

Figure S1. Bioinformatics analysis results. (A) SRAMP shows the presence of multiple m6A modification sites on the LINC00900 sequence. (B) m6A2Target displays that LINC00900 may bind to the YTHDF1 protein.

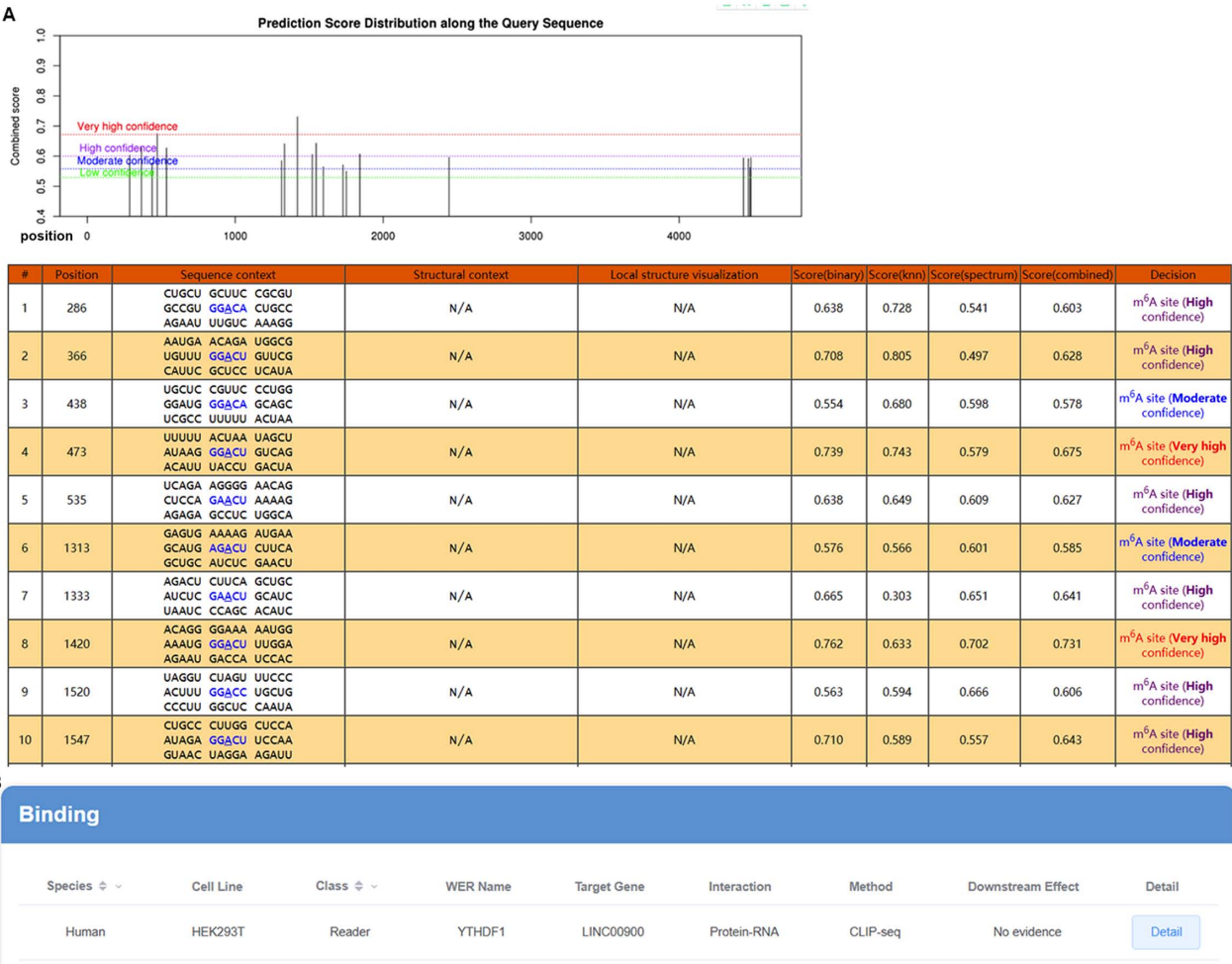


Figure S2. LINC00900 expression in glioma tissues and NBTs. On the basis of tumor type, 20 glioma tissues and adjacent tissues were divided into two groups: Glioblastoma (n=16) and astrocytoma (n=4). Data are presented as the mean \pm SD. *P<0.05, ***P<0.001. NBT, normal brain tissue; ns, not significant.

