Supplemental Procedures

Mice

All mice used in the study are on a C57BL/6 genetic background. *Mir155*$^{fl/fl}$ mice were created by Taconic by introducing loxP sites upstream and downstream of the miR-155 producing exon of *BIC* (schematics and sequence information in **Figure 4, S4** and **Table S1**). In brief, 30 μg of NotI-linearized final targeting vector DNA was electroporated into ~10^7 C57BL/6 ES cells and selected with 200 mg/ml G418. Two plates of G418 resistant ES clones (~192) were selected for screening. The primary ES screening was performed with 3' PCR and distal LoxP PCR. Approximately twenty potential targeted clones were identified from one plate. Six clones were expanded for further analysis. Upon completion of the ES clone expansion, additional Southern and PCR confirmation analysis was performed. Based on this analysis, all six expanded clones were confirmed for homologous recombination with single neo integration. Flp electroporations were performed on two clones. Two Neo deleted clones were identified and confirmed by PCR upon expansion (**Figure S4**).

Histological analyses

Spleen, liver and kidney samples were placed in a 10% formalin solution immediately after harvesting, fixed for 24 hours, rinsed in PBS and placed in 70% ethanol.

Flow Cytometry

Fluorophor-conjugated antibodies against CD45.1, CD45.2, CD11b, Gr1, CD4, CD3ε, CD8, CD62L, Icos, CD44 and CD69 (all from Biolegend) were used to stain RBC-

depleted splenocytes, LN cells, BM cells and peripheral blood cells. Germinal center B cells were identified by staining with antibodies against GL7 (ebioscience), FAS (BD Pharmagen), IgD (Biolegend) and B220 (Biolegend). The Tfh cells were identified by staining with antibodies against CD3ε, CD4, CXCR5 (ebioscience) and PD-1 (Biolegend), or CD3ε, CD4, Icos, PD-1 and Bcl6 (BD Pharmagen), and gating based on isotype or unstained controls.

ELISAs

Briefly, serum samples were added in a 5-fold serial dilution onto plates pre-coated with 4 μg/ml Ova. After incubation and washing, biotinylated anti-mouse IgG or IgG1 antibodies (SouthernBiotech) were added and incubated for 2 hrs at room temperature followed by 1 hr of Streptavidin-HRP (SouthernBiotech) incubation. Detection reagent and stop solution (eBioscience) were added according to the manufacturer's instructions, and the signal detected using a plate reader.

RNA Sequencing

For the RNA-seq experiments, $CD3\varepsilon^{+}CD4^{+}$ T cells were FACS sorted (using a BD FACSAria II) from the spleens of 10 months old mice of the indicated genotypes. In a separate experiment, $CD4^{+}$ T cells were first purified from both Wt and *Mir155*$^{-/-}$ mouse spleens on day 8 post Ova-immunization by using a $CD4^{+}$ T cell negative selection kit (Miltenyi). $CD4^{+}CXCR5^{+}PD1^{+}$ Tfh and $CD4^{+}CXCR5^{-}PD1^{-}$ non-Tfh cells were FACS sorted from Wt and *Mir155*$^{-/-}$ $CD4^{+}$ T cells (n=7 for each genotype per sample).

For the reference generation, Ensembl transcript annotations for mm10 were downloaded from the UCSC table browser (release 73). Gene annotations were created by merging transcripts with the same gene identifier using the USeq (v8.8.7) MergeUCSCGeneTable application. All possible splice junction sequences from each gene's transcripts were generated with the USeq (v8.8.7) MakeTranscriptome application using a radius of 46. These splice junction sequences were added to standard mm10 chromosome sequences and run through novoindex (v2.8) to create the transcriptome reference index.

For the RNA-Seq analyses, reads were aligned to the transcriptome reference index described above using Novoalign (v2.08.01), allowing up to 50 alignments for each read. The USeq (v8.8.7) SamTranscriptomeParser application was used to select the best alignment for each read and to convert the coordinates of reads aligning to splices back to genomic space. Differential gene expression was measured using the USeq (v8.8.3) DefinedRegionDifferentialSeq (DRDS) application, modified to report non-variance stabilized log2 ratios. Briefly, DRDS first determines the numbers of reads aligning to each gene annotation. DRDS then calls DESeq (v1.12.1), which normalizes the signal and determines differential expression.

Immunoblotting

$CD4^+$ T cells were isolated from mouse spleens using a $CD4^+$ T cell negative selection kit (Miltenyi). Cells were cultured in complete RPMI supplemented with plate-bound αCD3ε (5 μg/ml) and soluble αCD28 (2 μg/ml) for activation. RIPA buffer (50 mM Tris-HCl pH 7.4, 1% Nonidet P40, 150 mM NaCl, 1 mM EDTA, 10% sodium deoxycholate,

freshly added with 1 mM phenylmethylsulphonyl fluoride (PMSF), 1 mM Na_3VO_4 and 1 mM NaF) was used for lysis. Extract was used for Immunoblotting.

Ova Immunization

Eight days after immunization, mice were sacrificed and analyzed individually. Another group of mice was bled on days 14, 21 and 28 to detect Ova-specific total IgG or IgG1 antibodies. Mice were boosted on day 21 with Ova in PBS.

Figure S1, related to Figure 1

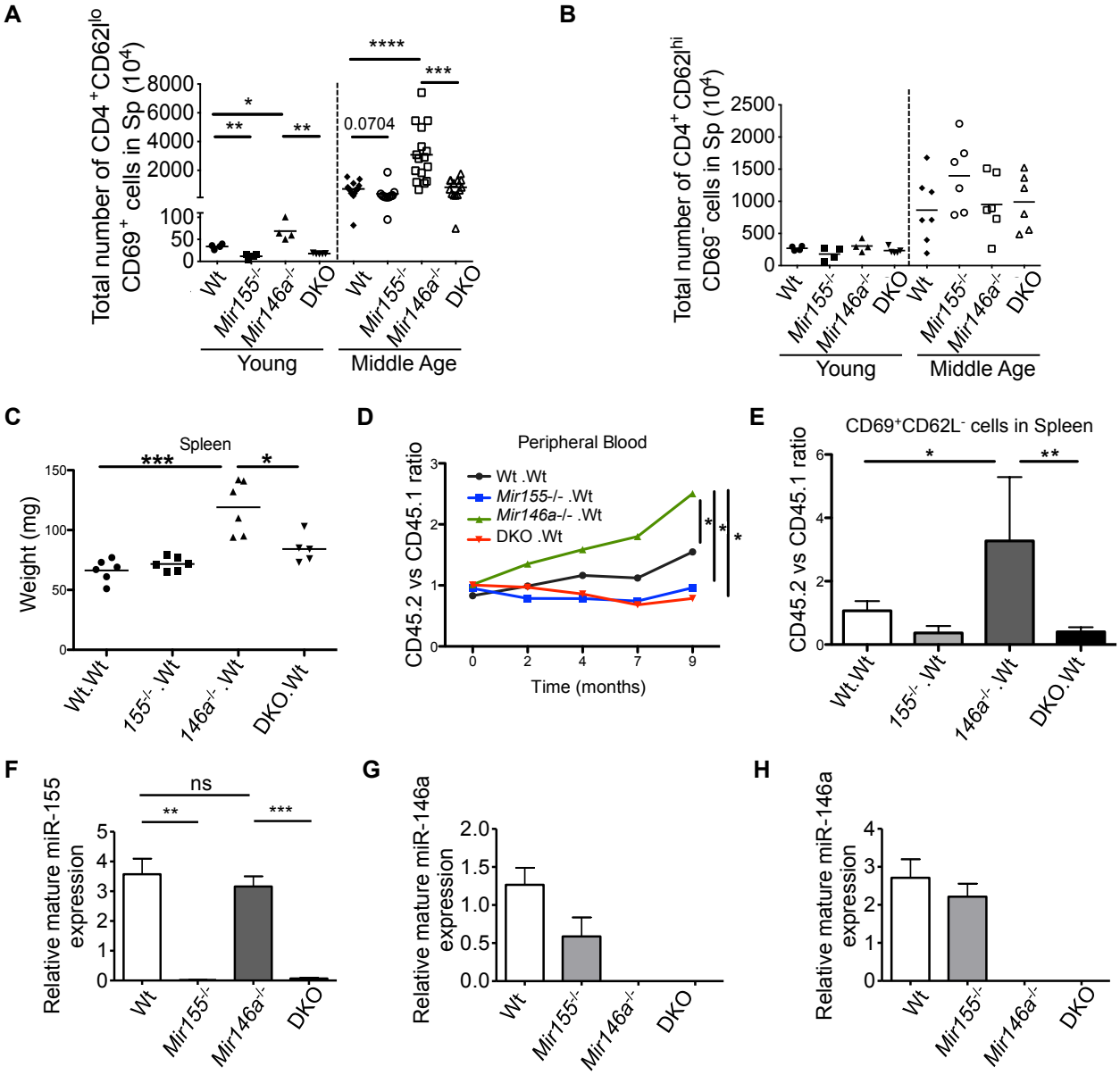

Figure S1, related to Figure 1. miR-155 is required for activated T cell expansion in *Mir146a*$^{-/-}$ mice. (**A-B**) Number of activated (CD69^{+}CD62L^{lo}) or naïve (CD69-CD62L^{hi}) CD4^{+} T cells in spleens from young and middle-aged mice. (**C**) Measured spleen weights at time of necropsy (10 months) following BM reconstitution with the indicated genotypes. (**D**) The ratio of CD45.2 (Wt or experimental BM) to CD45.1 (Wt control BM) WBCs in the peripheral blood of reconstituted mice were measured via flow cytometry at 0, 2, 4, 7, and 9 months of age. (**E**) CD45.2/CD45.1 ratio of activated CD4^{+} T cells (CD62L^{-} and CD69^{+}) in the spleens of 10-month old recipients. (**F-H**) Relative expression of mature miR-155 (F) and miR-146a in sorted B220^{+} B cells (H), or miR-146a in sorted CD4^{+} T cells (G), from the spleens of middle-aged mice.

Figure S2, related to Figure 2

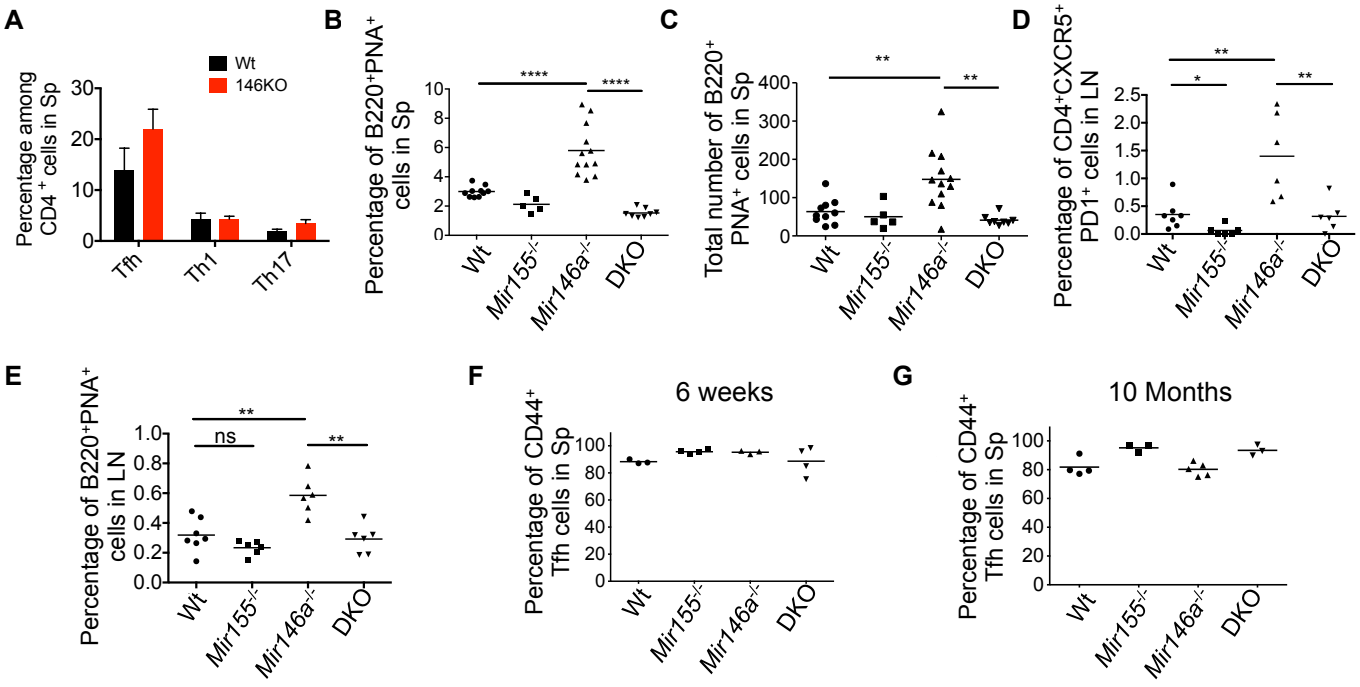

Figure S2, related to Figure 2. Tfh and GC B cell populations in Wt, *Mir155*$^{-/-}$, *Mir146a*$^{-/-}$ and DKO mice. (**A**) Average percentage of Tfh, Th1 and Th17 cells in middle-aged mice of the indicated genotypes as assessed by intracellular staining. (**B**) Average percentage of PNA^{+} GC B cells in middle-aged spleens. (**C**) Average total number of PNA^{+} GC B cells in middle-aged spleens. (**D**) Average percentage of Tfh cells in middle-aged LNs. (**E**) Average percentage of PNA^{+} GC B cells in middle-aged LNs. (**F**) Average percentage of CD44^{+} Tfh cells in young mice. (**G**) Average percentage of CD44^{+} Tfh in middle-aged mice.

