

Phenotype : C-reactive protein				sex-specific		beta±std error		best
rsid	RE	CV	GWAMA	SST(F)	SST(M)	female	male	methods
rs2794520	3.32e-23	2.11e-23	1.64e-22	1.28e-13	2.93e-11	0.314±0.042	0.291±0.043	RE,CV
rs2650000	1.71e-12	1.64e-12	8.09e-12	2.79e-06	8.65e-08	0.199±0.042	0.220±0.041	RE,CV
Phenotype : Glucose				sex-specific		beta±std error		best
rsid	RE	CV	GWAMA	SST(F)	SST(M)	female	male	methods
rs560887	5.30e-12	1.14e-12	1.39e-09	8.19e-06	4.83e-08	0.011±0.002	0.014±0.002	CV
rs7298683	2.01e-07	8.14e-05	7.23e-08	0.86718	5.92e-09	-0.0007±0.004	0.026±0.004	SST(M)
Phenotype : HDL				sex-specific		beta±std error		best
rsid	RE	CV	GWAMA	SST(F)	SST(M)	female	male	methods
rs2167079	4.46e-08	1.26e-06	5.06e-08	0.01838	9.78e-08	-0.024±0.010	-0.055±0.010	RE, GWAMA
rs7120118	4.62e-08	1.13e-06	5.07e-08	0.01679	1.15e-07	-0.024±0.010	-0.054±0.010	RE, GWAMA
rs1532085	3.53e-12	1.08e-11	2.98e-11	1.87e-06	2.25e-07	-0.048±0.010	-0.050±0.009	RE
rs3764261	4.15e-32	4.89e-32	2.88e-31	8.85e-16	3.63e-18	-0.090±0.011	-0.092±0.010	RE,CV
rs255049	5.26e-09	1.45e-08	3.94e-08	0.00014	5.85e-06	-0.047±0.012	-0.053±0.011	RE
rs1800961	2.39e-08	2.82e-08	8.96e-08	0.00051	6.29e-06	0.083±0.023	0.108±0.023	RE,CV
Phenotype : LDL				sex-specific		beta±std error		best
rsid	RE	CV	GWAMA	SST(F)	SST(M)	female	male	methods
rs646776	1.97e-15	4.17e-15	9.71e-15	8.36e-10	2.11e-07	0.169±0.027	0.166±0.031	RE
rs693	1.25e-11	2.97e-11	5.84e-11	8.81e-09	0.00013	-0.131±0.022	-0.103±0.026	RE
rs11668477	1.98e-08	4.04e-09	1.96e-08	0.00240	2.62e-07	0.090±0.029	0.179±0.034	CV
Phenotype : Triglyceride				sex-specific		beta±std error		best
rsid	RE	CV	GWAMA	SST(F)	SST(M)	female	male	methods
rs673548	2.61e-08	6.54e-08	2.21e-07	6.11e-06	0.00097	0.058±0.012	0.054±0.016	RE
rs1260326	1.64e-10	1.88e-10	1.49e-09	1.32e-06	2.10e-05	-0.057±0.011	-0.065±0.015	RE,CV
rs10096633	5.32e-08	1.98e-08	1.19e-07	0.00109	3.47e-06	0.062±0.019	0.113±0.024	CV

Table S3. Association mapping results of the NFBC data. We present 16 SNPs for which any method gave $P < 5 \times 10^{-8}$ in any of 10 phenotypes. For each SNP, the most significant p-value among the four methods (RE, CV, GWAMA, and SST) is in bold font. The “beta” column shows the effect sizes of male- and female-only studies and their estimated standard errors. For each significant association, we report the “best methods”, the set of methods whose p-value was less than two times the most significant p-value for each association.