

ESM Table 1. Power calculation for the MR analysis. The R^2 is the protein level variance explained by the lead SNP. The power for the MR-analysis was calculated by the free software (<https://sb452.shinyapps.io/power/>) for an odds ratio of 1.1 (or 0.9) using the study by Xue et al (21) with 62,892 T2D cases and 596,424 control persons and a significance level of $p=0.05$.

Gene	SNP rs-number	R^2	Power
EpiHealth GWAS (SNP-exposure associations)			
CCL16	rs11080369	0.205	100
CTSD	rs7122341	0.046	100
IDUA	rs3796622	0.291	100
IL-1Ra	rs4251961	0.027	96
LPL	rs325	0.054	100
TIM-1	rs6878069	0.213	100
VSIG2	rs11219769	0.029	97
GDF15	rs1227731	0.052	100
IL1RT1	rs1024794	0.0192	89
PON3	rs10487132	0.062	100
Previously published GWAS (SNP-exposure associations)			
CTSD	rs55861089	0.054	100
SELPLG	rs73191242	0.013	75
IDUA	rs3822020	0.220	100
CATZ	rs199825459	0.092	100

ENPP7	rs11871061	0.426	100
GDF15	rs45543339	0.102	100
IL-1Ra	rs6761276	0.027	96
TIM-1	rs6889164	0.059	100
Siglec-7	rs140185670	0.043	100

ESM Table 2. Odds ratio (OR), 95% confidence interval (CI) and p-value for the 29 proteins associated with prevalent diabetes in the validation analysis of the observational study in EpiHealth following adjustment for diabetes medication. Only the proteins with a false discovery rate (FDR) <5% in the validation step were included in the table.

Protein	Short name	OR	Lower 95%CI limit	Higher 95%CI limit	p-value
Cathepsin D	CTSD	1.79	1.38	2.32	9.56e-06
Hydroxyacid oxidase 1	HAOX1	1.69	1.28	2.24	0.0002564
Galectin-4	Gal-4	1.69	1.28	2.25	0.0002575
Lipoprotein lipase	LPL	0.55	0.4	0.77	0.0005328
Interleukin-1 receptor	IL-1ra	1.75	1.27	2.42	0.0006643

antagonist protein					
Gastric intrinsic factor	GIF	1.73	1.26	2.38	0.000752
Sialic acid-binding Ig-like lectin 7	SIGLEC7	1.64	1.22	2.21	0.0011108
Plasminogen activator inhibitor 1	PAI	1.65	1.22	2.24	0.0013094
Cathepsin Z	CTSZ	1.63	1.2	2.23	0.0018956
Cadherin-2	CDH2	1.56	1.16	2.11	0.0033674
Insulin-like Growth Factor-	IGFBP-2	0.64	0.47	0.88	0.0052053

Binding Protein 2					
Paraoxonase (PON 3)	PON3	0.66	0.49	0.9	0.008036
Tissue-type plasminogen activator	t-PA	1.63	1.13	2.35	0.0087763
Prostasin	PRSS8	1.52	1.07	2.14	0.0179974
P-selectin glycoprotein ligand 1	PSGL-1	1.49	1.07	2.07	0.0190852
Nodal modulator 1	NOMO1	1.4	1.05	1.88	0.0237439

ESM Table 3. Odds ratio (OR), 95% confidence interval (CI) and p-value for the 29 proteins associated with prevalent diabetes in the validation analysis in the main analysis. In this additional analysis, subjects with diabetic medication (n=67) were excluded. See table 2 for the abbreviations of the proteins. The proteins are given in same order as in table 2.

