

Supporting Information

IGF2BP2 Drives Thyroid Cancer Dedifferentiation Through m6A-Dependent STAT1 mRNA Destabilization

*Rui Chen¹†, Yi-xun Li¹†, Wei-lin Lu¹†, Ke-fei Wu¹, Yu-xin Wang¹, Zi-wen Wang¹, Yi-han Li¹,
Hai-yan Yang¹, Xu Zhang¹, Liang Shi¹, Dong Zhou^{2,3*}, Ying Wang^{4*}, Qiang Ding^{1*}*

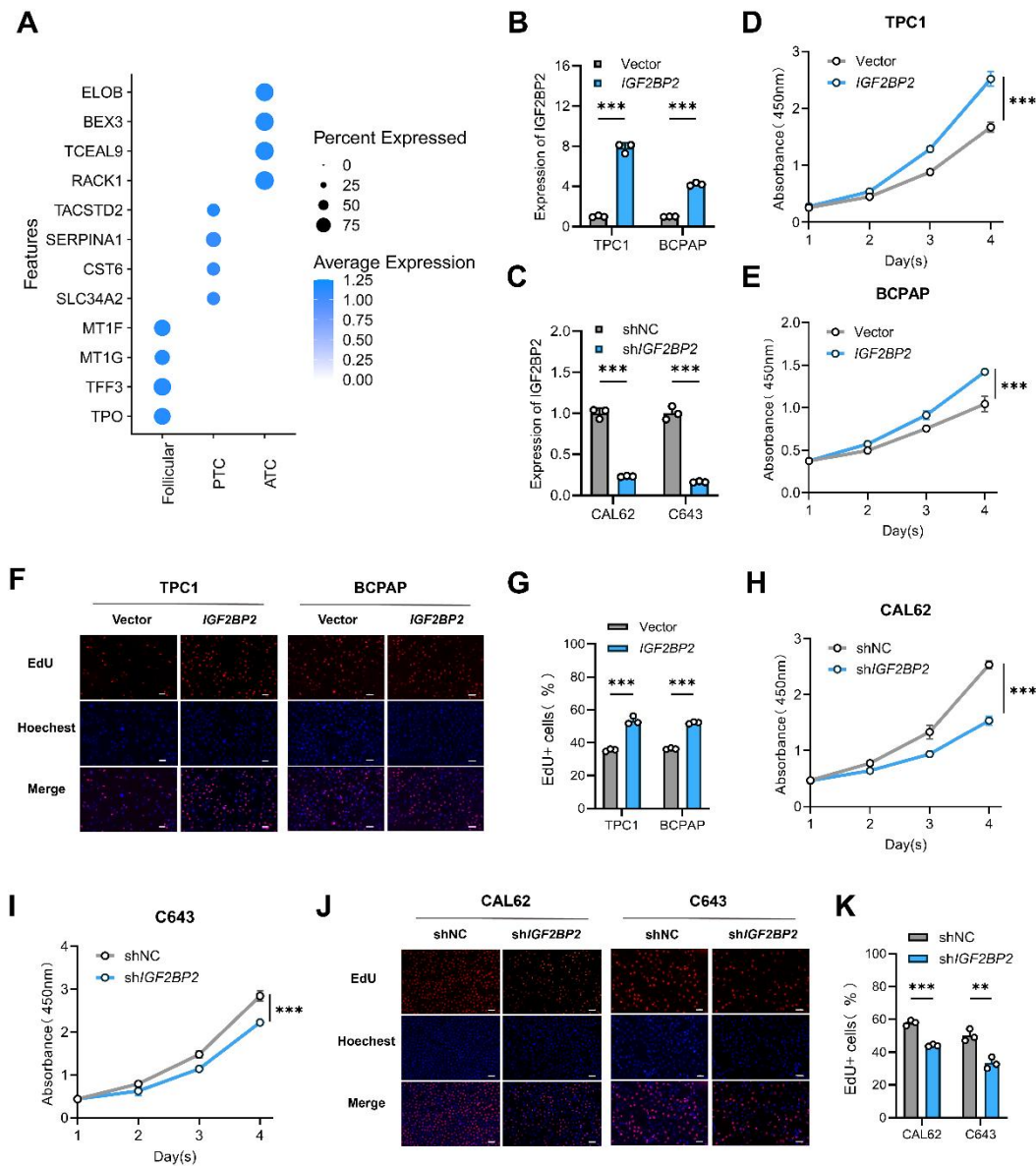


Fig. S1. (Related to Figure 2): IGF2BP2 promoted thyroid cancer proliferation

(A) The bubble plot illustrates genes specifically enriched in normal follicular, PTC, and ATC clusters. (B-C) The efficiency of stable *IGF2BP2* overexpression and knockdown cell lines. (D-G) CCK8 and EdU assays performed in TPC1-OE and BCPAP-OE cells. (H-K) CCK8 and EdU assays performed in CAL62-KD and C643-KD cells. *P* values were determined using a two-tailed unpaired Student's test (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$).

