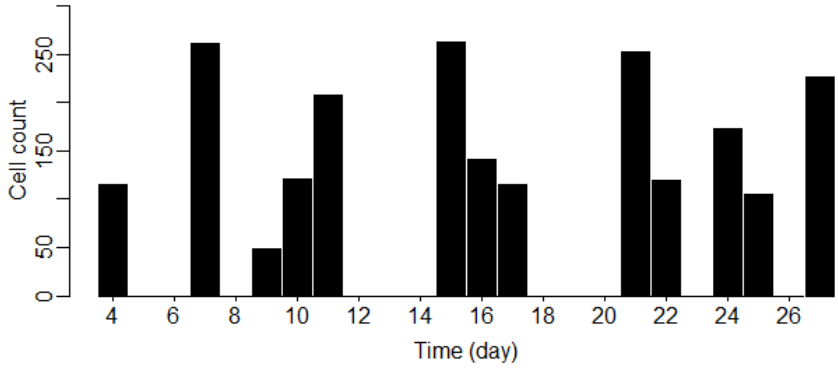

Figure S1. Distribution of number of cells sampled across the menstrual cycle. (Day: the day of menstrual cycle)

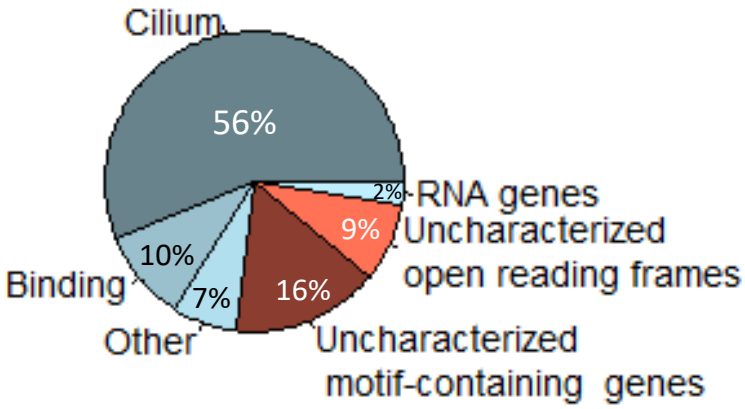

Figure S2. Classification and distribution of functional annotations for uniquely expressed genes in ciliated epithelium.

