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**Supplemental Methods. Technical details for UK Biobank GWAS, meta-analysis of UK Biobank and CKDGen GWAS, and PRS generation.**

**UK Biobank trans-ethnic GWAS**

We randomly selected 90% of the total 451,508 unrelated multi-ancestry UK Biobank individuals for conducting the GWAS (N=406,350). Excluded related individuals were defined as one individual in each pair within the third degree of relatedness determined based on kinship coefficients centrally calculated by UK Biobank.1 To ensure balance across different ethnic groups, the selection was stratified by the self-reported ethnic groups that were available in the UK Biobank, including EUR (British, Irish, White, or any other white background), AFR (African, Caribbean, Any other Black background, Black or Black British), SAS (Indian, Pakistani, Bangladeshi, Asian or Asian British, or any other Asian background), and EAS (Chinese). This led to a total of 390,694 EUR, 6,406 AFR, 7,979 SAS, 1,271 EAS participants for the GWAS. We conducted the GWAS in PLINK using an additive genetic model and adjusting for age, sex, diabetes, self-reported race, and the first 40 principal components (PCs) of genetic ancestry. PCA plot of the first 2 genetic PCs is shown in Supplemental Figure 3. The sample-size corrected genomic control (GC) inflation factor was 1.001 for this UK Biobank GWAS.

**Meta-analysis of UK Biobank and CKDGen GWAS**

We conducted a fixed-effects inverse variance weighted meta-analysis using METAL on the summary statistics from our UK Biobank GWAS and a meta-analysis by the CKDGen Consortium of the GWAS of eGFRcr including up to 765,348 multi-ethnic individuals (https://ckdgen.imbi.uni-freiburg.de/).2, 3 As the CKDGen consortium included the ARIC study (N=11,908), we adjusted the effect sizes of SNPs by re-conducting the meta-analysis removing ARIC data. This led to a total of 1,159,871 participants, including 949,116 whites, 166,997 East Asians, 21,338 South Asians, 17,459 African Americans, and 4,961 Hispanics. Since the sample-size corrected GC inflation factor was 1.004 for the CKDGen Consortium GWAS and 1.001 for the UK Biobank GWAS and potential population stratification was controlled through adjusting for PCs of genetic ancestry in the GWAS (first 40 PCs for the UK Biobank GWAS; number of PCs varies for the GWAS of participating studies in the CKDGen consortium), GC correction was not further applied in our meta-analysis. The sample-size corrected GC inflation factor for the overall meta-analysis was 1.0005. The Q-Q plot of this GWAS is shown in Supplemental Figure 4. By meta-analyzing with the UKB Biobank GWAS, the SNP heritability estimated using LD Score regression4 increased from 8.63% of the CKDGen Consortium meta-analysis alone to 12.01%. Effect sizes of SNPs after meta-analyzing the CKDGen and the UK Biobank were generally consistent with that of the CKDGen alone. The resulted meta-analysis identified 1,460 independent SNPs defined as squared pairwise correlations less than 0.1 that met genome-wide significance.

**Construction of trans-ethnic LD reference panel for PRS model development**

The LD reference panel for PRS model development was constructed based on 1000 Genomes individuals of multiple ethnic groups (N=608), including 498 EUR, 11 AFR, 11 SAS and 88 EAS, where the proportions of the various ethnic groups were consistent with those in the meta-analyzed UK Biobank and CKDGEN trans-ethnic GWAS summary statistics.

**Dataset for PRS tuning**

We used the remained 10% of the total 451,508 unrelated multi-ancestry UK Biobank individuals for turning parameters for the PRS models (N=45,158), which include 43,413 EUR, 715 AFR, 888 SAS and 142 EAS.

# **Supplemental Table 1. ICD-9/10 codes used for identifying chronic kidney disease and kidney failure.**

**(A) Chronic kidney disease (CKD)**

|  |  |  |
| --- | --- | --- |
| **ICD-9-code** | **Description** | **ICD-10-code** |
| 582 | Chronic glomerulonephritis | N03 |
| 583 | Nephritis and nephropathy |  |
| 585, 585.x where x≥3 | Chronic kidney disease | N18, N18.x where x≥3 |
| 586 | Renal failure | N19 |
| 587 | Renal sclerosis | N26 |
| 588 | Disorders resulting from impaired renal function | N25 |
| 403 | Hypertensive chronic kidney disease | I12 |
| 404 | Hypertensive heart and kidney disease | I13 |
| 593.9 | Unspecified disorder of the kidney and ureter |  |
| 250.4 | Diabetes with renal complications | E10.2, E11.2, E13.2 |
| V42.0 | Kidney replaced by transplant | Z94.0 |
| 55.6 | Transplant of kidney |  |
| 996.81 | Complications of transplanted kidney |  |
| V45.1a | Renal dialysis status | Z99.2 |
| V56 a | Admission for dialysis treatment or session | Z49 |
| 39.95a | Hemodialysis |  |
| 54.98a | Peritoneal dialysis |  |
|  | Encounter for adjustment and management of vascular access device | Z45.2 |

a Codes that are counted as incident CKD only if a concomitant acute kidney injury (AKI) code (ICD-9: 584.x, ICD-10: N17) is not present.

**(B) Kidney failure**

|  |  |  |
| --- | --- | --- |
| **ICD-9-code** | **Description** | **ICD-10-code** |
| V42.0 | Kidney replaced by transplant | Z94.0 |
| 55.6 | Transplant of kidney |  |
| 996.81 | Complications of transplanted kidney |  |
| V45.1a | Renal dialysis status | Z99.2 |
| V56 a | Admission for dialysis treatment or session | Z49 |
| 39.95a | Hemodialysis |  |
| 54.98a | Peritoneal dialysis |  |
|  | Encounter for adjustment and management of vascular access device | Z45.2 |
| 585.5 | Chronic kidney disease stage 5 | N18.5 |
| 585.6 | End stage renal disease | N18.6 |
| 586 | Renal failure | N19 |
| 403.01 | Hypertensive chronic kidney disease, malignant, with CKD 5 or ESRD |  |
| 403.91 | Hypertensive chronic kidney disease, with CKD 5 or ESRD | I12.0 |

a Codes that are not counted as incident kidney failure if: 1) for hospitalizations, a concurrent AKI code is present; 2) for deaths, if a concurrent AKI code is present without a concurrent CKD code.

# **Supplemental Table 2. Technical details of the polygenic risk scores.**

|  |  |  |  |
| --- | --- | --- | --- |
|  | **LDPred PRS** | **P+T PRS** | **Top SNPs PRS** |
| **Features** | Entire summary results of variants with rescaling weights based on LD structure, effect size, and estimated causal fraction | r2 and P value thresholds to restrict variants | r2 and genome-wide significant threshold to restrict variants |
| **Settings** | LD structure from 1000 Genome  % of causal variants = 30% | = 0.1  P = 0.05 | = 0.1  P = 5 |
| **No. of candidate SNPs** | ~ 1.5 million | ~ 1.5 million | ~ 1.5 million |
| **No. of included SNPs** | ~ 1.5 million | 40,042 | 1,460 |
| **Rescaling weights** | Yes | No | No |

PRS: polygenic risk score.

# **Supplemental Table 3. Adjusted proportion of the variance for estimated glomerular filtration rate (eGFR) and albumin to creatinine ratio (ACR) explained by polygenic risk scores (PRS) (N = 8,886).**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **eGFRcr** | | | **eGFRcys** | | | **eGFRcr-cys** | | | **ACR** | | |
| **LDPred PRS**a | **P+T PRS**a | **Top SNPs PRS**a | **LDPred PRS**a | **P+T PRS**a | **Simple PRS**a | **LDPred PRS**a | **P+T PRS**a | **Top SNPs PRS**a | **LDPred PRS**a | **P+T PRS**a | **Top SNPs PRS**a |
| **Visit 1** | 0.0787b | 0.0633 | 0.0505 |  |  |  |  |  |  |  |  |  |
| **Visit 2** | 0.0767 | 0.0653 | 0.0524 | 0.0289 | 0.0245 | 0.0182 | 0.06 | 0.0514 | 0.0398 |  |  |  |
| **Visit 3** | 0.0939 | 0.0784 | 0.062 | 0.0393 | 0.0311 | 0.024 | 0.0728 | 0.0593 | 0.0463 |  |  |  |
| **Visit 4** | 0.0786 | 0.0693 | 0.0474 | 0.0246 | 0.0219 | 0.0162 | 0.0582 | 0.0513 | 0.0364 | 0.0008 | 0.0011 | 0.0011 |
| **Visit 5** | 0.0551 | 0.0525 | 0.0427 | 0.0224 | 0.0196 | 0.0161 | 0.0391 | 0.0358 | 0.0293 | 0.0023 | 0.0018 | 0.0017 |
| **Visit 6** | 0.0641 | 0.0571 | 0.0485 | 0.0287 | 0.0267 | 0.0203 | 0.0477 | 0.0433 | 0.0349 | 0.0002 | 0.0001 | 0.0004 |

a LDPred PRS was constructed using LDPred algorithm, a Bayesian approach utilizes GWAS summary statistics to compute the posterior mean effect sizes for the genetic variants by assuming a prior of the joint effect sizes and incorporating the LD structure of the reference population. P+T PRS was constructed using ‘pruning and thresholding (P+T)’, which first prunes variants to only keep those who have absolute pairwise correlation weaker than a threshold within certain genetic distance and then filtered variants that have a P value larger than a pre-defined threshold of significance. Top SNPs score was constructed using the most commonly used level of absolute pairwise correlation for pruning and genome-wide significance level for thresholding.

b Proportion of the variance for eGFR explained by PRS with adjusting for age at the corresponded visit, sex, center, and first 10 genetic principal components for all such values.

eGFRcr, estimated glomerular filtration rate based on creatinine; eGFRcr-cys, estimated glomerular filtration rate based on creatinine and cystatin; eGFRcysr, estimated glomerular filtration rate based on cystatin.

# **Supplemental Table 4. Adjusted proportion of the variance for estimated glomerular filtration rate (eGFR) and albumin to creatinine ratio (ACR) explained by polygenic risk scores (PRS) among participants with African ancestry (N = 2,871).**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **eGFRcr** | | | **eGFRcys** | | | **eGFRcr-cys** | | | **ACR** | | |
| **LDPred PRS**a | **P+T PRS**a | **Top SNPs PRS**a | **LDPred PRS**a | **P+T PRS**a | **Simple PRS**a | **LDPred PRS**a | **P+T PRS**a | **Top SNPs PRS**a | **LDPred PRS**a | **P+T PRS**a | **Top SNPs PRS**a |
| **Visit 1** | 0.0144b | 0.007 | 0.0052 |  |  |  |  |  |  |  |  |  |
| **Visit 2** | 0.0255 | 0.0142 | 0.0078 | 0.0142 | 0.0064 | 0.0037 | 0.0236 | 0.0122 | 0.0074 |  |  |  |
| **Visit 3** | 0.0287 | 0.0153 | 0.0106 | 0.0157 | 0.0068 | 0.0032 | 0.0244 | 0.0122 | 0.0072 |  |  |  |
| **Visit 4** | 0.0357 | 0.0227 | 0.0152 | 0.0148 | 0.0075 | 0.006 | 0.0281 | 0.0166 | 0.0116 | 0.0002 | 0.00003 | 0.0012 |
| **Visit 5** | 0.0245 | 0.0149 | 0.0116 | 0.0162 | 0.0102 | 0.007 | 0.0215 | 0.0134 | 0.0098 | 0.003 | 0.0005 | 0.0006 |
| **Visit 6** | 0.0232 | 0.0175 | 0.0179 | 0.0073 | 0.0059 | 0.0106 | 0.0146 | 0.0113 | 0.0147 | 0.0004 | 0.0011 | 0.0004 |

a LDPred PRS was constructed using LDPred algorithm, a Bayesian approach utilizes GWAS summary statistics to compute the posterior mean effect sizes for the genetic variants by assuming a prior of the joint effect sizes and incorporating the LD structure of the reference population. P+T PRS was constructed using ‘pruning and thresholding (P+T)’, which first prunes variants to only keep those who have absolute pairwise correlation weaker than a threshold within certain genetic distance and then filtered variants that have a P value larger than a pre-defined threshold of significance. Top SNPs score was constructed using the most commonly used level of absolute pairwise correlation for pruning and genome-wide significance level for thresholding.

b Proportion of the variance for eGFR explained by PRS with adjusting for age at the corresponded visit, sex, center, and first 10 genetic principal components for all such values.

eGFRcr, estimated glomerular filtration rate based on creatinine; eGFRcr-cys, estimated glomerular filtration rate based on creatinine and cystatin; eGFRcysr, estimated glomerular filtration rate based on cystatin.

# **Supplemental Table 5. Risk for incident kidney diseases according to conventional risk factors of kidney diseases (N=8,886).**

|  |  |  |  |
| --- | --- | --- | --- |
|  |  | **Risk for incident kidney diseases per 1 unit increase of covariate** | |
| **Hazard ratios**  **(95% CI)** | **P value** |
| **Incident chronic kidney disease** | **Age, yearsa** | 1.07 (1.06, 1.08) | 1.69E-87 |
| **Femalea** | 0.78 (0.73, 0.85) | 1.97E-10 |
| **Body mass index, kg/m2 a** | 1.03 (1.02, 1.04) | 5.51E-15 |
|  | **Advanced educationa** | 0.91 (0.84, 0.98) | 1.89E-02 |
|  | **Current smokersa** | 1.34 (1.23, 1.47) | 1.16E-10 |
|  | **History of diabetesa** | 1.83 (1.62, 2.05) | 4.24E-24 |
|  | **History of hypertensiona** | 1.62 (1.49, 1.75) | 2.17E-31 |
|  | **History of CHDa** | 2.06 (1.77, 2.40) | 1.02E-20 |
| **Incident end stage kidney disease** | **Age, yearsa** | 1.06 (1.03, 1.10) | 4.87E-04 |
| **Femalea** | 0.47 (0.33, 0.69) | 8.56E-05 |
| **Body mass index, kg/m2 a** | 1.04 (1.00, 1.08) | 5.16E-02 |
| **Advanced educationa** | 0.78 (0.53, 1.15) | 2.05E-01 |
| **Current smokersa** | 2.10 (1.41, 3.13) | 2.76E-04 |
| **History of diabetesa** | 5.05 (3.44, 7.41) | 1.21E-16 |
| **History of hypertensiona** | 2.90 (1.99, 4.22) | 2.80E-08 |
|  | **History of CHDa** | 1.74 (0.99, 3.06) | 5.51E-02 |
| **Incident kidney failure** | **Age, yearsa** | 1.10 (1.08, 1.12) | 6.66E-24 |
| **Femalea** | 0.59 (0.48, 0.71) | 8.97E-08 |
| **Body mass index, kg/m2 a** | 1.04 (1.02, 1.06) | 7.06E-05 |
| **Advanced educationa** | 0.85 (0.69, 1.04) | 1.09E-01 |
| **Current smokersa** | 2.39 (1.94, 2.93) | 1.61E-16 |
| **History of diabetesa** | 3.21 (2.58, 4.01) | 3.53E-25 |
| **History of hypertensiona** | 2.09 (1.72, 2.54) | 1.80E-13 |
| **History of CHDa** | 3.16 (2.41, 4.14) | 7.71E-17 |
| **Incident acute kidney injury** | **Age, yearsa** | 1.09 (1.08, 1.10) | 8.92E-69 |
| **Femalea** | 0.67 (0.61, 0.74) | 2.29E-15 |
| **Body mass index, kg/m2 a** | 1.06 (1.05, 1.07) | 2.27E-29 |
| **Advanced educationa** | 0.85 (0.76, 0.94) | 1.82E-03 |
| **Current smokersa** | 2.09 (1.87, 2.34) | 7.26E-38 |
| **History of diabetesa** | 2.06 (1.78, 2.39) | 2.08E-22 |
| **History of hypertensiona** | 1.65 (1.48, 1.83) | 3.02E-20 |
|  | **History of CHDa** | 2.06 (1.68, 2.52) | 5.17E-12 |

a Models adjusted for LDpred PRS, age at baseline, sex, center, and first 10 genetic principal components, education, baseline body mass index, baseline smoking status, baseline history of hypertension, diabetes, and coronary heart disease.

# **Supplemental Table 6. Risk for incident kidney diseases according to polygenic risk scores of kidney function among participants who attended visit 4 (N=6,719).**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | **Risk for incident kidney diseases per 1 SD lower in PRS** | | | | | |
| **Ldpred PRS**a | | **P+T PRS**a | | **Top SNPs PRS**a | |
| **Hazard ratios**  **(95% CI)** | **P value** | **Hazard ratios**  **(95% CI)** | **P value** | **Hazard ratios**  **(95% CI)** | **P value** |
| **Chronic kidney disease** | **Model 1b** | 1.24 (1.19, 1.29) | 2.56E-22 | 1.23 (1.18, 1.29) | 1.93E-21 | 1.17 (1.12, 1.22) | 1.10E-12 |
| **Model 2b** | 1.23 (1.18, 1.29) | 2.86E-21 | 1.23 (1.18, 1.28) | 8.20E-21 | 1.18 (1.13, 1.24) | 5.60E-14 |
| **Model 3b** | 1.23 (1.18, 1.29) | 3.98E-21 | 1.23 (1.17, 1.28) | 2.63E-20 | 1.19 (1.14, 1.24) | 1.64E-14 |
|  | **Model 4b** | 1.15 (1.09, 1.2) | 8.43E-09 | 1.15 (1.10, 1.20) | 3.95E-09 | 1.11 (1.06, 1.17) | 3.01E-06 |
| **End stage kidney disease** | **Model 1b** | 1.20 (0.98, 1.45) | 7.35E-02 | 1.20 (0.99, 1.45) | 7.09E-02 | 1.02 (0.84, 1.24) | 8.16E-01 |
| **Model 2b** | 1.17 (0.96, 1.42) | 1.29E-01 | 1.20 (0.98, 1.46) | 7.57E-02 | 1.05 (0.86, 1.28) | 6.37E-01 |
| **Model 3b** | 1.15 (0.94, 1.41) | 1.63E-01 | 1.17 (0.96, 1.44) | 1.18E-01 | 1.05 (0.86, 1.29) | 6.04E-01 |
|  | **Model 4b** | 0.81 (0.65, 1.01) | 5.78E-02 | 0.87 (0.70, 1.08) | 2.07E-01 | 0.85 (0.69, 1.03) | 1.01E-01 |
| **Kidney failure** | **Model 1b** | 1.2 (1.08, 1.33) | 6.79E-04 | 1.20 (1.08, 1.33) | 4.73E-04 | 1.12 (1.01, 1.24) | 3.68E-02 |
| **Model 2b** | 1.18 (1.07, 1.31) | 1.74E-03 | 1.20 (1.08, 1.33) | 6.23E-04 | 1.13 (1.01, 1.25) | 2.61E-02 |
| **Model 3b** | 1.18 (1.06, 1.31) | 1.95E-03 | 1.20 (1.08, 1.33) | 6.53E-04 | 1.14 (1.02, 1.26) | 1.71E-02 |
|  | **Model 4b** | 0.96 (0.86, 1.08) | 5.11E-01 | 1.01 (0.90, 1.12) | 9.34E-01 | 0.98 (0.88, 1.09) | 7.28E-01 |
| **Acute kidney injury** | **Model 1b** | 1.06 (1.01, 1.12) | 2.59E-02 | 1.05 (1.00, 1.11) | 6.36E-02 | 1.00 (0.95, 1.06) | 9.49E-01 |
| **Model 2b** | 1.05 (1.00, 1.11) | 5.24E-02 | 1.05 (0.99, 1.10) | 8.13E-02 | 1.00 (0.95, 1.06) | 8.83E-01 |
| **Model 3b** | 1.05 (1.00, 1.11) | 5.77E-02 | 1.05 (0.99, 1.10) | 9.53E-02 | 1.01 (0.96, 1.06) | 8.03E-01 |
|  | **Model 4b** | 0.98 (0.92, 1.03) | 4.20E-01 | 0.98 (0.93, 1.03) | 4.25E-01 | 0.95 (0.90, 1.00) | 5.51E-02 |

a LDPred PRS was constructed using LDPred algorithm, a Bayesian approach utilizes GWAS summary statistics to compute the posterior mean effect sizes for the genetic variants by assuming a prior of the joint effect sizes and incorporating the LD structure of the reference population. P+T PRS was constructed using ‘pruning and thresholding (P+T)’, which first prunes variants to only keep those who have absolute pairwise correlation weaker than a threshold within certain genetic distance and then filtered variants that have a P value larger than a pre-defined threshold of significance. Top SNPs score was constructed using the most commonly used level of absolute pairwise correlation for pruning and genome-wide significance level for thresholding

b Model 1 adjusted for age at visit 4, sex, center, and first 10 genetic principal components; Model 2 adjusted for all covariates in model 1 and education, body mass index at visit 4, smoking status at visit 4, history of hypertension, diabetes, and coronary heart disease at visit 4; Model 3 adjusted for all covariates in model 2 and albumin-to-creatinine ratio (ACR) measured at visit 4; Model 4 adjusted for all covariates in model 3 and estimated glomerular filtration rate based on creatinine (eGFRcr) measured at visit 4.

