# Supplemental Figure

Figure S1

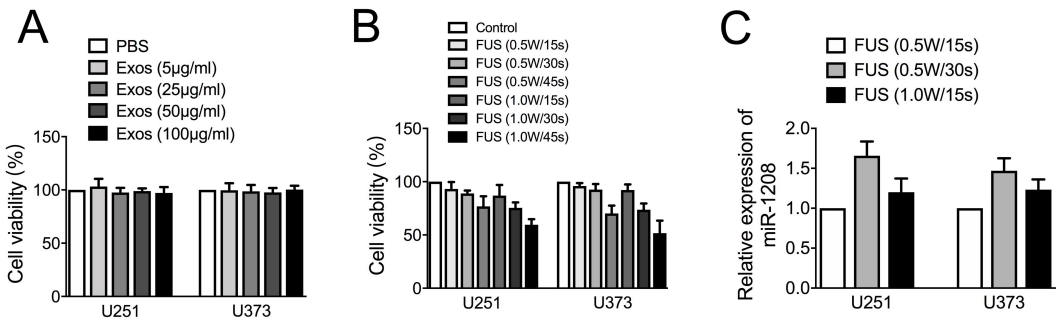


**Fig.S1 Cytotoxicity detection and ultrasonic parameter selection. A.** CCK-8 assay was used to detect the effects of exosomes on glioma cell viability at different concentrations. **B.** CCK-8 assay was used to detect the effects on glioma cell viability at different ultrasonic parameters. **C.** qRT-PCR was used to detect the miR-1208 expression of glioma cells after co-culture with Exos-miR1208 under different ultrasonic parameters. Data represent mean ± SD (n = 3, each group).

