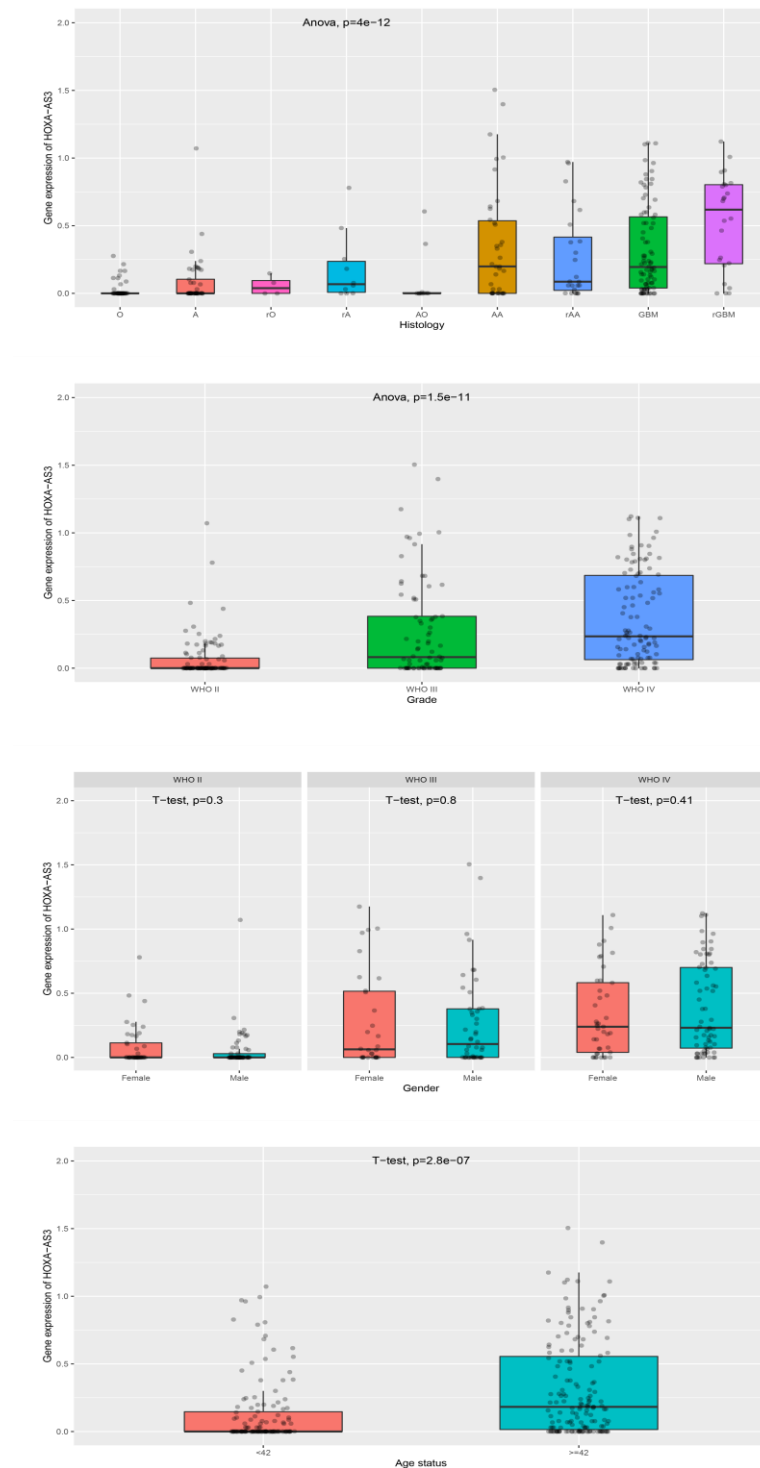