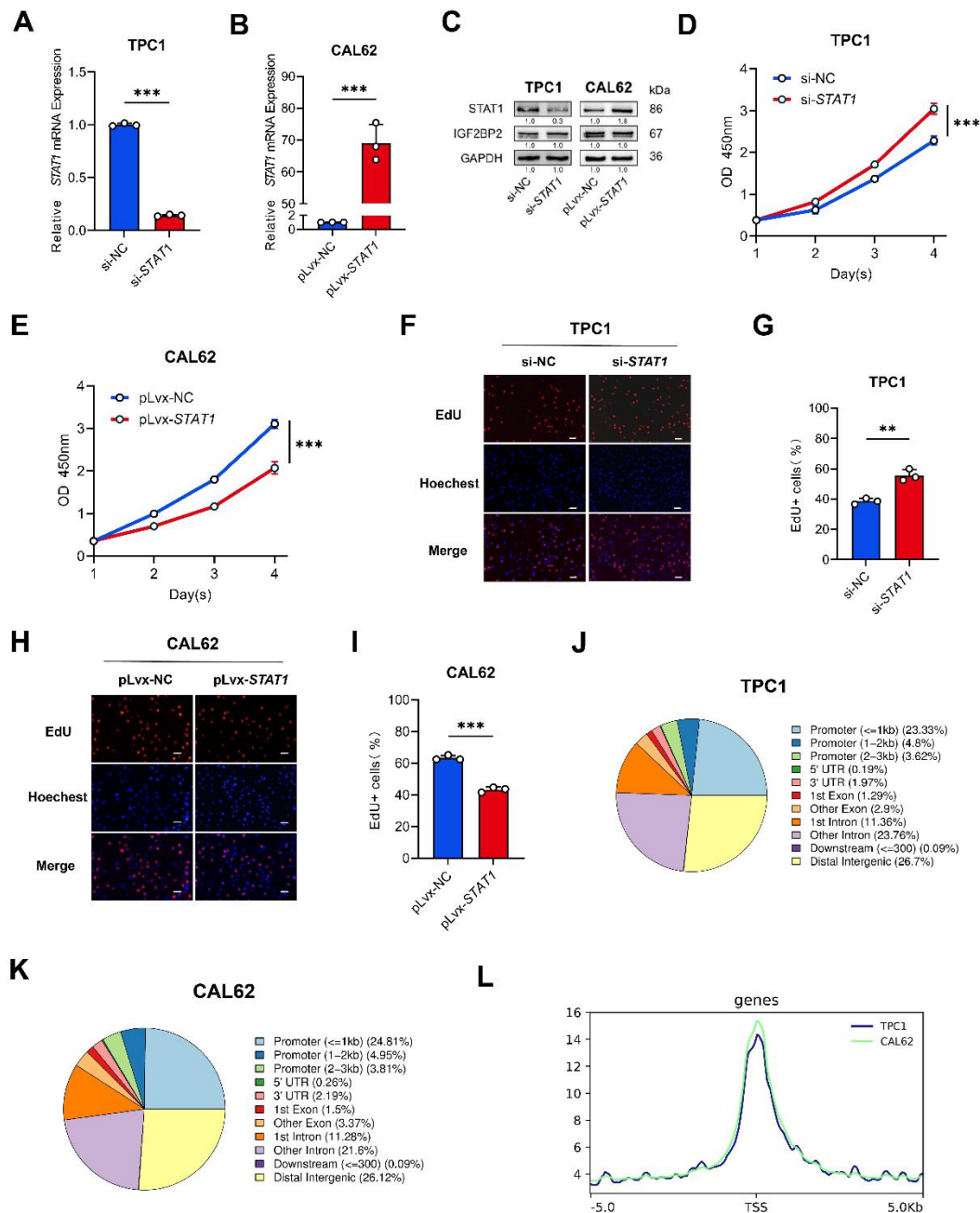


Fig. S2. (Related to Figure 6): STAT1 impaired the cell growth of thyroid cancer

(A-C) Wildtype TPC1 and CAL62 cells were transfected with *STAT1* targeted siRNAs and overexpression plasmids for 48 h. Transfection efficiency was verified by qRT-PCR (A-B) and western blot (C). (D) CCK8 assay using TPC1 transduced with *STAT1* siRNAs. (E) CCK8 assay using CAL62 transduced with *STAT1* overexpression plasmids. (F-G) EdU assays using TPC1 transduced with *STAT1* siRNAs. (H-I) EdU assays using CAL62

transduced with *STAT1* overexpression plasmids. (J-K) Pie chart of genome-wide distribution of upregulated STAT1 enrichment peaks in TPC1 and CAL62 cells. (L) The distribution density of STAT1-binding peaks around TSS in TPC1 and CAL62 cells. *P* values were determined using a two-tailed unpaired Student's test (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$).

