

Supplementary Figure 1

(A-D) qPCR analysis of the main m⁶A-associated methyltransferases and demethylases in BCa tissues (n = 32) and normal bladder tissues (n = 23).

(E) qPCR analysis of METTL14 in BCa tissues and normal bladder tissues from LEE Bladder in ONCOMINE database (Reporter: ILMN_1673037).

(F-G) qPCR and western blotting analysis of METTL14 in the normal urothelial cell line SVHUC-1 and five BCa cell lines (UMUC3, 5637, T24, J82 and EJ-M3).

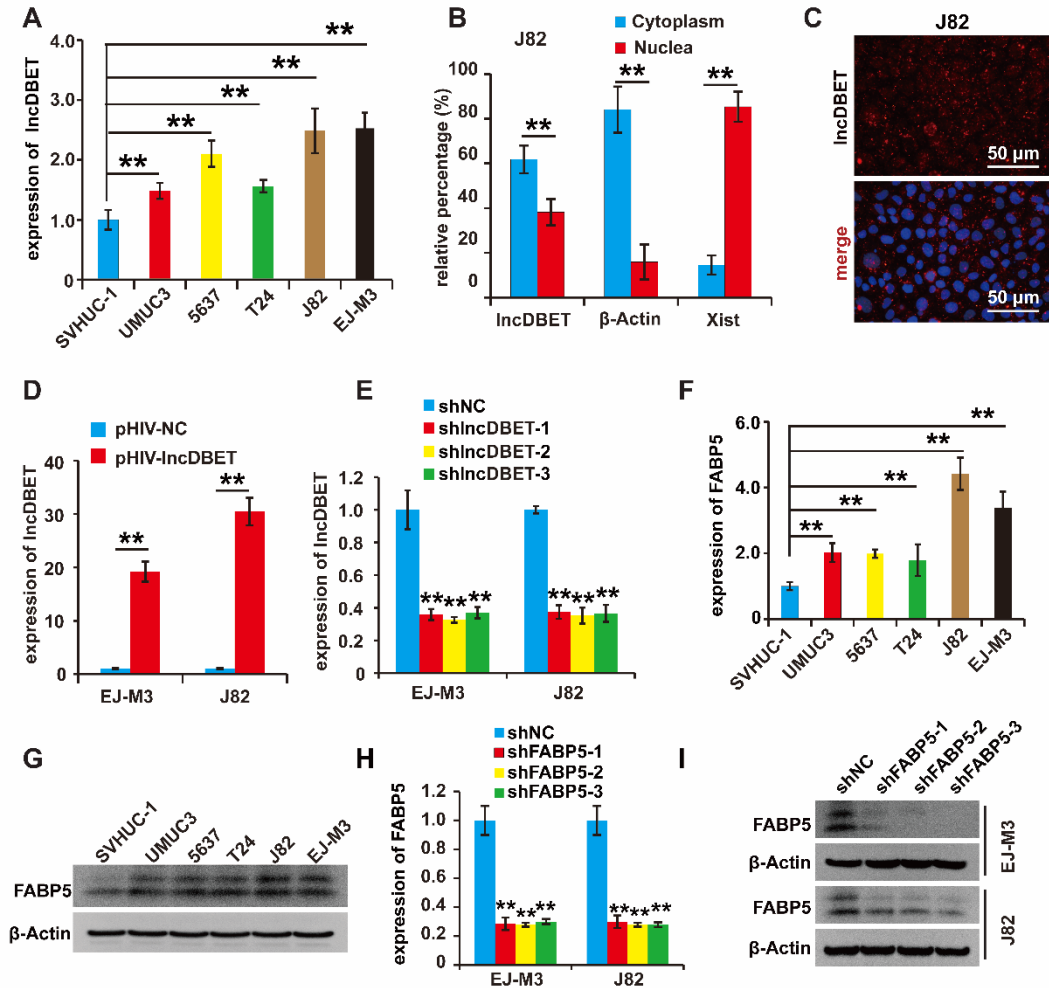
(H-I) qPCR and western blotting analysis of METTL14 in J82 and EJ-M3 cells transfected with pHIV-METTL14 or shMETTL14.