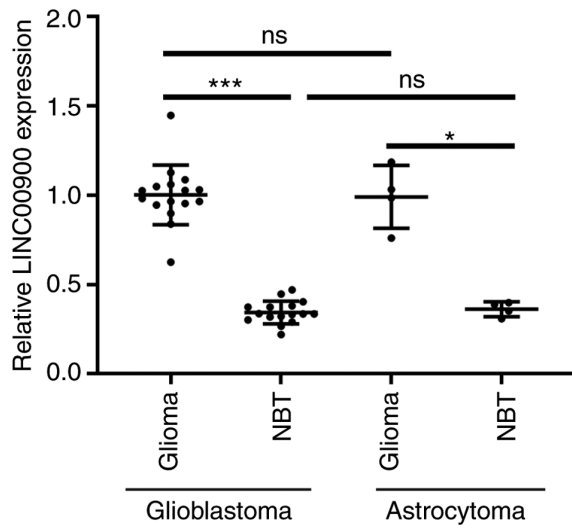


Figure S3. Induction and identification of GSCs. Human glioma cell lines (U87 and U251) were induced to GSCs (GSC-U87 and GSC-U251). (A) Tumor sphere formation assays of GSCs. Scale bars, 100 μ m. (B) Identification of GSCs by CD133 immunofluorescence. Scale bars, 50 μ m. (C) Identification of GSCs by western blot analysis of NANOG and OCT4. GSC, glioma stem cell.

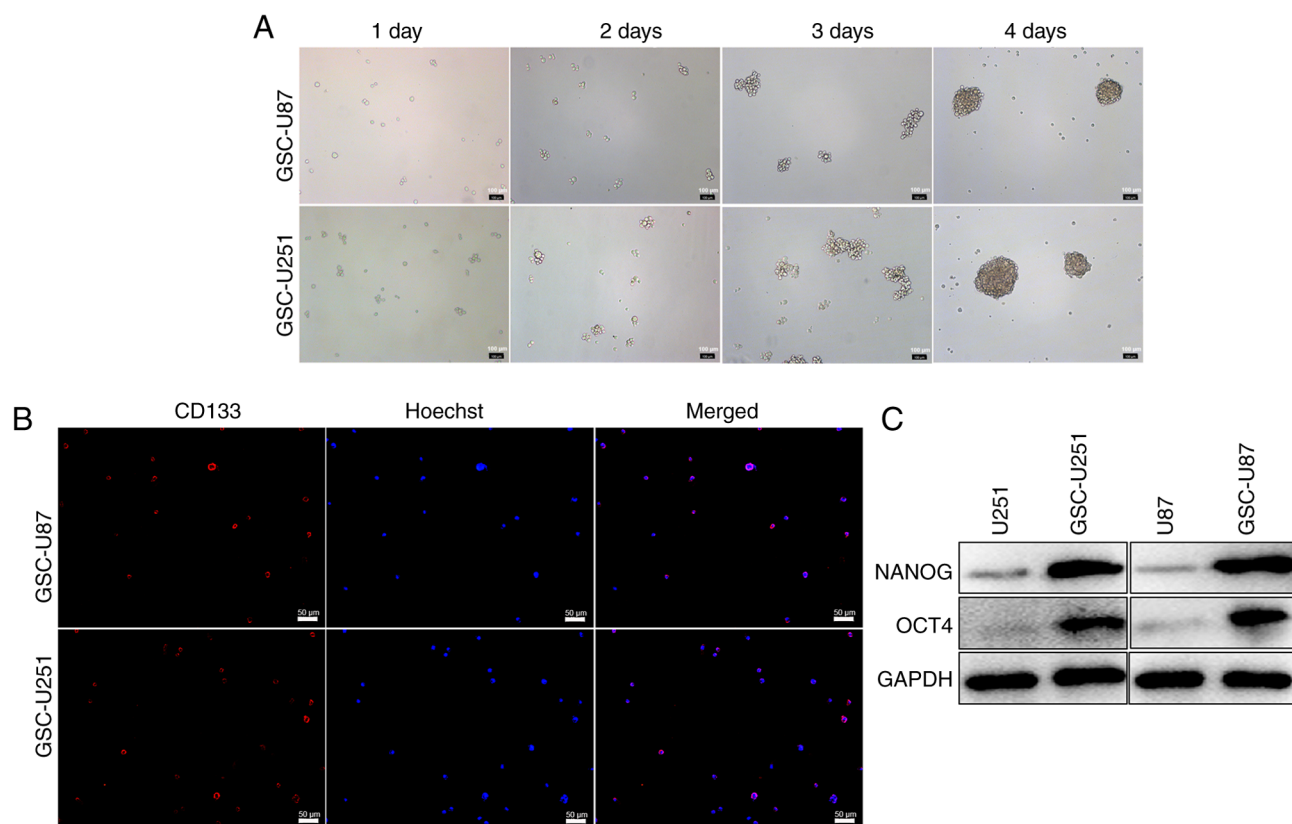


Figure S4. Induction and identification of GSCs. Human glioma cell lines (A172 and SHG44) were induced to GSCs (GSC-A172 and GSC-SHG44). (A) Tumor sphere formation assays of GSCs. Scale bars, 100 μ m. (B) Identification of GSCs by CD133 immunofluorescence. Scale bars, 50 μ m. GSC, glioma stem cell.

