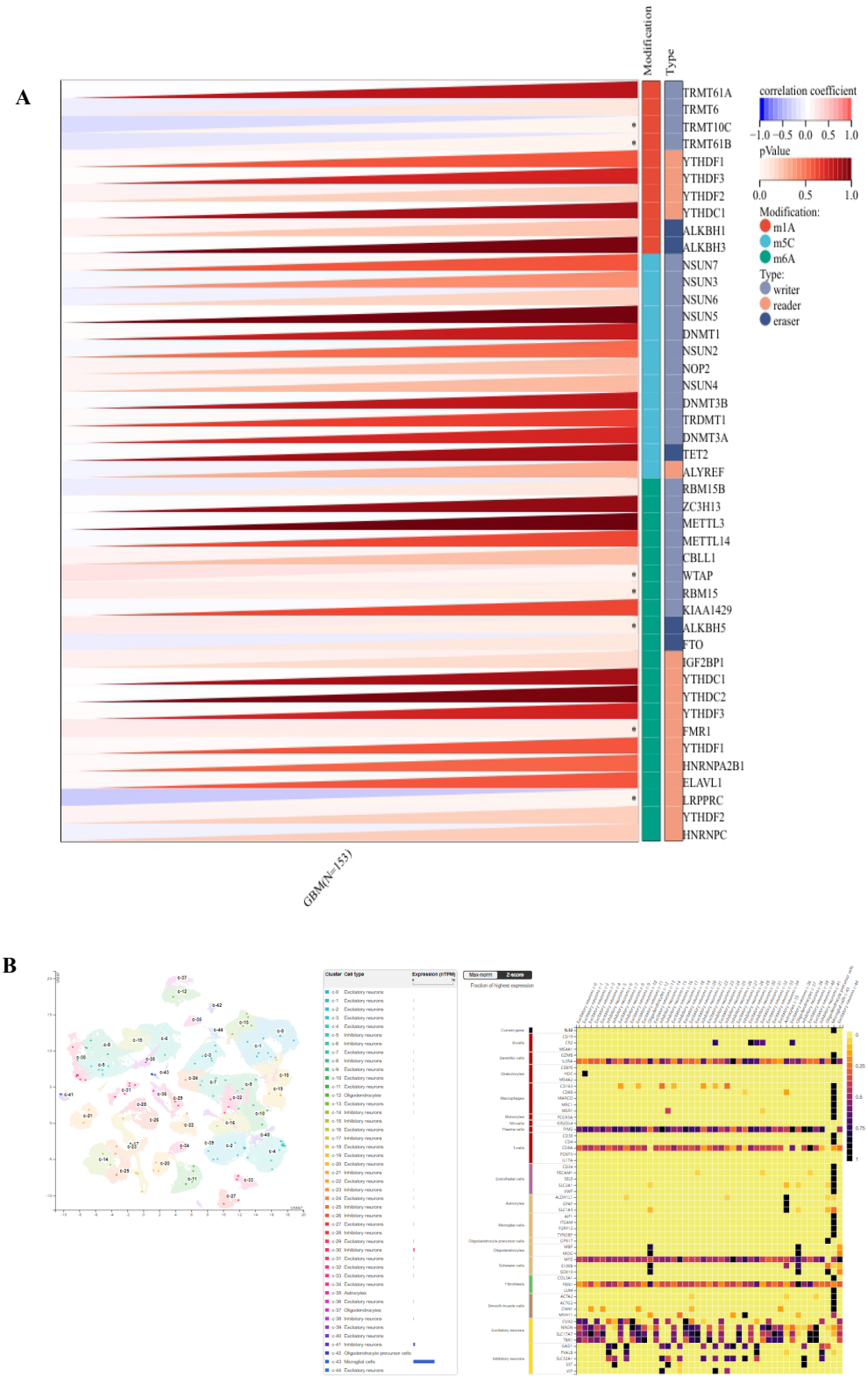

Supplementary Fig. 5. IL32 and RNA modification gene analysis (m6A, m5C, m1A). Expression profiles of IL32 and 44 RNA modification genes were extracted, and Pearson correlation analysis was conducted. Positive correlations were observed with METTL3 and TET2, while negative correlations were found with TRMT6, TRMT10C, and ELAVL1. Single-cell analysis from GSE156902 using Seurat showed IL32 was predominantly expressed in microglial clusters.IL32 expression is associated with epitranscriptomic regulators and is specifically enriched in microglial cells, suggesting its role in RNA modification–mediated immune modulation within the CNS.