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Supplemental Data

AID Produces DNA Double-Strand Breaks in Non-*Ig* Genes and Mature B Cell Lymphomas with Reciprocal Chromosome Translocations

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Figure S1. Western Blot for AID Protein in Pre-B and Follicular B Cells

Twenty μg of protein lysates from sorted pre-B and follicular B cells of the indicated genotypes were assayed in each lane.

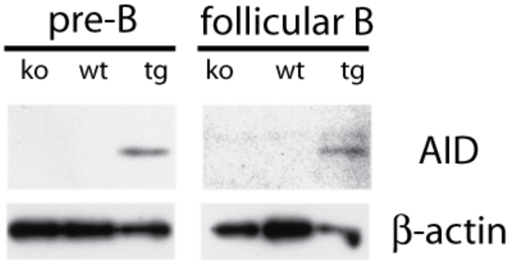

Figure S2. B Cell Development in *Igκ*AID Mice

Flow cytometric analysis of bone marrow leukocytes (A) and splenocytes (B) from age-matched wild type and *Igκ*AID mice reveals normal B lymphocyte development in *Igκ*AID mice. Immuno-staining was performed with the indicated markers. These figures are representative of three independent experiments.

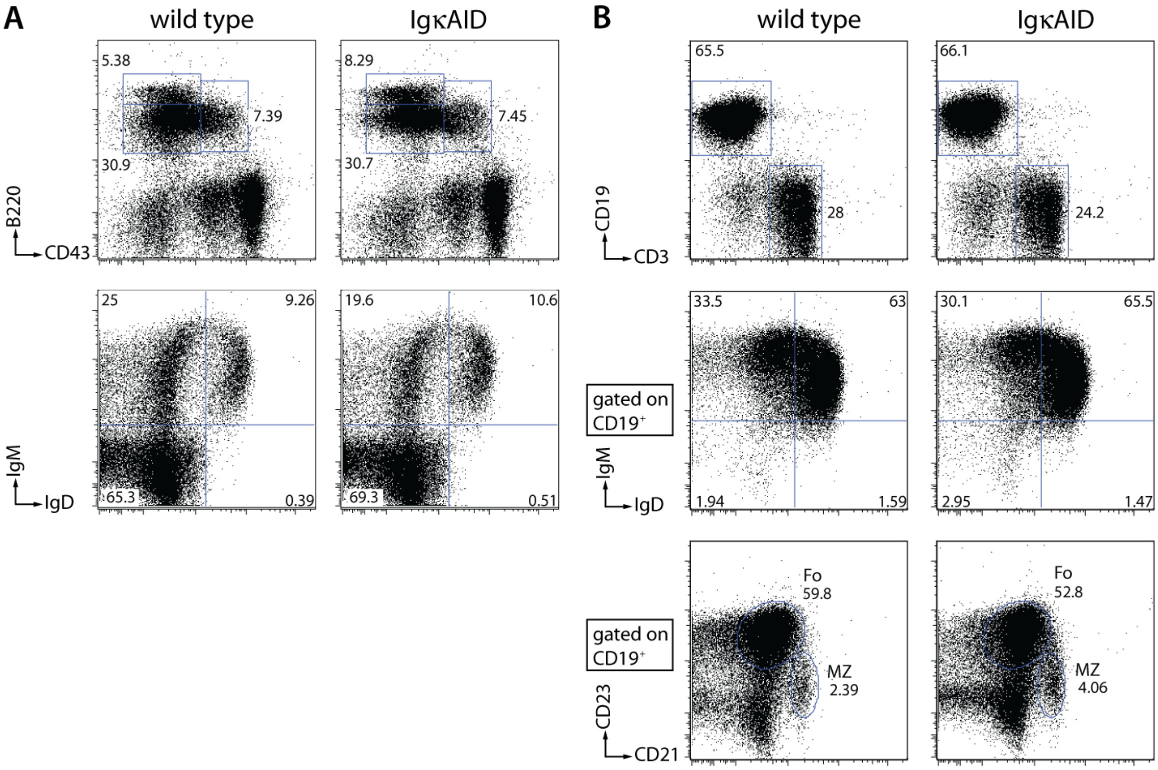

Figure S3. Serum Ig Isotypes

Serum titers of matched 9 week old *Igκ*AID and wild type mice were determined by ELISA as described (Dorsett et al., 2008).