(J-K) qPCR and western blotting analysis of FABP5 in J82 and EJ-M3 cells transfected with shMETTL14.

(L) CCK8 assay for the viability of J82 cell lines respectively transfected with shMETTL14 and pHIV-METTL14 and control shRNA(shNC)/pHIV-RNA (pHIV-NC).

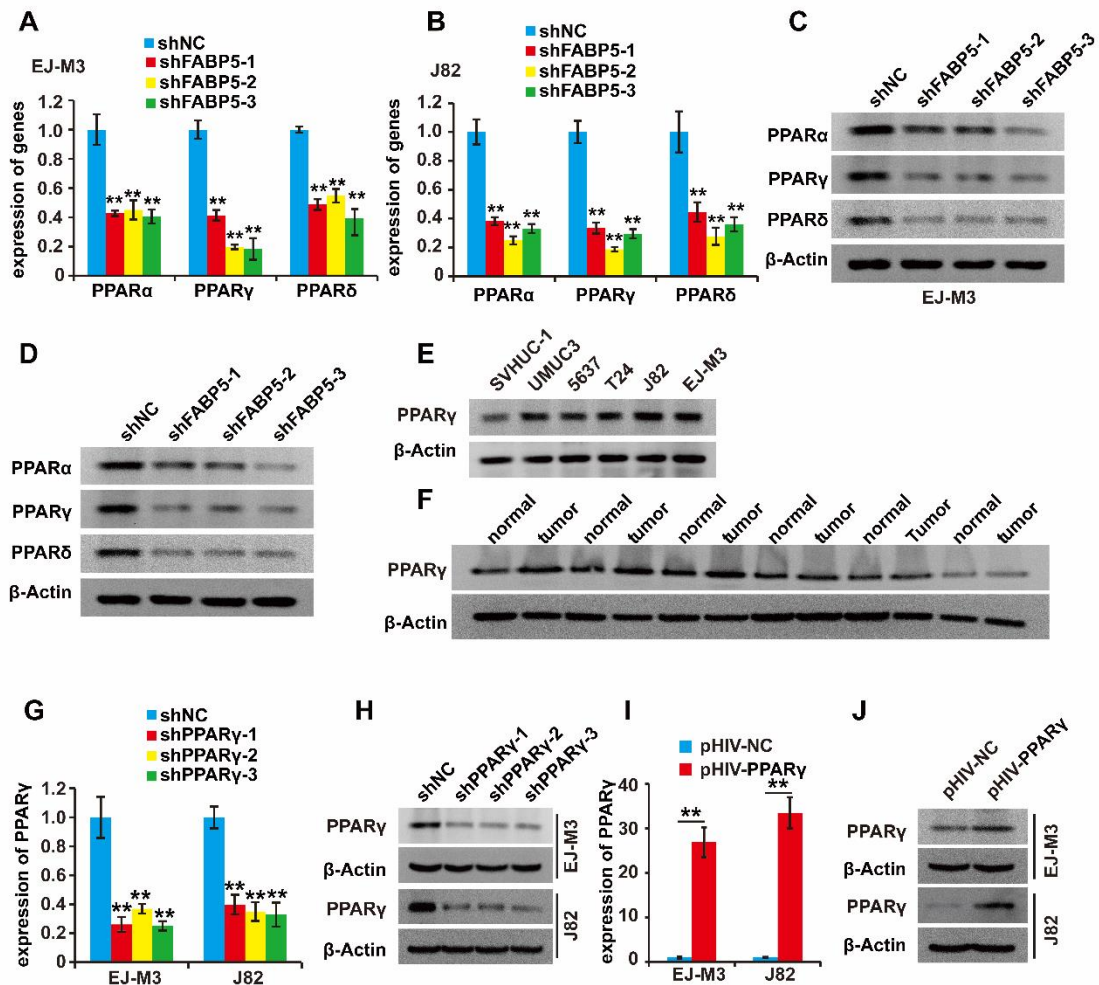
(M) Transwell, EdU and Flow cytometry assays for the migration, proliferation and apoptosis of

