Supplementary File S6: Volumes, T cell numbers, raw reads, total and unique TCRβ sequences from

laser-captured GC of pln (GST/SJL-H2s)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| GST  4 wks p.i. | mouse | GC | captured GC volume (x 107 µm3) | raw reads (x106) | total TCRβ sequences (x106) \* | unique TCRβ clonotypes | number of Tfh-clonotypes subjected to analysis \*\* |
| 1 | left | 4.68 | 1.74 | 0.86 | 1348 | 674 |
| right | 4.22 | 1.70 | 0.61 | 439 | 218 |
| 2 | left | 2.88 | 1.87 | 1.24 | 1328 | 662 |
| right | 4.09 | 2.27 | 0.64 | 1974 | 981 |
| 3 | left | 4.68 | 1.59 | 0.45 | 2275 | 1136 |
| right | 3.99 | 1.71 | 1.03 | 1125 | 562 |
| mean ± SD |  | 4.09 ± 0.66 | 1.81 ± 0.24 | 0.81 ± 0.29 | 1414 ± 648 | 706 ± 323 |

4-6 individual GC per pln were isolated by laser-microdissection and subjected to deep sequencing (GST/SJL-H2s). \* all sequences that appeared only once had been removed, \*\* only TCR sequences above the median were used for analysis