Figure S2

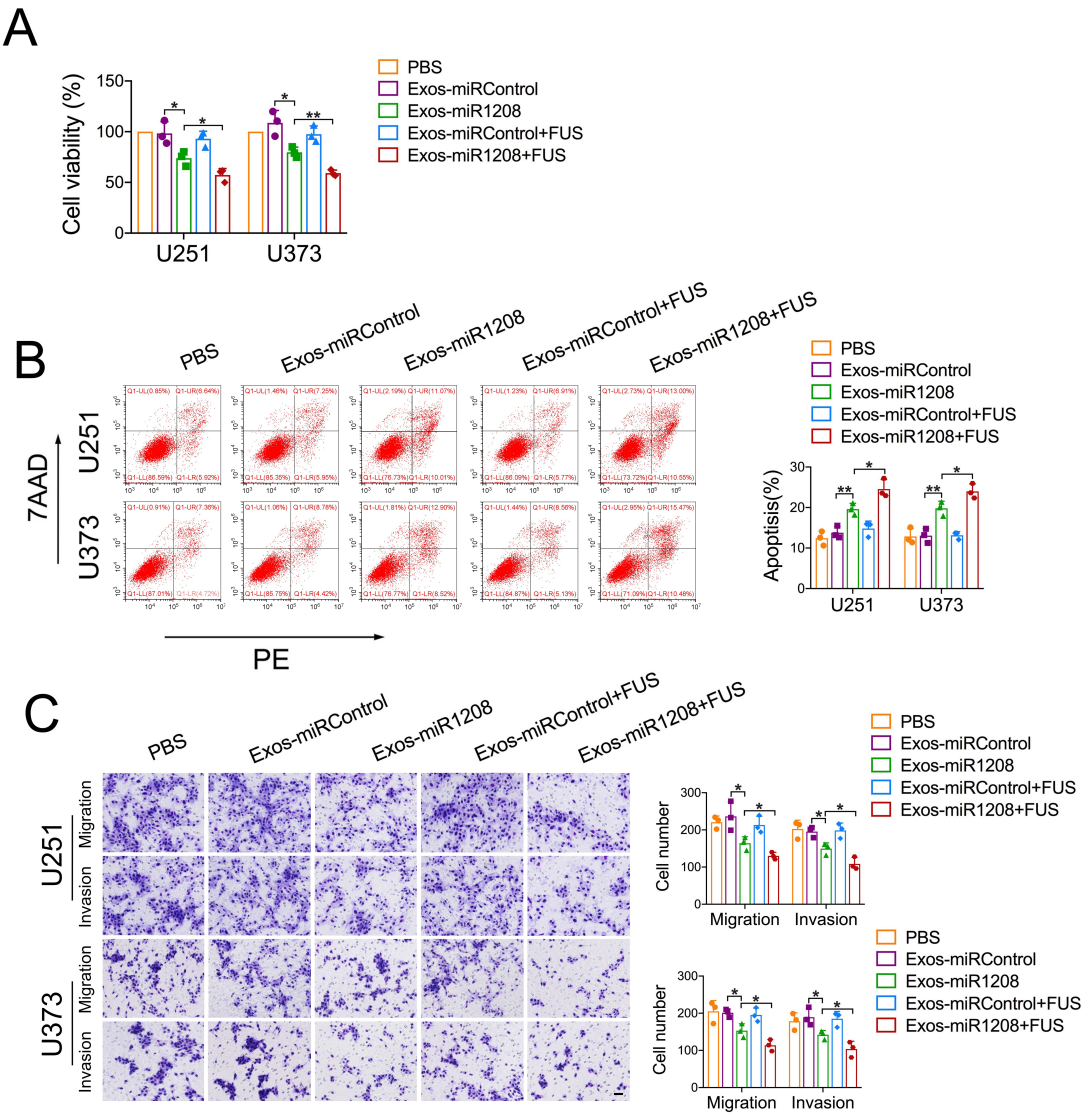


**Fig.S2 Exos-miR1208 combined with FUS inhibited the malignant biological behaviors of glioma cells. A.** The effects of Exos-miR1208 combined with FUS on glioma cell viability were determined by CCK-8 assay. **B.** The effects of Exos-miR1208 combined with FUS on glioma cell apoptosis were detected by flow cytometry. **C.** The effects of Exos-miR1208 combined with FUS on the migration and invasion ability of glioma cells were investigated by Transwell assay. Data are presented as the mean ± SD (n = 3, each group). **P* < 0.05, ***P* < 0.01. Scale bar of migration and invasion assays represent 40 μm.

