

SUPPLEMENTARY MATERIALS

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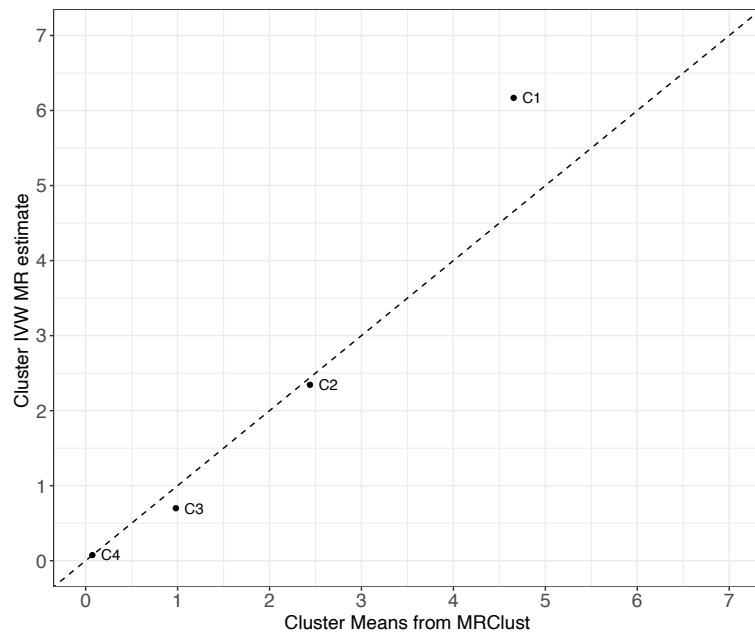
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Supplementary Table 1. UKB Participants' baseline characteristics

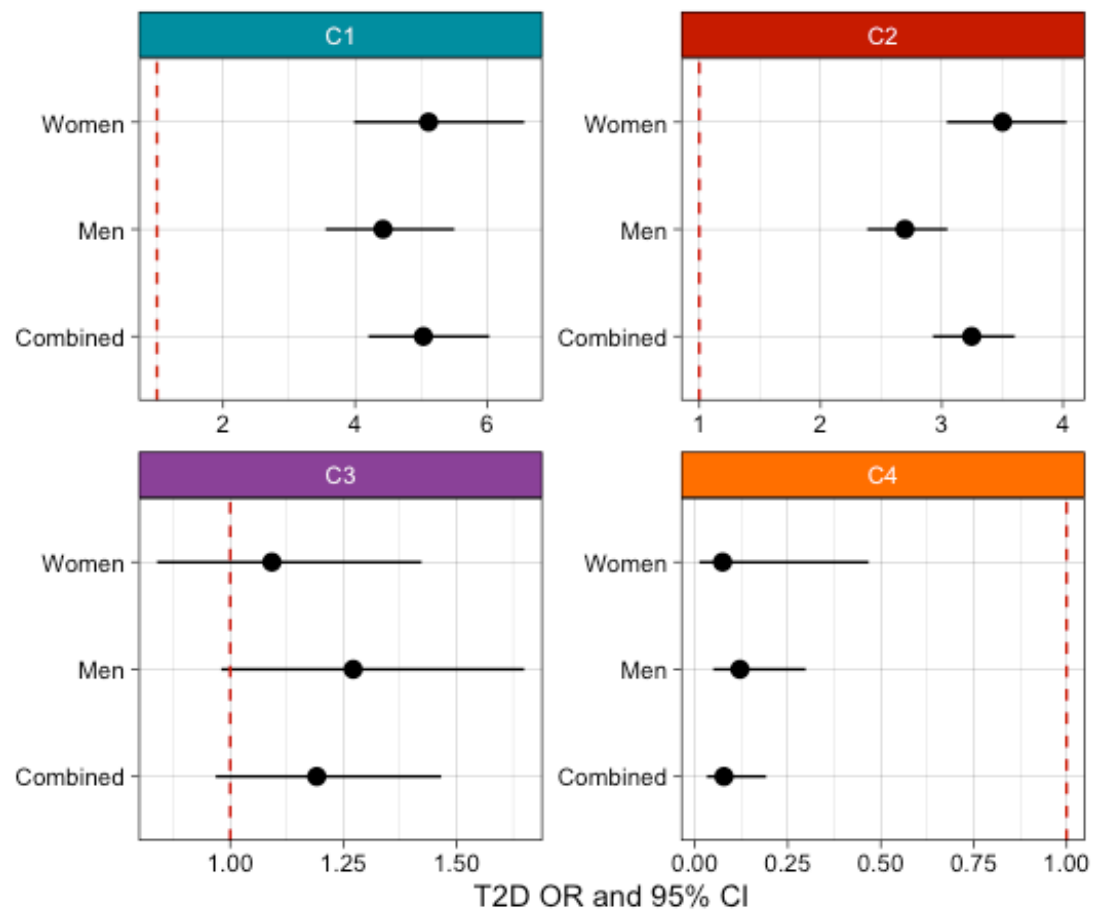
<i>Attribute</i>	<i>Females</i>	<i>Males</i>
<i>N (%)</i>	<i>194184 (53.8%)</i>	<i>166587</i>
<i>BMI (mean, SD)</i>	<i>27.04 (5.14)</i>	<i>27.85 (4.23)</i>
<i>Age (mean, SD)</i>	<i>56.68 (7.9)</i>	<i>57.13 (8.08)</i>
<i>Alcohol: Never</i>	<i>8368</i>	<i>2790</i>
<i>Previous</i>	<i>6927</i>	<i>5297</i>
<i>Current</i>	<i>178712</i>	<i>158360</i>
<i>Smoking: Never</i>	<i>115121</i>	<i>81400</i>
<i>Previous</i>	<i>61828</i>	<i>65014</i>
<i>Current</i>	<i>16587</i>	<i>19587</i>
<i>T2D: No</i>	<i>182033</i>	<i>148001</i>
<i>Yes</i>	<i>12151</i>	<i>18586</i>

