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AID Is Required for the Chromosomal Breaks in *c-myc* that Lead to *c-myc/IgH* Translocations

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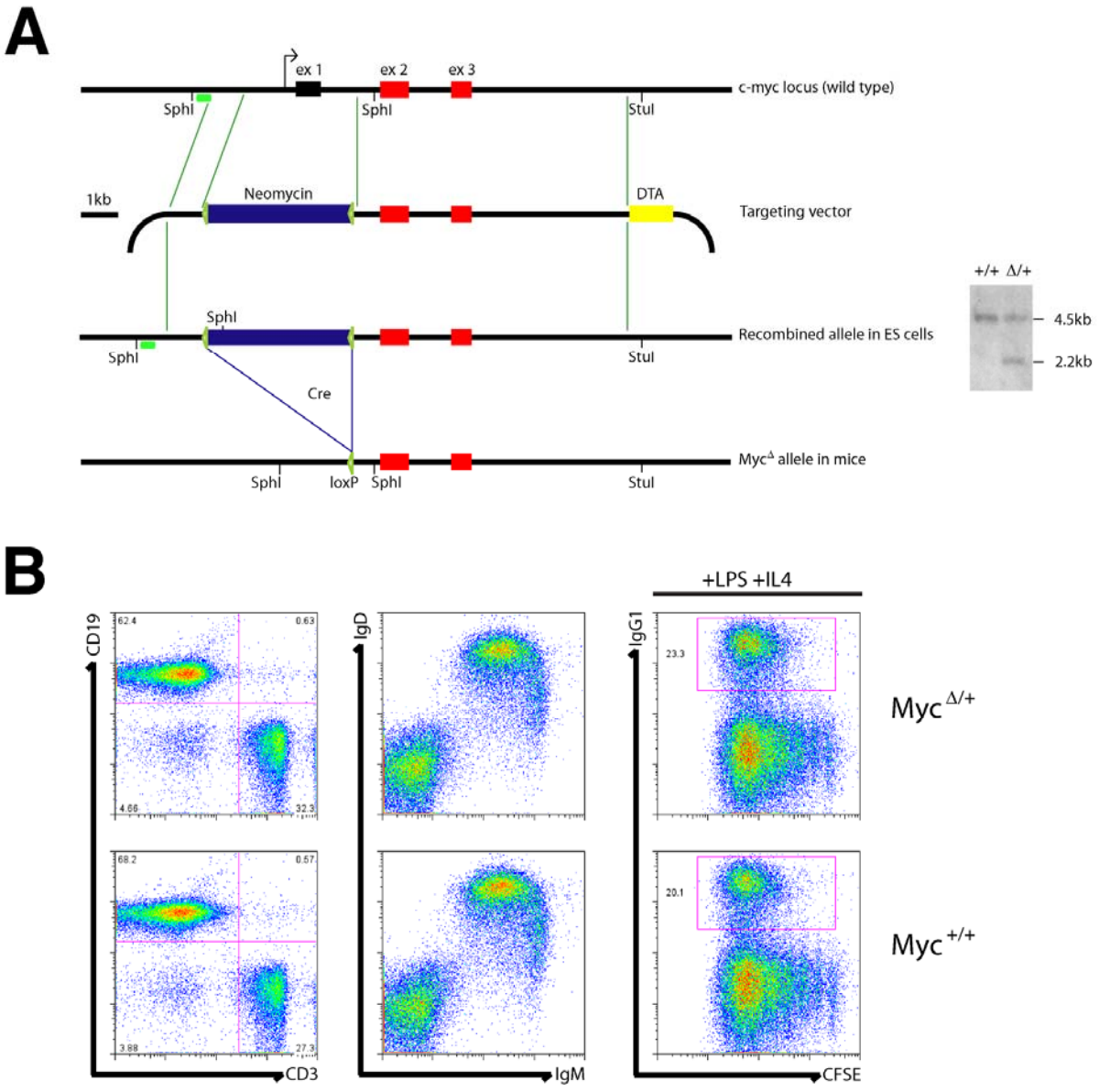


Figure S1. Knock-out strategy for the Myc$^{\Delta}$ allele.
(A) Targeting strategy is shown along with the genomic structure of the wild type murine *c-myc* locus, the targeting vector, the recombined allele in ES cells and in mice after removal of the neomycin-based ACN cassette (Bunting et al., 1999). Southern blot analysis of ES cell genomic DNA digested with SphI revealed proper integration upon hybridization with

a radiolabeled probe (PCR product of 5-CATTCTGACTCCTTTTGCCC-3 and 5-TCAGAGGTGGCTATTCAGTTGC-3), yielding fragments of the indicated sizes. Diphtheria toxin A (DTA) was used for negative selection. The following primers were used for generating the targeting vector: short arm of homology, 5-GGCGCGCCTCACAAATCCGAGAGCCACAAC-3 and 5-GGCCGGCCTGCGCAGTCCAGTAA-3; long arm of homology, 5-TTAATTAACACCCAGTGCTGAATCGCTGC-3 and 5-GCGGCCGCCACCACTCTGTAGGAAATGCC-3. For genotyping, 35 cycles of PCR (95C, 45 s; 59C, 45 s; and 72C, 2 min) were performed with primers 5-GTGAAAACCGACTGTGGCCCTGGAA-3, 5-GGGGAGGGGGTGTCAAATAATAAGA-3 and 5-CAACCGCAGATGAGGTCTATGC-3. The size of the wild type allele is 0.4 kb, the Myc^{Δ} allele is 0.3 kb. (B) Flow cytometric analysis of splenocytes from age-matched wild type ($Myc^{+/+}$) and mutant ($Myc^{\Delta/+}$) mice reveals normal B lymphocyte development and activation in $Myc^{\Delta/+}$ mice. Immuno-staining was performed with the indicated markers on total spleen cells (left and center panels) or on LPS and IL-4 activated B cells labeled with CFSE to track cell division (right panels). Representative of three independent experiments.

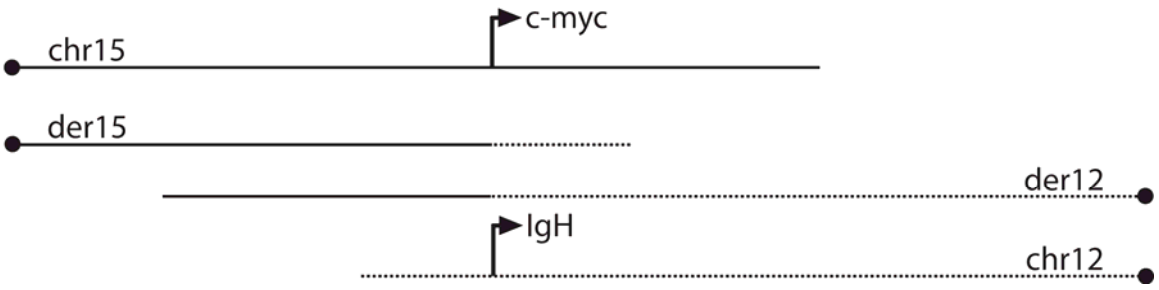


Figure S2. Diagram of balanced *c-myc/IgH* translocation.
Schematic representation of mouse chromosome 15 with *c-myc* transcribing towards the telomere and chromosome 12 with *IgH* transcribing towards the centromere. Centromeres are symbolized by circles. The derivative chromosomes der12 and der15, products of the balanced *c-myc/IgH* translocation, are also shown.