J82 cell lines respectively transfected with shMETTL14 and pHIV-METTL14 and control shRNA (shNC)/pHIV-RNA (pHIV-NC). UL, fragment and damaged cells; UR, late apoptosis and dead cells; LL, normal cells of negative control group; LR, early apoptotic cells. (N) HE staining analysis of the livers in metastasis tumor mice model injected EJ-M3 cells transfected with shMETTL14 or shNC through caudal vein. The bar was 20 μ m. Each experiment was repeated a minimum of three times. The symbol * denotes a significant difference ($P < 0.05$), while ** represents a highly significant difference ($P < 0.01$).



Supplementary Figure 2

- (A) qPCR analysis of lncDBET in the normal urothelial cell line SVHUC-1 and five BCa cell lines (UMUC3, 5637, T24, J82 and EJ-M3).
- (B) Localization analysis of lncDBET by biochemical fractionation in J82 cells. β -Actin (mostly in the cytoplasm) and Xist (mostly in the nuclei) are as control teams.
- (C) Localization analysis of lncDBET by fluorescence in situ hybridization (FISH) in J82 cells. Cell nuclei were counterstained with Hoechst (blue). Each experiment was repeated a minimum of three times. The symbol * denotes a significant difference ($P < 0.05$), while ** represents a highly significant difference ($P < 0.01$).
- (D-E) qPCR analysis of lncDBET in J82 and EJ-M3 cells transfected with pHIV-lncDBET or shlncDBET.
- (F) qPCR analysis of FABP5 in the normal urothelial cell line SVHUC-1 and five BCa cell lines (UMUC3, 5637, T24, J82 and EJ-M3).
- (G) Western blotting analysis of FABP5 in six paired cancer and adjacent normal tissues of BCa. β -Actin was used as the control.
- (H-I) qPCR and western blotting analysis of FABP5 in J82 and EJ-M3 cells transfected with shFABP5.



(A-D) qPCR and western blotting analysis of PPARs in J82 and EJ-M3 cells transfected with shFABP5.

(E-F) western blotting analysis of PPAR γ in BCa tissues and normal bladder tissues; and in the normal urothelial cell line SVHUC-1 and five BCa cell lines (UMUC3, 5637, T24, J82 and EJ-M3).