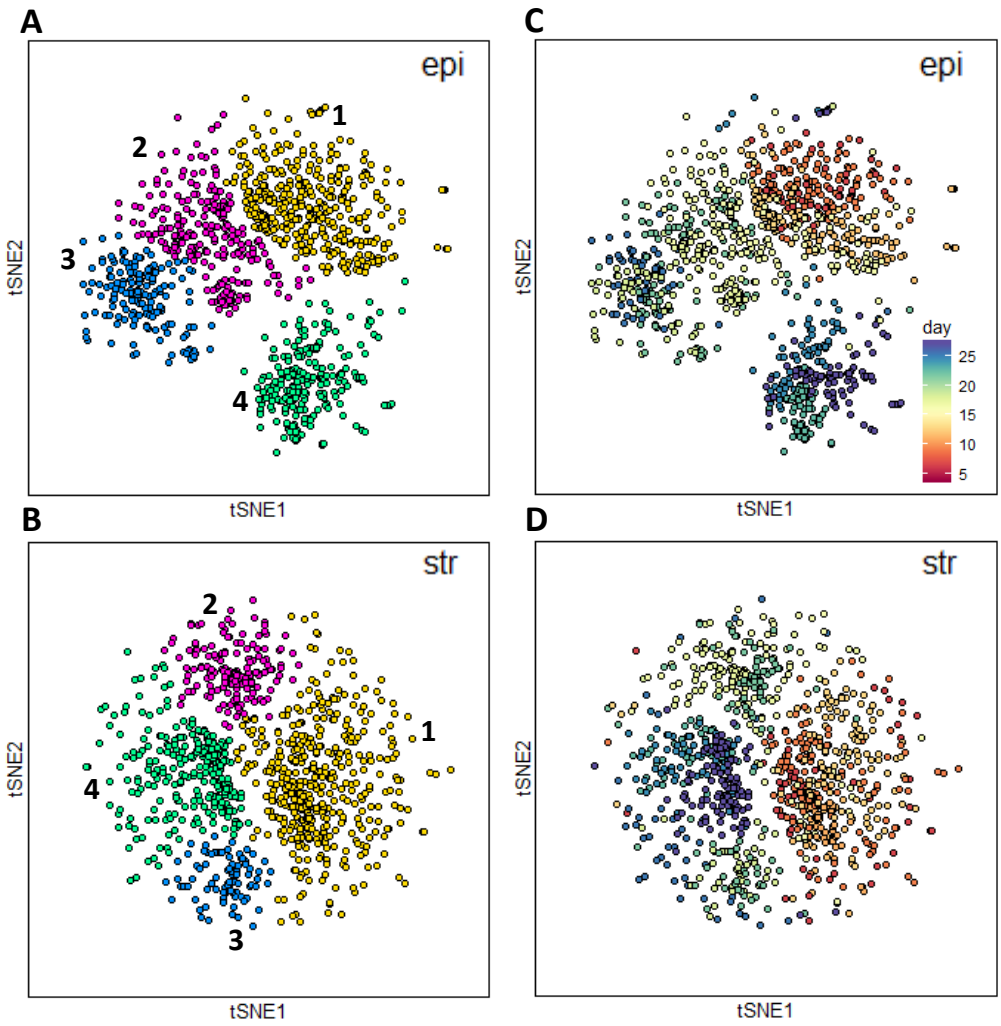

Figure S3. Unbiased definition of major phases of endometrial transformation across the menstrual cycle. A. B. Dimension reduction (tSNE) using whole transcriptome information and phase assignment using Ward's hierarchical agglomerative clustering method. **C. D.** tSNE cast with time. (epi: unciliated epithelium; str: stroma; day: the day of menstrual cycle)

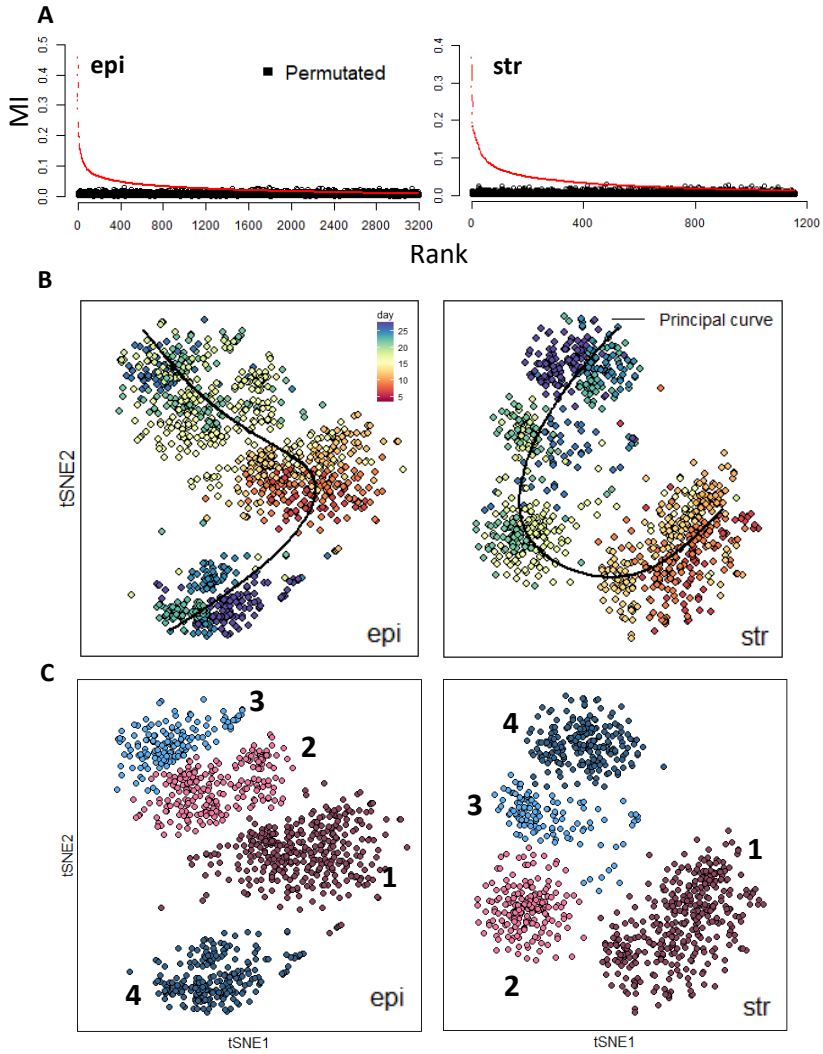

Figure S4. Constructing trajectories of endometrial transformation across the menstrual cycle via mutual information (MI) based approach. A. MI between expression of genes and time (red) or permutated time (black) for unciliated epithelium (epi) and stroma (str) cells. (Genes are ranked by MI) **B.** tSNE using time-associated genes and trajectories of endometrial transformation defined by principal curves. **C.** Phase assignment using Ward's hierarchical agglomerative clustering method.