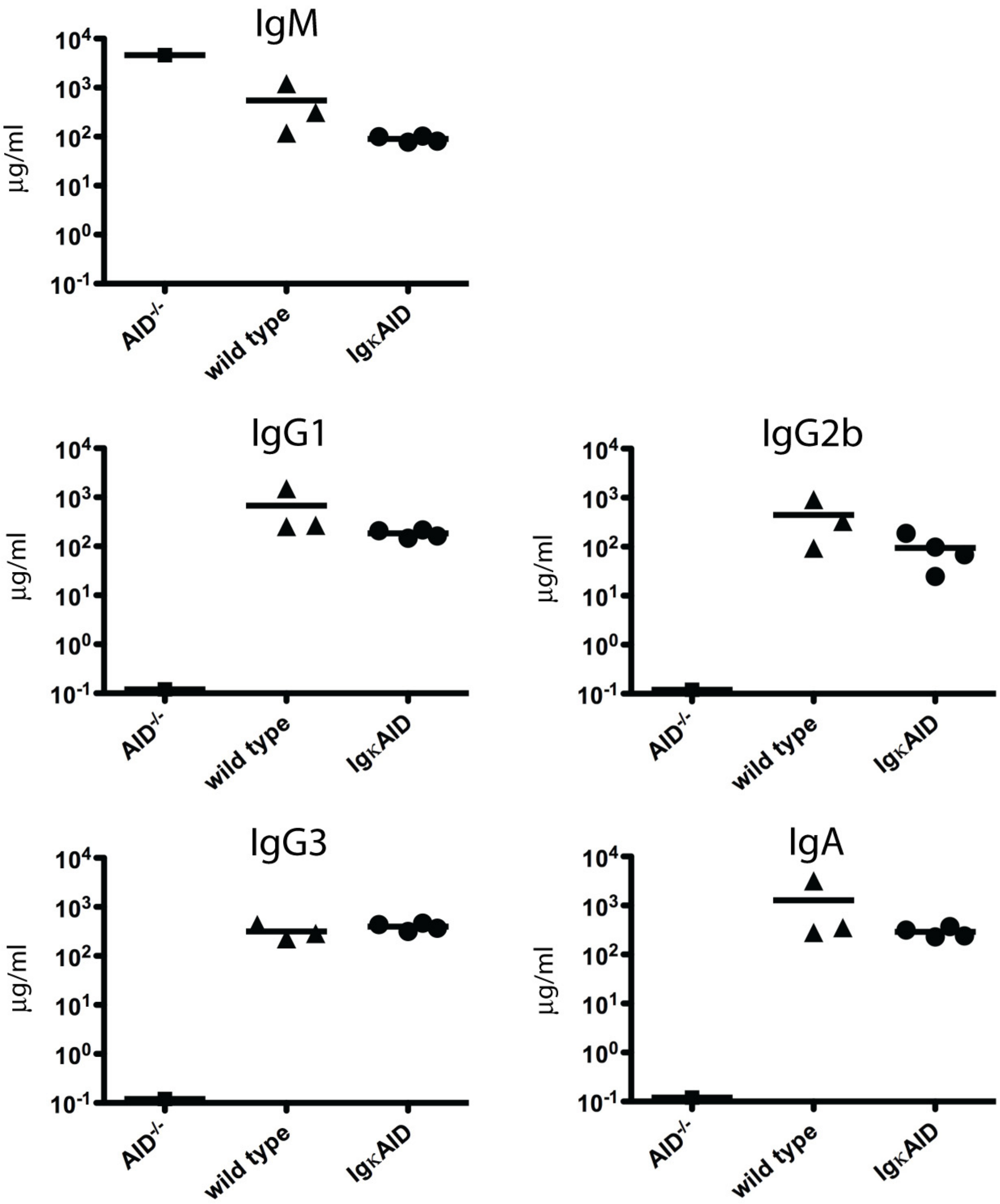

Figure S4. AID Nontarget Genes Are Expressed in Activated B Cells

cDNA from wild type B cells activated *in vitro* with LPS and IL-4 for four days was amplified with cross-intronic primers for *Taci* (5-CGCCATCTTCTGCTGTTTCTTG-3 and 5-AGCAGAAGCTACACGTTTCCACA-3), *Whsc1* (5-CCCCCTCCTGCCTCCCTG-3 and 5-CGTCGTCAATGTCAAACCACG-3), *H2Eα* (5-CCAGAGACCAGGATGCCGC-3 and 5-GTCCACCTTGGGGGTCAAAG-3), and *A20* (5- TGTGAAGATACGAGAGAGAACCCC-3 and 5-TGAAGAGGCAGATAAATCCCACC-3), resulting in amplicons of the expected sizes. gDNA is control genomic DNA from the same cells.

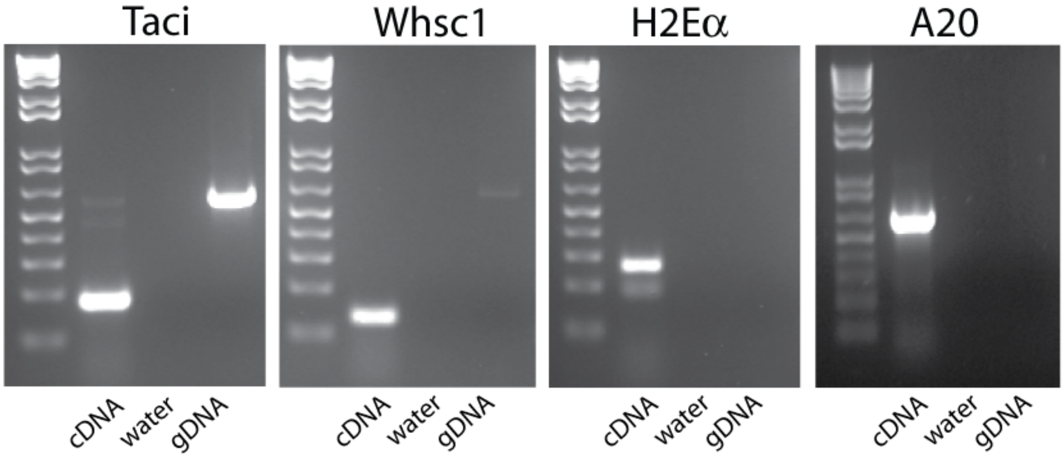

Figure S5. *Igκ*AID/p53$^{-/-}$ B Cell Lymphomas Are Heterogeneous in Phenotype

Flow cytometric analysis of representative *Igκ*AID/p53$^{-/-}$ B cell lymphomas with distinct karyotypes. As a comparison, one CD4^{+}CD8^{+} T cell lymphoma from a p53$^{-/-}$ control mouse is shown at the bottom.