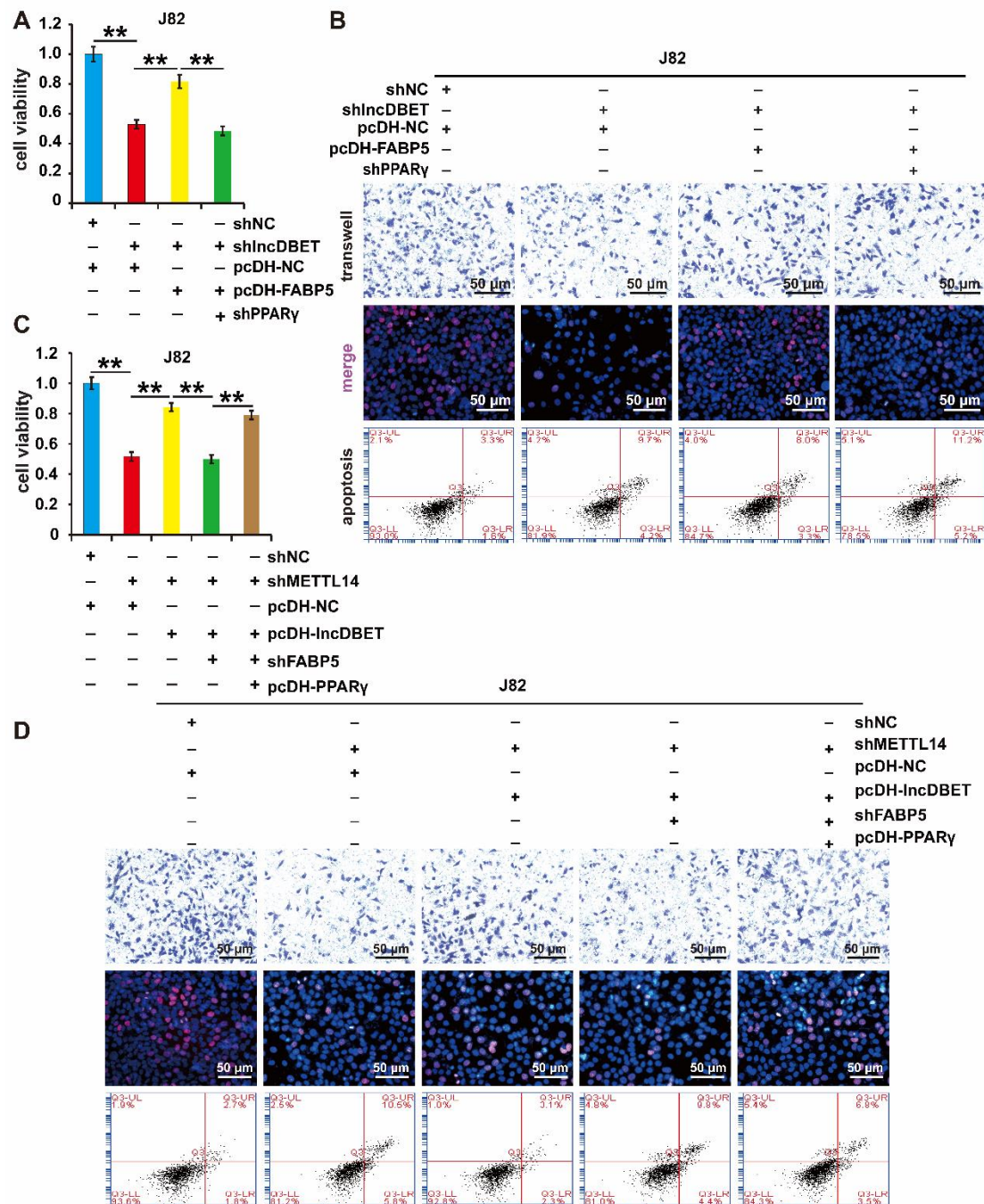
(G-J) qPCR and western blotting analysis of PPAR γ in J82 and EJ-M3 cells transfected with pHIV-PPAR γ or shPPAR γ .

Supplementary Figure 4

(A-B) CCK8, Transwell, EdU and flow cytometry assays for the viability, migration, proliferation and apoptosis of J82 cell lines transfected with shPPAR γ +pcDH-FABP5+shlncDBET, pcDH-FABP5+shlncDBET, pcDH-NC+shlncDBET and pcDH-NC+shNC.

(C-D) CCK8, Transwell, EdU and flow cytometry assays for the viability, migration, proliferation and apoptosis of J82 cell lines transfected with pcDH

PPAR γ +shFABP5+pcDHlncDBET+shMETTL14, shFABP5+pcDH-lncDBET+shMETTL14, pcDH-lncDBET+shMETTL14, pcDH-NC+shMETTL14 and pcDH-NC+shNC. Each experiment was repeated a minimum of three times. The symbol * denotes a significant difference ($P < 0.05$), while ** represents a highly significant difference ($P < 0.01$).



Supplementary Figure 4

(A-B) CCK8, Transwell, EdU and flow cytometry assays for the viability, migration, proliferation and apoptosis of J82 cell lines transfected with shPPAR γ +pcDH-FABP5+shlncDBET, pcDH-FABP5+shlncDBET, pcDH-NC+shlncDBET and pcDH-NC+shNC.

(C-D) CCK8, Transwell, EdU and flow cytometry assays for the viability, migration, proliferation and apoptosis of J82 cell lines transfected with pcDH PPAR γ +shFABP5+pcDHlncDBET+shMETTL14, shFABP5+pcDH-lncDBET+shMETTL14, pcDH-lncDBET+shMETTL14, pcDH-NC+shMETTL14 and pcDH-NC+shNC. Each experiment was repeated a minimum of three times. The symbol * denotes a significant difference ($P < 0.05$), while ** represents a highly significant difference ($P < 0.01$).

