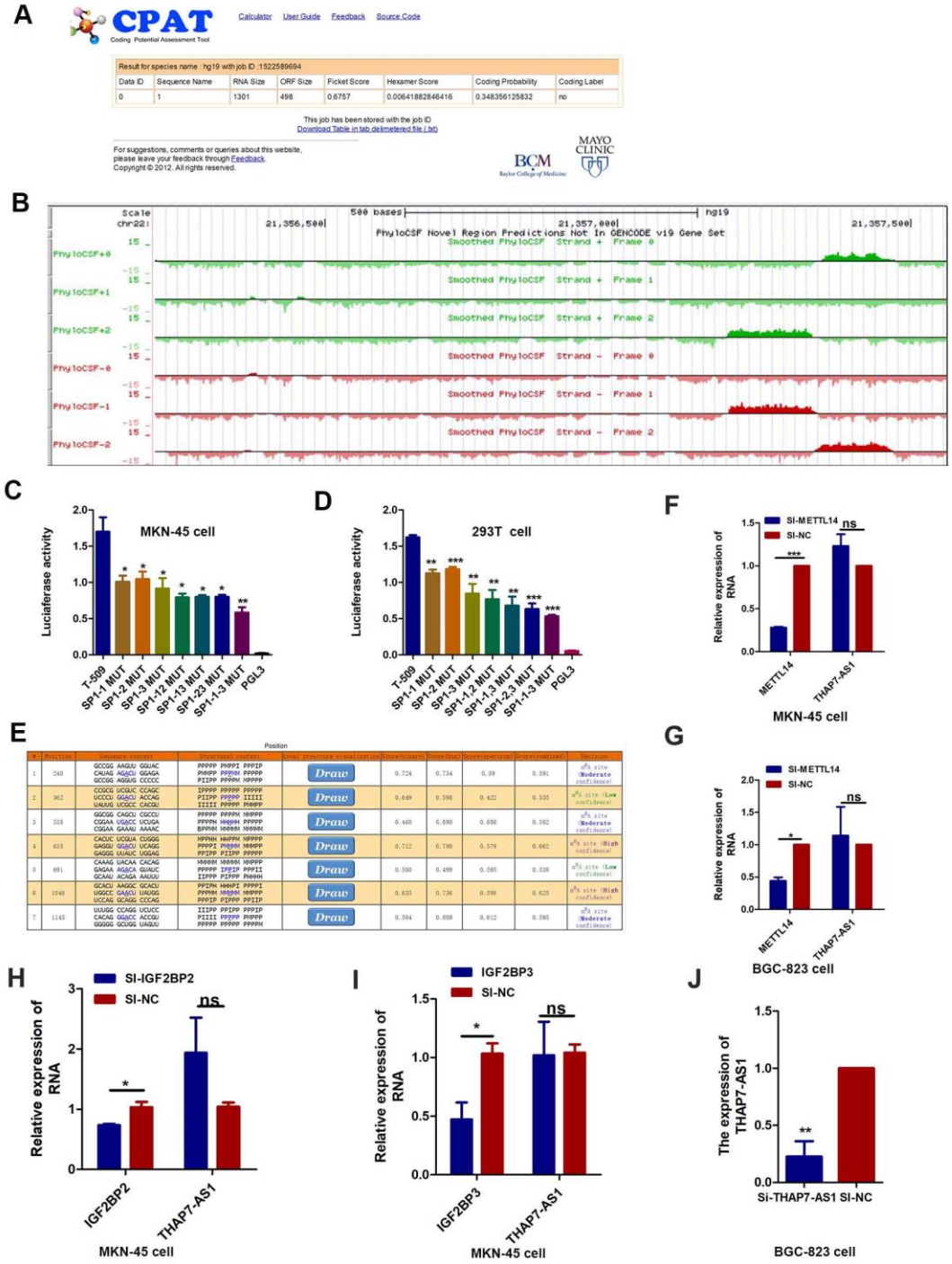
Supplementary Figure and Figure Legend



Supplementary Figure 1

(A). Coding-potential calculator Coding Potential Assessment Tool showed THAP7-AS1 has very weak protein-coding potential.

