

Figure S1. Shared DEGs between DOX-treated sgP130_siCTRL, sgP130_siP107, sgP130+sgRB1_siCTRL, and sgP130+sgRB1_siP107 HFF cells compared to the control cells. (A) UpSet plots of up- and down-regulated lncRNA and protein-coding genes between DOX-treated cells compared to control cells. (B) Enriched GO terms for the shared down-regulated protein-coding genes.

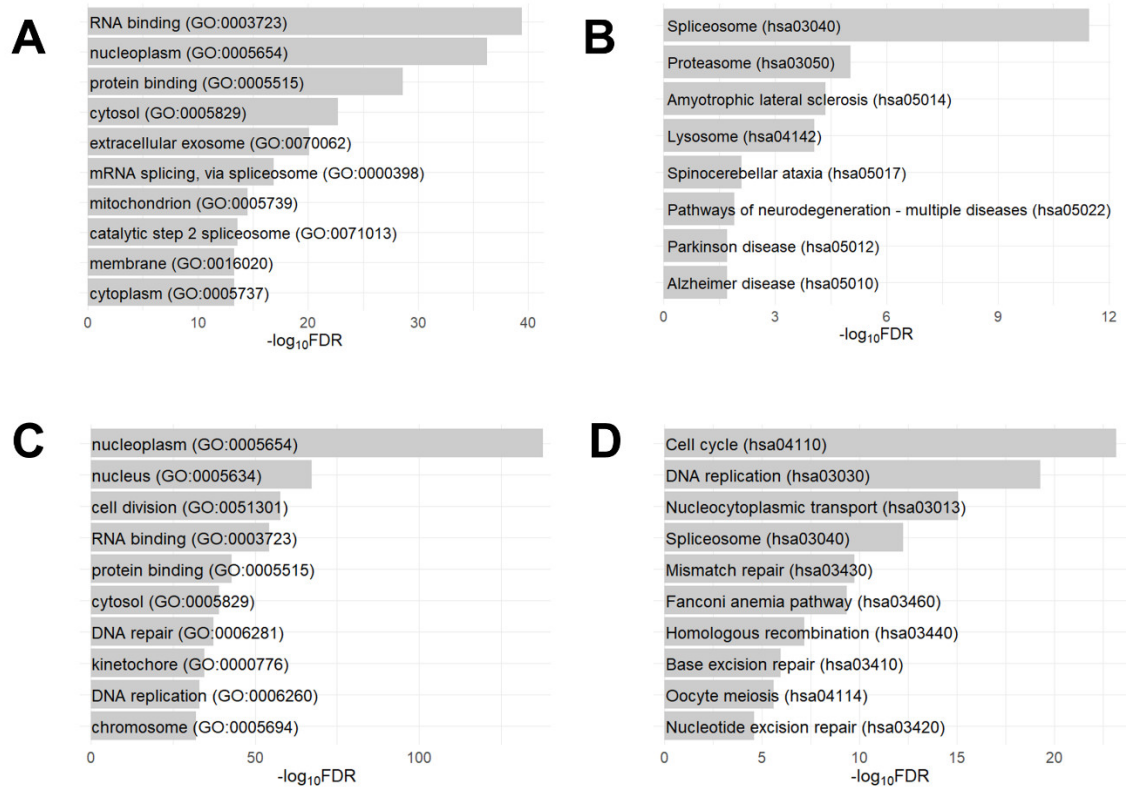


Figure S2. Expression correlation analysis of the differentially expressed lncRNA genes and protein-coding genes in DOX-induced senescent *PD-L1*⁺ and *PD-L1*⁻ cells compared to the control cells. (A) Enriched GO terms (top 10) and (B) KEGG pathways for the most significantly correlated protein-coding genes to the shared up-regulated lncRNA genes. (C) Top 10 enriched GO terms and (D) KEGG pathways for the most significantly correlated protein-coding genes to the shared down-regulated lncRNA genes.

