Table SI. Primers and probes used for PCR and colony screening

Technique	Oligonucleotide (5' to 3')	Description
PCR		
1st 5' J558	AGCCTGACATCTGAGGAC	1° PCR, heavy chain
1st 3' Eμ	GTGGTGTTTTGCTCAGCCTG	1° PCR, heavy chain
2nd 5' J558-EcoRI	CACGAATTCGCCTGACATCTGAGGACTCTGC	2° PCR, heavy chain
2nd 3' Eμ-ClaI	CACATCGATCAGCTACAAGTTTACCTAGTG	2° PCR, heavy chain
1st 5' Vκ4	CGCTTCAGTGGCAGTGGGTCTG	1° PCR, light chain
1st 3' Eκ	CAGGGTGAACGCCAAATGGCTG	1° PCR, light chain
2nd 5' Vκ4-EcoRI	CACGAATTCCTCTCACAATCAGCAGCATGGAGG	2° PCR, light chain
2nd 3' Eκ-ClaI	CACATCGATCAGCCGCGAGGTCACCCAGTTGTA	2° PCR, light chain
Hybridization		
JH139	CATCTGCCACACTCTGCATG	J_H1 probe
JH131	CAGGTCATGAAGGACTAGGG	J_H2 probe
Jκ168	CCGTTGTCTATGTCTGTGGC	J_K1 probe
Jκ169	TAGGGAGGGTTTTGTGGAGG	J_K2 probe

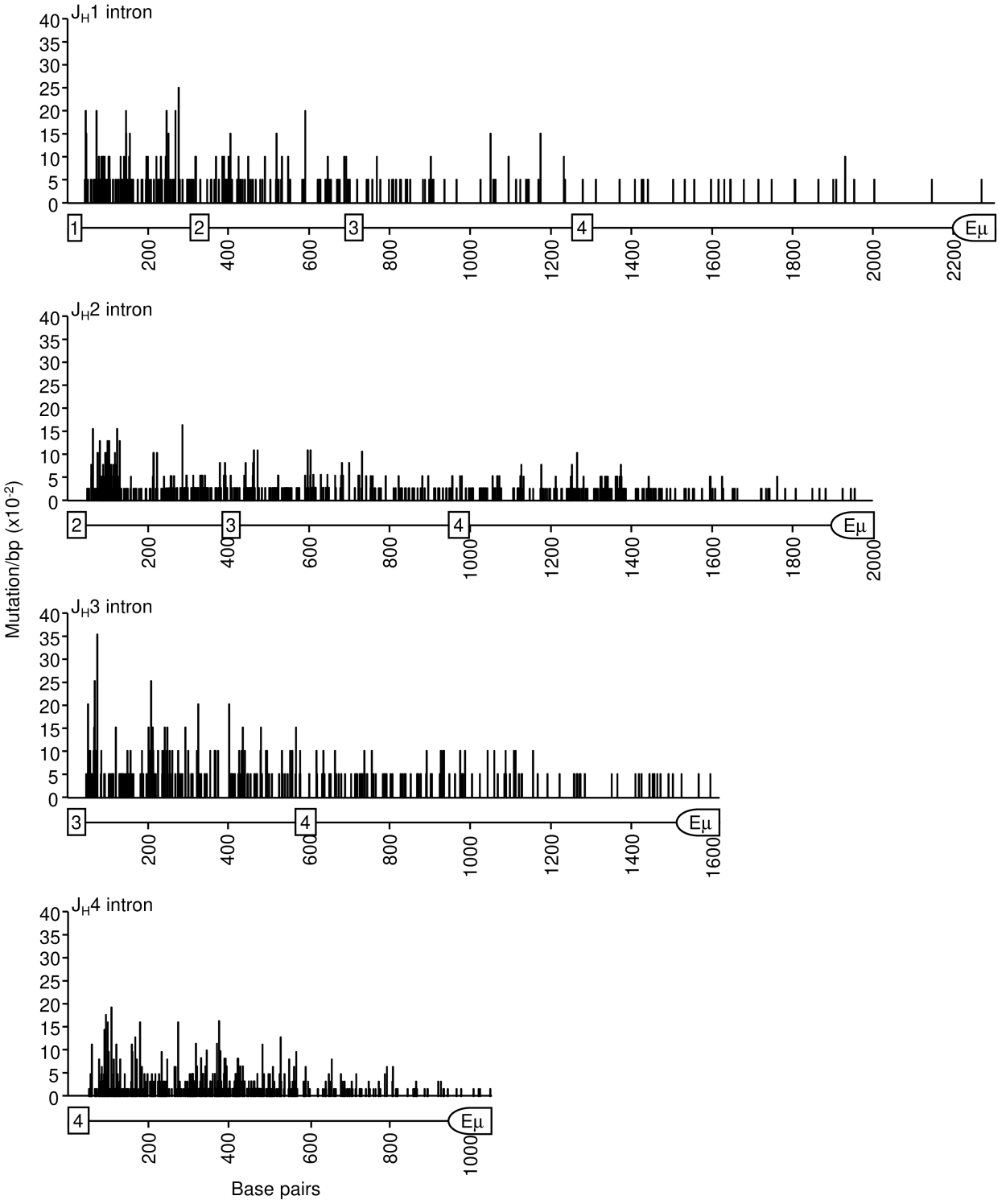

FIGURE S1. Mutational distribution in J_H intron sequences as in Fig. 2, aligned with the beginning of the utilized J segment. Black vertical lines represent the number of mutations/bp x 10^2 (y-axis) for each residue from VDJ clones utilizing J_H1, J_H2, J_H3, and J_H4 genes. X-axis depicts the distance from the utilized J segment to Eμ. Half circle shows the portion of the Eμ intronic enhancer that was sequenced.