Table S1 List of downregulated m⁶A modification lncRNAs from BCa m⁶A-lncRNA epitranscriptomic microarray

| Transcript_ID | Gene Symbol | Fold change (log₂-Scaled) | P value |
|----------------------|--------------------|---|----------------|
| ENST00000508732 | CTD-2536I1.1 | -2.616439873 | 0.000113278 |
| ENST00000561237 | TRIM69 | -0.850194954 | 0.037153064 |
| ENST00000534036 | RP11-2C23.1 | -1.154659005 | 0.001560242 |
| NR_045034 | APH1A | -0.621146107 | 0.012592951 |
| ENST00000477018 | CAV2 | -0.723778742 | 0.00886292 |
| NR_136745 | PAK3 | -0.592850896 | 0.020527123 |
| ENST00000599078 | CTD-2561J22.4 | -1.30673788 | 0.005164194 |
| NR_146773 | PTCSC1 | -3.606802095 | 0.014489763 |
| ENST00000627173 | LINC00891 | -1.610547232 | 0.019553424 |
| ENST00000630918 | DBET | -0.763805515 | 0.024079093 |
| ENST00000529416 | RP11-839D17.3 | -0.62509301 | 0.049543692 |
| ENST00000433997 | RP11-92C4.3 | -0.921497551 | 0.032014116 |

Table S2 List of Hypo-up lncRNAs from BCa m⁶A-lncRNA & lncRNA expression microarray

| Track_ID | log₂FC.x | log₂FC.y | P value | quadrant |
|-----------------|----------------------------|----------------------------|----------------|-----------------|
| DBET | 1.4636469 | -0.7613579 | 0.024079 | Hypo-up |
| GS1-278J22.1 | 1.0886827 | -1.2239234 | 0.169692 | Hypo-up |
| RP11-109E24.1 | 1.4728784 | -1.0958627 | 0.096076 | Hypo-up |
| RP11-353N4.6 | 2.0519077 | -0.8417021 | 0.264051 | Hypo-up |
| RP11-84G21.1 | 0.9415275 | -0.5917865 | 0.161864 | Hypo-up |
| RP11-92C4.3 | 0.8763188 | -0.9187676 | 0.032014 | Hypo-up |

m⁶A-lncRNA epitranscriptomic microarray and lncRNA expression microarray of BCa Hypo, down-regulated m⁶A modification;
up, quantitatively over-expressed.

Table S3 Quantitative expression of the six downregulated m⁶A modification lncRNAs from TCGA database

| Gene symbol | log ₂ FC | P value | Significance (Y/N) |
|-------------|---------------------|----------|--------------------|
| APH1A | 0.558132 | 1.89e-04 | N |
| LINC00891 | -4.167203 | 1.70e-18 | Y |
| DBET | 2.821098 | 3.25e-04 | Y |
| TRIM69 | -0.510902 | 2.23e-02 | N |
| CAV2 | -0.390410 | 2.47e-01 | N |
| PAK3 | -0.830588 | 1.18e-01 | N |

TCGA-BLCA transcript reads count data and clinical data were downloaded using TCGA bio-links R package, and lncRNA transcripts were screened using lncRNA data provided by Gene code website. Y, yes; N, no.

Table S4 Predicted m⁶A sites of lncDBET based on *Cui Lab*

| Position | Sequence context | Score (combined) | Decision |
|----------|--------------------------|------------------|-----------------------|
| 1 276 | GUGAA AAAAU AAACU | 0.56 | m ⁶ A site |
| | GCAGU GGACA GGUCG | | (Low confidence) |
| | UAAGC CAGAC UUCAU | | |
| 2 292 | CAGUG GACAG GCUGU | 0.57 | m ⁶ A site |
| | AAGCC AGACU UCAUC | | (Moderate confidence) |
| | AAAUU UCUGC ACCAA | | |
| 3 366 | AAAAC CCUAU UAAAC | 0.61 | m ⁶ A site |
| | GUCAC GGACA AGGCC | | (High confidence) |
| | AGAGU UUGAA UAUAC | | |
| 4 1577 | UCUAG GUCCA GGCCG | 0.54 | m ⁶ A site |
| | GUGAG AGACU CCACA | | (Low confidence) |
| | CCGCG GAGAA CUGCC | | |
| 5 1594 | GAGAG ACUCC ACACC | 0.56 | m ⁶ A site |
| | GCGGA GAACU GCCAU | | (Moderate confidence) |
| | UCUUU CCUGG GCAUC | | |

