Supplemental Material to:

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CRE promoter sites modulate alternative splicing via p300mediated histone acetylation

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Suppl.Fig.1



SUPPL. FIGURE 1: p300 affects alternative splicing of EDB exon. (A) Ratio of endogenous EDB included to excluded after p300 knockdown analyzed by RT-qPCR. The average of three experiments (normalized to NC siRNA) is shown including SEM, * indicates $p \le 0.05$ of the paired t-test with respect to cells treated with NC siRNA. (B) Ratio of EDB included or excluded mRNAs originated from the CMV driven mini-gene after p300 knockdown analyzed by RTqPCR. The average of three experiments (normalized to NC siRNA) is shown including SEM. (C) Western blot showing p300 knockdown efficiency and expression level of SR proteins after p300 knockdown using two different siRNAs. GAPDH is used as a loading control.











SUPPL. FIGURE 3: Splicing reporters. (A) Schemes of additional splicing reporters used in this study. (White boxes – promoter with CRE sites, grey boxes – constitutive exons, black lines – introns, black box – alternative EDB exon). (B) Analysis of EDB alternative splicing after deletion of various CRE sites within CMV promoter (black box – EDB exon, grey boxes – surrounding exons).

Suppl.Fig.4



SUPPL. FIGURE 4: Increase of acH4 after NaB treatment. Fold increase of H4 acetylation (normalized to H3 signal) after NaB treatment over non-treated cells. The gray dashed line represent level of H4 acetylation in non-treated cells. The average of three experiments is shown including SEM.