Figure S3

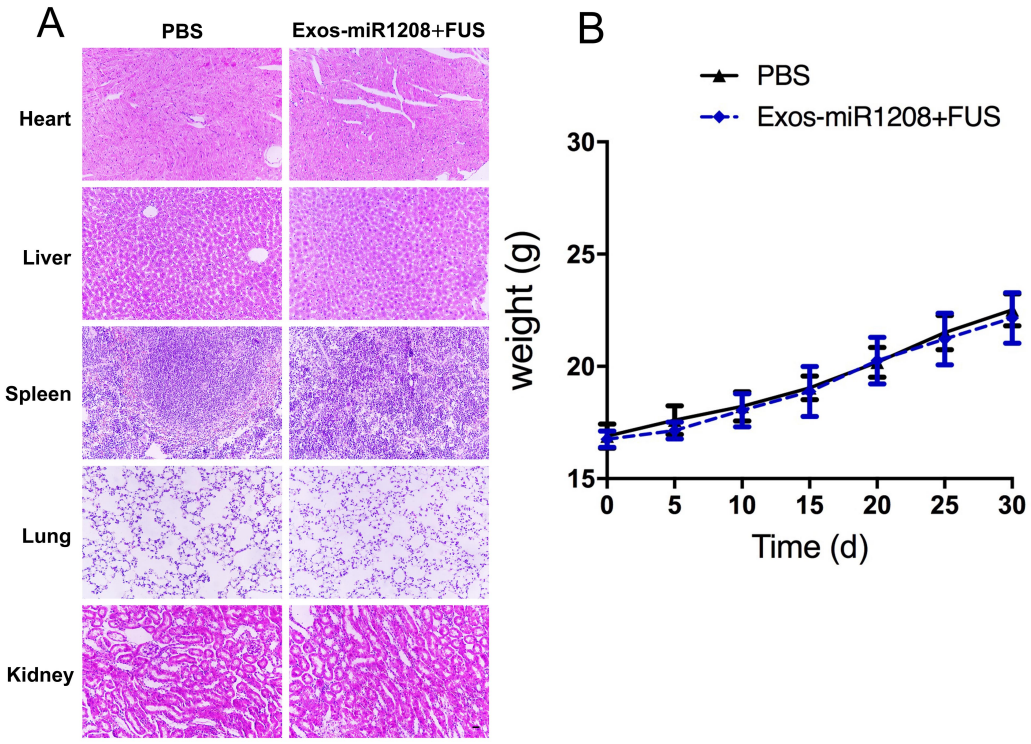


**Fig.S3 Exos-miR1208 combined with FUS had no significant harmful effects on healthy nude mice. A.** HE staining representative images of nude mice heart, liver, spleen, lung and kidney tissues. Scale bar represent 50 μm. **B.** Changes in body weight of nude mice. Data are presented as the mean ± SD (n = 3, each group).

Figure S4

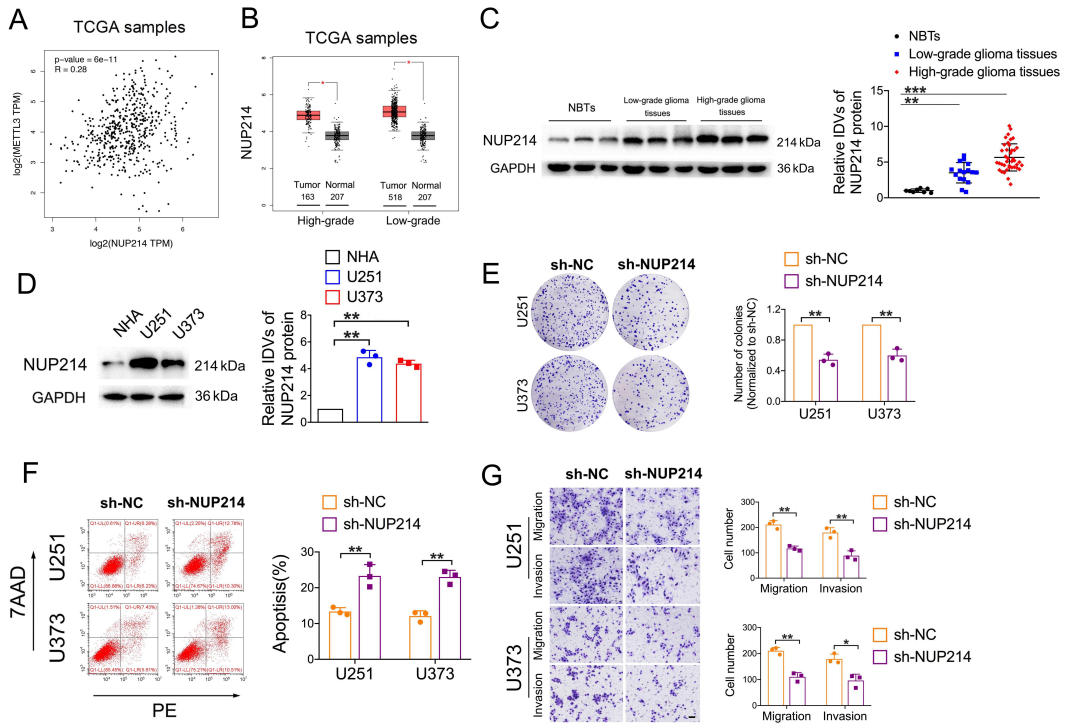


**Fig.S4 NUP214 plays an oncogenic role in glioma. A.** There is a positive correlation between METTL3 and NUP214 expression levels in glioma from TCGA samples. **B.** The expression levels of NUP214 in normal brain and glioma from TCGA samples. **C.** The expression levels of NUP214 were upregulated in glioma tissues. Data are presented as the mean ± SD (n = 8, NBTs; n = 16, Low-grade glioma tissues, including Grade I and Grade II; n = 40, High-grade glioma tissues, including Grade III and Grade IV). **D.** The expression levels of NUP214 were detected in NHA, U251 and U373 cells. Data are presented as the mean ± SD (n = 3, each group). $^{**}P < 0.01$, $^{***}P < 0.001$. **E-G.** Colony formation assay, flow cytometry analysis and migration and invasion assays were used to detected the impacts of NUP214 knockdown on biological behaviors of glioma cells. Data are presented as the mean ± SD (n = 3, each group). $^{*}P < 0.05$, $^{**}P < 0.01$. Scale bar of migration and invasion assays represent 40 μm.

