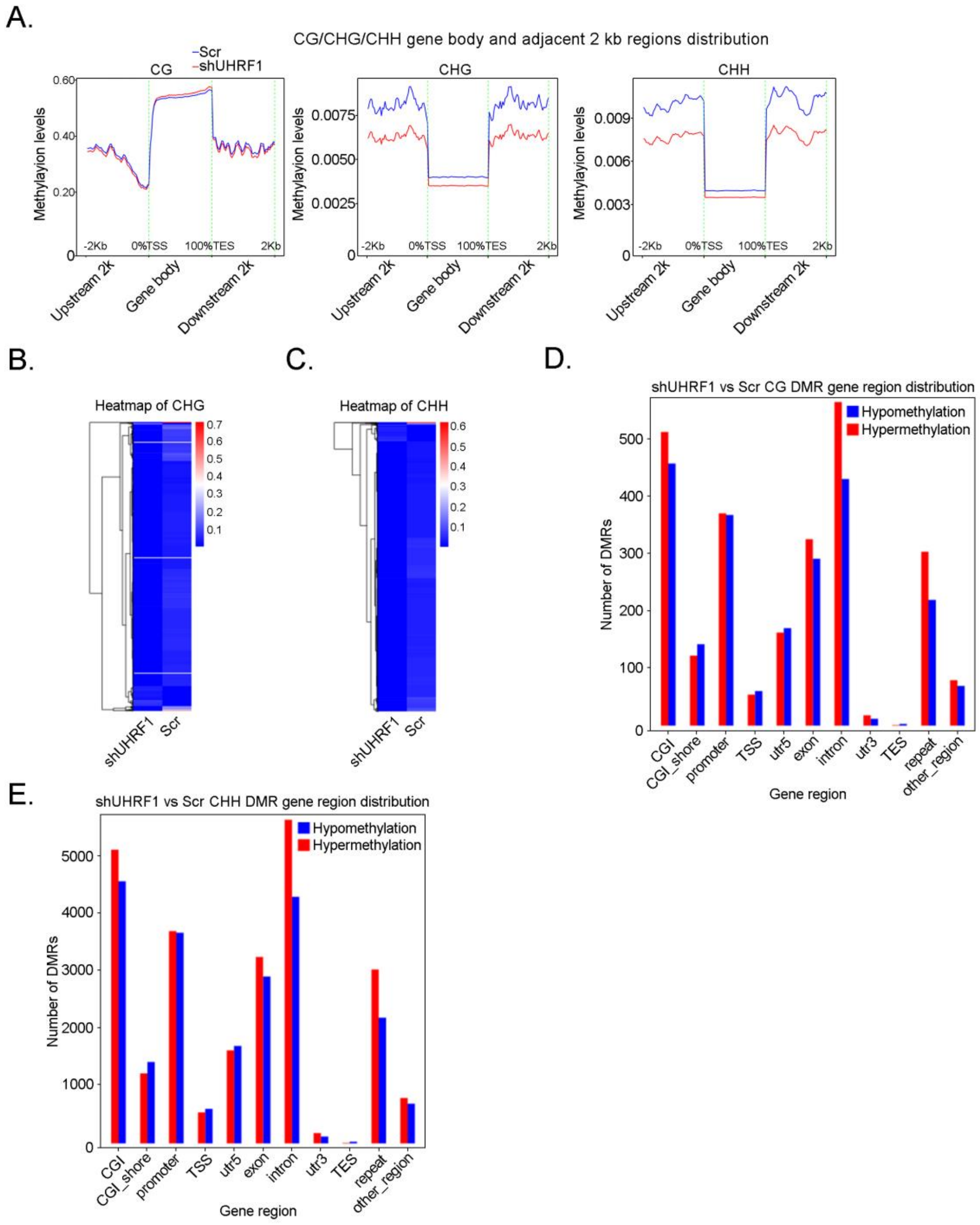
