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.
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 the 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.