

Supplemental Tables

Table S1. *L Chain Usage in 3H9.KI Hybridomas after cGVH Induction*

	dsDNA ⁺		dsDNA ⁻	
	3H9tg ⁺ = 17	3H9tg ⁻ = 9	3H9tg ⁺ = 3	3H9tg ⁻ = 9
L chain usage				
J κ 1	1 (6%)	1 (11%)	0	4 (44%)
J κ 2	3 (17%)	2 (22%)	1 (33%)	0
J κ 4	0	1 (11%)	0	1 (11%)
J κ 5	7 (41%)	2 (22%)	0	3 (33%)
λ 1	5 (29%)	0	0	1 (11%)
λ x				
V κ 38c	1 (5%) ^a	0	1 (33%)	0
V κ 32a	2 (11%) ^a	0	0	1 (11%) ^a

Analysis of the same monoclonal hybridomas shown in Table I. L chain rearrangement in hybridomas from the bm12→3H9(+) mouse. The high percentage of J κ 5 (41%) and λ usage (29%) found in dsDNA⁺3H9tg⁺ clones differs significantly from those expected for J κ 5 and λ ($P \leq 0.05$) usage (some of the 3H9.KI results have been already been published in reference 20 [listed in main text of article]).

^aRepresents dual L chain rearrangement. The κ and λ PCR assays were described previously (references 6, 18, 23, and 25 [listed in main text of article]).

Table S2. *L Chain Usage in 3H9/56R.KI IgM Hybridomas after cGVH Induction*

	dsDNA ⁺		dsDNA ⁻	
	56Rtg ⁺ = 16	56Rtg ⁻ = 2	56Rtg ⁺ = 2	56Rtg ⁻ = 2
L chain usage				
J κ 1	1 (6%)	0	1 (50%)	0
J κ 2	0	0	1 (50%)	1 (50%)
J κ 4	2 (12.5%)	1 (50%)	0	1 (50%)
J κ 5	5 (31.5%)	0	0	0
λ 1	1 (10%) ^a	0	0	1 (50%)
λ x	0	0	0	0
V κ 38c	10 (62%)	0	0	0
J1	1 (10%)			
J2	2 (20%)			
J4	6 (60%) ^a			
J5	1 (10%)			
V κ 32a	1 (6%) ^a	1 (50%) ^a	1 (50%) ^a	0

Analysis of the same monoclonal hybridomas shown in Table I. L chain rearrangement in IgM hybridomas from the bm12→56R(+) mouse.

^aRepresents dual L chain rearrangement. The κ and λ PCR assays were described previously (references 6, 18, 23, and 25 [listed in main text of article]).

Table S3. *L Chain Usage in 3H9/56R.KI IgG Hybridomas after cGVH Induction*

	dsDNA ⁺		dsDNA ⁻	
	56Rtg ⁺ = 0	56Rtg ⁻ = 38	56Rtg ⁺ = 0	56Rtg ⁻ = 18
L chain usage				
J κ 1		6 (16%)		0
J κ 2		11 (29%)		3 (17%)
J κ 4		8 (21%)		3 (17%)
J κ 5		3 (7%)		3 (17%)
λ 1		1 (2%)		0
λ x		0		0
V κ 38c		0		3 (17%)
V κ 32a		2 (5%) ^a		3 (17%) ^a

Analysis of the same monoclonal hybridomas shown in Table I. L chain rearrangement in IgG hybridomas from the bm12→56R(+) mouse. None of these clones show an L chain bias.

^aRepresents dual L chain rearrangement. The κ and λ PCR assays were described previously (references 6, 18, 23, and 25 [listed in main text of article]).