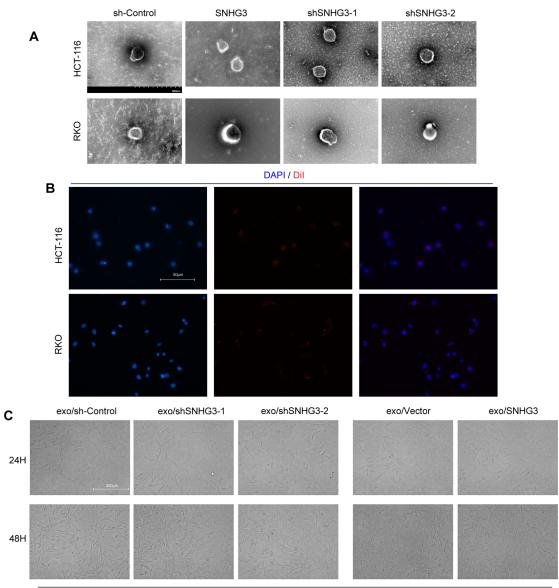
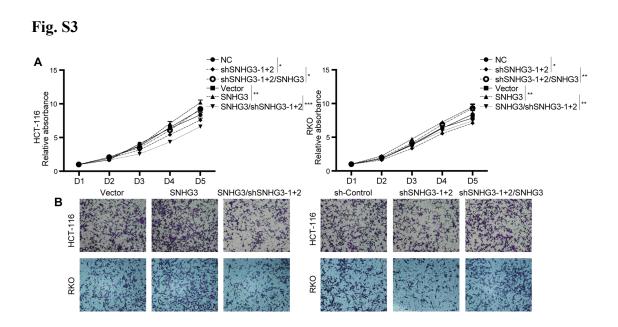


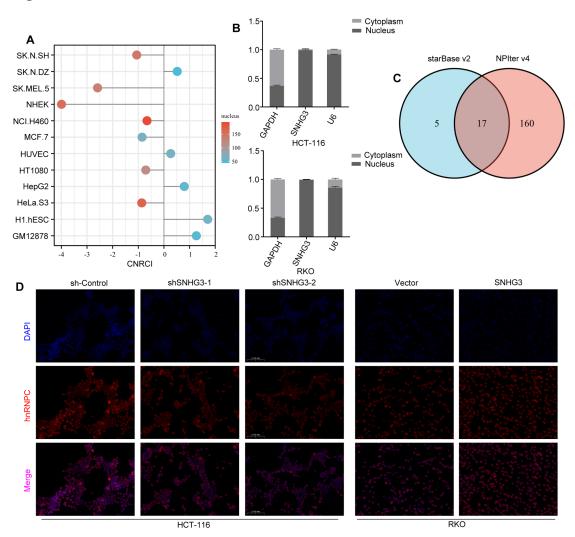
```
Fig. S2
```



RKO











Gene Symbol	MW (kDa)
CSTF2T	64
DDX54	99
DGCR8	100
ELAVL1	36
FMR1	71
hnRNPA1	38
hnRNPA2B1	37
hnRNPC	42
hnRNPM	77
IGF2BP1	65
IGF2BP2	66
IGF2BP3	63
LIN28B	30
RBFOX2	41
TAF15	62
TARDBP	44
U2AF2	53

Table S1 Proteins predicted by starBase v2 and NPIter v4

Legends of supplementary figures and table

Fig. S1 The differential expression of other top 10 lncRNAs in pan-cancer. A - I TCGA pan-cancer database was applied to analyze the differential expression of FENDRR, ABALON, VIMAS1, FAM157C, OR2A1AS1, ASMTLAS1, AC025164.1, AC098487.1 and LINC02256 in multiple cancers. *p < 0.05, **p < 0.01, ***p < 0.001.

Fig. S2 Exosomal SNHG3 affects the morphology of recipient CRC cells. A TEM image of purified exosomes from different groups. Scale bar=500 nm. **B** The internalization of DiI-labeled exosomes secreting by RKO cells was observed using an immunofluorescent microscope. Scale bar=200 μ m. C wt RKO cells were cocultured with exosomes for 24h and 48h respectively before observation.

Fig.S3 SNHG3 acts as a promoter during the progression of CRC. A and B CCK-8 assay and Transwell assay were applied to determine the oncogenic function of SNHG3. The error bar represents the mean \pm SD of three independent experiments. *p < 0.05, **p < 0.01, ***p < 0.001.

Fig. S4 SNHG3 is mainly located in the nucleus of CRC cells. A lncATLAS database indicated that SNHG3 is distributed in both the nucleus and cytoplasm. **B** Real-time PCR analyzed the level of SNHG3 in different cellular fractions of CRC cells which showed a high abundance in the cytoplasm. **C** StarBase v2 and NPIter v4 were used to predict the potential proteins interacted with SNHG3, the intersection was shown by

the venn plot. **D** Immunofluorescence staining exhibited the intracellular localization of hnRNPC in CRC cells.

Fig.S5 SNHG3 promotes the peritoneal metastasis of CRC cells through exosomes.

A High-SNHG3 exosomes-treated HCT 116 cells were injected to establish peritoneal metastasis models, and counts of metastatic lesions were analyzed. *p < 0.05, **p < 0.01.

Table S1 Summary of the proteins predicted to bind with SNHG3 using starBase v2and NPIter v4. The molecular weight of each protein was listed.