(B). PyhloCSF assay indicated low codon substitution frequency scores of THAP7-AS1.

(C-D). Luciferase activity of the THAP7-AS1 promoter was reduced when the three single site (SP1–1, SP1–2 and SP1–3), the two-site (SP1–1,2, SP1–1,3, SP1-2,3) and

the three-site (SP1–1-3) were mutated in MKN-45 cells (C) and 293T cells (D).

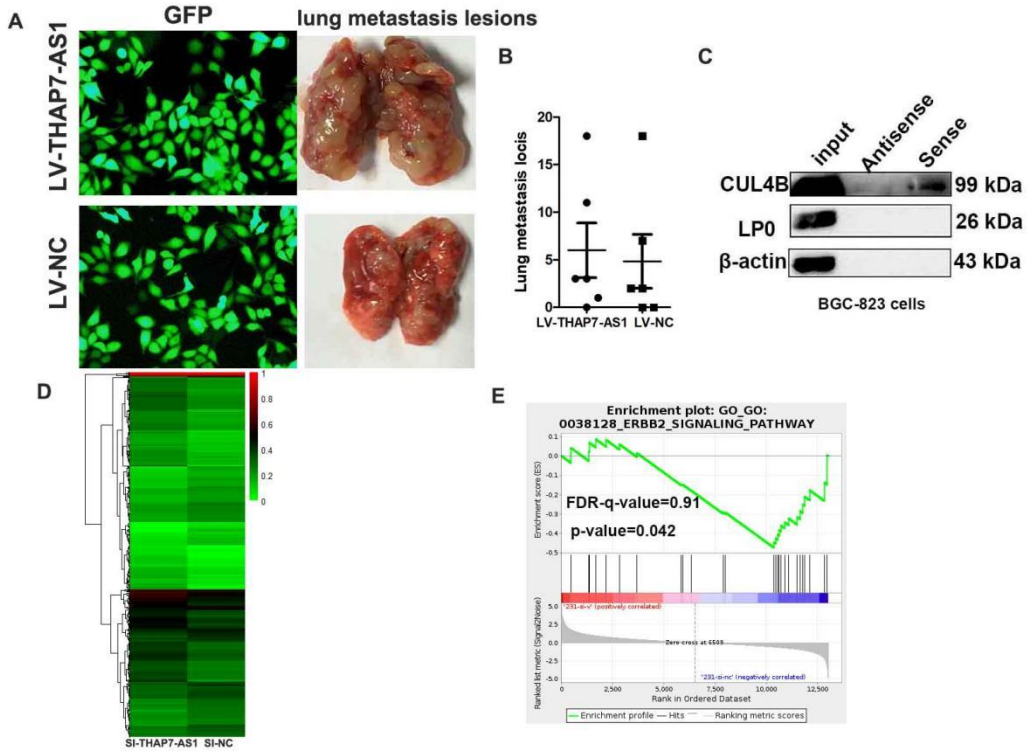
(E). SRAMP was used to predict m6A modification sites on the THAP7-AS1 sequences.

(F). Transcript levels of METTL14 and THAP7-AS1 in si-METTL14 and si-NC MKN-45 cells.

(G). Transcript levels of METTL14 and THAP7-AS1 in si-METTL14 and si-NC BGC-823 cells.

(H-I). Transcript levels of IGF2BP2-3 and THAP7-AS1 in si-IGF2BP2-3 and si-NC MKN-45 cells.

(J). The stably knockdown efficiency of THAP7-AS1 in BGC-823 cells.



Supplementary Figure 2

(A). LV-THAP7-AS1 or LV-NC was successfully transfected in MKN-45 cells, with GFP as marker gene (left). Representative lung metastasis locus was shown (right).

