=54929),SCAMP3(dist=63703),CLK2(dist=70592),HCN3(dist=85151),PKLR(dist=97017)
rs9333290	2	187227583	t	g	0.30	0.037	0.008	4.1E-06	3	46052	*ITGAV*	FAM171B(dist=39451)
rs13006483	2	187230995	t	g	0.30	0.035	0.008	6.7E-06	3	46052	*ITGAV*	FAM171B(dist=36039)
rs13001028	2	187255140	a	g	0.69	-0.034	0.008	9.9E-06	0	46052		ITGAV(dist=1266),FAM171B(dist=11894)
rs11678190	2	187268553	a	c	0.69	-0.035	0.008	8.7E-06	0	46052	*FAM171B*	ITGAV(dist=14679)
rs17750683	2	187328542	a	t	0.68	-0.035	0.008	4.6E-06	0	46052	*FAM171B*	ZSWIM2(dist=71910),ITGAV(dist=74668)
rs13026081	2	187334583	t	c	0.32	0.034	0.008	8.3E-06	0	46045	*FAM171B*	ZSWIM2(dist=65869),ITGAV(dist=80709)
rs4674086	2	201032130	t	c	0.46	0.028	0.006	8.7E-06	0	45053	*SPATS2L*	KCTD18(dist=29799),SGOL2(dist=66980)
rs9372871	6	127849645	t	c	0.89	-0.046	0.010	4.2E-06	2	45094	*SOGA3*	KIAA0408(dist=27417),C6orf58(dist=90367)
rs9372872	6	127849848	c	g	0.11	0.046	0.010	2.5E-06	0	46061	*SOGA3*	KIAA0408(dist=27620),C6orf58(dist=90164)
rs7739650	6	127850605	a	g	0.11	0.046	0.010	3.1E-06	2	46061	*SOGA3*	KIAA0408(dist=28377),C6orf58(dist=89407)
rs13220247	6	127850652	t	c	0.89	-0.046	0.010	3.4E-06	2	46061	*SOGA3*	KIAA0408(dist=28424),C6orf58(dist=89360)
rs9388580	6	127851073	t	c	0.89	-0.044	0.010	8.7E-06	6	46061	*SOGA3*	KIAA0408(dist=28845),C6orf58(dist=88939)
rs12668467	7	13598753	t	c	0.27	-0.043	0.009	4.1E-06	0	46061		
rs1801239	10	16959058	t	c	0.90	-0.054	0.012	4.4E-06	25	46061	*CUBN*	RSU1(dist=59599)
rs10795433	10	17009929	a	c	0.86	-0.045	0.010	8.7E-06	14	46061	*CUBN*	
rs2192224	15	24959369	t	g	0.13	0.048	0.011	6.1E-06	0	46061	*GABRG3*	LOC101928869(dist=26259)
rs7173577	15	53092295	a	g	0.45	-0.029	0.006	6.7E-06	0	46061		
rs1728867	15	53094106	a	g	0.45	-0.028	0.006	7.4E-06	0	46061		
rs951048	15	53094503	a	t	0.44	-0.028	0.006	7.8E-06	0	46061		
rs2414396	15	53094680	a	g	0.46	-0.029	0.006	4.1E-06	0	46061		
rs17818939	15	53096140	a	g	0.44	-0.028	0.006	9.9E-06	0	46061		
rs2899576	15	53107909	t	c	0.48	-0.029	0.006	5.7E-06	0	46035		
rs1528472	15	53108420	a	c	0.48	-0.030	0.007	3.1E-06	0	46056		
rs17238122	15	53109188	a	g	0.48	-0.030	0.007	4.8E-06	0	46054		
rs1528477	15	53111680	a	g	0.48	-0.030	0.007	6.6E-06	0	46061		
rs11858741	15	53112699	a	g	0.51	0.029	0.007	7.9E-06	0	46061		
rs4528660	18	3033516	t	c	0.91	-0.073	0.017	9.4E-06	3	33478		MYOM1(dist=23289),LPIN2(dist=31571),LOC727896 (dist=96895)

Supplementary Table 7: SNPs associated with UACR among individuals with diabetes with a p-value of <1E-05.