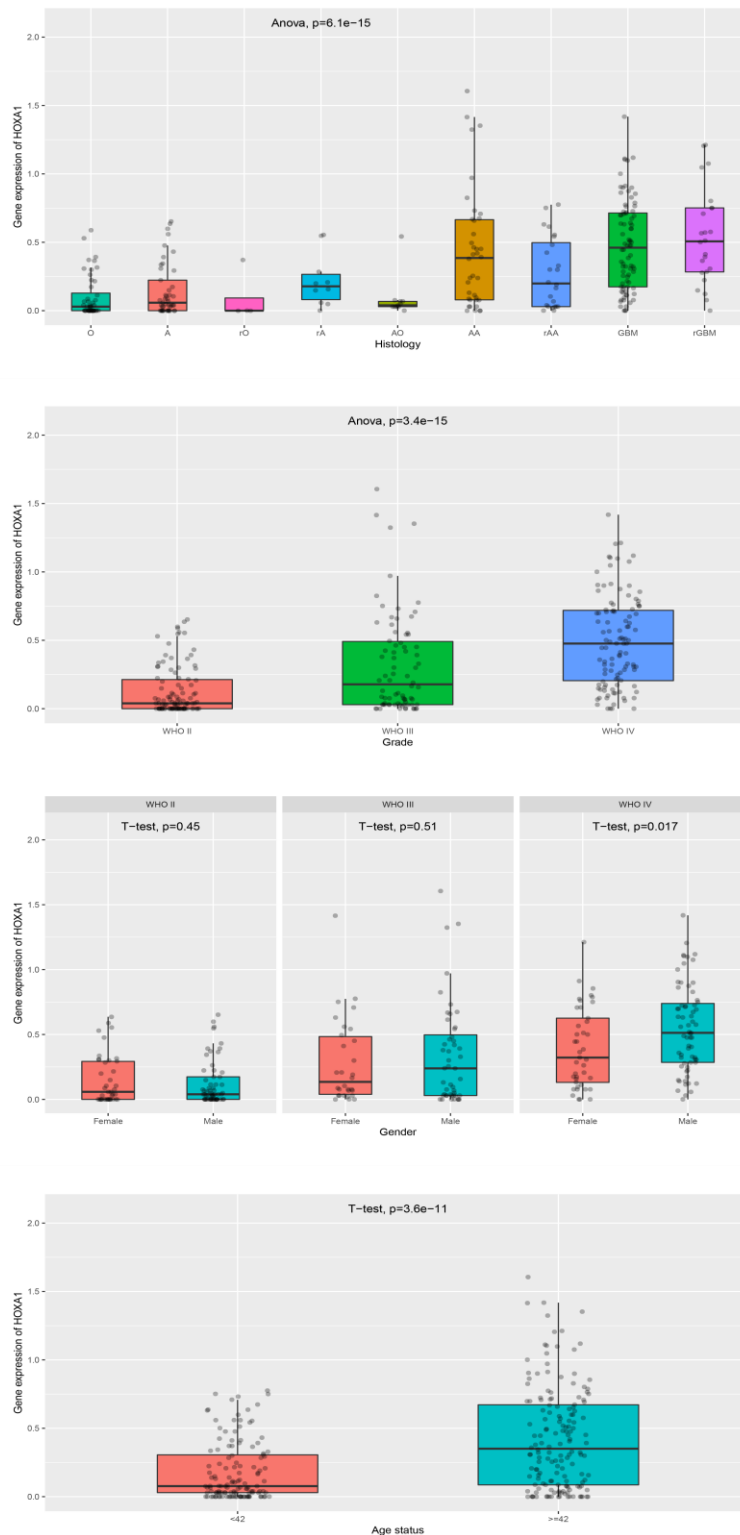


