Table S1: Sequences of preneoplastic *Myc:Igh* translocation sites from tissue culture

Clone Designation	Sequence	Tg/End	Polymorphic residues
	16,555 – 578* 1,419,586 – 562* (Sμ)		
der15.3.1[†]	TCCTGTGCTTTTGACACCTTTCTCA|CTCAGCCCAGCTCAGCTCACTCCAG	Tg[‡]	(6/6)
	16,842 - 818 1,421,882 - 858 (Sμ)		
18.10	AATCCCTTCTCCAAAGACCTCAGGA|GCTGAGCTGAGCTGGGGTGAGCTGA	Tg	(11/12)
	16,504 – 479 1,421,792 – 814 (Sμ)		
11.9	ACACAGGGAAAGACCACCAGATCTG|G|TGAGCTGAGCTGTGCTGGAGTGA	Tg	(13/13)
	15,085 – 061 (Sμ, 21 bp inversion[$],then 1,421,832)		
12.1	GTGGTGTGGAGGCGGCTCTTTCCCC|CAGCTCATCCCAGCTTACCCCAGCT	Tg	(9/9)
	16,694 – 670 1,421,922-946 (Sμ)		
10.1	CCTCCCGGTTTGACCCCTCAAAGGA|GGTGAGCTGAGCTGAGCTGGGGTGAG	Tg	(4/4)
	16,798 – 822 1,416,707 – 682 (Sμ)		
2.3	TCGCTTCGTGGTGGCCAAAGAAAGC|CCTAGGAACCACTTAAGAGTAAAAGC	End	(5/5)
8.1	ca. 15,133[¶] ca. 1,416,040	End	(9/9)
23-89-ml	ca. 16,471[¶] ca. 1,557,000 (Sγ2a)	Tg	(18/18)
	16,885 – 861 1,422,474 – 498 (Sμ)		
10.2	AGTCAGAAACTACGGAGCCTTCTCG|GGCCTGGTTGAGATGGTTCGAGATG	Tg	(3/3)
	16,915 - 891 1,421,516 - 540 (Sμ)		
15.5	GAAATTTAAATGCCCTCTCAGAGAC|CTGAGCTGAGCTGGGTGAGCTGAGC	Tg	(31/31)
	16,905 – 881 1,419,010 - 034 (Sμ)		
36.2	TGCCCTCTCAGAGACTGGTAAGTCA|TGGACTGTTCTGAGCTGAGATGAGC	Tg	(>31/31)
	16,796 – 772 1,419,079 – 055 (Sμ,152 bp inversion[$])		
37.3	ACCACGAAGCGACCTCCCGGTTTGA|GCTCACCCCAGCTCAGCTCACCCCA	Tg	(3/3)
	16,913 – 889 1,422,115 – 139 (Sμ)		
4.1	AATTTAAATGCCCTCTCAGAGACTG|AACTGAGCTGTGTGAGCTGAGCTGG	End	(4/4)
	15,085 – 061 1,419,559 – 535 (Sμ, 36 bp inversion[$])		
12.4	GTGGTGTGGAGGCGGCTCTTTCCCC|CAGCTCAGCTCACCCCAGCTCATCC	Tg	(51/52)
	17,095 – 071 1,421,631 – 655 (Sμ)		
6.3	AGCCCAACATCAAGTCCTAGTGCCG|TGAGCTGGGCTGAGCTGGGCTGAGC	Tg	(16/19)
	16,896 – 872 1,421,898 – 922 (Sμ)		
2.9	AGAGACTGGTAAGTCAGAGTCTACG|CTGGGGTGAGCTGAGCTGAGCTGGG	Tg	(7/7)
	16,208 – 184 1,421,908 – 932 (Sμ)		
21.10	GGCGGCAGGCTCGGAGGCAAAGCCC|CTGAGCTGAGCTGGGGTGAGCTGAG	Tg	(8/8)

[*] AC153008.4 is the Genbank accession number for the 25 bp of the *Myc* part of the translocation (left) and AJ851868.3 is the GenBank accession number for the *Igh* part (strain 129) of the translocation (right). Residue numbers from these accessions are shown above each sequence. The S region of origin is also shown above the sequence of the *Igh* part. For comparison to the endogenous *Igh* (C57BL/6) sequence, accession NT_166318.1 was used. A vertical line in each sequence notes the translocation site. Nucleotides between vertical lines represent insertions. Nucleotides that are underlined are shared between the *Igh* and *Myc* or *Pvt1* sequences.

Table 1 (continued)

[†]der 15.3.1, 18.10, etc. are the laboratory designations of the cloned translocation sequence. The first seven sequences are from transgenic line 995 B cells, "23-89-ml" is from transgenic line 820 B cells, and the last nine sequences are from transgenic line 556 B cells. The full sequences are available in GenBank, accessions JX080033-JX080049.

[‡]The transgenic (Tg) or endogenous (End) origin of the *Igh* sequence was determined by the examination of all potential polymorphic residues in the sequence. In the right-most column the number of residues that matched the "Tg" or "End" designation/number of polymorphic residues examined is shown in parentheses.

[§]In these translocation site sequences, there was a 21, 36, or 152 bp inversion of Sμ sequences at the exact translocation site, followed by Sμ in the orientation dictated by the PCR primers.

[¶]We did not determine the exact translocation site location by accurate sequences, as the translocation site was far removed from the sequencing primer. However, the residues shown are within 100 bp of the actual translocation site, and the Sμ sequences near the sequencing primer allowed unambiguous designation of transgenic or endogenous sequences.