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Table S1. Dataset description.

Phenotype	Consortium/First author	Participants	ICD-8 code	ICD-9 code	ICD-10 code	Adjustments	Web source/Pubmed ID
Type 2 diabetes (One-unit in log-transformed)	Vujkovic M et al. (2020)	148,726 cases, 965,732 controls				Age, sex, and the first 10 genetic principal components	32541925
Circulating protein level	deCODE/Ferkingstad et al. (2021)	35,559 Icelanders				Age, sex, and sample age	34857953
	UKB-PPP (UK Biobank Pharma Proteomics Project)/Sun et al. (2023)	54,219 European-ancestry individuals				Age, sex, batch, UKB center, UKB genetic array, time between blood sampling and measurement and the first 20 genetic principal components	37794186
	Fenland/Pietzner et al. (2021)	10,708 European-ancestry individuals				Age, sex, and the first ten genetic principal components and test site	34819519
Gastroesophageal reflux disease	FinnGen	26,184 cases, 320,387 controls		5301A	K21	Sex, age, genotyping batch and the first ten genetic principal components	FinnGen https://www.finnngen.fi/fi
	UK Biobank	14,223 cases, 369,275 controls			K21, K21.9	Sex, birth year, genotyping batch and first four principal components	UK Biobank https://www.leelabsg.org/resources
Gastric ulcer	FinnGen	1,307 cases, 287,137 controls		531	K25	Sex, age, genotyping batch and the first ten genetic principal components	FinnGen https://www.finnngen.fi/fi
	UK Biobank	4,109 cases, 401,5252 controls		531.1, 531.5, 531.7, 531.9	K25.1, K25.3, K25.5, K25.7, K25.9	Sex, birth year, genotyping batch and first four principal components	UK Biobank https://www.leelabsg.org/resources
Acute gastritis	FinnGen	2,370 cases, 320,387 controls	53500, 53501, 53502	535.0	K29.0, K29.1	Sex, age, genotyping batch and the first ten genetic principal components	FinnGen https://www.finnngen.fi/fi
	UK Biobank	1,184 cases, 378,124 controls		535	K29.0, K29.1	Sex, birth year, genotyping batch and first four principal components	UK Biobank https://www.leelabsg.org/resources
Chronic gastritis (Atrophic gastritis)	FinnGen	9,570 cases, 320,387 controls	53503	535.1, 535.4	K29.3, K29.4, K29.5	Sex, age, genotyping batch and the first ten genetic principal components	FinnGen https://www.finnngen.fi/fi
	UK Biobank	370 cases, 378,124 controls		535.1	K29.4	Sex, birth year, genotyping batch and first four principal components	UK Biobank https://www.leelabsg.org/resources
Irritable bowel syndrome	FinnGen	9,323 cases, 301,931 controls	56419	564.1	K58	Sex, age, genotyping batch and the first ten genetic principal components	FinnGen https://www.finnngen.fi/fi
	UK Biobank	5,548 cases, 334,783 controls		564.1	K58.0, K58.9	Sex, birth year, genotyping batch and first four principal components	UK Biobank https://www.leelabsg.org/resources
Diverticular disease of intestine	FinnGen	30,649 cases, 301,931 controls	562	562	K57	Sex, age, genotyping batch and the first ten genetic principal components	FinnGen https://www.finnngen.fi/fi
	UK Biobank	27,311 cases, 334,783 controls		562.0, 562.1	K57.0, K57.1, K57.2, K57.3, K57.4, K57.5, K57.8, K57.9	Sex, birth year, genotyping batch and first four principal components	UK Biobank https://www.leelabsg.org/resources
Cholelithiasis	FinnGen	37,041 cases, 330,903 controls	574	574	K80	Sex, age, genotyping batch and the first ten genetic principal components	FinnGen https://www.finnngen.fi/fi
	UK Biobank	13,777 cases, 391,307 controls		574.0, 574.1, 574.2	K80.0, K80.1, K80.2, K80.3, K80.4, K80.8	Sex, birth year, genotyping batch and first four principal components	UK Biobank https://www.leelabsg.org/resources
Cholecystitis	FinnGen	4,299 cases, 330,903 controls	574, 57500, 57501, 57502, 57503	574, 575.0, 575.1	K80, K81	Sex, age, genotyping batch and the first ten genetic principal components	FinnGen https://www.finnngen.fi/fi
	UK Biobank	2,761 cases, 391,307 controls		574.0, 574.1, 574.2, 575.0, 575.1	K80.0, K80.1, K80.2, K80.3, K80.4, K80.8, K81.0, K81.1, K81.8, K81.9	Sex, birth year, genotyping batch and first four principal components	UK Biobank https://www.leelabsg.org/resources
Nonalcoholic fatty liver disease	FinnGen	2,275 cases, 375,002 controls			K76.0	Sex, age, genotyping batch and the first ten genetic principal components	FinnGen https://www.finnngen.fi/fi
	UK Biobank	1,664 cases, 400,055 controls		571.5, 571.8, 571.9	K74.0, K74.1, K74.2, K76.0	Sex, birth year, genotyping batch and first four principal components	UK Biobank https://www.leelabsg.org/resources
Cirrhosis	FinnGen	3,970 cases, 373,307 controls	5719	571.5, 571.6	K74	Sex, age, genotyping batch and the first ten genetic principal components	FinnGen https://www.finnngen.fi/fi
	UK Biobank	2,895 cases, 400,055 controls		571.6	K74.3, K74.4, K74.5	Sex, birth year, genotyping batch and first four principal components	UK Biobank https://www.leelabsg.org/resources

ICD, International Classification of Diseases.

Table S2. Association of type 2 diabetes with ten gastrointestinal diseases.

Exposure	Outcomes	Database	n.snp	b.ivw	Inverse variance weighted					MR Egger					Weighted median					Weighted mode			
					se.ivw	pval.ivw	OR.ivw	FDR *	Q_pval	b.egger	se.egger	pval.egger	OR.egger	egger intercept	egger_pval	b.median	se.median	pval.median	OR.median	b.mode	se.mode	pval.mode	OR.mode
T2D	Acute gastritis	UK Biobank	225	0.185	0.059	0.002	1.20 (1.07, 1.35)	0.004	0.625	0.065	0.119	0.588	1.07 (0.84, 1.35)	0.008	0.246	0.177	0.117	0.128	1.19 (0.95, 1.50)	0.210	0.122	0.087	1.23 (0.97, 1.57)
T2D	Acute gastritis	Meta	225	0.092	0.035	0.010	1.10 (1.02, 1.17)	0.012	0.722	-0.034	0.073	0.643	0.97 (0.84, 1.11)	0.008	0.049	0.040	0.068	0.556	1.04 (0.91, 1.19)	0.030	0.072	0.676	1.03 (0.90, 1.19)
T2D	Acute gastritis	FinnGen	215	0.045	0.044	0.303	1.05 (0.96, 1.14)	0.303	0.225	-0.084	0.093	0.372	0.92 (0.77, 1.10)	0.008	0.117	-0.051	0.080	0.525	0.95 (0.81, 1.11)	-0.046	0.095	0.625	0.95 (0.79, 1.15)
T2D	Cholecystitis	UK Biobank	225	0.132	0.045	0.003	1.14 (1.05, 1.25)	0.006	0.001	0.087	0.091	0.338	1.09 (0.91, 1.30)	0.003	0.566	0.156	0.082	0.058	1.17 (0.99, 1.37)	0.116	0.085	0.171	1.12 (0.95, 1.33)
T2D	Cholecystitis	Meta	225	0.099	0.029	0.001	1.10 (1.04, 1.17)	0.002	4.88E-04	0.002	0.059	0.973	1.00 (0.89, 1.13)	0.006	0.061	0.080	0.054	0.136	1.08 (0.97, 1.20)	0.092	0.055	0.094	1.10 (0.98, 1.22)
T2D	Cholecystitis	FinnGen	215	0.073	0.038	0.053	1.08 (1.00, 1.16)	0.075	4.33E-04	-0.070	0.078	0.369	0.93 (0.80, 1.09)	0.009	0.037	0.006	0.064	0.921	1.01 (0.89, 1.14)	-0.030	0.072	0.673	0.97 (0.84, 1.12)
T2D	Cholelithiasis	UK Biobank	225	0.102	0.026	8.84E-05	1.11 (1.05, 1.17)	0.001	5.00E-19	0.016	0.052	0.763	1.02 (0.92, 1.13)	0.005	0.058	0.053	0.036	0.140	1.05 (0.98, 1.13)	0.071	0.038	0.062	1.07 (1.00, 1.16)
T2D	Cholelithiasis	Meta	224	0.077	0.021	3.12E-04	1.08 (1.04, 1.13)	0.001	6.57E-81	-0.020	0.043	0.637	0.98 (0.90, 1.07)	0.006	0.011	0.059	0.019	0.002	1.06 (1.02, 1.10)	0.048	0.022	0.032	1.05 (1.00, 1.10)
T2D	Cholelithiasis	FinnGen	215	0.067	0.023	0.003	1.07 (1.02, 1.12)	0.015	1.40E-62	-0.037	0.046	0.426	0.96 (0.88, 1.06)	0.006	0.011	0.032	0.021	0.124	1.03 (0.99, 1.08)	0.020	0.025	0.414	1.02 (0.97, 1.07)
T2D	Chronic gastritis (Atrophic gastritis)	UK Biobank	225	2.90E-04	0.106	0.998	1.00 (0.81, 1.23)	0.998	0.592	-0.206	0.213	0.335	0.81 (0.54, 1.24)	0.013	0.267	-0.164	0.193	0.397	0.85 (0.58, 1.24)	-0.130	0.241	0.591	0.88 (0.55, 1.41)
T2D	Chronic gastritis (Atrophic gastritis)	Meta	224	0.067	0.025	0.008	1.07 (1.02, 1.12)	0.012	0.001	0.041	0.053	0.433	1.04 (0.94, 1.16)	0.002	0.578	0.041	0.043	0.339	1.04 (0.96, 1.13)	0.039	0.041	0.347	1.04 (0.98, 1.13)
T2D	Chronic gastritis (Atrophic gastritis)	FinnGen	215	0.070	0.026	0.006	1.07 (1.02, 1.13)	0.018	0.001	0.053	0.053	0.319	1.05 (0.95, 1.17)	0.001	0.720	0.057	0.042	0.176	1.06 (0.97, 1.15)	0.058	0.042	0.172	1.06 (0.98, 1.15)
T2D	Cirrhosis	UK Biobank	225	0.127	0.054	0.018	1.14 (1.02, 1.26)	0.026	4.20E-17	-0.218	0.105	0.039	0.80 (0.65, 0.99)	0.022	1.99E-04	-0.107	0.069	0.120	0.90 (0.79, 1.03)	-0.147	0.090	0.103	0.86 (0.72, 1.03)
T2D	Cirrhosis	Meta	225	0.111	0.046	0.015	1.12 (1.02, 1.22)	0.017	4.93E-54	-0.128	0.092	0.166	0.88 (0.73, 1.05)	0.015	0.003	-0.029	0.043	0.504	0.97 (0.89, 1.06)	-0.092	0.060	0.131	0.91 (0.81, 1.03)
T2D	Cirrhosis	FinnGen	215	0.097	0.054	0.072	1.10 (0.99, 1.22)	0.090	7.13E-31	-0.049	0.112	0.664	0.95 (0.77, 1.19)	0.009	0.138	0.028	0.054	0.597	1.03 (0.93, 1.14)	-0.002	0.079	0.983	1.00 (0.85, 1.17)
T2D	Diverticular disease	UK Biobank	225	0.039	0.019	0.045	1.04 (1.00, 1.08)	0.050	6.72E-20	-0.113	0.038	0.003	0.89 (0.83, 0.96)	0.010	4.92E-06	-0.004	0.023	0.853	1.00 (0.95, 1.04)	-0.037	0.032	0.260	0.96 (0.90, 1.03)
T2D	Diverticular disease	Meta	225	0.034	0.016	0.035	1.04 (1.00, 1.07)	0.035	1.41E-36	-0.103	0.032	0.001	0.90 (0.85, 0.96)	0.009	1.47E-06	-0.014	0.019	0.473	0.99 (0.95, 1.02)	-0.041	0.023	0.670	0.96 (0.92, 1.00)
T2D	Diverticular disease	FinnGen	215	0.030	0.019	0.119	1.03 (0.99, 1.07)	0.133	5.63E-20	-0.094	0.039	0.017	0.91 (0.84, 0.98)	0.008	3.62E-04	-0.012	0.022	0.581	0.99 (0.95, 1.03)	-0.047	0.027	0.088	0.95 (0.90, 1.01)
T2D	Gastric ulcer	UK Biobank	225	0.120	0.032	1.85E-04	1.13 (1.06, 1.20)	0.001	0.539	0.117	0.065	0.071	1.12 (0.99, 1.28)	1.66E-04	0.962	0.143	0.065	0.027	1.15 (1.02, 1.31)	0.164	0.066	0.014	1.18 (1.03, 1.34)
T2D	Gastric ulcer	Meta	225	0.096	0.021	5.37E-06	1.10 (1.06, 1.15)	2.69E-05	0.086	0.055	0.046	0.238	1.06 (0.96, 1.16)	0.003	0.300	0.086	0.042	0.041	1.09 (1.00, 1.18)	0.077	0.046	0.097	1.08 (0.99, 1.18)
T2D	Gastric ulcer	FinnGen	215	0.073	0.028	0.009	1.08 (1.02, 1.14)	0.018	0.310	-0.007	0.059	0.909	0.99 (0.88, 1.11)	0.005	0.124	0.030	0.056	0.593	1.03 (0.92, 1.15)	0.013	0.060	0.833	1.01 (0.90, 1.14)
T2D	Gastroesophageal reflux disease	UK Biobank	225	0.057	0.020	0.006	1.06 (1.02, 1.10)	0.009	2.79E-04	-0.036	0.041	0.377	0.96 (0.89, 1.04)	0.004	0.009	0.016	0.028	0.576	1.02 (0.96, 1.07)	0.001	0.037	0.988	1.00 (0.93, 1.08)
T2D	Gastroesophageal reflux disease	Meta	225	0.045	0.015	0.002	1.05 (1.02, 1.08)	0.004	1.53E-10	-0.025	0.030	0.399	0.98 (0.92, 1.03)	0.004	0.007	0.014	0.019	0.456	1.01 (0.98, 1.05)	0.002	0.024	0.933	1.00 (0.96, 1.05)
T2D	Gastroesophageal reflux disease	FinnGen	215	0.038	0.017	0.027	1.04 (1.00, 1.07)	0.045	9.39E-08	-0.018	0.036	0.603	0.98 (0.92, 1.05)	0.003	0.070	-0.002	0.025	0.926	1.00 (0.95, 1.05)	0.000	0.030	0.999	1.00 (0.94, 1.06)
T2D	Irritable bowel syndrome	UK Biobank	225	0.069	0.032	0.029	1.07 (1.01, 1.14)	0.037	0.001	0.013	0.064	0.842	1.01 (0.89, 1.15)	0.004	0.310	0.102	0.053	0.054	1.11 (1.00, 1.23)	0.025	0.055	0.642	1.03 (0.92, 1.14)
T2D	Irritable bowel syndrome	Meta	225	0.069	0.021	0.001	1.07 (1.03, 1.12)	0.002	2.89E-05	-0.016	0.043	0.704	0.98 (0.90, 1.07)	0.005	0.024	0.053	0.036	0.139	1.05 (0.98, 1.13)	0.041	0.037	0.267	1.04 (0.97, 1.12)
T2D	Irritable bowel syndrome	FinnGen	215	0.065	0.025	0.008	1.07 (1.02, 1.12)	0.018	0.010	-0.037	0.051	0.471	0.96 (0.87, 1.07)	0.006	0.023	0.031	0.041	0.458	1.03 (0.95, 1.12)	0.042	0.048	0.383	1.04 (0.95, 1.14)
T2D	Nonalcoholic fatty liver disease	UK Biobank	225	0.239	0.067	3.97E-04	1.27 (1.11, 1.45)	0.001	1.23E-12	-0.176	0.132	0.184	0.84 (0.65, 1.09)	0.026	3.69E-04	0.103	0.086	0.231	1.11 (0.94, 1.31)	0.037	0.109	0.737	1.04 (0.84, 1.29)
T2D	Nonalcoholic fatty liver disease	Meta	225	0.307	0.060	2.94E-07	1.36 (1.21, 1.53)	2.94E-06	1.99E-53	0.010	0.121	0.932	1.01 (0.80, 1.28)	0.018	0.005	0.158	0.058	0.006	1.17 (1.05, 1.31)	0.014	0.078	0.858	1.01 (0.87, 1.18)
T2D	Nonalcoholic fatty liver disease	FinnGen	215	0.366	0.070	1.59E-07	1.44 (1.26, 1.65)	1.59E-06	1.33E-28	0.185	0.144	0.203	1.20 (0.91, 1.60)	0.011	0.153	0.176	0.073	0.017	1.19 (1.03, 1.38)	0.054	0.100	0.594	1.06 (0.87, 1.28)

*FDR performed by datasource

FDR, false discovery rate. CI, confidence interval

Table S3. Association of type 2 diabetes with deCODE plasma protein

Gene	Uniprot	nsnp	bw	sw	prval	CIlow	FOR_low	Q	val	egger	segger	prval_egger	CIlow_egger	egger	Interegger	prval_inter	semedian	prval_semedian	CIlow_semedian	bmode	semedian	prval_semedian	CIlow_semedian						
8897_38	BGAT3	Q47678	211	0.051	0.013	1.36E-04 (0.02, 0.08)	0.005	0.005	0.012	0.026	0.056	0.011	0.006	0.009	0.009	0.009	0.006	0.009	0.021	0.006	0.011	0.005	0.022	0.024	0.361	0.022	0.033	0.077	
11187_11	CLEC1E3	Q27429	211	0.046	0.015	3.9E-04 (0.02, 0.05)	0.005	0.005	0.012	0.026	0.056	0.011	0.006	0.009	0.009	0.009	0.006	0.009	0.021	0.006	0.011	0.005	0.022	0.024	0.361	0.022	0.033	0.077	
17836_17	S100A16	Q9P706	211	0.050	0.013	1.42E-04 (0.02, 0.08)	0.004	0.024	-0.020	0.026	0.472	-0.027	0.007	0.003	0.004	0.002	0.003	0.021	0.009	0.034	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04	
13614_16	CRABP1	Q92793	211	0.051	0.013	1.44E-04 (0.02, 0.08)	0.004	0.024	-0.020	0.026	0.472	-0.027	0.007	0.003	0.004	0.002	0.003	0.021	0.009	0.034	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04	
11440_58	SOCS3	Q92793	211	0.051	0.013	1.44E-04 (0.02, 0.08)	0.004	0.024	-0.020	0.026	0.472	-0.027	0.007	0.003	0.004	0.002	0.003	0.021	0.009	0.034	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04	
4152_58	KLHL1	Q92793	211	0.062	0.016	1.49E-04 (0.02, 0.09)	0.004	4.98E-12	0.043	0.033	0.193	0.04	0.022	0.011	0.009	0.008	0.002	0.010	0.006	0.022	0.006	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04
7741_14	KNO1	Q92793	211	0.062	0.016	1.49E-04 (0.02, 0.09)	0.004	4.98E-12	0.043	0.033	0.193	0.04	0.022	0.011	0.009	0.008	0.002	0.010	0.006	0.022	0.006	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04
5658_64	F1B3	P05160	211	0.051	0.014	1.56E-04 (0.02, 0.08)	0.004	0.002	0.011	0.026	0.080	0.011	0.006	0.009	0.009	0.009	0.009	0.006	0.009	0.021	0.006	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04
11219_95	F2FR3	Q92793	211	0.050	0.013	1.57E-04 (0.02, 0.08)	0.004	0.011	0.091	0.026	0.080	0.011	0.006	0.009	0.009	0.009	0.009	0.006	0.009	0.021	0.006	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04
10041_3	HNFA4	Q14258	211	0.051	0.013	1.58E-04 (0.02, 0.08)	0.004	0.003	0.007	0.026	0.080	0.011	0.006	0.009	0.009	0.009	0.009	0.006	0.009	0.021	0.006	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04
6089_17	GNB1L	Q92793	211	0.051	0.013	1.62E-04 (0.02, 0.08)	0.004	0.003	0.007	0.026	0.080	0.011	0.006	0.009	0.009	0.009	0.009	0.006	0.009	0.021	0.006	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04
8660_33	GRAP2	Q92793	211	0.058	0.015	1.74E-04 (0.02, 0.09)	0.004	1.63E-05	0.050	0.026	0.080	0.011	0.006	0.009	0.009	0.009	0.009	0.006	0.009	0.021	0.006	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04
18566_12	CR1	Q92793	211	0.058	0.015	1.74E-04 (0.02, 0.09)	0.004	1.63E-05	0.050	0.026	0.080	0.011	0.006	0.009	0.009	0.009	0.009	0.006	0.009	0.021	0.006	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04
33174_74	ERAA1	P58159	211	0.055	0.015	1.81E-04 (0.02, 0.09)	0.004	1.85E-06	0.050	0.026	0.080	0.011	0.006	0.009	0.009	0.009	0.009	0.006	0.009	0.021	0.006	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04
15324_25	HSB272	Q92793	211	0.055	0.015	1.85E-04 (0.02, 0.09)	0.004	6.07E-07	0.017	0.029	0.080	0.011	0.006	0.009	0.009	0.009	0.009	0.006	0.009	0.021	0.006	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04
5412_53	CD32	Q92793	211	0.046	0.012	1.91E-04 (0.02, 0.07)	0.005	0.28E	0.025	0.025	0.314	0.03	0.027	0.013	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011
3311_27	FCGR2B	P05845	211	0.060	0.016	1.93E-04 (0.02, 0.09)	0.005	5.98E-10	0.065	0.032	0.042	0.07	0.027	0.013	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011
8653_1	PLD2	Q04489	211	0.060	0.016	1.93E-04 (0.02, 0.09)	0.005	5.98E-10	0.065	0.032	0.042	0.07	0.027	0.013	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011
5307_12	FR	P00740	211	0.066	0.018	2.00E-04 (0.02, 0.10)	0.005	1.32E-19	0.111	0.035	0.176	0.03	0.028	0.016	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011
18698_198	TLR3	Q15455	211	0.044	0.012	2.01E-04 (0.02, 0.07)	0.005	0.351	0.034	0.024	0.184	0.03	0.028	0.016	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011
8221_1	ADPR	Q15455	211	0.045	0.012	2.06E-04 (0.02, 0.07)	0.005	0.620	0.015	0.025	0.185	0.03	0.028	0.016	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011
13842_44	HSPA9	P38844	211	0.043	0.012	2.18E-04 (0.02, 0.07)	0.005	0.169	0.021	0.024	0.393	0.02	0.037	0.023	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011
3093_23	TGFR3	Q03167	211	0.057	0.015	2.28E-04 (0.02, 0.09)	0.005	4.25E-07	0.028	0.030	0.381	0.03	0.039	0.023	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011
10613_33	CASC4	Q9P4E1	211	0.048	0.013	2.43E-04 (0.02, 0.07)	0.006	0.037	0.056	0.026	0.030	0.06	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011
10717_4	ACE	P12821	211	0.043	0.012	2.63E-04 (0.02, 0.07)	0.006	0.069	0.088	0.025	0.001	0.09	0.04	0.013	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011
7038_45	STR3A4	Q92187	211	0.043	0.012	2.63E-04 (0.02, 0.07)	0.006	0.069	0.088	0.025	0.001	0.09	0.04	0.013	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011
8233_2	THS	Q96UJ2	211	0.052	0.014	2.71E-04 (0.02, 0.08)	0.006	0.007	0.088	0.025	0.001	0.10	0.04	0.015	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011
17752_13	KCAL1	Q91015	211	0.052	0.014	2.74E-04 (0.02, 0.08)	0.006	1.65E-04	0.008	0.028	0.752	0.01	0.05	0.006	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003
7071_9	LR	Q15455	211	0.045	0.012	2.85E-04 (0.02, 0.08)	0.006	3.71E-07	0.029	0.029	0.335	0.01	0.033	0.015	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011
8009_33	SRFBP1	Q92793	211	0.045	0.012	2.85E-04 (0.02, 0.08)	0.006	3.71E-07	0.029	0.029	0.335	0.01	0.033	0.015	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011	0.011
13614_16	CRABP1	Q92793	211	0.051	0.013	1.44E-04 (0.02, 0.08)	0.004	0.024	-0.020	0.026	0.472	-0.027	0.007	0.003	0.004	0.002	0.003	0.021	0.009	0.034	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04	
11440_58	SOCS3	Q92793	211	0.051	0.013	1.44E-04 (0.02, 0.08)	0.004	0.024	-0.020	0.026	0.472	-0.027	0.007	0.003	0.004	0.002	0.003	0.021	0.009	0.034	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04	
4152_58	KLHL1	Q92793	211	0.062	0.016	1.49E-04 (0.02, 0.09)	0.004	4.98E-12	0.043	0.033	0.193	0.04	0.022	0.011	0.009	0.008	0.002	0.010	0.006	0.022	0.006	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04
7741_14	KNO1	Q92793	211	0.062	0.016	1.49E-04 (0.02, 0.09)	0.004	4.98E-12	0.043	0.033	0.193	0.04	0.022	0.011	0.009	0.008	0.002	0.010	0.006	0.022	0.006	0.011	0.005	0.022	0.024	0.902	-2.86E-03	0.05	0.04
5658_64	F1B3	P05160	211	0.051	0.014	1.56E-04 (0.02, 0.08)	0.004	0.002	0.011	0.026	0.080	0.011	0.006	0.009	0.009	0.009	0.009	0.00											

Table S3. Association of type 2 diabetes with deCODE plasma protein

SNP	Gene	Uniprot	nsnp	bw	sv	prv	cliv	FDR	Q_val	beqger	segger	prvsegger	egger	integger	prvmedian	semedian	prvmedian	clmedian	bmode	semode	prvmedian	clmedian		
14153.8	EPAS3	EPAS3	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.025	0.940	-1.91e-03 (0.05, 0.05)	0.002	0.102	0.007	0.21	0.78	0.01 (-0.03, 0.05)	0.015	0.222	0.488	0.02 (-0.03, 0.06)	
9212.2	CTSF	OR6K1	211	0.04	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.036	0.667	0.02 (-0.05, 0.09)	0.002	0.322	0.019	0.22	0.960	0.02 (-0.02, 0.06)	0.021	0.247	0.440	0.02 (-0.03, 0.07)
1329.39	NAP1L2	OR6U6	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
9480.7	DUSP9	OR6U7	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
8800.14	CLC7	OR6A7	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
5644.30	RNASEH2B	OR6U8	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
8874.53	TCF7	OR5Y03	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
9405.74	PSS2	P11465	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
11107.25	TENAC2	OR6P73	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
5658.53	ENDOU	P21128	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
14029.42	COPC2	PO1201	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
1024.52	SCGB3A1	OR6U91	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
17006.9	SRFBP2	OR6U92	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
17333.20	ACAD8	P11510	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
10782.2	KLRG2	ADN130	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
7173.141	BFI1	TMEM332	OR6U93	211	0.03	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
17482.19	BFI1	TMEM332	OR6U93	211	0.03	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
17329.2	BHD2	OR6U94	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
4335.20	BSI1	OR6U95	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
8811.103	GLEC3A	OR6U96	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
9363.11	CTSO	OR6U97	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
8898.17	TKOAS1	P24257	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
3077.66	F10	P00742	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
8415.90	CPN2	P22792	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
11352.168	TKOAS1	OR6U97	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
3184.25	F7	P08709	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
2788.50	MMF3	P08254	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
10514.5	TRIO1	OR6U98	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
12821.55	PP2R1A	P03253	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
17772.1	TGFB3L	OR6U99	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
5764.4	GALNT2	Q1044.1	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
7121.2	RNASEH2B	OR6U93	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
14178.18	CDKN3	P19687	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
8299.86	LRRA4	P59901	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
10643.16	CLRM3	OR6P87	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
1027.40	FNB1	OR6U99	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
16770.3	REG1B	P48304	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
11239.49	TPRSS3	OR6U99	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
13990.1	PI11488	OR6U99	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
7045.4	BNP3	Q12983	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
878.6	FAM171B	OR6P85	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
8918.23	CALB1	P05937	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.17e-03 (0.05, 0.05)
15427.16	LRP11	OR6U99	211	0.03	0.01	0.01	0.01	0.002	0.005	0.002	0.015	0.029	0.883	0.01 (-0.07, 0.05)	0.002	0.052	0.008	0.22	0.960	0.01 (-0.03, 0.05)	0.002	0.244	0.444	0.

Table S3. Association of type 2 diabetes with deCODE plasma protein

Gene	Chr	Gene	Uniprot	nsnp	Inverse variance weights				MR Egger				Weighted median				Weighted mode						
					b/w	se/bw	pval/iv	CI_low	FDR_low	Q_val	b/w	se/bw	pval/eg	CI_low	egger	interegger	pval/median	se/median	pval/median	CI_low	b_mode	se/median	pval/mode
15446_25	NR1G1	CD2207	21	0.029	0.015	0.050	0.033 (4.77e-05)	0.263	1.54E-07	0.008	0.029	0.774	0.011 (0.05, 0.07)	0.001	0.417	-0.009	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
15453_48	KRDL3	LOC101928	21	0.028	0.015	0.050	0.031 (4.12e-05)	0.263	1.54E-07	0.008	0.029	0.774	0.011 (0.05, 0.07)	0.001	0.417	-0.009	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
8719_145	UMK16	PLS112	21	0.023	0.012	0.050	0.032 (3.81e-05)	0.253	1.48E-07	0.008	0.029	0.774	0.011 (0.05, 0.07)	0.001	0.417	-0.009	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
12515_45	LMP2	OR2K2	21	0.023	0.012	0.050	0.033 (2.89e-05)	0.253	1.48E-07	0.008	0.029	0.774	0.011 (0.05, 0.07)	0.001	0.417	-0.009	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
8659_6	PNAP	LOC101928	21	0.023	0.012	0.050	0.033 (2.89e-05)	0.253	1.48E-07	0.008	0.029	0.774	0.011 (0.05, 0.07)	0.001	0.417	-0.009	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
5648_28	CTRB2	OGK1P1	21	0.182	0.093	0.050	0.181 (1.87e-04, 0.36)	0.255	0.005E+00	0.405	0.183	0.024	0.681 (0.41, 0.95, 0.78)	0.014	1.160	0.054	0.202	0.654	0.07 (0.05, 0.09)	0.058	0.022	0.101	0.08 (0.01, 0.14)
10771_9	TAXBP1	LOC101928	21	0.023	0.012	0.050	0.033 (2.89e-05)	0.253	1.48E-07	0.008	0.029	0.774	0.011 (0.05, 0.07)	0.001	0.417	-0.009	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
17557_33	SEPC3	GHSD4D	21	0.023	0.012	0.050	0.032 (3.85e-05)	0.255	1.70E-04	0.014	0.024	0.565	0.01 (0.06, 0.03)	0.012	0.774	-0.007	0.202	0.724	-0.01 (0.05, 0.03)	-0.011	0.025	0.668	-0.01 (0.06, 0.04)
8472_40	PML2	PA4967	21	0.029	0.015	0.050	0.033 (4.63e-05)	0.265	1.22E+05	0.072	0.029	0.913	0.027 (0.03, 0.12)	0.003	0.880	0.027	0.202	0.654	0.01 (0.05, 0.03)	0.040	0.024	0.096	0.04 (0.01, 0.09)
19177_7	MORC1	LOC101928	21	0.023	0.012	0.050	0.033 (2.89e-05)	0.253	1.48E-07	0.008	0.029	0.774	0.011 (0.05, 0.07)	0.001	0.417	-0.009	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
13813_23	AKS	OR5K9K	21	0.023	0.012	0.050	0.032 (1.10e-04)	0.257	1.81E-01	0.021	0.024	0.639	0.01 (0.06, 0.04)	0.012	0.101	0.021	0.202	0.654	0.03 (0.02, 0.08)	0.027	0.023	0.241	0.03 (0.02, 0.07)
15303_200	EDN3	PA1438	21	0.023	0.012	0.050	0.033 (1.03e-04)	0.257	1.57E-04	0.028	0.027	0.162	0.04 (0.09, 0.01)	0.004	0.006	-0.007	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
17350_13	CHMP2B	LOC101928	21	0.023	0.012	0.050	0.033 (2.89e-05)	0.253	1.48E-07	0.008	0.029	0.774	0.011 (0.05, 0.07)	0.001	0.417	-0.009	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
4283_3	RAN	PE2826	21	0.023	0.012	0.050	0.033 (2.89e-05)	0.253	1.48E-07	0.008	0.029	0.774	0.011 (0.05, 0.07)	0.001	0.417	-0.009	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
4217_49	HSD17B10	LOC101928	21	0.023	0.012	0.050	0.033 (2.89e-05)	0.253	1.48E-07	0.008	0.029	0.774	0.011 (0.05, 0.07)	0.001	0.417	-0.009	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
3302_58	CST7	OR7098	21	0.026	0.013	0.051	0.033 (1.37e-04)	0.257	0.007	0.055	0.028	0.304	-0.08 (0.11, -4.53e-03)	0.005	3.33E-04	0.018	0.202	0.654	0.02 (0.02, 0.08)	-0.050	0.026	0.855	-0.05 (0.10, 1.83e-04)
14128_121	FNX10	PO1566	21	0.023	0.012	0.050	0.032 (1.32e-04)	0.258	0.091	0.018	0.025	0.482	-0.02 (0.07, 0.03)	0.003	0.058	0.001	0.202	0.654	0.01 (0.05, 0.03)	0.005	0.024	0.832	0.01 (0.01, 0.04)
8532_1	ENTPF8	PT5354	21	0.023	0.012	0.050	0.033 (2.89e-05)	0.253	1.48E-07	0.008	0.029	0.774	0.011 (0.05, 0.07)	0.001	0.417	-0.009	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
2615_80	EFNA5	PS2803	21	0.028	0.014	0.051	0.033 (1.76e-04)	0.266	2.87E-04	0.017	0.029	0.555	0.02 (0.04, 0.07)	0.001	0.672	0.000	0.202	0.654	0.02 (0.02, 0.08)	0.001	0.026	0.993	0.02 (0.04, 0.05)
13116_25	CD177	OR8N03	21	0.022	0.011	0.050	0.032 (1.45e-04)	0.258	0.036	0.035	0.022	0.110	0.04 (0.09, 0.01)	-0.001	0.471	0.000	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
1659_11	TRH	PO3389	21	0.024	0.013	0.052	0.032 (1.17e-04)	0.265	0.040	0.025	0.024	0.025	0.02 (0.07, 0.02)	0.003	0.005	0.004	0.202	0.654	0.01 (0.05, 0.03)	0.004	0.024	0.866	0.03 (0.04, 0.05)
11122_97	SPG21	OR8N2D	21	0.023	0.012	0.050	0.032 (0.95, 1.84e-04)	0.259	0.228	0.068	0.024	0.047	0.07 (0.11, -0.02)	0.003	0.026	-0.044	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
14709_59	CDC	PO3389	21	0.023	0.012	0.050	0.032 (2.02e-04)	0.260	0.065	0.025	0.025	0.331	-0.02 (0.07, 0.02)	0.003	0.029	0.172	0.202	0.654	0.01 (0.05, 0.03)	0.018	0.023	0.438	0.02 (0.02, 0.03)
9565_80	CLMP	OR9H84	21	0.023	0.012	0.050	0.032 (2.07e-04)	0.260	0.275	0.025	0.024	0.292	-0.03 (0.07, 0.02)	0.003	0.021	0.003	0.202	0.654	0.01 (0.05, 0.03)	-0.003	0.024	0.899	-0.01 (0.03, 0.27e-03)
7196_21	FNW1	PO5001	21	0.022	0.011	0.050	0.032 (2.13e-04)	0.260	0.113	0.045	0.023	0.056	0.04 (0.09, 0.17e-04)	0.004	0.001	-0.003	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
16540_38	OPR12	PA7874	21	0.022	0.011	0.050	0.032 (2.58e-04)	0.262	0.144	0.021	0.023	0.036	0.04 (0.09, 0.17e-04)	0.004	0.001	-0.003	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
12766_33	GPR142	PO7501	21	0.022	0.011	0.050	0.032 (2.58e-04)	0.262	0.144	0.021	0.023	0.036	0.04 (0.09, 0.17e-04)	0.004	0.001	-0.003	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
16010_19	GPI1	PA2286	21	0.028	0.014	0.053	0.033 (3.49e-04)	0.263	3.54E+05	-0.052	0.028	0.182	-0.04 (0.11, 2.35e-03)	0.005	0.001	0.009	0.202	0.654	-0.01 (0.05, 0.03)	0.008	0.024	0.810	0.01 (0.04, 0.05)
10036_6	DUSP4	PO3389	21	0.024	0.013	0.052	0.032 (3.59e-04)	0.264	0.204	0.039	0.024	0.039	0.01 (0.06, 0.04)	0.004	0.003	0.001	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
18236_3	HSP190	OS3ZC6	21	0.023	0.012	0.050	0.033 (3.05e-04)	0.264	0.055	0.039	0.028	0.130	-0.02 (0.09, 0.01)	0.001	0.476	-0.056	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
10921_2	SPG21	OR8N2D	21	0.023	0.012	0.050	0.033 (3.05e-04)	0.264	0.055	0.039	0.028	0.130	-0.02 (0.09, 0.01)	0.001	0.476	-0.056	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
14623_26	SUMO3	PS5584	21	0.023	0.012	0.050	0.032 (0.05, 0.331e-04)	0.264	0.095	0.045	0.025	0.075	-0.05 (0.09, 3.80e-03)	0.001	0.302	-0.063	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
8993_151	RPM2	KA3353	21	0.023	0.012	0.050	0.032 (3.38e-04)	0.264	0.044	0.031	0.021	0.141	-0.03 (0.09, 0.05)	0.004	0.002	0.004	0.202	0.654	-0.01 (0.05, 0.03)	0.008	0.021	0.659	0.01 (0.03, 0.04)
15387_65	EHF	OR8N2C4	21	0.023	0.012	0.050	0.032 (3.38e-04)	0.264	0.044	0.031	0.021	0.141	-0.03 (0.09, 0.05)	0.004	0.002	0.004	0.202	0.654	-0.01 (0.05, 0.03)	0.008	0.021	0.659	0.01 (0.03, 0.04)
16756_30	GDF7	PT4295	21	0.022	0.011	0.050	0.032 (3.51e-04)	0.264	0.344	0.023	0.023	0.235	-0.02 (0.07, 0.02)	0.003	0.025	-0.007	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
1669_53	MAPK	OR1067	21	0.033	0.017	0.054	0.033 (5.25e-04)	0.264	1.03E-16	0.040	0.034	0.325	0.04 (0.03, 0.11)	0.002	0.795	0.009	0.202	0.654	0.01 (0.05, 0.03)	0.018	0.027	0.574	0.02 (0.04, 0.05)
1004_15	FRS3	OR1067	21	0.033	0.017	0.054	0.033 (5.25e-04)	0.264	1.03E-16	0.040	0.034	0.325	0.04 (0.03, 0.11)	0.002	0.795	0.009	0.202	0.654	0.01 (0.05, 0.03)	0.018	0.027	0.574	0.02 (0.04, 0.05)
7843_3	PCPT	OR1879	21	0.026	0.014	0.054	0.033 (4.01e-04)	0.264	0.107	0.033	0.027	0.163	0.01 (0.04, 0.07)	0.001	0.561	0.011	0.202	0.654	0.01 (0.05, 0.03)	-0.005	0.028	0.872	-0.05 (0.10, 3.23e-03)
10110_10	RLN2	LOC101928	21	0.023	0.012	0.050	0.033 (2.89e-05)	0.253	1.48E-07	0.008	0.029	0.774	0.011 (0.05, 0.07)	0.001	0.417	-0.009	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
11615_16	DAPF1	OR9N19	21	0.023	0.012	0.050	0.032 (0.05, 0.329e-04)	0.264	0.140	-0.036	0.025	0.155	-0.04 (0.09, 0.01)	0.001	0.561	-0.052	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
12976_49	SOX3B3	OR6004	21	0.022	0.011	0.050	0.032 (3.76e-04)	0.264	0.172	-0.055	0.023	0.918	-0.06 (0.10, -0.01)	0.005	1.48E-04	-0.016	0.202	0.654	-0.01 (0.05, 0.03)	-0.012	0.024	0.618	-0.01 (0.06, 0.04)
7099_17	GALNT1	OR10472	21	0.022	0.011	0.050	0.033 (0.03, 0.142e-04)	0.264	0.055	0.035	0.025	0.193	-0.01 (0.06, 0.04)	0.005	0.007	0.011	0.202	0.654	-0.01 (0.05, 0.03)	0.002	0.024	0.752	0.01 (0.03, 0.04)
12976_39	SFRP1																						

Table S3. Association of type 2 diabetes with deCODE plasma protein

Name	Gene	Uniprot	nsnp	Inverse variance weighted				MR Egger				Weighted median																
				b/w	se/w	pval/w	CI_low	CI_high	FDR_W	Q_val	egger	se_egger	pval_egger	CI_egger	egger	Interegger	pval_inter	se_median	pval_median	CI_median	b_median	se_md	pval_md	CI_md				
12684-19	PTPN23	PTN23	211	0.019	0.012	0.100	0.022	-0.346	0.034	0.365	0.101	0.010	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
13465-5	RCAN1	RCAN1	211	0.020	0.013	0.102	0.022	-0.346	0.034	0.365	0.101	0.010	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
5488-74	SMC2	SMC2	211	0.020	0.013	0.102	0.022	-0.346	0.034	0.365	0.101	0.010	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
16335-4	SRGAP2	SRGAP2	211	0.020	0.013	0.102	0.022	-0.346	0.034	0.365	0.101	0.010	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
16335-4	SRGAP2B	SRGAP2B	211	0.020	0.013	0.102	0.022	-0.346	0.034	0.365	0.101	0.010	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
8936-7	PMPA1	PMPA1	211	0.019	0.012	0.101	0.022	-0.346	0.034	0.366	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
1641-102	COL4A2	COL4A2	211	0.019	0.012	0.101	0.022	-0.346	0.034	0.366	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
12685-16	ILF2	ILF2	211	0.019	0.012	0.101	0.022	-0.346	0.034	0.366	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
19142-39	DNAH10	DNAH10	211	0.022	0.013	0.102	0.022	-0.346	0.034	0.366	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
10381-25	CNS1	CNS1	211	0.019	0.012	0.101	0.022	-0.346	0.034	0.366	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
8858-21	BATF3	BATF3	211	0.019	0.012	0.101	0.022	-0.346	0.034	0.366	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
11315-148	PRMT10	PRMT10	211	0.019	0.012	0.101	0.022	-0.346	0.034	0.366	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
11709-29	CPT1B	CPT1B	211	0.022	0.013	0.102	0.022	-0.346	0.034	0.366	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
11825-27	PRKAG2	PRKAG2	211	0.021	0.013	0.103	0.022	-0.346	0.034	0.368	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
12000-25	USP27	USP27	211	0.022	0.013	0.102	0.022	-0.346	0.034	0.368	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
12689-25	ACT5	ACT5	211	0.020	0.012	0.103	0.022	-0.346	0.034	0.368	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
17752-24	RC2	RC2	211	0.019	0.012	0.102	0.022	-0.346	0.034	0.368	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
1885-5	KCPI1	KCPI1	211	0.020	0.012	0.103	0.022	-0.346	0.034	0.368	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
8468-37	TAC4	TAC4	211	0.020	0.013	0.102	0.022	-0.346	0.034	0.368	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
9953-20	MIR34	MIR34	211	0.021	0.013	0.102	0.022	-0.346	0.034	0.368	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
7686-3	NBR1	NBR1	211	0.019	0.012	0.102	0.022	-0.346	0.034	0.368	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
9223-11	MANF	MANF	211	0.021	0.013	0.102	0.022	-0.346	0.034	0.368	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
8695-42	AFAP1L2	AFAP1L2	211	0.021	0.013	0.102	0.022	-0.346	0.034	0.368	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
8695-42	AFAP1L1	AFAP1L1	211	0.021	0.013	0.102	0.022	-0.346	0.034	0.368	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
8695-42	KIF14	KIF14	211	0.021	0.013	0.102	0.022	-0.346	0.034	0.368	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
12687-12	SRFBP1	SRFBP1	211	0.021	0.013	0.103	0.022	-0.346	0.034	0.368	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
13466-5	NEURL4	NEURL4	211	0.022	0.014	0.103	0.022	-0.346	0.034	0.368	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
1885-18	KIF8	KIF8	211	0.019	0.012	0.103	0.022	-0.346	0.034	0.368	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
10754-113	PROCR	PROCR	211	0.024	0.014	0.103	0.022	-0.346	0.034	0.369	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
7084-8	CEACAM6	CEACAM6	211	0.024	0.014	0.103	0.022	-0.346	0.034	0.369	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
15385-41	BA3	BA3	211	0.019	0.012	0.104	0.022	-0.346	0.034	0.371	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
9300-244	PCSK2	PCSK2	211	0.021	0.013	0.102	0.022	-0.346	0.034	0.371	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
5613-75	LCC2	LCC2	211	0.019	0.012	0.104	0.022	-0.346	0.034	0.372	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
12788-6	CATD	CATD	211	0.019	0.012	0.104	0.022	-0.346	0.034	0.372	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
18977-28	BARH1	BARH1	211	0.021	0.013	0.102	0.022	-0.346	0.034	0.372	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
11352-24	ORG2	ORG2	211	0.019	0.012	0.105	0.022	-0.346	0.034	0.372	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
7865-15	TM2A	TM2A	211	0.021	0.013	0.105	0.022	-0.346	0.034	0.373	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
603-64	TM2B3	TM2B3	211	0.021	0.013	0.105	0.022	-0.346	0.034	0.373	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
13812-58	HNFRNP3	HNFRNP3	211	0.019	0.012	0.105	0.022	-0.346	0.034	0.374	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
16975-6	EPOR	EPOR	211	0.021	0.013	0.102	0.022	-0.346	0.034	0.374	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
8304-50	TM2B3	TM2B3	211	0.024	0.015	0.105	0.022	-0.346	0.034	0.374	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004	0.221	0.865	-3.753	-0.04	0.003	0.894	3.056	-0.04	0.05
14123-34	C10orf46	C10orf46	211	0.019	0.012	0.106	0.022	-0.346	0.034	0.374	0.101	0.011	0.024	0.673	-0.011	0.006	0.042	0.165	-0.004									

Table S3. Association of type 2 diabetes with deCODE plasma protein

SNP/LogIC	Gene	Uniprot	nsnp	Inverse variance weighted				MR Egger				Weighted mode				Weighted mode							
				b/w	se/w	pval/w	CI_low	FOR_low	Q_val	begger	se_begger	pval_begger	CI_low	egger	Interegger	pval/inter	se/inter	pval/inter	CI_low	b/mode	se/mode	pval/mode	CI_low
7064_2	VAMPB	PR040	211	0.018	0.013	0.158	-0.02(0.01,0.04)	0.446	0.203	0.049	0.025	0.051	-0.05(0.10, -1.22e-06)	0.004	0.002	0.005	0.022	0.833	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
7033_125	RFCG	Q96444	211	0.003	0.002	0.157	-0.02(0.01,0.04)	0.446	0.203	0.049	0.025	0.051	-0.05(0.10, -1.22e-06)	0.004	0.002	0.005	0.022	0.833	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
8535_102	DMN	Q9EDU4	211	0.017	0.012	0.157	-0.02(0.01,0.04)	0.446	0.203	0.049	0.025	0.051	-0.05(0.10, -1.22e-06)	0.004	0.002	0.005	0.022	0.833	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
9638_148	TRAP	P58753	211	0.017	0.012	0.157	-0.02(0.01,0.04)	0.446	0.203	0.049	0.025	0.051	-0.05(0.10, -1.22e-06)	0.004	0.002	0.005	0.022	0.833	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
8644_138	ACTN2	Q96444	211	0.003	0.002	0.157	-0.02(0.01,0.04)	0.446	0.203	0.049	0.025	0.051	-0.05(0.10, -1.22e-06)	0.004	0.002	0.005	0.022	0.833	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
11383_58	AQP4	P55687	211	0.018	0.013	0.158	-0.02(0.01,0.04)	0.447	0.204	0.050	0.026	0.052	-0.06(0.11, -0.001)	0.003	0.003	0.004	0.023	0.834	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
16395_23	ZWNT1	Q96444	211	0.003	0.002	0.157	-0.02(0.01,0.04)	0.446	0.203	0.049	0.025	0.051	-0.05(0.10, -1.22e-06)	0.004	0.002	0.005	0.022	0.833	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
7991_24	FUT9	Q9Y231	211	0.018	0.013	0.158	-0.02(0.01,0.04)	0.447	0.204	0.050	0.026	0.052	-0.06(0.11, -0.001)	0.003	0.003	0.004	0.023	0.834	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
11684_32	FRZB	Q96444	211	0.003	0.002	0.157	-0.02(0.01,0.04)	0.446	0.203	0.049	0.025	0.051	-0.05(0.10, -1.22e-06)	0.004	0.002	0.005	0.022	0.833	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
12070_35	STAL2	Q96444	211	0.003	0.002	0.157	-0.02(0.01,0.04)	0.446	0.203	0.049	0.025	0.051	-0.05(0.10, -1.22e-06)	0.004	0.002	0.005	0.022	0.833	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
13740_51	FRZB	Q96444	211	0.003	0.002	0.157	-0.02(0.01,0.04)	0.446	0.203	0.049	0.025	0.051	-0.05(0.10, -1.22e-06)	0.004	0.002	0.005	0.022	0.833	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
14058_4	CGA	Q12015	211	0.016	0.011	0.159	-0.02(0.01,0.04)	0.447	0.204	0.050	0.026	0.052	-0.06(0.11, -0.001)	0.003	0.003	0.004	0.023	0.834	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
17432_25	HAT	Q12015	211	0.016	0.011	0.159	-0.02(0.01,0.04)	0.447	0.204	0.050	0.026	0.052	-0.06(0.11, -0.001)	0.003	0.003	0.004	0.023	0.834	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
17450_51	HARS	Q12015	211	0.016	0.011	0.159	-0.02(0.01,0.04)	0.447	0.204	0.050	0.026	0.052	-0.06(0.11, -0.001)	0.003	0.003	0.004	0.023	0.834	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
18327_31	HAT	Q12015	211	0.016	0.011	0.159	-0.02(0.01,0.04)	0.447	0.204	0.050	0.026	0.052	-0.06(0.11, -0.001)	0.003	0.003	0.004	0.023	0.834	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
4359_87	DYRK3	Q43781	211	0.017	0.012	0.159	-0.02(0.01,0.04)	0.447	0.204	0.050	0.026	0.052	-0.06(0.11, -0.001)	0.003	0.003	0.004	0.023	0.834	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
5599_88	PYX10X	Q96444	211	0.018	0.013	0.159	-0.02(0.01,0.04)	0.447	0.204	0.050	0.026	0.052	-0.06(0.11, -0.001)	0.003	0.003	0.004	0.023	0.834	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
14454_17	LITRA	Q12015	211	0.018	0.013	0.159	-0.02(0.01,0.04)	0.447	0.204	0.050	0.026	0.052	-0.06(0.11, -0.001)	0.003	0.003	0.004	0.023	0.834	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
16932_5	SULT1E1	P48888	211	0.018	0.013	0.160	-0.02(0.01,0.04)	0.448	0.204	0.051	0.027	0.053	-0.07(0.12, -0.001)	0.003	0.004	0.005	0.024	0.835	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
2677_77	MRC1	P22887	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
15598_17	CLA	Q12015	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
7082_2	BGN2T	Q96444	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
12376_85	CDON2	P55273	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
12543_76	ZNF560	Q96444	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
2987_37	HIST1H1C	P18403	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
13422_86	ENOX2	Q12015	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
8775_81	FAM24B	Q96444	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
11077_11	LS	P05133	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
7038_54	CSF1	P18403	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
4995_16	HPGD	P15428	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
1492_14	ADAM	Q96444	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
10618_10	LRP2	P98184	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
11334_7	LRFB3	Q75022	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
13554_78	REP1	Q96444	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
15235_14	GAP43	P17677	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
16290_16	ANKK4	P13873	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
16343_4	PTG2	Q96444	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
19187_21	STAMP	Q96444	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
1706_25	ZPA	Q96444	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
9128_34	FLRT3	Q96444	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
9562_93	SUSD1	Q96444	211	0.019	0.014	0.160	-0.02(0.01,0.04)	0.449	0.205	0.052	0.028	0.054	-0.08(0.13, -0.001)	0.004	0.005	0.006	0.025	0.836	-3.56(0.45,0.05,0.1)	0.002	0.024	0.833	1.99(0.33,0.04,0.05)
9504_48	GMBR2	Q96444	211	0.019	0.014	0.160																	

Table S3. Association of type 2 diabetes with deCODE plasma protein

Gene	Uniprot	nsnp	bw	sv	pr	cl	MD	Weighted median	se	Weighted median	se
Gene	Uniprot	nsnp	bw	sv	pr	cl	MD	Weighted median	se	Weighted median	se
18074.2	SERF2	RA1011	21	0.015	0.02	0.01	0.04	0.482	0.166	-0.039	0.024
18317.6	ZAP70	RA5403	21	0.017	0.02	0.01	0.04	0.482	0.166	-0.039	0.024
8009.1	THPO	24225	21	0.017	0.02	0.01	0.04	0.482	0.166	-0.039	0.024
8447.73	PTX3	26022	21	0.018	0.02	0.01	0.04	0.482	0.166	-0.039	0.024
2656.53	EDA	10338	21	0.018	0.02	0.01	0.04	0.482	0.166	-0.039	0.024
19637.9	CR1	PO8850	21	0.015	0.01	0.01	0.04	0.484	0.176	-0.015	0.023
10676.1	COL1E1	10338	21	0.015	0.02	0.01	0.04	0.484	0.176	-0.015	0.023
15350.5	UTR3	ORJUKP6	21	0.015	0.02	0.01	0.04	0.485	0.170	-0.038	0.024
5661.15	IL18	IL14118	21	0.016	0.02	0.01	0.04	0.485	0.178	-0.058	0.024
7901.38	POTEM	GNM7	21	0.015	0.02	0.01	0.04	0.486	0.170	-0.038	0.024
7139.14	SLFRK4	ORMS2	21	0.017	0.03	0.01	0.04	0.486	0.208	0.027	0.033
2860.59	CCDC28	CNR33	21	0.019	0.02	0.01	0.04	0.486	0.215	-0.118	0.030
12733.29	HNRPNB	ORF72	21	0.019	0.02	0.01	0.04	0.486	0.215	-0.118	0.030
4965.63	COTL1	IL10419	21	0.023	0.018	0.01	0.02	0.486	0.252	-0.016	0.035
10076.1	HPA02	CC252	21	0.012	0.02	0.01	0.04	0.486	0.245	0.024	0.033
5701.81	CLEC3B	PO5452	21	0.018	0.04	0.02	0.02	0.487	0.496	0.014	0.028
8941.11	SUMF1	ORNBK3	21	0.016	0.02	0.02	0.02	0.487	0.142	-0.025	0.025
14002.18	DOCK9	ORX29	21	0.012	0.02	0.02	0.04	0.487	0.134	-0.063	0.025
14021.81	MED4	ORJMK6	21	0.017	0.03	0.02	0.04	0.487	0.202	-0.023	0.030
18174.79	PDCD6B	ORJMK6	21	0.015	0.02	0.03	0.04	0.488	0.081	-0.041	0.025
7070.26	NEL	ORJMK6	21	0.015	0.02	0.03	0.04	0.488	0.222	0.014	0.024
18267.74	CARD17	OSXLAB	21	0.015	0.02	0.03	0.04	0.488	0.147	-0.042	0.024
19190.42	USEL2L	IL14533	21	0.017	0.03	0.02	0.04	0.488	0.009	-0.028	0.030
10022.207	POLH	ORJ253	21	0.015	0.01	0.04	0.04	0.488	0.270	0.015	0.033
15627.83	AKT1	ORJ253	21	0.016	0.02	0.02	0.04	0.488	0.079	-0.039	0.025
8614.3	SRBP1	ORJ253	21	0.017	0.03	0.02	0.04	0.489	0.035	-0.025	0.031
16887.76	PCTK1	ORJ596	21	0.016	0.02	0.04	0.04	0.490	0.127	-0.010	0.025
10830.55	ERHAB1	ORJ596	21	0.012	0.02	0.04	0.04	0.490	0.450	-0.033	0.023
12704.28	PCSK9	ORJ596	21	0.015	0.02	0.04	0.04	0.490	0.450	-0.033	0.023
18874.68	CEBPA	PA9715	21	0.015	0.02	0.01	0.04	0.490	0.404	-0.047	0.023
522.32	POE1A	ORJ596	21	0.015	0.02	0.04	0.04	0.490	0.404	-0.047	0.023
5337.64	CD86	PA4201	21	0.015	0.02	0.02	0.04	0.490	0.429	0.010	0.024
8119.14	MAMDC2	QZ084	21	0.017	0.02	0.02	0.04	0.490	0.255	-0.054	0.025
12571.14	ARL1	ORJ596	21	0.015	0.02	0.04	0.04	0.490	0.404	-0.047	0.023
17356.34	IL1F10	ORJ596	21	0.015	0.02	0.04	0.04	0.490	0.123	-0.023	0.024
8407.10	RS1	ORJ596	21	0.017	0.03	0.02	0.04	0.490	0.229	-0.043	0.025
8002.26	SERPINC1	ORJ596	21	0.015	0.02	0.04	0.04	0.490	1.502	-0.029	0.011
8927.6	CFTR7c3	EOCX11	21	0.015	0.02	0.02	0.04	0.491	0.155	-0.011	0.024
8616.2	CY14B2	ORJ596	21	0.015	0.02	0.04	0.04	0.491	0.155	-0.011	0.024
7071.23	MAN1B1	ORJMK7	21	0.017	0.03	0.02	0.04	0.492	0.002	-0.058	0.028
11348.132	PHAX2	IL5480	21	0.015	0.02	0.02	0.04	0.492	0.744	-0.044	0.024
11653.69	SLC49A8	ORJ596	21	0.015	0.02	0.04	0.04	0.492	0.002	-0.058	0.028
12705.9	IL1575	ORJ596	21	0.015	0.02	0.04	0.04	0.493	0.350	-0.044	0.023
12718.43	PRNA	ORJ253	21	0.013	0.02	0.04	0.04	0.493	0.044	-0.055	0.026
1847.52	CCL17	ORJ253	21	0.017	0.03	0.02	0.04	0.494	0.044	-0.055	0.026
18162.187	PKA	ORJMK7	21	0.016	0.03	0.02	0.04	0.494	0.044	-0.055	0.026
1682.52	CDNF	ORJMK7	21	0.015	0.02	0.04	0.04	0.494	0.044	-0.055	0.026
12535.2	XCC1	IL1887	21	0.015	0.02	0.04	0.04	0.495	0.608	-0.012	0.023
15300.96	PRCC14	ORJMK7	21	0.015	0.02	0.04	0.04	0.495	0.229	-0.058	0.025
8753.17	EZR	ORJ596	21	0.015	0.02	0.04	0.04	0.495	0.019	-0.019	0.024
13573.5	ARPC1	IL1545	21	0.015	0.02	0.04	0.04	0.496	0.043	-0.024	0.024
2855.49	MAPK3	PZ780	21	0.015	0.02	0.04	0.04	0.496	8.300	-0.042	0.004
5405.8	LRRC1	ORJ596	21	0.015	0.02	0.04	0.04	0.496	0.058	-0.018	0.024
2842.4	PRF31A2	ORJMK7	21	0.015	0.02	0.04	0.04	0.497	0.044	-0.025	0.030
18302.29	OTD2	ORJMK7	21	0.015	0.02	0.04	0.04	0.497	0.044	-0.025	0.030
8897.3	LRRF32A	ANM11	21	0.015	0.02	0.04	0.04	0.497	0.125	-0.049	0.024
12737.18	MMP7	OTZ721	21	0.017	0.03	0.02	0.04	0.497	0.044	-0.025	0.030
2627.2	UBA	ORJMK7	21	0.015	0.02	0.04	0.04	0.497	2.71E+07	-0.028	0.011
8897.2	UBA	ORJMK7	21	0.015	0.02	0.04	0.04	0.497	2.71E+07	-0.028	0.011
18202.22	CD37	PI1501	21	0.017	0.03	0.02	0.04	0.499	0.027	-0.058	0.025
3187.70	PEA3	IL14735	21	0.015	0.02	0.04	0.04	0.499	0.095	-0.058	0.025
13554.4	GNPNA7	ORJMK7	21	0.015	0.02	0.04	0.04	0.499	0.095	-0.058	0.025
10086.11	PIGFRA	IL16234	21	0.015	0.02	0.04	0.04	0.500	0.310	-0.006	0.024
15504.39	BDRG1	ORJMK7	21	0.015	0.02	0.04	0.04	0.501	0.259	-0.041	0.024
7217.76	UBA2	ORJMK7	21	0.015	0.02	0.04	0.04	0.501	0.688	-0.012	0.023
8834.58	CANX	PZ780	21	0.015	0.02	0.04	0.04	0.502	0.365	-0.039	0.023
10830.55	DEFB116	ORJMK7	21	0.015	0.02	0.04	0.04	0.502	0.688	-0.012	0.023
11391.69	MIK	ORJMK7	21	0.015	0.02	0.04	0.04	0.503	0.001	-0.046	0.028
12963.1	GNX17	ORJMK7	21	0.015	0.02	0.04	0.04	0.503	0.707	-0.024	0.023
14300.9	HNRPNB	ORJMK7	21	0.015	0.02	0.04	0.04	0.503	0.001	-0.046	0.028
17835.21	ANKRD13	PZ7216	21	0.015	0.02	0.04	0.04	0.503	0.338	-0.025	0.023
19141.22	DAP	ORJMK7	21	0.015	0.02	0.04	0.04	0.503	0.978	-0.005	0.021
1002.13	WDR9	ORJMK7	21	0.015	0.02	0.04	0.04	0.503	0.715	-0.005	0.021
4314.12	DCTP1	ORJMK7	21	0.015	0.02	0.04	0.04	0.503	0.001	-0.046	0.028
10356.21	JUN	ORJMK7	21	0.015	0.02	0.04	0.04	0.503	0.001	-0.046	0.028
13930.3	APC23	ORJMK7	21	0.015	0.02	0.04	0.04	0.503	0.999	-0.041	0.028
4128.27	POLR2C	ORJMK7	21	0.015	0.02	0.04	0.04	0.503	0.309	-0.042	0.023
5745.64	RIS	ORJMK7	21	0.015	0.02	0.04	0.04	0.503	0.309	-0.042	0.023
5196.7	NMT1	ORJMK7	21	0.015	0.02	0.04	0.04	0.504	0.258	-0.049	0.024
11862.7	XNP4	ORJMK7	21	0.015	0.02	0.04	0.04	0.505	0.055	-0.049	0.025
12984.9	TRNP4	ORJMK7	21	0.015	0.02	0.04	0.04	0.505	0.055	-0.049	0.025
14662.6	MPF1	ORJMK7	21	0.017	0.04	0.02	0.04	0.506	0.001	-0.038	0.027
10356.21	JUN	ORJMK7	21	0.015	0.02	0.04	0.04	0.506	0.001	-0.038	0.027
13624.17	NADK	ORJMK7	21	0.015	0.02	0.04	0.04	0.506	0.082	-0.028	0.025
14687.6	HLRC	ORJMK7	21	0.015	0.02	0.04	0.04	0.506	0.033	-0.044	0.024
17786.5	GEPR1	ORJMK7	21	0.015	0.02	0.04	0.04	0.506	0.033	-0.044	0.024
8584.1	HRC	PZ3327	21	0.015	0.02	0.04	0.04	0.506	0.882	-0.014	0.024
7855.108	MIR4	ORJMK7	21	0.015	0.02	0.04	0.04	0.507	0.001	-0.040	0.025
9016.21	ESRP1	ORJMK7	21	0.015	0.02	0.04	0.04	0.507	0.001	-0.040	0.025
13713.184	SEC22A	ORJMK7	21	0.015	0.02	0.04	0.04	0.507	0.157	-0.009	0.024
18952.54	PRM5A	ORJMK7	21	0.015	0.02	0.04	0.04	0.507	1.800	-0.021	0.011

Table S3. Association of type 2 diabetes with deCODE plasma protein

SNP	Gene	UnP	nsp	b/w	se/w	pval/w	CI/w	FDR	Q	pval	MR Egger	se/egger	pval/egger	CI/egger	egger	Interegger	pval/inter	se/median	pval/median	CI/median	b/med	se/med	pval/med	CI/med	
15436_40	RAMP1	CG0884	21	0.012	0.02	0.303	-0.01 (0.01, 0.03)	0.596	0.779	0.021	0.024	0.193	-0.03 (0.08, 0.02)	0.003	0.038	-0.031	0.020	0.124	-0.03 (0.07, 0.01)	-0.031	0.024	0.211	-0.03 (0.08, 0.02)		
16533_68	CFAP45	CG1989	21	0.012	0.02	0.338	-0.01 (0.01, 0.03)	0.627	0.729	0.023	0.025	0.151	-0.04 (0.08, 0.03)	0.003	0.035	0.022	0.041	-0.03 (0.07, 0.03)	-0.029	0.024	0.241	-0.03 (0.07, 0.03)			
18628_135	FMT	CG4978	21	0.012	0.02	0.303	-0.01 (0.04, 0.01)	0.598	0.335	0.024	0.024	0.143	-0.04 (0.08, 0.01)	0.001	0.287	-0.038	0.023	0.121	-0.04 (0.08, 0.01)	-0.027	0.023	0.246	-0.03 (0.07, 0.02)		
14051_54	FOXC2	CG4989	21	0.012	0.02	0.304	-0.01 (0.01, 0.03)	0.596	0.345	0.026	0.023	0.263	-0.03 (0.07, 0.02)	0.002	0.059	-0.011	0.019	0.181	-0.03 (0.08, 0.03)	-0.024	0.022	0.272	-0.02 (0.07, 0.02)		
12681_13	TMC3D3	CG2918	21	0.012	0.02	0.305	-0.01 (0.01, 0.03)	0.624	0.021	0.024	0.024	0.193	-0.04 (0.08, 0.04)	0.002	0.059	0.024	0.024	0.181	-0.04 (0.08, 0.04)	-0.024	0.022	0.272	-0.02 (0.07, 0.02)		
8956_56	SCARF2	CG0826	21	0.012	0.02	0.304	-0.01 (0.04, 0.01)	0.596	0.137	0.001	0.025	0.088	-0.04 (0.09, 0.05)	0.001	0.537	-0.019	0.020	0.463	-0.02 (0.07, 0.03)	-0.030	0.024	0.222	-0.03 (0.08, 0.02)		
1170_12	SUST1	CG1012	21	0.012	0.02	0.305	-0.01 (0.01, 0.03)	0.624	0.021	0.024	0.024	0.193	-0.04 (0.08, 0.04)	0.002	0.059	0.024	0.024	0.181	-0.04 (0.08, 0.04)	-0.024	0.022	0.272	-0.02 (0.07, 0.02)		
8933_84	MEF2C	CG0413	21	0.013	0.03	0.305	-0.01 (0.01, 0.04)	0.597	0.005	0.042	0.028	0.103	-0.04 (0.09, 0.01)	0.003	0.013	-0.010	0.020	0.543	-0.01 (0.05, 0.03)	-0.015	0.023	0.508	-0.02 (0.08, 0.03)		
15448_47	SDSMT1	CG13501	21	0.012	0.02	0.305	-0.01 (0.01, 0.03)	0.597	0.407	0.038	0.023	0.101	-0.04 (0.08, 0.01)	0.003	0.013	-0.009	0.021	0.646	-0.01 (0.05, 0.03)	-0.004	0.024	0.698	-0.01 (0.06, 0.04)		
17332_3	ADPRAL1	CG06448	21	0.012	0.02	0.307	-0.01 (0.01, 0.04)	0.611	0.021	0.024	0.024	0.193	-0.04 (0.08, 0.04)	0.002	0.059	0.024	0.024	0.181	-0.04 (0.08, 0.04)	-0.024	0.022	0.272	-0.02 (0.07, 0.02)		
19388_2	QSOX1	PS5289	21	0.013	0.03	0.305	-0.01 (0.01, 0.04)	0.598	0.002	0.119	0.026	0.471	-0.02 (0.07, 0.03)	0.002	0.155	0.004	0.024	0.870	0.386	-0.04 (0.04, 0.00)	-0.004	0.024	0.873	-0.384	-0.03 (0.05, 0.04)
8410_26	NLSL4	CG14841	21	0.012	0.02	0.308	-0.01 (0.01, 0.04)	0.598	0.002	0.032	0.026	0.223	-0.03 (0.08, 0.02)	0.003	0.045	-0.030	0.019	0.109	-0.03 (0.08, 0.01)	-0.036	0.022	0.111	-0.04 (0.09, 0.01)		
8501_4	SC2B2A	CG1660	21	0.012	0.02	0.308	-0.01 (0.01, 0.04)	0.598	0.002	0.032	0.026	0.223	-0.03 (0.08, 0.02)	0.003	0.045	-0.030	0.019	0.109	-0.03 (0.08, 0.01)	-0.036	0.022	0.111	-0.04 (0.09, 0.01)		
12432_23	CACYPB	CG0871	21	0.012	0.02	0.308	-0.01 (0.04, 0.01)	0.598	0.096	0.042	0.025	0.093	-0.04 (0.09, 0.01)	0.002	0.168	-0.052	0.021	0.104	-0.05 (0.09, 0.01)	-0.057	0.025	0.225	-0.06 (0.11, -0.01)		
4209_59	THY	CG19142	21	0.012	0.02	0.308	-0.01 (0.04, 0.01)	0.598	0.047	0.038	0.025	0.160	-0.04 (0.09, 0.01)	0.001	0.301	-0.040	0.024	0.160	-0.04 (0.09, 0.01)	-0.040	0.024	0.160	-0.04 (0.09, 0.01)		
8473_55	BPIFA1	CG08751	21	0.012	0.02	0.308	-0.01 (0.01, 0.04)	0.598	0.129	0.045	0.024	0.065	-0.04 (0.09, 2.58e-03)	0.004	0.007	-0.008	0.021	0.702	-0.01 (0.05, 0.03)	0.000	0.024	0.985	4.69e-04 (0.05, 0.05)		
8236_8	C12orf52	CG18201	21	0.012	0.02	0.308	-0.01 (0.01, 0.03)	0.598	0.788	0.016	0.023	0.075	-0.02 (0.06, 0.03)	0.002	0.158	0.021	0.023	0.302	-0.02 (0.06, 0.02)	0.021	0.026	0.411	0.02 (0.03, 0.07)		
8300_82	PKC14	CG12881	21	0.012	0.02	0.307	-0.01 (0.01, 0.03)	0.598	0.225	0.025	0.024	0.017	-0.03 (0.08, 0.03)	0.001	0.278	-0.046	0.020	0.020	-0.05 (0.08, 0.01)	-0.042	0.023	0.195	-0.04 (0.08, 4.50e-03)		
8017_8	SPR	PS5270	21	0.012	0.02	0.307	-0.01 (0.01, 0.03)	0.598	0.381	0.035	0.023	0.129	-0.04 (0.08, 0.01)	0.003	0.019	0.000	0.024	0.944	-1.82e-04 (0.05, 0.01)	-0.017	0.021	0.433	-0.02 (0.06, 0.03)		
12698_166	PRMT3	CG06078	21	0.012	0.02	0.307	-0.01 (0.01, 0.03)	0.598	0.005	0.029	0.028	0.272	-0.03 (0.08, 0.02)	0.003	0.062	0.004	0.020	0.834	4.20e-03 (0.04, 0.00)	-0.038	0.027	0.153	-0.04 (0.09, 0.01)		
19224_5	EP1AY	CG12162	21	0.012	0.02	0.307	-0.01 (0.01, 0.03)	0.599	0.030	0.048	0.026	0.180	-0.04 (0.08, 0.01)	0.002	0.146	-0.057	0.021	0.500	-0.01 (0.05, 0.01)	-0.058	0.027	0.229	-0.06 (0.11, -0.01)		
13735_1	RAP1GAP	PT1736	21	0.012	0.02	0.308	-0.01 (0.01, 0.03)	0.599	0.288	0.030	0.024	0.209	-0.03 (0.08, 0.02)	0.003	0.043	0.002	0.024	0.936	-1.91e-03 (0.04, 0.00)	-0.009	0.023	0.709	-0.01 (0.05, 0.04)		
18229_30	NCP1B	CG12162	21	0.013	0.03	0.308	-0.01 (0.01, 0.04)	0.599	0.018	0.035	0.025	0.160	-0.04 (0.08, 0.01)	0.002	0.027	0.014	0.021	0.500	-0.01 (0.05, 0.03)	-0.007	0.023	0.758	-0.01 (0.05, 0.04)		
11177_16	KRT5	P13647	21	0.013	0.03	0.308	-0.01 (0.04, 0.01)	0.600	0.005	0.051	0.028	0.045	-0.05 (0.10, 0.61e-04)	0.002	0.102	-0.031	0.023	0.195	-0.03 (0.08, 0.01)	-0.029	0.023	0.212	-0.03 (0.08, 0.02)		
12260_9	NTRC	CG18205	21	0.012	0.02	0.309	-0.01 (0.04, 0.01)	0.600	0.237	0.030	0.025	0.217	-0.03 (0.08, 0.02)	0.001	0.391	-0.028	0.022	0.204	-0.03 (0.07, 0.02)	-0.035	0.025	0.254	-0.03 (0.08, 0.01)		
18417_3	ASMT1	CG18889	21	0.013	0.03	0.308	-0.01 (0.01, 0.04)	0.600	0.049	0.058	0.025	0.050	-0.08 (0.10, 0.01)	0.004	0.001	-0.006	0.024	0.768	-0.01 (0.08, 0.04)	0.004	0.024	0.962	4.24e-03 (0.04, 0.05)		
7925_18	SMO2	ANCF2E2	21	0.012	0.02	0.308	-0.01 (0.01, 0.03)	0.600	0.101	0.089	0.024	0.024	-0.07 (0.12, 0.02)	0.005	1.20E-04	-0.029	0.020	0.244	-0.03 (0.07, 0.02)	-0.029	0.024	0.539	-0.03 (0.08, 0.02)		
11378_37	SYK	P34305	21	0.012	0.02	0.309	-0.01 (0.04, 0.01)	0.600	0.135	0.035	0.025	0.155	-0.04 (0.08, 0.01)	0.001	0.277	-0.004	0.024	0.151	-0.03 (0.08, 0.01)	-0.043	0.028	0.907	-0.04 (0.09, 0.01)		
15343_337	KMT1	CG12162	21	0.012	0.02	0.309	-0.01 (0.01, 0.03)	0.601	0.006	0.009	0.027	0.184	-0.04 (0.08, 0.01)	0.000	0.831	0.001	0.024	0.858	2.99e-03 (0.04, 0.00)	0.008	0.024	0.901	-0.01 (0.04, 0.00)		
13984_1	SLK	PC22087	21	0.013	0.03	0.309	-0.01 (0.01, 0.04)	0.601	0.015	0.011	0.025	0.005	-0.07 (0.12, 0.02)	0.005	1.20E-04	-0.017	0.021	0.425	-0.02 (0.06, 0.02)	-0.011	0.024	0.653	-0.01 (0.06, 0.04)		
1032_55	BST2	CG10562	21	0.012	0.02	0.309	-0.01 (0.01, 0.03)	0.602	0.002	0.002	0.025	0.180	-0.04 (0.08, 0.01)	0.002	0.056	-0.007	0.021	0.714	-0.01 (0.05, 0.03)	-0.005	0.024	0.714	-0.01 (0.05, 0.04)		
14047_78	BONF	PC23580	21	0.015	0.05	0.310	-0.02 (0.04, 0.01)	0.601	7.05E-06	0.055	0.029	0.082	-0.05 (0.10, 2.35e-03)	0.003	0.115	-0.044	0.020	0.053	0.05 (0.09, 6.75e-04)	-0.044	0.023	0.057	-0.04 (0.09, 1.04e-03)		
12786_51	GFPCD1	PC19858	21	0.012	0.02	0.311	-0.01 (0.04, 0.01)	0.603	0.205	0.025	0.022	0.302	-0.03 (0.07, 0.02)	0.001	0.530	-0.044	0.020	0.208	-0.04 (0.08, 4.88e-03)	-0.043	0.024	0.881	-0.04 (0.09, 0.01)		
8272_2	HSD17B4	PS6042	21	0.012	0.02	0.311	-0.01 (0.01, 0.03)	0.603	0.460	0.033	0.023	0.072	-0.03 (0.07, 0.02)	0.001	0.617	-0.011	0.020	0.023	0.017	-0.01 (0.05, 0.03)	-0.003	0.023	0.617	-0.01 (0.05, 0.03)	
10445_20	APOM	PS6445	21	0.016	0.06	0.311	-0.02 (0.05, 0.02)	0.603	4.85E-11	0.008	0.032	0.184	-0.01 (0.07, 0.06)	0.001	0.697	0.028	0.021	0.173	-0.01 (0.07, 0.01)	-0.038	0.028	0.166	0.04 (-0.02, 0.09)		
13377_3	CYB5B101	CG18201	21	0.014	0.04	0.311	-0.01 (0.01, 0.04)	0.603	0.003	0.003	0.027	0.194	-0.03 (0.08, 0.02)	0.003	0.036	-0.011	0.024	0.654	-0.01 (0.08, 0.04)	-0.042	0.025	0.940	-1.90e-03 (0.05, 0.05)		
14303_14	ACAD8	CG12162	21	0.012	0.02	0.312	-0.01 (0.01, 0.03)	0.603	0.132	0.012	0.024	0.184	-0.04 (0.08, 0.01)	0.002	0.059	0.028	0.020	0.834	-0.03 (0.08, 0.01)	-0.012	0.024	0.901	-0.01 (0.04, 0.00)		
11352_42	TRT	CG18201	21	0.012	0.02	0.312	-0.01 (0.01, 0.04)	0.604	0.042	0.031	0.025	0.215	-0.03 (0.08, 0.02)	0.003	0.042	0.003	0.024	0.699	-0.01 (0.05, 0.03)	-0.005	0.023	0.817	-0.01 (0.04, 0.05)		
16580_10	HSP9A	CG12162	21	0.012	0.02	0.312	-0.01 (0.01, 0.03)	0.604	0.002	0.002	0.025	0.184	-0.04 (0.08, 0.01)	0.002	0.059	0.028	0.020	0.834	-0.03 (0.08, 0.01)	-0.012	0.024	0.901			