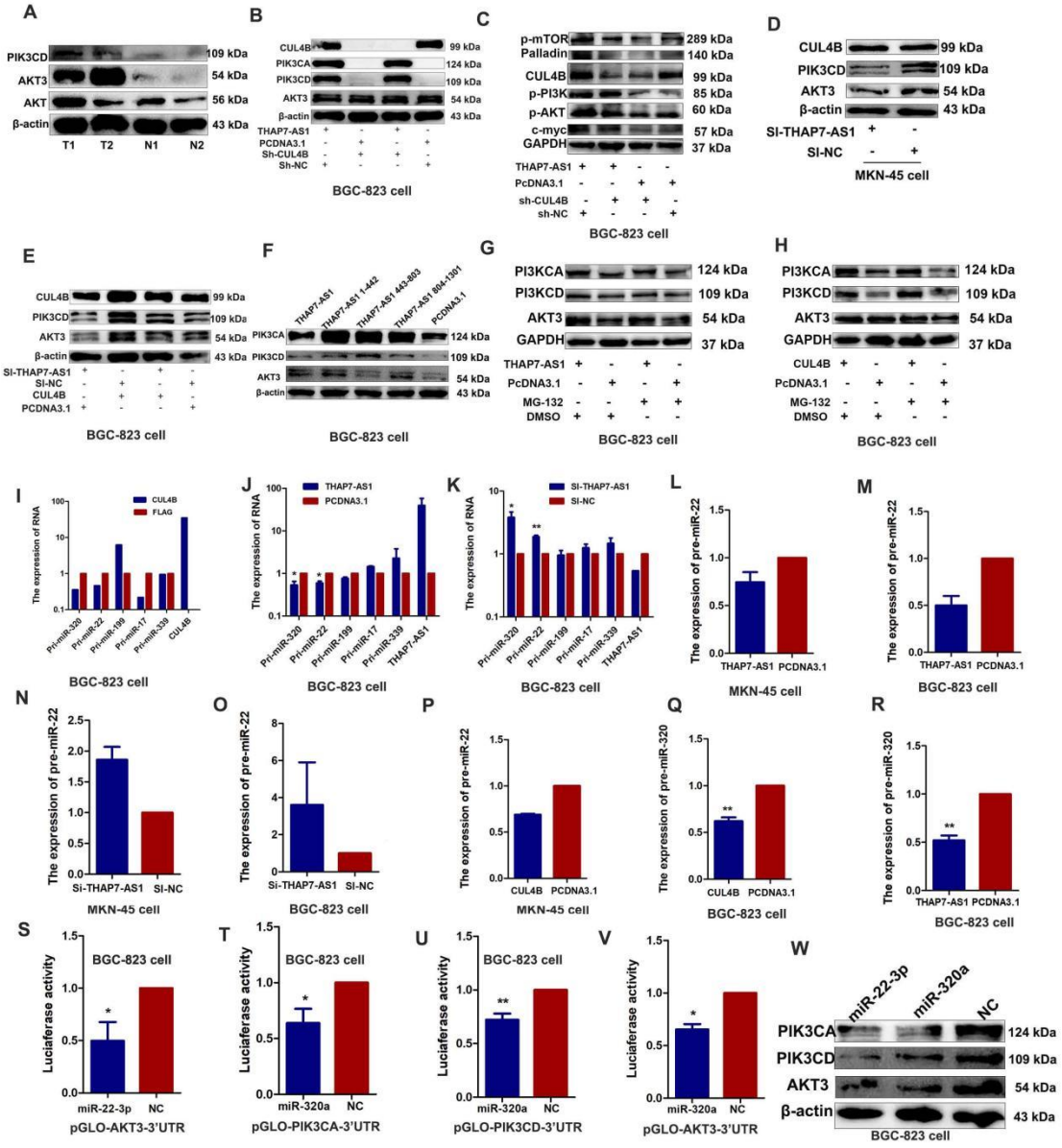
(B). The number of lung metastatic foci in the LV-THAP7-AS1 group was more than that in the LV-NC group.

(C). RNA-pulldown/Western blot analysi shows the specific interaction of CUL4B with THAP7-AS1 in BGC-823 cells.

(D). Heat maps to show the most differentially expressed genes in cancer cells with

THAP7-AS1 knockdown. Colored bands represented the change of the indicated gene expression: downregulation green and upregulation red.

(E) GSEA was performed to examine the expression of a set of THAP7-AS1-repressed genes in an RNA-Seq data set that profiled cancer cells with control or THAP7-AS1 knockdown. ERBB2 signaling pathway was enriched for downregulation upon THAP7-AS1knockdown.



