SUPPLEMENTARY DATA

**Supplementary Table 1.** Forward (F) and reverse (R) primers used for PCR quantification of mRNA transcripts encoding Gapdh, both isoforms of the beta chain constant region, Vβ9, Vβ13, Vβ15, and Vβ16. Gapdh was used as housekeeping control. Additional details are given in Methods.

| Genetic Element | Sequence |
|---|---|
| Real-time Primers | |
| Gapdh (F) | 5'-GCACCACCAACTGCTTAGCC-3' |
| Gapdh (R) | 5'-CTGAGTGGCAGTGATGGCAT-3' |
| Cβ (F) | 5'-TGCCAAGTGCAGTTCTATGG-3' |
| Cβ (R) | 5'-TTGTTGATAGGATGCTGAGGT-3' |
| Vβ4 (F) | 5'-GTTGCCTGGTCCTCTGTCTC-3' |
| Vβ4 (R) | 5'-TTGTGTCCTAGATGCTGTTCG-3' |
| Vβ9 (F) | 5'-TGTGATCTTCTGTCTTCTTGCAG-3' |
| Vβ9 (R) | 5'-CACTGGTTTTCCAACTCTTGC-3' |
| Vβ13 (F) | 5'-GGGCAGTGCTCTGTCTCCT-3' |
| Vβ13 (R) | 5'-TGGGTGACTCCAGTTTCAGA-3' |
| Vβ15 (F) | 5'-TGCTGCTTCTGCTACTTCTGG -3' |
| Vβ15 (R) | 5'-CCTGAACACCCTCAGTGTGAC-3' |
| Vβ16 (F) | 5'-GGCATCCAGACCCTCTGTT-3' |
| Vβ16 (R) | 5'-TGACTCCAGCATCTGCGTTA-3' |
| Vβ13 for Jβ (F) | 5'-TTGCTGTGAGGACTGAAGGA-3' |
| Vβ16 for Jβ (F) | 5'-CGATGGTAAAATTGGGGAGA-3' |
| Jβ 1.1 (R) | 5'-AACTGTCAGTCTCGTTCCTTTACC-3' |
| Jβ 1.2 (R) | 5'-GGGCCGAAGGTGTAGTCATA-3' |
| Jβ 1.3 (R) | 5'-CTTCCTTCACCAAAATAGAGCAC-3' |
| Jβ 1.4 (R) | 5'-CATGGCCGAAAAACAATCTT-3' |
| Jβ 1.5 (R) | 5'-CCGAGTCCCTTCTCCAAAAT-3' |
| Jβ 1.6 (R) | 5'-GTGCCTGCTGCAAAGTAGAG-3' |
| Jβ 2.1 (R) | 5'-GTGTCCCTGATCCGAAGAA-3' |
| Jβ 2.2 (R) | 5'-CAGCACTGTCAGCTTTGAGC-3' |
| Jβ 2.3 (R) | 5'-AACGGTCAGTCTGGTTCCTG-3' |
| Jβ 2.4 (R) | 5'-CTGCACCGAAGAACAAGGT-3' |
| Jβ 2.5 (R) | 5'-TGCCTGGTCCAAAGTACTGG-3' |
| Jβ 2.6 (R) | 5'-CGGGACCGAAATACTGCT-3' |
| | |
| Cloning and Sequencing Primers | |
| Vβ13 Cloning 1 (F) | 5'-GGGCAGTGCTCTGTCTCCT-3' |
| Vβ13 Cloning 1 (R) | 5'-TTGTTGATAGGATGCTGAGGT-3' |
| Vβ13 Cloning 2 (F) | 5'-TCGACACAGTTCTGTCTGAAAC-3' |
| Vβ13 Cloning 2 (R) | 5'-CCTTGTTTGAGCCATCAGAAGC-3' |
| | |

SUPPLEMENTARY DATA

**Supplementary Figure 1.** Correlation plot of Jβ usage from direct sequencing and qRT-PCR analysis. To exclude the possibility that skewing of individual CDR3 regions, as determined by direct sequencing of bacterial clones, was an artifact of PCR amplification of the insert or bacterial clone expansion we analyzed Jβ isotype abundance by qRT-PCR as described in Methods. Percent frequency of Jβ determined by sequencing was plotted against the percent frequency of Jβ determined by qRT-PCR. We observe a significant positive correlation of Jβ abundance by these two methods (Islets: R2=0.4425, p=0.018; spleen poly I:C: R2=0.5871, p=0.0037; spleen untreated: R2=0.3683, p=0.036). The significant positive correlation between Jβ usage determined by direct sequencing of clones and Jβ usage as determined by qRT-PCR indicates that our measurements of skewing and diversity from direct sequencing give an accurate measure of the true TCR repertoire diversity