Table S5 Analysis of candidate proteins binding to lncDBET based on ChIRP/MS

| Gene names | Score | log₂FC |
|-------------------|--------------|--------------------------|
| HRNR | 61.803 | 3.03212275 |
| POF1B | 28.942 | 2.06735177 |
| ALOX12B | 24.596 | 1.76272076 |
| FABP5 | 21.34 | 1.37605871 |
| FLG | 17.028 | 1.37605871 |
| SBSN | 13.415 | 1.37605871 |
| PRDX2 | 12.374 | 1.37605871 |
| HAL | 10.89 | 1.37605871 |

Table S6 The sequences of shRNAs

| Gene | Sequences |
|---------------|--|
| h-METTL14-1 | 5'- sense (5'-3') CCGGGGAACTCCCAACAGGATTTCCCTCGAGGGAAAT CCTGTTGGGAGTTCCTTTTTG-3' |
| | 5'- antisense (5'- 3') AATTCAAAAAGGAACTCCCAACAGGATTTCCCTCGAG GGAAATCCTGTTGGGAGTTCC-3' |
| h-shMETTL14-2 | 5'- sense (5'-3') CCGGGGATTTCTGTGGTGGAAAGGCTCGAGCCTTTC CACCACAGGAAATCCTTTTTG-3' |
| | 5'- antisense (5'- 3') AATTCAAAAAGGATTTCTGTGGTGGAAAGGCTCGAG CCTTCCACCACAGGAAATCC-3' |
| h-shMETTL14-3 | 5'- sense (5'-3') CCGGGTGGTGGAAAGGAAGCTTGTCTCGAGAACAA GCTTCCTTCCACCACTTTTTG-3' |
| | 5'- antisense (5'- 3') AATTCAAAAAGTGGTGGAAAGGAAGCTTGTCTCGA GAACAAGCTTCCTTCCACCAC-3' |
| h-shDBET-1 | 5'- sense (5'-3') CCGGGCTGTCTGTGGTATTGCAGTTCTCGAGAACTGC AATACCACAGACAGCTTTTTG-3' |
| | 5'- antisense (5'- 3') AATTCAAAAAGCTGTCTGTGGTATTGCAGTTCTCGAG AACTGCAATACCACAGACAGC3' |
| h-shDBET-2 | 5'- sense (5'-3') CCGGGCAGTTTCACTAGTGCTGTAGCTCGAGCTACAG CACTAGTGAAACTGCTTTTTG-3' |
| | 5'- antisense (5'- 3') AATTCAAAAAGCAGTTTCACTAGTGCTGTAGCTCGAG CTACAGCACTAGTGAAACTGC-3' |
| h-shDBET-3 | 5'- sense (5'-3') CCGGGCACTCCACATCAGGAGAGAACTCGAGTTCTCT CCTGATGTGGAGTGCTTTTTG-3' |
| | 5'- antisense (5'- 3') AATTCAAAAAGCACTCCACATCAGGAGAGAACTCGA GTTCTCTCCTGATGTGGAGTGC-3' |
| h-shFABP5-1 | 5'- sense (5'-3') CCGGGCATGACTCTGAGGAGTTATACTCGAGTATAAC TCCTCAGAGTCATGCTTTTTG-3' |