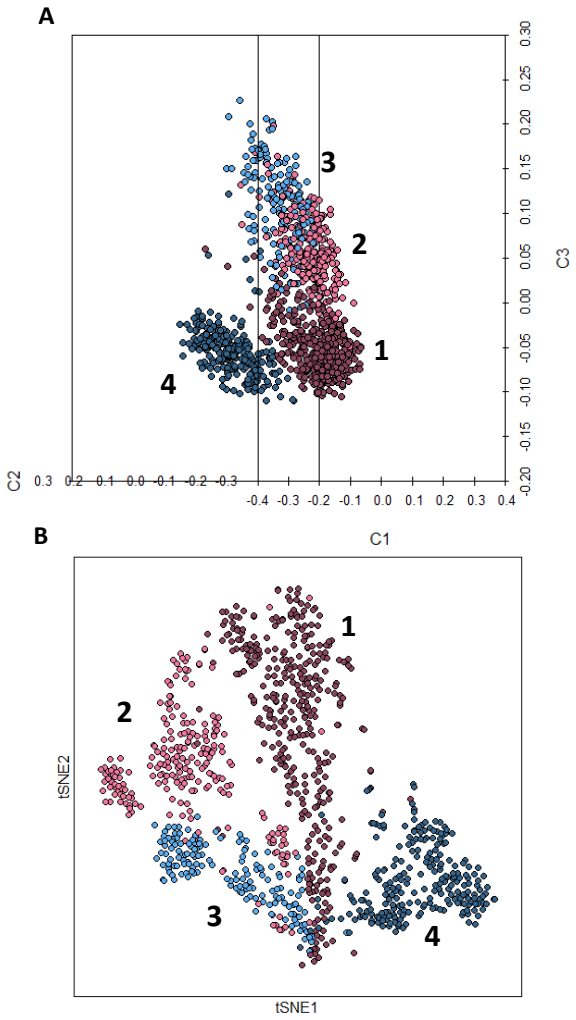

Figure S5. Discontinuity of phase 4 unciliated epithelium (epi) obtained using different analysis methods. A. First 3 components of multidimensional scaling on epi using whole transcriptome information. **B.** tSNE on top 50 principal components obtained via principal component analysis on whole transcriptome information. (Numbers 1-4: phase assignment determined in **Fig. S4C**)

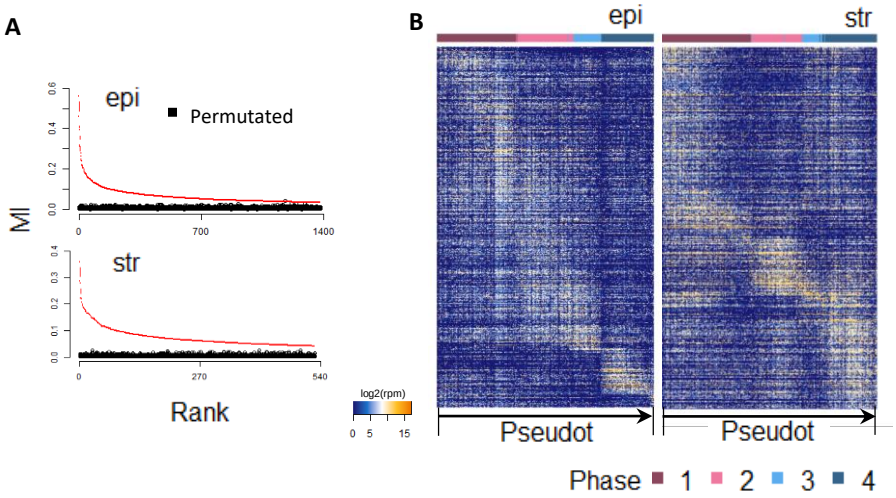

Figure S6. Global temporal transcriptome dynamics across the menstrual cycle. A. MI between expression of pseudotime-associated genes (FDR<1E-05) and pseudotime (red) or permutated pseudotime (black) for unciliated epithelium (epi) and stroma (str) cells. **B.** Dynamics of pseudotime associated genes across the trajectory of menstrual cycle.