Supplementary Figure 3

(A). LV-THAP7-AS1 enhanced the expression of PIK3CD, AKT3 and AKT in mice tumor xenografts, compared to that of the LV-NC group.

(B-C). Western blot analysis of the PI3K/AKT signaling downstream of THAP7-AS1

in BGC-823 cells expressing THAP7-AS1 or control cells with or without CUL4B knockdown.

(D). Western blot analysis of the different signaling downstream of THAP7-AS1 in GC cells expressing si-THAP7-AS1 or control cells.

(E). Western blot analysis of the PI3K/AKT signaling downstream of THAP7-AS1 in BGC-823 cells expressing si-THAP7-AS1 or control cells with or without transient transfection with PCDNA3.1-CUL4B.

(F). Western blot analysis of the THAP7-AS1 fragments mediated downstream PI3K/AKT signaling of THAP7-AS1/ CUL4B in BGC-823 cells.

(G-H). BGC-823 cells transfected with THAP7-AS1(G) or CUL4B (H) overexpression vector and control cells were treated with MG132 (5 mmol/L) or vehicle for 24 hours. Cell lysates were analyzed by Western blotting.

(I-K). Expression of primary miR-17, miR-19, miR-22-3p, miR-320a and miR-339 expression was assessed by RT–qPCR in BGC-823 cells respectively transfected with CUL4B (I), THAP7-AS1(J) and SI-THAP7-AS1(K).

(L-M). Expression of pre-miR-22 expression was assessed by RT–qPCR in MKN-45 cells (L) and BGC-823 cells (M) transfected with THAP7-AS1

(N-O). Expression of pre-miR-22 expression was assessed by RT–qPCR in MKN-45 cells (N) and BGC-823 cells (O) transfected with si-THAP7-AS1.

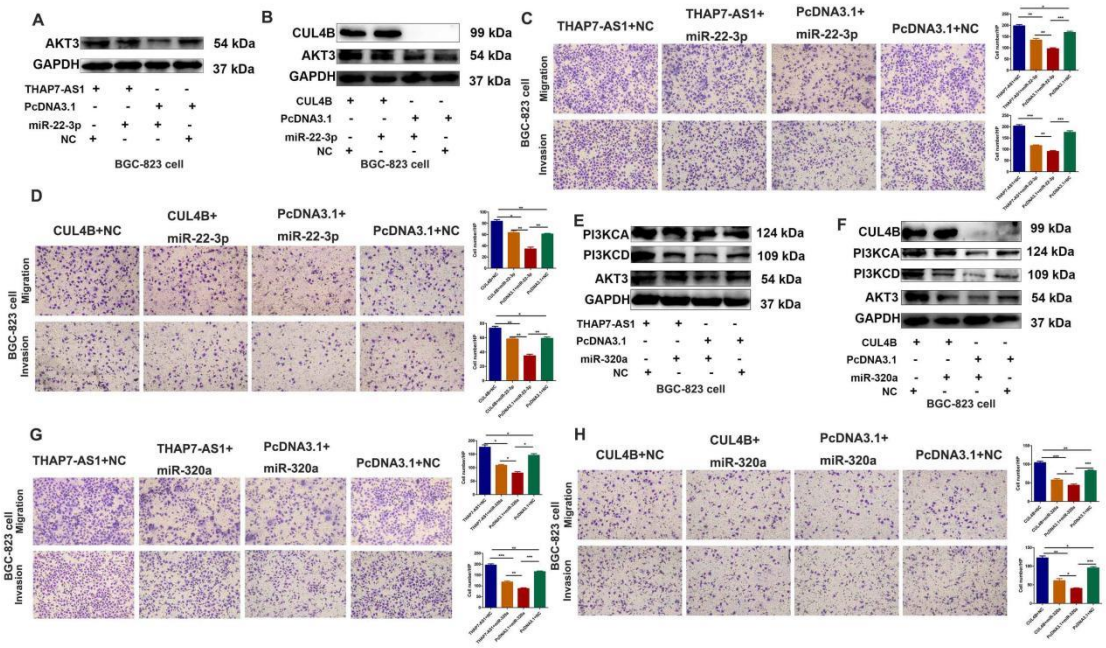
(P). Expression of pre-miR-22 expression was assessed by RT–qPCR in MKN-45 cells transfected with CUL4B.

