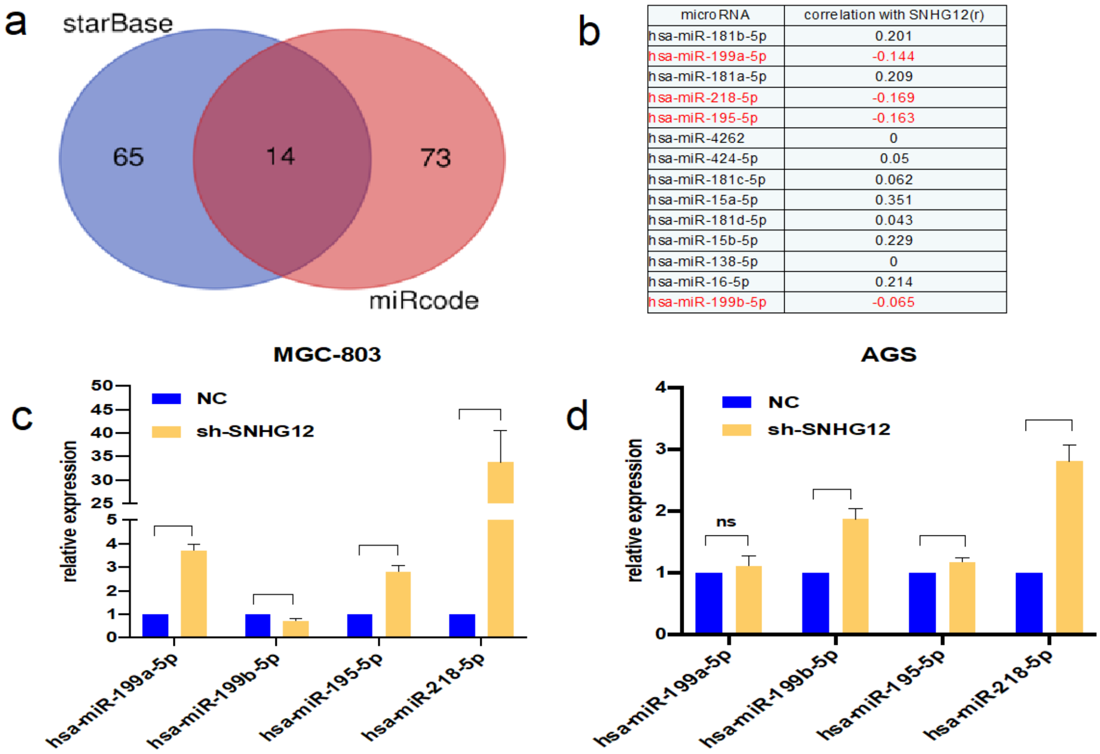
Additional file 1

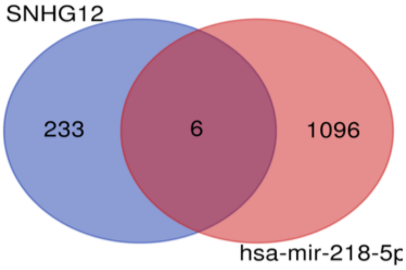
Figure S1. **Bioinformatics analysis and experimental verification suggest that SNHG12 could regulate miR-218-5p.** (**a**) Using bioinformatics databases (Starbase and miRcode), 14 miRNAs related to SNHG12 were identified. (**b**) According to the gastric cancer data in Starbase online databases, the correlation of the 14 miRNAs with SNHG12 were analyzed, and miR-199a-5p, miR-199b-5p, miR-195-5p and miR-218-5p were identified as negatively related to SNHG12 with low expression profile in GC (r refers to the correlation coefficient in Starbase online databases). (**c, d)** SNHG12 knockdown in MGC-803 and AGS revealed that the change in the expression of miR-218-5p was most significant among the 4 miRNAs.



microRNA	correlation with SNHG12(r)
hsa-miR-181b-5p	0.201
hsa-miR-199a-5p	-0.144
hsa-miR-181a-5p	0.209
hsa-miR-218-5p	-0.169
hsa-miR-195-5p	-0.163
hsa-miR-4262	0
hsa-miR-424-5p	0.05
hsa-miR-181c-5p	0.062
hsa-miR-15a-5p	0.351
hsa-miR-181d-5p	0.043
hsa-miR-15b-5p	0.229
hsa-miR-138-5p	0
hsa-miR-16-5p	0.214
hsa-miR-199b-5p	-0.065

Figure S2. Bioinformatics analysis indicated the target gene of miR-218-5p and SNHG12. (a) Using the databases TargetScan Human 7.2 and Starbase, 6 mRNAs were identified as the putative downstream genes of SNHG12 and miR-218-5p. (**b)** According to th GC data in Starbase online databases, the correlations of the 6 identified genes with SNHG12 and miR-218-5p were analyzed,, YWHAZ and RCC1 displayed high positive correlation with SNHG12, negative correlation with miR-218-5p, while YWHAZ was closely related with tumor metastasis. **(c, d, e)** The correlations between SNHG12, miR-218-5p and YWHAZ from the gastric cancer data in Starbase online databases.

a



b

mRNA	correlation with SNHG12 (r)	correlation with miR-218-5p (r)
YWHAZ	0.342	-0.384
SLC5A3	0.108	-0.141
RCC1	0.417	-0.259
BAZ2B	0.235	0.009
DDX6	0.072	0.052
ONECUT2	0.095	-0.065