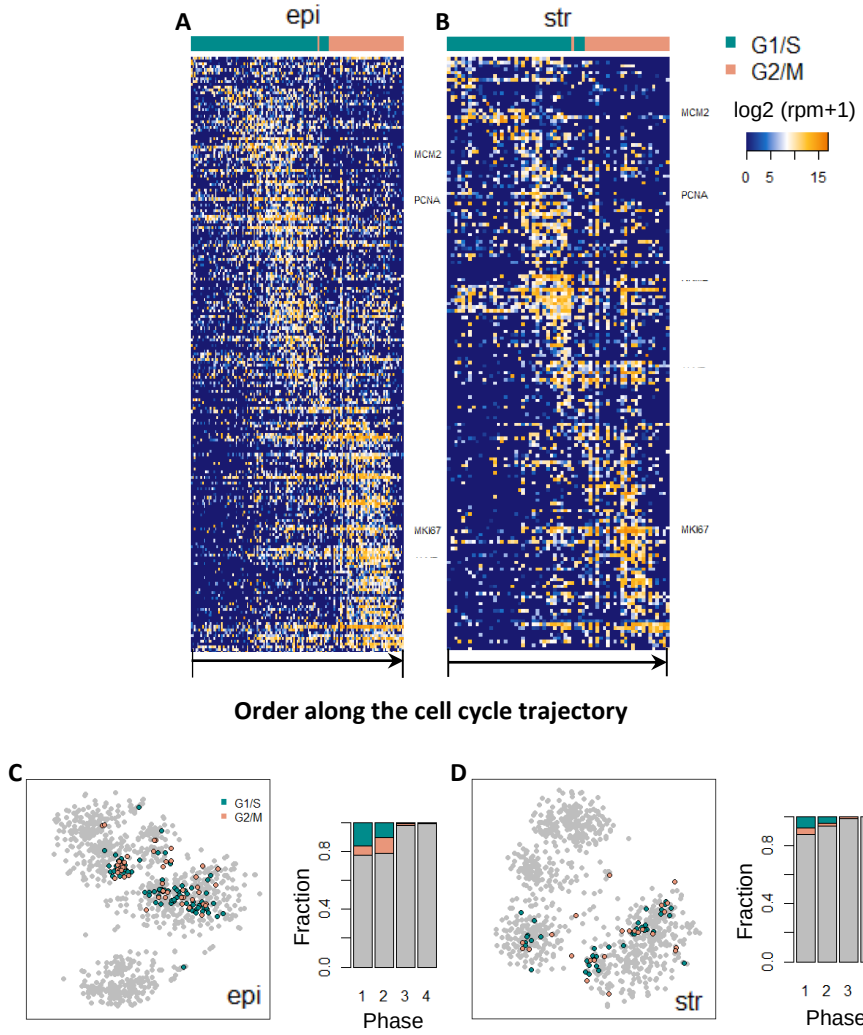

Figure S7. Cell cycle dynamics in human endometrium across the menstrual cycle. Endometrial G1/S and G2/M signatures in endometrial cycling for **(A)** unciliated epithelial (epi) and **(B)** stromal (str) cells. **C. D.** Distribution (left) and factional dynamics (right) of cycling cells across major phases of the menstrual cycle.