Table S3. Association of type 2 diabetes with deCODE plasma protein

Gene	Uniprot	nsnp	bw	bw	se_bw	prval	CI_low	CI_high	FOR_low	Q_val	egger	se_egger	prval_egger	CI_low_egger	CI_high_egger	egger	Interegger	prval_inter	se_inter	CI_low_inter	CI_high_inter	b_mede	se_mede	CI_low_mede	CI_high_mede		
14947.34	EIF3	FR5822	21	-0.11	0.012	0.350	-0.01	(-0.04, 0.01)	0.838	0.157	-0.037	0.025	0.147	-0.04	(-0.09, 0.01)	0.002	0.246	-0.044	0.021	0.032	-0.04	(-0.09, -3.82e-02)	-0.052	0.028	0.072	-0.05	(-0.11, 4.25e-03)
4444.4	PRPF	Q27275	21	-0.11	0.012	0.350	-0.01	(-0.04, 0.01)	0.838	0.157	-0.037	0.025	0.147	-0.04	(-0.09, 0.01)	0.002	0.246	-0.044	0.021	0.032	-0.04	(-0.09, -3.82e-02)	-0.052	0.028	0.072	-0.05	(-0.11, 4.25e-03)
17152.10	KRMA5	P43632	21	0.11	0.012	0.350	0.01	(0.01, 0.03)	0.638	0.174	-0.053	0.024	0.182	-0.05	(-0.10, 0.01)	0.004	0.002	-0.009	0.020	0.654	0.01	(0.05, 0.03)	-0.018	0.023	0.448	-0.02	(0.06, 0.03)
18826.7	PRMD3	P25788	21	0.11	0.012	0.350	0.01	(0.01, 0.03)	0.638	0.174	-0.053	0.024	0.182	-0.05	(-0.10, 0.01)	0.004	0.002	-0.009	0.020	0.654	0.01	(0.05, 0.03)	-0.018	0.023	0.448	-0.02	(0.06, 0.03)
14107.1	MTRFS	P14114	21	0.11	0.012	0.350	0.01	(0.01, 0.03)	0.638	0.174	-0.053	0.024	0.182	-0.05	(-0.10, 0.01)	0.004	0.002	-0.009	0.020	0.654	0.01	(0.05, 0.03)	-0.018	0.023	0.448	-0.02	(0.06, 0.03)
17222.57	REEG	Q68458	21	0.12	0.013	0.351	0.01	(0.01, 0.04)	0.839	0.046	-0.053	0.025	0.083	-0.05	(-0.10, -4.46e-02)	0.004	0.003	0.005	0.020	0.800	0.01	(0.03, 0.04)	0.000	0.023	0.987	-3.73e-04	(0.05, 0.04)
16919.35	GB	Q15403	21	0.11	0.012	0.351	0.01	(0.01, 0.03)	0.839	0.046	-0.053	0.025	0.083	-0.05	(-0.10, 0.02)	0.004	0.003	0.005	0.020	0.800	0.01	(0.03, 0.04)	0.000	0.023	0.987	-3.73e-04	(0.05, 0.04)
30554.34	IL4R	Z42434	21	0.11	0.011	0.351	0.01	(0.01, 0.03)	0.839	0.119	-0.044	0.024	0.083	-3.55e-03	(0.05, 0.04)	0.001	0.493	0.008	0.024	0.730	0.01	(0.05, 0.04)	0.004	0.023	0.848	4.48e-03	(0.04, 0.05)
14163.5	H2AF7	PC0755	21	0.12	0.012	0.351	0.01	(0.01, 0.03)	0.839	0.321	-0.044	0.023	0.059	-0.04	(-0.09, -1.35e-03)	0.003	0.007	-0.020	0.020	0.121	0.02	(-0.02, 0.02)	-0.017	0.024	0.495	-0.02	(0.06, 0.03)
1884.8	SSTA	Q43792	21	0.11	0.012	0.351	0.01	(0.01, 0.03)	0.839	0.046	-0.053	0.025	0.083	-0.05	(-0.10, 0.01)	0.004	0.003	0.005	0.020	0.800	0.01	(0.03, 0.04)	0.000	0.023	0.987	-3.73e-04	(0.05, 0.04)
12001.7	TPI1	Q07157	21	0.11	0.012	0.351	0.01	(0.01, 0.03)	0.839	0.429	-0.074	0.023	0.052	-0.07	(-0.12, 0.03)	0.004	0.003	-0.034	0.021	0.105	0.03	(-0.02, 0.01)	-0.035	0.026	0.173	-0.04	(0.09, 0.02)
17854.33	NAAT10	PI1227	21	0.11	0.012	0.352	0.01	(0.01, 0.03)	0.839	0.065	-0.045	0.025	0.078	-0.05	(-0.10, 0.01)	0.004	0.003	-0.009	0.020	0.725	0.01	(0.05, 0.03)	-0.042	0.025	0.998	-0.04	(0.09, 0.01)
1666.24	MFAP1	Q15811	21	0.11	0.012	0.352	0.01	(0.01, 0.03)	0.839	0.046	-0.053	0.025	0.083	-0.05	(-0.10, 0.01)	0.004	0.003	0.005	0.020	0.800	0.01	(0.03, 0.04)	0.000	0.023	0.987	-3.73e-04	(0.05, 0.04)
8589.13	CDCP1	Q895V8	21	0.12	0.013	0.352	0.01	(0.01, 0.04)	0.839	0.067	-0.035	0.026	0.178	-0.03	(-0.08, 0.02)	0.003	0.005	-0.009	0.024	0.705	0.01	(0.06, 0.04)	-0.009	0.024	0.727	-0.01	(0.04, 0.04)
14893.3	SEC13	P55739	21	0.11	0.012	0.352	0.01	(0.01, 0.03)	0.839	0.046	-0.053	0.025	0.083	-0.05	(-0.10, 0.02)	0.004	0.003	0.005	0.020	0.800	0.01	(0.03, 0.04)	0.000	0.023	0.987	-3.73e-04	(0.05, 0.04)
19869.17	KATZ	Q62830	21	0.11	0.012	0.352	0.01	(0.01, 0.03)	0.839	0.095	-0.055	0.025	0.083	-0.01	(0.04, 0.05)	0.004	0.003	0.005	0.020	0.800	0.01	(0.03, 0.04)	0.000	0.023	0.987	-3.73e-04	(0.05, 0.04)
9002.90	GAD45/GORTA8	Q15811	21	0.11	0.012	0.352	0.01	(0.01, 0.03)	0.839	0.145	-0.055	0.024	0.023	-0.05	(-0.10, -0.01)	0.004	0.002	-0.023	0.020	0.237	0.02	(-0.02, 0.02)	-0.016	0.023	0.481	-0.02	(0.06, 0.04)
10847.1	SUCF1B	Q20283	21	0.11	0.013	0.353	0.01	(0.01, 0.04)	0.839	0.031	-0.046	0.025	0.083	-0.01	(-0.10, 0.03)	0.004	0.006	-0.011	0.022	0.634	0.01	(0.05, 0.03)	-0.012	0.023	0.987	-3.73e-04	(0.05, 0.04)
15417.3	SRPNB5	P9852	21	-0.12	0.013	0.353	-0.01	(-0.04, 0.01)	0.839	0.002	-0.047	0.027	0.081	-0.05	(-0.10, 0.01)	0.002	0.139	-0.047	0.022	0.032	0.05	(-0.09, -4.02e-03)	-0.035	0.024	0.143	-0.03	(0.08, 0.01)
19025.21	ADH14	Q8R84	21	0.11	0.012	0.353	0.01	(0.01, 0.03)	0.839	0.839	0.027	0.023	0.918	2.41e-03	(0.04, 0.05)	0.001	0.877	0.006	0.023	0.734	0.01	(0.04, 0.05)	-0.011	0.023	0.620	0.01	(0.04, 0.03)
14149.9	IL30	Q82970	21	0.11	0.012	0.353	0.01	(0.01, 0.03)	0.840	0.049	-0.049	0.024	0.116	-0.04	(-0.09, 0.01)	0.004	0.007	-0.010	0.020	0.460	0.02	(0.06, 0.02)	-0.020	0.023	0.375	-0.02	(0.07, 0.01)
13711.10	CLTC	Q00610	21	0.11	0.012	0.354	0.01	(0.01, 0.03)	0.840	0.560	-0.043	0.023	0.086	-0.04	(-0.09, 0.01)	0.003	0.008	-0.010	0.020	0.619	0.01	(0.05, 0.03)	-0.020	0.023	0.384	-0.02	(0.06, 0.02)
10418.36	STK12	Q89892	21	0.11	0.012	0.355	0.01	(0.01, 0.03)	0.840	0.068	-0.049	0.024	0.116	-0.04	(-0.09, 0.01)	0.004	0.020	-0.017	0.020	0.460	0.02	(0.06, 0.02)	-0.020	0.023	0.375	-0.02	(0.07, 0.01)
18385.4	PSM10	U75832	21	-0.12	0.013	0.354	-0.01	(-0.04, 0.01)	0.840	0.100	-0.060	0.028	0.022	-0.06	(-0.11, -0.01)	0.003	0.034	-0.037	0.022	0.904	0.04	(0.08, 0.01)	-0.028	0.024	0.282	-0.03	(0.07, 0.02)
19154.41	SRPNB2	Q17093	21	-0.13	0.014	0.354	-0.01	(-0.04, 0.01)	0.840	0.003	-0.060	0.027	0.029	-0.08	(-0.11, -0.01)	0.003	0.046	-0.052	0.023	0.022	0.05	(-0.10, -0.01)	-0.048	0.024	0.046	-0.05	(0.09, -1.05e-03)
1452.17	LCK	P62932	21	0.11	0.012	0.354	0.01	(0.01, 0.03)	0.840	0.226	-0.030	0.024	0.205	-0.03	(-0.08, 0.02)	0.003	0.047	0.006	0.020	0.754	0.01	(0.03, 0.04)	-0.003	0.022	0.998	-2.79e-03	(0.05, 0.04)
4148.49	PAPPA	Q13219	21	-0.08	0.017	0.354	-0.02	(-0.05, 0.02)	0.840	6.85E-14	0.016	0.034	0.841	0.02	(0.05, 0.01)	-0.002	0.281	-0.022	0.025	0.931	0.02	(0.07, 0.03)	-0.000	0.027	0.993	2.77e-04	(0.07, 0.03)
8256.22	USX1	Q82827	21	0.11	0.012	0.354	0.01	(0.01, 0.04)	0.840	2.93E-04	-0.055	0.028	0.048	-0.06	(-0.11, -1.32e-02)	0.004	0.004	-0.007	0.020	0.749	0.01	(0.05, 0.03)	-0.030	0.027	0.273	-0.03	(0.08, 0.02)
105.10	CKX17	Q15811	21	0.11	0.012	0.354	0.01	(0.01, 0.04)	0.840	0.047	-0.059	0.025	0.083	-0.05	(-0.10, 0.01)	0.004	0.001	-0.020	0.020	0.634	0.01	(0.05, 0.03)	-0.018	0.022	0.375	-0.02	(0.07, 0.01)
4712.28	APCD	P05900	21	0.13	0.014	0.354	0.01	(0.01, 0.04)	0.841	1.75E-04	-0.055	0.027	0.048	-0.05	(-0.11, -8.95e-03)	0.004	0.005	-0.004	0.022	0.846	0.01	(0.05, 0.01)	-0.003	0.024	0.907	-2.78e-03	(0.05, 0.04)
9207.15	CDK2	Q72701	21	0.11	0.012	0.355	0.01	(0.01, 0.03)	0.840	0.046	-0.053	0.025	0.083	-0.05	(-0.10, 0.01)	0.004	0.003	0.005	0.020	0.800	0.01	(0.03, 0.04)	0.000	0.023	0.987	-3.73e-04	(0.05, 0.04)
8601.187	LRP1	Q07854	21	0.11	0.012	0.355	0.01	(0.01, 0.03)	0.841	0.572	-0.016	0.023	0.481	-0.02	(-0.06, 0.03)	0.002	0.176	-0.028	0.022	0.234	0.03	(-0.02, 0.02)	-0.018	0.023	0.434	-0.02	(0.06, 0.03)
13133.73	TBP4	Q82827	21	-0.14	0.015	0.356	-0.01	(-0.04, 0.02)	0.842	9.20E-08	0.028	0.030	0.346	0.03	(0.03, 0.03)	0.003	0.194	-0.014	0.027	0.610	0.01	(0.07, 0.04)	-0.021	0.028	0.708	-0.01	(0.07, 0.04)
14111.10	UREC4	Q15811	21	0.11	0.012	0.356	0.01	(0.01, 0.04)	0.842	0.046	-0.053	0.025	0.083	-0.05	(-0.10, 0.05)	0.004	0.005	0.006	0.020	0.800	0.01	(0.03, 0.04)	0.000	0.023	0.987	-3.73e-04	(0.05, 0.04)
3471.49	STK16	Q75166	21	0.12	0.013	0.356	0.01	(0.01, 0.04)	0.842	0.009	-0.024	0.026	0.017	-0.06	(-0.11, -0.01)	0.005	0.001	-0.007	0.022	0.741	0.01	(0.04, 0.05)	-0.006	0.023	0.806	-0.01	(0.05, 0.04)
5441.38	TNKS1	P19429	21	0.11	0.012	0.356	0.01	(0.01, 0.03)	0.842	0.118	-0.022	0.024	0.317	-0.02	(-0.07, 0.02)	0.002	0.099	-0.019	0.021	0.379	0.02	(-0.02, 0.02)	-0.029	0.024	0.234	-0.03	(0.08, 0.02)
900.59	CCL1	Q02812	21	0.11	0.012	0.356	0.01	(0.01, 0.03)	0.842	7.80E-04	-0.029	0.025	0.093	-0.05	(-0.10, 0.01)	0.004	0.009	-0.019	0.020	0.634	0.01	(0.05, 0.03)	-0.018	0.022	0.375	-0.02	(0.07, 0.01)
9532.5	WBP1L	Q82827	21	0.11	0.012	0.357	0.01	(0.01, 0.03)	0.842	0.280	-0.021	0.024	0.385	-0.02	(-0.07, 0.02)	0.002	0.116	-0.015	0.020	0.441	0.02	(-0.02, 0.02)	-0.040	0.027	0.143	-0.04	(0.09, 0.01)
4297.62	SPON1	Q82827	21	0.11	0.012	0.357	0.01	(0.01, 0.03)	0.842	0.046	-0.053	0.025	0.083	-0.05	(-0.10, 0.01)	0.004	0.003	0.005	0.020	0.800	0.01	(0.03, 0.04)	0.000	0.023	0.987	-3.73e-04	(0.05, 0.04)
13605.16	ANK10	Q82827	21	0.12	0.013	0.357	0.01	(0.01, 0.04)	0.842	0.046	-0.051	0.025	0.042	-0.05	(-0.10, -1.26e-02)	0.004	0.004	-0.016	0.020	0.438	0.02	(0.06, 0.02)	-0.013	0.023	0.583	-0.0	

Table S3. Association of type 2 diabetes with deCODE plasma protein

Gene	Chr	Uniprot	nsnp	Inverse variance weighted				MR Egger				Weighted median				Weighted mode							
				b/w	se_b/w	pval/iv	CI_low	FDR_IV	Q_val	begger	se_egger	pval/egger	CI_egger	egger	Interegger	pval/median	se_median	pval/median	CI_median	b_mode	se_mode	pval_mode	CI_mode
1607.56	PKLR	P30613	21	0.010	0.022	0.399	-0.01 (0.01, 0.03)	0.679	0.436	0.008	0.242	0.793	0.01 (0.04, 0.05)	0.002	0.853	-0.008	0.223	0.722	-0.01 (0.05, 0.04)	0.001	0.227	0.955	-1.49e-03 (0.05, 0.05)
1811.29	GATB1	P27274	21	0.010	0.013	0.249	0.01 (0.01, 0.03)	0.719	0.012	0.022	0.038	-0.05 (0.10, 0.354)	0.003	0.128	0.022	0.220	0.169	-0.02 (0.08, 0.03)	0.002	0.288	0.021	0.042	0.04 (0.02, 0.01)
3299.29	TNNT3	O84779	21	0.010	0.012	0.400	-0.01 (0.03, 0.01)	0.681	0.482	0.033	0.023	0.157	-0.03 (0.08, 0.01)	0.001	0.251	-0.047	0.019	0.016	-0.05 (0.09, 0.01)	-0.047	0.024	0.054	-0.05 (0.10, 0.47e-04)
7817.16	TNEM3	Q24249	21	-0.012	0.015	0.400	-0.01 (0.04, 0.02)	0.681	7.84E-07	0.014	0.029	0.621	0.01 (0.04, 0.07)	-0.002	0.287	-0.020	0.026	0.438	-0.02 (0.07, 0.03)	-0.005	0.025	0.858	-4.56e-03 (0.05, 0.02)
12786.44	NUGT3	P18989	21	0.010	0.013	0.249	0.01 (0.01, 0.03)	0.719	0.012	0.022	0.038	-0.05 (0.10, 0.354)	0.003	0.128	0.022	0.220	0.169	-0.02 (0.08, 0.03)	0.002	0.288	0.021	0.042	0.04 (0.02, 0.01)
7878.2	SEC6B1	P60488	21	0.010	0.012	0.401	-0.01 (0.03, 0.01)	0.682	0.533	0.039	0.023	0.093	-0.04 (0.08, 0.01)	0.003	0.016	-0.011	0.023	0.633	-0.01 (0.06, 0.03)	-0.007	0.022	0.747	-0.01 (0.05, 0.04)
10114.2	CD1A	O43768	21	0.010	0.012	0.401	-0.01 (0.03, 0.01)	0.682	0.533	0.039	0.023	0.093	-0.04 (0.08, 0.01)	0.003	0.016	-0.011	0.023	0.633	-0.01 (0.06, 0.03)	-0.007	0.022	0.747	-0.01 (0.05, 0.04)
14599.16	SEMAC6	OH9372	21	0.010	0.012	0.402	-0.01 (0.03, 0.01)	0.683	0.104	-0.039	0.024	0.105	-0.04 (0.09, 0.01)	0.003	0.019	-0.022	0.023	0.933	-0.03 (0.07, 0.01)	-0.022	0.024	0.348	-0.02 (0.07, 0.02)
16999.16	PTPIA2	Q12974	21	0.010	0.012	0.403	-0.01 (0.03, 0.01)	0.684	0.177	-0.043	0.025	0.085	-0.04 (0.09, 0.01)	0.002	0.126	-0.046	0.023	0.407	-0.05 (0.09, 0.04)	-0.047	0.025	0.601	-0.05 (0.10, 1.88e-03)
14299.2	NFATC1	Q86944	21	0.010	0.012	0.403	-0.01 (0.03, 0.01)	0.684	0.177	-0.043	0.025	0.085	-0.04 (0.09, 0.01)	0.002	0.126	-0.046	0.023	0.407	-0.05 (0.09, 0.04)	-0.047	0.025	0.601	-0.05 (0.10, 1.88e-03)
7786.48	CLEC2B	Q82478	21	0.010	0.012	0.403	-0.01 (0.03, 0.01)	0.684	0.060	-0.051	0.024	0.037	-0.05 (0.10, -0.347e-02)	0.004	0.004	-0.027	0.023	0.217	-0.03 (0.08, 0.02)	-0.009	0.025	0.713	-0.01 (0.06, 0.04)
10445.50	ANKRD27	Q8R9W4	21	0.010	0.012	0.403	-0.01 (0.03, 0.01)	0.684	1.139	-0.027	0.024	0.271	-0.03 (0.07, 0.02)	0.002	0.083	-0.011	0.022	0.627	-0.01 (0.05, 0.03)	-0.009	0.023	0.705	-0.01 (0.05, 0.04)
13062.4	EMG3	P27274	21	0.010	0.013	0.249	0.01 (0.01, 0.03)	0.719	0.012	0.022	0.038	-0.05 (0.10, 0.354)	0.003	0.128	0.022	0.220	0.169	-0.02 (0.08, 0.03)	0.002	0.288	0.021	0.042	0.04 (0.02, 0.01)
12616.60	PDXL2	Q8N253	21	0.010	0.012	0.404	-0.01 (0.03, 0.01)	0.685	0.034	-0.008	0.025	0.173	-0.01 (0.04, 0.06)	0.000	0.904	-0.017	0.020	0.388	-0.02 (0.06, 0.02)	-0.022	0.028	0.418	-0.02 (0.06, 0.03)
17734.13	EN3A	Q43768	21	0.010	0.012	0.401	-0.01 (0.03, 0.01)	0.682	0.091	-0.025	0.025	0.105	-0.03 (0.07, 0.02)	0.001	0.099	-0.019	0.025	0.645	-0.02 (0.07, 0.03)	-0.006	0.028	0.604	-0.01 (0.06, 0.04)
5018.88	PRDX6	P30041	21	-0.011	0.013	0.405	-0.01 (0.04, 0.01)	0.685	0.045	-0.039	0.028	0.130	-0.04 (0.09, 0.01)	0.002	0.205	-0.053	0.023	0.203	-0.05 (0.10, 0.01)	-0.054	0.026	0.037	-0.05 (0.10, -3.88e-03)
5912.87	AK1	O05688	21	-0.011	0.014	0.404	-0.01 (0.04, 0.02)	0.685	0.003	-0.040	0.027	0.139	-0.04 (0.09, 0.01)	0.002	0.220	-0.034	0.023	0.130	-0.03 (0.08, 0.01)	-0.037	0.025	0.137	-0.04 (0.09, 0.01)
11242.33	TM61	P18989	21	0.010	0.013	0.249	0.01 (0.01, 0.03)	0.719	0.012	0.022	0.038	-0.05 (0.10, 0.354)	0.003	0.128	0.022	0.220	0.169	-0.02 (0.08, 0.03)	-0.013	0.023	0.104	-0.04 (0.09, 0.01)	
17799.9	PGLS	O05336	21	0.010	0.012	0.405	-0.01 (0.04, 0.01)	0.685	0.106	-0.037	0.025	0.144	-0.04 (0.09, 0.01)	0.002	0.217	-0.037	0.023	0.125	-0.03 (0.08, 0.01)	-0.035	0.024	0.142	-0.03 (0.08, 0.01)
8362.17	MANBA	O04622	21	-0.034	0.041	0.405	-0.03 (0.11, 0.05)	0.685	0.00E+00	0.029	0.028	0.222	-0.06 (0.13, 0.13)	0.004	0.386	-0.027	0.022	0.220	-0.03 (0.08, 0.01)	-0.018	0.026	0.485	-0.02 (0.07, 0.03)
8364.7	TRFPLR	Q8R9S9	21	0.007	0.009	0.405	-0.01 (0.04, 0.02)	0.686	0.017	0.004	0.019	0.041	-0.04 (0.09, 0.01)	0.001	0.452	-0.004	0.015	0.787	-0.03 (0.08, 0.03)	-0.002	0.019	0.804	-0.03 (0.08, 0.03)
5021.13	PPA1	O15181	21	0.010	0.012	0.406	-0.01 (0.03, 0.01)	0.686	0.104	-0.031	0.025	0.217	-0.03 (0.08, 0.02)	0.003	0.059	-0.009	0.021	0.663	-0.01 (0.05, 0.03)	-0.018	0.024	0.502	-0.02 (0.06, 0.03)
5332.53	FOF1B	P17682	21	-0.012	0.014	0.406	-0.01 (0.04, 0.02)	0.686	1.29E-04	0.037	0.038	0.194	-0.04 (0.09, 0.01)	-0.003	0.047	-0.006	0.021	0.777	-0.01 (0.05, 0.03)	-0.013	0.026	0.814	-0.01 (0.06, 0.04)
5687.5	PKRCS3	P14314	21	0.010	0.012	0.406	-0.01 (0.03, 0.01)	0.686	0.074	-0.046	0.025	0.084	-0.05 (0.09, 0.24e-03)	0.002	0.091	-0.042	0.023	0.093	-0.03 (0.08, 0.14e-04)	-0.038	0.025	0.130	-0.04 (0.09, 0.01)
9049.2	SIL16A1	Q15427	21	0.010	0.012	0.406	-0.01 (0.03, 0.01)	0.686	0.292	-0.032	0.023	0.169	-0.03 (0.08, 0.01)	0.003	0.039	-0.009	0.024	0.716	-0.01 (0.04, 0.04)	-0.010	0.025	0.683	-0.01 (0.06, 0.04)
14034.29	HR23F	Q90475	21	0.010	0.012	0.406	-0.01 (0.03, 0.01)	0.686	1.19E-12	0.035	0.033	0.298	-0.01 (0.04, 0.10)	0.001	0.469	-0.035	0.025	0.156	-0.04 (0.08, 0.01)	-0.038	0.024	0.104	-0.04 (0.09, 0.01)
5007.17	MAPK14	O15639	21	0.010	0.012	0.407	-0.01 (0.03, 0.01)	0.686	0.320	-0.028	0.024	0.248	-0.03 (0.08, 0.02)	0.001	0.387	-0.038	0.023	0.177	-0.04 (0.08, 0.01)	-0.043	0.025	0.088	-0.04 (0.09, 0.01)
10589.29	MFSD1	P55001	21	0.011	0.013	0.407	-0.01 (0.03, 0.01)	0.686	0.018	-0.038	0.028	0.174	-0.04 (0.09, 0.02)	0.003	0.040	-0.005	0.023	0.841	-0.02 (0.06, 0.04)	0.001	0.025	0.960	-1.26e-03 (0.05, 0.05)
12415.12	CEP350	P18989	21	0.011	0.013	0.407	-0.01 (0.03, 0.01)	0.686	0.013	0.060	0.026	0.125	-0.01 (0.11, 0.01)	0.004	0.001	-0.021	0.022	0.417	-0.02 (0.06, 0.02)	-0.014	0.022	0.901	-0.02 (0.06, 0.02)
4840.73	CSF3	P09919	21	0.011	0.013	0.407	-0.01 (0.03, 0.01)	0.686	0.004	-0.012	0.027	0.646	-0.01 (0.06, 0.04)	0.001	0.314	-0.017	0.025	0.497	-0.02 (0.06, 0.04)	0.009	0.024	0.701	-0.01 (0.04, 0.06)
12014.19	FOF1B	P17682	21	0.010	0.012	0.406	-0.01 (0.04, 0.02)	0.686	0.017	0.003	0.017	0.041	-0.04 (0.09, 0.01)	0.001	0.452	-0.004	0.015	0.787	-0.03 (0.08, 0.03)	-0.002	0.019	0.804	-0.03 (0.08, 0.03)
7926.13	SPN13	Q20443	21	0.010	0.012	0.408	-0.01 (0.03, 0.01)	0.687	0.188	-0.029	0.024	0.221	-0.03 (0.08, 0.02)	0.002	0.061	-0.019	0.024	0.414	-0.02 (0.07, 0.03)	-0.020	0.025	0.435	-0.02 (0.07, 0.03)
14028.22	PKCZCA	Q09243	21	0.011	0.013	0.408	-0.01 (0.03, 0.01)	0.688	0.029	-0.058	0.025	0.279	-0.03 (0.11, 0.01)	0.004	0.002	-0.022	0.023	0.342	-0.02 (0.07, 0.02)	-0.016	0.023	0.472	-0.02 (0.06, 0.03)
19612.3	CSN1	Q86933	21	0.010	0.012	0.404	-0.01 (0.03, 0.01)	0.688	0.054	-0.011	0.024	0.159	-0.03 (0.08, 0.01)	0.003	0.017	-0.005	0.023	0.462	-0.02 (0.06, 0.03)	-0.017	0.023	0.601	-0.01 (0.06, 0.04)
5679.54	CSX2	P42127	21	0.015	0.018	0.409	-0.01 (0.02, 0.05)	0.689	2.11E+25	0.010	0.036	0.784	-0.01 (0.08, 0.06)	0.002	0.426	-0.015	0.021	0.496	-0.01 (0.05, 0.03)	-0.016	0.023	0.484	-0.02 (0.06, 0.03)
7801.1	COM42	Q8R9C9	21	0.011	0.014	0.409	-0.01 (0.03, 0.01)	0.689	0.003	-0.061	0.026	0.222	-0.06 (0.11, -0.11)	0.004	0.002	-0.004	0.022	0.698	-0.03 (0.08, 0.03)	-0.013	0.024	0.892	-3.26e-03 (0.04, 0.05)
8653.33	LYN	P07843	21	0.010	0.013	0.409	-0.01 (0.03, 0.01)	0.689	0.004	-0.024	0.026	0.222	-0.06 (0.11, -0.11)	0.004	0.002	-0.004	0.022	0.698	-0.03 (0.08, 0.03)	-0.013	0.024	0.892	-3.26e-03 (0.04, 0.05)
7207.4	AK1	O15181	21	0.010	0.012	0.410	-0.01 (0.03, 0.01)	0.689	0.374	-0.043	0.023	0.084	-0.04 (0.09, 0.224e-03)	0.003	0.009	-0.021	0.021	0.634	-0.02 (0.06, 0.02)	-0.018	0.023	0.427	-0.02 (0.06, 0.03)
7232.7	ESF3K	Q00434	21	0.010	0.012	0.410	-0.01 (0.03, 0.01)	0.689	7.50E-03	0.023	0.023	0.265	-0.02 (0.07, 0.02)	0.003	0.009	-0.021	0.021	0.634	-0.02 (0.06, 0.02)	-0.018	0.023	0.427	-0.02 (0.06, 0.03)
4420.7	RAM1	Q43184	21	0.010	0.012	0.410	-0.01 (0.03, 0.01)	0.689	0.408	-0.028	0.023	0.225	-0.03 (0.08, 0.02)	0.002	0.060	-0.011	0.022	0.919	-0.01 (0.05, 0.03)	-0.009	0.025	0.700	-0.01 (0.06, 0.04)
9044.1	CNTNAP3	Q8R9Y1	21	0.010	0.012	0.410	-0.01 (0.03, 0.01)	0.689	0.088	-0.035	0.024	0.152	-0.04 (0.08, 0.01)	0.003	0.035	-0.018	0.022	0.448	-0.02 (0.06, 0.03)	-0.009	0.023	0.687	-0.01 (0.06, 0.04)
9361.7	PCDH9L1	Q8R9Y1	21	0.010	0.012	0.410	-0.01 (0.03, 0.01)	0.689	0.088	-0.035	0.024	0.152	-0.04 (0.08, 0.01)	0.003	0.035	-0.018	0.022	0.448	-0.02 (0.06, 0.03)	-0.009	0.023	0.687	-0.01 (0.06, 0.04)
8913.22	SIGLEC11	Q8R9L6	21	0.010	0.012	0.410	-0.01 (0.03,																

Table S3. Association of type 2 diabetes with deCODE plasma protein

SNP	Gene	Chr	BP	Inverse variance weighted				MR Egger				Weighted mode				Weighted mode						
				beta	se_beta	p_val	CI_low	beta	se_beta	p_val	CI_low	beta	se_beta	p_val	CI_low	beta	se_beta	p_val	CI_low			
2578.87	CCL2	P13500	21	0.009	0.012	0.453	0.01	(0.01, 0.03)	0.723	0.107	0.000	0.225	0.094	1.99e-04	(0.05, 0.05)	0.001	0.685	-0.009	0.24	0.688	-0.01	(0.06, 0.04)
1202.2	KREM2	NR6900	21	0.009	0.012	0.452	0.01	(0.01, 0.03)	0.723	0.107	0.000	0.225	0.094	1.99e-04	(0.05, 0.05)	0.001	0.685	-0.009	0.24	0.688	-0.01	(0.06, 0.04)
3761.4	PTGS2	P35354	21	-0.009	0.012	0.453	0.01	(-0.03, 0.01)	0.723	0.108	-0.000	0.224	0.091	-0.008	(-0.13, -0.03)	0.004	0.001	-0.042	0.19	0.028	0.04	(-0.08, -0.50e-06)
9053.16	CRP2	P29243	21	-0.009	0.012	0.453	0.01	(-0.02, 0.03)	0.723	0.104	-0.004	0.225	0.084	-0.04	(-0.09, 0.01)	0.003	0.015	-0.020	0.22	0.36	-0.02	(-0.02, -0.02)
9379.248	EMR1D	Q10921	21	-0.009	0.012	0.453	0.01	(-0.01, 0.03)	0.723	0.105	-0.002	0.224	0.085	-0.02	(-0.07, 0.02)	0.002	0.022	-0.032	0.22	0.42	-0.03	(-0.02, 0.02)
9893.27	CAZ1	P45388	21	-0.009	0.012	0.453	0.01	(-0.03, 0.01)	0.723	0.105	-0.002	0.225	0.087	-0.02	(-0.07, 0.02)	0.002	0.022	-0.032	0.22	0.42	-0.03	(-0.02, 0.02)
10273.22	MATK	Q10921	21	-0.009	0.012	0.453	0.01	(-0.03, 0.01)	0.723	0.105	-0.002	0.225	0.087	-0.02	(-0.07, 0.02)	0.002	0.022	-0.032	0.22	0.42	-0.03	(-0.02, 0.02)
10854.17	LSMA	OY4240	21	-0.010	0.014	0.454	0.01	(-0.02, 0.04)	0.723	0.106	-0.004	0.224	0.086	-0.04	(-0.11, -0.04)	0.002	0.005	-0.014	0.23	0.538	-0.01	(-0.08, 0.03)
10858.77	OPB2A	Q29529	21	-0.009	0.012	0.454	0.01	(-0.03, 0.01)	0.723	0.106	-0.004	0.224	0.086	-0.04	(-0.11, -0.04)	0.002	0.005	-0.014	0.23	0.538	-0.01	(-0.08, 0.03)
10931	ANGPT1	OY9525	21	-0.009	0.012	0.454	0.01	(-0.03, 0.01)	0.723	0.106	-0.004	0.224	0.086	-0.04	(-0.11, -0.04)	0.002	0.005	-0.014	0.23	0.538	-0.01	(-0.08, 0.03)
11394.3	SULT1A3	P04988	21	-0.009	0.012	0.454	0.01	(-0.03, 0.01)	0.723	0.107	-0.002	0.225	0.087	-0.02	(-0.07, 0.02)	0.001	0.497	-0.047	0.20	0.032	0.05	(-0.09, -0.99e-04)
11399.7	LAP3	P28838	21	-0.009	0.012	0.455	0.01	(-0.03, 0.01)	0.723	0.107	-0.002	0.225	0.087	-0.02	(-0.07, 0.02)	0.001	0.360	-0.034	0.23	0.143	-0.03	(-0.08, 0.01)
11614.13	PHL1	Q10921	21	-0.009	0.012	0.455	0.01	(-0.03, 0.01)	0.723	0.107	-0.002	0.225	0.087	-0.02	(-0.07, 0.02)	0.001	0.360	-0.034	0.23	0.143	-0.03	(-0.08, 0.01)
11620.12	SPN1	OY9527	21	-0.010	0.013	0.455	0.01	(-0.02, 0.04)	0.723	0.103	-0.003	0.226	0.083	-0.04	(-0.11, -0.04)	0.002	0.020	-0.010	0.23	0.675	-0.01	(-0.08, 0.04)
12027.22	PAK6	Q10921	21	-0.009	0.012	0.455	0.01	(-0.03, 0.01)	0.723	0.106	-0.002	0.225	0.087	-0.02	(-0.07, 0.02)	0.001	0.448	-0.038	0.22	0.078	-0.04	(-0.08, 0.04)
12754.11	JAG1	P07850	21	-0.009	0.012	0.455	0.01	(-0.03, 0.01)	0.723	0.104	-0.002	0.225	0.087	-0.02	(-0.07, 0.02)	0.002	0.134	-0.005	0.21	0.803	-0.01	(-0.08, 0.04)
8235.48	CHGB	Q10921	21	-0.013	0.017	0.455	0.01	(-0.05, 0.02)	0.723	0.106	-0.004	0.224	0.086	-0.04	(-0.11, -0.04)	0.001	0.671	-0.033	0.23	0.899	-0.03	(-0.05, 0.01)
13029.27	CROT	Q10921	21	-0.009	0.012	0.455	0.01	(-0.03, 0.01)	0.723	0.106	-0.002	0.225	0.087	-0.02	(-0.07, 0.02)	0.001	0.260	-0.01	0.25	0.283	-0.02	(-0.07, 0.02)
13033.75	ADAM22	OP0101	21	-0.009	0.012	0.456	0.01	(-0.03, 0.02)	0.724	0.104	-0.001	0.224	0.087	-0.01	(-0.04, 0.06)	0.001	0.339	-0.000	0.25	1.000	0.00	(-0.05, 0.01)
10580.14	SFTA2	OB0100	21	-0.009	0.012	0.457	0.01	(-0.03, 0.02)	0.724	0.103	-0.002	0.224	0.087	-0.01	(-0.04, 0.06)	0.002	0.067	0.001	0.21	0.973	0.07	(-0.04, -0.04)
11444.49	POLR3F	Q10921	21	-0.009	0.012	0.457	0.01	(-0.03, 0.02)	0.724	0.103	-0.002	0.224	0.087	-0.01	(-0.04, 0.06)	0.002	0.067	0.001	0.21	0.973	0.07	(-0.04, -0.04)
12504.28	LMO1	P29536	21	-0.009	0.012	0.457	0.01	(-0.03, 0.02)	0.724	0.103	-0.002	0.224	0.087	-0.01	(-0.04, 0.06)	0.003	0.009	-0.016	0.22	0.448	-0.02	(-0.06, 0.03)
12623.24	TMC6	Q10921	21	-0.009	0.012	0.457	0.01	(-0.03, 0.02)	0.724	0.103	-0.002	0.224	0.087	-0.01	(-0.04, 0.06)	0.001	0.455	-0.017	0.21	0.999	-0.02	(-0.06, 0.03)
8004.15	GAD65	O14556	21	-0.009	0.012	0.457	0.01	(-0.03, 0.02)	0.724	0.109	-0.007	0.224	0.086	-0.04	(-0.06, 0.04)	0.001	0.446	-0.015	0.23	0.507	-0.02	(-0.06, 0.03)
13245.17	KCNK4	Q10921	21	-0.010	0.013	0.457	0.01	(-0.03, 0.02)	0.725	0.107	-0.005	0.226	0.083	-0.05	(-0.10, -0.04)	0.004	0.008	-0.024	0.22	0.284	-0.02	(-0.07, 0.02)
10530.8	PSMB8	P29072	21	-0.009	0.012	0.458	0.01	(-0.03, 0.01)	0.725	0.110	-0.001	0.224	0.086	-0.01	(-0.06, 0.02)	0.002	0.064	-0.014	0.22	0.529	-0.01	(-0.06, 0.03)
12794.6	NLRP4	O96922	21	-0.010	0.013	0.458	0.01	(-0.03, 0.02)	0.725	0.109	-0.003	0.225	0.083	-0.03	(-0.10, -0.04)	0.004	0.004	-0.024	0.22	0.284	-0.02	(-0.07, 0.02)
13452.113	SMX1	P0D303	21	-0.009	0.012	0.458	0.01	(-0.03, 0.01)	0.725	0.107	-0.002	0.225	0.083	-0.02	(-0.07, 0.02)	0.004	0.008	-0.024	0.22	0.284	-0.02	(-0.07, 0.02)
8235.95	SRFBP1	Q10921	21	-0.009	0.012	0.458	0.01	(-0.03, 0.01)	0.725	0.107	-0.002	0.225	0.083	-0.02	(-0.07, 0.02)	0.004	0.008	-0.024	0.22	0.284	-0.02	(-0.07, 0.02)
8528.95	EXTL2	Q10921	21	-0.009	0.013	0.458	0.01	(-0.03, 0.02)	0.725	0.103	-0.002	0.225	0.083	-0.02	(-0.07, 0.02)	0.004	0.003	-0.025	0.22	0.245	-0.03	(-0.06, 0.03)
8598.8	STK17B	Q10921	21	-0.009	0.013	0.458	0.01	(-0.03, 0.02)	0.725	0.103	-0.002	0.225	0.083	-0.02	(-0.07, 0.02)	0.004	0.003	-0.025	0.22	0.245	-0.03	(-0.06, 0.03)
8917.9	NRXN1	Q10921	21	-0.011	0.015	0.459	0.01	(-0.02, 0.04)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.000	0.785	-0.028	0.20	0.171	-0.03	(-0.07, 0.01)
12689.30	HECW1	Q10921	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	(-0.05, 0.04)
9642.2	CTNNA1	Q10921	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	(-0.05, 0.04)
11482.8	RFX2	Q13251	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	(-0.05, 0.04)
9086.3	CD55	Q13251	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	(-0.05, 0.04)
9086.3	CD55	Q13251	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	(-0.05, 0.04)
9086.3	CD55	Q13251	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	(-0.05, 0.04)
9086.3	CD55	Q13251	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	(-0.05, 0.04)
9086.3	CD55	Q13251	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	(-0.05, 0.04)
9086.3	CD55	Q13251	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	(-0.05, 0.04)
9086.3	CD55	Q13251	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	(-0.05, 0.04)
9086.3	CD55	Q13251	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	(-0.05, 0.04)
9086.3	CD55	Q13251	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	(-0.05, 0.04)
9086.3	CD55	Q13251	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	(-0.05, 0.04)
9086.3	CD55	Q13251	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	(-0.05, 0.04)
9086.3	CD55	Q13251	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	(-0.05, 0.04)
9086.3	CD55	Q13251	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	(-0.05, 0.04)
9086.3	CD55	Q13251	21	-0.009	0.013	0.459	0.01	(-0.03, 0.02)	0.725	0.103	-0.004	0.224	0.083	-0.04	(-0.06, 0.06)	0.004	0.002	-0.006	0.21	0.770	-0.01	

Table S3. Association of type 2 diabetes with deCODE plasma protein

SNP	Gene	UTP	nsnp	bw	se_bw	prval	CI_low	CI_high	FDR_low	Q_val	bagger	se_bagger	prval	CI_low	CI_high	egger	Interegger	prval	se_median	prval	CI_low	CI_high	b_mode	se_mode	prval	CI_low	CI_high		
160472	GRAP2	PT5791	21	0.008	0.102	0.503	0.01 (-0.02, 0.03)	0.755	0.448	0.304	0.025	0.167	0.03 (-0.08, 0.01)	0.003	0.049	0.021	0.020	0.294	0.02 (-0.02, 0.02)	0.003	0.294	0.02 (-0.02, 0.02)	-0.035	0.025	0.173	0.03 (-0.08, 0.01)	0.003		
14599_77	L1B	209687	21	0.008	0.102	0.503	0.01 (-0.02, 0.03)	0.755	0.448	0.304	0.025	0.167	0.03 (-0.08, 0.01)	0.003	0.049	0.021	0.020	0.294	0.02 (-0.02, 0.02)	0.003	0.294	0.02 (-0.02, 0.02)	-0.035	0.025	0.173	0.03 (-0.08, 0.01)	0.003		
5621_64	THSD1	QNS582	21	0.008	0.102	0.503	0.01 (-0.02, 0.03)	0.755	0.448	0.304	0.025	0.167	0.03 (-0.08, 0.01)	0.003	0.049	0.021	0.020	0.294	0.02 (-0.02, 0.02)	0.003	0.294	0.02 (-0.02, 0.02)	-0.035	0.025	0.173	0.03 (-0.08, 0.01)	0.003		
7035_81	NESD1	QZ381	21	0.011	0.016	0.002	-0.01 (-0.04, 0.02)	0.755	2.09E-10	0.016	0.032	0.680	0.02 (-0.05, 0.04)	0.002	0.344	0.007	0.026	0.761	0.01 (-0.04, 0.04)	0.002	0.761	0.01 (-0.04, 0.04)	0.007	0.026	0.761	0.01 (-0.04, 0.04)	0.002		
10430_31	BCL2L2	Q81945	21	0.008	0.102	0.503	0.01 (-0.02, 0.03)	0.755	0.602	-0.049	0.023	0.036	-0.05 (-0.09, -3.2E-02)	0.004	0.005	-0.025	0.022	0.255	0.02 (-0.07, 0.02)	0.019	0.255	0.02 (-0.07, 0.02)	-0.019	0.024	0.255	0.02 (-0.07, 0.02)	0.019		
5037_82	L1B	209687	21	0.008	0.102	0.503	0.01 (-0.02, 0.03)	0.755	0.448	0.304	0.025	0.167	0.03 (-0.08, 0.01)	0.003	0.049	0.021	0.020	0.294	0.02 (-0.02, 0.02)	0.003	0.294	0.02 (-0.02, 0.02)	-0.035	0.025	0.173	0.03 (-0.08, 0.01)	0.003		
109243_1	BCL2L2	Q81945	21	0.008	0.102	0.503	0.01 (-0.02, 0.03)	0.755	0.602	-0.049	0.023	0.036	-0.05 (-0.09, -3.2E-02)	0.004	0.005	-0.025	0.022	0.255	0.02 (-0.07, 0.02)	0.019	0.255	0.02 (-0.07, 0.02)	-0.019	0.024	0.255	0.02 (-0.07, 0.02)	0.019		
18905_5	KRT16	OR8779	21	0.008	0.102	0.503	0.01 (-0.02, 0.03)	0.755	0.423	0.006	0.023	0.789	0.01 (-0.04, 0.05)	0.000	0.940	0.014	0.020	0.175	0.01 (-0.05, 0.02)	0.010	0.175	0.01 (-0.05, 0.02)	0.010	0.023	0.175	0.01 (-0.05, 0.02)	0.010		
16407_35	TNKS1	Q45378	21	0.008	0.102	0.503	0.01 (-0.02, 0.03)	0.755	0.423	0.006	0.023	0.789	0.01 (-0.04, 0.05)	0.000	0.940	0.014	0.020	0.175	0.01 (-0.05, 0.02)	0.010	0.175	0.01 (-0.05, 0.02)	0.010	0.023	0.175	0.01 (-0.05, 0.02)	0.010		
168520_10	PDZK1	Q521W1	21	0.008	0.102	0.503	0.01 (-0.02, 0.03)	0.755	0.053	-0.057	0.025	0.02 (-0.06, -0.11, -0.01)	0.004	0.005	-0.029	0.022	0.145	0.03 (-0.07, 0.01)	0.021	0.145	0.03 (-0.07, 0.01)	-0.021	0.022	0.145	0.03 (-0.07, 0.01)	0.021			
18841_1	SRPNBL1	Q8U878	21	0.009	0.104	0.506	0.01 (-0.04, 0.02)	0.757	0.001	0.011	0.027	0.695	-0.01 (-0.06, 0.04)	0.000	0.945	-0.026	0.026	0.312	-0.03 (-0.02, 0.02)	-0.033	0.312	-0.03 (-0.02, 0.02)	-0.033	0.024	0.312	-0.03 (-0.02, 0.02)	-0.033		
10207_19	AKC	Q55263	21	0.009	0.104	0.506	0.01 (-0.04, 0.02)	0.757	0.001	0.011	0.027	0.695	-0.01 (-0.06, 0.04)	0.000	0.945	-0.026	0.026	0.312	-0.03 (-0.02, 0.02)	-0.033	0.312	-0.03 (-0.02, 0.02)	-0.033	0.024	0.312	-0.03 (-0.02, 0.02)	-0.033		
8259_9	LYSG6	Q8U878	21	-0.009	0.103	0.506	0.01 (-0.03, 0.02)	0.757	0.036	-0.066	0.025	0.009	-0.07 (-0.11, -0.02)	0.004	0.009	-0.043	0.020	0.034	0.04 (-0.08, -3.34E-04)	0.044	0.034	0.04 (-0.08, -3.34E-04)	0.044	0.025	0.034	0.04 (-0.08, -3.34E-04)	0.044		
9695_5	MTR1	Q15360	21	0.009	0.103	0.505	0.01 (-0.03, 0.02)	0.757	0.047	-0.049	0.025	0.05 (-0.05, 0.10, -0.02)	0.003	0.057	-0.028	0.020	0.161	0.03 (-0.07, 0.01)	-0.043	0.161	0.03 (-0.07, 0.01)	-0.043	0.022	0.161	0.03 (-0.07, 0.01)	-0.043			
2966_65	PCLP1	Q9Y240	21	0.010	0.104	0.508	0.01 (-0.02, 0.04)	0.758	2.14E-04	0.024	0.029	0.411	0.02 (-0.02, 0.03, 0.08)	-0.001	0.571	-0.003	0.025	0.904	0.298 (-0.05, 0.01)	-0.008	0.298	0.298 (-0.05, 0.01)	-0.008	0.022	0.298	0.298 (-0.05, 0.01)	-0.008		
12882_7	PANP1	Q81211	21	0.008	0.102	0.508	0.01 (-0.02, 0.03)	0.758	0.198	0.027	0.024	0.017	-0.06 (-0.10, -0.01)	0.004	0.002	0.013	0.022	0.566	0.01 (-0.06, 0.03)	-0.011	0.566	0.01 (-0.06, 0.03)	-0.011	0.024	0.566	0.01 (-0.06, 0.03)	-0.011		
19536_24	SCDH	Q45378	21	0.008	0.102	0.508	0.01 (-0.02, 0.03)	0.758	0.191	0.023	0.023	0.087	-0.04 (-0.08, 0.01)	0.003	0.019	-0.005	0.025	0.853	-0.04 (-0.08, 0.01)	-0.007	0.853	-0.04 (-0.08, 0.01)	-0.007	0.024	0.853	-0.04 (-0.08, 0.01)	-0.007		
3171_57	APC	P50587	21	-0.010	0.104	0.508	0.01 (-0.04, 0.02)	0.759	2.83E-05	-0.039	0.029	0.175	0.04 (-0.10, 0.02)	0.002	0.236	-0.041	0.024	0.087	0.04 (-0.08, 0.01)	-0.048	0.087	0.04 (-0.08, 0.01)	-0.048	0.025	0.087	0.04 (-0.08, 0.01)	-0.048		
16257_14	ROBO4	Q8W276	21	0.008	0.102	0.508	0.01 (-0.01, 0.03)	0.759	0.338	0.112	0.023	0.023	0.823	0.01 (-0.01, 0.03, 0.06)	0.000	0.848	-0.002	0.025	0.813	-0.06 (-0.05, 0.01)	-0.003	0.813	-0.06 (-0.05, 0.01)	-0.003	0.025	0.813	-0.06 (-0.05, 0.01)	-0.003	
11352_8	BTIC2	P43489	21	0.008	0.102	0.508	0.01 (-0.02, 0.04)	0.759	0.001	0.027	0.027	0.186	0.03 (-0.01, -4.1E-02)	0.004	0.005	-0.029	0.022	0.648	0.03 (-0.07, 0.01)	-0.021	0.648	0.03 (-0.07, 0.01)	-0.021	0.024	0.648	0.03 (-0.07, 0.01)	-0.021		
14675_20	PC3	P23588	21	-0.009	0.103	0.509	0.01 (-0.03, 0.02)	0.760	0.032	-0.051	0.026	0.048	-0.05 (-0.10, -3.8E-02)	0.003	0.056	-0.051	0.020	0.012	0.05 (-0.09, -0.01)	-0.063	0.056	0.012	0.05 (-0.09, -0.01)	-0.063	0.028	0.056	0.012	0.05 (-0.09, -0.01)	-0.063
5730_81	TNFRSF4	P43489	21	0.008	0.102	0.509	0.01 (-0.02, 0.03)	0.761	0.454	0.031	0.023	0.186	0.03 (-0.08, 0.01)	0.002	0.056	-0.016	0.020	0.244	0.02 (-0.05, 0.02)	-0.028	0.244	0.02 (-0.05, 0.02)	-0.028	0.028	0.244	0.02 (-0.05, 0.02)	-0.028		
12825_28	VAV1	P15488	21	0.008	0.102	0.510	0.01 (-0.03, 0.02)	0.761	0.117	-0.027	0.025	0.281	0.03 (-0.08, 0.02)	0.001	0.376	-0.038	0.022	0.084	0.04 (-0.08, 0.01)	-0.039	0.376	0.04 (-0.08, 0.01)	-0.039	0.028	0.376	0.04 (-0.08, 0.01)	-0.039		
11568_2	PKSFB	P81806	21	-0.009	0.103	0.510	0.01 (-0.03, 0.02)	0.761	0.016	-0.040	0.026	0.127	-0.04 (-0.09, 0.01)	0.002	0.167	-0.032	0.023	0.170	0.03 (-0.08, 0.01)	-0.035	0.167	0.03 (-0.08, 0.01)	-0.035	0.022	0.167	0.03 (-0.08, 0.01)	-0.035		
14693_10	FTL3	P48771	21	0.008	0.102	0.510	0.01 (-0.02, 0.03)	0.761	0.208	0.041	0.026	0.087	-0.04 (-0.08, 0.01)	0.003	0.019	-0.005	0.025	0.853	-0.04 (-0.08, 0.01)	-0.007	0.853	-0.04 (-0.08, 0.01)	-0.007	0.024	0.853	-0.04 (-0.08, 0.01)	-0.007		
17366_341	EEF1D	P29682	21	-0.009	0.103	0.510	0.01 (-0.03, 0.02)	0.761	0.056	-0.031	0.026	0.222	-0.04 (-0.08, 0.02)	0.001	0.290	-0.051	0.020	0.170	0.05 (-0.09, -0.01)	-0.050	0.290	0.05 (-0.09, -0.01)	-0.050	0.027	0.290	0.05 (-0.09, -0.01)	-0.050		
15322_39	CRADD	P78520	21	0.009	0.103	0.511	0.01 (-0.02, 0.03)	0.761	0.030	-0.013	0.026	0.608	-0.01 (-0.06, 0.04)	0.001	0.330	-0.020	0.022	0.368	-0.02 (-0.07, 0.02)	-0.021	0.368	-0.02 (-0.07, 0.02)	-0.021	0.024	0.368	-0.02 (-0.07, 0.02)	-0.021		
16969_15	COL2A1	P15488	21	0.009	0.103	0.511	0.01 (-0.02, 0.03)	0.761	0.001	0.019	0.027	0.608	-0.01 (-0.06, 0.04)	0.001	0.330	-0.020	0.022	0.368	-0.02 (-0.07, 0.02)	-0.021	0.368	-0.02 (-0.07, 0.02)	-0.021	0.024	0.368	-0.02 (-0.07, 0.02)	-0.021		
11402_17	MTC2	Q8W824	21	0.008	0.102	0.512	0.01 (-0.02, 0.03)	0.761	0.144	0.041	0.024	0.090	0.04 (-0.09, 0.01)	0.003	0.020	-0.025	0.021	0.252	0.02 (-0.07, 0.02)	-0.024	0.252	0.02 (-0.07, 0.02)	-0.024	0.024	0.252	0.02 (-0.07, 0.02)	-0.024		
14192_9	TRAF3	Q15360	21	0.009	0.104	0.509	0.01 (-0.03, 0.02)	0.761	0.001	0.011	0.027	0.695	-0.01 (-0.06, 0.04)	0.000	0.945	-0.026	0.026	0.312	-0.03 (-0.02, 0.02)	-0.033	0.312	-0.03 (-0.02, 0.02)	-0.033	0.024	0.312	-0.03 (-0.02, 0.02)	-0.033		
15414_316	LHDA	P00338	21	0.009	0.104	0.512	0.01 (-0.02, 0.04)	0.761	2.80E-04	-0.035	0.028	0.211	0.03 (-0.09, 0.02)	0.003	0.067	-0.023	0.023	0.331	0.03 (-0.07, 0.02)	-0.028	0.331	0.03 (-0.07, 0.02)	-0.028	0.028	0.331	0.03 (-0.07, 0.02)	-0.028		
18237_29	NR3C3	Q8U878	21	0.008	0.102	0.511	0.01 (-0.02, 0.03)	0.761	0.083	-0.055	0.024	0.030	-0.05 (-0.10, -0.01)	0.004	0.004	-0.037	0.021	0.080	0.04 (-0.08, -4.37E-04)	-0.029	0.080	0.04 (-0.08, -4.37E-04)	-0.029	0.023	0.080	0.04 (-0.08, -4.37E-04)	-0.029		
3656_7	WVF	Q15360	21	0.009	0.104	0.512	0.01 (-0.03, 0.02)	0.761	0.043	-0.031	0.024	0.176	0.04 (-0.09, 0.01)	0.003	0.076	-0.041	0.020	0.433	0.01 (-0.06, 0.03)	-0.029	0.433	0.01 (-0.06, 0.03)	-0.029	0.028	0.433	0.01 (-0.06, 0.03)	-0.029		
3356_50	CAT	P43166	21	0.008	0.102	0.512	0.01 (-0.02, 0.03)	0.761	0.258	0.116	0.024	0.517	-0.02 (-0.06, 0.03)	0.001	0.262	-0.012	0.022	0.574	0.01 (-0.06, 0.03)	-0.014	0.574	0.01 (-0.06, 0.03)	-0.014	0.028	0.574	0.01 (-0.06, 0.03)	-0.014		
8400_1	NMES1	Q8U878	21	0.008	0.102	0.512	0.01 (-0.02, 0.03)	0.761	0.142	-0.034	0.025	0.189	-0.03 (-0.08, 0.01)	0.002	0.219	-0.025	0.024	0.252	0.02 (-0.07, 0.02)	-0.024	0.252	0.02 (-0.07, 0.02)	-0.024	0.024	0.252	0.02 (-0.07, 0.02)	-0.024		
14645_253	GSTA4	P23588	21	0.009	0.103	0.512	0.01 (-0.02, 0.04)	0.761	0.001	0.011	0.027	0.695	-0.01 (-0.06, 0.04)	0.000	0.945	-0.026	0.026	0.312	-0.03 (-0.02, 0.02)	-0.033	0.312	-0.03 (-0.02, 0.02)	-0.033	0.024	0.312	-0.03 (-0.02, 0.02)	-0.033</		

Table S3. Association of type 2 diabetes with deCODE plasma protein

SNP	Gene	Uniprot	nsnp	bw	sv	pr	cl	MD	Weighted mode	Weighted mode													
rsid																							
3535_34	DKKI1	ENR007	211	-0.007	0.015	0.859	-0.01 (0.04, 0.02)	0.841	1.99E-05	0.046	0.229	0.115	-0.05 (0.10, 0.01)	0.003	0.117	-0.035	0.24	0.137	-0.04 (0.08, 0.01)	-0.038	0.205	0.158	-0.04 (0.08, 0.01)
7705_29	SH3BP2		211	0.005	0.012	0.859	0.01 (0.02, 0.03)	0.841	1.99E-05	0.046	0.229	0.115	-0.05 (0.10, 0.01)	0.003	0.117	-0.035	0.24	0.137	-0.04 (0.08, 0.01)	-0.038	0.205	0.158	-0.04 (0.08, 0.01)
8053_16	DNAH1B	ENR0188	211	0.005	0.012	0.859	0.01 (0.02, 0.03)	0.841	1.99E-05	0.046	0.229	0.115	-0.05 (0.10, 0.01)	0.003	0.117	-0.035	0.24	0.137	-0.04 (0.08, 0.01)	-0.038	0.205	0.158	-0.04 (0.08, 0.01)
8347_222	DNAAF1	ENR0188	211	0.005	0.012	0.859	0.01 (0.02, 0.03)	0.841	1.99E-05	0.046	0.229	0.115	-0.05 (0.10, 0.01)	0.003	0.117	-0.035	0.24	0.137	-0.04 (0.08, 0.01)	-0.038	0.205	0.158	-0.04 (0.08, 0.01)
12545_18	SNK1		211	0.005	0.012	0.859	0.01 (0.02, 0.03)	0.841	1.99E-05	0.046	0.229	0.115	-0.05 (0.10, 0.01)	0.003	0.117	-0.035	0.24	0.137	-0.04 (0.08, 0.01)	-0.038	0.205	0.158	-0.04 (0.08, 0.01)
9713_67	PQDRLR	Q15198	211	0.005	0.012	0.859	0.01 (0.02, 0.03)	0.841	1.99E-05	0.046	0.229	0.115	-0.05 (0.10, 0.01)	0.003	0.117	-0.035	0.24	0.137	-0.04 (0.08, 0.01)	-0.038	0.205	0.158	-0.04 (0.08, 0.01)
10177_52	GRP94		211	0.005	0.012	0.859	0.01 (0.02, 0.03)	0.841	1.99E-05	0.046	0.229	0.115	-0.05 (0.10, 0.01)	0.003	0.117	-0.035	0.24	0.137	-0.04 (0.08, 0.01)	-0.038	0.205	0.158	-0.04 (0.08, 0.01)
12711_19	GJAB	P48165	211	0.005	0.011	0.862	0.01 (0.02, 0.03)	0.843	0.240	-0.048	0.023	0.400	-0.05 (0.10, 0.01)	0.003	0.079	-0.004	0.023	0.855	-4.26E-03 (0.05, 0.0)	0.001	0.228	0.974	-8.39E-04 (0.05, 0.05)
19230_12	GSTT1	P70711	211	0.005	0.012	0.861	0.01 (0.02, 0.03)	0.843	0.208	-0.038	0.024	0.126	-0.04 (0.08, 0.01)	0.003	0.043	-0.005	0.020	0.799	-0.01 (0.04, 0.01)	-0.010	0.024	0.896	-0.01 (0.06, 0.04)
1335_14	PICK1	Q75634	211	0.005	0.012	0.861	0.01 (0.02, 0.03)	0.843	0.208	-0.038	0.024	0.126	-0.04 (0.08, 0.01)	0.003	0.043	-0.005	0.020	0.799	-0.01 (0.04, 0.01)	-0.010	0.024	0.896	-0.01 (0.06, 0.04)
3873_51	TPO	P70720	211	0.005	0.012	0.861	0.01 (0.02, 0.03)	0.843	0.155	-0.060	0.024	0.118	-0.04 (0.08, 0.01)	0.003	0.042	-0.002	0.019	0.897	-2.47E-03 (0.04, 0.0)	-0.025	0.023	0.286	-0.02 (0.07, 0.02)
3905_52	UBE2N	P10188	211	0.006	0.013	0.861	0.01 (0.03, 0.02)	0.843	0.028	-0.037	0.026	0.149	-0.04 (0.09, 0.01)	0.002	0.157	-0.038	0.022	0.102	-0.04 (0.08, 0.01)	-0.033	0.027	0.221	-0.03 (0.08, 0.02)
6306_20	CK2		211	0.005	0.012	0.862	0.01 (0.02, 0.03)	0.843	0.008	-0.074	0.026	0.149	-0.04 (0.09, 0.01)	0.002	0.157	-0.038	0.022	0.102	-0.04 (0.08, 0.01)	-0.033	0.027	0.221	-0.03 (0.08, 0.02)
12480_9	UTDUS	Q89674	211	0.006	0.013	0.862	0.01 (0.02, 0.03)	0.843	0.008	-0.074	0.026	0.149	-0.04 (0.09, 0.01)	0.002	0.157	-0.038	0.022	0.102	-0.04 (0.08, 0.01)	-0.033	0.027	0.221	-0.03 (0.08, 0.02)
5289_23	CNTN4	Q89462	211	0.005	0.012	0.862	0.01 (0.02, 0.03)	0.843	0.208	-0.045	0.026	0.051	-0.05 (0.10, 0.01)	0.003	0.078	-0.018	0.026	0.855	0.02 (0.03, 0.07)	0.012	0.023	0.91	0.01 (0.04, 0.04)
19286_35	GBP1	Q13283	211	0.005	0.012	0.862	0.01 (0.02, 0.03)	0.843	0.053	-0.058	0.025	0.122	-0.06 (0.11, 0.01)	0.003	0.016	-0.037	0.020	0.984	-0.04 (0.08, 0.21E-4)	-0.071	0.025	0.005	-0.07 (0.12, 0.02)
9386_42	TC9B	Q89822	211	0.005	0.012	0.862	0.01 (0.02, 0.03)	0.843	0.421	-0.035	0.024	0.134	-0.04 (0.08, 0.01)	0.002	0.139	-0.022	0.021	0.284	-0.02 (0.06, 0.02)	-0.018	0.023	0.434	-0.02 (0.06, 0.03)
2933_20	HLA	Q29678	211	0.005	0.012	0.862	0.01 (0.02, 0.03)	0.843	0.730	-0.033	0.025	0.139	-0.04 (0.08, 0.01)	0.002	0.139	-0.022	0.021	0.284	-0.02 (0.06, 0.02)	-0.018	0.023	0.434	-0.02 (0.06, 0.03)
11142_11	ANGPT1L	ENR541	211	0.006	0.014	0.864	0.01 (0.03, 0.02)	0.843	0.004	-0.007	0.027	0.174	-0.01 (0.05, 0.0)	0.001	0.578	-0.027	0.023	0.124	-0.03 (0.07, 0.02)	-0.018	0.026	0.484	-0.02 (0.07, 0.03)
13047_15	RSGP1	Q89474	211	0.005	0.012	0.864	0.01 (0.02, 0.03)	0.843	0.112	-0.048	0.024	0.151	-0.05 (0.10, 0.01)	0.003	0.013	-0.028	0.019	0.243	-0.03 (0.07, 0.02)	-0.018	0.026	0.484	-0.02 (0.07, 0.03)
13548_53	PPAP2C	Q11072	211	0.005	0.013	0.864	0.01 (0.02, 0.03)	0.843	0.003	-0.072	0.025	0.159	-0.02 (0.06, 0.02)	0.001	0.485	-0.026	0.020	0.202	-0.02 (0.06, 0.02)	-0.029	0.024	0.221	-0.03 (0.08, 0.02)
17154_2	PTGES3	ENR125	211	0.006	0.014	0.864	0.01 (0.02, 0.03)	0.843	0.001	-0.059	0.027	0.209	-0.08 (0.11, 0.01)	0.004	0.006	-0.017	0.022	0.428	-0.02 (0.06, 0.03)	-0.008	0.024	0.798	-0.01 (0.05, 0.04)
9620_87	L22R41	Q89997	211	0.005	0.012	0.864	0.01 (0.02, 0.03)	0.843	0.144	-0.074	0.024	0.033	-0.07 (0.12, 0.03)	0.004	0.001	-0.021	0.021	0.202	-0.02 (0.06, 0.02)	-0.031	0.024	0.205	-0.03 (0.08, 0.02)
5455_23	HSEB1	Q15043	211	0.006	0.014	0.864	0.01 (0.02, 0.03)	0.843	3.69E-05	0.003	0.029	0.928	-2.98E-03 (0.06, 0.05)	0.001	0.722	-0.019	0.020	0.345	-0.02 (0.06, 0.02)	-0.014	0.025	0.586	-0.01 (0.06, 0.04)
9625_56	SCARF2	Q89626	211	0.005	0.012	0.865	0.01 (0.02, 0.03)	0.843	0.665	-0.037	0.023	0.110	-0.04 (0.08, 0.01)	0.003	0.036	-0.009	0.019	0.625	-0.01 (0.05, 0.03)	-0.026	0.024	0.291	-0.03 (0.07, 0.02)
12584_5	GCA	Q29678	211	0.005	0.012	0.865	0.01 (0.02, 0.03)	0.844	0.020	-0.020	0.026	0.440	-0.07 (0.07, 0.03)	0.002	0.259	-0.028	0.024	0.265	-0.03 (0.07, 0.02)	-0.032	0.024	0.188	-0.03 (0.08, 0.02)
18610_3	GDH	P13150	211	0.005	0.012	0.865	0.01 (0.02, 0.03)	0.844	0.020	-0.020	0.026	0.440	-0.07 (0.07, 0.03)	0.002	0.259	-0.028	0.024	0.265	-0.03 (0.07, 0.02)	-0.032	0.024	0.188	-0.03 (0.08, 0.02)
3848_14	GAD65	P14448	211	0.005	0.012	0.865	0.01 (0.02, 0.03)	0.844	0.051	-0.034	0.026	0.170	-0.03 (0.08, 0.02)	0.002	0.199	-0.033	0.024	0.163	-0.03 (0.08, 0.02)	-0.025	0.025	0.315	-0.02 (0.07, 0.02)
9007_20	CAM4	Q89826	211	0.005	0.012	0.865	0.01 (0.02, 0.03)	0.844	0.697	-0.017	0.024	0.196	-0.02 (0.06, 0.02)	0.001	0.485	-0.026	0.020	0.202	-0.02 (0.06, 0.02)	-0.029	0.024	0.221	-0.03 (0.08, 0.02)
8033_57	LGH3	Q8H145	211	0.005	0.012	0.865	0.01 (0.02, 0.03)	0.844	0.217	-0.024	0.024	0.176	-0.02 (0.07, 0.03)	0.002	0.205	-0.017	0.021	0.420	-0.02 (0.06, 0.02)	-0.018	0.024	0.558	-0.02 (0.06, 0.03)
19135_5	INTSCL	Q89826	211	0.005	0.012	0.864	0.01 (0.02, 0.03)	0.843	0.003	-0.072	0.025	0.159	-0.02 (0.06, 0.02)	0.001	0.485	-0.026	0.020	0.202	-0.02 (0.06, 0.02)	-0.029	0.024	0.221	-0.03 (0.08, 0.02)
4429_51	CHST2	Q8G2X3	211	0.005	0.012	0.867	0.01 (0.02, 0.03)	0.845	0.387	-0.048	0.023	0.037	-0.05 (0.09, 0.032E-02)	0.003	0.008	-0.019	0.023	0.501	-0.02 (0.06, 0.03)	-0.008	0.024	0.727	-0.01 (0.05, 0.04)
8060_2	HP	P12723	211	0.005	0.012	0.867	0.01 (0.02, 0.03)	0.845	0.064	-0.009	0.027	0.147	-0.01 (0.04, 0.0)	0.001	0.544	-0.016	0.025	0.414	-0.02 (0.06, 0.03)	-0.018	0.025	0.481	-0.02 (0.07, 0.03)
10546_2	TSPYL	Q89496	211	0.005	0.012	0.868	0.01 (0.02, 0.03)	0.846	0.024	-0.024	0.024	0.463	-0.11 (0.11, 0.01)	0.002	0.107	-0.024	0.024	0.356	-0.02 (0.06, 0.02)	-0.018	0.025	0.481	-0.02 (0.07, 0.03)
9874_172	CALSI	P39059	211	0.006	0.015	0.869	0.01 (0.04, 0.02)	0.847	3.81E-05	0.029	0.029	0.324	-0.03 (0.09, 0.03)	0.001	0.372	-0.024	0.026	0.370	-0.02 (0.06, 0.03)	-0.031	0.026	0.234	-0.03 (0.08, 0.02)
12534_10	CALCOCCO	Q13137	211	0.006	0.015	0.869	0.01 (0.02, 0.03)	0.847	0.034	-0.061	0.025	0.107	-0.06 (0.11, 0.01)	0.004	0.003	-0.014	0.022	0.533	-0.03 (0.07, 0.02)	-0.015	0.028	0.554	-0.02 (0.07, 0.04)
10613_1	L18R49		211	0.005	0.012	0.869	0.01 (0.02, 0.03)	0.847	0.003	-0.022	0.024	0.163	-0.02 (0.06, 0.02)	0.001	0.403	-0.017	0.023	0.610	-0.02 (0.06, 0.02)	-0.024	0.027	0.610	-0.02 (0.07, 0.03)
3325_2	MAT2	Q00339	211	0.006	0.014	0.870	0.01 (0.03, 0.02)	0.847	0.002	-0.009	0.028	0.176	-0.01 (0.05, 0.0)	0.001	0.544	-0.016	0.022	0.476	-0.02 (0.06, 0.03)	-0.021	0.025	0.395	-0.02 (0.07, 0.03)
19189_2	USP14	Q15543	211	0.005	0.012	0.870	0.01 (0.02, 0.03)	0.847	0.003	-0.022	0.024	0.155	-0.02 (0.06, 0.02)	0.001	0.403	-0.017	0.023	0.610	-0.02 (0.06, 0.02)	-0.024	0.027	0.610	-0.02

Table S3. Association of type 2 diabetes with deCODE plasma protein

SNP	Gene	Uniprot	nsp	bw	sw	prval	clval	FDR	Q	val	beuger	segger	prval	clval	egger	Integger	prval	median	prval	clval	bmode	prval	clval	
9402.18	DCED11	ENR28	21	0.003	0.012	0.779	3.26e-03 (0.02, 0.03)	0.009	0.166	0.051	0.024	0.034	0.05e-04 (0.001, 0.01)	0.003	0.009	0.009	0.028	0.020	0.166	0.03 (0.07, 0.01)	-0.024	0.024	0.331	0.02 (0.07, 0.02)
9404.144	EPOH1	ENR22	21	0.003	0.012	0.779	3.26e-03 (0.02, 0.03)	0.009	0.203	0.048	0.024	0.034	0.05e-04 (0.001, 0.01)	0.003	0.009	0.009	0.028	0.020	0.166	0.03 (0.07, 0.01)	-0.024	0.024	0.331	0.02 (0.07, 0.02)
17455.42	FOLR1	P15328	21	0.004	0.013	0.781	3.62e-03 (0.02, 0.03)	0.007	0.034	0.041	0.026	0.058	0.01 (0.06, 0.04)	0.001	0.428	0.015	0.025	0.599	0.01 (0.04, 0.06)	0.013	0.025	0.605	0.01 (0.04, 0.06)	
9959.80	TMEM93	OR0428	21	0.003	0.012	0.781	3.62e-03 (0.02, 0.03)	0.007	0.067	0.046	0.026	0.088	0.07 (0.11, -0.02)	0.004	0.003	0.036	0.021	0.084	0.04 (0.06, 0.047e)	-0.037	0.023	0.110	-0.04 (0.08, 0.01)	
12071.35	SULT1B1	Q1301	21	0.003	0.012	0.781	3.62e-03 (0.02, 0.03)	0.007	0.034	0.041	0.026	0.058	0.01 (0.06, 0.04)	0.001	0.428	0.015	0.025	0.599	0.01 (0.04, 0.06)	0.013	0.025	0.605	0.01 (0.04, 0.06)	
14013.11	TANK	Q92844	21	0.003	0.012	0.783	3.48e-03 (0.02, 0.02)	0.008	0.044	0.037	0.025	0.135	0.04 (0.09, 0.01)	0.002	0.117	0.032	0.023	0.164	0.03 (0.08, 0.01)	-0.038	0.024	0.119	-0.04 (0.08, 0.01)	
12599.28	SCD5	P58819	21	0.003	0.012	0.783	3.48e-03 (0.02, 0.02)	0.008	0.044	0.037	0.025	0.135	0.04 (0.09, 0.01)	0.002	0.117	0.032	0.023	0.164	0.03 (0.08, 0.01)	-0.038	0.024	0.119	-0.04 (0.08, 0.01)	
26455.34	PKRIZ2	Q51153	21	0.003	0.012	0.782	3.22e-03 (0.02, 0.02)	0.008	0.415	0.053	0.023	0.023	0.02e-05 (0.00, 0.01)	0.003	0.013	0.037	0.022	0.102	0.04 (0.08, 0.01)	-0.044	0.025	0.079	-0.04 (0.08, 0.01)	
16099.99	ND2	Q14112	21	0.004	0.013	0.784	3.68e-03 (0.02, 0.03)	0.008	0.003	0.040	0.026	0.129	0.04 (0.09, 0.01)	0.003	0.005	0.031	0.021	0.137	0.03 (0.07, 0.01)	-0.045	0.026	0.079	-0.05 (0.10, 0.02)	
17327.3	CNPY3	Q91819	21	0.003	0.012	0.781	3.26e-03 (0.02, 0.03)	0.009	0.115	0.016	0.022	0.098	0.04 (0.09, 0.01)	0.003	0.011	0.036	0.024	0.162	0.01 (0.04, 0.06)	-0.045	0.026	0.079	-0.05 (0.10, 0.02)	
18877.15	CND2	Q99439	21	0.003	0.012	0.785	3.22e-03 (0.02, 0.02)	0.009	0.328	0.028	0.024	0.129	0.03 (0.07, 0.02)	0.002	0.223	0.033	0.022	0.137	0.03 (0.08, 0.01)	-0.032	0.025	0.194	-0.03 (0.08, 0.01)	
4301.58	TK1	Q14183	21	0.003	0.012	0.785	3.22e-03 (0.02, 0.02)	0.009	0.105	0.061	0.025	0.104	0.06 (0.11, -0.01)	0.004	0.007	0.026	0.024	0.269	0.03 (0.07, 0.02)	-0.012	0.023	0.623	0.01 (0.08, 0.01)	
9654.29	PITPNB	Q91819	21	0.003	0.012	0.781	3.26e-03 (0.02, 0.03)	0.009	0.062	0.027	0.022	0.098	0.04 (0.09, 0.01)	0.003	0.007	0.026	0.024	0.269	0.03 (0.07, 0.02)	-0.012	0.023	0.623	0.01 (0.08, 0.01)	
10390.21	ZNF373	OR5L27	21	0.003	0.012	0.788	3.21e-03 (0.02, 0.03)	0.009	0.246	0.048	0.024	0.048	0.05 (0.10, -0.01)	0.003	0.015	0.014	0.020	0.473	0.01 (0.05, 0.02)	-0.029	0.022	0.201	-0.03 (0.07, 0.01)	
12590.7	PSMB8	P28014	21	0.003	0.012	0.786	3.44e-03 (0.02, 0.02)	0.009	0.045	0.025	0.025	0.051	0.05 (0.10, 0.02)	0.003	0.023	0.021	0.024	0.385	0.03 (0.07, 0.02)	-0.010	0.024	0.088	-0.01 (0.06, 0.04)	
12808.103	CARHSP1	Q9Y2V2	21	0.003	0.012	0.789	3.17e-03 (0.02, 0.03)	0.009	0.129	0.028	0.025	0.280	0.03 (0.08, 0.02)	0.002	0.147	0.020	0.020	0.228	0.02 (0.06, 0.01)	-0.030	0.024	0.202	-0.03 (0.08, 0.01)	
12826.5	SLC6A5	Q92911	21	0.003	0.012	0.789	3.49e-03 (0.02, 0.03)	0.009	0.008	0.027	0.026	0.289	0.03 (0.08, 0.02)	0.002	0.187	0.022	0.023	0.342	0.02 (0.06, 0.01)	-0.035	0.024	0.142	-0.04 (0.08, 0.01)	
13111.78	BCIL1	P41482	21	0.003	0.012	0.789	3.16e-03 (0.02, 0.03)	0.009	0.120	0.045	0.024	0.051	0.05 (0.10, 0.02)	0.003	0.024	0.020	0.024	0.302	0.02 (0.06, 0.01)	-0.025	0.024	0.244	-0.03 (0.08, 0.01)	
13958.5	RBMA6	Q187V0	21	0.003	0.012	0.790	3.08e-03 (0.02, 0.03)	0.009	0.369	0.037	0.023	0.112	0.04 (0.09, 0.01)	0.003	0.046	0.032	0.024	0.143	0.03 (0.08, 0.01)	-0.042	0.023	0.071	-0.04 (0.08, 0.01)	
14098.28	CFM4	P49889	21	0.003	0.012	0.790	3.45e-03 (0.02, 0.03)	0.009	0.049	0.040	0.025	0.112	0.04 (0.09, 0.01)	0.003	0.046	0.032	0.024	0.143	0.03 (0.08, 0.01)	-0.042	0.023	0.071	-0.04 (0.08, 0.01)	
17453.34	CFP	P26689	21	0.003	0.012	0.789	3.78e-03 (0.02, 0.03)	0.009	1.87E-04	0.049	0.027	0.081	0.03 (0.07, 0.02)	0.003	0.027	0.013	0.023	0.151	0.01 (0.05, 0.02)	-0.013	0.024	0.887	0.01 (0.06, 0.04)	
18181.2	TSSC4	Q9Y5U2	21	0.003	0.012	0.789	3.18e-03 (0.02, 0.03)	0.009	0.089	0.046	0.025	0.083	0.05 (0.10, 0.02, 0.03)	0.003	0.022	0.021	0.019	0.263	0.02 (0.06, 0.02)	-0.040	0.023	0.084	-0.04 (0.08, 0.01)	
18302.204	ZWILCH	Q9H900	21	0.004	0.014	0.789	3.69e-03 (0.02, 0.03)	0.009	0.001	0.073	0.027	0.007	0.07 (0.13, -0.02)	0.005	0.001	0.013	0.023	0.561	0.01 (0.06, 0.04)	-0.009	0.024	0.988	0.01 (0.06, 0.04)	
18330.7	PSS2	Q96033	21	0.003	0.012	0.787	3.17e-03 (0.02, 0.03)	0.009	0.314	0.110	0.024	0.093	0.01 (0.06, 0.04)	0.001	0.541	0.006	0.023	0.809	0.01 (0.05, 0.04)	-0.001	0.024	0.954	-1.14 (0.05, 0.05)	
2734.49	NCR2	Q95844	21	0.003	0.012	0.788	3.12e-03 (0.02, 0.03)	0.009	0.313	0.050	0.023	0.034	0.05 (0.10, -0.01)	0.003	0.009	0.015	0.021	0.467	0.02 (0.06, 0.02)	-0.024	0.021	0.255	-0.02 (0.07, 0.02)	
9865.65	FRS3	P12034	21	0.003	0.012	0.788	3.13e-03 (0.02, 0.03)	0.009	0.322	0.038	0.023	0.103	0.04 (0.09, 0.01)	0.003	0.041	0.028	0.022	0.210	0.03 (0.07, 0.02)	-0.028	0.025	0.266	-0.03 (0.08, 0.02)	
3179.5	CTSC	P53634	21	0.003	0.012	0.786	3.22e-03 (0.02, 0.03)	0.009	0.241	0.053	0.024	0.028	0.05 (0.10, -0.01)	0.004	0.007	0.010	0.021	0.625	0.01 (0.05, 0.03)	-0.010	0.023	0.652	0.01 (0.05, 0.03)	
4430.1	ENTPD5	Q17585	21	0.003	0.012	0.790	3.18e-03 (0.02, 0.03)	0.009	0.092	0.029	0.025	0.008	0.07 (0.12, -0.02)	0.004	0.002	0.018	0.021	0.411	0.03 (0.07, 0.02)	-0.016	0.025	0.532	-0.02 (0.07, 0.02)	
5200.80	TYK2	Q91819	21	0.003	0.012	0.789	3.26e-03 (0.02, 0.03)	0.009	0.226	0.048	0.024	0.098	0.04 (0.09, 0.01)	0.003	0.017	0.036	0.024	0.175	0.04 (0.08, 0.01)	-0.052	0.020	0.295	0.01 (0.06, 0.04)	
5634.39	POU1F1	Q9H889	21	0.004	0.014	0.789	3.84e-03 (0.02, 0.03)	0.009	3.41E+05	0.056	0.028	0.047	0.06 (0.11, -1.86e-04)	0.004	0.014	0.028	0.020	0.163	0.03 (0.07, 0.01)	-0.058	0.025	0.023	-0.06 (0.11, -0.01)	
5910.40	JPH1	Q91819	21	0.003	0.012	0.789	3.26e-03 (0.02, 0.03)	0.009	0.062	0.027	0.022	0.117	0.03 (0.07, 0.02)	0.003	0.004	0.014	0.020	0.844	0.01 (0.05, 0.01)	-0.004	0.021	0.854	0.01 (0.05, 0.01)	
6998.106	ASPH	Q17587	21	0.003	0.012	0.789	3.15e-03 (0.02, 0.03)	0.009	0.326	0.039	0.024	0.102	0.04 (0.09, 0.01)	0.003	0.041	0.042	0.021	0.047	0.04 (0.08, 0.02)	-0.038	0.025	0.155	-0.04 (0.08, 0.01)	
8635.283	ZPNR	Q12956	21	0.003	0.012	0.789	3.54e-03 (0.02, 0.03)	0.009	0.105	0.039	0.024	0.091	0.07 (0.12, -0.02)	0.003	0.001	0.020	0.020	0.331	0.02 (0.06, 0.02)	-0.027	0.024	0.272	-0.03 (0.07, 0.02)	
9004.12	CACNA2D3	Q91819	21	0.003	0.012	0.789	3.26e-03 (0.02, 0.03)	0.009	0.233	0.043	0.024	0.102	0.04 (0.09, 0.01)	0.003	0.001	0.013	0.021	0.388	0.02 (0.06, 0.02)	-0.021	0.023	0.484	0.01 (0.06, 0.04)	
9004.12	RNF215	Q9Y157	21	0.003	0.012	0.790	3.16e-03 (0.02, 0.03)	0.009	0.026	0.065	0.025	0.101	0.06 (0.11, -0.02)	0.004	0.005	0.009	0.021	0.647	0.01 (0.05, 0.03)	-0.036	0.027	0.186	-0.04 (0.08, 0.02)	
9200.30	RMN3	Q9H727	21	0.003	0.012	0.789	3.18e-03 (0.02, 0.03)	0.009	0.227	0.052	0.024	0.032	0.05 (0.10, -0.01)	0.003	0.020	0.024	0.020	0.243	0.02 (0.06, 0.02)	-0.024	0.024	0.138	-0.02 (0.07, 0.02)	
9200.30	RNF215	Q9Y157	21	0.003	0.012	0.790	3.16e-03 (0.02, 0.03)	0.009	0.026	0.065	0.025	0.101	0.06 (0.11, -0.02)	0.004	0.005	0.009	0.021	0.647	0.01 (0.05, 0.03)	-0.036	0.027	0.186	-0.04 (0.08, 0.02)	
9534.39	POU1F1	Q9H889	21	0.004	0.014	0.789	3.84e-03 (0.02, 0.03)	0.009	3.41E+05	0.056	0.028	0.047	0.06 (0.11, -1.86e-04)	0.004	0.014	0.028	0.020	0.163	0.03 (0.07, 0.01)	-0.058	0.025	0.023	-0.06 (0.11, -0.01)	
9540.10	JPH1	Q91819	21	0.003	0.012	0.789	3.26e-03 (0.02, 0.03)	0.009	0.062	0.027	0.													