Figure S3, related to Figure 3

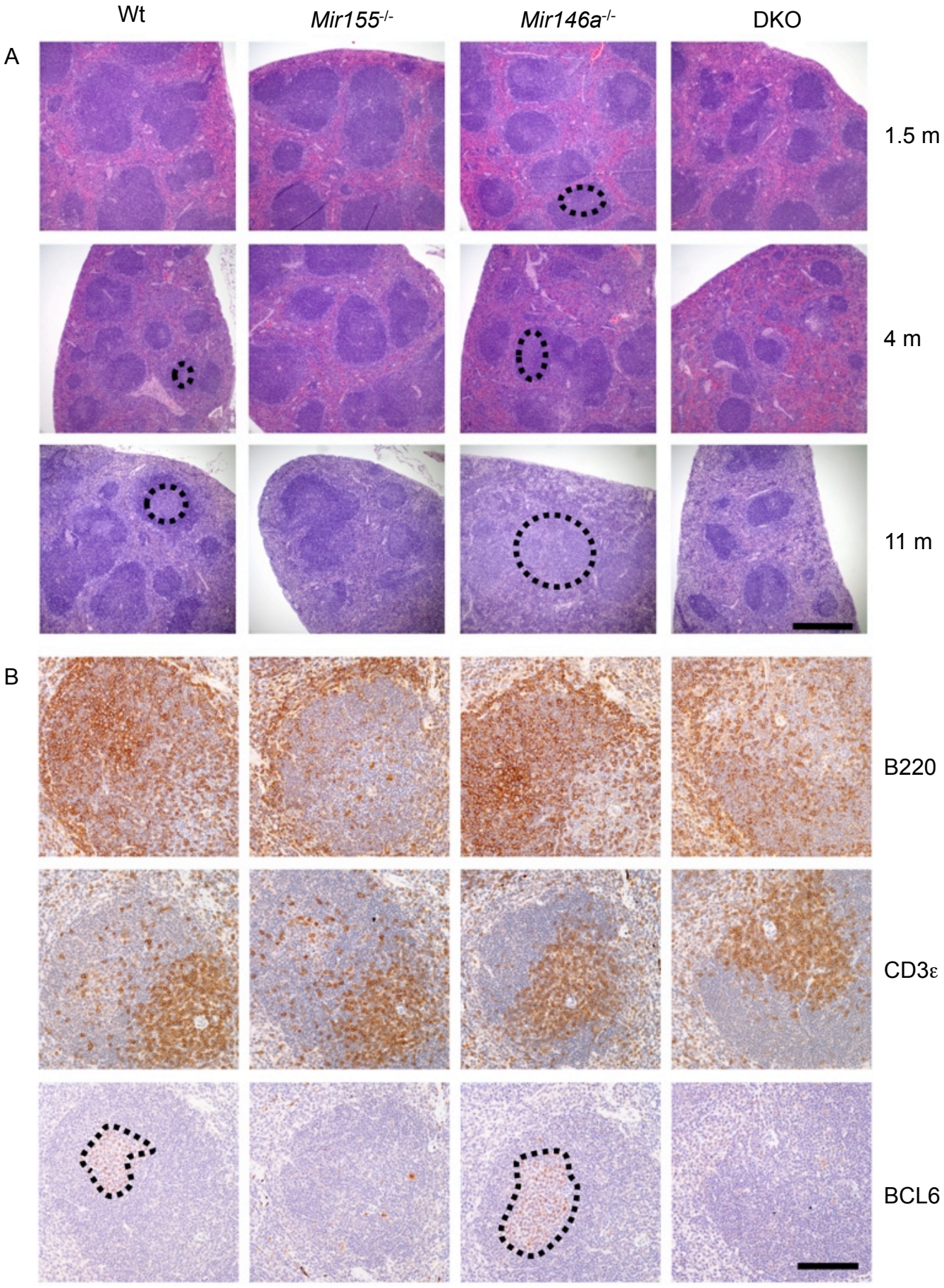

Figure S3, related to Figure 3. H&E staining and IHC of Wt, *Mir155*$^{-/-}$, *Mir146a*$^{-/-}$ and DKO mice. (**A**) Representative H&E staining of spleen sections from mice at the indicated ages (m=months). Examples of regions with germinal centers are indicated with a broken line. Scale bar: 400 microns. (**B**) Representative staining with the indicated antibodies on spleen sections from 1.5 months old mice of the indicated genotypes. Examples of regions with BCL6 staining are highlighted. Scale bar: 100 microns.

Figure S4, related to Figure 4

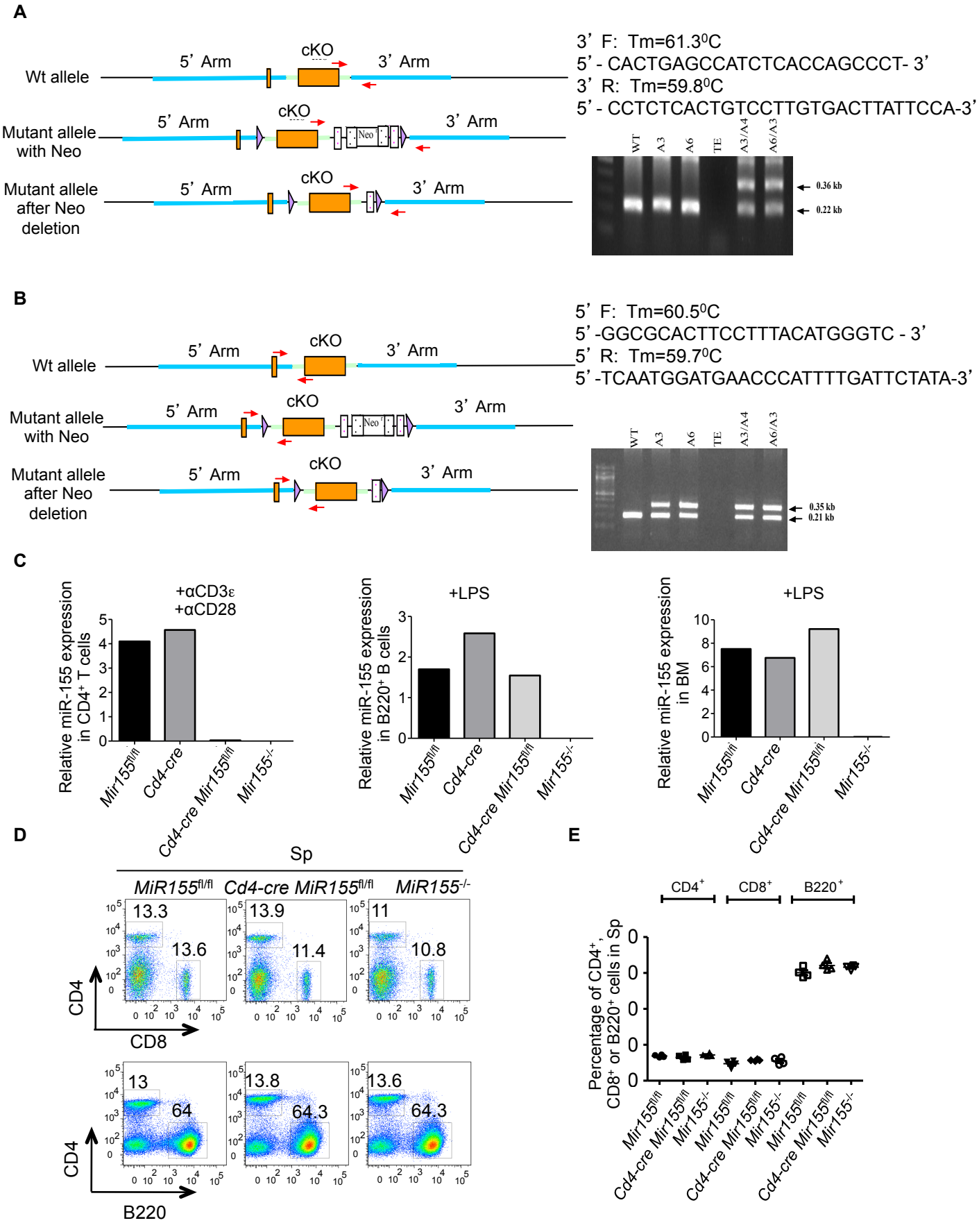

Figure S4, related to Figure 4. Validation of ES cell clones with a "floxed" miR-155 allele. (**A**) Schematic of the floxed miR-155 allele and location of primers used to genotype the 3' loxP site. Primer sequences used for PCR and an agarose gel demonstrating Wt vs. Mutant alleles are shown. A3 and A6 are two independent ES cell clones before removal of Neo, while A3/A4 and A6/A3 are clones after removal of Neo. (**B**) Same as in (A) but using primers that flank the 5' loxP site. Primers that amplify the 5' loxP site were used for genotyping. (**C**) $CD4^+$ T, $B220^+$ B and bone marrow cells were isolated from the indicated mice and activated by anti-CD3ε+anti-CD28 antibodies or LPS, as indicated. 24 hrs later, RNAs were extracted and subjected to QPCR analyses to quantify mature miR-155 expression. Expression values have been normalized to 5S values. (**D**) FACS plots showing the percentage of $CD4^+$, $CD8^+$ and $B220^+$ cells in indicated mouse spleens. (**E**) Average percentages of $CD4^+$, $CD8^+$ and $B220^+$ cells in the indicated mouse spleens.

