

Table S4. Overview of TCRV β sequencing results in brain and peripheral blood compartment.

Details of input samples and TCRV β sequencing results from sorted peripheral blood compartments (CFSE^{hi} and CFSE^{dim}) at day 7 of CFSE assay as well as brain lesions and brain infiltrates from two different MS patients. Frequency and counts of TCRV β sequences were only related and calculated according to productive sequences (in frame sequences). Irrelevant sequences such as unproductive sequences and sequences with CDR3 regions of less than four amino acids were excluded from analysis. The two independent experiments for MS patient 1 are indicated by (A) and (B), Related to Figure 5-6, Figure S5-S6 and Table S5.

patient	sample	characteristics (sorted cell number)	TCRseq method	productive TCRV β sequences		productive unique TCRV β sequences	
				nucleotide (total)	nucleotide (frequency)	common nucleotide (total)	common CDR3 amino acid, V-gene, J-gene (total)
1 (A)	PBMC CFSE ^{dim} 7AAD ⁻	proliferating (20.000 cells)	survey DNA	6377	34.73%	117	114
1 (B)	PBMC CFSE ^{dim} 7AAD ⁻	proliferating (20.000 cells)	survey DNA	27059	64.35%	406	391
1 (A)	PBMC CFSE ^{hi} 7AAD ⁻	non-proliferating (500.000 cells)	deep DNA	946304	80.30%	41274	38994
1 (B)	PBMC CFSE ^{hi} 7AAD ⁻	non-proliferating (500.000 cells)	deep DNA	433206	79.59%	15230	14465
1	brain lesion LI	tissue, late/low active lesion	survey DNA	141078	81.49%	1111	1062
1	brain lesion LIII	tissue, early/high active lesion	survey DNA	50522	65.90%	296	271
1	brain lesion LIV	tissue, early/medium active lesion	survey DNA	128655	74.57%	796	698
2	PBMC CFSE ^{dim} 7AAD ⁻	proliferating (20.000 cells)	survey DNA	45303	67.84%	513	492
2	PBMC CFSE ^{hi} 7AAD ⁻	non-proliferating (500.000 cells)	deep DNA	1409991	83.47%	60442	56362
2	brain-infiltrating cells	isolated brain- infiltrating cells	survey DNA	80347	76.05%	881	851