PRS: polygenic risk score

# **Supplemental Table 7. Associations of LDPred polygenic risk score for kidney function and estimated glomerular filtration rate with proteins significantly associated with LDPred polygenic risk score at both visit 3 (N=7,213) and visit 5 (N = 3,666)a.**

**(A) LDPred PRS, eGFR measured at visit 3, and proteins measured at visit 3**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Full name** | **Visit 3 Protein and LDPred PRSb,c** | | | **Visit 3 Protein and Visit 3 eGFRcr c** | | | **Visit 3 Protein and Visit 3 eGFRcysc** | | |
| **Correlation**e | **Beta (SE)** | **P** | **Correlation**e | **Beta (SE)** | **P** | **Correlation**e | **Beta (SE)** | **P** |
|  |  | **Positive significant correlations** | | | | | | | | |
| SPOCK2 | Testican-2 | 0.1148 | 0.039 (0.0038) | 1.83E-24 | 0.1951 | 0.0054 (0.0003) | 8.77E-68 | 0.1972 | 0.0042 (0.0002) | 9.18E-71 |
| PLG | Angiostatin | 0.0573 | 0.0142 (0.0027) | 1.39E-07 | 0.1669 | 0.0021 (0.0002) | 8.06E-22 | 0.2579 | 0.0033 (0.0002) | 3.44E-86 |
| HPRT1 | Hypoxanthine-guanine phosphoribosyltransferase | 0.0618 | 0.0144 (0.0028) | 1.89E-07 | 0.1418 | 0.0025 (0.0002) | 1.57E-28 | 0.169 | 0.0023 (0.0002) | 3.55E-41 |
| CA10 | Carbonic anhydrase-related protein 10 | 0.0587 | 0.0229 (0.0045) | 3.52E-07 | 0.1509 | 0.0039 (0.0004) | 1.92E-26 | 0.1723 | 0.0038 (0.0003) | 1.93E-40 |
| KL | Klotho | 0.055 | 0.0253 (0.0052) | 1.24E-06 | 0.0991 | 0.0039 (0.0004) | 9.15E-20 | 0.105 | 0.0033 (0.0003) | 4.23E-24 |
| Positive significant correlations, medianf | | 0.0587 | | | 0.1509 | | | 0.1723 | | |
|  |  | **Negative significant correlations** | | | | | | | | |
| CST3 | Cystatin-C | -0.1529 | -0.0411 (0.0029) | 2.31E-44 | -0.4811 | -0.009 (0.0002) | 0 | -0.677 | -0.0104 (0.0001) | 0 |
| COL15A1 | Collagen alpha-1(XV) chain | -0.1499 | -0.0368 (0.0028) | 1.86E-39 | -0.4171 | -0.0084 (0.0002) | 0 | -0.3766 | -0.0058 (0.0002) | 2.5E-254 |
| RNASE1 | Ribonuclease pancreatic | -0.1296 | -0.0746 (0.0062) | 4.51E-33 | -0.4341 | -0.0166 (0.0005) | 2.0E-253 | -0.577 | -0.0179 (0.0003) | 0 |
| DSC2 | Desmocollin-2 | -0.1256 | -0.0327 (0.0029) | 2.2E-29 | -0.3896 | -0.0076 (0.0002) | 4.4E-240 | -0.3408 | -0.0049 (0.0002) | 1.2E-165 |
| COL6A3 | Collagen alpha-3(VI) chain | -0.1187 | -0.0309 (0.0028) | 2.57E-27 | -0.3501 | -0.0064 (0.0002) | 1.3E-185 | -0.5068 | -0.0073 (0.0002) | 0 |
| TMED10 | Transmembrane emp24 domain-containing protein 10 | -0.1193 | -0.0378 (0.0035) | 4.26E-27 | -0.3768 | -0.0087 (0.0003) | 2.9E-213 | -0.5245 | -0.0095 (0.0002) | 0 |
| COL28A1 | Collagen alpha-1(XXVIII) chain | -0.1167 | -0.0329 (0.0031) | 2.29E-26 | -0.3534 | -0.0071 (0.0002) | 7.2E-181 | -0.5101 | -0.0081 (0.0002) | 0 |
| CD59 | CD59 glycoprotein | -0.1171 | -0.0319 (0.003) | 2.94E-26 | -0.3941 | -0.0078 (0.0002) | 1.8E-234 | -0.3382 | -0.0049 (0.0002) | 1.7E-154 |
| GM2A | Ganglioside GM2 activator | -0.1169 | -0.0345 (0.0032) | 3.95E-26 | -0.3897 | -0.0082 (0.0002) | 3.4E-219 | -0.4669 | -0.0076 (0.0002) | 0 |
| CDNF | Cerebral dopamine neurotrophic factor | -0.1216 | -0.0312 (0.003) | 1.47E-25 | -0.3566 | -0.0073 (0.0002) | 4.1E-209 | -0.1983 | -0.0029 (0.0002) | 6.99E-55 |
| TNFRSF1A | Tumor necrosis factor receptor superfamily member 1A | -0.1141 | -0.04 (0.0039) | 8.71E-25 | -0.393 | -0.0095 (0.0003) | 4.1E-210 | -0.5008 | -0.0097 (0.0002) | 0 |
| ART3 | Ecto-ADP-ribosyltransferase 3 | -0.1177 | -0.0469 (0.0047) | 1.25E-23 | -0.2788 | -0.0101 (0.0004) | 2.3E-161 | -0.045 | -0.0015 (0.0003) | 4.25E-07 |
| SELM | Selenoprotein M | -0.1084 | -0.0331 (0.0033) | 3.44E-23 | -0.3905 | -0.0081 (0.0003) | 2.4E-208 | -0.3691 | -0.0058 (0.0002) | 5.7E-174 |
| B2M | Beta-2-microglobulin | -0.1083 | -0.0301 (0.0031) | 2.12E-22 | -0.388 | -0.0074 (0.0002) | 1.5E-201 | -0.4931 | -0.0076 (0.0002) | 0 |
| EFNB2 | Ephrin-B2 | -0.1073 | -0.0324 (0.0035) | 1.28E-20 | -0.3532 | -0.0082 (0.0003) | 1.7E-195 | -0.3181 | -0.0056 (0.0002) | 2.5E-151 |
| LMAN2 | Vesicular integral-membrane protein VIP36 | -0.1048 | -0.0265 (0.0029) | 6.83E-20 | -0.3218 | -0.0061 (0.0002) | 5.2E-155 | -0.3681 | -0.0054 (0.0002) | 1.4E-206 |
| FSTL3 | Follistatin-related protein 3 | -0.0956 | -0.0281 (0.0031) | 1.2E-19 | -0.3423 | -0.0065 (0.0002) | 8.1E-154 | -0.4465 | -0.0067 (0.0002) | 4.5E-286 |
| FABP4 | Fatty acid-binding protein, adipocyte | -0.0906 | -0.0534 (0.006) | 1.23E-18 | -0.3044 | -0.0124 (0.0005) | 2.9E-145 | -0.3874 | -0.0121 (0.0004) | 7.2E-238 |
| SEPW1 | Selenoprotein W | -0.0959 | -0.032 (0.0036) | 1.9E-18 | -0.3183 | -0.0072 (0.0003) | 1.5E-133 | -0.312 | -0.0057 (0.0002) | 2.6E-141 |
| HSPB6 | Heat shock protein beta-6 | -0.0956 | -0.0404 (0.0046) | 2.26E-18 | -0.3341 | -0.0091 (0.0004) | 6.5E-134 | -0.3086 | -0.0063 (0.0003) | 5.1E-107 |
| MB | Myoglobin | -0.0986 | -0.0422 (0.0048) | 2.72E-18 | -0.2509 | -0.0093 (0.0004) | 1.1E-127 | -0.1043 | -0.0029 (0.0003) | 4.92E-22 |
| MYOC | Myocilin | -0.0995 | -0.0347 (0.004) | 6.69E-18 | -0.3036 | -0.0082 (0.0003) | 1.4E-143 | -0.2149 | -0.0043 (0.0002) | 5.08E-67 |
| IGFBP6 | Insulin-like growth factor-binding protein 6 | -0.0943 | -0.0235 (0.0027) | 9.28E-18 | -0.3139 | -0.0057 (0.0002) | 6.1E-150 | -0.2422 | -0.0032 (0.0002) | 8.14E-80 |
| COL18A1 | Endostatin | -0.089 | -0.0286 (0.0034) | 1.01E-16 | -0.2665 | -0.0061 (0.0003) | 3.7E-108 | -0.2652 | -0.0045 (0.0002) | 4.13E-98 |
| TNFRSF1B | Tumor necrosis factor receptor superfamily member 1B | -0.0922 | -0.0305 (0.0037) | 1.1E-16 | -0.3007 | -0.0069 (0.0003) | 5.3E-120 | -0.4723 | -0.0088 (0.0002) | 0 |
| RGMB | RGM domain family member B | -0.0969 | -0.022 (0.0026) | 1.14E-16 | -0.3045 | -0.0058 (0.0002) | 3E-165 | -0.1494 | -0.0021 (0.0002) | 2.02E-36 |
| LCN2 | Neutrophil gelatinase-associated lipocalin | -0.0938 | -0.036 (0.0044) | 1.95E-16 | -0.2589 | -0.0074 (0.0003) | 5.99E-98 | -0.2976 | -0.0068 (0.0003) | 4.2E-139 |
| PTGDS | Prostaglandin-H2 D-isomerase | -0.0887 | -0.0359 (0.0044) | 1.98E-16 | -0.3607 | -0.0093 (0.0003) | 5.1E-157 | -0.3399 | -0.0065 (0.0003) | 9.8E-131 |
| CFD | Complement factor D | -0.0885 | -0.0264 (0.0032) | 2.79E-16 | -0.2749 | -0.0057 (0.0003) | 1.1E-107 | -0.2996 | -0.0046 (0.0002) | 2E-119 |
| PPIC | Peptidyl-prolyl cis-trans isomerase C | -0.0929 | -0.0283 (0.0035) | 2.92E-16 | -0.2719 | -0.0063 (0.0003) | 7.4E-114 | -0.3251 | -0.0059 (0.0002) | 2.1E-168 |
| SMOC2 | SPARC-related modular calcium-binding protein 2 | -0.0895 | -0.0281 (0.0035) | 8.6E-16 | -0.2827 | -0.0066 (0.0003) | 3.1E-121 | -0.1853 | -0.0031 (0.0002) | 1.82E-44 |
| NBL1 | Neuroblastoma suppressor of tumorigenicity 1 | -0.0855 | -0.0314 (0.004) | 2.66E-15 | -0.3766 | -0.0095 (0.0003) | 2.9E-201 | -0.3767 | -0.0073 (0.0002) | 7E-199 |
| MFAP2 | Microfibrillar-associated protein 2 | -0.0903 | -0.0254 (0.0032) | 2.7E-15 | -0.2509 | -0.0051 (0.0003) | 2.52E-85 | -0.28 | -0.0043 (0.0002) | 6.8E-104 |
| RNASE6 | Ribonuclease K6 | -0.0856 | -0.038 (0.0049) | 5.73E-15 | -0.2812 | -0.0085 (0.0004) | 1.4E-105 | -0.3993 | -0.0097 (0.0003) | 2E-237 |
| CCL14 | C-C motif chemokine 14 | -0.0843 | -0.0415 (0.0053) | 6.66E-15 | -0.2645 | -0.0092 (0.0004) | 5.3E-104 | -0.3223 | -0.0085 (0.0003) | 1.7E-149 |
| ESAM | Endothelial cell-selective adhesion molecule | -0.0867 | -0.0247 (0.0032) | 1.19E-14 | -0.2935 | -0.006 (0.0003) | 2.9E-119 | -0.2428 | -0.0039 (0.0002) | 6.59E-86 |
| DNAJB12 | DnaJ homolog subfamily B member 12 | -0.0867 | -0.0327 (0.0042) | 1.28E-14 | -0.319 | -0.0086 (0.0003) | 3.1E-143 | -0.3283 | -0.0068 (0.0003) | 4.4E-152 |
| GABARAP | Gamma-aminobutyric acid receptor-associated protein | -0.0826 | -0.02 (0.0026) | 1.58E-14 | -0.3085 | -0.005 (0.0002) | 7.9E-126 | -0.4391 | -0.0058 (0.0001) | 6.8E-308 |
| UNC5B | Netrin receptor UNC5B | -0.0835 | -0.0259 (0.0034) | 1.92E-14 | -0.3227 | -0.0066 (0.0003) | 1.6E-132 | -0.3293 | -0.0052 (0.0002) | 2.6E-134 |
| WFDC1 | WAP four-disulfide core domain protein 1 | -0.0859 | -0.0308 (0.004) | 2.8E-14 | -0.3137 | -0.0077 (0.0003) | 1.7E-125 | -0.3575 | -0.007 (0.0002) | 8E-177 |
| MIA | Melanoma-derived growth regulatory protein | -0.0859 | -0.0269 (0.0035) | 2.93E-14 | -0.216 | -0.0053 (0.0003) | 2E-77 | -0.0955 | -0.0015 (0.0002) | 4.48E-12 |
| EFNA4 | Ephrin-A4 | -0.0877 | -0.0212 (0.0028) | 4.02E-14 | -0.2856 | -0.0052 (0.0002) | 4.2E-119 | -0.3333 | -0.0046 (0.0002) | 2.2E-164 |
| RARRES2 | Retinoic acid receptor responder protein 2 | -0.0811 | -0.0276 (0.0037) | 4.76E-14 | -0.2127 | -0.0054 (0.0003) | 2.32E-73 | -0.3435 | -0.0067 (0.0002) | 2E-200 |
| GAS1 | Growth arrest-specific protein 1 | -0.0849 | -0.0251 (0.0033) | 4.95E-14 | -0.3326 | -0.0069 (0.0003) | 2E-146 | -0.2843 | -0.0043 (0.0002) | 3.87E-94 |
| EFNA5 | Ephrin-A5 | -0.0831 | -0.0215 (0.0029) | 1.77E-13 | -0.3063 | -0.0058 (0.0002) | 1.6E-135 | -0.2857 | -0.004 (0.0002) | 5.2E-109 |
| CRABP2 | Cellular retinoic acid-binding protein 2 | -0.0842 | -0.0324 (0.0044) | 3.17E-13 | -0.28 | -0.0083 (0.0003) | 1.8E-119 | -0.3613 | -0.0084 (0.0003) | 1.3E-211 |
| UNC5C | Netrin receptor UNC5C | -0.08 | -0.0237 (0.0033) | 4.13E-13 | -0.247 | -0.0049 (0.0003) | 3.57E-78 | -0.243 | -0.0036 (0.0002) | 7.68E-71 |
| JAM2 | Junctional adhesion molecule B | -0.0805 | -0.0186 (0.0026) | 4.4E-13 | -0.2633 | -0.0043 (0.0002) | 2.81E-94 | -0.2662 | -0.0034 (0.0002) | 2.2E-99 |
| CD55 | Complement decay-accelerating factor | -0.0822 | -0.0198 (0.0027) | 5.12E-13 | -0.2368 | -0.0043 (0.0002) | 2.38E-85 | -0.1639 | -0.0021 (0.0002) | 6.61E-35 |
| EPHA2 | Ephrin type-A receptor 2 | -0.0791 | -0.0261 (0.0036) | 6.44E-13 | -0.2754 | -0.0059 (0.0003) | 7.89E-91 | -0.3183 | -0.0054 (0.0002) | 2.7E-128 |
| ATOX1 | Copper transport protein ATOX1 | -0.0762 | -0.0349 (0.0049) | 1.19E-12 | -0.2437 | -0.0073 (0.0004) | 1.26E-75 | -0.3091 | -0.008 (0.0003) | 2.8E-155 |
| TAGLN | Transgelin | -0.0713 | -0.0285 (0.004) | 1.21E-12 | -0.3513 | -0.0075 (0.0003) | 2.8E-118 | -0.2919 | -0.0041 (0.0002) | 1.86E-59 |
| TWSG1 | Twisted gastrulation protein homolog 1 | -0.0776 | -0.0157 (0.0022) | 1.47E-12 | -0.2736 | -0.0038 (0.0002) | 1E-101 | -0.2726 | -0.0029 (0.0001) | 5.8E-101 |
| CA3 | Carbonic anhydrase 3 | -0.0809 | -0.0505 (0.0071) | 1.62E-12 | -0.2173 | -0.0087 (0.0006) | 7.88E-51 | -0.1633 | -0.0045 (0.0004) | 4.41E-24 |
| TNFRSF1B | Tumor necrosis factor receptor superfamily member 1B | -0.0775 | -0.0263 (0.0037) | 1.67E-12 | -0.2628 | -0.006 (0.0003) | 2.29E-90 | -0.417 | -0.0078 (0.0002) | 3.7E-267 |
| CALCOCO2 | Calcium-binding and coiled-coil domain-containing protein 2 | -0.0805 | -0.0205 (0.0029) | 2.4E-12 | -0.1397 | -0.0032 (0.0002) | 2.06E-40 | -0.1282 | -0.0022 (0.0002) | 1.99E-33 |
| UNC5B | Netrin receptor UNC5B | -0.0776 | -0.0249 (0.0036) | 2.76E-12 | -0.289 | -0.0062 (0.0003) | 2.4E-104 | -0.3195 | -0.0053 (0.0002) | 2.2E-130 |
| VWC2 | Brorin | -0.0744 | -0.025 (0.0036) | 7.69E-12 | -0.2693 | -0.0064 (0.0003) | 1.1E-105 | -0.2584 | -0.0046 (0.0002) | 6.11E-90 |
| DLK1 | Protein delta homolog 1 | -0.0775 | -0.0417 (0.0061) | 9.59E-12 | -0.2185 | -0.0085 (0.0005) | 2.53E-66 | -0.1743 | -0.005 (0.0004) | 3.03E-38 |