Protein	OR	Lower 95%CI limit	Higher 95%CI limit	p-value
CTSD	1.61	1.18	2.20	0.002
ALDH1A1	1.40	1.01	1.95	0.041
IDUA	1.97	1.28	3.03	0.002
HAO1	1.43	0.99	2.06	0.055
Gal-4	1.16	0.82	1.62	0.399
GDF-15	1.05	0.69	1.60	0.821
LPL	0.73	0.47	1.13	0.159
IL-1ra	1.34	0.91	1.98	0.139
CTSO	1.08	0.75	1.56	0.687
SIGLEC7	1.25	0.86	1.82	0.249
PAI-1	1.92	1.31	2.84	9.2e-04
CCL16	1.92	1.15	3.21	0.012
SELE	1.57	1.03	2.40	0.036
CTSZ	1.49	1.02	2.18	0.040
ACE2	1.32	0.93	1.89	0.118
VSIG2	1.31	0.90	1.90	0.159

ENPP7	1.50	1.04	2.17	0.030
TR-AP	1.53	1.04	2.24	0.031
CDH2	1.25	0.85	1.85	0.252
IGFBP-2	0.65	0.43	0.96	0.030
FABP4	1.40	0.89	2.20	0.149
DDC	1.21	0.83	1.77	0.320
PON3	0.79	0.53	1.17	0.240
IL-1RT1	1.26	0.86	1.86	0.235
t-PA	2.50	1.51	4.16	3.8e-04
KIM-1	1.18	0.77	1.79	0.446
PRSS8	1.45	0.95	2.20	0.083
PSGL-1	1.24	0.83	1.85	0.295
NOMO1	0.96	0.66	1.38	0.808

ESM Table 4. Genotypes used as instrumental variables for all proteins where single nucleotide variants located within the respective protein's gene with genome-wide significant association ($P < 5 \times 10^{-8}$) with protein levels could be identified in EpiHealth and/or literature review. For protein abbreviations, see table 2.

Protein	Original SNP	Proxy/availability	Effect allele	Other allele	beta	SE	p-value
EpiHealth GWAS (SNP-exposure associations)							
CCL16	rs11080369	NA	C	A	-1.27	0.05	3.27e-98
CTSD	rs7122341	NA	C	T	-0.33	0.03	4.93e-18
IDUA	rs3796622	NA	C	T	0.64	0.02	1.84e-97
IL-1Ra	rs4251961	NA	C	T	-0.25	0.03	1.68e-15
LPL	rs325	NA	C	T	-0.60	0.05	2.84e-32
TIM-1	rs6878069	NA	G	A	-0.52	0.02	3.72e-74
VSIG2	rs11219769	NA	T	G	0.26	0.03	4.13e-15
GDF15	rs1227731	NA	A	G	0.47	0.04	1.97e-25
IL1RT1	rs1024794	NA	G	A	0.21	0.03	1.14e-12

PON3	rs10487132	NA	G	A	0.36	0.028	1.53e-34
Previously published GWAS (SNP-exposure associations)							
CTSD	rs55861089	rs72850969 (only T2D)	A	G	0.41	0.03	8.0e-26
SELPLG	rs73191242	rs8179151 (only T2D)	G	A	0.20	0.03	2.0e-12
IDUA	rs3822020	rs3796622 (only FG, HOMA-IR)	G	A	0.61	0.02	7.2e-148
CATZ	rs199825459	NA	G	A	2.20	0.12	2.6e-76
ENPP7	rs11871061	available for FG, HOMA-IR, no proxy in T2D	C	T	0.99	0.02	4.9e-531
GDF15	rs45543339	rs16982345 (only FG, HOMA-IR)	T	C	0.58	0.03	1.4e-99
IL-1Ra	rs6761276	available for FG, HOMA-IR, T2D	C	T	-0.19	0.02	1.5e-14
TIM-1	rs6889164	available for FG, HOMA-IR, T2D	C	T	-0.43	0.03	2.5e-59
Siglec-7	rs140185670	NA	C	G	-0.61	0.05	1.7e-36

ESM Table 5. Mendelian randomization analysis regarding causal effects of proteins on diabetes and two other related traits, fasting glucose and the HOMA insulin resistance index. In the upper part of the table are proteins for which a significant instrumental variable (IV) was found in EpiHealth given. In the lower part, IVs from the literature were used. FG= fasting glucose, HOMA= HOMA insulin resistance index, T2D= type 2 diabetes. For protein abbreviations, see table 2.

