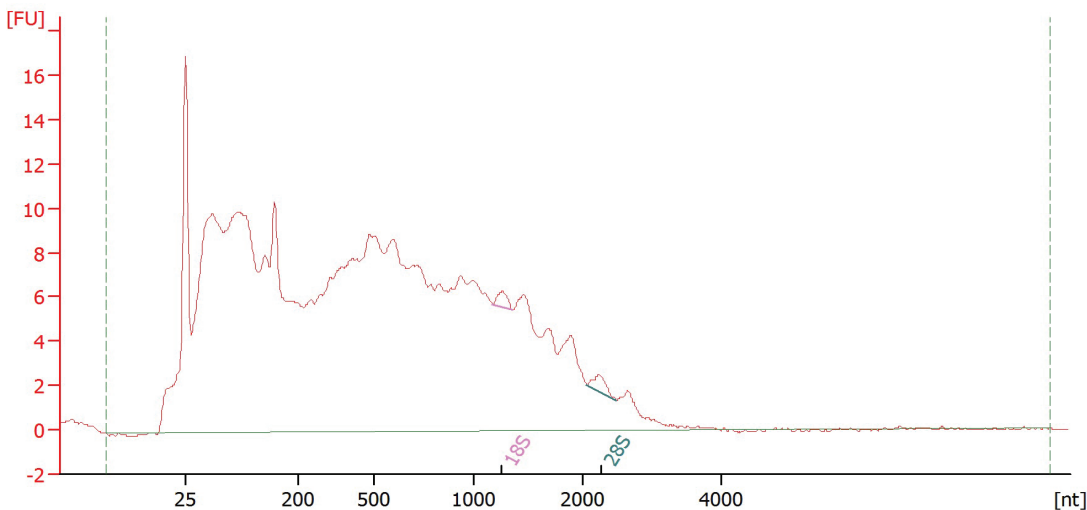
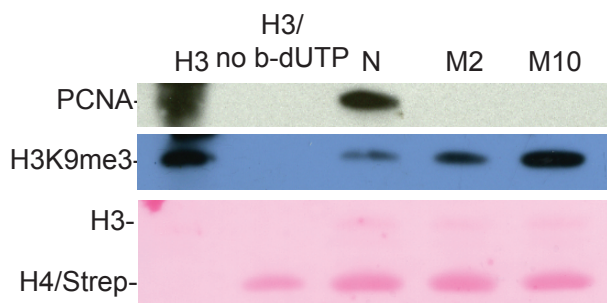


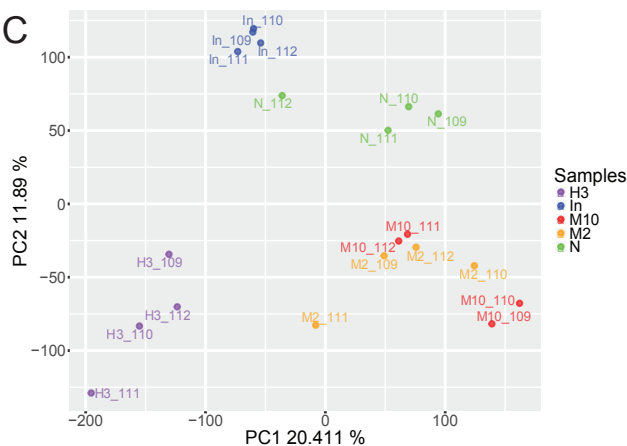
A



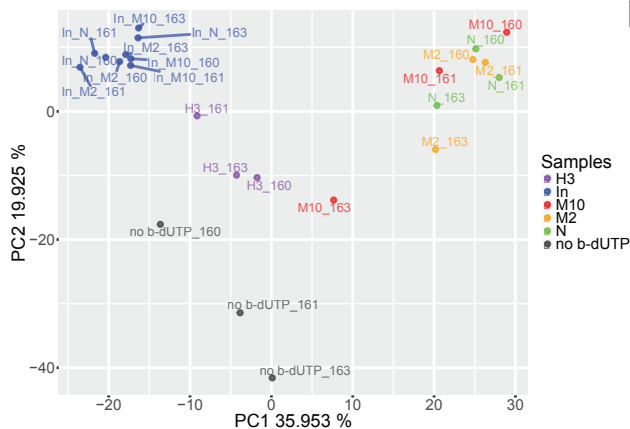
B



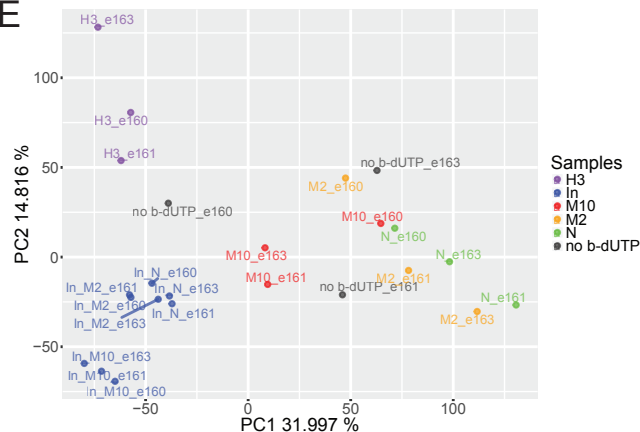
C



D



E



Supplementary Fig. S1 Controls for NCC RNA-seq pull down and read clustering A) RNA length from e160_M2 sample shown by bioanalyser Pico kit. X-axis indicate RNA length (nt=nucleotides) while Y-axis (FU=Fluorescence intensity). B) Westernblot of IPed protein from NCC samples (Histone 3 (H3), sample without biotin labelling (no b-dUTP), Nascent (N), 2 h (M2) and 10 h (M10) mature chromatin), Proliferating Cell Nuclear Antigen (PCNA, Abcam-ab29), Histone 3 Lysine 9 tri-methylation (H3K9me3, Abcam ab8898), ponceau staining indicating Histone 3 (H3), -4 (H4) and streptavidin beads. C) Principal component analysis (PCA) plot of long RNA-seq hg38 DERfinder analysis. D) PCA plot of short RNA-seq Rebase map analysis and E) hg38 map analysis.