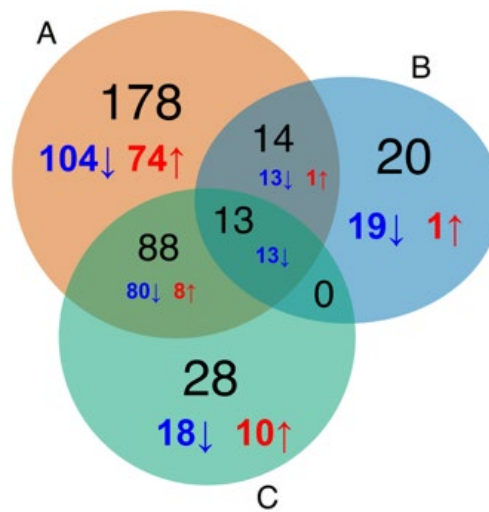


1 Supplementary material



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3 Figure S1. Venn diagram of DEGs in three analyses

4 Venn diagram showing the overlap of DEGs across three models: (A) age- and BMI-adjusted
 5 main model, (B) paired analysis, and (C) model additionally adjusted for cell type composition,
 6 gestational age at birth, and fetal sex (fully-adjusted model). Numbers indicate the number of
 7 DEGs in each set and their overlaps. Thirteen genes were consistently identified across all
 8 three analyses, including *AHSP*, *BPI*, *CAMP*, *DEFA3*, *F5*, *LCN2*, *LTF*, *MCEMP1*, *PGLYRP1*,
 9 *RETN*, *TENT5C* and *TLR5*. In each sector, the downregulated and upregulated genes were
 10 indicated by blue and red color, respectively.

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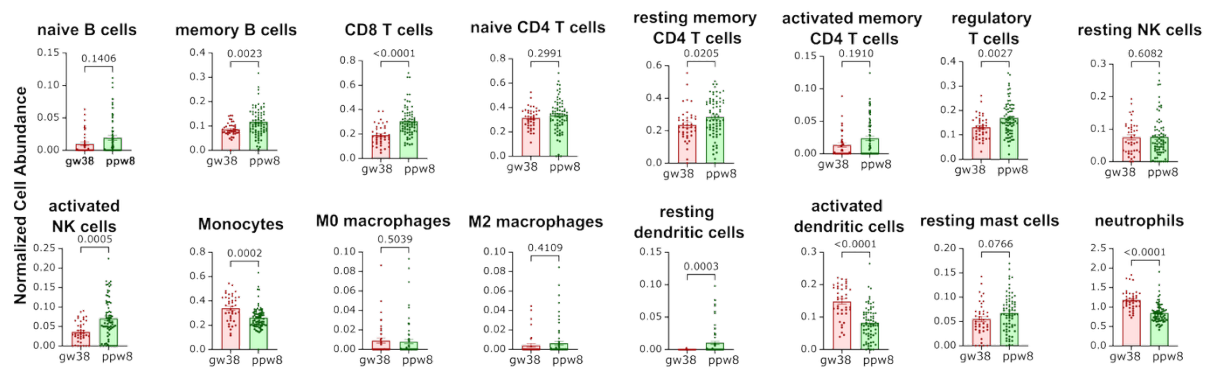


Figure S2. Comparison of deconvoluted cell-types between gw38 vs. ppw8.

Among 22 cell types deconvoluted using the model matrix, only 16 comparisons were performed due to the presence of too many zeros in plasma cells, follicular helper T cells, gamma delta T cells, macrophages, activated mast cells, and eosinophils. Women at ppw8 had higher abundance of memory B-cells, CD8+ cells, resting memory CD4+ cells, Tregs, activated NK cells, and resting dendritic cells ($p < 0.02$ for all), whereas women at gw38 had greater monocyte, activated dendritic cells, and neutrophil count ($p = 0.002$ for monocytes and $p < 0.001$ for activated dendritic cells and neutrophils).

