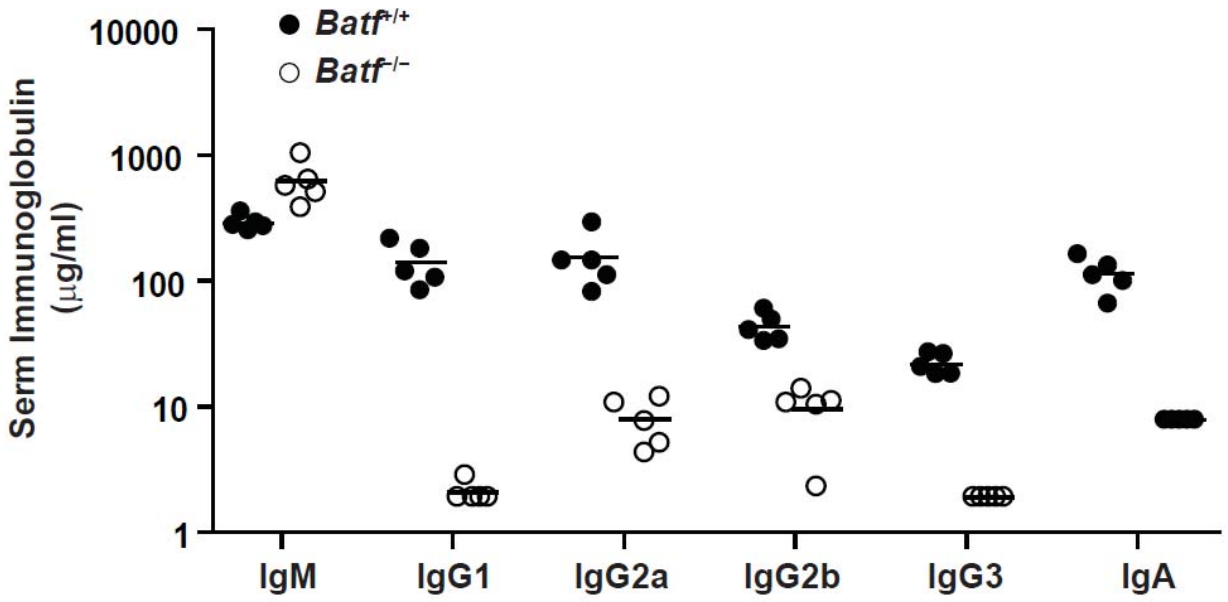
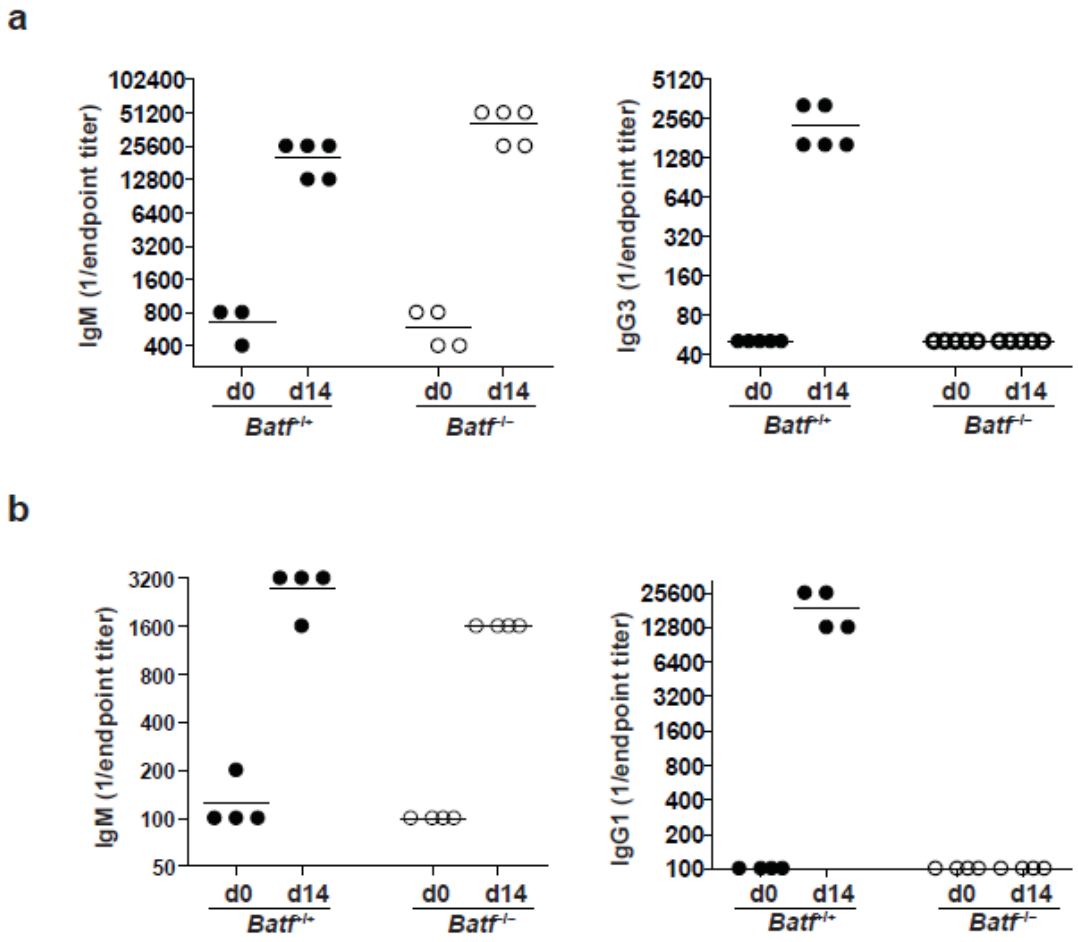
Supplementary Text and Figures

Supplementary Figure 1



Supplementary Fig. 1. *Batf*$^{-/-}$ mice have altered basal immunoglobulin titers. ELISA of basal serum immunoglobulin titers in unimmunized *Batf*$^{+/+}$ or *Batf*$^{-/-}$ mice.