Supplemental figure 1 Expression of *HOXA-AS3* in glioma tissues.



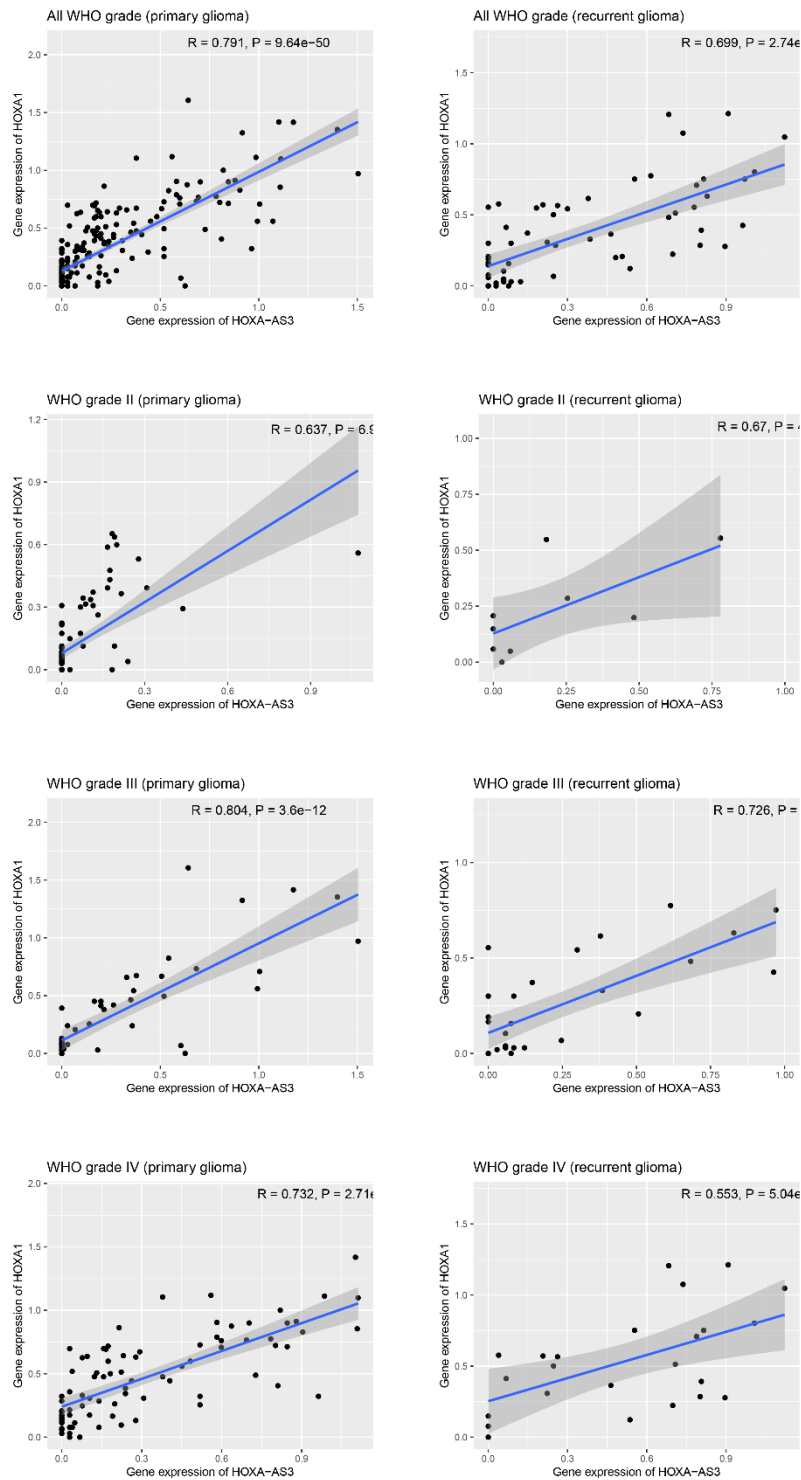
Expression of *HOXA-AS3* in glioma tissues was investigated based on “Histology”, “Grade”, “Gender”, and “Age status” in Chinese Glioma Genome Atlas

Supplemental figure 2 Expression of *HOXA1* in glioma tissues.



