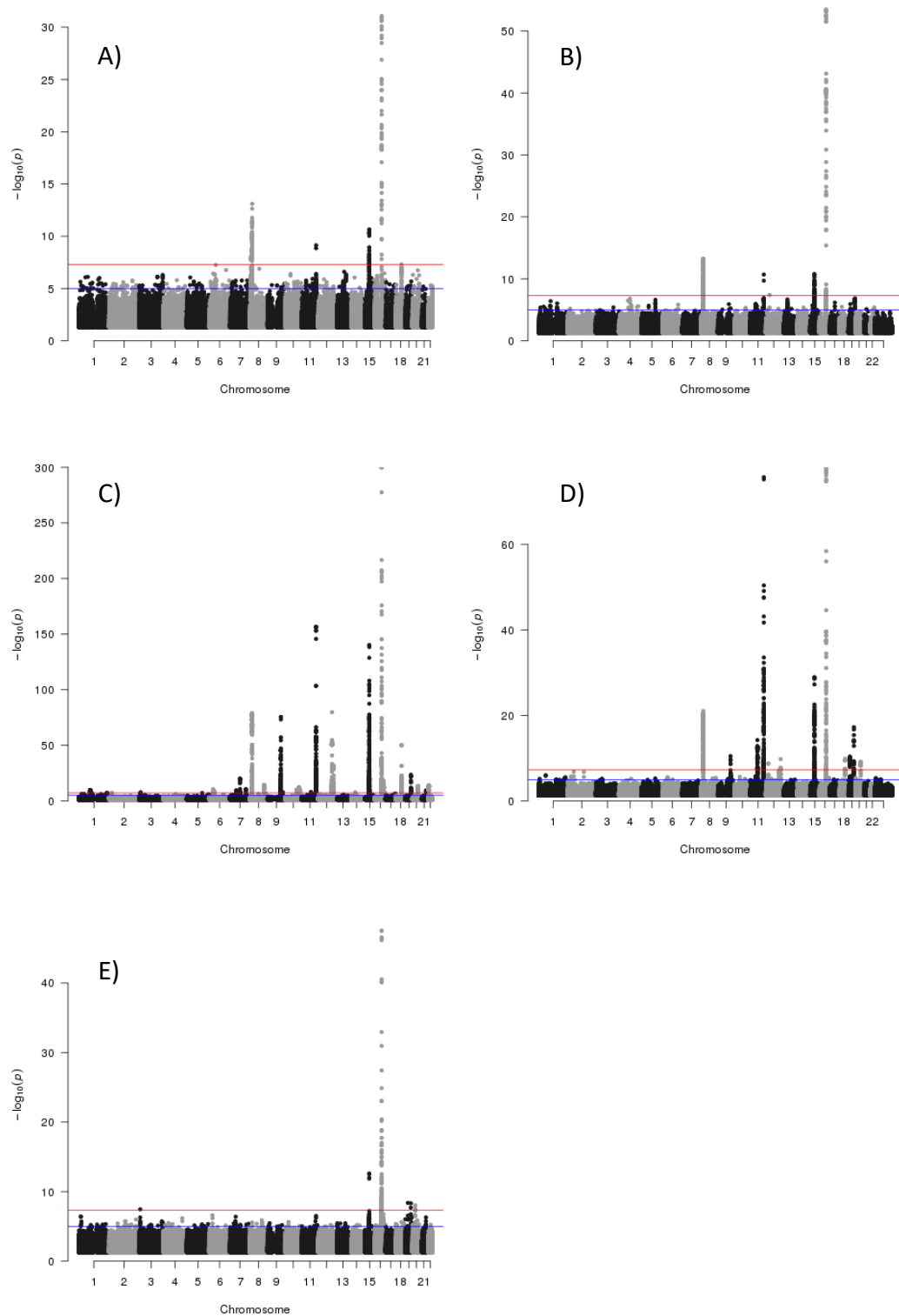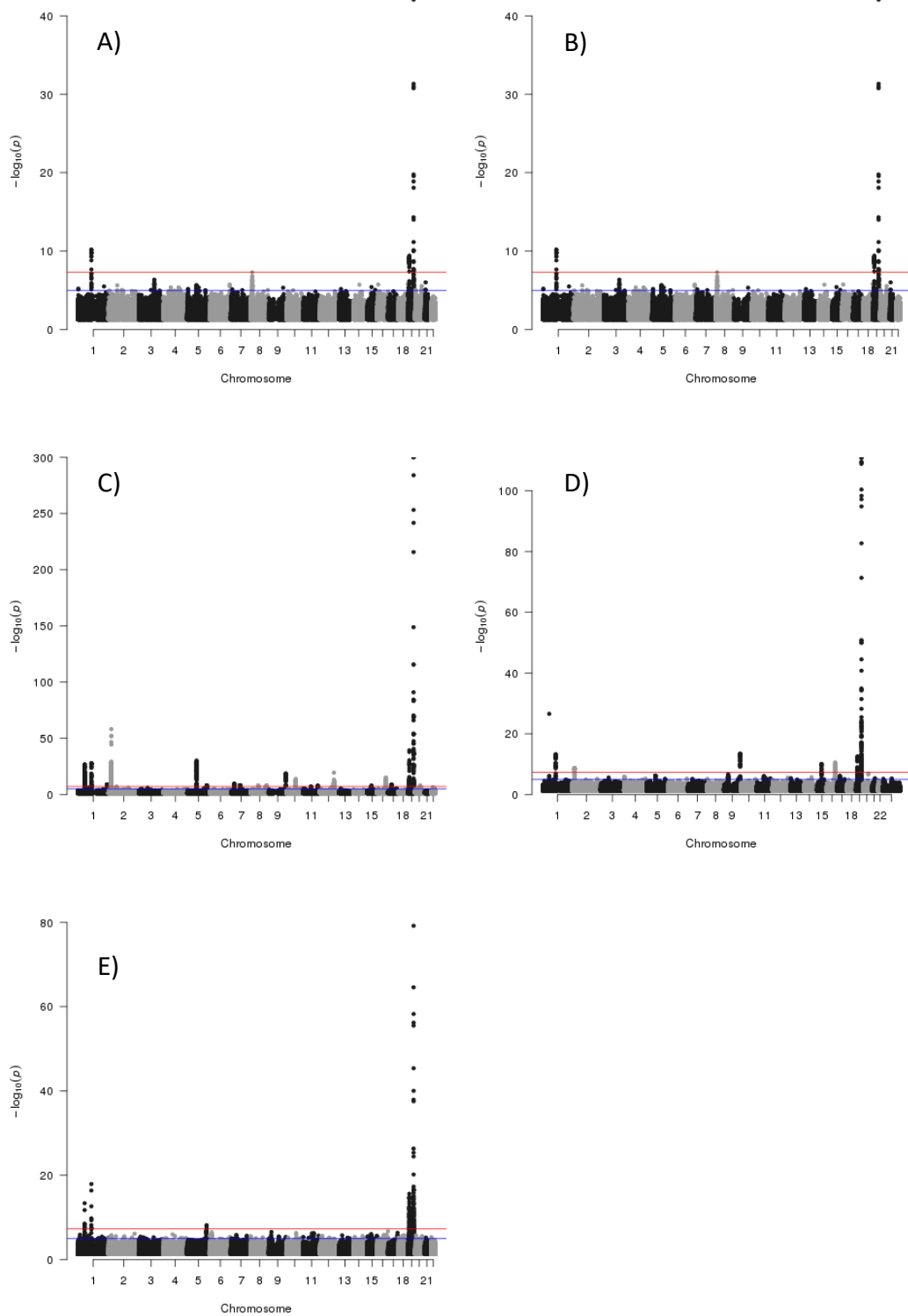