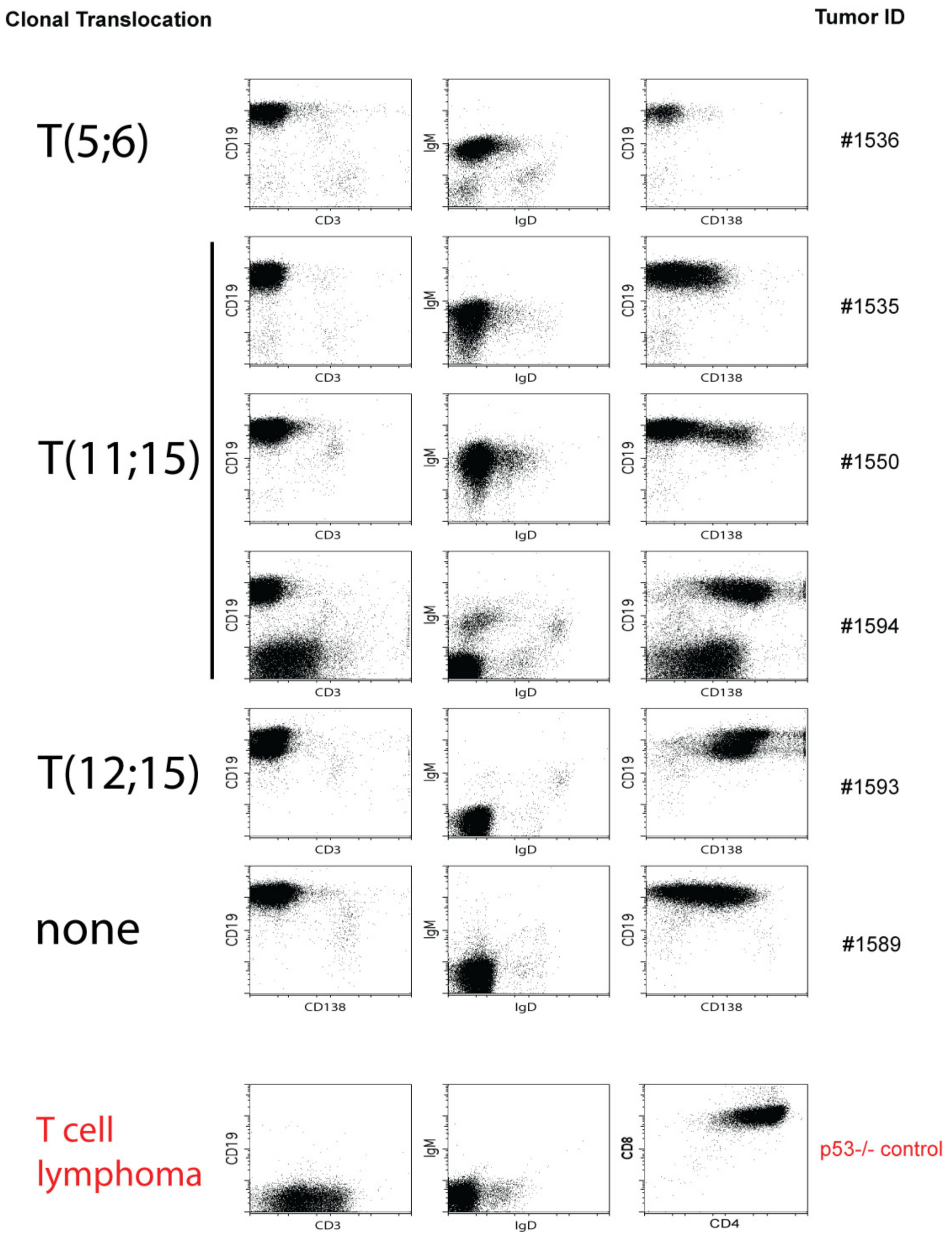

Figure S6. Identification of the T(5;6) Translocation Partners

(A) and (B) aCGH analysis of sorted chromosomes identifies the breakpoint in *Anxa4* (Chr6) and *Wdfy3* (Chr5). (C) and (D) RT-PCR detects hybrid transcripts between *Anxa4* and *Wdfy3* from both derivative chromosomes.

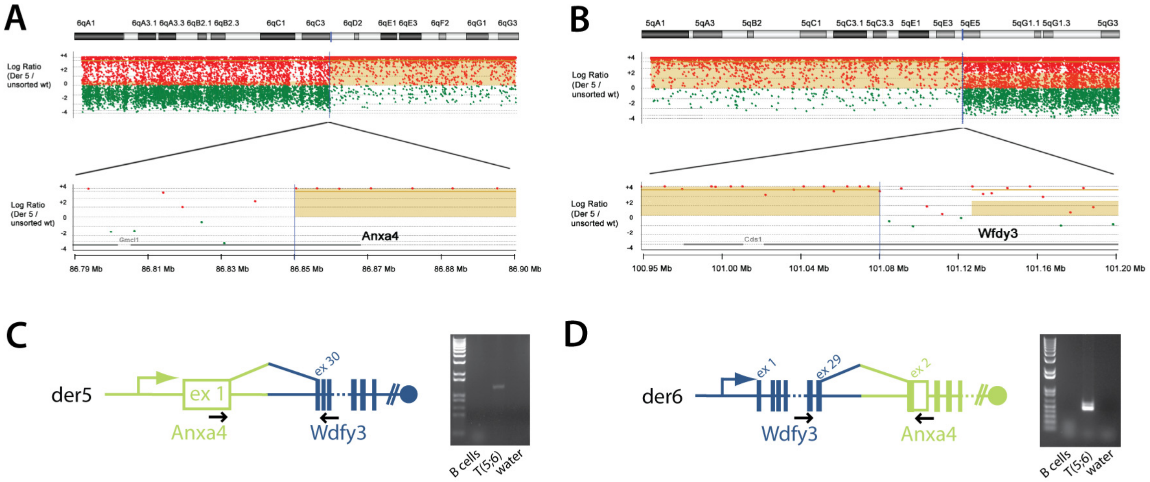

Figure S7. Model for the Processing of DNA Lesions Mediated by AID Leading to Deletions or Duplications at the Derivative Chromosomes

(A) AID induces a single-strand break (SSB), which is converted to a double-strand break (DSB). DNA ends are then resected prior to their joining to the translocation partner. The loss of nucleotides results in a deletion of sequence at the derivative chromosomes. (B) AID induces two SSBs. Single strands of DNA are filled-in and result in a duplication of sequence at the derivative chromosomes. See also Figure 4G and Supplemental Table S2.

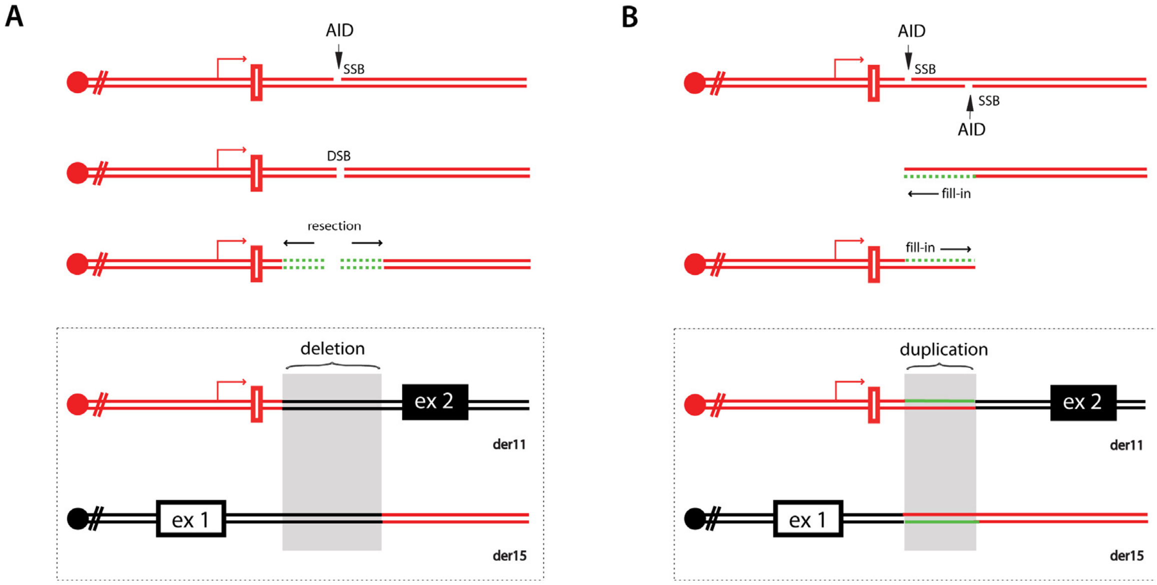

Figure S8. *miR-142* Mutations in Primary B Cells

Mutations at the *miR-142* locus (from Figure 5). Genotypes are color-coded, as indicated. Mutations from resting B cells are above, those from activated B cells are below the reference *miR-142* sequence (in black). Mutations from germinal center cells are bolded. Dashes indicate deletions. The *miR-142* sequence is boxed. DGYW/WRCH hotspots are underlined.

