

Table 4. Somatic hypermutation of J_H region in DLBCL, BLL, and FBL

Mouse	N	D _H	N	J _H	% clones mutated	J _H	D _H
K7	g	TCTACTATGATTAC	ctacggctattggtgtg	TACTATGCTATGGACTACT GGGGTC <u>GATGAACACCA</u> GCCACCGT <u>C</u> CTCA	23.3 (7/30)	J _H 4	DSP2.2
P2	ttat	TACTA	cgatgtagctaccc	TACTGGTACTTCGATGTCT GGGGCGCAGGGACCAC GGTCACCGTCTCCTCA	NM (2/2)	J _H 1	DSP2.n
K8	gttta	ATTAC	tacggtag	TAGTTTGACTACTGGGGC CAAGGCACCACTCTCACA GTCTCC <u>A</u> CA	20.0 (4/20)	J _H 2	DSP2.2

K7 J_H4: TACTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA

(1) G
(2) T
(3) A
(4) C
(5) C
(6) C
(7) A

Somatic mutations detected in BLL (K7), FBL (P2), and DLBCL (K8) tumor lines derived from *TCL1* transgenic mice. N-region additions flanking individual D_H gene segments are listed in lower case letters. The total variations detected from the germ-line J_H sequence in each tumor are underlined. Shown below the table are the positions of 7 mutations detected from 30 J_H region segments sequenced from tumor K7. All mutations were substitutions rather than insertions or deletions. Boldface underlined positions indicate transition-type mutations. The occurrence of four distinct transitions (Pyr → Pyr and Pur → Pur) and three independent transversions (Pyr → Pur and Pur → Pyr) is compatible with ongoing somatic hypermutation in this line. Mutations within

the D_H segments, 5' and 3' regions flanking the DJ_H segments were not observed. NM, not meaningful.