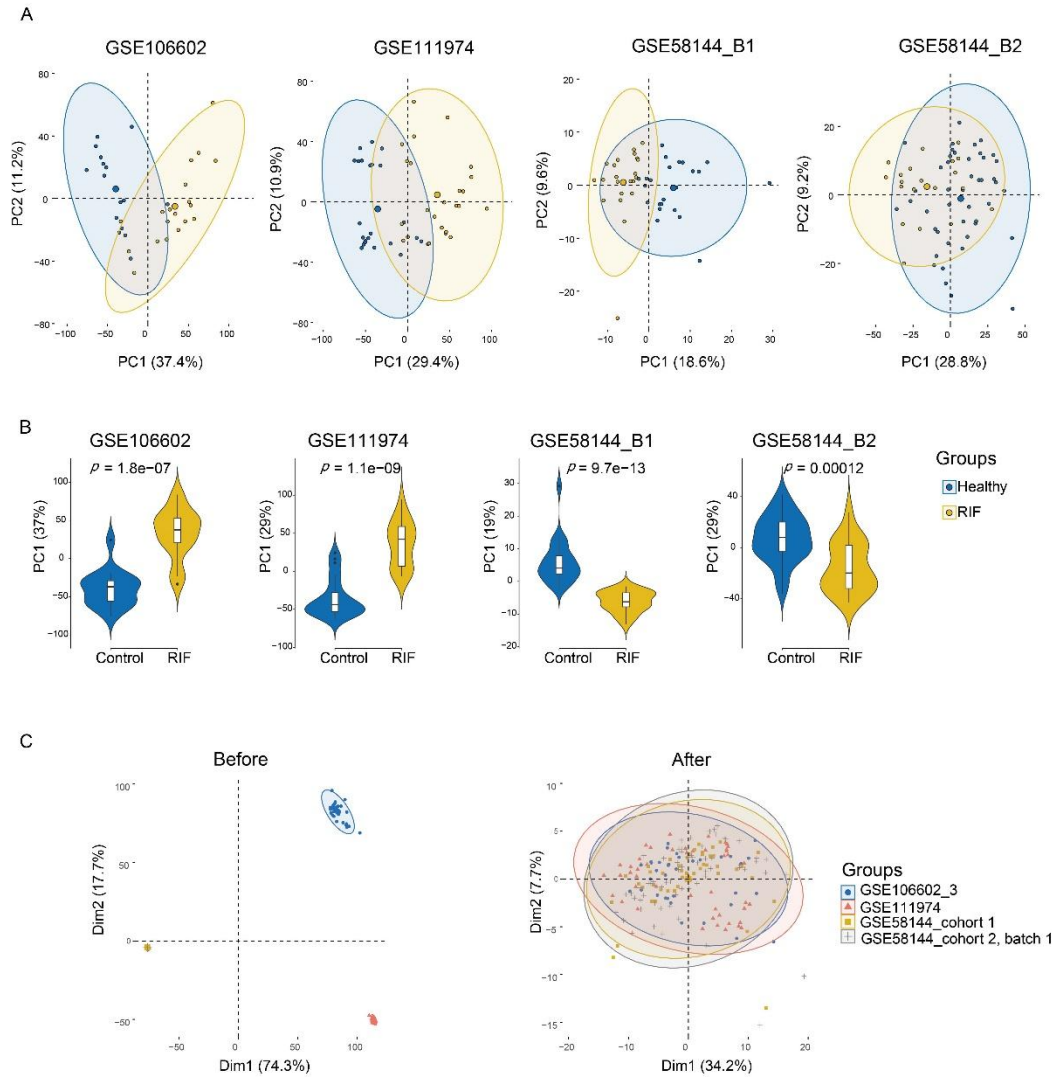
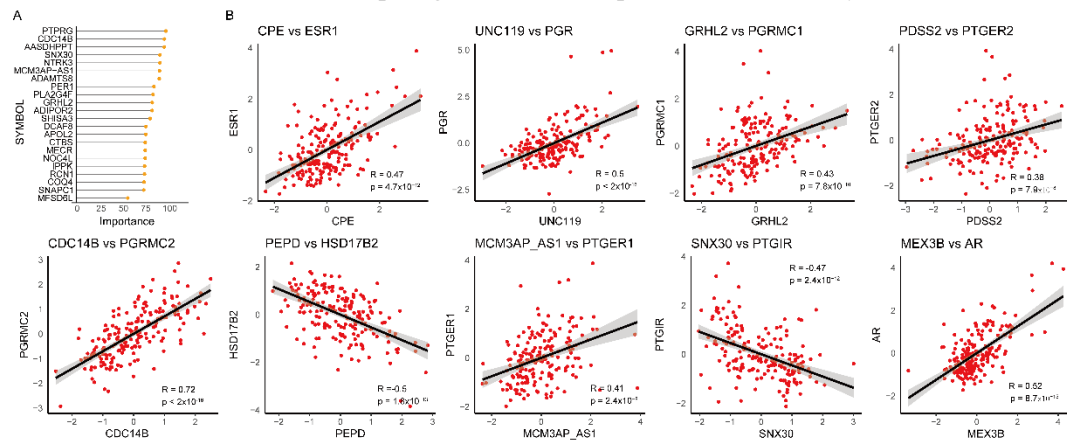


