Supplementary Table 1 Exposures source and description

Phenotype	Sample size	GWAS ID
bNGF	3531	ebi-a-GCST004421
CTACK	3631	ebi-a-GCST004420
Eotaxin	8153	ebi-a-GCST004460
FGFBasic	7565	ebi-a-GCST004459
GCSF	7904	ebi-a-GCST004458
GROa	3505	ebi-a-GCST004457
HGF	8292	ebi-a-GCST004449
IFNg	7701	ebi-a-GCST004456
IL-10	7681	ebi-a-GCST004444
IL-12p70	8270	ebi-a-GCST004439
IL-13	3557	ebi-a-GCST004443
IL-16	3483	ebi-a-GCST004430
IL-17	7760	ebi-a-GCST004442
IL-18	3636	ebi-a-GCST004441
IL-1b	3309	ebi-a-GCST004448
IL1ra	3638	ebi-a-GCST004447
IL-2	3475	ebi-a-GCST004455
IL2ra	3677	ebi-a-GCST004454
IL-4	8124	ebi-a-GCST004453
IL-5	3364	ebi-a-GCST004452
IL-6	8189	ebi-a-GCST004446
IL-7	3409	ebi-a-GCST004451
IL-8	3526	ebi-a-GCST004445
IL-9	3634	ebi-a-GCST004450
IP10	3685	ebi-a-GCST004440
MCP1	8293	ebi-a-GCST004438
MCP3	843	ebi-a-GCST004437
MCSF	840	ebi-a-GCST004436
MIF	3494	ebi-a-GCST004423
MIG	3685	ebi-a-GCST004435
MIP1a	3522	ebi-a-GCST004434
MIP1b	8243	ebi-a-GCST004433
PDGFbb	8293	ebi-a-GCST004432
RANTES	3421	ebi-a-GCST004431
SCF	8290	ebi-a-GCST004429
SCGFb	3682	ebi-a-GCST004428
SDF1a	5998	ebi-a-GCST004427
TNFa	3454	ebi-a-GCST004426
TNFb	1559	ebi-a-GCST004425
TRAIL	8186	ebi-a-GCST004424
VEGF	7118	ebi-a-GCST004422

ALM, appendicular lean mass; Hand grip strength, HGS;EWGSOP, European Working Group on Sarcopenia in Older People.
BDNF, brain-derived neurotrophic factor;
bNGF, beta-nerve growth factor;
CNTF, ciliary neurotrophic factor;
CTACK, cutaneous T-cell attracting chemokine;
FGFBasic, fibroblast growth factor basic;
GCSF, granulocyte colony-stimulating factor;
GROa, growth-regulated-alpha;
HGF, hepatocyte growth factor;
IFNb, interferon-beta;
IFNg, interferon-gamma;
IGF1, insulin-like growth factor 1;
IL, interleukin;
IP10, interferon gamma-induced protein 10;
LIF, leukemia inhibitory factor;
MCP1, monocyte chemoattractant protein-1;
MCP3, monocyte-specific chemokine 3;
MCSF1, Macrophage colony-stimulating factor 1;
MIF, macrophage migration inhibitory factor;
MIG, monokine induced by interferon gamma;
MIP1a, macrophage inflammatory protein-1a;
MIP1b, macrophage inflammatory protein-1b;
PDGFB, platelet-derived growth factor subunit A
PDGFB, platelet-derived growth factor subunit B
PDGFbb, platelet-derived growth factor BB;
RANTES, regulated upon activation normal T cell expressed and presumably secreted;
SCF, stem cell factor;
SCGFb, stem cell growth factor beta;
SDF1, stromal cell-derived factor-1
TNFa, tumor necrosis factor alpha;
TNFb, tumor necrosis factor beta;
TRAIL, TNF-related apoptosis inducing ligand;
VEGF, vascular endothelial growth factor;
VEGFD, vascular endothelial growth factor D

Supplementary Table 2 MR analysis of association between inflammatory factors and risk of diabetic nephropathy.

