

Inlay et al., <http://www.jem.org/cgi/doi/10.1084/jem.20052310>

Primer sequences

All sequences are listed 5' to 3'. Final concentrations used for real-time PCR reactions are listed in parentheses.

Real-time quantitative PCR analysis of DNA content.

Sequences for the β -actin gene (400 nM) are as follows: actin.gene.f (CGATGCCCTGAGGCTCTT) and actin.gene.r (TGGATGCCACAGGATTCCA).

Transcriptional analysis of WT and $\text{E}\mu\text{R}$ sorted B cell populations.

Sequences are as follows: $\text{C}\mu$ (200 nM), $\text{C}\mu 1$ (ACACCTGCCGTGTGGATCA) and $\text{C}\mu 2$ (GAGGAAGATGTCCG-GCAAAGG); GAPDH (100 nM), GAP.f (CCAGTATGACTCCACTCACG) and GAP.r (GACTCCACGACATACT-CAGC); β -actin transcription (400 nM), actin.mRNA.f (AGGCCAACCGTGAAAAGATG) and actin.mRNA.r (GCTGAGAAGCTGGCCAAAGA); mouse κ^0 germline transcription (400 nM), $\kappa^0\text{GT.f}$ (AGGAGGGTTTTTGTACAGC-CAGA) and $\kappa^0\text{GT.r}$ (TGGATGGTGGGAAGATGGAT); CD19 (400 nM), CD19.f (CTGACCATCGAGAGGCACGT) and CD19.r (GAGCCACACTGCTGACCTTG); $\text{V}_{\kappa 24-140}$ (400 nM), hf24.f (TGCCTGGTTTGTTCCTTGTCT) and hf24.r (GGCTTCAATTTGCCATGTTGA); $\text{V}_{\kappa 2-139}$ (400 nM), bd2.f (GTGCAATCTGGAGAGGAGCAG) and bd2.r (CCCTCCCTCTCACACAGACAC); $\text{V}_{\kappa 9-96}$ (400 nM), ce9.f (CCATGAAAGCAGAAGTGTGGG) and ce9.r (TCAC-CATGAGGAACATCTGGAG); $\text{V}_{\kappa 4-54}$ (400 nM), at4.f (AGTGGTTTTGATTGCAGTAGTCCAC) and at4.r (ATGA-CATTGTAAAGCAGAACACCC); $\text{V}_{\kappa 8-24}$ (400 nM), 8-24.f (TGGTTATACACTCTTCTCCATTTCAGC) and 8-24.r (GCATTTTCAGACATGGCACCTC); $\text{V}_{\kappa 21-1}$ (400 nM), 21-1.f (GAGGCTCAGTCTCTCAGTTCTCTCTT) and 21-1.r (GCTCTGTGTTGAGATGCAGGAG).

Real-time quantitative PCR analysis of unrearranged Igk loci.

Sequences for κGL (400 nM) are as follows: $\kappa\text{GL.f}$ (GCCTACCCACTGCTCTGTTC) and $\kappa\text{GL.r}$ (CGTTTGATTCCAGCTTGGT).

Semiquantitative rearrangement analysis.

Sequences are as follows: $\text{V}_{\kappa\text{D}}$, GGCTGCAGSTTCAGTGGCAGTGGRTCWGGRAC; K6, GACACTCCTGATGTTT-GGGAGTCTGAAC; MAR35, AACACTGGATAAAGCAGTTTATGCCCTTTC; iRS, GCCATGTAGATAACCATGGCTT-GCTGA; RS1, AGGACCCTAGTGGCAGCCAGGGTGGATC; and RS2, CATAACTGACTGTGCTGGCTGGGTTG.

Analysis of $\text{V}_{\kappa}\text{J}_{\kappa} 1$ junctions.

Sequences complementary to the endogenous mouse *Igk* locus are in capitals, and added sequences are in lowercase as follows: $\text{V}_{\kappa\text{D}}$.bam, ccggatcc-GGCTGCAGSTTCAGTGGCAGTGGRTCWGGRAC; and $\text{J}_{\kappa} 1$.eco, ggcgattCTTTGAGCATTCTGAAACTATCACTTGTG.

MSRE-QPCR.

Sequences are as follows: C_{κ} (400 nM), $\text{C}_{\kappa} 1$ (CAACTGTATCCATCTTCCCACCA) and $\text{C}_{\kappa} 2$ (GGCACCTCCAGATGT-TAACTGCT); q1 (400 nM), q1f (AAGATAAACTGAATGACCCAGAGGA) and q1r (TCTTCTCAGAGCTCCAGGCC); q2 (400 nM), q2f (TGAATCATACGTCAAGGCCAGA) and q2r (AGAGACCCCAAGGAGGGATC).

Bisulfite genomic sequencing.

Sequences that anneal to bisulfite-converted DNA are listed in capitals, and added sequences are listed in lowercase as follows: bis1.1, GGATAGAAAAGGGTTGAAGTTAAGTTTAGTT; bis2.1, CCTACCTAACCAATTAATAATCATATCAC; bis3.1, CCCTCTCACATTTTAAAATCACAATATTTAAC; bis4.1, CCTATCTCTTCCAAAATACTCTAATATTAACC; bis1.2eco, ggcgattcGGATGTGGGAGTAAATTTTGAAGATAAATTG; bis2.2bam, ggcgatCCATAACTTTTACTAAC-TATAAATTTTACCTC; bis3.2bam, ggcgatCTAAACTTTTACAAACTCCACCAAACCTCTC; and bis4.2bam, ggcgatCCAAACTAAACCTACTATATAAAACAAAACC.