Supplementary Table 2. Field codes of variables used

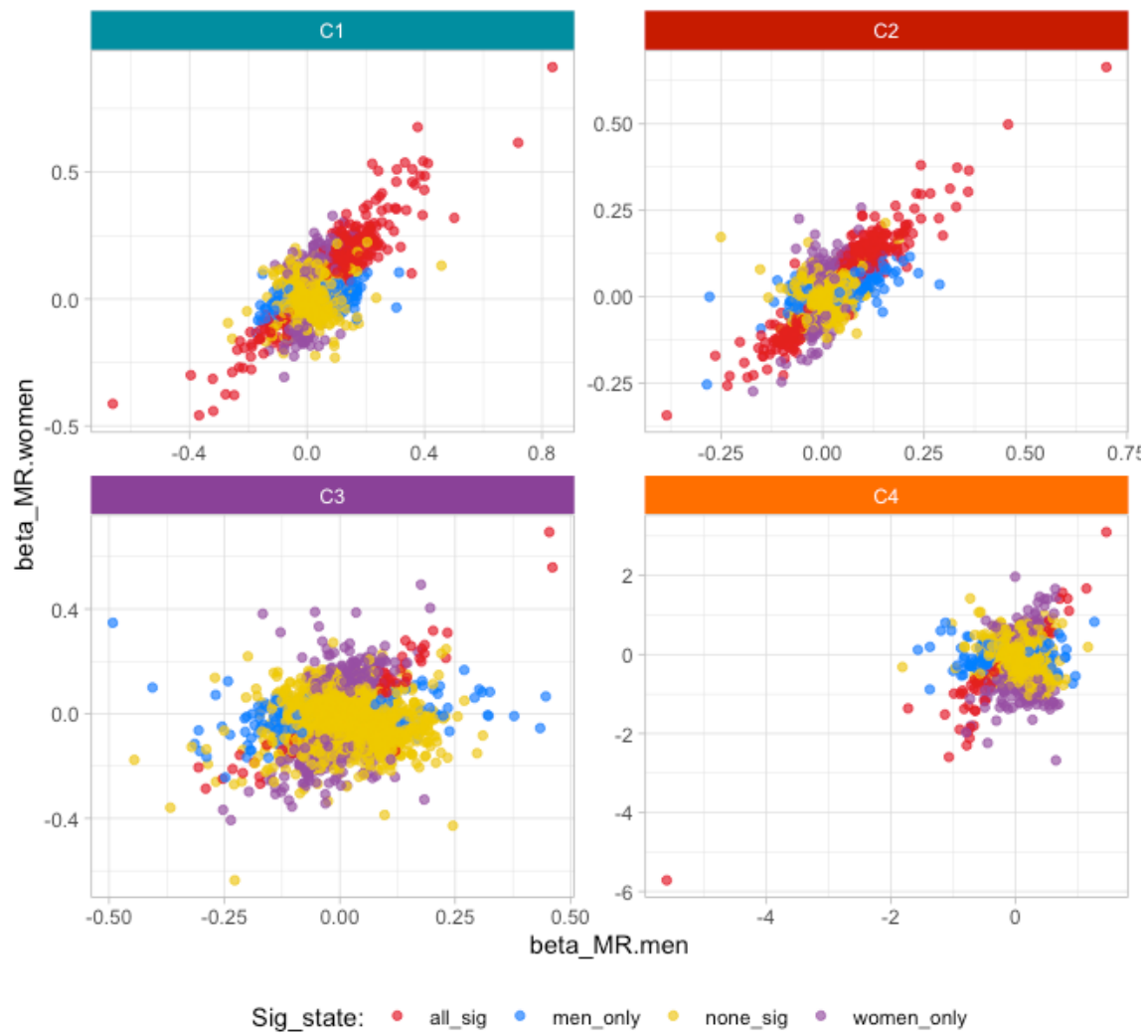
<i>Phenotype/ Variable</i>	<i>UKB Field code</i>
<i>Age</i>	<i>21022</i>
<i>Sex</i>	<i>30</i>
<i>BMI</i>	<i>23104</i>
<i>Smoking status</i>	<i>20116</i>
<i>Alcohol consumption</i>	<i>20117</i>
<i>Genetic Batch</i>	<i>22000</i>
<i>UKB centre</i>	<i>54</i>
<i>Type-2 diabetes</i>	<i>130708</i>
<i>Height</i>	<i>50</i>
<i>Weight</i>	<i>21002</i>
<i>Genetic principal components</i>	<i>22009</i>
<i>Proteomic data</i>	
<i>Participation in the PPP cohort</i>	<i>30903</i>
<i>Time to processing for proteins</i>	<i>Time to processing: Calculated as difference between olink processing start date and date of sample collection. Information provided in "resources" tab of Protein Biomarkers (https://biobank.ndph.ox.ac.uk/showcase/label.cgi?id=1839)</i>
<i>Protein assay batch number</i>	<i>30901</i>