Phenotype	nSNPs	MR-PRESSO				IVW				
		OR	95%CI	p_val	P_p_val	OR	95%CI	p_val	Q	Q_p_val
bNGF	7	0.92	0.75-1.12	0.457	0.17	0.92	0.78-1.08	0.315	9.595	0.142
CTACK	9	1.07	0.94-1.21	0.297	0.351	1.07	0.95-1.20	0.227	9.386	0.311
Eotaxin	16	1.04	0.91-1.19	0.545	0.278	1.04	0.92-1.18	0.488	8.828	0.221
FGFBasic	5	1.13	0.84-1.50	0.451	0.438	1.13	0.85-1.49	0.389	4.246	0.373
GCSF	8	1.03	0.85-1.25	0.718	0.548	1.03	0.84-1.27	0.725	6.110	0.526
GROa	10	1.02	0.96-1.08	0.514	0.836	1.02	0.94-1.10	0.613	5.011	0.833
HGF	7	0.94	0.76-1.16	0.608	0.489	0.94	0.76-1.17	0.607	5.433	0.489
IFNg	9	1.33	1.18-1.51	0.002	0.944	1.33	1.09-1.63	5.00E-03	2.952	0.937
IL-10	10	0.89	0.76-1.04	0.188	0.295	0.89	0.78-1.02	0.101	11.922	0.217
IL-12p70	10	0.94	0.85-1.05	0.332	0.69	0.94	0.84-1.05	0.34	7.825	0.551
IL-13	9	0.96	0.89-1.05	0.443	0.749	0.96	0.88-1.06	0.501	5.578	0.694
IL-16	10	0.89	0.80-1.01	0.104	0.3	0.89	0.81-0.99	0.043	11.222	0.26
IL-17	10	1.04	0.89-1.21	0.611	0.689	1.04	0.87-1.23	0.642	6.967	0.64
IL-18	15	0.96	0.89-1.03	0.281	0.884	0.96	0.88-1.05	0.395	8.028	0.887
IL-1b	5	0.86	0.69-1.06	0.245	0.544	0.86	0.69-1.06	0.172	4.032	0.401
IL1ra	6	0.88	0.75-1.03	0.182	0.56	0.88	0.73-1.05	0.171	3.909	0.562
IL-2	9	1.07	0.91-1.26	0.401	0.319	1.07	0.93-1.24	0.302	17.733	0.023
IL2ra	6	1.03	0.94-1.13	0.491	0.736	1.03	0.91-1.16	0.583	2.721	0.742
IL-4	9	0.96	0.77-1.20	0.772	0.33	0.96	0.78-1.18	0.747	9.253	0.321
IL-5	5	0.95	0.80-1.13	0.636	0.495	0.95	0.80-1.13	0.609	4.003	0.405
IL-6	5	0.98	0.82-1.18	0.906	0.776	0.98	0.75-1.28	0.932	1.861	0.761
IL-7	9	1.01	0.89-1.13	0.892	0.357	1.01	0.90-1.11	0.877	9.691	0.287
IL-8	4	1.02	0.91-1.15	0.645	0.834	1.02	0.82-1.27	0.791	0.816	0.845
IL-9	6	0.98	0.83-1.17	0.901	0.508	0.98	0.82-1.18	0.901	4.491	0.481
IP10	10	0.93	0.86-0.86	0.157	0.948	0.93	0.82-1.06	0.334	3.529	0.529
MCP1	14	1.07	0.96-1.19	0.208	0.83	1.07	0.94-1.22	0.281	8.651	0.798
MCP3	3	NA	NA	NA	NA	1.08	0.94-1.25	0.241	3.396	3.396
MCSF	8	0.99	0.83-1.18	0.961	0.188	0.96	0.86-1.07	0.515	17.347	0.015
MIF	6	1.07	1.00-1.13	0.051	0.995	1.07	0.90-1.26	0.397	0.547	0.991
MIG	13	0.98	0.87-1.10	0.796	0.42	0.98	0.87-1.10	0.787	32.349	0.002
MIP1a	7	1.07	0.95-1.20	0.278	0.83	1.07	0.91-1.26	0.401	2.986	0.81
MIP1b	17	0.92	0.86-0.98	0.026	0.699	0.92	0.85-0.98	0.022	13.859	0.609
PDGFbb	11	0.94	0.83-1.06	0.104	0.652	0.94	0.82-1.07	0.382	25.622	0.012
RANTES	9	0.99	0.85-1.16	0.973	0.287	0.99	0.86-1.14	0.969	9.835	0.276
SCF	9	1.25	1.12-1.39	0.004	0.966	1.25	1.02-1.52	2.70E-02	2.539	0.959
SCGFb	14	1.02	0.92-1.14	0.607	0.204	1.02	0.93-1.13	0.542	17.381	0.182
SDF1a	9	1.26	0.96-1.64	0.127	0.249	1.26	0.99-1.59	0.051	10.501	0.231

TNFa	3	NA	NA	NA	NA	1.05	0.82-1.36	0.649	12.54	0.013
TNFb	4	1.02	0.86-1.21	0.785	0.262	1.02	0.90-1.15	0.677	5.868	0.118
TRAIL	15	0.98	0.88-1.09	0.771	0.123	0.98	0.90-1.07	0.719	20.559	0.113
VEGF	10	0.98	0.91-1.07	0.809	0.544	0.98	0.90-1.08	0.818	7.716	0.562

P_p_val : MR-PRESSO global test; Q_p_val: Cochran’s Q-test.