Figure S5, related to Figure 4 and 5

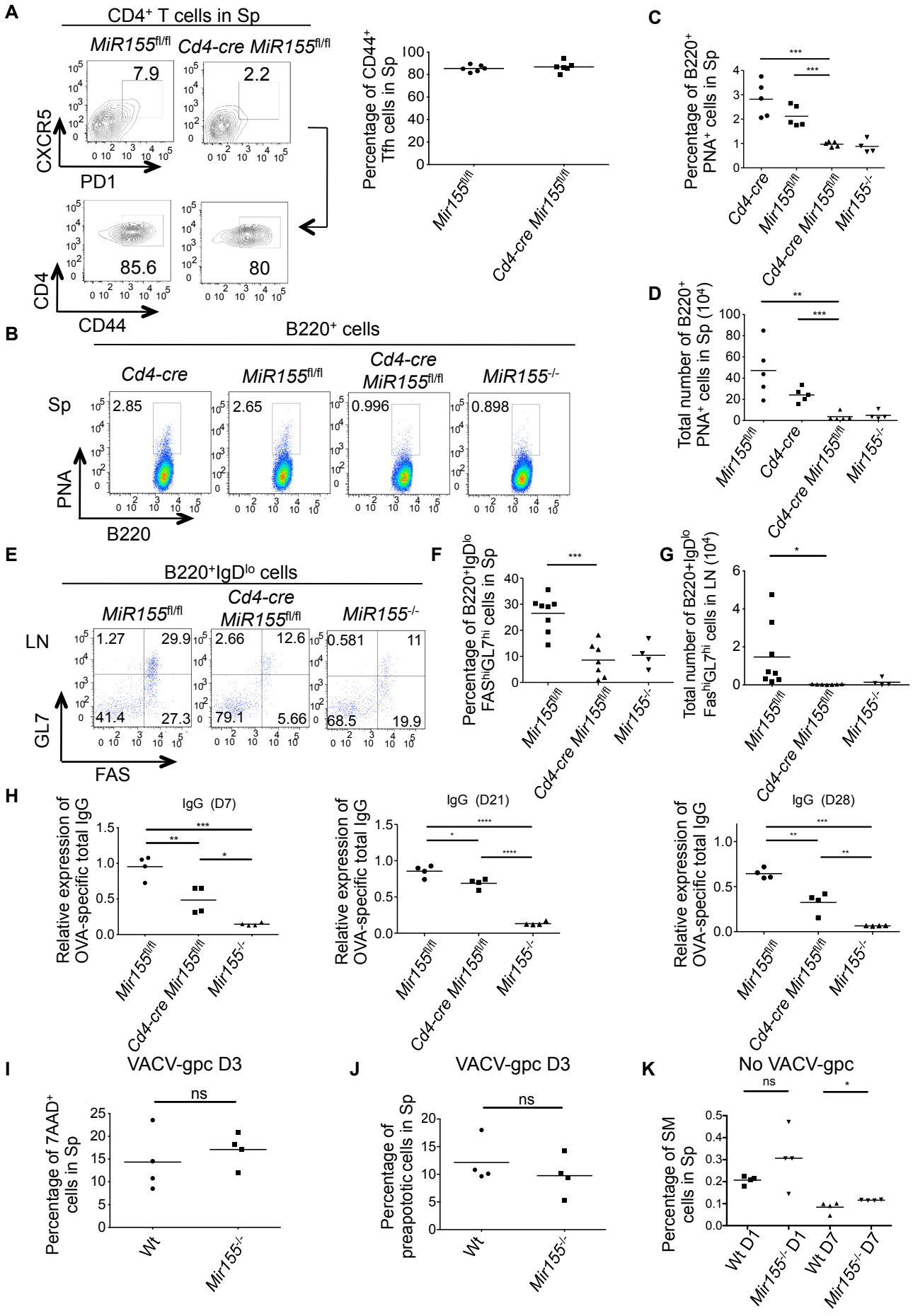

Figure S5, related to Figures 4 and 5. T cell-intrinsic role for miR-155 during Tfh cell development. (**A-H**) T cell-specific expression of miR-155 is required for proper antigen-specific responses by GC B cells. Mice were immunized with Ova in CFA for 8 days and then harvested. (**A**) FACS plots showing CD44 staining of Tfh cells from the indicated mouse spleens. Right panel shows the average percentage of $CD44^+$ cells among Tfh cells in mouse spleens. (**B**) FACS plots showing PNA staining of GC B cells in indicated mouse spleens. (**C**) Average percentage of PNA^+ cells in mouse spleens. (**D**) Average total number of PNA^+ cells in mice spleens. (**E**) FACS plots showing staining of GC B cells in LNs from the indicated genotypes. (**F**) Average percentage of GC B cells in mouse LNs. (**G**) Average total number of GC B cells in mouse LNs. (**H**) ELISA of relative concentrations of Ova-specific IgG antibody in the serum of Ova immunized mice from indicated time points. (**I**) Average percentage of Wt and *Mir155*$^{-/-}$ $7AAD^+CD4^+$ SM T cells in the indicated mouse spleens 3 days after VACV-gpc infection. (**J**) Average percentage of Wt and *Mir155*$^{-/-}$ $AnnexinV^+7AAD^-CD4^+$ SM T cells in the indicated mouse spleens 3 days after VACV-gpc infection. (**K**) Average percentage of SM cells in mouse spleens after adoptive transfer for the indicated periods of time.

Figure S6, related to Figure 6

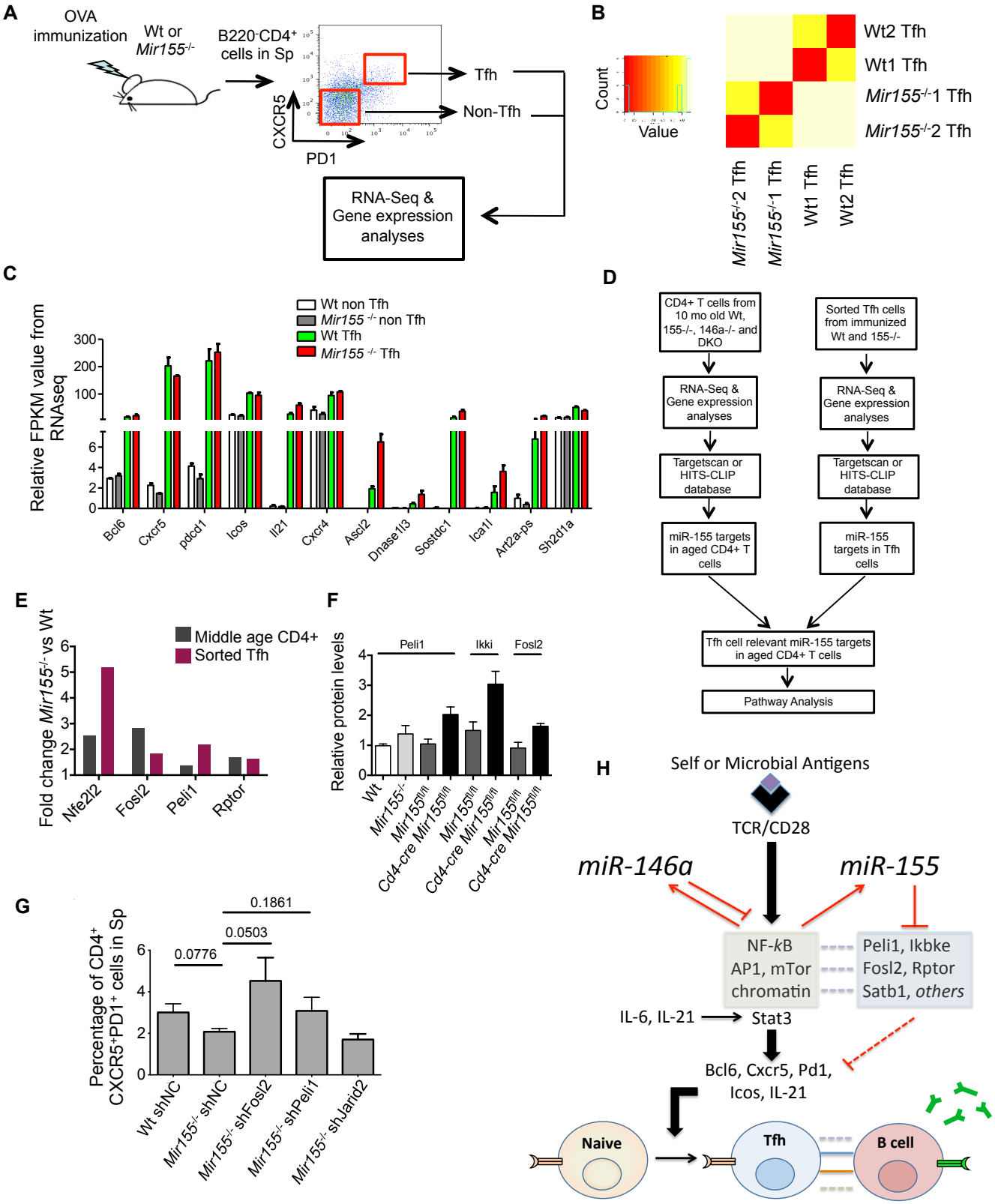

Figure S6, related to Figure 6. miR-155 targets in Tfh cells. (**A**) Schematic diagram showing the sorting of Tfh cells from immunized Wt and *Mir155*$^{-/-}$ mice. RNAs were extracted from indicated cell populations and subjected to RNA-Seq. (**B**) Gene clustering of RNA-Seq data is shown. The magnitude of the gene expression differences between any two groups is indicated by color, and the scale is shown. (**C**) Relative Tfh signature gene expression in sorted CD4^{+} Tfh cells from OVA immunized Wt and *Mir155*$^{-/-}$ mice based on RNA-Seq. (**D**) Schematic diagram of the approach used to identify Tfh cell-related miR-155 target genes in aged CD4^{+} T cells. (**E**) QPCR analyses of the indicated miR-155 target genes in CD4^{+} T cells from middle-aged Wt and *Mir155*$^{-/-}$ mice, or sorted CD4^{+}CXCR5^{+}PD1^{+} Tfh cells from both Ova-immunized Wt and *Mir155*$^{-/-}$ mice. Data are presented as fold changes between *Mir155*$^{-/-}$ and Wt cells. (**F**) Relative protein expression in Wt and *Mir155*-/- or *Cd4-cre Mir155*$^{fl/fl}$ CD4^{+} T cells, as indicated. (**G**) Average percentage of CXCR5^{+}PD1^{+} Tfh cells among CD3^{+}CD4^{+}TCRVβ11^{+} cells in the spleens following adoptive transfer with the indicated shRNA-containing Wt or *Mir155*$^{-/-}$ 2D2^{+} T cells and 7 days of immunization with MOG_{35-55}. n=3-4 mice per group. (**H**) Schematic diagram showing the potential pathways regulated by miR-155 and miR-146a during Tfh development. Dashed gray line indicates regulation of the pathway that could be either quantitative (repression or activation) or qualitative (e.g. altered heterodimer complexes). Dashed red inhibition line indicates indirect inhibition.

Figure S7, related to Figure 7

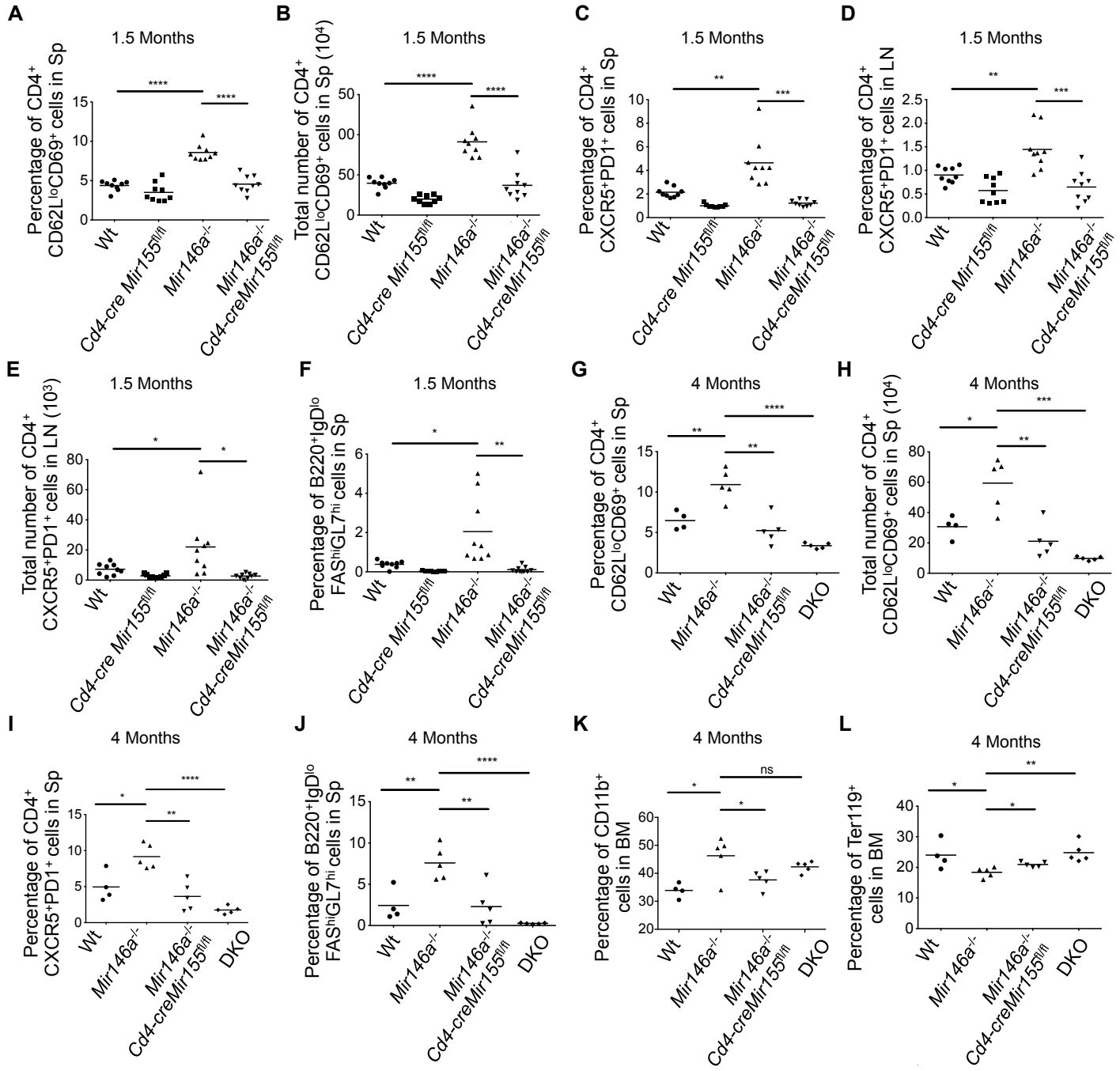

Figure S7, related to Figure 7. T cell-specific expression of miR-155 is required for activation of CD4$^+$ T cells and spontaneous accumulation of Tfh cells in *Mir146a*-/- mice. (**A-F**) Spleens and LNs were harvested from 1.5 months old mice of the indicated genotypes. (**A**) Average percentage of CD62L^{lo}CD69$^+$CD4$^+$ T cells in spleens. (**B**) Total number of CD4$^+$CD62L^{lo}CD69$^+$ T cells in spleens. (**C**) Average percentage of Tfh cells in spleens. (**D**) Average percentage of Tfh cells in LNs. (**E**) Total number of Tfh cells in LNs. (**F**) Average percentage of GC B cells in spleens. (**G-L**) Spleens and bone marrow were harvested from 4 month old mice of the indicated genotypes. (**G**) Average percentage of CD62L^{lo}CD69$^+$CD4$^+$ T cells in spleens. (**H**) Total number of CD4$^+$CD62L^{lo}CD69$^+$ T cells in spleens. (**I**) Average percentage of Tfh cells in spleens. (**J**) Average percentage of GC B cells in spleens. (**K**) Average percentage of CD11b$^+$ cells in the BM. (**L**) Average percentage of Ter119$^+$ cells in the BM.