| DLK1 | Protein delta homolog 1 | -0.0765 | -0.0442 (0.0065) | 1.36E-11 | -0.2262 | -0.0093 (0.0005) | 5.42E-70 | -0.1857 | -0.0056 (0.0004) | 5.76E-43 |
| CD46 | Membrane cofactor protein | -0.0749 | -0.0178 (0.0026) | 1.4E-11 | -0.2421 | -0.0043 (0.0002) | 4.39E-90 | -0.2577 | -0.0034 (0.0002) | 2.76E-97 |
| WFDC2 | WAP four-disulfide core domain protein 2 | -0.065 | -0.031 (0.0048) | 8.24E-11 | -0.2893 | -0.0078 (0.0004) | 7.6E-91 | -0.3899 | -0.0087 (0.0003) | 2.1E-194 |
| EPHB6 | Ephrin type-B receptor 6 | -0.0718 | -0.0169 (0.0026) | 8.89E-11 | -0.2274 | -0.0044 (0.0002) | 1.51E-98 | -0.168 | -0.0024 (0.0002) | 2.98E-49 |
| DCLK1 | Serine/threonine-protein kinase DCLK1 | -0.0748 | -0.026 (0.004) | 8.93E-11 | -0.1991 | -0.0054 (0.0003) | 6.46E-63 | -0.2091 | -0.0044 (0.0002) | 3.35E-69 |
| ASGR1 | Asialoglycoprotein receptor 1 | -0.0738 | -0.0212 (0.0033) | 1.98E-10 | -0.2175 | -0.0048 (0.0003) | 1.34E-70 | -0.3015 | -0.0052 (0.0002) | 6.6E-142 |
| LRP10 | Low-density lipoprotein receptor-related protein 10 | -0.072 | -0.017 (0.0027) | 2.07E-10 | -0.3042 | -0.005 (0.0002) | 1.7E-121 | -0.269 | -0.0033 (0.0002) | 3.97E-89 |
| EPHB4 | Ephrin type-B receptor 4 | -0.0715 | -0.0222 (0.0035) | 2.67E-10 | -0.2543 | -0.0056 (0.0003) | 4.14E-86 | -0.2586 | -0.0044 (0.0002) | 2.74E-89 |
| FABP3 | Fatty acid-binding protein, heart | -0.0611 | -0.0389 (0.0061) | 2.74E-10 | -0.1851 | -0.0095 (0.0005) | 1.34E-81 | -0.2872 | -0.0106 (0.0004) | 4E-173 |
| CAPG | Macrophage-capping protein | -0.0669 | -0.0362 (0.0058) | 4.86E-10 | -0.1979 | -0.0065 (0.0005) | 4.18E-43 | -0.2807 | -0.0076 (0.0004) | 5.6E-100 |
| SERPINF1 | Pigment epithelium-derived factor | -0.0732 | -0.0133 (0.0021) | 5.12E-10 | -0.207 | -0.0031 (0.0002) | 1.49E-73 | -0.2505 | -0.003 (0.0001) | 1.1E-113 |
| NPDC1 | Neural proliferation differentiation and control protein 1 | -0.0694 | -0.0217 (0.0035) | 5.13E-10 | -0.1954 | -0.0044 (0.0003) | 1.04E-53 | -0.2183 | -0.0037 (0.0002) | 1.74E-64 |
| JTB | Protein JTB | -0.0699 | -0.0158 (0.0026) | 6.71E-10 | -0.1859 | -0.0032 (0.0002) | 1.3E-52 | -0.1497 | -0.0018 (0.0002) | 5.19E-30 |
| IGFBP4 | Insulin-like growth factor-binding protein 4 | -0.069 | -0.0213 (0.0034) | 6.87E-10 | -0.1375 | -0.0034 (0.0003) | 1.79E-34 | -0.2318 | -0.0044 (0.0002) | 1.62E-95 |
| EFNA2 | Ephrin-A2 | -0.0697 | -0.0199 (0.0032) | 7.34E-10 | -0.2839 | -0.0058 (0.0003) | 5.9E-112 | -0.3221 | -0.0051 (0.0002) | 5.4E-145 |
| TNFRSF21 | Tumor necrosis factor receptor superfamily member 21 | -0.0693 | -0.0167 (0.0027) | 9.53E-10 | -0.1901 | -0.0036 (0.0002) | 2.12E-58 | -0.2484 | -0.0035 (0.0002) | 6.94E-96 |
| PI3 | Elafin | -0.0665 | -0.036 (0.0059) | 9.8E-10 | -0.2037 | -0.008 (0.0005) | 6.52E-63 | -0.2305 | -0.0071 (0.0004) | 2.58E-84 |
| PCOLCE | Procollagen C-endopeptidase enhancer 1 | -0.0687 | -0.0227 (0.0037) | 1.15E-09 | -0.2072 | -0.0046 (0.0003) | 2.11E-51 | -0.2085 | -0.0036 (0.0002) | 6.92E-54 |
| AIF1L | Allograft inflammatory factor 1-like | -0.0664 | -0.0191 (0.0031) | 1.19E-09 | -0.3092 | -0.0054 (0.0002) | 3.6E-102 | -0.3205 | -0.0044 (0.0002) | 6.7E-113 |
| ROR2 | Tyrosine-protein kinase transmembrane receptor ROR2 | -0.0678 | -0.0226 (0.0037) | 1.23E-09 | -0.286 | -0.0066 (0.0003) | 5.7E-110 | -0.2946 | -0.0052 (0.0002) | 1.9E-113 |
| CPLX2 | Complexin-2 | -0.0646 | -0.0266 (0.0044) | 1.42E-09 | -0.2839 | -0.0081 (0.0003) | 8.5E-117 | -0.1717 | -0.0031 (0.0003) | 6.49E-29 |
| DLK2 | Protein delta homolog 2 | -0.0642 | -0.0252 (0.0042) | 3.08E-09 | -0.2905 | -0.0078 (0.0003) | 7.2E-117 | -0.2236 | -0.0044 (0.0003) | 2.07E-62 |
| MXRA7 | Matrix-remodeling-associated protein 7 | -0.0661 | -0.0211 (0.0036) | 3.68E-09 | -0.2429 | -0.0056 (0.0003) | 1.92E-83 | -0.234 | -0.004 (0.0002) | 1.97E-73 |
| CD300A | CMRF35-like molecule 8 | -0.0654 | -0.0259 (0.0044) | 3.94E-09 | -0.2008 | -0.0052 (0.0004) | 1.19E-47 | -0.3053 | -0.0065 (0.0003) | 6E-129 |
| CD300C | CMRF35-like molecule 6 | -0.0648 | -0.0215 (0.0036) | 3.98E-09 | -0.148 | -0.0035 (0.0003) | 5.21E-32 | -0.2778 | -0.0053 (0.0002) | 4.5E-121 |
| CLMP | CXADR-like membrane protein | -0.0622 | -0.0253 (0.0044) | 6.55E-09 | -0.2243 | -0.0067 (0.0003) | 2.64E-82 | -0.2388 | -0.0053 (0.0003) | 7.24E-87 |
| LRP11 | Low-density lipoprotein receptor-related protein 11 | -0.0653 | -0.017 (0.0029) | 6.86E-09 | -0.2295 | -0.0044 (0.0002) | 1.5E-78 | -0.2431 | -0.0035 (0.0002) | 2.96E-82 |
| IL15RA | Interleukin-15 receptor subunit alpha | -0.0598 | -0.0243 (0.0042) | 1.13E-08 | -0.2545 | -0.0061 (0.0003) | 7.24E-72 | -0.3445 | -0.0069 (0.0003) | 5E-154 |
| MYL3 | Myosin light chain 3 | -0.0654 | -0.0535 (0.0094) | 1.29E-08 | -0.1901 | -0.0107 (0.0008) | 9.87E-45 | -0.0965 | -0.0034 (0.0006) | 1.06E-08 |
| IL18BP | Interleukin-18-binding protein | -0.0635 | -0.0221 (0.0039) | 1.3E-08 | -0.21 | -0.0044 (0.0003) | 1.99E-45 | -0.3404 | -0.0062 (0.0002) | 4.6E-152 |
| RNASE4 | Ribonuclease 4 | -0.062 | -0.0153 (0.0027) | 1.41E-08 | -0.2588 | -0.0046 (0.0002) | 4.4E-103 | -0.2649 | -0.0035 (0.0002) | 2.87E-96 |
| DDOST | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit | -0.0669 | -0.018 (0.0032) | 1.53E-08 | -0.2293 | -0.0046 (0.0003) | 1.12E-70 | -0.2301 | -0.0036 (0.0002) | 1.33E-72 |
| VIT | Vitrin | -0.064 | -0.022 (0.0039) | 1.67E-08 | -0.2417 | -0.0057 (0.0003) | 7.07E-74 | -0.2456 | -0.0046 (0.0002) | 4.26E-81 |
| TGFBR3 | Transforming growth factor beta receptor type 3 | -0.0651 | -0.0162 (0.0029) | 2.64E-08 | -0.1799 | -0.0037 (0.0002) | 5.77E-56 | -0.0927 | -0.0014 (0.0002) | 1.18E-13 |
| TNFRSF19 | Tumor necrosis factor receptor superfamily member 19 | -0.064 | -0.0227 (0.0041) | 2.67E-08 | -0.2841 | -0.0074 (0.0003) | 6.9E-111 | -0.2617 | -0.0051 (0.0003) | 2.14E-89 |
| SPON2 | Spondin-2 | -0.0599 | -0.0228 (0.0041) | 3.63E-08 | -0.2188 | -0.0057 (0.0003) | 1.71E-65 | -0.319 | -0.0066 (0.0002) | 3.5E-149 |
| CD93 | Complement component C1q receptor | -0.0627 | -0.0167 (0.0031) | 5.83E-08 | -0.1341 | -0.0033 (0.0002) | 1.77E-39 | -0.1857 | -0.0034 (0.0002) | 2.93E-69 |
| TREM1 | Triggering receptor expressed on myeloid cells 1 | -0.0579 | -0.0235 (0.0043) | 6.01E-08 | -0.2204 | -0.0054 (0.0003) | 2.07E-52 | -0.3302 | -0.0068 (0.0003) | 3.1E-144 |
| RETN | Resistin | -0.0603 | -0.0258 (0.0048) | 7.06E-08 | -0.2112 | -0.0068 (0.0004) | 1.81E-69 | -0.2422 | -0.006 (0.0003) | 8.5E-91 |
| MANSC1 | MANSC domain-containing protein 1 | -0.0615 | -0.0197 (0.0037) | 7.64E-08 | -0.1609 | -0.0039 (0.0003) | 3.03E-39 | -0.1886 | -0.0035 (0.0002) | 1.15E-52 |
| MAP2K2 | Dual specificity mitogen-activated protein kinase kinase 2 | -0.0576 | -0.031 (0.0058) | 8.72E-08 | -0.2286 | -0.008 (0.0005) | 3.14E-66 | -0.2525 | -0.0069 (0.0004) | 1.28E-81 |
| B4GALT1 | Beta-1,4-galactosyltransferase 1 | -0.0634 | -0.0125 (0.0023) | 8.81E-08 | -0.2378 | -0.0036 (0.0002) | 1.01E-81 | -0.1896 | -0.002 (0.0001) | 7.78E-45 |
| IGFLR1 | IGF-like family receptor 1 | -0.0566 | -0.0277 (0.0052) | 8.98E-08 | -0.252 | -0.0079 (0.0004) | 7.49E-80 | -0.3905 | -0.01 (0.0003) | 1.3E-222 |
| CPLX1 | Complexin-1 | -0.057 | -0.0188 (0.0035) | 9.13E-08 | -0.2524 | -0.0055 (0.0003) | 3E-83 | -0.1859 | -0.0027 (0.0002) | 3.04E-35 |
| PXDN | Peroxidasin homolog | -0.0597 | -0.0477 (0.009) | 1.21E-07 | -0.2027 | -0.011 (0.0007) | 4.03E-51 | -0.3277 | -0.0149 (0.0005) | 1.5E-160 |
| EPHA1 | Ephrin type-A receptor 1 | -0.0615 | -0.0303 (0.0058) | 1.48E-07 | -0.1813 | -0.0066 (0.0005) | 1.39E-44 | -0.2125 | -0.006 (0.0004) | 5.37E-62 |
| ROR1 | Inactive tyrosine-protein kinase transmembrane receptor ROR1 | -0.06 | -0.0193 (0.0037) | 1.79E-07 | -0.2255 | -0.005 (0.0003) | 1.02E-62 | -0.1544 | -0.0023 (0.0002) | 2.35E-22 |
| TMPO | Lamina-associated polypeptide 2, isoforms beta/gamma | -0.0569 | -0.0267 (0.0052) | 2.22E-07 | -0.2184 | -0.0066 (0.0004) | 1.38E-56 | -0.336 | -0.0088 (0.0003) | 1E-171 |
| XXYLT1 | Xyloside xylosyltransferase 1 | -0.0588 | -0.017 (0.0033) | 3.32E-07 | -0.2024 | -0.0043 (0.0003) | 7.71E-59 | -0.207 | -0.0033 (0.0002) | 8.24E-59 |
| SRL | Sarcalumenin | -0.0598 | -0.0238 (0.0047) | 3.81E-07 | -0.1838 | -0.0056 (0.0004) | 2.5E-49 | -0.1708 | -0.0039 (0.0003) | 1.96E-41 |
| UNC5D | Netrin receptor UNC5D | -0.0532 | -0.0226 (0.0045) | 5.44E-07 | -0.2337 | -0.0073 (0.0004) | 1.92E-90 | -0.0919 | -0.0018 (0.0003) | 2.83E-10 |
| VASN | Vasorin | -0.059 | -0.013 (0.0026) | 5.47E-07 | -0.1882 | -0.0033 (0.0002) | 7.55E-57 | -0.2238 | -0.0031 (0.0002) | 1.13E-85 |
| SMOC1 | SPARC-related modular calcium-binding protein 1 | -0.0528 | -0.0125 (0.0025) | 8.95E-07 | -0.2433 | -0.0035 (0.0002) | 7.45E-65 | -0.1798 | -0.0017 (0.0002) | 4.78E-26 |
| EFEMP1 | EGF-containing fibulin-like extracellular matrix protein 1 | -0.0427 | -0.0136 (0.0028) | 1.47E-06 | -0.2385 | -0.0034 (0.0002) | 3.41E-49 | -0.3549 | -0.0044 (0.0002) | 2.2E-142 |
| IL2RB | Interleukin-2 receptor subunit beta | -0.0571 | -0.0205 (0.0043) | 1.48E-06 | -0.1558 | -0.0048 (0.0003) | 1.16E-44 | -0.1624 | -0.0038 (0.0003) | 8.31E-47 |
| DPY30 | Protein dpy-30 homolog | -0.054 | -0.0226 (0.0047) | 1.55E-06 | -0.2077 | -0.0059 (0.0004) | 2.47E-54 | -0.2994 | -0.0073 (0.0003) | 3.4E-138 |
| PGRMC1 | Membrane-associated progesterone receptor component 1 | -0.0521 | -0.017 (0.0035) | 1.58E-06 | -0.136 | -0.0038 (0.0003) | 1.65E-40 | -0.1168 | -0.0023 (0.0002) | 3.26E-25 |
| SPINK7 | Serine protease inhibitor Kazal-type 7 | -0.0529 | -0.0227 (0.0047) | 1.64E-06 | -0.1937 | -0.0068 (0.0004) | 1.47E-70 | -0.0726 | -0.002 (0.0003) | 2.67E-11 |
| AMBP | Alpha-1-microglobulin | -0.0548 | -0.0146 (0.0031) | 2.3E-06 | -0.2113 | -0.004 (0.0002) | 4.13E-57 | -0.2833 | -0.0043 (0.0002) | 7.6E-114 |
| PENK | Proenkephalin-A | -0.0536 | -0.0375 (0.008) | 2.8E-06 | -0.1669 | -0.007 (0.0006) | 4.52E-27 | -0.2399 | -0.0086 (0.0005) | 2.08E-67 |
| CADM2 | Cell adhesion molecule 2 | -0.0501 | -0.0163 (0.0035) | 2.82E-06 | -0.1991 | -0.0047 (0.0003) | 5.47E-63 | -0.0646 | -0.0007 (0.0002) | 0.000789 |
| NEGR1 | Neuronal growth regulator 1 | -0.0495 | -0.0111 (0.0024) | 3.29E-06 | -0.1503 | -0.0025 (0.0002) | 1.51E-38 | -0.0375 | -0.0002 (0.0001) | 0.253267 |
| EWSR1 | RNA-binding protein EWS | -0.0489 | -0.0172 (0.0037) | 3.45E-06 | -0.2189 | -0.0047 (0.0003) | 4.23E-56 | -0.3301 | -0.0059 (0.0002) | 2.5E-148 |
| CCL23 | C-C motif chemokine 23 | -0.0557 | -0.0188 (0.0041) | 4.97E-06 | -0.1333 | -0.0037 (0.0003) | 4.65E-28 | -0.1123 | -0.0022 (0.0003) | 3.41E-17 |
| PSMB1 | Proteasome subunit beta type-1 | -0.0504 | -0.0218 (0.0049) | 8.23E-06 | -0.1788 | -0.0058 (0.0004) | 6.46E-48 | -0.1832 | -0.0045 (0.0003) | 3.42E-50 |
| APOF | Apolipoprotein F | -0.0515 | -0.0339 (0.0076) | 8.75E-06 | -0.2136 | -0.0097 (0.0006) | 2.54E-56 | -0.1101 | -0.0031 (0.0005) | 1.21E-10 |
| CCL23 | Ck-beta-8-1 | -0.0537 | -0.0207 (0.0047) | 9.66E-06 | -0.1609 | -0.0047 (0.0004) | 7.36E-36 | -0.1436 | -0.0031 (0.0003) | 8.25E-26 |
| NMB | Neuromedin-B | -0.0466 | -0.0147 (0.0033) | 9.81E-06 | -0.1714 | -0.0034 (0.0003) | 1.87E-37 | -0.1877 | -0.0027 (0.0002) | 4.62E-40 |
| Negative significant correlations, medianf | | -0.0720 | | | -0.2509 | | | -0.2661 | | |