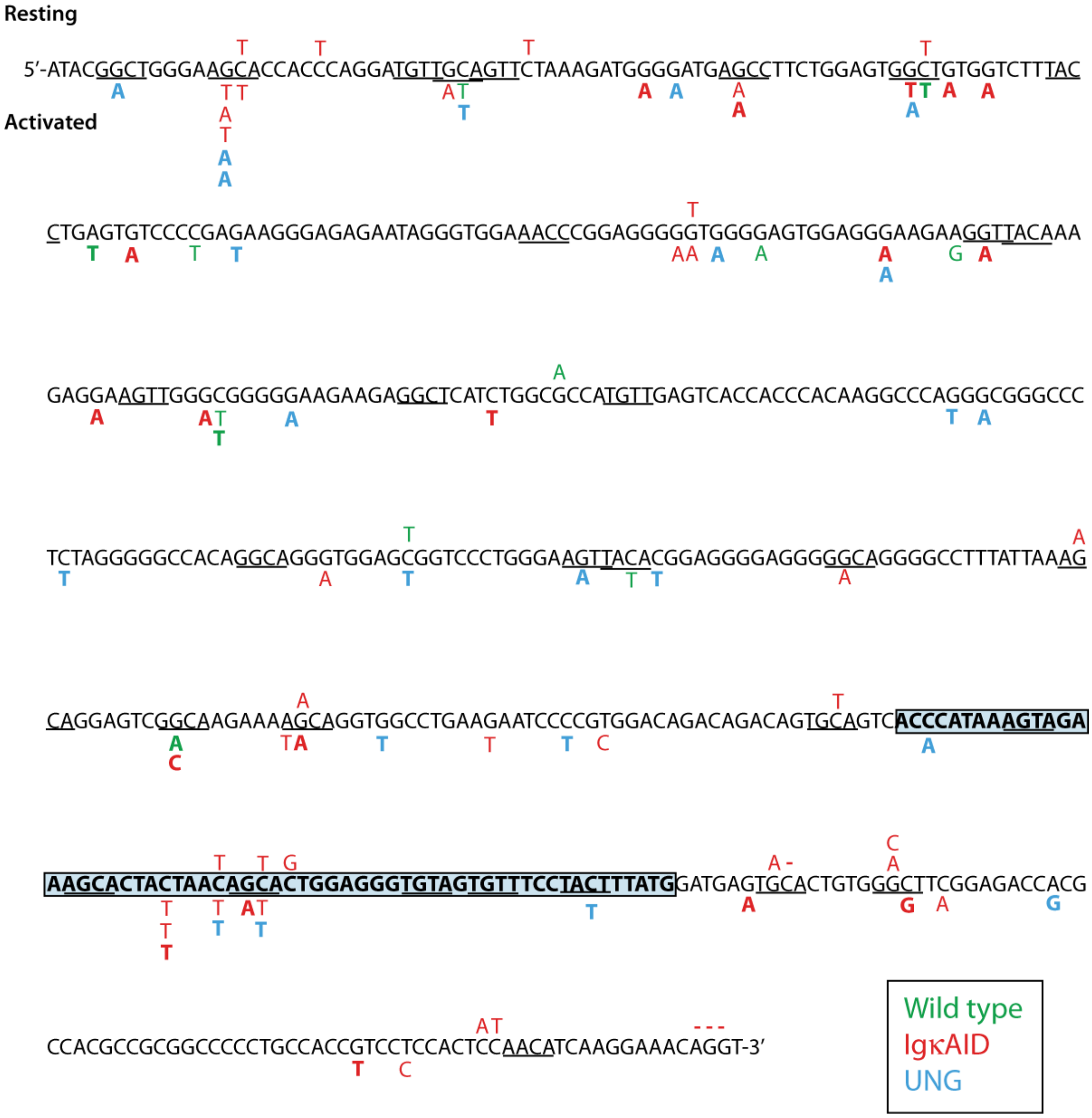

Figure S9. ***miR-142*** **Mutations at the Nontranslocated Allele in T(11;15)**

Mutations at the non-translocated *miR-142* allele of T(11;15) tumors (cumulative mutation rate: 60x10^{-4}). The non-translocated allele was amplified with primers external to the breakpoint region (5-TTGTCGCTGGTTTCCTGTCAG-3 and 5-AGTCAATAGGATGGCTCTGTGGG-3) and sequenced with a primer proximal to the *miR-142* sequence (5-AATGAGGGCGTGTGAGAGATGCTC-3). A total of 14 tumors were analyzed. The *miR-142* sequence is boxed. DGYW/WRCH hotspots are underlined.

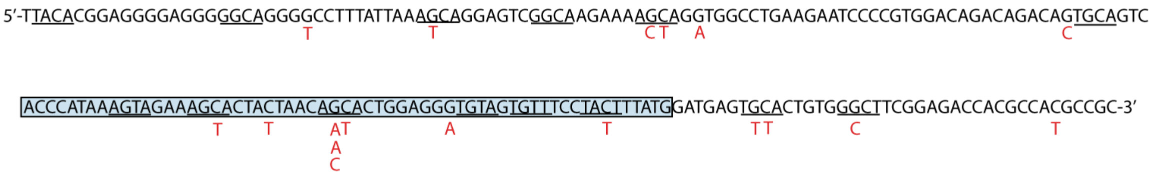

Table S1

Analysis of the breakpoints in *Igκ*AID/p53$^{-/-}$ lymphomas. 50 nucleotides surrounding each breakpoint (middle) are shown, with the homology to germline sequence (top and bottom) indicated by vertical bars. Microhomologies are yellow; insertions green; point mutations bolded in red. Shadowed in light grey are extended microhomologies if single nucleotides gaps are tolerated. Red sequences are *miR-142*, green are *Anxa4* and blue are *Wdfy3*.

T(12;15): der12 breakpoint

```
IgH Sμ      <  CAGCTCAGCTCAGCCCAGCTCAGCTCAGCTCACCCCAGCTCAGCTCACCC
               ||||||||||||||||||||||||
#1593          CAGCTCAGCTCAGCCCAGCTCAGCAATGTGCCCAGTCAACATAACTGTAC
                                       ||||||||||||||||||||||||||
c-myc       >  GGGGGGGGGGGTCGTTCTGGAAAGAATGTGCCCAGTCAACATAACTGTAC
```

T(12;15): der15 breakpoint

```
c-myc       >  TTCTGGAAAGAATGTGCCCAGTCAACATAACTGTACGACCAAAGGCAAAA
               ||||||||||||||||||||||||||
#1593          TTCTGGAAAGAATGTGCCCAGTCAACCCCAACTCAGCTCAGCTCACCCCA
                                       |||||| |||||||||||||||||||
IgH Sμ      <  GCTCACCCCAGCTCAGCTCAGCTCACCCCAGCTCAGCTCAGCTCACCCCA
```