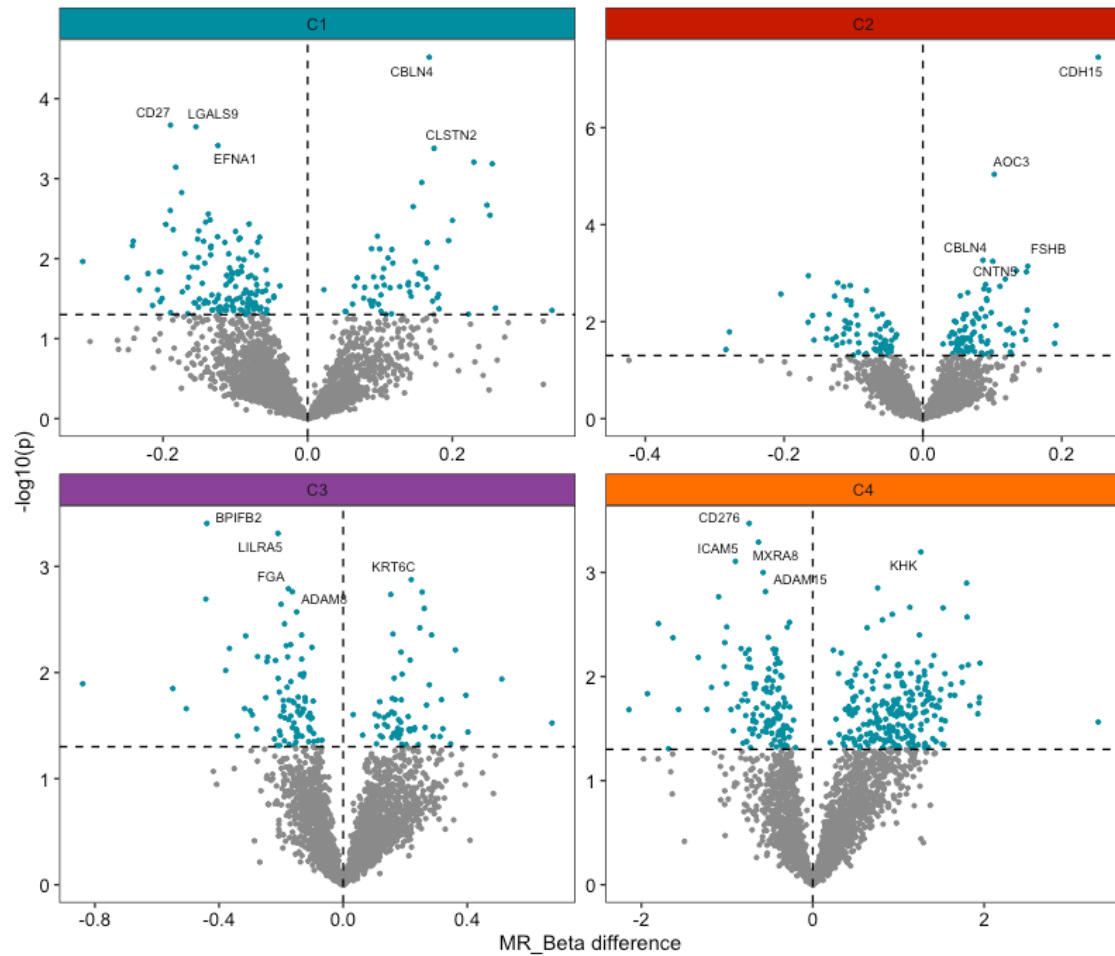
Supplementary Figure 1. A comparison of cluster means from MR-clust and the inverse-variance weighted (IVW) Mendelian randomization (MR) estimates. Values in the figure are presented as exponentiated cluster means (on X) and odds ratios (OR) for IVW MR estimates (on Y).



Supplementary Figure 2. Cluster-specific MR estimates for effect of BMI on T2D, from UKB in sex-combined and sex-stratified analyses.



Supplementary Figure 3. Cluster-specific MR estimates for effect of BMI on protein levels, sex-combined and sex-stratified analyses. Abbreviations: Sig_state = indicates whether a protein is significantly associated with BMI in males (men_only), females (women_only), both (all_sig), or neither (none_sig), with a significance threshold of $p < 0.05$.



Supplementary Figure 4. Difference between males and females in cluster-specific MR estimates for effect of BMI on protein levels. Blue points represent proteins with a significant ($p < 0.05$) difference between males and females, and grey points represent proteins with no significant difference.