| Trait | rs (dbSNP 129) | Chr-Position (build 36) | Gene | EAF (%) | Proxy ($r^2$) | N | Effect/P | Consistent direction | Reason for missing results |
|---|---|---|---|---|---|---|---|---|---|
| Fasting serum HDL-cholesterol | None | 17-39281652 | CD300LG | 3.5 | | | | | No proxy |
| Type 2 diabetes | rs7607980 | 2-165259447 | COBLL1 | 12.5 | | 22570 | 0.93 (0.87-0.99), *P*=0.016 | Y | |
| Type 2 diabetes | rs2296172 | 1-39608404 | MACF1 | 23.4 | | 22570 | 1.06 (1.01-1.11), *P*=0.016 | Y | |
| Type 2 diabetes | rs60980157 | 9-138355236 | GPSM1 | 24.6 | | | | | No proxy |
| Fasting serum triacylglycerol | rs41273264 | 6-31708085 | PRRC2A | 4.2 | | | | | No proxy |
| Obesity | rs11553746 | 2-262203 | ACP1 | 37.8 | | | | | No data for this trait |
| BMI | rs11553746 | 2-262203 | ACP1 | 37.8 | rs3791221 (1) | 123842 | P=0.093 | Y | |

Due to a minor overlap in samples between stage 3 and the GWAS meta-analysis data these data were not meta-analysed with stage 2 and stage 3 data and consequently they represent semi-independent replication. Data for type 2 diabetes were contributed by the DIAGRAM Consortium [27], data on BMI by GIANT Consortium [28] (http://www.broadinstitute.org/collaboration/giant/index.php/GIANT_consortium) and data on glycaemic traits were contributed by MAGIC investigators [29] and were downloaded from www.magicinvestigators.org. For two SNPs the lead SNPs were in the GWAS meta-analyses data while *in silico* replication for two SNPs was based on proxies. Here LD was estimated from data from the 1000 Genomes Project. Three SNPs had no good proxy ($r^2$ > 0.4). For one trait no GWAS data could be investigated.