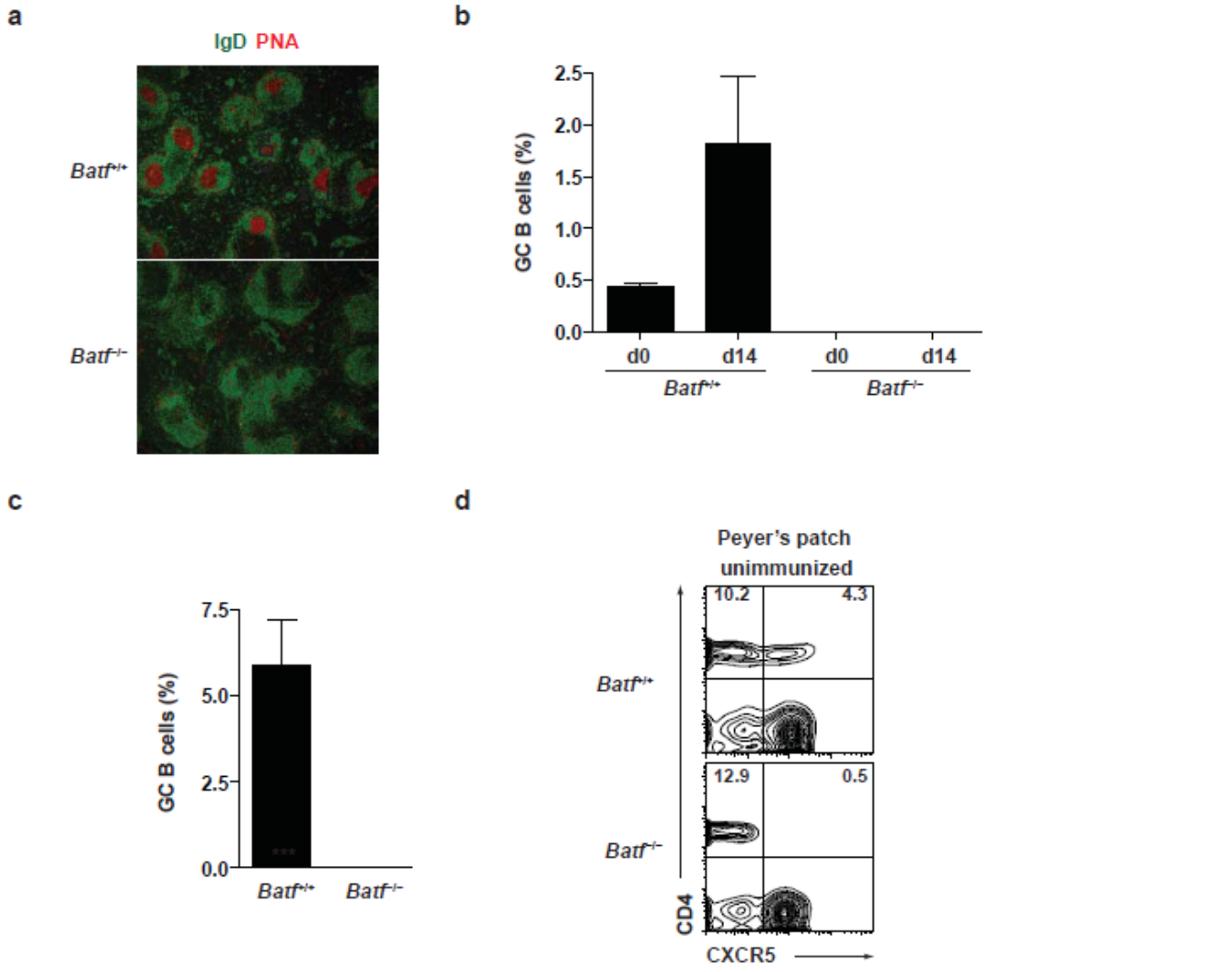
Supplementary Figure 2



Supplementary Fig. 2. *Batf*$^{-/-}$ mice have deficient antibody responses upon immunization. (**a**) TNP-specific antibody responses in *Batf*$^{-/-}$ mice immunized with TNP-Ficoll. TNP-specific IgM and IgG3 titers in serum obtained before (day 0) and on day 14 after immunization were measured by ELISA against plate-bound TNP-conjugated BSA. The TNP-specific titer is defined as the greatest dilution at which average optical density at 405 nm exceeds that of background by 1.5-fold. Each symbol represents an individual mouse; small horizontal bars indicate mean values. Data are representative of two experiments. (**b**) NP-specific antibody responses of *Batf*$^{-/-}$ mice immunized with NP-conjugated chicken γ-globulin in alum. NP-specific IgM and IgG1 titers in serum obtained before (day 0) and on

day 14 after immunization were measured by ELISA against plate-bound NP-conjugated BSA. Data are representative of two experiments.

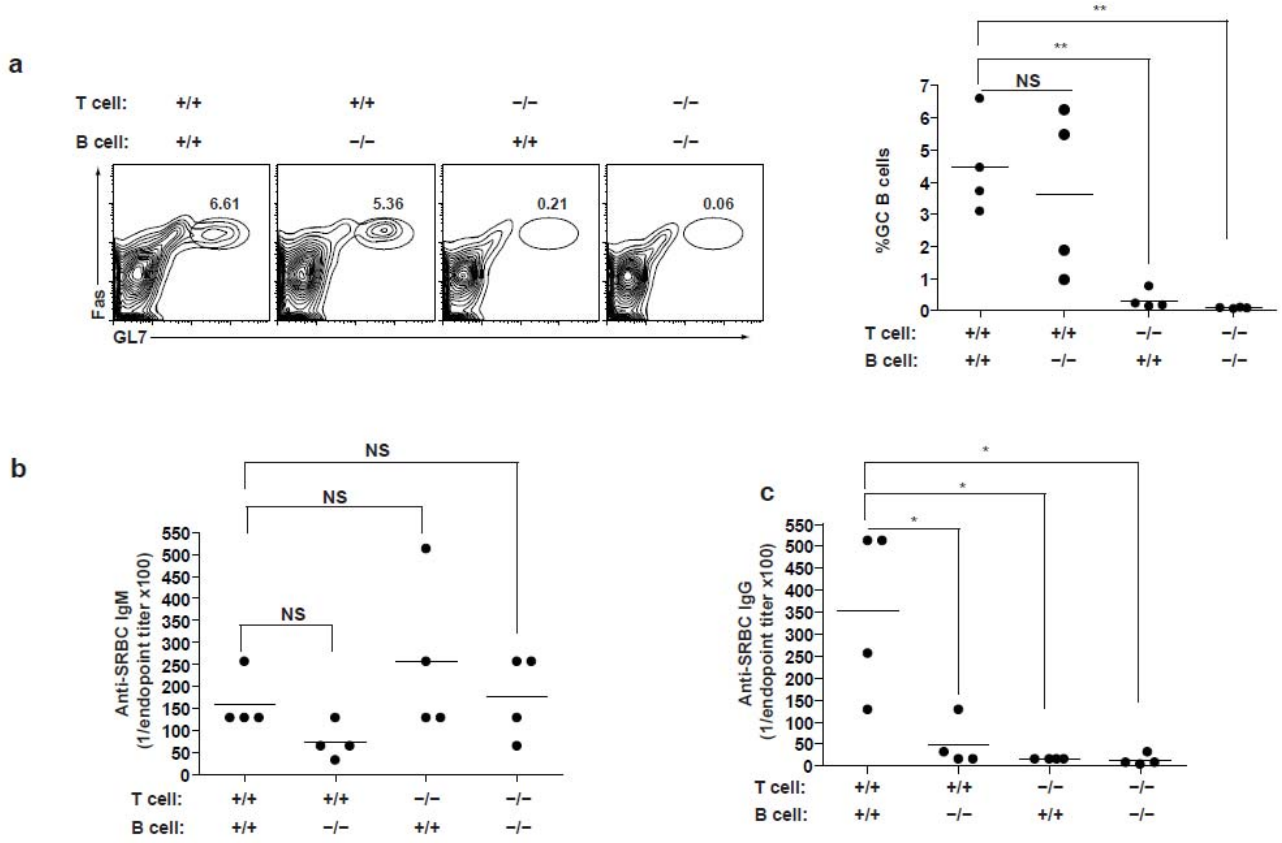
Supplementary Figure 3



Supplementary Fig. 3. *Batf*$^{-/-}$ mice have deficient germinal center B cell development. (**a**) Staining of germinal center in spleen sections prepared 10 d after immunization with sheep red blood cells (SRBC). The sections were stained with anti-IgD and peanut agglutinin (PNA). Original magnification, x100. Data are representative of two experiments. (**b**) Frequency of B220^{+}Fas^{+}GL7^{+} germinal center B cells in spleen before and 14 days after SRBC-immunization. Data are from 3 mice per group and are representative of two experiments. (**c**) Frequency of B220^{+}Fas^{+}GL7^{+} germinal center B cells in peyer's patches from unimmunized mice. Dare are from 3 mice per group and are representative of two

experiments. (**d**) FACS of CD4 and CXCR5 expression in Peyer's patches from unimmunized mice. Data are representative of three experiments.

