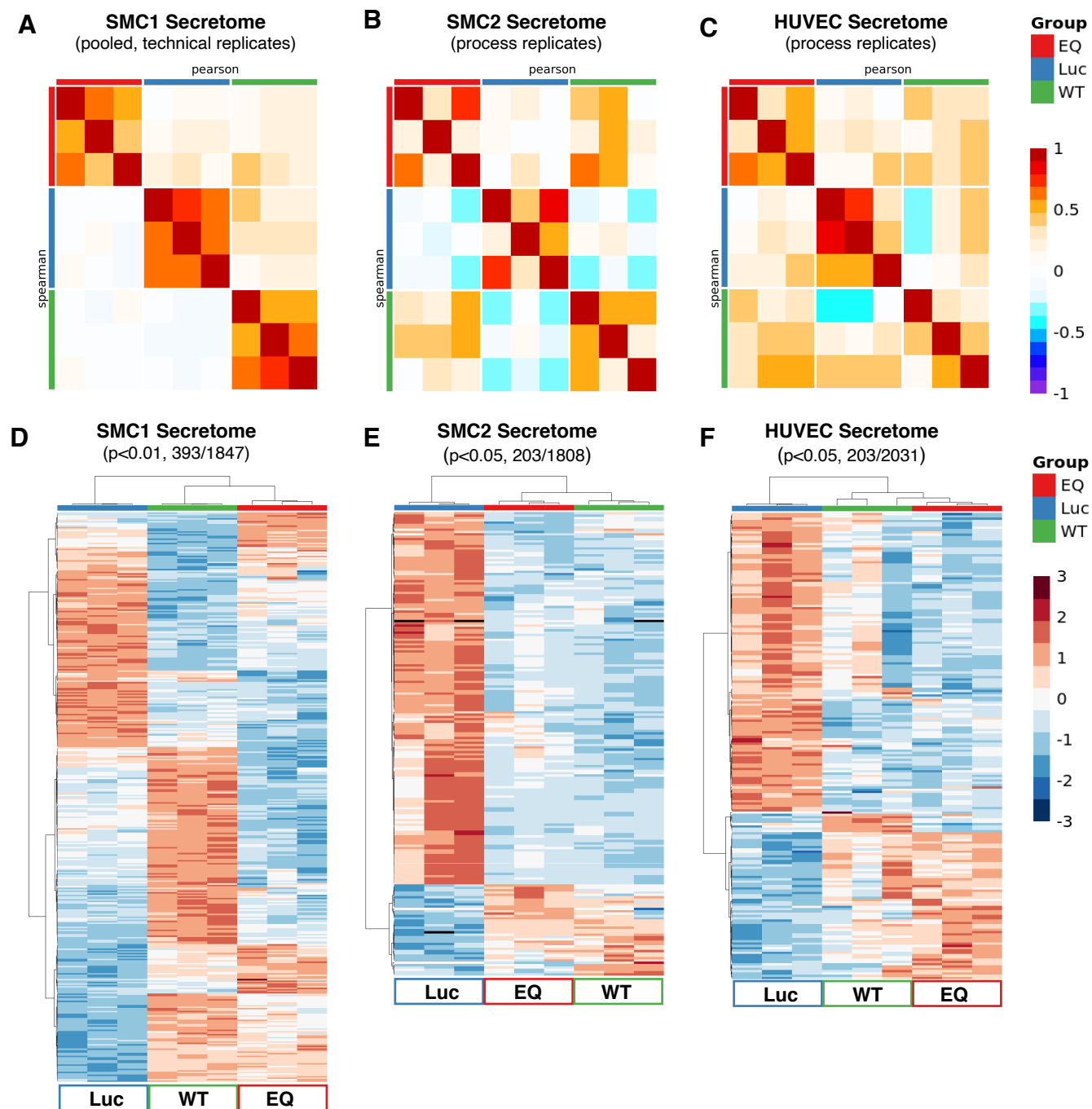


**Figure S4**



**Figure S4 Secretome replicate correlation plots and heatmaps for regulated proteins.** A-C, Similarity of secretome experimental replicates analyzed by Pearson (linear relationships) and Spearman (monotonic relationships) correlation plots generated by Protigy. For the total secretome analysis, a standard median normalization was used for the SMC1 technical replicates. SMC2 and HUVEC samples displayed greater diversity from biological replicates, therefore we applied median and median absolute deviation (M-MAD) to normalize the more variable secretome samples. D-F, Heatmap cluster analysis of regulated proteins from secretome experiments demonstrating greater clustering of WT and EQ compared to Luc replicates. The secretome heatmap dendrogram differs from the TAILS heatmap dendrogram and may be a product of Ad-ADAMTS7 expression rather than ADAMTS7 activity.