Supplemental Figure 1: Associations between Udler Cluster Polygenic Scores and Birthweight Percentile
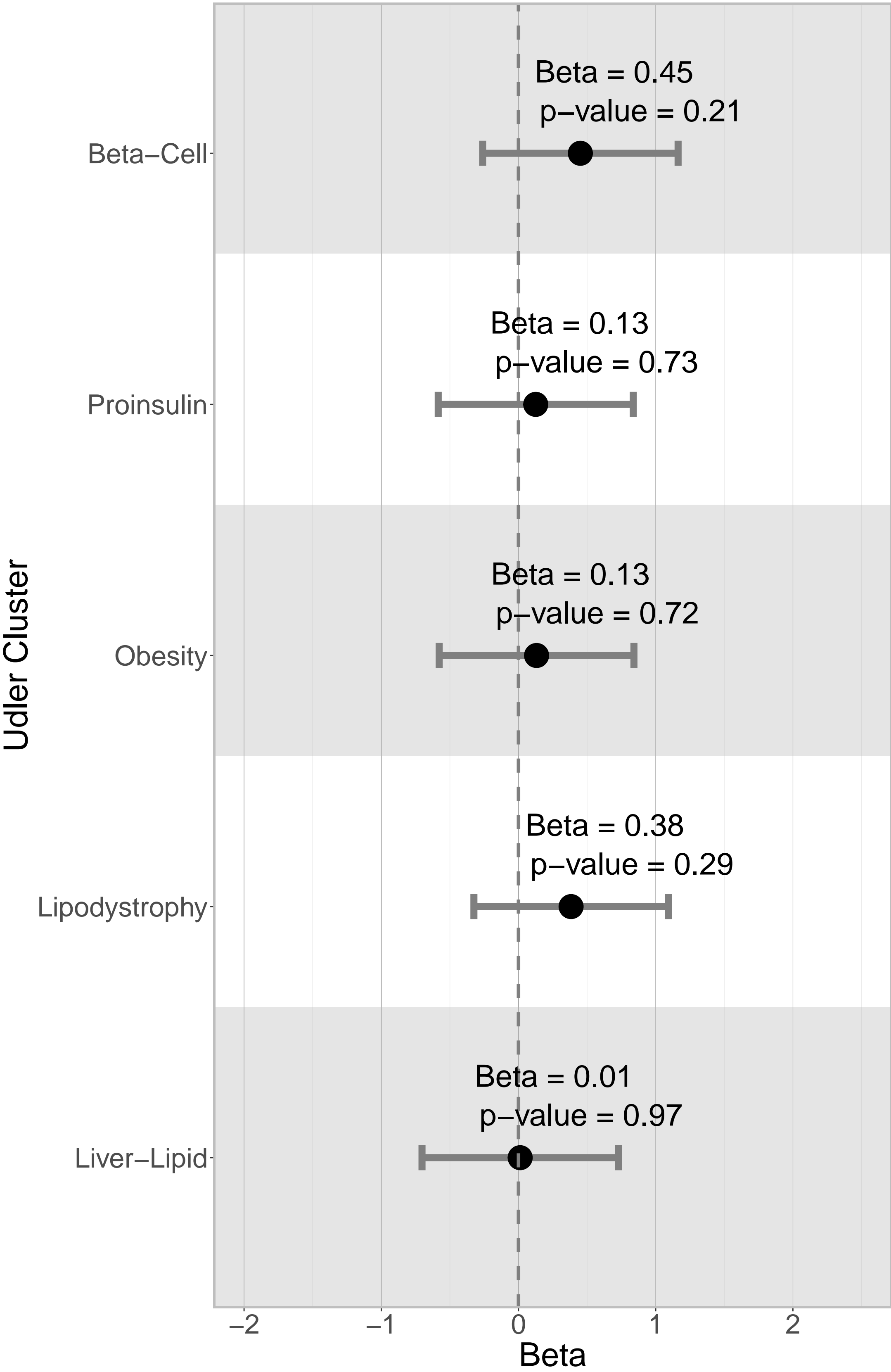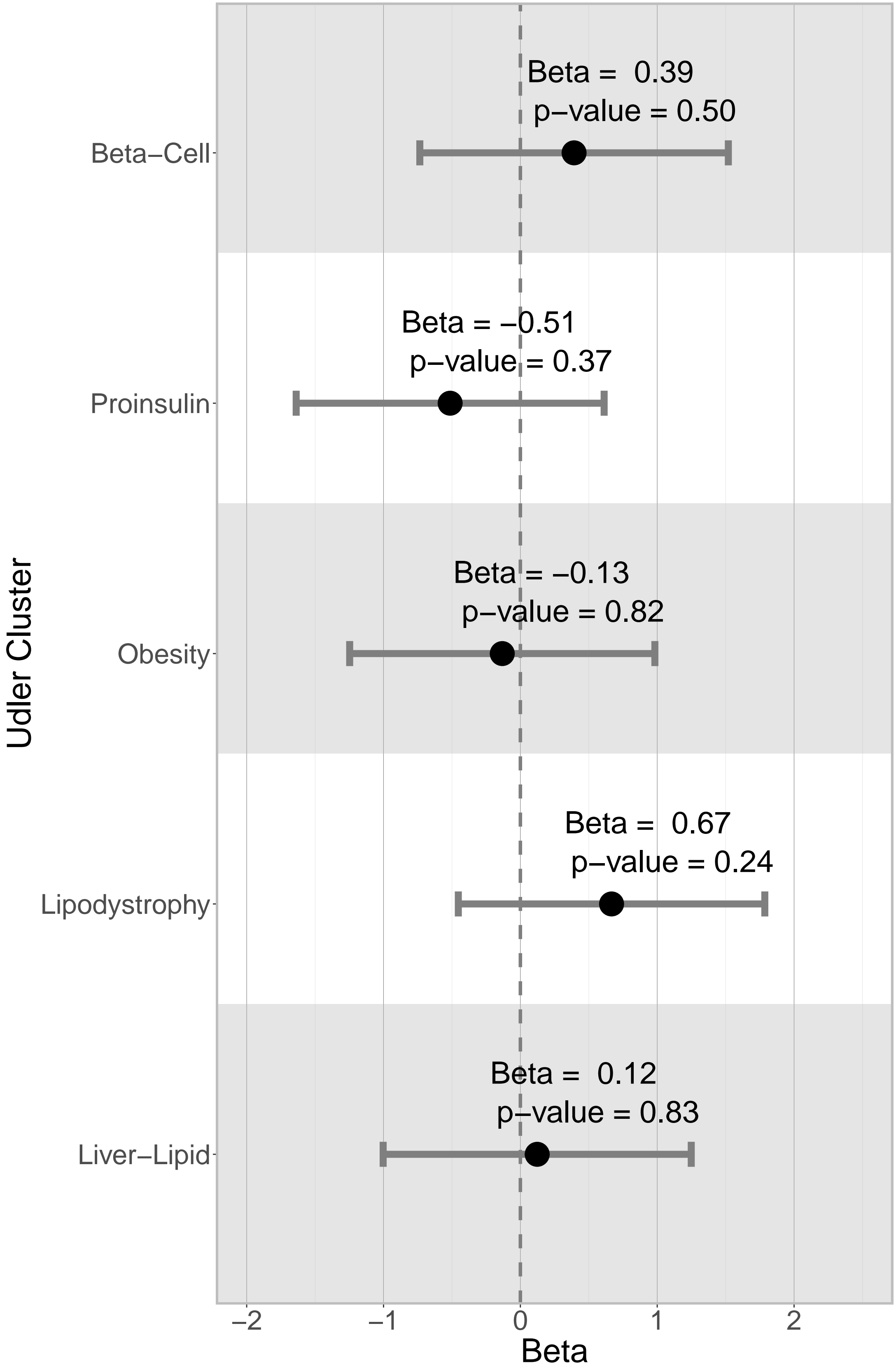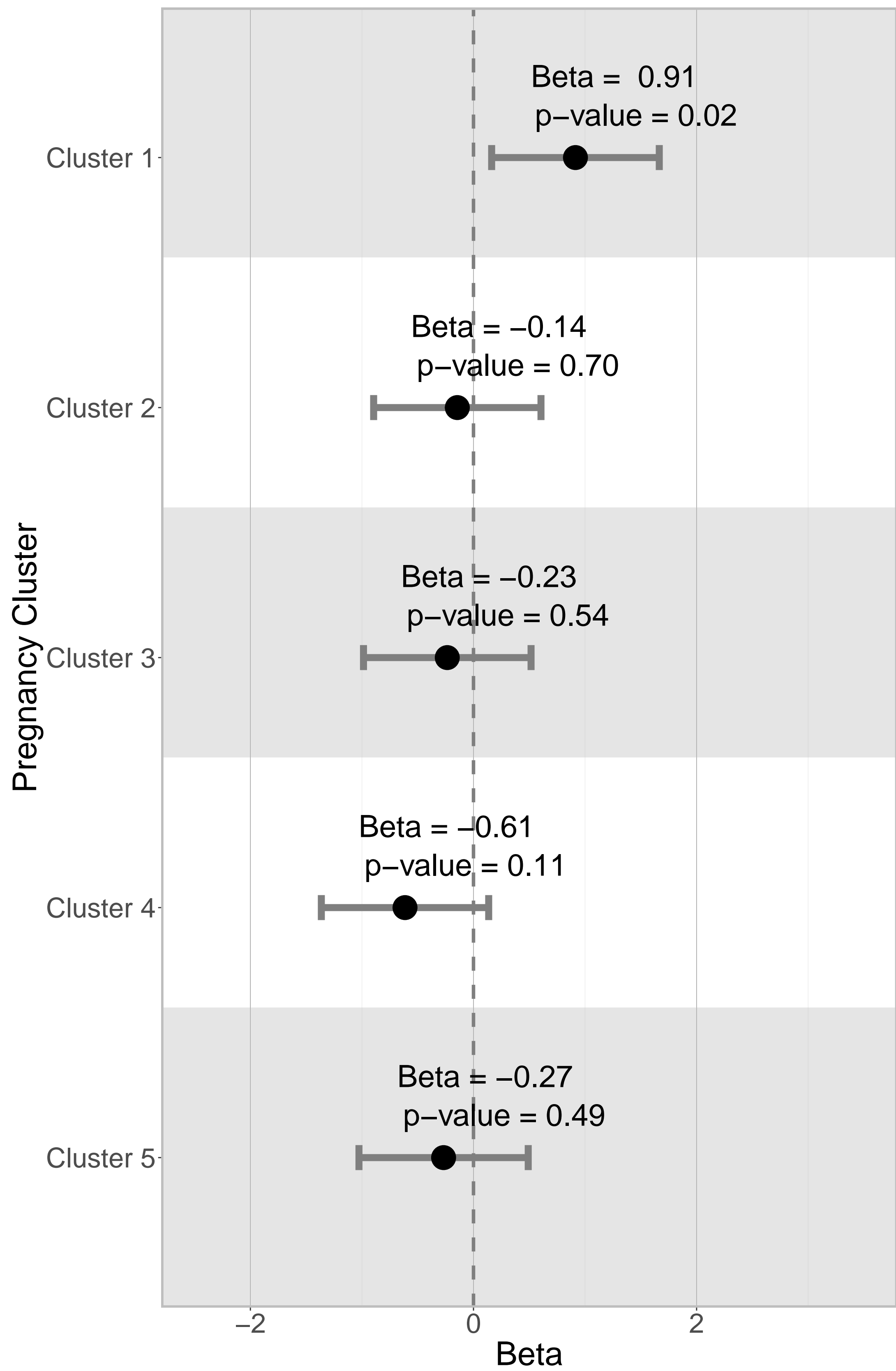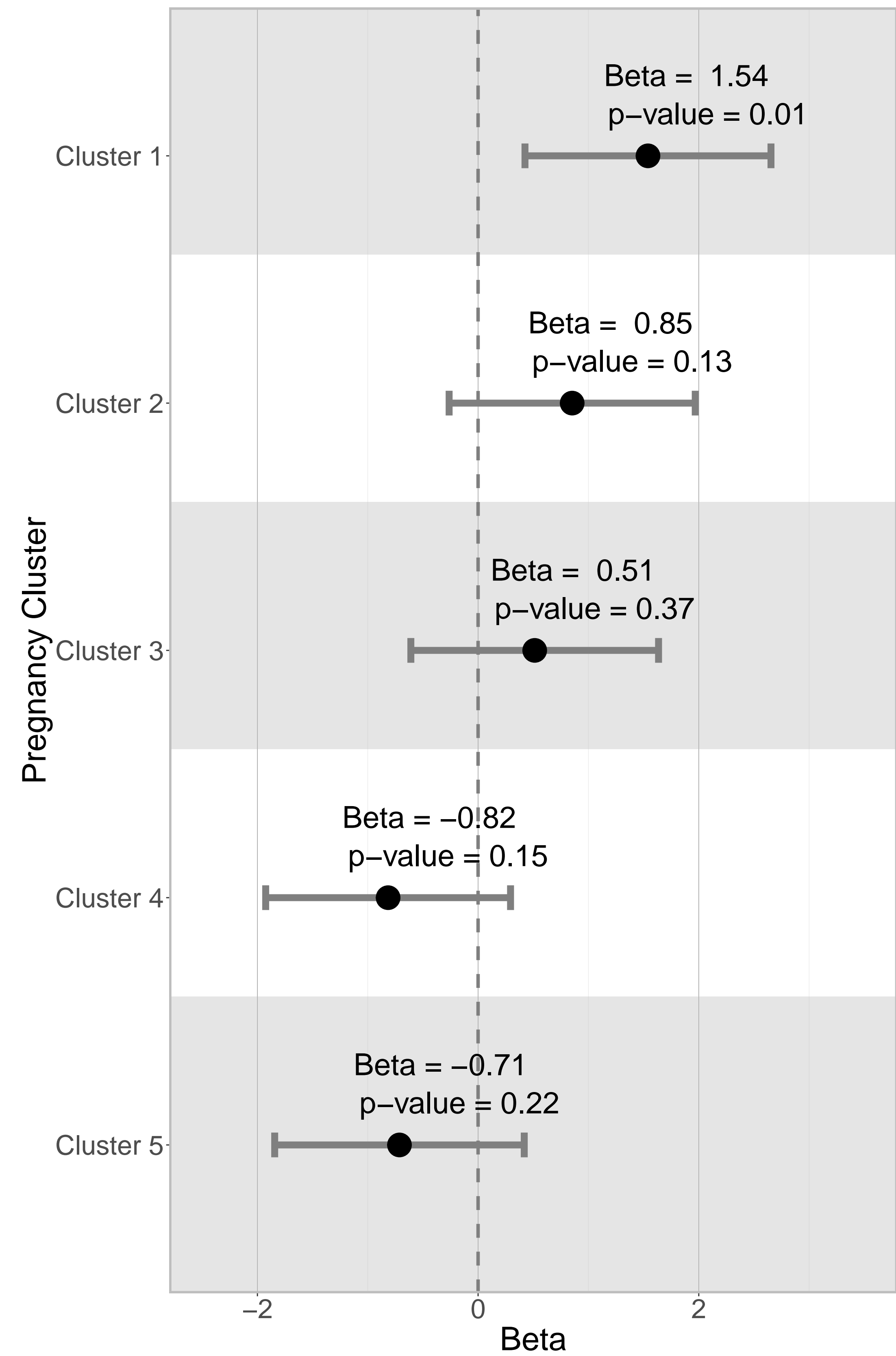

Here shown are the results from meta−analyses of associations between Udler Cluster Polygenic Scores and Birthweight Percentile. In the meta−analyses depicted in Panel A, all cohorts (Gen3G, HAPO−AC, HAPO−EU, HAPO−MA, HAPO−TH, and MGH[2]) are included. In the meta−analyses depicted in Panel B, cohorts with presumed European−predominant ancestry (Gen3G, HAPO−EU, and MGH[2]) are included. Prior to meta−analysis, associations from linear regression were adjusted for principal components and age. In the MGH[2] cohort we also adjusted for genotyping/imputation batch. Betas are depicted by black circles. Error bars provide the 95% confidence interval for the beta. P−values <0.01 were considered statistically significant.