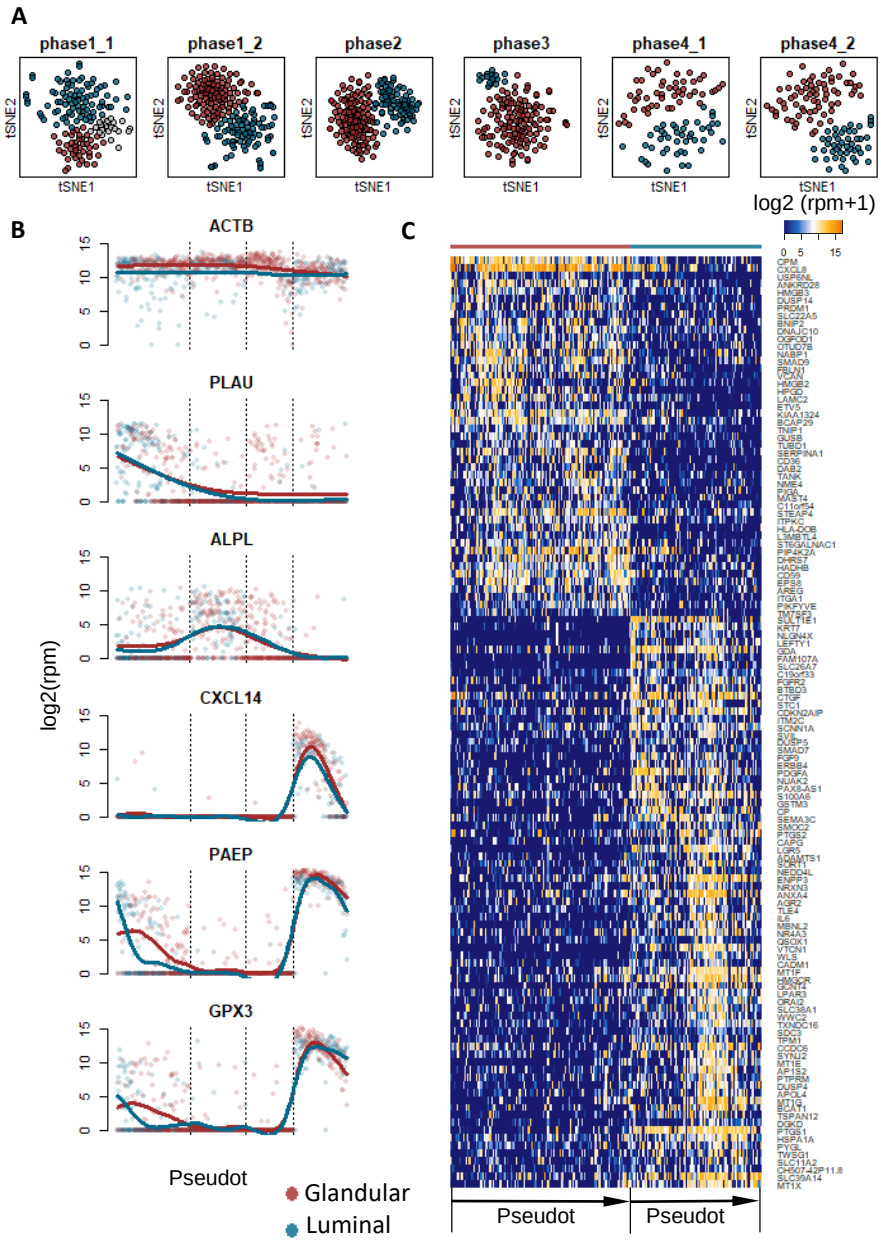

Figure S8. Deviation of subpopulations of unciliated epithelial cells through the trajectory of the menstrual cycle. A. Dimension reduction (tSNE) on unciliated epithelial cells at the major phases/sub-phases across the menstrual cycle. **B.** Dynamics of phase-defining and house keeping genes in subpopulations in unciliated epithelia across the menstrual cycle. (dashed lines: boundaries between 4 phases) **C**. Dynamics of differentially expressed genes between the two sub-populations during phase 2.

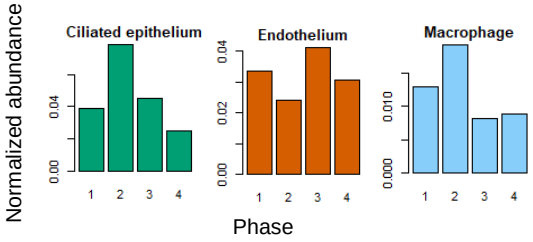

Figure S9. Phase-associated abundance of minor endometrial cell types. Abundance was normalized to total number of unciliated epithelial (ciliated epithelium) or stromal (endothelium, macrophage) single cells captured.

