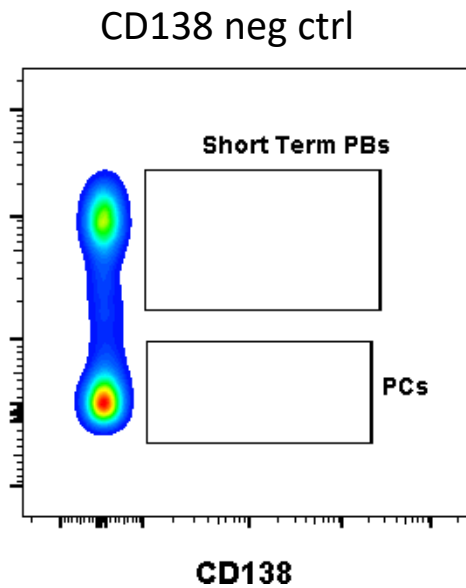
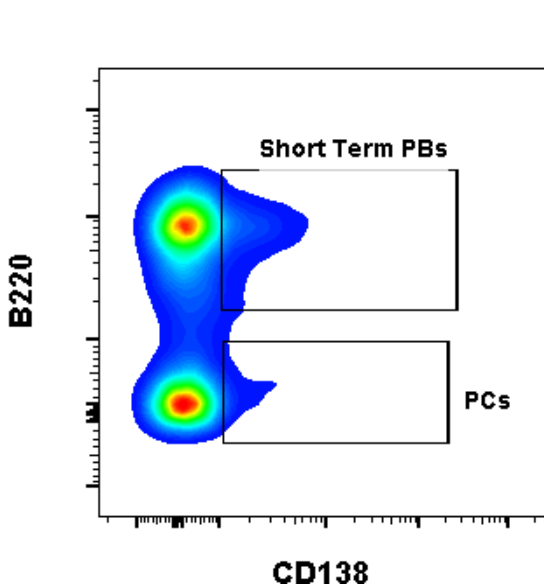
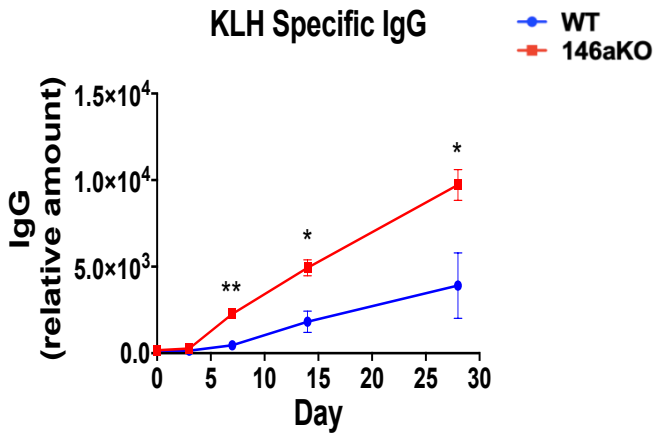


Regulation of T-Independent
B-Cell Responses by
MicroRNA-146a
King et al...