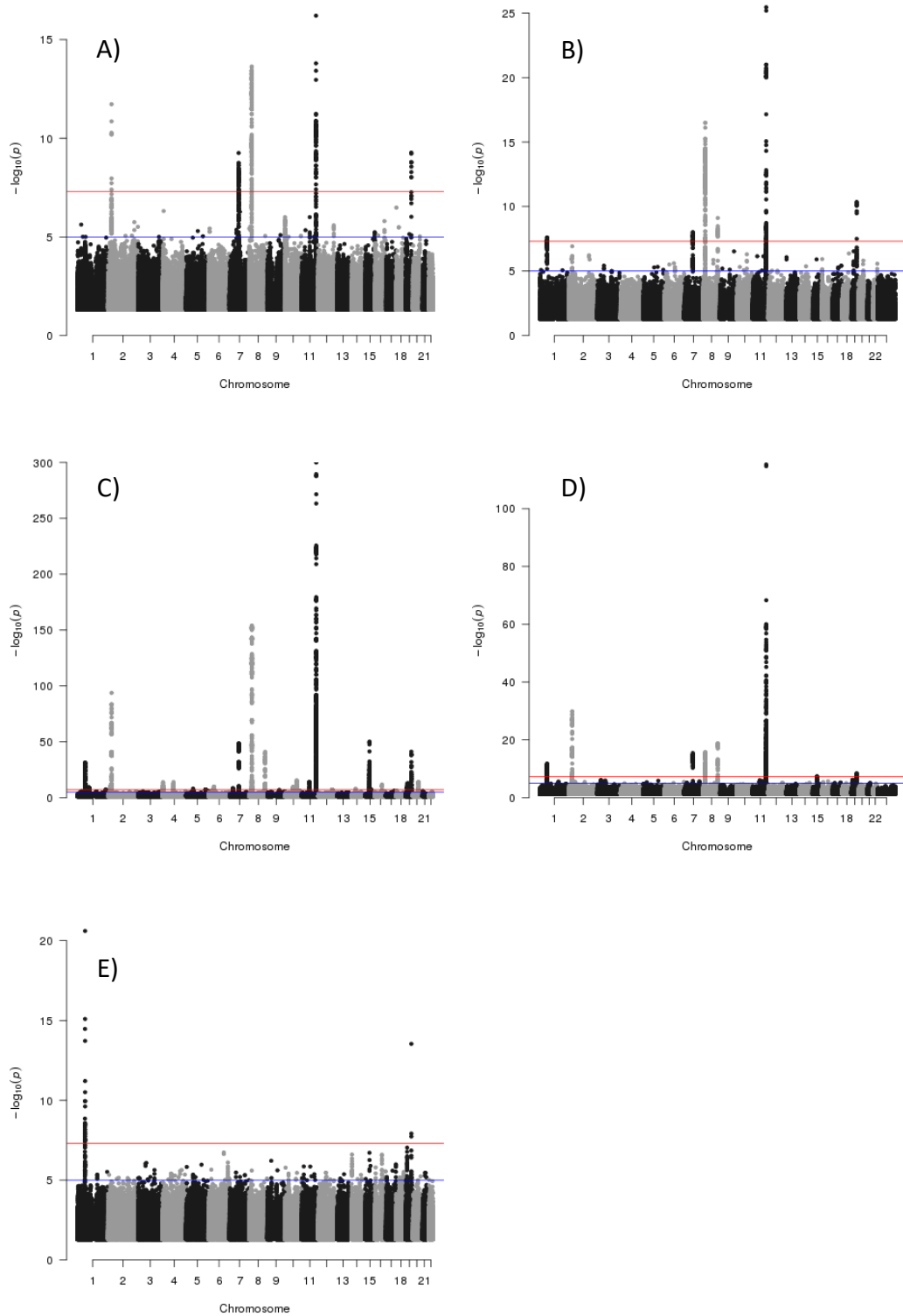# Supplementary figures and tables