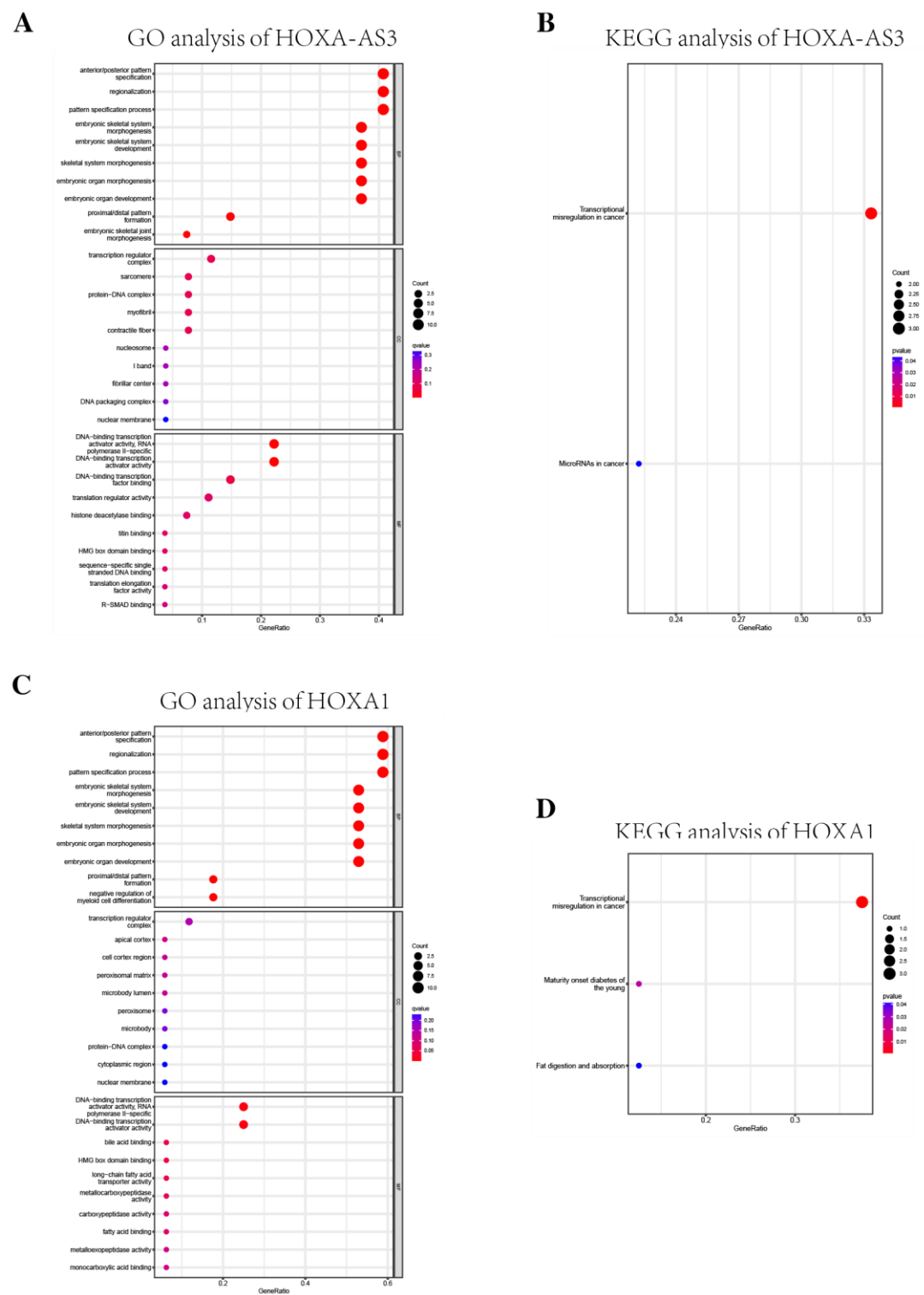
Expression of *HOXA1* in glioma tissues was investigated based on “Histology”, “Grade”, “Gender”, and “Age status” in Chinese Glioma Genome Atlas