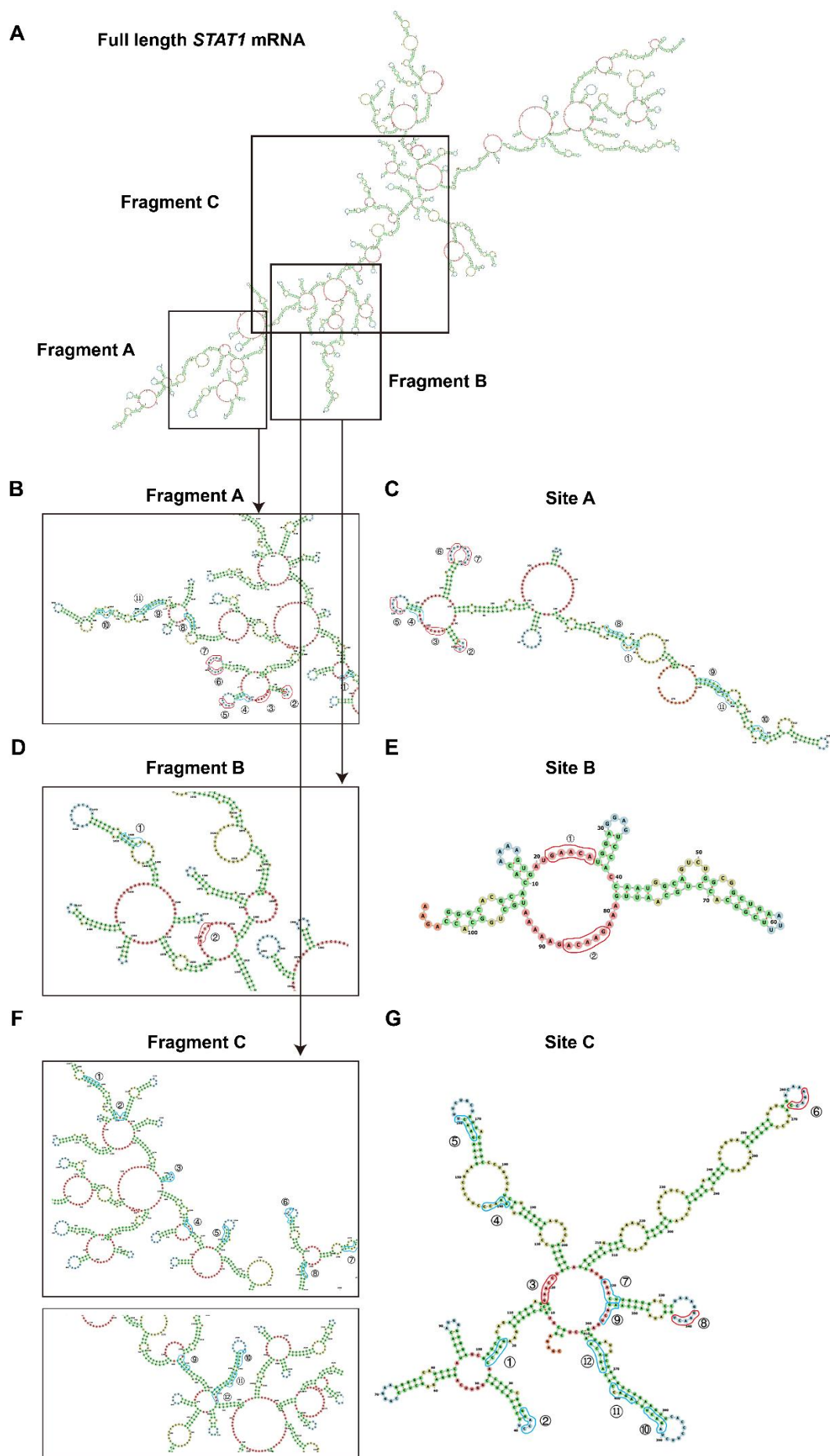


Fig. S3. (Related to Figure 7): Comparative *in silico* analysis of secondary structures for the *STAT1* m6A sites

(A) Secondary structures of the full-length *STAT1* mRNA were predicted using RNAfold (<http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAfold.cgi>). (B) The local RNA secondary structures of the high-confidence m6A site A within the full-length *STAT1* mRNA was predicted using RNAfold. (C) The local RNA secondary structures of the isolated site A was predicted using RNAfold. (D) The local RNA secondary structures of the high-confidence m6A site B within