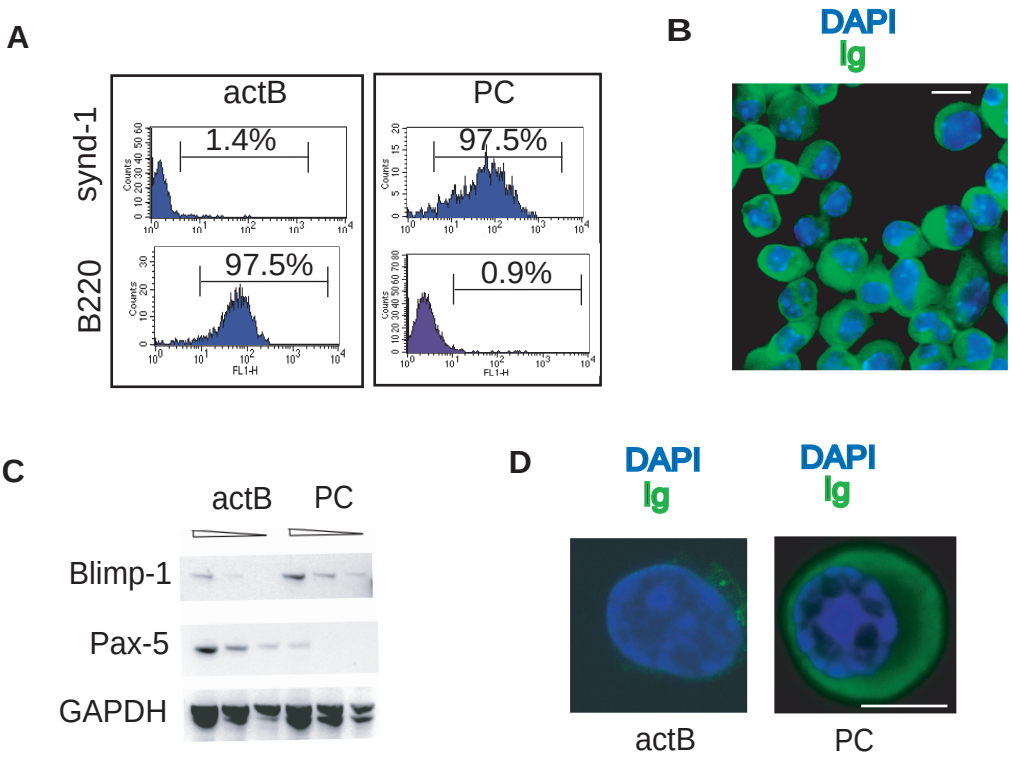

Figure S1. *In vitro* differentiation of plasma cells from splenic B cells

(**A**) Representative FACS analysis for syndecan-1 and B220 expression in the plasma cell (PC) culture following magnetic-bead selection. Levels were compared with an activated B cell (act B) control. (**B**) DAPI distribution (blue) and cytoplasmic immunoglobulin levels (green) in the purified plasma cell population. Abundant cytoplasmic Ig was detected in the cells. (**C**) RT-PCR analysis of Blimp-1 and Pax-5 expression carried out on RNA extracted from syndecan-1^{+}/B220^{-} plasma cells and CD19^{+} activated B cells. For quantitiation of transcript levels, PCRs were carried out on three serial dilutions of the template. (**D**) Following differentiation from the activated B cell stage (actB) chromatin in plasma cells (PC) becomes condense into DAPI-dense facultative heterochromatin.