**(B) LDPred PRS, eGFR measured at visit 5, and proteins measured at visit 5**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Full name** | | **Visit 5 Protein and LDPred PRSb,d** | | | | | **Visit 5 Protein and Visit 5 eGFRcrd** | | | | | **Visit 5 Protein and Visit 5 eGFRcysd** | | | | | |
| **Correlation** | **Beta (SE)** | | **P** | | **Correlation** | **Beta (SE)** | | **P** | | **Correlation** | | **Beta (SE)** | | **P** | |
|  |  | | **Positive significant correlations** | | | | | | | | | | | | | | | | |
| SPOCK2 | Testican-2 | | 0.1128 | 0.0418 (0.0064) | | 8.37E-11 | | 0.3976 | 0.0096 (0.0004) | | 6.00E-122 | | 0.4333 | | 0.009 (0.0003) | | 9.85E-147 | |
| KL | Klotho | | 0.0933 | 0.0426 (0.0079) | | 8.58E-08 | | 0.2571 | 0.0077 (0.0005) | | 2.31E-51 | | 0.3019 | | 0.0078 (0.0004) | | 1.67E-69 | |
| HPRT1 | Hypoxanthine-guanine phosphoribosyltransferase | | 0.0738 | 0.0223 (0.0045) | | 8.78E-07 | | 0.2950 | 0.0048 (0.0003) | | 6.48E-62 | | 0.2803 | | 0.0042 (0.0002) | | 2.10E-62 | |
| PLG | Angiostatin | | 0.0825 | 0.0171 (0.0035) | | 1.53E-06 | | 0.2734 | 0.0033 (0.0002) | | 7.74E-48 | | 0.3442 | | 0.0037 (0.0002) | | 7.82E-79 | |
| CA10 | Carbonic anhydrase-related protein 10 | | 0.0792 | 0.0291 (0.0063) | | 3.58E-06 | | 0.2416 | 0.0053 (0.0004) | | 8.92E-39 | | 0.3182 | | 0.0062 (0.0003) | | 4.99E-71 | |
| Positive significant correlations, medianf | | | 0.0825 | | | | | 0.2734 | | | | | 0.3182 | | | | | |
|  |  | | **Negative significant correlations** | | | | | | | | | | | | | | | | |
| CST3 | Cystatin-C | -0.1547 | | | -0.0552 (0.0054) | | 8.25E-24 | -0.7304 | | -0.015 (0.0003) | | 0 | | -0.8703 | | -0.0159 (0.0002) | | 0 | |
| COL15A1 | Collagen alpha-1(XV) chain | -0.1625 | | | -0.046 (0.0046) | | 3.64E-23 | -0.6275 | | -0.0112 (0.0002) | | 0 | | -0.5708 | | -0.0091 (0.0002) | | 1.93E-313 | |
| CD59 | CD59 glycoprotein | -0.1347 | | | -0.045 (0.005) | | 2.24E-19 | -0.5965 | | -0.0111 (0.0003) | | 1.64E-304 | | -0.5533 | | -0.0091 (0.0002) | | 1.11E-266 | |
| GM2A | Ganglioside GM2 activator | -0.1444 | | | -0.0569 (0.0063) | | 2.31E-19 | -0.6421 | | -0.015 (0.0003) | | 0 | | -0.6991 | | -0.0145 (0.0003) | | 0 | |
| TNFRSF1A | Tumor necrosis factor receptor superfamily member 1A | -0.1441 | | | -0.0577 (0.0065) | | 1.08E-18 | -0.6328 | | -0.0151 (0.0003) | | 0 | | -0.7100 | | -0.0151 (0.0003) | | 0 | |
| DSC2 | Desmocollin-2 | -0.1413 | | | -0.0491 (0.0056) | | 4.22E-18 | -0.6337 | | -0.0133 (0.0003) | | 0 | | -0.6052 | | -0.0112 (0.0003) | | 8.89E-323 | |
| ART3 | Ecto-ADP-ribosyltransferase 3 | -0.1217 | | | -0.0582 (0.0067) | | 6.59E-18 | -0.4533 | | -0.0128 (0.0004) | | 4.54E-207 | | -0.2375 | | -0.0062 (0.0004) | | 3.15E-60 | |
| EFNB2 | Ephrin-B2 | -0.1408 | | | -0.0479 (0.0056) | | 1.87E-17 | -0.5655 | | -0.0118 (0.0003) | | 4.93E-262 | | -0.5251 | | -0.0097 (0.0003) | | 7.08E-230 | |
| RNASE1 | Ribonuclease pancreatic | -0.1376 | | | -0.1037 (0.0122) | | 2.77E-17 | -0.6764 | | -0.0303 (0.0006) | | 0 | | -0.7862 | | -0.0313 (0.0004) | | 0 | |
| COL6A3 | Collagen alpha-3(VI) chain | -0.1447 | | | -0.0482 (0.0057) | | 3.75E-17 | -0.6145 | | -0.0129 (0.0003) | | 5.23E-317 | | -0.7037 | | -0.0132 (0.0002) | | 0 | |
| TMED10 | Transmembrane emp24 domain-containing protein 10 | -0.1383 | | | -0.059 (0.0071) | | 8.62E-17 | -0.6933 | | -0.018 (0.0003) | | 0 | | -0.7963 | | -0.0183 (0.0003) | | 0 | |
| COL28A1 | Collagen alpha-1(XXVIII) chain | -0.1382 | | | -0.0496 (0.006) | | 1.45E-16 | -0.6049 | | -0.0133 (0.0003) | | 3.74E-300 | | -0.7006 | | -0.0138 (0.0002) | | 0 | |
| LCN2 | Neutrophil gelatinase-associated lipocalin | -0.1323 | | | -0.06 (0.0075) | | 1.33E-15 | -0.4967 | | -0.0139 (0.0004) | | 1.12E-196 | | -0.5418 | | -0.0135 (0.0004) | | 2.24E-258 | |
| CDNF | Cerebral dopamine neurotrophic factor | -0.1204 | | | -0.0416 (0.0052) | | 1.56E-15 | -0.5404 | | -0.0107 (0.0003) | | 4.47E-248 | | -0.4012 | | -0.0069 (0.0003) | | 3.14E-127 | |
| FSTL3 | Follistatin-related protein 3 | -0.1291 | | | -0.0423 (0.0053) | | 1.90E-15 | -0.5862 | | -0.0112 (0.0003) | | 1.06E-263 | | -0.6781 | | -0.0115 (0.0002) | | 0 | |
| SELM | Selenoprotein M | -0.1169 | | | -0.0455 (0.0057) | | 2.47E-15 | -0.6084 | | -0.0126 (0.0003) | | 1.41E-295 | | -0.5979 | | -0.0109 (0.0003) | | 3.42E-292 | |
| B2M | Beta-2-microglobulin | -0.1237 | | | -0.0475 (0.006) | | 3.28E-15 | -0.6675 | | -0.0147 (0.0003) | | 0 | | -0.7559 | | -0.0147 (0.0002) | | 0 | |
| PXDN | Peroxidasin homolog | -0.1316 | | | -0.0908 (0.0115) | | 4.29E-15 | -0.6003 | | -0.0255 (0.0006) | | 9.65E-299 | | -0.7044 | | -0.0265 (0.0005) | | 0 | |
| CD55 | Complement decay-accelerating factor | -0.1186 | | | -0.033 (0.0043) | | 1.11E-14 | -0.4380 | | -0.0068 (0.0003) | | 5.54E-143 | | -0.3575 | | -0.0049 (0.0002) | | 3.66E-96 | |
| NBL1 | Neuroblastoma suppressor of tumorigenicity 1 | -0.1267 | | | -0.0681 (0.0088) | | 1.15E-14 | -0.6745 | | -0.0218 (0.0004) | | 0 | | -0.6762 | | -0.019 (0.0004) | | 0 | |
| LMAN2 | Vesicular integral-membrane protein VIP36 | -0.1202 | | | -0.0415 (0.0054) | | 1.36E-14 | -0.5818 | | -0.0116 (0.0003) | | 2.60E-282 | | -0.6133 | | -0.0109 (0.0002) | | 0 | |
| IGFBP6 | Insulin-like growth factor-binding protein 6 | -0.1088 | | | -0.0286 (0.0037) | | 1.60E-14 | -0.4328 | | -0.0062 (0.0002) | | 1.11E-154 | | -0.3647 | | -0.0047 (0.0002) | | 8.52E-118 | |
| MB | Myoglobin | -0.101 | | | -0.0547 (0.0073) | | 6.45E-14 | -0.4130 | | -0.0126 (0.0004) | | 1.27E-169 | | -0.2849 | | -0.008 (0.0004) | | 2.07E-86 | |
| RGMB | RGM domain family member B | -0.1152 | | | -0.0307 (0.0041) | | 1.04E-13 | -0.4920 | | -0.0075 (0.0002) | | 2.41E-192 | | -0.3779 | | -0.0051 (0.0002) | | 4.14E-110 | |
| MFAP2 | Microfibrillar-associated protein 2 | -0.1219 | | | -0.0383 (0.0052) | | 2.38E-13 | -0.4859 | | -0.009 (0.0003) | | 2.45E-169 | | -0.5207 | | -0.0086 (0.0003) | | 1.09E-206 | |
| TWSG1 | Twisted gastrulation protein homolog 1 | -0.1188 | | | -0.0283 (0.0039) | | 3.79E-13 | -0.5667 | | -0.008 (0.0002) | | 8.36E-250 | | -0.6029 | | -0.0074 (0.0002) | | 4.31E-298 | |
| TNFRSF1B | Tumor necrosis factor receptor superfamily member 1B | -0.1133 | | | -0.0508 (0.007) | | 4.35E-13 | -0.5315 | | -0.0135 (0.0004) | | 2.83E-216 | | -0.6549 | | -0.0149 (0.0003) | | 0 | |
| TNFRSF1B | Tumor necrosis factor receptor superfamily member 1B | -0.1186 | | | -0.0507 (0.007) | | 4.83E-13 | -0.4956 | | -0.0125 (0.0004) | | 4.63E-183 | | -0.6090 | | -0.0138 (0.0003) | | 2.77E-322 | |
| COL18A1 | Endostatin | -0.1159 | | | -0.0357 (0.0049) | | 5.14E-13 | -0.5416 | | -0.0096 (0.0003) | | 3.16E-220 | | -0.5732 | | -0.0089 (0.0002) | | 1.16E-256 | |
| RETN | Resistin | -0.1198 | | | -0.0494 (0.0068) | | 5.56E-13 | -0.3516 | | -0.0084 (0.0004) | | 2.02E-82 | | -0.3901 | | -0.0085 (0.0004) | | 1.30E-112 | |
| ROR2 | Tyrosine-protein kinase transmembrane receptor ROR2 | -0.118 | | | -0.0459 (0.0064) | | 8.83E-13 | -0.5376 | | -0.0123 (0.0004) | | 3.76E-213 | | -0.5614 | | -0.0113 (0.0003) | | 6.21E-247 | |
| EPHA2 | Ephrin type-A receptor 2 | -0.1065 | | | -0.0445 (0.0062) | | 9.23E-13 | -0.5039 | | -0.011 (0.0004) | | 4.60E-179 | | -0.5390 | | -0.0105 (0.0003) | | 7.15E-222 | |
| ESAM | Endothelial cell-selective adhesion molecule | -0.1083 | | | -0.0323 (0.0046) | | 4.01E-12 | -0.4823 | | -0.0082 (0.0003) | | 7.00E-178 | | -0.4412 | | -0.0065 (0.0002) | | 1.19E-147 | |
| TNFRSF21 | Tumor necrosis factor receptor superfamily member 21 | -0.105 | | | -0.0293 (0.0043) | | 6.61E-12 | -0.4081 | | -0.0063 (0.0003) | | 3.85E-120 | | -0.4190 | | -0.0057 (0.0002) | | 5.35E-134 | |
| CD46 | Membrane cofactor protein | -0.1078 | | | -0.0287 (0.0042) | | 9.35E-12 | -0.4917 | | -0.0074 (0.0002) | | 9.14E-176 | | -0.5017 | | -0.0066 (0.0002) | | 3.77E-186 | |
| PTGDS | Prostaglandin-H2 D-isomerase | -0.1098 | | | -0.0431 (0.0063) | | 9.38E-12 | -0.5897 | | -0.0134 (0.0003) | | 3.74E-273 | | -0.5922 | | -0.0119 (0.0003) | | 1.74E-285 | |
| WFDC1 | WAP four-disulfide core domain protein 1 | -0.1136 | | | -0.0433 (0.0064) | | 1.14E-11 | -0.5379 | | -0.0123 (0.0004) | | 1.08E-216 | | -0.5405 | | -0.0108 (0.0003) | | 3.02E-224 | |
| HSPB6 | Heat shock protein beta-6 | -0.0919 | | | -0.048 (0.0071) | | 1.33E-11 | -0.5076 | | -0.0128 (0.0004) | | 6.51E-186 | | -0.4937 | | -0.0109 (0.0004) | | 2.83E-180 | |
| EFNA5 | Ephrin-A5 | -0.1121 | | | -0.0342 (0.0051) | | 1.53E-11 | -0.5222 | | -0.0096 (0.0003) | | 7.39E-207 | | -0.5068 | | -0.0082 (0.0003) | | 9.21E-199 | |
| SRL | Sarcalumenin | -0.1148 | | | -0.0421 (0.0063) | | 2.45E-11 | -0.4580 | | -0.0108 (0.0004) | | 6.11E-167 | | -0.3738 | | -0.0078 (0.0003) | | 3.17E-111 | |
| TREM1 | Triggering receptor expressed on myeloid cells 1 | -0.0932 | | | -0.0451 (0.0068) | | 3.07E-11 | -0.4217 | | -0.0097 (0.0004) | | 4.48E-113 | | -0.4680 | | -0.0098 (0.0003) | | 1.03E-155 | |
| EFNA4 | Ephrin-A4 | -0.1143 | | | -0.0328 (0.0049) | | 3.68E-11 | -0.5355 | | -0.0097 (0.0003) | | 8.30E-225 | | -0.5568 | | -0.009 (0.0002) | | 2.98E-262 | |
| CFD | Complement factor D | -0.1081 | | | -0.0295 (0.0045) | | 5.51E-11 | -0.4101 | | -0.0066 (0.0003) | | 2.02E-118 | | -0.4065 | | -0.0059 (0.0002) | | 1.72E-124 | |
| B4GALT1 | Beta-1,4-galactosyltransferase 1 | -0.0903 | | | -0.0242 (0.0037) | | 7.53E-11 | -0.4407 | | -0.0058 (0.0002) | | 8.02E-138 | | -0.4314 | | -0.0051 (0.0002) | | 9.76E-140 | |
| FABP4 | Fatty acid-binding protein, adipocyte | -0.1079 | | | -0.0529 (0.0082) | | 1.07E-10 | -0.4937 | | -0.0156 (0.0005) | | 9.64E-212 | | -0.5664 | | -0.0156 (0.0004) | | 5.28E-296 | |
| UNC5B | Netrin receptor UNC5B | -0.1009 | | | -0.0346 (0.0053) | | 1.08E-10 | -0.5099 | | -0.0097 (0.0003) | | 1.73E-187 | | -0.5222 | | -0.0087 (0.0003) | | 1.15E-205 | |
| EPHB6 | Ephrin type-B receptor 6 | -0.097 | | | -0.0284 (0.0044) | | 1.43E-10 | -0.5061 | | -0.0079 (0.0003) | | 4.87E-185 | | -0.4816 | | -0.0065 (0.0002) | | 2.32E-162 | |
| CD300C | CMRF35-like molecule 6 | -0.1126 | | | -0.039 (0.0061) | | 1.55E-10 | -0.3838 | | -0.0083 (0.0004) | | 7.48E-103 | | -0.4669 | | -0.009 (0.0003) | | 6.25E-167 | |
| MANSC1 | MANSC domain-containing protein 1 | -0.1013 | | | -0.0331 (0.0052) | | 2.54E-10 | -0.3686 | | -0.0067 (0.0003) | | 3.27E-89 | | -0.3798 | | -0.0062 (0.0003) | | 7.80E-103 | |
| IL15RA | Interleukin-15 receptor subunit alpha | -0.0902 | | | -0.0422 (0.0067) | | 2.98E-10 | -0.4396 | | -0.0102 (0.0004) | | 2.04E-129 | | -0.5200 | | -0.011 (0.0003) | | 3.42E-207 | |
| GAS1 | Growth arrest-specific protein 1 | -0.0989 | | | -0.0321 (0.0051) | | 4.07E-10 | -0.4827 | | -0.0087 (0.0003) | | 1.22E-160 | | -0.4712 | | -0.0074 (0.0003) | | 1.02E-153 | |
| EPHB4 | Ephrin type-B receptor 4 | -0.0945 | | | -0.0332 (0.0053) | | 5.17E-10 | -0.4415 | | -0.0084 (0.0003) | | 4.51E-140 | | -0.4348 | | -0.0074 (0.0003) | | 1.18E-144 | |
| DCLK1 | Serine/threonine-protein kinase DCLK1 | -0.1024 | | | -0.0406 (0.0065) | | 5.65E-10 | -0.4399 | | -0.0106 (0.0004) | | 1.78E-148 | | -0.4479 | | -0.0096 (0.0003) | | 6.01E-163 | |
| CAPG | Macrophage-capping protein | -0.0918 | | | -0.0514 (0.0083) | | 6.02E-10 | -0.4178 | | -0.0114 (0.0005) | | 2.10E-103 | | -0.4728 | | -0.0113 (0.0004) | | 3.13E-137 | |
| PPIC | Peptidyl-prolyl cis-trans isomerase C | -0.1028 | | | -0.0354 (0.0057) | | 7.97E-10 | -0.4335 | | -0.0093 (0.0003) | | 1.57E-147 | | -0.4598 | | -0.0089 (0.0003) | | 1.81E-182 | |
| TNFRSF19 | Tumor necrosis factor receptor superfamily member 19 | -0.0944 | | | -0.044 (0.0072) | | 9.15E-10 | -0.4861 | | -0.0126 (0.0004) | | 4.04E-175 | | -0.4458 | | -0.0101 (0.0004) | | 3.27E-147 | |
| MYOC | Myocilin | -0.1032 | | | -0.0379 (0.0062) | | 1.29E-09 | -0.4303 | | -0.0103 (0.0004) | | 4.10E-155 | | -0.3091 | | -0.0066 (0.0003) | | 1.50E-80 | |
| UNC5C | Netrin receptor UNC5C | -0.0934 | | | -0.033 (0.0054) | | 1.32E-09 | -0.3872 | | -0.0073 (0.0003) | | 2.58E-100 | | -0.4023 | | -0.0068 (0.0003) | | 1.00E-114 | |
| CCL14 | C-C motif chemokine 14 | -0.104 | | | -0.0541 (0.0089) | | 1.34E-09 | -0.4783 | | -0.0153 (0.0005) | | 7.84E-168 | | -0.5550 | | -0.0159 (0.0004) | | 3.89E-251 | |
| MXRA7 | Matrix-remodeling-associated protein 7 | -0.0963 | | | -0.0381 (0.0063) | | 1.47E-09 | -0.5043 | | -0.0114 (0.0004) | | 1.20E-188 | | -0.4854 | | -0.0096 (0.0003) | | 1.52E-177 | |
