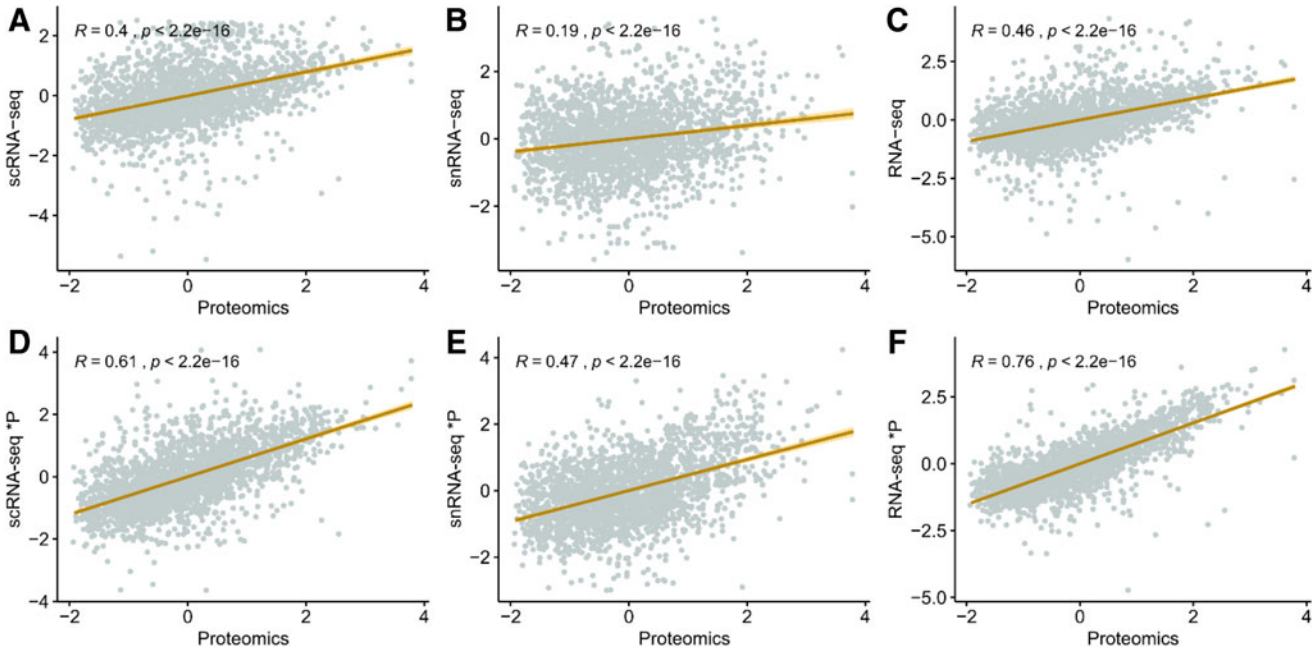
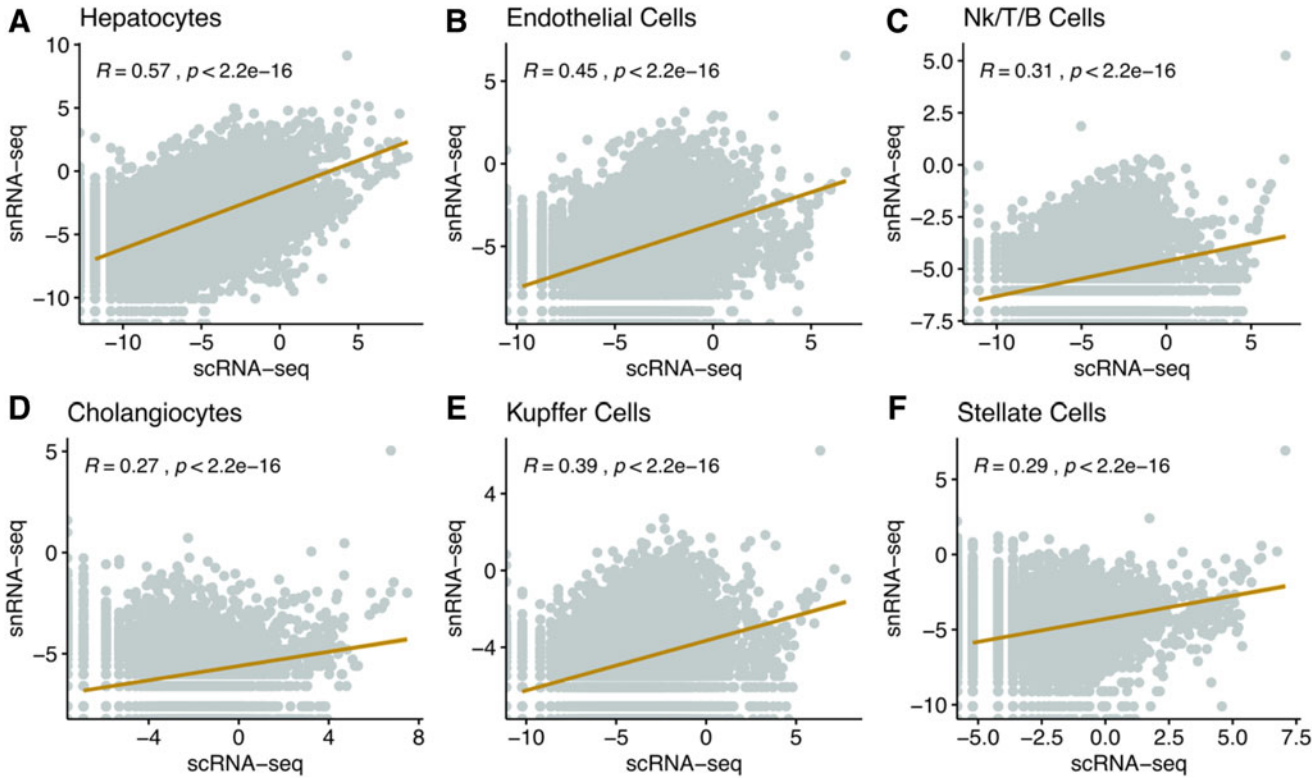


SUPPLEMENTARY FIG. S5. Pearson correlation analysis among transcriptomics and MS experiments. **(A)** Pearson correlation between $\log_2$-average *in silico* bulk scRNA-seq from five liver samples and MS proteomics from our study. **(B)** Pearson correlation between $\log_2$-average *in silico* bulk snRNA-seq and MS proteomics from our study. **(C)** Pearson correlation between $\log_2$-average number of reads of bulk RNA-seq from 175 liver samples and MS proteomics from our study. **(D)** Pearson correlation between $\log_2$-average *in silico* bulk scRNA-seq from five liver samples adjusted for gene-specific protein abundance estimation factors and MS proteomics from our study. **(E)** Pearson correlation between $\log_2$-average *in silico* bulk snRNA-seq adjusted for gene-specific protein abundance estimation factors and MS proteomics from our study. **(F)** Pearson correlation between $\log_2$-average number of reads of bulk RNA-seq from 175 liver samples adjusted for gene-specific protein abundance estimation factors and MS proteomics from our study. MS, mass spectrometry.



SUPPLEMENTARY FIG. S6. Cell type-specific correlation analysis between single-cell and single nuclei liver transcriptomics. Pearson correlation between $\log_2$-average *in silico* bulk scRNA-seq and $\log_2$-average *in silico* bulk snRNA-seq for shared cell types: **(A)** hepatocytes; **(B)** liver sinusoidal endothelial cells; **(C)** Nk/T/B cells; **(D)** cholangiocytes; **(E)** Kupffer cells; and **(F)** hepatic stellate cells. scRNA-seq, single-cell RNA sequencing.