

Description of supplementary files

Supplementary Data 1. Alternative splicing events in naïve B cells (related to Figure 4A).

This dataset contains genes with significantly altered alternative splicing events. Alternative splicing analysis was performed using rMATS. Statistical significance was assessed using a likelihood ratio test. P values were adjusted for multiple comparisons using the Benjamini–Hochberg procedure to control the false discovery rate (FDR). Splicing events with an FDR < 0.05 and an absolute change in percent spliced in ($|\Delta\text{PSI}|$) > 0.2 were considered significant.

Supplementary Data 2. Target genes with significant changes in alternative splicing (related to Supplementary Figure 5A).

Selection criteria: $|\Delta\text{PSI}|$ > 0.2, $P < 0.05$, and skipping junction count (SJC) in *Hnrnpa1^{ff} Hnrnpa2b1^{ff} Cd19^{Cre/+}* mice > 10. Alternative splicing analysis was performed using rMATS. Statistical significance was assessed using a likelihood ratio test. P values were adjusted for multiple comparisons using the Benjamini–Hochberg procedure to control the false discovery rate (FDR).

Supplementary Data 3. RNA-seq FPKM values of all genes in naïve B cells (related to Supplementary Figure 5J).

Expression profiles of all genes in naïve B cells isolated from the spleens of *Hnrnpa1^{ff} Hnrnpa2b1^{ff}* and *Hnrnpa1^{ff} Hnrnpa2b1^{ff} Cd19^{Cre/+}* mice.

Supplementary Data 4. List of differentially expressed genes in B cells stimulated with αIgM + αCD40 (related to Figure 6A).

Transcriptomic differential expression genes in B cells upon *Hnrnpa1* and *Hnrnpa2b1* deficiency following stimulation with αIgM + αCD40 for 48 hours.

Supplementary Data 5. Mass spectrometry data.

List of proteins identified by mass spectrometry following RNA pull-down using a 70-nt pre-mRNA fragment spanning exon 14 and intron 14 of EZH2 (EZH2) and its reverse complement sequence (E2-R).