Supplemental Table S1, related to Figure 4. Sequence of the Floxed mouse BIC allele (Homology arms in green, conditional knockout region in red. LoxP sites underlined. Frt sites in italics. Exons are bolded).

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3481  ATGTCTTTGA TAACTCAATC AGAAACTTAA AACTGGTTAC AGTGGCAAAG TTTGTTTGTA
      TACAGAAACT ATTGAGTTAG TCTTTGAATT TTGACCAATG TCACCGTTTC AAACAAACAT
3541  TGTATGTATA TGTGTGTGTA TGTATGTATG TATGTATGTA TGTATGTATG TATGTATGTA
      ACATACATAT ACACACACAT ACATACATAC ATACATACAT ACATACATAC ATACATACAT
3601  TGTATATGTG TGTATGTATG TATGTATGTA TGTATGTATG TATGTAGATA TATGTGTGTA
      ACATATACAC ACATACATAC ATACATACAT ACATACATAC ATACATCTAT ATACACACAT
3661  TATGTATATG ATGAAAGTTG AAGATGAGTA TGAATATGAT GCCCTTTCTT ACAGCTCCAA
      ATACATATAC TACTTTCAAC TTCTACTCAT ACTTATACTA CGGGAAAGAA TGTCGAGGTT
3721  AAGTTCATCT ACCCTACTCT GTATGTGTGT GTCTGTGTGT GTGTGTTATA TGTGTGAGAT
      TTCAAGTAGA TGGGATGAGA CATACACACA CAGACACACA CACACAATAT ACACACTCTA
3781  ACATGTGTGT GTGTGTGTTA CCACAAAAAA ATTACTAAAA ATAAAAAGAT CCAGTATAGG
      TGTACACACA CACACACAAT GGTGTTTTTT TAATGATTTT TATTTTTCTA GGTCATATCC
3841  ACATATTCTT CTCTGAGTAC CTTAGCTGAT AACATTTTCC CTGGCAAATC AGCAAGACTA
      TGTATAAGAA GAGACTCATG GAATCGACTA TTGTAAAAGG GACCGTTTAG TCGTTCTGAT
3901  GACAGATTGT GACATTCTAT GCCTCCCTTA TACCTCAAAA TATTATCCTG AAGAAAAGTC
      CTGTCTAACA CTGTAAGATA CGGAGGGAAT ATGGAGTTTT ATAATAGGAC TTCTTTTCAG
3961  TAATTATATT CTCCTGGAAT GTCCTTAGGT TTAGGCTATA CCACAGAGAA ATGGTGATAT
      ATTAATATAA GAGGACCTTA CAGGAATCCA AATCCGATAT GGTGTCTCTT TACCACTATA
4021  GCCACATAGT GAATGGGACC TGGACTTACG ATTTGTCTGA ACTAAATATA GTGCTTAAGG
      CGGTGTATCA CTTACCCTGG ACCTGAATGC TAAACAGACT TGATTTATAT CACGAATTCC
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4081  TTGGTCGAGA TTTTTACCTA AGGTCAAAAG AGTTGATTGC AATAGCAATT CCTAACATTA
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4141  TATTTTATTA TTTATTGAGA CGGGGTCCAA TATAGCCCAA GCTGACCCCA GAGGTGATAA
      ATAAAATAAT AAATAACTCT GCCCCAGGTT ATATCGGGTT CGACTGGGGT CTCCACTATT
4201  GTAATTGGGA ACAGCCCTGA GCTCATGATC CTCCTAAGTC CATCTCTCAA GTCCTGAGAT
      CATTAACCCT TGTCGGGACT CGAGTACTAG GAGGATTCAG GTAGAGAGTT CAGGACTCTA
4261  CAAAGGCTGC ACCAGTGTCC ATGTATGTGG TACTTGGGAA TCAAACCTAG GCTTTTCATG
      GTTTCCGACG TGGTCACAGG TACATACACC ATGAACCCTT AGTTTGGATC CGAAAAGTAC
4321  TAGATAGATG ATAGATAGAT AGATAGATAG ATAGATAGAT AGATAGATAG ATAGATAGAT
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4381  AGATAGGTGT GTATGTGTGC ACACATGTAT GTATATATGT AATATACATA TATATGTATA
      TCTATCCACA CATACACACG TGTGTACATA CATATATACA TTATATGTAT ATATACATAT
4441  TATGGCTATA CATATATATG TATATATGGC TATATATATA TAGCCAGATG TGGTGGTATA
      ATACCGATAT GTATATATAC ATATATACCG ATATATATAT ATCGGTCTAC ACCACCATAT
4501  TGGCTATAAT TCCAGAATTT GGGAGACTGA AGTGTAAGGT CATGAGTTCA AGGCCAGCCT
      ACCGATATTA AGGTCTTAAA CCCTCTGACT TCACATTCCA GTACTCAAGT TCCGGTCGGA
4561  AGGTTATATA GGGCAACCTT GGCTACCTAT ACTAAATATA TTCTTGGTAA TACCTTTATT
      TCCAATATAT CCCGTTGGAA CCGATGGATA TGATTTATAT AAGAACCATT ATGGAAATAA
4621  CAGATGGTAT CTTTAAAGGA TAGAAACAGA ACTTATAGAT AAGTTATTTA CTTAAATTGG
      GTCTACCATA GAAATTTCCT ATCTTTGTCT TGAATATCTA TTCAATAAAT GAATTTAACC
4681  AATGGGGTTA TGTAGGCACT CATGCACACA TGCACAGTTG CATATATTCT CCCTAATGGG
      TTACCCCAAT ACATCCGTGA GTACGTGTGT ACGTGTCAAC GTATATAAGA GGGATTACCC
4741  TCAATAATAT GGCATGAAGT AGAACACTAG AATCTTAATA GATTTACTGA GGACTTACTG
      AGTTATTATA CCGTACTTCA TCTTGTGATC TTAGAATTAT CTAAATGACT CCTGAATGAC
4801  AGTTCAATGC ACTATGAAGA GAAAAGGTAT TATTACAGTC TTTCTTTTGG CTGAAATAAA
      TCAAGTTACG TGATACTTCT CTTTTCCATA ATAATGTCAG AAAGAAAACC GACTTTATTT
4861  ATCCAAGATT GAAACTGTGT AATTCACAGA CTTTCCTCAT GAAACCAGCT CATCTGAGAA
      TAGGTTCTAA CTTTGACACA TTAAGTGTCT GAAAGGAGTA CTTTGGTCGA GTAGACTCTT
4921  AACAGCAAAG TTTAAAAAAG AAATACTATC AGTAAGTATG ATATATTTCC TTGGTTTGGA
      TTGTCGTTTC AAATTTTTTC TTTATGATAG TCATTCATAC TATATAAAGG AACCAAACCT
4981  AATTTCCAAG CCACGATATT CTGCCCTGTC AAAATATATT CACTGGGGAA TTTTTAACTT
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5041  GATGCATTTC TTTTGAACTT AATCACATTT CTACATCTAG CTGGTTTCAT TATTAAAGAA
      CTACGTAAAG AAAACTTGAA TTAGTGTAAA GATGTAGATC GACCAAAGTA ATAATTTCTT
5101  AAGAAAAGGT GGTTCCCCTC TGGTCCTAAA GGGAACCACA GACTTGAGTG ATGCTTGAAC
      TTCTTTTCCA CCAAGGGGAG ACCAGGATTT CCCTTGGTGT CTGAACTCAC TACGAACTTG
5161  TTCTAGGTTC GCGTACAGTA ACACTGAAAC CAGAAACTTG TGGGAGAAAT GTCACTTTAT
      AAGATCCAAG CGCATGTCAT TGTGACTTTG GTCTTTGAAC ACCCTCTTTA CAGTGAAATA
5221  CTGAGAGAGT AAAATCCAAC TCTAACAGGA AACAGCAAAT TCATCTTTTT TCTTTTTCTA
      GACTCTCTCA TTTTAGGTTG AGATTGTCCT TTGTCGTTTA AGTAGAAAAA AGAAAAAGAT
5281  AACCACTCTG CTGGAGACAA GTCCCTTGAG TCAGAGCTCT TTAAGGCGCA CTTCCTTTAC
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5341  ATGGGTCAAA CTGAAGCCAC CGGTTTGTGA GTCCCCAAAG GAATCACTGG AGGACAACAG
      TACCCAGTTT GACTTCGGTG GCCAAACACT CAGGGGTTTC CTTAGTGACC TCCTGTTGTC
5401  GAGCATTTTC AGATACCTTT CAGGATCCGG TACCAAAGGC CGCAATGGCC AAACCTGCAG
      CTCGTAAAAG TCTATGGAAA GTCCTAGGCC ATGGTTTCCG GCGTTACCGG TTTGGACGTC
5461  GAAGTACCAG AGCTCCCTAG GTTCTAGAAC CGGTGACGTT AAGCTCGAAT AACTTCGTAT
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5521  AATGTATGCT ATACGAAGTT ATCCTGCAGG TCGATCGAGA CCGTACGGCA GACCTGCCCT
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5581  GGCTGTACCC CCTATCTTGA AGAAAAAGAA AAACGAATAA GGTGAAAATC GCAACTACTA
      CCGACATGGG GGATAGAACT TCTTTTTCTT TTTGCTTATT CCACTTTTAG CGTTGATGAT
5641  TTTATAGAAT CAAAATGGGT TCATCCATTG AGTTTTAACT TTCAAAAATC ATAAAGTACC
      AAATATCTTA GTTTTACCCA AGTAGGTAAC TCAAAATTGA AAGTTTTTAG TATTTCATGG
5701  ATCCTAAATA TCTGAGATTT CTTGAATTGC CTAGTGACCT GTGGGATGTA CGTCAGAATA
      TAGGATTTAT AGACTCTAAA GAACTTAACG GATCACTGGA CACCCTACAT GCAGTCTTAT
5761  TTACCCAGAA CTGAAGTTGT GTCCTTTGAA CTTCAGCATT GTAGAACTAT GAACCGTGGC
      AATGGGTCTT GACTTCAACA CAGGAAACTT GAAGTCGTAA CATCTTGATA CTTGGCACCG
5821  TGTGTTAAAA ATGATACATG TATTCAAATA TTTCCACAGA ATTTAAAGTT TGATTTTATA
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5881  ATTAGTTTTT AAATTGCAAA CCTTACAAAA ATTTTCCAAA ATTTACTTAG AAGCATTTCA
      TAATCAAAAA TTTAACGTTT GGAATGTTTT TAAAAGGTTT TAAATGAATC TTCGTAAAGT
5941  GAGCTCTTTT CTTTCAAAGC TGAAGTCTAC CTTGCCTTCA GATTCATAAT CGTTCACTCT
      CTCGAGAAAA GAAAGTTTCG ACTTCAGATG GAACGGAAGT CTAAGTATTA GCAAGTGAGA
6001  ACTTTATAAC TAACTGTGTG CGTACACACA ACTATTTCTT TTTCTCTTTG CAGGTGCTGC
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6061  AAACCAGGAA GGGGAAGTGT GTGGTTTAAG TTGCATATCC CTTATCCTCT GGCTGCTGGA
      TTTGGTCCTT CCCCTTCACA CACCAAATTC AACGTATAGG GAATAGGAGA CCGACGACCT
6121  GGCTTGCTGA AGGCTGTATG CTGTTAATGC TAATTGTGAT AGGGGTTTTG GCCTCTGACT
      CCGAACGACT TCCGACATAC GACAATTACG ATTAACACTA TCCCCAAAAC CGGAGACTGA
6181  GACTCCTACC TGTTAGCATT AACAGGACAC AAGGCCTGTT ACTAGCACTC ACATGGAACA
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      TTACCGGTGG CACCCTCCTA CTGTTCAGGT TCTCAGTGGG ACGACCTACT TGCATCTACA
6301  CAGACTCTAT CATTTAATGT GCTAGTCATA ACCTGGTTAC TAGGATAGTC CACTGTAAGT
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6361  GTTACGATAA ATGTCATTTA AAAGATAGAT CAGCAGTATC CTAAACAACA TCTCAACTTC
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6421  AAGCCCACAT GTTTATTTTT TATCTTGAAT GGAAAGTGAA ACTTGTATCA TTTTTATTTC
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6481  AAAATTATGT TCATAACCAT CTTCAATGAT TCAACCAGAA TACAAAATGA ATGCACTAAA
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6541  AAGGACATTT CTATATTTCT GTAGTTAAAA TTCAGGACGG CCATTCTCGA CTGACATCTA
      TTCCTGTAAA GATATAAAGA CATCAATTTT AAGTCCTGCC GGTAAGAGCT GACTGTAGAT
6601  GGATTGTCTG GAATACCTCT TGTAAGACTT GGAATTGGCA TTTTTTCCAC ATTACAATGT
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6661  ATTAGTCAAC TTTGATTTAA AATTTGTAAC TCTTGTGTTT TAGTGTAAGG AAAAATTTAG
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6721  GGTTAGTGTT AGAGTTTAGG GCTAGGTAAG GAAAAACTGA GTCAACACTG AATGATTTTT
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6781  TTAAAATCTA TGAGCCAGCT GTTGGTAGTT TACTCCTTTA ATCCCAGCAC TCGGGAGGCA
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6841  GAGACAGGCA GATGGCTGAG TCGAAGGCCA ACCTGGTCTA CAGAGTGAGC TCCAGGACAG
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6901  CCTTAGCTAC ACAGAAAAAT GCCTTATCAA AAAATTAAGA AAATAAGATG AAGTATTAAA
      GGAATCGATG TGTCTTTTTA CGGAATAGTT TTTTAATTCT TTTATTCTAC TTCATAATTT
6961  AAGTGACATG ACAAATCATT CCTGAGGGCT ACCTATATAT TCCTCACACG GTATAAATAT
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7021  TTAATTTAAT TAATATTTAA TTTCAAATAT TCACATTTGA AATGAAACCC AAATCTGGGT
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7081  TCAAGCTTAC TGCTTTAGCT GCACAGTAAA GCTGTGTAGT AAGGAGACCC ACGTTTCCTA
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7141  CGCATTTCTT CATGAATGCG GATGAAACTT TACAAGGTTG GTGTGCAGCT CACTGGAGAT
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7201  GAACAACTCT TTGTAAGGTA ATAAAATCCC ACAGTGATGT CTTAAAGCCA ATCCAAAACT
      CTTGTTGAGA AACATTCCAT TATTTTAGGG TGTCACTACA GAATTTCGGT TAGGTTTTGA
7261  CACCCCGTTG CCTGACATAG GTAATAATTT GATATACAGA AGTTTAATGT TTGAATTCCT
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7321  ATGCAATTTT TCTCCACAGT GATATCACTG ACGAACACAT AGACAGCTGG ACTTGTTATA
      TACGTTAAAA AGAGGTGTCA CTATAGTGAC TGCTTGTGTA TCTGTCGACC TGAACAATAT
7381  TTTAATTTAT ACCTGTTCTT TTTTTTTTTT TTTAAAGACT TTTTATTTAT GTATATATAT
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7441  GTATATATAT ATTTATGTAT ATATGTAAGT ACACTGTAGC TGTCTTCAGA CACACCAGAA
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7501  GAGGGAGTCA GATCTTGTTA CGGATGGTTG TGAGCCACCA TGTGGTTGCT GGGATTTGAA
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7561  CTCTGGACCT TCGGAAGAGC AGTCGGGTGC TCTTACCCAC TGAGCCATCT CACCAGCCCT
      GAGACCTGGA AGCCTTCTCG TCAGCCCACG AGAATGGGTG ACTCGGTAGA GTGGTCGGGA
7621  AATTTATACC TGTTCTGATA GTTCTCCTGA ATATCTTGTC GTCGAC GAAG TTCCTATACT
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7681  TTCTAGAGAA TAGGAACTTC GGATCCACGA TTCGAGGGCC CCTGCAGGTC AATTCTACCG
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7741  GGTAGGGGAG GCGCTTTTCC CAAGGCAGTC TGGAGCATGC GCTTTAGCAG CCCCGCTGGG
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7801  CACTTGGCGC TACACAAGTG GCCTCTGGCC TCGCACACAT TCCACATCCA CCGGTAGGCG
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7861  CCAACCGGCT CCGTTCTTTG GTGGCCCCTT CGCGCCACCT TCTACTCCTC CCCTAGTCAG
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7921  GAAGTTCCCC CCCGCCCCGC AGCTCGCGTC GTGCAGGACG TGACAAATGG AAGTAGCACG
      CTTCAAGGGG GGGCGGGGCG TCGAGCGCAG CACGTCCTGC ACTGTTTACC TTCATCGTGC
7981  TCTCACTAGT CTCGTGCAGA TGGACAGCAC CGCTGAGCAA TGGAAGCGGG TAGGCCTTTG
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8041  GGGCAGCGGC CAATAGCAGC TTTGCTCCTT CGCTTTCTGG GCTCAGAGGC TGGGAAGGGG
      CCCGTCGCCG GTTATCGTCG AAACGAGGAA GCGAAAGACC CGAGTCTCCG ACCCTTCCCC
8101  TGGGTCCGGG GGCGGGCTCA GGGGCGGGCT CAGGGGCGGG GCGGGCGCCC GAAGGTCCTC
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8161  CGGAGGCCCG GCATTCTGCA CGCTTCAAAA GCGCACGTCT GCCGCGCTGT TCTCCTCTTC
      GCCTCCGGGC CGTAAGACGT GCGAAGTTTT CGCGTGCAGA CGGCGCGACA AGAGGAGAAG
8221  CTCATCTCCG GGCCTTTCGA CCTGCAGCCA ATATGGGATC GGCCATTGAA CAAGATGGAT
      GAGTAGAGGC CCGGAAAGCT GGACGTCGGT TATACCCTAG CCGGTAACTT GTTCTACCTA
8281  TGCACGCAGG TTCTCCGGCC GCTTGGGTGG AGAGGCTATT CGGCTATGAC TGGGCACAAC
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 8521  CGGGAAGGGA CTGGCTGCTA TTGGGCGAAG TGCCGGGGCA GGATCTCCTG TCATCTCACC
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 8581  TTGCTCCTGC CGAGAAAGTA TCCATCATGG CTGATGCAAT GCGGCGGCTG CATACGCTTG
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 8941  ATATTGCTGA AGAGCTTGGC GGCGAATGGG CTGACCGCTT CCTCGTGCTT TACGGTATCG
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 9001  CCGCTCCCGA TTCGCAGCGC ATCGCCTTCT ATCGCCTTCT TGACGAGTTC TTCTGAGGGG
       GGCGAGGGCT AAGCGTCGCG TAGCGGAAGA TAGCGGAAGA ACTGCTCAAG AAGACTCCCC
 9061  ATCGATCCGC TGTAAGTCTG CAGAAATTGA TGATCTATTA AACAATAAAG ATGTCCACTA
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 9121  AAATGGAAGT TTTTCCTGTC ATACTTTGTT AAGAAGGGTG AGAACAGAGT ACCTACATTT
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 9661  AGAGGTTCAC TAGTACTGGC CAATCGGCGC GCCATTGTCT TCCCTATAGC CAAATAAATG
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10021  ACAAAGTCAC AGAAAGCTAG GAACCCGCTG CGTTCTCTAC ATTACCCTCC AGCAGTTCCA
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10081  ATCAAAAGCT CTGAAATCAT AAAGCACTGT AACACCTACT GCATGCTTAG GCAAATCACT
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10141  TGCTCCATGT CTGTTTCTCC ATCAGTGTGT GTATCTCTGT GATGTAATTT TATTAAGGCT
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10201  TAGATGAAAT ACCACAAGAG GGAACACACT TTCTACCAGC ATTTAAGTGA TGAATACATA
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10261  CAAACCTTGA AACATGTATA AGTCCATAAT CTAAATCGAC GCAGCAGGCG TCCCTGGAAC
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10321  ACGCCACCTC CTCAGCTATC ATCCCACCCT AACCACCCAC ACAACCCAGA CGTGGCCAGC
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10381  AGGCTGGGTC TTCCCGGATG CCCAACTCTA CTAGCTGACC TCTTGGCATC ACAGATGGAT
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10441  TATTCCTGAC CAACATTTCC AGTCATTCCA AAAATTCTTG GAGTATGAGT TAAGGCTGGG
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       ATAAGGACTG GTTGTAAAGG TCAGTAAGGT TTTTAAGAAC CTCATACTCA ATTCCGACCC
10501  TGTGTTTGGA GTGGAGAGTA AGTAATGAGG AAGTTTGTGT GTGTGTGTGT GTGTGTGTGT
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10561  GTGTGTGTGT GTGTGTGTGT GTGAGTAAAG GAAGGGCAGC CCAATTTCGT GCACAGAAGA
       CACACACACA CACACACACA CACTCATTTC CTTCCCGTCG GGTTAAAGCA CGTGTCTTCT
10621  CTAAAGGGAA TGAAGCACTG AATTACATAG GATGACCTGG GCACAGACCA GCCCCTGAAG
       GATTTCCCTT ACTTCGTGAC TTAATGTATC CTACTGGACC CGTGTCTGGT CGGGGACTTC
10681  CCATTGGCTG AGAGTTAGAA AACAAGTTTT TCCTGGTCTT CATGTGGGAC TTCTAACAGT
       GGTAACCGAC TCTCAATCTT TTGTTCAAAA AGGACCAGAA GTACACCCTG AAGATTGTCA
10741  GAGAGCAGGG GCTGCCTCTG ACTGTTGCCT GCCTGTGGGA CCCTTTCAGG CTGCCTAATG
       CTCTCGTCCC CGACGGAGAC TGACAACGGA CGGACACCCT GGGAAAGTCC GACGGATTAC
10801  GGCTGCCTTG TCTAGCCTCA ACGAGAGAAG ATGTGCCTAG CCTTAACTGC AACTTTTTAT
       CCGACGGAAC AGATCGGAGT TGCTCTCTTC TACACGGATC GGAATTGACG TTGAAAAATA
10861  GCTAGGGCTG GTTGATATCC ATGGGAGGCC TCCCCTTTTC TGAAGAGAAA CAGAGTGGAT
       CGATCCCGAC CAACTATAGG TACCCTCCGG AGGGGAAAAG ACTTCTCTTT GTCTCACCTA
10921  GAGGTGGGAG AAAGGACTGG GAGGAGAGGA AGTTCTAGTC GGGATGTATA AGTAATTAGA
       CTCCACCCTC TTTCCTGACC CTCCTCTCCT TCAAGATCAG CCCTACATAT TCATTAATCT
10981  AAAAGATTTT TTGTAAAGAA ACTAACTAGG AAATAATTAG AAAAGGAAAC CCAGCTTTTC
       TTTTCTAAAA AACATTTCTT TGATTGATCC TTTATTAATC TTTTCCTTTG GGTCGAAAAG
11041  TTGCTCGCTC TCATCAGCTA AATAAACCTA GTAGCAGAGG TAGGACAGGA GAGAAAGCTG
       AACGAGCGAG AGTAGTCGAT TTATTTGGAT CATCGTCTCC ATCCTGTCCT CTCTTTCGAC
11101  GGACAGACTG AGGCACACAT AGAAACTGTG GCATAACAGT CATTTCCTGA GAATAAATGG
