Supplementary file 3. Tfh isolated by flow cytometry, T cell numbers, raw reads, total and unique TCRβ sequences (Ag1/SJLH2s)

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Ag14 wks p.i. | mouse | TfhCD4+/PD1high/CXCR5high | counted and estimated number of Tfh cells (x 104) | raw reads (x106) | total TCRβ sequences (x106)\* | unique TCRβ clonotypes | number of Tfh-clonotypes subjected to analysis>median \*\* |
| 1 | left | 4.3 | 2.0 | 1.68 | 11522 | 5744 |
| right | 5.0 | 2.2 | 1.76 | 13418 | 6615 |
| 2 | left | 4.5 | 2.0 | 1.68 | 11942 | 5891 |
| right | 3.6 | 2.1 | 1.89 | 12988 | 6489 |
| 3 | left | 5.0 | 1.8 | 1.43 | 8420 | 4181 |
| right | 5.0 | 2.4 | 2.2 | 11579 | 5768 |
| mean ± SD |  | 4.57 ± 0.56 | 2.08 ± 0.2 | 1.77 ±0.26 | 11644 ± 1758,15 | 5781,33 ± 868,38 |

Tfh were isolated from left and right pln and subjected subjected to deep sequencing. \* all sequences that appeared only once had been removed, \*\* only TCR sequences above the median were used for analysis