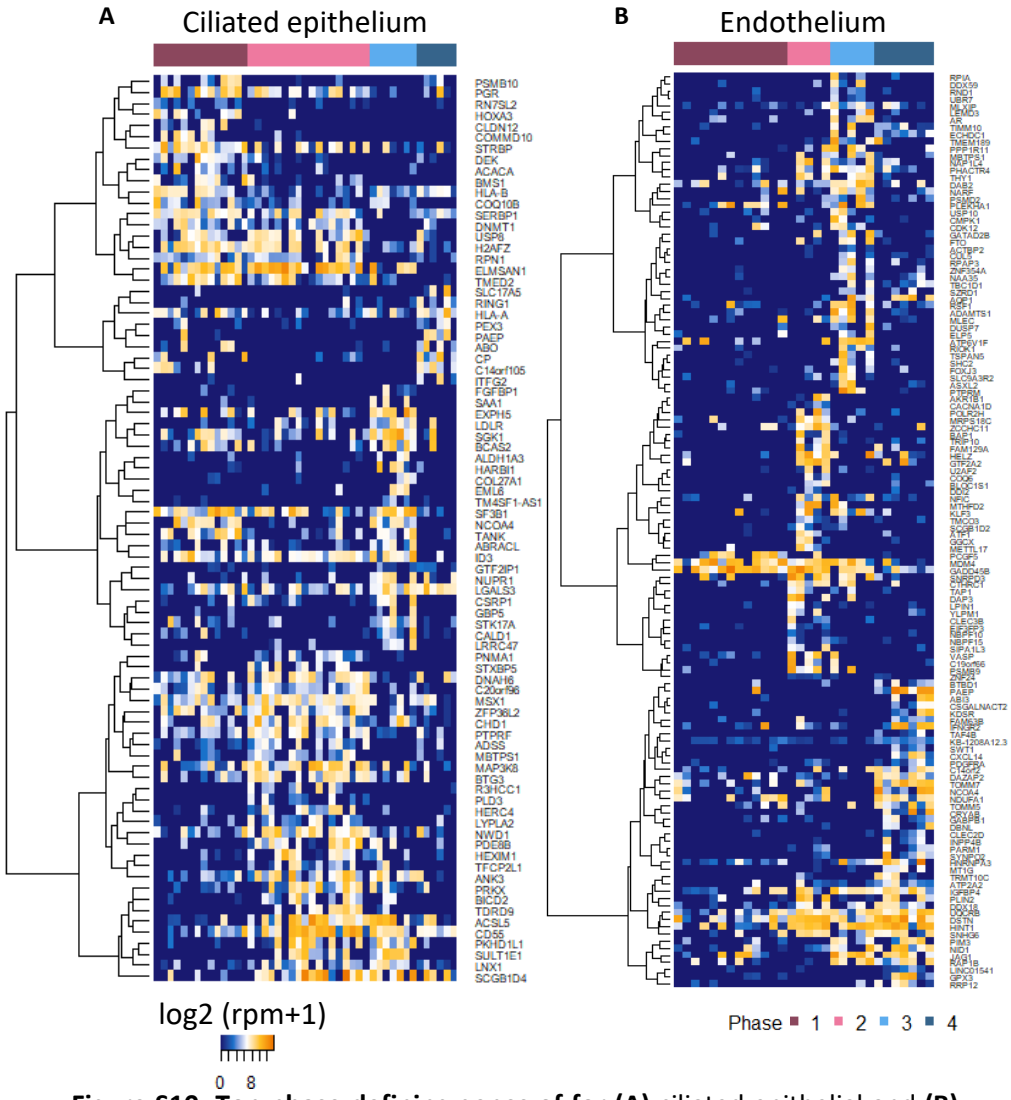

Figure S10. Top phase-defining genes of for (A) ciliated epithelial and **(B)** endothelial cells.

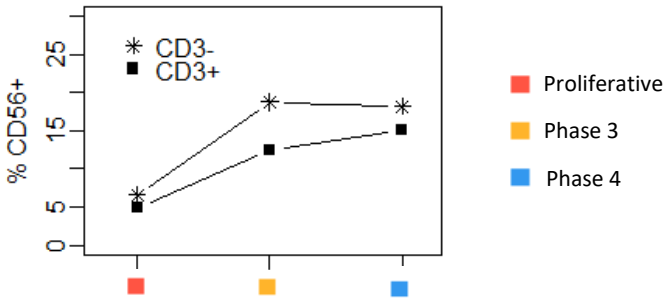

Figure S11. Percent of CD56+ cells in all CD3+ and CD3- lymphocytes across the menstrual cycle.