Supplemental figure 3 Positive correlation of HOXA-AS3 and HOXA1 expression in LGG

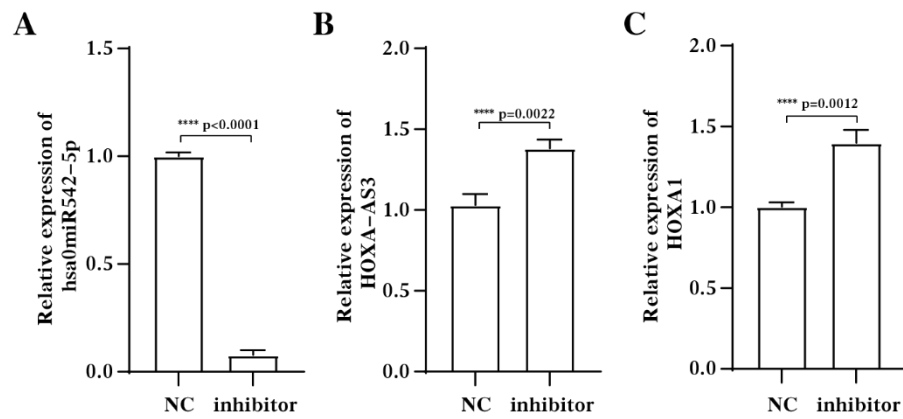


Correlation of HOXA-AS3 and HOXA1 expression in LGG was investigated by using the CGGA database with the Spearman's rho value.