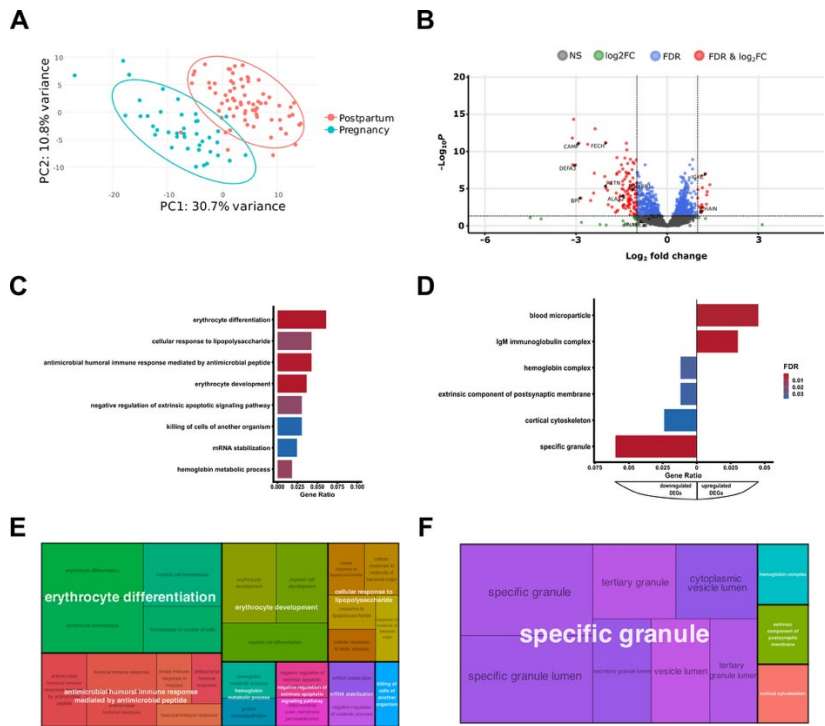


Figure S3. Results of analyses upon inclusion of additional covariates along with cell-type principal components.

A) Principal component analysis (PCA) of transcriptomic profiles. **B)** Volcano plot of DEGs in sensitivity model. The most significantly down-regulated DEGs included *CAMP*, *DEFA3*, *BPI*. Legend: red dots, statistically significant genes above FC threshold ($|\log_2FC| > 1$ and $FDR < 0.05$); blue dots, statistically significant genes under FC threshold ($|\log_2FC| < 1$ and $FDR < 0.05$); green dots, not statistically significant genes above FC threshold ($|\log_2FC| > 1$ and $FDR > 0.05$); grey dots, not statistically significant genes under FC threshold ($|\log_2FC| < 1$ and $FDR > 0.05$). **C)** Reduced representation of enriched Biological Processes (BP) for downregulated genes and **D)** Cellular Components (CC) for down- and up-regulated genes in ppw8 vs gw38. Bar length reflects the gene ratio (percentage of significant DEGs in the given ontology term). Color intensity represents FDR-adjusted p-values. **E)** Treemap of reduced GO Biological Processes (BP) terms of downregulated DEGs, **F)** Treemap of reduced GO Cellular Components (CC) terms of downregulated DEGs.

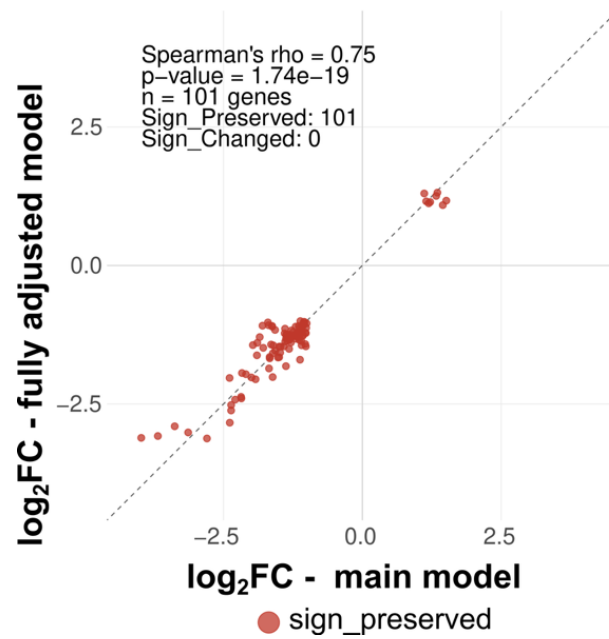


Figure S4: Preservation of differential expression estimates after additional covariate adjustment

Scatter plot comparing $\log_2\text{FC}$ estimates between the main age- and BMI-adjusted model and the fully adjusted model additionally including cell-type principal components, fetal sex, and gestational length. Each point represents a gene passing the significance criteria ($|\log_2\text{FC}| > 1$ and $\text{FDR} < 0.05$). The dashed diagonal line indicates identical $\log_2\text{FC}$ estimates between models. $\log_2\text{FC}$ direction was preserved for all 101 genes, common across two models, with no sign changes observed, and the estimates showed a strong positive correlation between models (Spearman's rho = 0.75, $p = 1.74 \times 10^{-19}$).