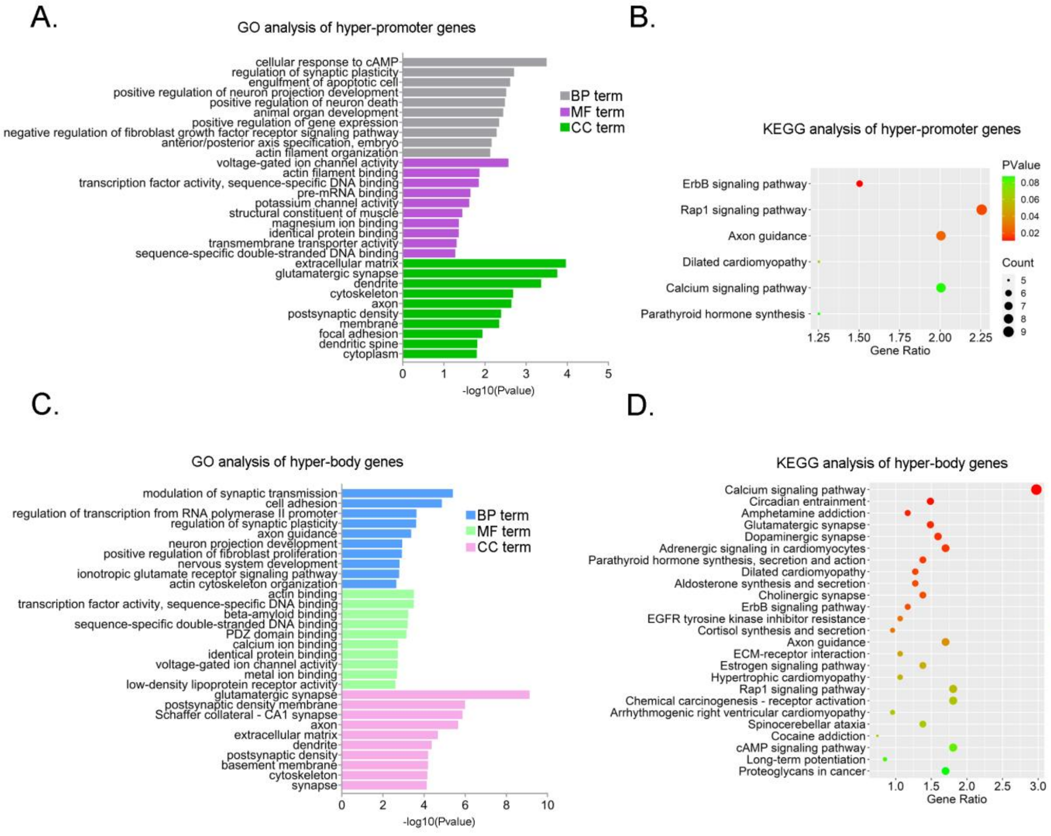
Supplementary Fig.1