| XXYLT1 | Xyloside xylosyltransferase 1 | -0.0979 | | | -0.0291 (0.0048) | | 1.57E-09 | -0.3410 | | -0.0058 (0.0003) | | 8.09E-78 | | -0.3364 | | -0.0051 (0.0003) | | 2.00E-79 | |
| TAGLN | Transgelin | -0.0775 | | | -0.038 (0.0064) | | 2.58E-09 | -0.5736 | | -0.0126 (0.0004) | | 2.15E-230 | | -0.5601 | | -0.0105 (0.0003) | | 3.27E-210 | |
| DNAJB12 | DnaJ homolog subfamily B member 12 | -0.1013 | | | -0.039 (0.0066) | | 2.93E-09 | -0.5364 | | -0.0128 (0.0004) | | 5.81E-224 | | -0.5541 | | -0.0117 (0.0003) | | 1.16E-252 | |
| GABARAP | Gamma-aminobutyric acid receptor-associated protein | -0.1069 | | | -0.0252 (0.0042) | | 2.96E-09 | -0.4869 | | -0.0075 (0.0002) | | 1.44E-177 | | -0.6207 | | -0.0083 (0.0002) | | 4.98E-315 | |
| JAM2 | Junctional adhesion molecule B | -0.1186 | | | -0.0227 (0.0038) | | 3.75E-09 | -0.4757 | | -0.0068 (0.0002) | | 4.07E-180 | | -0.4550 | | -0.0056 (0.0002) | | 1.03E-160 | |
| EFNA2 | Ephrin-A2 | -0.0943 | | | -0.0276 (0.0047) | | 6.20E-09 | -0.5312 | | -0.0091 (0.0003) | | 1.35E-216 | | -0.5529 | | -0.0084 (0.0002) | | 3.15E-251 | |
| SERPINF1 | Pigment epithelium-derived factor | -0.0983 | | | -0.0187 (0.0032) | | 6.38E-09 | -0.3319 | | -0.0043 (0.0002) | | 3.14E-95 | | -0.3629 | | -0.0042 (0.0002) | | 2.14E-126 | |
| CALCOCO2 | Calcium-binding and coiled-coil domain-containing protein 2 | -0.0901 | | | -0.0259 (0.0045) | | 7.23E-09 | -0.3562 | | -0.006 (0.0003) | | 4.21E-98 | | -0.3140 | | -0.0047 (0.0002) | | 2.57E-80 | |
| DLK2 | Protein delta homolog 2 | -0.0809 | | | -0.0386 (0.0067) | | 7.47E-09 | -0.4989 | | -0.012 (0.0004) | | 9.44E-185 | | -0.4489 | | -0.0094 (0.0003) | | 1.84E-148 | |
| UNC5B | Netrin receptor UNC5B | -0.0922 | | | -0.0312 (0.0054) | | 8.65E-09 | -0.4751 | | -0.0091 (0.0003) | | 3.90E-159 | | -0.5033 | | -0.0085 (0.0003) | | 5.09E-189 | |
| CRABP2 | Cellular retinoic acid-binding protein 2 | -0.1039 | | | -0.0409 (0.0071) | | 1.05E-08 | -0.4069 | | -0.0112 (0.0004) | | 8.88E-138 | | -0.4583 | | -0.0114 (0.0004) | | 1.33E-193 | |
| MAP2K2 | Dual specificity mitogen-activated protein kinase kinase 2 | -0.1024 | | | -0.0467 (0.0082) | | 1.16E-08 | -0.3862 | | -0.0117 (0.0005) | | 5.85E-113 | | -0.3532 | | -0.0089 (0.0004) | | 9.25E-87 | |
| DLK1 | Protein delta homolog 1 | -0.1001 | | | -0.0534 (0.0094) | | 1.41E-08 | -0.3515 | | -0.0122 (0.0006) | | 7.05E-92 | | -0.2881 | | -0.0087 (0.0005) | | 2.54E-61 | |
| LRP10 | Low-density lipoprotein receptor-related protein 10 | -0.0844 | | | -0.0245 (0.0043) | | 1.46E-08 | -0.4505 | | -0.0069 (0.0003) | | 5.60E-142 | | -0.4290 | | -0.0058 (0.0002) | | 1.05E-133 | |
| WFDC2 | WAP four-disulfide core domain protein 2 | -0.078 | | | -0.0383 (0.0068) | | 1.69E-08 | -0.5846 | | -0.0141 (0.0004) | | 1.56E-260 | | -0.6098 | | -0.0131 (0.0003) | | 2.05E-304 | |
| VASN | Vasorin | -0.0892 | | | -0.02 (0.0035) | | 1.85E-08 | -0.3395 | | -0.0046 (0.0002) | | 2.03E-92 | | -0.3392 | | -0.0041 (0.0002) | | 3.50E-98 | |
| PENK | Proenkephalin-A | -0.0898 | | | -0.0463 (0.0082) | | 1.87E-08 | -0.3396 | | -0.0091 (0.0005) | | 1.13E-66 | | -0.3779 | | -0.0089 (0.0004) | | 5.96E-85 | |
| DLK1 | Protein delta homolog 1 | -0.0988 | | | -0.0523 (0.0093) | | 2.03E-08 | -0.3443 | | -0.0118 (0.0006) | | 7.20E-88 | | -0.2819 | | -0.0084 (0.0005) | | 1.20E-58 | |
| NMB | Neuromedin-B | -0.0878 | | | -0.035 (0.0063) | | 2.38E-08 | -0.3680 | | -0.0079 (0.0004) | | 1.74E-85 | | -0.4005 | | -0.0074 (0.0003) | | 2.20E-102 | |
| EWSR1 | RNA-binding protein EWS | -0.0946 | | | -0.0331 (0.0059) | | 2.38E-08 | -0.3664 | | -0.0074 (0.0004) | | 6.73E-86 | | -0.4760 | | -0.0087 (0.0003) | | 1.23E-161 | |
| IL18BP | Interleukin-18-binding protein | -0.0789 | | | -0.0314 (0.0056) | | 2.41E-08 | -0.3747 | | -0.0072 (0.0003) | | 1.79E-88 | | -0.4523 | | -0.008 (0.0003) | | 6.75E-150 | |
| DDOST | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit | -0.0889 | | | -0.0295 (0.0053) | | 2.75E-08 | -0.3830 | | -0.0072 (0.0003) | | 5.18E-102 | | -0.3842 | | -0.0064 (0.0003) | | 1.92E-106 | |
| IL2RB | Interleukin-2 receptor subunit beta | -0.088 | | | -0.0396 (0.0071) | | 2.91E-08 | -0.2952 | | -0.0079 (0.0004) | | 1.08E-66 | | -0.3066 | | -0.0073 (0.0004) | | 2.14E-76 | |
| AMBP | Alpha-1-microglobulin | -0.1052 | | | -0.0221 (0.004) | | 4.33E-08 | -0.4258 | | -0.0063 (0.0002) | | 3.53E-136 | | -0.4805 | | -0.0063 (0.0002) | | 1.43E-189 | |
| VWC2 | Brorin | -0.0789 | | | -0.0286 (0.0053) | | 6.22E-08 | -0.4736 | | -0.0088 (0.0003) | | 1.70E-157 | | -0.4511 | | -0.0072 (0.0003) | | 3.25E-139 | |
| SPON2 | Spondin-2 | -0.0867 | | | -0.0342 (0.0063) | | 6.39E-08 | -0.4180 | | -0.0092 (0.0004) | | 2.84E-118 | | -0.5063 | | -0.0101 (0.0003) | | 1.57E-194 | |
| CADM2 | Cell adhesion molecule 2 | -0.0831 | | | -0.03 (0.0056) | | 7.64E-08 | -0.3653 | | -0.0072 (0.0003) | | 1.20E-91 | | -0.2654 | | -0.0041 (0.0003) | | 1.98E-38 | |
| EFEMP1 | EGF-containing fibulin-like extracellular matrix protein 1 | -0.0775 | | | -0.0243 (0.0046) | | 9.80E-08 | -0.4354 | | -0.0063 (0.0003) | | 2.16E-106 | | -0.5645 | | -0.0075 (0.0002) | | 6.01E-209 | |
| RNASE6 | Ribonuclease K6 | -0.0849 | | | -0.0479 (0.009) | | 1.16E-07 | -0.4655 | | -0.0148 (0.0005) | | 4.54E-152 | | -0.5481 | | -0.0156 (0.0004) | | 2.94E-236 | |
| VIT | Vitrin | -0.074 | | | -0.0303 (0.0057) | | 1.38E-07 | -0.3833 | | -0.008 (0.0004) | | 2.63E-105 | | -0.3584 | | -0.0067 (0.0003) | | 1.30E-98 | |
| IGFBP4 | Insulin-like growth factor-binding protein 4 | -0.1052 | | | -0.0247 (0.0047) | | 1.63E-07 | -0.3655 | | -0.0066 (0.0003) | | 3.38E-109 | | -0.4215 | | -0.0067 (0.0002) | | 1.18E-151 | |
| MIA | Melanoma-derived growth regulatory protein | -0.0785 | | | -0.0263 (0.005) | | 1.65E-07 | -0.2978 | | -0.0054 (0.0003) | | 1.65E-61 | | -0.1855 | | -0.0029 (0.0003) | | 2.70E-24 | |
| CD93 | Complement component C1q receptor | -0.0754 | | | -0.0239 (0.0046) | | 1.73E-07 | -0.2957 | | -0.0051 (0.0003) | | 4.17E-67 | | -0.2939 | | -0.0047 (0.0002) | | 8.05E-76 | |
| EPHA1 | Ephrin type-A receptor 1 | -0.1024 | | | -0.0433 (0.0083) | | 1.73E-07 | -0.2830 | | -0.0088 (0.0005) | | 5.36E-61 | | -0.3036 | | -0.0085 (0.0004) | | 1.19E-75 | |
| ASGR1 | Asialoglycoprotein receptor 1 | -0.0896 | | | -0.0304 (0.0059) | | 2.10E-07 | -0.4406 | | -0.0099 (0.0003) | | 1.62E-160 | | -0.4976 | | -0.01 (0.0003) | | 2.31E-227 | |
| SMOC1 | SPARC-related modular calcium-binding protein 1 | -0.0752 | | | -0.0258 (0.005) | | 2.47E-07 | -0.4404 | | -0.0074 (0.0003) | | 2.96E-120 | | -0.4244 | | -0.0061 (0.0003) | | 1.95E-109 | |
| TMPO | Lamina-associated polypeptide 2, isoforms beta/gamma | -0.0963 | | | -0.0424 (0.0082) | | 2.80E-07 | -0.3591 | | -0.0108 (0.0005) | | 4.41E-94 | | -0.4851 | | -0.0127 (0.0004) | | 5.88E-179 | |
| CLMP | CXADR-like membrane protein | -0.0948 | | | -0.0358 (0.007) | | 3.33E-07 | -0.4428 | | -0.0116 (0.0004) | | 1.82E-155 | | -0.4516 | | -0.0104 (0.0004) | | 1.13E-165 | |
| AIF1L | Allograft inflammatory factor 1-like | -0.0758 | | | -0.0252 (0.0049) | | 3.36E-07 | -0.4596 | | -0.0078 (0.0003) | | 1.84E-142 | | -0.4507 | | -0.0068 (0.0003) | | 2.82E-140 | |
| RARRES2 | Retinoic acid receptor responder protein 2 | -0.093 | | | -0.0286 (0.0056) | | 3.38E-07 | -0.4542 | | -0.0096 (0.0003) | | 3.38E-167 | | -0.5357 | | -0.01 (0.0003) | | 4.81E-252 | |
| NPDC1 | Neural proliferation differentiation and control protein 1 | -0.0822 | | | -0.0292 (0.0057) | | 3.73E-07 | -0.4681 | | -0.0097 (0.0003) | | 1.42E-162 | | -0.4648 | | -0.0083 (0.0003) | | 1.17E-158 | |
| PI3 | Elafin | -0.0748 | | | -0.0501 (0.0098) | | 3.90E-07 | -0.4154 | | -0.0155 (0.0006) | | 1.64E-138 | | -0.4343 | | -0.0148 (0.0005) | | 5.46E-171 | |
| MYL3 | Myosin light chain 3 | -0.0627 | | | -0.0748 (0.0148) | | 4.45E-07 | -0.2732 | | -0.0145 (0.0009) | | 1.26E-51 | | -0.1944 | | -0.009 (0.0008) | | 1.12E-26 | |
| APOF | Apolipoprotein F | -0.07 | | | -0.0514 (0.0102) | | 5.01E-07 | -0.4212 | | -0.0148 (0.0006) | | 2.01E-116 | | -0.3534 | | -0.0104 (0.0006) | | 3.06E-75 | |
| IGFLR1 | IGF-like family receptor 1 | -0.0805 | | | -0.0423 (0.0085) | | 6.88E-07 | -0.4744 | | -0.0143 (0.0005) | | 5.14E-160 | | -0.5687 | | -0.0153 (0.0004) | | 9.54E-259 | |
| TGFBR3 | Transforming growth factor beta receptor type 3 | -0.0736 | | | -0.0217 (0.0044) | | 7.55E-07 | -0.2723 | | -0.0042 (0.0003) | | 5.52E-50 | | -0.2333 | | -0.0032 (0.0002) | | 1.75E-37 | |
| DPY30 | Protein dpy-30 homolog | -0.0822 | | | -0.0343 (0.0069) | | 7.90E-07 | -0.3831 | | -0.01 (0.0004) | | 1.14E-115 | | -0.4664 | | -0.0106 (0.0004) | | 9.70E-177 | |
| CCL23 | C-C motif chemokine 23 | -0.0798 | | | -0.0301 (0.0061) | | 9.21E-07 | -0.3074 | | -0.0066 (0.0004) | | 5.15E-62 | | -0.2844 | | -0.0053 (0.0003) | | 1.40E-54 | |
| CPLX2 | Complexin-2 | -0.0854 | | | -0.0362 (0.0074) | | 9.21E-07 | -0.5110 | | -0.0135 (0.0004) | | 1.62E-192 | | -0.4491 | | -0.0096 (0.0004) | | 4.77E-125 | |
| JTB | Protein JTB | -0.0739 | | | -0.0215 (0.0044) | | 9.59E-07 | -0.3697 | | -0.0058 (0.0003) | | 5.11E-95 | | -0.3193 | | -0.0044 (0.0002) | | 2.69E-71 | |
| RNASE4 | Ribonuclease 4 | -0.0813 | | | -0.0202 (0.0041) | | 9.91E-07 | -0.4841 | | -0.0071 (0.0002) | | 8.89E-169 | | -0.4963 | | -0.0064 (0.0002) | | 2.33E-186 | |
| SPINK7 | Serine protease inhibitor Kazal-type 7 | -0.0768 | | | -0.0339 (0.007) | | 1.40E-06 | -0.4028 | | -0.0105 (0.0004) | | 4.92E-125 | | -0.2811 | | -0.0064 (0.0004) | | 1.35E-60 | |
| NEGR1 | Neuronal growth regulator 1 | -0.0647 | | | -0.018 (0.0037) | | 1.40E-06 | -0.2982 | | -0.0038 (0.0002) | | 3.86E-56 | | -0.1808 | | -0.0018 (0.0002) | | 1.09E-17 | |
| CCL23 | Ck-beta-8-1 | -0.0764 | | | -0.03 (0.0062) | | 1.53E-06 | -0.2799 | | -0.0059 (0.0004) | | 5.41E-49 | | -0.2538 | | -0.0047 (0.0003) | | 4.16E-41 | |
| FABP3 | Fatty acid-binding protein, heart | -0.0824 | | | -0.0436 (0.0091) | | 1.65E-06 | -0.4051 | | -0.0157 (0.0005) | | 1.78E-170 | | -0.4974 | | -0.0166 (0.0004) | | 2.90E-268 | |
| CA3 | Carbonic anhydrase 3 | -0.0637 | | | -0.0498 (0.0104) | | 1.80E-06 | -0.2696 | | -0.0087 (0.0007) | | 1.39E-37 | | -0.2631 | | -0.0075 (0.0006) | | 4.90E-37 | |
| CD300A | CMRF35-like molecule 8 | -0.0782 | | | -0.0314 (0.0066) | | 1.91E-06 | -0.3913 | | -0.009 (0.0004) | | 1.86E-102 | | -0.4707 | | -0.0098 (0.0003) | | 1.28E-165 | |
| SMOC2 | SPARC-related modular calcium-binding protein 2 | -0.0662 | | | -0.028 (0.0059) | | 2.02E-06 | -0.4313 | | -0.0088 (0.0004) | | 9.48E-126 | | -0.3614 | | -0.0063 (0.0003) | | 3.47E-82 | |
| ATOX1 | Copper transport protein ATOX1 | -0.0894 | | | -0.0381 (0.0081) | | 2.31E-06 | -0.3392 | | -0.0104 (0.0005) | | 2.25E-91 | | -0.4176 | | -0.0106 (0.0004) | | 2.52E-128 | |
| PCOLCE | Procollagen C-endopeptidase enhancer 1 | -0.0797 | | | -0.035 (0.0074) | | 2.51E-06 | -0.2922 | | -0.0081 (0.0005) | | 4.89E-65 | | -0.2694 | | -0.0064 (0.0004) | | 6.68E-54 | |
| CPLX1 | Complexin-1 | -0.0799 | | | -0.027 (0.0058) | | 3.28E-06 | -0.4821 | | -0.0099 (0.0003) | | 2.97E-166 | | -0.4301 | | -0.0072 (0.0003) | | 2.32E-114 | |
| UNC5D | Netrin receptor UNC5D | -0.0705 | | | -0.0303 (0.0065) | | 3.32E-06 | -0.4185 | | -0.0097 (0.0004) | | 3.72E-124 | | -0.3132 | | -0.0058 (0.0004) | | 9.98E-57 | |
| PGRMC1 | Membrane-associated progesterone receptor component 1 | -0.0881 | | | -0.0239 (0.0053) | | 5.51E-06 | -0.3592 | | -0.0074 (0.0003) | | 5.85E-108 | | -0.3449 | | -0.006 (0.0003) | | 3.98E-95 | |
| ROR1 | Inactive tyrosine-protein kinase transmembrane receptor ROR1 | -0.0677 | | | -0.024 (0.0053) | | 5.59E-06 | -0.3307 | | -0.0058 (0.0003) | | 4.83E-65 | | -0.2628 | | -0.0038 (0.0003) | | 2.61E-37 | |
| LRP11 | Low-density lipoprotein receptor-related protein 11 | -0.0742 | | | -0.0221 (0.0049) | | 5.61E-06 | -0.4706 | | -0.0082 (0.0003) | | 2.25E-163 | | -0.4846 | | -0.0075 (0.0002) | | 1.89E-182 | |
| PSMB1 | Proteasome subunit beta type-1 | -0.0778 | | | -0.0278 (0.0061) | | 5.81E-06 | -0.3854 | | -0.0086 (0.0004) | | 4.90E-108 | | -0.4015 | | -0.008 (0.0003) | | 2.61E-126 | |
| SEPW1 | Selenoprotein W | -0.0828 | | | -0.0297 (0.0067) | | 8.48E-06 | -0.3911 | | -0.0099 (0.0004) | | 3.30E-123 | | -0.4182 | | -0.0088 (0.0003) | | 3.00E-127 | |
| Negative significant correlations, medianf | | -0.0963 | | | | | | -0.4415 | | | | | | -0.4583 | | | | | |