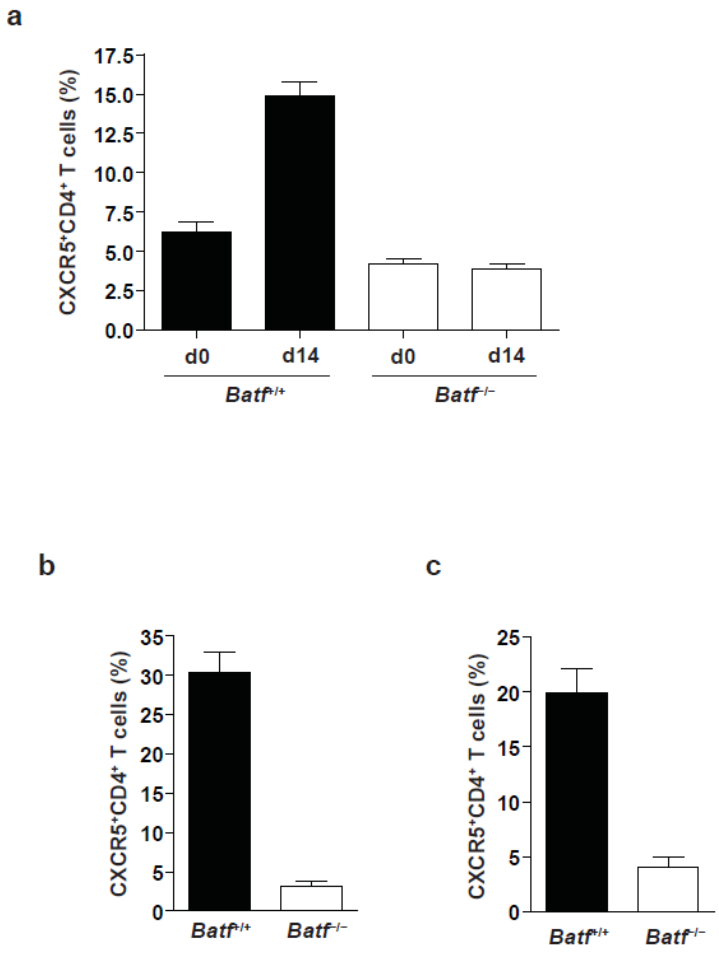
Supplementary Figure 4



Supplementary Fig. 4. Batf controls both B- and T-cell function required for antibody responses. $CD4^+$ T cells and B-cells were purified from *Batf*$^{+/+}$ or *Batf*$^{-/-}$ mice, mixed, and transferred into *Rag2*$^{-/-}$ mice as indicated. (**a**) Development of germinal center B cells in T-and B-cell reconstituted *Rag2*$^{-/-}$ mice 10 days after immunization with SRBC. Left panel; the cells were stained with anti-B220, anti-GL7, and anti-Fas. The data are gated on $B220^+$ cells. Right panel; The frequency of $B220^+Fas^+GL7^+$ cells from 4 mice per group. ***P*<0.005 (unpaired student *t*-test). NS; not significant. (**b** and **c**) SRBC-specific IgM (**b**) and IgG1 (**c**) antibody responses in T-B-cell-reconstituted *Rag2*$^{-/-}$ mice. The serum was collected 14 days after immunization with SRBC and anti-SRBC titer was determined by ELISA

as in Supplementary Figure 2. *P<0.05 (unpaired student t-test). NS; not significant. Data are representative of two experiments.

Supplementary Figure 5



Supplementary Fig. 5. Development of follicular helper T cells is defective in *Batf*$^{-/-}$ mice. (**a**) Frequency of CD4^{+}CXCR5^{+} T cells in spleen before or 14 days after immunization with SRBC. Data are from 3 mice per group and are representative of two experiments. (**b**) Frequency of CD4^{+}CXCR5^{+} T cells in peyer's patches from unimmunized mice. Dare are from 3 mice per group and are representative of two experiments. (**c**) Frequency of CD4^{+}CXCR5^{+} T cells in CD45.2 cells in spleens of SJL mice. SJL mice were transferred with CD4^{+}CD62L^{+} CD45.2^{+} cells from *Batf*$^{+/+}$ or *Batf*$^{-/-}$ mice

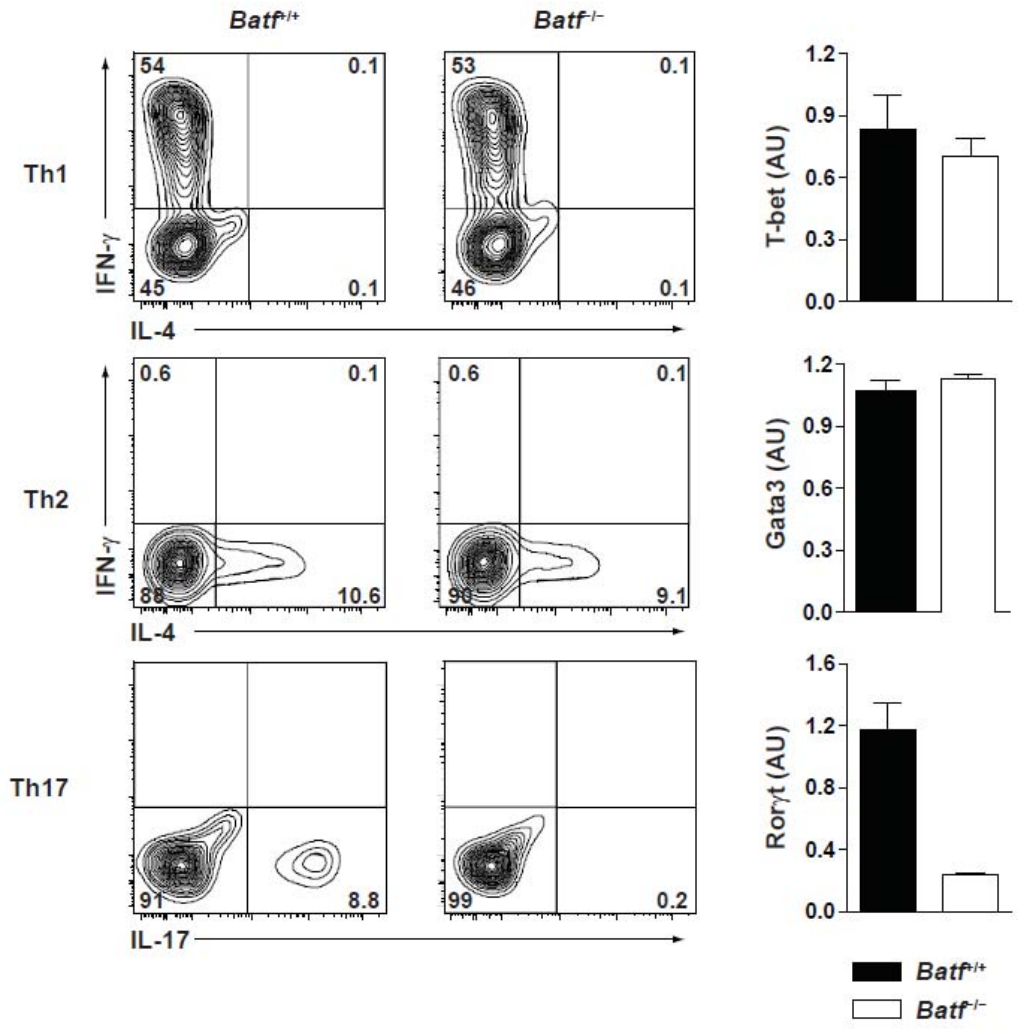
and immunized with SRBC 7 days before. Data are from 3 mice per group and representative of two experiments.

Supplementary Figure 6

Supplementary Fig. 6. Gene expression microarray analysis of activated *Batf*$^{+/+}$ or *Batf*$^{-/-}$ CD4^{+} T cells. Naïve CD4^{+} T cells were purified from *Batf*$^{+/+}$ or *Batf*$^{-/-}$ mice and cultured with anti-CD3/CD28 in the presence of IL-6, anti-IL-4, anti-IFN-γ, and anti-TGF-β. On day 1 or day3, cells were harvested,

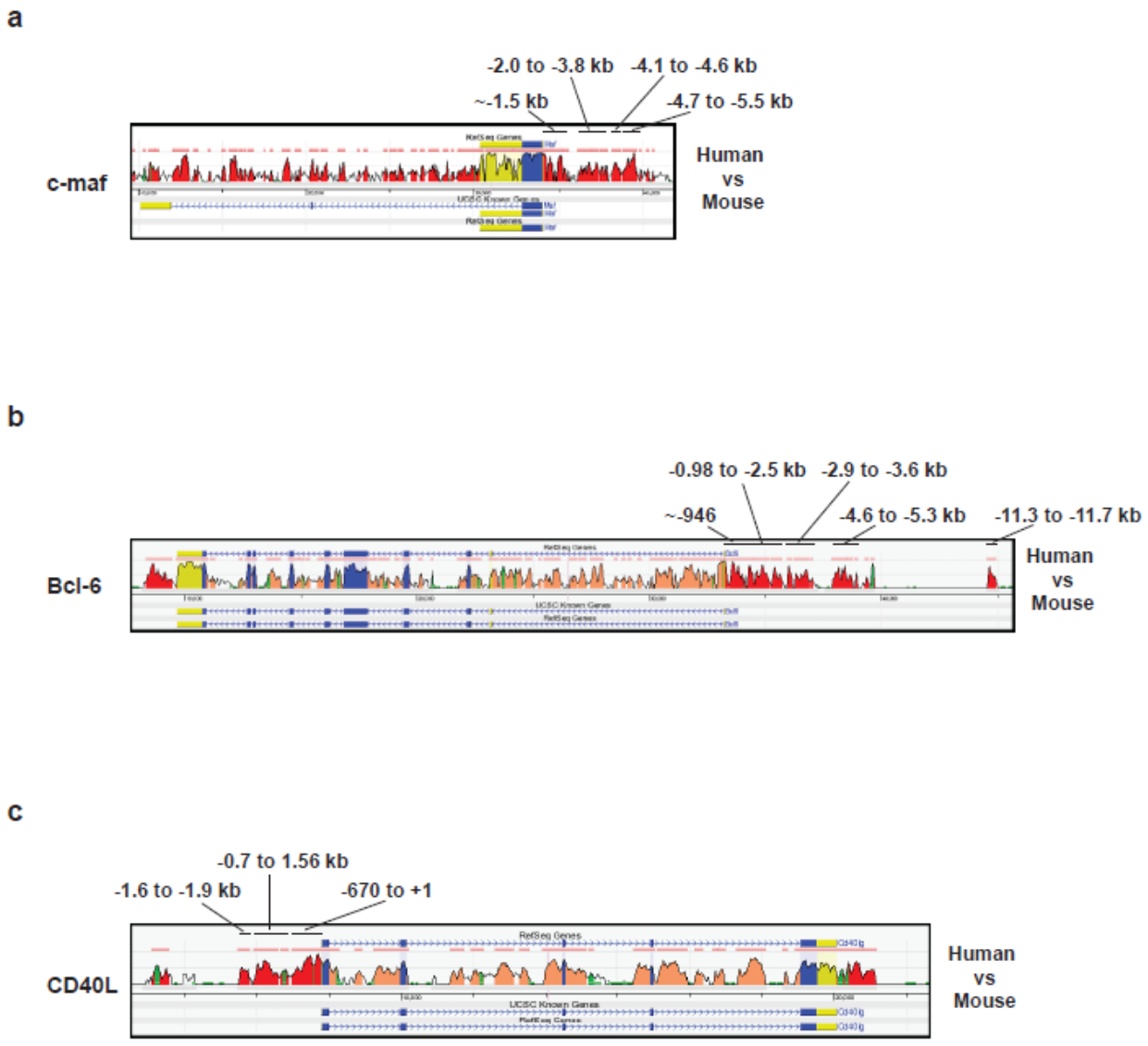
and RNA was prepared and subjected to gene expression microarray analysis. A representative heat map of genes differentially expressed at least 5-fold in *Batf*$^{+/+}$ or *Batf*$^{-/-}$ T cells is presented.