Supplementary Data

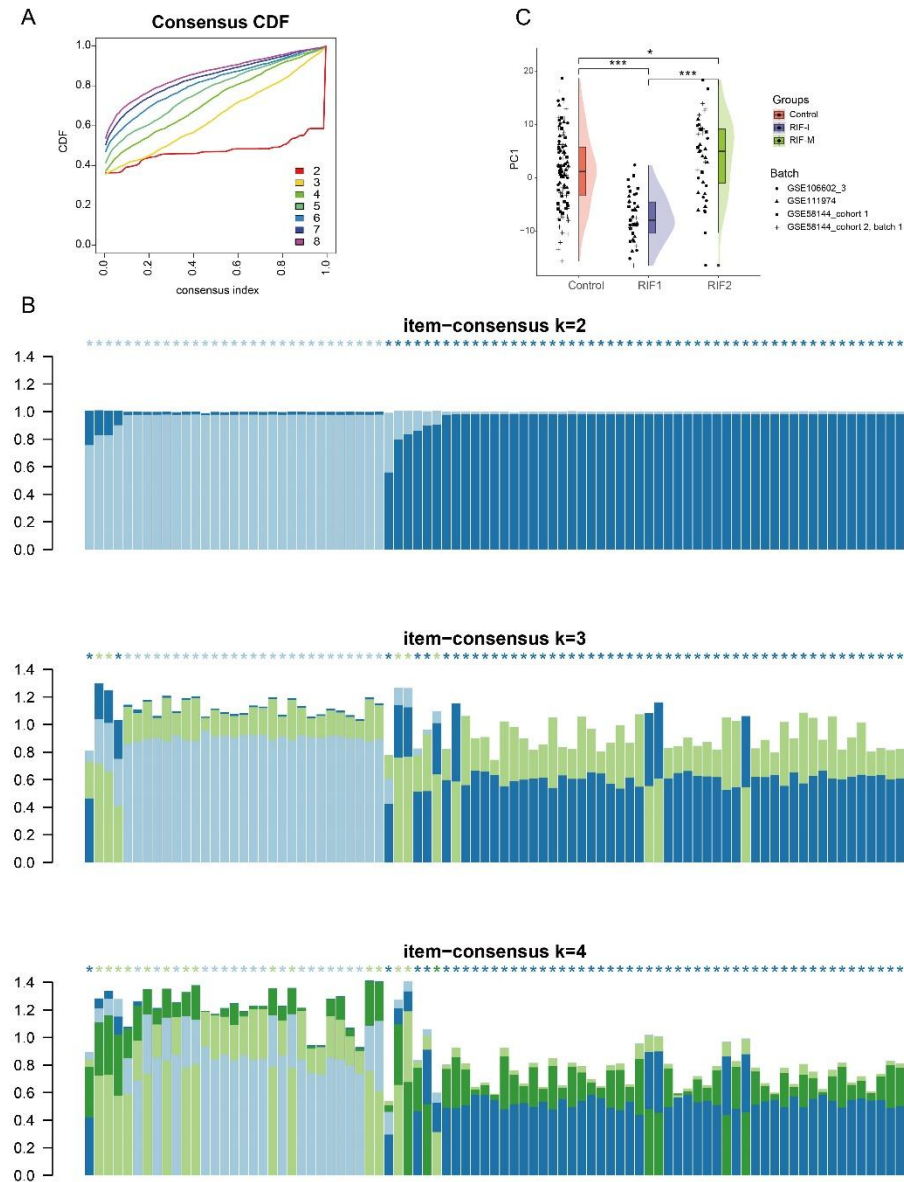
Supplementary Fig. S1. (A) 2D principal components analysis plot of GSE1106602, GSE111974, GSE58144 Batch 1, GSE58144 Batch 2, GSE71331 and In-house dataset. (B) Violin plots of PCA for GSE1106602, GSE111974, GSE58144_Batch 1, and GSE58144_Batch 2. (C) 2D plot of training datasets before and after batch effect removal.



