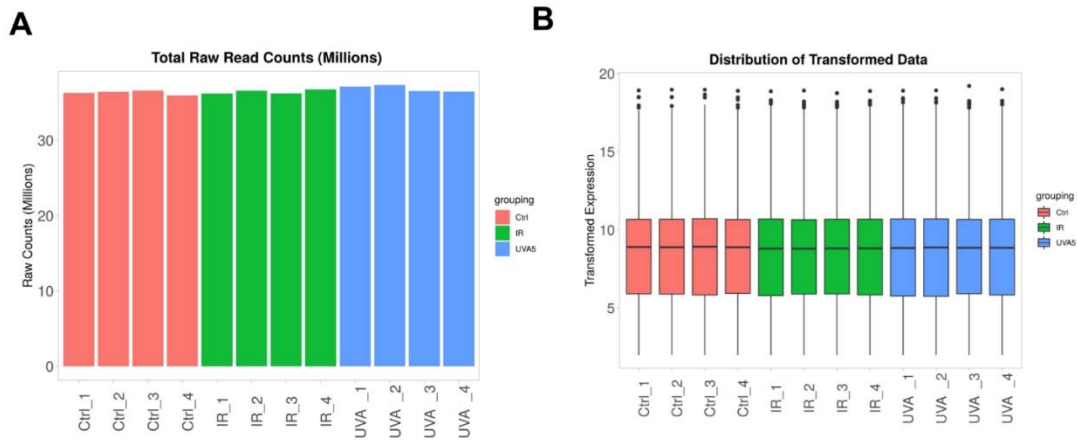
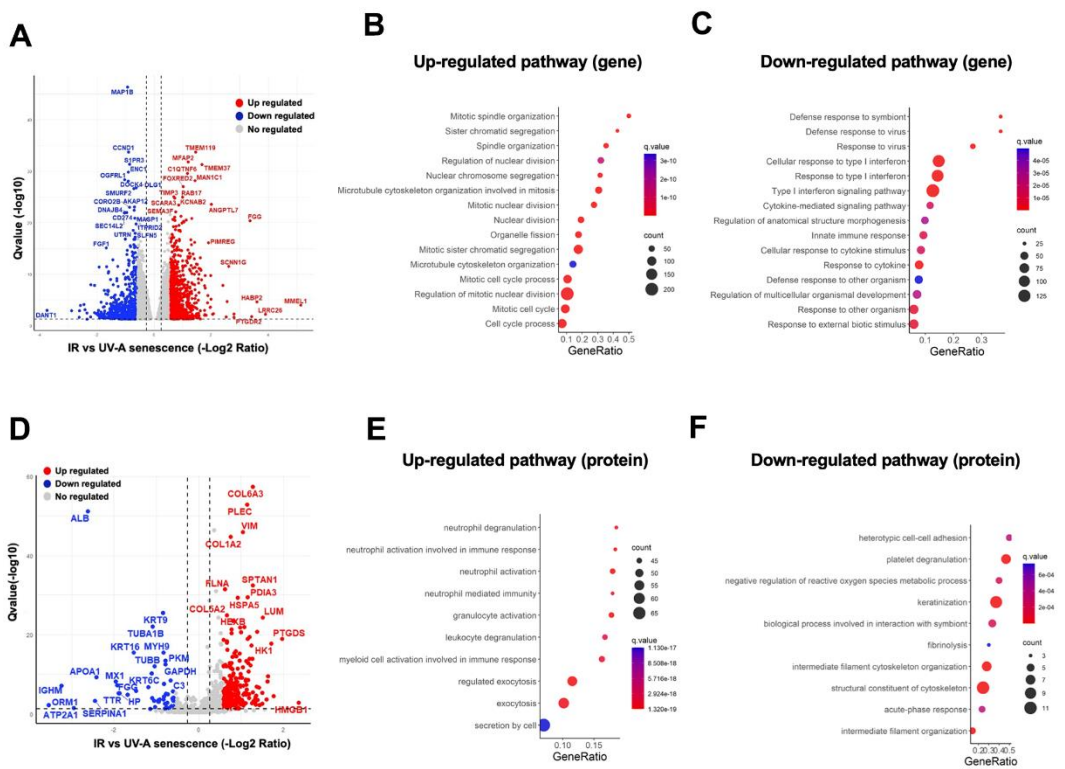


SUPPLEMENTARY FIGURES



Supplementary Figure 1. RNA-Seq data profile. (A) Total raw read counts of all RNA-Seq samples. (B) Distribution of transformed data of all RNA-Seq samples.



Supplementary Figure 2. Comparison of gene and protein expression patterns between UV-A- and IR-induced human senescent corneal endothelial cells. (A) Volcano plot comparing IR- and UV-A-induced senescent hCEnCs. Volcano plot showing Q-values (-log10) vs. fold change of (log2) IR- and UV-A-induced senescent hCEnCs. Blue, downregulated genes; red, up-regulated genes; and black, no significant change (fold change ≥ 2, q-value ≤ 0.05). (B, C) Gene ontology analysis of (B) up-regulated and (C) down-regulated genes comparing IR- and UV-A-induced senescent hCEnCs. (D) Volcano plot showing Q-values (-log10) vs. fold change of (log2) IR- and UV-A-induced senescent hCEnCs. Blue, downregulated proteins; red, upregulated proteins; and gray, no significant change (≥ 2 unique peptides, fold change ≥ 1.5, q-value ≤ 0.05). (E, F) Pathway and network analysis of secreted proteins that are significantly (E) increased and (F) decreased in the SASP from UV-A-induced senescent hCEnCs.