SNPID	chr	position (hg18)	Allele 1	Allele 2	Fre-quency Allele1	Effect	SE	p-value	I^2 %	Sample Size	In Gene	Genes Within 100kb [Closest Gene]
rs13427836	2	128744431	t	c	0.14	0.199	0.044	6.1E-06	10	5509	*HS6ST1*	UGGT1(dist=74712)
rs13428208	2	128744772	t	c	0.14	0.195	0.044	7.6E-06	10	5509	*HS6ST1*	UGGT1(dist=75053)
rs2405747	2	128748295	t	c	0.15	0.193	0.043	6.9E-06	14	5509	*HS6ST1*	UGGT1(dist=78576)
rs4662787	2	128752447	t	c	0.18	0.176	0.040	9.0E-06	0	5824	*HS6ST1*	UGGT1(dist=82728)
rs10183821	2	128753139	a	g	0.81	-0.169	0.038	9.3E-06	0	5825	*HS6ST1*	UGGT1(dist=83420)
rs13079877	3	2102845	a	g	0.45	0.148	0.033	5.6E-06	25	5825		CNTN4(dist=12705),CNTN4-AS2(dist=24248)
rs7634770	3	67012918	a	c	0.70	-0.142	0.030	2.7E-06	19	5825		[KBTBD8, dist=119174]
rs9876318	3	67014118	a	t	0.69	-0.144	0.030	2.0E-06	20	5824		[KBTBD8, dist=117974]
rs17738155	6	51264035	t	c	0.92	-0.241	0.053	5.9E-06	39	5825		[PKHD1, dist=324068]
rs947724	6	51274689	t	c	0.92	-0.239	0.053	7.5E-06	41	5825		[PKHD1, dist=313414]
rs7792461	7	29479920	t	g	0.39	0.130	0.029	5.1E-06	0	5825	*CHN2*	PRR15(dist=90032)
rs4722909	7	29481456	a	g	0.60	-0.134	0.029	3.2E-06	0	5823	*CHN2*	PRR15(dist=88496)
rs4722913	7	29482735	a	g	0.61	-0.131	0.029	4.2E-06	0	5825	*CHN2*	PRR15(dist=87217)
rs7798161	7	29483162	a	g	0.61	-0.130	0.029	4.7E-06	0	5825	*CHN2*	PRR15(dist=86790)
rs3828977	7	29486023	a	g	0.59	-0.131	0.029	4.9E-06	0	5825	*CHN2*	PRR15(dist=83929)
rs7922045	10	122991722	t	c	0.26	0.165	0.033	5.7E-07	0	5824		[FGFR2, dist=236111]
rs729014	10	122992796	t	c	0.15	0.202	0.043	2.4E-06	0	5825		[FGFR2, dist=235037]
rs649529	11	87647899	t	g	0.43	-0.147	0.033	9.3E-06	0	5825		CTSC(dist=18509),RAB38(dist=99616)

Supplementary Table 8: Discovery, replication and combined estimates for all index SNPs associated with UACR in diabetes in the discovery sample at p<1E-05

						discovery						replication						combined					
Marker	gene nearby	chr	position (hg18)	A 1	A 2	Freq A1	beta	SE	p-value	I^2 %	n	Freq A1	beta	SE	p-value	I^2 %	n	Freq A1	beta	SE	p-value	I^2 %	n
rs13427836	*HS6ST1*	2	128744431	t	c	0.14	0.20	0.04	6.1E-06	10	5509	0.15	0.16	0.07	3.13E-02	58	1890	0.15	0.19	0.04	6.31E-07	30	7399
rs13079877	*CNTN4*	3	2102845	a	g	0.45	0.15	0.03	5.6E-06	25	5825	0.50	0.04	0.05	5.16E-01	0	1880	0.46	0.12	0.03	2.40E-05	20	7705
rs9876318	*KBTBD8*	3	67014118	a	t	0.69	-0.14	0.03	2.0E-06	20	5824	0.69	0.08	0.06	1.56E-01	0	1897	0.69	-0.09	0.03	4.86E-04	37	7721
rs17738155	*PKHD1*	6	51264035	t	c	0.92	-0.24	0.05	5.9E-06	39	5825	0.92	0.06	0.10	5.30E-01	0	1896	0.92	-0.17	0.05	2.51E-04	42	7721
rs4722909	*CHN2*	7	29481456	a	g	0.60	-0.13	0.03	3.2E-06	0	5823	0.60	0.09	0.05	9.66E-02	40	1894	0.60	-0.08	0.03	9.92E-04	38	7717
rs7922045	*FGFR2*	10	122991722	t	c	0.26	0.17	0.03	5.7E-07	0	5824	0.23	-0.10	0.06	1.05E-01	35	1824	0.25	0.11	0.03	2.41E-04	39	7648
rs649529	*RAB38*	11	87647899	t	g	0.43	-0.15	0.03	9.3E-06	0	5825	0.43	-0.12	0.05	1.91E-02	0	1962	0.43	-0.14	0.03	5.84E-07	0	7787

A1 is the coded allele (effect allele), i.e. the beta corresponds to the effect by which UACR changes per each additional copy of the coded allele.
The I^2 statistic of the combined results was obtained from a separate analysis incorporating each discovery file with single GC-correction and the replication files. Standard error (SE) and p-value of the combined results are based on double-GC corrected results as described in the methods.

Supplementary Table 9: Association results for the index SNPs near *RAB38/CTSC* and in *HS6ST1* in the DCCT/EDIC Study

incident microalbuminuria (1244 individuals [268 cases]; primary endpoint)					
SNP	effect alelle	frequency of effect allele	effect	se	p-value
rs649529	T	0.42	0.04	0.09	0.64
rs13427836	T	0.14	-0.18	0.14	0.20
time to macroalbuminuria or ESRD (1304 individuals [133 cases]; secondary endpoint)					
SNP	effect alelle	frequency of effect allele	effect	se	p-value
rs649529	T	0.42	0.24	0.14	0.09
rs13427836	T	0.14	-0.31	0.22	0.16

Cox proportional hazards regression models were used to estimate hazard ratios after adjustment for cohort status (primary vs. secondary), treatment (intensive vs. conventional), cohort*treatment interaction (stratified by DCCT year of entry), age of diagnosis squared, sex, diabetes duration squared, body mass index, blood pressure, triglyceride, HDL-C, total cholesterol, smoking (all at baseline), as well as time-dependent updated mean A1C, and time-dependent indicators for hypertension diagnosis and treatment. Imputation quality (rs13427836) and call rate (rs649529) were both >=0.99.