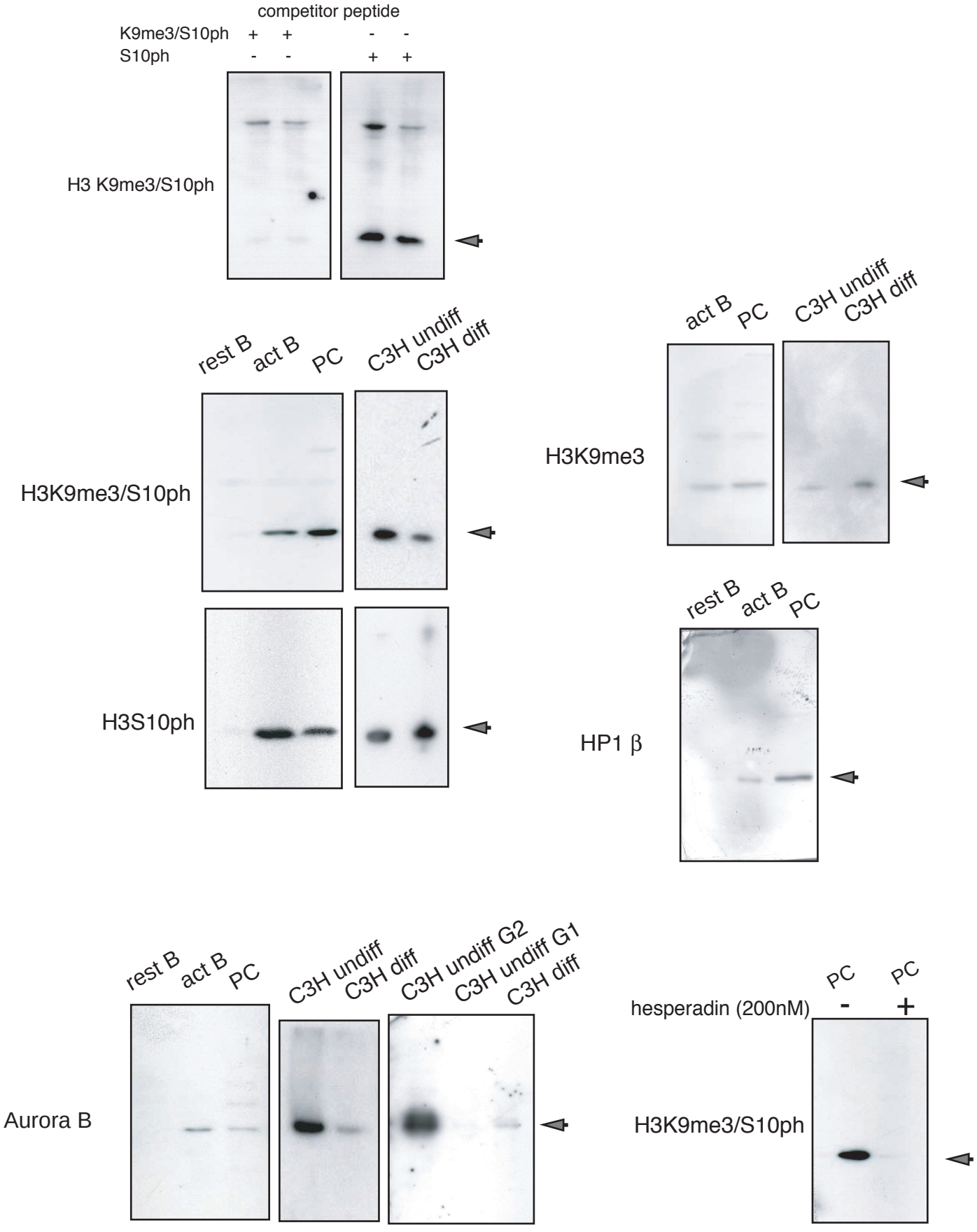

Figure S2. Full images of western blots shown in Fig. 1,3 and 4.