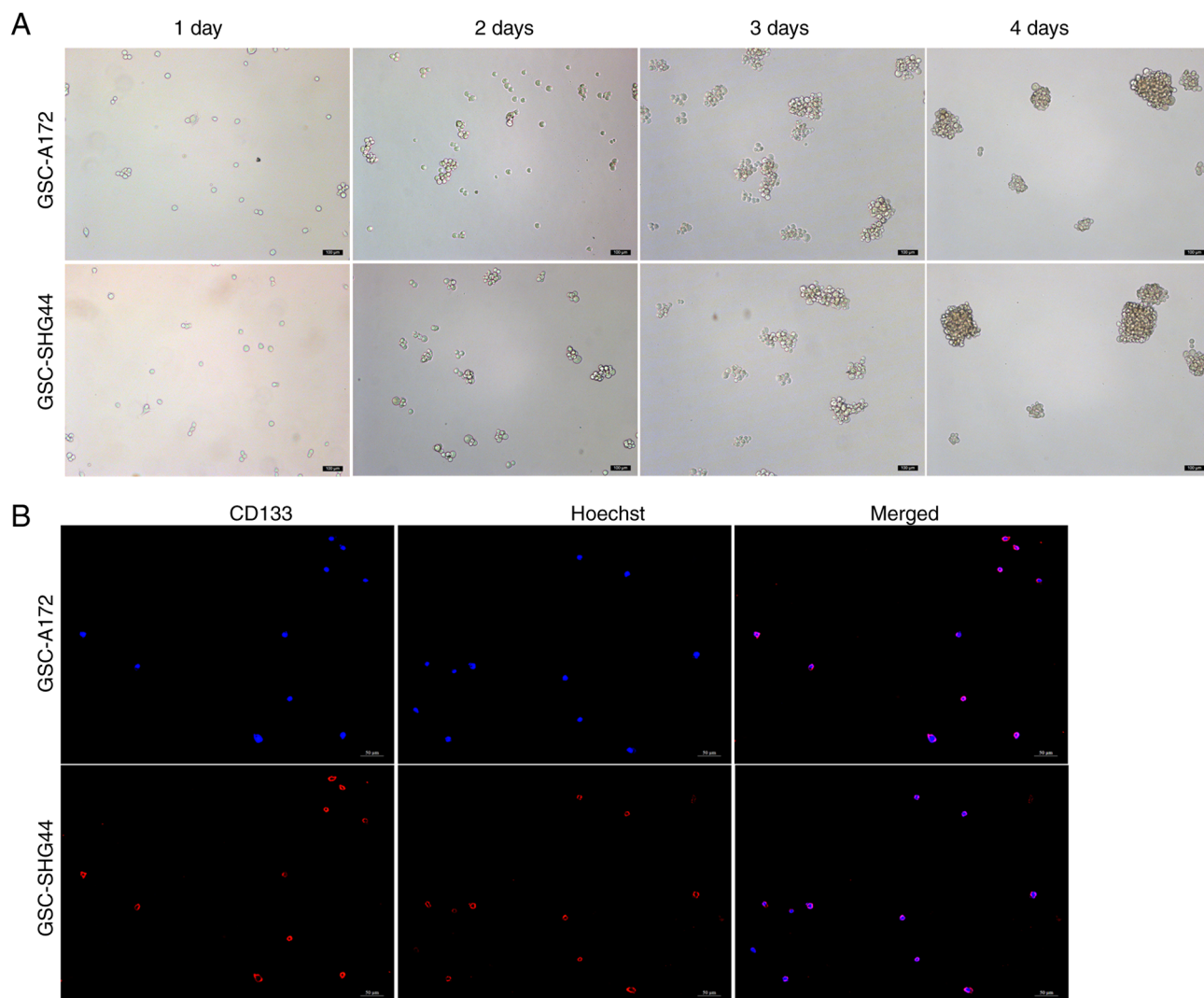


Figure S5. Overexpression/knockdown efficiency of LINC00900 and miR-1205. Overexpression/knockdown efficiency of LINC00900 in (A) GSC-U87 and (B) GSC-U251 cells. (Overexpression efficiency of miR-1205 in (C) GSC-U87 and (D) GSC-U251 cells. ###P<0.001 vs. LV-NC; &&P<0.01, &&&P<0.001 vs. LV-sh-NC; ***P<0.001 vs. mimics NC. GSC, glioma stem cell; LV, lentivirus; miR, microRNA; NC, negative control; sh, short hairpin.

