

Supplementary table 1. Genotyping details and quality control.

Study	Genotyping method	HWE P	Call Rate	Imputed	Other Info
WTCCC	Kbiosciences allele-specific PCR (KASPar)	> 0.05	> 0.95	No	
Dundee_Cases	Kbiosciences allele-specific PCR (KASPar)	0.36	0.94947	No	
Dundee_Ctrls	Kbiosciences allele-specific PCR (KASPar)	0.15	0.95043	No	
EFS-Y2D	Kbiosciences allele-specific PCR (KASPar)	0.93	0.9584	No	
Danish	Kbiosciences allele-specific PCR (KASPar)	0.99	0.963	No	
DGI_r20.9_rs12150660	MACH Imputation from Affymetrix GeneChip Human Mapping 500k Array Set	N/A	N/A	Yes - MACH rsqr 0.849	
Malmö_CC	Taqman	N/A	0.973	No	
FUSION_r20.9_rs12150660	MACH imputation from Illumina HumanHap 300	N/A	N/A	Yes - MACH rsqr 0.6955	
KORA	Taqman	N/A	0.977	No	Discordance rate in 115 routine duplicates = 0%
Cambridgeshire Case Control study	Taqman	> 0.05	> 0.97	No	100% concordance rate between duplicates (2.5-3.5% of samples)
ADDITION/ELY	Taqman	> 0.05	> 0.97	No	100% concordance rate between duplicates (2.5-3.5% of samples)
Norfolk/BOB Norfolk Diabetes Case Control Study	Taqman	> 0.05	> 0.97	No	100% concordance rate between duplicates (2.5-3.5% of samples)
DeCODE	Centaurus genotyping for 2052 individuals; For others: Imputation based on direct genotyping of 3872 Icelandic individuals	0.7	N/A	Yes, partly	
FUSION2	iPLEX Sequenom MassARRAY, Typer 4.0 calling algorithm	0.15	0.95	No	
METSIM	iPLEX Sequenom MassARRAY, Typer 4.0 calling algorithm	0.14	0.94	No	
DIAGEN	iPLEX Sequenom MassARRAY, Typer 4.0 calling algorithm	0.56	0.96	No	

N/A not available