Exposure	Outcome	IV estimate	SE	P-value
EpiHealth GWAS (SNP-exposure associations)				
	FG	-0.001	0.003	6.9E-01
CCL16	HOMA	0.005	0.006	4.6E-01
	T2D	-0.012	0.015	4.2E-01
CTSD	T2D	-0.012	0.029	6.8E-01
	FG	0.005	0.006	4.0E-01
IDUA	HOMA	0.000	0.007	9.8E-01
	FG	0.018	0.013	1.6E-01
IL1RA	HOMA	-0.004	0.017	8.1E-01
	T2D	0.004	0.030	8.9E-01
	FG	0.014	0.008	1.1E-01
LPL	HOMA	0.022	0.011	4.6E-02
	T2D	0.100	0.020	6.5E-07
	FG	-0.005	0.006	3.7E-01
TIM-1	HOMA	-0.010	0.007	1.8E-01
	T2D	0.024	0.015	1.2E-01
	FG	0.013	0.013	3.3E-01
VSIG2	HOMA	-0.004	0.017	8.1E-01
	T2D	0.007	0.034	8.5E-01
	FG	0.001	0.010	9.3E-01
GDF15	HOMA	0.009	0.013	5.1E-01
	FG	0.007	0.015	6.4E-01
IL1RT1	HOMA	-0.006	0.019	7.4E-01
	T2D	-0.030	0.038	4.4E-01
PON3	FG	0.014	0.009	1.2E-01

HOMA	0.001	0.012	9.2E-01
T2D	-0.020	0.022	3.6E-01

Previously published GWAS (SNP-exposure associations)

IDUA	FG	0.005	0.006	4.0E-01
	HOMA	-1.6E-04	0.008	9.8E-01
IL1ra	FG	0.006	0.016	7.0E-01
	HOMA	-0.006	0.022	7.9E-01
	T2D	-0.015	0.043	7.3E-01
GDF15	FG	-0.016	0.007	2.3E-02
	HOMA	0.001	0.010	9.1E-01
ENPP7	FG	0.003	0.004	4.8E-01
	HOMA	0.010	0.008	2.1E-01
TIM-1	FG	-0.041	0.024	8.3E-02
	HOMA	0.002	0.031	9.5E-01
	T2D	0.101	0.057	7.3E-02
CTSD	T2D	-0.031	0.034	3.6E-01
SELPLG	T2D	0.060	0.048	2.1E-01

ESM Table 6. Mendelian randomization analyses regarding the causal effect of three glucose-related traits, diabetes (T2D), fasting glucose (FG), and insulin resistance (HOMA-IR) on protein levels. Both the inverse variance weighted and the MR Egger estimated were calculated for each pair of glucose trait and protein.

Exposure	Outcome	No. SNPs	Method	IV estimate	SE	P-value	Heterogeneity P-value	Egger intercept P-value
T2D		120	Inverse variance weighted	-0.020	0.047	6.7E-01	3.2E-01	
			MR Egger	-0.154	0.117	1.9E-01	3.3E-01	0.217
FG	ACE2	29	Inverse variance weighted	-0.159	0.216	4.6E-01	9.3E-01	
			MR Egger	-0.089	0.396	8.2E-01	9.0E-01	0.835
HOMA-IR		9	Inverse variance weighted	1.931	1.228	1.2E-01	6.3E-02	
			MR Egger	-7.244	4.552	1.6E-01	2.4E-01	0.077
T2D	CCL16	120	Inverse variance weighted	0.001	0.045	9.9E-01	5.6E-01	
			MR Egger	-0.136	0.112	2.3E-01	5.8E-01	0.187
FG		29	Inverse variance weighted	-0.138	0.212	5.1E-01	7.4E-01	