Table S3. Association of type 2 diabetes with deCODE plasma protein

Gene	Chr	Gene/Protein	nsnp	bw	se	beta	prval	CI_low	CI_high	FDR_low	FDR_high	q_val	beqger	segger	prvalgger	CI_lowgger	CI_highgger	egger	Interegger	prvalInteregger	seMedian	prvalMedian	CI_lowMedian	CI_highMedian	b_mode	seMed	prvalMed	CI_lowMed	CI_highMed
19654.61	RFA	INT5308	211	0.002	0.12	0.839	2.34e-03	(0.62, 0.02)	0.932	0.765	0.029	0.023	0.209	0.03	0.027	0.007	(0.02, 0.02)	0.002	0.116	0.023	0.202	0.256	0.02	(0.02, 0.02)	-0.032	0.205	0.196	0.03	(0.08, 0.02)
17416.7	CABLES1	OR9K07	211	0.002	0.12	0.839	2.34e-03	(0.62, 0.02)	0.932	0.765	0.029	0.023	0.209	0.03	0.027	0.007	(0.02, 0.02)	0.002	0.116	0.023	0.202	0.256	0.02	(0.02, 0.02)	-0.032	0.205	0.196	0.03	(0.08, 0.02)
11312.179	FSTL1	IC12841	211	0.003	0.14	0.840	2.90e-03	(0.63, 0.03)	0.933	7.63E-05	0.012	0.029	0.867	0.01	0.027	0.001	(0.04, 0.07)	-0.001	0.703	0.015	0.025	0.568	0.01	(0.06, 0.04)	0.008	0.027	0.781	0.01	(0.05, 0.06)
10620.21	MSMB	11818	211	0.002	0.12	0.841	2.45e-03	(0.63, 0.02)	0.933	0.002	0.116	0.025	0.827	0.02	0.027	0.002	(0.04, 0.07)	0.001	0.405	0.019	0.025	0.312	0.02	(0.02, 0.02)	0.032	0.204	0.180	0.03	(0.01, 0.08)
11314.20	SLC2	OR9K04	211	0.002	0.12	0.842	2.65e-03	(0.63, 0.02)	0.933	0.002	0.116	0.025	0.827	0.02	0.027	0.002	(0.04, 0.07)	0.001	0.405	0.019	0.025	0.312	0.02	(0.02, 0.02)	0.032	0.204	0.180	0.03	(0.01, 0.08)
4137.57	LCS	ORH293	211	0.003	0.13	0.841	2.56e-03	(0.63, 0.02)	0.933	0.045	0.056	0.025	0.027	0.06	0.01	(0.10, 0.21)	0.003	0.014	0.025	0.020	0.203	0.02	(0.06, 0.01)	-0.032	0.022	0.158	0.03	(0.08, 0.01)	
11309.24	PYHFR	IC14145	211	0.002	0.12	0.844	2.35e-03	(0.63, 0.02)	0.933	0.001	0.119	0.028	0.814	0.03	0.027	0.001	(0.04, 0.07)	0.002	0.178	0.030	0.022	0.344	0.03	(0.03, 0.01)	0.004	0.021	0.844	0.01	(0.03, 0.01)
13068.139	CES	IC14518	211	0.002	0.12	0.841	2.37e-03	(0.63, 0.02)	0.933	0.058	0.063	0.025	0.011	0.06	0.01	(0.11, 0.21)	0.004	0.002	0.021	0.022	0.335	0.02	(0.02, 0.02)	-0.007	0.024	0.761	0.01	(0.05, 0.04)	
3132.1	VEGFC	P49767	211	0.002	0.12	0.841	2.39e-03	(0.63, 0.02)	0.933	0.064	0.041	0.025	0.140	0.04	0.025	0.102	(0.04, 0.09)	0.001	0.074	0.035	0.020	0.388	0.03	(0.07, 0.01)	-0.041	0.023	0.707	0.04	(0.09, 3.19e-03)
9478.56	PRPF43	OR9K08	211	0.002	0.12	0.842	2.58e-03	(0.63, 0.02)	0.933	0.086	0.041	0.025	0.140	0.04	0.025	0.102	(0.04, 0.09)	0.001	0.074	0.035	0.020	0.388	0.03	(0.07, 0.01)	-0.041	0.023	0.707	0.04	(0.09, 3.19e-03)
11198.37	CREBBL1	OR9K08A	211	0.002	0.12	0.842	2.31e-03	(0.63, 0.02)	0.933	0.433	0.034	0.025	0.140	0.04	0.025	0.102	(0.04, 0.09)	0.001	0.074	0.035	0.020	0.388	0.03	(0.07, 0.01)	-0.041	0.023	0.707	0.04	(0.09, 3.19e-03)
4152.10	AKR1A1	P14550	211	0.003	0.13	0.842	2.58e-03	(0.63, 0.02)	0.933	0.040	-0.029	0.026	0.103	0.03	0.027	0.00	(0.08, 0.02)	0.002	0.165	0.032	0.021	0.123	0.03	(0.07, 0.01)	-0.029	0.025	0.260	0.03	(0.08, 0.02)
8886.3	CTHRE6	OR9K09	211	0.002	0.12	0.843	2.30e-03	(0.63, 0.02)	0.933	8.88E-05	0.029	0.019	0.019	0.028	0.014	0.025	0.101	0.04	0.025	0.014	0.360	0.01	(0.06, 0.04)	0.017	0.026	0.815	0.01	(0.06, 0.04)	
12933.87	RPA	P49237	211	0.002	0.12	0.843	2.34e-03	(0.63, 0.02)	0.933	0.117	0.041	0.025	0.101	0.04	0.025	0.101	0.04	0.025	0.074	0.033	0.020	0.121	0.03	(0.07, 0.01)	-0.034	0.025	0.717	0.03	(0.08, 0.02)
12586.14	HEAT1	IC14145	211	0.002	0.12	0.844	2.55e-03	(0.63, 0.02)	0.933	0.011	0.028	0.026	0.08	0.02	0.03	(0.08, 0.02)	0.002	0.08	0.030	0.022	0.178	0.03	(0.07, 0.01)	-0.028	0.028	0.868	0.01	(0.03, 0.02)	
13991.47	EFGK3	OR4332	211	0.002	0.12	0.843	2.31e-03	(0.63, 0.02)	0.933	0.265	0.033	0.023	0.893E-05	0.028	0.033	0.893E-05	(0.13, 0.04)	0.005	6.96E-05	0.027	0.019	0.157	0.03	(0.08, 0.01)	-0.035	0.024	0.144	0.04	(0.08, 0.01)
14067.6	PK42	OR9939	211	0.003	0.13	0.843	2.55e-03	(0.63, 0.02)	0.933	0.030	-0.029	0.025	0.253	0.03	0.027	0.00	(0.08, 0.02)	0.002	0.150	0.021	0.019	0.279	0.02	(0.06, 0.02)	-0.044	0.025	0.704	0.04	(0.09, 4.07e-03)
5731.22	NOV	P95673	211	0.002	0.12	0.843	2.35e-03	(0.63, 0.02)	0.933	0.129	0.025	0.025	0.087	0.07	0.012	(0.12, 0.02)	0.004	0.003	0.037	0.030	0.068	0.04	(0.08, 2.46e-04)	-0.055	0.025	0.008	0.07	(0.11, 0.02)	
3504.58	HAMP	OR1672	211	0.002	0.12	0.843	2.40e-03	(0.63, 0.02)	0.933	0.288	0.019	0.025	0.495	0.02	0.027	0.00	(0.07, 0.03)	0.001	0.313	0.018	0.025	0.467	0.02	(0.07, 0.03)	-0.031	0.023	0.183	0.03	(0.08, 0.01)
3506.78	COL22	OR9K126	211	0.003	0.14	0.844	2.80e-03	(0.63, 0.03)	0.934	2.24E-04	-0.047	0.028	0.039	0.05	0.010	(0.10, 0.21)	0.003	0.041	0.029	0.020	0.144	0.03	(0.07, 0.01)	-0.042	0.026	0.113	0.04	(0.09, 0.01)	
14858.4	PTGFS2	OR9K177	211	0.002	0.12	0.845	2.34e-03	(0.63, 0.02)	0.935	0.093	0.025	0.033	0.025	0.03	0.025	0.03	(0.09, 0.01)	0.001	0.086	0.030	0.021	0.123	0.03	(0.07, 0.01)	-0.027	0.024	0.266	0.03	(0.07, 0.02)
8946.38	NR1H4	OR9K11	211	0.003	0.13	0.845	2.57e-03	(0.63, 0.02)	0.934	0.006	-0.060	0.026	0.020	0.08	0.01	(0.11, 0.21)	0.004	0.005	0.026	0.022	0.231	0.03	(0.07, 0.02)	-0.021	0.023	0.593	0.01	(0.06, 0.03)	
13516.48	EMC4	OR9K12	211	0.003	0.14	0.846	2.80e-03	(0.63, 0.03)	0.935	0.001	0.019	0.028	0.14	0.02	0.04	(0.07, 0.01)	0.001	0.385	0.010	0.026	0.087	0.01	(0.06, 0.04)	-0.016	0.027	0.588	0.02	(0.07, 0.04)	
16320.139	CD320	OR9K170	211	0.002	0.13	0.846	2.47e-03	(0.63, 0.02)	0.935	0.011	-0.018	0.025	0.475	0.02	0.017	(0.07, 0.03)	0.001	0.347	0.025	0.022	0.284	0.02	(0.07, 0.02)	-0.028	0.023	0.228	0.03	(0.07, 0.02)	
2182.83	CCLL2	OR9K43	211	0.002	0.12	0.846	2.29e-03	(0.63, 0.02)	0.935	0.140	-0.032	0.025	0.199	0.03	0.027	0.00	(0.08, 0.02)	0.002	0.187	0.027	0.022	0.215	0.03	(0.07, 0.02)	-0.028	0.023	0.219	0.03	(0.07, 0.02)
5831.52	HNRNK2P2292	OR9K12	211	0.003	0.14	0.846	2.63e-03	(0.63, 0.02)	0.935	0.005	0.071	0.026	0.007	0.07	0.012	(0.12, 0.02)	0.004	0.003	0.037	0.030	0.068	0.04	(0.08, 2.46e-04)	-0.055	0.025	0.008	0.07	(0.11, 0.02)	
8831.12	GSBP2	OR9K086	211	0.003	0.13	0.846	2.54e-03	(0.63, 0.02)	0.935	0.019	-0.046	0.026	0.075	0.05	0.010	(0.14, 0.33)	0.003	0.051	0.041	0.020	0.245	0.03	(0.07, 0.01)	-0.040	0.026	0.015	0.06	(0.12, 0.01)	
10893.43	KLRG2	OR9K150	211	0.002	0.13	0.849	2.45e-03	(0.63, 0.02)	0.935	0.009	-0.024	0.026	0.340	0.02	0.027	0.00	(0.07, 0.03)	0.002	0.225	0.029	0.022	0.193	0.03	(0.07, 0.01)	-0.020	0.024	0.398	0.02	(0.07, 0.03)
10772.21	CSGALNAC1	OR9K150	211	0.002	0.12	0.850	2.37e-03	(0.63, 0.02)	0.935	0.041	0.029	0.025	0.030	0.02	0.010	(0.07, 0.01)	0.001	0.273	0.028	0.020	0.215	0.03	(0.07, 0.02)	-0.024	0.024	0.260	0.03	(0.08, 0.01)	
13175.6	HMSD3	OR9K150	211	0.002	0.12	0.850	2.38e-03	(0.63, 0.02)	0.935	0.189	0.050	0.023	0.030	0.02	0.010	(0.10, 0.35e-06)	0.003	0.011	0.019	0.021	0.361	0.02	(0.06, 0.02)	-0.014	0.022	0.506	0.01	(0.06, 0.03)	
13473.55	ITPKA	P23677	211	0.002	0.12	0.850	2.22e-03	(0.63, 0.02)	0.935	0.080	-0.054	0.025	0.028	0.05	0.011	(0.11, 0.21)	0.003	0.015	0.008	0.019	0.264	0.01	(0.05, 0.03)	-0.030	0.024	0.215	0.03	(0.08, 0.02)	
15367.38	BPRF1	OR9K150	211	0.003	0.16	0.848	2.99e-03	(0.63, 0.03)	0.935	4.31E-09	0.033	0.031	0.914	0.03	0.031	0.377e-05	(0.06, 0.06)	0.000	0.989	0.025	0.022	0.263	0.03	(0.02, 0.02)	-0.022	0.028	0.435	0.02	(0.03, 0.08)
15415.8	LRRK3	OR9K150	211	0.002	0.13	0.848	2.63e-03	(0.63, 0.02)	0.935	0.011	0.022	0.013	0.109	0.02	0.013	(0.09, 0.03)	0.001	0.089	0.025	0.022	0.263	0.03	(0.02, 0.02)	-0.022	0.028	0.435	0.02	(0.03, 0.08)	
19132.1	MRLP2	OR9K150	211	0.002	0.12	0.848	2.23e-03	(0.63, 0.02)	0.935	0.189	-0.029	0.024	0.237	0.03	0.027	0.00	(0.08, 0.02)	0.002	0.142	0.020	0.024	0.986	0.25e-04	(0.05, 0.0)	0.004	0.022	0.853	0.11e-03	(0.04, 0.05)
2635.51	LAYN	OR9K150	211	0.002	0.13	0.850	2.45e-03																						

Table S3. Association of type 2 diabetes with deCODE plasma protein

Gene	Chr	Uniprot	nsnp	b/w	se/w	pr/w	cl/w	FDR	Q	val	egger	se/egger	pr/egger	cl/egger	egger	Intergenic	pr/Intergenic	cl/Intergenic	b/mode	se/mode	pr/mode	cl/mode		
19615_213	1	NTSC3A	CHRP90	211	0.001	0.012	0.901	-1.45e-03 (0.02, 0.02)	0.959	0.236	-0.027	0.024	0.257	-0.037 (0.07, 0.02)	0.002	0.214	-0.014	0.023	0.544	-0.011 (0.06, 0.03)	0.070	0.233	0.471 (0.02, 0.06)	
19640_2	1	PTH	019270	211	0.002	0.012	0.922	-1.43e-03 (0.02, 0.02)	0.969	0.165	-0.042	0.025	0.398	-0.10 (0.10, 0.21)	0.003	0.025	0.019	0.183	0.033	-0.037 (0.23, 0.24)	0.011	0.035	0.128	-0.031 (0.08, 0.01)
8522_22	1	GDF6	PN9905	211	0.001	0.012	0.901	1.46e-03 (0.02, 0.02)	0.959	0.270	-0.039	0.024	0.105	0.04 (0.09, 0.01)	0.003	0.052	-0.008	0.025	0.743	-0.01 (0.06, 0.04)	-0.009	0.024	0.707	-0.01 (0.05, 0.04)
8310_6	1	ZGFR	OR9D40	211	0.001	0.011	0.901	1.42e-03 (0.02, 0.02)	0.959	0.085	0.011	0.024	0.162	0.01 (0.04, 0.06)	0.001	0.850	-0.008	0.025	0.716	-0.01 (0.05, 0.03)	-0.010	0.022	0.665	-0.01 (0.05, 0.03)
11551_16	1	HMG20B	019322	211	0.002	0.012	0.922	-1.43e-03 (0.02, 0.02)	0.969	0.165	-0.042	0.025	0.398	-0.10 (0.10, 0.21)	0.003	0.025	0.019	0.183	0.033	-0.037 (0.23, 0.24)	0.011	0.035	0.128	-0.031 (0.08, 0.01)
19170_25	1	POLE3	GN9F99	211	0.001	0.012	0.902	1.45e-03 (0.02, 0.02)	0.959	0.056	0.025	0.025	0.025	0.08 (0.10, 0.01)	0.004	0.008	-0.027	0.021	0.196	-0.03 (0.07, 0.01)	-0.029	0.024	0.228	-0.03 (0.08, 0.02)
845_19	1	ATP18A	019322	211	0.002	0.012	0.902	1.41e-03 (0.02, 0.02)	0.959	0.056	0.025	0.025	0.025	0.08 (0.10, 0.01)	0.004	0.008	-0.027	0.021	0.196	-0.03 (0.07, 0.01)	-0.029	0.024	0.228	-0.03 (0.08, 0.02)
106594_18	1	PRR16	019322	211	0.001	0.012	0.903	1.43e-03 (0.02, 0.02)	0.959	0.262	-0.029	0.024	0.225	-0.03 (0.08, 0.02)	0.002	0.140	-0.028	0.023	0.193	-0.03 (0.07, 0.02)	-0.013	0.023	0.573	-0.01 (0.06, 0.03)
10832_24	1	BALGH1	OR9U9X	211	0.002	0.016	0.904	1.50e-03 (0.02, 0.03)	0.959	1.73E-10	0.013	0.031	0.679	0.01 (0.05, 0.07)	0.001	0.583	0.003	0.025	0.919	2.58e-03 (0.06, 0.00)	0.000	0.028	0.755	0.01 (0.04, 0.06)
13895_15	1	EMC1	019322	211	0.001	0.012	0.902	1.43e-03 (0.02, 0.02)	0.959	0.013	0.013	0.013	0.013	0.013 (0.01, 0.01)	0.001	0.013	0.013	0.013	0.013	0.013 (0.01, 0.01)	-0.010	0.023	0.665	-0.01 (0.06, 0.03)
14197_2	1	PRDM1	019322	211	0.001	0.012	0.904	1.43e-03 (0.02, 0.02)	0.959	0.084	-0.063	0.025	0.011	-0.06 (0.11, -0.02)	0.004	0.003	-0.028	0.003	0.222	-0.03 (0.08, 0.03)	-0.016	0.022	0.474	-0.02 (0.06, 0.03)
5457_5	1	COLL12C	OR9U2C	211	0.002	0.013	0.903	1.54e-03 (0.02, 0.03)	0.959	0.148	0.034	0.026	0.202	0.03 (0.02, 0.00)	0.002	0.159	0.011	0.027	0.681	-0.01 (0.04, 0.06)	-0.010	0.022	0.714	-0.01 (0.06, 0.04)
19600_11	1	HNT1	019322	211	0.001	0.012	0.904	1.43e-03 (0.02, 0.02)	0.959	0.164	0.044	0.024	0.144	0.04 (0.09, 0.03)	0.002	0.168	0.033	0.024	0.168	0.03 (0.08, 0.03)	-0.011	0.021	0.621	-0.01 (0.06, 0.04)
8544_33	1	NELL1	029232	211	0.002	0.014	0.903	1.67e-03 (0.02, 0.03)	0.959	0.021	-0.035	0.027	0.195	0.04 (0.09, 0.02)	0.002	0.116	-0.020	0.025	0.621	-0.02 (0.07, 0.03)	-0.017	0.025	0.511	-0.02 (0.07, 0.03)
8456_19	1	KLK4	P07388	211	0.001	0.012	0.903	1.42e-03 (0.02, 0.02)	0.959	0.369	-0.031	0.023	0.023	-0.03 (0.08, 0.02)	0.002	0.017	-0.017	0.023	0.453	-0.02 (0.08, 0.03)	-0.014	0.023	0.453	-0.01 (0.07, 0.04)
10684_1	1	OR9U41	019322	211	0.001	0.012	0.903	1.43e-03 (0.02, 0.02)	0.959	0.204	-0.041	0.024	0.089	-0.04 (0.09, 0.01)	0.004	0.058	0.014	0.021	0.599	-0.01 (0.05, 0.03)	-0.022	0.024	0.358	-0.02 (0.07, 0.02)
12221_3	1	CNDNC2	PA4773	211	0.002	0.013	0.903	1.55e-03 (0.02, 0.03)	0.960	0.204	-0.059	0.025	0.019	-0.06 (0.11, -0.01)	0.004	0.005	-0.028	0.023	0.233	-0.03 (0.07, 0.02)	-0.023	0.023	0.319	-0.02 (0.07, 0.02)
17099_43	1	TM6SF8	019322	211	0.002	0.012	0.905	1.41e-03 (0.02, 0.02)	0.960	0.314	-0.020	0.024	0.052	-0.02 (0.07, 0.03)	0.001	0.366	-0.014	0.024	0.545	-0.01 (0.06, 0.03)	-0.006	0.024	0.444	-0.01 (0.06, 0.04)
5082_51	1	IL1RAPL2	OR9N90	211	0.001	0.012	0.905	1.40e-03 (0.02, 0.02)	0.960	0.341	-0.049	0.023	0.035	-0.05 (0.10, -0.37e-03)	0.003	0.012	-0.029	0.020	0.132	-0.03 (0.07, 0.01)	-0.023	0.023	0.327	-0.02 (0.07, 0.02)
11608_22	1	DNAH6	019322	211	0.001	0.012	0.906	1.40e-03 (0.02, 0.02)	0.960	0.051	-0.045	0.025	0.072	-0.05 (0.09, 0.38e-03)	0.003	0.032	-0.030	0.020	0.195	-0.03 (0.07, 0.01)	-0.052	0.023	0.402	-0.05 (0.10, -0.01)
13896_6	1	LINC11	019322	211	0.001	0.012	0.906	1.59e-03 (0.02, 0.02)	0.961	0.013	0.046	0.026	0.190	-0.03 (0.08, 0.02)	0.003	0.053	0.022	0.023	0.163	-0.03 (0.08, 0.02)	-0.046	0.023	0.592	-0.05 (0.09, 0.45e-05)
2831_5	1	XRCPC	P12956	211	0.002	0.013	0.906	1.51e-03 (0.02, 0.03)	0.961	0.031	-0.044	0.025	0.083	-0.04 (0.09, 0.01)	0.003	0.038	-0.033	0.020	0.110	-0.03 (0.07, 0.01)	-0.035	0.024	0.150	-0.03 (0.08, 0.01)
5317_23	1	HTR4	043464	211	0.001	0.012	0.907	1.39e-03 (0.02, 0.02)	0.961	0.153	-0.022	0.025	0.190	-0.03 (0.08, 0.02)	0.002	0.146	-0.028	0.020	0.163	-0.03 (0.08, 0.01)	-0.041	0.023	0.133	-0.04 (0.09, 0.04)
4132_27	1	FST	P19883	211	0.001	0.012	0.907	1.38e-03 (0.02, 0.02)	0.961	0.084	-0.053	0.025	0.034	-0.05 (0.10, -0.37e-03)	0.003	0.012	-0.027	0.020	0.171	-0.03 (0.07, 0.01)	-0.033	0.023	0.143	-0.03 (0.08, 0.01)
13519_112	1	ARHGAP25	OR9W76	211	0.002	0.012	0.908	1.35e-03 (0.02, 0.02)	0.962	0.326	-0.038	0.023	0.109	-0.04 (0.08, 0.01)	0.002	0.055	-0.023	0.024	0.340	-0.02 (0.07, 0.02)	-0.020	0.023	0.378	-0.02 (0.07, 0.02)
13871_40	1	TM6SF8	019322	211	0.002	0.016	0.910	1.81e-03 (0.03, 0.03)	0.963	1.33E-07	0.023	0.492	-0.02 (0.09, 0.03)	0.001	0.432	-0.040	0.021	0.058	0.04 (0.08, 0.144e-04)	-0.058	0.025	0.304	-0.01 (0.06, 0.04)	
13880_3	1	NAB2	O15742	211	0.001	0.012	0.910	1.33e-03 (0.02, 0.02)	0.963	0.212	-0.051	0.024	0.032	-0.05 (0.10, -0.45e-03)	0.003	0.011	-0.029	0.020	0.160	-0.03 (0.07, 0.01)	-0.034	0.022	0.121	-0.03 (0.08, 0.01)
12451_52	1	BACH1	O14867	211	0.001	0.012	0.910	1.47e-03 (0.02, 0.03)	0.963	0.018	-0.025	0.025	0.008	-0.07 (0.12, -0.02)	0.005	0.001	-0.024	0.022	0.264	-0.02 (0.07, 0.02)	-0.025	0.025	0.319	-0.02 (0.07, 0.02)
1344_141	1	TBP1	019322	211	0.001	0.012	0.912	1.34e-03 (0.02, 0.02)	0.963	0.062	-0.033	0.025	0.134	-0.02 (0.07, 0.01)	0.002	0.148	-0.040	0.020	0.165	-0.04 (0.08, 0.135e-04)	-0.049	0.023	0.595	-0.05 (0.10, 2.38e-03)
12578_13	1	RF3	PE1204	211	0.002	0.013	0.913	1.27e-03 (0.02, 0.02)	0.965	0.219	-0.017	0.024	0.471	-0.02 (0.06, 0.03)	0.003	0.440	-0.011	0.025	0.651	-0.01 (0.06, 0.04)	0.000	0.022	0.989	-0.00 (0.04, 0.04)
12004_5	1	GMEB2	019322	211	0.001	0.012	0.913	1.27e-03 (0.02, 0.02)	0.965	0.028	-0.033	0.025	0.190	-0.03 (0.08, 0.02)	0.002	0.028	-0.033	0.025	0.686	-0.02 (0.07, 0.02)	-0.023	0.023	0.444	-0.02 (0.07, 0.02)
13042_7	1	KCN10A	O16322	211	0.001	0.012	0.912	1.29e-03 (0.02, 0.02)	0.965	0.153	-0.050	0.024	0.039	-0.05 (0.10, -0.27e-03)	0.003	0.014	-0.020	0.020	0.299	-0.02 (0.06, 0.02)	-0.029	0.024	0.220	-0.03 (0.08, 0.02)
15670_15	1	C12orf23	019322	211	0.001	0.012	0.913	1.40e-03 (0.02, 0.03)	0.965	0.034	-0.070	0.025	0.006	-0.07 (0.12, -0.02)	0.004	0.001	-0.026	0.024	0.273	-0.03 (0.07, 0.02)	-0.020	0.021	0.342	-0.02 (0.06, 0.02)
16002_31	1	OCAD1	019322	211	0.001	0.012	0.913	1.45e-03 (0.02, 0.03)	0.965	0.028	-0.028	0.024	0.039	-0.04 (0.09, 0.01)	0.003	0.017	-0.017	0.020	0.160	-0.03 (0.07, 0.01)	-0.011	0.023	0.342	-0.02 (0.06, 0.02)
19620_16	1	DLG2	O15751	211	0.001	0.013	0.913	1.41e-03 (0.02, 0.02)	0.965	0.028	-0.028	0.026	0.284	-0.03 (0.08, 0.02)	0.002	0.239	-0.042	0.022	0.684	-0.01 (0.04, 0.28e-04)	-0.054	0.027	0.552	-0.05 (0.11, 2.12e-04)
3434_34	1	FN1	O21751	211	0.001	0.012	0.913	1.26e-03 (0.02, 0.02)	0.965	0.127	-0.025	0.024	0.297	-0.03 (0.07, 0.02)	0.002	0.231	-0.049	0.023	0.885	-0.01 (0.05, 0.04)	-0.009	0.023	0.885	-0.01 (0.05, 0.04)
1001_60	1	PKSIN	OR9W62	211	0.001	0.012	0.913	1.41e-03 (0.02, 0.02)	0.965	0.029	-0.028	0.024	0.039	-0.04 (0.09, 0.01)	0.003	0.023	-0.028	0.020	0.293	-0.02 (0.06, 0.02)	-0.023	0.023	0.444	-0.02 (0.07, 0.02)
8715_4	1	ABHD14	OR9UJ0	211	0.001	0.013	0.914	1.44e-03 (0.02, 0.03)	0.965	0.065	-0.063	0.026	0.109	-0.06 (

Table S3. Association of type 2 diabetes with deCODE plasma protein

Protein	Gene	UniProt	nsnp	Inverse variance weighted				MR Egger				Weighted median				Weighted mode								
				b/w	se_iw	pval_iw	CI_low	FDR_iw	Q_val	egger	se_egger	pval_egger	CI_egger	se_median	pval_median	CI_median	b_mode	se_mode	pval_mode	CI_mode				
9413_79	LPK	OSVXJ0	211	0.001	0.013	0.968	-5.35e-04 (0.03, 0.02)	0.988	0.000	0.068	0.028	0.008	-0.07 (0.11, -0.02)	0.004	0.003	-0.035	0.020	0.077	-0.04 (0.07, 3.76e-4)	-0.034	0.023	0.140	-0.03 (0.08, 0.01)	
12651_44	GABARAP	Q9H988	211	0.001	0.013	0.967	-5.45e-04 (0.03, 0.03)	0.988	0.000	0.068	0.028	0.022	-0.08 (0.11, -0.01)	0.004	0.009	-0.038	0.031	0.069	-0.04 (0.08, 2.95e-4)	-0.040	0.023	0.084	-0.04 (0.08, 0.01)	
12626_19	MOB1A	Q9H859	211	0.000	0.012	0.968	4.70e-04 (0.02, 0.02)	0.989	0.003	0.028	0.025	0.283	-0.03 (0.08, 0.02)	0.002	0.217	-0.009	0.024	0.697	0.01 (0.06, 0.04)	-0.005	0.022	0.834	-4.70e-03 (0.05, 0.04)	
19601_15	ASB9	Q9H9X3	211	0.001	0.020	0.968	8.08e-04 (0.04, 0.04)	0.989	2.77E-41	0.012	0.040	0.291	-0.07 (0.07, 0.09)	0.001	0.744	-0.030	0.020	0.133	-0.03 (0.07, 0.01)	-0.040	0.028	0.120	-0.04 (0.09, 0.01)	
13590_9	COLKALBP	Q9H974	211	0.001	0.013	0.969	-5.02e-04 (0.03, 0.02)	0.989	0.004	0.029	0.014	0.084	-0.04 (0.09, 0.01)	0.003	0.048	-0.029	0.021	0.175	-0.03 (0.07, 0.01)	-0.033	0.029	0.203	-0.03 (0.08, 0.02)	
7242_14	YSTM4	Q9H900	211	0.001	0.013	0.969	-5.05e-04 (0.03, 0.02)	0.989	0.032	-0.057	0.025	0.025	-0.08 (0.11, -0.01)	0.004	0.010	-0.022	0.023	0.348	-0.02 (0.07, 0.02)	-0.018	0.024	0.508	-0.02 (0.06, 0.03)	
19195_85	RPS5	P48782	211	0.000	0.013	0.970	-4.86e-04 (0.02, 0.02)	0.990	0.042	-0.058	0.025	0.020	-0.08 (0.11, -0.01)	0.004	0.007	-0.026	0.020	0.682	-0.02 (0.07, 0.01)	-0.058	0.026	0.308	-0.06 (0.12, 0.03)	
11226_16	UBES3A	Q05086	211	0.000	0.012	0.971	-4.35e-04 (0.02, 0.02)	0.990	0.129	0.034	0.025	0.165	-0.03 (0.08, 0.01)	0.002	0.107	-0.033	0.020	0.102	-0.03 (0.07, 0.01)	-0.025	0.024	0.309	-0.02 (0.07, 0.02)	
12830_4	SAP18	Q04422	211	0.000	0.012	0.971	-4.23e-04 (0.02, 0.02)	0.990	0.124	-0.063	0.024	0.101	-0.06 (0.11, -0.02)	0.004	0.003	-0.023	0.020	0.288	-0.02 (0.07, 0.02)	-0.014	0.022	0.522	-0.01 (0.06, 0.03)	
16180_2	PKMT1	Q9H971	211	0.000	0.012	0.971	-4.22e-04 (0.02, 0.02)	0.990	0.223	0.033	0.024	0.230	-0.05 (0.10, 0.29e-02)	0.002	0.108	-0.033	0.011	0.162	-0.03 (0.07, 0.01)	-0.032	0.021	0.612	-0.03 (0.07, 0.01)	
19333_4	HNRNPK	P61978	211	0.000	0.013	0.971	-4.81e-04 (0.03, 0.03)	0.990	0.007	-0.043	0.026	0.104	-0.04 (0.09, 0.01)	0.003	0.055	-0.029	0.020	0.056	-0.04 (0.08, 9.37e-4)	-0.047	0.024	0.505	-0.05 (0.09, 2.90e-04)	
2761_49	FCF1B	Q9H993	211	0.000	0.012	0.971	-4.28e-04 (0.02, 0.02)	0.990	0.155	-0.054	0.024	0.024	-0.05 (0.10, -0.01)	0.003	0.009	-0.025	0.019	0.188	-0.02 (0.06, 0.01)	-0.029	0.022	0.152	-0.03 (0.07, 0.01)	
742_5	CPN1	Q9H989	211	0.000	0.012	0.971	-4.28e-04 (0.02, 0.02)	0.990	0.052	-0.048	0.025	0.021	-0.05 (0.10, 0.01)	0.003	0.042	-0.026	0.020	0.245	-0.03 (0.07, 0.02)	-0.021	0.025	0.203	-0.03 (0.08, 0.02)	
8853_2	GLO1C4A	Q9H9M7	211	0.000	0.012	0.970	-4.43e-04 (0.02, 0.02)	0.990	0.057	-0.067	0.025	0.027	-0.05 (0.10, -0.02)	0.004	0.002	-0.020	0.022	0.352	-0.02 (0.06, 0.02)	-0.015	0.023	0.535	-0.01 (0.06, 0.03)	
5801_72	HSP	P01138	211	0.000	0.013	0.972	-4.58e-04 (0.02, 0.02)	0.990	0.013	-0.015	0.026	0.056	-0.02 (0.07, 0.04)	0.001	0.484	-0.027	0.021	0.190	-0.03 (0.07, 0.01)	-0.025	0.022	0.631	-0.03 (0.07, 0.02)	
6580_29	P2P	P20742	211	0.000	0.013	0.972	-4.84e-04 (0.03, 0.03)	0.990	0.001	-0.050	0.028	0.054	-0.05 (0.10, 0.54e-04)	0.003	0.027	-0.032	0.021	0.129	-0.03 (0.07, 0.01)	-0.022	0.023	0.344	-0.02 (0.07, 0.02)	
9883_29	GLP1	Q04780	211	0.000	0.013	0.972	-4.85e-04 (0.03, 0.03)	0.990	0.014	-0.039	0.028	0.137	-0.04 (0.09, 0.01)	0.002	0.089	-0.032	0.019	0.100	-0.03 (0.07, 0.01)	-0.037	0.023	0.116	-0.04 (0.08, 0.01)	
11140_56	COL1A1	P20452	211	0.001	0.015	0.972	-5.33e-04 (0.03, 0.03)	0.990	4.34E-07	0.033	0.030	0.280	0.03 (0.03, 0.03)	0.002	0.294	0.014	0.027	0.055	0.01 (0.04, 0.01)	-0.007	0.027	0.965	-0.01 (0.06, 0.05)	
8885_41	RAP2A	P10114	211	0.000	0.012	0.973	-3.93e-04 (0.02, 0.02)	0.991	0.174	0.003	0.024	0.916	2.52e-03 (0.04, 0.05)	0.000	0.888	-0.015	0.025	0.547	0.01 (0.06, 0.03)	-0.014	0.027	0.611	-0.01 (0.07, 0.04)	
12742_160	TMEM8	A6NDV4	211	0.000	0.011	0.973	-3.59e-04 (0.02, 0.02)	0.991	0.126	0.030	0.024	0.178	-0.02 (0.08, 0.02)	0.002	0.148	-0.026	0.020	0.215	-0.03 (0.07, 0.02)	-0.017	0.022	0.442	-0.02 (0.06, 0.03)	
15588_1	DC	Q92774	211	0.000	0.014	0.973	-3.48e-04 (0.03, 0.03)	0.991	0.004	-0.036	0.027	0.188	-0.04 (0.09, 0.02)	0.002	0.115	0.018	0.023	0.061	-0.02 (0.06, 0.02)	-0.002	0.025	0.937	1.55e-03 (0.05, 0.04)	
19148_58	TMM6A	Q96220	211	0.000	0.012	0.973	-3.96e-04 (0.02, 0.02)	0.991	0.085	-0.010	0.025	0.683	-0.01 (0.06, 0.04)	0.001	0.624	-0.032	0.021	0.118	-0.03 (0.07, 0.01)	-0.034	0.024	0.165	-0.03 (0.08, 0.01)	
19186_15	RPS19	Q9H919	211	0.000	0.013	0.974	-4.28e-04 (0.03, 0.03)	0.991	0.015	-0.075	0.025	0.003	-0.08 (0.13, -0.03)	0.005	0.001	-0.037	0.020	0.487	-0.04 (0.08, 2.55e-4)	-0.044	0.024	0.074	-0.04 (0.09, 4.09e-03)	
19251_56	SRGN	P10124	211	0.000	0.013	0.974	-4.17e-04 (0.03, 0.03)	0.991	0.024	-0.034	0.028	0.181	-0.03 (0.08, 0.02)	0.002	0.126	-0.045	0.022	0.041	-0.05 (0.09, -1.87e-2)	-0.051	0.024	0.035	-0.05 (0.10, -3.81e-03)	
2505_49	GFP3	Q9H909	211	0.000	0.012	0.974	-3.90e-04 (0.02, 0.02)	0.991	0.135	-0.052	0.024	0.035	-0.05 (0.10, -3.87e-02)	0.003	0.014	-0.022	0.024	0.377	-0.02 (0.06, 0.03)	-0.015	0.028	0.590	-0.01 (0.07, 0.04)	
3010_53	TSLP	Q9H908	211	0.000	0.012	0.975	-3.74e-04 (0.02, 0.02)	0.991	0.185	-0.054	0.024	0.027	-0.05 (0.10, -0.01)	0.003	0.011	-0.025	0.020	0.265	-0.03 (0.08, 0.01)	-0.027	0.023	0.244	-0.03 (0.07, 0.02)	
5343_74	CPE	P16870	211	0.001	0.016	0.974	-5.08e-04 (0.03, 0.03)	0.991	1.27E-10	-0.078	0.031	0.101	-0.08 (0.14, -0.02)	0.005	0.004	-0.011	0.024	0.639	-0.01 (0.06, 0.04)	-0.011	0.024	0.640	-0.01 (0.06, 0.04)	
5693_26	SIRPB2	Q9JKA9	211	0.000	0.013	0.974	-4.18e-04 (0.03, 0.02)	0.991	0.018	-0.073	0.025	0.004	-0.07 (0.12, -0.02)	0.005	0.001	-0.030	0.020	0.124	-0.03 (0.07, 0.01)	-0.047	0.024	0.053	-0.05 (0.10, 3.59e-04)	
8544_60	MFT1	Q9H986	211	0.000	0.013	0.975	-3.97e-04 (0.03, 0.02)	0.991	0.020	-0.048	0.025	0.057	-0.05 (0.10, 1.08e-02)	0.003	0.029	-0.023	0.021	0.262	-0.02 (0.06, 0.02)	-0.018	0.022	0.412	-0.02 (0.06, 0.03)	
13482_14	CNO17	A5YKX6	211	0.000	0.013	0.975	-3.97e-04 (0.03, 0.02)	0.991	0.035	-0.043	0.025	0.089	-0.04 (0.09, 0.01)	0.003	0.051	-0.021	0.019	0.267	-0.02 (0.06, 0.02)	-0.028	0.028	0.201	-0.03 (0.08, 0.02)	
7103_37	COSBP2	Q9H9E3	211	0.000	0.012	0.976	-3.49e-04 (0.02, 0.02)	0.992	0.146	-0.047	0.024	0.056	-0.05 (0.10, 9.21e-04)	0.003	0.028	-0.040	0.020	0.043	-0.04 (0.08, 3.17e-2)	-0.034	0.023	0.055	-0.04 (0.09, 1.38e-03)	
12532_10	CAS	P23280	211	0.000	0.014	0.977	-3.98e-04 (0.03, 0.03)	0.992	0.007	-0.087	0.028	0.001	0.05 (0.04, 0.04)	0.002	0.198	0.034	0.025	0.020	0.188	0.03 (0.04, 0.08)	0.054	0.025	0.033	0.05 (0.47e-03, 0.01)
3350_40	CKB1B	P61024	211	0.000	0.012	0.977	-3.27e-04 (0.02, 0.02)	0.992	0.171	-0.038	0.024	0.121	-0.04 (0.09, 0.01)	0.002	0.070	-0.034	0.021	0.109	-0.03 (0.07, 0.01)	-0.028	0.023	0.239	-0.03 (0.07, 0.02)	
14474_63	PACNSB	Q9H958	211	0.000	0.013	0.978	-3.20e-04 (0.02, 0.02)	0.992	0.281	-0.058	0.024	0.013	-0.08 (0.13, -0.01)	0.004	0.004	-0.016	0.020	0.364	-0.02 (0.06, 0.02)	-0.042	0.024	0.884	-0.04 (0.08, 0.01)	
18402_1	AMMECR1	Q6DCAD	211	0.000	0.013	0.977	-3.78e-04 (0.03, 0.03)	0.992	0.005	-0.043	0.026	0.107	-0.04 (0.09, 0.01)	0.003	0.065	-0.028	0.021	0.214	-0.03 (0.07, 0.02)	-0.039	0.024	0.107	-0.04 (0.09, 0.01)	
18834_50	TM22	Q21980	211	0.000	0.013	0.978	-3.58e-04 (0.03, 0.03)	0.992	0.021	-0.042	0.026	0.105	-0.04 (0.09, 0.01)	0.003	0.059	-0.022	0.019	0.251	-0.02 (0.06, 0.02)	-0.049	0.027	0.065	-0.05 (0.10, 2.82e-03)	
8696_21	FOXP2	Q9H985	211	0.000	0.012	0.978	-3.23e-04 (0.02, 0.02)	0.992	0.266	-0.029	0.023	0.031	-0.05 (0.10, -4.79e-02)	0.003	0.012	-0.013	0.020	0.558	-0.01 (0.06, 0.03)	-0.019	0.023	0.816	-0.01 (0.05, 0.03)	
10045_47	CUL3	Q13818	211	0.000	0.012	0.978	-3.20e-04 (0.02, 0.02)	0.992	0.141	-0.048	0.024	0.051	-0.05 (0.10, -1.63e-02)	0.003	0.025	-0.023	0.020	0.247	-0.02 (0.06, 0.02)	-0.037	0.023	0.120	-0.04 (0.08, 0.01)	
11201_19	CKX10	Q92778	211	0.000	0.012	0.979	-3.55e-04 (0.02, 0.02)	0.992	0.016	-0.024	0.024	0.370	-0.02 (0.07, 0.03)	0.001	0.292	-0.028	0.024	0.048	-0.01 (0.06, 0.03)	-0.014	0.024	0.865	-0.01 (0.06, 0.03)	
18214_2	GCLM	P48507	211	0.000	0.013	0.980	-3.24e-04 (0.02, 0.02)	0.993	0.042	-0.027	0.028	0.286	-0.03 (0.08, 0.02)	0.002	0.211	-0.028	0.021	0.213	-0.03 (0.07, 0.01)	-0.035	0.026	0.171	-0.04 (0.09, 0.02)	
3060_43	CS	P02748	211	0.000	0.013	0.980	-3.79e-04 (0.03, 0.03)	0.993	2.22E-05	-0.033	0.029	0.029	-0.03 (0.09, 0.02)	0.002	0.197	-0.012	0.027	0.650	-0.01 (0.07, 0.04)	-0.021	0.025	0.407	-0.02 (0.07, 0.03)	
4475_22	ZFP70	Q9H943	211	0.000	0.013	0.980	-3.41e-04 (0.02, 0.02)	0.993	0.033	-0.045	0.025	0.013												

Table S4. Association of type 2 diabetes with UKB-PPP plasma protein.

UnProt	Gene	OD	Inverse variance				MR Egger				Weighted median																		
			nsp	blw	seblw	pvalblw	CI_low	CI_high	FDR_blw	p_val	egger	pval_egger	CI_egger	egger	Inter_egger	se_weighted	pval_weighted	CI_weighted	bmode	se_mode	pval_mode	CI_mode							
DBP107	FNLR1	OD20506	132	0.033	0.013	0.003	0.01	0.006	0.077	0.003	0.029	0.01	0.04	0.06	0.01	0.368	0.022	0.25	0.36	0.02	0.037	0.011	0.228	0.065	0.01	0.04	0.06		
P10147	CCL3	OD20510	132	0.035	0.014	0.002	0.01	0.008	0.129	0.002	0.59	0.02	0.04	0.05	0.001	0.019	0.014	0.02	0.33	0.02	0.037	0.011	0.228	0.065	0.01	0.04	0.06		
P10147	CDG8	OD21265	132	0.039	0.015	0.010	0.04	0.017	0.080	0.47E-09	0.016	0.029	0.57	0.02	0.04	0.003	0.028	0.015	0.20	0.43	0.02	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P0262K	ADGR2	OD20588	132	0.040	0.016	0.011	0.04	0.017	0.081	4.1E-05	0.016	0.030	0.25	0.03	0.029	0.003	0.053	0.005	0.17	0.53	0.01	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P14005	L3E	OD20592	132	0.041	0.017	0.012	0.04	0.018	0.082	4.1E-05	0.016	0.030	0.25	0.03	0.029	0.003	0.053	0.005	0.17	0.53	0.01	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P06240	PLN1	OD20835	132	0.039	0.015	0.011	0.04	0.017	0.083	3.44E-08	0.016	0.030	0.25	0.03	0.029	0.003	0.053	0.005	0.17	0.53	0.01	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
DM517	SLITR5	OD20596	132	0.042	0.018	0.013	0.04	0.019	0.108	0.003	0.18	0.03	0.03	0.03	0.001	0.029	0.014	0.02	0.34	0.02	0.037	0.011	0.228	0.065	0.01	0.04	0.06		
P30409	ATF5D1	OD20597	132	0.031	0.012	0.011	0.03	0.010	0.084	0.343	0.020	0.024	0.43	0.02	0.04	0.003	0.068	0.001	0.22	0.06	0.06	0.02	0.011	0.061	0.025	0.06	0.01	0.11	
P12830	CDH1	OD20553	132	0.052	0.021	0.011	0.05	0.021	0.084	2.41E-06	0.045	0.040	0.20	0.03	0.12	0.003	0.337	0.005	0.23	0.01	0.06	0.01	0.05	0.023	0.02	0.05	0.01	0.11	
P47470	DOAH1	OD20598	132	0.035	0.014	0.012	0.04	0.016	0.086	0.002	0.08	0.02	0.40	0.02	0.04	0.003	0.068	0.001	0.22	0.06	0.06	0.02	0.011	0.061	0.025	0.06	0.01	0.11	
OT5558	ENTPD5	OD21040	132	0.042	0.017	0.011	0.04	0.017	0.084	1.70E-11	0.015	0.032	0.24	0.01	0.03	0.002	0.327	0.003	0.25	0.30	0.02	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P03462	NRP2	OD21081	132	0.041	0.016	0.011	0.04	0.017	0.084	1.27E-17	0.047	0.032	0.14	0.05	0.11	0.003	0.335	0.004	0.23	0.01	0.06	0.01	0.05	0.023	0.02	0.05	0.01	0.11	
P05567	TGSI1	OD20576	132	0.035	0.014	0.012	0.04	0.016	0.085	0.003	0.07	0.02	0.40	0.02	0.04	0.003	0.068	0.001	0.22	0.06	0.06	0.02	0.011	0.061	0.025	0.06	0.01	0.11	
P49023	PNP	OD20822	132	0.032	0.012	0.011	0.03	0.010	0.084	3.88E-04	0.024	0.024	0.33	0.02	0.02	0.002	0.700	0.003	0.23	0.14	0.03	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P15423	CXCL1	OD20576	132	0.042	0.018	0.012	0.04	0.017	0.085	1.84E-15	0.056	0.052	0.63	0.02	0.12	0.011	0.609	0.04	0.23	0.09	0.04	0.02	0.037	0.011	0.228	0.065	0.01	0.04	0.06
P08727	ROR1B	OD20598	132	0.032	0.013	0.012	0.03	0.010	0.085	0.44	0.033	0.025	0.17	0.03	0.02	0.003	0.979	0.006	0.20	0.75	0.01	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
OT5340	KCDB2	OD20163	132	0.028	0.010	0.012	0.03	0.010	0.087	4.48E-08	0.037	0.020	0.70	0.03	0.02	0.003	0.544	0.024	0.18	0.11	0.02	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P11117	ESFR	OD21445	132	0.031	0.015	0.012	0.04	0.016	0.091	2.07E-10	0.004	0.028	0.85	0.02	0.03	0.003	0.989	0.011	0.22	0.67	0.01	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P18627	LAC3	OD21315	132	0.034	0.014	0.012	0.03	0.010	0.087	1.74E-05	0.047	0.027	0.81	0.05	0.01	0.01	0.590	0.025	0.22	0.22	0.03	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
D15123	ANGPT2	OD21463	132	0.036	0.014	0.012	0.04	0.016	0.088	4.15E-08	0.001	0.027	0.91	0.06	0.04	0.003	0.920	0.010	0.23	0.12	0.03	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P14687	BCAT1	OD20322	132	0.031	0.013	0.012	0.03	0.010	0.089	0.001	0.15	0.024	0.40	0.02	0.03	0.003	0.516	0.009	0.23	0.20	0.03	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P24001	L3E	OD20592	132	0.044	0.018	0.012	0.04	0.018	0.089	2.97E-24	0.021	0.034	0.54	0.02	0.02	0.003	0.423	0.020	0.24	0.19	0.02	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
DM517	SLIT1	OD20596	132	0.041	0.017	0.012	0.04	0.018	0.089	0.003	0.18	0.026	0.47	0.02	0.03	0.003	0.919	0.007	0.19	0.22	0.01	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
OT5197	EPH8B	OD20882	132	0.029	0.012	0.012	0.03	0.010	0.089	0.141	0.044	0.024	0.62	0.04	0.02	0.003	0.448	0.047	0.23	0.42	0.02	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P35556	FRP2	OD30974	132	0.030	0.012	0.013	0.03	0.011	0.090	0.980	0.030	0.023	0.15	0.03	0.02	0.003	0.990	0.024	0.24	0.31	0.02	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P05027	MMY7	OD20987	132	0.029	0.015	0.013	0.03	0.011	0.090	0.604	0.016	0.023	0.44	0.02	0.03	0.003	0.968	0.022	0.23	0.34	0.02	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
EW0C01	MRP1	OD31420	132	0.030	0.012	0.013	0.03	0.011	0.091	0.280	0.033	0.023	0.19	0.03	0.02	0.003	0.858	0.005	0.23	0.20	0.03	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P43490	NAMPT	OD21227	132	0.030	0.012	0.013	0.03	0.011	0.091	0.062	0.008	0.025	0.79	0.01	0.04	0.003	0.302	0.009	0.23	0.81	0.01	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
OT1972	ROSI	OD21024	132	0.030	0.012	0.013	0.03	0.011	0.091	3.26E-07	0.029	0.027	0.15	0.03	0.02	0.003	0.855	0.000	0.23	0.36	0.02	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P44546	SRFB	OD21352	132	0.030	0.012	0.013	0.03	0.011	0.091	0.683	0.034	0.023	0.14	0.03	0.02	0.003	0.830	0.021	0.23	0.38	0.02	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P25442	ROSI	OD21024	132	0.030	0.012	0.013	0.03	0.011	0.091	1.81E-08	0.015	0.028	0.60	0.01	0.03	0.003	0.812	0.000	0.23	0.38	0.02	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
OM907	VSIG2	OD21371	132	0.032	0.013	0.013	0.03	0.011	0.094	0.002	0.23	0.025	0.37	0.02	0.03	0.003	0.681	0.032	0.24	0.17	0.03	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P81172	DYLL1	OD20925	132	0.029	0.012	0.014	0.03	0.011	0.097	0.005	0.05	0.027	0.81	0.01	0.04	0.003	0.222	0.009	0.19	0.68	0.01	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P02926	NEB	OD20578	132	0.032	0.013	0.013	0.03	0.011	0.097	0.002	0.08	0.023	0.78	0.01	0.03	0.003	0.678	0.001	0.19	0.61	0.01	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
OM908	CFHR5	OD20716	132	0.041	0.016	0.014	0.04	0.017	0.097	9.00E-21	0.040	0.032	0.21	0.04	0.02	0.003	0.969	0.048	0.22	0.32	0.03	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
DMW23	SLAMF7	OD20602	132	0.033	0.013	0.014	0.03	0.011	0.098	2.20E-07	0.044	0.028	0.90	0.04	0.01	0.01	0.812	0.013	0.23	0.45	0.01	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P11278	LAMP1	OD21116	132	0.031	0.013	0.013	0.03	0.011	0.098	0.002	0.08	0.023	0.78	0.01	0.03	0.003	0.678	0.001	0.19	0.61	0.01	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
OM214	LOC102888	132	0.031	0.013	0.013	0.03	0.011	0.098	1.85E-10	0.010	0.025	0.62	0.01	0.03	0.003	0.311	0.042	0.20	0.07	0.04	0.02	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P02703	MTR	OD20576	132	0.031	0.013	0.013	0.03	0.011	0.098	0.002	0.08	0.023	0.78	0.01	0.03	0.003	0.678	0.001	0.19	0.61	0.01	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
OT2432	COL1A1	OD20335	132	0.038	0.016	0.015	0.04	0.017	0.104	1.1E-05	0.065	0.030	0.03	0.07	0.12	0.001	0.297	0.297	0.23	0.14	0.06	0.01	0.054	0.022	0.04	0.05	0.01	0.11	
DM242	LAC2	OD20592	132	0.030	0.012	0.015	0.03	0.011	0.104	1.18E-04	0.020	0.024	0.36	0.02	0.03	0.003	0.838	0.022	0.23	0.38	0.02	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
P08267	HERP	OD21040	132	0.034	0.015	0.014	0.04	0.018	0.104	0.002	0.08	0.023	0.78	0.01	0.03	0.003	0.678	0.001	0.19	0.61	0.01	0.037	0.011	0.228	0.065	0.01	0.04	0.06	
OP2228	LACR1	OD21387	132	0.034	0.015	0.014	0.04	0.018	0.104	5.18E-05	0.011	0.027	0.95	0.01	0.04	0.003	0.503	0.015	0.20	0.1									

Table S4. Association of type 2 diabetes with UKG-PPP plasma protein.

UnProt	Gene	OID	Inverse variance				MR Egger				Weighted median																
			nsp	b/w	se/w	CI_low	CI_high	FDR_IVW	Q	val	egger	se/egger	CI_low	CI_high	b/mod	se/mod	CI_low	CI_high									
09JEXK1	CTSF	0021500	192	0.037	0.018	0.042	0.034	0.17(-0.03, 0.07)	0.11	1.25E-31	0.077	0.036	0.032	0.011	0.15	0.022	0.195	0.076	0.221	4.30E-04	0.08	0.023	0.004	0.007	0.022	0.11	
P24371	FCAR	0020564	192	0.022	0.013	0.047	0.023	0.15(-0.03, 0.05)	0.21	1.86E-05	0.077	0.036	0.032	0.011	0.15	0.022	0.195	0.076	0.221	4.30E-04	0.08	0.023	0.004	0.007	0.022	0.11	
P27550	LRRF1	0030751	192	-0.025	0.012	0.042	-0.023	0.02(-0.05, 0.27E-07)	0.11	4.56E-04	-0.029	0.024	0.232	0.033	-0.008	0.022	0.196	0.077	0.222	4.30E-04	0.08	0.023	0.004	0.007	0.022	0.11	
P27550	NRC1	0020568	192	0.024	0.012	0.042	0.023	0.02(0.17(-0.04, 0.05))	0.11	0.005	-0.002	0.223	0.033	0.032	0.011	0.15	0.022	0.195	0.076	0.221	4.30E-04	0.08	0.023	0.004	0.007	0.022	0.11
P27550	PRKRI	0020568	192	0.024	0.012	0.042	0.023	0.02(0.17(-0.04, 0.05))	0.11	0.005	-0.002	0.223	0.033	0.032	0.011	0.15	0.022	0.195	0.076	0.221	4.30E-04	0.08	0.023	0.004	0.007	0.022	0.11
09VW97	RBOB1	0020374	192	0.034	0.017	0.042	0.033	0.12(0.03, 0.07)	0.11	3.08E-18	0.055	0.027	0.887	0.033	0.087	0.007	0.044	0.022	0.291	0.005	0.022	0.826	0.033	0.087	0.007	0.044	
015391	TLR1	0020568	192	0.024	0.012	0.042	0.023	0.02(0.17(-0.04, 0.05))	0.11	0.005	-0.002	0.223	0.033	0.032	0.011	0.15	0.022	0.195	0.076	0.221	4.30E-04	0.08	0.023	0.004	0.007	0.022	0.11
09PM1	LRRP2B	0020374	192	0.028	0.014	0.042	0.023	0.03(0.03, 0.05)	0.12	0.004	0.022	0.227	0.041	0.022	0.027	0.141	0.022	0.195	0.076	0.221	4.30E-04	0.08	0.023	0.004	0.007	0.022	0.11
06K76	MYO6	0030717	192	0.034	0.017	0.043	0.033	0.10(0.03, 0.07)	0.11	7.21E-28	0.019	0.032	0.800	0.033	0.087	0.007	0.044	0.022	0.291	0.005	0.022	0.826	0.033	0.087	0.007	0.044	
09WV03	CHCHD10	0020568	192	0.022	0.013	0.047	0.023	0.02(0.17(-0.04, 0.05))	0.11	0.005	-0.002	0.223	0.033	0.032	0.011	0.15	0.022	0.195	0.076	0.221	4.30E-04	0.08	0.023	0.004	0.007	0.022	0.11
099972	BIOC	0021211	192	-0.029	0.014	0.043	-0.03	0.03(-0.06, 4.8E-07)	0.11	9.69E-09	-0.013	0.027	0.629	0.033	0.027	0.141	0.022	0.195	0.076	0.221	4.30E-04	0.08	0.023	0.004	0.007	0.022	0.11
012544	ZDNR	0020683	192	0.043	0.021	0.043	0.04	0.12(0.03, 0.19)	0.11	2.21E-05	0.028	0.042	0.499	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044	
09M278	CHL1	0020721	192	0.022	0.013	0.047	0.023	0.02(0.17(-0.04, 0.05))	0.11	0.005	-0.002	0.223	0.033	0.032	0.011	0.15	0.022	0.195	0.076	0.221	4.30E-04	0.08	0.023	0.004	0.007	0.022	0.11
09HBE5	L2MR	0030441	192	0.024	0.012	0.044	0.023	0.02(0.03, 0.05)	0.12	0.005	0.022	0.227	0.041	0.022	0.027	0.141	0.022	0.195	0.076	0.221	4.30E-04	0.08	0.023	0.004	0.007	0.022	0.11
P25295	PRK1	0020568	192	0.024	0.012	0.044	0.023	0.02(0.17(-0.04, 0.05))	0.11	0.005	-0.002	0.223	0.033	0.032	0.011	0.15	0.022	0.195	0.076	0.221	4.30E-04	0.08	0.023	0.004	0.007	0.022	0.11
P28907	CD38	0021316	192	0.023	0.011	0.044	0.023	0.02(0.23(-0.04, 0.05))	0.11	4.47E-06	0.001	0.022	0.586	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044	
09P186	PLB1	0030310	192	0.023	0.012	0.044	0.023	0.02(0.03, 0.05)	0.12	1.81E-11	0.009	0.022	0.679	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044	
013410	ETNA11	0020568	192	0.023	0.012	0.044	0.023	0.02(0.23(-0.04, 0.05))	0.11	0.005	-0.002	0.223	0.033	0.032	0.011	0.15	0.022	0.195	0.076	0.221	4.30E-04	0.08	0.023	0.004	0.007	0.022	0.11
015683	KITN	0030410	192	-0.028	0.014	0.045	-0.03	0.03(-0.06, 4.8E-07)	0.11	2.42E-06	0.013	0.027	0.634	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044	
017121	KIT	0020370	192	-0.028	0.014	0.045	-0.03	0.03(-0.06, 4.8E-07)	0.11	2.42E-06	0.013	0.027	0.634	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044	
09HCL5	PREB	0020939	192	0.029	0.015	0.046	0.024	0.02(0.03, 0.05)	0.12	0.005	0.022	0.502	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044		
015116	L2MR	0021210	192	-0.024	0.012	0.046	-0.02	0.02(-0.05, 4.0E-06)	0.12	0.005	0.006	0.225	0.033	0.032	0.011	0.15	0.022	0.195	0.076	0.221	4.30E-04	0.08	0.023	0.004	0.007	0.022	0.11
09M278	COL1A1	0020398	192	-0.029	0.014	0.046	-0.03	0.03(-0.06, 4.45E-07)	0.11	4.02E-07	-0.004	0.027	0.611	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044	
09JURP4	DMK1	0020284	192	0.021	0.011	0.046	0.023	0.02(0.03, 0.05)	0.12	5.27E-18	0.024	0.030	0.427	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044	
P21588	NTF5	0021498	192	0.028	0.013	0.046	0.023	0.03(0.03, 0.05)	0.12	1.08E-07	0.019	0.026	0.478	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044	
P15684	TGFB	0020939	192	0.028	0.014	0.047	0.023	0.03(0.03, 0.05)	0.12	1.43E-08	0.013	0.027	0.508	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044	
09WV04	PTFB	0030504	192	0.028	0.014	0.047	0.023	0.03(0.03, 0.05)	0.12	1.68E-04	0.006	0.027	0.833	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044	
P01992	ERC1	0031222	192	0.024	0.012	0.042	0.023	0.02(0.03, 0.05)	0.12	0.005	0.021	0.545	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044		
P11927	CTN1	0020937	192	0.024	0.012	0.042	0.023	0.02(0.03, 0.05)	0.12	0.005	0.021	0.545	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044		
P01133	EGF	0020288	192	-0.028	0.014	0.048	-0.03	0.03(-0.06, 4.44E-07)	0.11	3.82E-05	-0.012	0.027	0.652	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044	
09WV15	GMAPT	0020945	192	0.029	0.015	0.048	0.024	0.02(0.03, 0.05)	0.12	0.005	0.021	0.545	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044		
09WV19	LYC6	0020945	192	0.032	0.016	0.048	0.024	0.03(0.03, 0.05)	0.12	0.005	0.021	0.545	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044		
P11521	SCG2	0020400	192	0.029	0.015	0.049	0.024	0.03(0.03, 0.05)	0.12	0.005	0.021	0.545	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044		
0126301	DEFB4DEFB4L1	0020937	192	0.029	0.015	0.049	0.024	0.03(0.03, 0.05)	0.12	0.005	0.021	0.545	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044		
09KX74	RSPQ1	0021415	192	-0.027	0.014	0.050	-0.03	0.03(-0.06, 4.79E-07)	0.11	0.005	0.021	0.545	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044		
09L313	HSD17B4	0030579	192	0.043	0.022	0.050	0.04	0.12(0.03, 0.19)	0.11	7.17E-10	0.029	0.047	0.830	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044	
043898	SIGLEC5	0020939	192	0.029	0.015	0.050	0.024	0.03(0.03, 0.05)	0.12	0.005	0.021	0.545	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044		
09M477	HSD17B4	0030579	192	0.043	0.022	0.050	0.04	0.12(0.03, 0.19)	0.11	7.17E-10	0.029	0.047	0.830	0.033	0.105	0.011	0.074	0.003	0.220	0.005	0.022	0.826	0.033	0.087	0.007	0.044	
09M477	HSD17B4	0030579	192	0.043	0.022	0.050	0.04	0.1																			

Table S4. Association of type 2 diabetes with UKB-PPP plasma protein.