T(11;15): der11 breakpoints

```
miR-142     >  AGGGTGTAGTGTTTCCTACTTTATGGATGAGTGCACTGTGGGCTTCGGAG
               ||||||||||||||||||||||||||
#1461          AGGGTGTAGTGTTTCCTACTTTATGGGACCGACACGGAGGTGCGTCCCGC
                                      |||||||||||||||||||||||||||
c-myc       >  AGCTTGGTGCATTTCTGACAGCCTGGGACCGACACGGAGGTGCGTCCCGC
```

```
miR-142     >  GGCCAGGCTCCCCGAAAGACCTTCATGGCTCCCCCAAAGCACGGTGCTTC
               |||||||||||||||||||||||||
#1550          GGCCAGGCTCCCCGAAAGACCTTCACCCTGCACCCAGTGCTGAATCGCTG
                                        |||||||||||||||||||||||||
c-myc       >  ACCCTCGGCGGGGAGAGGGAAGACGCCCTGCACCCAGTGCTGAATCGCTG
```

```
miR-142     >  GGATGGGTAAGGGTCACGGGGCCCTCAACACTAATAAAGAATGGACTGGT
               ||||||||||||||||| |||||||
#1561          GGATGGGTAAGGGTCACAGGGCCCTGATGTTACCGATTCGTTGACTTGGG
                                        ||||| |||||||||||||||||||
c-myc       >  TGAGGAGAAGCAAAATTGGGACAGGGATGTGACCGATTCGTTGACTTGGG
```

```
miR-142     >  GAAAGACCTTCATGGCTCCCCCAAAGCACGGTGCTTCCTGACCCCTGATA
               |||||||||||||||||||||||||
#1583          GAAAGACCTTCATGGCTCCCCCAAATTCTGACTTACCAGTCTCTGAGAGG
                                        |||||||||||||||||||||||||
c-myc       >  TTTGGGAGCGAGAAGGCTCCGTAGCTTCTGACTTACCAGTCTCTGAGAGG
```

```
miR-142     >  GCGGTCCCTGGGAAGTTACACGGAGGGGAGGGGGCAGGGGCCTTTATTAA
               ||||||||||||||||||||||||
#1584          GCGGTCCCTGGGAAGTTACACGGAATAGCTTAGCTGCTACCCTCGGCGGG
                                              |||||||||||||||||||
c-myc       >  CGGTGAGTCGTGATCTGAGCGGTTCCGTAACAGCTGCTACCCTCGGCGGG
```

```
miR-142     >  AAGGGAGCCGGATGGATGGGTAAGGGTCACGGGGCCCTCAACACTAATAA
               |||||||||||||||||||||||||||
#1592          AAGGGAGCCGGATGGATGGGTAAGGGTAGCGCAGTGAGGAGAAGCAAAAT
                                         ||||||||||||||||||||||||
c-myc       >  CGCGGCACTAGGACTTGATGTTGGGCTAGCGCAGTGAGGAGAAGCAAAAT
```

```
miR-142    >  TGGACAGACAGACAGTGCAGTCACCCATAGAAAGCACTACTAACAGCACT
              ||||||||||||||||||||||||||
#1595         TGGACAGACAGACAGTGCAGTCACCCGCTGAAAGGGGAGTGGTTCAGGAT
                                       |||||||||||||||||||||||||
c-myc      >  CACACACACACTTGGAAGTACAGCACGCTGAAAGGGGAGTGGTTCAGGAT

miR-142    >  AGCTGGGAACCTAACCCAGGGCTTTGCGCTTACCATTGAGCTAAATCCCC
              |||||||||||||||||||||||
#1613         AGCTGGGAACTTAACCCAGGGCTGGAATTGGGACAGGGATGTGACCGATT
                                       |||||||||||||||||||||||||
c-myc      >  GGGCTAGCGCAGTGAGGAGAAGCAAAATTGGGACAGGGATGTGACCGATT

miR-142    >  CTTGGGCCACCGGAAGTAGACTTTGTAGCAACGTGAAGAAAGGGTATGAG
              ||||||||||||||||||||||||
#1673         CTTGGGCCACCGGAAGTAGACTTTAAGTCTTTCTTCCATTCCTGTGCTTT
                                       |||||||||||||||||||||||||
c-myc      >  CTTGAATGTAGCGGCCGGTTAGGACAGTCTTTCTTCCATTCCTGTGCTTT

miR-142    >  GGGCCTTTATTAAAGCAGGAGTCGGCAAGAAAAGCAGGTGGCCTGAAGAA
              ||||||||||||||||||||||||||
#1674         GGGCCTTTATTAAAGCAGGAGTCGGCCACACACACACACACACACACACA
                                       |||||||||||||||||||||||||
c-myc      >  AAAAGAGTGCATGCCTCCCCCCCAACCACACACACACACACACACACACA

miR-142    >  GCTTCGGAGACCACGCCACGCCGCGGCCCCCTGCCACCGTCCTCCACTCC
              |||||||||||||||||||||||||||
#1714         GCTTCGGAGACCACGCCACGCCGCGGCATTAGGACTTGATGTTGGGCTAG
                                  |||||||| |||||||||||||||||||||
c-myc      >  GTAAAATTTAAGCCTGACCCCCGCGGCACTAGGACTTGATGTTGGGCTAG
```