Supplementary Figure 7



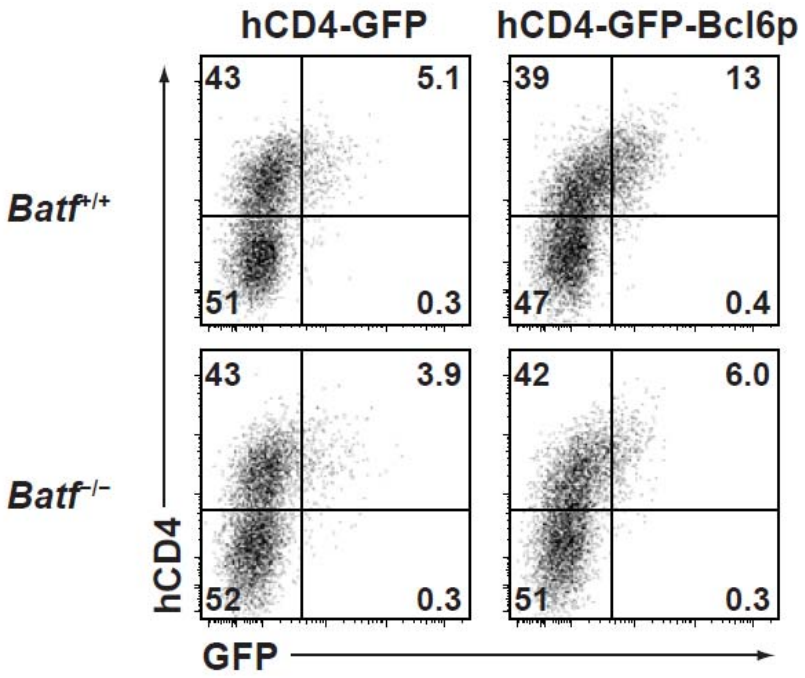
Supplementary Fig. 7. Th2 response is normal in *Batf*$^{-/-}$ CD4^{+} T cells. Naïve CD4^{+} T cells were purified from *Batf*$^{+/+}$ or *Batf*$^{-/-}$ mice and stimulated with anti-CD3/CD28 in the presence of IL-12, IFN-γ and anti-IL-4 (Th1), IL-4, anti-IFN-γ (Th2), or IL-6, TGF-β, anti-IL-4, anti-IFN-γ (Th17). At day 5, cells were harvested and re-stimulated with PMA and ionomycine for 4 hours Expression of intracellular IL-4, IFN-γ, and IL-17 was examined by FACS. Expression of T-bet, GATA-3, RORγt mRNA was measured by q-PCR.

Supplementary Figure 8



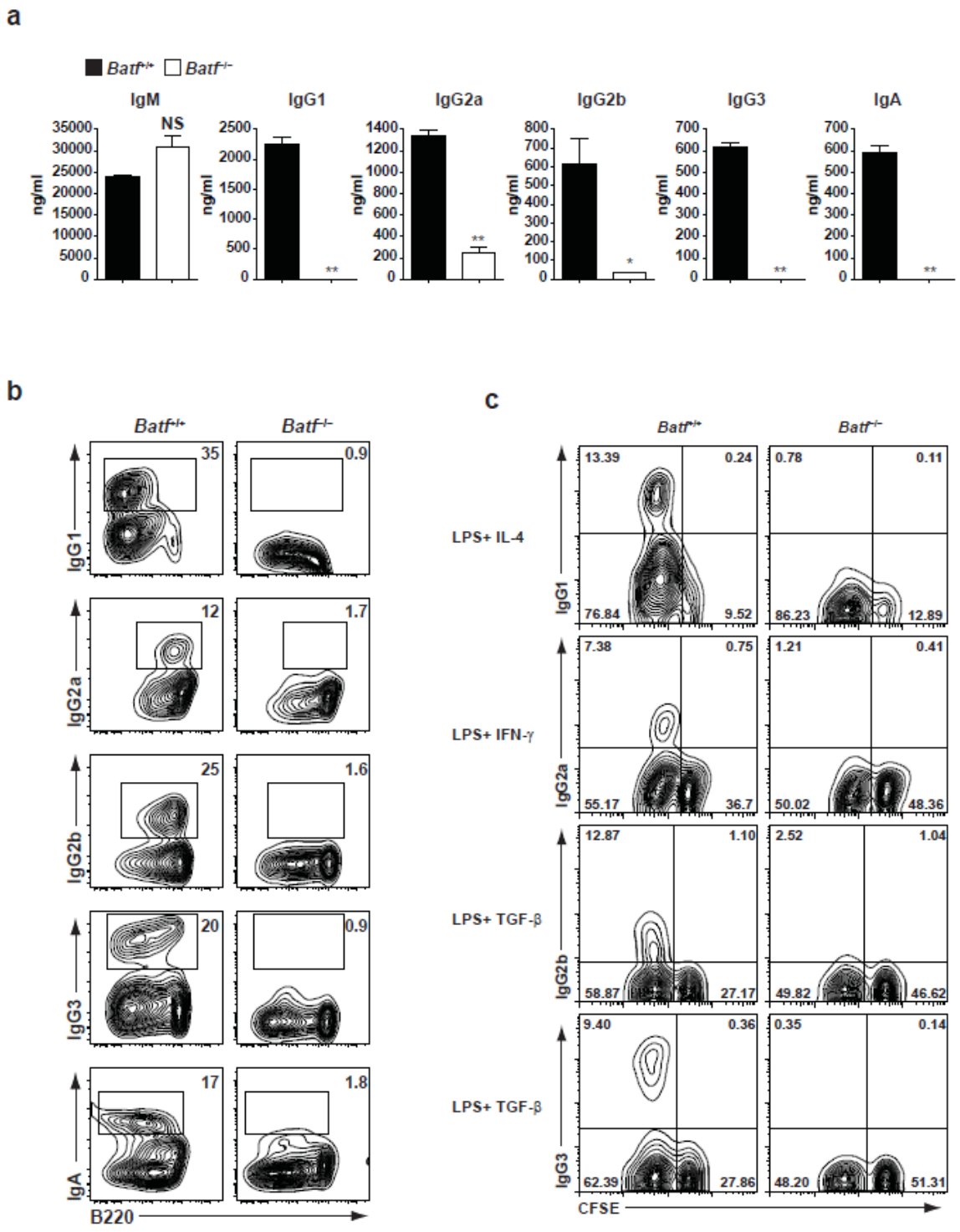
Supplementary Fig. 8. Conserved non-coding regions in Bcl-6 and c-Maf. Shown are vista alignment plots displaying the sequence similarity between human and mouse c-Maf (**a**), Bcl-6 (**b**), and CD40L (**c**) loci. The sequences within these indicated conserved regions were analyzed for identification of potential Batf binding sites.