the full-length *STAT1* mRNA was predicted using RNAfold. (E) The local RNA secondary structures of the isolated site B was predicted using RNAfold. (F) The local RNA secondary structures of the high-confidence m6A site C within the full-length *STAT1* mRNA was predicted using RNAfold. (G) The local RNA secondary structures of the isolated site C was predicted using RNAfold. Accessible RRACH motifs are highlighted in red, while inaccessible motifs are colored blue.

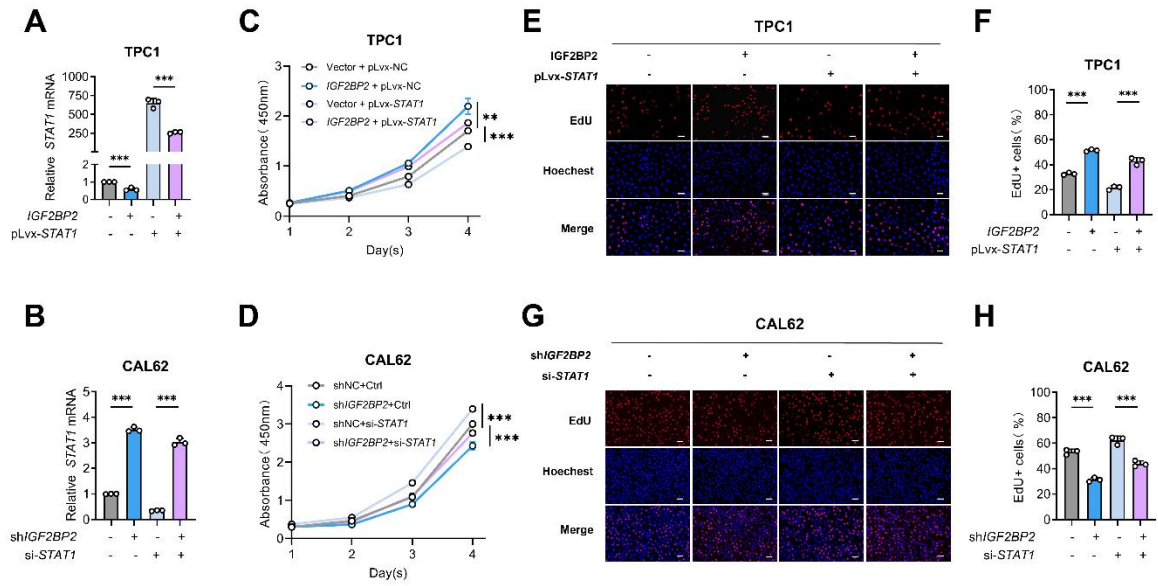


Fig. S4. (Related to Figure 8): STAT1 reversed the vicious proliferation promoted by IGF2BP2 in thyroid cancer