Supplementary Fig. 1 CHG context and CHH context methylation characteristic analysis of UHRF1-shRNA and scramble MCF-7 cells. A methylation level of CG context, CHG context and CHH context in the gene body and adjacent 2 kb regions distribution are shown. TSS, transcription initiation site; TES, transcription termination site. B and C Cluster heatmap of the CHG (B) and CHH (C). D and E The CG (D) and CHH (E) context DMR gene region distribution.

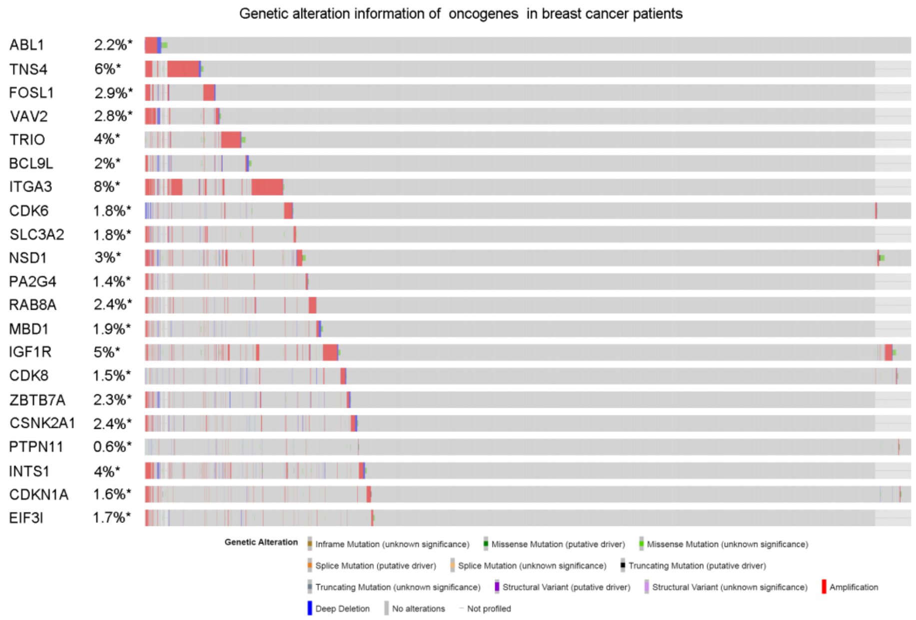
Supplementary Fig.2



Supplementary Fig. 2 GO and KEGG enrichment analysis of the hypermethylated promoters and hypermethylated gene bodies. A and B GO (A) and KEGG (B) enrichment analyses of the hypermethylated promoter genes are shown. C and D GO (C) and KEGG (D) enrichment analysis of the hypermethylated body genes.

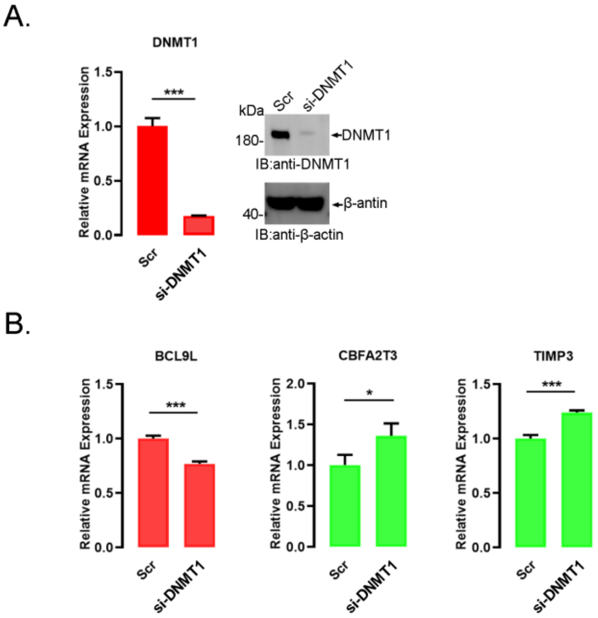
Supplementary Fig.3

A.