Supplementary Figure 9



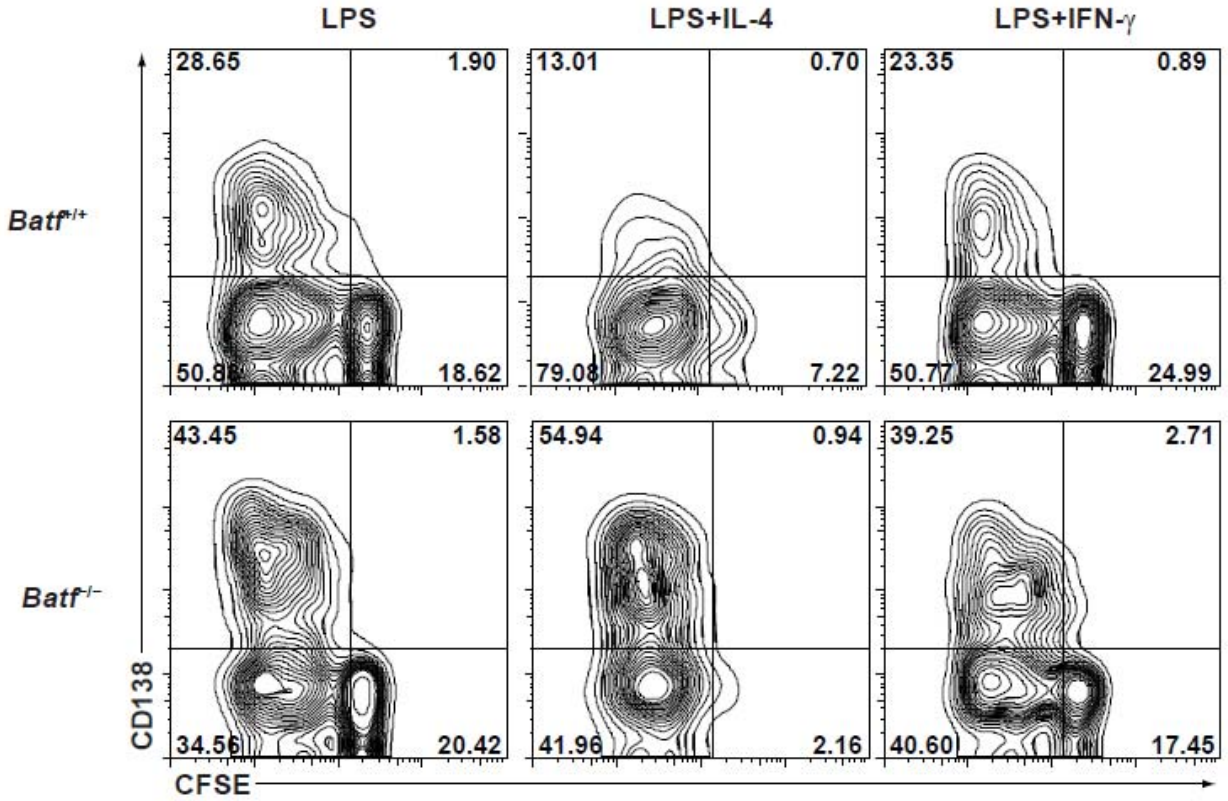
Supplementary Fig. 9. Bcl-6 promoter activity in activated $CD4^+$ T cells. $CD4^+$ T cells were cultured with anti-CD3 and anti-CD28 in the presence of IL-6, anti-IL-4, anti-IFN-γ, and anti-TGF-β and infected with hCD4-pA GFP-RV (left) or hCD4-pA GFP-Bcl-6-promoter-RV (right). hCD4 and GFP expression was examined on day 3 after stimulation. Data are from two independent experiments.

Supplementary Figure 10



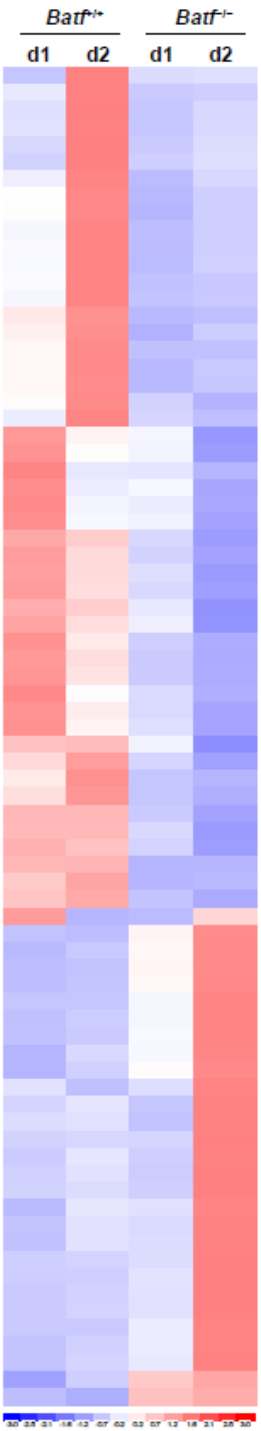
Supplementary Fig. 10. *Batf*$^{-/-}$ B cells proliferate normally but do not express switched Immunoglobulin. (**a**) Immunoglobulin titers in supernatants of cultures of *Batf*$^{+/+}$ or *Batf*$^{-/-}$ B-cells stimulated for 7 days with LPS alone (IgM and IgG3), LPS plus IL-4 (IgG1), LPS plus IFN-γ (IgG2a), or LPS plus TGF-β (IgG2b and IgA). Data are representative of three experiments with three pairs of *Batf*$^{+/+}$ or *Batf*$^{-/-}$ B-cells. **P*<0.01 and ***P*<0.0001 (unpaired student *t*-test). NS; not significant. Data are from three independent experiments (mean and s.e.m.). (**b**) FACS of immunoglobulin expression by *Batf*$^{+/+}$ or *Batf*$^{-/-}$ B-cells stimulated for 4 days with LPS alone (IgG3), LPS plus IL-4 (IgG1), LPS plus IFN-γ (IgG2a), LPS plus TGF-β and BAFF (IgG2b), or LPS plus IL-5, TGF-β, APRIL, and Retinoic acid (IgA). Data are representative of three experiments. (**c**) Splenic B cells from *Batf*$^{+/+}$ or *Batf*$^{-/-}$ mice were labeled with CFSE and cultured for 4 days with LPS alone (IgG3), LPS plus IL-4 (IgG1), LPS plus IFN-γ (IgG2a), or LPS plus TGF-β (Ig2b). CFSE dilution and surface immunoglobulin expression were examined by FACS. Data are representative of three experiments.

Supplementary Figure 11



Supplementary Fig. 11. *Batf*$^{-/-}$ B cells differentiate into CD138^{+} plasma cells. B-cells were purified from spleens of *Batf*$^{+/+}$ or *Batf*$^{-/-}$ mice, labeled with CFSE, and cultured for 4 days with LPS alone, LPS plus IL-4, or LPS plus IFN-γ. CFSE dilution and CD138 expression were examined by FACS. Data are representative of three experiments.