a Proteins were identified through linear regression of LDPred PRS for kidney function on 4,877 proteins measured at visit 3 and visit 5 with adjusting for age at the corresponded visits, sex, center, and first 10 genetic principal components. A total of 108 proteins were significantly associated with LDPred PRS at both visit 3 and visit 5. The threshold of significance was Bonferroni corrected: p = 1.02 × 10-5. Visit 3 was conducted during 1993-1995 when the mean age of study population was 60.4 years and visit 5 was conducted during 2011-2013 when the mean age of study population was 75.9 years.

b LDPred PRS was constructed using LDPred algorithm, a Bayesian approach utilizes GWAS summary statistics to compute the posterior mean effect sizes for the genetic variants by assuming a prior of the joint effect sizes and incorporating the LD structure of the reference population.

c Linear regression of LDPred PRS, eGFRcr measured at visit 3, and eGFRcys measured at visit 3 on proteins measured at visit 3, with adjusting for age at visit 3, sex, center, and first 10 genetic principal components.

d Linear regression of LDPred PRS, eGFRcr measured at visit 5, and eGFRcys measured at visit 5 on proteins measured at visit 5, with adjusting for age at visit 5, sex, center, and first 10 genetic principal components.

e P values of Wilcoxon signed rank test for the comparison between correlations of proteins with LDPred PRS and with eGFR were 5.14E-23for eGFRcr and 1.17E-21for eGFRcys at visit 3, and were 7.38E-23 for eGFRcr and 5.28E-22 for eGFRcys at visit 5.

f P values of Wilcoxon signed rank test for the comparison between visit 3 and visit 5 correlations of proteins with LDPred PRS was 4.74E-19, and that of proteins with eGFR were 3.9E-21 for eGFRcr and 2.13E-18 for eGFRcys.

eGFRcr: estimated glomerular filtration rate based on creatinine; eGFRcys: estimated glomerular filtration rate based on cystatin C; PRS: polygenic risk score.

# **Supplemental Table 8. Causal mediation effects of estimated glomerular filtration rate measured based on creatinie on proteins significantly associated with LDPred polygenic risk score at both visit 3 (N=7,213) and visit 5 (N = 3,666)a,b.**

**(A) LDPred PRS, eGFRcr measured at visit 3, and proteins measured at visit 3**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  |  | **Total Effects** | | **Average direct effects** | |
|  |  | **Beta (95% CI)** | **P** | **Beta (95% CI)** | **P** |
|  |  | **Positive total effect** | | | |
| SPOCK2 | Testican-2 | 0.0386 (0.0315, 0.0468) | <2E-16 | 0.0171 (0.0102, 0.0248) | <2E-16 |
| PLG | Angiostatin | 0.0153 (0.0103, 0.0206) | <2E-16 | 0.0066 (0.0016, 0.0129) | 0.02 |
| HPRT1 | Hypoxanthine-guanine phosphoribosyltransferase | 0.0141 (0.0089, 0.0189) | <2E-16 | 0.0038 (-0.0014, 0.0085) | 0.2 |
| CA10 | Carbonic anhydrase-related protein 10 | 0.0244 (0.0167, 0.0327) | <2E-16 | 0.0083 (0.0004, 0.0182) | 0.04 |
| KL | Klotho | 0.0274 (0.0189, 0.0398) | <2E-16 | 0.0119 (0.0037, 0.0227) | 0.02 |
|  |  | **Negative total effect** | | | |
| CST3 | Cystatin-C | -0.0413 (-0.0474, -0.0367) | <2E-16 | -0.0017 (-0.0065, 0.0028) | 0.52 |
| COL15A1 | Collagen alpha-1(XV) chain | -0.0362 (-0.0413, -0.0313) | <2E-16 | 0.0004 (-0.0047, 0.0051) | 0.86 |
| RNASE1 | Ribonuclease pancreatic | -0.0757 (-0.0883, -0.0625) | <2E-16 | -0.003 (-0.0151, 0.0087) | 0.62 |
| DSC2 | Desmocollin-2 | -0.0323 (-0.0374, -0.0281) | <2E-16 | 0.0015 (-0.0037, 0.0063) | 0.54 |
| COL6A3 | Collagen alpha-3(VI) chain | -0.0323 (-0.0372, -0.0272) | <2E-16 | -0.0042 (-0.0101, 0.0009) | 0.16 |
| TMED10 | Transmembrane emp24 domain-containing protein 10 | -0.0385 (-0.0466, -0.0311) | <2E-16 | -0.0005 (-0.0071, 0.006) | 0.9 |
| COL28A1 | Collagen alpha-1(XXVIII) chain | -0.0336 (-0.0403, -0.0262) | <2E-16 | -0.0027 (-0.0088, 0.0037) | 0.44 |
| CD59 | CD59 glycoprotein | -0.0316 (-0.0376, -0.0237) | <2E-16 | 0.0032 (-0.0029, 0.0098) | 0.28 |
| GM2A | Ganglioside GM2 activator | -0.035 (-0.0412, -0.0288) | <2E-16 | 0.001 (-0.0052, 0.0087) | 0.7 |
| CDNF | Cerebral dopamine neurotrophic factor | -0.0298 (-0.0356, -0.0248) | <2E-16 | 0.0029 (-0.0032, 0.0081) | 0.38 |
| TNFRSF1A | Tumor necrosis factor receptor superfamily member 1A | -0.0394 (-0.0456, -0.0327) | <2E-16 | 0.003 (-0.0047, 0.0097) | 0.44 |
| ART3 | Ecto-ADP-ribosyltransferase 3 | -0.0446 (-0.0551, -0.0354) | <2E-16 | -0.0001 (-0.0095, 0.0104) | 0.96 |
| SELM | Selenoprotein M | -0.0319 (-0.0384, -0.0261) | <2E-16 | 0.0048 (-0.0017, 0.0102) | 0.1 |
| B2M | Beta-2-microglobulin | -0.0311 (-0.0363, -0.0241) | <2E-16 | 0.002 (-0.0045, 0.0084) | 0.44 |
| EFNB2 | Ephrin-B2 | -0.0311 (-0.0374, -0.0242) | <2E-16 | 0.0059 (0, 0.0118) | 0.06 |
| LMAN2 | Vesicular integral-membrane protein VIP36 | -0.026 (-0.0316, -0.0207) | <2E-16 | 0.0012 (-0.0052, 0.0064) | 0.68 |
| FSTL3 | Follistatin-related protein 3 | -0.028 (-0.0332, -0.0225) | <2E-16 | 0.0009 (-0.0042, 0.0068) | 0.72 |
| FABP4 | Fatty acid-binding protein, adipocyte | -0.055 (-0.0673, -0.0439) | <2E-16 | 0.0003 (-0.0122, 0.0127) | 0.82 |
| SEPW1 | Selenoprotein W | -0.0321 (-0.0389, -0.0259) | <2E-16 | -0.0006 (-0.0073, 0.0065) | 0.86 |
| HSPB6 | Heat shock protein beta-6 | -0.0396 (-0.0473, -0.0317) | <2E-16 | 0.0008 (-0.0074, 0.0078) | 0.86 |
| MB | Myoglobin | -0.0415 (-0.0507, -0.0313) | <2E-16 | -0.0002 (-0.0104, 0.0106) | 0.98 |
| MYOC | Myocilin | -0.0331 (-0.0399, -0.0261) | <2E-16 | 0.0036 (-0.0031, 0.0116) | 0.32 |
| IGFBP6 | Insulin-like growth factor-binding protein 6 | -0.0234 (-0.0278, -0.0195) | <2E-16 | 0.0021 (-0.002, 0.007) | 0.52 |
| COL18A1 | Endostatin | -0.0287 (-0.0347, -0.0217) | <2E-16 | -0.0018 (-0.0081, 0.0045) | 0.64 |
| TNFRSF1B | Tumor necrosis factor receptor superfamily member 1B | -0.0309 (-0.0387, -0.0245) | <2E-16 | -0.0008 (-0.0088, 0.0055) | 0.88 |
| RGMB | RGM domain family member B | -0.0203 (-0.0259, -0.0162) | <2E-16 | 0.0056 (0.0002, 0.0104) | 0.06 |
| LCN2 | Neutrophil gelatinase-associated lipocalin | -0.0352 (-0.0438, -0.0276) | <2E-16 | -0.003 (-0.012, 0.0049) | 0.52 |
| PTGDS | Prostaglandin-H2 D-isomerase | -0.0368 (-0.0474, -0.0274) | <2E-16 | 0.0045 (-0.0051, 0.0144) | 0.32 |
| CFD | Complement factor D | -0.0266 (-0.0324, -0.0193) | <2E-16 | -0.0015 (-0.0062, 0.0055) | 0.58 |
| PPIC | Peptidyl-prolyl cis-trans isomerase C | -0.0283 (-0.0347, -0.022) | <2E-16 | -0.0007 (-0.0062, 0.0057) | 0.8 |
| SMOC2 | SPARC-related modular calcium-binding protein 2 | -0.0266 (-0.0347, -0.0207) | <2E-16 | 0.0028 (-0.0048, 0.0101) | 0.48 |
| NBL1 | Neuroblastoma suppressor of tumorigenicity 1 | -0.0309 (-0.0392, -0.0238) | <2E-16 | 0.0128 (0.0056, 0.0205) | <2E-16 |
| MFAP2 | Microfibrillar-associated protein 2 | -0.0254 (-0.0307, -0.0188) | <2E-16 | -0.0031 (-0.0092, 0.0039) | 0.36 |
| RNASE6 | Ribonuclease K6 | -0.0378 (-0.0467, -0.0276) | <2E-16 | -0.0003 (-0.0089, 0.0096) | 0.92 |
| CCL14 | C-C motif chemokine 14 | -0.0426 (-0.0553, -0.0335) | <2E-16 | -0.0023 (-0.0151, 0.0088) | 0.74 |
| ESAM | Endothelial cell-selective adhesion molecule | -0.0235 (-0.0285, -0.0177) | <2E-16 | 0.0035 (-0.0027, 0.0097) | 0.3 |
| DNAJB12 | DnaJ homolog subfamily B member 12 | -0.032 (-0.0423, -0.0244) | <2E-16 | 0.0068 (-0.0031, 0.0147) | 0.18 |
| GABARAP | Gamma-aminobutyric acid receptor-associated protein | -0.0202 (-0.0239, -0.0156) | <2E-16 | 0.002 (-0.0027, 0.0057) | 0.42 |
| UNC5B | Netrin receptor UNC5B | -0.025 (-0.0316, -0.0179) | <2E-16 | 0.005 (-0.0014, 0.0126) | 0.24 |
| WFDC1 | WAP four-disulfide core domain protein 1 | -0.0301 (-0.0381, -0.0225) | <2E-16 | 0.0043 (-0.0042, 0.0122) | 0.32 |
| MIA | Melanoma-derived growth regulatory protein | -0.0259 (-0.033, -0.0195) | <2E-16 | -0.0034 (-0.0119, 0.0044) | 0.36 |
| EFNA4 | Ephrin-A4 | -0.02 (-0.0254, -0.013) | <2E-16 | 0.0033 (-0.0027, 0.0105) | 0.34 |
| RARRES2 | Retinoic acid receptor responder protein 2 | -0.0287 (-0.0354, -0.0214) | <2E-16 | -0.0057 (-0.0124, 0.0018) | 0.14 |
| GAS1 | Growth arrest-specific protein 1 | -0.0242 (-0.03, -0.0181) | <2E-16 | 0.0069 (0.0002, 0.013) | 0.06 |
| EFNA5 | Ephrin-A5 | -0.0202 (-0.0245, -0.0137) | <2E-16 | 0.0061 (0.0007, 0.0117) | <2E-16 |
| CRABP2 | Cellular retinoic acid-binding protein 2 | -0.0323 (-0.041, -0.0237) | <2E-16 | 0.0047 (-0.0045, 0.0131) | 0.32 |
| UNC5C | Netrin receptor UNC5C | -0.0235 (-0.03, -0.0173) | <2E-16 | -0.0021 (-0.0087, 0.0043) | 0.58 |
| JAM2 | Junctional adhesion molecule B | -0.018 (-0.0223, -0.0129) | <2E-16 | 0.001 (-0.0035, 0.0061) | 0.74 |
| CD55 | Complement decay-accelerating factor | -0.0186 (-0.0235, -0.0138) | <2E-16 | 0.0004 (-0.0048, 0.0057) | 0.8 |
| EPHA2 | Ephrin type-A receptor 2 | -0.0258 (-0.0321, -0.0195) | <2E-16 | 0.0002 (-0.0068, 0.0065) | 0.96 |
| ATOX1 | Copper transport protein ATOX1 | -0.0353 (-0.043, -0.027) | <2E-16 | -0.0036 (-0.0109, 0.007) | 0.5 |
| TAGLN | Transgelin | -0.0276 (-0.0335, -0.0203) | <2E-16 | 0.0061 (-0.0003, 0.0133) | 0.08 |
| TWSG1 | Twisted gastrulation protein homolog 1 | -0.0157 (-0.0204, -0.0116) | <2E-16 | 0.0012 (-0.0031, 0.0052) | 0.72 |
| CA3 | Carbonic anhydrase 3 | -0.0482 (-0.0612, -0.0348) | <2E-16 | -0.0116 (-0.0252, 0.0009) | 0.08 |
| TNFRSF1B | Tumor necrosis factor receptor superfamily member 1B | -0.0271 (-0.0329, -0.02) | <2E-16 | -0.0009 (-0.0077, 0.0067) | 0.84 |
| CALCOCO2 | Calcium-binding and coiled-coil domain-containing protein 2 | -0.0211 (-0.0267, -0.0149) | <2E-16 | -0.0081 (-0.015, -0.0013) | 0.02 |
| UNC5B | Netrin receptor UNC5B | -0.0235 (-0.0306, -0.0173) | <2E-16 | 0.0044 (-0.0033, 0.011) | 0.2 |
| VWC2 | Brorin | -0.0244 (-0.0314, -0.0173) | <2E-16 | 0.0047 (-0.0023, 0.0111) | 0.22 |
| DLK1 | Protein delta homolog 1 | -0.0394 (-0.0518, -0.0284) | <2E-16 | -0.0023 (-0.0172, 0.0099) | 0.74 |
| DLK1 | Protein delta homolog 1 | -0.0421 (-0.0545, -0.0311) | <2E-16 | -0.001 (-0.014, 0.0098) | 0.92 |
| CD46 | Membrane cofactor protein | -0.0175 (-0.0221, -0.0123) | <2E-16 | 0.0014 (-0.0039, 0.0064) | 0.56 |
| WFDC2 | WAP four-disulfide core domain protein 2 | -0.0292 (-0.039, -0.0185) | <2E-16 | 0.0057 (-0.0038, 0.0157) | 0.26 |
| EPHB6 | Ephrin type-B receptor 6 | -0.0166 (-0.0202, -0.0118) | <2E-16 | 0.0033 (-0.0015, 0.0076) | 0.16 |
| DCLK1 | Serine/threonine-protein kinase DCLK1 | -0.0258 (-0.0334, -0.019) | <2E-16 | -0.0023 (-0.0103, 0.0062) | 0.64 |
| ASGR1 | Asialoglycoprotein receptor 1 | -0.0212 (-0.0275, -0.0148) | <2E-16 | -0.0002 (-0.0067, 0.0071) | 0.96 |
| LRP10 | Low-density lipoprotein receptor-related protein 10 | -0.0156 (-0.0195, -0.0104) | <2E-16 | 0.0072 (0.0028, 0.0126) | <2E-16 |
| EPHB4 | Ephrin type-B receptor 4 | -0.0213 (-0.0278, -0.0141) | <2E-16 | 0.004 (-0.0021, 0.0114) | 0.24 |
| FABP3 | Fatty acid-binding protein, heart | -0.041 (-0.0526, -0.0299) | <2E-16 | 0.0011 (-0.0108, 0.0132) | 0.84 |
| CAPG | Macrophage-capping protein | -0.0371 (-0.049, -0.0271) | <2E-16 | -0.0095 (-0.0206, 0.0013) | 0.1 |
| SERPINF1 | Pigment epithelium-derived factor | -0.0139 (-0.0176, -0.0105) | <2E-16 | 0 (-0.004, 0.004) | 1 |
| NPDC1 | Neural proliferation differentiation and control protein 1 | -0.0224 (-0.0293, -0.0164) | <2E-16 | -0.0038 (-0.0111, 0.0023) | 0.4 |
| JTB | Protein JTB | -0.0153 (-0.0205, -0.0102) | <2E-16 | -0.0013 (-0.0074, 0.0042) | 0.62 |
| IGFBP4 | Insulin-like growth factor-binding protein 4 | -0.0218 (-0.0298, -0.0156) | <2E-16 | -0.0075 (-0.016, -0.0011) | 0.02 |
| EFNA2 | Ephrin-A2 | -0.0187 (-0.0256, -0.0125) | <2E-16 | 0.0079 (0.0009, 0.0141) | <2E-16 |
| TNFRSF21 | Tumor necrosis factor receptor superfamily member 21 | -0.0158 (-0.0211, -0.0103) | <2E-16 | -0.0001 (-0.0057, 0.0055) | 0.9 |
| PI3 | Elafin | -0.0348 (-0.0461, -0.0263) | <2E-16 | 0.0007 (-0.0105, 0.0099) | 0.96 |
| PCOLCE | Procollagen C-endopeptidase enhancer 1 | -0.022 (-0.03, -0.0153) | <2E-16 | -0.002 (-0.0102, 0.0052) | 0.62 |
| AIF1L | Allograft inflammatory factor 1-like | -0.0182 (-0.0246, -0.0117) | <2E-16 | 0.0065 (-0.0001, 0.0128) | 0.1 |
| ROR2 | Tyrosine-protein kinase transmembrane receptor ROR2 | -0.022 (-0.0291, -0.0144) | <2E-16 | 0.0084 (0.0008, 0.0171) | 0.04 |
| CPLX2 | Complexin-2 | -0.0258 (-0.0342, -0.0163) | <2E-16 | 0.0116 (0.0024, 0.0209) | 0.04 |
| DLK2 | Protein delta homolog 2 | -0.0242 (-0.0331, -0.0164) | <2E-16 | 0.0122 (0.0038, 0.0199) | <2E-16 |
| MXRA7 | Matrix-remodeling-associated protein 7 | -0.0212 (-0.0284, -0.0148) | <2E-16 | 0.0042 (-0.0026, 0.0113) | 0.28 |
| CD300A | CMRF35-like molecule 8 | -0.0252 (-0.032, -0.0185) | <2E-16 | -0.0029 (-0.0106, 0.0046) | 0.58 |
| CD300C | CMRF35-like molecule 6 | -0.0221 (-0.0266, -0.0156) | <2E-16 | -0.0077 (-0.0147, -0.0017) | <2E-16 |
| CLMP | CXADR-like membrane protein | -0.0262 (-0.033, -0.0189) | <2E-16 | 0.0043 (-0.0029, 0.0122) | 0.28 |
| LRP11 | Low-density lipoprotein receptor-related protein 11 | -0.0157 (-0.022, -0.0099) | <2E-16 | 0.0044 (-0.002, 0.0106) | 0.1 |
| IL15RA | Interleukin-15 receptor subunit alpha | -0.024 (-0.0307, -0.0157) | <2E-16 | 0.0037 (-0.0033, 0.0112) | 0.34 |
| MYL3 | Myosin light chain 3 | -0.0512 (-0.0687, -0.0354) | <2E-16 | -0.0048 (-0.0219, 0.0121) | 0.6 |
| IL18BP | Interleukin-18-binding protein | -0.0221 (-0.0301, -0.0135) | <2E-16 | -0.003 (-0.0103, 0.0058) | 0.46 |
| RNASE4 | Ribonuclease 4 | -0.0151 (-0.0202, -0.0101) | <2E-16 | 0.0063 (0.0003, 0.012) | 0.06 |
| DDOST | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit | -0.0177 (-0.0243, -0.0116) | <2E-16 | 0.0028 (-0.003, 0.0095) | 0.48 |
| VIT | Vitrin | -0.02 (-0.0278, -0.0132) | <2E-16 | 0.0062 (-0.0022, 0.0131) | 0.16 |
| TGFBR3 | Transforming growth factor beta receptor type 3 | -0.0148 (-0.0201, -0.0096) | <2E-16 | 0.0019 (-0.0035, 0.0076) | 0.5 |
| TNFRSF19 | Tumor necrosis factor receptor superfamily member 19 | -0.022 (-0.0296, -0.0146) | <2E-16 | 0.0117 (0.0046, 0.0196) | <2E-16 |
| SPON2 | Spondin-2 | -0.022 (-0.0292, -0.0146) | <2E-16 | 0.0039 (-0.0052, 0.0116) | 0.36 |
| CD93 | Complement component C1q receptor | -0.0161 (-0.022, -0.0108) | <2E-16 | -0.002 (-0.0081, 0.0043) | 0.56 |
| TREM1 | Triggering receptor expressed on myeloid cells 1 | -0.0234 (-0.0315, -0.0134) | <2E-16 | 0.0005 (-0.0092, 0.0111) | 0.9 |
| RETN | Resistin | -0.0245 (-0.0312, -0.0178) | <2E-16 | 0.0058 (-0.0016, 0.0136) | 0.14 |
| MANSC1 | MANSC domain-containing protein 1 | -0.0202 (-0.0278, -0.0134) | <2E-16 | -0.0031 (-0.0113, 0.004) | 0.48 |
| MAP2K2 | Dual specificity mitogen-activated protein kinase kinase 2 | -0.0294 (-0.0404, -0.0184) | <2E-16 | 0.0066 (-0.0052, 0.0183) | 0.32 |
| B4GALT1 | Beta-1,4-galactosyltransferase 1 | -0.0119 (-0.0164, -0.0073) | <2E-16 | 0.0047 (0.0003, 0.0099) | 0.06 |
| IGFLR1 | IGF-like family receptor 1 | -0.0284 (-0.0395, -0.0193) | <2E-16 | 0.0077 (-0.0039, 0.0176) | 0.22 |
| CPLX1 | Complexin-1 | -0.018 (-0.026, -0.0118) | <2E-16 | 0.007 (-0.0009, 0.0139) | 0.06 |
| PXDN | Peroxidasin homolog | -0.0466 (-0.0631, -0.0276) | <2E-16 | 0.002 (-0.0149, 0.0223) | 0.9 |
| EPHA1 | Ephrin type-A receptor 1 | -0.0301 (-0.0428, -0.0161) | <2E-16 | -0.001 (-0.0137, 0.0135) | 0.94 |
| ROR1 | Inactive tyrosine-protein kinase transmembrane receptor ROR1 | -0.0178 (-0.0246, -0.0099) | <2E-16 | 0.005 (-0.0023, 0.0133) | 0.18 |
| TMPO | Lamina-associated polypeptide 2, isoforms beta/gamma | -0.0257 (-0.0377, -0.0151) | <2E-16 | 0.0042 (-0.0061, 0.0138) | 0.44 |
| XXYLT1 | Xyloside xylosyltransferase 1 | -0.0157 (-0.0211, -0.0091) | <2E-16 | 0.0039 (-0.0033, 0.0111) | 0.26 |
| SRL | Sarcalumenin | -0.0217 (-0.0319, -0.0122) | <2E-16 | 0.0034 (-0.0068, 0.0119) | 0.54 |
| UNC5D | Netrin receptor UNC5D | -0.0211 (-0.0313, -0.012) | <2E-16 | 0.0128 (0.0027, 0.0229) | 0.02 |
| VASN | Vasorin | -0.0123 (-0.0167, -0.0072) | <2E-16 | 0.0028 (-0.0028, 0.0086) | 0.28 |
| SMOC1 | SPARC-related modular calcium-binding protein 1 | -0.0125 (-0.0175, -0.0078) | <2E-16 | 0.0032 (-0.0018, 0.0084) | 0.34 |
| EFEMP1 | EGF-containing fibulin-like extracellular matrix protein 1 | -0.014 (-0.0197, -0.009) | <2E-16 | 0.0009 (-0.0044, 0.0059) | 0.86 |
| IL2RB | Interleukin-2 receptor subunit beta | -0.0202 (-0.0281, -0.0111) | <2E-16 | 0.0016 (-0.0059, 0.0103) | 0.82 |
| DPY30 | Protein dpy-30 homolog | -0.023 (-0.034, -0.0124) | <2E-16 | 0.0037 (-0.0077, 0.0151) | 0.5 |
| PGRMC1 | Membrane-associated progesterone receptor component 1 | -0.0158 (-0.0227, -0.0093) | <2E-16 | 0.0013 (-0.0069, 0.0085) | 0.64 |
| SPINK7 | Serine protease inhibitor Kazal-type 7 | -0.0208 (-0.0307, -0.0116) | <2E-16 | 0.0106 (0.001, 0.0219) | 0.04 |
| AMBP | Alpha-1-microglobulin | -0.0151 (-0.0203, -0.0091) | <2E-16 | 0.0029 (-0.0026, 0.0085) | 0.36 |
| PENK | Proenkephalin-A | -0.0366 (-0.0486, -0.0242) | <2E-16 | -0.0061 (-0.0202, 0.0069) | 0.42 |
| CADM2 | Cell adhesion molecule 2 | -0.0151 (-0.0215, -0.0083) | <2E-16 | 0.0067 (0.0006, 0.0129) | 0.04 |
| NEGR1 | Neuronal growth regulator 1 | -0.0104 (-0.0152, -0.0056) | <2E-16 | 0.0006 (-0.0046, 0.0052) | 0.74 |
| EWSR1 | RNA-binding protein EWS | -0.0173 (-0.0243, -0.0094) | <2E-16 | 0.0045 (-0.0023, 0.0132) | 0.38 |
| CCL23 | C-C motif chemokine 23 | -0.0191 (-0.0275, -0.012) | <2E-16 | -0.0036 (-0.0134, 0.0039) | 0.48 |
| PSMB1 | Proteasome subunit beta type-1 | -0.0198 (-0.0274, -0.0101) | <2E-16 | 0.0064 (-0.0019, 0.0158) | 0.16 |
| APOF | Apolipoprotein F | -0.0312 (-0.0434, -0.018) | <2E-16 | 0.0131 (0.0003, 0.0268) | 0.02 |
| CCL23 | Ck-beta-8-1 | -0.0191 (-0.0294, -0.0108) | <2E-16 | 0.0019 (-0.0072, 0.011) | 0.74 |
| NMB | Neuromedin-B | -0.0147 (-0.0198, -0.0087) | <2E-16 | 0.0007 (-0.0063, 0.0065) | 0.8 |

