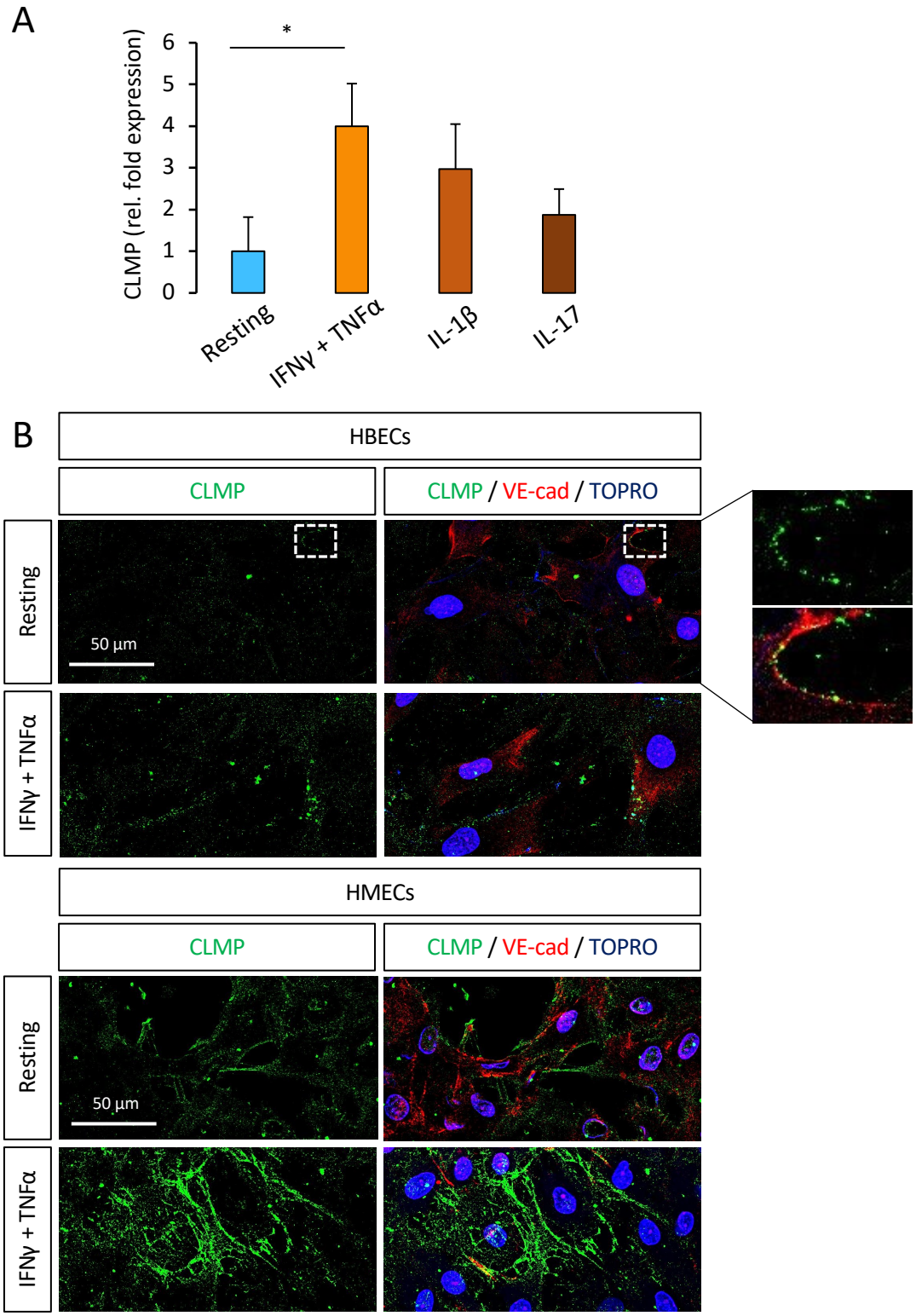
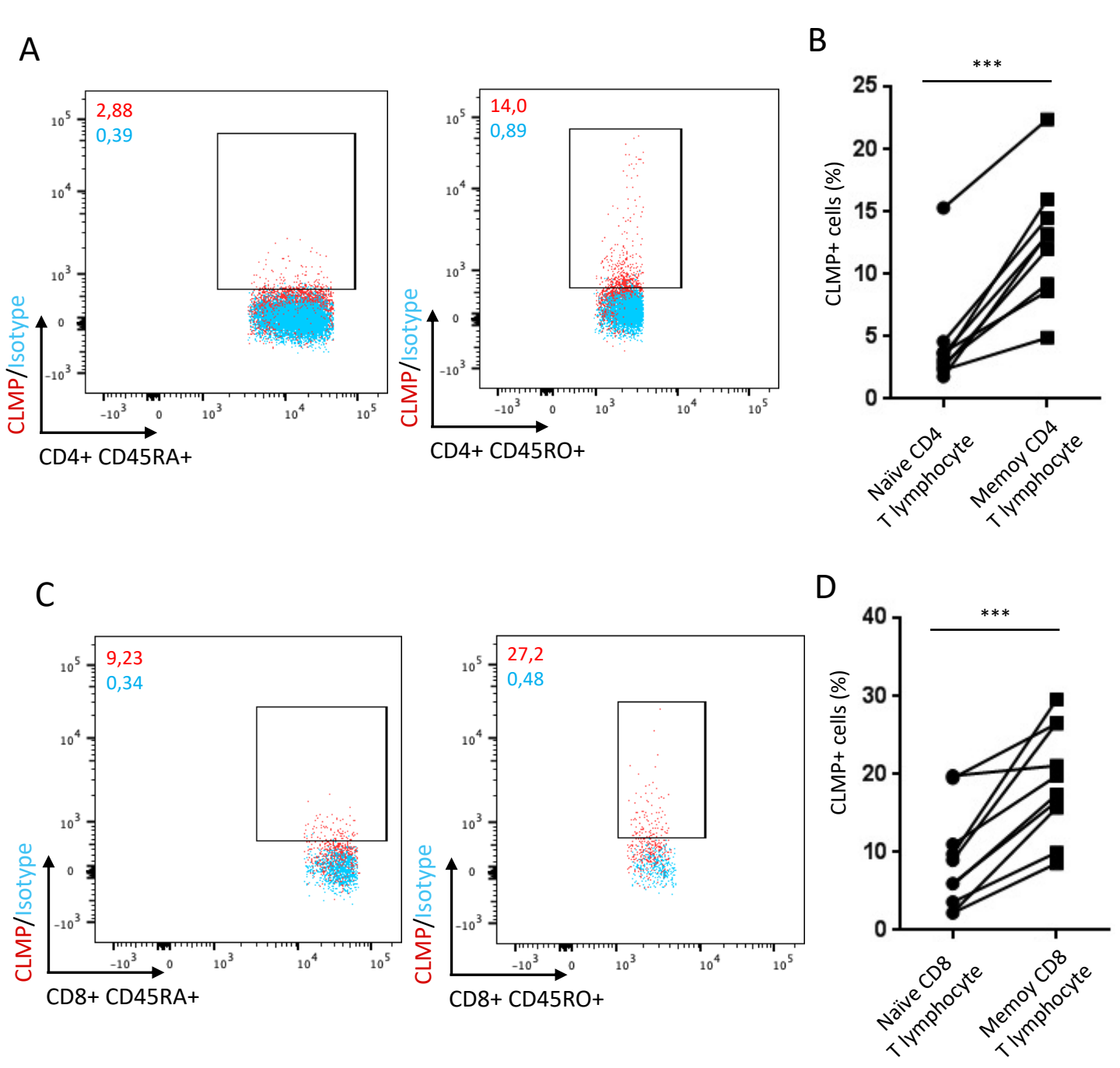
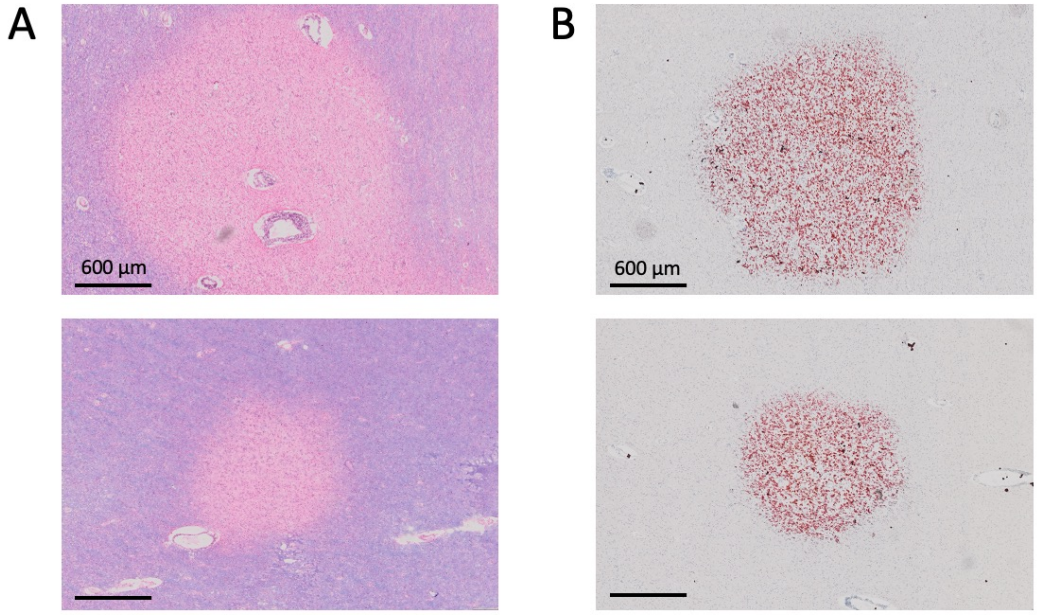


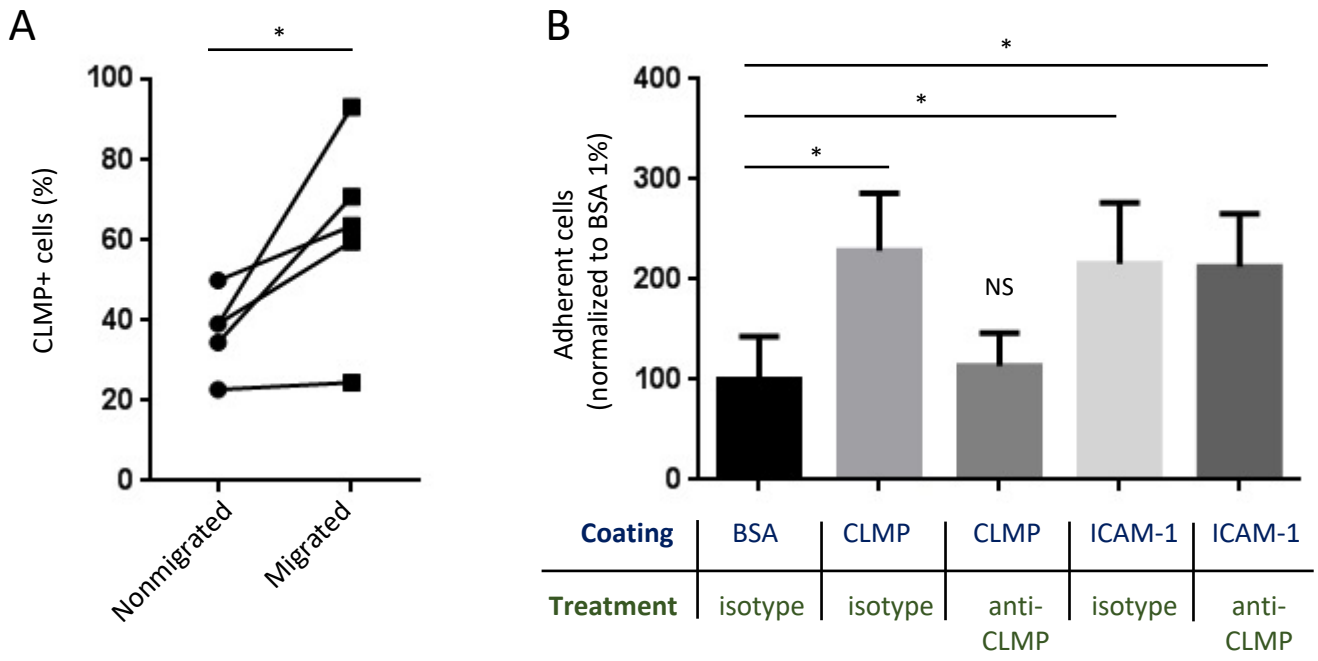
eFigure 1: (A) Quantitative PCR analysis of CLMP mRNA expression relative to 18S ribosomal RNA in HBECS (n=3; mean ± SEM; *$P < 0.05$, by Friedman test with Dunn's post hoc test). **(B)** CLMP (green) and VE-cadherin (VE-cad; red) on the surface of HBECs and HMECs, untreated or treated for 24h with TNF-α and IFN-γ, by confocal microscopy; nuclei are stained with TOPRO-3 (blue). Scale bar: 50 µm.



eFigure 2: Representative dot plots and quantification of flow cytometry analysis of CLMP expression by memory and naïve CD4+ T lymphocytes **(A and B)** and memory and naïve CD8+ T lymphocytes **(C and D)**, obtained from peripheral blood of MS patients; corresponding quantification (n=9-10; ***$P < 0.001$ by paired t-test).



eFigure 3: Autopsy-derived MS CNS materials were stained with Luxol fast blue Haematoxylin and Eosin (LHE, panel **A**) and Oil Red O (ORO, panel **B**) to identify active lesions.



eFigure 4: (A) Expression of CLMP on nonmigrated (recovered from the upper chamber) versus migrated (recovered from the lower chamber) CD14+ monocytes, as analyzed by flow cytometry; n =5 per group. *P < 0.05 by paired t test. **(B)** Amount of CFSE-labeled T cells adhering to coated rhCLMP or rhICAM-1, normalized to BSA 1%, according to fluorescence intensity as assessed by plate-reader; n=4 per group. *P < 0.05 by one-way ANOVA followed by Dunnett's multiple comparison test.