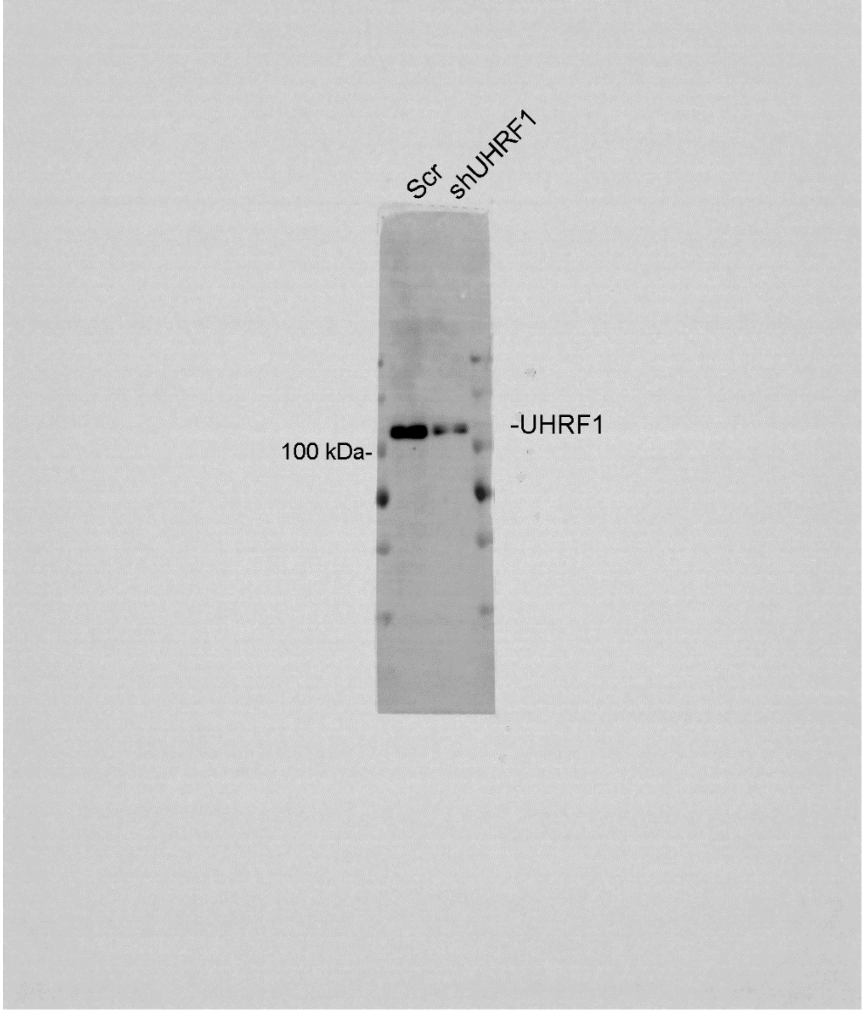
Supplementary Fig. 3 A visual summary of the oncogene genetic alterations in breast cancer patients using data from the cBio Cancer Genomics Portal.