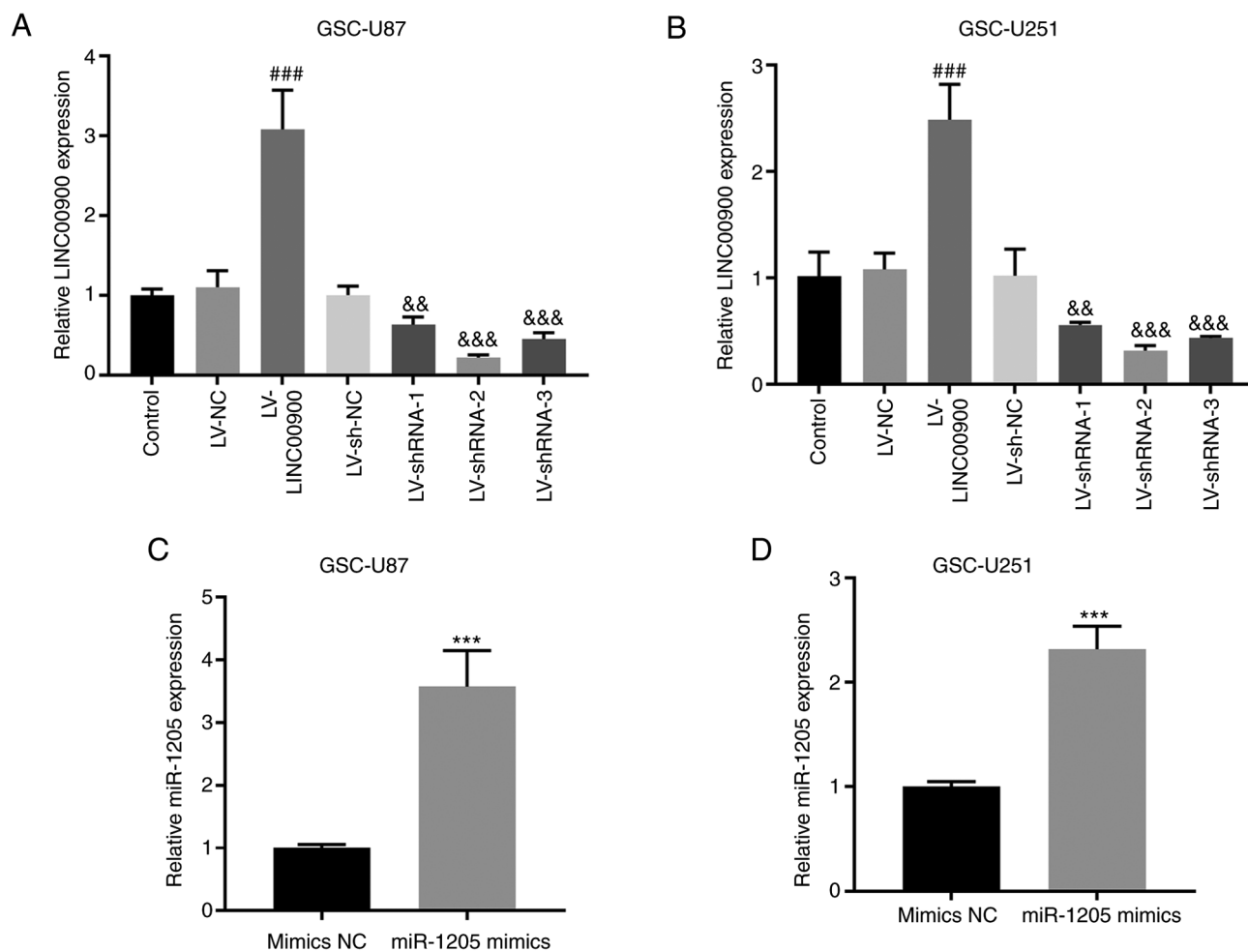


Figure S6. miR-1205 and STAT3 expression in glioma tissues. (A) Measurement of miR-1205 expression in glioma tissues and NBTs by RT-qPCR. (B) Western blotting was used to measure STAT3 protein expression in glioma tissues and NBTs. (C) RT-qPCR was used to measure STAT3 mRNA expression in glioma tissues and NBTs. Data are presented as the mean \pm SD. *** $P < 0.001$. miR, microRNA; NBT, normal brain tissue; RT-qPCR, reverse transcription-quantitative PCR.