       CCTGTCTGAC TCCGTGTGTA TCTTTGACAC CGTATTGTCA GTAAAGGACT CTTATTTACC
11161  TCAGGGCATG AAAGAATGGG GAAACTTGAA GTAAAATACA AGTGGGAAAA ACACGCGAAC
       AGTCCCGTAC TTTCTTACCC CTTTGAACTT CATTTTATGT TCACCCTTTT TGTGCGCTTG
11221  GAAGGAAATT AAATAAATAC AGCTCAAAAT TCCTAAGTGA GCAGACCCAC TAAGGACCAA
       CTTCCTTTAA TTTATTTATG TCGAGTTTTA AGGATTCACT CGTCTGGGTG ATTCCTGGTT
11281  GAGACCGGCA CAGCTACAGA ATGTCAGAAT CCCGTAACAA CAAAAGCAAG GTCCCACAAG
       CTCTGGCCGT GTCGATGTCT TACAGTCTTA GGGCATTGTT GTTTTCGTTC CAGGGTGTTC
11341  TGTCCAGCAC AGAGCTTCAG GTTAAAATCA GACAAGAACC AGGCTGTCAG TCTTGTCAGC
       ACAGGTCGTG TCTCGAAGTC CAATTTTAGT CTGTTCTTGG TCCGACAGTC AGAACAGTCG
11401  ATTGTCACTT GCCAGAAGCC AACTGGGCTC TTTCTGAGTC CTGATAGGAA ACTGTTTTCA
       TAACAGTGAA CGGTCTTCGG TTGACCCGAG AAAGACTCAG GACTATCCTT TGACAAAAGT
11461  AAATAGAATT CCGTATCTAG TCAAACAGCT GCTCAAAGCC AGCACAGCTA AAAGCCGGTG
       TTTATCTTAA GGCATAGATC AGTTTGTCGA CGAGTTTCGG TCGTGTCGAT TTTCGGCCAC
11521  TAGGCACCCA GTTCACCTTG CCTTACGGAT TTTCCCCTAG GAAGGCAGTG GGGAACAGCT
       ATCCGTGGGT CAAGTGGAAC GGAATGCCTA AAAGGGGATC CTTCCGTCAC CCCTTGTCGA
11581  CTAGGGAATG AGAGCCGGGC CTAGTGAATT TCGGTATATG ATATTTTTAT TTACAACATT
       GATCCCTTAC TCTCGGCCCG GATCACTTAA AGCCATATAC TATAAAAATA AATGTTGTAA
11641  TTCATAATAA TGTTTATTAC ATATGTGTAT ATATATACAC ACACACACAT ATATATATAC
       AAGTATTATT ACAAATAATG TATACACATA TATATATGTG TGTGTGTGTA TATATATATG
11701  ATATATATAT ACATACATAT ATATATACAC ACACACACAC ACACACATAT ATATATATAT
       TATATATATA TGTATGTATA TATATATGTG TGTGTGTGTG TGTGTGTATA TATATATATA
11761  ATATATAATC TAAAAAGAGA AAACTAGTTT TGGAGGCTAG CATCTGGTAG CATCTAACAG
       TATATATTAG ATTTTTCTCT TTTGATCAAA ACCTCCGATC GTAGACCATC GTAGATTGTC
11821  AACTCCGCTA CCAGAATGCA AACTTATCCA GGTATCCCTG CGGGCGGCAG CACCTGTGAG
       TTGAGGCGAT GGTCTTACGT TTGAATAGGT CCATAGGGAC GCCCGCCGTC GTGGACACTC
11881  AGTAGAGCAG CCTTGGTAAG ATCACCTGCA CTCTCTATGG TGATGAAACA GAAACACTGT
       TCATCTCGTC GGAACCATTC TAGTGGACGT GAGAGATACC ACTACTTTGT CTTTGTGACA
11941  CTTAACAAGT GGGAATTAAA TAAGATGCTC ACACCCTAAT TCTAGGACTT GGAAGGCAGA
       GAATTGTTCA CCCTTAATTT ATTCTACGAG TGTGGGATTA AGATCCTGAA CCTTCCGTCT
12001  GGCAGGAGGG CTGCATAGCC AGTTCCAGAC CAGGTTTAAC TACACACTGA GACGCTGGCT
       CCGTCCTCCC GACGTATCGG TCAAGGTCTG GTCCAAATTG ATGTGTGACT CTGCGACCGA
12061  CAAATAAAAC AACAGAGAAG CTCCGGGGAG GGAGGGGCCT AGGGGTGCTT AACACACTGG
       GTTTATTTTG TTGTCTCTTC GAGGCCCCTC CCTCCCCGGA TCCCCACGAA TTGTGTGACC
12121  CACATAGTAG CGACACAGTT AACAGCATCG CCCATCTGCA AACACATTAT TTCGAACATG
       GTGTATCATC GCTGTGTCAA TTGTCGTAGC GGGTAGACGT TTGTGTAATA AAGCTTGTAC
12181  GATGTTTACT AGAGCACTCT TTAAACAGCC CAAACTGGCG CACACACAGT GTATTTTCCC
       CTACAAATGA TCTCGTGAGA AATTTGTCGG GTTTGACCGC GTGTGTGTCA CATAAAAGGG
12241  ATGTGTCTAT CCATGGGGAG GAGGCGCATG GACCTCCTTA AAGTCTGTAT CTGCAGAGCA
       TACACAGATA GGTACCCCTC CTCCGCGTAC CTGGAGGAAT TTCAGACATA GACGTCTCGT
12301  GGGACAAACA CACATTGTAT TAAAAGCTTT TATTTTAATT TACTCTACAA GTTTAAATTT
       CCCTGTTTGT GTGTAACATA ATTTTCGAAA ATAAAATTAA ATGAGATGTT CAAATTTAAA
12361  TAGAACACTA CTGGGTGGAT TCGGTGTTCT CTGTCTGTCT GACTTCATCT TCAGTTACCT
       ATCTTGTGAT GACCCACCTA AGCCACAAGA GACAGACAGA CTGAAGTAGA AGTCAATGGA
12421  GTGAAGACAG CAACAGTTTT ACTCCTCCGG CTCTTTCAGC CCACCCTGTG CACAGTTCAA
       CACTTCTGTC GTTGTCAAAA TGAGGAGGCC GAGAAAGTCG GGTGGGACAC GTGTCAAGTT
12481  CCCCCACTCC CCCTCCTGTG AAGACCTGTC CCACTTCCTT CAGGAATTAT CACAGAGTTT
       GGGGGTGAGG GGGAGGACAC TTCTGGACAG GGTGAAGGAA GTCCTTAATA GTGTCTCAAA
12541  AACAACAACA AAACAAGTTC CGATATAAAC CACCAAGTGT GGCCATTAAA AACTATATAA
       TTGTTGTTGT TTTGTTCAAG GCTATATTTG GTGGTTCACA CCGGTAATTT TTGATATATT
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12601  CAGAAGGCAT ATTAACGTAG GCTTCCTAAG TTTCTCACCT TATTCTTATC TATAAAACAA
       GTCTTCCGTA TAATTGCATC CGAAGGATTC AAAGAGTGGA ATAAGAATAG ATATTTTGTT
12661  AAGCATTACT ATGAGAAAAT TAGCAGGAGG GAAACACAGG GTATTCTTCA TCAATGTGTC
       TTCGTAATGA TACTCTTTTA ATCGTCCTCC CTTTGTGTCC CATAAGAAGT AGTTACACAG
12721  TTACTGCGGT CGCGACGCGT GCTAGCCCGG GCGCCTAGTT ATTAATAGTA ATCAATTACG
       AATGACGCCA GCGCTGCGCA CGATCGGGCC CGCGGATCAA TAATTATCAT TAGTTAATGC
12781  GGGTCATTAG TTCATAGCCC ATATATGGAG TTCCGCGTTA CATAACTTAC GGTAAATGGC
       CCCAGTAATC AAGTATCGGG TATATACCTC AAGGCGCAAT GTATTGAATG CCATTTACCG
12841  CCGCCTGGCT GACCGCCCAA CGACCCCCGC CCATTGACGT CAATAATGAC GTATGTTCCC
       GGCGGACCGA CTGGCGGGTT GCTGGGGGCG GGTAACTGCA GTTATTACTG CATACAAGGG
12901  ATAGTAACGC CAATAGGGAC TTTCCATTGA CGTCAATGGG TGGAGTATTT ACGGTAAACT
       TATCATTGCG GTTATCCCTG AAAGGTAACT GCAGTTACCC ACCTCATAAA TGCCATTTGA
12961  GCCCACTTGG CAGTACATCA AGTGTATCAT ATGCCAAGTA CGCCCCCTAT TGACGTCAAT
       CGGGTGAACC GTCATGTAGT TCACATAGTA TACGGTTCAT GCGGGGGATA ACTGCAGTTA
13021  GACGGTAAAT GGCCCGCCTG GCATTATGCC CAGTACATGA CCTTATGGGA CTTTCCTACT
       CTGCCATTTA CCGGGCGGAC CGTAATACGG GTCATGTACT GGAATACCCT GAAAGGATGA
13081  TGGCAGTACA TCTACGTATT AGTCATCGCT ATTACCATGG TCGAGGTGAG CCCCACGTTC
       ACCGTCATGT AGATGCATAA TCAGTAGCGA TAATGGTACC AGCTCCACTC GGGGTGCAAG
13141  TGCTTCACTC TCCCCATCTC CCCCCCCTCC CCACCCCCAA TTTTGTATTT ATTTATTTTT
       ACGAAGTGAG AGGGGTAGAG GGGGGGGAGG GGTGGGGGTT AAAACATAAA TAAATAAAAA
13201  TAATTATTTT GTGCAGCGAT GGGGGCGGGG GGGGGGGGGG GGCGCGCGCC AGGCGGGGCG
       ATTAATAAAA CACGTCGCTA CCCCCGCCCC CCCCCCCCCC CCGCGCGCGG TCCGCCCCGC
13261  GGGCGGGGCG AGGGGCGGGG CGGGGCGAGG CGGAGAGGTG CGGCGGCAGC CAATCAGAGC
       CCCGCCCCGC TCCCCGCCCC GCCCCGCTCC GCCTCTCCAC GCCGCCGTCG GTTAGTCTCG
13321  GGCGCGCTCC GAAAGTTTCC TTTTATGGCG AGGCGGCGGC GGCGGCGGCC CTATAAAAAG
       CCGCGCGAGG CTTTCAAAGG AAAATACCGC TCCGCCGCCG CCGCCGCCGG GATATTTTTC
13381  CGAAGCGCGC GGCGGGCGGC TGCGACCTGC AGGTCCTCGC CATGGACCCT GATGATGTTG
       GCTTCGCGCG CCGCCCGCCG ACGCTGGACG TCCAGGAGCG GTACCTGGGA CTACTACAAC
13441  TTGATTCTTC TAAATCTTTT GTGATGGAAA ACTTTTCTTC GTACCACGGG ACTAAACCTG
       AACTAAGAAG ATTTAGAAAA CACTACCTTT TGAAAAGAAG CATGGTGCCC TGATTTGGAC
13501  GTTATGTAGA TTCCATTCAA AAAGGTATAC AAAAGCCAAA ATCTGGTACA CAAGGAAATT
       CAATACATCT AAGGTAAGTT TTTCCATATG TTTTCGGTTT TAGACCATGT GTTCCTTTAA
13561  ATGACGATGA TTGGAAAGGG TTTTATAGTA CCGACAATAA ATACGACGCT GCGGGATACT
       TACTGCTACT AACCTTTCCC AAAATATCAT GGCTGTTATT TATGCTGCGA CGCCCTATGA
13621  CTGTAGATAA TGAAAACCCG CTCTCTGGAA AAGCTGGAGG CGTGGTCAAA GTGACGTATC
       GACATCTATT ACTTTTGGGC GAGAGACCTT TTCGACCTCC GCACCAGTTT CACTGCATAG
13681  CAGGACTGAC GAAGGTTCTC GCACTAAAAG TGGATAATGC CGAAACTATT AAGAAAGAGT
       GTCCTGACTG CTTCCAAGAG CGTGATTTTC ACCTATTACG GCTTTGATAA TTCTTTCTCA
13741  TAGGTTTAAG TCTCACTGAA CCGTTGATGG AGCAAGTCGG AACGGAAGAG TTTATCAAAA
       ATCCAAATTC AGAGTGACTT GGCAACTACC TCGTTCAGCC TTGCCTTCTC AAATAGTTTT
13801  GGTTCGGTGA TGGTGCTTCG CGTGTAGTGC TCAGCCTTCC CTTCGCTGAG GGGAGTTCTA
       CCAAGCCACT ACCACGAAGC GCACATCACG AGTCGGAAGG GAAGCGACTC CCCTCAAGAT
13861  GCGTTGAATA TATTAATAAC TGGGAACAGG CGAAAGCGTT AAGCGTAGAA CTTGAGATTA
       CGCAACTTAT ATAATTATTG ACCCTTGTCC GCTTTCGCAA TTCGCATCTT GAACTCTAAT
13921  ATTTTGAAAC CCGTGGAAAA CGTGGCCAAG ATGCGATGTA TGAGTATATG GCTCAAGCCT
       TAAAACTTTG GGCACCTTTT GCACCGGTTC TACGCTACAT ACTCATATAC CGAGTTCGGA
13981  GTGCAGGAAA TCGTGTCAGG CGATCTCTTT GTGAAGGAAA CCTTACTTCT GTGGTGTGAC
       CACGTCCTTT AGCACAGTCC GCTAGAGAAA CACTTCCTTT GGAATGAAGA CACCACACTG
14041  ATAATTGGAC AAACTACCTA CAGAGATTTA AAGCTCTAAG GTAAATATAA AATTTTTAAG
       TATTAACCTG TTTGATGGAT GTCTCTAAAT TTCGAGATTC CATTTATATT TTAAAAATTC
14101  TGTATAATGT GTTAAACTAC TGATTCCTAA TTGTTTGTGT ATTTTAGATT CCAACCTATG
       ACATATTACA CAATTTGATG ACTAAGGATT AACAAACACA TAAAATCTAA GGTTGGATAC
14161  GAACTGATGA ATGGGAGCAG TGGTGGAATG CAGATCCACT AGGATCTAAC TTGTTTATTG
       CTTGACTACT TACCCTCGTC ACCACCTTAC GTCTAGGTGA TCCTAGATTG AACAAATAAC
14221  CAGCTTATAA TGGTTACAAA TAAAGCAATA GCATCACAAA TTTCACAAAT AAAGCATTTT
       GTCGAATATT ACCAATGTTT ATTTCGTTAT CGTAGTGTTT AAAGTGTTTA TTTCGTAAAA
14281  TTTCACTGCA TTCTAGTTGT GGTTTGTCCA AACTCATCAA TGTATCTTAT CATGTCTGGA
       AAAGTGACGT AAGATCAACA CCAAACAGGT TTGAGTAGTT ACATAGAATA GTACAGACCT
14341  TCGTAGTTCT AGAGCGGACC GAGGGGGCCC GTACTACGCC TTAAGTGAGT CGTATTACGG
       AGCATCAAGA TCTCGCCTGG CTCCCCCGGG CATGATGCGG AATTCACTCA GCATAATGCC
14401  ACTGGCCGTC GTTTTACAAC GTCGTGACTG GGAAAACCCT GGCGTTACCC AACTTAATCG
       TGACCGGCAG CAAAATGTTG CAGCACTGAC CCTTTTGGGA CCGCAATGGG TTGAATTAGC
14461  CCTTGCAGCA CATCCCCCTT TCGCCAGCTG GCGTAATAGC GAAGAGGCCC GCACCGATCG
       GGAACGTCGT GTAGGGGGAA AGCGGTCGAC CGCATTATCG CTTCTCCGGG CGTGGCTAGC
14521  CCCTTCCCAA CAGTTGCGCA GCCTGAATGG CGAATGGCGC TTCGCTTGGT AATAAAGCCC
       GGGAAGGGTT GTCAACGCGT CGGACTTACC GCTTACCGCG AAGCGAACCA TTATTTCGGG
14581  GCTTCGGCGG GCTTTTTTTT GTTAACTACG TCAGGTGGCA CTTTTCGGGG AAATGTGCGC
       CGAAGCCGCC CGAAAAAAAA CAATTGATGC AGTCCACCGT GAAAAGCCCC TTTACACGCG
14641  GGAACCCCTA TTTGTTTATT TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA
       CCTTGGGGAT AAACAAATAA AAAGATTTAT GTAAGTTTAT ACATAGGCGA GTACTCTGTT
14701  TAACCCTGAT AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT TCAACATTTC
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       ATTGGGACTA TTTACGAAGT TATTATAACT TTTTCCTTCT CATACTCATA AGTTGTAAAG
14761  CGTGTCGCCC TTATTCCCTT TTTTGCGGCA TTTTGCCTTC CTGTTTTTGC TCACCCAGAA
       GCACAGCGGG AATAAGGGAA AAAACGCCGT AAAACGGAAG GACAAAAACG AGTGGGTCTT
14821  ACGCTGGTGA AAGTAAAAGA TGCTGAAGAT CAGTTGGGTG CACGAGTGGG TTACATCGAA
       TGCGACCACT TTCATTTTCT ACGACTTCTA GTCAACCCAC GTGCTCACCC AATGTAGCTT
14881  CTGGATCTCA ACAGCGGTAA GATCCTTGAG AGTTTTCGCC CCGAAGAACG TTCTCCAATG
       GACCTAGAGT TGTCGCCATT CTAGGAACTC TCAAAAGCGG GGCTTCTTGC AAGAGGTTAC
14941  ATGAGCACTT TTAAAGTTCT GCTATGTGGC GCGGTATTAT CCCGTGTTGA CGCCGGGCAA
       TACTCGTGAA AATTTCAAGA CGATACACCG CGCCATAATA GGGCACAACT GCGGCCCGTT
15001  GAGCAACTCG GTCGCCGCAT ACACTATTCT CAGAATGACT TGGTTGAGTA CTCACCAGTC
       CTCGTTGAGC CAGCGGCGTA TGTGATAAGA GTCTTACTGA ACCAACTCAT GAGTGGTCAG
15061  ACAGAAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAT TATGCAGTGC TGCCATAACC
       TGTCTTTTCG TAGAATGCCT ACCGTACTGT CATTCTCTTA ATACGTCACG ACGGTATTGG
15121  ATGAGTGATA ACACTGCGGC CAACTTACTT CTGACAACGA TCGGAGGACC GAAGGAGCTA
       TACTCACTAT TGTGACGCCG GTTGAATGAA GACTGTTGCT AGCCTCCTGG CTTCCTCGAT
15181  ACCGCTTTTT TGCACAACAT GGGGGATCAT GTAACTCGCC TTGATCGTTG GGAACCGGAG
       TGGCGAAAAA ACGTGTTGTA CCCCCTAGTA CATTGAGCGG AACTAGCAAC CCTTGGCCTC
15241  CTGAATGAAG CCATACCAAA CGACGAGCGT GACACCACGA TGCCTGTAGC AATGGCAACA
       GACTTACTTC GGTATGGTTT GCTGCTCGCA CTGTGGTGCT ACGGACATCG TTACCGTTGT
15301  ACGTTGCGCA AACTATTAAC TGGCGAACTA CTTACTCTAG CTTCCCGGCA ACAATTAATA
       TGCAACGCGT TTGATAATTG ACCGCTTGAT GAATGAGATC GAAGGGCCGT TGTTAATTAT
15361  GACTGGATGG AGGCGGATAA AGTTGCAGGA CCACTTCTGC GCTCGGCCCT TCCGGCTGGC
       CTGACCTACC TCCGCCTATT TCAACGTCCT GGTGAAGACG CGAGCCGGGA AGGCCGACCG
15421  TGGTTTATTG CTGATAAATC TGGAGCCGGT GAGCGTGGGT CTCGCGGTAT CATTGCAGCA
       ACCAAATAAC GACTATTTAG ACCTCGGCCA CTCGCACCCA GAGCGCCATA GTAACGTCGT
15481  CTGGGGCCAG ATGGTAAGCC CTCCCGTATC GTAGTTATCT ACACGACGGG GAGTCAGGCA
       GACCCCGGTC TACCATTCGG GAGGGCATAG CATCAATAGA TGTGCTGCCC CTCAGTCCGT
15541  ACTATGGATG AACGAAATAG ACAGATCGCT GAGATAGGTG CCTCACTGAT TAAGCATTGG
       TGATACCTAC TTGCTTTATC TGTCTAGCGA CTCTATCCAC GGAGTGACTA ATTCGTAACC
15601  TAACTGTCAG ACCAAGTTTA CTCATATATA CTTTAGATTG ATTTACCCCG GTTGATAATC
       ATTGACAGTC TGGTTCAAAT GAGTATATAT GAAATCTAAC TAAATGGGGC CAACTATTAG
15661  AGAAAAGCCC CAAAAACAGG AAGATTGTAT AAGCAAATAT TTAAATTGTA AACGTTAATA
       TCTTTTCGGG GTTTTTGTCC TTCTAACATA TTCGTTTATA AATTTAACAT TTGCAATTAT
15721  TTTTGTTAAA ATTCGCGTTA AATTTTTGTT AAATCAGCTC ATTTTTTAAC CAATAGGCCG
       AAAACAATTT TAAGCGCAAT TTAAAAACAA TTTAGTCGAG TAAAAAATTG GTTATCCGGC
15781  AAATCGGCAA AATCCCTTAT AAATCAAAAG AATAGCCCGA GATAGGGTTG AGTGTTGTTC
       TTTAGCCGTT TTAGGGAATA TTTAGTTTTC TTATCGGGCT CTATCCCAAC TCACAACAAG
15841  CAGTTTGGAA CAAGAGTCCA CTATTAAAGA ACGTGGACTC CAACGTCAAA GGGCGAAAAA
       GTCAAACCTT GTTCTCAGGT GATAATTTCT TGCACCTGAG GTTGCAGTTT CCCGCTTTTT
15901  CCGTCTATCA GGGCGATGGC CCACTACGTG AACCATCACC CAAATCAAGT TTTTTGGGGT
       GGCAGATAGT CCCGCTACCG GGTGATGCAC TTGGTAGTGG GTTTAGTTCA AAAAACCCCA
15961  CGAGGTGCCG TAAAGCACTA AATCGGAACC CTAAAGGGAG CCCCCGATTT AGAGCTTGAC
       GCTCCACGGC ATTTCGTGAT TTAGCCTTGG GATTTCCCTC GGGGGCTAAA TCTCGAACTG
16021  GGGGAAAGCG AACGTGGCGA GAAAGGAAGG GAAGAAAGCG AAAGGAGCGG GCGCTAGGGC
       CCCCTTTCGC TTGCACCGCT CTTTCCTTCC CTTCTTTCGC TTTCCTCGCC CGCGATCCCG
16081  GCTGGCAAGT GTAGCGGTCA CGCTGCGCGT AACCACCACA CCCGCCGCGC TTAATGCGCC
       CGACCGTTCA CATCGCCAGT GCGACGCGCA TTGGTGGTGT GGGCGGCGCG AATTACGCGG
16141  GCTACAGGGC GCGTAAAAGG ATCTAGGTGA AGATCCTTTT TGATAATCTC ATGACCAAAA
       CGATGTCCCG CGCATTTTCC TAGATCCACT TCTAGGAAAA ACTATTAGAG TACTGGTTTT
16201  TCCCTTAACG TGAGTTTTCG TTCCACTGAG CGTCAGACCC CGTAGAAAAG ATCAAAGGAT
       AGGGAATTGC ACTCAAAAGC AAGGTGACTC GCAGTCTGGG GCATCTTTTC TAGTTTCCTA
16261  CTTCTTGAGA TCCTTTTTTT CTGCGCGTAA TCTGCTGCTT GCAAACAAAA AAACCACCGC
       GAAGAACTCT AGGAAAAAAA GACGCGCATT AGACGACGAA CGTTTGTTTT TTTGGTGGCG
16321  TACCAGCGGT GGTTTGTTTG CCGGATCAAG AGCTACCAAC TCTTTTTCCG AAGGTAACTG
       ATGGTCGCCA CCAAACAAAC GGCCTAGTTC TCGATGGTTG AGAAAAAGGC TTCCATTGAC
16381  GCTTCAGCAG AGCGCAGATA CCAAATACTG TTCTTCTAGT GTAGCCGTAG TTAGGCCACC
       CGAAGTCGTC TCGCGTCTAT GGTTTATGAC AAGAAGATCA CATCGGCATC AATCCGGTGG
16441  ACTTCAAGAA CTCTGTAGCA CCGCCTACAT ACCTCGCTCT GCTAATCCTG TTACCAGTGG
       TGAAGTTCTT GAGACATCGT GGCGGATGTA TGGAGCGAGA CGATTAGGAC AATGGTCACC
16501  CTGCTGCCAG TGGCGATAAG TCGTGTCTTA CCGGGTTGGA CTCAAGACGA TAGTTACCGG
       GACGACGGTC ACCGCTATTC AGCACAGAAT GGCCCAACCT GAGTTCTGCT ATCAATGGCC
16561  ATAAGGCGCA GCGGTCGGGC TGAACGGGGG GTTCGTGCAC ACAGCCCAGC TTGGAGCGAA
       TATTCCGCGT CGCCAGCCCG ACTTGCCCCC CAAGCACGTG TGTCGGGTCG AACCTCGCTT
16621  CGACCTACAC CGAACTGAGA TACCTACAGC GTGAGCTATG AGAAAGCGCC ACGCTTCCCG
       GCTGGATGTG GCTTGACTCT ATGGATGTCG CACTCGATAC TCTTTCGCGG TGCGAAGGGC
16681  AAGGGAGAAA GGCGGACAGG TATCCGGTAA GCGGCAGGGT CGGAACAGGA GAGCGCACGA
       TTCCCTCTTT CCGCCTGTCC ATAGGCCATT CGCCGTCCCA GCCTTGTCCT CTCGCGTGCT
16741  GGGAGCTTCC AGGGGGAAAC GCCTGGTATC TTTATAGTCC TGTCGGGTTT CGCCACCTCT
       CCCTCGAAGG TCCCCCTTTG CGGACCATAG AAATATCAGG ACAGCCCAAA GCGGTGGAGA
16801  GACTTGAGCG TCGATTTTTG TGATGCTCGT CAGGGGGGCG GAGCCTATGG AAAAACGCCA
       CTGAACTCGC AGCTAAAAAC ACTACGAGCA GTCCCCCCGC CTCGGATACC TTTTTGCGGT
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16861  GCAACGCGGC CTTTTTACGG TTCCTGGCCT TTTGCTGGCC TTTTGCTCAC ATGTAATGTG
       CGTTGCGCCG GAAAAATGCC AAGGACCGGA AAACGACCGG AAAACGAGTG TACATTACAC
16921  AGTTAGCTCA CTCATTAGGC ACCCCAGGCT TTACACTTTA TGCTTCCGGC TCGTATGTTG
       TCAATCGAGT GAGTAATCCG TGGGGTCCGA AATGTGAAAT ACGAAGGCCG AGCATACAAC
16981  TGTGGAATTG TGAGCGGATA ACAATTTCAC ACAGGAAACA GCTATGACCA TGATTACGCC
       ACACCTTAAC ACTCGCCTAT TGTTAAAGTG TGTCCTTTGT CGATACTGGT ACTAATGCGG
17041  AAGCTACGTA ATACGACTCA CTAG
       TTCGATGCAT TATGCTGAGT GATC
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Supplemental Table S2, related to Figure 6. miR-155 targets in Tfh cells.