			MR Egger	0.038	0.388	9.2E-01	7.1E-01	0.593
			Inverse variance					
HOMA-IR		9	weighted	2.284	1.058	3.1E-02	1.8E-01	
			MR Egger	-6.139	3.891	1.6E-01	4.8E-01	0.062
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			Inverse variance					
T2D		120	weighted	0.080	0.050	1.1E-01	1.2E-01	
			MR Egger	-0.102	0.124	4.1E-01	1.5E-01	0.113
			Inverse variance					
FG	CTSD	29	weighted	-0.117	0.231	6.1E-01	3.4E-01	
			MR Egger	-0.139	0.431	7.5E-01	2.9E-01	0.950
			Inverse variance					
HOMA-IR		9	weighted	1.670	0.920	7.0E-02	6.6E-01	
			MR Egger	0.499	4.053	9.1E-01	5.6E-01	0.775
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			Inverse variance					
T2D		120	weighted	0.042	0.050	3.9E-01	4.0E-02	
			MR Egger	-0.179	0.123	1.5E-01	6.0E-02	0.053
			Inverse variance					
FG	CTSZ	29	weighted	-0.298	0.214	1.6E-01	4.4E-01	
			MR Egger	0.135	0.388	7.3E-01	4.8E-01	0.195
			Inverse variance					
HOMA-IR		9	weighted	1.597	0.884	7.1E-02	9.1E-01	
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			MR Egger	1.148	3.890	7.8E-01	8.6E-01	0.909
			Inverse variance					
T2D		120	weighted	-0.088	0.051	8.3E-02	1.5E-02	
			MR Egger	-0.249	0.127	5.3E-02	1.8E-02	0.172
			Inverse variance					
FG	FABP4	29	weighted	-0.762	0.212	3.3E-04	9.6E-01	
			MR Egger	-0.652	0.389	1.1E-01	9.5E-01	0.740
			Inverse variance					
HOMA-IR		9	weighted	-1.370	1.204	2.5E-01	6.3E-02	
			MR Egger	-7.936	5.056	1.6E-01	1.1E-01	0.224
			Inverse variance					
T2D		120	weighted	-0.033	0.045	4.5E-01	9.2E-01	
			MR Egger	-0.028	0.112	8.0E-01	9.1E-01	0.961
			Inverse variance					
FG	GDF15	29	weighted	-0.406	0.231	7.9E-02	2.3E-01	
			MR Egger	-0.597	0.429	1.8E-01	2.1E-01	0.600
			Inverse variance					
HOMA-IR		9	weighted	1.110	0.884	2.1E-01	8.9E-01	
			MR Egger	1.478	3.893	7.2E-01	8.2E-01	0.925
			Inverse variance					
T2D	Gal4	120	weighted	-0.059	0.075	4.3E-01	5.2E-23	

			MR Egger	-0.038	0.190	8.4E-01	3.1E-23	0.902
			Inverse variance					
FG		29	weighted	0.048	0.228	8.3E-01	2.5E-01	
			MR Egger	0.166	0.426	7.0E-01	2.1E-01	0.745
			Inverse variance					
HOMA-IR		9	weighted	0.607	1.099	5.8E-01	1.3E-01	
			MR Egger	-4.339	4.801	4.0E-01	1.5E-01	0.325
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			Inverse variance					
T2D		120	weighted	-0.005	0.050	9.2E-01	5.8E-02	
			MR Egger	-0.303	0.123	1.5E-02	1.2E-01	0.009
			Inverse variance					
FG	HAOX1	29	weighted	-0.180	0.263	4.9E-01	5.6E-02	
			MR Egger	0.108	0.487	8.3E-01	5.1E-02	0.487
			Inverse variance					
HOMA-IR		9	weighted	0.224	0.904	8.0E-01	5.4E-01	
			MR Egger	-5.968	3.978	1.8E-01	7.4E-01	0.154
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			Inverse variance					
T2D		120	weighted	0.058	0.050	2.5E-01	6.1E-02	
	IDUA		MR Egger	0.112	0.126	3.8E-01	5.5E-02	0.638
			Inverse variance					
FG		29	weighted	0.032	0.217	8.8E-01	7.8E-01	