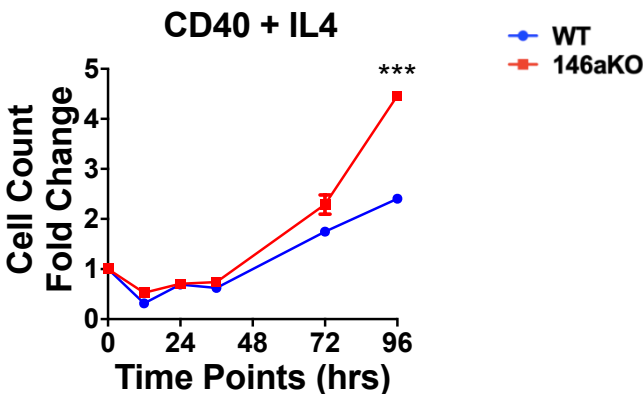
Supplement



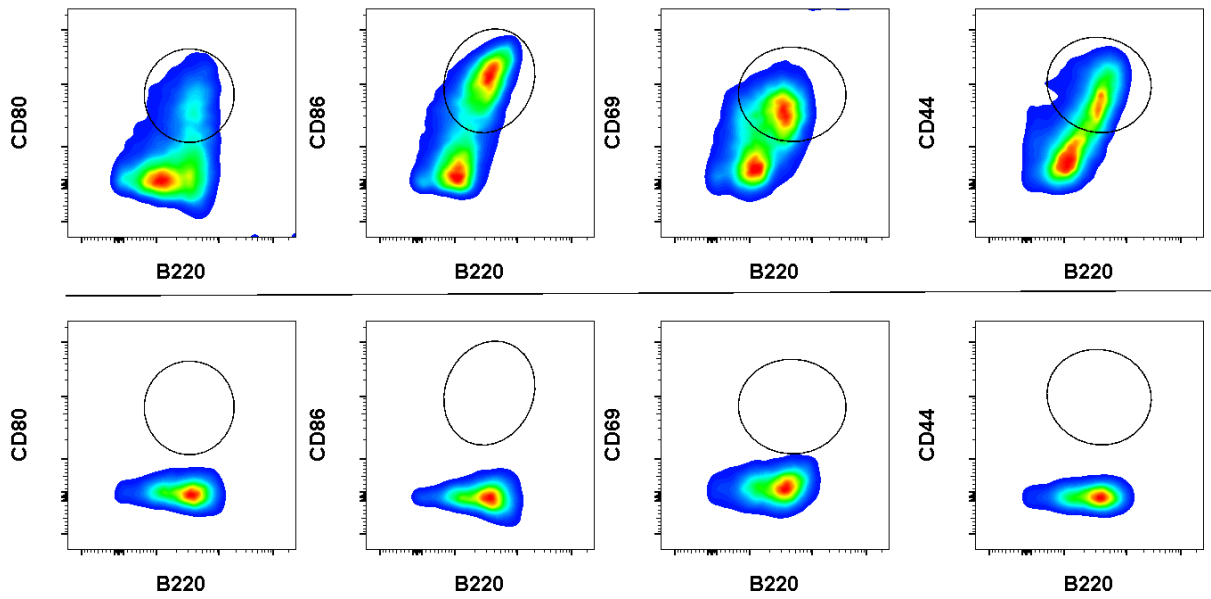
Supplement 1: Representative FACS plot of splenic plasma cell subsets from primary immunization response to T-independent antigen (left) vs. B220+CD138- negative staining control (right).



Supplement 2A: miR-146aKO B-cells have higher peptide specific IgG secretion in response to T-dependent antigen than WT. After *in vivo* immunization with T-dependent antigen Keyhole Limpet Hemocyanin (TNP-KLH), KLH specific IgG responses were higher in miR-146aKO than in WT (*t* test; **P* ≤ 0.05, ***P* < 0.01). n = 3 mice/group. Data represent mean ± SEM.

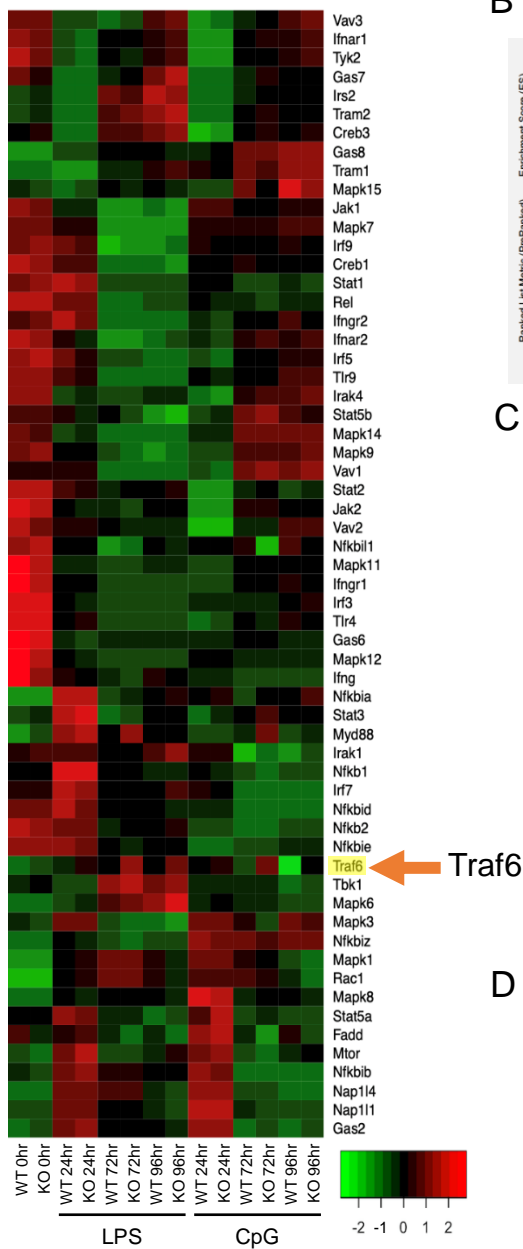


Supplement 2B: MiR-146aKO splenic B-cells activated with T-dependent stimuli have higher cell counts than WT. B-cells were stimulated with anti-CD40 (5ug/ml) along with IL-4 (5ng/ml). Representative of 3 mice/group in duplicates or triplicates, confirmed in 2 independent experiments. (*t* test; ****P* < 0.001).