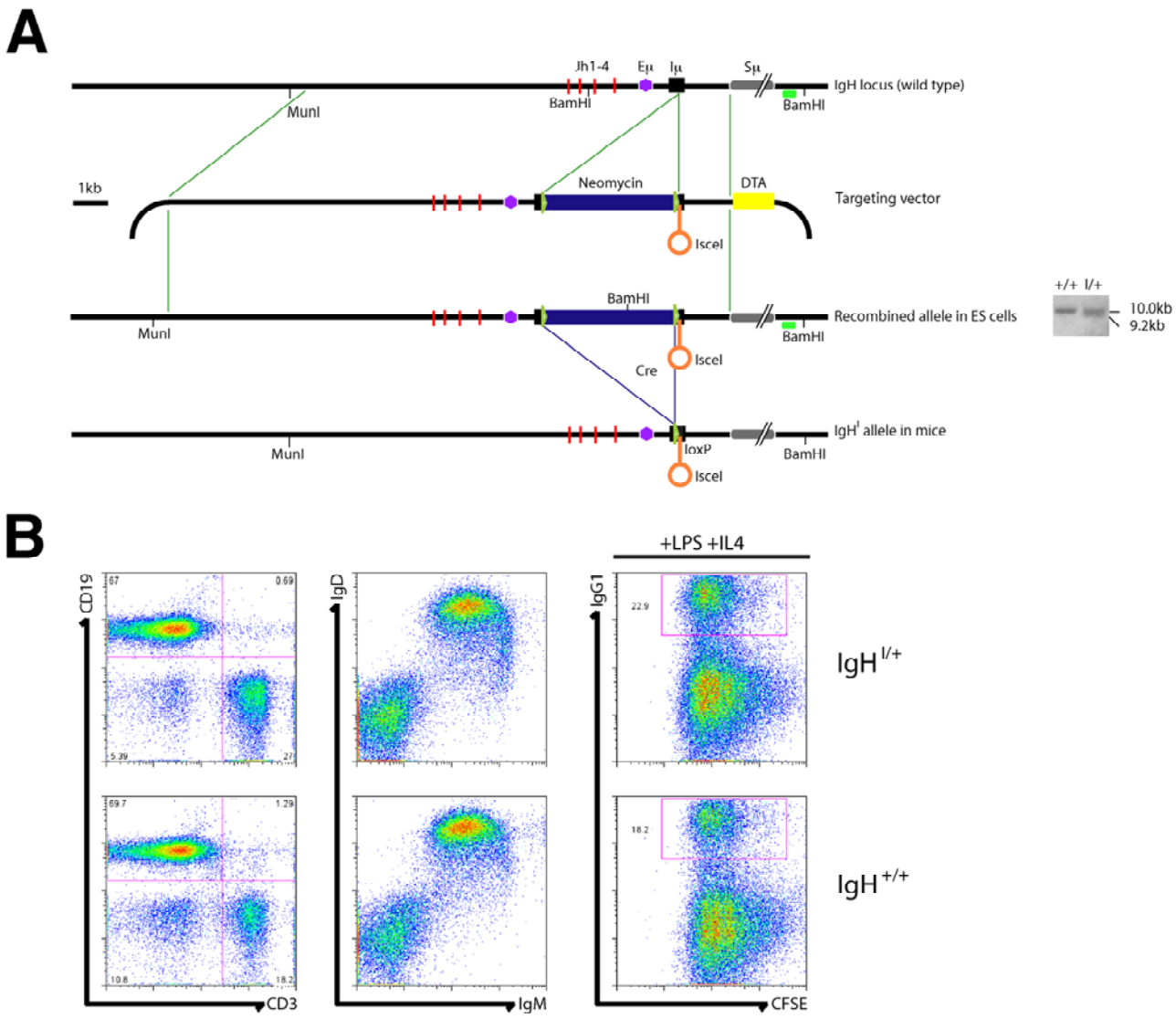


Figure S3. Knock-in strategy for the IgH^{I} allele.
(A) The targeting strategy is shown along with the genomic structure of the wild type murine *IgH* locus, the targeting vector, the recombined allele in ES cells and in mice after removal of the neomycin-based ACN cassette (Bunting et al., 1999). Southern blot analysis of ES cell genomic DNA digested with BamHI revealed proper integration upon hybridization with a radiolabeled probe (PCR product of 5- AAATGAGGAAGGCTGAGCAAGG-3 and 5-AGGAAGGTGGGTTATGTTGGGG-3), yielding fragments of the indicated sizes. Diphtheria toxin A (DTA) was used for negative selection. The following primers were used for generating the targeting vector and introducing the I-SceI recognition sequence: long arm of homology, 5- GGCGCGCCGATGAGAGCAGTGTAGGTCTATGGG-3 and 5-GGCCGGCCCAGAAGCCACAACCATACATTCC-3; short arm of homology, 5-GCGGCCGCAGTTACGCTAGGGATAACAGGGTAATATAGCCACCCATCCACCTGGCTGC-3 (I-SceI site is underlined) and 5-GCGGCCGCATTCCAGTTTGGCTCATCTCG-3. For genotyping, 35 cycles of PCR (95C, 45 s; 56C, 45 s; and 72C, 30 s) were performed with primers 5-TGGGAATGTATGGTTGTGGCTTC-3 and

5-GGAGAGGTCCAGAGTCTTTGTGTG-3. The size of the wild type allele is 0.1 kb, the IgH^{I} allele is 0.25 kb. (B) Flow cytometric analysis of spleen cells from age-matched wild type ($IgH^{+/+}$) and mutant ($IgH^{I/+}$) mice reveals normal B lymphocyte development and activation in $IgH^{I/+}$ mice. Immuno-staining was performed with the indicated markers on total spleen cells (left and center panels) or on LPS and IL-4 activated B cells labeled with CFSE to track cell division (right panels). Representative of two independent experiments.

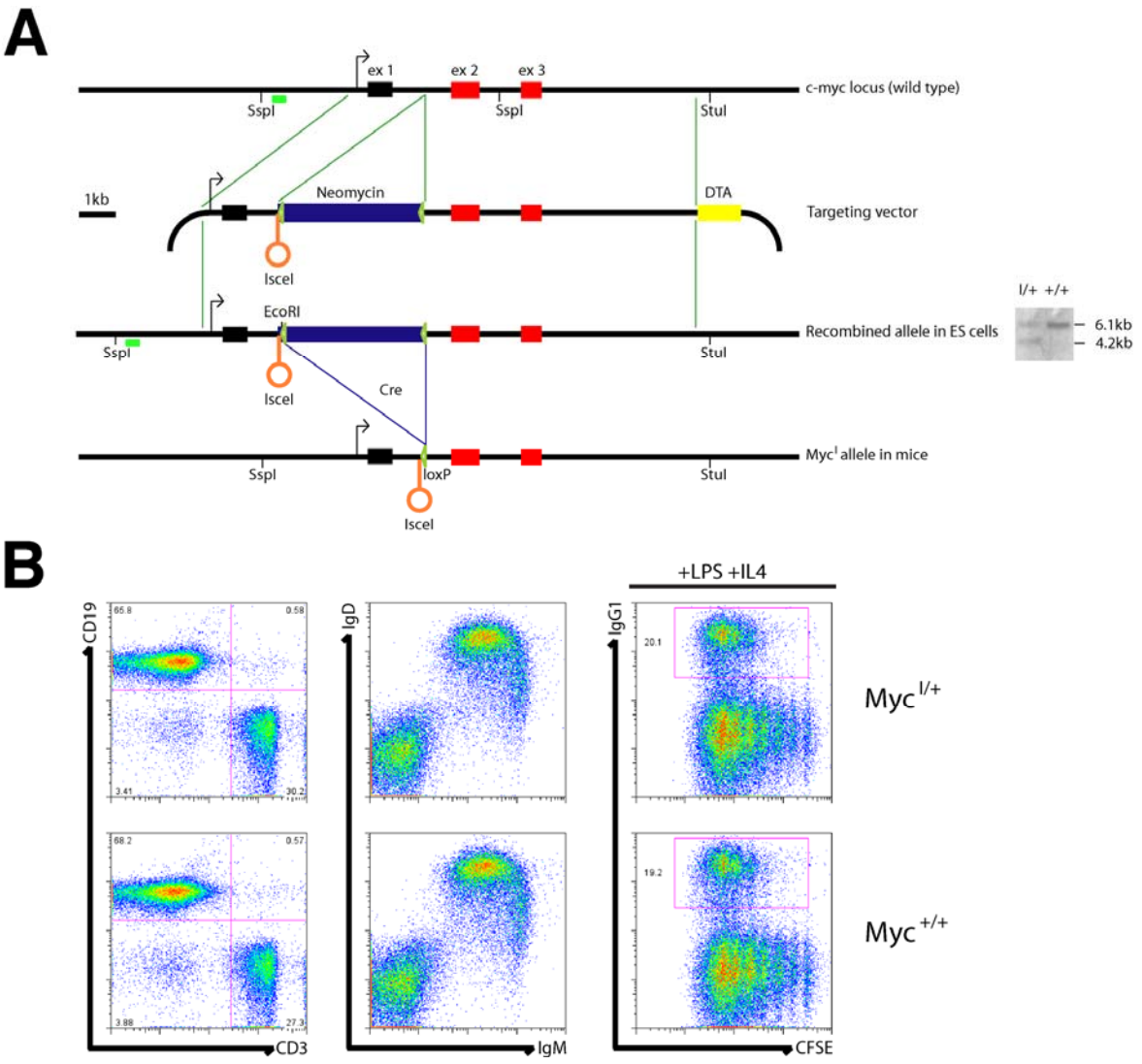


Figure S4. Knock-in strategy for the Myc^{I} allele.
(A) The targeting strategy is shown along with the genomic structure of the wild type murine *c-myc* locus, the targeting vector, the recombined allele in ES cells and in mice after removal of the neomycin-based ACN cassette (Bunting et al., 1999). Southern blot analysis of ES cell genomic DNA digested with SspI revealed proper integration upon hybridization with a radiolabeled probe (PCR product of 5-CATTCTGACTCCTTTTGCCC-3 and 5-TCAGAGGTGGCTATTCAGTTGC-3), yielding fragments of the indicated sizes. Diphtheria toxin A (DTA) was used for negative selection. The following primers were used for generating the targeting vector and introducing the I-SceI recognition sequence: short arm of homology, 5- GGCCGGCCGGGAGACCTACAGGGGAAAGAGCCG-3 and 5-GGCCGGCCATTACCCTGTTATCCCTACAGGGCGTCTTCCCTCTCCCCG-3 (I-SceI site is underlined); long arm of homology, 5-TTAATTAACACCCAGTGCTGAATCGCTGC-3 and 5-GCGGCCGCCACCACTCTGTAGGAAATGCC-3. For genotyping, 35 cycles of PCR (95C, 45 s; 58C, 45 s; and 72C, 45 s) were performed with primers 5-TTGGGGGAAACCAGAGGGAATCC-3 and 5-GGGAGGGGGTGTCAAATAATAAGAG-3. The size of the wild type allele is 0.25 kb, the Myc^{I} allele is 0.35 kb.(B) Flow cytometric analysis of spleen cells from age-

