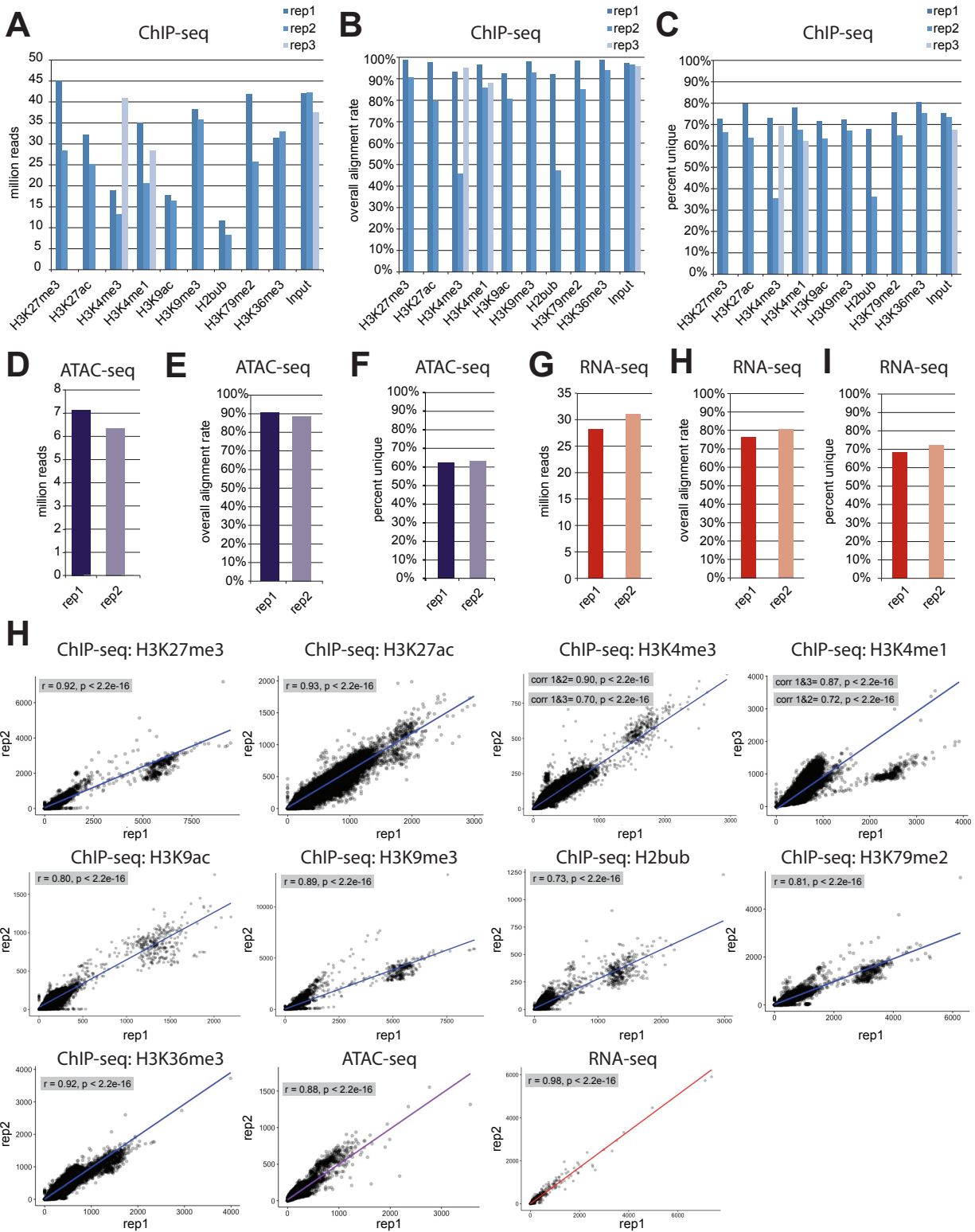




Supplemental Figure S3. ChIP-, ATAC-, and RNA-sequencing quality control. (A) Sequencing depth (millions of reads) for ChIP-seq biological replicates for each antibody. (B) Overall alignment, and (C) percent unique reads for each ChIP-seq sample. Note H3K4me1 and H3K4me3 have three replicates, while the other samples have two. (D-I) Similar to (A-C) but for ATAC-seq and RNA-seq replicates. Alignments and read mapping statistics were obtained with Bowtie2 (Langmead B, Salzberg S., 2012) for ChIP and ATAC-seq, and HISAT2 (Kim et al., 2015) for RNA-seq. (H) Pearson correlations of biological replicate coverage for each data set across 600 bp sliding windows, coverage calculated using 'genomecov' in Bedtools and pearson correlations calculated and plotted in R.