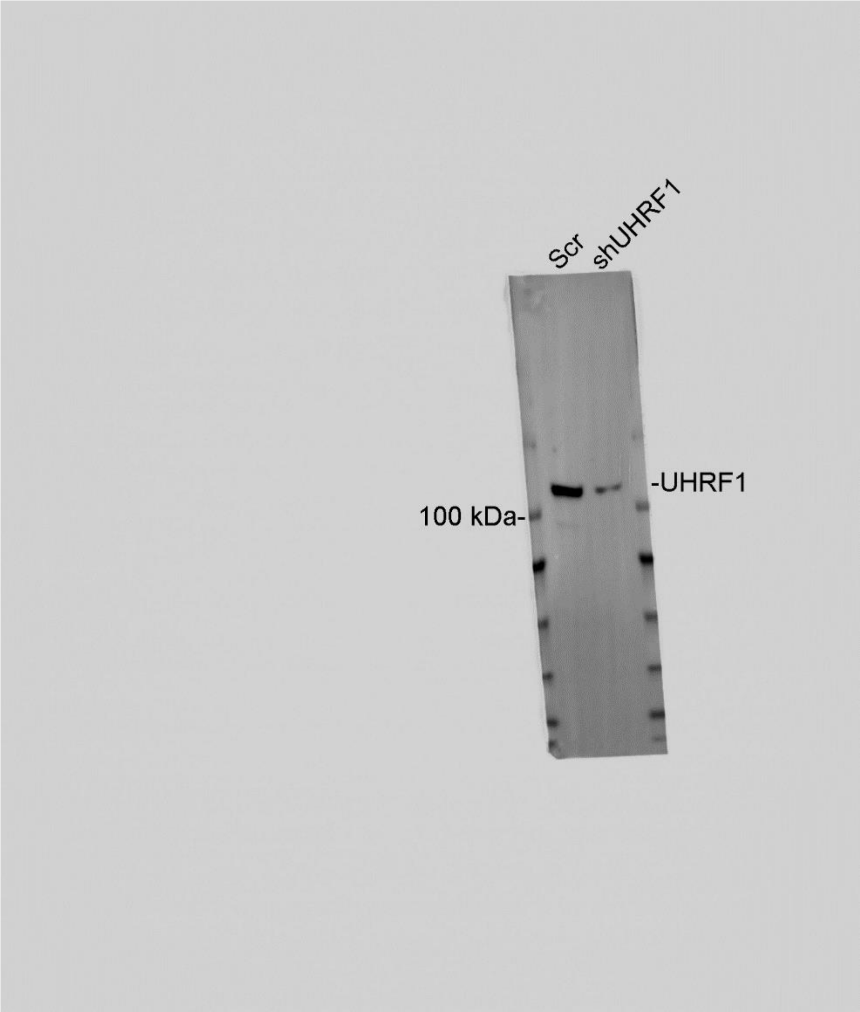
Supplementary Fig.4



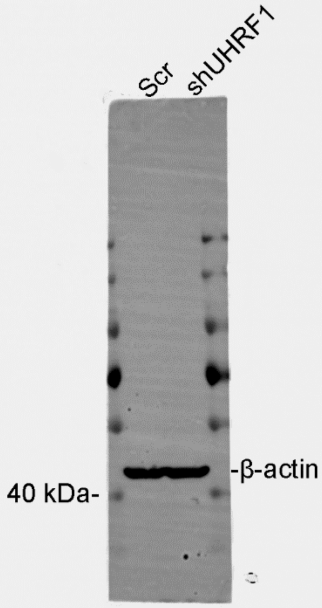
Supplementary Fig. 4 A MCF-7 cells were transfected with the DMNT1 siRNA or scramble siRNA (as a control) for 72 h and were analyzed by qRT–PCR (left) or immunoblotting (right). B qRT–PCR validation of the oncogene and TSGs. Red represents the oncogenes, and green represents the TSGs. The data are shown as the mean ± SD from three independent experiments. *p <0.05, ***p <0.01.