matched wild type ($Myc^{+/+}$) and mutant ($Myc^{I/+}$) mice reveals normal B lymphocyte development and activation in $Myc^{I/+}$ mice. Immuno-staining was performed with the indicated markers on total spleen cells (left and center panels) or on LPS and IL-4 activated B cells labeled with CFSE to track cell division (right panels). Representative of two independent experiments.

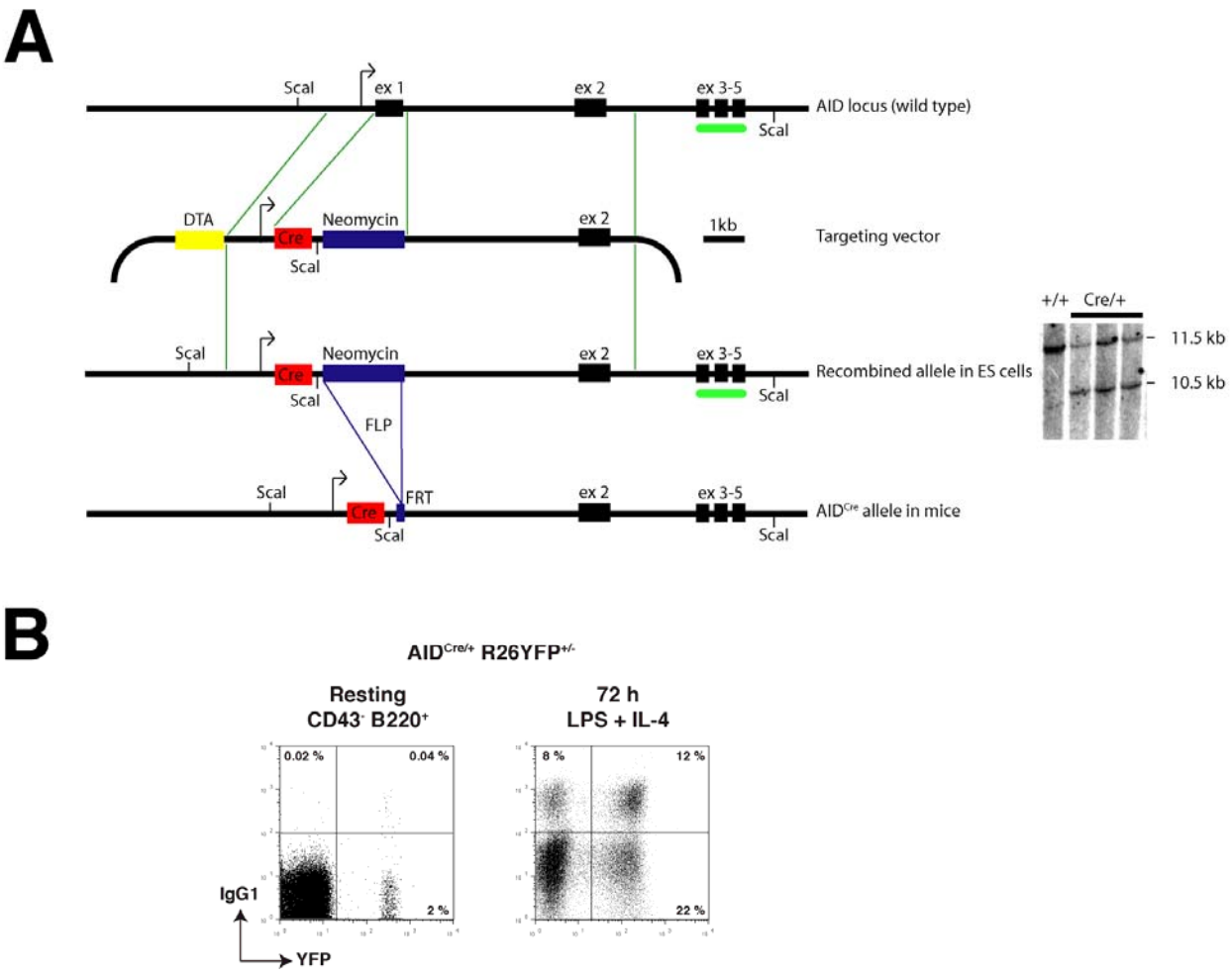


Figure S5. Targeted insertion of Cre recombinase into the mouse *aicda* locus (AID$^{Cre/+}$ mice).

The targeting strategy is shown along with the genomic structure of the wild type murine *aicda* locus, the targeting vector, the recombined allele in ES cells and in mice after germline deletion of the selection cassette by crossing with FLPer mice. The inserted Cre recombinase DNA contains a nuclear localization signal, an SV40 T-antigen intron and an HSV thymidine kinase polyA signal. Expression of the neomycin resistance gene is driven by the PGK promoter. To increase the frequency of targeting, the neomycin DNA lacked a polyA and included the splice donor sequence of AID's exon 2. Southern blot analysis of ES cell genomic DNA digested with ScaI revealed proper integration upon hybridization with a radiolabeled probe (amplified with primers 5-CTGGCTGCCACGTGGAATTGTTG-3 and 5-TCCCAACATACGAAATGCATCTC-3), yielding fragments of the indicated sizes. Diphtheria toxin A (DTA) was used for negative selection. The following primers were used for generating the targeting vector: short arm of homology, 5-ATAAGAATGCGGCCGCACATTCAGAGCAAGCCGCAGTGGTG-3 and 5-CCTTAATTAATAGTACTCCAAATCTCAGGACAAGTCAAGGC-3; long arm of homology, 5-CCATTAATTAAGCAGAGCTAGAGCCGGCTTGTGGTAATAAC-3 and 5-GGCGCGCCGTGACTGTAATAACTGCAATCGTAATAGG-3; Cre recombinase DNA, combined PCR with the products of 5-GGCATAAAACTGAGTGTAACAAACGGAAGGAAC-3 and 5-

GACACCTTCCTCTTCTTCTTGGGCATATCGGTCTCCAGCGTGACTTTCTTG-3 with 5-CAAGAAAGTCACGCTGGAGACCGATATGCCCAAGAAGAAGAGGAAGGTGTC-3 and 5-CCTTAATTAATACGCGTCGATCGAGTACTCGACCGAACAAACGACCCAACAC-3. The frt-flanked Neomycin cassette was removed in vivo by crossing to FLPer mice (a gift by Dr. Susan Dymecki (Rodriguez et al., 2000)). For genotyping, 35 cycles of PCR (95C, 45 s; 57C, 45 s; and 72C, 1 min) were performed with primers 5-GGACCCAACCCAGGAGGCAGATGT-3, 5-CACTCGTTGCATCGACCGGTAATG-3 and 5-CCTCTAAGGCTTCGCTGTTATTACCAC-3. The wild type allele is 0.5 kb, the AID^{Cre} allele is 0.3 kb. (B) Flow cytometric analysis of splenic B cells from $AID^{Cre/+}$, ROSA26-STOP-$YFP^{+/-}$ (Srinivas et al., 2001) mice prior and after stimulation with LPS and IL-4 shows regulated activity of Cre.