UnProt	Gene	Chr	OD	Inverse variance co-kriging				MR Egger				Weighted median				Weighted mode													
				nsp	b/w	se/w	pval/w	CI_low	CI_high	FDR_low	U	pval	egger	se/egger	pval/egger	CI_egger	egger	se/egger	pval/egger	CI_egger									
DTF85	GIPC2	03	0115	0.07	0.12	0.155	0.02	0.01	0.04	0.474	0.018	0.024	0.879	-0.01	0.06	0.04	0.022	0.181	-0.012	0.200	0.556	-0.01	0.05	0.03	0.004	0.022	0.842	4.43e-03	(0.04, 0.05)
P1484	PCG1	02	0101	0.02	0.03	0.154	0.02	0.01	0.04	0.474	0.018	0.024	0.879	-0.01	0.06	0.04	0.022	0.181	-0.012	0.200	0.556	-0.01	0.05	0.03	0.004	0.022	0.842	4.43e-03	(0.04, 0.05)
GRMUM5	NEBF	03	0214	0.05	0.156	0.02	0.01	0.05	0.475	1.72E-05	0.024	0.288	0.02	-0.03	0.08	0.000	0.878	0.006	0.023	0.785	-0.01	0.05	0.04	0.005	0.021	0.991	-2.89e-04	(0.05, 0.05)	
P21860	ENEB	02	0201	0.14	0.157	0.02	0.01	0.05	0.478	8.27E-08	0.035	0.227	0.00	0.03	0.02	0.009	0.517	0.048	0.021	0.202	0.05	0.01	0.09	0.004	0.023	1.13e	0.01	(0.01, 0.08)	
D69971	CD160	06	0201	0.02	0.157	0.02	0.01	0.05	0.478	8.27E-08	0.035	0.227	0.00	0.03	0.02	0.009	0.517	0.048	0.021	0.202	0.05	0.01	0.09	0.004	0.023	1.13e	0.01	(0.01, 0.08)	
P05113	L5	02	0201	0.12	0.157	0.02	0.01	0.05	0.478	8.27E-08	0.035	0.227	0.00	0.03	0.02	0.009	0.517	0.048	0.021	0.202	0.05	0.01	0.09	0.004	0.023	1.13e	0.01	(0.01, 0.08)	
DT4278	RMH9	02	0101	0.02	0.157	0.02	0.01	0.05	0.478	8.27E-08	0.035	0.227	0.00	0.03	0.02	0.009	0.517	0.048	0.021	0.202	0.05	0.01	0.09	0.004	0.023	1.13e	0.01	(0.01, 0.08)	
FR3252	ADAM5	02	0101	0.03	0.159	0.02	0.01	0.04	0.481	3.58E-04	-0.022	0.268	0.35	0.02	0.07	0.003	0.068	0.024	0.023	0.289	0.02	0.01	0.04	0.012	0.021	0.431	0.02	(0.02, 0.06)	
DMC42	RNF49	02	0101	0.02	0.159	0.02	0.01	0.04	0.481	3.58E-04	-0.022	0.268	0.35	0.02	0.07	0.003	0.068	0.024	0.023	0.289	0.02	0.01	0.04	0.012	0.021	0.431	0.02	(0.02, 0.06)	
DMC42	CSH1	02	0101	0.02	0.159	0.02	0.01	0.04	0.481	3.58E-04	-0.022	0.268	0.35	0.02	0.07	0.003	0.068	0.024	0.023	0.289	0.02	0.01	0.04	0.012	0.021	0.431	0.02	(0.02, 0.06)	
NR718	KLK1	03	0102	0.20	0.160	0.02	0.01	0.05	0.484	4.73E-08	-0.028	0.227	0.43	-0.03	0.08	0.003	0.051	-0.001	0.018	0.471	-1.23e	-0.03	0.04	0.003	0.021	0.899	2.95e-03	(0.04, 0.04)	
I12421	MSLN	02	0101	0.14	0.160	0.02	0.01	0.05	0.484	4.73E-08	-0.028	0.227	0.43	-0.03	0.08	0.003	0.051	-0.001	0.018	0.471	-1.23e	-0.03	0.04	0.003	0.021	0.899	2.95e-03	(0.04, 0.04)	
P049819	PDGFA	02	0101	0.02	0.160	0.02	0.01	0.05	0.484	4.73E-08	-0.028	0.227	0.43	-0.03	0.08	0.003	0.051	-0.001	0.018	0.471	-1.23e	-0.03	0.04	0.003	0.021	0.899	2.95e-03	(0.04, 0.04)	
P16422	EPCAM	02	0201	0.16	0.161	0.02	0.01	0.05	0.485	2.14E-10	0.030	0.227	0.43	-0.03	0.08	0.003	0.051	-0.001	0.018	0.471	-1.23e	-0.03	0.04	0.003	0.021	0.899	2.95e-03	(0.04, 0.04)	
DL0178	CLU2	02	0102	0.162	0.162	0.02	0.01	0.05	0.489	0.029	-0.021	0.256	0.06	0.01	0.09	0.003	0.050	0.006	0.015	0.242	0.02	0.01	0.04	0.003	0.021	0.899	2.95e-03	(0.04, 0.04)	
P25378	ELAVL4	02	0101	0.02	0.163	0.02	0.01	0.04	0.490	0.001	0.011	0.225	0.65	0.01	0.04	0.006	0.070	0.023	0.025	0.364	0.02	0.01	0.04	0.003	0.021	0.899	2.95e-03	(0.04, 0.04)	
PS6499	FAM3B	02	0101	0.03	0.163	0.02	0.01	0.04	0.490	1.50E-05	0.021	0.225	0.48	0.02	0.03	0.006	0.070	0.023	0.025	0.364	0.02	0.01	0.04	0.003	0.021	0.899	2.95e-03	(0.04, 0.04)	
SNMWR5	TOP11	02	0101	0.02	0.163	0.02	0.01	0.04	0.490	1.50E-05	0.021	0.225	0.48	0.02	0.03	0.006	0.070	0.023	0.025	0.364	0.02	0.01	0.04	0.003	0.021	0.899	2.95e-03	(0.04, 0.04)	
DMC237	PP1R12B	02	0101	0.02	0.164	0.02	0.01	0.04	0.491	0.463	0.008	0.223	0.79	0.01	0.04	0.005	0.070	0.023	0.025	0.364	0.02	0.01	0.04	0.003	0.021	0.899	2.95e-03	(0.04, 0.04)	
DMC237	CDON	02	0101	0.02	0.165	0.02	0.01	0.04	0.492	9.01E-08	0.011	0.228	0.82	0.01	0.04	0.005	0.070	0.023	0.025	0.364	0.02	0.01	0.04	0.003	0.021	0.899	2.95e-03	(0.04, 0.04)	
P14410	CTLA4	02	0101	0.02	0.165	0.02	0.01	0.04	0.492	9.01E-08	0.011	0.228	0.82	0.01	0.04	0.005	0.070	0.023	0.025	0.364	0.02	0.01	0.04	0.003	0.021	0.899	2.95e-03	(0.04, 0.04)	
NR718	GRN	02	0101	0.02	0.164	0.02	0.01	0.04	0.492	2.82E-07	0.019	0.230	0.82	0.01	0.04	0.005	0.070	0.023	0.025	0.364	0.02	0.01	0.04	0.003	0.021	0.899	2.95e-03	(0.04, 0.04)	
PS4370	PNLRP1	02	0101	0.02	0.164	0.02	0.01	0.04	0.492	2.82E-07	0.019	0.230	0.82	0.01	0.04	0.005	0.070	0.023	0.025	0.364	0.02	0.01	0.04	0.003	0.021	0.899	2.95e-03	(0.04, 0.04)	
P14411	CSF2	02	0101	0.04	0.165	0.02	0.01	0.05	0.492	0.002	-0.005	0.268	0.81	-4.62e	-0.03	0.05	0.001	0.299	0.013	0.021	0.359	0.01	0.05	0.03	0.017	0.024	0.470	-0.02	(-0.03, 0.03)
P22307	SCF2	02	0101	0.02	0.165	0.02	0.01	0.04	0.493	0.633	0.016	0.223	0.49	0.02	0.03	0.006	0.065	0.006	0.023	0.791	-0.01	0.05	0.04	0.006	0.028	0.816	0.01	(0.01, 0.06)	
P44775	TDGF2	02	0101	0.02	0.165	0.02	0.01	0.04	0.493	0.633	0.016	0.223	0.49	0.02	0.03	0.006	0.065	0.006	0.023	0.791	-0.01	0.05	0.04	0.006	0.028	0.816	0.01	(0.01, 0.06)	
DMC237	FCRL6	02	0201	0.05	0.166	0.02	0.01	0.05	0.493	1.01E-17	0.019	0.228	0.50	0.02	0.04	0.007	0.069	0.011	0.019	0.551	0.01	0.05	0.04	0.006	0.028	0.816	0.01	(0.01, 0.06)	
P12326	PCL	02	0101	0.04	0.166	0.02	0.01	0.05	0.494	1.83E-07	-0.003	0.228	0.91	-3.36e	-0.03	0.05	0.001	0.327	-0.003	0.021	-3.45e	-0.03	0.04	0.006	0.028	0.816	0.01	(0.01, 0.06)	
DT512	ZNF1	02	0101	0.02	0.166	0.02	0.01	0.04	0.494	1.83E-07	-0.003	0.228	0.91	-3.36e	-0.03	0.05	0.001	0.327	-0.003	0.021	-3.45e	-0.03	0.04	0.006	0.028	0.816	0.01	(0.01, 0.06)	
P02776	FCF2	02	0201	0.16	0.169	0.02	0.01	0.05	0.492	1.58E-11	-0.029	0.231	0.33	-0.03	0.09	0.003	0.294	0.014	0.024	0.541	-0.01	0.05	0.03	0.016	0.023	0.901	-0.02	(-0.06, 0.03)	
D69971	MESFP1	02	0101	0.02	0.169	0.02	0.01	0.04	0.492	1.58E-11	-0.029	0.231	0.33	-0.03	0.09	0.003	0.294	0.014	0.024	0.541	-0.01	0.05	0.03	0.016	0.023	0.901	-0.02	(-0.06, 0.03)	
P29475	NSG1	02	0101	0.01	0.171	0.02	0.01	0.04	0.506	0.052	-0.001	0.224	0.966	-1.01e	-0.03	0.05	0.001	0.418	-0.018	0.021	0.443	-0.02	0.03	0.03	0.006	0.025	0.804	-0.01	(0.01, 0.04)
I01419	MORC3	02	0101	0.02	0.171	0.02	0.01	0.04	0.506	0.052	-0.001	0.224	0.966	-1.01e	-0.03	0.05	0.001	0.418	-0.018	0.021	0.443	-0.02	0.03	0.03	0.006	0.025	0.804	-0.01	(0.01, 0.04)
DT2941	RABEP1	02	0101	0.02	0.171	0.02	0.01	0.04	0.506	0.052	-0.001	0.224	0.966	-1.01e	-0.03	0.05	0.001	0.418	-0.018	0.021	0.443	-0.02	0.03	0.03	0.006	0.025	0.804	-0.01	(0.01, 0.04)
P31764	STO2	02	0101	0.02	0.171	0.02	0.01	0.04	0.506	0.052	-0.001	0.224	0.966	-1.01e	-0.03	0.05	0.001	0.418	-0.018	0.021	0.443	-0.02	0.03	0.03	0.006	0.025	0.804	-0.01	(0.01, 0.04)
I12428	TRM2	02	0101	0.02	0.171	0.02	0.01	0.04	0.506	0.052	-0.001	0.224	0.966	-1.01e	-0.03	0.05	0.001	0.418	-0.018	0.021	0.443	-0.02	0.03	0.03	0.006	0.025	0.804	-0.01	(0.01, 0.04)
P31721	ACSL1	02	0101	0.02	0.171	0.02	0.01	0.04	0.506	0.052	-0.001	0.224	0.966	-1.01e	-0.03	0.05	0.001	0.418	-0.018	0.021	0.443	-0.02	0.03	0.03	0.006	0.025	0.804	-0.01	(0.01, 0.04)
D69628	PKP1	02	0101	0.02	0.171	0.02	0.01	0.04	0.506	0.052	-0.001	0.224	0.966	-1.01e	-0.03	0.05	0.001	0.418											

Table S4. Association of type 2 diabetes with UKB-PPP plasma protein.

UnProt	Gene	OD	Inverse variance (log2, log2)				MR Egger				Weighted median				Weighted mode										
			nsp	b/w	se/w	pval/w	CI/w	FDR/w	CI/w	bagger	se/bagger	pval/bagger	CI/bagger	egger	bagger	se/bagger	pval/bagger	CI/bagger	bmode	se/bmode	pval/bmode	CI/bmode			
072324	LYSMD3	OC039650	192	0.10	0.13	0.388	0.01	(0.01, 0.04)	0.737	0.029	0.118	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
P12872	MLN	OC039650	192	0.10	0.13	0.388	0.01	(0.01, 0.04)	0.737	0.029	0.118	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
08NFF7	UCD1030	OC039650	192	0.10	0.13	0.388	0.01	(0.01, 0.04)	0.737	0.029	0.118	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
06ZP24	PTHD1	OC031216	192	0.10	0.12	0.385	0.01	(0.01, 0.04)	0.737	0.028	0.118	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
06K165	FLKDC1	OC031216	192	0.10	0.12	0.385	0.01	(0.01, 0.04)	0.737	0.028	0.118	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
017798	SMAD2	OC031353	192	0.10	0.12	0.385	0.01	(0.01, 0.04)	0.737	0.028	0.118	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
022233	CD33	OC030983	192	0.10	0.12	0.385	0.01	(0.01, 0.04)	0.737	0.028	0.118	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
08M120	MRH21	OC030891	192	0.10	0.11	0.387	0.01	(0.01, 0.03)	0.737	0.027	0.118	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
09H465	TC1D17	OC020844	192	0.10	0.11	0.388	0.01	(0.01, 0.03)	0.737	0.027	0.118	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
P09851	TON1	OC020847	192	0.10	0.11	0.388	0.01	(0.01, 0.03)	0.737	0.027	0.118	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
043597	SPRY2	OC020475	192	0.10	0.12	0.388	0.01	(0.01, 0.04)	0.738	0.030	0.119	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
06ZVL6	KIAA1549L	OC031312	192	0.10	0.12	0.389	0.01	(0.01, 0.03)	0.738	0.031	0.120	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
06ZLJL	PKRAB1	OC020887	192	0.10	0.12	0.389	0.01	(0.01, 0.03)	0.738	0.031	0.120	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
042768	WAS	OC031279	192	0.10	0.11	0.389	0.01	(0.01, 0.04)	0.738	0.030	0.120	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
014552	CASQ2	OC030983	192	0.10	0.12	0.390	0.01	(0.01, 0.03)	0.739	0.031	0.120	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
06UMF0	ICAM5	OC021045	192	0.10	0.12	0.390	0.01	(0.01, 0.03)	0.739	0.031	0.120	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
014349	BIRC4	OC021217	192	0.10	0.11	0.390	0.01	(0.01, 0.04)	0.739	0.031	0.120	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
P44109	CRKL	OC020350	192	0.10	0.12	0.391	0.01	(0.01, 0.04)	0.739	0.030	0.120	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
014344	ADAM10	OC021045	192	0.10	0.11	0.394	0.01	(0.01, 0.03)	0.740	0.030	0.121	0.028	0.742	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
P17151	AKT2	OC031652	89	0.10	0.19	0.392	0.02	(0.05, 0.02)	0.740	0.033	0.120	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
007507	DPT	OC020276	192	0.10	0.12	0.396	0.01	(0.02, 0.03)	0.740	0.033	0.120	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
PS1452	DUSP3	OC020827	192	0.10	0.12	0.394	0.01	(0.04, 0.02)	0.740	0.034	0.120	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
09F2K7	OC030533	192	0.10	0.12	0.394	0.01	(0.04, 0.02)	0.740	0.034	0.120	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)			
06ZLJL	FNL2	OC030719	192	0.10	0.12	0.395	0.01	(0.02, 0.04)	0.740	0.036	0.122	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
P09859	OC020455	192	0.10	0.12	0.392	0.01	(0.03, 0.01)	0.740	0.036	0.122	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)			
P09859	OC020455	192	0.10	0.12	0.392	0.01	(0.03, 0.01)	0.740	0.036	0.122	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)			
09E882	KALL1	OC021339	192	0.10	0.12	0.394	0.01	(0.04, 0.02)	0.740	0.036	0.122	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
P09851	NFC	OC030888	192	0.10	0.12	0.394	0.01	(0.01, 0.03)	0.740	0.036	0.122	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
P01198	PHF21	OC030888	192	0.10	0.12	0.394	0.01	(0.01, 0.03)	0.740	0.036	0.122	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
015113	PCCOLCE	OC020384	192	0.10	0.12	0.396	0.02	(0.08, 0.02)	0.740	0.031	0.124	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
071587	NACTR2	OC030533	192	0.10	0.12	0.396	0.01	(0.04, 0.02)	0.740	0.033	0.124	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
075711	OC030533	192	0.10	0.12	0.395	0.01	(0.03, 0.01)	0.740	0.033	0.124	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)			
012765	SCRN1	OC020542	192	0.10	0.12	0.396	0.01	(0.03, 0.01)	0.740	0.033	0.124	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
027096	SPRSD2	OC030533	192	0.10	0.12	0.396	0.01	(0.03, 0.01)	0.740	0.033	0.124	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
PS5022	TL3	OC030624	192	0.10	0.12	0.395	0.01	(0.01, 0.03)	0.740	0.033	0.124	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
09F184S	STC3	OC021285	192	0.10	0.12	0.393	0.01	(0.04, 0.02)	0.740	0.034	0.124	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
09F426	TRCB	OC030533	192	0.10	0.12	0.393	0.01	(0.04, 0.02)	0.740	0.034	0.124	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
PS5288	THOP1	OC021034	18	0.10	0.22	0.396	0.02	(0.03, 0.06)	0.740	0.191	0.062	0.035	0.993	0.06	(0.01, 0.13)	0.05	1.04	0.043	(0.06, 0.01)	0.049	0.28	0.145	0.04	(0.01, 0.10)	
09F426	TRCB	OC030533	192	0.10	0.12	0.393	0.01	(0.04, 0.02)	0.740	0.034	0.124	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
P12931	SCR1	OC021521	192	0.10	0.11	0.397	0.01	(0.04, 0.01)	0.741	0.030	0.118	0.028	0.847	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
P04216	CHST1	OC021050	192	0.10	0.12	0.397	0.01	(0.02, 0.04)	0.741	0.030	0.118	0.028	0.847	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)	0.023	0.25	0.345	0.022	(0.03, 0.07)
09F426	TRCB	OC030533	192	0.10	0.12	0.393	0.01	(0.04, 0.02)	0.740	0.034	0.124	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
09F426	TRCB	OC030533	192	0.10	0.12	0.393	0.01	(0.04, 0.02)	0.740	0.034	0.124	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
09F426	TRCB	OC030533	192	0.10	0.12	0.393	0.01	(0.04, 0.02)	0.740	0.034	0.124	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)		
09F426	TRCB	OC030533	192	0.10	0.12	0.393	0.01	(0.04, 0.02)	0.740	0.034	0.124	0.032	0.899	0.011	(0.06, 0.07)	0.022	0.367	0.011	(0.06, 0.07)	0.					

Table S4. Association of type 2 diabetes with UKB-PPP plasma protein.

UnProt	Gene	OD	nsnp	Inverse variance co-ordinates				MR Egger				Weighted median				Weighted mode											
				b_low	se_low	p_val_low	CI_low	FDR_low	Q_val	loggger	segger	pvalgger	CIegger	egger	beta_egger	se_val	p_val	beta	se_mode	p_val	beta	se_mode	p_val				
U14843	ITPR1	OD30216	192	-0.010	0.014	0.465	-0.01 (0.04, 0.02)	0.789	8.12E-05	0.024	0.028	0.933	-0.022	(-0.08, 0.03)	0.001	0.576	0.002	0.026	0.934	2.15e-03	(0.05, 0.05)	0.002	0.25	0.933	2.15e-03	(0.05, 0.05)	
D28445	LEI8E4	OD20928	192	-0.008	0.015	0.481	0.01 (0.02, 0.04)	0.789	2.27E-05	0.007	0.006	0.917	0.017	(0.01, 0.02)	0.001	0.620	0.002	0.024	0.744	0.03	(0.04, 0.03)	0.001	0.015	0.917	0.017	(0.01, 0.02)	
D93639	NPTN	OD21235	192	-0.009	0.012	0.465	-0.01 (0.03, 0.01)	0.789	6.17E-09	0.024	0.029	0.933	-0.022	(-0.08, 0.03)	0.002	0.627	-0.035	0.021	0.101	-0.04	(0.08, 0.01)	0.003	0.038	0.933	-0.022	(-0.08, 0.03)	
P20774	DN	OD21123	192	-0.009	0.013	0.464	-0.01 (0.02, 0.03)	0.789	6.28E-09	0.025	0.017	0.922	-0.022	(-0.08, 0.03)	0.003	0.622	-0.040	0.017	0.117	-0.036	(0.04, 0.03)	0.003	0.024	0.922	-0.022	(-0.08, 0.03)	
P11286	PPY	OD21123	192	-0.009	0.013	0.464	-0.01 (0.02, 0.03)	0.789	6.28E-09	0.025	0.017	0.922	-0.022	(-0.08, 0.03)	0.003	0.622	-0.040	0.017	0.117	-0.036	(0.04, 0.03)	0.003	0.024	0.922	-0.022	(-0.08, 0.03)	
D06689	RAD51	OD21254	192	-0.009	0.012	0.465	-0.01 (0.02, 0.03)	0.789	5.21E-05	0.023	0.025	0.933	-0.022	(-0.08, 0.03)	0.001	0.574	0.007	0.024	0.707	0.01	(0.04, 0.05)	0.006	0.023	0.933	-0.022	(-0.08, 0.03)	
U15043	STK4	OD21254	192	-0.009	0.012	0.465	-0.01 (0.02, 0.03)	0.789	5.21E-05	0.023	0.025	0.933	-0.022	(-0.08, 0.03)	0.001	0.574	0.007	0.024	0.707	0.01	(0.04, 0.05)	0.006	0.023	0.933	-0.022	(-0.08, 0.03)	
Q6UX82	CXCL12	OD21252	192	0.010	0.013	0.467	0.01 (0.02, 0.04)	0.791	1.28E-07	0.013	0.026	0.906	0.010	(0.01, 0.04)	0.006	0.868	0.016	0.022	0.459	0.02	(0.03, 0.06)	0.010	0.024	0.906	0.010	(0.01, 0.04)	
D93703	MRFSP5	OD21268	192	-0.009	0.012	0.467	-0.01 (0.01, 0.03)	0.791	0.85E-06	0.006	0.023	0.901	-0.011	(-0.05, 0.04)	0.001	0.485	-0.013	0.024	0.589	-0.01	(0.06, 0.03)	-0.013	0.024	0.901	-0.011	(-0.05, 0.04)	
P78560	CRADD	OD21268	192	-0.009	0.012	0.467	-0.01 (0.01, 0.03)	0.791	0.85E-06	0.006	0.023	0.901	-0.011	(-0.05, 0.04)	0.001	0.485	-0.013	0.024	0.589	-0.01	(0.06, 0.03)	-0.013	0.024	0.901	-0.011	(-0.05, 0.04)	
D06705	HMOX2	OD21268	192	-0.010	0.014	0.468	-0.01 (0.04, 0.02)	0.791	2.75E-06	0.006	0.026	0.819	-0.011	(-0.05, 0.06)	0.001	0.485	-0.013	0.023	0.938	-0.01	(0.04, 0.05)	0.007	0.024	0.819	-0.011	(-0.05, 0.06)	
P12270	TRIP1	OD30143	128	0.010	0.014	0.468	0.01 (0.02, 0.04)	0.791	0.39E-03	0.026	0.221	-0.031	0.028	(-0.07, 0.03)	0.003	0.059	0.000	0.026	0.988	1.16e-04	(0.04, 0.05)	-0.016	0.025	0.026	0.988	1.16e-04	(0.04, 0.05)
D26884	CEP43	OD21268	192	-0.009	0.012	0.467	-0.01 (0.02, 0.04)	0.791	0.39E-03	0.026	0.221	-0.031	0.028	(-0.07, 0.03)	0.003	0.059	0.000	0.026	0.988	1.16e-04	(0.04, 0.05)	-0.016	0.025	0.026	0.988	1.16e-04	(0.04, 0.05)
P34813	EPHK2	OD20219	192	0.010	0.014	0.469	0.01 (0.02, 0.04)	0.792	2.81E-04	0.018	0.027	0.912	0.012	(0.02, 0.04)	0.002	0.230	0.011	0.028	0.679	0.01	(0.04, 0.06)	0.001	0.027	0.912	0.012	(0.02, 0.04)	
P10209	PRKAC3	OD20221	192	0.010	0.014	0.469	0.01 (0.01, 0.03)	0.792	0.86E-05	0.023	0.027	0.933	0.012	(0.01, 0.04)	0.002	0.230	0.011	0.028	0.679	0.01	(0.04, 0.06)	0.001	0.027	0.933	0.012	(0.02, 0.04)	
Q8BU17	SERPINA1	OD20221	192	-0.008	0.011	0.470	-0.01 (0.03, 0.01)	0.792	3.61E-08	0.038	0.022	0.906	-0.014	(-0.08, 0.03)	0.001	0.015	-0.019	0.018	0.298	-0.02	(0.02, 0.05)	0.020	0.021	0.906	-0.014	(-0.08, 0.03)	
P01588	EGP	OD20222	192	0.010	0.014	0.471	0.01 (0.02, 0.04)	0.793	0.00E+00	0.048	0.026	0.808	0.005	(0.01, 0.035-03)	0.004	0.011	-0.032	0.020	0.102	-0.03	(0.07, 0.01)	0.030	0.024	0.808	0.005	(0.01, 0.035-03)	
D05966	TRNFRS14	OD20222	192	0.010	0.014	0.471	0.01 (0.02, 0.04)	0.793	0.00E+00	0.048	0.026	0.808	0.005	(0.01, 0.035-03)	0.004	0.011	-0.032	0.020	0.102	-0.03	(0.07, 0.01)	0.030	0.024	0.808	0.005	(0.01, 0.035-03)	
P22748	CD4	OD20241	87	-0.015	0.021	0.472	-0.02 (0.06, 0.03)	0.793	3.52E-05	0.019	0.036	0.922	-0.022	(-0.08, 0.03)	0.002	0.238	0.001	0.027	0.934e-04	(0.05, 0.05)	0.007	0.025	0.922	-0.022	(-0.08, 0.03)		
P04234	C3D	OD20242	192	-0.009	0.012	0.475	-0.01 (0.02, 0.03)	0.793	0.37E-09	0.009	0.024	0.787	-0.011	(-0.06, 0.04)	0.001	0.401	-0.012	0.024	0.627	-0.01	(0.04, 0.05)	-0.011	0.023	0.787	-0.011	(-0.06, 0.04)	
D02949	CEACAM1	OD20242	192	-0.009	0.012	0.475	-0.01 (0.02, 0.03)	0.793	0.37E-09	0.009	0.024	0.787	-0.011	(-0.06, 0.04)	0.001	0.401	-0.012	0.024	0.627	-0.01	(0.04, 0.05)	-0.011	0.023	0.787	-0.011	(-0.06, 0.04)	
U14055	COL9A2	OD21255	192	-0.009	0.012	0.474	-0.01 (0.01, 0.03)	0.793	0.57E-04	0.026	0.023	0.925	-0.013	(-0.07, 0.02)	0.002	0.089	0.000	0.025	0.988	4.60e-04	(0.05, 0.05)	0.002	0.024	0.925	-0.013	(-0.07, 0.02)	
D03889	EDF1	OD21010	192	0.010	0.014	0.472	0.01 (0.02, 0.04)	0.793	0.00E+00	0.029	0.027	0.725	0.011	(0.06, 0.04)	0.001	0.399	0.009	0.024	0.767	0.01	(0.04, 0.02)	0.004	0.024	0.725	0.011	(0.06, 0.04)	
D06447	EVI5	OD30519	192	-0.009	0.013	0.475	-0.01 (0.04, 0.02)	0.793	0.00E+00	0.019	0.026	0.465	-0.022	(-0.07, 0.03)	0.001	0.671	-0.020	0.024	0.402	-0.02	(0.07, 0.02)	-0.027	0.024	0.465	-0.022	(-0.07, 0.03)	
P25992	GUCY2C	OD31318	192	-0.009	0.012	0.474	-0.01 (0.01, 0.03)	0.793	0.25E-07	0.027	0.026	0.933	-0.022	(-0.08, 0.03)	0.001	0.362	-0.017	0.019	0.380	-0.02	(0.05, 0.02)	-0.025	0.028	0.933	-0.022	(-0.08, 0.03)	
P20702	ITGAK	OD31325	192	-0.009	0.012	0.475	-0.01 (0.02, 0.04)	0.793	0.00E+00	0.011	0.030	0.911	-0.011	(-0.06, 0.04)	0.001	0.359	0.001	0.020	0.968	0.04e-04	(0.04, 0.04)	-0.008	0.028	0.911	-0.011	(-0.06, 0.04)	
P11137	MAP2	OD31318	192	-0.009	0.013	0.472	-0.01 (0.02, 0.04)	0.793	0.00E+00	0.007	0.026	0.780	-0.011	(-0.04, 0.06)	0.001	0.362	-0.017	0.019	0.380	-0.02	(0.05, 0.02)	-0.025	0.028	0.780	-0.011	(-0.06, 0.04)	
U14986	MESD	OD21299	192	-0.010	0.013	0.473	-0.01 (0.04, 0.02)	0.793	0.00E+00	0.019	0.026	0.844	-0.022	(-0.07, 0.03)	0.001	0.371	-0.010	0.024	0.677	-0.01	(0.04, 0.04)	-0.022	0.028	0.844	-0.022	(-0.07, 0.03)	
D01514	MORF4L2	OD21299	192	-0.010	0.013	0.473	-0.01 (0.04, 0.02)	0.793	0.00E+00	0.019	0.026	0.844	-0.022	(-0.07, 0.03)	0.001	0.371	-0.010	0.024	0.677	-0.01	(0.04, 0.04)	-0.022	0.028	0.844	-0.022	(-0.07, 0.03)	
P02166	NESD	OD21299	192	-0.010	0.013	0.473	-0.01 (0.04, 0.02)	0.793	0.00E+00	0.019	0.026	0.844	-0.022	(-0.07, 0.03)	0.001	0.371	-0.010	0.024	0.677	-0.01	(0.04, 0.04)	-0.022	0.028	0.844	-0.022	(-0.07, 0.03)	
D17674	MOF	OD21299	192	-0.010	0.013	0.473	-0.01 (0.04, 0.02)	0.793	0.00E+00	0.019	0.026	0.844	-0.022	(-0.07, 0.03)	0.001	0.371	-0.010	0.024	0.677	-0.01	(0.04, 0.04)	-0.022	0.028	0.844	-0.022	(-0.07, 0.03)	
P28922	RPTD	OD20570	192	-0.009	0.013	0.473	-0.01 (0.04, 0.02)	0.793	0.00E+00	0.018	0.025	0.744	-0.022	(-0.07, 0.03)	0.002	0.207	-0.020	0.023	0.401	-0.02	(0.03, 0.07)	-0.020	0.026	0.744	-0.022	(-0.07, 0.03)	
D94446	WTKO	OD20570	192	-0.009	0.013	0.473	-0.01 (0.04, 0.02)	0.793	0.00E+00	0.018	0.025	0.744	-0.022	(-0.07, 0.03)	0.002	0.207	-0.020	0.023	0.401	-0.02	(0.03, 0.07)	-0.020	0.026	0.744	-0.022	(-0.07, 0.03)	
P05121	SERPINE1	OD21015	192	-0.009	0.013	0.472	-0.01 (0.03, 0.02)	0.793	0.00E+00	0.008	0.025	0.739	-0.011	(-0.06, 0.04)	0.001	0.366	-0.008	0.023	0.733	-0.01	(0.05, 0.04)	-0.024	0.026	0.739	-0.011	(-0.06, 0.04)	
P18474	TRM1	OD20533	192	-0.009	0.013	0.474	-0.01 (0.03, 0.02)	0.793	0.01E-02	0.010	0.025	0.703	-0.011	(-0.06, 0.04)	0.001	0.366	-0.008	0.023	0.733	-0.01	(0.05, 0.04)	-0.024	0.026	0.703	-0.011	(-0.06, 0.04)	
D06814	ABHD14B	OD20533	192	-0.009	0.013	0.474	-0.01 (0.03, 0.02)	0.793	0.01E-02	0.010	0.025	0.703	-0.011	(-0.06, 0.04)	0.001	0.366	-0.008	0.023	0.733	-0.01	(0.05, 0.04)	-0.024	0.026	0.703	-0.011	(-0.06, 0.04)	
P11338	COL1	OD20533	192	-0.009	0.013	0.474	-0.01 (0.03, 0.02)	0.793	0.01E-02	0.010	0.025	0.703	-0.011	(-0.06, 0.04)	0.001	0.366	-0.008	0.023	0.733	-0.01	(0.05, 0.04)	-0.024	0.026	0.703	-0.011	(-0.06, 0.04)	
U13388	TOM2D	OD30353	192	-0.010	0.014	0.478	-0.01 (0.02, 0.04)	0.795	2.38E-05	0.019	0.028	0.884	-0.022	(-0.07, 0.03)	0.002	0.214	-0.005	0.025	0.932	0.01	(0.04, 0.04)	0.000	0.025	0.884	-0.022	(-0.07, 0.03)	
D07700	OTC	OD20242	192	-0.009	0.012	0.478	-0.01 (0.02, 0.04)	0.795	0.00E+00	0.019	0.028	0.884	-0.022	(-0.07, 0.03)	0.002	0.214	-0.005	0.025	0.932	0.01	(0.04, 0.04)	0.000	0.025	0.884	-0.022	(-0.07, 0.03)	
P02848	ACE	OD30727	192	0.010	0.014	0.479	0.01 (0.09, 0.19)	0.796	0.00E+00	0.037	0.136	0.787	0.014	(0.23, 0.30)	0.001	0.913	-0.002	0.019	0.908	-0.22	(0.04, 0.04)	0.014					

Table S4. Association of type 2 diabetes with UKB-PPP plasma protein.

UnPrFid	Gene	OD	nsnp	Inverse variance co-kriging				MR Egger				Weighted median				Weighted mode													
				beta	se	pval	CI_low	CI_high	FDR_low	beta	se	pval	CI_low	CI_high	beta	se	pval	CI_low	CI_high	beta	se	pval	CI_low	CI_high					
09UNNS	PROCR	0301349	48	-0.12	0.22	0.543	-0.01	(0.5, 0.03)	0.832	0.618	0.34	0.30	0.289	0.03	(-0.09, 0.03)	0.002	0.345	-0.025	0.288	0.33	0.02	(-0.06, 0.03)	-0.027	0.272	0.312	-0.03	(-0.06, 0.03)		
09TE4S	DT11	0203069	192	-0.08	0.13	0.546	-0.01	(0.02, 0.02)	0.832	0.106	0.06	0.028	0.134	0.006	(-0.01, 0.01)	0.002	0.927	0.014	0.022	0.883	0.12	0.01	(-0.01, 0.03)	-0.012	0.283	0.431	-0.01	(-0.06, 0.03)	
013451	KPFR5	0200937	192	-0.08	0.13	0.545	-0.01	(0.03, 0.02)	0.832	0.201	-0.003	0.225	0.884	-0.336	0.05	(0.05, 0.05)	0.000	0.835	0.006	0.025	0.812	0.01	(-0.06, 0.04)	-0.020	0.236	0.438	-0.02	(-0.07, 0.03)	
026445	MKBP	0203028	192	-0.08	0.13	0.548	-0.01	(0.03, 0.02)	0.832	0.016	-0.043	0.226	1.100	-0.04	(0.09, 0.01)	0.002	1.120	-0.037	0.024	1.121	-0.04	(-0.08, 0.01)	-0.036	0.225	0.553	-0.04	(-0.09, 0.01)		
054117	KXPH1	0200449	192	-0.08	0.13	0.546	-0.01	(0.03, 0.02)	0.832	0.028	0.028	0.228	0.028	0.028	(0.02, 0.02)	0.000	0.927	0.014	0.022	0.883	0.12	0.01	(-0.01, 0.03)	-0.012	0.283	0.431	-0.01	(-0.06, 0.03)	
013976	PRKG1	0203062	192	-0.08	0.13	0.545	-0.01	(0.03, 0.02)	0.832	0.006	-0.020	0.228	0.442	0.02	(0.03, 0.07)	0.001	0.993	0.017	0.024	0.979	0.02	0.02	(-0.06, 0.03)	-0.038	0.233	0.106	-0.04	(-0.08, 0.01)	
025245	RC14	0203096	192	-0.08	0.13	0.550	-0.02	(0.04, 0.07)	0.832	3.165	1.12	0.864	0.55	0.28	0.04	(0.14, 0.16)	0.003	0.268	0.040	0.024	0.998	0.04	0.01	(-0.02, 0.06)	0.037	0.220	0.434	0.04	(-0.06, 0.03)
026111	SFTPA2	0201218	192	-0.08	0.13	0.544	-0.01	(0.02, 0.03)	0.832	2.01E-04	0.918	0.225	0.483	0.02	(0.03, 0.07)	0.001	0.644	0.037	0.017	0.032	0.04	(0.15e-03, 0.07)	0.046	0.254	0.051	0.05	(0.17e-04, 0.09)		
098585	TSPAN15	0203095	192	-0.07	0.12	0.547	-0.01	(0.02, 0.03)	0.832	0.144	-0.013	0.225	0.980	0.01	(-0.06, 0.04)	0.001	0.330	-0.022	0.020	0.290	0.02	(-0.06, 0.02)	-0.037	0.208	0.179	-0.04	(-0.08, 0.02)		
096512	AKM2D	0201176	192	-0.07	0.12	0.546	-0.01	(0.02, 0.03)	0.832	0.104	0.025	0.225	0.980	0.01	(-0.06, 0.04)	0.001	0.330	-0.022	0.020	0.290	0.02	(-0.06, 0.02)	-0.037	0.208	0.179	-0.04	(-0.08, 0.02)		
015169	AKM1	0120582	192	-0.07	0.12	0.547	-0.01	(0.02, 0.03)	0.833	0.077	0.003	0.224	0.913	2.63e-03	(0.07, 0.05)	0.001	0.864	0.007	0.020	0.745	0.01	(0.03, 0.05)	0.000	0.025	0.991	2.85e-04	(0.05, 0.05)		
030705	CKAP4	0202017	192	-0.09	0.15	0.547	-0.01	(0.02, 0.04)	0.833	3.53E-09	-0.055	0.228	0.949	-0.06	(-0.11, -0.06e-04)	0.004	0.008	-0.030	0.020	1.45	-0.03	(-0.07, 0.01)	-0.017	0.021	0.416	-0.02	(-0.06, 0.02)		
026101	RAB2B	0201082	192	-0.08	0.13	0.547	-0.01	(0.02, 0.03)	0.832	1.93E-02	0.022	0.228	0.811	0.00	(-0.06, 0.05)	0.003	0.024	0.007	0.471	0.01	0.01	(-0.04, 0.04)	-0.012	0.023	0.881	3.4e-03	(0.04, 0.05)		
026177	EYF7Y7	0203085	192	-0.09	0.15	0.548	-0.01	(0.03, 0.05)	0.835	1.78E-28	-0.036	0.228	0.841	-0.01	(-0.06, 0.04)	0.001	0.554	-0.015	0.022	0.440	-0.02	(-0.06, 0.03)	-0.009	0.023	0.685	-0.01	(-0.06, 0.04)		
042702	IFLN4	0203096	192	-0.08	0.13	0.550	-0.02	(0.04, 0.07)	0.835	3.16E-11	0.864	0.55	0.28	0.04	(0.14, 0.16)	0.003	0.268	0.040	0.024	0.998	0.04	0.01	(-0.02, 0.06)	0.037	0.220	0.434	0.04	(-0.06, 0.03)	
020783	NTP3	0202091	192	-0.08	0.13	0.551	-0.01	(0.02, 0.04)	0.835	3.29E-04	0.945	0.027	0.901	0.05	(0.01, 0.10)	0.002	1.106	0.043	0.020	0.034	0.04	(0.27e-03, 0.08)	0.035	0.023	0.135	0.03	(0.02, 0.08)		
016233	PNLP1	0203063	192	-0.19	0.31	0.550	-0.02	(0.04, 0.08)	0.835	8.29E-18	0.074	0.861	0.225	0.07	(0.05, 0.19)	0.003	0.291	0.034	0.023	1.42	0.03	(-0.01, 0.08)	0.030	0.025	0.230	0.03	(0.02, 0.08)		
026174	SRPN21	0203096	192	-0.07	0.12	0.555	-0.01	(0.02, 0.03)	0.835	0.981	0.007	0.023	0.778	0.01	(0.04, 0.05)	0.001	0.493	0.022	0.021	0.288	0.02	(-0.02, 0.06)	0.028	0.028	0.291	0.03	(0.02, 0.08)		
026558	WASF1	0202091	192	-0.08	0.13	0.551	-0.01	(0.02, 0.03)	0.835	0.001	-0.009	0.226	0.740	-0.01	(-0.06, 0.04)	0.000	0.978	0.008	0.023	0.471	0.01	(0.04, 0.05)	-0.005	0.023	0.810	-0.01	(-0.06, 0.04)		
016971	CD36	0203045	192	-0.09	0.15	0.552	-0.01	(0.02, 0.04)	0.836	1.24E-09	-0.008	0.029	0.790	-0.01	(-0.06, 0.04)	0.001	0.510	-0.017	0.021	1.416	-0.02	(-0.06, 0.02)	-0.010	0.023	0.695	-0.01	(-0.06, 0.04)		
022511	NTYA	0203014	192	-0.07	0.12	0.552	-0.01	(0.02, 0.03)	0.836	0.407	-0.022	0.023	0.100	0.04	(0.03, 0.05)	0.002	0.944	-0.028	0.022	0.641	-0.02	(-0.06, 0.02)	-0.023	0.023	0.683	-0.02	(-0.06, 0.04)		
026127	NLGN1	0203090	192	-0.07	0.12	0.552	-0.01	(0.02, 0.03)	0.836	0.275	0.014	0.024	0.552	0.01	(-0.03, 0.08)	0.000	0.729	0.005	0.025	0.827	0.01	(-0.04, 0.05)	-0.021	0.024	0.391	0.02	(0.03, 0.07)		
017518	ARHCA1	0202092	192	-0.07	0.12	0.553	-0.01	(0.02, 0.03)	0.837	0.228	-0.040	0.024	0.100	0.04	(0.03, 0.05)	0.003	0.024	0.009	0.025	0.733	0.01	(-0.04, 0.06)	0.003	0.023	0.681	3.4e-03	(0.04, 0.05)		
098960	LTAH4	0201452	192	-0.07	0.12	0.554	-0.01	(0.02, 0.03)	0.838	0.778	-0.051	0.022	0.023	0.05	(-0.10, 0.01)	0.003	0.022	-0.016	0.023	0.493	0.02	(-0.06, 0.03)	-0.014	0.024	0.560	-0.01	(-0.06, 0.03)		
043896	KIFIC	0203163	192	-0.07	0.12	0.555	-0.01	(0.02, 0.03)	0.838	0.258	-0.045	0.023	0.058	0.04	(0.09, -0.22e-03)	0.003	0.011	-0.042	0.020	0.038	0.04	(-0.08, -0.22e-03)	-0.047	0.022	0.033	-0.05	(-0.08, -0.13e-04)		
043378	PTN9B	0203037	192	-0.07	0.12	0.555	-0.01	(0.02, 0.03)	0.838	0.981	0.007	0.023	0.778	0.01	(0.04, 0.05)	0.001	0.493	0.022	0.021	0.288	0.02	(-0.02, 0.06)	0.028	0.028	0.291	0.03	(0.02, 0.08)		
012888	TSP3BP1	0203040	192	-0.10	0.16	0.556	-0.01	(0.02, 0.04)	0.839	3.39E-12	0.007	0.322	0.825	0.01	(-0.06, 0.07)	0.000	0.924	0.031	0.024	0.208	0.03	(-0.08, 0.02)	-0.045	0.023	0.050	-0.04	(-0.08, -0.19e-04)		
062574	LYPD3	0201230	192	-0.10	0.17	0.557	-0.01	(0.04, 0.02)	0.840	8.39E-28	0.044	0.033	0.176	0.04	(0.02, 0.11)	0.003	0.054	0.022	0.019	0.227	0.02	(-0.02, 0.06)	0.020	0.022	0.356	0.02	(0.02, 0.06)		
026176	TRAF3IP1	0203096	192	-0.07	0.12	0.557	-0.01	(0.02, 0.03)	0.840	2.45E-09	0.029	0.023	0.285	0.01	(-0.06, 0.07)	0.001	0.350	0.024	0.027	0.621	0.02	(-0.02, 0.06)	0.033	0.023	0.683	0.02	(0.03, 0.08)		
026128	BKIP1	0202094	192	-0.07	0.12	0.558	-0.01	(0.02, 0.03)	0.842	0.400	0.008	0.024	0.748	0.01	(-0.04, 0.06)	0.001	0.488	0.015	0.021	0.440	0.02	(-0.03, 0.06)	0.005	0.024	0.847	-0.05	(-0.09, 0.04)		
026178	CLEC2C	0203096	192	-0.07	0.12	0.558	-0.01	(0.02, 0.03)	0.842	0.022	0.022	0.024	0.100	0.04	(0.03, 0.05)	0.002	0.027	0.027	0.471	0.01	(-0.04, 0.06)	0.003	0.023	0.681	3.4e-03	(0.04, 0.05)			
026129	DCLD2L	0202044	192	-0.11	0.18	0.563	-0.01	(0.05, 0.03)	0.842	1.31E-33	0.003	0.036	0.925	0.34e-03	(0.07, 0.07)	0.001	0.648	0.021	0.023	0.348	0.02	(-0.02, 0.07)	0.025	0.023	0.275	0.02	(0.02, 0.07)		
098665	PSDEFA1	0202034	192	-0.08	0.14	0.564	-0.01	(0.02, 0.02)	0.842	4.61E-07	-0.020	0.228	0.489	-0.02	(-0.08, 0.03)	0.001	0.818	-0.008	0.025	0.741	-0.01	(-0.06, 0.04)	-0.013	0.027	0.577	-0.01	(-0.06, 0.03)		
026125	EBAG9	0203096	192	-0.07	0.12	0.564	-0.01	(0.02, 0.03)	0.842	0.024	0.024	0.024	0.485	0.02	(0.03, 0.04)	0.001	0.024	0.024	0.485	0.02	(0.03, 0.04)	0.001	0.024	0.485	0.02	(0.03, 0.04)			
042892	FCF1	0202091	192	-0.14	0.24	0.560	-0.01	(0.06, 0.03)	0.842	1.54E-75	-0.001	0.047	0.988	-0.29	(-0.09, 0.09)	0.001	0.740	-0.019	0.023	0.410	-0.02	(-0.06, 0.07)	-0.027	0.023	0.238	0.03	(0.02, 0.07)		
097285	FARSA	0203087	192	-0.08	0.14	0.563	-0.01	(0.02, 0.03)	0.842	0.003	-0.027	0.228	0.307	-0.03	(-0.08, 0.02)	0.002	0.124	-0.005	0.020	0.802	0.01	(-0.03, 0.03)	-0.009	0.028	0.706	-0.01	(-0.06, 0.04)		
026179	EM1	0201233	192	-0.07	0.12	0.563	-0.01	(0.02, 0.03)	0.842	0.012	0.023	0.228	0.307	-0.03	(-0.08, 0.02)	0.002	0.124	-0.005	0.020	0.802	0.01	(-0.03, 0.03)	-0.009	0.028	0.706	-0.01	(-0.06, 0.04)		
026171	FN1	0203077	192	-0.07	0.12	0.563	-0.01	(0.02, 0.03)	0.842	0.022	-0.021	0.024	0.389	-0.02	(-0.07, 0.03)	0.002	0.175	-0.012	0.022	0.604	-0.01	(-0.06, 0.03)	-0.012	0.023	0.609	-0.01	(-0.06, 0.03)		
015293	GADD45B	0203096	192	-0.07	0.12	0.563	-0.01	(0.02, 0.03)	0.842	0.002	0.023	0.228	0.307	-0.03	(-0.08, 0.02)	0.002	0.124	-0.005	0.020	0.802	0.01	(-0.03, 0.03)	-0.009	0.028	0.706	-0.01	(-0.06, 0.04)		
016665	FN1A	0203025	192	-0.07	0.12	0.561	-0.01	(0.02, 0.02)	0.842	0.427	-0.023	0.024	0.322	0.02	(0.07, 0.03)	0.001	0.417	-0.03											

Table S4. Association of type 2 diabetes with UKB-PPP plasma protein.

UnProt	Gene	OD	Inverse variance meta-analysis				MR Egger				Weighted median				Weighted mode									
			n	nsnp	bl/w	se/blw	beta	CI_low	CI_high	FDR_low	bl/w	se/blw	beta	CI_low	CI_high	FDR_low	bl/w	se/blw	beta	CI_low	CI_high	FDR_low		
P09397	HMSB	0021385	192	-0.006	0.011	0.624	0.01	(0.62, 0.03)	0.888	0.138	0.027	0.379	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
073349	ATP11B1	0023042	192	-0.007	0.014	0.628	0.01	(0.62, 0.03)	0.879	0.138	0.027	0.379	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
070201	C10orf79	0023018	192	-0.008	0.013	0.626	0.01	(0.62, 0.03)	0.889	0.137	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026X00	C12orf75	0023018	192	-0.007	0.014	0.625	0.01	(0.62, 0.03)	0.889	0.138	0.027	0.379	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
017862	CD226	0023018	192	-0.007	0.014	0.625	0.01	(0.62, 0.03)	0.889	0.138	0.027	0.379	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
016773	KYAT1	0023022	192	-0.007	0.013	0.626	0.01	(0.62, 0.03)	0.889	0.137	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
014271	NBL1	0023018	192	-0.007	0.014	0.625	0.01	(0.62, 0.03)	0.889	0.138	0.027	0.379	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
P20155	SPINK2	0023027	192	-0.008	0.012	0.625	0.01	(0.62, 0.03)	0.889	0.138	0.027	0.379	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
P08913	ADRA2	0023067	192	-0.006	0.012	0.627	0.01	(0.62, 0.03)	0.889	0.137	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
043423	ANCSD3	0023018	192	-0.007	0.014	0.625	0.01	(0.62, 0.03)	0.889	0.138	0.027	0.379	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
019338	CAP3	0023126	192	-0.010	0.012	0.629	0.01	(0.63, 0.05)	0.889	0.138	0.027	0.379	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026S92	CRACR2A	0021249	192	-0.007	0.014	0.629	0.01	(0.63, 0.05)	0.889	0.138	0.027	0.379	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026811	EVL1	0023039	192	-0.007	0.014	0.629	0.01	(0.63, 0.05)	0.889	0.138	0.027	0.379	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
06JWUW0	LCN15	0023102	192	-0.007	0.014	0.628	0.01	(0.63, 0.05)	0.889	0.138	0.027	0.379	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
P5470	LOXL4	0023074	192	-0.008	0.012	0.628	0.01	(0.63, 0.05)	0.889	0.138	0.027	0.379	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026V35	NUDT15	0023102	192	-0.008	0.012	0.629	0.01	(0.63, 0.05)	0.889	0.138	0.027	0.379	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
P01210	PENK	0023066	192	-0.011	0.023	0.628	0.01	(0.63, 0.05)	0.889	0.138	0.027	0.379	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
P03668	AK1	0023092	192	-0.009	0.015	0.635	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
020552	AKAP12	0023071	192	-0.008	0.013	0.636	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
P23435	KLHL21	0023081	192	-0.008	0.012	0.633	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
020701	CDOLDF	0023089	192	-0.009	0.014	0.631	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
P38962	CDN1A	0023119	192	-0.007	0.014	0.633	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
020701	CDN1A	0023119	192	-0.007	0.014	0.633	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026WU2	CHAC2	0023230	192	-0.008	0.013	0.636	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026H30	DHDH2	0023103	192	-0.008	0.013	0.632	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
P04992	HDM1	0023098	192	-0.008	0.013	0.635	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026N97	LZBR1	0023049	192	-0.008	0.013	0.635	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
P03533	LRPAP1	0023159	192	-0.013	0.026	0.631	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
P43357	MAGE2	0023031	192	-0.007	0.014	0.631	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026V79	MCR3	0023274	192	-0.007	0.014	0.631	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026W03	MTF3	0023103	192	-0.007	0.014	0.631	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
043776	NARS1	0023105	192	-0.007	0.014	0.633	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
P16066	NRF1	0023016	192	-0.008	0.012	0.633	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
P07296	NUDC	0023098	192	-0.008	0.012	0.633	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026V33	SH3BP1	0023149	192	-0.008	0.012	0.636	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
P61266	STK18	0023034	192	-0.008	0.013	0.632	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
P02844	TANK	0023074	192	-0.008	0.013	0.632	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026R92	TSPG1	0023042	192	-0.008	0.012	0.633	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026S41	STO31A3	0023042	192	-0.008	0.012	0.633	0.01	(0.63, 0.05)	0.870	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026V18	CRTP	0023042	192	-0.008	0.012	0.638	0.01	(0.63, 0.05)	0.871	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026H44	RESF4	0023128	192	-0.005	0.012	0.638	0.01	(0.63, 0.05)	0.871	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
P41735	TKNT	0023099	192	-0.005	0.012	0.640	0.01	(0.63, 0.05)	0.871	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026V88	MIRA	0023115	192	-0.008	0.014	0.640	0.01	(0.63, 0.05)	0.871	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026V43	ANKK1	0023197	192	-0.008	0.014	0.641	0.01	(0.63, 0.05)	0.871	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001	0.455	0.029	0.627	0.01	(0.61, 0.07)	0.024	0.272	0.02	(0.62, 0.07)
026V83	NTG2	0023103	192	-0.008	0.014	0.641	0.01	(0.63, 0.05)	0.871	0.135	0.027	0.380	0.02	(0.62, 0.07)	0.001									

Table S4. Association of type 2 diabetes with UKB-PPP plasma protein.

UnProt	Gene	OD	nsnp	Inverse variance				MR Egger				Weighted mode				Weighted mode											
				beta	se_beta	pval_ivw	CI_low	CI_high	pval	egger	se_egger	pval_egger	CI_low	CI_high	se_weighted	pval_weighted	CI_low	CI_high	se_weighted	pval_weighted	CI_low	CI_high					
097175	CXCL14	0202458	192	0.001	0.11	0.708	-1.56e-03	(0.02, 0.03)	0.001	0.148	0.003	0.223	0.807	0.266e-03	(0.04, 0.05)	0.000	0.939	-0.011	0.221	0.613	-0.01	(0.02, 0.03)	-0.007	0.222	0.771	-0.01	(0.02, 0.04)
097994	EDMD2	0203138	192	0.005	0.12	0.735	-4.58e-03	(0.02, 0.03)	0.013	0.263	0.012	0.023	0.611	(0.04, 0.08)	0.002	0.912	-0.022	0.228	0.412	-0.02	(0.02, 0.03)	-0.022	0.228	0.851	-0.02	(0.04, 0.04)	
098011	ENPEP	0203302	192	-0.005	0.13	0.708	-4.90e-03	(0.02, 0.02)	0.001	0.008	0.023	0.225	0.322	-0.02	(0.07, 0.03)	0.001	0.403	-0.007	0.224	0.786	-0.01	(0.05, 0.04)	-0.023	0.223	0.319	-0.02	(0.07, 0.02)
098090	KSRF9	0202167	17	-0.015	0.440	0.707	-0.01	(-0.09, 0.06)	0.001	2.696e-04	0.063	0.026	0.226	0.02	(0.03, 0.16)	0.010	0.042	-0.022	0.228	0.415	0.02	(0.02, 0.03)	-0.023	0.228	0.528	0.02	(0.04, 0.06)
098167	MERTK	0202657	192	0.005	0.12	0.735	-4.58e-03	(0.02, 0.03)	0.013	0.263	0.012	0.023	0.611	(0.04, 0.08)	0.002	0.912	-0.022	0.228	0.412	-0.02	(0.02, 0.03)	-0.022	0.228	0.851	-0.02	(0.04, 0.04)	
098338	SIGLEC9	0202190	192	-0.007	0.107	0.708	-0.01	(-0.04, 0.03)	0.001	1.075e-05	-0.007	0.024	0.630	-0.01	(0.07, 0.06)	0.000	0.981	-0.008	0.215	0.701	-0.01	(0.04, 0.02)	-0.011	0.218	0.554	-0.01	(0.05, 0.02)
098422	SMAD3	0202020	36	-0.002	0.174	0.711	-0.01	(-0.05, 0.03)	0.003	0.025	0.025	0.025	0.629	-0.01	(0.05, 0.04)	0.000	0.981	-0.008	0.215	0.701	-0.01	(0.04, 0.02)	-0.011	0.218	0.554	-0.01	(0.05, 0.02)
098537	CCM2B21	0202120	192	0.005	0.12	0.708	-4.58e-03	(0.02, 0.03)	0.001	1.075e-05	-0.007	0.024	0.630	-0.01	(0.07, 0.06)	0.000	0.981	-0.008	0.215	0.701	-0.01	(0.04, 0.02)	-0.011	0.218	0.554	-0.01	(0.05, 0.02)
098598	BABAM1	0203466	192	-0.004	0.12	0.710	-4.49e-03	(0.02, 0.02)	0.002	0.851	-0.016	0.023	0.504	-0.02	(0.08, 0.03)	0.001	0.578	-0.028	0.224	0.281	-0.03	(0.07, 0.02)	-0.034	0.224	0.184	-0.03	(0.08, 0.01)
098635	NELL2	0203035	192	-0.005	0.12	0.735	-4.58e-03	(0.02, 0.03)	0.013	0.263	0.012	0.023	0.611	(0.04, 0.08)	0.002	0.912	-0.022	0.228	0.412	-0.02	(0.02, 0.03)	-0.022	0.228	0.851	-0.02	(0.04, 0.04)	
098644	B2M	0203035	192	-0.005	0.13	0.711	-4.78e-03	(0.02, 0.02)	0.002	0.062	-0.060	0.025	0.515	-0.06	(-0.11, -0.01)	0.004	0.009	-0.029	0.222	0.080	-0.04	(0.08, 0.04)	-0.023	0.228	0.035	-0.18	(0.03, 0.02)
098658	ITGA7	0203275	192	0.005	0.14	0.714	-0.01	(-0.02, 0.03)	0.003	1.21E+06	-0.041	0.028	0.124	-0.04	(-0.09, 0.01)	0.003	0.053	-0.023	0.221	0.275	-0.02	(0.02, 0.02)	-0.018	0.221	0.422	-0.02	(0.02, 0.03)
098666	CLTA	0203116	192	-0.004	0.12	0.735	-4.58e-03	(0.02, 0.03)	0.013	0.263	0.012	0.023	0.611	(0.04, 0.08)	0.002	0.912	-0.022	0.228	0.412	-0.02	(0.02, 0.03)	-0.022	0.228	0.851	-0.02	(0.04, 0.04)	
098685	EDM1	0203109	192	0.005	0.14	0.713	-0.01	(-0.02, 0.03)	0.003	4.79E+09	0.007	0.028	0.792	0.01	(0.05, 0.06)	0.000	0.930	-0.018	0.222	0.414	0.02	(0.02, 0.02)	-0.007	0.221	0.753	0.01	(0.04, 0.05)
098691	LY8RA	0202020	36	-0.002	0.174	0.711	-0.01	(-0.05, 0.03)	0.003	0.025	0.014	0.054	0.714	-0.01	(-0.06, 0.08)	0.002	0.458	-0.007	0.228	0.677	-0.01	(0.05, 0.04)	-0.005	0.220	0.151	-0.01	(0.06, 0.03)
098760	L33	0202428	192	-0.004	0.12	0.714	-4.42e-03	(0.02, 0.02)	0.003	0.833	-0.050	0.023	0.535	-0.05	(-0.10, -0.36e-03)	0.002	0.025	-0.024	0.221	0.251	-0.02	(0.02, 0.02)	-0.032	0.223	0.165	-0.03	(0.08, 0.01)
098781	LGALS3	0202028	192	0.005	0.14	0.714	-0.01	(-0.02, 0.03)	0.003	8.57E+13	-0.009	0.026	0.733	-0.01	(-0.06, 0.04)	0.001	0.536	-0.015	0.222	0.508	-0.01	(-0.03, 0.06)	-0.016	0.223	0.484	0.02	(0.03, 0.06)
098823	MYH4	0203035	192	-0.002	0.12	0.735	-4.58e-03	(0.02, 0.03)	0.013	0.263	0.012	0.023	0.611	(0.04, 0.08)	0.002	0.912	-0.022	0.228	0.412	-0.02	(0.02, 0.03)	-0.022	0.228	0.851	-0.02	(0.04, 0.04)	
098827	NEMO	0203078	192	0.005	0.13	0.713	-4.94e-03	(0.02, 0.03)	0.003	0.001	-0.014	0.028	0.602	-0.01	(-0.06, 0.04)	0.001	0.407	-0.016	0.224	0.511	-0.02	(0.08, 0.03)	-0.019	0.222	0.392	-0.02	(0.08, 0.02)
098828	STOML2	0203183	192	0.005	0.13	0.714	-4.82e-03	(0.02, 0.03)	0.003	0.048	0.016	0.028	0.540	-0.02	(0.03, 0.07)	0.001	0.620	-0.005	0.226	0.682	-0.04	(-0.06, 0.05)	-0.007	0.225	0.784	-0.01	(0.06, 0.04)
098829	TLR4	0203035	192	-0.005	0.12	0.735	-4.58e-03	(0.02, 0.03)	0.013	0.263	0.012	0.023	0.611	(0.04, 0.08)	0.002	0.912	-0.022	0.228	0.412	-0.02	(0.02, 0.03)	-0.022	0.228	0.851	-0.02	(0.04, 0.04)	
098843	CCT5	0203210	192	-0.005	0.14	0.716	-4.94e-03	(0.02, 0.02)	0.004	0.002	-0.016	0.028	0.551	-0.02	(-0.07, 0.04)	0.001	0.613	-0.011	0.228	0.679	-0.01	(-0.06, 0.04)	-0.012	0.224	0.818	-0.01	(0.06, 0.04)
098845	EXTL1	0203014	192	-0.004	0.12	0.735	-4.27e-03	(0.02, 0.02)	0.004	0.108	-0.004	0.024	0.616	-0.01	(-0.06, 0.04)	0.000	0.981	-0.004	0.223	0.309	-0.02	(0.07, 0.02)	-0.036	0.227	0.179	-0.04	(0.04, 0.02)
098846	OR8M40	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012	0.224	0.775	-0.01	(0.05, 0.04)
098847	OR8M50	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012	0.224	0.775	-0.01	(0.05, 0.04)
098848	OR8M51	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012	0.224	0.775	-0.01	(0.05, 0.04)
098849	OR8M52	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012	0.224	0.775	-0.01	(0.05, 0.04)
098850	OR8M53	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012	0.224	0.775	-0.01	(0.05, 0.04)
098851	OR8M54	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012	0.224	0.775	-0.01	(0.05, 0.04)
098852	OR8M55	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012	0.224	0.775	-0.01	(0.05, 0.04)
098853	OR8M56	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012	0.224	0.775	-0.01	(0.05, 0.04)
098854	OR8M57	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012	0.224	0.775	-0.01	(0.05, 0.04)
098855	OR8M58	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012	0.224	0.775	-0.01	(0.05, 0.04)
098856	OR8M59	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012	0.224	0.775	-0.01	(0.05, 0.04)
098857	OR8M60	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012	0.224	0.775	-0.01	(0.05, 0.04)
098858	OR8M61	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012	0.224	0.775	-0.01	(0.05, 0.04)
098859	OR8M62	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012	0.224	0.775	-0.01	(0.05, 0.04)
098860	OR8M63	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012	0.224	0.775	-0.01	(0.05, 0.04)
098861	OR8M64	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012	0.224	0.775	-0.01	(0.05, 0.04)
098862	OR8M65	0203134	192	-0.005	0.14	0.716	-0.01	(-0.03, 0.02)	0.004	0.001	-0.028	0.027	0.233	-0.01	(-0.08, 0.02)	0.001	0.311	-0.006	0.225	0.815	-0.01	(0.05, 0.04)	-0.012				

Table S4. Association of type 2 diabetes with UKG-PPP plasma protein.

UnProt	Gene	OID	nsnp	lnv		rs		pval		CI		MR Egger		Weighted median		Weighted mode											
				b/w	se/w	b/w	se/w	pval	CI	FDR _W	p _{val}	egger	se/egger	se/egger	pval	CI	b/mode	se/mode	pval	CI							
Q04999	PDEF	Q030084	192	-0.003	0.012	0.796	-1.31e-03	(0.03, 0.02)	0.939	0.670	0.209	0.223	0.211	0.02	0.192	-0.012	0.225	0.643	-0.01	(0.06, 0.04)	-0.008	0.224	0.738	-0.01	(0.06, 0.04)		
Q06003	PCOL2	Q030086	192	-0.003	0.012	0.790	-2.22e-03	(0.02, 0.03)	0.938	0.676	0.184	0.205	0.179	0.02	0.192	0.005	0.225	0.643	-0.01	(0.06, 0.05)	-0.008	0.224	0.738	-0.01	(0.06, 0.05)		
Q08200	PNMA1	Q030194	192	-0.003	0.013	0.795	-3.36e-03	(0.02, 0.02)	0.939	0.646	-0.014	0.225	0.584	-0.01	(0.06, 0.04)	0.001	0.628	-0.018	0.224	0.643	-0.02	(0.06, 0.03)	-0.016	0.224	0.515	-0.02	(0.06, 0.03)
Q09422	PNMA2	Q030482	192	-0.003	0.012	0.795	-3.36e-03	(0.02, 0.03)	0.939	0.617	-0.004	0.223	0.649	-0.01	(0.06, 0.05, 0.04)	0.000	0.705	-0.008	0.225	0.738	-0.01	(0.06, 0.04)	-0.001	0.225	0.955	-1.46e-03	(0.05, 0.05)
Q10244	PRSS2	Q030483	192	-0.003	0.012	0.795	-3.36e-03	(0.02, 0.03)	0.939	0.617	-0.004	0.223	0.649	-0.01	(0.06, 0.05, 0.04)	0.000	0.705	-0.008	0.225	0.738	-0.01	(0.06, 0.04)	-0.001	0.225	0.955	-1.46e-03	(0.05, 0.05)
Q10477	SRVZL	Q030050	192	-0.003	0.012	0.802	-3.03e-03	(0.02, 0.03)	0.939	0.605	-0.007	0.225	0.783	-0.01	(0.04, 0.08)	0.000	0.854	-0.012	0.224	0.619	-0.01	(0.06, 0.04)	-0.001	0.226	0.985	-1.15e-03	(0.05, 0.05)
Q10541	TFAP5	Q030050	192	-0.003	0.012	0.802	-3.03e-03	(0.02, 0.03)	0.939	0.605	-0.007	0.225	0.783	-0.01	(0.04, 0.08)	0.000	0.854	-0.012	0.224	0.619	-0.01	(0.06, 0.04)	-0.001	0.226	0.985	-1.15e-03	(0.05, 0.05)
Q10543	TGFB2	Q030050	192	-0.004	0.013	0.788	-3.58e-03	(0.02, 0.02)	0.939	0.608	-0.007	0.226	0.794	-0.01	(0.06, 0.04)	0.000	0.885	-0.008	0.225	0.738	-0.01	(0.06, 0.04)	-0.015	0.223	0.523	-0.01	(0.06, 0.03)
Q10678	TNFSF11B	Q030852	192	-0.003	0.012	0.788	-3.58e-03	(0.02, 0.03)	0.939	0.604	0.025	0.224	0.295	0.02	(0.02, 0.07)	0.001	0.289	0.040	0.222	0.601	0.04	(1.82e-05, 0.08)	0.043	0.225	0.088	0.04	(0.01, 0.09)
Q11788	TNFSF11B	Q030852	192	-0.003	0.012	0.788	-3.58e-03	(0.02, 0.03)	0.939	0.604	0.025	0.224	0.295	0.02	(0.02, 0.07)	0.001	0.289	0.040	0.222	0.601	0.04	(1.82e-05, 0.08)	0.043	0.225	0.088	0.04	(0.01, 0.09)
Q14386	TNXL1	Q030182	192	-0.004	0.014	0.799	-3.65e-03	(0.02, 0.02)	0.939	1.475	0.014	0.228	0.704	0.01	(0.04, 0.07)	0.001	0.551	-0.005	0.224	0.834	-0.01	(0.05, 0.04)	0.002	0.234	0.941	1.81e-03	(0.05, 0.05)
Q14931	USP31	Q030128	192	-0.003	0.011	0.801	-2.87e-03	(0.03, 0.02)	0.939	0.458	-0.007	0.227	0.707	-0.01	(0.05, 0.04)	0.000	0.845	-0.005	0.223	0.839	-0.00	(0.05, 0.04)	-0.009	0.223	0.892	-0.01	(0.05, 0.04)
Q15061	USP31	Q030128	192	-0.003	0.011	0.801	-2.87e-03	(0.03, 0.02)	0.939	0.458	-0.007	0.227	0.707	-0.01	(0.05, 0.04)	0.000	0.845	-0.005	0.223	0.839	-0.00	(0.05, 0.04)	-0.009	0.223	0.892	-0.01	(0.05, 0.04)
Q15061	USP31	Q030128	192	-0.004	0.013	0.789	-3.52e-03	(0.02, 0.02)	0.939	0.608	-0.018	0.228	0.680	-0.02	(0.07, 0.02)	0.000	0.845	-0.022	0.224	0.639	-0.02	(0.07, 0.02)	-0.017	0.223	0.483	-0.02	(0.06, 0.03)
Q15061	USP31	Q030128	192	-0.004	0.013	0.789	-3.52e-03	(0.02, 0.02)	0.939	0.608	-0.018	0.228	0.680	-0.02	(0.07, 0.02)	0.000	0.845	-0.022	0.224	0.639	-0.02	(0.07, 0.02)	-0.017	0.223	0.483	-0.02	(0.06, 0.03)
Q15061	USP31	Q030128	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.223	0.760	-0.01	(0.05, 0.04)
Q15172	PP2R2A	Q030150	192	-0.003	0.013	0.803	-3.22e-03	(0.02, 0.03)	0.940	0.608	-0.008	0.226	0.807	-0.01	(0.06, 0.04)	0.001	0.694	-0.002	0.224	0.929	0.02	(0.05, 0.05)	-0.009	0.2			

Table S4. Association of type 2 diabetes with UKB-PPP plasma protein.

Protein	UnProt	Gene	OID	Inverse variance weighted				MR Egger				Weighted median				Weighted mode										
				nsp	b/w	se	ci_low	ci_high	FDR_low	ci_low	ci_high	egger	inter	egger	preval	median	preval	median	preval	median						
09J15	TAGLN3	LOC13225	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.969	0.310	0.024	0.585	0.011	0.039	0.019	0.025	0.441	0.022	0.037	0.013	0.024	0.598	0.010	0.034	0.026	
09K378	GOLGA3	LOC13226	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.969	0.310	0.024	0.585	0.011	0.039	0.019	0.025	0.441	0.022	0.037	0.013	0.024	0.598	0.010	0.034	0.026	
09K644	MSLN1	LOC13229	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.969	0.310	0.024	0.585	0.011	0.039	0.019	0.025	0.441	0.022	0.037	0.013	0.024	0.598	0.010	0.034	0.026	
09N763	STAU1	LOC13310	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.969	0.310	0.024	0.585	0.011	0.039	0.019	0.025	0.441	0.022	0.037	0.013	0.024	0.598	0.010	0.034	0.026	
09N783	MICAL2L	LOC13311	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.969	0.310	0.024	0.585	0.011	0.039	0.019	0.025	0.441	0.022	0.037	0.013	0.024	0.598	0.010	0.034	0.026	
09A979	SEC31A	LOC13329	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.970	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09M270	SH2	LOC13330	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.970	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09K684	KIRREL1	LOC13331	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.970	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09B670	ATP10V2	LOC13332	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.970	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
091225	FRS3	LOC13333	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.970	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09S110	HMPV2	LOC13334	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.970	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09JUA7	L3CA	LOC13342	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.970	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09K009	OTL07B	LOC13344	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.970	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
04A363	PSCA	LOC13347	192	-0.001	0.10	0.092	-1.34e-03	(0.02, 0.02)	0.970	7.73E-16	0.005	0.199	0.001	0.003	0.004	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09S223	SEPTIN8	LOC13348	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.970	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09KX55	DNAJC5	LOC13347	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.970	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09V778	GIGZF	LOC13362	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.970	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09B841	DNAJL2	LOC13363	192	-0.001	0.10	0.092	-1.34e-03	(0.02, 0.02)	0.971	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09B674	GICF1	LOC13364	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.971	7.44E-47	0.000	0.386	0.001	0.003	0.004	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09I268	DIS3	LOC13460	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.971	1.20E-04	0.027	0.280	0.003	0.008	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09WVW3	PFB1	LOC13461	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.971	2.00E-07	0.007	0.296	0.003	0.008	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09B729	RNKG	LOC13474	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.971	9.31E-23	0.035	0.300	0.003	0.008	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09B292	SLC13A1	LOC13475	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.971	0.000	0.005	0.285	0.001	0.004	0.005	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09K749	SNK2	LOC133174	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.971	0.016	-0.008	0.268	0.002	0.003	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09H9P3	USP28	LOC13428	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.971	0.040	-0.007	0.284	0.002	0.003	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09K444	L34	LOC13398	192	-0.001	0.10	0.092	-1.34e-03	(0.02, 0.02)	0.971	0.053	0.017	0.300	0.002	0.003	0.004	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09S155	OSGEP	LOC13376	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.971	2.07E-05	0.028	0.282	0.003	0.008	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09I268	DIS3	LOC13460	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.972	0.124	0.012	0.325	0.003	0.008	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09I276	TRIOH	LOC13462	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.972	2.34E-05	0.007	0.287	0.003	0.008	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09I705	ENPEP	LOC13315	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.972	0.107	0.009	0.323	0.003	0.008	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09I505	RDI1	LOC13393	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.972	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09I505	RDI1	LOC13393	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.972	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09I505	RDI1	LOC13393	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.972	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09I505	RDI1	LOC13393	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.972	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09I505	RDI1	LOC13393	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.972	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09I505	RDI1	LOC13393	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.972	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09I505	RDI1	LOC13393	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.972	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09I505	RDI1	LOC13393	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.972	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09I505	RDI1	LOC13393	192	-0.002	0.12	0.088	-1.74e-03	(0.02, 0.03)	0.972	0.003	-0.006	0.283	-0.001	0.008	0.005	0.004	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002
09I505	RDI1	LOC13393	192																							

Table S4. Association of type 2 diabetes with UKB-PPP plasma protein.

Protein	Gene	OID	Inverse variance weighted				MR Egger				Weighted median																
			n SNP	b _{IVW}	se _{IVW}	CI _{IVW}	FDR _{IVW}	Q	p _{egger}	se _{egger}	p _{val} egger	CI _{egger}	egger	Inte	egger	val _{median}	se _{median}	p _{val} median	CI _{median}	b _{mode}	se _{mode}	p _{val} mode	CI _{mode}				
D9Y275	TNFSF18B	OD20272	192	0.000	0.013	0.975	4.09e-04	(0.03, 0.03)	0.995	9.04E-05	-0.038	0.025	0.133	0.04	(-0.09, 0.01)	0.002	0.076	0.011	0.622	0.624	0.01	(0.03, 0.05)	0.002	0.025	0.936	1.99e-03	(0.05, 0.05)
P22033	MMKIT	OD30159	192	0.000	0.014	0.976	4.22e-04	(0.03, 0.03)	0.995	0.003	-0.022	0.027	0.419	0.02	(0.07, 0.03)	0.001	0.355	-0.025	0.624	0.284	-0.03	(0.07, 0.02)	0.001	0.024	0.385	-0.02	(0.07, 0.03)
D8YVW5	RNF168	OD30506	192	0.000	0.012	0.977	3.51e-04	(0.02, 0.02)	0.996	0.496	-0.001	0.023	0.951	1.45e-03	(-0.05, 0.04)	0.000	0.956	-0.011	0.622	0.607	-0.01	(0.05, 0.03)	-0.006	0.023	0.810	-0.01	(-0.05, 0.04)
D00273	DFFA	OD20620	192	0.000	0.013	0.977	3.70e-04	(0.03, 0.03)	0.996	0.013	0.004	0.025	0.881	0.79e-03	(0.05, 0.05)	0.000	0.848	0.011	0.622	0.611	0.01	(0.03, 0.05)	-0.009	0.023	0.700	-0.01	(-0.05, 0.04)
P41166	CAT	OD31265	192	0.000	0.012	0.978	3.33e-04	(0.02, 0.02)	0.996	0.380	-0.026	0.024	0.265	0.03	(0.07, 0.02)	0.002	0.199	-0.021	0.622	0.342	-0.02	(0.05, 0.02)	-0.010	0.028	0.696	-0.01	(-0.05, 0.04)
P04179	SOD2	OD20114	192	0.000	0.016	0.978	4.50e-04	(0.03, 0.03)	0.996	2.52E-16	-0.024	0.032	0.451	-0.02	(0.09, 0.04)	0.001	0.388	-0.018	0.624	0.502	-0.02	(0.06, 0.03)	-0.036	0.025	0.153	-0.04	(-0.08, 0.01)
D01007	BRN1E1	OD30347	192	0.000	0.012	0.979	3.19e-04	(0.02, 0.02)	0.996	0.271	-0.019	0.024	0.444	0.02	(0.07, 0.03)	0.001	0.380	0.008	0.623	0.725	0.01	(0.04, 0.05)	0.001	0.023	0.950	1.45e-03	(0.04, 0.04)
Q07AE3	GAD45GPI1	OD30237	192	0.000	0.015	0.979	3.52e-04	(0.03, 0.03)	0.996	4.81E-06	-0.022	0.029	0.447	-0.02	(-0.08, 0.03)	0.001	0.384	-0.021	0.624	0.378	-0.02	(0.07, 0.03)	-0.024	0.022	0.295	-0.02	(-0.07, 0.02)
Q12287	NMI	OD30178	192	0.000	0.013	0.980	3.55e-04	(0.03, 0.03)	0.996	3.98E-04	0.019	0.026	0.467	0.02	(0.03, 0.07)	-0.001	0.405	0.023	0.622	0.284	0.02	(0.02, 0.07)	0.005	0.023	0.825	0.01	(0.04, 0.05)
D8A248	PKP1	OD30221	192	0.000	0.014	0.980	3.53e-04	(0.03, 0.03)	0.996	2.37E-09	-0.031	0.028	0.260	-0.03	(-0.09, 0.02)	0.002	0.194	-0.032	0.624	0.173	-0.03	(0.04, 0.01)	-0.036	0.026	0.172	-0.04	(-0.08, 0.01)
P19957	P13	OD20326	192	0.000	0.011	0.980	2.77e-04	(0.02, 0.02)	0.996	0.104	0.005	0.023	0.818	0.01	(0.04, 0.05)	0.000	0.799	0.015	0.623	0.519	0.01	(0.03, 0.06)	0.016	0.023	0.484	0.02	(0.03, 0.06)
D2L426	PRSS35	OD30193	192	0.000	0.012	0.979	3.03e-04	(0.02, 0.02)	0.996	3.23E-09	0.002	0.023	0.938	1.74e-03	(0.04, 0.05)	0.000	0.944	0.006	0.618	0.758	0.01	(0.03, 0.04)	-0.004	0.019	0.825	4.27e-03	(0.03, 0.04)
P53814	SMTN	OD30154	192	0.000	0.013	0.980	3.11e-04	(0.03, 0.03)	0.996	0.019	-0.011	0.025	0.668	0.01	(0.06, 0.04)	0.001	0.627	-0.003	0.624	0.890	-3.37e-03	(0.05, 0.04)	-0.014	0.024	0.547	-0.01	(-0.06, 0.03)
P62072	TMEM10	OD30358	192	0.000	0.013	0.981	3.14e-04	(0.03, 0.03)	0.997	0.005	-0.035	0.026	0.171	-0.04	(-0.09, 0.02)	0.002	0.114	-0.026	0.624	0.290	-0.03	(0.07, 0.02)	-0.032	0.024	0.176	-0.03	(-0.08, 0.01)
P33419	MMT1	OD31021	192	0.000	0.013	0.983	2.84e-04	(0.03, 0.03)	0.997	0.025	-0.022	0.025	0.951	1.57e-03	(-0.05, 0.05)	0.000	0.932	0.014	0.624	0.961	0.01	(0.03, 0.06)	0.000	0.023	0.991	2.77e-04	(0.05, 0.05)
Q07D43	PTPRH	OD31433	192	0.000	0.018	0.983	3.82e-04	(0.03, 0.03)	0.997	2.73E-39	0.017	0.034	0.615	0.02	(0.05, 0.08)	-0.001	0.565	-0.009	0.621	0.671	-0.01	(0.05, 0.03)	-0.014	0.022	0.538	-0.01	(-0.06, 0.03)
Q07204	THBD	OD20231	192	0.000	0.020	0.982	4.40e-04	(0.04, 0.04)	0.997	5.75E-45	-0.037	0.038	0.344	-0.04	(-0.11, 0.04)	0.002	0.284	-0.001	0.622	0.974	-7.21e-04	(0.04, 0.04)	-0.009	0.022	0.671	-0.01	(-0.05, 0.03)
P21964	COMT	OD20086	192	0.000	0.013	0.984	2.61e-04	(0.03, 0.03)	0.998	0.012	-0.007	0.025	0.787	0.01	(0.05, 0.04)	0.000	0.762	-0.002	0.622	0.911	-2.48e-03	(0.05, 0.04)	-0.002	0.023	0.929	-2.06e-03	(0.05, 0.04)
D56F21	BRDT	OD30179	192	0.000	0.018	0.984	3.49e-04	(0.03, 0.03)	0.998	3.99E-18	-0.012	0.034	0.715	-0.01	(-0.08, 0.05)	0.001	0.678	-0.029	0.621	1.164	-0.03	(0.07, 0.01)	-0.020	0.024	0.407	-0.02	(-0.07, 0.03)
P47674	OMP	OD30385	192	0.000	0.012	0.984	2.38e-04	(0.02, 0.02)	0.998	0.216	0.004	0.024	0.163	0.03	(0.01, 0.08)	-0.002	0.105	0.031	0.622	0.169	0.03	(0.02, 0.07)	0.001	0.025	0.208	0.03	(0.02, 0.08)
P05543	CNP	OD30285	192	0.000	0.013	0.985	2.59e-04	(0.03, 0.03)	0.998	0.007	-0.007	0.026	0.783	0.01	(0.06, 0.04)	0.000	0.738	-0.008	0.625	0.737	-0.01	(0.06, 0.04)	-0.014	0.024	0.547	-0.01	(-0.06, 0.03)
D98W61	DDA1	OD30126	192	0.000	0.012	0.985	2.27e-04	(0.02, 0.02)	0.998	0.783	-0.021	0.023	0.369	-0.02	(-0.07, 0.02)	0.001	0.300	-0.017	0.622	0.425	-0.02	(0.06, 0.03)	-0.019	0.024	0.430	-0.02	(-0.07, 0.03)
P05519	ABL1	OD21280	192	0.000	0.013	0.989	1.78e-04	(0.03, 0.03)	0.998	0.003	-0.038	0.026	0.128	-0.04	(-0.09, 0.01)	0.002	0.077	-0.029	0.623	0.222	-0.03	(0.07, 0.02)	-0.033	0.023	0.140	-0.03	(-0.08, 0.01)
Q07E58	ADAMTS15	OD21275	192	0.000	0.015	0.989	1.22e-04	(0.03, 0.03)	0.998	4.89E-07	-0.103	0.027	2.31E-04	0.10	(-0.16, 0.05)	0.000	0.962	-0.003	0.625	1.145	-0.04	(0.05, 0.01)	-0.040	0.023	0.084	-0.04	(-0.09, 0.01)
P54819	AK2	OD31142	192	0.000	0.013	0.987	2.17e-04	(0.03, 0.03)	0.998	0.005	-0.007	0.026	0.795	0.01	(0.06, 0.04)	0.000	0.754	-0.012	0.624	0.603	-0.01	(0.06, 0.03)	-0.018	0.023	0.443	-0.02	(-0.06, 0.03)
D6LXK1	CRELD2	OD20075	192	0.000	0.014	0.988	2.35e-04	(0.03, 0.03)	0.998	3.59E-06	-0.034	0.026	0.207	-0.03	(-0.08, 0.02)	0.002	0.139	-0.023	0.621	0.290	-0.02	(0.06, 0.03)	-0.023	0.022	0.291	-0.02	(-0.07, 0.02)
D43102	EIF4G3	OD31022	192	0.000	0.013	0.989	1.81e-04	(0.02, 0.02)	0.998	0.037	-0.029	0.025	0.242	-0.03	(-0.08, 0.02)	0.002	0.170	-0.012	0.623	0.474	-0.02	(0.06, 0.03)	-0.025	0.024	0.293	-0.03	(-0.07, 0.02)
P55010	EIF5	OD30156	192	0.000	0.012	0.989	1.75e-04	(0.02, 0.02)	0.998	0.644	-0.023	0.023	0.328	-0.02	(-0.07, 0.02)	0.001	0.254	-0.022	0.624	0.363	-0.02	(0.07, 0.03)	-0.033	0.023	0.184	-0.03	(-0.08, 0.01)
D14964	HIS5	OD21176	192	0.000	0.014	0.987	2.31e-04	(0.03, 0.03)	0.998	0.002	0.018	0.027	0.489	0.02	(0.03, 0.07)	0.001	0.424	0.015	0.624	0.540	0.01	(0.03, 0.06)	0.006	0.025	0.815	0.01	(0.04, 0.05)
P22304	DIS	OD20819	192	0.000	0.014	0.988	2.39e-04	(0.03, 0.03)	0.998	3.75E-04	0.073	0.026	0.037	0.07	(0.02, 0.12)	0.005	0.001	0.046	0.621	0.031	0.05	(0.04e-03, 0.09)	0.044	0.024	0.083	0.04	(2.11e-03, 0.09)
P05372	LYPLAL2	OD30817	192	0.000	0.012	0.989	1.87e-04	(0.02, 0.02)	0.998	0.320	-0.002	0.024	0.943	1.73e-03	(-0.05, 0.05)	0.000	0.927	0.013	0.624	0.587	0.01	(0.03, 0.06)	0.017	0.025	0.496	0.02	(0.03, 0.07)
P54727	RAD23B	OD21166	192	0.000	0.014	0.989	1.82e-04	(0.03, 0.03)	0.998	0.005	-0.001	0.026	0.972	0.34e-04	(-0.05, 0.05)	0.000	0.960	0.001	0.625	0.997	1.04e-03	(-0.05, 0.05)	-0.014	0.023	0.550	-0.01	(-0.06, 0.03)
P04808	RLN1	OD30995	192	0.000	0.012	0.989	1.60e-04	(0.02, 0.02)	0.998	0.006	-0.018	0.024	0.458	-0.02	(-0.07, 0.03)	0.001	0.382	-0.000	0.624	0.998	1.17e-04	(-0.05, 0.05)	-0.002	0.023	0.922	-2.23e-03	(-0.05, 0.05)
D9H8E7	VCPMT1	OD31176	192	0.000	0.014	0.989	1.85e-04	(0.03, 0.03)	0.998	0.003	0.026	0.027	0.335	0.03	(0.03, 0.08)	0.002	0.264	0.005	0.624	0.837	0.01	(0.04, 0.05)	0.014	0.023	0.553	0.01	(0.03, 0.06)
D6NXT1	ANKRD54	OD21162	192	0.000	0.013	0.994	9.36e-05	(0.02, 0.02)	0.999	0.045	0.022	0.025	0.831	0.02	(0.03, 0.07)	-0.001	0.288	0.020	0.623	0.387	0.02	(0.03, 0.07)	0.015	0.023	0.528	0.01	(0.03, 0.06)
D9HEU7	C10AL11C1	OD30180	192	0.000	0.012	0.992	1.19e-04	(0.02, 0.02)	0.999	0.473	-0.027	0.023	0.252	-0.03	(-0.07,												

Table S5. Association of type 2 diabetes with Finnish plasma protein.