Supplementary Figure 1: Manhattan plot for SNP associations with HDL cholesterol levels, for A) eMerge, B) UKHLS, C) Biobank Japan, D) China Kadoorie Biobank, E) APCDR-Uganda

Supplementary Figure 2: Manhattan plot for SNP associations with LDL cholesterol levels, for A) eMerge, B) UKHLS, C) Biobank Japan, D) China Kadoorie Biobank, E) APCDR-Uganda

Supplementary Figure 3: Manhattan plot for SNP associations with triglyceride levels, for A) eMerge, B) UKHLS, C) Biobank Japan, D) China Kadoorie Biobank, E) APCDR-Uganda

Supplementary Table 1: Trans-ethnic genetic correlation estimates and p-values for a test whether the genetic correlation is 1 for each lipid biomarker in one study with each lipid biomarkers in the other study

biomarker	correlation	standard error	p-value*
GLGC2013 (European) – China Kadoorie Biobank			
HDL-HDL	0.999	-	-
LDL-LDL	0.778	0.300	0.460
TG-TG	0.999	-	-
HDL - LDL	0.068	0.229	0.000
HDL - TG	-0.550	0.176	0.000
LDL - HDL	-0.238	0.143	0.000
LDL - TG	0.473	0.155	0.001
TG - HDL	-0.741	0.162	0.000
TG - LDL	-0.226	0.195	0.000
GLGC2013 (European) – Biobank Japan			
HDL-HDL	0.999	0.081	0.999
LDL-LDL	0.959	0.138	0.765
TG-TG	0.961	0.066	0.555
HDL - LDL	-0.055	0.097	0.000
HDL - TG	-0.592	0.130	0.000
LDL - HDL	-0.277	0.150	0.000
LDL - TG	0.294	0.056	0.000
TG - HDL	-0.481	0.176	0.000
TG - LDL	-0.038	0.091	0.000
China Kadoorie Biobank – Biobank Japan			
HDL-HDL	0.999	-	-
LDL-LDL	0.871	0.225	0.566
TG-TG	0.999	-	-
HDL - LDL	0.085	0.141	0.000
HDL - TG	-0.618	0.151	0.000
LDL - HDL	0.290	0.185	0.000
LDL - TG	0.180	0.169	0.000
TG - HDL	-0.862	0.186	0.000
TG - LDL	-0.097	0.153	0.000

