Table S2: Sequences of *Myc:Igh* translocation sites from tumors

Tumor	Sequence*	Tg/End	Polymorphic residues
	16,905 – 881 1,419,010 – 034 (Sμ)		
4816	TGCCCTCTCAGAGACTGGTAAGTCA|TGGACTGTTCTGAGCTGAGATGAGC	Tg	(24/24[†])
	23,286,370 – 394[‡] 1,586,911 – 935 (Sα)		
74219	TGACGGTTGATCAGTGACAATGTAG|TGAGCTGAGCTAAACTAGGCTGAAA	Tg[§]	
	23,288,305 – 329[‡] 1,418,724 – 700 (Sμ[¶])		
74163	TTCTGAAAACAGGAATATGTGCAAG|CAAGCTTTATGAGTCTGGCCTTCTC	Tg[§]	
	15,709 - 684 1,537,648 - 672 (Sγ2b)		
79130	TACTCCGGCTCCGGGGTGTAAACAG|AGCACTGGGCCTTTCCAGAACTAAT	Tg[§]	
	15,283 – 314 1,555,377 - 357 (Sγ2a)		
79130	TACGTGGCAGTGAGTTGCTGAGTAA|CCCAGATTCCCCATAGCTGCTCTGC	Tg[§]	
	23,295,296 – 6,018[‡] 1,509,641 - 618 (Sγ1)		
79134	CTTTCTTCCAGGCTAATTCATATTT|G|TTATCACAGGGCTCAGCTGCCTT	Tg[§]	
	16,786 - 762 1,587,313 – 337 (Sα)		
1854	GACCTCCCGGTTTGACCCCTCAAAG|CTGAGCTGGGCCTAAGATGGACTTG	Tg[§]	
	16,340 – 364 1,416,532 – 508 (Sμ)		
1854	CCCAGGCTCCGGGGAGGGAATTTTT|CTCCTTCCAACAAATGAAGTTTTAA	Tg[§]	

*The organization of this Table is identical to Table S1. Relevant GenBank accession numbers are listed in the footnotes to Table S1. Tumor 4816 was derived from transgenic line 995. Tumors 74219 and 74163 were derived from transgenic line 820. Tumors 79130 and 79134 were derived from transgenic line 336. Tumor 1854 was derived from transgenic line 556. These sequences are available in GenBank, accessions JX080050-JX080057.

[†]The alignment of the Sμ part of the translocation from the tumor in mouse 4816 required two deletions relative to the germline sequences. The first was at residue 1,419,156 and was 90 bp for the 129 sequence and 105 bp for the C57BL/6 sequence. The second deletion was at residue 1,419,441 and was 2145 bp for the 129 sequence and 145 bp for the C57BL/6 sequence. These putative deletions resulted in the best alignments for both 129 and C57BL/6.

[‡]Chr 15 sequence (*Pvt1*) is from accession NT_039621.7. Consistent with the sequence of the translocation site, Pvt1-Cα transcripts (1) were amplified from the RNA of tumor #74219 and #79134. Pvt1-Cα transcripts were also cloned from the RNA of tumor #74163.

[§]These tumors were derived from mice with an endogenous *Igh*[a] allele, and therefore the origin of the *Igh* part of the translocation cannot be determined from sequence polymorphisms. The "Tg" designation is derived from two-color FISH.

[¶]213 bp of Sμ (the 3' end of the Sμ sequence is joined to 5' end of the *Pvt1* sequence) is followed by 84 bp of Sγ1 sequence (the 3' end of the Sγ1 sequence is joined to the 5' of end of the Sμ sequence). The Sγ1 sequence is followed by Sα sequences (joined to Sγ1 5' to 5'). The orientation of the Sμ and Sγ1 sequences relative to one another and to the Sα sequences suggest that the Sμ and Sγ1 sequences are derived from a switch deletion circle.

1. Huppi K, Siwarski D (1994) Chimeric transcripts with an open reading frame are generated as a result of translocation to the Pvt-1 region in mouse B-cell tumors. *Int. J. Cancer* 15**:**648-651.