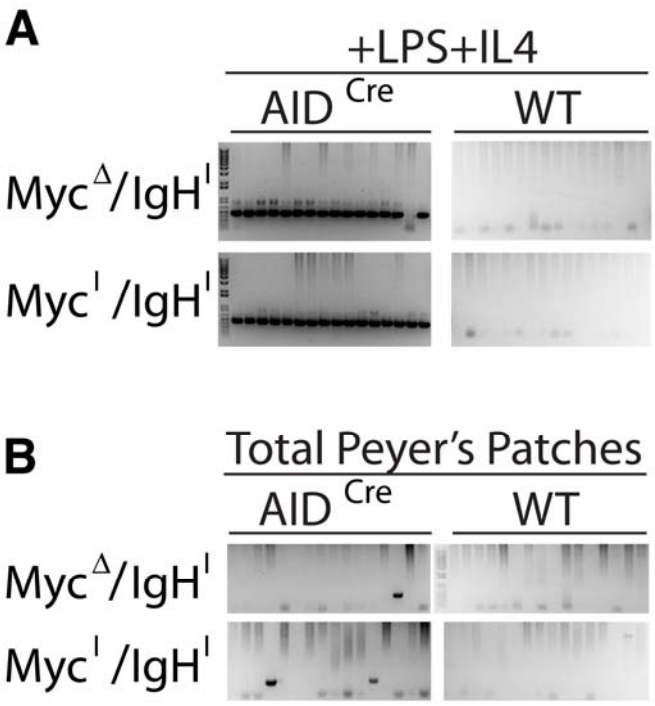


Figure S6. AID^{Cre} mediated translocations *in vivo*.
(A) Agarose gel with 0.5 kb PCR products corresponding to precise loxP-to-loxP *c-myc/IgH* translocations (as verified by sequencing). B cells of the indicated genotypes were stimulated with LPS and IL-4. 100,000 cells were assayed in each lane. (B) Agarose gel with 0.5 kb PCR products corresponding to precise loxP-to-loxP *c-myc/IgH* translocations (as verified by sequencing). DNA from total Peyer's Patches from mice with the indicated genotypes were analyzed. 100,000 cells were assayed in each lane.

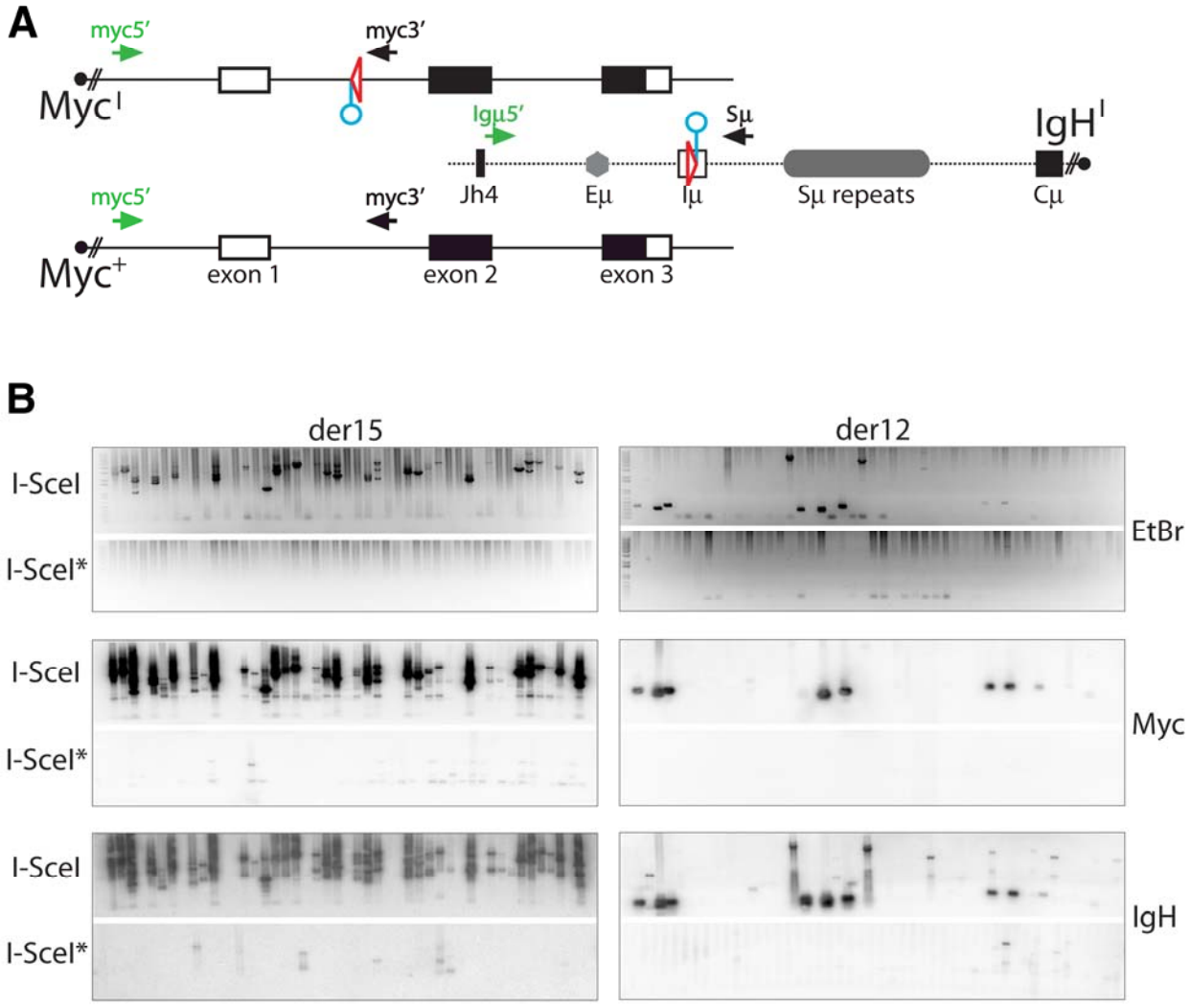


Figure S7. I-SceI induced translocations in AID deficient B lymphocytes: Southern Blot.

(A) Schematic representation of the Myc^{I}, Myc^{+} and IgH^{I} alleles with the PCR primers for detecting der12 and der15 *c-myc/IgH* translocations. Circles point to recognition sequences for I-SceI. (B) I-SceI rescues translocation in the absence of AID. Representative ethidium bromide (EtBr) stained agarose gels from Figure 4B were Southern blotted and oligo-probed for *c-myc* and *IgH*, as indicated, to verify translocations.

