

Supplement Material

For

Gene-based elevated triglycerides and T2D risk in the Women's Genome Health Study

Running title: Triglyceride, Genetics and Type 2 Diabetes

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Supplemental Table I Updated 127 TG-associated SNPs quality control information in the WGHS

SNP	POSITION	Nearest Gene	Effect Allele	Other Allele	EAFF_WGHS	Published effect estimate
rs1077514	1:23766233	<i>ASAP3:Intron</i>	T	C	0.85965	0.019
rs12748152	1:27138393	<i>PIGV:Intergenic</i>	T	C	0.07840	0.031
rs16826069	1:39797055	<i>MACF1:Ile39Val</i>	G	A	0.21588	0.025
rs4660293	1:40028180	<i>PABPC4:Intron</i>	G	A	0.23605	0.024
rs10889353	1:63118196	<i>DOCK7:Intron</i>	A	C	0.66714	0.077
rs1011731	1:172346548	<i>DNM3:Intron</i>	G	A	0.42462	0.015
rs2785990	1:219687432	<i>LYPLAL1:Intergenic</i>	T	C	0.67293	0.016
rs2785980	1:219700519	<i>LYPLAL1:Intergenic</i>	T	C	0.67646	0.016
rs10489615	1:230304988	<i>GALNT2:Intron</i>	A	G	0.38141	0.039
rs6749689	2:20396122	<i>EPHA2:Intergenic</i>	T	C	0.44297	0.016
rs1367117	2:21263900	<i>APOB:Thr98Ile</i>	A	G	0.31864	0.023
rs1049817	2:27550967	<i>GTF3C2:Pro783Pro</i>	A	G	0.61854	0.056
rs1260333	2:27748624	<i>PTPN14:Intergenic</i>	A	G	0.45328	0.095
rs7607980	2:165551201	<i>COBLL1:Asn939Asp</i>	T	C	0.87549	0.045
rs3769823	2:202122995	<i>CASP8:Lys14Arg</i>	G	A	0.71022	0.017
rs1344642	2:219555262	<i>STK36:Arg583Gln</i>	G	A	0.55902	0.015
rs1801282	3:12393125	<i>PPARG:Pro12Ala</i>	C	G	0.87383	0.023
rs13326165	3:52532118	<i>STAB1:Intron</i>	G	A	0.79654	0.02
rs9311651	3:57528503	<i>DNAH12:Val32Ala</i>	A	G	0.83795	0.021
rs645040	3:135926622	<i>RFX5:Intergenic</i>	T	G	0.77924	0.023
rs6818397	4:3434885	<i>RGS12:Intron</i>	T	G	0.40778	0.021
rs3748034	4:3446091	<i>HGFAC:Ala218Ser</i>	T	G	0.14640	0.035
rs16844401	4:3449652	<i>HGFAC:Arg509His</i>	A	G	0.07423	0.03
rs6831256	4:3473139	<i>DOK7:Intron</i>	G	A	0.42323	0.021
rs442177	4:88030261	<i>AFF1:Intron</i>	T	G	0.58753	0.031
rs13133548	4:89740128	<i>FAM13A:Intron</i>	A	G	0.46191	0.014
rs1126673	4:100045616	<i>ADH4:Val374Ile</i>	T	C	0.69046	0.017