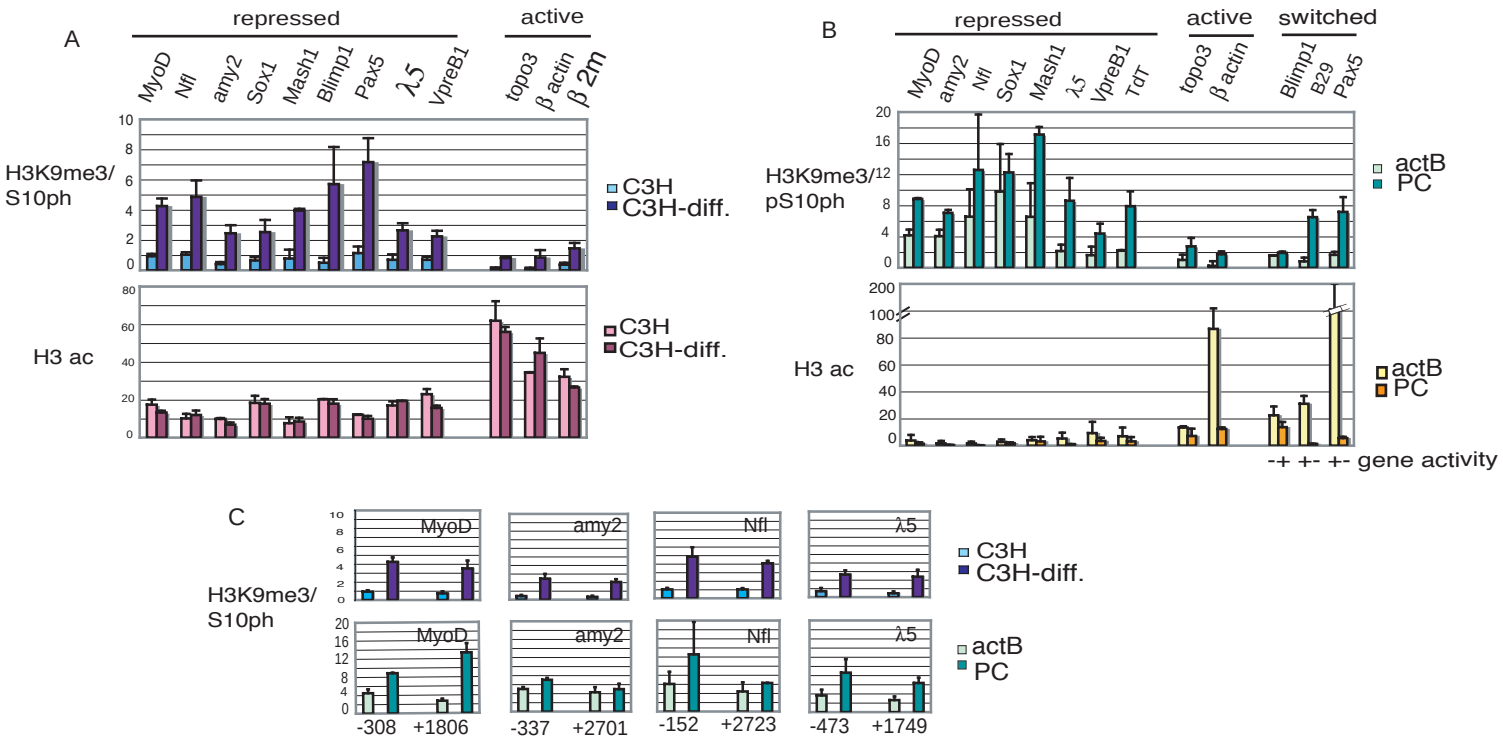

Figure S3. H3 K9me3/S10ph is enriched at the promoters of silent genes following differentiation. (**A**) ChIP analysis performed on formaldehyde fixed chromatin from undifferentiated (C3H) and differentiated (C3H-diff) C3H10T1/2 cells. The ChIP was carried out using anti-H3K9me3/S10ph and anti-acetylated H3. ChIP with anti-FLAG antibody and non-specific rabbit IgG were used as background controls and resulted in negligible immunoprecipitation (not shown). *y* axis= percentage of the input that was precipitated by the specific antibody calculated by the equation: $2^{-\text{average CT IP}} / 2^{-\text{average CT input}}$ x 100/input dilution factor, where the input dilution factor is the ratio between the amount of chromatin used for immunoprecipitation and for input chromatin. The percentage of the input that was precipitated was the average of at least two independent immunoprecipitations and error bars indicate standard deviations. (**B**) ChIP analysis of activated B cells and *in vitro* differentiated plasma cells was carried out on micrococcal nuclease digested chromatin. As a background control, immunoprecipitation was also carried out with a non-specific IgG antibody. Background values were low and only the enrichment for the specific antibody above the background is shown. (**C**) Four of the silent genes analysed by ChIP were further characterised using primers located within the transcribed region (numbers indicate position relative to the transcription start site).

