Supplementary Fig 1. **Flowchart of study design and application of 2-sample Mendelian randomisation (MR) in infer the causal association between n6 PUFA synthesis and T2D risk or insulin disposition index (DI).** In Sample 1, summary-level data of single nucleotide polymorphisms (SNPs) associated with our exposure of interest (i.e., n6 PUFA synthesis) were identified for use as instrumental variables. These SNPs were then pruned and cross referenced with Sample 2 studies/consortia, which had summary-level data of SNPs associated with our outcomes of interest (i.e., insulin disposition index and type-2 diabetes). We these two sets of data, we then performed our analysis using the Wald Ratio.

A screenshot of a cell phone

Description automatically generated