rs13107325	4:103188709	<i>SLC39A8:Ala391Thr</i>	T	C	0.06839	0.034
rs4311394	5:53300662	<i>ARL15:Intron</i>	G	A	0.25441	0.018
rs459193	5:55806751	<i>ASPM:Intergenic</i>	G	A	0.75341	0.023
rs9686661	5:55861786	<i>ASPM:Intergenic</i>	T	C	0.19671	0.042
rs4976033	5:67714246	<i>IGFN1:Intergenic</i>	G	A	0.42309	0.018
rs26008	5:131008194	<i>FNIP1:Gln620Arg</i>	T	C	0.06400	0.028
rs6882076	5:156390297	<i>TIMD4:Upstream</i>	C	T	0.63332	0.038
rs1501908	5:156398169	<i>ATP1A2:Intergenic</i>	C	G	0.63443	0.038
rs3130564	6:31101674	<i>PSORS1C1:Intron</i>	C	T	0.78902	0.033
rs2844480	6:31564821	<i>F5:Intergenic</i>	T	C	0.19720	0.023
rs1057373	6:32813279	<i>TAP1:Utr3</i>	A	C	0.08756	0.03
rs998584	6:43757896	<i>SH2D5:Intergenic</i>	A	C	0.47433	0.034
rs6905288	6:43758873	<i>SH2D5:Intergenic</i>	A	G	0.56028	0.033
rs9472138	6:43811762	<i>SH2D5:Intergenic</i>	C	T	0.71293	0.02
rs2745353	6:127452935	<i>RSPO3:Intron</i>	T	C	0.52864	0.02
rs643381	6:139839423	<i>TXNIP:Intergenic</i>	C	A	0.48562	0.023
rs12208357	6:160543148	<i>SLC22A1:Arg61Cys</i>	T	C	0.07532	0.032
rs1564348	6:160578860	<i>SLC22A1:Intron</i>	C	T	0.16127	0.02
rs7758229	6:160840252	<i>SLC22A3:Intron</i>	T	G	0.32667	0.018
rs4410790	7:17284577	<i>NCSTN:Intergenic</i>	C	T	0.624	0.015
rs4722551	7:25991826	<i>HMCN1:Intergenic</i>	T	C	0.83825	0.026
rs2240466	7:72856269	<i>BAZ1B:Intron</i>	G	A	0.88122	0.12
rs1178979	7:72856430	<i>BAZ1B:Intron</i>	T	C	0.80273	0.096
rs35332062	7:73012042	<i>MLXIPL:Ala358Val</i>	G	A	0.87100	0.12
rs38855	7:116358044	<i>MET:Intron</i>	A	G	0.53139	0.014
rs4731702	7:130433384	<i>SNX27:Intergenic</i>	C	T	0.51161	0.027
rs972283	7:130466854	<i>SNX27:Intergenic</i>	G	A	0.52348	0.027
rs4841132	8:9183596	<i>NECAP2:Intergenic</i>	A	G	0.08719	0.035
rs11776767	8:10683929	<i>PINX1:Intron</i>	C	G	0.37553	0.022
rs3947	8:11702375	<i>CTSB:Utr3</i>	A	G	0.26004	0.024
rs4921914	8:18272438	<i>PGLYRP4:Intergenic</i>	C	T	0.22212	0.035
rs1495741	8:18272881	<i>PGLYRP4:Intergenic</i>	G	A	0.22269	0.035