(A-B) The TPC1-OE cells were transfected with pLv $\times$ -*STAT1* plasmids and CAL62-KD cells were interfered with si-*STAT1*, confirmed by qRT-PCR. (C) CCK8 assays showing the rescue effect of *STAT1* overexpression on TPC1-OE cells. (D) CCK8 assays showing the rescue effect of *STAT1* interference on CAL62-KD cells. (E-F) EdU assays showing the rescue effect of *STAT1* overexpression on TPC1-OE cells. (G-H) EdU assays showing the rescue effect of *STAT1* interference on CAL62-KD cells. *P* values were determined using a two - tailed unpaired Student's test (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$).

Table S1.

The sequence information of Lentivirus, and siRNA. Related to Methods.

shRNA sequences (5'-3')	
shIGF2BP2	ACAGGACUGUCCGUGCUAUTT
siRNA (5'-3')	
si-STAT1	CCCTGAAGTATCTGTATCCAA
si-CNOT1-1	TGCCTATTTGGTGGTATAATT
si-CNOT1-2	CATTCAACATTCCCTTATAAA

Table S2.**The sequence information of qPCR primers. Related to Methods.**

qPCR primer sequence (5'-3')		
ACTIN	Forward	CATGTACGTTGCTATCCAGGC
	Reverse	CTCCTTAATGTCACGCACGAT
IGF2BP2	Forward	AGTGAATTGTCATGGGAAAATCA
	Reverse	CAACGGCGGTTTCTGTGTC
STAT1	Forward	CAGCTTGACTCAAAATTCCTGGA
	Reverse	TGAAGATTACGCTTGCTTTTCCT
TSHR	Forward	GGAATGGGGTGTTCGTCTCC
	Reverse	GCGTTGAATATCCTTGCAGGT
TPO	Forward	GCCAACAAGCGGAGTGATTG
	Reverse	GGGCAGCATGTAAGGGAGAC
FOX E1	Forward	CACGGTGGACTTCTACGGG
	Reverse	GGACACGAACCGATCTATCCC
PAX8	Forward	ATCCGGCCTGGAGTGATAGG
	Reverse	TGGCGTTTGTAGTCCCCAATC
NKX2.1	Forward	AGCACACGACTCCGTTCTC
	Reverse	GCCCACTTTCTTGTAGCTTTCC
SLC5A5	Forward	GCAGTACATTGTAGCCACGAT
	Reverse	TGCAGATAATTCCGGTGGACA
SLC26A4	Forward	GCTCCCCAAATACCGAGTCAA
	Reverse	CACCACTGGAAAAGGTCCAAC
CD133	Forward	AGTCGGAAACTGGCAGATAGC
	Reverse	GGTAGTGTTGTACTGGGCCAAT
SOX2	Forward	TGGACAGTTACGCGCACAT
	Reverse	CGAGTAGGACATGCTGTAGGT
OCT4	Forward	CTGGGTTGATCCTCGGACCT
	Reverse	CCATCGGAGTTGCTCTCCA
NANOG	Forward	AAGGTCCCGGTCAAGAAACAG
	Reverse	CTTCTGCGTCACACCATTGC
CNOT1	Forward	ACTTCCTTGACACGCTGAAGA
	Reverse	ATTGGCTGCAGCTTTATCAGA
Methylation-specific primers (5'-3')		
STAT1	Forward	GCCCAGAGATTTATGGTCTCGT
	Reverse	CAGGCTCTTGATTTTCATGCTCT

Table S3.

The sequence information of Luciferase. Related to Methods.

Plasmids: Luciferase sequence (5'-3') in Fig. 6	
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NKX2.1

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 GGAAGCCGGCGGAGGGAG

Plasmids: Luciferase sequence (5'-3') in Fig. 7

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 GATGAATATGACTTCAAATGCAAAACCTTGCAGAAC
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