SomaLogic Gene	Protein	nsnp	Inverse variance weighted			MR Egger			Weighted median			Weighted mode							
			b/w	se/w	p/w	CI/w	FDR_ZW	Q	pval	egger	intercept	se/median	se/plasma	b/mode	se/mode	se/CI/mode			
12730_30	APDF	236	-0.132	0.022	2.29E-09	-0.13 (-0.18, -0.09)	1.05E-05	0.001	-0.057	0.044	0.032	0.168	0.028	0.028	-0.10 (-0.19, -0.01)				
12732_38	PCBP	236	0.127	0.022	3.32E-09	0.13 (0.08, 0.18)	1.05E-05	0.001	0.103	0.044	0.032	0.168	0.028	0.028	0.10 (0.02, 0.18)				
8469_41	IGFBP2	236	-0.140	0.024	4.42E-09	-0.14 (-0.19, -0.09)	1.05E-05	1.84E-07	-0.035	0.048	0.041	0.041	-0.111	0.033	0.001 -0.11 (-0.16, -0.06)				
4763_31	AFM	236	0.109	0.019	1.72E-08	0.11 (0.07, 0.15)	2.14E-05	0.114	0.077	0.041	0.060	0.080	0.283	0.048	0.040 0.283 (0.08, 0.41)				
2948_58	GHR	236	0.095	0.019	1.52E-08	0.09 (0.05, 0.13)	2.14E-05	0.073	0.047	0.041	0.060	0.080	0.283	0.048	0.040 0.283 (0.08, 0.41)				
10665_19	SLTRK3	SLK3	236	-0.123	0.024	2.46E-07	-0.12 (-0.17, -0.07)	2.04E-04	1.53E-08	0.027	0.047	0.571	0.033	-0.077	0.012	-0.077 0.033 (-0.12, 0.01)			
8408_2	INHBC	NHBC	236	0.090	0.019	2.11E-08	0.09 (0.05, 0.13)	0.001	1.99E-011	0.039	0.070	0.013	0.077	0.012	0.034 0.060 0.060 (-0.07, 0.05)				
8007_19	CTSB	CTBP	236	0.090	0.019	2.11E-08	0.09 (0.05, 0.13)	0.001	1.99E-011	0.039	0.070	0.013	0.077	0.012	0.034 0.060 0.060 (-0.07, 0.05)				
17386_23	ADH1A	ADH1A	236	0.104	0.022	3.61E-06	0.10 (0.06, 0.15)	0.002	3.03E-05	0.001	0.045	0.180	0.060	-0.033	0.15	0.057	0.038 0.137 (0.06, 0.21)		
3708_62	ADM2	ADM2	236	-0.084	0.018	3.91E-08	-0.08 (-0.12, -0.05)	0.002	3.03E-05	0.001	0.045	0.180	0.060	-0.033	0.15	0.057	0.038 0.137 (0.06, 0.21)		
15592_24	GUSB	BCU1	236	0.097	0.020	1.52E-08	0.09 (0.05, 0.13)	0.002	3.03E-05	0.001	0.045	0.180	0.060	-0.033	0.15	0.057	0.038 0.137 (0.06, 0.21)		
8325_37	ADH4	ADH4	236	0.099	0.022	8.85E-06	0.10 (0.06, 0.14)	0.003	8.29E-06	0.059	0.044	0.180	0.060	-0.033	0.15	0.057	0.038 0.137 (0.06, 0.21)		
8337_65	PTFR	PTFR	236	0.083	0.019	2.72E-08	0.08 (0.05, 0.12)	0.003	2.96E-06	0.059	0.044	0.180	0.060	-0.033	0.15	0.057	0.038 0.137 (0.06, 0.21)		
3554_24	ADPOD	Adiponectin	236	-0.100	0.024	1.06E-05	-0.10 (-0.14, -0.06)	0.004	1.64E-11	0.022	0.045	0.612	0.022	0.045	0.029	0.114 -0.05 (-0.10, 0.01)			
3343_1	ACY1	Ameyasyl	236	0.091	0.021	1.35E-05	0.09 (0.05, 0.13)	0.004	2.80E-05	0.094	0.042	0.227	0.080	0.118	0.039	0.039 0.079 0.035 (0.02, 0.01, 0.15)			
9416_37	CPIR	CPIR	236	0.091	0.021	1.35E-05	0.09 (0.05, 0.13)	0.004	2.80E-05	0.094	0.042	0.227	0.080	0.118	0.039	0.039 0.079 0.035 (0.02, 0.01, 0.15)			
8590_23	ICT1	ICT1	236	0.090	0.020	1.84E-05	0.09 (0.05, 0.13)	0.005	4.07E-07	0.087	0.040	0.332	0.022	0.040	0.042	0.051	0.033 0.066 0.051 (0.01, 0.02)		
11424_4	PHAT	PHAT	236	0.093	0.022	2.28E-05	0.09 (0.05, 0.14)	0.006	0.001	0.075	0.045	0.057	0.071	0.016	0.001	0.628	0.058	0.040 0.149 (0.08, 0.22, 0.14)	
10979_39	GH2	GH2	236	-0.076	0.018	2.58E-05	-0.08 (-0.11, -0.04)	0.006	4.94E-06	-0.023	0.036	0.444	0.022	0.036	0.031	0.246 -0.04 (-0.10, 0.02)			
2212_69	FLM	FLM	236	0.075	0.018	2.56E-05	0.08 (0.04, 0.11)	0.006	5.98E-06	0.036	0.036	0.315	0.044	-0.033	0.11	0.021	0.215 0.069 0.202 (0.07, 0.13)		
3220_40	RET	RET	236	0.078	0.019	2.84E-05	0.08 (0.04, 0.11)	0.007	4.66E-06	0.023	0.038	0.535	0.022	0.036	0.003	0.094	0.026	0.034 0.445 (0.04, 0.09)	
17386_23	DC1M121	DC1M121	236	0.086	0.021	3.46E-05	0.08 (0.04, 0.13)	0.008	3.03E-06	0.024	0.041	0.562	0.022	0.041	0.069	0.045	0.034 0.178 (0.02, 0.11)		
3362_81	CHREL1	CHREL1	236	0.074	0.018	4.23E-05	0.07 (-0.11, -0.04)	0.009	0.95E-02	0.020	0.039	0.607	0.022	0.039	0.003	0.113	0.050	0.036 0.160 -0.05 (-0.12, 0.02)	
18914_104	CD14	CD14	236	-0.072	0.018	5.25E-05	-0.07 (-0.11, -0.04)	0.011	1.00E-06	0.038	0.099	5.84E-03	0.077	0.077	-0.004	0.028	0.018	0.031 0.684 -0.02 (-0.08, 0.04)	
18342_2	PSAT1	SERP	236	0.087	0.022	5.64E-05	0.09 (0.04, 0.13)	0.011	9.40E-05	0.050	0.040	0.949	0.022	0.040	0.032	0.078	0.039	0.053 0.08 (0.01, 0.16)	
6049_84	PTFRS	PTFRS	236	-0.094	0.023	5.87E-05	-0.09 (-0.14, -0.05)	0.011	1.61E-05	-0.026	0.047	0.85E-03	0.122	0.077	-0.004	0.095	0.049	0.029 -0.05 (-0.13, 0.03)	
9235_3	PLKDC1	PLKDC1	236	0.073	0.020	6.33E-05	0.07 (-0.11, -0.04)	0.012	0.084	0.070	0.039	0.707	0.022	0.040	0.002	0.924	0.065	0.037 0.076 -0.07 (-0.14, 0.01)	
12918_50	AKR1C1	Akrivastin	236	0.077	0.019	6.63E-05	0.08 (0.04, 0.12)	0.012	0.93E-06	0.039	0.041	0.849	0.022	0.040	0.069	0.038	0.115 0.08 (0.02, 0.13)		
17138_8	GSTA1	GSTA1	236	-0.081	0.020	8.38E-05	-0.08 (-0.12, 0.01)	0.014	0.042	0.051	0.041	0.220	0.055	0.033	0.002	0.407	0.049	0.036 0.170 0.05 (-0.02, 0.12)	
4929_55	SHBG	SHBG	236	-0.082	0.021	8.59E-05	-0.08 (-0.12, 0.01)	0.014	1.50E-06	0.042	0.042	0.933	0.022	0.040	-0.005	0.919	0.079	0.029 0.008 -0.08 (-0.14, -0.02)	
8313_27	CBAT1	CBAT1	236	0.075	0.019	8.96E-05	0.08 (0.04, 0.12)	0.015	1.42E-06	0.039	0.041	0.849	0.022	0.040	0.015	0.142	0.068	0.011 0.01 (0.08, 0.02)	
4559_84	KYNU	KYNU	236	0.075	0.019	8.96E-05	0.08 (0.04, 0.12)	0.015	1.42E-06	0.039	0.041	0.849	0.022	0.040	0.015	0.142	0.068	0.011 0.01 (0.08, 0.02)	
8699_53	CPCLT	CPCLT	236	-0.089	0.023	1.06E-04	-0.09 (-0.13, -0.04)	0.016	8.94E-09	-0.048	0.048	0.322	0.053	-0.043	0.028	0.286	-0.073	0.039 0.058 -0.07 (-0.15, 0.01)	
7124_18	ENB	ENB	236	0.088	0.020	2.81E-04	0.09 (0.05, 0.13)	0.016	8.94E-09	0.048	0.048	0.322	0.053	0.043	0.028	0.286	-0.073	0.039 0.058 -0.07 (-0.15, 0.01)	
11676_137	ENOB	ENOB	236	-0.087	0.023	1.80E-04	-0.09 (-0.13, 0.01)	0.023	0.114	0.043	0.038	0.260	0.044	-0.033	0.12	0.038	0.041	0.348 0.04 (-0.17, 0.12)	
14101_23	CNTFR	CNTFR	236	0.086	0.021	3.46E-04	0.08 (0.04, 0.13)	0.023	0.041	0.041	0.041	0.324	0.044	-0.033	0.12	0.038	0.041	0.348 0.04 (-0.17, 0.12)	
19241_31	HERP5	HERP5	236	0.077	0.020	1.72E-04	0.08 (0.04, 0.12)	0.023	0.009	0.079	0.041	0.057	0.044	-0.033	0.12	0.038	0.041	0.348 0.04 (-0.17, 0.12)	
7860_9	HERP4	HERP4	236	0.072	0.019	1.76E-04	0.07 (0.03, 0.11)	0.023	0.080	0.041	0.041	0.324	0.044	-0.033	0.12	0.038	0.041	0.348 0.04 (-0.17, 0.12)	
8497_10	RS1	RS1	236	0.072	0.019	1.76E-04	0.07 (0.03, 0.11)	0.023	0.080	0.041	0.041	0.324	0.044	-0.033	0.12	0.038	0.041	0.348 0.04 (-0.17, 0.12)	
11416_23	DOX	DOX	236	0.072	0.019	2.22E-04	0.07 (0.03, 0.11)	0.028	0.353	0.099	0.040	0.018	0.099	0.022	0.041	0.056	0.093	0.041	0.023 0.099 0.07 (-0.01, 0.14)
11912_35	FBXL4	FBXL4	236	-0.077	0.021	7.77E-04	-0.08 (-0.12, -0.04)	0.028	0.009	-0.015	0.040	0.732	0.021	0.041	-0.001	0.506	0.093	0.039 0.147 -0.06 (-0.12, 0.02)	
13460_4	CHAD	CHAD	236	0.086	0.021	2.97E-04	0.09 (0.05, 0.13)	0.028	0.119	0.040	0.041	0.324	0.044	-0.033	0.12	0.038	0.041	0.348 0.04 (-0.17, 0.12)	
13933_26	NAB1	NAB1	236	0.069	0.019	2.44E-04	0.07 (0.03, 0.11)	0.028	0.196	0.035	0.039	0.375	0.033	-0.041	0.11	0.021	0.321	0.036	0.035 0.312 0.04 (-0.03, 0.11)
15826_29	ADH1C	ADH1C	236	0.085	0.023	2.86E-04	0.08 (0.04, 0.13)	0.028	1.73E-08	0.059	0.047	0.209	0.038	0.033	0.022	0.538	0.070	0.039 0.076 -0.07 (-0.14, 0.01)	
15591_28	CPK1	CPK1	236	0.087	0.022	3.05E-04	0.09 (0.05, 0.13)	0.028	1.83E-02	0.038	0.042	0.396	0.022	0.040	0.022	0.608	0.038	0.042 0.184 -0.02 (0.11, 0.07)	
16763_11	LECT2	LECT2	236	0.077	0.021	3.05E-04	0.08 (0.04, 0.12)	0.028	0.203	-0.017	0.042	0.680	0.022	0.040	0.006	0.011	0.095	0.039	0.016 0.09 (0.02, 0.17)
18397_5	AKR1C4	AKR1C4	236	0.079	0.022	3.05E-04	0.08 (0.04, 0.12)	0.028	8.60E-06	0.033	0.044	0.458	0.033	0.033	0.022	0.919	0.077	0.034 0.612 0.02 (-0.05, 0.08)	
18208_12	GLU	GLU	236	0.077	0.021	3.05E-04	0.08 (0.04, 0.12)	0.028	8.60E-06	0.033	0.044	0.458	0.033	0.033	0.022	0.919	0.077	0.034 0.612 0.02 (-0.05, 0.08)	
2837_3	MET	MET	236	-0.115	0.023	3.07E-04	-0.12 (-0.18, -0.05)	0.028	4.02E-04	0.001	0.064	0.88E-03	0.111	0.044	-0.008	0.423	0.023	0.034 0.501 -0.02 (-0.08, 0.04)	
2950_57	IGFBP1	IGFBP1	236	0.071	0.019	2.35E-04	0.07 (0.03, 0.11)	0.028	0.90E-04	0.041	0.041	0.914	0.022	0.040	0.003	0.603	0.043	0.033 0.200 0.04 (-0.02, 0.12)	
3550_25	SEPPOR1	SEPPOR1	236	0.080	0.022	3.03E-04	0.08 (0.04, 0.12)	0.028	6.95E-05	0.068	0.041	0.922	0.022						

Table S5. Association of type 2 diabetes with Ferland plasma protein.

SomaLogScore	Protein	rsnp	Inverse variance weighted				MR Egger				Weighted median				Weighted mode								
			b	se	ci_low	ci_high	b	se	ci_low	ci_high	b	se	ci_low	ci_high	b	se	ci_low	ci_high					
12845	SNX17	SNX17	0.26	0.052	0.19	0.055	0.05 (0.02, 0.09)	0.130	0.400	0.038	0.038	0.134 (0.04, 0.11)	0.001	0.071	0.023	0.032	0.457	0.02 (0.04, 0.09)	0.014	0.039	0.715	0.01 (0.06, 0.23)	
15460	DPPI4	DPPI4	0.26	0.052	0.19	0.055	0.05 (0.02, 0.09)	0.130	0.400	0.038	0.038	0.134 (0.04, 0.11)	0.001	0.071	0.023	0.032	0.457	0.02 (0.04, 0.09)	0.014	0.039	0.715	0.01 (0.06, 0.23)	
6898	49	THNSFA1	LIGHT	0.26	0.052	0.19	0.055	0.05 (0.02, 0.09)	0.130	0.400	0.038	0.038	0.134 (0.04, 0.11)	0.001	0.071	0.023	0.032	0.457	0.02 (0.04, 0.09)	0.014	0.039	0.715	0.01 (0.06, 0.23)
15460	DPPI4	DPPI4	LIGHT	0.26	0.052	0.19	0.055	0.05 (0.02, 0.09)	0.130	0.400	0.038	0.038	0.134 (0.04, 0.11)	0.001	0.071	0.023	0.032	0.457	0.02 (0.04, 0.09)	0.014	0.039	0.715	0.01 (0.06, 0.23)
8353	15	SCN2B	SCN2B	0.26	0.052	0.19	0.055	0.05 (0.02, 0.09)	0.130	0.400	0.038	0.038	0.134 (0.04, 0.11)	0.001	0.071	0.023	0.032	0.457	0.02 (0.04, 0.09)	0.014	0.039	0.715	0.01 (0.06, 0.23)
18434	141	TBPL1	TBPL1	0.26	0.051	0.18	0.055	0.05 (0.02, 0.09)	0.131	0.412	0.041	0.039	0.287 (0.04, 0.12)	0.001	0.072	0.014	0.032	0.664 (0.10, 0.08)	0.025	0.043	0.568	0.02 (0.07, 0.11)	
6274	15	WSD2D	WSD2D	0.26	0.052	0.18	0.055	0.05 (0.02, 0.09)	0.131	0.412	0.041	0.039	0.287 (0.04, 0.12)	0.001	0.072	0.014	0.032	0.664 (0.10, 0.08)	0.025	0.043	0.568	0.02 (0.07, 0.11)	
8327	26	DPPE2	DPPE2	0.26	0.052	0.18	0.055	0.05 (0.02, 0.09)	0.131	0.412	0.041	0.039	0.287 (0.04, 0.12)	0.001	0.072	0.014	0.032	0.664 (0.10, 0.08)	0.025	0.043	0.568	0.02 (0.07, 0.11)	
10557	6	TELX2	TELX2	0.26	0.054	0.19	0.055	0.05 (0.02, 0.09)	0.132	0.428	0.047	0.040	0.881 (0.01, 0.07)	0.003	0.178	0.026	0.032	0.414 (0.03, 0.04)	0.009	0.042	0.971	0.1566 (0.08, 0.08)	
10554	23	IGL1	IGL1	0.26	0.054	0.19	0.055	0.05 (0.02, 0.09)	0.133	0.438	0.053	0.041	0.394 (0.04, 0.05, 12)	0.001	0.587	0.007	0.035	0.846 (0.01, 0.04, 0.09)	0.017	0.047	0.679	0.02 (0.06, 0.10)	
10561	5	PSYBP1	PSYBP1	0.26	0.054	0.19	0.055	0.05 (0.02, 0.09)	0.133	0.438	0.053	0.041	0.394 (0.04, 0.05, 12)	0.001	0.587	0.007	0.035	0.846 (0.01, 0.04, 0.09)	0.017	0.047	0.679	0.02 (0.06, 0.10)	
10753	31	ADAM1	ADAM1	0.26	0.054	0.19	0.055	0.05 (0.02, 0.09)	0.133	0.438	0.053	0.041	0.394 (0.04, 0.05, 12)	0.001	0.587	0.007	0.035	0.846 (0.01, 0.04, 0.09)	0.017	0.047	0.679	0.02 (0.06, 0.10)	
14636	25	HRSMP12	Ribonuclease	0.26	0.063	0.223	0.055	0.05 (0.02, 0.11)	0.133	0.496	0.053	0.048	0.342 (0.04, 0.05, 13)	0.001	0.624	0.040	0.036	0.270 (0.04, 0.03, 0.17)	0.023	0.037	0.655	0.05 (0.10, 0.25)	
15468	14	CFHR1	PHR1	0.26	0.052	0.18	0.055	0.05 (0.02, 0.09)	0.133	0.428	0.047	0.040	0.881 (0.01, 0.07)	0.003	0.178	0.026	0.032	0.414 (0.03, 0.04)	0.009	0.042	0.971	0.1566 (0.08, 0.08)	
15483	37	AGRN	Aggrin	0.26	0.064	0.223	0.055	0.05 (0.02, 0.11)	0.133	0.496	0.053	0.048	0.342 (0.04, 0.05, 13)	0.001	0.624	0.040	0.036	0.270 (0.04, 0.03, 0.17)	0.023	0.037	0.655	0.05 (0.10, 0.25)	
15489	11	ATRN	Ahrn	0.26	0.054	0.19	0.055	0.05 (0.02, 0.09)	0.133	0.438	0.053	0.041	0.394 (0.04, 0.05, 12)	0.001	0.587	0.007	0.035	0.846 (0.01, 0.04, 0.09)	0.017	0.047	0.679	0.02 (0.06, 0.10)	
17758	79	DCXR	DCXR	0.26	0.056	0.20	0.055	0.05 (0.02, 0.09)	0.133	0.452	0.056	0.041	0.688 (0.02, 0.06, 0.12)	0.002	0.275	0.020	0.032	0.325 (0.02, 0.08, 0.04)	0.018	0.037	0.876	0.02 (0.06, 0.10)	
19175	18	MARCKSL1	MARCKSL1	0.26	0.058	0.21	0.055	0.05 (0.02, 0.11)	0.133	0.476	0.060	0.042	0.857 (0.01, 0.09, 0.08)	0.003	0.167	0.048	0.033	0.141 (0.05, 0.12, 0.02)	0.016	0.038	0.876	0.02 (0.06, 0.10)	
6038	12	JTB	JTB	0.26	0.052	0.18	0.055	0.05 (0.02, 0.09)	0.133	0.428	0.047	0.040	0.881 (0.01, 0.07)	0.003	0.178	0.026	0.032	0.414 (0.03, 0.04)	0.009	0.042	0.971	0.1566 (0.08, 0.08)	
10820	21	MSSM	PSP-9A	0.26	0.050	0.18	0.055	0.05 (0.02, 0.09)	0.134	0.407	0.043	0.036	0.086 (0.06, 0.13, 0.01)	0.001	0.689	0.058	0.032	0.066 (0.06, 0.12, 3.78e-4)	0.057	0.038	0.143	0.06 (0.13, 0.02)	
14747	9	CRFL1	CRFL1	0.26	0.053	0.19	0.055	0.05 (0.02, 0.09)	0.134	0.410	0.045	0.041	0.020 (0.10, 0.18, 0.02)	0.003	0.233	0.049	0.037	0.184 (0.05, 0.12, 0.02)	0.067	0.041	0.165	0.07 (0.15, 0.01)	
11286	78	VAMP	SELS	0.26	0.051	0.18	0.055	0.05 (0.02, 0.09)	0.134	0.407	0.043	0.036	0.086 (0.06, 0.13, 0.01)	0.001	0.689	0.058	0.032	0.066 (0.06, 0.12, 3.78e-4)	0.057	0.038	0.143	0.06 (0.13, 0.02)	
13883	27	CRYZ	QOR	0.26	0.053	0.19	0.055	0.05 (0.02, 0.09)	0.137	0.211	0.041	0.040	0.309 (0.04, 0.04, 12)	0.001	0.728	0.060	0.033	0.073 (0.06, 0.11, 0.12)	0.053	0.042	0.208	0.05 (0.03, 0.14)	
13810	9	MAGE10	MAGE10	0.26	0.053	0.19	0.055	0.05 (0.02, 0.09)	0.138	0.251	0.020	0.039	0.622 (0.02, 0.06, 0.10)	0.002	0.328	0.010	0.032	0.983 (1.50e-03, 0.06, 0.0)	0.009	0.044	0.832	0.01 (0.06, 0.09)	
19863	3	SEZL2	SEZL2	0.26	0.057	0.21	0.057	0.06 (0.02, 0.10, 0.02)	0.138	0.261	0.041	0.038	0.04 (0.04, 0.12)	0.006	0.006	0.022	0.034	0.508 (0.02, 0.08, 0.04)	0.026	0.039	0.502	0.03 (0.10, 0.05)	
8373	54	DLK1	DLK1	0.26	0.070	0.225	0.060	0.07 (-0.12, 0.02, 0.08)	0.138	0.336	0.133	0.022	0.051	0.683 (0.02, 0.12, 0.08)	0.003	0.285	0.044	0.038	0.247 (-0.04, 0.12, 0.03)	0.024	0.039	0.532	0.02 (0.10, 0.05)
9213	24	FTCD	FTCD	0.26	0.060	0.222	0.060	0.06 (0.02, 0.10)	0.138	0.366	0.044	0.047	0.285 (0.05, 0.04, 0.13)	0.001	0.734	0.023	0.039	0.560 (0.02, 0.05, 0.10)	0.026	0.038	0.462	0.03 (0.05, 0.10)	
15442	140	SFSB1	SFSB1	0.26	0.059	0.20	0.059	0.05 (0.02, 0.10)	0.139	0.344	0.043	0.043	0.047 (0.04, 0.12)	0.001	0.734	0.023	0.039	0.560 (0.02, 0.05, 0.10)	0.026	0.038	0.462	0.03 (0.05, 0.10)	
2681	23	HGF	HGF	0.26	0.059	0.20	0.059	0.05 (0.02, 0.10)	0.139	0.344	0.043	0.043	0.047 (0.04, 0.12)	0.001	0.734	0.023	0.039	0.560 (0.02, 0.05, 0.10)	0.026	0.038	0.462	0.03 (0.05, 0.10)	
5708	18	LEAP2	LEAP2	0.26	0.068	0.224	0.067	0.07 (0.02, 0.11)	0.143	0.966	0.104	0.049	0.283 (0.05, 0.04, 0.13)	0.001	0.748	0.035	0.032	0.273 (0.04, 0.03, 0.10)	0.031	0.045	0.485	0.03 (0.06, 0.12)	
15422	66	ENO2	ENO2	0.26	0.058	0.20	0.058	0.05 (0.02, 0.10)	0.143	0.966	0.104	0.049	0.283 (0.05, 0.04, 0.13)	0.001	0.748	0.035	0.032	0.273 (0.04, 0.03, 0.10)	0.031	0.045	0.485	0.03 (0.06, 0.12)	
17817	22	DDIT4	DDIT4	0.26	0.068	0.224	0.067	0.07 (0.02, 0.11)	0.146	0.017	0.013	0.043	0.763 (0.01, 0.07, 0.10)	0.003	0.227	0.040	0.037	0.280 (0.04, 0.03, 0.11)	0.043	0.043	0.318	0.04 (0.04, 0.13)	
3040	43	CFP	CFP	0.26	0.058	0.20	0.058	0.05 (0.02, 0.10)	0.146	0.017	0.013	0.043	0.763 (0.01, 0.07, 0.10)	0.003	0.227	0.040	0.037	0.280 (0.04, 0.03, 0.11)	0.043	0.043	0.318	0.04 (0.04, 0.13)	
6062	43	NSC	Tensin	0.26	0.058	0.20	0.058	0.05 (0.02, 0.10)	0.148	0.005	0.018	0.043	0.014 (-0.22, 0.05)	0.005	0.032	0.106	0.036	0.003 (-0.11, 0.08, 0.04)	0.094	0.040	0.202	0.09 (0.17, 0.02)	
1042	14	INSL5	Insulin	0.26	0.049	0.18	0.057	0.05 (0.02, 0.09)	0.148	0.228	0.011	0.038	0.777 (0.01, 0.09, 0.08)	0.002	0.241	0.034	0.034	0.814 (-3.7e-03, 0.07)	0.013	0.038	0.731	0.01 (0.09, 0.06)	
3235	50	WRKNC2	WRKNC2	0.26	0.051	0.19	0.057	0.05 (0.02, 0.09)	0.149	0.134	0.042	0.040	0.296 (0.04, 0.04, 12)	0.006	0.007	0.032	0.324 (0.03, 0.09, 0.03)	0.011	0.043	0.805	0.01 (0.07, 0.02)		
8871	37	TRAPP3	TRAPP3	0.26	0.052	0.19	0.057	0.05 (0.02, 0.09)	0.149	0.134	0.042	0.040	0.296 (0.04, 0.04, 12)	0.006	0.007	0.032	0.324 (0.03, 0.09, 0.03)	0.011	0.043	0.805	0.01 (0.07, 0.02)		
16320	59	MAGEA8	MAGEA8	0.26	0.051	0.19	0.057	0.05 (0.02, 0.09)	0.149	0.134	0.042	0.040	0.296 (0.04, 0.04, 12)	0.006	0.007	0.032	0.324 (0.03, 0.09, 0.03)	0.011	0.043	0.805	0.01 (0.07, 0.02)		
11457	53	GALE	GALE	0.26	0.068	0.225	0.067	0.07 (0.02, 0.11)	0.150	7.01e-11	0.019	0.051	0.710 (0.02, 0.08, 0.12)	0.003	0.286	0.101	0.040	0.102 (0.02, 0.18)	0.027	0.041	0.308	0.09 (0.09, 0.17)	
14718	18	CDKN3	CDKN3	0.26	0.058	0.202	0.057	0.06 (0.02, 0.10, 0.02)	0.150	0.044	0.023	0.043	0.584 (0.02, 0.08, 0.11)	0.005	0.031	0.045	0.040	0.259 (-0.04, 0.12, 0.03)	0.022	0.041	0.585	0.02 (0.10, 0.06)	
17474	108	VEGFA	VEGFA	0.26	0.058	0.202	0.057	0.06 (0.02, 0.10, 0.02)	0.150	0.044	0.023	0.043	0.584 (0.02, 0.08, 0.11)	0.005	0.031	0.045	0.040	0.259 (-0.04, 0.12, 0.03)	0.022	0.041	0.585	0.02 (0.10, 0.06)	
18928	10	S100Y	S100Y	0.26	0.053	0.202	0.057	0.06 (0.02, 0.10, 0.02)	0.151	0.005	0.004	0.039	0.997 (1.31e-04, 0.08, 0.08)	0.003	0.124	0.016	0.036	0.653 (0.02, 0.09, 0.05)	0.042	0.040	0.295	0.04 (0.12, 0.04)	
8352	28	SIGLEC2	SIGLEC2	0.26	0.059	0.202	0.057	0.06 (0.02, 0.10, 0.02)	0.151	0.005	0.004	0.039	0.997 (1.31e-04, 0.08, 0.08)	0.003	0.124	0.016	0.036	0.653 (0.02, 0.09, 0.05)	0.042	0.040	0.295	0.04 (0.12, 0.04)	
8617	29	CEP350	CEP350	0.26	0.088	0.233	0.067	0.07 (0.02, 0.11)	0.151	3.29e-48	0.051	0.066	0.441 (0.05, 0.08, 0.16)	0.002									

Table S5. Association of type 2 diabetes with Ferland plasma protein.

SomaLogicGene	Protein	tsp	Inverse variance weighted		MR Egger		Weighted median		Weighted mode															
			b/w	se/w	pval/IV	CI/w	FDR_ZW	Q1	pval	se/egger	pval/egger	se/median	pval/median	b.mode	se.mode	pval/mode	CI/mode							
2879.9	SERPNA3	a1-Antitrypsin	0.19	0.019	0.016	-0.05 (-0.08, -0.01)	0.213	0.127	0.003	0.451	0.956	0.258 (-0.08, 0.08)	-0.003	0.167	0.059	0.41	0.151	-0.06 (-0.14, 0.02)	-0.065	0.41	0.118	-0.07 (-0.15, 0.02)		
12391.27	POSD2		0.22	0.022	0.018	-0.05 (-0.08, -0.01)	0.213	0.127	0.003	0.451	0.956	0.258 (-0.08, 0.08)	-0.003	0.167	0.059	0.41	0.151	-0.06 (-0.14, 0.02)	-0.065	0.41	0.118	-0.07 (-0.15, 0.02)		
13116.5	SMOC1	SMOC1	0.26	0.049	0.020	0.016	-0.05 (-0.09, 0.01)	0.213	0.127	0.004	0.41	0.270	-0.05 (-0.13, 0.04)	0.000	0.919	0.070	0.035	0.046	-0.07 (-0.14, -0.12e-01)	0.001	0.440	0.205	-0.05 (-0.13, 0.03)	
5882.34	EEF1B2	EEF1-beta	0.26	0.045	0.019	0.016	0.04 (-0.01, 0.08)	0.214	0.091	0.048	0.038	0.028	0.08 (0.01, 0.16)	-0.002	0.227	0.003	0.031	0.935	0.252	0.03 (0.06, 0.0)	0.000	0.441	0.996	-2.13e-04 (0.08, 0.08)
8636.30	DOX		0.26	0.045	0.019	0.016	0.04 (-0.01, 0.08)	0.214	0.091	0.048	0.038	0.028	0.08 (0.01, 0.16)	-0.002	0.227	0.003	0.031	0.935	0.252	0.03 (0.06, 0.0)	0.000	0.441	0.996	-2.13e-04 (0.08, 0.08)
11967.23	DNK1	ZNF10	0.26	0.047	0.019	0.016	0.05 (0.01, 0.08)	0.215	0.063	0.112	0.039	0.041	0.011 (0.04, 0.19)	-0.004	0.554	0.093	0.034	0.06	0.09 (0.03, 0.16)	0.002	0.440	0.024	0.09 (0.01, 0.17)	
16831.7	DOX1	DOX1	0.26	0.044	0.019	0.016	0.05 (0.01, 0.08)	0.215	0.063	0.112	0.039	0.041	0.011 (0.04, 0.19)	-0.004	0.554	0.093	0.034	0.06	0.09 (0.03, 0.16)	0.002	0.440	0.024	0.09 (0.01, 0.17)	
8324.3	OST2		0.26	0.047	0.019	0.016	0.05 (0.01, 0.08)	0.215	0.063	0.112	0.039	0.041	0.011 (0.04, 0.19)	-0.004	0.554	0.093	0.034	0.06	0.09 (0.03, 0.16)	0.002	0.440	0.024	0.09 (0.01, 0.17)	
8220.15	C10orf55	CJ35	0.26	0.047	0.019	0.016	0.05 (-0.08, 0.01)	0.216	0.764	0.078	0.039	0.046	0.08 (-0.15, 1.71e-03)	0.002	0.349	0.077	0.039	0.04	-0.08 (-0.15, -1.97e-01)	-0.009	0.442	0.037	-0.09 (-0.17, 0.01)	
2888.49	CT	CT	0.26	0.050	0.021	0.017	-0.05 (-0.09, 0.01)	0.216	0.044	-0.022	0.044	0.596	-0.02 (-0.11, 0.06)	-0.002	0.449	0.059	0.038	0.161	-0.05 (-0.13, 0.02)	-0.013	0.441	0.755	-0.01 (-0.09, 0.07)	
18007.87	KRDL1	KOL1	0.26	0.048	0.019	0.017	-0.05 (-0.09, 0.01)	0.217	0.181	0.042	0.043	0.045	0.08 (0.01, 0.16)	-0.002	0.449	0.059	0.038	0.161	-0.05 (-0.13, 0.02)	-0.013	0.441	0.755	-0.01 (-0.09, 0.07)	
5755.29	GP	GP	0.26	0.046	0.019	0.017	-0.05 (-0.09, 0.01)	0.217	0.213	-0.050	0.041	0.219	-0.05 (-0.13, 0.03)	0.000	0.919	0.036	0.037	0.007	-0.04 (-0.11, 0.03)	-0.038	0.439	0.331	-0.04 (-0.11, 0.04)	
5105.2	RTHAR	Negce	0.26	0.052	0.022	0.017	0.05 (0.01, 0.1)	0.217	0.002	0.006	0.044	0.895	0.01 (-0.08, 0.09)	0.000	0.225	0.020	0.040	0.619	0.02 (-0.06, 0.10)	0.040	0.440	0.329	0.04 (-0.04, 0.12)	
7655.11	NFB9	Prm5	0.26	0.046	0.019	0.017	-0.05 (-0.09, 0.01)	0.219	0.001	-0.022	0.041	0.575	0.01 (-0.10, 0.06)	-0.002	0.451	0.099	0.030	0.764	0.01 (-0.07, 0.05)	0.022	0.441	0.912	0.02 (-0.07, 0.11)	
7179.89	NFASC	NFASC	0.26	0.057	0.024	0.017	0.06 (0.01, 0.1)	0.220	1.696	0.147	0.048	0.003	0.14 (0.03, 0.24)	-0.005	0.936	0.054	0.042	0.240	0.05 (-0.03, 0.14)	0.068	0.444	0.123	0.07 (-0.02, 0.15)	
15333.11	SDF2	SDF2	0.26	0.047	0.019	0.017	-0.05 (-0.09, 0.01)	0.220	0.441	-0.056	0.039	0.156	0.06 (-0.15, 0.02)	-0.005	0.974	0.038	0.037	0.340	0.04 (-0.11, 0.04)	-0.061	0.444	0.153	-0.06 (-0.14, 0.02)	
15540.54	TAGLN	TAGLN	0.26	0.048	0.019	0.017	-0.05 (-0.09, 0.01)	0.220	1.102	0.006	0.038	0.041	0.04 (0.08, 0.08)	0.003	0.445	0.028	0.032	0.202	0.03 (0.01, 0.05)	-0.019	0.437	0.612	0.02 (-0.09, 0.05)	
5744.12	MENT	CA056	0.26	0.113	0.048	0.017	-0.11 (-0.21, -0.02)	0.220	657E-184	0.045	0.096	0.638	-0.05 (-0.23, 0.14)	-0.004	0.443	0.030	0.039	0.451	-0.03 (-0.11, 0.05)	-0.026	0.441	0.526	-0.03 (-0.11, 0.05)	
15311.44	DCN3	DCN3	0.26	0.045	0.019	0.017	-0.05 (-0.09, 0.01)	0.220	0.840	0.066	0.038	0.348	0.04 (-0.14, 0.11)	-0.005	0.751	0.016	0.031	0.917	0.02 (0.05, 0.09)	-0.012	0.441	0.979	0.06 (-0.02, 0.08)	
5744.12	MENT	FLRT1	0.26	0.043	0.018	0.017	0.04 (0.01, 0.08)	0.220	0.144	0.046	0.039	0.237	0.05 (-0.03, 0.12)	-0.004	0.943	0.001	0.029	0.966	-1.23e-03 (-0.06, 0)	-0.045	0.440	0.259	0.04 (-0.12, 0.03)	
4697.59	CSF2	GM-CSF	0.26	0.051	0.021	0.017	-0.05 (-0.09, 0.01)	0.220	0.010	-0.030	0.043	0.488	-0.01 (-0.11, 0.05)	-0.001	0.577	-0.002	0.040	0.433	-0.03 (-0.11, 0.05)	-0.044	0.441	0.284	-0.04 (-0.12, 0.04)	
8596.6	PIANP	PIANP	0.26	0.042	0.018	0.017	-0.05 (-0.09, 0.01)	0.220	0.142	0.003	0.038	0.800	0.16 (-0.03, 0.07, 0.08)	-0.003	0.440	0.036	0.037	0.325	-0.01 (-0.11, 0.04)	-0.042	0.437	0.835	0.05 (-0.13, 0.02)	
15573.110	NCAN	CSPG3	0.26	0.056	0.024	0.017	-0.06 (-0.10, 0.01)	0.221	2.316	0.105	0.047	0.467	0.03 (-0.06, 0.1)	-0.006	0.028	0.001	0.033	0.986	-1.34e-03 (-0.07, 0)	-0.002	0.441	0.956	2.30e-03 (0.08, 0.08)	
10825.12	VSG10	VSG10	0.26	0.045	0.019	0.018	-0.05 (-0.09, 0.01)	0.224	0.656	0.034	0.039	0.386	0.03 (-0.04, 0.1)	-0.005	0.919	0.008	0.036	0.811	-0.01 (-0.08, 0.06)	-0.013	0.441	0.756	-0.01 (-0.09, 0.07)	
7225.31	MMST1	PRM1	0.26	0.050	0.021	0.018	-0.05 (-0.09, 0.01)	0.227	0.017	-0.043	0.043	0.322	0.04 (-0.13, 0.04)	-0.005	0.838	0.007	0.039	0.859	-0.01 (-0.08, 0.07)	-0.015	0.443	0.733	-0.01 (-0.10, 0.07)	
3415.61	BSP	BSP	0.26	0.051	0.022	0.018	-0.05 (-0.09, 0.01)	0.227	0.000	0.000	0.044	0.997	1.38e-04 (-0.09, 0.09)	-0.003	0.176	0.028	0.040	0.485	-0.03 (-0.11, 0.05)	-0.025	0.439	0.522	-0.03 (-0.10, 0.05)	
8698.60	TNR8	Tensin-x	0.26	0.058	0.025	0.018	-0.06 (-0.11, 0.01)	0.227	8.79E-05	-0.020	0.017	0.684	-0.02 (-0.11, 0.07)	-0.002	0.397	0.015	0.015	0.872	0.01 (-0.08, 0.08)	0.008	0.444	0.866	0.01 (-0.08, 0.10)	
7050.5	NEGR1	NEGR1	0.26	0.058	0.025	0.018	-0.06 (-0.11, 0.01)	0.227	8.79E-05	-0.020	0.017	0.684	-0.02 (-0.11, 0.07)	-0.002	0.397	0.015	0.015	0.872	0.01 (-0.08, 0.08)	0.008	0.444	0.866	0.01 (-0.08, 0.10)	
12461.8	SIRT5	SIRT5	0.26	0.046	0.019	0.018	-0.05 (-0.09, 0.01)	0.229	0.001	-0.003	0.040	0.937	-3.77e-03 (-0.08, 0.08)	-0.003	0.221	-0.007	0.037	0.856	-0.01 (-0.08, 0.07)	-0.038	0.442	0.363	-0.04 (-0.12, 0.04)	
1315.15	OPD2	OPD2	0.26	0.049	0.020	0.018	-0.05 (-0.09, 0.01)	0.229	0.001	-0.003	0.040	0.937	-3.77e-03 (-0.08, 0.08)	-0.003	0.221	-0.007	0.037	0.856	-0.01 (-0.08, 0.07)	-0.038	0.442	0.363	-0.04 (-0.12, 0.04)	
6022.57	NELL2	NELL2	0.26	0.043	0.018	0.019	-0.04 (-0.08, 0.01)	0.230	0.057	0.039	0.898	0.01 (-0.07, 0.08)	-0.003	0.160	-0.008	0.033	0.809	-0.01 (-0.07, 0.08)	-0.011	0.439	0.772	-0.01 (-0.09, 0.06)		
7784.8	RNKL1	Kinmeneg	0.26	0.050	0.021	0.019	0.05 (0.01, 0.09)	0.233	0.036	0.046	0.433	0.287	0.05 (0.01, 0.11)	0.000	0.913	0.010	0.039	0.607	0.17 (-0.22e-03, 0.1)	0.061	0.440	0.128	0.06 (-0.02, 0.14)	
12530.8	ARSP2	ARSP2	0.26	0.050	0.021	0.019	0.05 (0.01, 0.09)	0.234	0.065	0.046	0.433	0.287	0.05 (0.01, 0.11)	0.000	0.913	0.010	0.039	0.607	0.17 (-0.22e-03, 0.1)	0.061	0.440	0.128	0.06 (-0.02, 0.14)	
12514.16	METTL1	METTL1	0.26	0.075	0.032	0.019	0.07 (0.01, 0.14)	0.235	1.44E-040	0.064	0.089	0.091	0.11 (-0.02, 0.24)	-0.002	0.529	0.124	0.035	3.72E-04	0.12 (0.06, 0.19)	0.129	0.441	0.020	0.13 (0.05, 0.21)	
15793.12	ARSP2	ARSP2	0.26	0.050	0.021	0.019	0.05 (0.01, 0.09)	0.235	0.065	0.046	0.433	0.287	0.05 (0.01, 0.11)	0.000	0.913	0.010	0.039	0.607	0.17 (-0.22e-03, 0.1)	0.061	0.440	0.128	0.06 (-0.02, 0.14)	
15530.33	EPH4	EPH4	0.26	0.047	0.019	0.019	-0.05 (-0.09, 0.01)	0.235	0.043	0.008	0.041	0.844	0.01 (-0.07, 0.09)	-0.003	0.118	-0.024	0.036	0.493	-0.02 (-0.09, 0.05)	-0.022	0.438	0.564	-0.02 (-0.10, 0.05)	
8633.58	CDH7	CDH7	0.26	0.042	0.018	0.019	0.04 (-0.01, 0.08)	0.236	0.603	0.035	0.036	0.333	0.04 (-0.04, 0.01)	-0.000	0.826	0.120	0.037	0.887	0.01 (-0.05, 0.07)	-0.008	0.440	0.840	-0.01 (-0.09, 0.07)	
5240.69	DLL1	DLL1	0.26	0.045	0.019	0.019	0.04 (-0.01, 0.08)	0.237	0.142	0.003	0.038	0.348	0.04 (-0.14, 0.06)	-0.004	0.447	0.016	0.031	0.917	0.02 (0.05, 0.09)	-0.012	0.441	0.979	0.06 (-0.02, 0.08)	
4537.60	NLNAX	NLNAX	0.26	0.045	0.019	0.020	-0.04 (-0.08, 0.01)	0.237	0.302	0.021	0.039	0.602	0.02 (-0.06, 0.1)	-0.004	0.057	0.010	0.038	0.797	-0.01 (-0.09, 0.07)	-0.007	0.440	0.869	-0.01 (-0.09, 0.07)	
18841.1	SNRPB	SNRPB	0.26	0.044	0.019	0.020	-0.04 (-0.08, 0.01)	0.238	0.058	0.018	0.041	0.655	0.02 (-0.11, 0.07)	-0.004	0.079	0.023	0.031	0.464	-0.02 (-0.08, 0.04)	-0.005	0.439	0.899	-0.01 (-0.09, 0.07)	
10756.34	LOC3	LOC3	0.26	0.046	0.020	0.020	-0.05 (-0.09, 0.01)	0.240	0.249	0.045	0.038	0.950	0.01 (-0.11, 0.07)	-0.004	0.496	0.048	0.039	0.460	-0.05 (-0.13, 0.02)	-0.013	0.441	0.938	-0.05 (-0.13, 0.02)	
7638.30	LMAN2	Lectin, man	0.26	0.051	0.022	0.020	0.05 (0.01, 0.09)	0.239	0.005	-0.020	0.044	0.641	-0.02 (-0.11, 0.07)	-0.004	0.062	0.020	0.037	0.593	0.02 (0.05, 0.09)	0.027	0.441	0.505	0.03 (0.01, 0.07)	
8653.132	DNAX1	DNAX1	0.26	0.045	0.019	0.020	0.05 (0.01, 0.09)	0.239	0.132	-0.008	0.041	0.848	-0.01 (-0.09, 0.07)	-0.004	0.137	0.009	0.037	0.804	-0.0					

Table S5. Association of type 2 diabetes with Finnish plasma protein.

SomaLogGE	Protein	tsp	Inverse variance weighted				MR Egger				Weighted median				Weighted mode											
			b1w	se1w	pval1w	CI1w	FDR_ZW	Q	b1w	se1w	pval1w	CI1w	b1w	se1w	pval1w	CI1w	b1w	se1w	pval1w	CI1w						
8008_12	DNAJB12	DJB12	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
9191_2	TFPI	TFPI	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
9211_19	SRPFP1	PFDF	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
10342_55	SRPFP1	PFDF	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
11192_168	TM6SF1	TM6SF1	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
11426_58	SOCS3	SOCS3	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
15326_64	GBP1	GBP1	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
17822_37	REGR	REGR	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
5459_33	CST3	CYN7	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
6252_62	SCGB1A1	Secretoglobin	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
6901_28	EGLN1	EGLN1	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
13307_51	TRAD	TRADD	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
5035_35	TYMS	TYMS	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
6690_49	TUT1	TUT1	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
15398_24	FCGR3A	FcR1a	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
8697_3	LRRRC12	LRR12	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
12452_32	SUW42H2	SUW42H2	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
18917_53	AMV2A	Pancreatic	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
18554_50	TM6SF1	TM6SF1	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
7003_4	GALNT10	GLT10	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
7828_1	DCLK1	DCLK1	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
7887_154	STGALNA1A	STGALNA1A	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
9332_6	DEFB3	DEFB3	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
9359_9	DLK2	EGLF9	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
12802_1	GRAP	GRAP	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
8853_2	CLEC4A	CLEC4A	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
9370_69	GGH	GGH	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
13893_6	FOXP3	FOXP3	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
4549_78	FUT5	FUT5	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
5644_60	RNASE4	RNASE4	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
11552_27	PFARCB1	PFARCB1	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
7108_37	OOSP2	PLACL1	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
9231_23	IMPAD1	IMPAD1	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
10424_31	NPPD	NPPD	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
10515_2	HSPG2	HSPG2	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
12708_91	LMBL1	LMBL1	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
13614_6	CREBBP	CREBBP	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002	0.874	-0.44	0.39	0.257	-0.04	(-0.12, 0.03)	-0.051	0.40	0.197	-0.05	(-0.13, 0.03)
17175_5	HAP2	HAP2	0.28	-0.40	0.19	0.034	-0.04	(-0.08, -2.93e-02)	0.309	0.427	-0.035	0.387	0.673	(0.11, 0.04)	0.002											

Table S5. Association of type 2 diabetes with Ferland plasma protein.

Locus	SNP	Protein	rsnp	Inverse variance weights				MR Egger				Weighted median				Weighted mode																
				b/w	se/bw	pval/iw	OR	FOR_Z	Q	pval	segger	pval/egger	egger	integger	pval/integger	se/integger	pval/median	b.mode	se.mode	pval/med	Cmode											
12999.134	CCDC50	CCDC50	226	0.034	0.017	0.059	0.13	-0.28	0.07	0.396	0.000	0.13	0.039	0.737	0.01	0.08	0.09	0.001	0.532	-0.004	0.322	0.001	-3.95e-03	0.07	0.0	0.008	0.037	0.822	0.01	0.06	0.08	
13003.7	HFDSD	HFDSD	226	0.034	0.017	0.059	0.13	-0.28	0.07	0.396	0.000	0.13	0.039	0.737	0.01	0.08	0.09	0.001	0.532	-0.004	0.322	0.001	-3.95e-03	0.07	0.0	0.008	0.037	0.822	0.01	0.06	0.08	
15827.20	FOXL2	FOXL2	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.554	0.034	0.039	0.372	0.03	-0.04	0.11	0.000	0.895	0.016	0.337	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
15830.20	RODR	RODR	226	0.040	0.021	0.081	0.04	-0.08	0.03	0.396	2.836	0.06	0.041	0.06	0.01	-0.08	0.11	0.000	0.895	0.016	0.337	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
16780.6	HSP1A1	HSP1A1	226	0.034	0.017	0.059	0.13	-0.28	0.07	0.396	0.000	0.13	0.039	0.737	0.01	0.08	0.09	0.001	0.532	-0.004	0.322	0.001	-3.95e-03	0.07	0.0	0.008	0.037	0.822	0.01	0.06	0.08	
17346.61	FDSP	FDSP	226	0.040	0.021	0.081	0.04	-0.08	0.03	0.396	0.014	-0.036	0.043	0.405	0.04	-0.12	0.05	0.000	0.895	0.016	0.337	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
17346.61	FDSP	FDSP	226	0.040	0.021	0.081	0.04	-0.08	0.03	0.396	0.014	-0.036	0.043	0.405	0.04	-0.12	0.05	0.000	0.895	0.016	0.337	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
17785.11	ROL	ROL	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.723	0.007	0.037	0.847	0.01	-0.08	0.08	0.000	0.895	0.016	0.337	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
18061.26	HSP1B	HSP1B	226	0.039	0.021	0.086	0.04	-0.17	0.03	0.396	0.005	0.025	0.042	0.553	0.02	-0.06	0.11	0.001	0.699	0.015	0.338	0.009	0.611	0.01	-0.09	0.09	-0.015	0.38	0.63	0.01	-0.09	0.06
2558.51	POMA	E-endorphin	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.579	0.032	0.039	0.419	0.03	-0.05	0.11	0.004	0.846	0.029	0.338	0.009	0.611	0.01	-0.09	0.09	0.034	0.43	0.26	0.03	-0.12	
2590.63	MPD	MPD	226	0.035	0.018	0.060	0.04	-0.16	0.03	0.396	0.441	0.016	0.016	0.151	0.01	-0.12	0.05	0.003	0.846	0.029	0.338	0.009	0.611	0.01	-0.09	0.09	0.034	0.43	0.26	0.03	-0.12	
2838.2	TNFSF4	CD40 Ligand	226	0.037	0.020	0.059	0.04	-0.08	0.03	0.396	0.575	-0.025	0.039	0.532	-0.02	-0.10	0.05	0.001	0.721	-0.015	0.440	0.007	-0.02	-0.08	0.09	0.001	0.39	0.97	1.42e-03	-0.08	0.08	
2970.60	AREG	AREG	226	0.034	0.018	0.060	0.04	-0.16	0.03	0.396	0.481	0.028	0.037	0.448	0.03	-0.04	0.10	0.000	0.847	-0.011	0.331	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
3348.49	BMF1	BMF1	226	0.034	0.018	0.060	0.04	-0.16	0.03	0.396	0.084	0.050	0.039	0.156	0.03	-0.13	0.05	0.001	0.677	0.020	0.331	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
3403.1	TPS28	TPS28	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	2.229	0.001	0.040	0.978	0.09	-0.08	0.08	0.002	0.286	0.037	0.441	0.009	0.611	0.01	-0.09	0.09	0.034	0.43	0.26	0.03	-0.12	
5020.2	PAM	PAM	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.006	0.010	0.123	0.165	0.17	-0.41	0.07	0.000	0.599	0.011	0.332	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
5632.6	CRAC1	CRAC1	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.005	0.025	0.040	0.565	0.02	-0.10	0.05	0.000	0.846	0.029	0.338	0.009	0.611	0.01	-0.09	0.09	0.034	0.43	0.26	0.03	-0.12	
6533.20	DNAH2B	DNAH2B	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.281	0.013	0.040	0.752	0.01	-0.07	0.09	-0.003	0.159	0.005	0.337	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
6571.5	C11orf78	C11orf78	226	0.034	0.018	0.060	0.04	-0.16	0.03	0.396	0.066	0.025	0.040	0.752	0.01	-0.07	0.09	0.001	0.534	0.013	0.332	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
7196.21	FNW	FNW	226	0.037	0.020	0.059	0.04	-0.08	0.03	0.396	0.588	-0.022	0.039	0.587	-0.02	-0.10	0.05	0.001	0.679	-0.021	0.339	0.009	0.588	-0.02	-0.10	0.05	0.008	0.39	0.83	0.01	-0.08	0.07
8222.49	CHDR3	CHDR3	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.511	-0.002	0.038	0.984	-1.79	-0.08	0.07	0.002	0.305	-0.007	0.336	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
8632.25	BS12	BS12	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.006	0.025	0.040	0.752	0.01	-0.07	0.09	0.001	0.534	0.013	0.332	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
8907.8	CNHR3	CNHR3	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.538	0.006	0.038	0.984	-1.79	-0.08	0.07	0.002	0.305	-0.007	0.336	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9297.12	BSG2B	BSG2B	226	0.039	0.021	0.081	0.04	-0.17	0.03	0.396	0.118	0.022	0.042	0.600	0.02	-0.08	0.10	0.004	0.094	-0.018	0.337	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9432.27	FST	FST	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.274	0.026	0.039	0.323	0.03	-0.05	0.10	0.001	0.850	0.025	0.332	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9327.3	LYPD1	LYPD1	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.666	0.011	0.039	0.777	0.01	-0.07	0.09	-0.003	0.184	-0.038	0.330	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9327.3	LYPD1	LYPD1	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.666	0.011	0.039	0.777	0.01	-0.07	0.09	-0.003	0.184	-0.038	0.330	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9327.3	LYPD1	LYPD1	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.666	0.011	0.039	0.777	0.01	-0.07	0.09	-0.003	0.184	-0.038	0.330	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9327.3	LYPD1	LYPD1	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.666	0.011	0.039	0.777	0.01	-0.07	0.09	-0.003	0.184	-0.038	0.330	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9327.3	LYPD1	LYPD1	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.666	0.011	0.039	0.777	0.01	-0.07	0.09	-0.003	0.184	-0.038	0.330	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9327.3	LYPD1	LYPD1	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.666	0.011	0.039	0.777	0.01	-0.07	0.09	-0.003	0.184	-0.038	0.330	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9327.3	LYPD1	LYPD1	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.666	0.011	0.039	0.777	0.01	-0.07	0.09	-0.003	0.184	-0.038	0.330	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9327.3	LYPD1	LYPD1	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.666	0.011	0.039	0.777	0.01	-0.07	0.09	-0.003	0.184	-0.038	0.330	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9327.3	LYPD1	LYPD1	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.666	0.011	0.039	0.777	0.01	-0.07	0.09	-0.003	0.184	-0.038	0.330	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9327.3	LYPD1	LYPD1	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.666	0.011	0.039	0.777	0.01	-0.07	0.09	-0.003	0.184	-0.038	0.330	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9327.3	LYPD1	LYPD1	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.666	0.011	0.039	0.777	0.01	-0.07	0.09	-0.003	0.184	-0.038	0.330	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9327.3	LYPD1	LYPD1	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.666	0.011	0.039	0.777	0.01	-0.07	0.09	-0.003	0.184	-0.038	0.330	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9327.3	LYPD1	LYPD1	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.666	0.011	0.039	0.777	0.01	-0.07	0.09	-0.003	0.184	-0.038	0.330	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9327.3	LYPD1	LYPD1	226	0.036	0.019	0.061	0.04	-0.16	0.03	0.396	0.666	0.011	0.039	0.777	0.01	-0.07	0.09	-0.003	0.184	-0.038	0.330	0.007	0.677	0.02	-0.08	0.09	0.039	0.40	0.38	0.04	0.11	
9327.3	LYPD1	LYPD1</																														

Table S5. Association of type 2 diabetes with Ferland plasma protein.

SomaLogic Gene	Protein	rsnp	Inverse variance weighted		MR Egger		Weighted median		Weighted mode									
			b1w	se1w	pval1w	OR1w	b2w	se2w	pval2w	OR2w	b3w	se3w	pval3w	OR3w				
3388_58	PAK7	PAK7	0.26	0.033	0.019	0.079	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
6246_12	CDMP2	CDMP2	0.26	0.033	0.019	0.079	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
5730_50	FXN1	FXN1	0.26	0.032	0.018	0.079	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
6470_19	BCBL1	Bcl11	0.26	0.038	0.021	0.080	-0.04	-0.08	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
6658_58	SCXCL10	SCXCL10	0.26	0.038	0.021	0.080	-0.04	-0.08	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
6606_61	KISS1	KISS1	0.26	-0.040	0.023	0.079	-0.04	-0.08	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
6918_18	KCK1	CCKN	0.26	-0.033	0.019	0.081	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
7621_1	C1D	C1D	0.26	0.033	0.019	0.079	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
8308_24	MXRA7	MXRA7	0.26	-0.037	0.021	0.077	-0.04	-0.08	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
8388_24	SPAST	SPAST	0.26	0.034	0.019	0.079	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
8398_42	FA2H	FA2H	0.26	0.033	0.019	0.079	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
8843_34	MYRF	MYRF	0.26	0.034	0.020	0.078	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
8867_21	MURF	MURF	0.26	0.032	0.018	0.078	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
8745_20	EFHE2	EFHE2	0.26	0.033	0.019	0.079	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
10047_12	NCF2	NCF2	0.26	0.037	0.021	0.081	-0.04	-0.08	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
10447_18	PMP30	LCTP3	0.26	0.033	0.019	0.079	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
10880_135	LCTL	LCTL	0.26	0.034	0.020	0.082	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
12685_108	RUVBL1	RUVBL1	0.26	0.033	0.019	0.079	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
13360_2	UAF1	Sperm-ase	0.26	0.036	0.021	0.080	-0.04	-0.08	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
2201_17	COL1A1	Endostatin	0.26	-0.034	0.019	0.081	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
3874_6	UBR3L	UBR3L	0.26	0.032	0.018	0.082	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
7125_18	CCDC9B	CCDC9B	0.26	0.033	0.019	0.079	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
17152_10	KIR2D5A	KIR2D5A	0.26	0.036	0.021	0.082	-0.04	-0.08	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
10003_15	ZNFX1	ZNFX1	0.26	-0.034	0.020	0.083	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
10070_22	PLCG2	PLCG2	0.26	0.032	0.018	0.083	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
11549_6	ISL1	ISL1	0.26	-0.033	0.019	0.082	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
12638_113	SMYD2	SMYD2	0.26	-0.033	0.019	0.082	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
12711_35	SUL1B1	SUL1B1	0.26	-0.033	0.019	0.082	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
12681_63	USP21	USP21	0.26	0.033	0.019	0.082	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
11713_179	FSTL1	FSTL1	0.26	-0.041	0.023	0.083	-0.04	-0.08	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
16240_6	OMP	OMP	0.26	0.033	0.019	0.082	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
18893_26	GPR56	GPR56	0.26	0.033	0.019	0.083	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
5028_58	RFS3	RFS3	0.26	0.037	0.021	0.082	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
5028_58	CCL11	CCR1	0.26	0.037	0.021	0.082	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
8795_48	TRPC	TRPC	0.26	0.031	0.018	0.081	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
10569_28	FMRF2	FMRF2	0.26	0.032	0.019	0.081	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
13076_4	FXR1	FXR1	0.26	0.032	0.019	0.083	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
13116_8	TMEM132D	TMEM132D	0.26	0.034	0.020	0.083	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
3152_3	CNDP2	CNDP2	0.26	0.033	0.019	0.081	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
7988_18	IL2RA	IL2RA	0.26	-0.034	0.020	0.083	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
8085_18	NALG2	NALG2	0.26	-0.035	0.020	0.083	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
8085_18	TMEM128B	TMEM128B	0.26	-0.035	0.020	0.083	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
17460_51	Mx1	Mx1	0.26	0.036	0.021	0.084	-0.04	-0.08	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
3714_49	KMK	KMK	0.26	0.032	0.018	0.084	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
3867_49	SEZSL2	SEZSL2	0.26	0.033	0.019	0.084	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
7121_2	SYT7	SYT7	0.26	-0.034	0.020	0.084	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
9125_23	MASP3	MASP3	0.26	0.033	0.019	0.084	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
15441_6	GK2A	GK2A	0.26	-0.041	0.024	0.084	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
6732_7	YBX2	YBX2	0.26	0.036	0.021	0.084	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
6459_6	PSG9	PSG9	0.26	-0.034	0.020	0.084	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
8712_15	NLGN2	NLGN2	0.26	0.033	0.019	0.084	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
12503_5	SPFN1	SPFN1	0.26	0.033	0.019	0.085	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
2522_53	FRFR1	FRFR1	0.26	-0.032	0.020	0.085	-0.03	-0.07	-0.43	0.029	0.401	0.008	0.043	0.087	-0.01	-0.08	0.08	0.08
12620_3	SEPTIN1	SEPTIN1	0.26	0.032	0.019	0.085	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
12683_156	DYPL5	DYPL5	0.26	0.034	0.020	0.085	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
12904_180	CN2P2	CN2P2	0.26	0.033	0.019	0.085	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
11909_32	TCEAL8	TCEAL8	0.26	0.033	0.019	0.085	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
4712_18	AP0D	AP0D	0.26	0.032	0.019	0.085	0.033	0.32	-0.07	0.079	0.429	0.189	0.019	0.039	0.021	0.022	0.06	0.10
6425_24	MRP1																	

Table S5. Association of type 2 diabetes with Ferndal plasma protein.

SomaLogicGene	Protein	rnsnp	Inverse variance weighted				MR Egger				Weighted median				Weighted mode																
			b1w	se1w	pval1w	CI1w	FOR_ZW	Q	pval	begger	se_begger	pval_begger	egger	inter_egger	se_egger	pval_egger	b_mode	se_mode	pval_mode	CI_mode											
12717.65	TOX3	TOX3	0.26	0.030	0.018	0.103	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
13430.59	SLC14A11	SLC14A11	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
13499.30	COG1	COG1	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
14112.40	REL1	REL1	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
15437.11	RAMPS1	RAMPS1	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
16785.45	DEF5A3	DEF5A3	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
17183.11	ANAK5	ANAK5	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
17365.7	CCBL1	KAT5	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
19195.85	RPS5	R5S	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
2590.69	ROR1	ROR1	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
3798.19	ANKK1L4	ANKK1L4	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
4971.1	CTSB	CTSB	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
6896.2	CD1262	CD1262	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
8273.15	CD3E	CD3E	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
8525.17	DUSP13	DUSP13	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
17773.26	NAP3	NAP3	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
4124.24	NAPPA	NAPPA	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
9962.1	CDHR5	MUC2L	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
8620.35	ADAM30	ADAM30	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
3600.2	CHIT1	Chitinase3	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
4829.43	RFN3	STRATIFIN	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
16590.38	OPN1	OPN1	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
15430.21	RND3	RND3	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
9644.24	C7orf99	C7orf99	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
8545.156	C22orf6	C22orf6	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
19229.92	HOMER1	HOMER1	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
8024.64	TPST2	TPST2	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
16892.7	CLSTN2	CLSTN2	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
6369.82	DEAF1	DEAF1	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
8121.3	SEMA6B	SEMA6B	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
12018.14	TPK1	TPK1	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
13436.54	MAZ	MAZ	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
15391.114	GAS6	GAS6	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
17989.12	WBP2	WBP2	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
18303.39	NRGN	NRGN	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
18707.55	ELP2	ELP2	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
7868.15	CRTM	CRTM	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.354	0.044	0.037	0.707	0.011	0.066	0.099	0.001	0.629	0.020	0.030	0.517	-0.022	0.028	0.064	0.044	0.043	0.207	-0.055	0.144	0.003
10085.25	STAR	STAR	0.26	0.032	0.019	0.102	0.033	0.011	0.077	0.456	0.																				

Table S5. Association of type 2 diabetes with Ferland plasma protein.

Gene	Protein	rsnp	Inverse variance weighted		MR Egger		Weighted median		Weighted mode																		
			b1w	se.b1w	pval.iw	CI.iw	FOR_ZW	Q_val	begger	se.begger	pval.egger	CI.egger	egger	se.egger	pval.wmedian	CI.wmedian	b.mode	se.mode	pval.wmode	CI.wmode							
1181.73	TYMP	TP	226	-0.027	0.18	0.130	-0.03	(-0.08, 0.01)	0.499	0.233	-0.068	0.037	0.177	(0.14, 0.21)	0.003	0.216	0.046	0.38	0.233	-0.05	(-0.12, 0.03)	-0.045	0.034	0.188	-0.05	(-0.11, 0.02)	
1543.5	PNOC	PNOC	226	-0.027	0.18	0.130	-0.03	(-0.08, 0.01)	0.499	0.233	-0.068	0.037	0.177	(0.14, 0.21)	0.003	0.216	0.046	0.38	0.233	-0.05	(-0.12, 0.03)	-0.045	0.034	0.188	-0.05	(-0.11, 0.02)	
11146.4	TBX21	TBX22	226	-0.029	0.19	0.131	0.03	(-0.01, 0.07)	0.501	0.234	0.028	0.041	0.492	(0.43, 0.55)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)	
9547.29	EMD1	EMD1	226	-0.029	0.19	0.131	0.03	(-0.01, 0.07)	0.501	0.234	0.028	0.041	0.492	(0.43, 0.55)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)	
10035.6	DUSP4	DUSP4	226	-0.029	0.19	0.131	0.03	(-0.01, 0.07)	0.501	0.234	0.028	0.041	0.492	(0.43, 0.55)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)	
5699.26	SIRPB	SIRPB	226	-0.027	0.18	0.131	0.03	(-0.01, 0.06)	0.501	0.234	0.028	0.041	0.492	(0.43, 0.55)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)	
14085.11	CD8	CD8	226	-0.031	0.021	0.131	-0.03	(-0.07, 0.01)	0.502	0.230	-0.029	0.042	0.487	(0.43, 0.51)	0.005	0.952	0.224	0.35	0.815	-0.02	(-0.08, 0.04)	-0.081	0.040	0.129	-0.06	(-0.14, 0.02)	
12800.7	ARRBP2	ARRBP2	226	-0.031	0.021	0.131	-0.03	(-0.07, 0.01)	0.502	0.230	-0.029	0.042	0.487	(0.43, 0.51)	0.005	0.952	0.224	0.35	0.815	-0.02	(-0.08, 0.04)	-0.081	0.040	0.129	-0.06	(-0.14, 0.02)	
1569.15	COL2A1	Collagen II	226	-0.033	0.022	0.132	-0.03	(-0.08, 0.01)	0.504	0.234	0.032	0.044	0.470	(0.43, 0.51)	0.004	0.991	-0.078	0.35	0.027	-0.08	(-0.15, 0.01)	-0.069	0.040	0.882	0.07	(-0.15, 0.01)	
2797.56	AFOPB	AFOPB	226	-0.048	0.032	0.132	-0.03	(-0.11, 0.01)	0.504	0.234	-0.042	0.044	0.518	-0.04	(-0.10, 0.08)	0.000	0.910	0.118	0.38	0.634	0.02	(-0.06, 0.09)	-0.024	0.040	0.551	0.02	(-0.05, 0.10)
5032.64	SRRP1	SRRP1	226	-0.029	0.19	0.131	0.03	(-0.01, 0.07)	0.504	0.234	0.028	0.041	0.492	(0.43, 0.55)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)	
11126.102	TRIO	TRIO	226	-0.029	0.19	0.131	0.03	(-0.01, 0.07)	0.504	0.234	0.028	0.041	0.492	(0.43, 0.55)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)	
12408.33	RAB22A	RAB22A	226	-0.027	0.18	0.133	0.03	(-0.01, 0.06)	0.504	0.234	0.027	0.041	0.492	(0.43, 0.55)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)	
14121.24	TRHRST9	TRHRST9	226	-0.027	0.18	0.133	0.03	(-0.01, 0.06)	0.504	0.234	0.027	0.041	0.492	(0.43, 0.55)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)	
3328.58	CADMI	Nectin-like	226	-0.028	0.18	0.133	0.03	(-0.01, 0.06)	0.504	0.234	0.027	0.041	0.492	(0.43, 0.55)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)	
1455.7	TNSI	Tensin	226	-0.029	0.19	0.133	0.03	(-0.01, 0.07)	0.504	0.234	0.027	0.041	0.492	(0.43, 0.55)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)	
10075.75	ACAD8	ACAD8	226	-0.027	0.18	0.133	0.03	(-0.01, 0.06)	0.504	0.234	0.027	0.041	0.492	(0.43, 0.55)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)	
12432.29	CACYP8	CACYP8	226	-0.027	0.18	0.133	0.03	(-0.01, 0.06)	0.504	0.234	0.027	0.041	0.492	(0.43, 0.55)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)	
4899.2	AGR2	AGR2	226	-0.029	0.19	0.134	0.03	(-0.01, 0.07)	0.506	0.237	0.008	0.039	0.839	0.01	(-0.07, 0.09)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)
6255.74	CPY1M1	CPY1M1	226	-0.029	0.19	0.134	0.03	(-0.01, 0.07)	0.506	0.237	0.008	0.039	0.839	0.01	(-0.07, 0.09)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)
9579.263	MANKS4	MANKS4	226	-0.064	0.056	0.138	-0.08	(-0.18, 0.03)	0.506	0.237	-0.064	0.056	0.138	-0.08	(-0.18, 0.03)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)
4911.49	GSTP1	Glutathione	226	-0.028	0.19	0.134	0.03	(-0.01, 0.07)	0.506	0.237	0.008	0.039	0.839	0.01	(-0.07, 0.09)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)
9470.15	METTL24	METTL24	226	-0.028	0.19	0.134	0.03	(-0.01, 0.07)	0.506	0.237	0.008	0.039	0.839	0.01	(-0.07, 0.09)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)
10396.6	MOI1	MOI1	226	-0.029	0.19	0.134	0.03	(-0.01, 0.07)	0.507	0.237	0.009	0.040	0.840	0.01	(-0.07, 0.09)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)
18218.48	CNR1P1	CNR1P1	226	-0.029	0.19	0.135	0.03	(-0.01, 0.07)	0.507	0.237	0.009	0.040	0.840	0.01	(-0.07, 0.09)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)
3412.7	BCL2L1	Bcl-2	226	-0.027	0.18	0.135	0.03	(-0.01, 0.06)	0.508	0.238	0.008	0.039	0.839	0.01	(-0.07, 0.09)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)
12732.13	MPPT	MPPT	226	-0.029	0.19	0.135	0.03	(-0.01, 0.07)	0.508	0.238	0.009	0.040	0.840	0.01	(-0.07, 0.09)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)
5128.53	SLAMF6	SLAMF6	226	-0.028	0.19	0.135	0.03	(-0.01, 0.07)	0.508	0.238	0.009	0.040	0.840	0.01	(-0.07, 0.09)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)
18289.16	CCL15	MIP-5	226	-0.033	0.022	0.135	-0.03	(-0.08, 0.01)	0.508	0.238	-0.044	0.037	0.539	-0.03	(-0.11, 0.06)	0.000	0.985	-0.021	0.44	0.632	-0.02	(-0.11, 0.06)	-0.012	0.043	0.784	-0.01	(-0.10, 0.07)
12248.46	SARS2	SARS2	226	-0.029	0.19	0.135	0.03	(-0.01, 0.07)	0.508	0.238	0.009	0.040	0.840	0.01	(-0.07, 0.09)	0.001	0.965	0.101	0.41	0.801	0.01	(-0.07, 0.09)	0.019	0.042	0.681	0.02	(-0.06, 0.10)
17775.8	TAGLN3	TAGLN3	226	-0.029	0.19	0.136	0.03	(-0.01, 0.07)	0.509	0.241	0.028	0.039	0.840	(0.78, 0.91)	0.000	0.985	-0.021	0.44	0.632	-0.02	(-0.11, 0.06)	-0.012	0.043	0.784	-0.01	(-0.10, 0.07)	
12729.12	PSH2G	PSH2G	226	-0.028	0.19	0.136	0.03	(-0.01, 0.06)	0.509	0.241	0.028	0.039	0.840	(0.78, 0.91)	0.000	0.985	-0.021	0.44	0.632	-0.02	(-0.11, 0.06)	-0.012	0.043	0.784	-0.01	(-0.10, 0.07)	
11421.10	EHOD4	EHOD4	226	-0.028	0.19	0.136	0.03	(-0.01, 0.06)	0.509	0.241	0.028	0.039	0.840	(0.78, 0.91)	0.000	0.985	-0.021	0.44	0.632	-0.02	(-0.11, 0.06)	-0.012	0.043	0.784	-0.01	(-0.10, 0.07)	
12832.10	ASH2L	ASH2L	226	-0.028	0.19	0.136	0.03	(-0.01, 0.06)	0.509	0.241	0.028	0.039	0.840	(0.78, 0.91)	0.000	0.985	-0.021	0.44	0.632	-0.02	(-0.11, 0.06)	-0.012	0.043	0.784	-0.01	(-0.10, 0.07)	
14992.20	SH2B3	SH2B3	226	-0.028	0.19	0.136	0.03	(-0.01, 0.06)	0.509	0.241	0.028	0.039	0.840	(0.78, 0.91)	0.000	0.985	-0.021	0.44	0.632	-0.02	(-0.11, 0.06)	-0.012	0.043	0.784	-0.01	(-0.10, 0.07)	
3810.50	FCGR	FCGR	226	-0.028	0.19	0.136	0.03	(-0.01, 0.06)	0.510	0.241	0.028	0.039	0.840	(0.78, 0.91)	0.000	0.985	-0.021	0.44	0.632	-0.02	(-0.11, 0.06)	-0.012	0.043	0.784	-0.01	(-0.10, 0.07)	
8553.68	CFAR5	CFAR5	226	-0.029	0.19	0.137	0.03	(-0.01, 0.07)	0.510	0.241	0.028	0.039	0.840	(0.78, 0.91)	0.000	0.985	-0.021	0.44	0.632	-0.02	(-0.11, 0.06)	-0.012	0.043	0.784	-0.01	(-0.10, 0.07)	
8047.222	DEFB129	DEFB129	226	-0.029	0.19	0.137	0.03	(-0.01, 0.07)	0.510	0.241	0.028	0.039	0.840	(0.78, 0.91)	0.000	0.985	-0.021	0.44	0.632	-0.02	(-0.11, 0.06)	-0.012	0.043	0.784	-0.01	(-0.10, 0.07)	
8089.173	NR4A1	NR4A1	226	-0.029	0.19	0.137	0.03	(-0.01, 0.07)	0.510	0.241	0.028	0.039	0.840	(0.78, 0.91)	0.000	0.985	-0.021	0.44	0.632	-0.02	(-0.11, 0.06)	-0.012	0.043	0.784	-0.01	(-0.10, 0.07)	
9025.5	AHSP	AHSP	226	-0.029	0.19	0.137	0.03	(-0.01, 0.07)	0.510	0.241	0.028	0.039	0.840	(0.78, 0.91)	0.000	0.985	-0.021	0.44	0.632	-0.02	(-0.11, 0.06)	-0.012	0.043	0.784	-0.01	(-0.10, 0.07)	
12343.14	ACAP2	ACAP2	226	-0.029	0.19	0.138	0.03	(-0.01, 0.07)	0.511	0.241	0.028	0.039	0.840	(0.78, 0.91)	0.000	0.985	-0.021	0.44	0.632	-0.02	(-0.11, 0.06)	-0.012	0.043	0.784	-0.01	(-0.10, 0.07)	
18707.7	PPA2	PPA2	226	-0.027																							

Table S5. Association of type 2 diabetes with Fenland plasma protein.