rs2081687	8:59388565	<i>IGSF9:Intergenic</i>	T	C	0.34043	0.019
rs2954029	8:126490972	<i>AMPD1:Intergenic</i>	A	T	0.53641	0.08
rs2954033	8:126493746	<i>AMPD1:Intergenic</i>	A	G	0.30890	0.082
rs2954038	8:126507389	<i>AMPD1:Intergenic</i>	C	A	0.30582	0.087
rs3927680	9:16887366	<i>OR6P1:Intergenic</i>	T	A	0.39992	0.018
rs1883025	9:107664301	<i>ABCA1:Intron</i>	C	T	0.74439	0.022
rs1935	10:64927823	<i>JMJD1C:Glu2299Asp</i>	C	G	0.51238	0.029
rs12355784	10:65121565	<i>JMJD1C:Intron</i>	C	A	0.51154	0.03
rs7901016	10:74637326	<i>CCDC109A:Intron</i>	C	T	0.05031	0.042
rs2068888	10:94839642	<i>C1orf106:Intergenic</i>	G	A	0.54792	0.032
rs2255141	10:113933886	<i>GPAM:Intron</i>	G	A	0.71153	0.019
rs2792751	10:113940329	<i>GPAM:Ile43Val</i>	C	T	0.71133	0.02
rs7940646	10:113940329	<i>GPAM:Ile43Val</i>	C	T	0.68239	0.016
rs2167079	11:10669228	<i>MRVI1:Intron</i>	C	T	0.70480	0.02
rs174546	11:47270255	<i>ACP2:Arg29Gln</i>	T	C	0.33592	0.052
rs174547	11:61569830	<i>FADS1:Utr3</i>	C	T	0.33587	0.052
rs174550	11:61570783	<i>FADS1:Intron</i>	C	T	0.33582	0.052
rs11820589	11:61571478	<i>FADS1:Intron</i>	A	G	0.06483	0.19
rs10047462	11:116633862	<i>BUD13:Pro148Leu</i>	G	T	0.10347	0.11
rs10892063	11:116722041	<i>SIK3:Intron</i>	A	C	0.36044	0.058
rs4149056	11:116896155	<i>SIK3:Intron</i>	C	T	0.15772	0.029
rs1106766	12:21331549	<i>SLCO1B1:Val174Ala</i>	C	T	0.77240	0.03
rs10861661	12:57809456	<i>CFH:Intergenic</i>	C	A	0.23852	0.019
rs11057401	12:107174646	<i>RIC8B:Intron</i>	T	A	0.68156	0.028
rs7157785	12:124427306	<i>CCDC92:Ser70Cys</i>	T	G	0.16251	0.023
rs3803357	14:64235556	<i>NPR1:Intergenic</i>	C	A	0.49745	0.017
rs3742970	15:40751555	<i>BAHD1:Gln298Lys</i>	A	C	0.08886	0.038
rs10468017	15:43622265	<i>LCMT2:Arg142Ser</i>	T	C	0.27708	0.034
rs1532085	15:58678512	<i>SNX27:Intergenic</i>	A	G	0.37324	0.031
rs1800588	15:58683366	<i>SNX27:Intergenic</i>	T	C	0.21611	0.047
rs7200543	15:58723675	<i>SNX27:Intergenic</i>	G	A	0.30366	0.024
rs1135999	16:15129970	<i>PDXDC1:Leu736Leu</i>	G	A	0.30336	0.024

rs1421085	16:15131962	<i>NTAN1:Ser287Pro</i>	C	T	0.40600	0.019
rs9989419	16:53800954	<i>FTO:Intron</i>	A	G	0.39543	0.019
rs173539	16:56985139	<i>OR10K2:Intergenic</i>	C	T	0.68007	0.034
rs247616	16:56988044	<i>OR10K2:Intergenic</i>	C	T	0.68535	0.036
rs3764261	16:56989590	<i>OR10K2:Intergenic</i>	C	A	0.68314	0.036
rs9939224	16:56993324	<i>OR10K2:Intergenic</i>	T	G	0.20006	0.034
rs7499892	16:57002732	<i>CETP:Intron</i>	T	C	0.17689	0.04
rs5880	16:57006590	<i>CETP:Intron</i>	C	G	0.05201	0.039
rs2000999	16:57015091	<i>CETP:Ala390Pro</i>	A	G	0.19786	0.021
rs2925979	16:72108093	<i>HPR:Intron</i>	T	C	0.29772	0.029
rs7946	16:81534790	<i>CMIP:Intron</i>	C	T	0.26372	0.016
rs12453522	17:17409560	<i>PEMT:Val12Met</i>	G	A	0.17257	0.021
rs11871606	17:41931375	<i>CD300LG:Thr194Ala</i>	A	C	0.49982	0.016
rs2292642	17:45732774	<i>KPNB1:Intron</i>	C	T	0.38870	0.02
rs4129767	17:76395430	<i>PGS1:Gly172Gly</i>	G	A	0.50195	0.015
rs489693	18:57882787	<i>DVL1:Intergenic</i>	A	C	0.32544	0.015
rs12970134	18:57882787	<i>DVL1:Intergenic</i>	A	G	0.26918	0.017
rs891088	18:57884750	<i>DVL1:Intergenic</i>	A	G	0.73804	0.017
rs7248104	19:7184762	<i>INSR:Intron</i>	G	A	0.59212	0.02
rs7255436	19:7224431	<i>INSR:Intron</i>	C	A	0.47088	0.019
rs58542926	19:8433196	<i>ANGPTL4:Intron</i>	C	T	0.92458	0.12
rs731839	19:19379549	<i>TM6SF2:Glu167Lys</i>	G	A	0.33978	0.015
rs8182584	19:33899065	<i>PEPD:Intron</i>	T	G	0.38135	0.016
rs157580	19:33909710	<i>PEPD:Intron</i>	A	G	0.61120	0.047
rs769449	19:45395266	<i>TOMM40:Intron</i>	A	G	0.11769	0.35
rs7412	19:11350874	<i>LOC55908:Gln121Stp</i>	T	C	0.08537	0.12
rs439401	19:45412079	<i>APOE:Arg176Cys</i>	C	T	0.63052	0.075
rs445925	19:45414451	<i>ATP13A2:Intergenic</i>	A	G	0.10465	0.12
rs492602	19:45415640	<i>ATP13A2:Intergenic</i>	G	A	0.48041	0.018
rs2287922	19:49206417	<i>FUT2:Ala69Ala</i>	A	G	0.49222	0.019
rs2280401	19:49232226	<i>RASIP1:Arg601Cys</i>	G	A	0.83758	0.02
rs7679	19:50000009	<i>RPS11:Intron</i>	C	T	0.18876	0.053