T(11;15): der15 breakpoints

```
c-myc      >  ACCGACACGGAGGTGCGTCCCGCCCGCCAATCCCCGGCGGCGATCGCAAC
              |||||||||||||||||||||||
#1461         ACCGACACGGAGGTGCGTCCCGCACCCTTTATTAAAGCAGGAGTCGGCAA
                                       |||||||||||||||||||||||||
miR-142    >  TTACACGGAGGGGAGGGGGCAGGGGCCTTTATTAAAGCAGGAGTCGGCAA

c-myc      >  GGGAATTTTTGTCTATTTGGGGACAGTGTTCTCTGCCTCTGCCCGCGATC
              |||||||||||||||||||||||
#1535         GGGAATTTTTGTCTATTTGGGGAGAGTAGGGAGGAGTTGCGAGAGTGGGA
                                   |||||||||||||||||||||||||||||
miR-142    >  AGCTCTTAGGGAGGAGGGCCAGAGAGTAGGGAGGAGTTGCGAGAGTGGGA

c-myc      >  GAGAAGGCTCCGTAGCTTCTGACTTACCAGTCTCTGAGAGGGCATTTAAA
              |||||||||||||| |||||||||||||
#1583         GAGAAGGCTCCGTAACTTCTGACTTACCCCTGATACTTGGGGAGACACCA
                                       |||||||||||||||||||||||||
miR-142    >  CTCCCCCAAAGCACGGTGCTTCCTGACCCCTGATACTTGGGGAGACACCA

c-myc      >  AAGACTGCGGTGAGTCGTGATCTGAGCGGTTCCGTAACAGCTGCTACCCT
              |||||||||||||||||||||||||
#1584         AAGACTGCGGTGAGTCGTGATCTGAATCCCCGTGGACAGACAGACAGTGC
                                     |||||||||||||||||||||||||||
miR-142    >  GCAAGAAAAGCAGGTGGCCTGAAGAATCCCCGTGGACAGACAGACAGTGC

c-myc      >  GCACTAGGACTTGATGTTGGGCTAGCGCAGTGAGGAGAAGCAAAATTGGG
              ||||||||||||||||||||||||||
#1592         GCACTAGGACTTGATGTTGGGCTAGCACTAATAAAGAATGGACTGGTTTC
                                       |||||||||||||||||||||||||
miR-142    >  TGGGTAAGGGTCACGGGGCCCTCAACACTAATAAAGAATGGACTGGTTTC
```

```
c-myc         > GCTGACGCTGACCCGGCCGGTTGGACATTCTTGCTTTGCTACATTAATTG
                ||||||||||||||||||||||||||
#1594           GCTGACGCTGACCCGGCCGGTTGGACCAGAGAGTAGGGAGGAGTTGCGAG
                                         |||||||||||||||||||||||||
miR-142       > AGTCTCTAGCTCTTAGGGAGGAGGGCCAGAGAGTAGGGAGGAGTTGCGAG

c-myc         > AAGGCTCCGTAGCTTCTGACTTACCAGTCTCTGAGAGGGCATTTAAATTT
                ||||||||||||||||||||||||
#1613           AAGGCTCCGTAGCTTCTGACTTACGCTAAATCCCCAACCCCATCTTTTAA
                                        ||||||||||||||||||||||||||
miR-142       > CCAGGGCTTTGCGCTTACCATTGAGCTAAATCCCCAACCCCATCTTTTAA

c-myc         > TTTGAAGCGGGGTTCCCGAGGTTACTATGGGCTGACGCTGACCCGGCCGG
                |||||||||||||||||||||||||
#1673           TTTGAAGCGGGGTTCCCGAGGTTACCGTAAAATGGTTGTCTGCCTCCCAA
                                          |||||| |||||||||||||||||
miR-142       > GTTTTCTGATGGTCTTGAGTGGCCCTGTAAAAGGGTTGTCTGCCTCCCAA

c-myc         > AAAAATAGTGATCGTAGTAAAATTTAAGCCTGACCCCCGCGGCACTAGGA
                ||||||||||||||||||||||||
#1674           AAAAATAGTGATCGTAGTAAAATTCGTGTCCAGGCATTTTTTCCACGCAA
                                         ||| |||||||||||||||||||||
miR-142       > ACAGTGAGACTGGTATCGGCAAGTGGTGCCCAGGCATTTTTTCCACGCAA

c-myc         > GTGTAGAAGGGAGGTGTCTCTTATTATTTGACACCCCCTCCCCTTTTATT
                |||||||||||||||||||||||||
#1676           GTGTAGAAGGGAGGTGTCTCTTATTCGGAGACCACGCCACGCCGCGGCCC
                                       |||||||||||||||||||||||||||
miR-142       > TTATGGATGAGTGCACTGTGGGCTTCGGAGACCACGCCACGCCGCGGCCC

c-myc         > TGATCGTAGTAAAATTTAAGCCTGACCCCCGCGGCACTAGGACTTGATGT
                |||||||||||||||||||||||||
#1714           TGATCGTAGTAAAATTTAAGCCTGAGTGCACTGTGGGCTTCGGAGACCAC
                                      ||||||||||||||||||||||||||||
miR-142       > GTAGTGTTTCCTACTTTATGGATGAGTGCACTGTGGGCTTCGGAGACCAC
```

T(5;6): der5 breakpoint

```
Anxa4         > CACATAGAGAACATGGGATCTGAATGAAGACCTTTTGCTCCCATGCAAGT
                |||||||||||||||||||||||||
#1536         > CACATAGAGAACATGGGATCTGAATTCACACTTTTAACTACTTGGAAGAG
                                         |||||||||||||||||||||||||
Wdfy3         > TTTAGCAACCAGGGTATGATTTTGCTCACACTTTTAACTACTTGGAAGAG
```

T(5;6): der6 breakpoint

```
Wdfy3         > CAGGGTATGATTTTGCTCACACTTTTAACTACTTGGAAGAGGAATTCTTA
                ||||||||||||||||||||||
#1536         > CAGGGTATGATTTTGCTCACACCTTTTGCTCCCATGCAAGTGACCTGGAC
                                    ||||||||||||||||||||||||||||||
Anxa4         > AACATGGGATCTGAATGAAGACCTTTTGCTCCCATGCAAGTGACCTGGAC
```

Table S2

Analysis of loss or gain of sequence at the breakpoints in *Igκ*AID/p53$^{-/-}$ lymphomas. Nucleotides surrounding each breakpoint are shown, with the homology of either derivative chromosomes (top and bottom) to germline sequence (middle) indicated by vertical bars. Insertions are underlined. Red sequences are *miR-142*, green are *Anxa4* and blue are *Wdfy3*.

T(12;15): #1593

```
                          16 bp duplication in c-myc

der15       …GGGGGGGGGTCGTTCTGGAAAGAATGTGCCCAGTCAACCCCAACTCAGCTCAGCTCACCC…
             ||||||||||||||||||||||||||||||||||||||
c-myc       …GGGGGGGGGTCGTTCTGGAAAGAATGTGCCCAGTCAACATAACTGTACTAACTGTACGAC…
                                   ||||||||||||||||||||||||||||||||||||||
der12       …GCTCAGCTCAGCCCAGCTCAGCAATGTGCCCAGTCAACATAACTGTACTAACTGTACGAC…


                          362 bp deletion in IgH-Sμ

der15       …GGGGGGGGGGGTCGTTCTGGAAAGAATGTGCCCAGTCAACCCCAACTCAGCTCAGCTCAC…
                                                   |||||| |||||||||||||||
IgH-Sμ      …CAGCTCAGCTCAGCCCAGCTCAGCTCAGCTC...GCTCACCCCAGCTCAGCTCAGCTCAC…
             ||||||||||||||||||||||||
der12       …CAGCTCAGCTCAGCCCAGCTCAGCAATGTGCCCAGTCACATAACTGTACTAACTGTACGA…
```