Figure S5

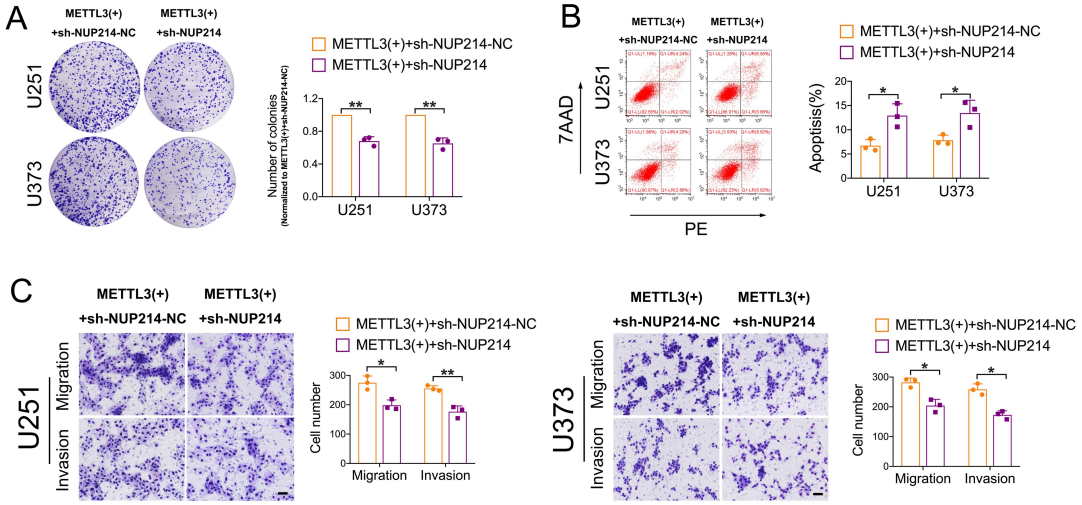


**Fig.S5 NUP214 knockdown significantly reversed the promotive effects of METTL3 overexpression on biological behaviors of glioma cells. A-C.** Colony formation assay, flow cytometry analysis and migration and invasion assays were used to detected the impacts on biological behaviors of glioma cells co-transfection with METTL3 overexpression and NUP214 knockdown. Data are presented as the mean ± SD (n = 3, each group). **P* < 0.05, ***P* < 0.01. Scale bar of migration and invasion assays represent 40 μm.