rs6062343	20:44576502	<i>PCIF1:Utr3</i>	G	A	0.55395	0.018
rs738322	22:38546033	<i>TCEA2:Intron</i>	A	G	0.51948	0.02
rs5757251	22:38569006	<i>PLA2G6:Intron</i>	A	G	0.36881	0.016
rs738409	22:39100128	<i>NPR1:Intergenic</i>	C	G	0.77495	0.018

EAF_WGHS: effect allele frequency in the Women's Genome Health Study cohort. Published effect estimate:

Supplemental Table II Association of TG with the incidence of T2DM across tertiles of GRS in the WGHS (total sample)

	Model	1st GRS tertile			2nd GRS tertile			3rd GRS tertile			<i>P</i> _{interaction}
		HR	HR (95% CIs)		HR	HR (95% CIs)		HR	HR (95% CIs)		
Triglycerides (mmol/L)	Basic	1.87	1.75	2.00	1.75	1.65	1.86	1.66	1.57	1.75	0.0012
	Full	1.45	1.34	1.57	1.38	1.28	1.49	1.37	1.29	1.46	0.1734
TRLP (nmol/l)	Basic	1.01	1.01	1.01	1.01	1.00	1.01	1.01	1.01	1.01	0.2951
	Full	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.01	0.9597
	Full + TG	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.4674
Very large TRLP (nmol/l)	Basic	1.66	1.54	1.78	1.49	1.39	1.59	1.50	1.42	1.58	0.0336
	Full	1.40	1.29	1.52	1.26	1.15	1.37	1.30	1.22	1.39	0.1595
	Full + TG	1.14	1.02	1.28	1.00	0.89	1.12	1.09	0.99	1.20	0.2062
Large TRLP (nmol/l)	Basic	1.19	1.17	1.22	1.15	1.13	1.18	1.14	1.13	1.16	0.0018
	Full	1.09	1.07	1.12	1.07	1.05	1.10	1.07	1.05	1.09	0.1106
	Full + TG	1.01	0.98	1.05	0.99	0.96	1.03	0.97	0.93	1.00	0.0415
Medium TRLP (nmol/l)	Basic	1.03	1.02	1.03	1.03	1.02	1.03	1.02	1.02	1.03	0.0526
	Full	1.01	1.00	1.01	1.01	1.00	1.01	1.01	1.00	1.01	0.3606
	Full + TG	0.98	0.97	0.99	0.99	0.98	0.99	0.98	0.97	0.99	0.2207
Small TRLP (nmol/l)	Basic	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.012
	Full	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.2549
	Full + TG	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.5224
Very small TRLP (nmol/l)	Basic	1.01	1.01	1.01	1.01	1.01	1.01	1.01	1.01	1.01	0.2737
	Full	1.01	1.00	1.01	1.00	1.00	1.01	1.01	1.01	1.01	0.2099
	Full + TG	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.01	0.7023
TRLZ (nm)	Basic	1.07	1.06	1.08	1.06	1.05	1.07	1.07	1.06	1.07	0.5759
	Full	1.04	1.03	1.05	1.03	1.02	1.04	1.04	1.03	1.05	0.4683
	Full + TG	1.03	1.01	1.04	1.01	1.00	1.02	1.02	1.00	1.03	0.1947
TRLTG (mmol/l)	Basic	2.56	2.27	2.89	2.05	1.87	2.25	2.06	1.88	2.26	0.0027
	Full	1.59	1.38	1.83	1.43	1.27	1.62	1.46	1.30	1.64	0.1842
	Full + TG	0.82	0.64	1.06	0.72	0.57	0.92	0.76	0.61	0.94	0.1214