			MR Egger	0.217	0.397	5.9E-01	7.6E-01	0.584
			Inverse variance					
HOMA-IR		9	weighted	0.909	0.903	3.1E-01	6.5E-01	
			MR Egger	-1.435	3.973	7.3E-01	5.9E-01	0.564
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			Inverse variance					
T2D		120	weighted	-0.135	0.049	6.2E-03	4.1E-02	
			MR Egger	0.124	0.122	3.1E-01	7.4E-02	0.023
			Inverse variance					
FG	IGFBP2	29	weighted	-0.007	0.214	9.7E-01	4.3E-01	
			MR Egger	-0.359	0.392	3.7E-01	4.3E-01	0.294
			Inverse variance					
HOMA-IR		9	weighted	-2.919	0.882	9.4E-04	7.1E-01	
			MR Egger	0.673	3.883	8.7E-01	7.1E-01	0.374
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			Inverse variance					
T2D		120	weighted	0.016	0.044	7.2E-01	5.4E-01	
			MR Egger	0.064	0.112	5.7E-01	5.2E-01	0.641
			Inverse variance					
FG	IL1RT1	29	weighted	0.098	0.230	6.7E-01	2.3E-01	
			MR Egger	0.054	0.430	9.0E-01	1.9E-01	0.903
			Inverse variance					
HOMA-IR		9	weighted	0.766	0.881	3.8E-01	4.8E-01	

			MR Egger	-0.842	3.981	8.4E-01	3.9E-01	0.691
			Inverse variance					
T2D		120	weighted	-0.058	0.051	2.5E-01	7.2E-02	
			MR Egger	-0.323	0.126	1.1E-02	1.2E-01	0.024
			Inverse variance					
FG	IL1ra	29	weighted	-0.632	0.221	4.2E-03	8.5E-01	
			MR Egger	-0.047	0.404	9.1E-01	9.3E-01	0.097
			Inverse variance					
HOMA-IR		9	weighted	-0.082	1.101	9.4E-01	1.8E-01	
			MR Egger	-4.082	4.941	4.4E-01	1.7E-01	0.433
			Inverse variance					
T2D		120	weighted	-0.133	0.047	5.1E-03	2.7E-01	
			MR Egger	-0.044	0.119	7.1E-01	2.7E-01	0.421
			Inverse variance					
FG	LPL	29	weighted	-0.397	0.244	1.0E-01	1.7E-01	
			MR Egger	-0.144	0.452	7.5E-01	1.5E-01	0.511
			Inverse variance					
HOMA-IR		9	weighted	-2.809	0.950	3.1E-03	3.6E-01	
			MR Egger	-2.837	4.471	5.5E-01	2.7E-01	0.995
			Inverse variance					
T2D	PAI	120	weighted	0.017	0.051	7.4E-01	1.4E-02	

			MR Egger	-0.128	0.128	3.2E-01	1.6E-02	0.219
			Inverse variance					
FG		29	weighted	-0.571	0.212	7.0E-03	7.9E-01	
			MR Egger	-0.085	0.389	8.3E-01	8.5E-01	0.148
			Inverse variance					
HOMA-IR		9	weighted	0.737	0.935	4.3E-01	3.5E-01	
			MR Egger	-8.579	3.893	6.3E-02	8.9E-01	0.044
			Inverse variance					
T2D		120	weighted	-0.181	0.050	3.0E-04	3.1E-02	
			MR Egger	0.064	0.124	6.1E-01	5.4E-02	0.033
			Inverse variance					
FG	PON3	29	weighted	0.185	0.229	4.2E-01	2.6E-01	
			MR Egger	-0.069	0.423	8.7E-01	2.4E-01	0.479
			Inverse variance					
HOMA-IR		9	weighted	-3.731	0.884	2.5E-05	9.4E-01	
			MR Egger	-0.802	3.891	8.4E-01	9.4E-01	0.465
			Inverse variance					
T2D		120	weighted	-0.032	0.049	5.2E-01	9.9E-02	
	PRSS8		MR Egger	-0.405	0.118	8.4E-04	2.8E-01	0.001
			Inverse variance					
FG		29	weighted	-0.172	0.223	4.4E-01	3.7E-01	