(Q-R). Expression of pre-miR-320a expression was assessed by RT–qPCR in BGC-823 respectively transfected with CUL4B (Q) and sh-CUL4B (R).

(S). The results indicated a decrease in luciferase activity in BGC-823 cells transfected with PGLO-AKT3-3'UTR and miR-22-3p.

(T-V). Luciferase activity showed a decrease in BGC-823 cells transfected with PGLO-PIK3CA-3'UTR (T), PGLO-PIK3CD-3'UTR (U), PGLO-AKT3-3'UTR (V) and miR-320a.

(W). Western blot analyses were performed to confirm the PIK3CA, PIK3CD and AKT3 expression in BGC-823 cells transfected with miR-22-3p or miR-320a mimics.



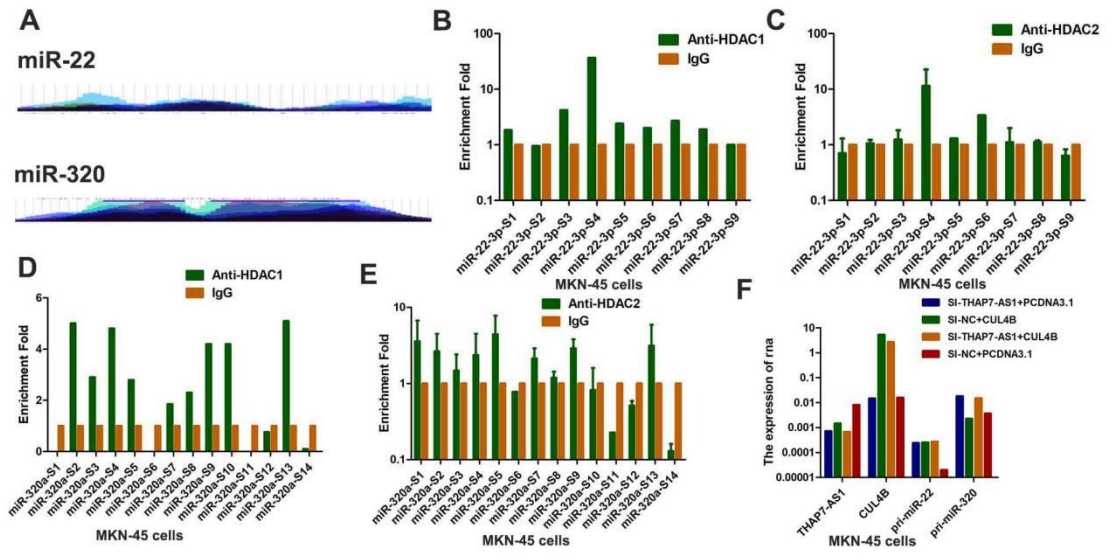
Supplementary Figure 4

(A-B).Western blotting analysis of the AKT3 in BGC-823 cells overexpressing THAP7-AS1(A) or CUL4B(B) with or without transient transfection with miR-22-3p mimics.

(C-D).Migration and invasion abilities of BGC-823 cells transiently transfected with indicated RNA and plasmid were observed. (×100)

(E-F).Western blotting analysis of the PIK3CA, PIK3CD and AKT3 in BGC-823cells overexpressing THAP7-AS1 (E) or CUL4B (F) with or without transient transfection with miR-320a mimics.

(G-H).Migration and invasion abilities of BGC-823 cells transiently transfected with indicated RNA and plasmid were observed. (×100)



Supplementary Figure 5

(A). ENCODE Histone Modification Tracks embedded in UCSC Genome Browser (UC Santa Cruz, CA, USA) found histone methylation enrichment peaks in the surrounding miR-22-3p and miR-320a promoter region.

(B-E). ChIP assays of miR-22-3p (B-C) or miR-320 (D-E) promoter primers in MKN-45 cells using indicated antibodies.

(F). RT-qPCR assay was performed to detect primary miR-22-3p and miR-320a in MKN-45 cells transiently transfected with indicated RNA and plasmid.