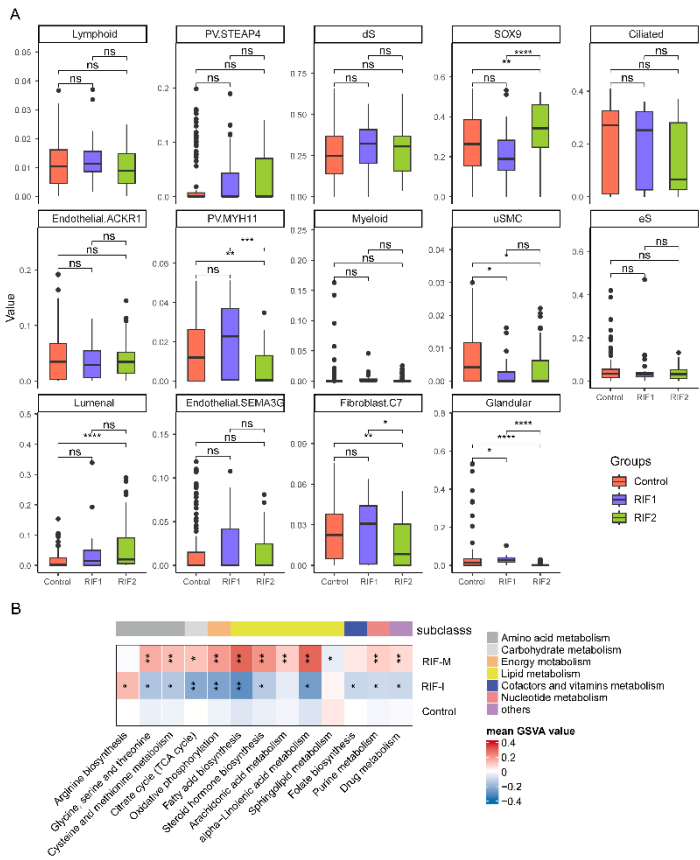
Supplementary Fig. S2. RIF-DEGs with importance scores greater than 50, along with the correlations between hormone receptor genes and the expression levels of key RIF-DEGs.