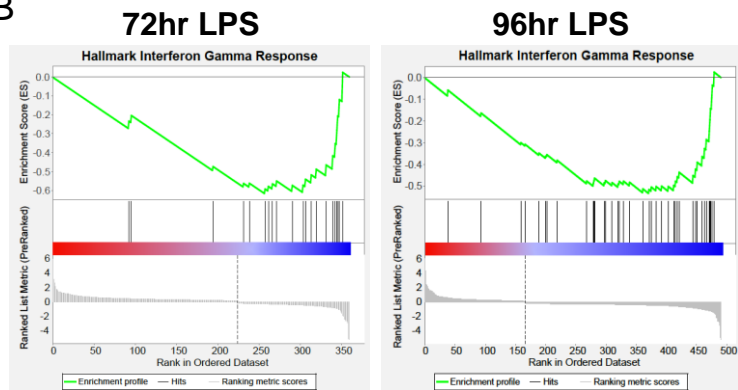


Supplement 3. Representative FACS plots for splenic B220+ cell surface activation markers (top panel) with FMOs (bottom panel).

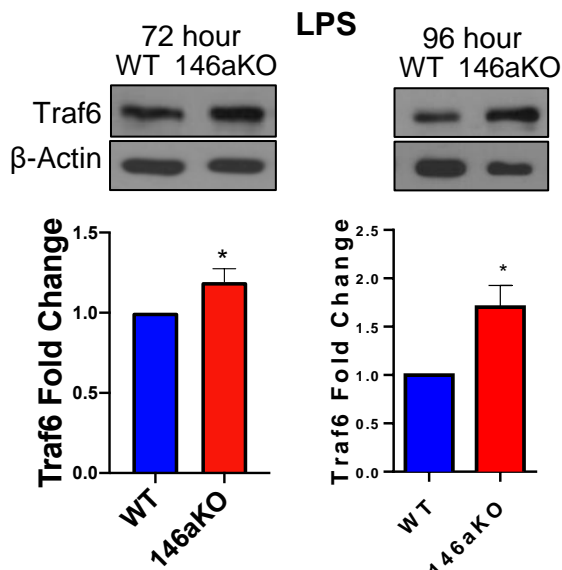
A



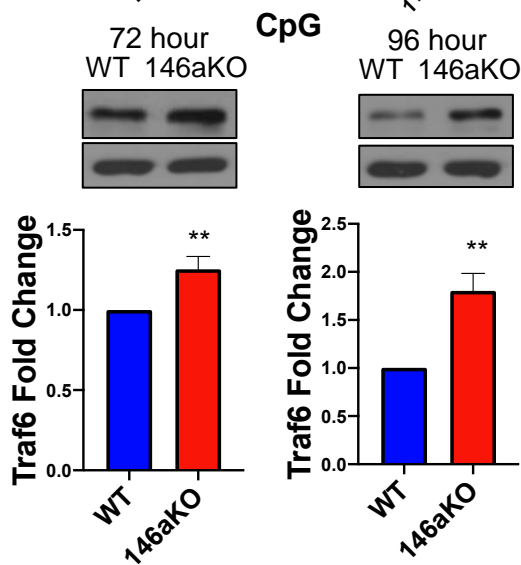
B



C

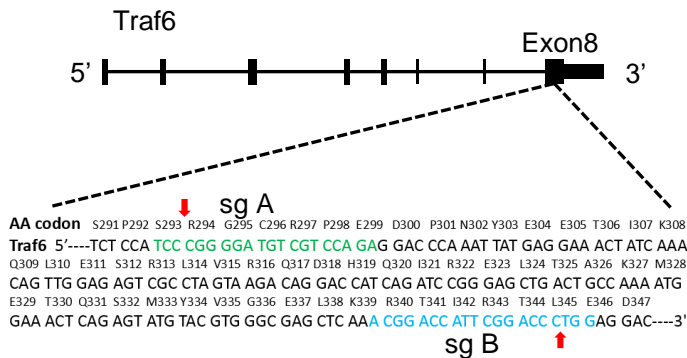


D

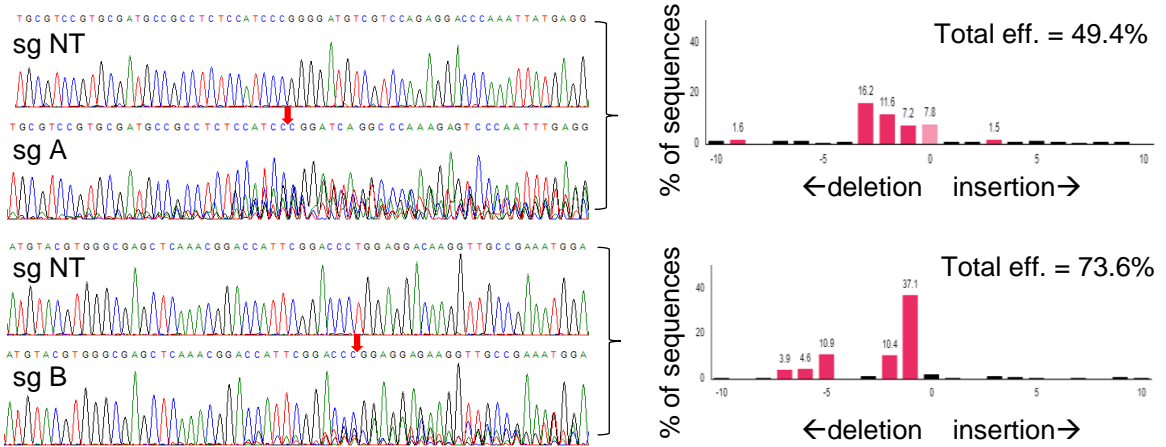


Supplement 4: *Traf6* expression increases with T-independent antigen stimulation of B-cells. (A) Heatmap from the RNA-Seq data showing differentially expressed IFN targeted genes. miR-146a molecular target, *Traf6*, is highlighted in yellow. (B) Gene set enrichment analysis (GSEA) of genes differentially expressed between WT and miR-146aKO activated B-cells shows enrichment in Interferon γ pathways. 72hrs Normalized Enrichment Score: -1.96; FDR q value: 0.0. 96hrs Normalized Enrichment Score: -1.85; FDR q value: 0.046. (C) Protein expression via Western Blot of TRAF6 in B-cells when stimulated with LPS and (D) CpG. t test; * $P < 0.05$, ** $P < 0.01$. Data represent mean \pm SEM. Graphs combine 3 independent experiments (n = 3-4 mice/group/exp).

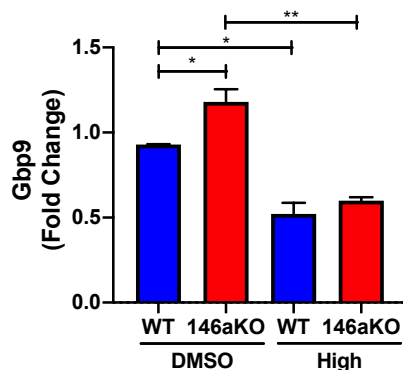
A



B



C