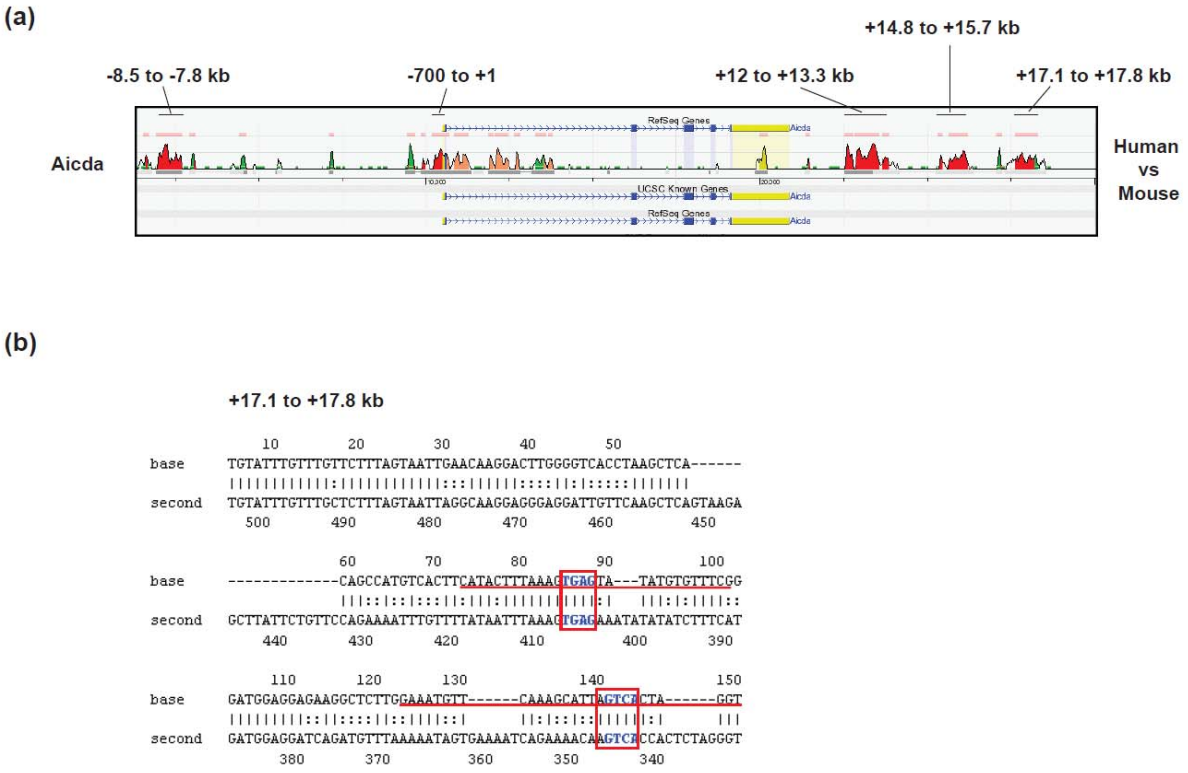
Supplementary Figure 12



Nupr1: nuclear protein 1
Igh-3 /// Ighg: immunoglobulin heavy chain 3 (serum IgG2b) /// Immunoglobulin heavy chain (gamma polypeptide)
Aicda: activation-induced cytidine deaminase
Ighg: Immunoglobulin heavy chain (gamma polypeptide)
Pnkd: paroxysmal nonkinesiogenic dyskinesia
Tg: thyroglobulin
Niban: niban protein
Bhlhb2: basic helix-loop-helix domain containing, class B2
AI324046: expressed sequence AI324046
Ighg1: immunoglobulin heavy constant gamma 1 (G1m marker)
Niban: niban protein
AI324046: expressed sequence AI324046
Igh-6: Immunoglobulin heavy chain complex
Igh-6: Immunoglobulin heavy chain complex
1700048O20Rik: RIKEN cDNA 1700048O20 gene
LOC100046232 /// Nfil3: nuclear factor, interleukin 3, regulated /// similar to NFIL3/E4BP4 transcription factor
Igh /// Ighg: immunoglobulin heavy chain complex /// Immunoglobulin heavy chain (gamma polypeptide)
Auh: AU RNA binding protein/enoyl-coenzyme A hydratase
Auh: AU RNA binding protein/enoyl-coenzyme A hydratase
Fgl2: fibrinogen-like protein 2
Fgl2: fibrinogen-like protein 2
Cxcr7: chemokine (C-X-C motif) receptor 7
Nedd4: neural precursor cell expressed, developmentally down-regulated gene 4
Ifit1: interferon-induced protein with tetratricopeptide repeats 1
Hba-a1 /// Hba-a2: hemoglobin alpha, adult chain 1 /// hemoglobin alpha, adult chain 2
Hbb-b1 /// Hbb-b2: hemoglobin, beta adult major chain /// hemoglobin, beta adult minor chain
1110032F04Rik: RIKEN cDNA 1110032F04 gene
Bat2d: BAT2 domain containing 1
Rtp4: receptor transporter protein 4
Ccl22: chemokine (C-C motif) ligand 22
Ifi44: interferon-induced protein 44
Il6: interleukin 6
Mx1: myxovirus (influenza virus) resistance 1
Ifih1: interferon induced with helicase C domain 1
Gypc: glycophorin C
BIC noncoding mRNA, complete sequence
Cxcl10 /// LOC100045000: chemokine (C-X-C motif) ligand 10 /// similar to Small inducible cytokine B10 precur...
Oasl1: 2'-5' oligoadenylate synthetase-like 1
Ifit3: interferon-induced protein with tetratricopeptide repeats 3
Ddx6: DEAD (Asp-Glu-Ala-Asp) box polypeptide 6
EG545728 /// EG623898 /// Speer1-ps1: spermatogenesis associated glutamate (E)-rich protein 1, pseudogene 1...
Gatm: glycine amidinotransferase (L-arginine:glycine amidinotransferase)
Cdk5r1: cyclin-dependent kinase 5, regulatory subunit (p35) 1
LOC100048346 /// Usp18: ubiquitin specific peptidase 18 /// similar to ubiquitin specific protease UBP43
Mx2: myxovirus (influenza virus) resistance 2
Cpd: carboxypeptidase D
Batf: basic leucine zipper transcription factor, ATF-like
Irf7: interferon regulatory factor 7
Cdk5r1: cyclin-dependent kinase 5, regulatory subunit (p35) 1
Rgs13: regulator of G-protein signaling 13
Zyx: zyxin
Tns3: tensin 3
Serpinb7: serine (or cysteine) peptidase inhibitor, clade B, member 7
Kit: kit oncogene
D0H4S114: DNA segment, human D4S114
Upb1: ureidopropionase, beta
OTTMUSG00000000971: predicted gene, OTTMUSG00000000971
Slamf9: SLAM family member 9
Il10: interleukin 10
Ccl3: chemokine (C-C motif) ligand 3
AA517650: expressed sequence AA517650
Smok3a /// Smok3b: sperm motility kinase 3A /// sperm motility kinase 3B
Sdc1: syndecan 1
Lag3: lymphocyte-activation gene 3
Sdc1: syndecan 1
Adamts16: a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 16
Gadd45g: growth arrest and DNA-damage-inducible 45 gamma
Lrrc8a /// Phyhd1: phytanoyl-CoA dioxygenase domain containing 1 /// leucine rich repeat containing 8A
Mm.210787.1
2010300C02Rik: RIKEN cDNA 2010300C02 gene
Wnt10a: wingless related MMTV integration site 10a
Phlda1: pleckstrin homology-like domain, family A, member 1
Pdcd1: programmed cell death 1
Ccl4: chemokine (C-C motif) ligand 4
Chst1: carbohydrate (keratan sulfate Gal-6) sulfotransferase 1
Crisp3: cysteine-rich secretory protein 3
Jun: Jun oncogene
S100a6: S100 calcium binding protein A6 (calcyclin)

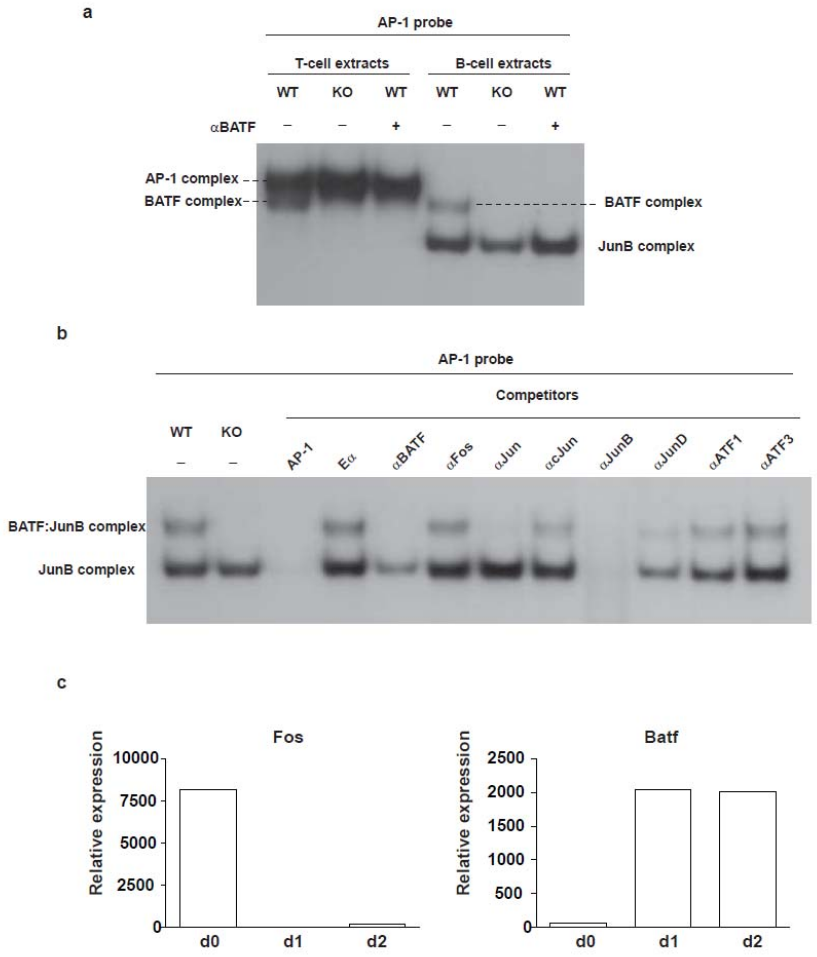
Supplementary Fig. 12. Gene expression microarray analysis of activated *Batf*$^{+/+}$ or *Batf*$^{-/-}$ B cells. B cells were purified from *Batf*$^{+/+}$ or *Batf*$^{-/-}$ mice and cultured with LPS. On day 1 or day2, cells were harvested and subjected to gene expression microarray analysis. A representative heat map of genes differentially expressed at least 5-fold in *Batf*$^{+/+}$ or *Batf*$^{-/-}$ B cells is presented.