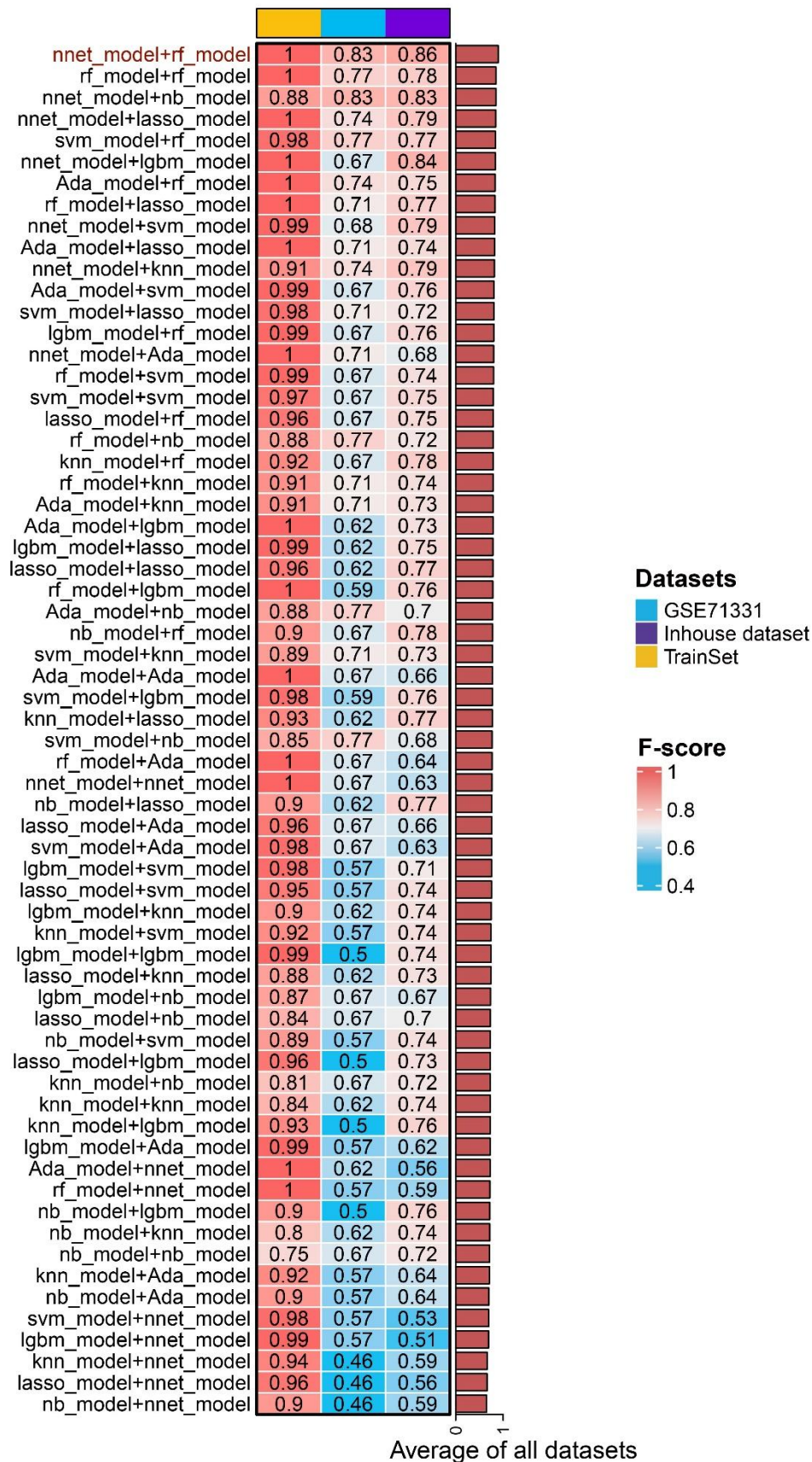
Supplementary Fig. S3. (A) The cumulative distribution frequency curve of RIF samples. (B) The item-consensus plot of RIF sample. (C) The raincloud plot shows the difference among RIF subtypes and control group through PCA.



Supplementary Fig S4. Analysis of endometrial cell infiltration and GSVA scores for specific metabolic pathways across RIF subtypes and the control group.



Supplementary Fig S5. Heatmap display the F-scores of 64 machine learning models used to predict RIF status across different datasets.



Supplementary Fig S6. (A) Principal component analysis of RIF patients based on MetaRIF classifiers including genes. (B) Boxplot representing the senescence scores among control, RIF-I, and RIF-M groups.