Supplemental figure 4 GO functional and KEGG pathway enrichment analysis

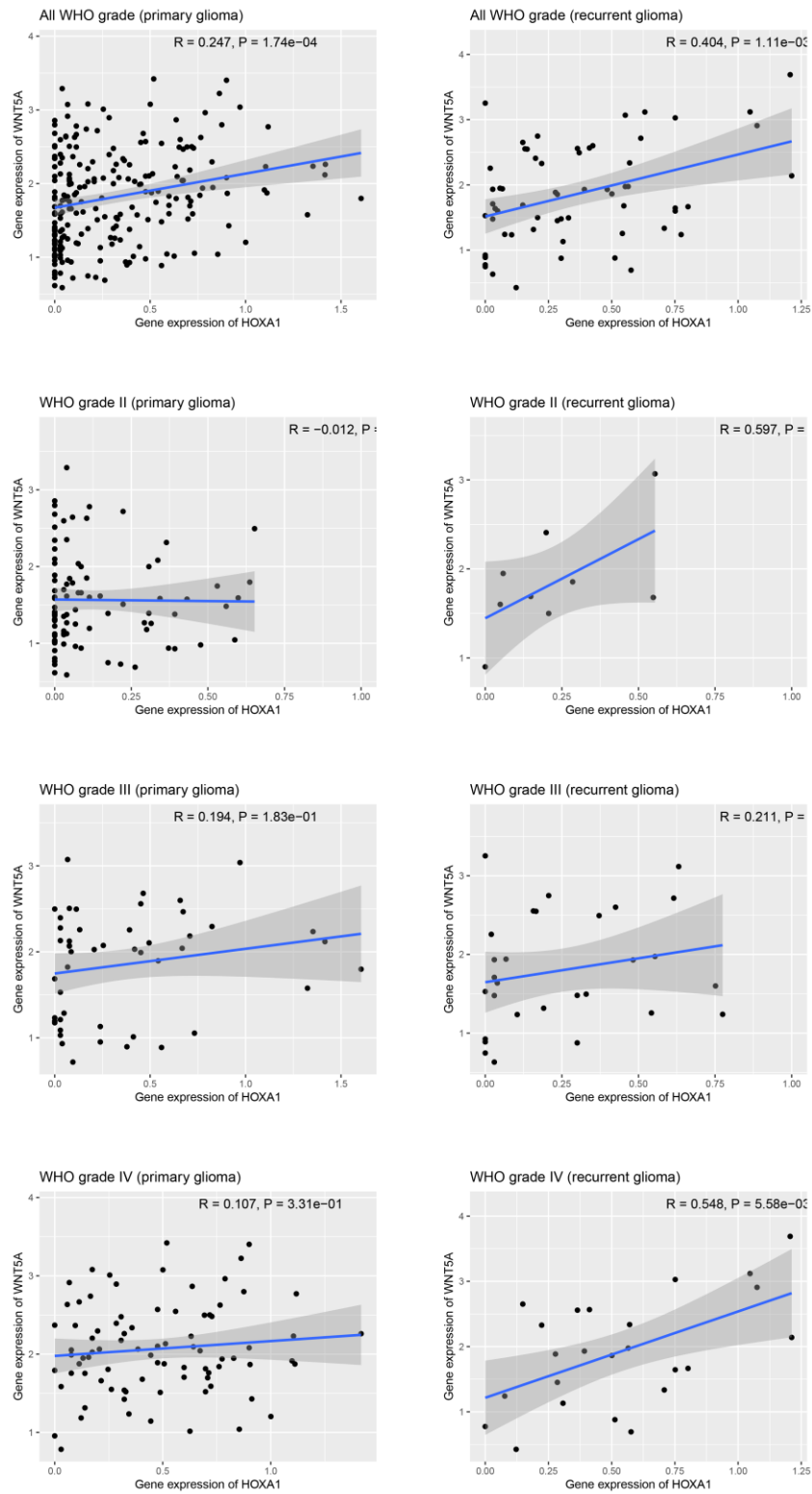


Supplemental figure 5 Silenced hsa-miR-542-5p led to increased expression of HOXA-AS3 and HOXA1 in U373 cells.