* When the estimate is close to the boundary of 1, popcorn cannot compute the standard error and p-value

Supplementary Table 2: Associations of polygenic scores based on established lipid-associated loci and levels of each of the other lipid biomarkers in UKHLS, HELIC-MANOLIS, -Pomak, and APCDR-Uganda using a linear mixed model analysis.

score - trait	p-value	correlation	SE (β)
APCDR-Uganda			
HDL - LDL	2.34E-01	-1.49E-02	1.25E-02
HDL - TG	2.49E-01	-1.44E-02	1.25E-02
LDL - HDL	6.75E-10	-7.73E-02	1.25E-02
LDL - TG	7.27E-04	4.22E-02	1.25E-02
TG - HDL	6.81E-01	-5.13E-03	1.25E-02
TG - LDL	1.86E-04	-4.67E-02	1.25E-02
UKHLS			
HDL - LDL	2.02E-07	-5.26E-02	1.01E-02
HDL - TG	1.63E-12	-7.20E-02	1.02E-02
LDL - HDL	3.97E-07	-5.16E-02	1.01E-02
LDL - TG	4.07E-01	8.45E-03	1.02E-02
TG - HDL	1.67E-39	-1.34E-01	1.01E-02
TG - LDL	2.47E-01	1.17E-02	1.01E-02
HELIC-Pomak			
HDL - LDL	1.97E-02	-7.22E-02	3.09E-02
HDL - TG	4.96E-05	-1.28E-01	3.10E-02
LDL - HDL	6.00E-02	-6.08E-02	3.18E-02
LDL - TG	9.18E-01	3.43E-03	3.19E-02
TG - HDL	6.16E-07	-1.57E-01	3.05E-02
TG - LDL	1.70E-02	7.39E-02	3.08E-02
HELIC-MANOLIS			
HDL - LDL	7.56E-01	9.19E-03	2.96E-02
HDL - TG	2.13E-03	-9.36E-02	3.01E-02
LDL - HDL	4.42E-01	-2.29E-02	2.97E-02
LDL - TG	9.64E-01	-1.36E-03	3.03E-02
TG - HDL	1.25E-05	-1.33E-01	2.98E-02
TG - LDL	9.56E-01	-1.63E-03	2.98E-02

Supplementary Table 3: Study description and mean levels of HDL-cholesterol, LDL-cholesterol and triglycerides (TG) in mmol/l

study	acronym	population	array	N SNPs genotyped, imputed	N samples	%female	mean age	mean HDL	mean LDL	mean TG
UK Household Longitudinal Study[1]	**UKHLS**	British	HumanCoreExome	248K, 26M	9,962	44	52	1.55	3.02	1.81
electronic MEdical Records and GEnomics[2]	**eMERGE**	European ancestry	GWAS arrays, Metabochip	17.6M	14,528	43	61	1.33	2.80	1.77
Global Lipids Genetics Consortium[3]	**GLGC2013** (meta-analysis)	European ancestry	23 studies GWAS arrays, 37 Metabochip	200K, 2.5M	188,577					
Global Lipids Genetics Consortium[4]	**GLGC2017** (meta-analysis)	European ancestry	HumanExome	242,289	237,050					
African Partnership for Chronic Disease Research - Uganda[5]	**APCDR-Uganda**	Ugandan	HumanOmni2.5	2.2M, 20M	6,407	56	34	1.02	2.05	1.18
China Kadoorie Biobank[6]	**CKB**	Chinese	Custom Affymetrix Axiom Array	701K/830K, 10M	21,295	62	60	1.37	2.19	1.69
RIKEN Biobank Japan[7]	**BBJ**	Japanese	HumanOmniExpress	6M	162,255	63	43	1.42	3.38	1.50
Hellenic Isolated Cohorts[8,9]	**HELIC-MANOLIS, -Pomak**	Isolated Greek populations	Whole-genome sequencing	24M	1,641, 1,945	42,34	62,45	1.28, 1.18	3.27, 3.09	1.61, 1.58

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