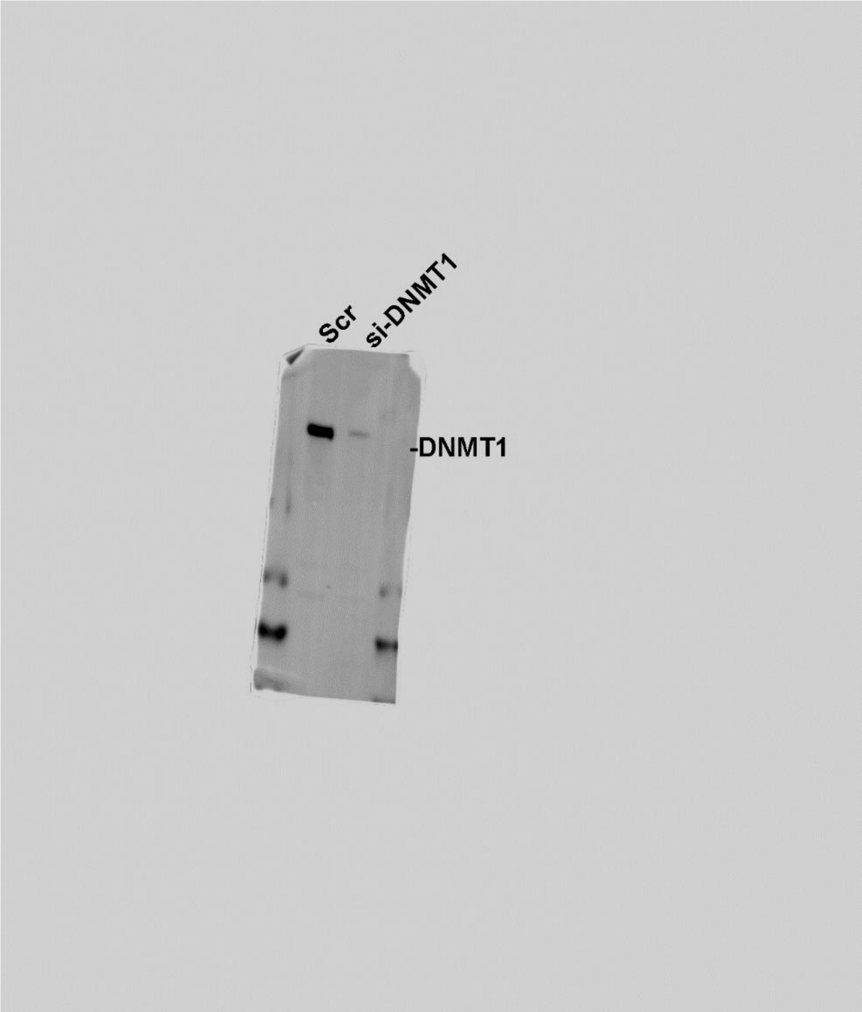
Supplementary Fig.5




Scr
shUHRF1
-UHRF1
100 kDa-


Scr
shUHRF1
40 kDa-
-β-actin
unrelated


Scr
shUHRF1
-β-actin
40 kDa-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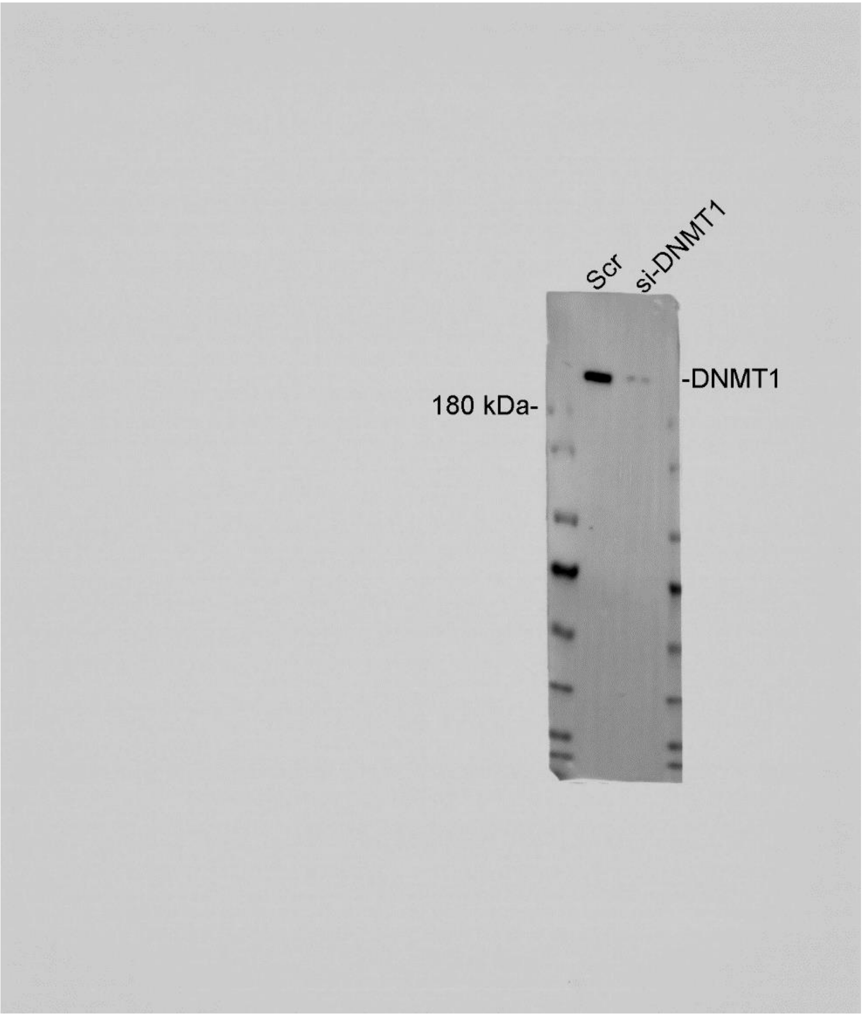
si-DNMT1
-DNMT1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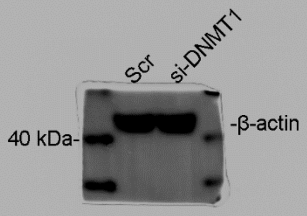