Supplementary Figure13



Supplementary Fig. 13. Conserved non-coding regions in AID locus. (**a**) Vista alignment plot displaying the sequence similarity between human and mouse AID locus. The conserved regions that were used for identification of potential Batf binding sites are shown. (**b**) Sequence alignment of a region of +17.1 to +17.8 kB. The conserved TGAG/C sequences are shown in blue in red boxes and the probes that were used for this region are underlined with red lines.

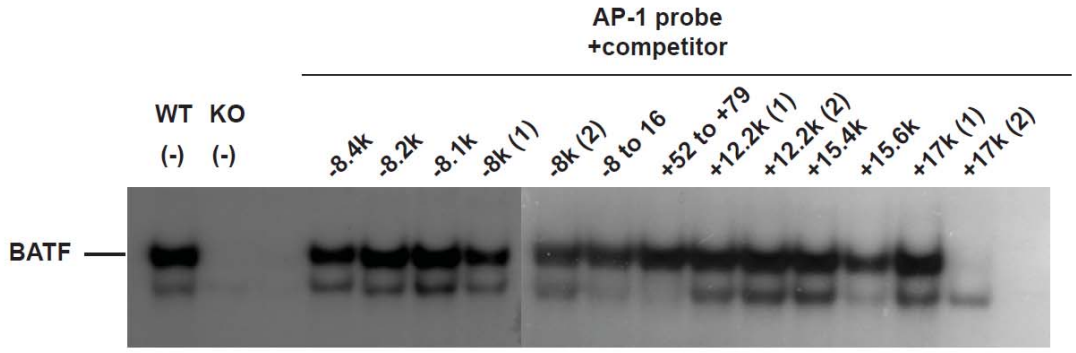
Supplementary Figure 14



Supplementary Fig. 14. EMSA assay for Batf binding in B cells. (**a**) Nuclear extracts were prepared from T cells that were activated with αCD3/αCD28 for 1 day or B cells that were activated with LPS plus IL-4 for 1 day and were analyzed for DNA binding ability to a consensus AP-1 probe by EMSA. (**b**) B cell nuclear extracts were analyzed for DNA binding ability to a consensus AP-1 probe in the presence of AP-1 or Eα oligos or the indicated antibodies. (**c**) Microarray data from B cells presented in Supplementary figure 12 of B cells activated with LPS and harvested on day 1 (D1) or day 2 (D2) after activation was normalized with microarray data of unstimulated B cells (D0) purified at the same

time. Shown are the normalized expression values exported from dCHIP analysis software for Fos and Batf on the indicated day.

Supplementary Figure 15



Supplementary Fig. 15. Identification of potential Batf binding sites AID locus. B cells purified from *Batf*$^{+/+}$ or *Batf*$^{-/-}$ mice were cultured with LPS plus IL-4 for 24 hours. Nuclear extracts were analyzed for DNA binding ability to a consensus AP-1 probe by EMSA. Annealed double-stranded oligonucleotides, between 29 and 32 bp in length, from the indicated regions of AID locus were used as competitors. Data are representative of two experiments.

Supplementary Table 1. Primers for real-time qRT-PCR and ChIP-qPCR

	Forward primer	Reverse primer
Real-time qRT-PCR primers		
c-maf	5'-AGCAGTTGGTGACCATGTCG-3'	5'-TGGAGATCTCCTGCTTGAGG-3'
Bcl-6	5'-AGGCCTCCTTCCGCTACAAG-3'	5'-CAAATGTTACAGCGATAGGGTTTCT-3'
Blimp-1	5'-TCTGTTCAAGCCGAGGCATCC-3'	5'-TCTTGGGAACTGTGTCATTAG-3'
CXCR5	5'-CGACATCAGACAGTGACCAGCC-3'	5'-GTCCTGTAGGGGAATCTCCGTG-3'
IL-21	5'-GCCAAACTCAAGCCATCAAACC-3'	5'-TTCTCATACGAATCACAGGAAGGG-3'
IRF4	5'-GCCCAACAAGCTAGAAAG-3'	5'-TCTCTGAGGGTCTGGAAACT-3'
AID	5'-TGCTACGTGGTGAAGAGGAG-3'	5'-TCCCAGTCTGAGATGTAGCG-3'
HPRT	5'-AGCCTAAGATGAGCGCAAGT-3'	5'-TTACTAGGCAGATGGCCACA-3'
Germline transcripts		
Iμ-Cμ	5'-ACCTGGGAATGTATGGTTGTGGCTT-3'	5'-TCTGAACCTTCAAGGATGCTCTTG-3'
Iγ3-Cγ3	5'-AACTACTGCTACCACCACCACCAG-3'	5'-ACCAAGGGATAGACAGATGGGG-3'
Iγ1-Cγ1	5'-GGCCCTTCCAGATCTTTGAG-3'	5'-ATGGAGTTAGTTTGGGCAGCA-3'
Iγ2b-Cγ2b	5'-GATGGGGAGGAGTTGGCAGAT-3'	5'-CGGAGGAACCAGTTGTATC-3'
Iγ2a-Cγ2a	5'-GCTGATGTACCTACCGAGAGA-3'	5'-GCTGGGCCAGGTGCTCGAGGTT-3'
Iα-Cα	5'-CAAGAAGGAGAAGGTGATTCAG-3'	5'-GAGCTGGTGGGAGTGTCAGTG-3'
Post switch transcripts		
Iμ-Cγ3	5'-CTCGGTGGCTTTGAAGGAAC-3'	5'-ACCAAGGGATAGACAGATGGGG-3'
Iμ-Cγ1	5'-ACCTGGGAATGTATGGTTGTGGCTT-3'	5'-ATGGAGTTAGTTTGGGCAGCA-3'
Iμ-Cγ2b	5'-ACCTGGGAATGTATGGTTGTGGCTT-3'	5'-CGGAGGAACCAGTTGTATC-3'
Iμ-Cγ2a	5'-ACCTGGGAATGTATGGTTGTGGCTT-3'	5'-GCTGGGCCAGGTGCTCGAGGTT-3'
Iμ-Cα	5'-ACCTGGGAATGTATGGTTGTGGCTT-3'	5'-TAATCGTGAATCAGGCAG-3'
ChIP-qPCR		
Iμ	5'-GCAGGTCGGCTGGACTAACT-3'	5'-CAACCTTGTTCCCTTAATTTTGCT-3'
Iγ3	5'-CTACTGCCTCTTCTCTTACCCTGAA-3'	5'-TCCTTGGGTGTAGAGACACTGTCA-3'
Iγ1	5'-CAGGTGCACAGAGAAACAGGAGTA-3'	5'-GTGAGGCGGTACCCTTGAGA-3'
Iγ2b	5'-TGGGGCAAGGACTGTGAATC-3'	5'-GGCTCTCTCCAGTCTCTCAGCT-3'
Iγ2a	5'-GATCCCTGCCCAGCTTCTCT-3'	5'-TGCTCCGGCTTCTGACTGT-3'
Iα	5'-ACACACCTGTCTCCACCACA-3'	5'-TGGCTGGAAGCTGTTTTTCT-3'
HS3A	5'-CACACACTGGGCTGCAACTG-3'	5'-TGTCTCCATTCTGTGCCTCTGA-3'
HS1,2	5'-CCAGTTATCACCACTGCTGGAA-3'	5'-GTGTTGAGCCACCCATCCTT-3'
HS3B	5'-CCTTTCTGATGAAGCCCTGTCT-3'	5'-CAGCTATTCTGGCAGAGGACTAGA-3'
HS4	5'-GCCAGGGCCTTCTAACCAA-3'	5'-GGTTCAGCTCATGGCTTCTCA-3'