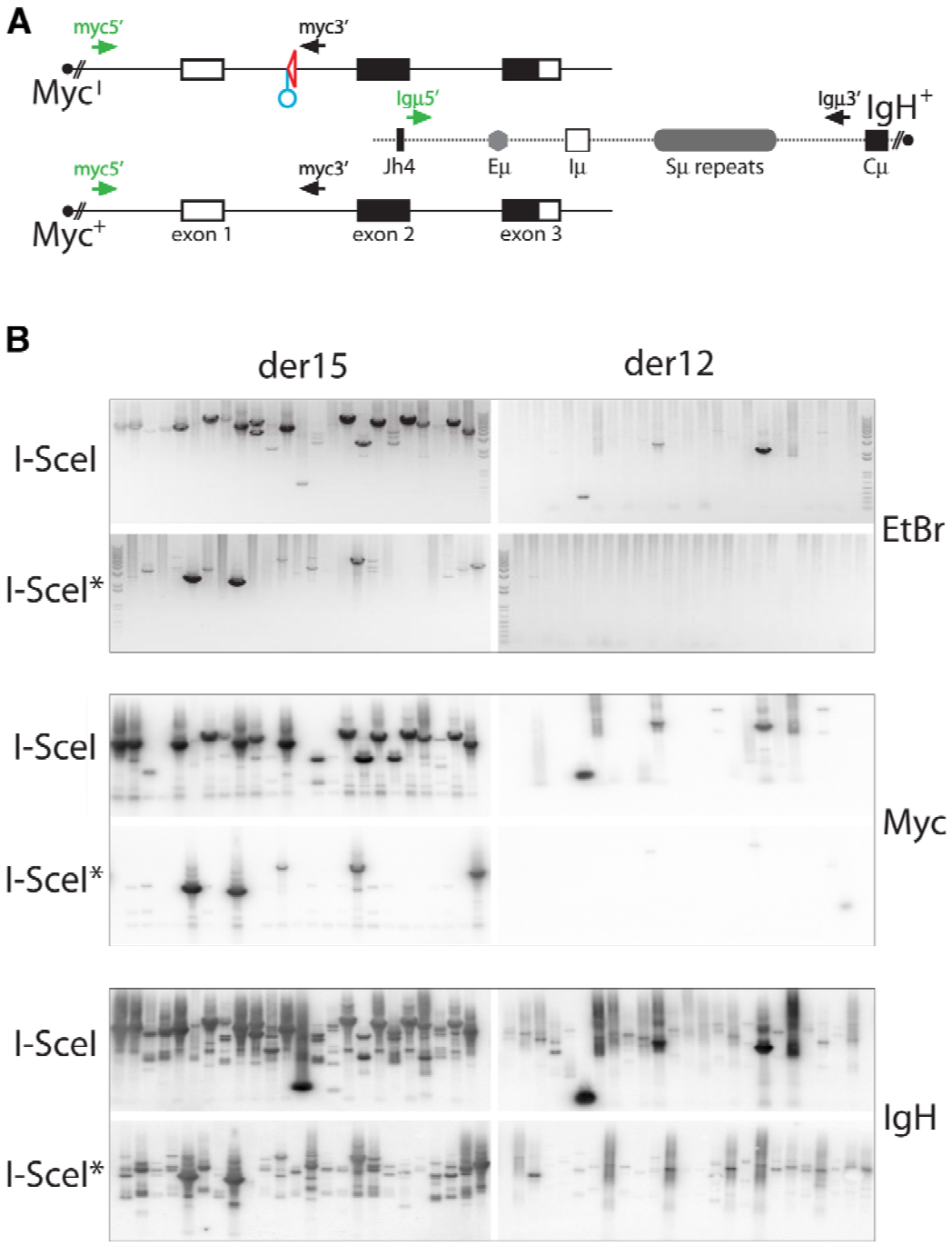


Figure S8. I-SceI mediated translocations in Myc$^{I/+}$, AID proficient B lymphocytes: Southern Blot.

(A) Schematic representation of the Myc^{I}, Myc^{+} and IgH^{+} alleles with the PCR primers for detecting der12 and der15 *c-myc/IgH* translocations. Circles point to recognition sequences for I-SceI. (B) I-SceI mediated translocations in the presence of AID. Representative ethidium bromide (EtBr) stained agarose gels from Figure 5B were Southern blotted and oligo-probed for *c-myc* and *IgH*, as indicated, to verify translocations. Myc$^{I/+}$ B cells were stimulated with LPS and IL-4 and infected with retroviruses encoding I-SceI or I-SceI* control. 100,000 cells were assayed in each lane.

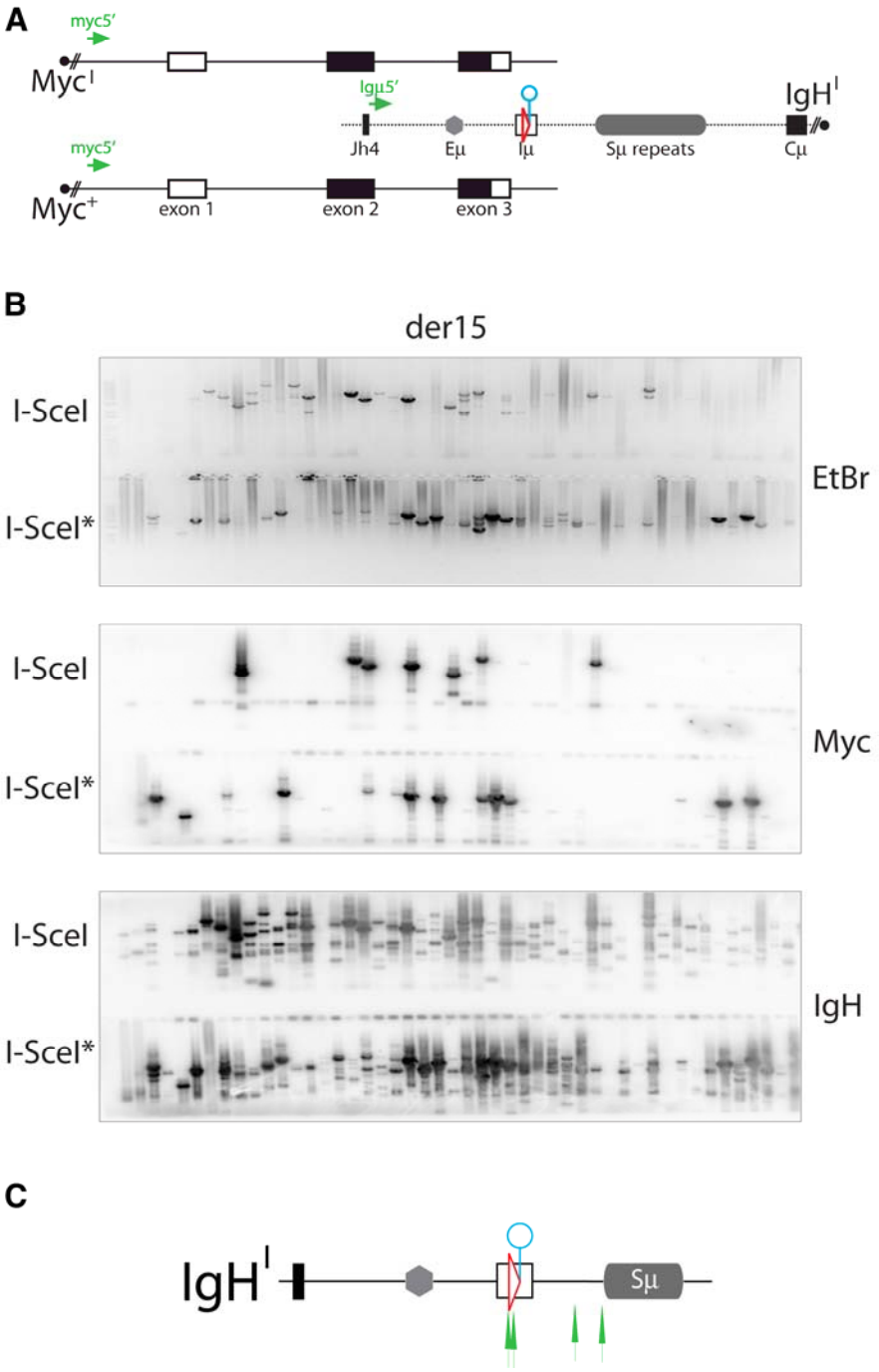


Figure S9. I-SceI mediated translocations in IgH$^{I/+}$, AID proficient B lymphocytes. (A) Schematic representation of the Myc^{+} and IgH^{I} alleles with the PCR primers for detecting der15 *c-myc/IgH* translocations. Circles point to recognition sequences for I-SceI. (B) I-SceI mediated translocations in the presence of AID. Representative ethidium bromide (EtBr) stained agarose gel with PCR products corresponding to *c-myc/IgH* translocations was Southern blotted and oligo-probed for *c-myc* and *IgH*, as indicated, to identify translocations. IgH$^{I/+}$ B cells were stimulated with LPS and IL-4 and infected with retroviruses encoding I-SceI or I-SceI* control. 100,000 cells were assayed in each lane. Two independent experiments. (C) Map of translocation breakpoints from stimulated IgH$^{I/+}$ B cells infected with I-SceI. Arrows point to *c-myc/IgH* der15 breakpoints at the IgH^{I} allele.

