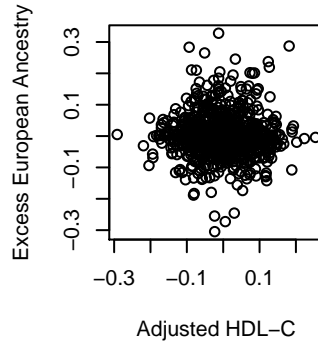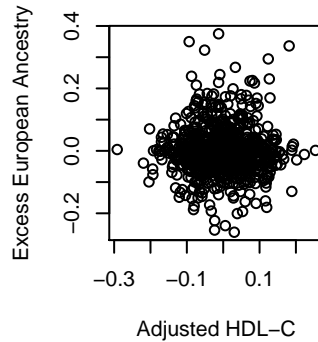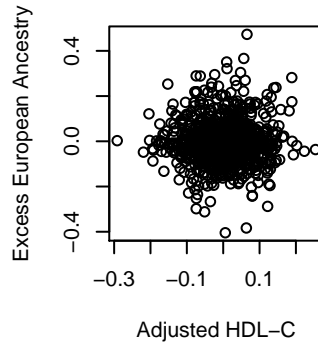## ScatterPlot of Excess European ancestry at marker D8S1136 and adjusted HDL−C

ScatterPlot of Excess European ancestry at marker D8S1113 and adjusted HDL−C

ScatterPlot of Excess European ancestry at marker GATA193A07 and adjusted HDL−C

Supplementary Table 1. Marker locations with the most significant regression on ancestry for the trait LDL-C.

DNAME	Cytological and Genetic (cM) Location	Estimated (r_l)	Marker Names
D3S2427	3q26.31(188.29)	-2.35	GATA22F11
D4S2367	4q13.2(78.43)	-2.33	GATA24H01
D4S3248	4q13.1(72.52)	-2.24	GATA28F03
D3S1763	3q26.1(176.54)	-2.21	GATA3H01
D3S2418	3q28(215.84)	-2.19	ATA22E01
D7S1824	7q34(149.9)	-2.13	GATA32C12
D4S1627	4p13(60.16)	-2.10	GATA7D01
D3S1311	3q29(224.88)	-2.08	AFM254VE1
D3S1744	3q24(161.04)	-2.06	GATA3C02
D7S3061	7q31.32(128.41)	-1.96	GGAA6D03
D11S1984	11p15.5(2.11)	2.00	GGAA17G05
Unknown	11p15(33.02)	2.00	ATA34E08
D13S793	13q32.1(76.26)	2.01	GATA43H03
D14S588	14q24.1(75.61)	2.02	GGAA4A12
D2S1391	2q32.1(186.21)	2.05	GATA65C03
D21S1437	21q21.1(13.05)	2.21	GGAA3C07
D21S1432	21q21.1(2.99)	2.57	GATA11C12

Supplementary Table 2. Marker locations with the most significant regression on ancestry for the trait HDL-C.

DNAME	Cytological and Genetic (cM) Location	Estimated (r_i)	Marker Names
D8S1136	8q13.1(82.26)	-4.13	GATA41A01
D8S1113	8q12.1(77.89)	-3.01	GGAA8G07
Unknown	14q31.2(95.89)	-3.00	GATA193A07
D14S606	14q31.1(91.62)	-2.61	GATA30A03
D8S2324	8q21.11(94.08)	-2.45	GATA14E09
D10S1208	10p11.21(63.3)	-2.34	ATA5A04
D14S588	14q24.1(75.61)	-2.33	GGAA4A12
D10S1426	10p11.23(59.03)	-2.17	GATA73E11
D8S1110	8q11.23(67.27)	-2.04	GATA8G10
D4S2366	4p16.1(12.93)	-2.01	GATA22G05
D5S2849	5p15.33(7.77)	2.00	GATA145D10
D17S784	17q25.3(116.86)	2.03	AFM044XG3
Unknown	12q23.2(109.47)	2.05	PAH
D12S1300	12q23.1(104.12)	2.12	GATA85A04
D15S816	15q26.2(100.59)	2.14	GATA73F01
D17S1301	17q25.1(100.02)	2.16	GATA28D11
D9S930	9q32(120.04)	2.16	GATA48D07
D6S1021	6q16.3(112.2)	2.28	ATA11D10
D6S474	6q21(118.64)	2.37	GATA31
D9S910	9q22.33(104.48)	2.69	ATA18A07
D9S938	9q31.1(110.93)	2.69	GGAA22E01

Supplementary Table 3. Marker locations with the most significant regression on ancestry for the trait TG

DNAME	Cytological and Genetic (cM) Location	Estimated (r_l)	Marker Names
D15S652	15q26.1(90.02)	-2.75	ATA24A08
D15S816	15q26.2(100.59)	-2.69	GATA73F01
D15S659	15q21.1(43.47)	-2.40	GATA63A03
D21S1446	21q22.3(57.77)	-2.24	GATA70B08
D15S643	15q22.2(52.33)	-2.18	GATA50G06
D15S655	15q25.3(82.84)	-2.07	ATA28G05
D17S784	17q25.3(116.86)	-2.03	AFM044XG3
D9S938	9q31.1(110.93)	-2.00	GGAA22E01
D5S1456	5q35.1(174.8)	1.99	GATA11A11
D11S2371	11q13.4(76.13)	2.06	GATA90D07
D2S1399	2q22.3(152.04)	2.15	GGAA20G04
D8S1132	8q23.1(119.22)	2.19	GATA26E03
D8S2324	8q21.11(94.08)	2.24	GATA14E09
D8S1136	8q13.1(82.26)	2.31	GATA41A01
D8S1113	8q12.1(77.89)	2.31	GGAA8G07
D8S1128	8q24.21(139.53)	2.43	GATA21C12
D11S2002	11q14.1(85.48)	2.46	GATA30G01
D8S592	8q24.11(125.27)	2.48	GATA6B02
D8S373	8q24.3(164.47)	2.53	UT721
D8S1179	8q24.13(135.08)	2.59	GATA7G07