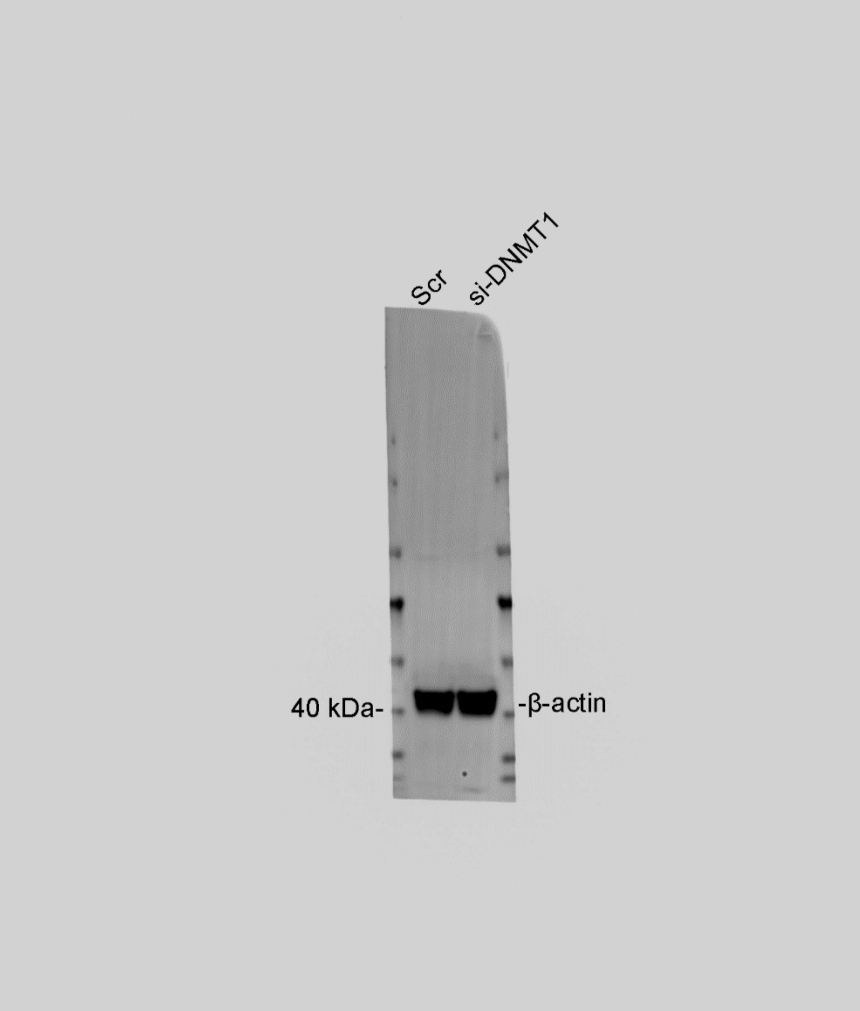
si-DNMT1
180 kDa-
-DNMT1


Scr
si-DNMT1
40 kDa-
-β-actin



Supplementary Fig.5 Full length Western blots showing protein levels of UHRF1, DNMT1 and β -actin. The gel was transferred to a membrane, and the membrane were cut prior to hybridisation with antibodies.