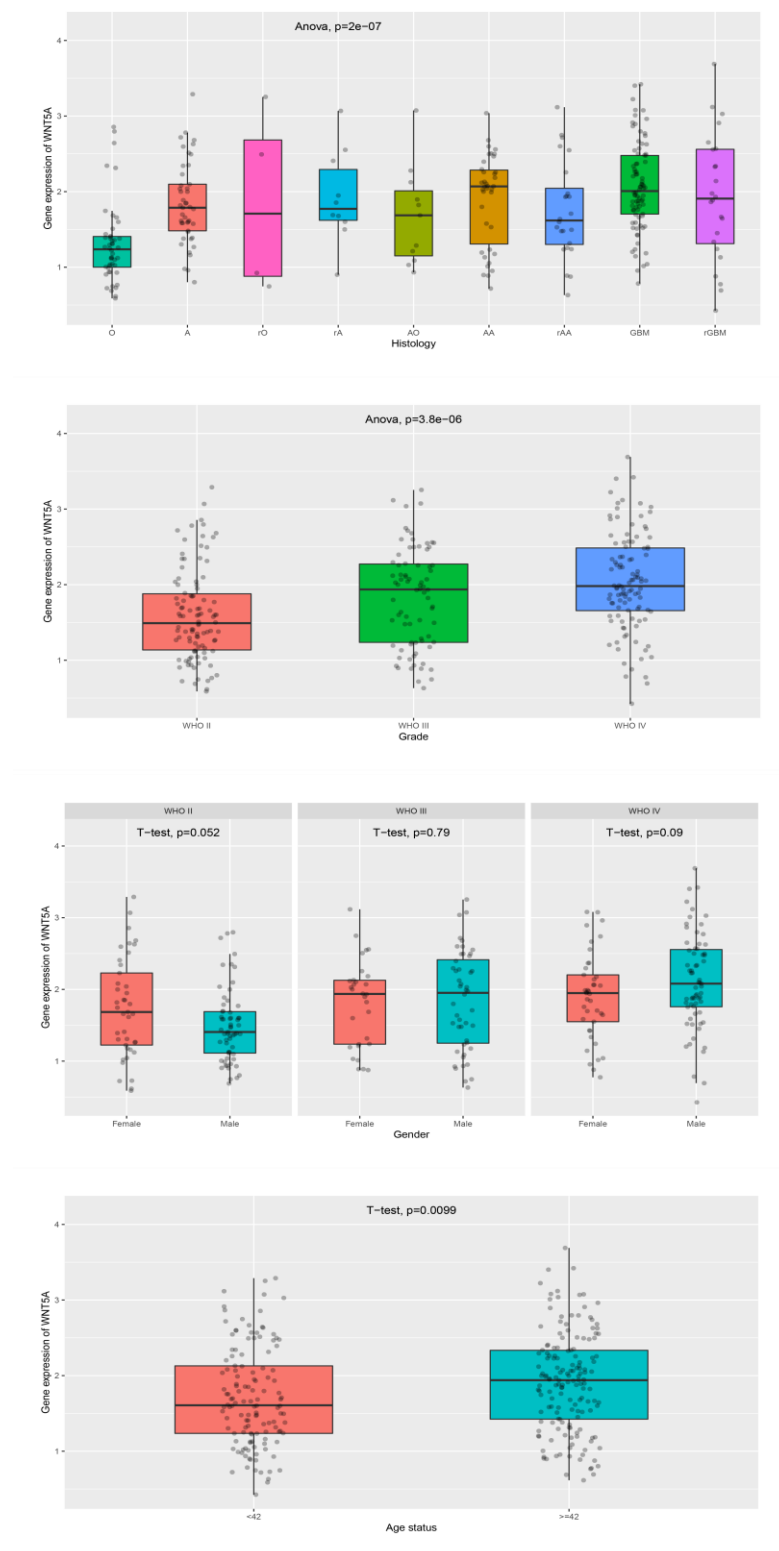


U373 cells were treated with miRNA inhibitor (20 nM) for 24 hours, then cells were collected for hsa-miR-542-5p (A), HOXA-AS3 (B), and HOXA1 (C) detection.

Supplemental figure 6 Positive correlation of HOXA1 and WNT5A expression in LGG

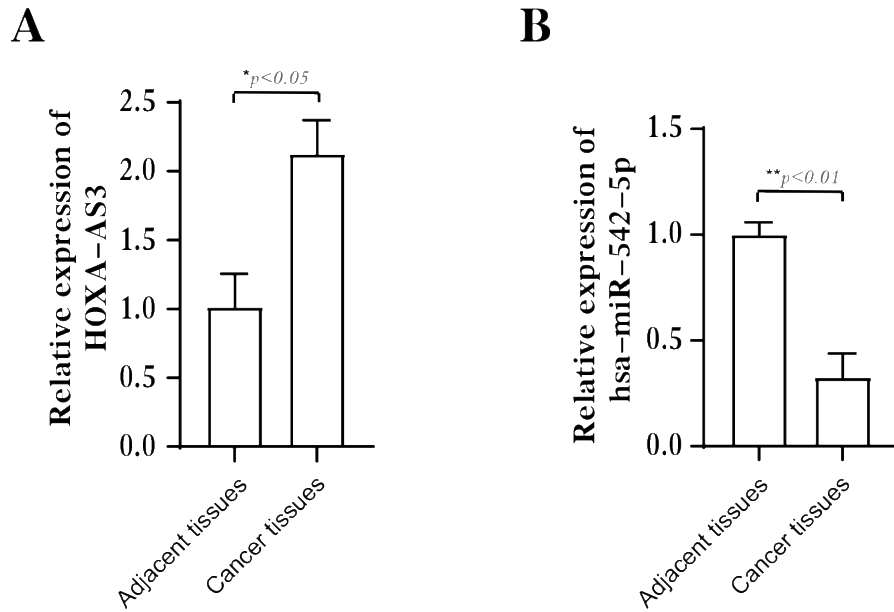


Supplemental figure 7 Expression of *WNT5A* in glioma tissues.



