

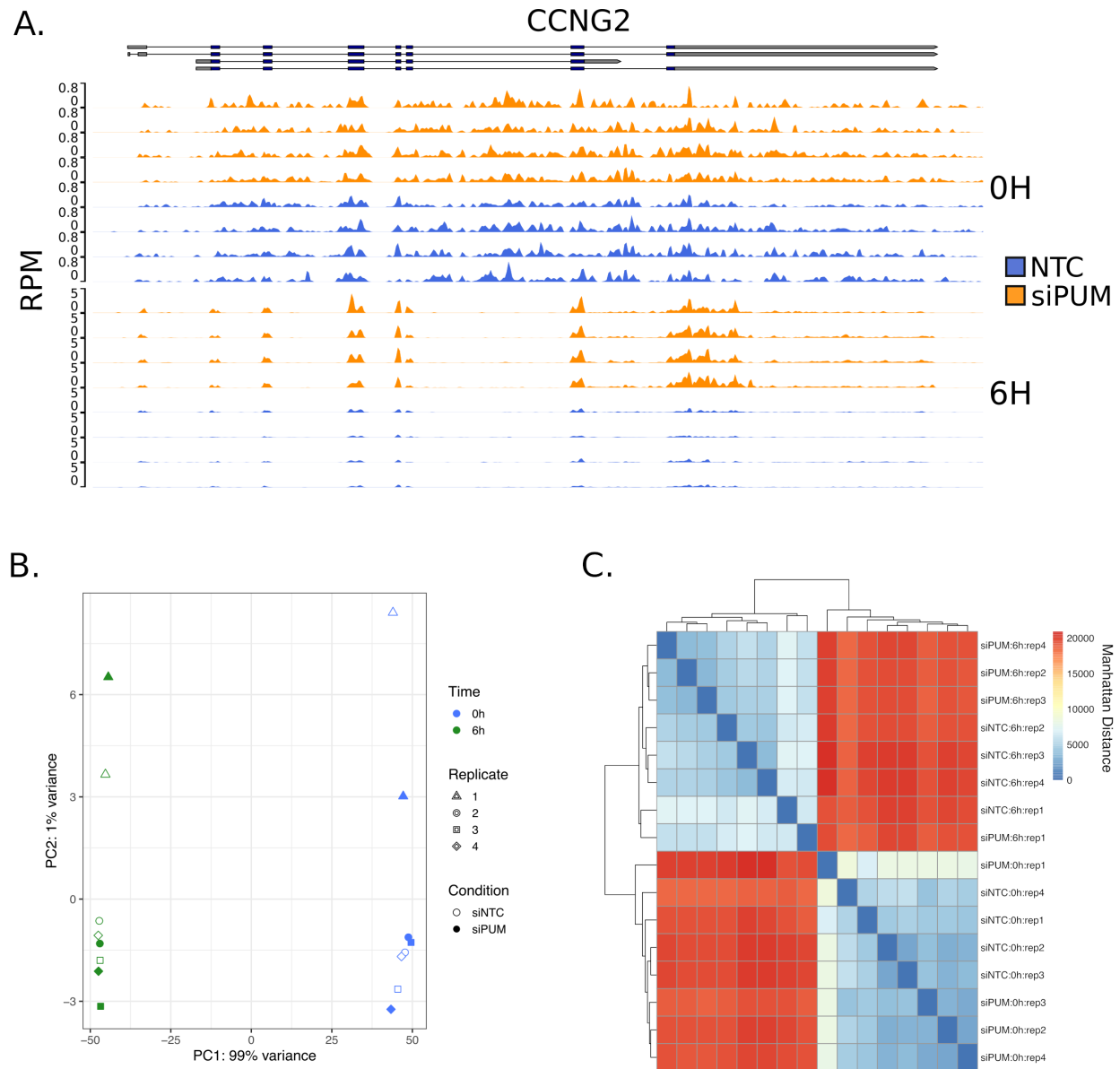


Figure S2: Reproducibility of Bru-seq and BruChase-seq. **A)** Breakout of four biological replicates for each time and condition for *CCNG2* (See Figure 1B for overlaid replicates). Read coverage is shown in read per million (RPM). Traces for the siPUM condition are in orange whereas traces for the siNTC condition are shown in blue. Known isoforms for *CCNG2* are represented above. Read coverage for each replicate is shown as the average in 30 bp windows over the region shown (chr4:78077800-78092000, hg19). Coverage plots were generated using pyGenomeTracks [104]. **B)** PCA analysis of normalized count matrices for each replicate. Count matrices were normalized using the variance stabilized counts while taking the design matrix into account as recommended by the DESeq2 documentation [47]. **C)** Heatmap of hierarchically clustered samples based on the Manhattan distance between samples in the variance stabilized count matrix.