GeneID	GeneName	Fold (KO Tfh/Wt Tfh)
ENSMUSG00000022687	Boc	4.132471013
ENSMUSG00000020303	Stc2	3.56824407
ENSMUSG00000020607	Fam84a	2.901785139
ENSMUSG00000024673	Ms4a1	2.84088474
ENSMUSG00000000266	Mid2	2.48974778
ENSMUSG00000016239	Lonrf3	2.442990071
ENSMUSG00000033855	Ston1	2.427239553
ENSMUSG00000035678	Tnfsf9	2.18540581
ENSMUSG00000052062	Pard3b	1.901509966
ENSMUSG00000029135	Fosl2	1.834219505
ENSMUSG00000025231	Sufu	1.714252053
ENSMUSG00000053477	Tcf4	1.631977424
ENSMUSG00000031342	Gpm6b	1.624162789
ENSMUSG00000038518	Jarid2	1.595074557
ENSMUSG00000036986	Pml	1.584578904
ENSMUSG00000027394	Ttl	1.569198575
ENSMUSG00000031642	Sh3rf1	1.540609963
ENSMUSG00000030557	Mef2a	1.539563208
ENSMUSG00000036959	Bcorl1	1.533549708
ENSMUSG00000059005	Hnrnpa3	1.531220914
ENSMUSG00000022272	Myo10	1.524470528
ENSMUSG00000020716	Nf1	1.518882534
ENSMUSG00000022462	Slc38a2	1.515038651
ENSMUSG00000052155	Acvr2a	1.494249438
ENSMUSG00000022698	Naa50	1.494238873
ENSMUSG00000030265	Kras	1.485442849
ENSMUSG00000048796	Cyb561d1	1.480012294
ENSMUSG00000038679	Trps1	1.476525682
ENSMUSG00000052707	Tnrc6a	1.46288146
ENSMUSG00000054693	Adam10	1.462129971
ENSMUSG00000020612	Prkar1a	1.455590762
ENSMUSG00000028945	Rheb	1.45360465
ENSMUSG00000020780	Srp68	1.444017874
ENSMUSG00000020849	Ywhae	1.442014059
ENSMUSG00000015839	Nfe2l2	1.436223028
ENSMUSG00000062866	Phactr2	1.433196872
ENSMUSG00000045730	Adrb2	1.425026996

