A

$D_\beta 1$-$J_\beta 1.1$ SJ	Rag1^{+/+}	Rag1[KI/KI]
Precise joints	31/35 (89%)	26/33 (79%)
Imprecise joints	4/35 (11%)	7/33 (21%)
N nucleotides	4/4 (100%)	7/7 (100%)
Deletion	0/4 (0%)	1/7 (14%)

B

$D_\beta 1$-$J_\beta 1.6$ CJ	Rag1^{+/+}	Rag1[KI/KI]
Deletion within $D_\beta 1$	24/35 (69% -4.88bp)	28/31 (90% -4.46bp ns)
P/N addition at DJ junction	26/35 (74% +2.50bp)	21/31 (68% +3.38bp ns)
Deletion within $J_\beta 1.6$	31/35 (89% -5.42bp)	21/31 (68% -12.40bp**)

C

$D_\beta 1$-$J_\beta 2.7$ CJ	Rag1^{+/+}	Rag1[KI/KI]
Deletion within $D_\beta 1$	28/30 (93% -3.50bp)	25/29 (86% -6.00bp ns)
P/N addition at DJ junction	23/30 (77% +2.17bp)	7/29 (24% +4.71bp***)
Deletion within $J_\beta 2.7$	25/30 (83% -5.28bp)	26/29 (90% -4.31bp ns)

Supplementary Figure 2. Comparison of recombination products between RAG1[KI/KI] and RAG1^{+/+} mice. The number of each joint out of the total number analyzed is shown. The frequency of each joint is expressed as the percentage in parentheses. The average length of additions or deletions was calculated only for the junctions with additions or deletions. The statistical tests refer to the average length added or deleted. (**A**) Comparison of $D_\beta 1$-$J_\beta 1.1$ signal joints. (**B**) Comparison of $D_\beta 1$-$J_\beta 1.6$ coding joints (mean $\pm$ SEM; **P < 0.01 by Student's t-test; N.S., no significance). (**C**) Comparison of $D_\beta 1$-$J_\beta 2.7$ coding joints (mean $\pm$ SEM; ***P < 0.001 by Student's t-test; N.S., no significance).