| | | |
|----------------------|-------------------|---|
| | antisense (5'-3') | 5'- AATTCAAAAAGCATGACTCTGAGGAGTTATACTCGAG TATAACTCCTCAGAGTCATGC-3' |
| | sense (5'-3') | 5'- CCGGGCTTCTCATCACTGAGTAAATCTCGAGATTTAC TCAGTGATGAGAAGCTTTTTTG-3' |
| h-shFABP5-2 | antisense (5'-3') | 5'- AATTCAAAAAGCTTCTCATCACTGAGTAAATCTCGAG ATTTACTCAGTGATGAGAAGC-3' |
| | sense (5'-3') | 5'- CCGGGCAGTATTCTCCCTCTCAATTCTCGAGAATTGA GAGGGAGAATACTGCTTTTTTG-3' |
| h-shFABP5-3 | antisense (5'-3') | 5'- AATTCAAAAAGCAGTATTCTCCCTCTCAATTCTCGAG AATTGAGAGGGAGAATACTGC-3' |
| | sense (5'-3') | 5'- CCGGGCCCGGCTCGGCCCGACCCGGCTCGAGCCGGGT CGGGCCGAGCCGGGCTTTTTTG-3' |
| h-shPPAR γ -1 | antisense (5'-3') | 5'- AATTCAAAAAGCCCGGCTCGGCCCGACCCGGCTCGA GCCGGGTCGGGCCGAGCCGGGC-3' |
| | sense (5'-3') | 5'- CCGGGCTCGGCCCGACCCGGCTCCGCTCGAGCGGAGC CGGGTCGGGCCGAGCTTTTTTG-3' |
| h-shPPAR γ -2 | antisense (5'-3') | 5'- AATTCAAAAAGCTCGGCCCGACCCGGCTCCGCTCGAG CGGAGCCGGGTCGGGCCGAGC-3' |
| | sense (5'-3') | 5'-CCGGGGGTCGGCCTCGAGGACACCGCTCGAG CGGTGTCCTCGAGGCCGACCTTTTTTG-3' |
| h-shPPAR γ -3 | antisense (5'-3') | 5'- AATTCAAAAAGGGTCGGCCTCGAGGACACCGCTCGA GCGGTGTCCTCGAGGCCGACCC-3' |

Table S7 Primers used in this study

| Gene | primer | Sequence |
|-------------------|---------------|---------------------------------|
| h-METTL3 | Forward | 5'- TTTTCCGGTTAGCCTTCGGG -3' |
| | Reverse | 5'- GATAGAGCTCCACGTGTCCG-3' |
| h-METTL14 | Forward | 5'- ACCTGGAAGAGTGTGTTTACGA -3' |
| | Reverse | 5'- TGTGAGCCAGCCTTTGTTCT-3' |
| h-WTAP | Forward | 5'- AAATCAACTCAGTGC GGGGT-3' |
| | Reverse | 5'- CGGGAACCCACAGTTCGATT-3' |
| h-FTO | Forward | 5'- GTCTCCCAGGTTGATAAGGCA-3' |
| | Reverse | 5'- GTTCGGGCAATTCGTGACTG-3' |
| h-ALKBH5 | Forward | 5'- AGTTCAGTCTTCTGCTCGCC-3' |
| | Reverse | 5'- AGGAACTGTGGACATGGCAG -3' |
| h-lncDBET | Forward | 5'- AAAGACCGGGACTCGGGTT -3' |
| | Reverse | 5'- CCACGCGGAAACCAAAATCA -3' |
| h-FABP5 | Forward | 5'- TGGCCAAGCCAGATTGTATCA-3' |
| | Reverse | 5'- CTGATGCTGAACCAATGCACC-3' |
| h-PPAR α | Forward | 5'- AAGCTGTCACCACAGTAGCTTG -3' |
| | Reverse | 5'- AACGAATCGCGTTGTGTGAC -3' |
| h-PPAR δ | Forward | 5'- TGACAGTGTGGGGAAGTGTC -3' |
| | Reverse | 5'- GATCCTGCATGCTCAGTCAGT -3' |
| h-PPAR γ | Forward | 5'- AGAAAACCAAGGGACCCGAA -3' |
| | Reverse | 5'- AGAGAGGGTCCCATTTCGA -3' |
| h- β -actin | Forward | 5'- CATTCCAAATATGAGATGCGTTGT-3' |
| | Reverse | 5'- TGTGGACTTGGGAGAGGACT-3' |