TRLTC (mmol/l)	Basic	4.65	3.54	6.11	3.55	2.80	4.50	3.82	3.03	4.82	0.131
	Full	1.88	1.38	2.55	1.68	1.27	2.23	1.91	1.46	2.50	0.6667
	Full + TG	0.84	0.58	1.21	0.74	0.52	1.06	0.87	0.62	1.22	0.2438

Basic model was adjusted with age, PCs, VE and ASA; Fully adjusted model was adjusted with basic model + BMI, HDL; Full + TG: fully adjusted model + TG.

Supplemental Table III Association of TG-associated SNPs with T2DM incidence across two levels of TG (≤ 1.287 vs ≥ 1.287) in fasting sample

SNP	Low TG Level				High TG Level			
	HR	Lower 95% CI	Higher 95 % CI	P	HR	Lower 95%	Higher 95 % CI	P
rs12748152	1.13	0.87	1.48	0.360	1.11	0.95	1.29	0.188
rs2131925	0.93	0.80	1.08	0.352	0.94	0.86	1.02	0.150
rs4846914	1.03	0.88	1.19	0.743	0.93	0.85	1.01	0.101
rs1260326	0.90	0.77	1.05	0.180	1.01	0.93	1.10	0.833
rs2972146	0.99	0.85	1.16	0.916	1.00	0.92	1.10	0.944
rs645040	1.05	0.88	1.26	0.590	1.03	0.93	1.14	0.570
rs6831256	0.93	0.80	1.08	0.343	1.04	0.96	1.14	0.342
rs442177	0.79	0.68	0.92	0.002	1.09	1.00	1.19	0.057
rs9686661	0.86	0.70	1.05	0.142	0.97	0.87	1.08	0.591
rs6882076	1.12	0.96	1.31	0.148	1.02	0.94	1.12	0.600
rs998584	1.01	0.84	1.23	0.893	1.05	0.94	1.18	0.369
rs719726	1.13	0.97	1.33	0.113	0.96	0.88	1.05	0.367
rs4719841	1.02	0.88	1.19	0.772	0.98	0.90	1.07	0.647
rs13238203	0.00	0.00	0.53	0.032	0.26	0.00	16.02	0.523
rs17145738	0.92	0.74	1.15	0.455	0.95	0.83	1.09	0.443
rs38855	1.03	0.89	1.20	0.665	0.96	0.88	1.04	0.311
rs11776767	1.07	0.91	1.25	0.413	0.91	0.83	0.99	0.036
rs1495741	1.08	0.90	1.29	0.395	1.03	0.93	1.14	0.576
rs12678919	1.07	0.84	1.36	0.605	0.90	0.78	1.03	0.132
rs2954029	1.09	0.94	1.26	0.264	0.98	0.90	1.07	0.721
rs1832007	1.08	0.88	1.33	0.466	1.06	0.94	1.19	0.353
rs10761731	0.94	0.81	1.10	0.441	0.95	0.87	1.04	0.244
rs2068888	0.99	0.85	1.14	0.836	0.98	0.90	1.06	0.564
rs174546	1.03	0.88	1.20	0.746	0.86	0.79	0.94	0.001
rs964184	0.84	0.65	1.07	0.156	0.71	0.63	0.81	<.0001
rs11613352	0.93	0.78	1.10	0.374	0.97	0.87	1.07	0.483
rs4765127	1.05	0.90	1.23	0.529	1.02	0.93	1.12	0.680
rs2412710	0.83	0.44	1.58	0.569	1.30	0.99	1.71	0.064
rs2929282	1.06	0.72	1.55	0.772	1.11	0.91	1.35	0.311
rs1532085	1.09	0.94	1.27	0.275	0.96	0.88	1.04	0.320
rs3198697	0.97	0.79	1.19	0.760	1.00	0.89	1.13	0.949
rs11649653	0.99	0.84	1.18	0.932	1.03	0.93	1.14	0.524
rs1121980	1.07	0.92	1.25	0.356	0.99	0.91	1.08	0.890
rs3764261	0.92	0.77	1.09	0.322	0.92	0.83	1.02	0.126
rs8077889	1.06	0.89	1.27	0.515	0.92	0.83	1.02	0.106
rs7248104	1.01	0.87	1.17	0.934	1.02	0.94	1.11	0.611
rs10401969	0.70	0.56	0.89	0.003	0.87	0.73	1.03	0.094
rs731839	1.00	0.85	1.18	0.995	1.09	1.00	1.19	0.064
rs6065906	0.87	0.71	1.06	0.166	0.99	0.89	1.10	0.820