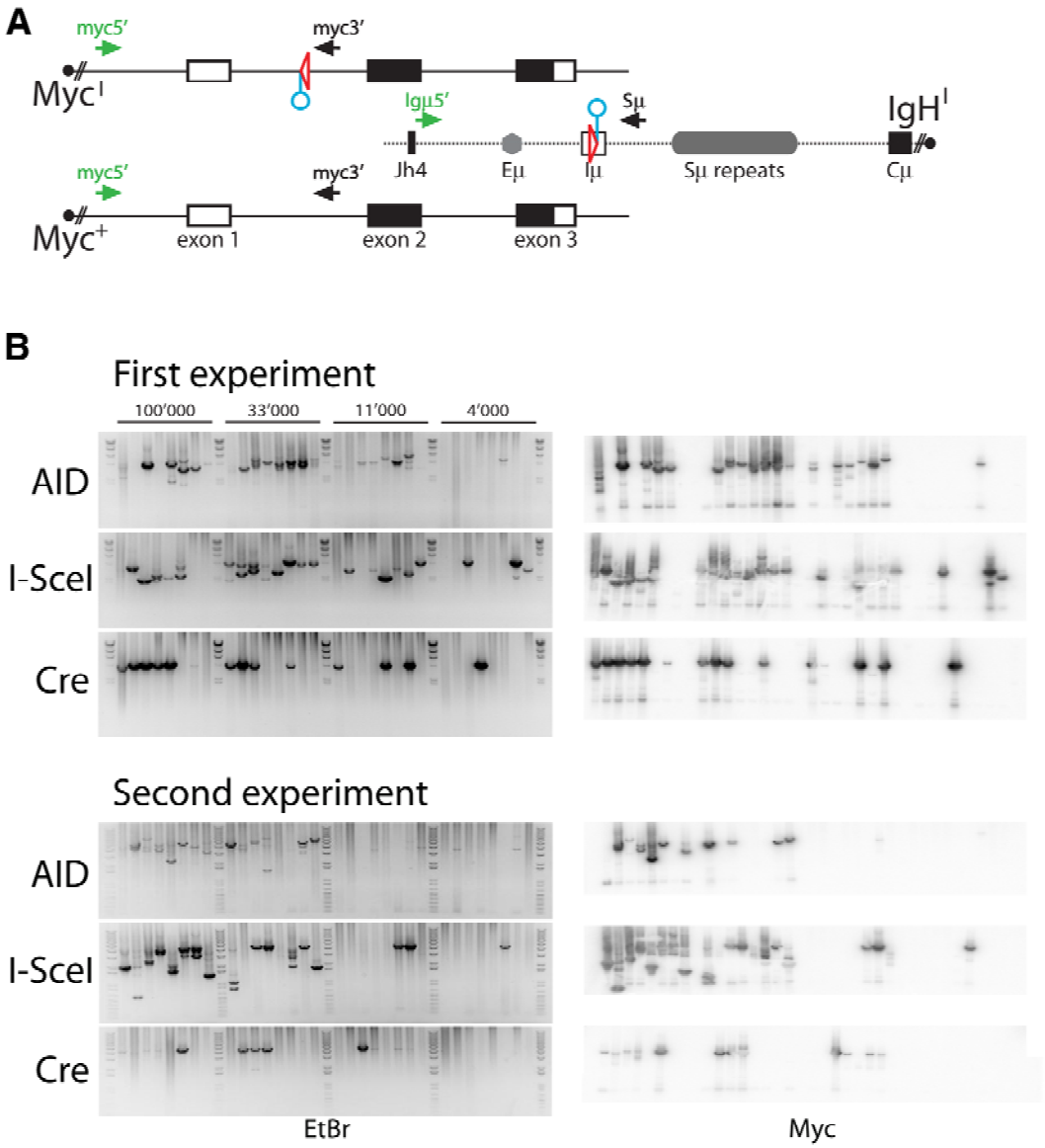


Figure S10. Comparing translocations by retroviral AID, I-SceI and Cre in AID$^{-/-}$ cells: Southern Blot.
(A) Schematic representation of the Myc^{I}, Myc^{+} and IgH^{I} alleles with the PCR primers for detecting der15 *c-myc/IgH* translocations. Triangles represent loxP sites, circles point to recognition sequences for I-SceI. (B) AID, I-SceI, or Cre mediated translocations in the absence of AID. Ethidium bromide (EtBr) stained agarose gels from two independent experiments were blotted and oligo-probed for *c-myc*, as indicated, to identify translocations (see also figure 6B).

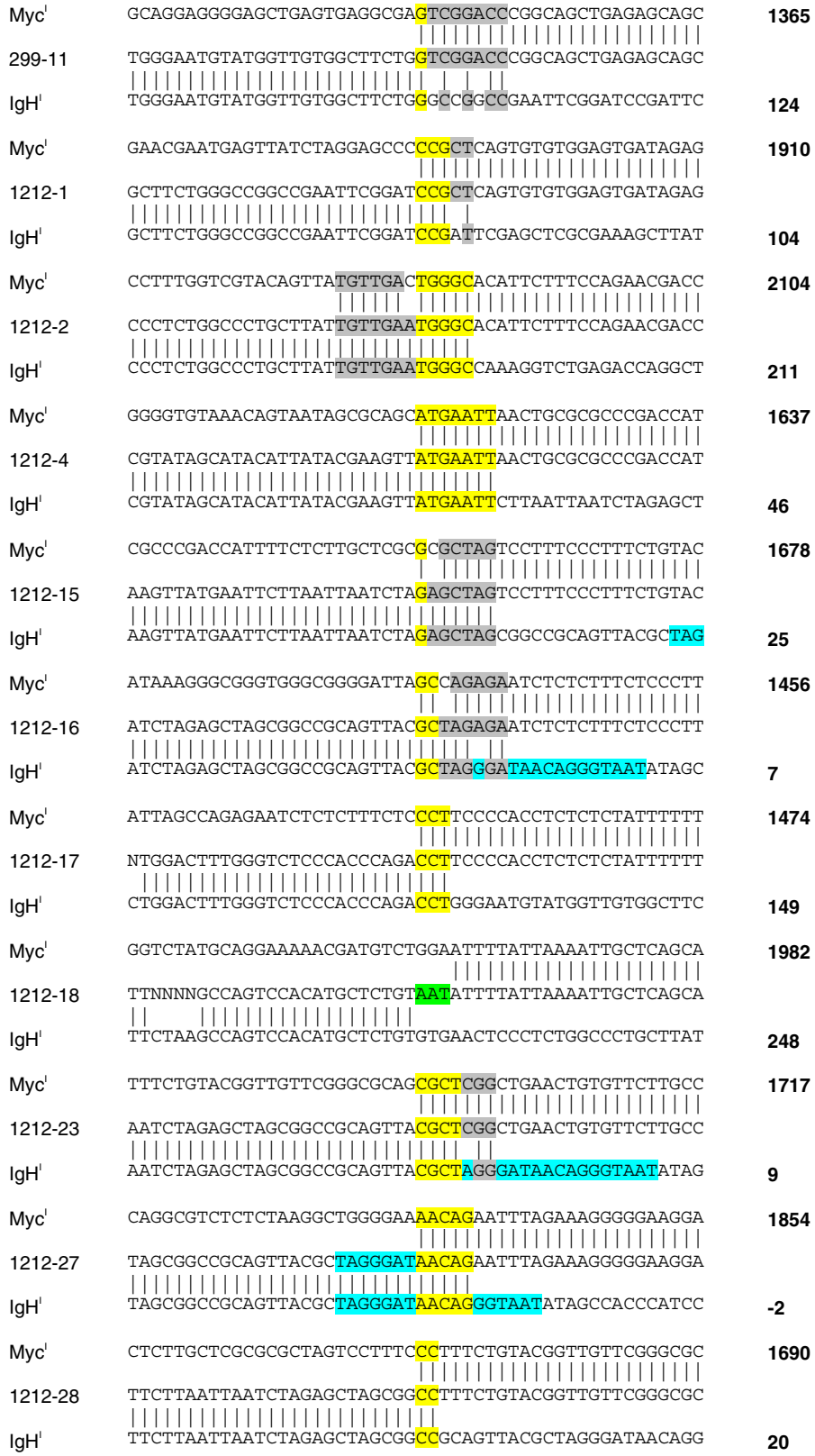
Table S1. Summary of mutation data in *c-myc*.

Genotype	Retrovirus	Frequency of unique mutations[1]	Mutations at C/G (%)[2]	Transitions at C/G (%)[3]
Wild type	-	0.3×10^{-4} (87'890)[4]	33.3	100
$AID^{-/-}$	AID	1.2×10^{-4} (101'541)[5]	66.7	75
$AID^{-/-}$	empty	$<0.07 \times 10^{-4}$ (136'800)[4,5]	-	-

[1] Frequency of unique mutations (number of analyzed nucleotides).
[2] Percentage of mutations at C or G.
[3] Percentage of C or G mutations that are transitions.
[4] $p = 0.08$ with Student's T-Test.
[5] $p = 0.0005$ with Student's T-Test.

Table S2. Translocation breakpoints from Myc$^{I/+}$ IgH$^{I/+}$ AID$^{-/-}$ B cells infected with I-SceI. 50 nucleotides surrounding each breakpoint are shown, with the homology to germline sequence indicated by vertical bars. I-SceI site sequences are highlighted in blue, insertions are green, microhomologies are yellow. Shadowed in light grey are extended microhomologies if single nucleotides gaps are tolerated. Numbers on the right indicate the distance in base pairs between the breakpoint and the center of the corresponding I-SceI allele. The top 8 sequences are from der12, the remaining 13 from der15 translocations.

