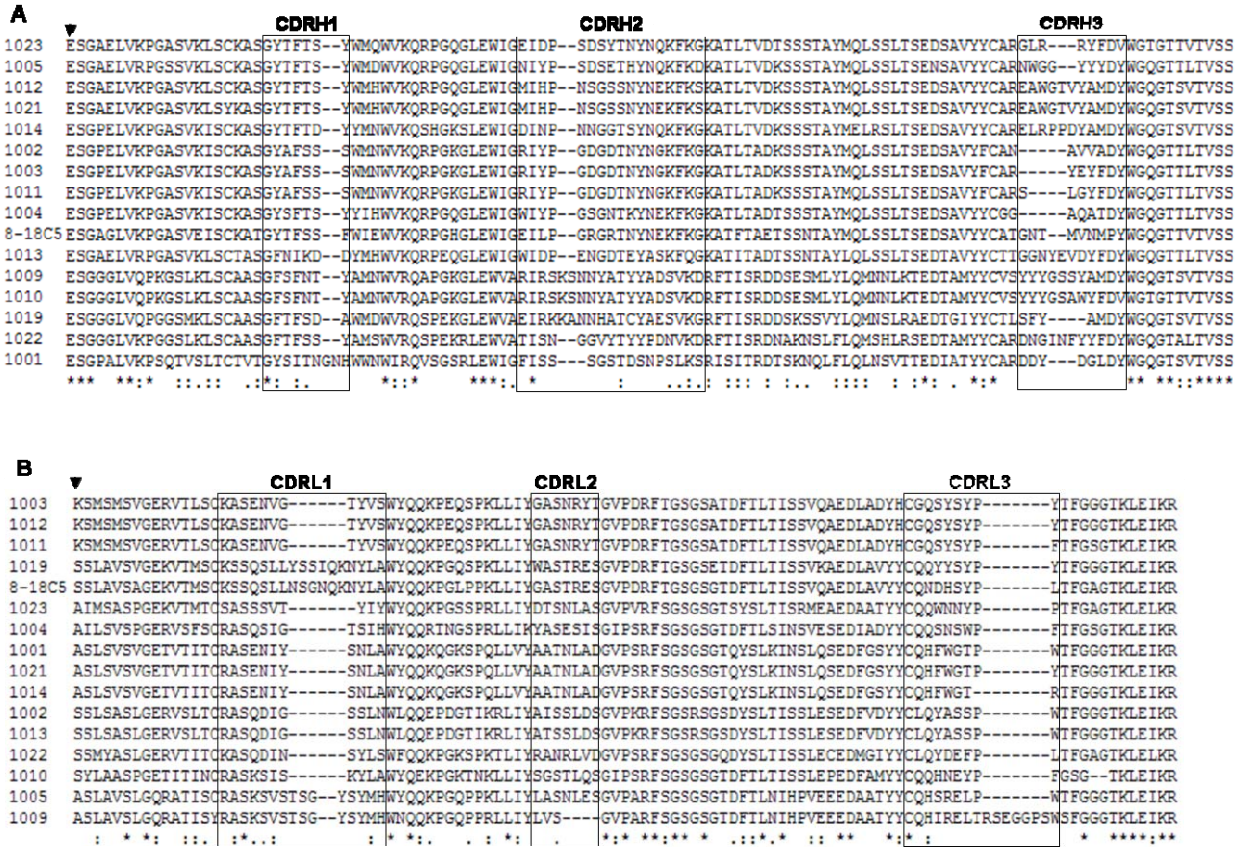

Figure S1. Sequence alignment of the V_H (A) and V_L (B) domain sequences of the mAbs indicates a diverse repertoire. Amino acid sequences of V_H and V_L domains of anti hMOG mAbs and 8-18C5 were aligned using the Clustal-W (http://www.ebi.ac.uk/Tools/msa/clustalw2/). The numbering is based on Kabat database (1). Arrowhead indicates sixth and ninth residue from the N-terminus in V_H and $V_{L,}$ respectively. Primer encoded sequences are not shown. CDRs are shown boxed.

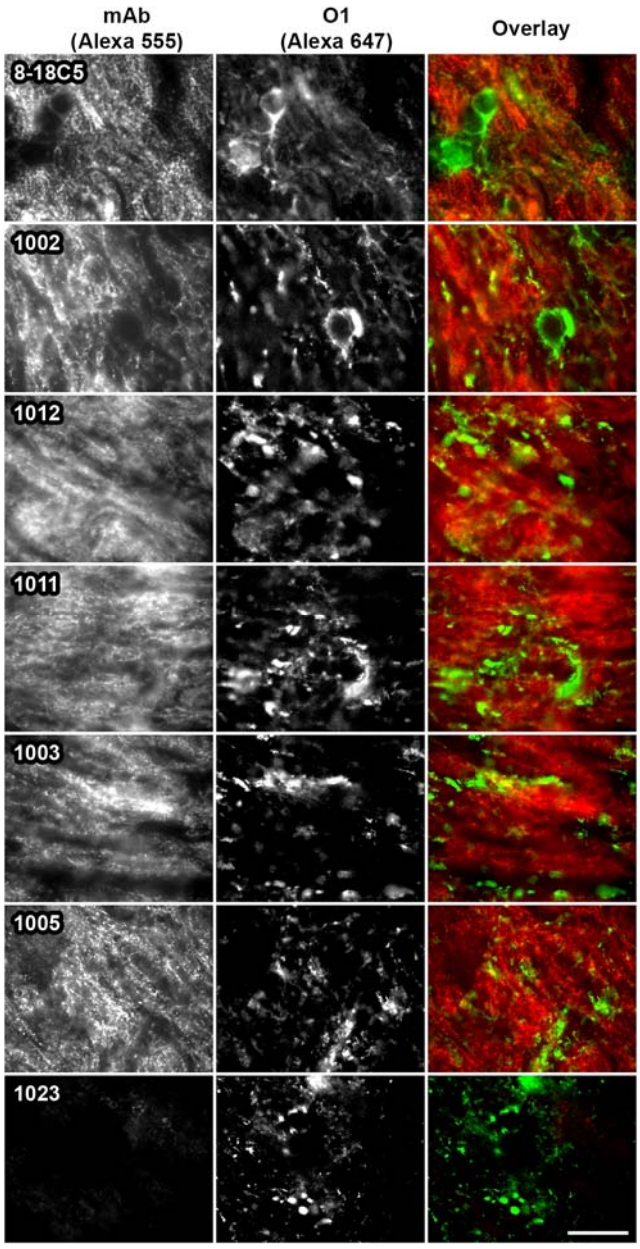

Figure S2. Staining patterns of the anti-MOG mAbs that exacerbate EAE are similar. Spinal cord sections of C57BL/6 mice were co-stained with 50 μg/ml Alexa 555-labeled anti-MOG antibodies (pseudocolored red in overlay) and Alexa 647-labeled anti-oligodendrocyte marker O1 (pseudocolored green in overlay). Each image for the EAE-exacerbating mAbs was adjusted individually to similar intensity levels. MAb 1023 stains at background levels and was used as control (images for staining by mAb 1005 and mAb 1023 were processed analogously). Scale bar represents 20 μm.

REFERENCES

1. Kabat, E. A., T. T. Wu, H. M. Perry, K. S. Gottesman, and C. Foeller. 1991. *Sequences of proteins of immunological interest*. U.S. Dept. of Health and Human Services.