			MR Egger	0.073	0.413	8.6E-01	3.4E-01	0.484
			Inverse variance					
HOMA-IR		9	weighted	-0.054	0.899	9.5E-01	9.9E-01	
			MR Egger	0.111	3.957	9.8E-01	9.8E-01	0.967
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			Inverse variance					
T2D		120	weighted	0.027	0.046	5.5E-01	9.0E-01	
			MR Egger	-0.133	0.115	2.5E-01	9.2E-01	0.131
			Inverse variance					
FG	PSGL1	29	weighted	-0.029	0.217	8.9E-01	9.5E-01	
			MR Egger	0.182	0.398	6.5E-01	9.5E-01	0.532
			Inverse variance					
HOMA-IR		9	weighted	0.572	0.904	5.3E-01	6.9E-01	
			MR Egger	-0.927	3.978	8.2E-01	6.0E-01	0.710
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			Inverse variance					
T2D		120	weighted	0.007	0.100	9.5E-01	2.4E-65	
			MR Egger	0.077	0.252	7.6E-01	1.3E-65	0.761
			Inverse variance					
FG	SELE	29	weighted	0.176	0.212	4.1E-01	9.3E-01	
			MR Egger	0.317	0.388	4.2E-01	9.1E-01	0.667
			Inverse variance					
HOMA-IR		9	weighted	2.335	0.883	8.2E-03	8.2E-01	

			MR Egger	4.767	3.887	2.6E-01	7.9E-01	0.541
			Inverse variance					
T2D		120	weighted	-0.014	0.045	7.6E-01	7.8E-01	
			MR Egger	0.042	0.115	7.2E-01	7.7E-01	0.598
			Inverse variance					
FG	TIM	29	weighted	0.093	0.216	6.7E-01	8.8E-01	
			MR Egger	0.351	0.396	3.8E-01	8.7E-01	0.444
			Inverse variance					
HOMA-IR		9	weighted	1.103	0.901	2.2E-01	6.3E-01	
			MR Egger	-4.535	3.967	2.9E-01	7.8E-01	0.188
			Inverse variance					
T2D		120	weighted	0.102	0.045	2.2E-02	7.5E-01	
			MR Egger	-0.040	0.112	7.2E-01	7.7E-01	0.171
			Inverse variance					
FG	TRAP	29	weighted	0.200	0.212	3.5E-01	7.7E-01	
			MR Egger	-0.036	0.389	9.3E-01	7.5E-01	0.476
			Inverse variance					
HOMA-IR		9	weighted	1.711	1.272	1.8E-01	3.6E-02	
			MR Egger	-5.461	5.295	3.4E-01	7.4E-02	0.207
			Inverse variance					
T2D	VSIG2	120	weighted	-0.026	0.046	5.7E-01	4.7E-01	

			MR Egger	-0.235	0.115	4.2E-02	5.5E-01	0.048
			Inverse variance					
FG		29	weighted	-0.323	0.216	1.4E-01	5.3E-01	
			MR Egger	0.103	0.396	8.0E-01	5.6E-01	0.212
			Inverse variance					
HOMA-IR		9	weighted	0.396	0.901	6.6E-01	6.4E-01	
			MR Egger	-4.580	3.967	2.9E-01	7.3E-01	0.239
			Inverse variance					
T2D		120	weighted	0.085	0.051	9.7E-02	9.2E-03	
			MR Egger	-0.144	0.127	2.6E-01	1.6E-02	0.052
			Inverse variance					
FG	tPA	29	weighted	-0.048	0.211	8.2E-01	8.6E-01	
			MR Egger	-0.335	0.387	4.0E-01	8.5E-01	0.386
			Inverse variance					
HOMA-IR		9	weighted	2.293	1.065	3.1E-02	1.7E-01	
			MR Egger	-3.689	4.440	4.3E-01	2.4E-01	0.209
			Inverse variance					
T2D		120	weighted	-0.026	0.057	6.4E-01	2.5E-03	
	ALDH1A1		MR Egger	0.278	0.139	4.8E-02	7.2E-03	0.019
			Inverse variance					
FG		29	weighted	0.335	0.236	1.6E-01	3.4E-01	