rs5756931	0.89	0.76	1.04	0.132	0.90	0.82	0.98	0.021
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Models were adjusted for age, BMI, HDL and PCs.

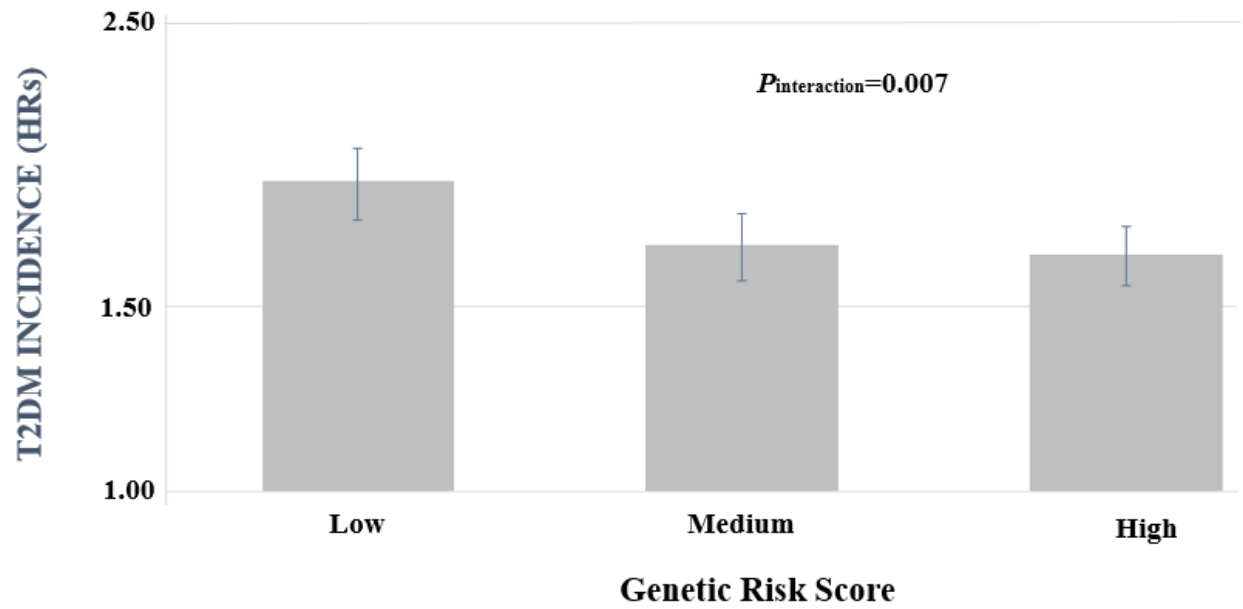
Supplemental Table IV Association of TG with the incidence of T2DM across tertiles of GRS based upon 34 SNPs (T2DM associated SNPs excluded) in the WGHS