Figure S6

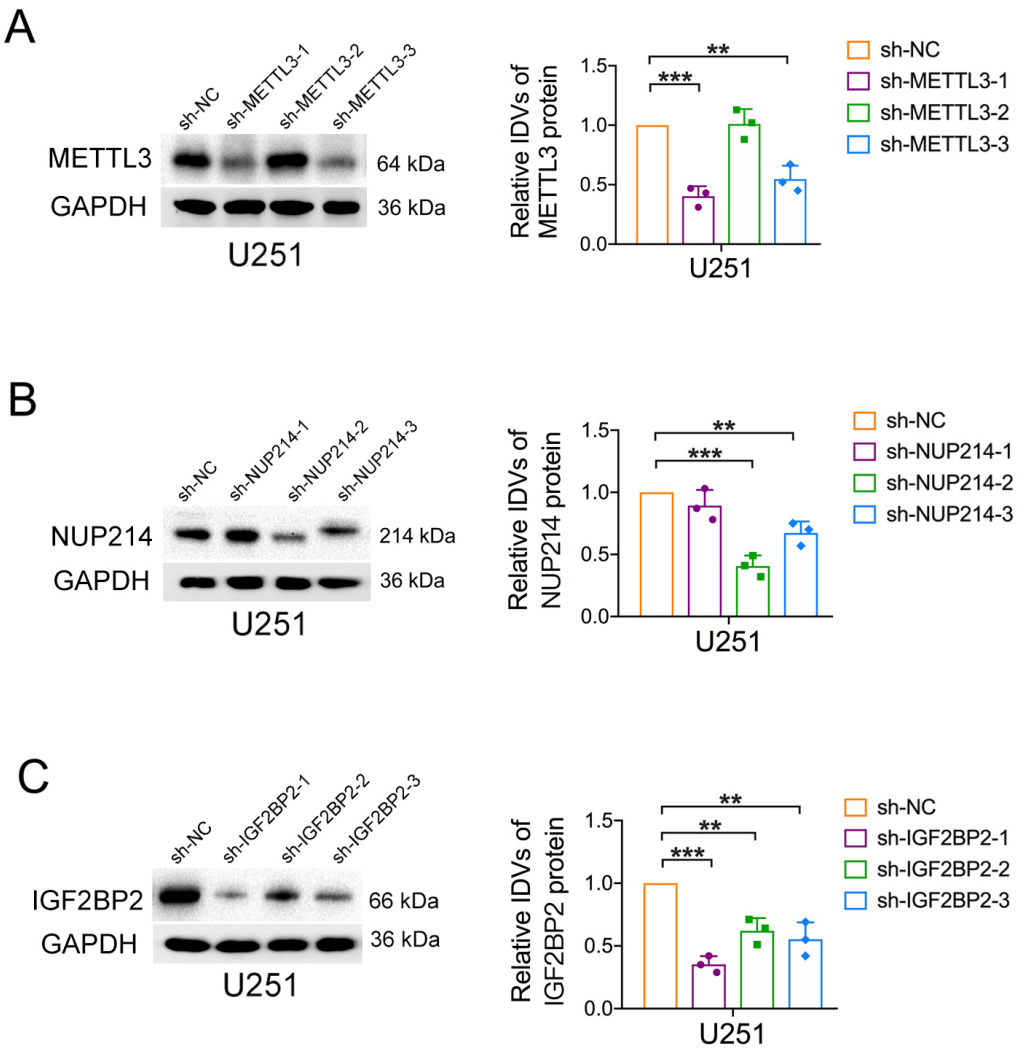


**Fig.S6 The knockdown efficacy was detected by western blot. A.** Western blot was used to examine the expression of METTL3 in glioma cells treated with shRNA against three different target sequences of METTL3, and sh-METTL3-1 was manifested with highest knockdown efficiency. Data are presented as the mean ±SD (n = 3, each group). $^{**}P < 0.01$, $^{***}P < 0.001$. **B.** Western blot was used to examine the expression of NUP214 in glioma cells treated with shRNA against three different target sequences of NUP214, and sh-NUP214-2 was manifested with highest knockdown efficiency. Data are presented as the mean ± SD (n = 3, each group). $^{**}P < 0.01$, $^{***}P < 0.001$. **C.** Western blot was used to examine the expression of IGF2BP2 in glioma cells treated with shRNA against three different target sequences of IGF2BP2, and sh-IGF2BP2-1 was manifested with highest knockdown efficiency. Data are presented as the mean ± SD (n = 3, each group). $^{**}P < 0.01$, $^{***}P < 0.001$.