Supplement 5: Traf6 sgRNAs for CRISPR/Cas9. (A) sgRNAs (sg A and B) location on Exon 8 of *Traf6*. AA codon sequence indicates the detail location. (B) TIDE analysis of engrafted primary bone marrow cells transduced with sg NT, A, and B (GFP+ mCherry+ cells) respectively. Left panel is the sequence, red arrows show the position of double strand breaks (DSBs) that should be introduced by CRISPR/Cas9; right panel is the TIDE results, total eff. means sum for all the types of gene editing. (C) RT-qPCR of downstream *Traf6* gene, *Gbp9*, in LPS-stimulated B-cells treated with DMSO or high dose of C25-140. t test; * $P < 0.05$, ** $P < 0.01$.

Supplementary Table 1. List of antibody stains used in FACS analysis.

Antigen	Clone
B220	RA3-6B2
CD21	7E9
CD23	B3B4
CD80	16-10A1
CD86	GL-1
CD69	H1.2F3
CD44	IM7
CD40	HM40-3
CD138	281-2
CD93	AA4.1
GL7	GL7
CD95	SA367H8
IgD	11-26c.2a
CD3e	145-2C11
CD11b	M1/70
Ly-6c	HK1.4

Supplementary Table 2. sgRNA and primer sequences used in this study.

sgRNA	Sequence
sg A (F)	TTTGTCTGGACGACATCCCCGGGA
sg A (R)	AAACTCCCGGGGATGTCGTCCAGA
sg B (F)	TTTGACGGACCATTTCGGACCCTGG
sg B (R)	AAACCCAGGGTCCGAATGGTCCGT
sg NT (F)	TTTGCGAGGTATTCGGCTCCGCG
sg NT (R)	AAACCGCGGAGCCGAATACCTCG
m-Traf6-F	GCACAAGTGCCCAGTTGAC
m-Traf6-R	TGCAAAATTGTCGGGAAACAGT
m-Cd72-F	CATACCCTCGGAAGTCTGGA
m-Cd72-R	GCCTCCACTTCTTGCTCATC
m-Ccng1-F	TAAGTGGCCGAGATTTGACC
m-Ccng1-R	ATGGTCTCAGGAATCGTTGG
m-Gbp9-F	TGTGCAGTCTCAGACCAAGG
m-Gbp9-R	AAGCACACTTAGGGCGAAGA