Supplemental Table I. Primer and probe sequences for *BCL2/IGH*-PCR of alternative *BCL2* breakpoints

Test tube 1		
	MBR 1	CTCTGTGGCATTATTGCATTA
	MBR 2	CCTAAGAAAAACCTGGATGTC
Test tube 2		
	MCR 1	CAAGCGCCCAATAAATAGCAG
	MCR 2	GGAGTGGAAAGGAAGGACAAT
	MCR 3	AAATCCAAAATCAAATATGTG
Test tube 3		
	3'MBR 1	AGCACCTGCTGGATACAACAC
	3'MBR 2	TGACAGAGCAAAACATGAACA
	3'MBR 3	TGTAATGACTGGGGAGCAAAT
	3'MBR 4	CTGGTTGGCGTGGTTTAGAGA
	5'MCR	CTGAAAGAAACGAAAGCAACA
	ICR	AGTGAGAGTGCAGAATCTGAC
JH primers		
	JH 1	AGCACCTGTCCCCAAGTCTGA
	JH 2	GTGCCTGGACAGAGAAGACTG
	JH 3	AGAGAAAGGAGGCAGAAGGAA
	JH 4	AAGCAGGAGAGAGGTTGTGAG
	JH 5	AAAATGCCTCCAAGACTCTGA
	JH 6	GAAAACAAAGGCCCTAGAGTG
JH MGB probe		CTGAGGAGACGGTGACC

Supplemental Methods: The PCR for alternative *BCL2/IGH* breakpoints was done as a multiplex PCR. *BCL2* primers (test tubes 1, 2 and 3) were combined with all six *JH* primers and the *JH* MGB probe. Cycling conditions and reagents were identical to the MBR-PCR. For PCR-positive tumor samples, the respective *BCL2* and *IGH* primers were identified and used for analysis of corresponding blood samples.

Supplemental Table II. *BCL2*-MBR translocation sequences from blood of control patients who did not develop follicular lymphoma (FL)

Case no.	Translocation frequency per 100,000 cells	*BCL2*-MBR break-point*	Nontemplated N nucleotides	N length (bp)	*JH* gene	*IGH* break-point†	PCR fragment length (bp)
Control 1	1.6	3053	CCGCTGAACCCA	12	6	2948	153
Control 2	0.1	3056	TTCTGACGGACTCCAAGACTGGAATTGATCATTAT	35	6	2959	166
Control 3‡	0.4	3056	TGGGGACTAC	10	6	2967	134
Control 4§	0.7	3056	TTGCGAGCAGGGTGAT	16	6	2968	139
Control 5	0.4	3109	GGGA	4	6	2959	188
Control 6	0.1	3112	GGGGGCCGGTCATTGGGGTTCGG	23	6	2949	219
Control 4§	0.7	3114	ATTCGTTCACCCCACGGACTTGACCT	26	6	2968	209
Control 7	0.1	3146	CCGTCCGGGATGGAGCA	17	6	2953	246
Control 8	0.4	3154	GCAAGTAAAAGCTTAGAGAT	20	5	2368	239
Control 9	0.2	3162	TCCTCGGACCG	11	3	1537	247

* *BCL2* sequence based on GenBank accession number M14745.

† *IGH* sequence based on GenBank accession number J00256.

‡ Sequence identical to Case no. MBR1 blood DNA amplified in an adjacent well.

§ Two different sequences isolated from the same patient.