Supplementary Table 2. Oligos for EMSA

	Top (sequence 5' to 3')	Bottom (sequence 5' to 3')
c-maf		
-47 to -70	GGGCAAGCTGGCTCACCCGCTGGCCA	GGGTGGCCAGCGGGTGAGCCAGCTTG
-951 to -980	GGCACGGGTGCTATAAAACTCAGCAAT	GGAATTGCTGAGTTTTATAGCACCCGT
-1.0 k	GGCGGAGAGTGCCAGTCAATTTCCCATT	GGAAATGGGAAATTGACTGGCACTCTCC
-1.1 k (1)	GGGCTGTGATTGACAGCTCCGAAAAGTTT	AGGAAACTTTTCGGAGCTGTCAATCACAG
-1.1 k (2)	GGTGTCCCAGCTGACAGTCAGCTGATTGG	GGCCCAATCAGCTGACTGTCAGCTGGGAC
-2.7 k	GGTGGCGCTGTTGAGGTAAAAACCAA	GAGTTGGTTTTTACCTCAACAGCGCC
-2.9 k	GGACAGGCACAGGTCTCTCAGCCAGAA	GGTATTCTGGCTGAGAGACCTGTGCCTG
-3.1 k	GGCGAAGTCAGGATTTTCTGAGAATTA	AGGTAATTCTCAGAAAATCCTGACTTC
-3.2 k	GGCTTAATATATGACTTAAGTGTCCGA	GGTTCGGACACTTAAGTCATATATTAA
-3.5 k	GGTCACCTCAGTATTGACATAGTCTT	GTGAAGACTATGTCAATACTGAGGTG
-4.3 k	GGTGCTAAATTAAAATGAGTGCTTGCA	GGTTGCAAGCACTCATTTTAATTTAGC
-4.5 k	GGGTTGAACTGGTCAATAATGACAAGCG	GTGCGCTTGTCATTATTGACCAGTTCAA
-5.4 k	GGCAGAAATATATTCTCAGGCATAATG	GTGCATTATGCCTGAGAATATATTTCT
-5.5 k	GAGTAATTCATGAAGTGACTATTTATG	GAGCATAAATAGTCACTTCATGAATTA
Bcl-6		
-339 to -368	GGCAAATTAGTTCTCAGAATTCCAGAG	GGCCTCTGGAATTCTGAGAACTAATTT
-300 to -331	GGTACAGCGAAGACGCCGACGTCACGGAG	GGGCTCCGTGACGTCGGCGTCTTCGCTGT
-276 to -304	GGCCCACGTGACGGCGGCGGAGCGGG	GGGCCCGCTCCGCCGCCGTCACGTGG
-2.3 kb	GGATCAATTTGACAAAGTCACCGTGT	GGACACGGTGACTTTGTCAAATTGA
-2.4 kb	GGAATACTCTAAAATGAGAGGGAAGGGG	GGTCCCCTTCCCTCTCATTTTAGAGTAT
-1.7 kb (1)	GAGTCTCACTCATCCAGGGATGAGTAGGAG	GGCCTCCTACTCATCCCTGGATGAGTGAGA
-1.2 kb	GGAATTTCCTGAGAGTCAACAGTAACAGA	GGCTCTGTTACTGTTGACTCTCAGGAAAT
-1.8 kb	GGCCAGAACAGCCTGACCTTTGAAAGA	GGCTCTTTCAAAGGTCAGGCTGTTCTG
-1.7 kb (2)	GGATATTATTTAGCTCACACCCTTCTTG	GGGCAAGAAGGGTGTGAGCTAAATAATA
-2.9 kb	GGGTTTGAGGTATGAGAAGGGTAAATT	GGGAATTTACCCTTCTCATACCTCAAA
-3.5 kb	GGAGTCCCCGATCCTGAGTATTAGCAA	TGGTTGCTAATACTCAGGATCGGGGAC
-4.9 kb	GGCACCCTGAGTTTACAAATACTCAAGTCC	GGGAGGGACTTGAGTATTTGTAAACTCAGG
-5.1 kb	GGTAGGCTTATGCAGAGTCAGGTGTACAG	GGTCTGTACACCTGACTCTGCATAAGCCT
-5.3 kb	GGGACGGTTTGATGACTTGAATTTCAG	GGCCTGAAATTCAAGTCATCAAACCGT
-5.3 kb (2)	GGCCTCTGCAGCCTGACCTCAGGGGA	GCGTCCCCTGAGGTCAGGCTGCAGAG
-11.7 kb	GGATTTTGATAACTCACTCATCACTTC	GGTGAAGTGATGAGTGAGTTATCAAAA
-11.6 kb	GGAAGAGTAAAGTTAGCTCAGAATAATTG	GAGCAATTATTCTGAGCTAACTTTACTCT

Supplementary Table 2 (cont.)

	Top (sequence 5' to 3')	Bottom (sequence 5' to 3')
CD40L		
-38 to -64	GGCCACTTTGACAGTCTTCTCATGCTG	AGGCAGCATGAGAAGACTGTCAAAGTG
-62 to -89	GCTCTTAACTAATCCTGAGTAAGGCGGC	GTGGCCGCCTTACTCAGGATTAGTTAAG
-367 to -392	GGTAGTGGACTCATTTGTCACTTTCCTT	GGCAAGGAAAGTGACAAATGAGTCCACT
-507 to -532	GGATCAAAGTCCTGAGAAGCAATTAAGG	GGCCCTTAATTGCTTCTCAGGACTTTGA
-541 to -565	GGTAGAAAGATTTTATTGAGCTTAGAG	GGTCTCTAAGCTCAATAAAATCTTTCT
-564 to -588	GGCATGTAGTTTTGACTAGTAAAGCTA	GGCTAGCTTTACTAGTCAAAACTACAT
-1.0 kb	GGAATCATTTGGAAAACTCATTTCATA	GGCTATGAAATGAGTTTTCCAAATGAT
-1.1 k	GCGAAAACAGTGTCACAACCTGAGGTG	GGCCACCTCAGGTTGTGACACTGTTTT
-1.4 k	GGAACCAATGCTTCTGACTTGACTGAT	GTGATCAGTCAAGTCAGAAGCATTGGT
AID		
-8.4 kb	GGGCCACAAAGTGAGAAAAACAAAAAT	GCGATTTTTGTTTTTCTCACTTTGTGG
-8.2 kb	GTGACCCGAGGAGTCATGTCTGAGTGT	GGCACACTCAGACATGACTCCTCGGGT
-8.1 kb	GCGAAACCTCACCTGTGTGTCTCATAGG	GGCCCTATGAGACACACAGGTGAGGTTT
-8.0 kb (1)	GGCTCGATTTCCAAGTCACAGTATTTTT	GGCAAAAATACTGTGACTTGGAAATCGA
-8.0 kb (2)	GGCAATAGAAGTTAATGAGGGGAAAGAGA	GGTTCTCTTTCCCCTCATTAACTTCTATT
-8 to -16	GGGCCAGTGCTCTGTCACACAACAG	GTGCTGTTGTGTGACAGAGCACTGG
+52 to +79	GAGACTTTGAGGGAGTCAAGAAAGTCACG	GAGCGTGACTTTCTTGACTCCCTCAAAGT
+12.2 kb (1)	GGTAAGTCTACAAGAGGAGTCAGTTTAGA	GGGTCTAAACTGACTCCTCTTGTAGACTT
+12.2 kb (2)	GGTTAGACCCCTAGTGTTGTCAGAGTGTG	GGTCACACTCTGACAACACTAGGGGTCTA
+15.4 kb	GAGGGAACCTTAGTGGAGTCACAGGCCA	GGATGGCCTGTGACTCCACTAAGGTTCC
+15.6 kb	GGGGTTTTAAGACTGTCATGGTCCATGC	GGTGCATGGACCATGACAGTCTTAAAAC
+17 kb (1)	GGCATACTTTAAAGTGAGTATATGTGTT	GGAAACACATATACTCACTTTAAAGTAT
+17 kb (2)	GGAATGTTCAAAGCATTAGTCACTAGGT	GTGACCTAGTGACTAATGCTTTGAACAT