

Table 2. CDR3 length of heavy and light chain rearrangements in pol  $\lambda$ - and pol  $\mu$ / pol  $\lambda$ -double deficient mice

Ig gene Rearrangement <sup>a</sup>	mice	CDR3 length in bp (number of sequences)			CDR3 size range in bp
		Total sequences	In frame sequences	Out of frame sequences	Total sequences
V <sub>H</sub> DJ <sub>H4</sub>	+/+	38.6 (39)	37.7 (25)	40.4 (14)	21-54
	pol $\lambda$ -/-	33.6 (41)	34.9 (27)	31.5 (14)	12-51
	pol $\mu$ / pol $\lambda$ -/-	34.6 (77)	34.9 (63)	31.1 (15)	(0) <sup>b</sup> -51
V <sub>H</sub> DJ <sub>H1</sub>	+/+	40.9 (60)	41.5 (36)	39.9 (24)	10-54
	pol $\lambda$ -/-	35.7 (73)	36.2 (55)	34.1 (18)	19-54
	pol $\mu$ /pol $\lambda$ -/-	35.5 (94)	35.5 (82)	36.6 (12)	15-52
V $\kappa$ -J $\kappa$ 1	+/+ <sup>c</sup>	27.2 (35)	27.2 (14)	27.2 (21)	23-30
	pol $\lambda$ -/-	27.7 (36)	27.2 (15)	28.0 (21)	22-32
	pol $\mu$ -/- <sup>c</sup>	21.2 (40)	21.0 (13)	21.3 (27)	7-32
	pol $\mu$ /pol $\lambda$ -/-	18.0 (88)	19.2 (22)	17.4 (66)	(0) <sup>b</sup> -30
V $\kappa$ 41-J $\kappa$ 1	+/+ <sup>c</sup>	27.3 (25)	27.2 (16)	27.4 (9)	21-31
	pol $\mu$ -/- <sup>c</sup>	17.2 (35)	17.4 (14)	17.1 (21)	(0) <sup>b</sup> -30
	pol $\mu$ /pol $\lambda$ -/-	19.1 (41)	22.8 (17)	17.9 (24)	(0) <sup>b</sup> -30

a) Rearrangements were studied in sorted B220<sup>+</sup>/IgM<sup>-</sup> bone marrow cells.

b) 0 in parenthesis stands for deletions extending in the framework region.

c) Data taken from Bertocci et al., 2003.