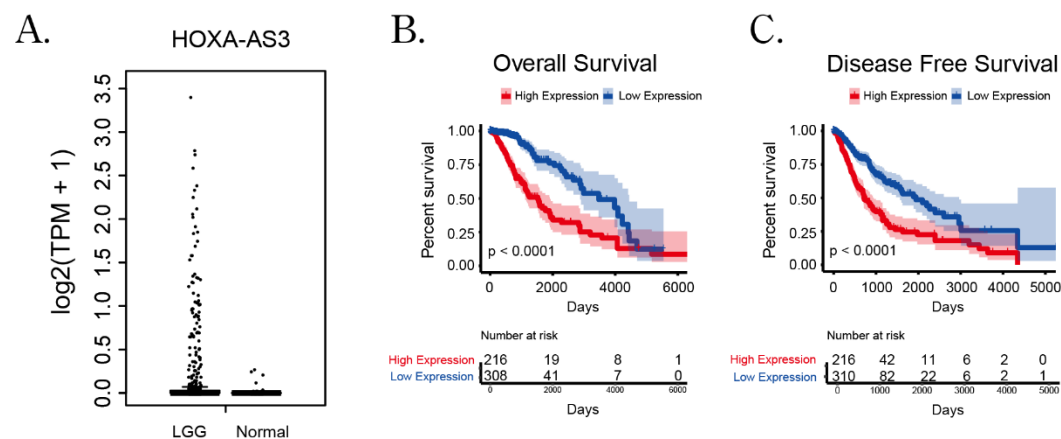
Expression of *WNT5A* in glioma tissues was investigated based on “Histology”, “Grade”, “Gender”, and “Age status” in Chinese Glioma Genome Atlas

Supplemental figure 8 Expression of *HOXA-AS3* and *hsa-miR-542-5p* in glioma tissues.



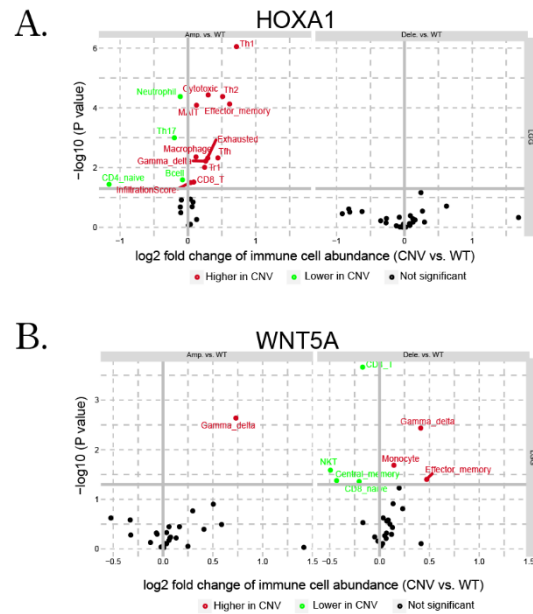
Expression of *HOXA-AS3* (A) and *hsa-miR-542-5p* (B) in glioma tissues and the corresponding adjacent tissues in patients, n=3 in each group.

Supplemental figure 9 High level of HOXA-AS3 indicated a poor outcome in LGG patients.



The expression level of HOXA-AS3 (A) in LGG patients and corresponding control was analyzed by using the Lnc2Cancer 3.0 database, and the Kaplan-Meier survival analysis was performed to investigate the OS (B) and DFS (C) of HOXA-AS3 in LGG.

Supplemental figure 10 Higher copy number variations (CNVs) of HOXA1 and WNT5A were associated with tumor-associated macrophages in LGG.



The correlation between immune infiltration with gene set CNV in LGG was analyzed by using the GSCA. Gene set CNV of HOXA1 (A) and WNT5A (B), and correlates with immune infiltration was shown in supplemental figure 4.