Supplementary 3.

Loss of H3 active methylation marks is specific to promoters and transcribed regions. ChIP analysis of Grp78 and Chop upstream (-1kB), core promoter (TSS) and transcribed regions (+1kB); CyclinA2 (+1kB) and Pcna (+1.7kB) transcribed regions with growing NIH-3T3 infected with the indicated adenoviruses as in Fig. 3. The antibodies are listed on the right and fold enrichment was calculated as described for Fig. 3.