Myc^{I}	AGTTATAAGCTTTCGCGAGCTCGAATCGGATCCGAATTCTTAATTAACAC	75
285-1	GGCTTACCATTTGCGGTGCCTGGTTTCGGATCCGAATTCTTAATTAACAC	
IgH^{I}	GGCTTACCATTTGCGGTGCCTGGTTTCGGAGAGGTCCAGAGTCTTTGTGT	95
Myc^{I}	TAACAGGGTAATGGCCGGCCCAAGGGCGAATTCATAACTTCGTATAATGT	22
285-3	GTGCCTGGTTTCGGAGAGGTCCAGAGCGAATTCATAACTTCGTATAATGT	
IgH^{I}	GTGCCTGGTTTCGGAGAGGTCCAGAGTCTTTGTGTGGAATTGTTCCTTCA	84
Myc^{I}	ACAGGGTAATGGCCGGCCCAAGGGCGAATTCATAACTTCGTATAATGTA	24
285-4	AATTGTTCCTTCAAAGATTAATTAAGAATTCATAACTTCGTATAATGTA	
IgH^{I}	AATTGTTCCTTCAAAGCCACCGAGGCTGGCTGGTCCATGAGCAGCCAGG	57
Myc^{I}	GAAGACGCCCTGTAGGGATAACAGGGTAATGGCCGGCCCAAGGGCGAAT	4
285-7	GGTGGATGGGTGGCTATATTACCCTGTAATGGCCGGCCCAAGGGCGAAT	
IgH^{I}	GGTGGATGGGTGGCTATATTACCCTGTTATCCCTAGCGTAACTGCGGCC	-1
Myc^{I}	TTAACACCCAGTGCTGAATCGCTGCAGGGTCTCTGGTGCAGTGGCGTCG	118
285-8	TGGAATTGTTCCTTCAAAGCCACCGAGGGTCTCTGGTGCAGTGGCGTCA	
IgH^{I}	TGGAATTGTTCCTTCAAAGCCACCGAGGCTGGCTGGTCCATGAGCAGCC	48
Myc^{I}	TTCGCGAGCTCGAATCGGATCCGAATTCTTAATTAACACCCAGTGCTGA	86
285-9	TGGATGGGTGGCTATATTACCCTGTTTCTTAATTAACACCCAGTGCTGA	
IgH^{I}	TGGATGGGTGGCTATATTACCCTGTTATCCCTAGCGTAACTGCGGCCGC	-2
Myc^{I}	CTTCGTATAATGTATGCTATACGAAGTTATAAGCTTTCGCGAGCTCGAAT	51
285-10	GGTGGATGGGTGGCTATATTACCCTGTTATAAGCTTTCGCGAGCTCGAAT	
IgH^{I}	GGTGGATGGGTGGCTATATTACCCTGTTATCCCTAGCGTAACTGCGGCCG	-4
Myc^{I}	ACAGGGTAATGGCCGGCCCAAGGGCGAATTCATAACTTCGTATAATGTAT	24
299-2	AAGCCACCGAGGCTGGCTGGTCCATGAATTCATAACTTCGTATAATGTAT	
IgH^{I}	AAGCCACCGAGGCTGGCTGGTCCATGAGCAGCCAGGTGGATGGGTGGCTA	33
Myc^{I}	CAAAAGGCAGATTCCCCCCCCCCCCACACACACACTCCAGCACCTCCGG	2178
299-5	TCTAGAGCTAGCGGCCGCAGTTACGCACACACACACTCCAGCACCTCCGG	
IgH^{I}	TCTAGAGCTAGCGGCCGCAGTTACGCTAGGGATAACAGGGTAATATAGCC	10
Myc^{I}	GCTCCGGGGTGTAAACAGTAATAGCGCAGCATGAATTAACTGCGCGCCCG	1632
299-8	CTCTGTGTGAACTCCCTCTGGCCCTGCAGCATGAATTAACTGCGCGCCCG	
IgH^{I}	CTCTGTGTGAACTCCCTCTGGCCCTGCTTATTGTTGAATGGGCCAAAGGT	231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IgH
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124
Myc
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1910
1212-1
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IgH
GCTTCTGGGCCGGCCGAATTCGGATCCGATTCGAGCTCGCGAAAGCTTAT
104
Myc
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2104
1212-2
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211
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1678
1212-15
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IgH
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25
Myc
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1456
1212-16
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IgH
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7
Myc
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1474
1212-17
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IgH
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149
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1982
1212-18
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248
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1212-23
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IgH
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9
Myc
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1212-27
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IgH
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-2
Myc
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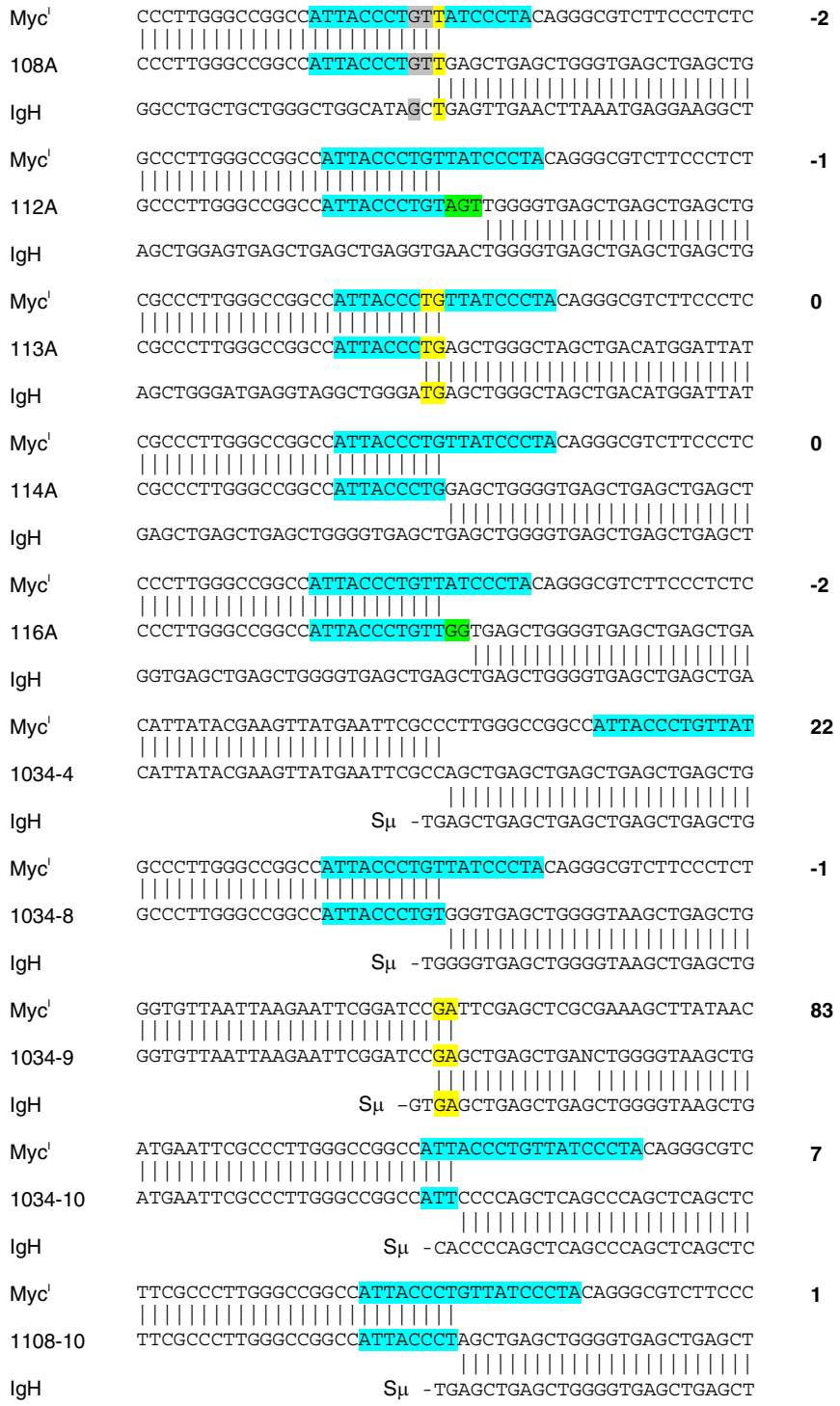
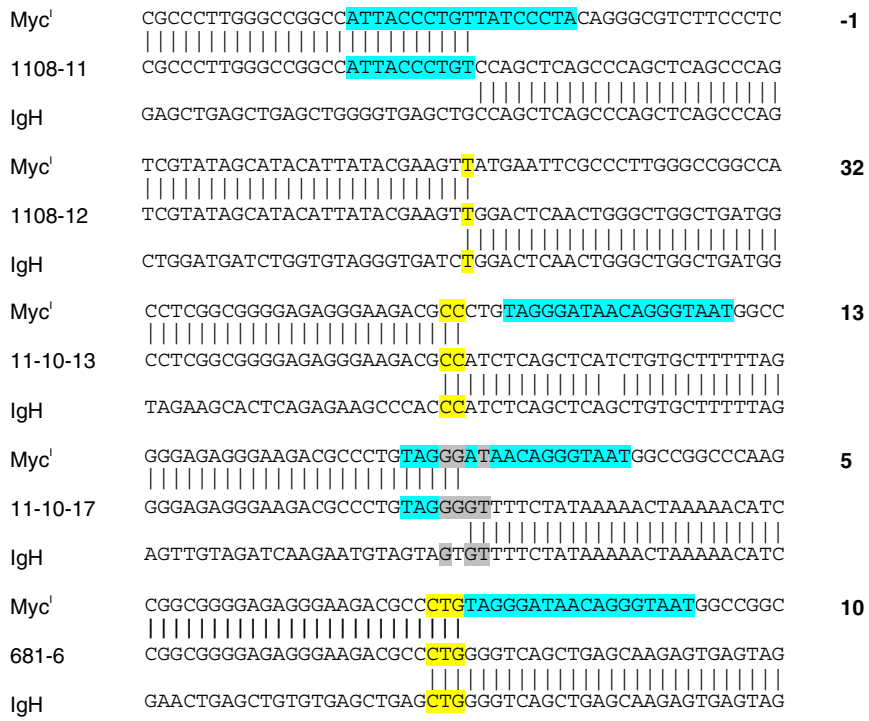
1690
1212-28
TTCTTAATTAATCTAGAGCTAGCGGCCTTTCTGTACGGTTGTTCGGGCGC
IgH
TTCTTAATTAATCTAGAGCTAGCGGCCGCAGTTACGCTAGGGATAACAGG
20