Figure S7

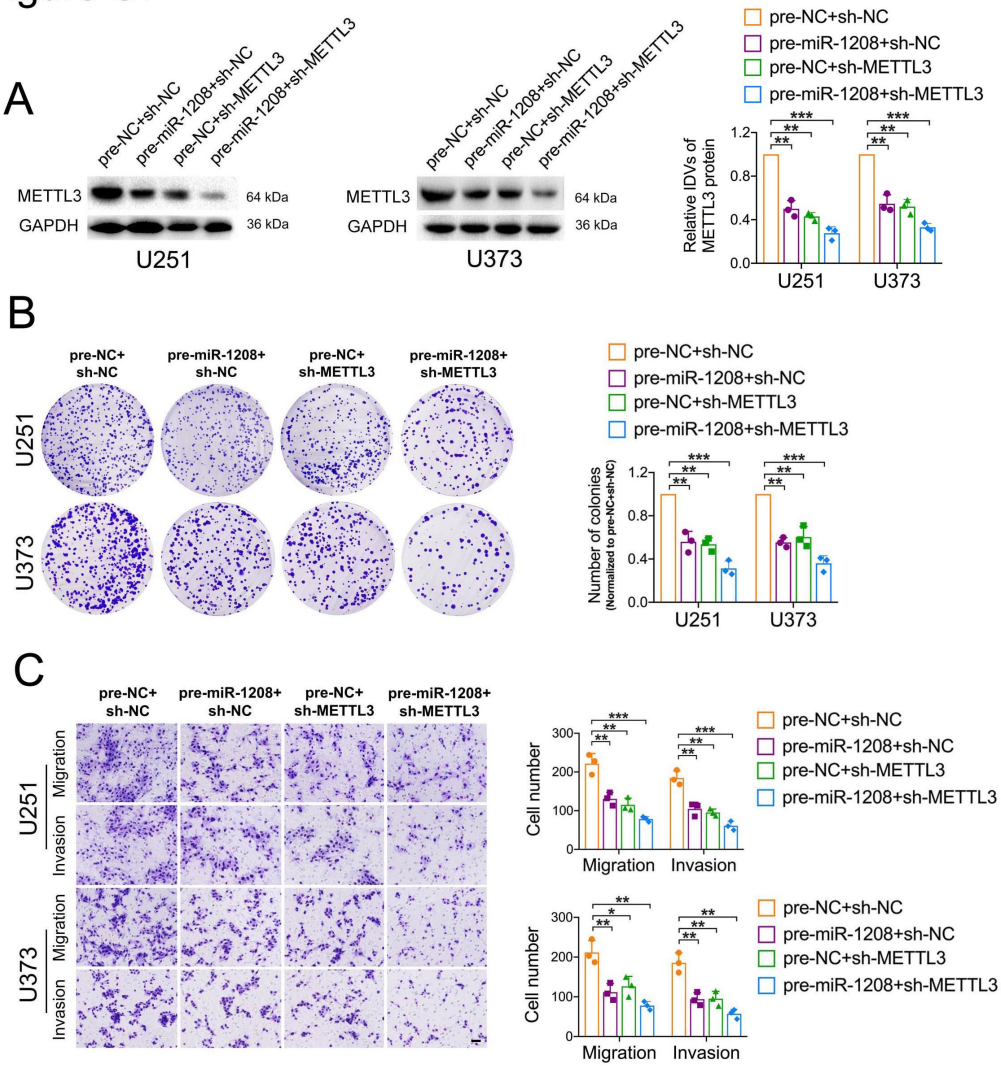


**Fig.S7 MiR-1208 overexpression or METTL3 knockdown significantly repressed malignant biological behaviors of glioma cells. A.** Western blot was used to examine the expression of METTL3 in glioma cells treated with miR-1208 overexpression, METTL3 knockdown or co-transfection with miR-1208 overexpression and METTL3 knockdown. Data are presented as the mean ±SD (n = 3, each group). $^{**}P < 0.01$, $^{***}P < 0.001$. **B-C.** Colony formation assay and migration and invasion assays were used to detected the impacts on biological behaviors of glioma cells treated with miR-1208 overexpression, METTL3 knockdown or co-transfection with miR-1208 overexpression and METTL3 knockdown. Data are presented as the mean ± SD (n = 3, each group). $^{*}P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$. Scale bar of migration and invasion assays represent 40 μm.

**Table S1. Sequences of shRNA template.**

| Gene | | Target sequence(5'->3') |
|---|---|---|
| METTL3 | Target 1 | GCTGCACTTCAGACGAATTAT |
| | Target 2 | GCCTTAACATTGCCCACTGAT |
| | Target 3 | CGTCAGTATCTTGGGCAAGTT |
| NUP214 | Target 1 | GCTGTCAAAGTCAACCTTAGT |
| | Target 2 | GGAAATCACCATCAGTGATGA |
| | Target 3 | GCAGGGACATCAGTGGAAAGA |
| IGF2BP2 | Target 1 | CTTAACCAGTGCAGAAGTCAT |
| | Target 2 | GGTGCCTGCAGCGGTAATATA |
| | Target 3 | AGTGAAGCTGGAAGCGCATAT |

**Table S2. Primers used for qRT-PCR.**

| Primer | Gene | Sequence (5'->3') |
|---|---|---|
| Primer | miR-1208 | F: GCTGCGTCACTGTTCAGACA |
| | | R: AGTGCAGGGTCCGAGGTATT |
| | U6 | F: TGGAACGCTTCACGAATTTGCG |
| | | R: GGAACGATACAGAGAAGATTAGC |