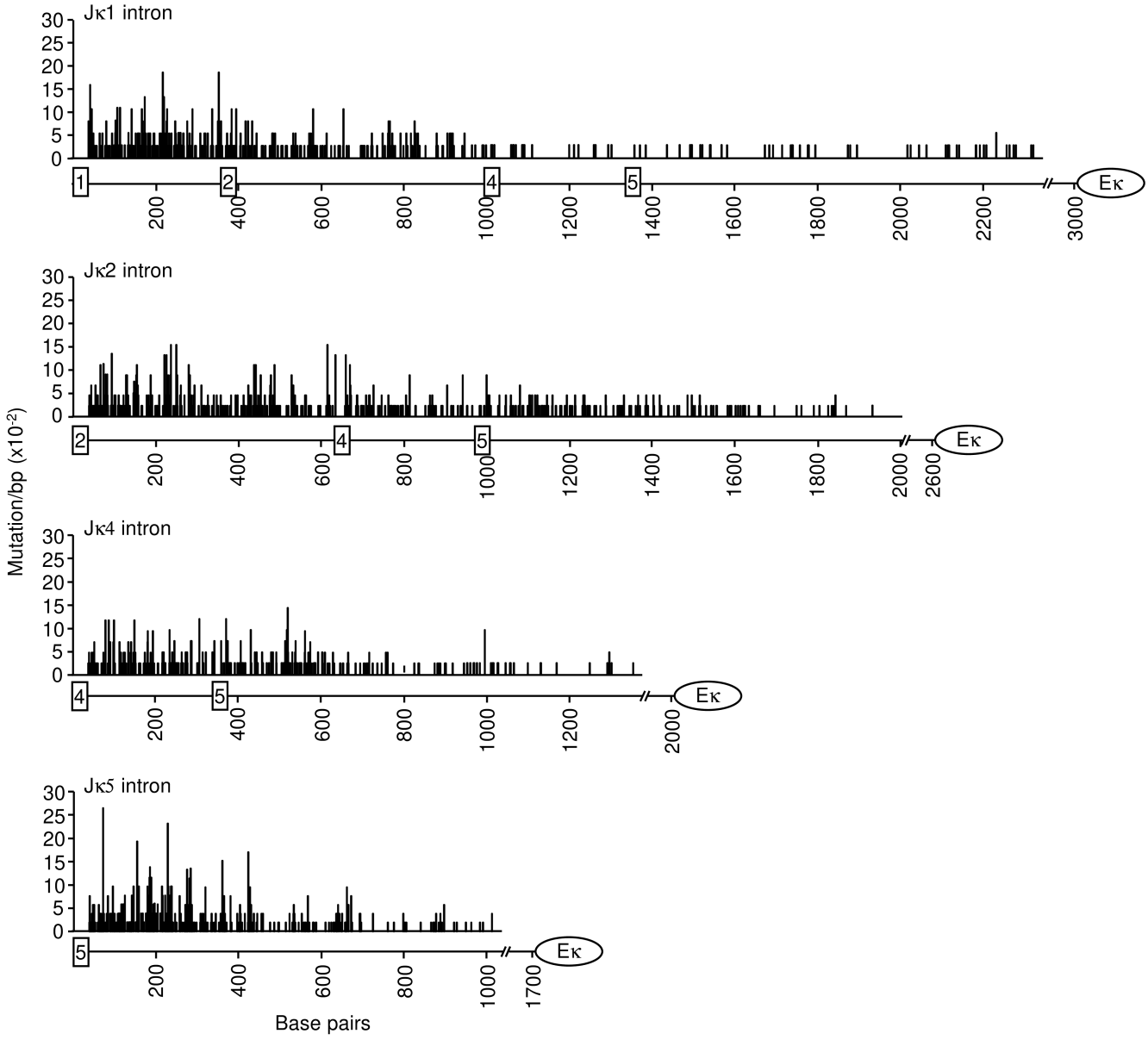

FIGURE S2. Mutational distribution in J_κ intron sequences as in Fig. 3, aligned with the beginning of the utilized J segment. Black vertical lines represent the number of mutations/bp x 10^2 (y-axis) for each residue from VJ clones utilizing $J_\kappa1$, $J_\kappa2$, $J_\kappa4$, and $J_\kappa5$ genes. X-axis depicts the distance from the utilized J segment to Eκ. Circle shows the position of the Eκ intronic enhancer.