Table S3. Translocation breakpoints from Myc$^{I/+}$ B cells infected with I-SceI. 50 nucleotides surrounding each breakpoint are shown, with the homology to germline sequence indicated by vertical bars. I-SceI site sequences are highlighted in blue, insertions are green, microhomologies are yellow. Shadowed in light grey are extended microhomologies if single nucleotides gaps are tolerated. In 5 cases the breakpoint falls in the repetitive switch μ region, but cannot be precisely mapped. Numbers on the right indicate the distance in base pairs between the breakpoint and the center of the I-SceI site at the Myc^{I} allele. The top 12 sequences are from der12, the remaining 3 from der15 translocations.

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IgH
GAGCTGAGCTGAGCTGGGGTGAGCTGCCAGCTCAGCCCAGCTCAGCCCAG
Myc
TCGTATAGCATACATTATACGAAGTTATGAATTCGCCCTTGGGCCGGCCA
32
1108-12
TCGTATAGCATACATTATACGAAGTTGGACTCAACTGGGCTGGCTGATGG
IgH
CTGGATGATCTGGTGTAGGGTGATCTGGACTCAACTGGGCTGGCTGATGG
Myc
CCTCGGCGGGGAGAGGGAAGACGCCCTGTAGGGATAACAGGGTAATGGCC
13
11-10-13
CCTCGGCGGGGAGAGGGAAGACGCCATCTCAGCTCATCTGTGCTTTTTAG
IgH
TAGAAGCACTCAGAGAAGCCCACCCATCTCAGCTCAGCTGTGCTTTTTAG
Myc
GGGAGAGGGAAGACGCCCTGTAGGGATAACAGGGTAATGGCCGGCCCAAG
5
11-10-17
GGGAGAGGGAAGACGCCCTGTAGGGGTTTTCTATAAAAACTAAAAACATC
IgH
AGTTGTAGATCAAGAATGTAGTAGTGTTTTCTATAAAAACTAAAAACATC
Myc
CGGCGGGGAGAGGGAAGACGCCCTGTAGGGATAACAGGGTAATGGCCGGC
10
681-6
CGGCGGGGAGAGGGAAGACGCCCTGGGGTCAGCTGAGCAAGAGTGAGTAG
IgH
GAACTGAGCTGTGTGAGCTGAGCTGGGGTCAGCTGAGCAAGAGTGAGTAG

Table S4. Translocation breakpoints from uninfected wild type B cells. 50 nucleotides surrounding each breakpoint are shown, with the homology to germline sequence indicated by vertical bars. Insertions are green, microhomologies are yellow. Shadowed in light grey are extended microhomologies if single nucleotides gaps are tolerated. In 4 cases the breakpoint falls in the repetitive switch μ region, but cannot be precisely mapped. The top 5 sequences are from der12, the remaining 6 from der15 translocations.

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Myc      CTAGCGCAGTGAGGAGAAGCAAAATTGGGACAGGGATGTGACCGATTCGT
                                   ||||||||||||||||||||||||||
931-1    TCAGCTCACCCCAGCTCAGCTCACCTGGGACAGGGATGTGACCGATTCGT
         |||||||||||||||||||||||||
IgH      TCAGCTCACCCCAGCTCAGCTCACCCC - Sμ

Myc      CAGATCTGGTGGTCTTTCCCTGTGTTCTTTCTGCGTCTTGAATGTAGCGG
                                   ||||||||||||||||||||||||||
931-4    TCACCCTAGNTCAGCTCACCCCAGCTCTTTCTGCGTCTTGAATGTAGCGG
         |||||||| |||||||||||||||||
IgH      TCACCCTAGCTCAGCTCACCCCAGCTCAG - Sμ

Myc      TGAGGGGTCAAACCGGGAGGTCGCTTCGTGGTGGCCAAAGAAAGCCCTTG
                                   ||||||||||||||||||||||||||
931-6    AAGCACTCAGAGAAGCCCACCCATCTCGTGGTGGCCAAAGAAAGCCCTTG
         ||||||||||||||||||||||||||||
IgH      AAGCACTCAGAGAAGCCCACCCATCTCAGCTCAGCTGTGCTTTTTAGAGC

Myc      TTTGGGAGCGAGAAGGCTCCGTAGCTTCTGACTTACCAGTCTCTGAGAGG
                                   ||||||||||||||||||||||||||
931-7    TCACCCTAGCTCAGCTCACCCCAGATTCTGACTTACCAGTCTCTGAGAGG
         |||||||||||||||||||||||||
IgH      TCACCCTAGCTCAGCTCACCCCAGCTCA - Sμ

Myc      TCGCTTCGTGGTGGCCAAAGAAAGCCCTTGGAATCCTGAGGTCTTTGGAG
                                   ||||||||||||||||||||||||||
931-8    CAGCTCAGCTCAGCTCAGCCCAGCTCCTTGGAATCCTGAGGTCTTTGGAG
         ||||||||||||||||||||||||||
IgH      CAGCTCAGCTCAGCTCAGCCCAGCTCAGCTCAGCTCACCCCAGCTCAGCT

Myc      TTCTGACTTACCAGTCTCTGAGAGGGCATTTAAATTTCAGCTTGGTGCAT
         ||||||||||||||||||||||||||
237      TTCTGACTTACCAGTCTCTGAGAGGATGCATCGGATACTGTATAAATGCT
                                   ||||||||||||||||||||||||||
IgH      GTGCCCCACTCCACTCTTTGTCCCTATGCATCGGATACTGTATAAATGCT

Myc      CAGTTAATTCATGCTGCGCTATTACTGTTTACACCCCGGAGCCGGAGTAC
         ||||||||||||||||||||||||||
268      CAGTTAATTCATGCTGCGCTATTACCCAGCTCAGCTCACCCTAGCTCAGC
                                    ||||||||||||||||||||||||||||
IgH      CTCACCCCAGCTTAGCTCAGCTCACCCAGCTCAGCTCACCCTAGCTCAGC

Myc      AAACCCCGGTAAGCACAGATCTGGTGGTCTTTCCCTGTGTTCTTTCTGCG
         ||||||||||||||||||||||||||
274      AAACCCCGGTAAGCACAGATCTGGTTTTCTCAATTCTGTACAGCTGTGGC
                                   ||||||||||||||||||||||||||
IgH      TGGCCTCAACTGCAGGTCTCTATTCTTTCTCAATTCTGTACAGCTGTGGC

Myc      GGTTAGGACAGTCTTTCTTCCATTCCTGTGCTTTTGACACTTTTCTCAAG
         ||||||||||||||||||||||||||
276      GGTTAGGACAGTCTTTCTTCCATTCATCCGCCCAATCTAGCTGATTTGTC
IgH                                ||||||||||||||||||||||||||
         GGTCCCCTGAAGCTGATCTGCCAGGATCCGCCCAATCTAGCTGATTTGTC

Myc      TCTCTGAGAGGGCATTTAAATTTCAGCTTGGTGCATTTCTGACAGCCTGG
         ||||||||||||||||||||||||||
278      TCTCTGAGAGGGCATTTAAATTTCAACTCATTAAACCACATTGAGTNGTA
                                   || |||||||||||||||||| |||
IgH      GAAGTACATTTACTGGCAACTTCAAATTCATTAAACCACATTGAGTTGTA
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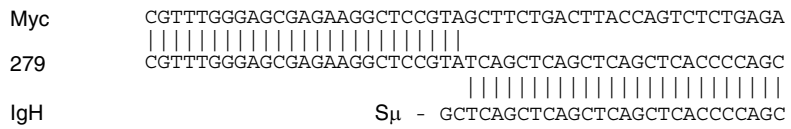

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