Supplementary Table 1

qRT–PCR primers used in this study:

primer sequence	amplicon size (bp)
UHRF1-F: 5’-GTCGGATCATCTTCGTGGAC-3’	310
UHRF1-R: 5’-AGTACCACCTCGCTGGCAT-3’	
PA2G4-F: 5’-CTGGTCGCTCTTCAAAGGGG-3’	474
PA2G4-R: 5’-CGGTACTGAGCCTGTGTGAG-3’	
EIF3I-F: 5’-ATGCGGACGTAACCATCTTC-3’	163
EIF3I-R: 5’-CCACAACTTCCACCAGGATT-3’	
VAV2-F: 5’-CTTTGTTCTGCGCGATGCT-3’	75
VAV2-R: 5’-TCGATGTGCGAGACTTTGGA-3’	
ABL1-F: 5’-GCCTAAGACCCGGAGCTTTTCA-3’	72
ABL1-R: 5’-TGTATGATTTTGTGGCCAGTGGAG-3’	
CDK6-F: 5’-AACTTCCACGAAAAAGAGGCTT-3’	132
CDK6-R: 5’-CCAGATGGCTCTAACCTCAGT-3’	
SLC3A2-F: 5’-GTCTTCCGCCACCTTGATCTT-3’	110
SLC3A2-R: 5’-TGAATGAGTTAGAGCCCGAGA-3’	
BCL9L-F: 5’-CAGTACAGGCAGCACAGAGAC-3’	159
BCL9L-R: 5’-CCACAGGCCAGCCTACTCTT-3’	
ZBTB7A-F: 5’-GTTCTTCAGGTCGTAGTTGTG-3’	134
ZBTB7A-R: 5’-AGTGCAACATCTGCAAGGTC-3’	

CBFA2T3-F:	5’-ACATCTGGAGGAAGGCTGAAGAG-3’	132
CBFA2T3-R:	5’-GCTCCATCTTGGCACGCT-3’	
PPP2R1B-F:	5’-CAGCTGGGTGTGGAATTCTT-3’	199
PPP2R1B-R:	5’-GTTGTTGGTGGCAGCTTCTC-3’	
TGFB1-F:	5’-AGGCTCCAAATATAGGGGCAGGGTC-3’	156
TGFB1-R:	5’-GGATACCAACTATTGCTTCAGCTCC-3’	
TIMP3-F:	5’-TGCTCTCTGTCTCTTTTTTCAGCTT-3’	142
TIMP3-R:	5’-CTACAGTGTGTTGTCTGCTGCTTTT-3’	
DNMT3A-F:	5’-CAATAATCTCCTTGACCTTGG-3’	115
DNMT3A-R:	5’-GAAGAGAAGAATCCCTACAAAG-3’	
PRKCD-F:	5’-CCCTGTTTCACCAATCCCCA-3’	88
PRKCD-R:	5’-TGCCTCACCGATTCAAGGTC-3’	
LRP1B-F:	5’-CCAAGAGGACGAGAGGCACA-3’	72
LRP1B-R:	5’-CCCCAAAGAGCAGCAAGTCT-3’	
FAM172A-F:	5’-AGAGCCTCGTATCTTTTCTGGT-3’	133
FAM172A-R:	5’-TGAACCGCCTCTTGATTTTCC-3’	
DNMT1-F:	5’-CCATCAGGCATTCTACCA-3’	132
DNMT1-R:	5’-CGTTCTCCTTGTCTTCTCT-3’	
GAPDH-F:	5’-GGCTGTTGTCATACTTCTCATGG-3’	197
GAPDH-R:	5’-GGAGCGAGATCCCTCCAAAAT-3’	

siRNA sequence:

si-DNMT1 sense: 5’-CAAUGAGACUGACAUCAAA-3’ si-DNMT1 antisense: 5’-GUUACUCUGACUGUAGUUU-3’