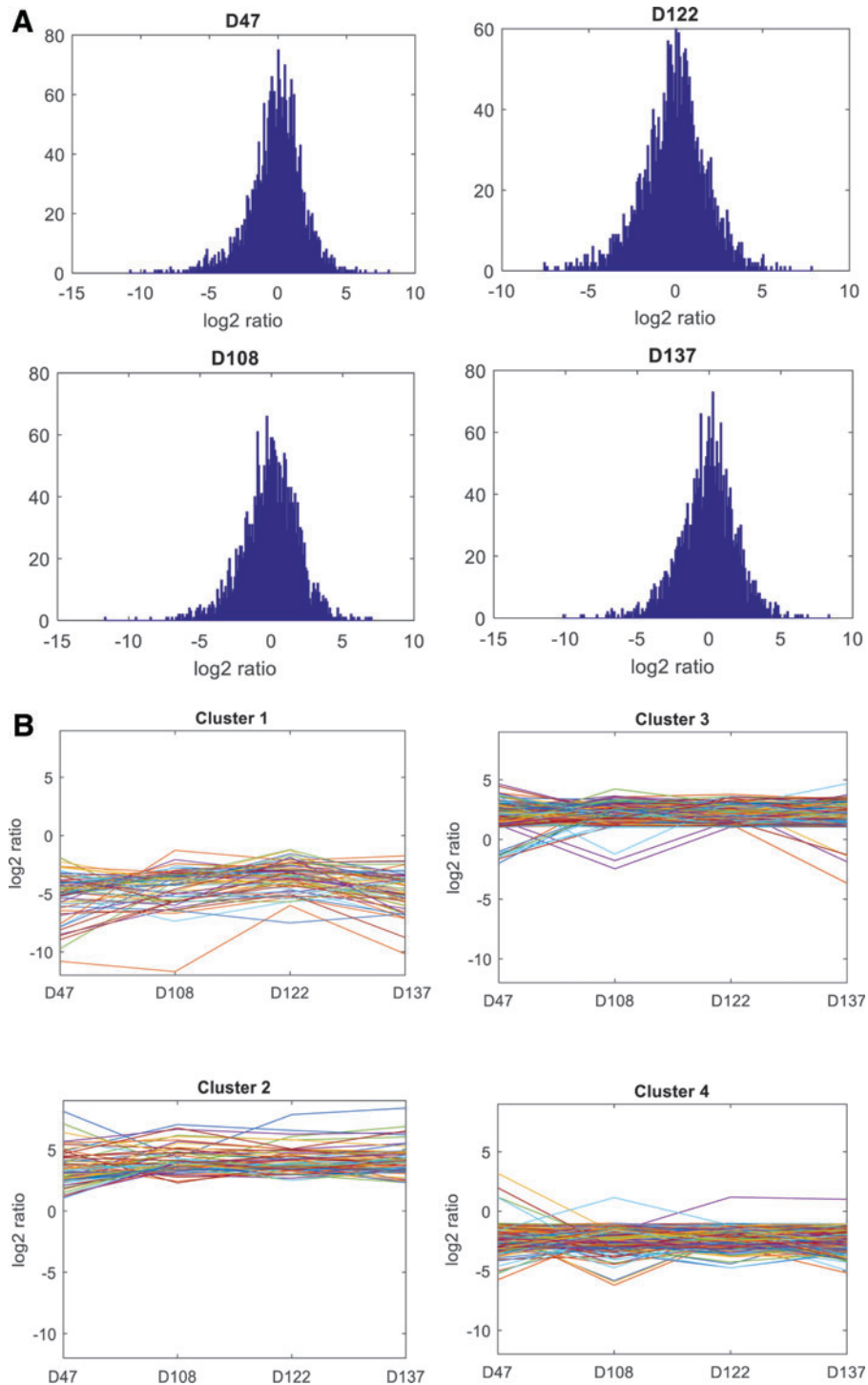


## Supplementary Data



**SUPPLEMENTARY FIG. S1.** Bioinformatics processing of quantitative mass spectrometry of human ovarian tissue from developmental days 47, 108, 122, and 137 in comparison to cortex tissue from an adult. **(A)** Log<sub>2</sub>-ratios generated normal distributions after filtering, and **(B)** Self-organizing map clustering analysis identified *top* upregulated and down-regulated protein groups. Clusters 1 and 2 were chosen to identify protein pathways with significant changes across all fetal stages in comparison to adult tissue.