T(11;15): #1461

```
                          27 bp duplication in c-myc

der15       …GTGCATTTCTGACAGCCTGGGACCGACACGGAGGTGCGTCCCGCACCCTTTATTAAAGC…
             ||||||||||||||||||||||||||||||||||||||||||||
c-myc       …GTGCATTTCTGACAGCCTGGGACCGACACGGAGGTGCGTCCCGCCCGCCAATCCCCGGC…
                              ||||||||||||||||||||||||||||||||||||||||||
der11       …TAGTGTTTCCTACTTTATGGGACCGACACGGAGGTGCGTCCCGCCCGCCAATCCCCGGC…


                          136 bp duplication in miR-142

der15       …ACACGGAGGTGCGTCCCGCACCCTTTATTA...ACTTTATGGATGAGTGCACTGTGGGC…
                                  ||||||||||||||||||||||||||||||||||||||
miR-142     …CACGGAGGGAGGGGGCAGGGGCCTTTATTA...ACTTTATGGATGAGTGCACTGTGGGC…
             ||||||||||||||||||||||||||||||||||||||||||
der11       …CACGGAGGGAGGGGGCAGGGGCCTTTATTA...ACTTTATGGGACCGACACGGAGGTGC…
```

T(11;15): #1583

```
                          12 bp duplication in c-myc

der15       …TTTGGGAGCGAGAAGGCTCCGTAACTTCTGACTTACCCCTGATACTTGGGGAGACACCA…
             ||||||||||||||||||||||| |||||||||||||
c-myc       …TTTGGGAGCGAGAAGGCTCCGTAGCTTCTGACTTACCAGTCTCTGAGAGGGCATTTAAA…
                                      ||||||||||||||||||||||||||||||||||
der11       …GAAAGACCTTCATGGCTCCCCCAAATTCTGACTTACCAGTCTCTGAGAGGGCATTTAAA…


                          15 bp deletion in miR-142

der15       …GCGTTTGGGAGCGAGAAGGCTCCGTAACTTCTGACTTACCCCTGATACTTGGGGAGACA…
                                                  ||||||||||||||||||||||
miR-142     …AGACCTTCATGGCTCCCCCAAAGCACGGTGCTTCCTGACCCCTGATACTTGGGGAGACA…
             ||||||||||||||||||||||
der11       …AGACCTTCATGGCTCCCCCAAATTCTGACTTACCAGTCTCTGAGAGGGCATTTAAATTT…
```

T(11;15): #1584

13 bp deletion in c-myc

```
der15       ...GACTGCGGTGAGTCGTGATCTGAATCCCCGTGGACAGACAGACAGTGCAGTCACCCATAA...
               |||||||||||||||||||||||
c-myc       ...GACTGCGGTGAGTCGTGATCTGAGCGGTTCCGTAACAGCTGCTACCCTCGGCGGGGAGAG...
                                                   ||||||||||||||||||||||||
der11       ...GTGGAGCGGTCCCTGGGAAGTTACACGGAATAGCTTAGCTGCTACCCTCGGCGGGGAGAG...
```

60 bp deletion in miR-142

```
der15       ...CGCCCCTGAATTGCTAGGAAGACTGCGGTGAGTCGTGATCTGAATCCCCGTGGACAGACA...
                                                        |||||||||||||||||||
miR-142     ...TCCCTGGGAAGTTACACGGAGGGGAGGGG...TGGCCTGAAGAATCCCCGTGGACAGACA...
               ||||||||||||||||||||
der11       ...TCCCTGGGAAGTTACACGGAATAGCTTAGCTGCTACCCTCGGCGGGGAGAGGGAAGACGC...
```

T(11;15): #1592

4 bp duplication in c-myc

```
der15       ...ACCCCCGCGGCACTAGGACTTGATGTTGGGCTAGCACTAATAAAGAATGGACTGGTTTC...
               |||||||||||||||||||||||||||||||||||
c-myc       ...ACCCCCGCGGCACTAGGACTTGATGTTGGGCTAGCGCAGTGAGGAGAAGCAAAATTGGG...
                                              ||||||||||||||||||||||||||||
der11       ...TCGAGAAGGGAGCCGGATGGATGGGTAAGGGTAGCGCAGTGAGGAGAAGCAAAATTGGG...
```

14 bp deletion in miR-142

```
der15       ...GACCCCCGCGGCACTAGGACTTGATGTTGGGCTAGCACTAATAAAGAATGGACGGTTTC...
                                                  ||||||||||||||||||||||||
miR-142     ...GCCGGATGGATGGGTAAGGGTCACGGGGCCCTCAACACTAATAAAGAATGGACGGTTTC...
               |||||||||||||||||||||
der11       ...GCCGGATGGATGGGTAAGGGTAGCGCAGTGAGGAGAAGCAAAATTGGGACAGGGATGTG...
```

T(11;15): #1613

227 bp deletion in c-myc

```
der15       ...AAGGCTCCGTAGCTTCTGACTTACGCTAAATCCCCAACCCATCTTTTAAATCTACAGAAT...
               ||||||||||||||||||||||||
c-myc       ...AAGGCTCCGTAGCTTCTGACTTACCAGTCT...AGCAAAATTGGGACAGGGATGTGACCG...
                                                     ||||||||||||||||||||||
der11       ...TGTTTTTTGGGGAAGCTGGGAACCTAACCCAGGGCTGGAATTGGGACAGGGATGTGACCG...
```

16 bp deletion in miR-142

```
der15       ...GCGTTTGGGAGCGAGAAGGCTCCGTAGCTTCTGACTTACGCTAAATCCCCAACCCCATCT...
                                                      |||||||||||||||||||||
miR-142     ...AGCTGGGAACCTAACCCAGGGCTTTGCGCTTACCATTGAGCTAAATCCCCAACCCCATCT...
               |||||||||||||||||||||||
der11       ...AGCTGGGAACCTAACCCAGGGCTGGAATTGGGACAGGGATGTGACCGATTCGTTGACTTG...
```

T(11;15): #1673

159 bp duplication in c-myc

```
der15   …AATGTAGCGGCCGGTTAGGACAGTCTTT...AGGTTACCGTAAAATGGTTGTCTGCCTCC…
         ||||||||||||||||||||||||||||||||||||||
c-myc   …AATGTAGCGGCCGGTTAGGACAGTCTTT...AGGTTACTATGGGCTGACGCTGACCCGGC…
                              |||||||||||||||||||||||||||||||||||||||
der11   …GGCCACCGGAAGTAGACTTTAAGTCTTT...AGGTTACTATGGGCTGACGCTGACCCGGC…
```

304 bp deletion in miR-142

```
der15   …AACCGGGATGCATTTTGAAGCGGGGTTCCCGAGGTTACCGTAAAATGGTTGTCTGCCTCC…
                                                |||||| ||||||||||||||
miR-142 …GGGCCACCGGAAGTAGACTTTGTAGCAAC...TGGCCCTGTAAAAGGGTTGTCTGCCTCC…
         |||||||||||||||||||||
der11   …GGGCCACCGGAAGTAGACTTTAAGTCTTTCTTCCATTCCTGTGCTTTTGACACTTTTCTC…
```