SomaLogicGene	Protein	rsnp	b/w		se/w		pval/w		CI/w		MR Egger		Weighted median		Weighted mode		
			low	high	low	high	low	high	low	high	low	high	low	high	low	high	
8321_27	ZNF43	ZNF43	0.26	-0.27	0.20	0.182	-0.03	(-0.07, 0.01)	0.544	0.998	0.010	0.039	0.802	-0.01	(-0.09, 0.07)	-0.001	0.910
13559_36	ATP11A3	ATP11A3	0.26	-0.27	0.20	0.182	-0.03	(-0.07, 0.01)	0.544	0.998	0.010	0.039	0.802	-0.01	(-0.09, 0.07)	-0.001	0.910
6227_18	KLK10	Kalherin-10	0.26	-0.30	0.22	0.182	-0.03	(-0.07, 0.01)	0.544	4.29E-04	-0.223	0.044	0.599	-0.02	(-0.11, 0.06)	0.000	0.849
8454_38	ARHGAP24	Rho-GDIA	0.26	-0.28	0.20	0.182	-0.03	(-0.07, 0.01)	0.544	0.004	0.007	0.041	0.859	-0.01	(-0.07, 0.09)	0.000	0.910
7755_37	ITGB5	ITGB5	0.26	-0.28	0.20	0.182	-0.03	(-0.07, 0.01)	0.544	0.008	0.008	0.041	0.859	-0.01	(-0.07, 0.09)	0.000	0.910
8932_17	PRSS57	PRSS57	0.26	-0.29	0.21	0.182	-0.03	(-0.07, 0.01)	0.544	0.001	-0.013	0.042	0.759	-0.01	(-0.11, 0.07)	-0.001	0.668
11154_6	SIT1	SIT1	0.26	-0.27	0.19	0.182	-0.03	(-0.07, 0.01)	0.544	0.361	-0.033	0.039	0.394	-0.03	(-0.10, 0.04)	0.004	0.777
18265_18	ZNF34	ZNF34	0.26	-0.28	0.19	0.182	-0.03	(-0.07, 0.01)	0.544	0.811	-0.033	0.039	0.394	-0.03	(-0.10, 0.04)	0.004	0.777
8951_162	CSPG4	CSPG4	0.26	-0.30	0.22	0.182	-0.03	(-0.07, 0.01)	0.544	0.010	-0.009	0.044	0.829	-0.01	(-0.10, 0.08)	0.002	0.296
19001_15	ASB9	ASB9	0.26	-0.28	0.20	0.182	-0.03	(-0.07, 0.01)	0.545	0.043	-0.013	0.041	0.829	-0.01	(-0.10, 0.08)	0.002	0.296
8409_11	TSPB1	TRB1	0.26	-0.28	0.19	0.182	-0.03	(-0.07, 0.01)	0.546	0.335	0.238	0.039	0.487	0.03	(0.05, 0.10)	-0.003	0.105
11531_24	C10orf54	G24	0.26	-0.26	0.19	0.182	-0.03	(-0.07, 0.01)	0.547	0.232	0.001	0.039	0.973	0.02	(0.06, 0.08)	-0.002	0.466
14083_25	SEH1A1	SPS4	0.26	-0.28	0.19	0.182	-0.03	(-0.07, 0.01)	0.547	0.038	0.011	0.039	0.973	0.02	(0.06, 0.08)	-0.002	0.466
7851_30	ANKRD46	ANKRD46	0.26	-0.27	0.19	0.182	-0.03	(-0.07, 0.01)	0.547	0.773	0.035	0.039	0.373	0.03	(0.04, 0.11)	0.000	0.815
13056_1	RMI1	RMI1	0.26	-0.28	0.19	0.182	-0.03	(-0.07, 0.01)	0.549	0.214	0.012	0.039	0.751	0.01	(0.04, 0.09)	0.001	0.680
19125_26	PRKAR2A	KAP2	0.26	-0.27	0.19	0.182	-0.03	(-0.07, 0.01)	0.549	0.863	-0.020	0.040	0.651	-0.02	(-0.10, 0.06)	0.000	0.845
17204_17	PNMT	PNMT	0.26	-0.27	0.20	0.182	-0.03	(-0.07, 0.01)	0.549	0.346	-0.018	0.040	0.657	-0.02	(-0.10, 0.06)	0.001	0.790
16886_28	DISCAL1	DISC1	0.26	-0.28	0.19	0.182	-0.03	(-0.07, 0.01)	0.551	0.753	0.058	0.038	0.204	0.03	(0.04, 0.04)	0.001	0.686
2991_9	IL1R1	IL1R1	0.26	-0.26	0.19	0.182	-0.03	(-0.07, 0.01)	0.551	0.328	0.059	0.038	0.119	0.06	(-0.13, 0.13)	-0.005	0.100
7266_4	SERPINA9	SAP9	0.26	-0.25	0.18	0.182	-0.03	(-0.07, 0.01)	0.551	0.273	0.030	0.038	0.418	0.03	(-0.04, 0.12)	-0.003	0.089
8590_102	DAC1	DAC1	0.26	-0.27	0.19	0.182	-0.03	(-0.07, 0.01)	0.551	0.863	-0.020	0.040	0.651	-0.02	(-0.10, 0.06)	0.000	0.897
8885_8	CACNA2D2	CAC2D2	0.26	-0.30	0.22	0.182	-0.03	(-0.07, 0.01)	0.551	0.001	0.031	0.044	0.480	0.03	(-0.06, 0.12)	-0.004	0.109
9366_54	IL21R	IL21R	0.26	-0.26	0.19	0.182	-0.03	(-0.07, 0.01)	0.551	0.460	-0.015	0.038	0.696	-0.01	(-0.09, 0.06)	0.003	0.216
8590_102	DAC1	DAC1	0.26	-0.27	0.19	0.182	-0.03	(-0.07, 0.01)	0.551	0.863	-0.020	0.040	0.651	-0.02	(-0.10, 0.06)	0.000	0.897
18193_165	MORF4L1	MOL1	0.26	-0.28	0.19	0.182	-0.03	(-0.07, 0.01)	0.551	0.462	-0.001	0.038	0.975	-0.17	(-0.08, 0.07)	-0.002	0.453
18914_188	FA2H	FA2H	0.26	-0.28	0.19	0.182	-0.03	(-0.07, 0.01)	0.551	0.496	-0.002	0.038	0.960	-0.19	(-0.07, 0.08)	-0.002	0.454
8007_7	SCLEC4E	Siglec4e	0.26	-0.27	0.19	0.182	-0.03	(-0.07, 0.01)	0.551	0.009	0.014	0.038	0.914	0.01	(0.01, 0.07)	-0.001	0.610
9017_58	LCT	LPH	0.26	-0.28	0.19	0.182	-0.03	(-0.07, 0.01)	0.554	0.019	0.002	0.041	0.987	0.17	(-0.08, 0.08)	-0.002	0.404
10748_216	PCDHB2	PCDHB2	0.26	-0.26	0.19	0.182	-0.03	(-0.07, 0.01)	0.555	0.304	-0.051	0.039	0.190	0.05	(-0.13, 0.13)	-0.002	0.023
15307_38	DEFRA	HSD-2	0.26	-0.27	0.19	0.182	-0.03	(-0.07, 0.01)	0.555	0.100	0.005	0.039	0.924	0.01	(0.01, 0.02)	0.002	0.244
19575_4	EPOF	EPOF	0.26	-0.27	0.20	0.182	-0.03	(-0.07, 0.01)	0.555	0.802	-0.057	0.039	0.149	-0.06	(-0.13, 0.02)	-0.002	0.380
3115_64	MAPK1	MAPK1	0.26	-0.25	0.18	0.182	-0.03	(-0.07, 0.01)	0.555	0.738	0.019	0.038	0.604	0.02	(-0.05, 0.09)	0.000	0.851
7154_22	LEC1	LEC1	0.26	-0.27	0.19	0.182	-0.03	(-0.07, 0.01)	0.555	0.101	0.005	0.038	0.924	0.01	(0.01, 0.02)	0.002	0.244
12386_16	CRYSD	CRYSD	0.26	-0.29	0.21	0.182	-0.03	(-0.07, 0.01)	0.556	0.017	-0.010	0.043	0.819	-0.01	(-0.09, 0.07)	-0.001	0.602
1147_22	SLC33A3	SLC33A3	0.26	-0.28	0.19	0.182	-0.03	(-0.07, 0.01)	0.556	0.189	-0.015	0.038	0.829	-0.01	(-0.09, 0.07)	-0.001	0.602
4908_6	ENK	Endoglin	0.26	-0.30	0.22	0.182	-0.03	(-0.07, 0.01)	0.556	4.55E-05	0.336	0.044	0.411	0.04	(-0.02, 0.12)	-0.004	0.084
7789_182	PRDX4	PRDX4	0.26	-0.28	0.19	0.182	-0.03	(-0.07, 0.01)	0.556	0.172	0.061	0.040	0.123	0.06	(-0.05, 0.14)	-0.002	0.304
2381_52	CS	CS	0.26	-0.28	0.19	0.182	-0.03	(-0.07, 0.01)	0.556	0.038	0.010	0.038	0.950	0.01	(0.01, 0.02)	0.002	0.414
6060_2	PIP	PIP	0.26	-0.29	0.21	0.182	-0.03	(-0.07, 0.01)	0.557	0.002	0.014	0.043	0.754	0.01	(-0.07, 0.10)	-0.003	0.253
10830_5	HATP2	HAT2	0.26	-0.27	0.20	0.182	-0.03	(-0.07, 0.01)	0.558	0.458	-0.038	0.039	0.356	0.04	(-0.11, 0.04)	0.004	0.066
11190_129	MYL1	MYL1	0.26	-0.29	0.19	0.182	-0.03	(-0.07, 0.01)	0.558	0.211	0.009	0.038	0.924	0.01	(0.01, 0.02)	0.002	0.244
11951_233	NHEJ1	NHEJ1	0.26	-0.28	0.19	0.182	-0.03	(-0.07, 0.01)	0.558	0.246	0.013	0.038	0.290	0.04	(-0.03, 0.12)	-0.001	0.655
12767_164	FLI	FLI	0.26	-0.25	0.18	0.182	-0.03	(-0.07, 0.01)	0.558	0.427	-0.031	0.037	0.412	-0.03	(-0.10, 0.04)	0.000	0.808
8695_9	DEFB12	DEFB12	0.26	-0.28	0.19	0.182	-0.03	(-0.07, 0.01)	0.558	0.456	-0.039	0.038	0.950	-0.02	(-0.10, 0.06)	-0.001	0.680
8482_18	HLI	HGH	0.26	-0.27	0.19	0.182	-0.03	(-0.07, 0.01)	0.558	0.640	-0.045	0.039	0.256	0.04	(-0.12, 0.03)	0.001	0.597
16933_3	FADD	FADD	0.26	-0.29	0.19	0.182	-0.03	(-0.07, 0.01)	0.558	0.167	0.045	0.040	0.264	0.05	(-0.03, 0.12)	0.005	0.441
1815_38	RTD4	RTD4	0.26	-0.27	0.19	0.182	-0.03	(-0.07, 0.01)	0.558	0.048	0.048	0.038	0.950	0.01	(0.01, 0.02)	0.002	0.244
18401_18	ALKBK3	ALKBK3	0.26	-0.25	0.19	0.182	-0.03	(-0.07, 0.01)	0.558	0.261	0.021	0.038	0.586	0.02	(-0.05, 0.10)	0.000	0.897
4642_62	GPC3	Glypican-3	0.26	-0.29	0.21	0.182	-0.03	(-0.07, 0.01)	0.558	0.004	0.063	0.042	0.137	0.06	(-0.02, 0.15)	-0.008	0.013
5002_11	MSN	MSN	0.26	-0.27	0.19	0.182	-0.03	(-0.07, 0.01)	0.558	0.045	0.035	0.042	0.972	0.01	(0.01, 0.02)	0.002	0.244
5354_11	KRT18	Keratin-18	0.26	-0.28	0.19	0.182	-0.03	(-0.07, 0.01)	0.558	0.898	-0.021	0.038	0.582	-0.02	(-0.06, 0.10)	-0.000	0.877
7921_55	FJX1	FJX1	0.26	-0.28	0.19	0.182	-0.03	(-0.07, 0.01)	0.558	0.147	-0.028	0.040	0.692	-0.04	(-0.13, 0.05)	-0.001	0.605
8633_84	MEF2C	MEF2C	0.26	-0.25	0.18	0.182	-0.03	(-0.07, 0.01)	0.558	0.251	-0.012	0.037	0.752	-0.01	(-0.09, 0.07)	-0.001	0.602
2714_78	AMP1	AMP2	0.26	-0.29	0.21	0.182	-0.03	(-0.07, 0.01)	0.558	0.009	0.072	0.043	0.094	0.07	(-0.01, 0.16)	-0.003	0.249
7911_29	SCAB1	SCAB1	0.26	-0.28	0.19	0.182	-0.03	(-0.07, 0.01)	0.558	0.005	0.005	0.038	0.960	-0.01	(-0.09, 0.07)	-0.001	0.605
12562_1	PKN1	PKN1	0.26	-0.24	0.18	0.182	-0.03	(-0.07, 0.01)	0.558	0.632	-0.040	0.035	0.905	-0.22	(-0.07, 0.07)	-0.002	0.360
13339_131	KCNK11	KCNK11	0.26	-0.27	0.19	0.182	-0.03	(-0.07, 0.01)	0.560	0.299	0.012	0.040	0.774	0.01	(-0.07, 0.09)	0.001	0.689
16323_5	NRXN3	NRXN3	0.26	-0.27	0.19	0.182	-										

Table S5. Association of type 2 diabetes with Ferland plasma protein.

SomaLogic Gene	Protein	rnp	Inverse variance weighted				MR Egger				Weighted median				Weighted mode														
			b1w	se.b1w	pval.b1w	CI_low	FOR_Irw	b1w	se.b1w	pval.b1w	CI_low	egger	egger	egger	egger	b.mode	se.mode	pval.mode	CI_low										
13717.15	FCN2	FCN2	0.26	0.029	0.023	0.198	0.033	0.027	0.591	9.06E-05	0.075	0.046	0.104	0.077	0.019	-0.003	0.253	0.091	0.039	0.021	0.099	0.117	0.111	0.044	0.012	0.11	0.02	0.20	
6250.53	MPH24	MPH24	0.26	0.029	0.023	0.198	0.033	0.027	0.591	9.06E-05	0.075	0.046	0.104	0.077	0.019	-0.003	0.253	0.091	0.039	0.021	0.099	0.117	0.111	0.044	0.012	0.11	0.02	0.20	
10667.78	CD181	CD181	0.26	0.029	0.023	0.198	0.033	0.027	0.591	9.06E-05	0.075	0.046	0.104	0.077	0.019	-0.003	0.253	0.091	0.039	0.021	0.099	0.117	0.111	0.044	0.012	0.11	0.02	0.20	
9008.51	SOOT2	SOOT2	0.26	0.029	0.023	0.198	0.033	0.027	0.591	9.06E-05	0.075	0.046	0.104	0.077	0.019	-0.003	0.253	0.091	0.039	0.021	0.099	0.117	0.111	0.044	0.012	0.11	0.02	0.20	
8303.02	CLD1010	CLD1010	0.26	0.029	0.023	0.198	0.033	0.027	0.591	9.06E-05	0.075	0.046	0.104	0.077	0.019	-0.003	0.253	0.091	0.039	0.021	0.099	0.117	0.111	0.044	0.012	0.11	0.02	0.20	
8631.33	ERMAP	ERMAP	0.26	0.029	0.023	0.198	0.033	0.027	0.591	9.06E-05	0.075	0.046	0.104	0.077	0.019	-0.003	0.253	0.091	0.039	0.021	0.099	0.117	0.111	0.044	0.012	0.11	0.02	0.20	
13388.57	PCPK1	PCPK1	0.26	0.029	0.023	0.198	0.033	0.027	0.591	9.06E-05	0.075	0.046	0.104	0.077	0.019	-0.003	0.253	0.091	0.039	0.021	0.099	0.117	0.111	0.044	0.012	0.11	0.02	0.20	
6460.50	DDY18B	DDY18B	0.26	0.029	0.023	0.198	0.033	0.027	0.591	9.06E-05	0.075	0.046	0.104	0.077	0.019	-0.003	0.253	0.091	0.039	0.021	0.099	0.117	0.111	0.044	0.012	0.11	0.02	0.20	
8480.29	ELFEMP1	ELFEMP1	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
9004.24	LDRAD4	CRO1	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
12880.1	SVGA	SVGA	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
18322.15	JMJD6	JMJD6	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
5726.50	FCRL1	FCRL1	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
8075.121	KIAA1024	K1024	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
8766.29	LILRA5	LILRA5	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
8657.72	ERLEC1	ATPB	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
10548.14	PLD3	PLD3	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
11633.89	AHSA1	AHSA1	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
12515.45	UC2C	UC2C	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
17756.69	DCTD	DCTD	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
2747.3	ULBP3	ULBP3	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
3336.50	TFPI	TFPI	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
7975.97	UNC5A	UNC5A	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
8070.88	DLG4	DLG4	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
8336.33	ITIH2	ITIH2	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
13588.11	ANXAA9	ANXAA9	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
2833.20	KLK4	Kallistatin 4	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
1111.7	TRKE	TRKE	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
12406.119	DIRAS3	ARH1	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
13882.47	CSFR	CSFR	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
17411.55	LFZL1	LFZL1	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
19276.124	SNRPG	RUCG	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
3391.10	PKNOX	PKNOX	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
5261.13	ABL2	ABL2	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
5493.17	WNK3	WNK3	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
6554.12	GNAT2	GNAT2	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
6870.23	SEM3	SEM3	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
8448.38	BAD	Bad	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
10526.22	HSP2D	HSP2D	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
3290.50	PRR4	CD109	0.26	0.030	0.024	0.200	0.033	0.028	0.593	4.36E-08	0.074	0.048	0.123	0.077	0.022	0.003	0.296	0.045	0.038	0.027	0.104	0.123	0.078	0.038	0.043	0.08	0.15	2.98	0.33
3822.54	MAPKAPK4	MAPKAPK4	0.26	0.030	0.024																								

Table S5. Association of type 2 diabetes with Ferland plasma protein.

Locus	Protein	rsnp	Inverse variance weighted		MR Egger		Weighted median		Weighted mode	
			b	se	b	se	b	se	b	se
12603.67	PABP4	PABP4	2.06	0.222	0.18	0.235	0.02	0.01	0.06	0.008
18186.15	TARD	TARD	0.48	0.031	0.18	0.023	0.02	0.01	0.01	0.001
6907.17	TMC5A	TMC5A	0.28	-0.026	0.22	0.235	-0.02	0.02	0.01	0.001
7100.4	LARR2	LARR2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8950.4	CLCA2	CLCA2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
4717.55	L3	L3	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
11965.58	ZNF23	ZNF23	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
12844.83	ADSS	PURHA2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
12684.28	DIM1	DIM1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
5813.58	EMO1	Epo	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
7695.52	QSOX1	QSOX2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
9758.17	RSX4	RSX4	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
12373.73	TRAB2	TRAB2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
18864.7	PRSS3	TR3	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
4851.25	L1A	L1a	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
19156.73	HOPX	HOPX	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
12585.39	ERCDC1	ERCDC1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
1830.1	ITLN1	Omentin	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
2696.55	L4	L4	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
3875.82	ARD3A	ARD3A	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
12647.52	SETD2	SETD2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
3420.21	CAN1	Catecholamin	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8999.19	CEACAM3	CEAM3	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
13113.7	SFP1	Osteopontin	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
15589.1	CC	POU3f1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8975.70	THOC1	THOC1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
9883.97	PRSS35	PRSS35	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
10584.7	NDR45A	NDR45A	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
11596.47	ZNF50	ZNF50	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
13098.93	FGF2	VEGF-D	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
16585.16	BGN2T4	BGN2T4	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
3033.57	LGALS2	Galectin-2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
7625.27	YWHQ4	14-3-3 β	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8036.75	FSH1	FSH1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8454.31	RPM3	RPM3	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8454.31	RPM3	RPM3	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8454.31	RPM3	RPM3	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
7981.20	B3GALT6	B3GALT6	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
14024.19	EDA	EDA	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
14067.5	PNP2	PNP2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
5589.66	MNPP3	MNPP3	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
7018.10	TRP1	TRP1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
7175.4	PCDHGA2	PCDHGA2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
7958.11	MNOS1	MOS1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8881.93	PGRC2	PGRC2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
9274.3	CPA2	CPA2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
9669.8	SLC22A16	S22AG	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
4396.54	IFNL1	IFN-lambda3	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
7007.24	TRAPPC4	TRAPPC4	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
10666.7	RNTP2	GNPTG	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
17516.7	RAB2A	Rab2a	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
17819.30	FAH1D1	FAH1D1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
18925.24	PSMA5	Proteasome	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
18442.1	GMPF2	GMPF2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
3050.7	VWF	VWF	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
4499.78	CHST15	ST4S6	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8075.21	FAM20A	FAM20A	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
3024.18	SERPINF2	42-Angiopo	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
9388.18	MCEE	MCEE	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
17221.1	LCF1	LCF1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
19219.71	NFTF-2	NFTF-2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
4246.40	LIGCAM	NCCAM1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
7020.20	TNFRSF10	TNFRSF10	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8082.15	EVAI8	FTIB8	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
6282.14	L1TRB	L1-TRB	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8374.5	NSFR	NSFR	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
11185.145	GCH1	GCH1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
11645.9	PHN1A	PHN1A	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
15089.87	BTC	BTC	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
14192.31	PODCL2	PODCL2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
16863.47	NANP	NANP	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
6981.6	CTSLB3	ES1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8054.6	NXPH3	NXPH3	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
7960.53	ADAM29	ADAM29	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8637.8	MFRP3L	MFR3L	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
9317.4	LRRK25	LRRK25	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
9636.18	EDM3A	EDM3A	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
9577.26	SYT2	SYT2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
13987.14	TNFRD1	Thioredoxin	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8391.12	DEFB15	DEFB15	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
13548.53	PLD3	PLD3	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
7897.75	DLG3	DLG3	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
12451.82	BACH1	BACH1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
12667.2	GBA	GUAD	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
3042.2	MDA	Myoglobin	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8758.13	BDI1	BDI1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8676.20	ALDOC	aldolase C	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
3823.9	MATK	MATK	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
4131.72	FNI	Fibrinogen	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
5687.5	PRKCSH	GLUB	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
7127.3	AP2A2	AP2A2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
13545.15	ADAM29	ADAM29	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
19333.4	HNRNPK1	HNRNPK1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
10716.25	PSMD5	PSMD5	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
19252.67	PSMB2	PSB2	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
3206.4	LYVE1	LYVE1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
8326.20	BMF4	BMF4	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
2972.57	BMP7	BMP7	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
18309.18	CSF1	CSF1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
11275.94	LFBP1	LFBP1	0.28	-0.023	0.19	0.235	-0.02	0.01	0.01	0.001
11616.9	HSF1									

Table S5. Association of type 2 diabetes with Ferland plasma protein.

SomaLogE Gene	Protein	tsp	Inverse variance weighted		MR Egger		Weighted median		Weighted mode	
			b	se	b	se	b	se	b	se
1828.34	FLRT3	FLRT3	0.21	0.19	0.273	0.02 (0.2, 0.06)	0.668	0.374	0.101	0.09 (0.09, 0.07)
15372.43	BRD2	BRD2	0.26	0.19	0.168	0.02 (0.15, 0.08)	0.668	0.374	0.101	0.09 (0.09, 0.07)
18012.26	ARL1	ARL1	0.26	0.21	0.020	0.02 (0.02, 0.00)	0.668	0.374	0.101	0.09 (0.09, 0.07)
15012.67	AK1	Mykinesin	0.26	0.20	0.018	0.274 -0.02 (0.05, 0.02)	0.668	0.374	0.101	0.09 (0.09, 0.07)
12923.51	KRT17	KRT17	0.26	0.20	0.018	0.274 -0.02 (0.05, 0.02)	0.668	0.374	0.101	0.09 (0.09, 0.07)
4982.54	PL3	Ela1n	0.26	0.20	0.022	0.274 -0.02 (0.07, 0.02)	0.668	0.374	0.101	0.09 (0.09, 0.07)
17749.20	UBE2B	UBE2B	0.26	0.20	0.021	0.275 -0.02 (0.08, 0.02)	0.670	0.375	0.102	0.09 (0.09, 0.07)
1519.34	CPB2	TAF11	0.26	0.20	0.019	0.277 -0.02 (0.07, 0.02)	0.671	0.376	0.102	0.09 (0.09, 0.07)
5825.49	IFNGR1	IFNGR1	0.26	0.20	0.019	0.275 -0.02 (0.08, 0.02)	0.671	0.376	0.102	0.09 (0.09, 0.07)
11659.31	CLNT1	CLNT1	0.26	0.20	0.018	0.276 -0.02 (0.08, 0.02)	0.671	0.376	0.102	0.09 (0.09, 0.07)
14519.16	ZNF323	ZNF323	0.26	0.20	0.019	0.277 -0.02 (0.08, 0.02)	0.671	0.376	0.102	0.09 (0.09, 0.07)
8905.20	KCMB3	KCMB3	0.26	0.20	0.024	0.276 0.03 (0.02, 0.07)	0.671	0.376	0.102	0.09 (0.09, 0.07)
13041.47	TRAF4	TRAF4	0.26	0.20	0.021	0.276 -0.02 (0.08, 0.02)	0.671	0.376	0.102	0.09 (0.09, 0.07)
15343.2	PFZD2	PFZD2	0.26	0.20	0.021	0.276 -0.02 (0.08, 0.02)	0.671	0.376	0.102	0.09 (0.09, 0.07)
13393.46	DERL1	DERL1	0.26	0.20	0.019	0.277 -0.02 (0.08, 0.02)	0.673	0.377	0.102	0.09 (0.09, 0.07)
12980.31	RANBP2	RANBP2	0.26	0.20	0.020	0.279 -0.02 (0.08, 0.02)	0.673	0.377	0.102	0.09 (0.09, 0.07)
14037.18	RANBP3	RANBP3	0.26	0.20	0.019	0.277 -0.02 (0.08, 0.02)	0.673	0.377	0.102	0.09 (0.09, 0.07)
17343.6	SNPH	SNPH	0.26	0.20	0.019	0.278 -0.02 (0.08, 0.02)	0.673	0.377	0.102	0.09 (0.09, 0.07)
16302.2	SPAT7	Spenn-pro2	0.26	0.20	0.021	0.279 -0.02 (0.08, 0.02)	0.673	0.377	0.102	0.09 (0.09, 0.07)
18294.12	CCDC25	CCDC25	0.26	0.20	0.021	0.278 -0.02 (0.08, 0.02)	0.673	0.377	0.102	0.09 (0.09, 0.07)
18874.86	CEBPA	CEBPA	0.26	0.20	0.020	0.279 -0.02 (0.08, 0.02)	0.673	0.377	0.102	0.09 (0.09, 0.07)
15564.61	IRF4	IRF4	0.26	0.20	0.021	0.279 -0.02 (0.08, 0.02)	0.673	0.377	0.102	0.09 (0.09, 0.07)
4900.8	C3	C3	0.26	0.20	0.022	0.279 0.02 (0.02, 0.06)	0.673	0.377	0.102	0.09 (0.09, 0.07)
4979.34	DPT	DERM	0.26	0.20	0.020	0.278 -0.02 (0.08, 0.02)	0.673	0.377	0.102	0.09 (0.09, 0.07)
8230.36	CEP1	CEP1	0.26	0.20	0.019	0.276 -0.02 (0.08, 0.02)	0.673	0.377	0.102	0.09 (0.09, 0.07)
6304.8	C10orf1	C10orf1	0.26	0.20	0.025	0.273 -0.03 (0.07, 0.02)	0.673	0.377	0.102	0.09 (0.09, 0.07)
8988.106	ASPH	HAH	0.26	0.20	0.021	0.278 -0.02 (0.08, 0.02)	0.673	0.377	0.102	0.09 (0.09, 0.07)
8333.20	C11orf4	CKO4	0.26	0.20	0.019	0.279 0.02 (0.02, 0.06)	0.673	0.377	0.102	0.09 (0.09, 0.07)
10024.44	HOGA1	HOGA1	0.26	0.20	0.021	0.279 0.02 (0.02, 0.06)	0.673	0.377	0.102	0.09 (0.09, 0.07)
12814.17	RNCP3	RBM10	0.26	0.20	0.020	0.279 -0.02 (0.08, 0.02)	0.673	0.377	0.102	0.09 (0.09, 0.07)
18915.26	ITPA	Protein-tyrosin	0.26	0.20	0.019	0.279 0.02 (0.02, 0.06)	0.673	0.377	0.102	0.09 (0.09, 0.07)
8315.5	DEFB119	DEFB119	0.26	0.20	0.021	0.279 -0.02 (0.08, 0.02)	0.673	0.377	0.102	0.09 (0.09, 0.07)
17749.20	CHORD1	CAT15	0.26	0.20	0.020	0.280 0.02 (0.02, 0.06)	0.673	0.377	0.102	0.09 (0.09, 0.07)
10349.59	RNF2	RLA2	0.26	0.20	0.021	0.280 0.02 (0.02, 0.06)	0.673	0.377	0.102	0.09 (0.09, 0.07)
12442.4	RHOV	RHOV	0.26	0.20	0.019	0.281 -0.02 (0.08, 0.02)	0.674	0.378	0.102	0.09 (0.09, 0.07)
15433.9	SNZ	SNZ	0.26	0.20	0.017	0.280 0.02 (0.08, 0.02)	0.674	0.378	0.102	0.09 (0.09, 0.07)
17329.2	SAH1	SAH1	0.26	0.20	0.020	0.280 0.02 (0.08, 0.02)	0.674	0.378	0.102	0.09 (0.09, 0.07)
17329.2	SAH2	SAH2	0.26	0.20	0.022	0.281 0.02 (0.02, 0.06)	0.674	0.378	0.102	0.09 (0.09, 0.07)
17704.74	HSPH1	HSPH1	0.26	0.20	0.019	0.280 0.02 (0.08, 0.02)	0.674	0.378	0.102	0.09 (0.09, 0.07)
3182.38	ENTPD1	CD39	0.26	0.20	0.019	0.280 0.02 (0.08, 0.02)	0.674	0.378	0.102	0.09 (0.09, 0.07)
4874.3	ANG	Angiogenin	0.26	0.20	0.019	0.281 0.02 (0.02, 0.06)	0.674	0.378	0.102	0.09 (0.09, 0.07)
4656.2	EREG	EREG	0.26	0.20	0.019	0.280 0.02 (0.08, 0.02)	0.674	0.378	0.102	0.09 (0.09, 0.07)
7818.10	ADRM	GBP6	0.26	0.20	0.019	0.281 0.02 (0.02, 0.06)	0.674	0.378	0.102	0.09 (0.09, 0.07)
7922.5	GBP6	ADRM	0.26	0.20	0.021	0.281 -0.02 (0.08, 0.02)	0.674	0.378	0.102	0.09 (0.09, 0.07)
12427.8	CCDC28	CCDC28	0.26	0.20	0.019	0.281 -0.02 (0.08, 0.02)	0.674	0.378	0.102	0.09 (0.09, 0.07)
13231.90	IGHG3	IgkL, Kapp	0.26	0.20	0.021	0.282 0.02 (0.02, 0.06)	0.674	0.378	0.102	0.09 (0.09, 0.07)
5653.23	PRSS3	PRSS3	0.26	0.20	0.020	0.282 -0.02 (0.08, 0.02)	0.674	0.378	0.102	0.09 (0.09, 0.07)
8051.3	ARHGFB1	ARHGFB1	0.26	0.20	0.019	0.282 -0.02 (0.08, 0.02)	0.674	0.378	0.102	0.09 (0.09, 0.07)
9108.87	LYSM4	LYSM4	0.26	0.20	0.019	0.282 0.02 (0.02, 0.06)	0.674	0.378	0.102	0.09 (0.09, 0.07)
10054.3	GAN	GAN	0.26	0.20	0.019	0.283 -0.02 (0.08, 0.02)	0.675	0.379	0.102	0.09 (0.09, 0.07)
15524.30	PSMA2	PSMA2	0.26	0.20	0.019	0.283 -0.02 (0.08, 0.02)	0.675	0.379	0.102	0.09 (0.09, 0.07)
3222.11	SEMA3A	Semaphorin	0.26	0.20	0.020	0.283 0.02 (0.02, 0.06)	0.675	0.379	0.102	0.09 (0.09, 0.07)
8715.5	ALPPL2	ALPPL2	0.26	0.20	0.020	0.283 -0.02 (0.08, 0.02)	0.675	0.379	0.102	0.09 (0.09, 0.07)
8715.5	CASA	Cemaphorin	0.26	0.20	0.021	0.283 0.02 (0.02, 0.06)	0.675	0.379	0.102	0.09 (0.09, 0.07)
13491.40	PDEBD	PDEBD	0.26	0.20	0.019	0.284 0.02 (0.02, 0.06)	0.675	0.379	0.102	0.09 (0.09, 0.07)
10199.3	POU2F1	POU2F1	0.26	0.20	0.019	0.284 0.02 (0.02, 0.06)	0.675	0.379	0.102	0.09 (0.09, 0.07)
5061.27	ICOLG3	ICOLG3	0.26	0.20	0.021	0.284 -0.02 (0.08, 0.02)	0.675	0.379	0.102	0.09 (0.09, 0.07)
5133.17	TGFR12	TGFR- β II	0.26	0.20	0.020	0.284 0.02 (0.02, 0.06)	0.675	0.379	0.102	0.09 (0.09, 0.07)
8715.5	LOC101928	LOC101928	0.26	0.20	0.019	0.285 -0.02 (0.08, 0.02)	0.675	0.379	0.102	0.09 (0.09, 0.07)
11140.56	COX1A1	COX1A1	0.26	0.20	0.024	0.283 -0.02 (0.07, 0.02)	0.677	0.381	0.104	0.09 (0.09, 0.07)
11846.4	CHST9	Carbohydrate	0.26	0.20	0.023	0.286 0.03 (0.02, 0.07)	0.677	0.382	0.104	0.09 (0.09, 0.07)
8715.5	ENK1	ENK1	0.26	0.20	0.020	0.286 0.03 (0.02, 0.07)	0.677	0.382	0.104	0.09 (0.09, 0.07)
14334.3	RCVRN	RECO	0.26	0.20	0.022	0.285 -0.02 (0.08, 0.02)	0.677	0.382	0.104	0.09 (0.09, 0.07)
18339.207	PSMB3	PSB3	0.26	0.20	0.019	0.286 0.02 (0.02, 0.06)	0.677	0.382	0.104	0.09 (0.09, 0.07)
18373.8	CEACAM6	CEACAM6	0.26	0.20	0.019	0.286 0.02 (0.02, 0.06)	0.677	0.382	0.104	0.09 (0.09, 0.07)
18933.4	TM64	TM64	0.26	0.20	0.019	0.286 -0.02 (0.08, 0.02)	0.677	0.382	0.104	0.09 (0.09, 0.07)
3324.51	LY9	LY9	0.26	0.20	0.018	0.285 -0.02 (0.08, 0.02)	0.677	0.382	0.104	0.09 (0.09, 0.07)
4831.4	SELL	Selectin	0.26	0.20	0.019	0.286 0.02 (0.02, 0.06)	0.677	0.382	0.104	0.09 (0.09, 0.07)
7945.10	SEMA6	Semaphorin	0.26	0.20	0.022	0.286 0.02 (0.02, 0.06)	0.677	0.382	0.104	0.09 (0.09, 0.07)
9256.78	NPTX1	NPTX1	0.26	0.20	0.021	0.285 -0.02 (0.08, 0.02)	0.677	0.382	0.104	0.09 (0.09, 0.07)
11444.49	PORLRF	PORLRF	0.26	0.20	0.019	0.285 -0.02 (0.08, 0.02)	0.677	0.382	0.104	0.09 (0.09, 0.07)
5663.18	PFV1	PFV1	0.26	0.20	0.021	0.287 -0.02 (0.08, 0.02)	0.678	0.383	0.104	0.09 (0.09, 0.07)
3652.1	ACT1	ACT1	0.26	0.20	0.019	0.288 0.02 (0.02, 0.06)	0.678	0.383	0.104	0.09 (0.09, 0.07)
13745.10	PKD2	PKD2	0.26	0.20	0.021	0.287 -0.02 (0.08, 0.02)	0.678	0.383	0.104	0.09 (0.09, 0.07)
17456.53	GOLM1	GOLM1	0.26	0.20	0.020	0.288 0.02 (0.02, 0.06)	0.678	0.383	0.104	0.09 (0.09, 0.07)
2637.77	MRG1	MRG1	0.26	0.20	0.020	0.287 0.02 (0.02, 0.06)	0.678	0.383	0.104	0.09 (0.09, 0.07)
4471.50	TM3	TM3	0.26	0.20	0.024	0.288 -0.02 (0.07, 0.02)	0.679	0.384	0.104	0.09 (0.09, 0.07)
5201.50	PDEA3	PDEA3	0.26	0.20	0.019	0.288 0.02 (0.02, 0.06)	0.679	0.384	0.104	0.09 (0.09, 0.07)
8506.54	TMED10	TMED10	0.26	0.20	0.019	0.288 0.02 (0.02, 0.06)	0.679	0.384	0.104	0.09 (0.09, 0.07)
9936.27	LNK1	LNK1	0.26	0.20	0.023	0.288 0.02 (0.02, 0.06)	0.679	0.384	0.104	0.09 (0.09, 0.07)
14135.3	RXRP1	RXRP1	0.26	0.20	0.019	0.289 0.02 (0.02, 0.06)	0.679	0.384	0.104</	

Table S5. Association of type 2 diabetes with Ferndal plasma protein.

SomaLogic Gene	CD320	Protein	nsnp	Inverse variance weighted				MR Egger				Weighted median				Weighted mode										
				b1w	se.b1w	pval.i1w	CI_low	CI_high	FOR_Iw	Q pval	begger	se.begger	pval.egger	CI_low	CI_high	b.mode	se.mode	CI_low	CI_high							
16303236	158	CD320	226	-0.021	0.021	0.310	-0.022	(-0.08, 0.02)	0.695	0.101	-0.045	0.443	0.296	(-0.13, 0.04)	0.001	0.532	-0.056	0.332	0.083	-0.068	(-0.12, 0.01)	-0.114	0.042	0.007	-0.11	(-0.20, -0.03)
6590_54	CB22B	CB22B	226	-0.019	0.019	0.311	-0.020	(-0.08, 0.02)	0.696	0.101	-0.045	0.443	0.296	(-0.13, 0.04)	0.001	0.532	-0.056	0.332	0.083	-0.068	(-0.12, 0.01)	-0.114	0.042	0.007	-0.11	(-0.20, -0.03)
10773_58	LEPRLP	PLM1	226	-0.019	0.019	0.311	-0.020	(-0.08, 0.02)	0.696	0.101	-0.045	0.443	0.296	(-0.13, 0.04)	0.001	0.532	-0.056	0.332	0.083	-0.068	(-0.12, 0.01)	-0.114	0.042	0.007	-0.11	(-0.20, -0.03)
6273_58	CD320	CD320	226	-0.019	0.019	0.311	-0.020	(-0.08, 0.02)	0.696	0.101	-0.045	0.443	0.296	(-0.13, 0.04)	0.001	0.532	-0.056	0.332	0.083	-0.068	(-0.12, 0.01)	-0.114	0.042	0.007	-0.11	(-0.20, -0.03)
12450_42	PMK1	PMK1	226	-0.019	0.019	0.311	-0.020	(-0.08, 0.02)	0.696	0.101	-0.045	0.443	0.296	(-0.13, 0.04)	0.001	0.532	-0.056	0.332	0.083	-0.068	(-0.12, 0.01)	-0.114	0.042	0.007	-0.11	(-0.20, -0.03)
12705_9	HERC1	HERC1	226	-0.019	0.019	0.311	-0.020	(-0.08, 0.02)	0.696	0.101	-0.045	0.443	0.296	(-0.13, 0.04)	0.001	0.532	-0.056	0.332	0.083	-0.068	(-0.12, 0.01)	-0.114	0.042	0.007	-0.11	(-0.20, -0.03)
5255_22	PDE4D	PDE4D	226	-0.020	0.020	0.312	-0.021	(-0.08, 0.02)	0.697	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
19814_8	TCM1	Hou1-2	226	-0.020	0.020	0.312	-0.021	(-0.08, 0.02)	0.697	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
9782_14	VASP	VASP	226	-0.019	0.019	0.312	-0.020	(-0.08, 0.02)	0.697	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
14132_21	HLLA2	HLLA2	226	-0.019	0.019	0.312	-0.020	(-0.08, 0.02)	0.697	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
10088_38	CS3	CS3	226	-0.019	0.019	0.312	-0.020	(-0.08, 0.02)	0.697	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
10772_21	CSMANGCAGT2		226	-0.019	0.019	0.312	-0.020	(-0.08, 0.02)	0.697	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
11530_37	HMB3	HMB3	226	-0.019	0.019	0.312	-0.020	(-0.08, 0.02)	0.697	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
11540_37	FOXC4	FOXC4	226	-0.019	0.019	0.312	-0.020	(-0.08, 0.02)	0.697	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
12838_28	DUSP15	DUSP15	226	-0.020	0.020	0.312	-0.021	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
13384_110H	FUN1B	FUN1B	226	-0.019	0.019	0.312	-0.020	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
13615_10	NCK2	NCK2	226	-0.019	0.019	0.312	-0.020	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
13621_31	AP2A2	AP2A2	226	-0.018	0.018	0.314	-0.020	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
13680_2	OC1	OC1	226	-0.018	0.018	0.314	-0.020	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
18166_4	RHOB	RHOB	226	-0.019	0.019	0.315	-0.020	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
18184_28	GMP5	GMP5	226	-0.019	0.019	0.315	-0.020	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
19175_27	FAM83B	FAM83B	226	-0.019	0.019	0.315	-0.020	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
3078_1	PIGF	PIGF	226	-0.019	0.019	0.315	-0.020	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
3903_49	SNX4	Sorting nexin 4	226	-0.018	0.018	0.315	-0.020	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
4650_34	LCK	LCK	226	-0.019	0.019	0.315	-0.020	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
4891_50	GCG	Gucyasein	226	-0.020	0.020	0.315	-0.021	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
5109_24	NRCAM	N-CAM	226	-0.022	0.022	0.315	-0.022	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
5204_20	CSNK2A1	CSK2A1	226	-0.020	0.020	0.315	-0.021	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
7875_86	PLEK	PLEK	226	-0.019	0.019	0.315	-0.020	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
8171_11	CSRP3	CSRP3	226	-0.019	0.019	0.315	-0.020	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
8234_8	TWIST1	TWIST1	226	-0.019	0.019	0.315	-0.020	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
9255_5	LITC7	LITC7	226	-0.019	0.019	0.315	-0.020	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
15509	NAGLU	NAGLU	226	-0.019	0.019	0.315	-0.020	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
10371_14	MGAT1	MGAT1	226	-0.019	0.019	0.315	-0.020	(-0.08, 0.02)	0.698	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
10847_1	SIGLEC15	SIG15	226	-0.020	0.020	0.317	-0.022	(-0.08, 0.02)	0.699	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
10874_2	BAE2	BAE2	226	-0.019	0.019	0.317	-0.021	(-0.08, 0.02)	0.699	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
8511_17	F19A4	F19A4	226	-0.019	0.019	0.317	-0.021	(-0.08, 0.02)	0.699	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
8274_74	STM7K	STM7K	226	-0.019	0.019	0.317	-0.021	(-0.08, 0.02)	0.699	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
8946_38	NR1H4	NR1H4	226	-0.019	0.019	0.317	-0.021	(-0.08, 0.02)	0.699	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
9838_4	SMAD1	SMAD1	226	-0.018	0.018	0.317	-0.021	(-0.08, 0.02)	0.699	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0.20, -0.03)
10916_44	PLA2R1	PLA2R1	226	-0.021	0.021	0.319	-0.022	(-0.08, 0.02)	0.699	0.102	-0.046	0.444	0.297	(-0.13, 0.04)	0.001	0.533	-0.057	0.333	0.084	-0.069	(-0.12, 0.01)	-0.115	0.043	0.008	-0.11	(-0

Table S5. Association of Type 2 diabetes with Ferndal plasma protein.

SomaLogE	Enzyme	rnp	b/w	Inverse variance weighted		MR Egger		Weighted median		Weighted mode													
				b/w	se/bw	pval/iv	CI_low	FOR_low	iv	bagger	segger	pval/egger	se.ed	pval/med	b.mode	se.mode	pval/mode	b.mode	se.mode	pval/mode			
4884_83	ESD	Enestrin D	226	0.017	0.19	0.384	0.02 (0.02, 0.05)	0.737	0.153	-0.015	0.40	0.769	-0.02 (0.09, 0.06)	0.002	0.365	0.003	0.43	0.849	0.271 (0.08, 0.10)	-0.008	0.424	0.848	-0.01 (0.09, 0.08)
6221_6	TPPRL1		226	0.017	0.19	0.384	0.02 (0.02, 0.05)	0.737	0.153	-0.015	0.40	0.769	-0.02 (0.09, 0.06)	0.002	0.365	0.003	0.43	0.849	0.271 (0.08, 0.10)	-0.008	0.424	0.848	-0.01 (0.09, 0.08)
17848_6	DRG1		226	0.016	0.18	0.384	0.02 (0.02, 0.05)	0.737	0.147	-0.018	0.036	0.630	-0.02 (0.09, 0.05)	0.002	0.293	-0.006	0.029	0.829	-0.01 (0.08, 0.05)	-0.013	0.040	0.743	-0.01 (0.09, 0.07)
8962_5	HDLR3	DRG3	226	0.020	0.023	0.384	0.02 (0.02, 0.06)	0.737	5.20E-05	0.034	0.046	0.488	0.03 (0.08, 0.12)	0.001	0.733	0.017	0.472	0.879	0.02 (0.07, 0.10)	0.021	0.041	0.818	0.02 (0.07, 0.10)
3813_3	PNL	407	226	0.017	0.19	0.385	0.02 (0.02, 0.05)	0.738	0.158	-0.015	0.036	0.630	-0.02 (0.09, 0.05)	0.002	0.293	-0.006	0.029	0.829	-0.01 (0.08, 0.05)	-0.013	0.040	0.743	-0.01 (0.09, 0.07)
8604_39	COL20A1	COXA1	226	-0.017	0.19	0.385	-0.02 (0.02, 0.02)	0.738	0.118	0.008	0.042	0.856	0.01 (-0.07, 0.09)	-0.002	-0.488	0.038	0.038	0.292	0.04 (-0.03, 0.11)	0.031	0.041	0.455	0.03 (-0.05, 0.10)
4477_32	CKL13	WPCF1	226	-0.017	0.19	0.385	-0.02 (0.02, 0.02)	0.738	0.106	-0.005	0.041	0.971	-0.01 (-0.09, 0.08)	-0.001	0.738	0.005	0.037	0.884	-0.01 (0.07, 0.08)	-0.009	0.048	0.859	-0.01 (0.09, 0.08)
9931_20	KRT1	Keratin-1	226	0.016	0.19	0.387	0.02 (0.02, 0.05)	0.741	0.158	-0.008	0.037	0.823	-0.01 (0.08, 0.07)	0.002	0.453	-0.007	0.038	0.855	-0.01 (0.08, 0.07)	-0.029	0.038	0.444	-0.03 (-0.10, 0.04)
19329_31	HRP3	HPK3	226	0.016	0.19	0.388	0.02 (0.02, 0.05)	0.741	0.141	0.033	0.040	0.409	0.03 (0.05, 0.11)	0.001	0.630	0.012	0.348	0.741	0.01 (0.06, 0.09)	0.016	0.039	0.677	0.02 (0.06, 0.09)
2730_54	PP3P	NAP-2	226	0.016	0.19	0.388	0.02 (0.02, 0.05)	0.741	0.225	0.019	0.042	0.268	0.03 (0.06, 0.08)	0.001	0.403	0.017	0.348	0.741	0.01 (0.06, 0.09)	0.016	0.039	0.677	0.02 (0.06, 0.09)
3284_75	BMN	BGN	226	-0.017	0.20	0.388	-0.02 (0.02, 0.02)	0.741	0.039	-0.016	0.040	0.685	-0.02 (0.10, 0.06)	0.000	0.980	-0.012	0.037	0.742	-0.01 (0.08, 0.06)	-0.026	0.039	0.504	-0.03 (-0.10, 0.05)
8424_289	CTNNA1	C-actinin	226	0.017	0.19	0.387	0.02 (0.02, 0.05)	0.741	0.783	-0.034	0.039	0.362	-0.03 (0.11, 0.04)	0.003	0.134	0.000	0.040	0.992	-0.18 (-0.04, 0.00)	0.007	0.041	0.860	-0.01 (0.07, 0.09)
16367_74	CARD17	CARD17	226	0.017	0.19	0.389	0.02 (0.02, 0.05)	0.743	0.865	-0.054	0.038	0.101	-0.07 (0.13, 0.02)	0.004	0.035	0.008	0.040	0.835	-0.01 (0.08, 0.07)	-0.017	0.046	0.818	-0.02 (0.10, 0.06)
7082_2	B3GNT6	B3GNT6	226	0.019	0.22	0.389	0.02 (0.02, 0.06)	0.743	0.027	-0.033	0.045	0.461	-0.03 (0.12, 0.05)	0.003	0.181	0.022	0.042	0.992	0.02 (0.06, 0.10)	0.010	0.041	0.811	0.01 (0.07, 0.09)
8470_213	RNASEH1	RNASEH1	226	-0.018	0.21	0.390	-0.02 (0.02, 0.02)	0.743	0.027	-0.039	0.042	0.362	-0.03 (0.12, 0.05)	0.001	0.557	0.006	0.031	0.775	-0.01 (0.08, 0.07)	-0.008	0.041	0.825	-0.10 (0.18, 0.11)
8014_39	MANEA		226	-0.018	0.21	0.390	-0.02 (0.02, 0.02)	0.744	0.037	-0.046	0.042	0.268	0.05 (0.10, 0.04)	0.004	0.077	0.011	0.039	0.911	0.03 (0.08, 0.07)	0.008	0.041	0.818	0.01 (0.07, 0.09)
12493_42	OTUB2	OTUB2	226	0.016	0.18	0.390	0.02 (0.02, 0.05)	0.744	0.144	-0.010	0.039	0.778	-0.01 (0.09, 0.07)	0.002	0.446	0.015	0.033	0.839	-0.02 (0.08, 0.05)	-0.023	0.040	0.569	-0.02 (-0.10, 0.06)
10704_91	LIMP	LRMP2	226	0.015	0.18	0.392	0.02 (0.02, 0.05)	0.744	0.368	0.050	0.029	0.267	0.03 (0.05, 0.11)	-0.002	0.338	0.052	0.039	0.184	0.02 (0.02, 0.13)	0.002	0.042	0.569	-0.02 (-0.10, 0.06)
10708_3	GNRH2	GNH2	226	-0.017	0.19	0.392	-0.02 (0.02, 0.02)	0.744	0.685	-0.039	0.039	0.319	-0.04 (0.11, 0.04)	0.001	0.510	0.009	0.035	0.787	0.01 (0.06, 0.08)	0.015	0.041	0.708	0.02 (0.06, 0.10)
11103_24	HSPB1	HSP 27	226	0.016	0.19	0.393	0.02 (0.02, 0.05)	0.744	0.422	0.025	0.039	0.526	0.02 (0.05, 0.10)	-0.001	0.804	0.001	0.032	0.862	-0.70 (-0.04, 0.00)	0.004	0.039	0.925	3.70 (-0.07, 0.08)
11405_150	CARD9	CARD9	226	0.016	0.19	0.393	0.02 (0.02, 0.05)	0.744	0.049	-0.066	0.041	0.111	-0.07 (0.15, 0.01)	0.005	0.020	0.068	0.033	0.868	0.01 (0.06, 0.07)	-0.007	0.045	0.845	0.02 (-0.10, 0.06)
11592_1	ELAVL1	ELAV1	226	0.016	0.18	0.392	0.02 (0.02, 0.05)	0.744	0.999	-0.003	0.037	0.941	-2.76 (-0.08, 0.07)	0.001	0.566	-0.013	0.031	0.662	-0.01 (0.07, 0.05)	-0.027	0.040	0.505	-0.03 (-0.10, 0.05)
13405_61	SPFNK2	ISK2	226	-0.016	0.19	0.393	-0.02 (0.02, 0.02)	0.744	0.425	0.001	0.038	0.978	0.06 (0.07, 0.08)	0.000	0.606	0.010	0.040	0.796	-0.01 (0.08, 0.07)	-0.045	0.038	0.241	-0.04 (-0.12, 0.03)
13554_9	CNPNK1	CNPK1	226	0.015	0.18	0.392	0.02 (0.02, 0.05)	0.744	0.877	0.010	0.037	0.793	0.01 (-0.08, 0.08)	0.000	0.864	0.000	0.039	0.977	-0.87 (-0.04, 0.00)	-0.007	0.037	0.844	-0.01 (0.08, 0.07)
17769_28	PCNP	PCNP	226	0.016	0.18	0.392	0.02 (0.02, 0.05)	0.744	0.507	0.024	0.036	0.512	-0.02 (0.05, 0.10)	-0.001	0.797	-0.032	0.032	0.320	-0.03 (0.08, 0.03)	-0.029	0.037	0.441	-0.03 (-0.10, 0.04)
18237_29	NR3P	NR3P	226	-0.017	0.19	0.392	-0.02 (0.02, 0.02)	0.744	0.444	-0.003	0.039	0.944	-2.76 (-0.08, 0.07)	0.001	0.686	0.012	0.034	0.720	0.01 (0.05, 0.08)	-0.016	0.038	0.671	-0.02 (0.09, 0.06)
18392_19	MAT2B	MAT2B	226	0.016	0.19	0.391	0.02 (0.02, 0.05)	0.744	0.901	0.025	0.042	0.562	0.03 (0.08, 0.11)	0.000	0.837	0.011	0.035	0.765	-0.01 (0.08, 0.08)	0.002	0.040	0.642	-0.03 (0.08, 0.08)
19190_4	UBE2L6	UBE2L6	226	0.016	0.19	0.391	0.02 (0.02, 0.05)	0.744	0.884	-0.002	0.038	0.953	-2.22 (-0.08, 0.07)	0.001	0.581	0.012	0.038	0.754	0.01 (0.06, 0.09)	0.026	0.038	0.472	0.03 (0.04, 0.10)
3392_68	AKT3	PKB alpha	226	-0.016	0.19	0.393	-0.02 (0.02, 0.02)	0.744	0.905	-0.003	0.038	0.930	-3.36 (-0.07, 0.08)	0.000	0.455	-0.029	0.032	0.377	-0.03 (0.08, 0.03)	-0.039	0.038	0.385	-0.04 (-0.11, 0.04)
3432_21	EPHA3	EPHA3	226	-0.016	0.19	0.393	-0.02 (0.02, 0.02)	0.744	0.452	0.021	0.039	0.944	-2.22 (-0.08, 0.07)	0.000	0.455	-0.029	0.032	0.377	-0.03 (0.08, 0.03)	-0.039	0.038	0.385	-0.04 (-0.11, 0.04)
4481_34	CAA	CAA	226	-0.017	0.20	0.393	-0.02 (0.02, 0.02)	0.744	0.908	-0.038	0.042	0.382	-0.04 (0.12, 0.04)	0.001	0.555	-0.019	0.035	0.580	-0.02 (0.08, 0.05)	-0.030	0.040	0.462	-0.03 (-0.11, 0.05)
5246_6	PI3K2	gPI3K	226	-0.021	0.20	0.391	-0.02 (0.02, 0.02)	0.744	0.955	-0.058	0.039	0.162	-0.06 (0.13, 0.02)	0.002	0.261	-0.035	0.039	0.380	-0.03 (0.11, 0.04)	-0.047	0.048	0.222	-0.06 (-0.12, 0.03)
8440_31	MFAP5	MFAP5	226	-0.016	0.19	0.393	0.02 (0.02, 0.05)	0.744	0.903	0.041	0.039	0.944	-2.22 (-0.08, 0.07)	0.000	0.455	-0.029	0.032	0.377	-0.03 (0.08, 0.03)	-0.039	0.038	0.385	-0.04 (-0.11, 0.04)
9754_33	HDAC3	HDAC3	226	-0.017	0.19	0.390	-0.02 (0.02, 0.02)	0.744	0.264	-0.021	0.040	0.598	-0.02 (0.10, 0.06)	0.000	0.896	0.000	0.041	0.995	2.39 (0.04, 0.00)	0.000	0.041	0.887	-0.01 (0.07, 0.09)
11669_39	SLOC5A1	SOSA1	226	-0.016	0.19	0.393	0.02 (0.02, 0.02)	0.744	0.672	0.000	0.038	0.999	3.06 (0.05, 0.08)	0.001	0.625	0.011	0.033	0.743	0.01 (0.05, 0.08)	0.018	0.041	0.674	0.02 (0.06, 0.10)
11669_39	MAPK11	MK11	226	0.018	0.22	0.393	0.02 (0.02, 0.06)	0.744	0.006	0.065	0.043	0.135	0.07 (0.02, 0.15)	-0.003	0.217	0.074	0.037	0.048	0.07 (0.39, 0.04)	0.117	0.074	0.042	0.01 (0.27, 0.03)
10539_30	CD92E	CD92E	226	-0.017	0.19	0.392	-0.02 (0.02, 0.02)	0.744	0.207	-0.007	0.039	0.687	-0.01 (0.07, 0.08)	0.000	0.606	0.010	0.040	0.796	-0.01 (0.08, 0.07)	-0.045	0.038	0.241	-0.04 (-0.12, 0.03)
14005_2	CHD7	CHD7	226	-0.019	0.22	0.394	-0.02 (0.02, 0.02)	0.744	0.004	-0.034	0.044	0.444	-0.03 (0.12, 0.05)	0.001	0.623	-0.058	0.039	0.137	-0.06 (0.13, 0.02)	-0.033	0.042	0.228	-0.05 (-0.13, 0.03)
14100_63	C10C	C10C	226	-0.016	0.19	0.394	-0.02 (0.02, 0.02)	0.744	0.440	0.011	0.039	0.783	0.01 (0.07, 0.09)	-0.002	0.423	-0.045	0.038	0.236	-0.05 (0.12, 0.03)	-0.035	0.043	0.419	-0.03 (-0.12, 0.05)
16588_10	HSP9A	HSP9A	226	0.016	0.19	0.392	0.02 (0.02, 0.05)	0.744	0.262	-0.068	0.040	0.189	-0.07 (0.15, 0.01)	0.004	0.423	-0.045	0.038	0.236	-0.05 (0.12, 0.03)	-0.035	0.043	0.419	-0.03 (-0.12, 0.05)
3505_5	LA1	Lymphotixin	226	-0.018	0.19	0.393	-0.02 (0.02, 0.02)	0.744	0.038	-0.017	0.038	0.647	-0.02 (0.09, 0.09)	0.000	0.968	-0.039	0.037	0.282	-0.04 (0.11, 0.03)	-0.039	0.038	0.307	-0.04 (-0.11, 0.04)
8357_83	CEL3A	ELAB3	226	0.017	0.19	0.394	0.02 (0.02, 0.05)	0.744	0.808	0.018	0.039	0.643	0.02 (0.06, 0.09)	0.000	0.968	-0.039	0.037	0.282	-0.04 (0.11, 0.03)	-0.039	0.038	0.307	-0.04 (-0.11, 0.04)
7790_21	LF	LF	226	0.015	0.18	0.392	0.02 (0.02, 0.05)	0.744	0.910	0.012	0.039	0.823	0.07 (0.05, 0.15)	0.000	0.972	0.009	0.039	0.847	0.03 (0.04, 0.11)	0.012	0.040	0.844	0.03 (0.05, 0.13)

Table S5. Association of type 2 diabetes with Ferland plasma protein.

SomaLogicGene	Protein	rsnp	b/w		pval/w		CI/w		MR Egger		Weighted median		Weighted mode					
			beta	se	pval	ci_low	ci_high	beta	se	beta	se	beta	se					
17384_10_HFKM	KFPF	226	-0.013	0.018	0.471	-0.02 (0.02, 0.05)	0.792	0.005	-0.025	0.038	0.121	-0.02 (0.10, 0.05)	0.010	0.037	0.779	-0.01 (0.08, 0.06)		
11342_58_FLDC2	FLDC2	226	-0.013	0.018	0.471	-0.02 (0.02, 0.05)	0.792	0.005	-0.025	0.038	0.121	-0.02 (0.10, 0.05)	0.010	0.037	0.779	-0.01 (0.08, 0.06)		
15455_40_ADM15	ADM15	226	-0.014	0.019	0.472	-0.01 (0.05, 0.02)	0.793	0.007	0.031	0.042	0.454	0.03 (0.05, 0.11)	-0.003	0.213	0.030	0.903	0.31 (0.07, 0.07)	
11400_25_TEN3	TEN3	226	-0.014	0.020	0.472	-0.01 (0.05, 0.02)	0.793	0.009	-0.030	0.049	0.454	-0.03 (0.11, 0.05)	-0.001	0.651	0.022	0.909	0.67 (-0.02, 0.07)	
5762_35_SPAH1B	SPAH1B	226	-0.015	0.020	0.472	-0.01 (0.05, 0.02)	0.793	0.007	0.031	0.042	0.454	0.03 (0.05, 0.11)	-0.003	0.213	0.030	0.903	0.31 (0.07, 0.07)	
6439_9_CPLZ	CPLZ	226	-0.014	0.019	0.472	-0.01 (0.05, 0.02)	0.793	0.008	-0.060	0.042	0.152	-0.06 (0.14, 0.02)	-0.003	0.200	0.090	0.034	0.009	-0.09 (-0.16, -0.02)
7193_14_SFRZ	SFRZ	226	-0.014	0.019	0.472	-0.01 (0.05, 0.02)	0.793	0.013	0.035	0.038	0.357	0.03 (0.04, 0.11)	-0.003	0.142	0.107	0.032	0.599	0.02 (-0.05, 0.08)
8692_10_STEAS3	STEAS3	226	-0.014	0.019	0.472	-0.01 (0.05, 0.02)	0.793	0.013	0.035	0.038	0.357	0.03 (0.04, 0.11)	-0.003	0.142	0.107	0.032	0.599	0.02 (-0.05, 0.08)
10001_7_VRF1	c-Raf	226	-0.013	0.018	0.474	-0.01 (0.05, 0.02)	0.793	0.014	0.035	0.038	0.357	0.03 (0.04, 0.11)	-0.003	0.142	0.107	0.032	0.599	0.02 (-0.05, 0.08)
11176_21_SAF1	SVEP1	226	-0.016	0.022	0.473	-0.02 (0.05, 0.02)	0.793	0.014	-0.022	0.044	0.614	-0.02 (0.11, 0.05)	-0.003	0.983	0.040	0.036	0.920	-3.66 (0.03, 0.07)
11881_8_AGR1	NURF	226	-0.016	0.022	0.473	-0.02 (0.05, 0.02)	0.793	0.014	-0.022	0.044	0.614	-0.02 (0.11, 0.05)	-0.003	0.983	0.040	0.036	0.920	-3.66 (0.03, 0.07)
12540_25_RHRG	RHOG	226	-0.013	0.018	0.474	-0.01 (0.05, 0.02)	0.793	0.013	-0.030	0.038	0.428	-0.03 (0.10, 0.04)	-0.003	0.191	0.133	0.032	0.694	-0.01 (-0.08, 0.05)
18163_3_LDRAP1	ARH1	226	-0.013	0.019	0.473	-0.01 (0.05, 0.02)	0.793	0.013	-0.030	0.038	0.428	-0.03 (0.10, 0.04)	-0.003	0.191	0.133	0.032	0.694	-0.01 (-0.08, 0.05)
8701_81_CLEC3B	Tetraspanin	226	-0.013	0.019	0.473	-0.01 (0.05, 0.02)	0.793	0.013	-0.030	0.038	0.428	-0.03 (0.10, 0.04)	-0.003	0.191	0.133	0.032	0.694	-0.01 (-0.08, 0.05)
5731_1_SPNK6	SKG	226	-0.015	0.021	0.474	-0.02 (0.05, 0.02)	0.793	0.013	-0.030	0.038	0.428	-0.03 (0.10, 0.04)	-0.003	0.191	0.133	0.032	0.694	-0.01 (-0.08, 0.05)
9773_21_PGG1	PGM1	226	-0.015	0.021	0.474	-0.02 (0.05, 0.02)	0.793	0.013	-0.030	0.038	0.428	-0.03 (0.10, 0.04)	-0.003	0.191	0.133	0.032	0.694	-0.01 (-0.08, 0.05)
1648_9_MYBPC1	MYBPC1	226	-0.015	0.021	0.474	-0.02 (0.05, 0.02)	0.793	0.013	-0.030	0.038	0.428	-0.03 (0.10, 0.04)	-0.003	0.191	0.133	0.032	0.694	-0.01 (-0.08, 0.05)
8556_5_ENPP5	ENPP5	226	-0.014	0.020	0.474	-0.01 (0.05, 0.02)	0.793	0.013	-0.030	0.038	0.428	-0.03 (0.10, 0.04)	-0.003	0.191	0.133	0.032	0.694	-0.01 (-0.08, 0.05)
2614_28_EFNAA	Efnv4a1b	226	-0.013	0.018	0.475	-0.01 (0.05, 0.02)	0.793	0.013	-0.030	0.038	0.428	-0.03 (0.10, 0.04)	-0.003	0.191	0.133	0.032	0.694	-0.01 (-0.08, 0.05)
3148_49_CXCL2	Cxcl2	226	-0.014	0.020	0.475	-0.01 (0.05, 0.02)	0.793	0.013	-0.030	0.038	0.428	-0.03 (0.10, 0.04)	-0.003	0.191	0.133	0.032	0.694	-0.01 (-0.08, 0.05)
3285_23_C1R	C1r	226	-0.015	0.021	0.475	-0.02 (0.05, 0.02)	0.794	0.014	-0.008	0.043	0.858	-0.01 (0.09, 0.08)	-0.003	0.843	0.022	0.442	0.597	-0.02 (-0.10, 0.06)
10452_2_AGA	AGA	226	-0.013	0.018	0.475	-0.01 (0.05, 0.02)	0.794	0.013	-0.030	0.038	0.428	-0.03 (0.10, 0.04)	-0.003	0.191	0.133	0.032	0.694	-0.01 (-0.08, 0.05)
12692_56_DOT1L	DOT1L	226	-0.014	0.020	0.476	-0.01 (0.05, 0.02)	0.795	0.014	-0.008	0.043	0.858	-0.01 (0.09, 0.08)	-0.003	0.843	0.022	0.442	0.597	-0.02 (-0.10, 0.06)
11187_11_CLEC2A	CL2A	226	-0.014	0.019	0.477	-0.01 (0.05, 0.02)	0.795	0.013	-0.001	0.039	0.989	0.28 (-0.04, 0.08)	-0.001	0.667	0.007	0.441	0.857	-0.01 (-0.08, 0.07)
13392_12_NSF	NSF	226	-0.014	0.019	0.477	-0.01 (0.05, 0.02)	0.795	0.013	-0.001	0.039	0.989	0.28 (-0.04, 0.08)	-0.001	0.667	0.007	0.441	0.857	-0.01 (-0.08, 0.07)
8807_13_SNK1	SNK1	226	-0.014	0.019	0.477	-0.01 (0.05, 0.02)	0.795	0.013	-0.001	0.039	0.989	0.28 (-0.04, 0.08)	-0.001	0.667	0.007	0.441	0.857	-0.01 (-0.08, 0.07)
3291_30_FICER2	CD33	226	-0.015	0.022	0.477	-0.02 (0.05, 0.03)	0.795	0.009	-0.050	0.044	0.251	-0.05 (0.14, 0.04)	-0.002	0.358	0.029	0.441	0.479	-0.03 (-0.11, 0.05)
10754_113_PRR20	PRR20	226	-0.015	0.022	0.477	-0.02 (0.05, 0.03)	0.795	0.009	-0.050	0.044	0.251	-0.05 (0.14, 0.04)	-0.002	0.358	0.029	0.441	0.479	-0.03 (-0.11, 0.05)
11196_31_COL6A3	Collagen a3	226	-0.015	0.022	0.481	-0.02 (0.05, 0.03)	0.795	0.011	-0.073	0.044	0.094	-0.07 (0.16, 0.01)	-0.004	0.127	0.024	0.441	0.553	-0.02 (-0.10, 0.06)
12641_3_INPBP8	RPE2	226	-0.013	0.018	0.481	-0.01 (0.05, 0.02)	0.795	0.011	-0.073	0.044	0.094	-0.07 (0.16, 0.01)	-0.004	0.127	0.024	0.441	0.553	-0.02 (-0.10, 0.06)
12713_36R6R19	R6R19	226	-0.013	0.018	0.481	-0.01 (0.05, 0.02)	0.795	0.011	-0.073	0.044	0.094	-0.07 (0.16, 0.01)	-0.004	0.127	0.024	0.441	0.553	-0.02 (-0.10, 0.06)
12735_39_CSD2E1	CSD2E1	226	-0.013	0.018	0.482	-0.01 (0.05, 0.02)	0.795	0.011	-0.073	0.044	0.094	-0.07 (0.16, 0.01)	-0.004	0.127	0.024	0.441	0.553	-0.02 (-0.10, 0.06)
13671_40_ELANE	Elastase	226	-0.014	0.019	0.481	-0.01 (0.05, 0.02)	0.795	0.011	-0.073	0.044	0.094	-0.07 (0.16, 0.01)	-0.004	0.127	0.024	0.441	0.553	-0.02 (-0.10, 0.06)
13726_19_ERP29	ERP29	226	-0.014	0.019	0.481	-0.01 (0.05, 0.02)	0.795	0.011	-0.073	0.044	0.094	-0.07 (0.16, 0.01)	-0.004	0.127	0.024	0.441	0.553	-0.02 (-0.10, 0.06)
14021_81_MED4	MED4	226	-0.014	0.020	0.479	-0.01 (0.05, 0.02)	0.795	0.014	-0.004	0.039	0.921	3.96 (-0.07, 0.08)	-0.001	0.604	0.017	0.039	0.672	-0.02 (-0.08, 0.06)
14037_6_EB56	EB56	226	-0.014	0.020	0.479	-0.01 (0.05, 0.02)	0.795	0.014	-0.004	0.039	0.921	3.96 (-0.07, 0.08)	-0.001	0.604	0.017	0.039	0.672	-0.02 (-0.08, 0.06)
14324_56_SMC3	CSPG6	226	-0.014	0.020	0.479	-0.01 (0.05, 0.02)	0.795	0.014	-0.004	0.039	0.921	3.96 (-0.07, 0.08)	-0.001	0.604	0.017	0.039	0.672	-0.02 (-0.08, 0.06)
16394_6_LGR4	LGR4	226	-0.014	0.019	0.480	-0.01 (0.05, 0.02)	0.795	0.011	-0.002	0.039	0.920	0.02 (0.10, 0.06)	-0.003	0.933	0.027	0.034	0.431	-0.03 (-0.09, 0.04)
16110_3_GDI1	GDI1	226	-0.013	0.018	0.479	-0.01 (0.05, 0.02)	0.795	0.011	-0.002	0.039	0.920	0.02 (0.10, 0.06)	-0.003	0.933	0.027	0.034	0.431	-0.03 (-0.09, 0.04)
16865_02_TAF15	RBPV56	226	-0.013	0.018	0.478	-0.01 (0.05, 0.02)	0.795	0.011	-0.002	0.039	0.920	0.02 (0.10, 0.06)	-0.003	0.933	0.027	0.034	0.431	-0.03 (-0.09, 0.04)
18174_79_PDCD8P1	PDCD8	226	-0.012	0.017	0.481	-0.01 (0.05, 0.02)	0.795	0.011	-0.002	0.039	0.920	0.02 (0.10, 0.06)	-0.003	0.933	0.027	0.034	0.431	-0.03 (-0.09, 0.04)
18262_219_ACAD11	ACAD11	226	-0.013	0.019	0.479	-0.01 (0.05, 0.02)	0.795	0.011	-0.002	0.039	0.920	0.02 (0.10, 0.06)	-0.003	0.933	0.027	0.034	0.431	-0.03 (-0.09, 0.04)
2966_55_L1ER1A	SCGF-beta	226	-0.015	0.021	0.481	-0.01 (0.05, 0.02)	0.795	0.011	-0.002	0.039	0.920	0.02 (0.10, 0.06)	-0.003	0.933	0.027	0.034	0.431	-0.03 (-0.09, 0.04)
2993_1_CLEP1	L1R-Br	226	-0.013	0.019	0.482	-0.01 (0.05, 0.02)	0.795	0.011	-0.002	0.039	0.920	0.02 (0.10, 0.06)	-0.003	0.933	0.027	0.034	0.431	-0.03 (-0.09, 0.04)
3067_07_CDFP	CDFP	226	-0.013	0.019	0.482	-0.01 (0.05, 0.02)	0.795	0.011	-0.002	0.039	0.920	0.02 (0.10, 0.06)	-0.003	0.933	0.027	0.034	0.431	-0.03 (-0.09, 0.04)
3647_49_TLR4	TLR4-AM2-2	226	-0.015	0.021	0.480	-0.01 (0.05, 0.02)	0.795	0.011	-0.002	0.039	0.920	0.02 (0.10, 0.06)	-0.003	0.933	0.027	0.034	0.431	-0.03 (-0.09, 0.04)
5067_5_L2R2A	L2R2P	226	-0.014	0.020	0.481	-0.01 (0.05, 0.02)	0.795	0.011	-0.002	0.039	0.920	0.02 (0.10, 0.06)	-0.003	0.933	0.027	0.034	0.431	-0.03 (-0.09, 0.04)
6562_13_VASN	VASN	226	-0.014	0.020	0.481	-0.01 (0.05, 0.02)	0.795	0.011	-0.002	0.039	0.920	0.02 (0.10, 0.06)	-0.003	0.933	0.027	0.034	0.431	-0.03 (-0.09, 0.04)
6739_75_KRTAP4	KTAP4	226	-0.014	0.020	0.481	-0.01 (0.05, 0.02)	0.795	0.011	-0.002	0.039	0.920	0.02 (0.10, 0.06)	-0.003	0.933	0.027	0.034	0.431	-0.03 (-0.09, 0.04)
7148_42_MLXN1																		

Table S5. Association of type 2 diabetes with Finland plasma protein.