	Model	1st GRS tertile			2nd GRS tertile			3rd GRS tertile			Pinteraction
		HR	HR (95% CIs)		HR	HR (95% CIs)		HR	HR (95% CIs)		
Triglycerides (mmol/L)	Basic	2.06	1.91	2.23	1.72	1.60	1.85	1.59	1.49	1.70	<0.0001
	Full	1.63	1.49	1.79	1.42	1.30	1.54	1.28	1.18	1.38	0.0001
TRLP (nmol/l)	Basic	1.01	1.01	1.01	1.01	1.00	1.01	1.01	1.00	1.01	0.0123
	Full	1.00	1.00	1.01	1.00	1.00	1.00	1.00	1.00	1.00	0.1402
	Full + TG	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.0443
VLTRLP (nmol/l)	Basic	1.86	1.69	2.05	1.48	1.36	1.60	1.55	1.44	1.68	0.0484
	Full	1.61	1.44	1.80	1.26	1.15	1.39	1.30	1.19	1.42	0.024
	Full + TG	1.18	1.02	1.38	1.00	0.88	1.14	1.14	1.01	1.29	0.0162
LTRLP (nmol/l)	Basic	1.21	1.18	1.24	1.16	1.13	1.18	1.13	1.11	1.15	0.0002
	Full	1.11	1.08	1.14	1.08	1.06	1.11	1.05	1.02	1.07	0.0035
	Full + TG	0.99	0.95	1.04	1.00	0.95	1.04	0.97	0.93	1.01	0.001
MTRLP (nmol/l)	Basic	1.03	1.02	1.04	1.02	1.02	1.03	1.02	1.01	1.02	0.004
	Full	1.01	1.00	1.02	1.01	1.00	1.02	1.00	0.99	1.01	0.0173
	Full + TG	0.98	0.97	0.99	0.98	0.97	0.99	0.98	0.97	0.98	0.0028
STRLP (nmol/l)	Basic	1.00	1.00	1.01	1.00	1.00	1.00	1.00	0.99	1.00	0.0008
	Full	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.99	1.00	0.0507
	Full + TG	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.1667
VSTRLP (nmol/l)	Basic	1.01	1.01	1.01	1.01	1.01	1.01	1.01	1.01	1.01	0.6691
	Full	1.01	1.00	1.01	1.00	1.00	1.01	1.01	1.00	1.01	0.4935
	Full + TG	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.01	0.9765
TRLZ (nm)	Basic	1.06	1.05	1.08	1.06	1.05	1.07	1.07	1.06	1.08	0.8731
	Full	1.04	1.03	1.05	1.04	1.03	1.05	1.04	1.02	1.05	0.4952
	Full + TG	1.02	1.00	1.03	1.02	1.01	1.03	1.03	1.01	1.04	0.1788
TRLTG (mmol/l)	Basic	2.77	2.39	3.20	2.00	1.80	2.23	1.88	1.69	2.10	0.0002
	Full	1.71	1.44	2.02	1.47	1.28	1.69	1.28	1.11	1.48	0.0105