**(B) LDPred PRS, eGFRcr measured at visit 5, and proteins measured at visit 5**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  |  | **Total Effects** | | **Average direct effects** | |
|  |  | **Beta (95% CI)** | **P** | **Beta (95% CI)** | **P** |
|  |  | **Positive total effect** | | | |
| SPOCK2 | Testican-2 | 0.0423 (0.0309, 0.0536) | <2E-16 | 0.0013 (-0.009, 0.0113) | 0.84 |
| PLG | Angiostatin | 0.017 (0.0101, 0.0235) | <2E-16 | 0.0027 (-0.0044, 0.009) | 0.44 |
| HPRT1 | Hypoxanthine-guanine phosphoribosyltransferase | 0.0225 (0.0149, 0.0331) | <2E-16 | 0.0018 (-0.0054, 0.0116) | 0.64 |
| CA10 | Carbonic anhydrase-related protein 10 | 0.0295 (0.0156, 0.0407) | <2E-16 | 0.007 (-0.0061, 0.0188) | 0.24 |
| KL | Klotho | 0.0424 (0.029, 0.0577) | <2E-16 | 0.0101 (-0.0052, 0.0272) | 0.24 |
|  |  | **Negative total effect** | | | |
| CST3 | Cystatin-C | -0.0568 (-0.0678, -0.0471) | <2E-16 | 0.0091 (0.0013, 0.0153) | 0.04 |
| COL15A1 | Collagen alpha-1(XV) chain | -0.0459 (-0.0567, -0.0364) | <2E-16 | 0.0027 (-0.0057, 0.0112) | 0.44 |
| RNASE1 | Ribonuclease pancreatic | -0.1013 (-0.1229, -0.0746) | <2E-16 | 0.0302 (0.0151, 0.0495) | <2E-16 |
| DSC2 | Desmocollin-2 | -0.0492 (-0.0613, -0.0379) | <2E-16 | 0.0087 (0.0012, 0.018) | 0.04 |
| COL6A3 | Collagen alpha-3(VI) chain | -0.0479 (-0.0558, -0.0365) | <2E-16 | 0.0083 (0.0004, 0.0167) | 0.04 |
| TMED10 | Transmembrane emp24 domain-containing protein 10 | -0.0598 (-0.0721, -0.0459) | <2E-16 | 0.0203 (0.0092, 0.0298) | <2E-16 |
| COL28A1 | Collagen alpha-1(XXVIII) chain | -0.0495 (-0.0619, -0.0365) | <2E-16 | 0.0081 (-0.002, 0.018) | 0.18 |
| CD59 | CD59 glycoprotein | -0.0447 (-0.0541, -0.0357) | <2E-16 | 0.0038 (-0.0044, 0.0113) | 0.44 |
| GM2A | Ganglioside GM2 activator | -0.0565 (-0.0693, -0.0456) | <2E-16 | 0.0077 (-0.0024, 0.0181) | 0.14 |
| CDNF | Cerebral dopamine neurotrophic factor | -0.042 (-0.05, -0.0347) | <2E-16 | 0.0041 (-0.0037, 0.013) | 0.44 |
| TNFRSF1A | Tumor necrosis factor receptor superfamily member 1A | -0.0586 (-0.0685, -0.0461) | <2E-16 | 0.0068 (-0.0034, 0.0181) | 0.16 |
| ART3 | Ecto-ADP-ribosyltransferase 3 | -0.0578 (-0.0708, -0.0439) | <2E-16 | -0.0028 (-0.015, 0.0089) | 0.76 |
| SELM | Selenoprotein M | -0.0454 (-0.0544, -0.0333) | <2E-16 | 0.0096 (-0.0002, 0.0172) | 0.06 |
| B2M | Beta-2-microglobulin | -0.0472 (-0.0587, -0.0377) | <2E-16 | 0.0181 (0.0098, 0.025) | <2E-16 |
| EFNB2 | Ephrin-B2 | -0.0481 (-0.0587, -0.0372) | <2E-16 | 0.0027 (-0.0073, 0.0122) | 0.58 |
| LMAN2 | Vesicular integral-membrane protein VIP36 | -0.0413 (-0.0525, -0.0297) | <2E-16 | 0.0099 (0.0017, 0.0194) | 0.04 |
| FSTL3 | Follistatin-related protein 3 | -0.0423 (-0.0517, -0.034) | <2E-16 | 0.006 (-0.0037, 0.0136) | 0.18 |
| FABP4 | Fatty acid-binding protein, adipocyte | -0.0536 (-0.0674, -0.0381) | <2E-16 | 0.0143 (0.0014, 0.0282) | 0.04 |
| SEPW1 | Selenoprotein W | -0.0305 (-0.0418, -0.0197) | <2E-16 | 0.0136 (0.0007, 0.0237) | 0.04 |
| HSPB6 | Heat shock protein beta-6 | -0.0481 (-0.0608, -0.0339) | <2E-16 | 0.0075 (-0.0054, 0.0207) | 0.28 |
| MB | Myoglobin | -0.0552 (-0.0674, -0.0403) | <2E-16 | -0.0008 (-0.0109, 0.0107) | 0.86 |
| MYOC | Myocilin | -0.0392 (-0.0487, -0.0272) | <2E-16 | 0.006 (-0.0064, 0.0166) | 0.26 |
| IGFBP6 | Insulin-like growth factor-binding protein 6 | -0.0287 (-0.0358, -0.0218) | <2E-16 | -0.0023 (-0.0096, 0.0052) | 0.7 |
| COL18A1 | Endostatin | -0.0354 (-0.0435, -0.0265) | <2E-16 | 0.0063 (-0.0017, 0.015) | 0.16 |
| TNFRSF1B | Tumor necrosis factor receptor superfamily member 1B | -0.0514 (-0.0612, -0.0403) | <2E-16 | 0.0077 (-0.0027, 0.0173) | 0.16 |
| RGMB | RGM domain family member B | -0.0306 (-0.0377, -0.0236) | <2E-16 | 0.0019 (-0.0053, 0.0079) | 0.5 |
| LCN2 | Neutrophil gelatinase-associated lipocalin | -0.0592 (-0.0732, -0.0476) | <2E-16 | -0.0001 (-0.013, 0.0118) | 1 |
| PTGDS | Prostaglandin-H2 D-isomerase | -0.0429 (-0.053, -0.0315) | <2E-16 | 0.016 (0.0066, 0.0267) | <2E-16 |
| CFD | Complement factor D | -0.0291 (-0.0385, -0.0222) | <2E-16 | -0.0011 (-0.0083, 0.0068) | 0.82 |
| PPIC | Peptidyl-prolyl cis-trans isomerase C | -0.0355 (-0.0437, -0.0269) | <2E-16 | 0.0056 (-0.0034, 0.0147) | 0.2 |
| SMOC2 | SPARC-related modular calcium-binding protein 2 | -0.0291 (-0.0401, -0.0169) | <2E-16 | 0.0099 (-0.0025, 0.0212) | 0.1 |
| NBL1 | Neuroblastoma suppressor of tumorigenicity 1 | -0.069 (-0.0858, -0.0549) | <2E-16 | 0.0277 (0.0126, 0.0383) | <2E-16 |
| MFAP2 | Microfibrillar-associated protein 2 | -0.0385 (-0.0497, -0.0282) | <2E-16 | 0.0002 (-0.0086, 0.009) | 0.98 |
| RNASE6 | Ribonuclease K6 | -0.0482 (-0.0654, -0.0302) | <2E-16 | 0.0171 (0.001, 0.0354) | 0.04 |
| CCL14 | C-C motif chemokine 14 | -0.0557 (-0.0733, -0.0359) | <2E-16 | 0.0111 (-0.0045, 0.0284) | 0.2 |
| ESAM | Endothelial cell-selective adhesion molecule | -0.033 (-0.0407, -0.0244) | <2E-16 | 0.003 (-0.0039, 0.0112) | 0.5 |
| DNAJB12 | DnaJ homolog subfamily B member 12 | -0.0394 (-0.0535, -0.0256) | <2E-16 | 0.0167 (0.0049, 0.0273) | <2E-16 |
| GABARAP | Gamma-aminobutyric acid receptor-associated protein | -0.0255 (-0.0315, -0.0184) | <2E-16 | 0.0075 (0.0012, 0.015) | 0.04 |
| UNC5B | Netrin receptor UNC5B | -0.0349 (-0.0471, -0.0259) | <2E-16 | 0.0076 (-0.0042, 0.0166) | 0.08 |
| WFDC1 | WAP four-disulfide core domain protein 1 | -0.0434 (-0.0544, -0.0292) | <2E-16 | 0.0104 (0.0007, 0.0216) | 0.04 |
| MIA | Melanoma-derived growth regulatory protein | -0.0258 (-0.0333, -0.0183) | <2E-16 | -0.0029 (-0.0105, 0.0047) | 0.56 |
| EFNA4 | Ephrin-A4 | -0.0336 (-0.0424, -0.0243) | <2E-16 | 0.0093 (0.0026, 0.0176) | <2E-16 |
| RARRES2 | Retinoic acid receptor responder protein 2 | -0.0285 (-0.0403, -0.0182) | <2E-16 | 0.014 (0.0039, 0.0227) | 0.02 |
| GAS1 | Growth arrest-specific protein 1 | -0.0323 (-0.0422, -0.0229) | <2E-16 | 0.0053 (-0.0045, 0.0129) | 0.3 |
| EFNA5 | Ephrin-A5 | -0.0345 (-0.0436, -0.0257) | <2E-16 | 0.0076 (-0.0008, 0.0152) | 0.1 |
| CRABP2 | Cellular retinoic acid-binding protein 2 | -0.0404 (-0.0508, -0.0239) | <2E-16 | 0.0083 (-0.0028, 0.0244) | 0.18 |
| UNC5C | Netrin receptor UNC5C | -0.0322 (-0.0404, -0.0218) | <2E-16 | -0.0006 (-0.0096, 0.0097) | 0.9 |
| JAM2 | Junctional adhesion molecule B | -0.0234 (-0.0314, -0.0148) | <2E-16 | 0.0065 (-0.001, 0.0145) | 0.1 |
| CD55 | Complement decay-accelerating factor | -0.033 (-0.0396, -0.0256) | <2E-16 | -0.0038 (-0.0116, 0.003) | 0.34 |
| EPHA2 | Ephrin type-A receptor 2 | -0.0435 (-0.0566, -0.031) | <2E-16 | 0.0043 (-0.0079, 0.0159) | 0.54 |
| ATOX1 | Copper transport protein ATOX1 | -0.038 (-0.0525, -0.0221) | <2E-16 | 0.0076 (-0.0057, 0.0215) | 0.36 |
| TAGLN | Transgelin | -0.0387 (-0.0502, -0.0264) | <2E-16 | 0.0172 (0.0057, 0.028) | <2E-16 |
| TWSG1 | Twisted gastrulation protein homolog 1 | -0.0288 (-0.0355, -0.0208) | <2E-16 | 0.0061 (0.0005, 0.013) | 0.04 |
| CA3 | Carbonic anhydrase 3 | -0.0501 (-0.0684, -0.0311) | <2E-16 | -0.0145 (-0.0319, 0.0052) | 0.2 |
| TNFRSF1B | Tumor necrosis factor receptor superfamily member 1B | -0.0521 (-0.0661, -0.0376) | <2E-16 | 0.0024 (-0.0092, 0.0176) | 0.72 |
| CALCOCO2 | Calcium-binding and coiled-coil domain-containing protein 2 | -0.0256 (-0.0324, -0.018) | <2E-16 | 0.0005 (-0.0068, 0.0077) | 0.94 |
| UNC5B | Netrin receptor UNC5B | -0.0317 (-0.0416, -0.0208) | <2E-16 | 0.0085 (-0.0006, 0.02) | 0.08 |
| VWC2 | Brorin | -0.0289 (-0.0382, -0.0203) | <2E-16 | 0.0098 (0.0011, 0.0206) | 0.04 |
| DLK1 | Protein delta homolog 1 | -0.0512 (-0.0694, -0.0306) | <2E-16 | -0.0008 (-0.0205, 0.0159) | 0.84 |
| SEMG2 | Protein delta homolog 1 | -0.0522 (-0.0708, -0.0336) | <2E-16 | -0.0003 (-0.0169, 0.0158) | 0.96 |
| CD46 | Membrane cofactor protein | -0.0292 (-0.0365, -0.0208) | <2E-16 | 0.0029 (-0.0046, 0.0106) | 0.54 |
| WFDC2 | WAP four-disulfide core domain protein 2 | -0.0374 (-0.0529, -0.0263) | <2E-16 | 0.0248 (0.014, 0.0353) | <2E-16 |
| EPHB6 | Ephrin type-B receptor 6 | -0.0283 (-0.036, -0.0202) | <2E-16 | 0.0059 (-0.0012, 0.0133) | 0.16 |
| DCLK1 | Serine/threonine-protein kinase DCLK1 | -0.0414 (-0.0568, -0.0303) | <2E-16 | 0.0048 (-0.0091, 0.0186) | 0.46 |
| ASGR1 | Asialoglycoprotein receptor 1 | -0.0306 (-0.0436, -0.0206) | <2E-16 | 0.0126 (-0.0001, 0.0229) | 0.08 |
| LRP10 | Low-density lipoprotein receptor-related protein 10 | -0.0254 (-0.0336, -0.0174) | <2E-16 | 0.0048 (-0.0025, 0.0112) | 0.3 |
| EPHB4 | Ephrin type-B receptor 4 | -0.0342 (-0.0437, -0.0245) | <2E-16 | 0.0024 (-0.0056, 0.0102) | 0.58 |
| FABP3 | Fatty acid-binding protein, heart | -0.043 (-0.0604, -0.0274) | <2E-16 | 0.0265 (0.0113, 0.0398) | <2E-16 |
| CAPG | Macrophage-capping protein | -0.0523 (-0.0662, -0.0405) | <2E-16 | -0.0032 (-0.0187, 0.0097) | 0.74 |
| SERPINF1 | Pigment epithelium-derived factor | -0.0185 (-0.0241, -0.0127) | <2E-16 | -0.0004 (-0.0062, 0.0047) | 0.88 |
| NPDC1 | Neural proliferation differentiation and control protein 1 | -0.0285 (-0.0383, -0.0181) | <2E-16 | 0.0143 (0.0053, 0.0247) | <2E-16 |
| JTB | Protein JTB | -0.0208 (-0.0278, -0.0134) | <2E-16 | 0.0043 (-0.0027, 0.0115) | 0.28 |
| IGFBP4 | Insulin-like growth factor-binding protein 4 | -0.0248 (-0.0332, -0.0159) | <2E-16 | 0.0044 (-0.0046, 0.0131) | 0.34 |
| EFNA2 | Ephrin-A2 | -0.0279 (-0.0341, -0.0201) | <2E-16 | 0.0131 (0.0067, 0.0218) | <2E-16 |
| TNFRSF21 | Tumor necrosis factor receptor superfamily member 21 | -0.0284 (-0.0368, -0.0214) | <2E-16 | -0.0016 (-0.0097, 0.004) | 0.64 |
| PI3 | Elafin | -0.0499 (-0.0688, -0.0296) | <2E-16 | 0.0184 (-0.0017, 0.0375) | 0.1 |
| PCOLCE | Procollagen C-endopeptidase enhancer 1 | -0.0348 (-0.0455, -0.0201) | <2E-16 | 0.0004 (-0.0112, 0.0142) | 0.98 |
| AIF1L | Allograft inflammatory factor 1-like | -0.0247 (-0.0328, -0.0166) | <2E-16 | 0.0099 (0.0011, 0.0179) | 0.02 |
| ROR2 | Tyrosine-protein kinase transmembrane receptor ROR2 | -0.0471 (-0.0593, -0.0339) | <2E-16 | 0.0068 (-0.0054, 0.0184) | 0.26 |
| CPLX2 | Complexin-2 | -0.0352 (-0.0508, -0.0182) | <2E-16 | 0.0248 (0.0105, 0.0377) | <2E-16 |
| DLK2 | Protein delta homolog 2 | -0.037 (-0.0478, -0.0237) | <2E-16 | 0.0155 (0.0018, 0.0288) | 0.02 |
| MXRA7 | Matrix-remodeling-associated protein 7 | -0.0379 (-0.0496, -0.0258) | <2E-16 | 0.0122 (0.0015, 0.0251) | 0.04 |
| CD300A | CMRF35-like molecule 8 | -0.0316 (-0.0442, -0.0182) | <2E-16 | 0.0076 (-0.0062, 0.0194) | 0.32 |
| CD300C | CMRF35-like molecule 6 | -0.0387 (-0.049, -0.0268) | <2E-16 | -0.0026 (-0.0117, 0.0075) | 0.6 |
| CLMP | CXADR-like membrane protein | -0.0368 (-0.0526, -0.0227) | <2E-16 | 0.0153 (0.0038, 0.0262) | 0.02 |
| LRP11 | Low-density lipoprotein receptor-related protein 11 | -0.0227 (-0.032, -0.014) | <2E-16 | 0.0143 (0.0062, 0.0228) | <2E-16 |
| IL15RA | Interleukin-15 receptor subunit alpha | -0.0431 (-0.0558, -0.0291) | <2E-16 | 0.0009 (-0.0126, 0.0128) | 0.86 |
| MYL3 | Myosin light chain 3 | -0.0752 (-0.1127, -0.0504) | <2E-16 | -0.0148 (-0.0546, 0.014) | 0.34 |
| IL18BP | Interleukin-18-binding protein | -0.0316 (-0.0434, -0.0198) | <2E-16 | -0.0009 (-0.0121, 0.0099) | 0.86 |
| RNASE4 | Ribonuclease 4 | -0.02 (-0.0282, -0.0123) | <2E-16 | 0.0117 (0.0042, 0.0201) | <2E-16 |
| DDOST | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit | -0.0299 (-0.0407, -0.0185) | <2E-16 | 0.0017 (-0.0088, 0.0112) | 0.74 |
| VIT | Vitrin | -0.0304 (-0.0402, -0.0199) | <2E-16 | 0.0046 (-0.0057, 0.0139) | 0.46 |
| TGFBR3 | Transforming growth factor beta receptor type 3 | -0.0225 (-0.0314, -0.0133) | <2E-16 | -0.0047 (-0.0131, 0.0039) | 0.24 |
| TNFRSF19 | Tumor necrosis factor receptor superfamily member 19 | -0.0433 (-0.0577, -0.0318) | <2E-16 | 0.0117 (-0.0003, 0.0261) | 0.06 |
| SPON2 | Spondin-2 | -0.0355 (-0.0454, -0.026) | <2E-16 | 0.0049 (-0.0047, 0.0147) | 0.36 |
| CD93 | Complement component C1q receptor | -0.0236 (-0.0338, -0.0163) | <2E-16 | -0.0018 (-0.0117, 0.0056) | 0.76 |
| TREM1 | Triggering receptor expressed on myeloid cells 1 | -0.0462 (-0.0568, -0.0341) | <2E-16 | -0.0041 (-0.0149, 0.0079) | 0.5 |
| RETN | Resistin | -0.0491 (-0.0602, -0.038) | <2E-16 | -0.014 (-0.0256, -0.0015) | 0.04 |
| MANSC1 | MANSC domain-containing protein 1 | -0.0332 (-0.0431, -0.0212) | <2E-16 | -0.0048 (-0.0142, 0.0056) | 0.34 |
| MAP2K2 | Dual specificity mitogen-activated protein kinase kinase 2 | -0.047 (-0.0619, -0.0313) | <2E-16 | 0.0034 (-0.0116, 0.0175) | 0.68 |
| B4GALT1 | Beta-1,4-galactosyltransferase 1 | -0.0239 (-0.03, -0.018) | <2E-16 | 0.0012 (-0.0044, 0.0067) | 0.8 |
| IGFLR1 | IGF-like family receptor 1 | -0.043 (-0.0601, -0.0265) | <2E-16 | 0.0198 (0.0064, 0.0351) | 0.02 |
| CPLX1 | Complexin-1 | -0.027 (-0.0379, -0.0166) | <2E-16 | 0.0176 (0.0056, 0.0268) | <2E-16 |
| PXDN | Peroxidasin homolog | -0.0893 (-0.1092, -0.0687) | <2E-16 | 0.0219 (0.0061, 0.0386) | <2E-16 |
| EPHA1 | Ephrin type-A receptor 1 | -0.0427 (-0.0557, -0.0307) | <2E-16 | -0.0056 (-0.018, 0.0089) | 0.34 |
| ROR1 | Inactive tyrosine-protein kinase transmembrane receptor ROR1 | -0.0239 (-0.0343, -0.0148) | <2E-16 | 0.0013 (-0.0095, 0.0114) | 0.84 |
| TMPO | Lamina-associated polypeptide 2, isoforms beta/gamma | -0.0438 (-0.0581, -0.0289) | <2E-16 | 0.0032 (-0.01, 0.0168) | 0.74 |
| XXYLT1 | Xyloside xylosyltransferase 1 | -0.0293 (-0.0376, -0.0174) | <2E-16 | -0.0048 (-0.0129, 0.0059) | 0.36 |
| SRL | Sarcalumenin | -0.0417 (-0.0564, -0.0294) | <2E-16 | 0.0049 (-0.0065, 0.0156) | 0.36 |
| UNC5D | Netrin receptor UNC5D | -0.0317 (-0.0438, -0.0194) | <2E-16 | 0.0117 (0.001, 0.023) | 0.02 |
| VASN | Vasorin | -0.0199 (-0.0263, -0.0142) | <2E-16 | -0.0002 (-0.0073, 0.0062) | 0.94 |
| SMOC1 | SPARC-related modular calcium-binding protein 1 | -0.0256 (-0.0363, -0.0162) | <2E-16 | 0.0068 (-0.0028, 0.0158) | 0.18 |
| EFEMP1 | EGF-containing fibulin-like extracellular matrix protein 1 | -0.0243 (-0.0314, -0.0167) | <2E-16 | 0.0036 (-0.0051, 0.0114) | 0.38 |
| IL2RB | Interleukin-2 receptor subunit beta | -0.0407 (-0.0542, -0.0271) | <2E-16 | -0.007 (-0.0203, 0.0064) | 0.26 |
| DPY30 | Protein dpy-30 homolog | -0.0349 (-0.0471, -0.0218) | <2E-16 | 0.0088 (-0.0034, 0.0213) | 0.16 |
| PGRMC1 | Membrane-associated progesterone receptor component 1 | -0.0233 (-0.0328, -0.0133) | <2E-16 | 0.0091 (-0.0005, 0.0183) | 0.08 |
| SPINK7 | Serine protease inhibitor Kazal-type 7 | -0.0326 (-0.0482, -0.0198) | <2E-16 | 0.0139 (0.001, 0.0265) | 0.04 |
| AMBP | Alpha-1-microglobulin | -0.0224 (-0.03, -0.0152) | <2E-16 | 0.0052 (-0.0008, 0.0119) | 0.18 |
| PENK | Proenkephalin-A | -0.0457 (-0.0613, -0.0316) | <2E-16 | -0.0067 (-0.0253, 0.0066) | 0.36 |
| CADM2 | Cell adhesion molecule 2 | -0.031 (-0.0416, -0.0215) | <2E-16 | 0.0007 (-0.0092, 0.0107) | 0.88 |
| NEGR1 | Neuronal growth regulator 1 | -0.0183 (-0.0257, -0.0117) | <2E-16 | -0.0021 (-0.0104, 0.0056) | 0.58 |
| EWSR1 | RNA-binding protein EWS | -0.0328 (-0.0436, -0.0216) | <2E-16 | -0.0012 (-0.0111, 0.0092) | 0.88 |
| CCL23 | C-C motif chemokine 23 | -0.0308 (-0.0452, -0.0175) | <2E-16 | -0.0027 (-0.0164, 0.0091) | 0.68 |
| PSMB1 | Proteasome subunit beta type-1 | -0.0279 (-0.04, -0.0182) | <2E-16 | 0.0101 (-0.003, 0.0203) | 0.12 |
| APOF | Apolipoprotein F | -0.0518 (-0.0672, -0.0353) | <2E-16 | 0.0134 (-0.0031, 0.028) | 0.14 |
| CCL23 | Ck-beta-8-1 | -0.0308 (-0.0442, -0.0198) | <2E-16 | -0.0056 (-0.0162, 0.0052) | 0.38 |
| NMB | Neuromedin-B | -0.0345 (-0.0479, -0.0228) | <2E-16 | -0.0006 (-0.0136, 0.0117) | 0.86 |