ENSMUSG00000027522	Stx16	1.417934175
ENSMUSG00000021109	Hif1a	1.413589472
ENSMUSG00000026464	Zc3h11a	1.409026602
ENSMUSG00000020134	Peli1	1.390659016
ENSMUSG00000059474	Mbtd1	1.388926966
ENSMUSG00000042349	Ikbke	1.374892289
ENSMUSG00000005371	Fbxo11	1.367102012
ENSMUSG00000040848	Sft2d2	1.355026569
ENSMUSG00000025583	Rptor	1.354645351
ENSMUSG00000047879	Usp14	1.345762271
ENSMUSG00000032688	Malt1	1.345399894
ENSMUSG00000033209	Ttc28	1.343441062
ENSMUSG00000016534	Lamp2	1.332914831
ENSMUSG00000024143	Rhoq	1.332582239
ENSMUSG00000069895	Atxn1l	1.331801472
ENSMUSG00000027189	Trim44	1.328798565
ENSMUSG00000033610	Pank1	1.325132572
ENSMUSG00000006527	Sfmbt1	1.323970264
ENSMUSG00000032216	Nedd4	1.321111964
ENSMUSG00000052302	Tbc1d30	1.320894342
ENSMUSG00000042390	Gatad2b	1.320015875
ENSMUSG00000034560	A230046K03Rik	1.317313057
ENSMUSG00000048787	Dcun1d3	1.315573816
ENSMUSG00000005871	Apc	1.31373844
ENSMUSG00000063663	Brwd3	1.309838825
ENSMUSG00000031309	Rps6ka3	1.303179342
ENSMUSG00000027351	Spred1	1.300165448
ENSMUSG00000032846	Zswim6	1.298247907
ENSMUSG00000073725	Lmbrd1	1.288794784
ENSMUSG00000028403	Zdhhc21	1.283790153
ENSMUSG00000048118	Arid4a	1.282609173
ENSMUSG00000025626	Phf6	1.281033452
ENSMUSG00000023927	Satb1	1.280430032
ENSMUSG00000027523	Gnas	1.261838129
ENSMUSG00000042599	Kdm7a	1.258831269
ENSMUSG00000049470	Aff4	1.253888792
ENSMUSG00000021377	Dek	1.252301923
ENSMUSG00000004994	Ccdc130	1.250746955
ENSMUSG00000034247	Plekhm1	1.249459449
ENSMUSG00000024095	Hnrpll	1.246636795
ENSMUSG00000031016	Wee1	1.245243301