Accession	Protein	rnp	Inverse variance weighted		MR Egger		Weighted median		Weighted mode													
			b/w	se/w	pval/iv	CI/w	FOR_ZW	Q1	b/egger	se/egger	pval/egger	CI/egger	egger	inter	se/median	pval/median	b/mode	se/mode	pval/mode	CI/mode		
14074_2	SH2C	SH2C	0.23	0.020	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
14519_8	ZNF252	ZNF252	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
16046_12	GRAP2	GRAP2	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
2874_24	RPS27A	Ubltin1	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
3321_2	SLA	SLA	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
3342_76	ABL2	ABL2	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
3381_24	LYN	LYN	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
4430_44	COL1E1	Col1e1	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
5230_99	HMGCR	HMGCR	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
5467_15	HSP90AB1	HSP90	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
7695_108	MRAP	MRAP	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
8378_3	LDC1	LDC1	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
8426_102	NMI	NMI	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
8450_36	ACYP1	PCAP3P	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
8649_13	APEX1	APEX1	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
8673_75	ESRRB	Erbp1	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
8684_70	PCDH8	PCDH8	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
8951_36	FXR1	FXR1	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
9203_25	RFXC	RFXC	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
9703_74	MATN4	MATN4	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
9711_40	JPH4	JPH4	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
9823_2	FBP2	FBP2	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
19150_20	PRPS2P	KPR2	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
13790_43	HDLBP	VIGLN	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
13240_170	SHANK1	SHANK1	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
2796_52	FGA	Fibrogene	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
9628_98	LDC1	LDC1	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
11571_75	KLRK1	KLRK2	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
7038_45	STR3A4	SIAD	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
11273_176	IGTST2B	GSTT2	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
11470_9	RELB	RELB	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
11550_94	BCAP29	BAP29	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
16247_7	PN1	PN1	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
19135_5	NLSCL	CYBB	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
8247_9	SIRPB1	SIRPB1	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
8535_102	NTSCL	NTSCL	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
8536_102	DNMKN	Dermokine	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
9802_27	PLML2	PLML2	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
15335_118	FABP2	FABP2	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
16090_99	NID2	NID2	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
16875_13	MAOGB1	MGN2	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
16897_8	MIR45	MIR45	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
3872_2	TPT1	TCTP	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
10705_14	STGALNA5	SIATC	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
14209_28	APBB1	APBB1	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
12936_38	RLBP1	RLBP1	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
19367_34	DCI	D3D2	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
8609_25	CAV3	CAV3	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
5629_58	KLRK1	KLRK2A	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
9501_4	PRRP6	PRRP6	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
2848_6	PLK3	DK	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0.037
12433_8	ARL11	ARL11	0.23	0.012	0.518	0.017	0.035	0.815	0.662	0.16	0.039	0.022	-0.06	0.09	0.924	0.004	0.339	0.917	-4.55e-03	0.008	0.014	0

Table S5. Association of type 2 diabetes with Ferland plasma protein.

SomaLogIC gene	Protein	tsp	Inverse variance weighted				MR Egger				Weighted median				Weighted mode				
			b1w	se1w	b2w	se2w	b1w	se1w	b2w	se2w	b1w	se1w	b2w	se2w	b1w	se1w	b2w	se2w	
12827.37	RG53	RG53	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
13330.10	USO1		0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
13890.10	pyruvate car		0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
13999.10	SH3B1	SH3B1	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
17747.45	TRAF1	TRAF1	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
2741.22	SIGLEC6	Siglec-6	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
3844.24	NACA	NACA	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
4654.60	MAPT	MAP2	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
9757.29	ENAH	ENAH	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
13685.35	PP2R2A	PP2A, subunit	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
14684.17	CANX2	CANX	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
16828.8	COL6A1	Collagen a1	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
3172.28	ARSB	ARSB	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
5317.33	HTRA2	HTRA2	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
6285.71	MLEC	KO152	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
10700.10	RSF11	RSF11	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
14070.56	ITSR		0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
14124.6	EFNA2	Ephrin-A2	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
17916.22	SUCY1	SUCY1	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
15686.49	INHBC		0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
12746.4	CYTH4	CYTH4	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
2911.27	MDK	SKIVIN	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
4981.6	DSC3	DSC3	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
5100.53	SCARB2	LAMP II	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
6632.42	ITGAS	ITGA8	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
13822.16	PPP2R2A	ZAS2	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
14158.17	ANXAS	Annexin V	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
2652.15	RFP1	RFP	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
4413.3	SLP1	SLP1	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
10722.13	SLY1	RSK9K	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
17728.61	CHMP2	CHMP2A	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
4673.13	L6	L6	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
10723.02	SETD2	SETD2	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
6020.52	UTS2	Utriosin-1b	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
15503.29	LFYF2	Leu-4	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
17520.170	MLF1	MLF1	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
8043.153	COMP	COMP	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
13688.30	PSMD4	PSMD4	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
4127.15	CS	CS	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
5272.55	SHC3	SHC3	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
12975.8	HMBG3	HMBG3	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
16188.12	CATM	CATM	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
13485.48	HCAR2	HCAR2	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
13322.25	CHEP1R	NEPR1	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
15482.98	CO3A	CO3A	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
16584.44	FAM	FAM1	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
2794.60	SOD1	SOD1	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
5014.49	NCK1	NCK1	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
5070.76	TNFRSF8	DR3	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
5070.76	TNFRSF8	DR3	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
5070.76	TNFRSF8	DR3	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
5070.76	TNFRSF8	DR3	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
5070.76	TNFRSF8	DR3	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
5070.76	TNFRSF8	DR3	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
5070.76	TNFRSF8	DR3	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
5070.76	TNFRSF8	DR3	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
5070.76	TNFRSF8	DR3	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
5070.76	TNFRSF8	DR3	0.20	0.10	0.20	0.10	0.01	0.03	0.05	0.83	0.67	0.01	0.03	0.01	0.03	0.01	0.03	0.01	0.03
5070.7																			

Table S5. Association of type 2 diabetes with Ferland plasma protein.

SomaLogic	Protein	Enzyme	rnp	b/w	Inverse variance weighted				MR Egger				Weighted median				Weighted mode						
					se	se,2w	pval,1w	CI,1w	FOR,2w	Q	pval	se,2w	pval,1w	CI,1w	se	pval	se,2w	pval,1w	CI,1w	se,mode	pval,mode	CI,mode	
13726_4	CD80	B7	226	-0.009	0.020	0.655	0.01 (-0.03, 0.05)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
13337_75	CAND1	CAND1	226	-0.009	0.020	0.655	0.01 (-0.03, 0.05)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
15805_1	RXN1	Keratin-16	226	-0.009	0.020	0.655	0.01 (-0.03, 0.05)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
18398_5	FXR1	Farnesyl transferase-1	226	-0.009	0.020	0.655	0.01 (-0.03, 0.05)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
16504_22	DTYRK	Protein tyrosine kinase	226	-0.009	0.020	0.655	0.01 (-0.03, 0.05)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
2682_58	HSP40	HSP60	226	-0.009	0.020	0.655	0.01 (-0.03, 0.05)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
3024_1	GFP1	GFP	226	-0.009	0.020	0.655	0.01 (-0.03, 0.05)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
6082_51	L1EARL1	L1EARL1	226	-0.009	0.020	0.655	0.01 (-0.03, 0.05)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
6361_49	PTFR3	PTFR3	226	-0.009	0.020	0.655	0.01 (-0.03, 0.05)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
6997_32	RAB2B	RAB2B	226	-0.011	0.024	0.653	0.01 (-0.03, 0.04)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
6957_19	ADRM1	ADRM1	226	-0.009	0.020	0.655	0.01 (-0.03, 0.05)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
8974_28	KCNMB2	p15 ^{INK4b}	226	-0.009	0.020	0.655	0.01 (-0.03, 0.05)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
11662_1	IDCC3C	IDCC3C	226	-0.009	0.020	0.655	0.01 (-0.03, 0.05)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
16905_5	PDSEA	PDSEA	226	-0.009	0.020	0.655	0.01 (-0.03, 0.05)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
8878_48	YTHDC1	YTHDC1	226	-0.009	0.020	0.655	0.01 (-0.03, 0.05)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
9116_1	PSD2	PSD2	226	-0.009	0.020	0.655	0.01 (-0.03, 0.05)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
10202_14	KRDL5A	KRDL5A	226	-0.009	0.020	0.655	0.01 (-0.03, 0.05)	0.878	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
17364_8	SNRR2B	SNRR2B	226	-0.008	0.018	0.657	0.01 (-0.03, 0.04)	0.879	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
18202_14	SRH1	SRH1	226	-0.008	0.018	0.657	0.01 (-0.03, 0.04)	0.879	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
19169_38	FIBP	FIBP	226	-0.008	0.018	0.657	0.01 (-0.03, 0.04)	0.879	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
3630_27	CAZM3	Neurin-like 1	226	-0.008	0.018	0.657	0.01 (-0.03, 0.04)	0.879	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
8670_38	NPM1	NPM1	226	-0.008	0.018	0.657	0.01 (-0.03, 0.04)	0.879	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
9753_17	EZR	EZR	226	-0.008	0.018	0.657	0.01 (-0.03, 0.04)	0.879	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
7879_12	CYP3A4	Cytochrome P450 3A4	226	-0.009	0.021	0.658	0.01 (-0.03, 0.05)	0.879	0.77	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
12706_2	CD42BPB	CD42BPB	226	-0.009	0.021	0.658	0.01 (-0.03, 0.05)	0.879	0.77	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
2571_12	IGFBP3	IGFBP3	226	-0.008	0.018	0.658	0.01 (-0.03, 0.04)	0.879	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
8458_11	SNCA	α-Synuclein	226	-0.008	0.018	0.658	0.01 (-0.03, 0.04)	0.879	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
8730_22	CHDC	CHDC	226	-0.009	0.021	0.658	0.01 (-0.03, 0.05)	0.879	0.77	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
12895_62	KLHL12	KLHL12	226	-0.008	0.018	0.658	0.01 (-0.03, 0.04)	0.879	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
19334_52	TXNDC12	TXNDC12	226	-0.008	0.018	0.658	0.01 (-0.03, 0.04)	0.879	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
2962_50	PTPLH	PTPLH	226	-0.008	0.018	0.658	0.01 (-0.03, 0.04)	0.879	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
3809_3	FGFR3	FGFR3	226	-0.008	0.018	0.658	0.01 (-0.03, 0.04)	0.879	0.78	0.04	0.09	0.589	0.854 (-0.08, 0.08)	0.001	0.815	0.040	0.326	0.249	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
9445_44	C18orf8	C18orf8	226	-0.009	0.021	0.659	0.01 (-0.03, 0.05)	0.880	0.80	0.04	0.10	0.600	0.924 (-0.04, 0.04)	0.001	0.816	0.040	0.327	0.250	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
7305_28	LARGE	LARGE	226	-0.009	0.021	0.659	0.01 (-0.03, 0.05)	0.880	0.80	0.04	0.10	0.600	0.924 (-0.04, 0.04)	0.001	0.816	0.040	0.327	0.250	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
10608_9	HTH1	HIS1	226	-0.008	0.018	0.661	0.01 (-0.03, 0.04)	0.880	0.80	0.04	0.10	0.600	0.924 (-0.04, 0.04)	0.001	0.816	0.040	0.327	0.250	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
12516_26	NPST	NPST	226	-0.008	0.018	0.661	0.01 (-0.03, 0.04)	0.880	0.80	0.04	0.10	0.600	0.924 (-0.04, 0.04)	0.001	0.816	0.040	0.327	0.250	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
13642_90	KPNA4	KPNA4	226	-0.008	0.018	0.661	0.01 (-0.03, 0.04)	0.880	0.80	0.04	0.10	0.600	0.924 (-0.04, 0.04)	0.001	0.816	0.040	0.327	0.250	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
12982_18	ITPA3	ITPA3	226	-0.008	0.018	0.661	0.01 (-0.03, 0.04)	0.880	0.80	0.04	0.10	0.600	0.924 (-0.04, 0.04)	0.001	0.816	0.040	0.327	0.250	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
13942_90	ITPA3	ITPA3	226	-0.008	0.018	0.661	0.01 (-0.03, 0.04)	0.880	0.80	0.04	0.10	0.600	0.924 (-0.04, 0.04)	0.001	0.816	0.040	0.327	0.250	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
12475_18	PKB	PKB	226	-0.008	0.018	0.661	0.01 (-0.03, 0.04)	0.880	0.80	0.04	0.10	0.600	0.924 (-0.04, 0.04)	0.001	0.816	0.040	0.327	0.250	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
5735_54	C1GALT1C1C	C1GALT1C1C	226	-0.021	0.049	0.661	0.02 (-0.07, 0.12)	0.880	0.80	0.04	0.10	0.600	0.924 (-0.04, 0.04)	0.001	0.816	0.040	0.327	0.250	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
8973_23	FCRL4	FCRL4	226	-0.009	0.022	0.661	0.01 (-0.03, 0.05)	0.880	0.80	0.04	0.10	0.600	0.924 (-0.04, 0.04)	0.001	0.816	0.040	0.327	0.250	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
10955_4	CLEC4E	CLEC4E	226	-0.009	0.022	0.661	0.01 (-0.03, 0.05)	0.880	0.80	0.04	0.10	0.600	0.924 (-0.04, 0.04)	0.001	0.816	0.040	0.327	0.250	0.04 (-0.03, 0.11)	0.032	0.40	0.425	0.03 (-0.05, 0.11)
16847_39																							

Table S5. Association of type 2 diabetes with Finland plasma protein.

SomaLigase	Protein	nsnp	Inverse variance weights		MR Egger		Weighted median		Weighted mode														
			b/w	se/bw	pval/IV	CI/w	FOR_IV	b/w	begger	seegger	pval/egger	CI/egger	b/w	se/w	pval/w	CI/w							
4545.53	DNAJ19	DnaJ19	226	0.005	0.18	0.797	4.85e-03 (0.03, 0.04)	0.932	0.249	0.005	0.077	0.897	4.85e-03 (0.07, 0.08)	0.001	0.995	0.044	0.31	0.161	-0.041 (0.11, 0.02)	0.001	0.938	0.178	-0.05 (0.03, 0.02)
13482.14	CNTN1	CNTN1	226	0.005	0.18	0.797	4.85e-03 (0.03, 0.04)	0.932	0.249	0.005	0.077	0.897	4.85e-03 (0.07, 0.08)	0.001	0.995	0.044	0.31	0.161	-0.041 (0.11, 0.02)	0.001	0.938	0.178	-0.05 (0.03, 0.02)
9003.59	MARCO	MARCO	226	0.005	0.19	0.797	4.98e-03 (0.03, 0.04)	0.932	0.192	0.010	0.041	0.813	-0.01 (0.09, 0.07)	0.001	0.679	0.007	0.038	0.862	0.01 (0.07, 0.08)	-0.003	0.338	0.933	3.25e-03 (0.08, 0.07)
12358.6	ISBP1	ISBP1	226	0.005	0.18	0.797	4.72e-03 (0.03, 0.04)	0.932	0.249	0.010	0.041	0.813	-0.01 (0.09, 0.07)	0.001	0.679	0.007	0.038	0.862	0.01 (0.07, 0.08)	-0.003	0.338	0.933	3.25e-03 (0.08, 0.07)
7740.33	FATE1	FATE1	226	0.005	0.18	0.797	4.72e-03 (0.03, 0.04)	0.932	0.249	0.010	0.041	0.813	-0.01 (0.09, 0.07)	0.001	0.679	0.007	0.038	0.862	0.01 (0.07, 0.08)	-0.003	0.338	0.933	3.25e-03 (0.08, 0.07)
4270.47	PSMA2	PSA2	226	0.006	0.221	0.798	0.01 (0.04, 0.05)	0.932	0.006	-0.019	0.043	0.680	-0.02 (0.10, 0.07)	0.002	0.514	0.011	0.040	0.776	0.01 (0.07, 0.09)	0.032	0.442	0.450	0.03 (0.05, 0.11)
17331.38	KREM1	KREM1	226	0.006	0.223	0.798	0.01 (0.04, 0.05)	0.932	0.006	-0.019	0.043	0.680	-0.02 (0.10, 0.07)	0.002	0.514	0.011	0.040	0.776	0.01 (0.07, 0.09)	0.032	0.442	0.450	0.03 (0.05, 0.11)
6699.39	EFEA	EFEA	226	0.006	0.223	0.798	0.01 (0.04, 0.05)	0.932	0.006	-0.019	0.043	0.680	-0.02 (0.10, 0.07)	0.002	0.514	0.011	0.040	0.776	0.01 (0.07, 0.09)	0.032	0.442	0.450	0.03 (0.05, 0.11)
6528.95	EXTL2	EXTL2	226	0.006	0.222	0.799	0.01 (0.04, 0.05)	0.932	0.010	-0.029	0.043	0.509	-0.03 (0.11, 0.06)	0.002	0.365	0.028	0.040	0.484	-0.03 (0.11, 0.05)	-0.041	0.039	0.293	0.04 (-0.12, 0.04)
11485.4	GPR135	GPR135	226	0.005	0.200	0.801	-4.93e-03 (0.04, 0.03)	0.933	0.183	-0.078	0.041	0.058	-0.04 (-0.16, 0.07)	0.005	0.400	-0.042	0.035	0.237	-0.04 (-0.11, 0.03)	-0.048	0.041	0.233	-0.03 (0.03, 0.03)
11837.7	RORC	RORC	226	0.005	0.200	0.801	-4.93e-03 (0.04, 0.03)	0.933	0.183	-0.078	0.041	0.058	-0.04 (-0.16, 0.07)	0.005	0.400	-0.042	0.035	0.237	-0.04 (-0.11, 0.03)	-0.048	0.041	0.233	-0.03 (0.03, 0.03)
12475.48	CLCS	CLCS	226	0.005	0.200	0.801	-4.93e-03 (0.04, 0.03)	0.933	0.183	-0.078	0.041	0.058	-0.04 (-0.16, 0.07)	0.005	0.400	-0.042	0.035	0.237	-0.04 (-0.11, 0.03)	-0.048	0.041	0.233	-0.03 (0.03, 0.03)
14070.71	SKL	SKL	226	0.004	0.177	0.800	-4.42e-03 (0.04, 0.03)	0.933	0.360	-0.101	0.036	0.875	-0.01 (0.08, 0.05)	0.001	0.532	-0.006	0.036	0.876	-0.01 (0.08, 0.06)	-0.005	0.338	0.897	4.85e-03 (0.07, 0.08)
17400.71	ACOR8	ACOR8	226	0.005	0.199	0.800	-4.72e-03 (0.04, 0.03)	0.933	0.178	-0.008	0.039	0.815	-0.01 (0.08, 0.07)	0.001	0.706	0.006	0.035	0.814	-0.04 (0.10, 0.03)	-0.038	0.030	0.407	0.04 (-0.11, 0.04)
17688.27	TBC2B	TBC2B	226	0.005	0.199	0.800	-4.85e-03 (0.04, 0.03)	0.933	0.178	-0.008	0.039	0.815	-0.01 (0.08, 0.07)	0.001	0.706	0.006	0.035	0.814	-0.04 (0.10, 0.03)	-0.038	0.030	0.407	0.04 (-0.11, 0.04)
6443.65	CCM1	CCM1	226	0.006	0.218	0.801	4.50e-03 (0.04, 0.03)	0.933	0.122	-0.025	0.038	0.512	-0.02 (0.10, 0.05)	0.002	0.375	-0.004	0.028	0.253	-0.03 (0.08, 0.02)	-0.046	0.038	0.248	-0.05 (0.10, 0.04)
4907.56	FCM4	FCM4	226	0.006	0.218	0.801	4.50e-03 (0.04, 0.03)	0.933	0.122	-0.025	0.038	0.512	-0.02 (0.10, 0.05)	0.002	0.375	-0.004	0.028	0.253	-0.03 (0.08, 0.02)	-0.046	0.038	0.248	-0.05 (0.10, 0.04)
8086.15	CHRDL2	CHRDL2	226	0.005	0.199	0.800	-4.72e-03 (0.04, 0.03)	0.933	0.405	-0.038	0.038	0.347	-0.04 (-0.11, 0.04)	0.002	0.348	-0.027	0.034	0.433	-0.03 (0.08, 0.04)	-0.006	0.040	0.890	-0.01 (0.08, 0.08)
7690.72	BGN2T	BGN2T	226	0.008	0.300	0.801	0.01 (0.05, 0.04)	0.933	0.855	-0.293	0.060	0.311	0.11 (0.01, 0.23)	-0.006	0.003	0.040	0.391	0.03 (0.04, 0.11)	0.055	0.042	0.944	0.05 (0.05, 0.14)	
8045.3	KRDL3	KRDL3	226	0.005	0.200	0.801	-4.93e-03 (0.04, 0.03)	0.933	0.227	-0.007	0.041	0.884	-0.01 (0.09, 0.07)	0.000	0.954	-0.014	0.042	0.745	-0.01 (-0.10, 0.07)	-0.022	0.047	0.966	2.00e-03 (0.09, 0.09)
8346.9	DPPT	DPPT	226	0.005	0.199	0.801	-4.89e-03 (0.04, 0.03)	0.933	0.420	-0.008	0.038	0.843	-0.01 (0.07, 0.08)	0.000	0.931	-0.010	0.036	0.790	-0.01 (0.08, 0.08)	-0.003	0.037	0.969	2.98e-03 (0.08, 0.07)
12462.20	SETMAR	SETMAR	226	0.005	0.199	0.801	-4.89e-03 (0.04, 0.03)	0.933	0.420	-0.008	0.038	0.843	-0.01 (0.07, 0.08)	0.000	0.931	-0.010	0.036	0.790	-0.01 (0.08, 0.08)	-0.003	0.037	0.969	2.98e-03 (0.08, 0.07)
14011.17	S100A11	S100A11	226	0.005	0.199	0.801	-4.89e-03 (0.04, 0.03)	0.933	0.168	-0.006	0.041	0.877	-0.01 (0.09, 0.07)	0.000	0.987	-0.002	0.043	0.963	-0.04 (-0.13, 0.05)	-0.013	0.049	0.785	0.01 (0.08, 0.11)
3489.9	CNTF	CNTF	226	0.005	0.199	0.802	-4.70e-03 (0.04, 0.03)	0.933	0.915	-0.021	0.038	0.578	-0.02 (0.09, 0.05)	0.001	0.619	-0.031	0.039	0.449	-0.03 (-0.11, 0.05)	-0.046	0.041	0.261	-0.05 (0.13, 0.03)
13304.75	RSPD3	RSPD3	226	0.005	0.199	0.803	4.76e-03 (0.04, 0.03)	0.934	0.936	-0.003	0.038	0.442	-0.03 (0.10, 0.05)	0.002	0.304	-0.035	0.033	0.285	-0.04 (-0.13, 0.03)	-0.044	0.040	0.278	0.04 (-0.12, 0.03)
18285.6	SVP	SVP	226	0.005	0.200	0.803	4.86e-03 (0.04, 0.03)	0.934	0.583	-0.035	0.039	0.380	-0.03 (0.11, 0.04)	0.002	0.249	-0.020	0.040	0.852	-0.23 (-0.33, 0.06)	-0.001	0.037	0.976	-1.13e-03 (0.07, 0.07)
18285.24	OC2H	OC2H	226	0.005	0.200	0.803	4.86e-03 (0.04, 0.03)	0.934	0.583	-0.035	0.039	0.380	-0.03 (0.11, 0.04)	0.002	0.249	-0.020	0.040	0.852	-0.23 (-0.33, 0.06)	-0.001	0.037	0.976	-1.13e-03 (0.07, 0.07)
6713.4	LRP11	LRP11	226	0.005	0.199	0.804	-4.76e-03 (0.04, 0.03)	0.934	0.210	0.053	0.040	0.182	0.05 (0.02, 0.13)	-0.004	0.094	0.032	0.035	0.353	0.03 (0.04, 0.10)	0.032	0.039	0.414	0.03 (0.04, 0.11)
11516.7	FABP1	FABP1	226	0.005	0.201	0.804	0.01 (0.04, 0.05)	0.934	0.028	0.020	0.042	0.638	0.02 (0.06, 0.10)	0.001	0.687	0.005	0.037	0.885	0.01 (0.07, 0.08)	0.004	0.039	0.921	3.85e-03 (0.07, 0.08)
12381.20	CBR1	CBR1	226	0.005	0.201	0.804	0.01 (0.04, 0.05)	0.934	0.028	0.020	0.042	0.638	0.02 (0.06, 0.10)	0.001	0.687	0.005	0.037	0.885	0.01 (0.07, 0.08)	0.004	0.039	0.921	3.85e-03 (0.07, 0.08)
8845.2	ADAMTSS3	ADAMTSS3	226	0.005	0.199	0.805	-4.78e-03 (0.04, 0.03)	0.935	0.028	0.020	0.042	0.500	0.03 (0.05, 0.10)	-0.002	0.359	0.008	0.041	0.845	-0.01 (0.07, 0.09)	-0.014	0.042	0.731	-0.01 (0.10, 0.07)
13574.50	RND3	RND3	226	0.005	0.202	0.806	0.01 (0.04, 0.05)	0.936	0.016	-0.044	0.043	0.311	-0.04 (0.13, 0.04)	0.003	0.191	0.028	0.040	0.508	-0.03 (0.05, 0.10)	-0.009	0.040	0.833	-0.01 (0.10, 0.08)
10589.7	ROSL1	ROSL1	226	0.005	0.202	0.806	0.01 (0.04, 0.05)	0.936	0.016	-0.044	0.043	0.311	-0.04 (0.13, 0.04)	0.003	0.191	0.028	0.040	0.508	-0.03 (0.05, 0.10)	-0.009	0.040	0.833	-0.01 (0.10, 0.08)
10333.10	CANL1	CANL1	226	0.005	0.202	0.806	0.01 (0.04, 0.05)	0.936	0.016	-0.044	0.043	0.311	-0.04 (0.13, 0.04)	0.003	0.191	0.028	0.040	0.508	-0.03 (0.05, 0.10)	-0.009	0.040	0.833	-0.01 (0.10, 0.08)
9053.3	CACTL5	CACTL5	226	0.005	0.202	0.806	0.01 (0.04, 0.05)	0.936	0.016	-0.044	0.043	0.311	-0.04 (0.13, 0.04)	0.003	0.191	0.028	0.040	0.508	-0.03 (0.05, 0.10)	-0.009	0.040	0.833	-0.01 (0.10, 0.08)
13062.4	GMFG	GMFG	226	0.005	0.199	0.807	-4.61e-03 (0.04, 0.03)	0.936	0.480	-0.007	0.038	0.853	-0.01 (0.08, 0.07)	0.001	0.724	-0.024	0.039	0.538	-0.02 (0.10, 0.05)	-0.028	0.041	0.528	-0.03 (0.11, 0.05)
15440.57	PMK2	PMK2	226	0.005	0.199	0.807	-4.74e-03 (0.04, 0.03)	0.936	0.156	-0.011	0.041	0.791	-0.01 (0.09, 0.07)	0.001	0.863	-0.028	0.035	0.459	-0.03 (0.08, 0.04)	-0.014	0.039	0.729	-0.01 (0.09, 0.06)
17172.19	STATH	STATH	226	0.005	0.199	0.807	-4.74e-03 (0.04, 0.03)	0.936	0.156	-0.011	0.041	0.791	-0.01 (0.09, 0.07)	0.001	0.863	-0.028	0.035	0.459	-0.03 (0.08, 0.04)	-0.014	0.039	0.729	-0.01 (0.09, 0.06)
10280.8	PSMB8	PSMB8	226	0.005	0.199	0.808	-4.73e-03 (0.04, 0.03)	0.936	0.534	0.026	0.039	0.510	0.03 (0.05, 0.10)	-0.002	0.369	0.020	0.040	0.615	0.02 (0.06, 0.10)	0.019	0.041</		

Table S5. Association of type 2 diabetes with Ferland plasma protein.		Inverse variance weighted		MR Egger		Weighted median		Weighted mode												
SNP	Gene	Protein	rsnp	b2w	se.b2w	pval.iw	CI.iw	FOR_ZW	Q1	lower	se.egger	pval.egger	se.med	pval.med	b.mode	se.mode	pval.mode	CI.mode		
12854.3	TEAD3	TEAD3	226	-0.003	0.020	0.897	2.53e-03 (0.04, 0.04)	0.966	0.109	0.045	0.042	0.776	0.05 (0.04, 0.1)	-0.003	0.028	-0.004	0.040	0.915	-4.29e-03 (0.08, 0)	
14151.4	ISG15	ISG15	226	-0.003	0.020	0.901	2.53e-03 (0.04, 0.04)	0.966	0.109	0.045	0.042	0.776	0.05 (0.04, 0.1)	-0.003	0.028	-0.004	0.040	0.915	-4.29e-03 (0.08, 0)	
18919.10	HMG2A	HMG2A	226	-0.002	0.019	0.900	-2.40e-03 (0.04, 0.03)	0.966	0.178	0.003	0.040	0.933	-3.39e-03 (0.08, 0.08)	-0.000	0.027	-0.040	0.037	0.275	-0.04 (0.11, 0.03)	
2516.23	CH25H	CH25H	226	-0.003	0.027	0.897	3.48e-03 (0.05, 0.06)	0.966	7.77e-16	0.052	0.040	0.831	0.05 (0.05, 0.1)	-0.003	0.027	-0.040	0.036	0.534	0.02 (0.09, 0.08)	
3455.4	KLHL6	KLHL6	226	-0.002	0.019	0.899	-2.46e-03 (0.04, 0.04)	0.966	0.182	0.003	0.040	0.933	-3.39e-03 (0.08, 0.08)	-0.000	0.027	-0.040	0.037	0.275	-0.04 (0.11, 0.03)	
3628.3	MP2K2	MP2K2	226	-0.002	0.019	0.899	-2.46e-03 (0.04, 0.04)	0.966	0.182	0.003	0.040	0.933	-3.39e-03 (0.08, 0.08)	-0.000	0.027	-0.040	0.037	0.275	-0.04 (0.11, 0.03)	
4138.25	L2P2	L2P2	226	-0.002	0.018	0.899	-2.46e-03 (0.04, 0.04)	0.966	0.182	0.003	0.040	0.933	-3.39e-03 (0.08, 0.08)	-0.000	0.027	-0.040	0.037	0.275	-0.04 (0.11, 0.03)	
4598.24	RSPD2	RSPD2	226	-0.002	0.019	0.899	-2.46e-03 (0.04, 0.04)	0.966	0.182	0.003	0.040	0.933	-3.39e-03 (0.08, 0.08)	-0.000	0.027	-0.040	0.037	0.275	-0.04 (0.11, 0.03)	
5743.82	CART3	CART3	226	-0.002	0.019	0.899	-2.46e-03 (0.04, 0.04)	0.966	0.182	0.003	0.040	0.933	-3.39e-03 (0.08, 0.08)	-0.000	0.027	-0.040	0.037	0.275	-0.04 (0.11, 0.03)	
6526.77	OBP2A	OBP2A	226	-0.002	0.019	0.898	-2.45e-03 (0.04, 0.03)	0.966	0.165	0.007	0.040	0.899	0.01 (0.07, 0.09)	-0.001	0.028	-0.037	0.044	0.933	-0.02 (0.10, 0.04)	
8242.9	CLCFLC1	CLCFLC1	226	-0.002	0.019	0.898	-2.45e-03 (0.04, 0.03)	0.966	0.165	0.007	0.040	0.899	0.01 (0.07, 0.09)	-0.001	0.028	-0.037	0.044	0.933	-0.02 (0.10, 0.04)	
8634.58	Calnexin	Calnexin	226	-0.002	0.019	0.898	-2.45e-03 (0.04, 0.03)	0.966	0.165	0.007	0.040	0.899	0.01 (0.07, 0.09)	-0.001	0.028	-0.037	0.044	0.933	-0.02 (0.10, 0.04)	
13931.22	PANX1	PANX1	226	-0.002	0.019	0.900	-2.44e-03 (0.04, 0.04)	0.966	0.805	0.001	0.039	0.986	-6.61e-04 (0.08, 0.07)	0.000	0.026	0.001	0.040	0.986	6.81e-04 (0.08, 0.07)	
17973.34	CAS9	CAS9	226	-0.002	0.019	0.901	-2.35e-03 (0.04, 0.04)	0.966	0.729	0.004	0.038	0.955	-0.02 (0.10, 0.05)	0.002	0.026	0.005	0.037	0.955	-0.01 (0.08, 0.08)	
8269.327	ARSK	ARSK	226	-0.003	0.024	0.901	2.97e-03 (0.04, 0.05)	0.966	4.11e-07	0.097	0.048	0.942	0.10 (0.13e-03, 0.19)	-0.002	0.023	-0.058	0.037	0.117	0.06 (0.11, 0.13)	
8599.147	ARLKB	ARLKB	226	-0.003	0.024	0.901	2.97e-03 (0.04, 0.05)	0.966	4.11e-07	0.097	0.048	0.942	0.10 (0.13e-03, 0.19)	-0.002	0.023	-0.058	0.037	0.117	0.06 (0.11, 0.13)	
16756.30	GP77	GP77	226	-0.002	0.020	0.902	-2.39e-03 (0.04, 0.04)	0.967	0.528	0.012	0.037	0.912	-0.01 (0.09, 0.06)	-0.004	0.016	-0.028	0.035	0.448	0.03 (0.04, 0.1)	
17852.5	PPM1E	PPM1E	226	-0.002	0.019	0.901	-2.33e-03 (0.04, 0.03)	0.966	0.755	0.006	0.038	0.881	-0.01 (0.08, 0.07)	-0.000	0.026	0.000	0.039	0.942	0.01 (0.08, 0.07)	
17852.5	PPM1E	PPM1E	226	-0.002	0.019	0.901	-2.33e-03 (0.04, 0.03)	0.966	0.755	0.006	0.038	0.881	-0.01 (0.08, 0.07)	-0.000	0.026	0.000	0.039	0.942	0.01 (0.08, 0.07)	
17852.5	PPM1E	PPM1E	226	-0.002	0.019	0.901	-2.33e-03 (0.04, 0.03)	0.966	0.755	0.006	0.038	0.881	-0.01 (0.08, 0.07)	-0.000	0.026	0.000	0.039	0.942	0.01 (0.08, 0.07)	
17781.19	GMPL7	GMPL7	226	-0.003	0.021	0.903	-2.52e-03 (0.04, 0.04)	0.967	0.044	-0.057	0.041	0.169	-0.06 (0.14, 0.02)	0.003	0.010	-0.053	0.031	0.084	-0.05 (0.11, 0.01)	
12403.30	RAB39B	RAB39B	226	-0.003	0.021	0.903	-2.52e-03 (0.04, 0.04)	0.968	0.023	-0.028	0.042	0.538	-0.03 (0.11, 0.06)	0.001	0.022	-0.011	0.041	0.787	-0.01 (0.08, 0.07)	
16482.1	HMDH3	HMDH3	226	-0.002	0.020	0.904	-2.35e-03 (0.04, 0.04)	0.968	0.065	0.026	0.042	0.532	0.03 (0.08, 0.11)	-0.001	0.022	-0.004	0.040	0.723	-0.01 (0.08, 0.07)	
2992.59	L17RA	L17RA	226	-0.002	0.019	0.904	-2.33e-03 (0.04, 0.04)	0.968	0.423	0.003	0.039	0.930	3.48e-03 (0.07, 0.08)	0.000	0.026	0.000	0.038	0.938	0.318	0.04 (0.10, 0.11)
9187.2	HMGN1	HMGN1	226	-0.002	0.019	0.904	-2.30e-03 (0.04, 0.04)	0.968	0.162	0.000	0.040	0.990	-4.89e-04 (0.08, 0.08)	-0.000	0.026	0.000	0.039	0.942	0.02 (0.05, 0.1)	
8412.52	ACVR2B	ACVR2B	226	-0.002	0.021	0.903	-2.57e-03 (0.04, 0.04)	0.968	0.041	0.012	0.043	0.771	0.01 (0.07, 0.07)	-0.001	0.026	-0.001	0.040	0.912	0.01 (0.08, 0.1)	
19392.6	DOAH1	DOAH1	226	-0.002	0.019	0.905	-2.30e-03 (0.04, 0.04)	0.968	0.420	-0.001	0.039	0.891	-8.26e-04 (0.08, 0.08)	-0.000	0.026	-0.001	0.039	0.946	-2.64e-03 (0.08, 0.08)	
5183.53	PRKAA1	PRKAA1	226	-0.002	0.019	0.906	-2.27e-03 (0.04, 0.04)	0.968	0.538	0.022	0.039	0.952	0.02 (0.05, 0.1)	-0.001	0.026	-0.001	0.040	0.985	0.01 (0.07, 0.07)	
6512.16	HINT2	HINT2	226	-0.002	0.019	0.906	-2.27e-03 (0.04, 0.04)	0.968	0.538	0.022	0.039	0.952	0.02 (0.05, 0.1)	-0.001	0.026	-0.001	0.040	0.985	0.01 (0.07, 0.07)	
11513.92	CD38	CD38	226	-0.002	0.019	0.906	-2.27e-03 (0.04, 0.04)	0.969	0.420	-0.035	0.039	0.370	-0.04 (0.11, 0.04)	0.002	0.026	0.002	0.034	0.984	-0.01 (0.08, 0.07)	
10608.34	TOR1AIP1	TOR1AIP1	226	-0.002	0.020	0.909	-2.25e-03 (0.04, 0.04)	0.969	0.014	-0.038	0.040	0.337	-0.04 (0.12, 0.04)	0.003	0.024	0.029	0.041	0.944	-0.04 (0.10, 0.07)	
12943.6	ZNF140	ZNF140	226	-0.002	0.019	0.909	-2.25e-03 (0.04, 0.04)	0.969	0.376	0.009	0.039	0.929	0.01 (0.07, 0.07)	-0.000	0.026	-0.001	0.039	0.952	0.01 (0.07, 0.07)	
13449.25	SFR3A	SFR3A	226	-0.002	0.019	0.909	-2.25e-03 (0.04, 0.04)	0.969	0.376	0.009	0.039	0.929	0.01 (0.07, 0.07)	-0.000	0.026	-0.001	0.039	0.952	0.01 (0.07, 0.07)	
14291.09	TRAF3IP1	TRAF3IP1	226	-0.002	0.019	0.909	-2.25e-03 (0.04, 0.04)	0.969	0.376	0.009	0.039	0.929	0.01 (0.07, 0.07)	-0.000	0.026	-0.001	0.039	0.952	0.01 (0.07, 0.07)	
14061.48	ITRAF1	ITRAF1	226	-0.002	0.020	0.909	-2.24e-03 (0.04, 0.04)	0.969	0.465	0.002	0.040	0.951	2.44e-03 (0.08, 0.08)	0.000	0.026	0.000	0.040	0.942	0.02 (0.05, 0.1)	
14129.1	FNRF1	FNRF1	226	-0.002	0.020	0.908	-2.29e-03 (0.04, 0.04)	0.969	0.225	0.012	0.041	0.771	0.01 (0.07, 0.09)	-0.001	0.026	-0.001	0.040	0.923	0.04 (0.03, 0.09)	
14523.28	SUMO3	SUMO3	226	-0.002	0.020	0.908	-2.29e-03 (0.04, 0.04)	0.969	0.225	0.012	0.041	0.771	0.01 (0.07, 0.09)	-0.001	0.026	-0.001	0.040	0.923	0.04 (0.03, 0.09)	
17483.3	ARHGAP5	ARHGAP5	226	-0.002	0.018	0.907	-2.10e-03 (0.04, 0.03)	0.969	0.709	0.018	0.036	0.619	0.02 (0.09, 0.05)	-0.001	0.026	-0.001	0.036	0.930	0.130	-0.05 (0.11, 0.01)
18746.31	RBP4	RBP4	226	-0.003	0.022	0.908	-2.55e-03 (0.05, 0.04)	0.969	1.140e-05	0.036	0.044	0.418	0.04 (0.05, 0.12)	-0.002	0.026	-0.002	0.039	0.952	0.01 (0.08, 0.07)	
19551.216	PLKND1	PLKND1	226	-0.002	0.019	0.904	-2.17e-03 (0.04, 0.04)	0.969	0.275	0.043	0.040	0.827	0.01 (0.07, 0.07)	-0.001	0.026	-0.001	0.040	0.929	0.02 (0.05, 0.1)	
3312.54	FCGR1A	FCGR1A	226	-0.002	0.019	0.907	-2.21e-03 (0.04, 0.04)	0.969	0.135	0.030	0.040	0.450	0.03 (0.05, 0.11)	-0.002	0.021	-0.012	0.037	0.745	-0.01 (0.08, 0.07)	
7208.60	ARSL4C4	ARSL4C4	226	-0.002	0.019	0.909	-2.19e-03 (0.04, 0.04)	0.969	0.396	0.010	0.039	0.650	0.02 (0.07, 0.09)	-0.001	0.026	-0.001	0.040	0.935	0.160	0.05 (0.12, 0.02)
7835.2	BNIP1	BNIP1	226	-0.002	0.019	0.909	-2.19e-03 (0.04, 0.04)	0.969	0.396	0.010	0.039	0.650	0.02 (0.07, 0.09)	-0.001	0.026	-0.001	0.040	0.935	0.160	0.05 (0.12, 0.02)
8382.10	MRPL3	MRPL3	226	-0.002	0.020	0.907	-2.27e-03 (0.04, 0.04)	0.969	0.886	0.040	0.039	0.311	0.04 (0.12, 0.05)	-0.003	0.021	-0.033	0.035	0.214	0.04 (0.10, 0.11)	
8382.10	MRPL3	MRPL3	226	-0.002	0.020	0.907	-2.27e-03 (0.04, 0.04)	0.969	0.886	0.040	0.039	0.311	0.04 (0.12, 0.05)	-0.003	0.021	-0.033	0.035	0.214	0.04 (0.10, 0.11)	
8382.10	MRPL3	MRPL3	226	-0.002	0.020	0.907	-2.27e-03 (0.04, 0.04)	0.969	0.886	0.040	0.039	0.311	0.04 (0.12, 0.05)	-0.003	0.021	-0.033	0.035	0.214	0.04 (0.10, 0.11)	
8598.30	PER1	PER1	226	-0.002	0.018	0.908	-2.14e-03 (0.04, 0.03)	0.969	0.396											

Table S5. Association of type 2 diabetes with Finland plasma protein.

SomaLogic	Protein	rnp	b/w	Inverse variance weighted		MR Egger		Weighted median		Weighted mode			
				se,ivw	pval,ivw	CI_low	CI_high	se,ivw	pval,ivw	se,mode	pval,mode		
13374.4	DEFB13	DB13	1	0.001	0.019	0.849	1.25e-03 (0.04, 0.04)	0.881	0.362	0.024	0.440	0.022	0.05 (0.10, 0.10)
17320.3	S10A10	CD141	1	0.001	0.019	0.849	1.25e-03 (0.04, 0.04)	0.881	0.362	0.024	0.440	0.022	0.05 (0.10, 0.10)
18165.1	UBR2	UBR2	1	0.001	0.019	0.849	1.25e-03 (0.04, 0.04)	0.881	0.362	0.024	0.440	0.022	0.05 (0.10, 0.10)
19306.20	IGJ	IGJ	1	0.001	0.019	0.849	1.25e-03 (0.04, 0.04)	0.881	0.362	0.024	0.440	0.022	0.05 (0.10, 0.10)
16748.12	RHBB	RHBB	1	0.001	0.019	0.849	1.25e-03 (0.04, 0.04)	0.881	0.362	0.024	0.440	0.022	0.05 (0.10, 0.10)
2627.23	LCR1L	Fractalkin	1	0.001	0.019	0.849	1.25e-03 (0.04, 0.04)	0.881	0.362	0.024	0.440	0.022	0.05 (0.10, 0.10)
5091.28	LYR2	IL-4	1	0.001	0.022	0.851	1.36e-03 (0.04, 0.04)	0.882	0.001	0.036	0.048	0.046	0.022 (0.06, 0.06)
5096.75	CD5	CD5	1	0.001	0.019	0.849	1.25e-03 (0.04, 0.04)	0.881	0.362	0.024	0.440	0.022	0.05 (0.10, 0.10)
5969.10	NM1	Nucleoside	1	0.001	0.019	0.849	1.25e-03 (0.04, 0.04)	0.881	0.362	0.024	0.440	0.022	0.05 (0.10, 0.10)
8838.10	CASCA	CASCA	1	0.002	0.037	0.851	2.27e-03 (0.07, 0.07)	0.882	6.99e-77	0.019	0.074	0.004	0.033 (0.09, 0.09)
9234.45	MFAP2	MFAP2	1	0.001	0.019	0.849	1.25e-03 (0.04, 0.04)	0.881	0.362	0.024	0.440	0.022	0.05 (0.10, 0.10)
9582.93	SUSD1	SUSD1	1	0.001	0.020	0.850	1.22e-03 (0.04, 0.04)	0.882	0.129	0.007	0.042	0.070	0.011 (0.07, 0.07)
12295.86	DAR32	SYND	1	0.001	0.018	0.851	1.10e-03 (0.04, 0.04)	0.882	0.133	-0.020	0.038	0.067	0.022 (0.09, 0.09)
1865.60	SNR1P	SNR1P	1	0.001	0.019	0.849	1.25e-03 (0.04, 0.04)	0.881	0.362	0.024	0.440	0.022	0.05 (0.10, 0.10)
17337.1	YY1	YY1	1	0.001	0.018	0.853	1.10e-03 (0.04, 0.04)	0.883	0.327	-0.045	0.038	0.232	0.05 (0.10, 0.10)
2647.56	GDI2	Flav-GDP-P	1	0.001	0.018	0.853	1.03e-03 (0.04, 0.04)	0.883	0.620	-0.028	0.035	0.422	0.03 (0.10, 0.10)
6433.57	FAM20A	FAM20A	1	0.001	0.019	0.853	1.03e-03 (0.04, 0.04)	0.883	0.165	0.000	0.038	0.299	0.04 (0.10, 0.10)
11231.12	FDX1L	ADXL	1	0.001	0.019	0.854	1.11e-03 (0.04, 0.04)	0.884	0.882	0.040	0.039	0.306	0.04 (0.10, 0.10)
11096.57	NM1T1	NM1T1	1	0.001	0.019	0.854	1.10e-03 (0.04, 0.04)	0.884	0.004	-0.024	0.038	0.554	0.02 (0.10, 0.10)
17450.51	HARS	HuH4yJRN	1	0.001	0.019	0.855	1.05e-03 (0.04, 0.04)	0.884	0.654	0.001	0.038	0.986	0.04 (0.10, 0.10)
15299.102	MESDC2	MESDC2	1	0.001	0.018	0.856	9.92e-04 (0.04, 0.04)	0.885	0.701	-0.022	0.038	0.545	0.02 (0.09, 0.09)
5213.35	ND1	NM1T1	1	0.001	0.019	0.856	9.97e-04 (0.04, 0.04)	0.885	0.105	-0.045	0.038	0.228	0.04 (0.10, 0.10)
9176.3	MUC1	MUC1	1	0.001	0.021	0.856	1.17e-03 (0.04, 0.04)	0.885	0.018	0.017	0.042	0.097	0.07 (0.15, 0.15)
19289.29	UROD	DCUP	1	0.001	0.019	0.857	1.05e-03 (0.04, 0.04)	0.885	0.728	-0.028	0.039	0.467	0.03 (0.10, 0.10)
12033.54	HEM2	HEM2	1	0.001	0.019	0.857	9.97e-04 (0.04, 0.04)	0.885	0.246	0.039	0.050	0.104	0.04 (0.11, 0.11)
18613.3	CDM1T	CAD17	1	0.001	0.024	0.857	1.28e-03 (0.05, 0.05)	0.885	1.18e-06	0.058	0.048	0.255	0.05 (0.14, 0.14)
17335.18	VAMP2	VAMP2	1	0.001	0.020	0.857	1.05e-03 (0.04, 0.04)	0.885	0.465	-0.035	0.039	0.382	0.03 (0.11, 0.11)
19033.64	PET117	PET117	1	0.001	0.019	0.858	1.13e-03 (0.04, 0.04)	0.885	0.073	0.004	0.042	0.821	0.06 (0.08, 0.08)
19560.23	PANP	PLX4	1	0.001	0.022	0.858	1.17e-03 (0.04, 0.04)	0.886	2.40e-05	0.007	0.045	0.875	0.01 (0.08, 0.10)
2819.50	BCAM	BCAM	1	0.001	0.027	0.858	1.42e-03 (0.05, 0.05)	0.886	1.11e-19	0.013	0.055	0.818	0.01 (0.09, 0.12)
14345.4	PNP	PNP	1	0.001	0.019	0.858	1.13e-03 (0.04, 0.04)	0.886	0.049	0.018	0.041	0.821	0.06 (0.08, 0.08)
17797.1	CUL1	CUL1	1	0.001	0.019	0.859	9.74e-04 (0.04, 0.04)	0.886	0.495	0.043	0.038	0.285	0.04 (0.10, 0.12)
3434.54	FN1	FN1	1	0.001	0.019	0.859	9.82e-04 (0.04, 0.04)	0.886	0.841	0.048	0.039	0.881	0.01 (0.07, 0.08)
6940.18	CPH3	CPH3	1	0.001	0.019	0.859	9.82e-04 (0.04, 0.04)	0.886	0.414	0.004	0.038	0.881	0.01 (0.07, 0.08)
8019.43	V5C2	V5C2	1	0.001	0.019	0.859	9.82e-04 (0.04, 0.04)	0.886	0.813	0.043	0.038	0.281	0.04 (0.12, 0.13)
3040.59	JPH1	JPH1	1	0.001	0.019	0.859	9.82e-04 (0.04, 0.04)	0.886	0.813	0.043	0.038	0.281	0.04 (0.12, 0.13)
4440.8	PDPK1	PDPK1	1	0.001	0.018	0.860	9.11e-04 (0.04, 0.04)	0.886	0.586	0.012	0.038	0.736	0.01 (0.08, 0.08)
10613.33	CASCA	CASCA	1	0.002	0.040	0.863	1.88e-03 (0.08, 0.08)	0.886	2.77e-11	-0.012	0.080	0.878	0.01 (0.17, 0.14)
13303.5	SEC7M1	SEC7M1	1	0.001	0.019	0.863	1.14e-03 (0.04, 0.04)	0.886	0.428	0.003	0.041	0.821	0.06 (0.11, 0.11)
17320.19	AASBP	AASBP	1	0.001	0.018	0.863	8.61e-04 (0.04, 0.04)	0.886	0.762	0.002	0.037	0.987	0.15 (0.07, 0.07)
17336.54	CR2L2	CR2L2	1	0.001	0.020	0.862	9.37e-04 (0.04, 0.04)	0.886	0.484	0.070	0.039	0.977	0.07 (0.19, 0.15)
18290.5	ANKK4	ANKK4	1	0.001	0.019	0.862	9.37e-04 (0.04, 0.04)	0.886	0.209	0.009	0.038	0.987	0.01 (0.06, 0.06)
19590.46	SFP2	SFP2	1	0.001	0.022	0.862	1.06e-03 (0.04, 0.04)	0.886	0.001	-0.039	0.045	0.377	0.04 (0.13, 0.15)
4382.54	FGF12	FGF12	1	0.001	0.019	0.861	9.14e-04 (0.04, 0.04)	0.886	0.067	0.049	0.040	0.225	0.05 (0.13, 0.13)
7090.17	GALNT1	GALNT1	1	0.001	0.019	0.861	9.07e-03 (0.04, 0.04)	0.886	0.405	0.017	0.044	0.172	0.02 (0.10, 0.11)
7105.7	SCARB2	CABL2	1	0.001	0.018	0.861	8.94e-04 (0.04, 0.04)	0.886	0.594	-0.042	0.037	0.253	0.04 (0.11, 0.13)
9600.55	THSD7A	THSD7A	1	0.001	0.020	0.862	9.30e-04 (0.04, 0.04)	0.886	0.523	0.133	0.040	0.752	0.01 (0.06, 0.09)
9625.56	CLARET	CLARET	1	0.001	0.019	0.862	9.30e-04 (0.04, 0.04)	0.886	0.256	0.047	0.038	0.621	0.02 (0.09, 0.07)
13984.23	DDX25	DDX25	1	0.001	0.019	0.863	8.86e-04 (0.04, 0.04)	0.887	0.369	0.035	0.039	0.372	0.04 (0.11, 0.11)
9907.216	TNKS	Tanycytes	1	0.001	0.019	0.863	8.86e-04 (0.04, 0.04)	0.887	0.563	0.038	0.039	0.855	0.01 (0.07, 0.08)
16330.7	PSM2	PSM2	1	0.001	0.019	0.863	8.86e-04 (0.04, 0.04)	0.887	0.894	0.037	0.039	0.855	0.01 (0.07, 0.08)
18678.15	GREM1	GREM1	1	0.001	0.023	0.864	1.03e-03 (0.04, 0.05)	0.887	1.70e-04	-0.012	0.045	0.791	0.01 (0.10, 0.18)
18696.25	CLRN3	CLRN3	1	0.001	0.018	0.864	8.59e-04 (0.04, 0.04)	0.887	0.885	0.036	0.041	0.848	0.02 (0.06, 0.07)
5749.53	LGPS	LGPS	1	0.001	0.023	0.865	1.00e-03 (0.04, 0.05)	0.887	0.864	0.096	0.045	0.036	0.10 (0.10, 0.18)
8479.4	MLP10	MLP10	1	0.001	0.021	0.865	8.31e-04 (0.04, 0.04)	0.888	0.120	0.006	0.041	0.881	0.01 (0.07, 0.09)
9012.22	CTSF	CTSF	1	0.001	0.019	0.865	8.31e-04 (0.04, 0.04)	0.888	0.004	-0.039	0.041	0.881	0.01 (0.07, 0.09)
3038.9	ITAC	ITAC	1	0.001	0.021	0.866	8.79e-04 (0.04, 0.04)	0.888	0.006	0.011	0.042	0.790	0.01 (0.09, 0.07)
3603.80	CLCTA	CLCTA	1	0.001	0.020	0.866	8.51e-04 (0.04, 0.04)	0.888	0.007	0.019	0.040	0.635	0.02 (0.06, 0.10)
6040.10	RSPD1	RSPD1	1	0.001	0.019	0.866	8.51e-04 (0.04, 0.04)	0.888	0.004	-0.039	0.041	0.881	0.01 (0.07, 0.09)
7779.86	CHST1	CHST1	1	0.001	0.030	0.866	1.29e-03 (0.06, 0.06)	0.888	4.47e-33	0.026	0.061	0.670	0.03 (0.15, 0.19)
17403.14	AGTR8	lyso-GD3	1	0.001	0.019	0.867	7.55e-04 (0.04, 0.04)	0.888	0.057	0.007	0.040	0.863	0.01 (0.07, 0.09)
18327.5	SNXS	SNXS	1	0.001	0.020	0.867	9.47e-04 (0.04, 0.04)	0.888	0.524	0.037	0.041	0.863	0.02 (0.06, 0.07)
19817.5	PTGSR	lyso-GD3	1	0.001	0.019	0.867	7.92e-04 (0.04, 0.04)	0.888	0.050	-0.037	0.042	0.376	0.04 (0.12, 0.14)
4993.16	GSTA3	GSTA3	1	0.001	0.020	0.868	7.94e-04 (0.04, 0.04)	0.888	0.174	-0.005	0.041	0.910	0.06 (0.09, 0.08)
5319.58	TMED4	TMED4	1	0.001	0.019	0.868	7.94e-04 (0.04, 0.04)	0.888	0.304	0.041	0.040	0.863	0.01 (0.07, 0.09)
3346.72	AURKB	AURKB	1	0.001	0.019	0.869	7.86e-04 (0.04, 0.04)	0.889	0.364	-0.040	0.040	0.910	0.04 (0.12, 0.14)
10580.14	SFTA2	SFTA2	1	0.001	0.019	0.869	7.86e-04 (0.04, 0.04)	0.889	0.603	0.032	0.041	0.910	0.04 (0.12, 0.14)
15164.16	SLC42A2	SLC42A2	1	0.001	0.019	0.869	7.86e-04 (0.04, 0.04)	0.889	0.230	0.022	0.039	0.863	0.02 (0.09, 0.07)
17355.56	SYT4	SYT4	1	0.001	0.018	0.870	6.76e-04 (0.04, 0.04)	0.889	0.633	-0.042	0.038	0.248	0.04 (0.11, 0.13)
12532.28	CDCA4	UBR1	1	0.001	0.019	0.870	7.30e-04 (0.04, 0.04)	0.889	0.862	0.049	0.040	0.863	0.04 (0.12, 0.14)
18622.2	QDNF	QDNF	1	0.001	0.019	0.869	8.59e-04 (0.04, 0.04)	0.889	0.903	0.032	0.039	0.863	0.02 (0.09, 0.07)
9116.28	HPCAD3	HECA2	1	0.001	0.019	0.871	7.09e-04 (0.04, 0.04)	0.890	0.296	-0.055	0.040	0.170	0.05 (0.13, 0.13)
9027.36	TPK3	TPK3	1	0.001	0.019	0.871	7.09e-04 (0.04, 0.04)	0.890	0.807	0.037	0.040	0.863	0.01 (0.07, 0.09)
6447.73	PTX3	PTX3	1	0.001	0.022	0.872	7.87e-04 (0.04, 0.04)	0.890	0.009	0.035	0.044	0.421	0.04 (0.12, 0.15)
8045.27	GPX7</												

Table S6. Association of putative type 2 diabetes-associated proteins in deCODE with gastrointestinal diseases.

Index SNP	Somalogic	UniProt	Gene	GI outcomes	FDR	b	se	pval	OR (95% CI)	snp_r2.exposure	snp_r2.outcome	correct_causal_direction	steiger_pval
rs1229984	9834_62	P00325	ADH1B	Cirrhosis	0.003	0.719	0.183	8.99E-05	2.05 (1.43,2.94)	0.001	1.97E-05	TRUE	2.17E-09
rs2602844	8325_37	P08319	ADH4	Cholelithiasis	0.017	0.229	0.067	0.001	1.26 (1.01,1.23)	0.005	1.47E-05	TRUE	6.15E-34
rs35246623	4435_66	Q6UWU6	ENPP7	Cholelithiasis	0.013	0.038	0.011	4.19E-04	1.04 (1.02,1.06)	0.025	1.60E-05	TRUE	2.00E-183
rs10952549	3431_54	P21709	EPHA1	Cholecystitis	0.036	-0.140	0.043	0.001	0.87 (0.80,0.95)	0.025	1.46E-05	TRUE	2.28E-183
rs34356500	15562_24	P08236	GUSB	Nonalcoholic fatty liver disease	0.003	0.654	0.167	8.61E-05	1.92 (1.39,2.67)	0.008	1.98E-05	TRUE	3.42E-56
rs11809759	10462_14	P00325	ADH1B	Gastric ulcer	0.020	-0.941	0.261	3.18E-04	0.39 (0.23,0.65)	0.008	1.88E-05	TRUE	9.57E-10
rs2228603	15573_110	O14594	NCAN	Nonalcoholic fatty liver disease	8.58E-17	-1.092	0.124	1.34E-18	0.34 (0.26,0.43)	0.012	9.93E-05	TRUE	1.06E-74
rs2228603	15573_110	O14592	NCAN	Cirrhosis	1.18E-08	-0.625	0.187	1.85E-10	0.54 (0.44,0.68)	0.012	5.21E-05	TRUE	6.80E-59
rs1212100	9829_91	Q06520	SULT2A1	Cholelithiasis	8.19E-44	0.683	0.048	1.28E-45	1.98 (1.80,2.18)	0.011	2.62E-04	TRUE	8.04E-61
rs1212100	9829_91	Q06520	SULT2A1	Cholecystitis	0.036	0.374	0.111	0.001	1.45 (1.17,1.81)	0.011	1.54E-05	TRUE	6.07E-78
rs35894069	5939_42	O43508	TNFSF12	Diverticular disease	0.018	0.102	0.028	2.78E-04	1.11 (1.05,1.17)	0.025	1.92E-05	TRUE	1.20E-181
rs10403399	3232_28	P13686	ACPF5	Chronic gastritis (Atrophic gastritis)	0.192	0.218	0.073	0.003	1.24 (1.08,1.43)	0.018	1.27E-05	TRUE	7.49E-127
rs10403399	3232_28	P13686	ACPF5	Cholecystitis	0.666	-0.138	0.084	0.100	0.87 (0.74,1.03)	0.018	3.69E-06	TRUE	3.35E-130
rs10403399	3232_28	P13686	ACPF5	Nonalcoholic fatty liver disease	0.795	-0.138	0.112	0.218	0.97 (0.89,1.05)	0.018	1.95E-06	TRUE	1.29E-131
rs10403399	3232_28	P13686	ACPF5	Cholelithiasis	0.788	-0.034	0.035	0.341	0.97 (0.90,1.04)	0.018	1.18E-06	TRUE	3.99E-132
rs10403399	3232_28	P13686	ACPF5	Gastric ulcer	0.849	-0.054	0.071	0.451	0.95 (0.82,1.09)	0.018	8.20E-07	TRUE	7.07E-132
rs10403399	3232_28	P13686	ACPF5	Acute gastritis	0.939	0.149	0.118	0.209	1.16 (0.92,1.46)	0.018	2.25E-06	TRUE	8.70E-131
rs10403399	3232_28	P13686	ACPF5	Gastroesophageal reflux disease	0.949	0.015	0.037	0.682	1.02 (0.94,1.09)	0.018	2.26E-07	TRUE	4.93E-133
rs10403399	3232_28	P13686	ACPF5	Irritable bowel syndrome	0.993	0.020	0.060	0.732	1.02 (0.91,1.15)	0.018	1.85E-07	TRUE	2.15E-132
rs10403399	3232_28	P13686	ACPF5	Diverticular disease	1.000	0.000	0.033	1.000	1.00 (0.94,1.07)	0.018	5.65E-11	TRUE	1.21E-133
rs10403399	3232_28	P13686	ACPF5	Cirrhosis	1.000	0.009	0.085	0.920	1.01 (0.85,1.19)	0.018	1.32E-08	TRUE	3.87E-134
rs148804382	3343_1	Q03154	ACY1	Diverticular disease	0.238	0.101	0.045	0.025	1.11 (1.01,1.21)	0.014	7.22E-06	TRUE	6.78E-103
rs148804382	3343_1	Q03154	ACY1	Cholelithiasis	0.582	0.084	0.050	0.091	1.09 (0.99,1.20)	0.014	3.70E-06	TRUE	1.01E-104
rs148804382	3343_1	Q03154	ACY1	Gastroesophageal reflux disease	0.773	0.043	0.052	0.410	1.04 (0.94,1.16)	0.014	9.34E-07	TRUE	3.97E-106
rs148804382	3343_1	Q03154	ACY1	Cholecystitis	0.847	0.021	0.021	0.929	1.02 (0.95,1.23)	0.014	6.75E-08	TRUE	4.43E-101
rs148804382	3343_1	Q03154	ACY1	Acute gastritis	0.964	0.034	0.164	0.838	1.03 (0.75,1.43)	0.014	5.94E-08	TRUE	3.33E-107
rs148804382	3343_1	Q03154	ACY1	Cirrhosis	1.000	-0.111	0.115	0.338	0.90 (0.71,1.12)	0.014	1.18E-06	TRUE	3.13E-106
rs148804382	3343_1	Q03154	ACY1	Nonalcoholic fatty liver disease	0.981	0.031	0.151	0.839	1.03 (0.77,1.39)	0.014	5.29E-08	TRUE	9.89E-108
rs148804382	3343_1	Q03154	ACY1	Chronic gastritis (Atrophic gastritis)	0.993	0.014	0.116	0.906	1.01 (0.81,1.27)	0.014	1.99E-08	TRUE	1.98E-107
rs148804382	3343_1	Q03154	ACY1	Irritable bowel syndrome	-0.002	0.052	0.082	0.855	0.95 (0.85,1.07)	0.014	1.11E-10	TRUE	3.20E-107
rs148804382	3343_1	Q03154	ACY1	Cholecystitis	0.983	0.024	0.115	0.835	1.02 (0.82,1.28)	0.014	5.97E-08	TRUE	2.16E-107
rs11534419	6379_62	Q86TH1	ADAMTSL2	Gastroesophageal reflux disease	0.773	0.070	0.071	0.323	1.07 (0.93,1.23)	0.005	1.36E-06	TRUE	7.56E-35
rs11534419	6379_62	Q86TH1	ADAMTSL2	Gastric ulcer	0.741	-0.131	0.133	0.324	0.88 (0.68,1.14)	0.005	1.40E-06	TRUE	9.46E-35
rs11534419	6379_62	Q86TH1	ADAMTSL2	Cirrhosis	0.798	-0.242	0.160	0.131	0.79 (0.57,1.07)	0.005	2.91E-06	TRUE	2.06E-34
rs11534419	6379_62	Q86TH1	ADAMTSL2	Cholelithiasis	0.823	-0.041	0.066	0.534	0.96 (0.84,1.09)	0.005	5.15E-07	TRUE	2.22E-35
rs11534419	6379_62	Q86TH1	ADAMTSL2	Cholecystitis (Atrophic gastritis)	0.841	-0.173	0.107	0.193	0.81 (0.65,1.01)	0.005	1.32E-06	TRUE	1.63E-34
rs11534419	6379_62	Q86TH1	ADAMTSL2	Acute gastritis	0.964	-0.024	0.222	0.913	0.98 (0.63,1.51)	0.005	1.65E-08	TRUE	8.06E-36
rs11534419	6379_62	Q86TH1	ADAMTSL2	Nonalcoholic fatty liver disease	0.981	-0.016	0.210	0.939	0.98 (0.65,1.49)	0.005	7.84E-09	TRUE	5.04E-36
rs11534419	6379_62	Q86TH1	ADAMTSL2	Irritable bowel syndrome	0.993	0.031	0.112	0.779	1.03 (0.83,1.28)	0.005	1.20E-07	TRUE	1.78E-35
rs11534419	6379_62	Q86TH1	ADAMTSL2	Cholecystitis	0.983	0.032	0.157	0.838	1.03 (0.76,1.41)	0.005	5.75E-08	TRUE	9.05E-36
rs11534419	6379_62	Q86TH1	ADAMTSL2	Diverticular disease	1.000	0.031	0.064	0.522	1.00 (0.91,1.17)	0.005	3.60E-07	TRUE	2.49E-35
rs1229984	9834_62	P00325	ADH1B	Nonalcoholic fatty liver disease	0.306	0.524	0.240	0.067	1.69 (1.06,2.70)	0.001	6.12E-06	TRUE	8.21E-10
rs1229984	9834_62	P00325	ADH1B	Cholelithiasis	0.664	-0.112	0.083	0.179	0.89 (0.76,1.05)	0.001	2.33E-06	TRUE	7.06E-11
rs1229984	9834_62	P00325	ADH1B	Gastric ulcer	0.715	0.181	0.153	0.236	1.20 (0.89,1.62)	0.001	2.02E-06	TRUE	6.92E-11
rs1229984	9834_62	P00325	ADH1B	Chronic gastritis (Atrophic gastritis)	0.843	0.320	0.226	0.156	1.38 (0.88,2.14)	0.001	2.84E-06	TRUE	9.34E-11
rs1229984	9834_62	P00325	ADH1B	Gastroesophageal reflux disease	0.959	-0.014	0.083	0.866	0.99 (0.84,1.16)	0.001	3.89E-08	TRUE	1.42E-11
rs1229984	9834_62	P00325	ADH1B	Cholecystitis	-0.098	0.066	0.096	0.292	1.02 (0.54,1.92)	0.001	1.53E-07	TRUE	4.89E-11
rs1229984	9834_62	P00325	ADH1B	Irritable bowel syndrome	0.993	-0.051	0.133	0.704	0.95 (0.73,1.23)	0.001	2.21E-07	TRUE	2.28E-11
rs1229984	9834_62	P00325	ADH1B	Cholecystitis	0.983	0.036	0.185	0.845	1.04 (0.72,1.49)	0.001	5.26E-08	TRUE	1.48E-11
rs1229984	9834_62	P00325	ADH1B	Diverticular disease	1.000	0.000	0.068	0.995	1.00 (0.87,1.14)	0.001	4.38E-11	TRUE	1.18E-11
rs2602844	8325_37	P08319	ADH4	Cholecystitis	0.256	0.364	0.162	0.024	1.44 (1.05,1.98)	0.005	6.99E-06	TRUE	4.95E-35
rs2602844	8325_37	P08319	ADH4	Gastroesophageal reflux disease	0.689	0.085	0.072	0.237	1.09 (0.95,1.25)	0.005	1.92E-06	TRUE	2.71E-36
rs2602844	8325_37	P08319	ADH4	Chronic gastritis	-0.192	0.703	0.066	0.159	0.92 (0.63,1.36)	0.005	2.89E-06	TRUE	6.84E-36
rs2602844	8325_37	P08319	ADH4	Cirrhosis	0.798	-0.249	0.163	0.127	0.78 (0.57,1.07)	0.005	2.97E-06	TRUE	4.67E-36
rs2602844	8325_37	P08319	ADH4	Nonalcoholic fatty liver disease	0.795	-0.256	0.216	0.236	0.77 (0.51,1.18)	0.005	1.82E-06	TRUE	1.96E-36
rs2602844	8325_37	P08319	ADH4	Acute gastritis	0.964	-0.221	0.227	0.329	0.80 (0.51,1.25)	0.005	1.35E-06	TRUE	1.86E-36
rs2602844	8325_37	P08319	ADH4	Chronic gastritis (Atrophic gastritis)	0.993	0.007	0.139	0.963	1.01 (0.77,1.32)	0.005	3.50E-09	TRUE	1.34E-37
rs2602844	8325_37	P08319	ADH4	Irritable bowel syndrome	0.993	-0.050	0.114	0.658	0.95 (0.76,1.19)	0.005	2.96E-07	TRUE	5.90E-37
rs2602844	8325_37	P08319	ADH4	Cholecystitis	1.000	-0.077	0.066	0.319	1.01 (0.85,1.14)	0.005	1.32E-06	TRUE	1.63E-37
rs143257534	3554_24	O15848	ADIPOQ	Cholecystitis	0.171	0.228	0.086	0.008	1.26 (1.06,1.49)	0.020	9.56E-06	TRUE	1.67E-141
rs143257534	3554_24	O15848	ADIPOQ	Cirrhosis	0.363	0.190	0.087	0.030	1.21 (1.02,1.44)	0.020	6.07E-06	TRUE	3.30E-143
rs143257534	3554_24	O15848	ADIPOQ	Nonalcoholic fatty liver disease	0.635	0.174	0.115	0.129	1.19 (0.95,1.49)	0.020	2.96E-06	TRUE	1.01E-144
rs143257534	3554_24	O15848	ADIPOQ	Cholelithiasis	0.788	0.033	0.036	0.357	1.03 (0.96,1.11)	0.020	1.10E-06	TRUE	4.68E-146
rs143257534	3554_24	O15848	ADIPOQ	Chronic gastritis (Atrophic gastritis)	0.072	0.064	0.064	0.522	1.00 (0.93,1.07)	0.020	1.28E-06	TRUE	6.62E-145
rs143257534	3554_24	O15848	ADIPOQ	Gastric ulcer	0.849	0.054	0.073	0.454	1.06 (0.92,1.22)	0.020	0.80E-07	TRUE	1.20E-145
rs143257534	3554_24	O15848	ADIPOQ	Gastroesophageal reflux disease	0.937	0.019	0.039	0.619	1.02 (0.95,1.10)	0.020	3.38E-07	TRUE	1.20E-146
rs143257534	3554_24	O15848	ADIPOQ	Acute gastritis	0.964	-0.009	0.121	0.940	0.99 (0.78,1.26)	0.020	8.02E-09	TRUE	2.14E-147
rs143257534	3554_24	O15848	ADIPOQ	Irritable bowel syndrome	0.993	0.044	0.061	0.472	1.04 (0.93,1.18)	0.020	7.97E-07	TRUE	3.33E-145
rs143257534	3554_24	O15848	ADIPOQ	Diverticular disease	1.000	0.011	0.034	0.744</					

Table S6. Association of putative type 2 diabetes-associated proteins in deCODE with gastrointestinal diseases.