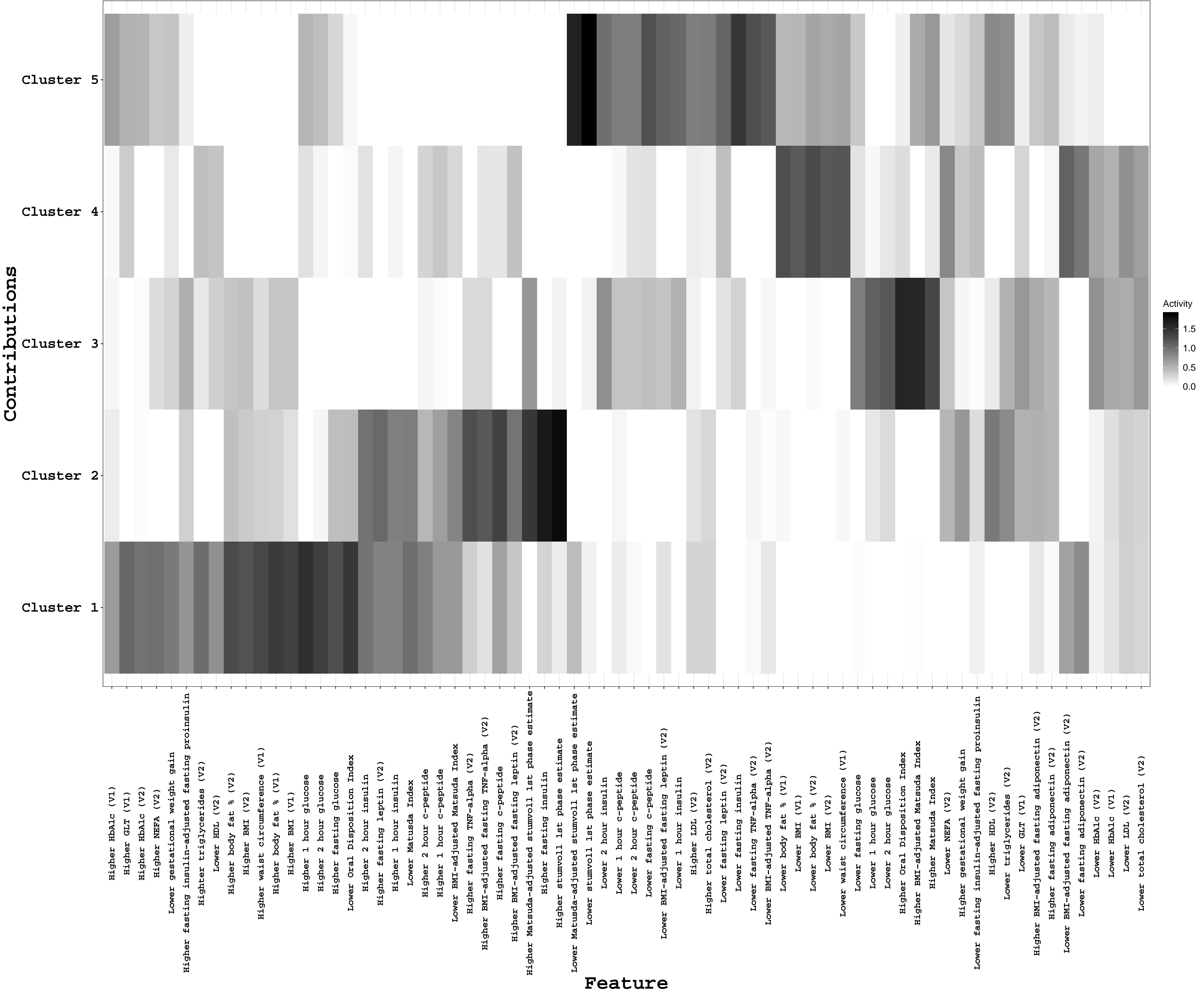**Supplemental Figure 1: Associations between Pregnancy Cluster Polygenic Scores and Birthweight Percentile**
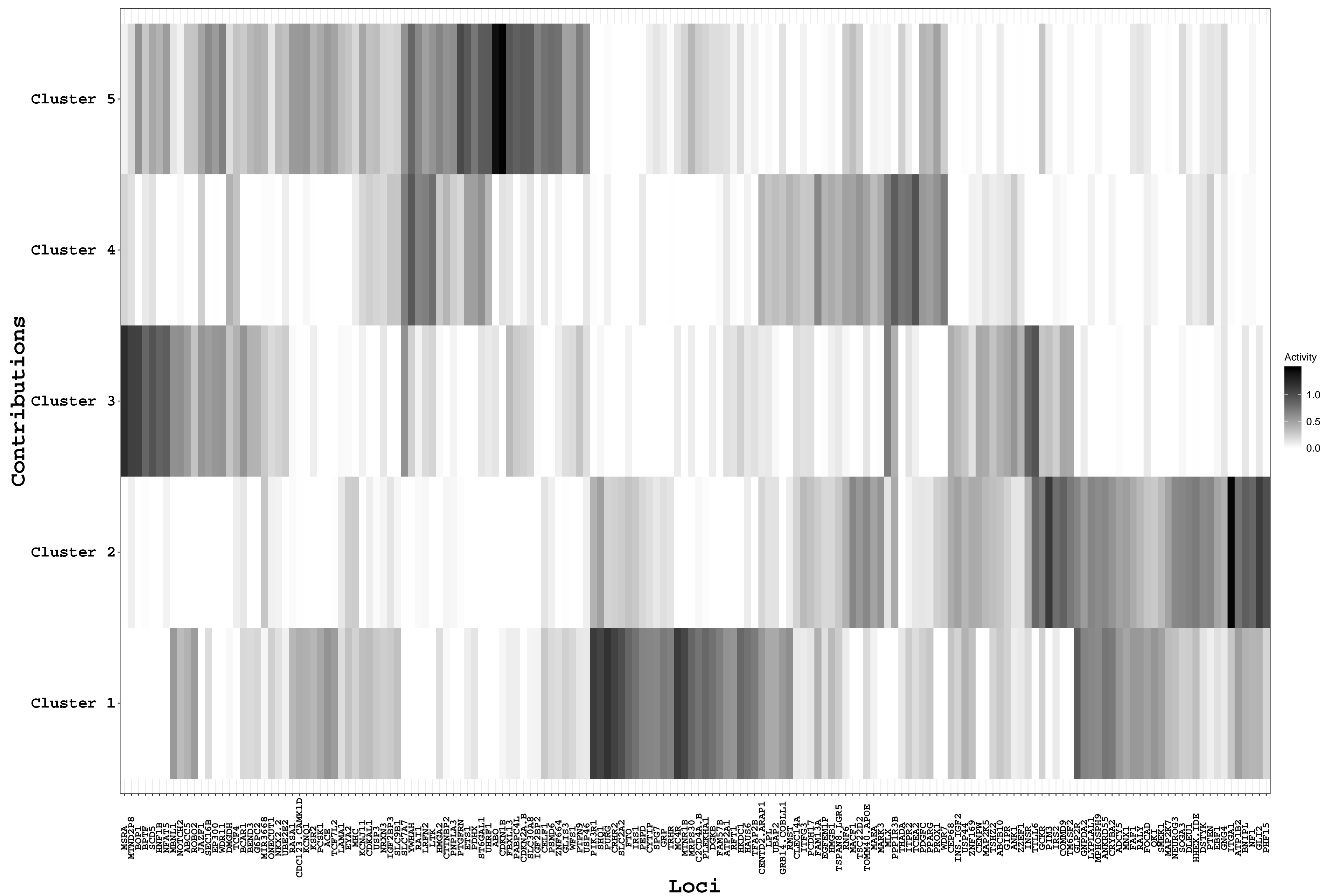

Here shown are the results from meta–analyses of associations between Pregnancy Cluster Polygenic Scores and Birthweight Percentile. In the meta–analyses depicted in Panel A, all cohorts (Gen3G, HAPO–AC, HAPO–EU, HAPO–MA, HAPO–TH, and MGH[2]) are included. In the meta–analyses depicted in Panel B, cohorts with presumed European–predominant ancestry (Gen3G, HAPO–EU, and MGH[2]) are included. Prior to meta–analysis, associations from linear regression were adjusted for principal components and age. In the MGH[2] cohort we also adjusted for genotyping/imputation batch. Betas are depicted by black circles. Error bars provide the 95% confidence interval for the beta. P–values <0.01 were considered statistically significant.