			MR Egger	0.368	0.438	4.1E-01	2.8E-01	0.928
			Inverse variance					
HOMA-IR		9	weighted	-2.179	0.959	2.3E-02	2.9E-01	
			MR Egger	6.527	4.452	1.9E-01	5.9E-01	0.086
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			Inverse variance					
T2D		120	weighted	0.026	0.054	6.4E-01	2.0E-02	
			MR Egger	0.103	0.136	4.5E-01	1.8E-02	0.534
			Inverse variance					
FG	CDH2	29	weighted	-0.010	0.268	9.7E-01	9.3E-02	
			MR Egger	0.088	0.497	8.6E-01	7.2E-02	0.816
			Inverse variance					
HOMA-IR		9	weighted	-1.206	1.076	2.6E-01	1.5E-01	
			MR Egger	9.483	4.452	7.1E-02	5.3E-01	0.044
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			Inverse variance					
T2D		120	weighted	0.022	0.052	6.7E-01	9.5E-02	
			MR Egger	0.232	0.128	7.3E-02	1.2E-01	0.077
			Inverse variance					
FG	CTSO	29	weighted	0.009	0.300	9.8E-01	1.5E-02	
			MR Egger	-0.164	0.555	7.7E-01	1.1E-02	0.712
			Inverse variance					
HOMA-IR		9	weighted	-1.827	0.877	3.7E-02	6.7E-01	
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			MR Egger	4.873	4.455	3.1E-01	8.4E-01	0.169
			Inverse variance					
T2D		120	weighted	0.030	0.048	5.3E-01	4.6E-01	
			MR Egger	0.077	0.120	5.2E-01	4.4E-01	0.670
			Inverse variance					
FG	DDC	29	weighted	-0.067	0.234	7.8E-01	3.5E-01	
			MR Egger	-0.123	0.435	7.8E-01	3.0E-01	0.878
			Inverse variance					
HOMA-IR		9	weighted	-0.701	0.875	4.2E-01	8.3E-01	
			MR Egger	6.354	4.448	2.0E-01	9.8E-01	0.150
			Inverse variance					
T2D		120	weighted	-0.007	0.061	9.1E-01	2.9E-05	
			MR Egger	0.229	0.151	1.3E-01	5.8E-05	0.092
			Inverse variance					
FG	ENPP7	29	weighted	-0.048	0.340	8.9E-01	6.8E-04	
			MR Egger	-0.657	0.609	2.9E-01	1.2E-03	0.245
			Inverse variance					
HOMA-IR		9	weighted	-2.013	0.979	4.0E-02	2.6E-01	
			MR Egger	7.672	4.449	1.3E-01	6.5E-01	0.062
			Inverse variance					
T2D	NOMO1	120	weighted	-0.027	0.056	6.3E-01	5.0E-03	

			MR Egger	0.210	0.139	1.3E-01	8.7E-03	0.065
			Inverse variance					
FG		29	weighted	0.031	0.243	9.0E-01	2.7E-01	
			MR Egger	-0.076	0.449	8.7E-01	2.3E-01	0.778
			Inverse variance					
HOMA-IR		9	weighted	-1.942	1.024	5.8E-02	2.1E-01	
			MR Egger	9.960	4.457	6.1E-02	8.4E-01	0.030
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			Inverse variance					
T2D		120	weighted	-0.028	0.048	5.7E-01	3.9E-01	
			MR Egger	0.186	0.120	1.2E-01	4.6E-01	0.054
			Inverse variance					
FG	SIGLEC7	29	weighted	0.310	0.292	2.9E-01	2.5E-02	
			MR Egger	0.709	0.532	2.0E-01	2.5E-02	0.378
			Inverse variance					
HOMA-IR		9	weighted	-0.763	0.877	3.8E-01	6.2E-01	
			MR Egger	4.882	4.456	3.1E-01	7.1E-01	0.237
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ESM Figure 1. Pearson's correlation coefficient for relationships between the 29 proteins identified as being related to diabetes.