Index SNP	Somalogic	UniProt	Gene	GI outcomes	FDR	b	se	pval	OR (95% CI)	snp_r2.exposure	snp_r2.outcome	correct_causal_direction	steiger_pval
rs28590506	13460_4	O15335	CHAD	Cholelithiasis	0.983	0.109	0.369	0.768	1.11 (0.54,2.30)	0.001	1.77E-07	TRUE	1.47E-08
rs28590506	13460_4	O15335	CHAD	Diverticular disease	1.000	-0.001	0.148	0.996	1.00 (0.88,1.17)	0.004	2.92E-07	TRUE	1.81E-06
rs28590506	13460_4	O15335	CHAD	Cirrhosis	1.000	0.109	0.375	0.772	1.11 (0.53,2.32)	0.001	1.08E-07	TRUE	1.38E-08
rs1908671	9416_77	P14384	CPM	Cholelithiasis	0.256	0.454	0.194	0.020	1.57 (1.08,2.31)	0.004	7.47E-06	TRUE	1.94E-25
rs1908671	9416_77	P14384	CPM	Gastric ulcer	0.708	0.228	0.164	0.164	1.26 (0.91,1.73)	0.004	2.78E-06	TRUE	2.76E-26
rs1908671	9416_77	P14384	CPM	Nonalcoholic fatty liver disease	0.795	0.239	0.259	0.204	1.39 (0.84,2.31)	0.004	2.07E-06	TRUE	1.29E-26
rs1908671	9416_77	P14384	CPM	Cholelithiasis	0.788	0.081	0.082	0.323	1.08 (0.92,1.27)	0.004	1.26E-06	TRUE	7.04E-27
rs1908671	9416_77	P14384	CPM	Diverticular disease	0.913	0.079	0.077	0.305	0.99 (0.93,1.06)	0.004	1.52E-06	TRUE	1.17E-26
rs1908671	9416_77	P14384	CPM	Chronic gastritis (Atrophic gastritis)	0.859	0.136	0.173	0.430	1.15 (0.82,1.61)	0.004	8.77E-07	TRUE	6.13E-27
rs1908671	9416_77	P14384	CPM	Gastroesophageal reflux disease	0.959	0.007	0.087	0.937	1.01 (0.85,1.19)	0.004	7.81E-09	TRUE	1.03E-27
rs1908671	9416_77	P14384	CPM	Acute gastritis	0.964	0.029	0.274	0.917	1.03 (0.60,1.76)	0.004	1.59E-08	TRUE	1.24E-27
rs1908671	9416_77	P14384	CPM	Irritable bowel syndrome	0.924	0.168	0.138	0.225	1.18 (0.90,1.55)	0.004	2.28E-06	TRUE	2.43E-26
rs1908671	9416_77	P14384	CPM	Cirrhosis	1.000	-0.001	0.197	0.860	1.00 (0.88,1.17)	0.004	2.09E-11	TRUE	7.22E-26
rs2645398	8007_19	P07858	CTSB	Cholelithiasis	0.077	-0.080	0.032	0.059	0.91 (0.86,0.97)	0.025	1.00E-05	TRUE	2.34E-185
rs2645398	8007_19	P07858	CTSB	Cirrhosis	0.304	-0.185	0.079	0.019	1.20 (1.03,1.41)	0.025	7.04E-06	TRUE	1.25E-186
rs2645398	8007_19	P07858	CTSB	Chronic gastritis (Atrophic gastritis)	0.859	-0.050	0.066	0.444	0.95 (0.84,1.08)	0.025	8.27E-07	TRUE	6.75E-190
rs2645398	8007_19	P07858	CTSB	Acute gastritis	0.964	0.119	0.109	0.273	1.13 (0.91,1.40)	0.025	1.71E-06	TRUE	6.98E-189
rs2645398	8007_19	P07858	CTSB	Nonalcoholic fatty liver disease	0.910	0.102	0.104	0.327	1.10 (0.90,1.36)	0.025	1.23E-06	TRUE	3.08E-190
rs2645398	8007_19	P07858	CTSB	Gastroesophageal reflux disease	0.959	0.006	0.035	0.860	1.01 (0.94,1.08)	0.025	4.42E-08	TRUE	8.18E-192
rs2645398	8007_19	P07858	CTSB	Gastric ulcer	0.967	0.007	0.066	0.912	1.01 (0.88,1.15)	0.025	1.73E-08	TRUE	1.52E-191
rs2645398	8007_19	P07858	CTSB	Irritable bowel syndrome	0.993	0.033	0.055	0.551	1.03 (0.93,1.15)	0.025	5.46E-07	TRUE	1.62E-189
rs2645398	8007_19	P07858	CTSB	Cholelithiasis	0.996	-0.003	0.078	0.969	1.00 (0.86,1.16)	0.025	2.15E-09	TRUE	3.43E-192
rs2645398	8007_19	P07858	CTSB	Diverticular disease	1.000	-0.008	0.031	0.792	0.99 (0.93,1.05)	0.025	1.02E-07	TRUE	4.15E-191
rs55861089	5508_62	P07339	CTSD	Gastric ulcer	0.368	0.202	0.085	0.018	1.22 (1.03,1.45)	0.018	8.03E-06	TRUE	1.44E-130
rs55861089	5508_62	P07339	CTSD	Cholelithiasis	0.018	0.133	0.089	0.122	1.08 (0.78,1.32)	0.018	3.07E-07	TRUE	2.47E-133
rs55861089	5508_62	P07339	CTSD	Chronic gastritis (Atrophic gastritis)	0.859	0.069	0.098	0.485	1.07 (0.88,1.30)	0.018	6.90E-07	TRUE	1.27E-134
rs55861089	5508_62	P07339	CTSD	Acute gastritis	0.939	0.246	0.144	0.087	1.28 (0.96,1.69)	0.018	4.17E-06	TRUE	3.48E-132
rs55861089	5508_62	P07339	CTSD	Gastroesophageal reflux disease	0.959	0.100	0.045	0.818	1.01 (0.92,1.10)	0.018	7.19E-08	TRUE	6.29E-136
rs55861089	5508_62	P07339	CTSD	Diverticular disease	0.958	0.029	0.039	0.464	1.03 (0.95,1.11)	0.018	8.66E-07	TRUE	2.07E-134
rs55861089	5508_62	P07339	CTSD	Nonalcoholic fatty liver disease	0.018	0.133	0.089	0.122	1.08 (0.78,1.32)	0.018	2.25E-08	TRUE	1.48E-133
rs55861089	5508_62	P07339	CTSD	Gastric ulcer	1.000	0.081	0.101	0.422	1.08 (0.89,1.32)	0.018	7.28E-07	TRUE	4.70E-135
rs55861089	5508_62	P07339	CTSD	Irritable bowel syndrome	0.993	0.006	0.072	0.928	1.01 (0.87,1.16)	0.018	1.29E-08	TRUE	1.73E-135
rs55861089	5508_62	P07339	CTSD	Cholelithiasis	0.996	0.006	0.100	0.951	1.01 (0.83,1.23)	0.018	4.91E-09	TRUE	2.58E-136
rs10900074	9278_9	P48061	CXCL12	Cholelithiasis	0.248	0.244	0.113	0.031	1.28 (1.02,1.59)	0.002	5.96E-06	TRUE	1.47E-112
rs1023264	3516_60	P48061	CXCL12	Chronic gastritis (Atrophic gastritis)	0.589	0.267	0.115	0.020	1.31 (1.04,1.63)	0.002	7.87E-06	TRUE	3.86E-48
rs1023264	3516_60	P48061	CXCL12	Cholelithiasis	0.787	0.047	0.087	0.587	1.07 (0.97,1.18)	0.002	2.59E-06	TRUE	1.85E-49
rs10900074	9278_9	P48061	CXCL12	Cholelithiasis	0.718	0.362	0.270	0.181	1.44 (0.84,2.44)	0.002	2.45E-06	TRUE	4.86E-13
rs1023264	3516_60	P48061	CXCL12	Gastroesophageal reflux disease	0.757	0.062	0.058	0.284	1.06 (0.95,1.19)	0.002	1.57E-06	TRUE	5.34E-50
rs10900074	9278_9	P48061	CXCL12	Irritable bowel syndrome	0.798	0.314	0.192	0.101	1.37 (0.94,1.99)	0.002	4.14E-06	TRUE	1.06E-12
rs1023264	3516_60	P48061	CXCL12	Cholelithiasis	0.823	0.039	0.055	0.476	1.04 (0.93,1.16)	0.002	6.56E-07	TRUE	1.18E-50
rs10900074	9278_9	P48061	CXCL12	Chronic gastritis (Atrophic gastritis)	0.859	0.079	0.234	0.044	1.09 (0.76,1.59)	0.002	8.33E-07	TRUE	2.07E-13
rs1023264	3516_60	P48061	CXCL12	Acute gastritis	0.941	-0.298	0.184	0.104	0.74 (0.52,1.08)	0.002	3.76E-06	TRUE	1.26E-49
rs1023264	3516_60	P48061	CXCL12	Cholelithiasis	0.942	-0.092	0.130	0.478	0.91 (0.71,1.18)	0.002	6.87E-07	TRUE	1.66E-50
rs1023264	3516_60	P48061	CXCL12	Nonalcoholic fatty liver disease	0.931	-0.162	0.173	0.349	0.85 (0.61,1.19)	0.002	1.12E-06	TRUE	2.26E-50
rs10900074	9278_9	P48061	CXCL12	Gastroesophageal reflux disease	0.959	0.014	0.121	0.907	1.01 (0.80,1.29)	0.002	1.73E-08	TRUE	6.71E-14
rs10900074	9278_9	P48061	CXCL12	Cholelithiasis	0.964	0.195	0.381	0.608	1.22 (0.88,1.68)	0.002	3.77E-07	TRUE	1.39E-13
rs10900074	9278_9	P48061	CXCL12	Chronic gastritis (Atrophic gastritis)	0.909	0.097	0.097	0.499	1.07 (0.91,1.26)	0.002	2.97E-09	TRUE	1.54E-19
rs10900074	9278_9	P48061	CXCL12	Nonalcoholic fatty liver disease	0.981	-0.031	0.360	0.930	0.97 (0.48,1.96)	0.002	7.96E-09	TRUE	5.90E-14
rs1023264	3516_60	P48061	CXCL12	Irritable bowel syndrome	0.993	-0.003	0.092	0.976	1.00 (0.83,1.19)	0.002	1.13E-09	TRUE	3.43E-51
rs1023264	3516_60	P48061	CXCL12	Diverticular disease	1.000	0.016	0.052	0.759	1.02 (0.92,1.12)	0.002	1.42E-07	TRUE	6.17E-51
rs1023264	3516_60	P48061	CXCL12	Cirrhosis	1.000	0.043	0.132	0.745	1.04 (0.81,1.35)	0.002	1.37E-07	TRUE	3.31E-51
rs10900074	9278_9	P48061	CXCL12	Cirrhosis	1.000	-0.121	0.274	0.658	0.89 (0.52,1.51)	0.002	2.90E-07	TRUE	1.03E-13
rs10900074	9278_9	P48061	CXCL12	Diverticular disease	0.900	-0.022	0.037	0.803	1.00 (0.92,1.09)	0.002	8.89E-10	TRUE	1.22E-14
rs12948284	17758_79	Q724W1	DCXR	Gastroesophageal reflux disease	0.544	-0.167	0.086	0.051	0.85 (0.71,1.00)	0.003	5.22E-06	TRUE	2.91E-25
rs12948284	17758_79	Q724W1	DCXR	Gastric ulcer	0.708	0.225	0.162	0.165	1.25 (0.91,1.72)	0.003	2.79E-06	TRUE	1.01E-25
rs12948284	17758_79	Q724W1	DCXR	Cirrhosis	0.798	0.270	0.194	0.164	1.31 (0.90,1.92)	0.003	2.47E-06	TRUE	6.20E-26
rs12948284	17758_79	Q724W1	DCXR	Irritable bowel syndrome	0.798	-0.231	0.135	0.088	0.79 (0.61,1.03)	0.003	4.45E-06	TRUE	2.82E-25
rs12948284	17758_79	Q724W1	DCXR	Cholelithiasis	0.823	0.065	0.080	0.419	1.07 (0.91,1.25)	0.003	8.36E-07	TRUE	1.73E-26
rs12948284	17758_79	Q724W1	DCXR	Chronic gastritis (Atrophic gastritis)	0.967	0.069	0.166	0.587	1.07 (0.97,1.18)	0.003	2.51E-07	TRUE	1.85E-27
rs12948284	17758_79	Q724W1	DCXR	Acute gastritis	0.964	-0.253	0.270	0.348	0.78 (0.46,1.32)	0.003	1.26E-06	TRUE	3.36E-26
rs12948284	17758_79	Q724W1	DCXR	Diverticular disease	0.939	-0.059	0.076	0.434	0.94 (0.81,1.09)	0.003	8.83E-07	TRUE	2.42E-26
rs12948284	17758_79	Q724W1	DCXR	Nonalcoholic fatty liver disease	0.981	-0.080	0.256	0.753	1.08 (0.66,1.79)	0.003	1.28E-07	TRUE	5.62E-27
rs12948284	17758_79	Q724W1	DCXR	Cholelithiasis	0.996	-0.017	0.192	0.931	0.98 (0.88,1.13)	0.003	1.01E-08	TRUE	4.00E-27
rs78111814	9175_48	O60469	DSCAM	Cholelithiasis	0.756	0.049	0.069	0.291	1.07 (0.96,1.19)	0.010	3.01E-06	TRUE	1.08E-15
rs78111814	9175_48	O60469	DSCAM	Chronic gastritis (Atrophic gastritis)	0.741	-0.100	0.101	0.323	0.90 (0.74,1.10)	0.010	1.41E-06	TRUE	2.21E-75
rs78111814	9175_48	O60469	DSCAM	Cirrhosis	0.798	-0.160	0.122	0.187	0.85 (0.67,1.08)	0.010	2.23E-06	TRUE	2.49E-75
rs78111814	9175_48	O60469	DSCAM	Chronic gastritis (Atrophic gastritis)	0.859	-0.089	0.096	0.351	0.91 (0.76,1.10)	0.010	1.23E-06	TRUE	1.42E-75
rs78111814	9175_48	O60469	DSCAM	Acute gastritis	0.964	-0.152	0.165	0.357	0.86 (0.62,1.19)	0.010	1.21E-06	TRUE	1.50E-75
rs78111814	9175_48	O60469	DSCAM	Gastroesophageal reflux disease	0.959	0.009	0.053	0.871	1.01 (0.91,1.12)	0.010	3.56E-08	TRUE	4.85E-77
rs78111814</													

Table S6. Association of putative type 2 diabetes-associated proteins in deCODE with gastrointestinal diseases.

Index SNP	SomaLogic	UniProt	Gene	GI outcomes	FDR	se	pval	OR (95% CI)	snp_r2.exposure	snp_r2.outcome	correct_causal	direction	steiger_pval
rs3780126	9370_69	C92820	GGH	Diverticular disease	0.649	0.030	0.024	2.09 (1.03, 3.81)	0.025	2.32E-06	TRUE		2.78E-188
rs3780126	9370_69	C92820	GGH	Gastric ulcer	0.700	0.068	0.051	0.54 (0.39, 0.77)	0.025	2.62E-06	TRUE		4.75E-168
rs3780126	9370_69	C92820	GGH	Acute gastritis	0.964	0.076	0.085	0.367 (0.18, 0.72)	0.025	1.16E-06	TRUE		2.01E-189
rs3780126	9370_69	C92820	GGH	Nonalcoholic fatty liver disease	0.981	0.005	0.080	0.948 (0.1, 8.6)	0.025	5.38E-09	TRUE		1.08E-192
rs3780126	9370_69	C92820	GHR	Cirrhosis	1.000	-0.030	0.061	0.627 (0.3, 1.0)	0.025	3.01E-07	TRUE		1.40E-191
rs4610468	2948_58	P10912	GHR	Gastroesophageal reflux disease	0.567	-0.128	0.068	0.662 (0.3, 1.1)	0.013	4.77E-06	TRUE		2.96E-94
rs4610468	2948_58	P10912	GHR	Gastric ulcer	0.708	0.217	0.120	0.172 (0.06, 0.57)	0.013	4.67E-06	TRUE		4.51E-94
rs4610468	2948_58	P10912	GHR	Acute gastritis	0.939	0.110	0.110	0.164 (0.06, 0.41)	0.013	2.75E-06	TRUE		1.97E-95
rs4610468	2948_58	P10912	GHR	Nonalcoholic fatty liver disease	0.878	-0.196	0.188	0.297 (0.07, 1.1)	0.013	1.40E-06	TRUE		3.43E-96
rs4610468	2948_58	P10912	GHR	Cholelithiasis	0.947	0.009	0.071	0.903 (0.1, 8.8)	0.013	1.87E-08	TRUE		6.51E-98
rs4610468	2948_58	P10912	GHR	Cholecystitis	0.942	-0.093	0.147	0.527 (0.1, 2.2)	0.013	5.48E-07	TRUE		1.19E-96
rs4610468	2948_58	P10912	GHR	Chronic gastritis (Atrophic gastritis)	0.993	-0.008	0.397	0.984 (0.4, 2.1)	0.013	5.98E-10	TRUE		1.02E-97
rs4610468	2948_58	P10912	GHR	Irritable bowel syndrome	0.993	-0.009	0.109	0.933 (0.3, 2.3)	0.013	1.02E-06	TRUE		3.42E-97
rs4610468	2948_58	P10912	GHR	Diverticular disease	1.000	0.012	0.053	0.811 (0.1, 5.1)	0.013	7.80E-08	TRUE		3.33E-97
rs4610468	2948_58	P10912	GHR	Cirrhosis	1.000	0.027	0.143	0.851 (0.3, 2.1)	0.013	4.46E-08	TRUE		7.94E-98
rs76829642	13697_51	P21695	GD1	Cholecystitis	0.718	0.326	0.253	0.198 (0.04, 0.8)	0.001	2.27E-06	TRUE		1.48E-09
rs76829642	13697_51	P21695	GD1	Cholelithiasis	0.906	-0.042	0.111	0.709 (0.3, 1.5)	0.001	1.82E-07	TRUE		4.01E-10
rs76829642	13697_51	P21695	GD1	Gastric ulcer	0.953	0.086	0.212	0.684 (0.2, 1.6)	0.001	2.39E-07	TRUE		4.77E-10
rs76829642	13697_51	P21695	GD1	Gastroesophageal reflux disease	0.953	-0.009	0.099	0.933 (0.3, 2.3)	0.001	1.02E-06	TRUE		2.96E-10
rs76829642	13697_51	P21695	GD1	Acute gastritis	0.964	-0.194	0.368	0.599 (0.2, 1.0)	0.001	3.94E-07	TRUE		5.56E-10
rs76829642	13697_51	P21695	GD1	Nonalcoholic fatty liver disease	0.981	0.023	0.332	0.945 (0.2, 5.3)	0.001	6.13E-09	TRUE		2.64E-10
rs76829642	13697_51	P21695	GD1	Cirrhosis	1.000	-0.181	0.252	0.473 (0.1, 1.3)	0.001	6.60E-07	TRUE		6.27E-10
rs76829642	13697_51	P21695	GD1	Chronic gastritis (Atrophic gastritis)	0.993	-0.033	0.270	0.902 (0.3, 2.5)	0.001	2.13E-08	TRUE		3.12E-10
rs76829642	13697_51	P21695	GD1	Irritable bowel syndrome	0.993	0.115	0.162	0.528 (0.1, 2.3)	0.001	6.11E-07	TRUE		7.15E-10
rs76829642	13697_51	P21695	GD1	Diverticular disease	0.993	0.068	0.096	0.874 (0.3, 2.4)	0.001	3.82E-07	TRUE		4.77E-10
rs10985149	16607_78	P06396	GSN	Acute gastritis	0.964	0.019	0.132	0.887 (0.2, 3.2)	0.009	2.86E-08	TRUE		2.05E-71
rs10985149	16607_78	P06396	GSN	Chronic gastritis (Atrophic gastritis)	0.993	0.004	0.075	0.954 (0.1, 8.7)	0.009	4.82E-09	TRUE		1.38E-71
rs10985149	16607_78	P06396	GSN	Cholecystitis	0.717	0.134	0.095	0.156 (0.01, 1.9)	0.009	2.77E-06	TRUE		2.06E-69
rs10985149	16607_78	P06396	GSN	Cholelithiasis	0.713	0.047	0.309	0.228 (0.05, 0.9)	0.009	1.88E-06	TRUE		5.28E-70
rs10985149	16607_78	P06396	GSN	Chronic gastritis (Atrophic gastritis)	0.993	-0.064	0.068	0.569 (0.1, 2.4)	0.009	5.49E-07	TRUE		6.23E-71
rs10985149	16607_78	P06396	GSN	Diverticular disease	1.000	-0.021	0.039	0.591 (0.1, 1.0)	0.009	1.06E-07	TRUE		1.43E-70
rs10985149	16607_78	P06396	GSN	Gastric ulcer	0.708	0.143	0.081	0.076 (0.01, 0.9)	0.009	4.54E-06	TRUE		1.34E-68
rs10985149	16607_78	P06396	GSN	Gastroesophageal reflux disease	0.837	-0.029	0.042	0.489 (0.1, 1.5)	0.009	6.52E-07	TRUE		1.25E-70
rs10985149	16607_78	P06396	GSN	Irritable bowel syndrome	0.924	0.080	0.067	0.231 (0.08, 0.5)	0.009	2.20E-06	TRUE		2.72E-69
rs10985149	16607_78	P06396	GSN	Nonalcoholic fatty liver disease	0.981	-0.068	0.128	0.592 (0.1, 2.0)	0.009	3.68E-07	TRUE		4.04E-71
rs2144693	17138_8	P08263	GSTA1	Cholecystitis	0.669	-0.039	0.104	0.669 (0.2, 1.9)	0.025	2.15E-06	TRUE		2.12E-189
rs2144693	17138_8	P08263	GSTA1	Gastric ulcer	0.708	-0.100	0.061	0.099 (0.0, 0.8)	0.025	3.93E-06	TRUE		3.37E-187
rs2144693	17138_8	P08263	GSTA1	Gastroesophageal reflux disease	0.773	-0.026	0.032	0.415 (0.1, 1.0)	0.025	9.15E-07	TRUE		4.72E-190
rs2144693	17138_8	P08263	GSTA1	Chronic gastritis (Atrophic gastritis)	0.843	-0.084	0.063	0.183 (0.02, 1.4)	0.025	2.51E-06	TRUE		2.56E-188
rs2144693	17138_8	P08263	GSTA1	Acute gastritis	0.964	0.104	0.102	0.304 (0.1, 0.9)	0.025	1.50E-06	TRUE		4.47E-189
rs2144693	17138_8	P08263	GSTA1	Nonalcoholic fatty liver disease	0.981	-0.055	0.096	0.565 (0.1, 2.4)	0.025	4.22E-07	TRUE		2.51E-191
rs2144693	17138_8	P08263	GSTA1	Irritable bowel syndrome	0.993	0.001	0.051	0.988 (0.1, 9.0)	0.025	1.23E-10	TRUE		3.22E-191
rs2144693	17138_8	P08263	GSTA1	Cholecystitis	0.983	-0.019	0.027	0.794 (0.1, 4.1)	0.025	9.22E-08	TRUE		1.40E-191
rs2144693	17138_8	P08263	GSTA1	Cirrhosis	1.000	-0.013	0.073	0.861 (0.1, 6.1)	0.025	4.04E-08	TRUE		2.10E-192
rs2144693	17138_8	P08263	GSTA1	Diverticular disease	1.000	0.009	0.029	0.749 (0.1, 3.5)	0.025	1.54E-07	TRUE		1.61E-191
rs34356500	15562_24	P08236	GUSB	Cholecystitis	0.265	0.273	0.125	0.029 (0.1, 0.3)	0.008	6.86E-06	TRUE		1.87E-58
rs34356500	15562_24	P08236	GUSB	Diverticular disease	0.469	-0.066	0.063	0.545 (0.1, 2.1)	0.008	4.37E-06	TRUE		6.20E-59
rs34356500	15562_24	P08236	GUSB	Gastroesophageal reflux disease	0.589	-0.096	0.056	0.086 (0.01, 0.8)	0.008	4.09E-06	TRUE		3.71E-59
rs34356500	15562_24	P08236	GUSB	Gastric ulcer	0.715	-0.126	0.106	0.231 (0.08, 0.7)	0.008	2.07E-06	TRUE		8.86E-60
rs34356500	15562_24	P08236	GUSB	Cirrhosis	0.798	0.181	0.126	0.152 (0.04, 0.5)	0.008	2.62E-06	TRUE		7.45E-60
rs34356500	15562_24	P08236	GUSB	Irritable bowel syndrome	0.798	-0.134	0.088	0.128 (0.07, 0.2)	0.008	3.52E-06	TRUE		5.02E-59
rs34356500	15562_24	P08236	GUSB	Cholelithiasis	0.823	0.036	0.052	0.493 (0.1, 1.9)	0.008	5.99E-07	TRUE		6.04E-61
rs34356500	15562_24	P08236	GUSB	Chronic gastritis (Atrophic gastritis)	0.959	-0.023	0.019	0.519 (0.1, 2.0)	0.008	1.79E-06	TRUE		6.73E-60
rs34356500	15562_24	P08236	GUSB	Acute gastritis	0.939	0.264	0.176	0.133 (0.02, 0.8)	0.008	3.21E-06	TRUE		2.38E-59
rs3828998	2771_35	P08833	IGFBP1	Cholelithiasis	0.664	0.126	0.098	0.196 (0.01, 3.7)	0.003	2.15E-06	TRUE		3.14E-19
rs3828998	2771_35	P08833	IGFBP1	Gastric ulcer	0.708	-0.303	0.195	0.120 (0.04, 0.5)	0.003	3.48E-06	TRUE		7.41E-19
rs3828998	2771_35	P08833	IGFBP1	Acute gastritis	0.939	-0.446	0.326	0.172 (0.04, 0.7)	0.003	2.67E-06	TRUE		4.94E-19
rs3828998	2771_35	P08833	IGFBP1	Chronic gastritis (Atrophic gastritis)	0.881	-0.098	0.203	0.531 (0.1, 2.3)	0.003	3.29E-07	TRUE		8.21E-20
rs3828998	2771_35	P08833	IGFBP1	Gastroesophageal reflux disease	0.939	0.039	0.104	0.708 (0.1, 3.1)	0.003	2.19E-06	TRUE		2.12E-189
rs3828998	2771_35	P08833	IGFBP1	Nonalcoholic fatty liver disease	0.981	0.161	0.309	0.602 (0.1, 6.4)	0.003	3.48E-07	TRUE		7.04E-20
rs3828998	2771_35	P08833	IGFBP1	Irritable bowel syndrome	0.993	0.052	0.164	0.751 (0.1, 4.5)	0.003	1.52E-07	TRUE		1.77E-20
rs3828998	2771_35	P08833	IGFBP1	Cholecystitis	0.983	0.085	0.231	0.715 (0.1, 3.0)	0.003	1.83E-07	TRUE		6.05E-20
rs3828998	2771_35	P08833	IGFBP1	Diverticular disease	1.000	0.005	0.092	0.955 (0.1, 8.4)	0.003	5.22E-09	TRUE		3.84E-20
rs3828998	2771_35	P08833	IGFBP1	Chronic gastritis (Atrophic gastritis)	0.939	-0.034	0.016	0.261 (0.07, 0.9)	0.003	4.10E-07	TRUE		3.03E-20
rs4674100	8469_41	P18065	IGFBP2	Gastroesophageal reflux disease	0.589	0.264	0.151	0.081 (0.01, 0.7)	0.001	4.18E-06	TRUE		3.33E-08
rs4674100	8469_41	P18065	IGFBP2	Cholecystitis	0.823	-0.382	0.338	0.258 (0.03, 1.2)	0.001	1.76E-06	TRUE		1.55E-08
rs4674100	8469_41	P18065	IGFBP2	Chronic gastritis (Atrophic gastritis)	0.859	0.176	0.285	0.537 (0.1, 2.6)	0.001	5.36E-07	TRUE		8.37E-09
rs4674100	8469_41	P18065	IGFBP2	Gastric ulcer	0.967	-0.065	0.285	0.819 (0.4, 1.5)	0.001	7.73E-08	TRUE		5.17E-09
rs4674100	8469_41	P18065	IGFBP2	Cholelithiasis	0.947	0.019	0.141	0.891 (0.2, 3.1)	0.001	2.25E-08	TRUE		4.11E-09
rs4674100	8469_41	P18065	IGFBP2	Acute gastritis	0.913	-0.084	0.123	0.474 (0.1, 1.8)	0.001	8.21E-08	TRUE		6.20E-09
rs4674100	8469_41	P18065	IGFBP2	Cirrhosis	1.000	-0.338	0.343	0.325 (0.1, 0.9)	0.001	1.25E-06	TRUE		1.18E-08
rs4674100	8469_41	P18065	IGFBP2	Nonalcoholic fatty liver disease	0.981	0.384	0.451	0.394 (0.1, 1.1)	0.				

Table S6. Association of putative type 2 diabetes-associated proteins in deCODE with gastrointestinal diseases.

Index SNP	SomaLogIC	UnIProt	Gene	GI outcomes	FDR	b	se	pval	OR (95% CI)	snp_r2.exposure	snp_r2.outcome	correct_causal_direction	steiger_pval
rs2228603	15573_110	O14594	NCAN	Cholelithiasis	0.823	0.033	0.042	0.436	1.03 (0.95,1.12)	0.012	7.89E-07	TRUE	1.31E-88
rs2228603	15573_110	O14594	NCAN	Chronic gastritis (Atrophic gastritis)	0.851	-0.092	0.061	0.841	0.99 (0.88,1.1)	0.025	1.54E-06	TRUE	1.0E-197
rs2228603	15573_110	O14594	NCAN	Cholelithiasis	0.942	0.082	0.100	0.411	1.09 (0.89,1.32)	0.012	9.31E-07	TRUE	2.93E-88
rs2228603	15573_110	O14594	NCAN	Acute gastritis	0.964	0.080	0.140	0.568	1.08 (0.82,1.43)	0.012	4.66E-07	TRUE	1.48E-88
rs2228603	15573_110	O14594	NCAN	Diverticular disease	1.000	-0.012	0.040	0.756	0.99 (0.91,1.07)	0.012	1.37E-07	TRUE	5.20E-89
rs6656887	7179_69	O94856	NFASC	Chronic gastritis (Atrophic gastritis)	0.859	0.033	0.052	0.529	1.03 (0.93,1.15)	0.025	5.57E-07	TRUE	2.78E-190
rs6656887	7179_69	O94856	NFASC	Cholelithiasis	0.909	-0.008	0.025	0.753	0.99 (0.95,1.04)	0.025	1.29E-07	TRUE	5.95E-192
rs6656887	7179_69	O94856	NFASC	Chronic gastritis (Atrophic gastritis)	0.953	0.049	0.079	0.691	1.02 (0.93,1.12)	0.025	2.28E-07	TRUE	9.87E-191
rs6656887	7179_69	O94856	NFASC	Gastroesophageal reflux disease	0.959	-0.008	0.026	0.771	0.99 (0.94,1.04)	0.025	1.89E-11	TRUE	1.65E-191
rs6656887	7179_69	O94856	NFASC	Acute gastritis	0.964	-0.041	0.082	0.615	0.96 (0.82,1.13)	0.025	3.60E-07	TRUE	1.52E-190
rs6656887	7179_69	O94856	NFASC	Nonalcoholic fatty liver disease	0.981	0.017	0.077	0.823	1.02 (0.87,1.18)	0.025	6.45E-08	TRUE	2.89E-192
rs6656887	7179_69	O94856	NFASC	Irritable bowel syndrome	0.993	-0.012	0.041	0.766	0.99 (0.91,1.07)	0.025	1.33E-07	TRUE	2.15E-190
rs6656887	7179_69	O94856	NFASC	Cholelithiasis	0.983	-0.012	0.058	0.841	0.99 (0.88,1.1)	0.025	5.80E-08	TRUE	5.64E-192
rs6656887	7179_69	O94856	NFASC	Cirrhosis	1.000	-0.020	0.059	0.736	0.98 (0.87,1.1)	0.025	1.47E-07	TRUE	5.86E-192
rs6656887	7179_69	O94856	NFASC	Diverticular disease	1.000	-0.004	0.023	0.872	1.00 (0.95,1.04)	0.025	3.80E-08	TRUE	2.11E-191
rs198379	7655_11	P16860	NPPB	Acute gastritis	0.964	0.044	0.097	0.651	1.04 (0.86,1.26)	0.025	2.92E-07	TRUE	1.10E-190
rs198379	7655_11	P16860	NPPB	Chronic gastritis (Atrophic gastritis)	0.881	0.029	0.060	0.633	1.03 (0.91,1.16)	0.025	3.21E-07	TRUE	1.05E-190
rs198379	7655_11	P16860	NPPB	Cholelithiasis	0.942	0.044	0.069	0.527	1.04 (0.91,1.20)	0.025	5.51E-07	TRUE	1.51E-190
rs198379	7655_11	P16860	NPPB	Cirrhosis	0.238	0.064	0.029	0.225	1.07 (1.01,1.13)	0.025	6.40E-06	TRUE	7.64E-187
rs198379	7655_11	P16860	NPPB	Cirrhosis	1.000	-0.048	0.070	0.488	0.95 (0.83,1.09)	0.025	6.13E-07	TRUE	5.02E-191
rs198379	7655_11	P16860	NPPB	Diverticular disease	0.649	0.037	0.028	0.181	1.04 (0.98,1.1)	0.025	2.63E-06	TRUE	4.74E-188
rs198379	7655_11	P16860	NPPB	Gastric ulcer	0.715	0.066	0.058	0.257	1.07 (0.95,1.20)	0.025	1.85E-06	TRUE	1.18E-188
rs198379	7655_11	P16860	NPPB	Gastroesophageal reflux disease	0.643	-0.039	0.031	0.201	0.96 (0.91,1.02)	0.025	2.21E-06	TRUE	8.31E-189
rs198379	7655_11	P16860	NPPB	Irritable bowel syndrome	0.798	0.072	0.049	0.140	1.07 (0.98,1.18)	0.025	3.34E-06	TRUE	5.67E-187
rs198379	7655_11	P16860	NPPB	Nonalcoholic fatty liver disease	0.769	0.039	0.062	0.780	0.99 (0.86,1.13)	0.025	9.40E-07	TRUE	4.04E-189
rs7289344	15511_37	O95502	NPTXR	Cholelithiasis	0.077	0.037	0.013	0.006	1.04 (1.01,1.06)	0.025	9.62E-06	TRUE	1.65E-185
rs7289344	15511_37	O95502	NPTXR	Cirrhosis	0.883	-0.040	0.035	0.251	0.96 (0.90,1.03)	0.025	1.69E-06	TRUE	8.35E-190
rs7289344	15511_37	O95502	NPTXR	Chronic gastritis (Atrophic gastritis)	0.843	0.031	0.025	0.208	1.03 (0.98,1.08)	0.025	2.23E-06	TRUE	1.60E-188
rs7289344	15511_37	O95502	NPTXR	Acute gastritis	0.964	0.051	0.046	0.269	1.05 (0.98,1.15)	0.025	1.75E-06	TRUE	7.54E-189
rs7289344	15511_37	O95502	NPTXR	Cholelithiasis	0.229	0.042	0.029	0.942	1.03 (0.96,1.10)	0.025	9.85E-07	TRUE	5.90E-189
rs7289344	15511_37	O95502	NPTXR	Gastric ulcer	0.953	-0.012	0.029	0.884	0.99 (0.93,1.05)	0.025	2.40E-07	TRUE	1.06E-190
rs7289344	15511_37	O95502	NPTXR	Diverticular disease	0.939	0.011	0.014	0.439	1.01 (0.98,1.04)	0.025	8.61E-07	TRUE	1.12E-189
rs7289344	15511_37	O95502	NPTXR	Gastroesophageal reflux disease	0.959	0.003	0.015	0.840	1.00 (0.97,1.03)	0.025	5.52E-08	TRUE	9.36E-192
rs7289344	15511_37	O95502	NPTXR	Irritable bowel syndrome	0.993	-0.006	0.024	0.799	0.99 (0.95,1.04)	0.025	1.01E-11	TRUE	1.66E-190
rs7289344	15511_37	O95502	NPTXR	Nonalcoholic fatty liver disease	0.998	0.000	0.046	0.998	1.00 (0.91,1.10)	0.025	1.07E-07	TRUE	7.35E-193
rs844124	11313_100	P61457	PCBD1	Gastroesophageal reflux disease	0.181	0.047	0.018	0.181	1.05 (0.95,1.16)	0.025	2.19E-05	TRUE	4.08E-191
rs844124	11313_100	P61457	PCBD1	Nonalcoholic fatty liver disease	0.309	0.438	0.198	0.027	1.55 (1.05,2.28)	0.006	6.30E-06	TRUE	5.35E-45
rs844124	11313_100	P61457	PCBD1	Cholelithiasis	0.823	0.045	0.063	0.468	1.05 (0.93,1.18)	0.006	6.95E-07	TRUE	6.67E-47
rs844124	11313_100	P61457	PCBD1	Chronic gastritis (Atrophic gastritis)	0.859	0.100	0.130	0.441	1.11 (0.86,1.43)	0.006	8.40E-07	TRUE	1.26E-46
rs844124	11313_100	P61457	PCBD1	Cholelithiasis	0.880	0.145	0.149	0.330	1.16 (0.86,1.55)	0.006	1.31E-06	TRUE	1.99E-46
rs844124	11313_100	P61457	PCBD1	Acute gastritis	0.939	-0.482	0.209	0.021	0.62 (0.41,0.93)	0.006	7.60E-06	TRUE	1.63E-44
rs844124	11313_100	P61457	PCBD1	Gastric ulcer	0.939	0.125	0.125	0.369	1.07 (0.98,1.17)	0.006	8.27E-08	TRUE	1.55E-47
rs844124	11313_100	P61457	PCBD1	Irritable bowel syndrome	0.924	0.126	0.105	0.230	1.13 (0.92,1.39)	0.006	2.21E-06	TRUE	8.65E-46
rs844124	11313_100	P61457	PCBD1	Diverticular disease	1.000	0.002	0.059	0.979	1.00 (0.89,1.12)	0.006	1.36E-09	TRUE	1.33E-47
rs844124	11313_100	P61457	PCBD1	Cirrhosis	1.000	0.043	0.150	0.775	1.04 (0.78,1.40)	0.006	1.07E-07	TRUE	1.65E-47
rs575280	4459_68	Q16549	PCSK7	Chronic gastritis (Atrophic gastritis)	0.704	-0.110	0.060	0.066	0.90 (0.80,1.01)	0.025	4.76E-06	TRUE	6.47E-187
rs575280	4459_68	Q16549	PCSK7	Cholelithiasis	0.969	-0.069	0.069	0.889	1.01 (0.95,1.07)	0.025	1.36E-06	TRUE	1.89E-187
rs575280	4459_68	Q16549	PCSK7	Cholelithiasis	0.947	-0.005	0.029	0.863	0.99 (0.94,1.05)	0.025	4.04E-08	TRUE	2.51E-192
rs575280	4459_68	Q16549	PCSK7	Gastroesophageal reflux disease	0.959	0.003	0.031	0.928	1.00 (0.94,1.07)	0.025	1.04E-08	TRUE	4.54E-192
rs575280	4459_68	Q16549	PCSK7	Acute gastritis	0.964	0.025	0.098	0.798	1.03 (0.85,1.24)	0.025	9.35E-08	TRUE	3.08E-191
rs575280	4459_68	Q16549	PCSK7	Gastric ulcer	0.967	-0.006	0.059	0.924	0.99 (0.89,1.12)	0.025	1.33E-08	TRUE	1.39E-191
rs575280	4459_68	Q16549	PCSK7	Nonalcoholic fatty liver disease	0.981	-0.055	0.093	0.558	0.95 (0.79,1.14)	0.025	4.41E-07	TRUE	2.71E-191
rs575280	4459_68	Q16549	PCSK7	Chronic gastritis (Atrophic gastritis)	0.950	0.001	0.071	0.490	1.05 (0.95,1.17)	0.025	6.41E-07	TRUE	5.35E-191
rs575280	4459_68	Q16549	PCSK7	Irritable bowel syndrome	0.993	0.009	0.050	0.854	1.01 (0.92,1.11)	0.025	5.08E-08	TRUE	1.01E-190
rs575280	4459_68	Q16549	PCSK7	Diverticular disease	1.000	0.006	0.028	0.822	1.01 (0.95,1.06)	0.025	7.15E-08	TRUE	3.13E-191
rs748844	3216_2	P01833	PIGR	Gastric ulcer	0.886	0.061	0.103	0.554	1.06 (0.87,1.30)	0.008	5.05E-07	TRUE	1.77E-60
rs748844	3216_2	P01833	PIGR	Acute gastritis	0.939	0.219	0.173	0.205	1.25 (0.89,1.75)	0.008	2.30E-06	TRUE	1.88E-59
rs748844	3216_2	P01833	PIGR	Gastroesophageal reflux disease	0.894	-0.031	0.055	0.573	0.97 (0.87,1.08)	0.008	4.32E-07	TRUE	1.09E-60
rs748844	3216_2	P01833	PIGR	Gastroesophageal reflux disease	0.942	-0.042	0.077	0.893	0.96 (0.78,1.18)	0.008	2.19E-05	TRUE	4.42E-61
rs748844	3216_2	P01833	PIGR	Cholelithiasis	0.906	-0.018	0.051	0.722	0.98 (0.89,1.09)	0.008	1.67E-07	TRUE	3.60E-61
rs748844	3216_2	P01833	PIGR	Cholelithiasis	0.942	0.085	0.122	0.487	1.09 (0.86,1.38)	0.008	6.59E-07	TRUE	1.75E-60
rs748844	3216_2	P01833	PIGR	Nonalcoholic fatty liver disease	0.981	0.133	0.164	0.417	1.14 (0.83,1.57)	0.008	8.50E-07	TRUE	1.64E-60
rs748844	3216_2	P01833	PIGR	Irritable bowel syndrome	0.993	0.082	0.087	0.345	1.09 (0.92,1.29)	0.008	1.37E-06	TRUE	1.08E-59
rs748844	3216_2	P01833	PIGR	Cirrhosis	-0.020	0.004	0.012	0.124	0.99 (0.77,1.28)	0.008	3.04E-08	TRUE	1.70E-61
rs748844	3216_2	P01833	PIGR	Diverticular disease	1.000	0.020	0.049	0.679	1.02 (0.93,1.12)	0.008	2.82E-07	TRUE	9.25E-61
rs2020921	2212_69	P00750	PLAT	Gastric ulcer	0.708	0.130	0.101	0.199	1.14 (0.93,1.39)	0.018	2.38E-06	TRUE	1.37E-134
rs2020921	2212_69	P00750	PLAT	Cholelithiasis	0.713	-0.064	0.054	0.234	0.94 (0.84,1.04)	0.018	1.83E-06	TRUE	1.24E-135
rs2020921	2212_69	P00750	PLAT	Gastroesophageal reflux disease	0.773	0.047	0.056	0.400	1.05 (0.94,1.17)	0.018	9.71E-07	TRUE	5.17E-136
rs2020921	2212_69	P00750	PLAT	Irritable bowel syndrome	0.798	0.123	0.088	0.162	1.13 (0.95,1.34)	0.018	2.99E-06	TRUE	8.44E-134
rs2020921	2212_69	P00750	PLAT	Acute gastritis	0.834								

Table S6. Association of putative type 2 diabetes-associated proteins in deCODE with gastrointestinal diseases.

Index SNP	SomalLogic	UniProt	Gene	GI outcomes	FDR *	b	se	pval	OR (95% CI)	snp_r2.exposure	snp_r2.outcome	correct_causal_direction	steiger_pval
rs2695234	5660_51	P08294	SOD3	Diverticular disease	0.649	0.032	0.024	0.176	1.03 (0.99,1.08)	0.025	2.62E-06	TRUE	4.70E-188
rs2695234	5660_51	P08294	SOD3	Irritable bowel syndrome	0.798	-0.072	0.042	0.088	0.93 (0.86,1.01)	0.025	4.48E-06	TRUE	2.85E-186
rs2695234	5660_51	P08294	SOD3	Chronic gastritis (Atrophic gastritis)	0.881	-0.025	0.050	0.613	0.97 (0.88,1.08)	0.025	3.61E-07	TRUE	1.26E-190
rs2695234	5660_51	P08294	SOD3	Cholelithiasis	0.923	0.006	0.025	0.822	1.01 (0.96,1.06)	0.025	6.99E-08	TRUE	3.40E-192
rs2695234	5660_51	P08294	SOD3	Acute gastritis	0.964	0.018	0.083	0.831	1.02 (0.86,1.20)	0.025	6.53E-08	TRUE	2.35E-191
rs2695234	5660_51	P08294	SOD3	Gastric ulcer	0.967	-0.003	0.050	0.956	1.00 (0.90,1.10)	0.025	4.23E-09	TRUE	1.08E-191
rs2695234	5660_51	P08294	SOD3	Nonalcoholic fatty liver disease	0.981	-0.021	0.079	0.787	0.98 (0.84,1.14)	0.025	9.38E-08	TRUE	3.85E-192
rs2695234	5660_51	P08294	SOD3	Cirrhosis	1.000	-0.052	0.061	0.387	0.95 (0.84,1.07)	0.025	9.81E-07	TRUE	1.47E-190
rs2695234	5660_51	P08294	SOD3	Cholecystitis	0.983	0.021	0.059	0.727	1.02 (0.91,1.15)	0.025	1.67E-07	TRUE	2.47E-191
rs72722045	15447_45	Q00796	SORD	Cirrhosis	0.304	-0.213	0.088	0.016	0.81 (0.68,0.96)	0.019	7.48E-06	TRUE	4.04E-141
rs72722045	15447_45	Q00796	SORD	Gastroesophageal reflux disease	0.643	0.058	0.039	0.134	1.06 (0.98,1.14)	0.019	3.05E-06	TRUE	1.04E-142
rs72722045	15447_45	Q00796	SORD	Cholelithiasis	0.821	-0.031	0.036	0.385	0.97 (0.90,1.04)	0.019	9.77E-07	TRUE	1.25E-144
rs72722045	15447_45	Q00796	SORD	Gastric ulcer	0.876	0.046	0.073	0.534	1.05 (0.91,1.21)	0.019	5.62E-07	TRUE	2.09E-144
rs72722045	15447_45	Q00796	SORD	Chronic gastritis (Atrophic gastritis)	0.881	-0.037	0.074	0.815	0.96 (0.83,1.11)	0.019	3.54E-07	TRUE	7.26E-145
rs72722045	15447_45	Q00796	SORD	Acute gastritis	0.964	0.031	0.122	0.798	1.03 (0.81,1.31)	0.019	9.24E-08	TRUE	2.11E-145
rs72722045	15447_45	Q00796	SORD	Nonalcoholic fatty liver disease	0.981	-0.070	0.116	0.543	0.93 (0.74,1.17)	0.019	4.75E-07	TRUE	2.72E-145
rs72722045	15447_45	Q00796	SORD	Irritable bowel syndrome	0.993	0.068	0.061	0.264	1.07 (0.95,1.21)	0.019	1.90E-06	TRUE	1.13E-142
rs72722045	15447_45	Q00796	SORD	Cholecystitis	0.983	-0.042	0.087	0.629	0.96 (0.81,1.14)	0.019	3.19E-07	TRUE	4.01E-145
rs72722045	15447_45	Q00796	SORD	Diverticular disease	1.000	-0.012	0.035	0.734	0.99 (0.92,1.06)	0.019	1.84E-07	TRUE	4.03E-145
rs212100	9829_91	Q06520	SULT2A1	Gastric ulcer	0.715	-0.112	0.094	0.236	0.89 (0.74,1.08)	0.011	2.04E-06	TRUE	1.54E-81
rs212100	9829_91	Q06520	SULT2A1	Cirrhosis	0.873	-0.136	0.113	0.232	0.87 (0.70,1.09)	0.011	1.84E-06	TRUE	4.39E-82
rs212100	9829_91	Q06520	SULT2A1	Chronic gastritis (Atrophic gastritis)	0.906	-0.035	0.098	0.722	0.97 (0.80,1.17)	0.011	1.79E-07	TRUE	3.62E-83
rs212100	9829_91	Q06520	SULT2A1	Gastroesophageal reflux disease	0.959	-0.017	0.050	0.727	0.98 (0.89,1.08)	0.011	1.66E-07	TRUE	2.62E-83
rs212100	9829_91	Q06520	SULT2A1	Acute gastritis	0.981	-0.004	0.157	0.981	1.00 (0.73,1.36)	0.011	8.68E-10	TRUE	9.64E-84
rs212100	9829_91	Q06520	SULT2A1	Nonalcoholic fatty liver disease	0.981	0.079	0.149	0.597	1.08 (0.91,1.45)	0.011	3.60E-07	TRUE	3.03E-83
rs212100	9829_91	Q06520	SULT2A1	Irritable bowel syndrome	0.993	-0.021	0.079	0.793	0.98 (0.84,1.14)	0.011	1.05E-07	TRUE	5.54E-83
rs212100	9829_91	Q06520	SULT2A1	Diverticular disease	1.000	-0.007	0.044	0.882	0.99 (0.91,1.08)	0.011	3.16E-08	TRUE	1.80E-83
rs59178722	3009_3	Q03167	TGFBR3	Gastroesophageal reflux disease	0.643	0.121	0.084	0.152	1.13 (0.96,1.33)	0.003	2.78E-06	TRUE	3.77E-24
rs59178722	3009_3	Q03167	TGFBR3	Cholelithiasis	0.788	0.080	0.080	0.317	1.08 (0.93,1.27)	0.003	1.30E-06	TRUE	1.21E-24
rs59178722	3009_3	Q03167	TGFBR3	Cirrhosis	0.873	0.233	0.192	0.224	1.26 (0.87,1.84)	0.003	1.89E-06	TRUE	1.84E-24
rs59178722	3009_3	Q03167	TGFBR3	Chronic gastritis (Atrophic gastritis)	0.843	0.212	0.159	0.183	1.24 (0.90,1.69)	0.003	2.50E-06	TRUE	3.43E-24
rs59178722	3009_3	Q03167	TGFBR3	Gastric ulcer	0.849	0.114	0.161	0.479	1.12 (0.82,1.54)	0.003	7.30E-07	TRUE	9.13E-25
rs59178722	3009_3	Q03167	TGFBR3	Diverticular disease	0.939	-0.066	0.077	0.388	0.94 (0.81,1.09)	0.003	1.08E-06	TRUE	1.29E-24
rs59178722	3009_3	Q03167	TGFBR3	Acute gastritis	0.964	0.191	0.267	0.474	1.21 (0.72,2.04)	0.003	7.30E-07	TRUE	8.87E-25
rs59178722	3009_3	Q03167	TGFBR3	Nonalcoholic fatty liver disease	0.981	0.121	0.255	0.636	1.13 (0.89,1.46)	0.003	2.89E-07	TRUE	3.74E-25
rs59178722	3009_3	Q03167	TGFBR3	Irritable bowel syndrome	0.993	0.129	0.134	0.338	1.14 (0.87,1.48)	0.003	1.41E-06	TRUE	2.04E-24
rs59178722	3009_3	Q03167	TGFBR3	Cholecystitis	0.983	0.042	0.190	0.824	1.04 (0.72,1.51)	0.003	6.63E-08	TRUE	2.56E-25
rs35894069	5939_42	Q43508	TNFSF12	Gastroesophageal reflux disease	0.773	-0.026	0.031	0.406	0.97 (0.92,1.04)	0.025	9.35E-07	TRUE	5.00E-190
rs35894069	5939_42	Q43508	TNFSF12	Acute gastritis	0.939	-0.126	0.100	0.207	0.88 (0.73,1.07)	0.025	2.27E-06	TRUE	2.06E-188
rs35894069	5939_42	Q43508	TNFSF12	Cholelithiasis	0.884	0.014	0.030	0.649	1.01 (0.96,1.07)	0.025	2.78E-07	TRUE	1.49E-191
rs35894069	5939_42	Q43508	TNFSF12	Chronic gastritis (Atrophic gastritis)	0.887	0.025	0.062	0.889	1.03 (0.91,1.16)	0.025	2.25E-07	TRUE	6.36E-191
rs35894069	5939_42	Q43508	TNFSF12	Gastric ulcer	0.953	-0.030	0.059	0.819	0.97 (0.86,1.09)	0.025	3.60E-07	TRUE	1.94E-190
rs35894069	5939_42	Q43508	TNFSF12	Nonalcoholic fatty liver disease	0.981	-0.016	0.094	0.866	0.98 (0.82,1.18)	0.025	3.77E-08	TRUE	2.09E-192
rs35894069	5939_42	Q43508	TNFSF12	Irritable bowel syndrome	0.993	0.031	0.050	0.539	1.03 (0.93,1.14)	0.025	5.81E-07	TRUE	1.84E-189
rs35894069	5939_42	Q43508	TNFSF12	Cholecystitis	0.996	0.006	0.070	0.936	1.01 (0.88,1.15)	0.025	8.51E-09	TRUE	4.40E-192
rs35894069	5939_42	Q43508	TNFSF12	Cirrhosis	1.000	-0.004	0.071	0.958	1.00 (0.87,1.15)	0.025	3.85E-09	TRUE	9.84E-193
rs4794183	3235_50	Q8TEU8	WFIKN2	Gastroesophageal reflux disease	0.128	0.068	0.023	0.003	1.07 (1.02,1.12)	0.025	1.20E-05	TRUE	3.43E-184
rs4794183	3235_50	Q8TEU8	WFIKN2	Cholecystitis	0.717	0.077	0.051	0.133	1.08 (0.98,1.19)	0.025	3.10E-06	TRUE	3.71E-188
rs4794183	3235_50	Q8TEU8	WFIKN2	Diverticular disease	0.801	0.022	0.020	0.288	1.02 (0.98,1.06)	0.025	1.62E-06	TRUE	7.29E-189
rs4794183	3235_50	Q8TEU8	WFIKN2	Chronic gastritis (Atrophic gastritis)	0.843	0.065	0.044	0.139	1.07 (0.98,1.16)	0.025	3.08E-06	TRUE	6.45E-188
rs4794183	3235_50	Q8TEU8	WFIKN2	Cholelithiasis	0.918	-0.006	0.021	0.784	0.99 (0.95,1.04)	0.025	9.28E-08	TRUE	4.42E-192
rs4794183	3235_50	Q8TEU8	WFIKN2	Gastric ulcer	0.967	-0.008	0.043	0.846	0.99 (0.91,1.08)	0.025	5.36E-08	TRUE	2.62E-191
rs4794183	3235_50	Q8TEU8	WFIKN2	Acute gastritis	0.964	0.006	0.072	0.332	1.01 (0.87,1.16)	0.025	1.02E-06	TRUE	1.01E-191
rs4794183	3235_50	Q8TEU8	WFIKN2	Nonalcoholic fatty liver disease	0.981	0.037	0.069	0.586	1.04 (0.91,1.19)	0.025	3.80E-07	TRUE	2.09E-191
rs4794183	3235_50	Q8TEU8	WFIKN2	Irritable bowel syndrome	0.993	0.031	0.036	0.386	1.03 (0.96,1.11)	0.025	1.16E-06	TRUE	9.98E-189
rs4794183	3235_50	Q8TEU8	WFIKN2	Cirrhosis	1.000	-0.016	0.052	0.764	0.98 (0.89,1.09)	0.025	1.16E-07	TRUE	4.51E-192

* False discovery rate (FDR) based on Benjamini-Hochberg approach and performed by each gastrointestinal outcomes.

Table S7. Association of putative type 2 diabetes-associated proteins in UKB-PPP with gastrointestinal diseases.

Index SNP	Gene	UniProt	OID	GI outcomes	b	se	pval	OR (95% CI)	snp_r2.exp	snp_r2.out	correct_ca	steiger_pval
rs1614972	ADH1B	P00325	OID30612	Cirrhosis	0.595	0.408	0.145	1.81 (0.82,4.03)	0.001	2.71E-06	TRUE	1.53E-07
rs75045569	EPHA1	P21709	OID20677	Cholecystitis	0.044	0.091	0.629	1.05 (0.87,1.25)	0.014	3.20E-07	TRUE	1.52E-159
rs34356500	GUSB	P08236	OID20296	Nonalcoholic fatty liver disease	0.742	0.189	8.61E-05	2.10 (1.45,3.04)	0.006	1.98E-05	TRUE	1.20E-57
rs11809759	INSL5	Q9Y5Q6	OID31448	Gastric ulcer	-0.300	0.083	3.18E-04	0.74 (0.63,0.87)	0.011	1.88E-05	TRUE	2.39E-111
rs3761077	NCAN	O14594	OID21055	Nonalcoholic fatty liver disease	-1.195	0.155	1.07E-14	0.30 (0.22,0.41)	0.008	7.67E-05	TRUE	5.77E-79
rs3761077	NCAN	O14594	OID21055	Cirrhosis	-0.737	0.121	1.09E-09	0.48 (0.38,0.61)	0.008	4.76E-05	TRUE	1.93E-82
rs212100	SULT2A1	Q06520	OID20508	Cholelithiasis	0.383	0.027	1.28E-45	1.47 (1.39,1.55)	0.017	0.000262	TRUE	9.48E-145
rs212100	SULT2A1	Q06520	OID20508	Cholecystitis	0.209	0.062	8.03E-04	1.23 (1.09,1.39)	0.017	1.54E-05	TRUE	1.78E-176
rs4968200	TNFSF12	O43508	OID20624	Diverticular disease	0.140	0.032	1.08E-05	1.15 (1.08,1.22)	0.017	2.78E-05	TRUE	3.65E-172

CI, confidence interval; GI, gastrointestinal; OR, odd ratio.

Table S8. Association of putative type 2 diabetes-associated proteins in Fenland with gastrointestinal diseases.

Index SNP	SomaLogic Gene	Protein	Description	GI outcomes	b	se	pval	OR (95% CI)	snp_r2.exp	snp_r2.out	correct	ca	steiger_pval
rs1229984	9834-62	ADH1B	ADH1B	Alcohol dehydrogenase 1B	Cirrhosis	1.249	0.319	8.96E-05 3.49 (1.87,6.51)	0.004	1.97E-05	TRUE		3.20E-10
rs1800759	8325-37	ADH4	ADH4	Alcohol dehydrogenase 4	Cholelithiasis	0.183	0.069	8.54E-03 1.20 (1.05,1.38)	0.006	8.85E-06	TRUE		4.89E-15
rs41277428	3431-54	EPHA1	EphA1	Ephrin type-A receptor 1	Cholecystitis	-0.015	0.024	0.542 0.99 (0.94,1.03)	0.082	5.11E-07	TRUE		1.11E-199
rs9530	15562-24	GUSB	BGLR	Beta-glucuronidase	Nonalcoholic fatty liver disease	0.582	0.159	2.51E-04 1.79 (1.31,2.44)	0.013	1.72E-05	TRUE		2.01E-29
rs11809759	10462-14	INSL5	INSL5	Insulin-like peptide INSL5	Gastric ulcer	-0.507	0.141	3.18E-04 0.60 (0.46,0.79)	0.005	1.88E-05	TRUE		1.23E-12
rs2228603	15573-110	NCAN	CSPG3	Neurocan core protein	Nonalcoholic fatty liver disease	-1.268	0.144	1.34E-18 0.28 (0.21,0.37)	0.014	9.93E-05	TRUE		3.02E-29
rs2228603	15573-110	NCAN	CSPG3	Neurocan core protein	Cirrhosis	-0.725	0.114	1.85E-10 0.48 (0.39,0.61)	0.014	5.21E-05	TRUE		1.20E-30
rs10426201	9829-91	SULT2A1	SULT 2A1	Bile salt sulfotransferase	Cholelithiasis	0.497	0.039	1.28E-36 1.64 (1.52,1.77)	0.018	0.000208	TRUE		8.19E-36
rs10426201	9829-91	SULT2A1	SULT 2A1	Bile salt sulfotransferase	Cholecystitis	0.302	0.092	1.03E-03 1.35 (1.13,1.62)	0.018	1.48E-05	TRUE		5.68E-42
rs62061198	5939-42	TNFSF12	TWEAK	Tumor necrosis factor ligand superfamily member 12	Diverticular disease	0.046	0.018	8.55E-03 1.05 (1.01,1.08)	0.082	1.00E-05	TRUE		2.99E-196

CI, confidence interval; GI, gastrointestinal; OR, odd ratio.

Table S9. Colocalization analysis of identified protein-gastrointestinal pairs in deCODE, UKB-PPP, and Fenland.

					window ± 500kb						window ± 1000kb					
Database	SomaLogic	Gene	UniProt	GI outcomes	nsnps	PP.H0.abf	PP.H1.abf	PP.H2.abf	PP.H3.abf	PP.H4.abf	nsnps	PP.H0.abf	PP.H1.abf	PP.H2.abf	PP.H3.abf	PP.H4.abf
deCODE	9834_62	ADH1B	P00325	Cirrhosis	5991	7.42E-07	1.19E-06	3.29E-02	0.052	0.915	11147	6.53E-07	1.11E-06	0.026	0.043	0.931
deCODE	8325_37	ADH4	P08319	Cholelithiasis	5983	8.85E-34	3.70E-34	4.25E-01	0.177	0.397	11068	9.64E-34	5.03E-34	0.419	0.218	0.363
deCODE	4435_66	ENPP7	Q6UWV6	Cholelithiasis	6793	0	0	2.20E-03	0.981	0.017	12899	0	0	0.003	0.969	0.028
deCODE	3431_54	EPHA1	P21709	Cholecystitis	3167	0	0	0.777	0.207	0.016	6699	0	0	0.670	0.317	0.013
deCODE	15562_24	GUSB	P08236	Nonalcoholic fatty liver disease	5782	3.08E-104	1.47E-103	1.71E-01	0.813	0.017	11340	3.38E-104	1.78E-103	0.157	0.826	0.017
deCODE	10462_14	INSL5	Q9Y5Q6	Gastric ulcer	5033	1.46E-07	5.90E-08	1.69E-01	0.068	0.763	10053	1.12E-07	8.46E-08	0.129	0.097	0.774
deCODE	15573_110	NCAN	O14594	Cirrhosis	4665	3.66E-100	1.19E-86	3.07E-14	1.000	1.93E-07	10375	3.55E-100	1.25E-86	2.83E-14	1.000	1.91E-07
deCODE	15573_110	NCAN	O14594	Nonalcoholic fatty liver disease	4665	3.60E-103	1.18E-86	3.02E-17	0.992	0.008	10374	4.60E-103	1.24E-86	3.67E-17	0.991	0.009
deCODE	9829_91	SULT2A1	Q06520	Cholecystitis	6065	4.03E-82	2.17E-82	2.39E-01	0.128	0.633	10900	3.81E-82	3.75E-82	0.207	0.203	0.589
deCODE	9829_91	SULT2A1	Q06520	Cholelithiasis	6067	1.30E-122	1.16E-83	7.71E-42	0.006	0.994	10903	6.06E-123	8.80E-84	3.29E-42	0.004	0.996
deCODE	5939_42	TNFSF12	O43508	Diverticular disease	5059	0	0	2.96E-03	0.997	0.001	10354	0	0	0.004	0.996	0.001
Database	OID	Gene	UniProt	Outcomes	nsnps	PP.H0.abf	PP.H1.abf	PP.H2.abf	PP.H3.abf	PP.H4.abf	nsnps	PP.H0.abf	PP.H1.abf	PP.H2.abf	PP.H3.abf	PP.H4.abf
UKB-PPP	OID30612	ADH1B	P00325	Cirrhosis	4098	1.43E-33	1.77E-33	0.359319	0.446	0.195	8694	1.32E-33	1.97E-33	0.328	0.491	0.181
UKB-PPP	OID20677	EPHA1	P21709	Cholecystitis	2621	3.05E-165	6.35E-166	0.818744	0.171	0.011	4374	2.79E-165	9.05E-166	0.748	0.243	0.009
UKB-PPP	OID20296	GUSB	P08236	Nonalcoholic fatty liver disease	4968	3.76E-64	1.87E-63	4.37E-02	0.216	0.740	8665	3.68E-64	2.02E-63	0.043	0.234	0.723
UKB-PPP	OID31448	INSL5	Q9Y5Q6	Gastric ulcer	3783	3.46E-124	8.02E-125	0.170214	0.039	0.791	8647	2.65E-124	1.43E-124	0.130	0.069	0.800
UKB-PPP	OID21055	NCAN	O14594	Cirrhosis	3957	7.06E-109	2.30E-95	3.07E-14	1.000	4.78E-08	7922	6.27E-109	2.30E-95	0.000	1.000	4.25E-08
UKB-PPP	OID21055	NCAN	O14594	Nonalcoholic fatty liver disease	3957	6.78E-112	2.29E-95	2.95E-17	0.999	0.001	7922	7.96E-112	2.30E-95	0.000	0.999	0.001
UKB-PPP	OID20508	SULT2A1	Q06520	Cholecystitis	5172	1.58E-300	7.33E-301	0.206033	0.095	0.699	8618	1.46E-300	1.31E-300	0.190	0.171	0.638
UKB-PPP	OID20508	SULT2A1	Q06520	Cholelithiasis	5172	0.00E+00	2.94E-302	4.30E-42	0.003	0.997	8618	0	2.30E-302	0	0.002	0.998
UKB-PPP	OID20624	TNFSF12	O43508	Diverticular disease	4512	0.00E+00	0.00E+00	2.80E-03	0.997	4.85E-04	8024	0	0.E+00	0.003	0.996	0.001
Database	SomaLogic	Gene	UniProt	Outcomes	nsnps	PP.H0.abf	PP.H1.abf	PP.H2.abf	PP.H3.abf	PP.H4.abf	nsnps	PP.H0.abf	PP.H1.abf	PP.H2.abf	PP.H3.abf	PP.H4.abf
Fenland	9834_62	ADH1B	P00325	Cirrhosis	3772	4.97E-07	6.22E-07	2.92E-02	0.036	0.935	6433	4.94E-07	6.62E-07	0.029	0.038	0.933
Fenland	8325-37	ADH4	P08319	Cholelithiasis	3764	1.81E-10	3.95E-11	0.730824	0.159	0.110	6082	1.76E-10	4.47E-11	0.713	0.180	0.107
Fenland	3431-54	EPHA1	P21709	Cholecystitis	1612	0	0	0.887437	0.095	0.017	3888	0	0	0.818	0.166	0.016
Fenland	15562_24	GUSB	P08236	Nonalcoholic fatty liver disease	1874	1.53E-26	2.26E-26	9.09E-02	0.134	0.775	4645	1.11E-26	6.44E-26	0.064	0.373	0.562
Fenland	10462-14	INSL5	Q9Y5Q6	Gastric ulcer	3160	2.06E-09	5.54E-10	0.135	0.036	0.829	5793	2.03E-09	7.60E-10	0.134	0.049	0.817
Fenland	15573-110	NCAN	O14594	Cirrhosis	2333	1.24E-41	4.54E-28	2.73E-14	1.000	1.77E-07	5412	1.24E-41	4.55E-28	2.73E-14	1.000	1.77E-07
Fenland	15573-110	NCAN	O14594	Nonalcoholic fatty liver disease	2333	1.56E-44	4.50E-28	3.44E-17	0.992	0.008	5412	1.56E-44	4.52E-28	3.44E-17	0.992	0.008
Fenland	9829-91	SULT2A1	Q06520	Cholecystitis	3701	1.58E-39	4.61E-40	0.277111	0.080	0.643	6158	1.45E-39	8.79E-40	0.254	0.153	0.593
Fenland	9829_91	SULT2A1	Q06520	Cholelithiasis	3701	1.45E-79	2.30E-40	2.54E-41	0.039	0.961	6158	1.44E-79	2.28E-40	2.52E-41	0.039	0.961
Fenland	5939_42	TNFSF12	O43508	Diverticular disease	2727	0	4.9406564E-03	3.31E-03	0.996	3.88E-04	5816	0	4.9406564E-03	0.003	0.996	3.88E-04

Table S10. Mediation analysis of identified protein between type 2 diabetes and gastrointestinal diseases in deCODE, UKB-PPP, and Fenland.

Database	Index SNP	SomaLogic	UniProt	Gene	Outcomes	b (T2D-GI)	se (T2D-GI)	pval (T2D-GI)	b (T2D-protein)	se (T2D-protein)	pval (T2D-protein)	b (protein-GI)	se (protein-GI)	pval (protein-GI)	Mediation *	b_mediation	se_mediation	p_mediation	Proportion mediation estimate	se_proportion mediation	Mediation proportion (95% CI)
deCODE	rs1229984	9834_62	P00325	ADH1B	Cirrhosis	0.111	0.046	0.015	0.067	0.014	9.32E-07	0.719	0.183	8.96E-05	Yes	0.048	0.016	0.002	0.429	0.140	0.140 (0.43,0.70,36)
deCODE	rs2602844	8325_37	P08319	ADH4	Cholelithiasis	0.077	0.021	3.12E-04	0.122	0.015	1.36E-15	0.229	0.067	0.001	Yes	0.028	0.009	0.002	0.362	0.115	0.115 (0.36,0.58,76)
deCODE	rs35246623	4435_66	Q6UWV6	ENPP7	Cholelithiasis	0.077	0.021	3.12E-04	0.077	0.013	2.18E-09	0.038	0.011	4.19E-04	Yes	0.003	0.001	0.003	0.038	0.013	0.013 (0.37,0.62,27)
deCODE	rs10952549	3431_54	P21709	EPHA1	Cholecystitis	0.099	0.029	0.001	0.051	0.013	7.01E-05	-0.140	0.043	0.001	No	NA	NA	NA	NA	NA	NA
deCODE	rs34356500	15562_24	P08236	GUSB	Nonalcoholic fatty liver disease	0.307	0.060	2.94E-07	0.121	0.018	6.46E-12	0.654	0.167	8.61E-05	Yes	0.079	0.023	0.001	0.256	0.075	0.075 (0.87,40.42)
deCODE	rs11809759	10462_14	Q9Y5Q6	INSL5	Gastric ulcer	0.096	0.021	5.37E-06	0.038	0.012	0.001	-0.941	0.261	3.18E-04	No	NA	NA	NA	NA	NA	NA
deCODE	rs2228603	15573_110	O14594	NCAN	Cirrhosis	0.111	0.046	0.015	-0.057	0.017	0.001	-0.625	0.098	1.85E-10	Yes	0.035	0.012	0.003	0.318	0.109	0.109 (0.50,53.05)
deCODE	rs2228603	15573_110	O14594	NCAN	Nonalcoholic fatty liver disease	0.307	0.060	2.94E-07	-0.057	0.017	0.001	-1.092	0.124	1.34E-18	Yes	0.062	0.020	0.002	0.201	0.065	0.065 (0.20,32.91)
deCODE	rs212100	9829_91	Q06520	SULT2A1	Cholecystitis	0.099	0.029	0.001	0.082	0.014	1.43E-08	0.374	0.111	0.001	Yes	0.031	0.011	0.004	0.309	0.107	0.107 (0.99,51.83)
deCODE	rs212100	9829_91	Q06520	SULT2A1	Cholelithiasis	0.077	0.021	3.12E-04	0.082	0.014	1.43E-08	0.683	0.048	1.28E-45	Yes	0.056	0.011	1.39E-07	0.728	0.138	0.138 (0.45,70.99,88)
deCODE	rs35894069	5939_42	O43508	TNFSF12	Diverticular disease	0.034	0.016	0.035	-0.047	0.013	3.57E-04	0.102	0.028	2.78E-04	No	NA	NA	NA	NA	NA	NA
UKB-PPP	rs1614972	OID30612	P00325	ADH1B	Cirrhosis	0.111	0.046	0.015	0.093	0.017	1.02E-07	0.595	0.408	0.145	Yes	0.055	0.039	0.159	0.496	0.353	0.353 (0.118,75)
UKB-PPP	rs75045569	OID20677	P21709	EPHA1	Cholecystitis	0.099	0.029	0.001	0.032	0.015	0.028	0.044	0.091	0.029	Yes	0.001	0.003	0.637	0.014	0.031	0.031 (0.44)
UKB-PPP	rs34356500	OID20296	P08236	GUSB	Nonalcoholic fatty liver disease	0.307	0.060	2.94E-07	0.092	0.021	1.59E-05	0.742	0.189	8.61E-05	Yes	0.068	0.023	0.004	0.221	0.076	0.076 (0.21,37.04)
UKB-PPP	rs11809759	OID31448	Q9Y5Q6	INSL5	Gastric ulcer	0.096	0.021	5.37E-06	0.073	0.018	6.11E-05	-0.300	0.083	3.18E-04	No	NA	NA	NA	NA	NA	NA
UKB-PPP	rs3761077	OID21055	O14594	NCAN	Cirrhosis	0.111	0.046	0.015	-0.090	0.021	2.88E-05	-0.737	0.121	1.09E-09	Yes	0.066	0.019	0.001	0.594	0.172	0.172 (0.53,93.12)
UKB-PPP	rs3761077	OID21055	O14594	NCAN	Nonalcoholic fatty liver disease	0.307	0.060	2.94E-07	-0.090	0.021	2.88E-05	-1.195	0.155	1.07E-14	Yes	0.107	0.029	2.34E-04	0.349	0.095	0.095 (0.31,53.50)
UKB-PPP	rs212100	OID20508	Q06520	SULT2A1	Cholecystitis	0.099	0.029	0.001	0.067	0.015	1.20E-05	0.209	0.062	0.001	Yes	0.014	0.005	0.008	0.141	0.053	0.053 (0.72,24.49)
UKB-PPP	rs212100	OID20508	Q06520	SULT2A1	Cholelithiasis	0.077	0.021	3.12E-04	0.067	0.015	1.20E-05	0.383	0.027	1.28E-45	Yes	0.026	0.006	2.89E-05	0.332	0.079	0.079 (0.66,48.82)
UKB-PPP	rs4968200	OID20624	O43508	TNFSF12	Diverticular disease	0.034	0.016	0.035	-0.068	0.017	7.11E-05	0.140	0.032	1.08E-05	No	NA	NA	NA	NA	NA	NA
Fenland	rs1229984	9834_62	P00325	ADH1B	Cirrhosis	0.111	0.046	0.015	0.041	0.019	0.027	1.249	0.319	8.96E-05	Yes	0.051	0.027	0.054	0.459	0.238	0.238 (0.92,64)
Fenland	rs1800759	8325_37	P08319	ADH4	Cholelithiasis	0.077	0.021	3.12E-04	0.099	0.022	6.89E-06	0.183	0.069	0.009	Yes	0.018	0.008	0.023	0.234	0.103	0.103 (0.20,43.61)
Fenland	rs41277428	3431_54	P21709	EPHA1	Cholecystitis	0.099	0.029	0.001	0.040	0.019	0.029	-0.015	0.024	0.542	No	NA	NA	NA	NA	NA	NA
Fenland	rs9530	15562_24	P08236	GUSB	Nonalcoholic fatty liver disease	0.307	0.060	2.94E-07	0.107	0.023	5.39E-06	0.652	0.159	2.51E-04	Yes	0.062	0.022	0.004	0.202	0.071	0.071 (0.31,34.06)
Fenland	rs11809759	10462_14	Q9Y5Q6	INSL5	Gastric ulcer	0.096	0.021	5.37E-06	0.053	0.019	0.007	-0.507	0.141	3.18E-04	No	NA	NA	NA	NA	NA	NA
Fenland	rs2228603	15573_110	O14594	NCAN	Cirrhosis	0.111	0.046	0.015	-0.056	0.024	0.017	-0.725	0.114	1.85E-10	Yes	0.041	0.018	0.026	0.367	0.165	0.165 (0.41,69.03)
Fenland	rs2228603	15573_110	O14594	NCAN	Nonalcoholic fatty liver disease	0.307	0.060	2.94E-07	-0.056	0.024	0.017	-1.268	0.144	1.34E-18	Yes	0.072	0.031	0.022	0.233	0.101	0.101 (0.23,28.34,0.43,16)
Fenland	rs10426201	9829_91	Q06520	SULT2A1	Cholecystitis	0.099	0.029	0.001	0.055	0.021	0.009	0.302	0.092	0.001	Yes	0.017	0.008	0.041	0.168	0.082	0.082 (0.71,32.86)
Fenland	rs10426201	9829_91	Q06520	SULT2A1	Cholelithiasis	0.077	0.021	3.12E-04	0.055	0.021	0.009	0.497	0.039	1.28E-36	Yes	0.027	0.011	0.010	0.356	0.139	0.139 (0.64,0.62,86)
Fenland	rs62061198	5939_42	O43508	TNFSF12	Diverticular disease	0.034	0.016	0.035	-0.057	0.021	0.008	0.046	0.018	0.009	No	NA	NA	NA	NA	NA	NA

* Mediation effect exist or not, se, standard error

Table S11. Appraisal of druggability.

Uniport	Gene	Target name	Pipeline	Drug name	Indication/associated conditions
Q06520	SULT2A1	Bile salt sulfotransferase	Approved	Abiraterone*	An antiandrogen used in the treatment of metastatic castration-resistant prostate cancer and metastatic high-risk castration-sensitive prostate cancer.
				Tamoxifen*	A selective estrogen receptor modulator used to treat estrogen receptor positive breast cancer, reduce the risk of invasive breast cancer following surgery, or reduce the risk of breast cancer in high-risk women.
				Prasterone*	A steroid formulated as a vaginal insert indicated for the treatment of moderate to severe dyspareunia associated with menopausal vulvar and vaginal atrophy.
				Palbociclib*	An endocrine-based chemotherapeutic agent used in combination with other antineoplastic agents to treat HER2-negative and HR-positive advanced or metastatic breast cancer.
			In clinical trials	Dehydroepiandrosterone (Launched) †	Menopause
				Adenosine 3',5'-diphosphate* †	NA
				Aetiocolanalone*	NA
				Mercuric iodide*	NA
Preclinical	Bentflurain (Phase 3) †	NA			
	3-alpha-hydroxy-5-beta-androstan-17-one †	NA			
			Propacetamol*	A paracetamol prodrug of intravenous administration used to control fever and pain of perioperative period in multimodal analgesia therapy.	
P00325	ADH1B	Alcohol dehydrogenase 1B	Approved	NADH*	Some evidence suggests that NADH might be useful in treating Parkinson's disease, chronic fatigue syndrome, Alzheimer's disease and cardiovascular disease.
				Fomepizole*	An antidote for ethylene glycol (such as antifreeze) or methanol poisoning, or for use in suspected ethylene glycol or methanol ingestion, either alone or in combination with hemodialysis
				Glycerin*	A solvent, emollient, pharmaceutical agent, and sweetening agent.
			In clinical trials	Ethanol*	For therapeutic neurolysis of nerves or ganglia for the relief of intractable chronic pain in such conditions as inoperable cancer and trigeminal neuralgia (tic douloureux), in patients for whom neurosurgical procedures are contraindicated.
				N-Benzylformamide*	NA
				4-Iodopyrazole*	NA
				Cyclohexanol*	NA
				N-Heptylformamide*	NA
Nicotinamide adenine dinucleotide phosphate*	NA				
Coenzyme-I (Phase 2) †	NA				
P08319	ADH4	Alcohol dehydrogenase 4	Approved	NADH*	Some evidence suggests that NADH might be useful in treating Parkinson's disease, chronic fatigue syndrome, Alzheimer's disease and cardiovascular disease.
				Ethanol*	For therapeutic neurolysis of nerves or ganglia for the relief of intractable chronic pain in such conditions as inoperable cancer and trigeminal neuralgia (tic douloureux), in patients for whom neurosurgical procedures are contraindicated.
			In clinical trials	Cyclohexylformamide*	NA
			Coenzyme-I (Phase 2) †	NA	
Q6UWV6	ENPP7	Ectonucleotide pyrophosphatase/phosphodiesterase family member 7	Druggable §	NA	NA
P21709	EPHA1	Ephrin type-A receptor 1	Approved	Fostamatinib* Vandetanib †	Fostamatinib is a spleen tyrosine kinase inhibitor used to treat chronic immune thrombocytopenia after attempting one other treatment. Medullary thyroid cancer (MTC)
Q9Y5Q6	INSL5	Insulin-like peptide INSL5	Not listed as druggable target §	NA	NA
O14594	NCAN	Neurocan core protein	Approved	Hyaluronic-acid †	Osteoarthritis, interstitial cystitis (IC)
P08236	GUSB	Beta-glucuronidase	Approved	Chondroitin sulfate* Tyropanoic acid *	Symptomatic treatment of Arthritis, backache, muscle pain, muscle ache. For use in cholecystography (X-ray diagnosis/imaging of gallstones).
O43508	TNFSF12	Tumor necrosis factor ligand superfamily member 12	In clinical trials	RO-5458640 (Phase 1) † BLIB-023 (Phase 2) †	Neoplasms Lupus Nephritis; Arthritis, Rheumatoid

* Identified in DrugBank

† Identified in ChEMBL databases

‡ Identified in Connectivity Map

§ Identified in Dependency Map

NA, not available