Supplemental Figure 2A: Heat Maps Generated in bNMF Clustering of Variants and Glycemic Traits in Pregnancy
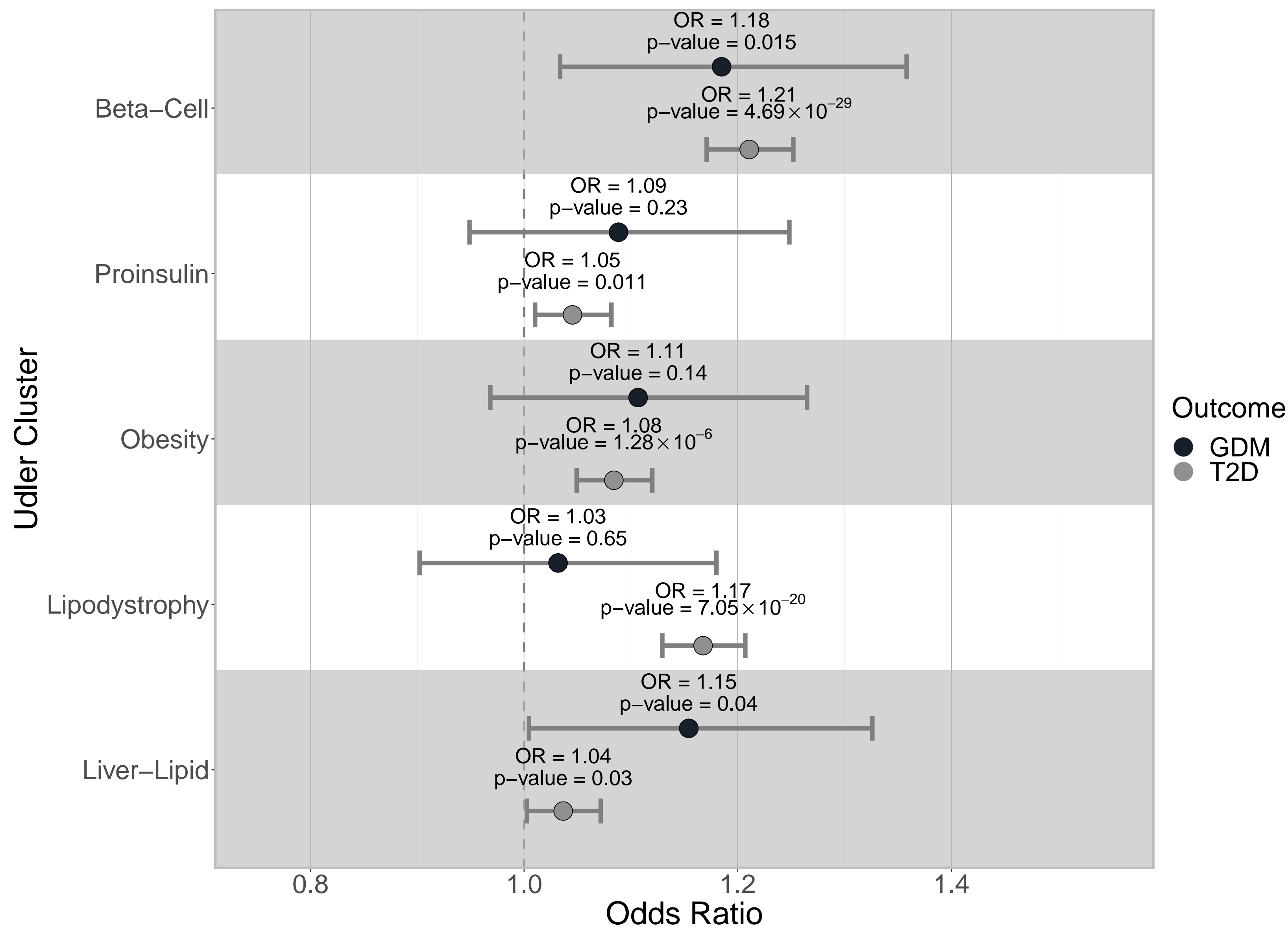
Supplemental Figure 2B: Heat Maps Generated in bNMF Clustering of Variants and Glycemic Traits in Pregnancy
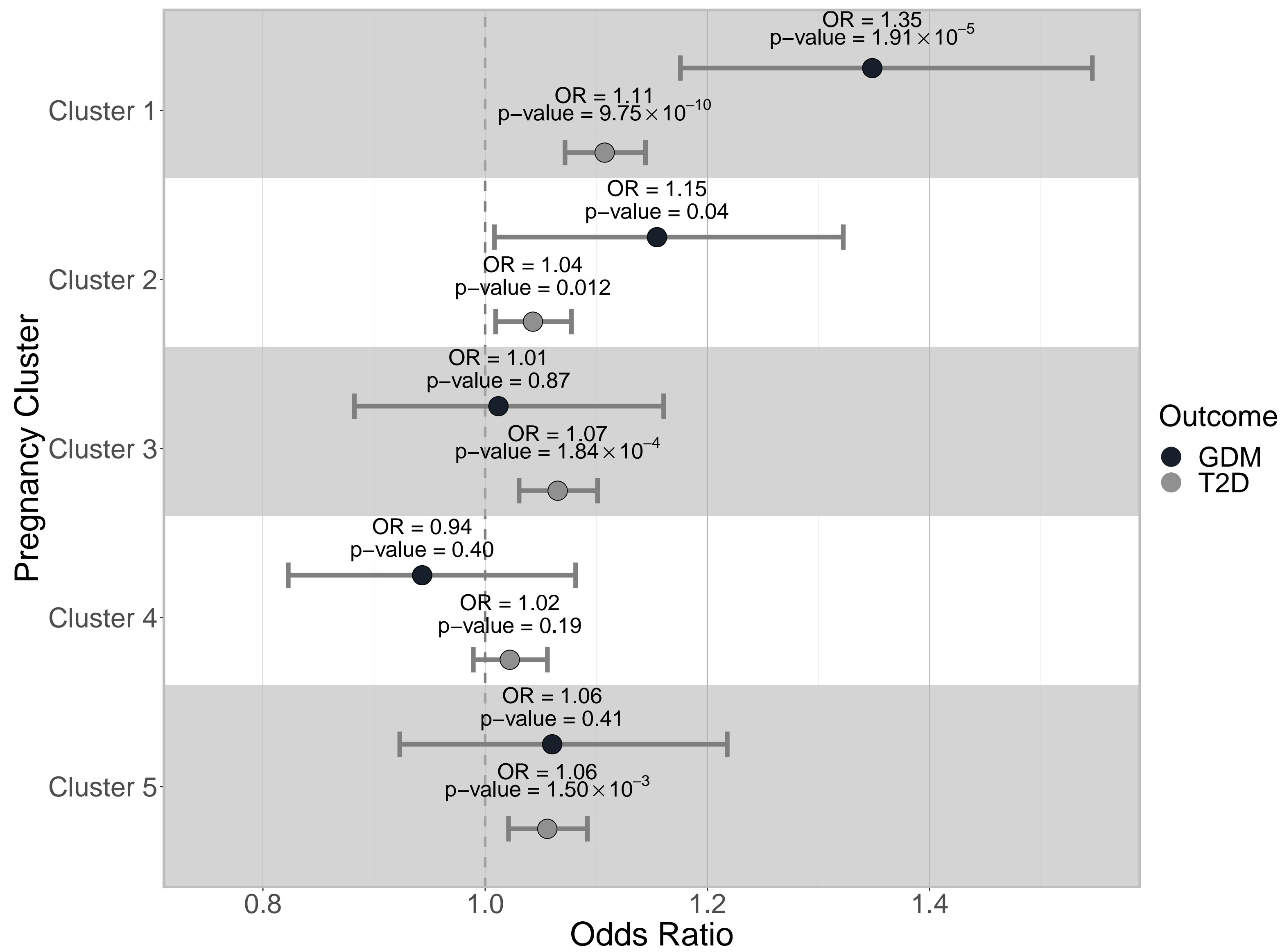
Supplemental Figure 3: Comparison of Cluster Polygenetic Score Associations with GDM and T2D in Presumed European Ancestry−Predominant Cohorts

Here we compare the association of each cluster (A: Udler Clusters; B: Pregnancy Clusters) with GDM (presumed European−predominant ancestry meta−analyses) and T2D (from a case−control set of participants in the Partners Biobank). Associations from logistic regression were adjusted for principal components and age. In MGH[2] and Partners Biobank we also adjusted for genotyping/imputation batch. OR=Odds Ratio, depicted by circles. Error bars provide the 95% confidence interval for the OR. P−values < 0.01 were considered statistically significant.