a Proteins were identified through linear regression of LDPred PRS for kidney function on 4,877 proteins measured at visit 3 and visit 5 with adjusting for age at the corresponded visits, sex, center, and first 10 genetic principal components. A total of 132 proteins were significantly associated with LDPred PRS at both visit 3 and visit 5. The threshold of significance was Bonferroni corrected: p = 1.02 × 10-5. Visit 3 was conducted during 1993-1995 when the mean age of study population was 60.4 years and visit 5 was conducted during 2011-2013 when the mean age of study population was 75.9 years.

b Causal mediation effects of eGFRcr on the association between PRS and proteins were evaluated using the ‘mediation’ R package and with adjusting for age, sex, center, and first 10 genetic PCs. The simulation type was the quasi-Bayesian Monte Carlo method based on normal approximation and the number of simulation was 100. Total effects without considering the mediation effects of eGFRcr and average direct effects with considering the mediation effects were presented.

eGFRcr: estimated glomerular filtration rate based on creatinine; PRS: polygenic risk score

**Supplemental Figure 1. Flow chart of subjects included in the study.**

N=7,213

Study population for evaluating the association between PRS and proteomic measurements

N= 11,478

15,792 participants enrolled in the ARIC at baseline in 1987-1989

N= 8,886

Study population for evaluating the associations of PRS with estimated glomerular filtration rate (eGFR) and kidney diseases

Exclusion: 459 participants who were one of the close relative pairs (determined by the proportion of their genomes identical-by-state (IBS)).

Exclusion: 2,133 participants who did not have valid genetic information for creating polygenic risk scores (PRS).

N= 9,345

Exclusion: 4,314 participants whose self-reported race groups were not White

Exclusion: 1,673 participants without proteomic data at visit 3measurements.

|  |  |  |
| --- | --- | --- |
| **P + T PRS**a **vs. LDPred PRS**a | **Top SNPs PRS**a **vs. LDPred PRS** | **Top SNPs PRS vs. P + T PRS** |
|  |  |  |

# **Supplemental Figure 2.** **Scatter plots of polygenic risk scores (PRS) with locally weighted smoothing (LOESS) regression line.**

LDPred PRS was constructed using LDPred algorithm, a Bayesian approach utilizes GWAS summary statistics to compute the posterior mean effect sizes for the genetic variants by assuming a prior of the joint effect sizes and incorporating the LD structure of the reference population. P+T PRS was constructed using ‘pruning and thresholding (P+T)’, which first prunes variants to only keep those who have absolute pairwise correlation weaker than a threshold within certain genetic distance and then filtered variants that have a P value larger than a pre-defined threshold of significance. Top SNPs score was constructed using the most commonly used level of absolute pairwise correlation for pruning and genome-wide significance level for thresholding.



**Supplemental Figure 3.** **10-fold cross validation** **Area under the curve (AUC) performances for predicting incident CKD for each of the seven models.** Models incorporating PRS are shown as solid lines. Green line indicate only with PRS; orange lines indicate modifiable covariates (education, baseline BMI, baseline smoking status, baseline history of hypertension) with or without PRS; purple lines indicate all covariates (modifiable covariates plus age, sex, center, and baseline history of diabetes, and CHD) with or without PRS; pink lines indicate all covariates plus eGFR with or without PRS. BMI: body mass index; CHD: coronary heart disease; CKD: chronic kidney disease; eGFR: estimated glomerular filtration rate; PRS: LDPred polygenic risk score.

Chart, scatter chart

Description automatically generated

# **Supplemental Figure 4. Population substructure shown by the first two principal components of genetic ancestry among participants included in the UK Biobank GWAS.** A total of 406,350 multi-ethnic participants was included for the GWAS, including 390,694 EUR, 6,406 AFR, 7,979 SAS, 1,271 EAS participants. Race was self-reported. EUR: British, Irish, White, Any other white background; AFR: African, Caribbean, Any other Black background, Black or Black British; SAS: Indian, Pakistani, Bangladeshi, Asian or Asian British, Any other Asian background; EAS: Chinese.



# **Supplemental Figure 5. Quantile–quantile plots for the meta-analysis of UK Biobank and CKDGen GWAS.**

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