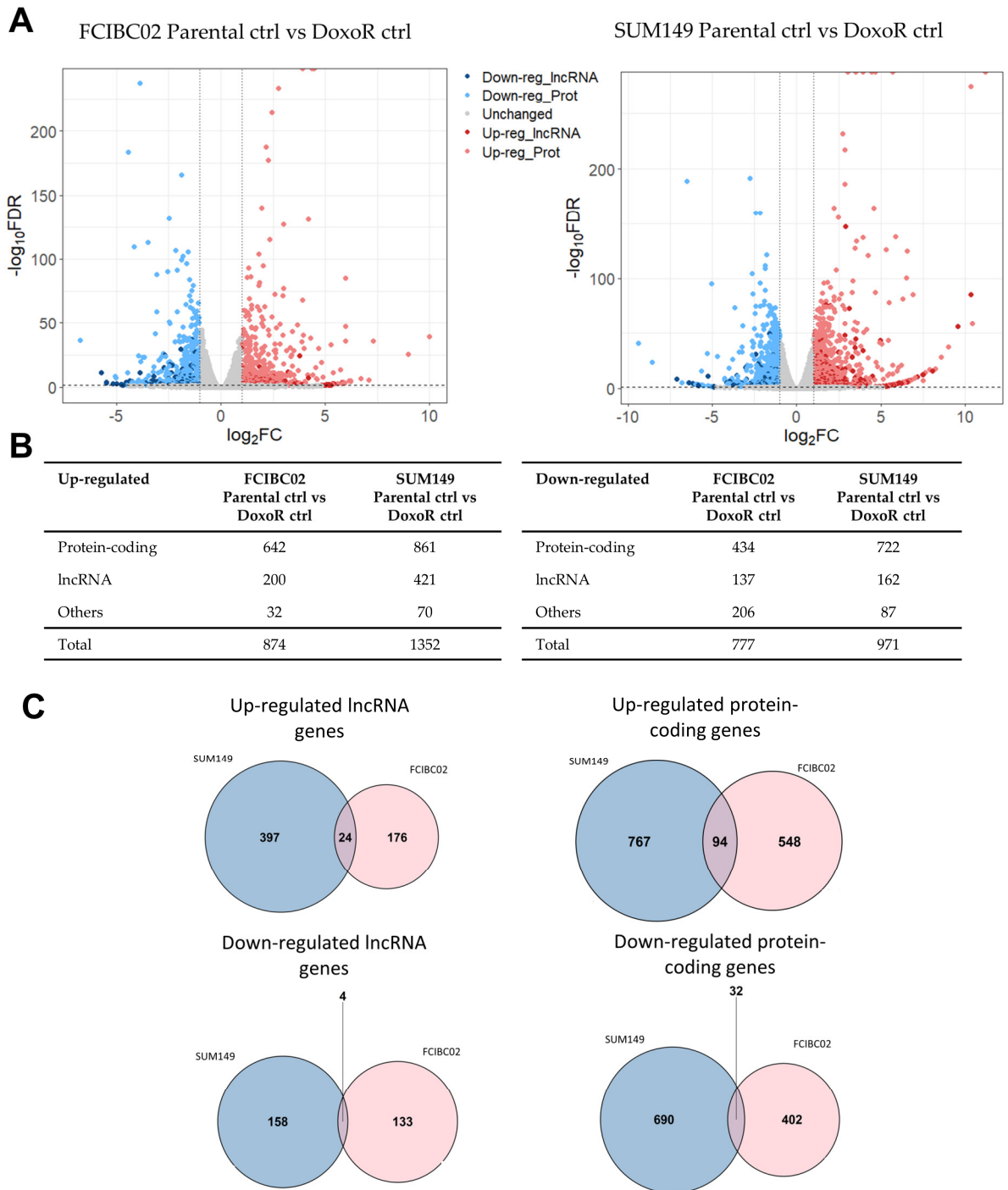


Figure S3. RNA-seq data analysis of DOX-resistant IBC cells (FCIBC02 and SUM149 cells) compared to control cells. (A) Volcano plot of differentially expressed genes based on the threshold values of 2-fold change and FDR < 0.05. (B) Number of differentially expressed lncRNA, protein-coding and other types of genes. (C) Venn diagrams of shared up- and down-regulated lncRNA and protein-coding genes between DOX-resistant IBC FCIBC02 and SUM149 cells compared to the control cells (p -value < 0.0001).