T(11;15): #1674

802 bp deletion in c-myc

```
der15   …ATAGTGATCGTAGTAAAATTCGTGTCCAGGCATTTTTTCACGCAACATGGCCGCCATTTC…
         ||||||||||||||||||||
c-myc   …ATAGTGATCGTAGTAAAATTTAAGCCTGA...CCCCCCAACCACACACACACACACACAC…
                                                 ||||||||||||||||||||
der11   …AGGGGAGGGGGCAGGGGCCTTTATTAAAGGCAGGAGTCGGCCACACACACACACACACAC…
```

544 bp duplication in miR-142

```
der15   …GTGATCGTAGTAAAATTCGTGTCCAGG...GAGTCGGCAAGAAAAGCAGGTGGCCTGAAG…
                           ||| ||||||||||||||||||||||||||||||||||||||
miR-142 …GACTGGTATCGGCAAGTGGTGCCCAGG...GAGTCGGCAAGAAAAGCAGGTGGCCTGAAG…
         ||||||||||||||||||||||||||||||||||||||
der11   …GACTGGTATCGGCAAGTGGTGCCCAGG...GAGTCGGCCACACACACACACACACACACA…
```

T(11/15); #1714

3 bp deletion in c-myc

```
der15   …TAGTGATCGTAGTAAAATTTAAGCCTGAGTGCACTGTGGGCTTCGGAGACCACGCCACGC…
         ||||||||||||||||||||||||||||
c-myc   …TAGTGATCGTAGTAAAATTTAAGCCTGACCCCCGCGGCACTAGGACTTGATGTTGGGCTA…
                                        |||||||| ||||||||||||||||||||
der11   …GTGCACTGTGGGCTTCGGAGACCACGCCACGCCGCGGCATTAGGACTTGATGTTGGGCTA…
```

41 bp duplication in miR-142

```
der15   …AATTTAAGCCTGAGTGCACTGTGGGCTTCGGAGACCACGCCACGCCGCGGCCCCCTGCCA…
                   ||||||||||||||||||||||||||||||||||||||||||||||||||
miR-142 …ACTTTATGGATGAGTGCACTGTGGGCTTCGGAGACCACGCCACGCCGCGGCCCCCTGCCA…
         |||||||||||||||||||||||||||||||||||||||||||||||||||
der11   …ACTTTATGGATGAGTGCACTGTGGGCTTCGGAGACCACGCCACGCCGCGGCATTAGGACT…
```

T(5;6): #1536

4 bp deletion in Anxa4

```
der5      ...CCACATAGAGAACATGGGATCTGAATTCACACTTTTAACTACTTGGAAGAGGAATTCTTA...
             ||||||||||||||||||||||||||
Anxa4     ...CCACATAGAGAACATGGGATCTGAATGAAGACCTTTTGCTCCCATGCAAGTGACCTGGAC...
                                           ||||||||||||||||||||||||||||||
der6      ...TTTTAGCAACCAGGGTATGATTTTGCTCACACCTTTTGCTCCCATGCAAGTGACCTGGAC...
```

6 bp duplication in Wdfy3

```
der5      ...GGTACCACATAGAGAACATGGGATCTGAATTCACACTTTTAACTACTTGGAAGAGGAATT...
                                           ||||||||||||||||||||||||||||||
Wdfy3     ...CGATTTTTAGCAACCAGGGTATGATTTTGCTCACACTTTTAACTACTTGGAAGAGGAATT...
             ||||||||||||||||||||||||||||||||||||
der6      ...CGATTTTTAGCAACCAGGGTATGATTTTGCTCACACCTTTTGCTCCCATGCAAGTGACCT...
```

Table S3
Chromosome aberrations detected in wild type (n=500) and in 250 additional *Igk*AID primary B cells (see Figure 6).

Metaphase ID	**wild type**
1	*T(3;11), Dic(8;8)*
2	*T(5;6)*
3	*Reciprocal T(18;19)*
Metaphase ID	***Igκ*AID**
12	Dic(12;16)
13	T(12;13)
14	Dic(12;16)
15	T(10;12), Dic(10;12)
16	T(9;16), T(3;4), T(11;17), Dic(4;11), Dic(3;4), Dic(7;19)
17	T(2;16)
18	T(2;12)
19	T(12;16)
20	Dic(4;11)
21	T(8;16), Dic(4;11)
22	Dic(11;15)
23	Dic(13;13)
24	T(1;13)
25	T(13;17), Dic(12;13)
26	T(2;13)

Table S4

Summary of sequence information (unique mutations/sequenced nucleotides).
The number of independent reads is indicated in parentheses.

	IgV_H	Sμ	c-myc	Taci	Whsc1	H2Eα	A20	miR-142	Anxa4	Wdfy3
AID$^{-/-}$ resting	1/40860 (90)	2/26600 (50)	5/70225 (84)	n.d.	n.d.	n.d.	n.d.	1/42450 (75)	n.d.	n.d.
AID$^{-/-}$ activated	1/19068 (42)	1/50008 (94)	7/77325 (94)	n.d.	n.d.	n.d.	n.d.	9/105842 (187)	n.d.	n.d.
Wild type resting	1/40406 (89)	7/50540 (95)	6/80595 (93)	n.d.	n.d.	n.d.	n.d.	2/52638 (93)	n.d.	n.d.
Wild type activated	2/37682 (83)	7/45752 (86)	3/46500 (93)	1/47150 (82)	n.d.	n.d.	n.d.	6/45280 (90)	n.d.	n.d.
IgκAID resting	30/39952 (88)	235/46284 (87)	3/42140 (68)	n.d.	n.d.	n.d.	n.d.	20/44148 (78)	n.d.	n.d.
IgκAID activated	32/40406 (89)	258/44688 (84)	21/148210 (178)	0/50025 (87)	1/53768 (94)	1/32289 (47)	2/43200 (48)	19/24338 (38)	2/72354 (93)	2/59432 (92)
AID$^{-/-}$ germinal center	n.d.	n.d.	3/75938 (86)	n.d.	n.d.	n.d.	n.d.	5/22074 (39)	n.d.	n.d.
Wild type Germinal center	n.d.	n.d.	3/51392 (60)	n.d.	n.d.	n.d.	n.d.	4/47544 (84)	n.d.	n.d.
IgκAID Germinal center	n.d.	n.d.	45/82087 (94)	n.d.	n.d.	n.d.	n.d.	18/23772 (42)	n.d.	n.d.
UNG$^{-/-}$ Germinal center	n.d.	n.d.	21/73494 (84)	n.d.	n.d.	n.d.	n.d.	23/49242 (87)	n.d.	n.d.

n.d. = not determined