ENSMUSG00000029684	Wasl	1.245216518
ENSMUSG00000047888	Tnrc6b	1.24465774
ENSMUSG00000029004	Mll5	1.243020466
ENSMUSG00000021277	Traf3	1.238129802
ENSMUSG00000020918	Kat2a	1.233963072
ENSMUSG00000032413	Rasa2	1.228470829
ENSMUSG00000024969	Mark2	1.223552546
ENSMUSG00000022285	Ywhaz	1.22078065
ENSMUSG00000038342	Mlxip	1.220723661
ENSMUSG00000041528	Rnf123	1.217797469
ENSMUSG00000022663	Atg3	1.21660915
ENSMUSG00000029178	Klf3	1.212518534
ENSMUSG00000021488	Nsd1	1.212306842
ENSMUSG00000024241	Sos1	1.208561735
ENSMUSG00000037674	Rfx7	1.20590725

Supplemental Table S3, related to Figure 6. miR-155 targets in CD4$^+$ T cells from middle aged mice.

GeneID	GeneName	Fold(DKO/WT)	Fold(155KO/WT)	Fold(146KO/WT)
ENSMUSG00000022272	Myo10	2.331431916	2.455943208	1.040814644
ENSMUSG00000052040	Klf13	2.293345153	2.140585557	1.134085436
ENSMUSG00000023927	Satb1	1.753170089	2.119641237	-2.123911717
ENSMUSG00000056493	Foxk1	2.122844505	2.049143189	1.177268668
ENSMUSG00000047712	Ust	1.357459015	2.030804131	-2.009690169
ENSMUSG00000039087	Rreb1	1.990078721	2.003146727	1.00555831
ENSMUSG00000029135	Fosl2	1.810604192	1.938201454	1.163551873
ENSMUSG00000048796	Cyb561d1	1.6461751	1.806782568	1.183826453
ENSMUSG00000037896	Rcor1	1.616575625	1.734108057	1.063441255
ENSMUSG00000045730	Adrb2	1.476483874	1.733787336	-1.358271346
ENSMUSG00000020918	Kat2a	1.460721661	1.714166146	1.050074461
ENSMUSG00000018076	Med13l	1.736410739	1.707203809	-1.018280643
ENSMUSG00000041235	Chd7	1.402127263	1.683182605	-1.152584937
ENSMUSG00000029196	Tada2b	1.624537222	1.682953948	1.095369352
ENSMUSG00000035696	Rnf38	1.591433584	1.602117389	1.119839481
ENSMUSG00000020593	Lpin1	1.612429519	1.577333363	-1.106345796
ENSMUSG00000015839	Nfe2l2	1.210530643	1.575118642	-1.171658912
ENSMUSG00000042349	Ikbke	1.448399717	1.569226387	1.093022947
ENSMUSG00000025026	Add3	1.395044227	1.549231703	-1.27170831
ENSMUSG00000042599	Kdm7a	1.308522127	1.545562365	-1.171988595
ENSMUSG00000031137	Fgf13	1.268552229	1.537266242	-1.184140386
ENSMUSG00000041961	Znrf3	1.616055561	1.534306839	-1.554512481
ENSMUSG00000020134	Peli1	1.300818987	1.53384283	1.08185986
ENSMUSG00000031309	Rps6ka3	1.667626554	1.53208449	-1.05203863
ENSMUSG00000020198	Ap3d1	1.448209079	1.511043926	1.02235682
ENSMUSG00000029016	Clcn6	1.548078619	1.5039673	1.092543915
ENSMUSG00000024642	Tle4	1.376390815	1.503573027	-1.193613766
ENSMUSG00000006585	Cdt1	1.476242162	1.474086413	1.111798415
ENSMUSG00000020941	Map3k14	1.382172615	1.467698363	-1.475561447
ENSMUSG00000026464	Zc3h11a	1.262214148	1.463216684	1.115516876
ENSMUSG00000003382	Etv3	1.24487937	1.44431808	-1.309482391
ENSMUSG00000027394	Ttl	1.390026705	1.442646129	1.071066102
ENSMUSG00000022387	Brd1	1.28245713	1.430638627	-1.12757029
ENSMUSG00000026361	Cdc73	1.396501729	1.42101281	1.135182151
ENSMUSG00000025612	Bach1	1.32784858	1.420055711	-1.165951833
ENSMUSG00000027522	Stx16	1.29407602	1.418086661	1.181498092
ENSMUSG00000049470	Aff4	1.325354751	1.396103288	-1.127437649
ENSMUSG00000078515	Ddi2	1.299912982	1.390122576	1.06998946
ENSMUSG00000026288	Inpp5d	1.327572886	1.387980068	1.170072496

ENSMUSG00000025583	Rptor	1.53709262	1.381652415	1.120688701
ENSMUSG00000051675	Trim32	1.216310022	1.37186213	-1.07658812
ENSMUSG00000045005	Fzd5	1.205762729	1.363341439	1.118656148
ENSMUSG00000021277	Traf3	1.287966483	1.357344162	1.151881702
ENSMUSG00000003882	Il7r	1.204859507	1.352716094	-1.289626916
ENSMUSG00000021488	Nsd1	1.337974138	1.345900558	1.024598788
ENSMUSG00000001280	Sp1	1.341300231	1.341849323	1.176540669
ENSMUSG00000026335	Pam	1.434857733	1.328979776	1.157721514
ENSMUSG00000037926	Ssh2	1.24064617	1.324864274	-1.091289633
ENSMUSG00000069895	Atxn1l	1.489072946	1.318525104	1.196667726
ENSMUSG00000003345	Csnk1g2	1.316242673	1.313048922	-1.006804118
ENSMUSG00000026028	Trak2	1.344302542	1.30566628	1.015419713
ENSMUSG00000039615	Stub1	1.308449442	1.29151876	1.017423574
ENSMUSG00000037824	Tspan14	1.299464346	1.287960207	-1.443989648
ENSMUSG00000057230	Aak1	1.22066489	1.278568247	-1.13042255
ENSMUSG00000094483	Purb	1.224462143	1.277469857	1.105740188
ENSMUSG00000074748	Atxn7l3b	1.244765112	1.277197045	1.039735064
ENSMUSG00000040848	Sft2d2	1.365935348	1.275904191	-1.000255111
ENSMUSG00000032846	Zswim6	1.230379047	1.274611604	1.144202253
ENSMUSG00000043411	Usp48	1.209453565	1.274201552	1.067266717
ENSMUSG00000032035	Ets1	1.247165375	1.258059678	-1.09858344
ENSMUSG00000033237	Arid2	1.317316892	1.24794774	-1.054503717
ENSMUSG00000055200	Sertad3	1.312583043	1.238857869	1.11202553
ENSMUSG00000074221	Zfp568	1.225266054	1.216741478	-1.359511608

Supplemental Table S4, related to Figure 6. shRNA targeting sequences and quantitative PCR (qPCR) Primers.

Gene	**Targeting sequence**	
Fosl2	TCCTAGTGAGCTTCCTTTCTT	
Peli1	ACGGTGGTGGTTGAATATACT	
Gene	**Forward Primer Sequence**	**Reverse Primer Sequence**
BCL6	CCTGTGAAATCTGTGGCACTCG	CGCAGTTGGCTTTTGTGACG
CXCR5	GACCTTCAACCGTGCCTTTCTC	GAACTTGCCCTCAGTCTGTAATCC
IL21	GCTCCACAAGATGTAAAGGGGC	CCACGAGGTCAATGATGAATGTC
ICOS	CAGGAGAAATCAATGGCTCGG	TTGGTCTTGGTGAGTTCGCAG
NFE2L2	TAGATGACCATGAGTCGCTTGC	GCCAAACTTGCTCCATGTCC
RPTOR	TTTGTCTACGACTGTTCCAATGC	GCTACCTCTAGTTCCTGCTCC
FOSL2	CCAGCAGAAGTTCCGGGTAG	GTAGGGATGTGAGCGTGGATA
PELI1	GCCCCAGTAAAATATGGCGAA	CCCCATTTGCCTTAGGTCTTT
L32	AAGCGAAACTGGCGGAAAC	TAACCGATGTTGGGCATCAG