	Full + TG	0.71	0.56	0.92	0.71	0.53	0.94	0.71	0.54	0.92	0.0016
TRLTC (mmol/l)	Basic	5.17	3.81	7.03	3.14	2.38	4.14	2.83	2.16	3.69	0.0043
	Full	2.07	1.47	2.91	1.49	1.08	2.06	1.33	0.97	1.83	0.0617
	Full + TG	0.64	0.42	0.97	0.53	0.35	0.82	0.66	0.44	0.98	0.0091

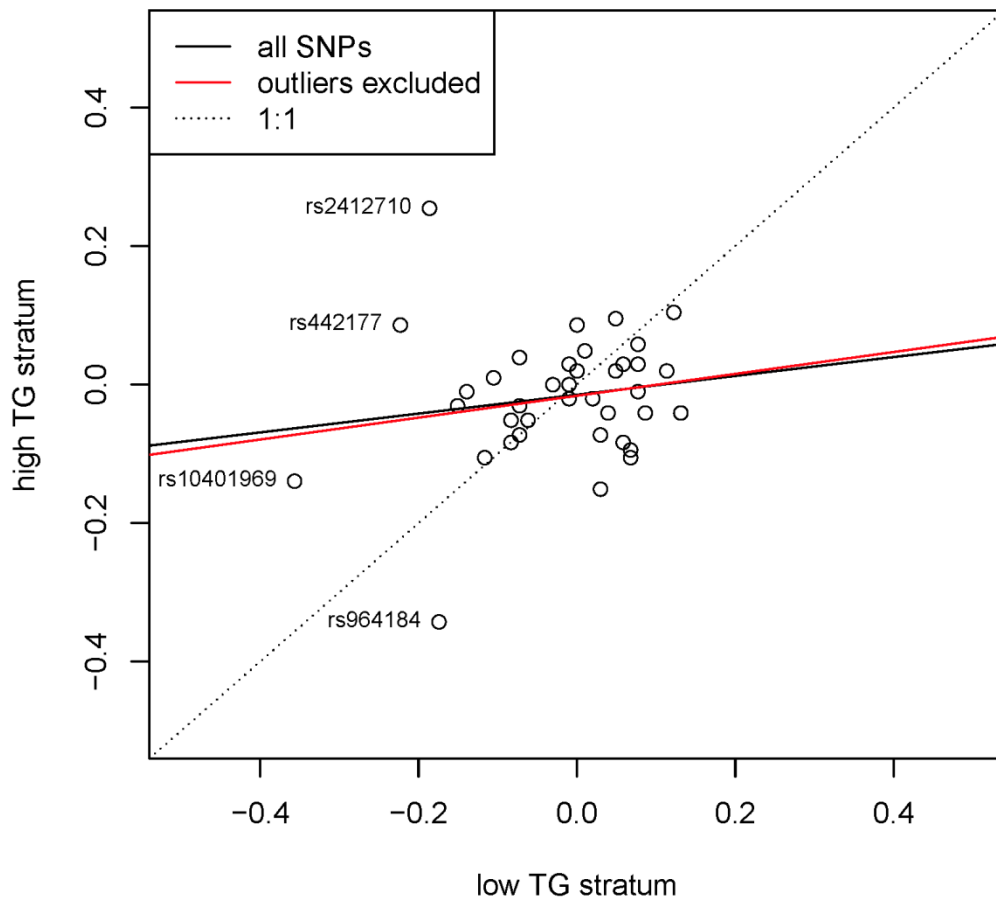
Basic model was adjusted with age and PCs

Fully adjusted model was adjusted with basic model + BMI, HDL; Full + TG: Fully adjusted model + TG



Supplementary Figure I Association of TG with T2DM incidence across TG-wGRS tertiles in the WGHS fasting sample (N= 15,813).

WGHS T2DM beta coefficients in high v. low TG strata



Supplementary Figure II Association of TG-associated SNPs with T2DM incidence across two levels of TG (low TG stratum ≤ 1.287 vs high TG stratum ≥ 1.287) in the fasting sample of the WGHS cohort. “Outliers” refers to SNPs judged to have disproportionate influence on the regression fit by virtue of at least one of several diagnostic measures (Methods)