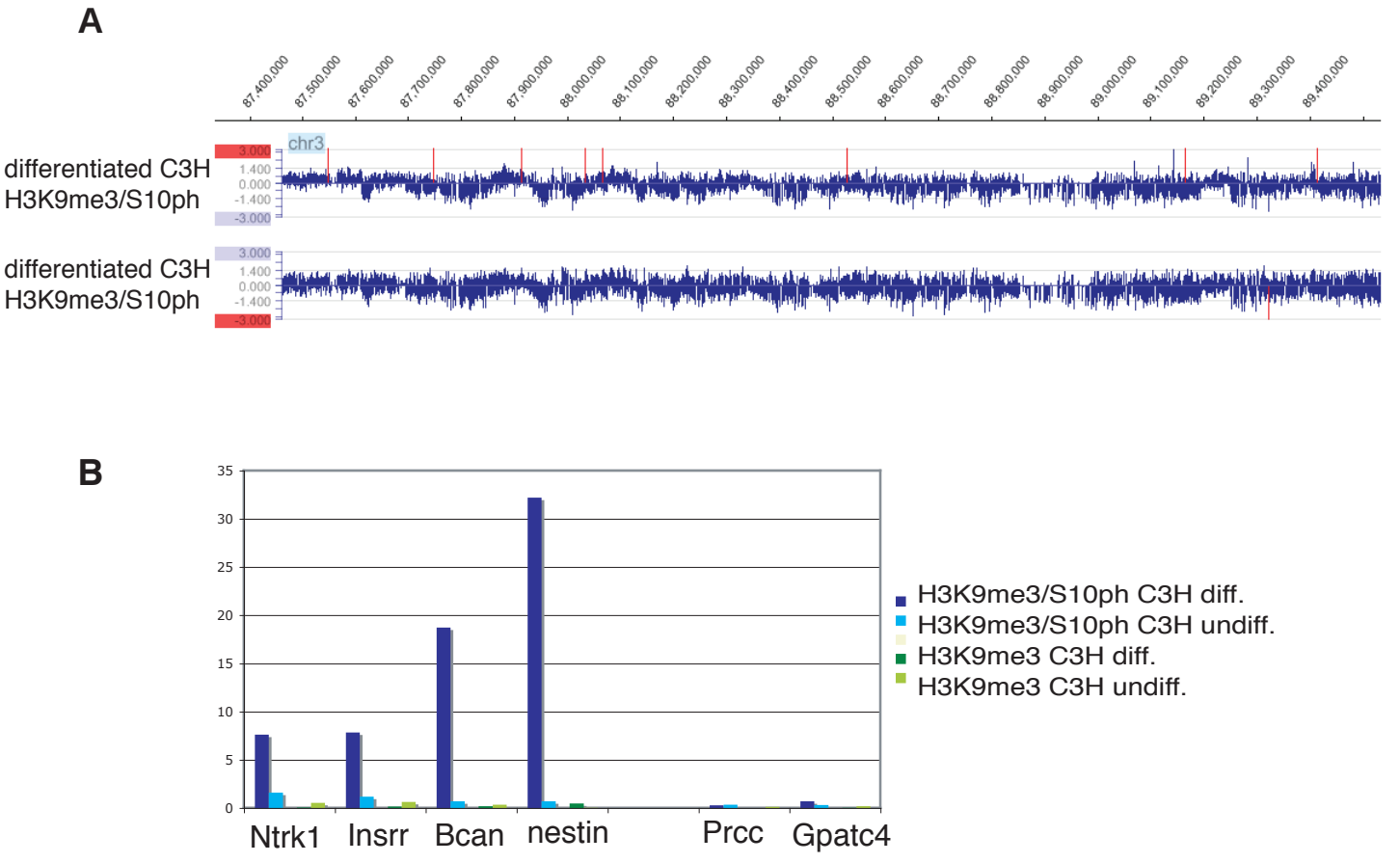

Figure S4. Reproducibility and validation of the microarray analysis by real-time PCR. (**A**) The $\log_2$IP/input signal ratios along the 2 Mb region for H3K9me3/S10ph in differentiated C3H10T1/2 cells is represented by bars. The profile obtained with two independent immunoprecipitation is shown. (**B**) The unamplified DNA obtained by ChIP and used for the microarray analysis after amplification was analysed by real-time PCR using primers within the coding region of six genes of the 2 Mb region. The *y* axis represents the fold enrichment over the input. The real-time PCR confirmed enrichment for H3K9me3/S10ph on genes (Ntrk1, Insrr, Bcan, nestin) found to be enriched by microarray analysis.