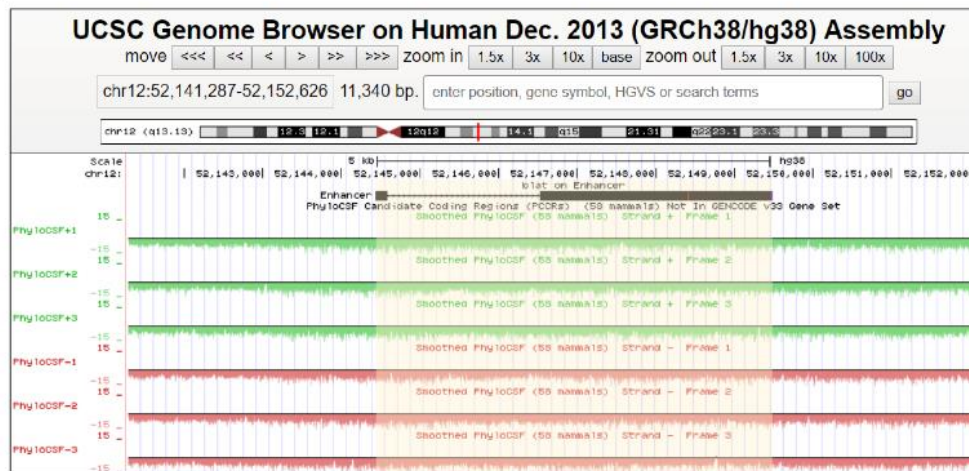


Figure S1.

A

ID	C/NC	CODING POTENTIAL SCORE	EVIDENCE	UTR-DB HITS	RNA-DB HITS
enhancer	noncoding (weak)	-0.587351	detail	search	search

B

C

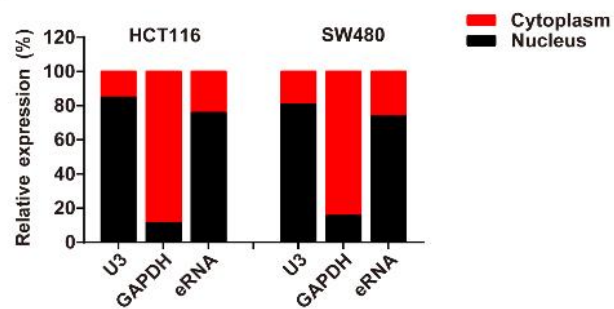


Figure S2.

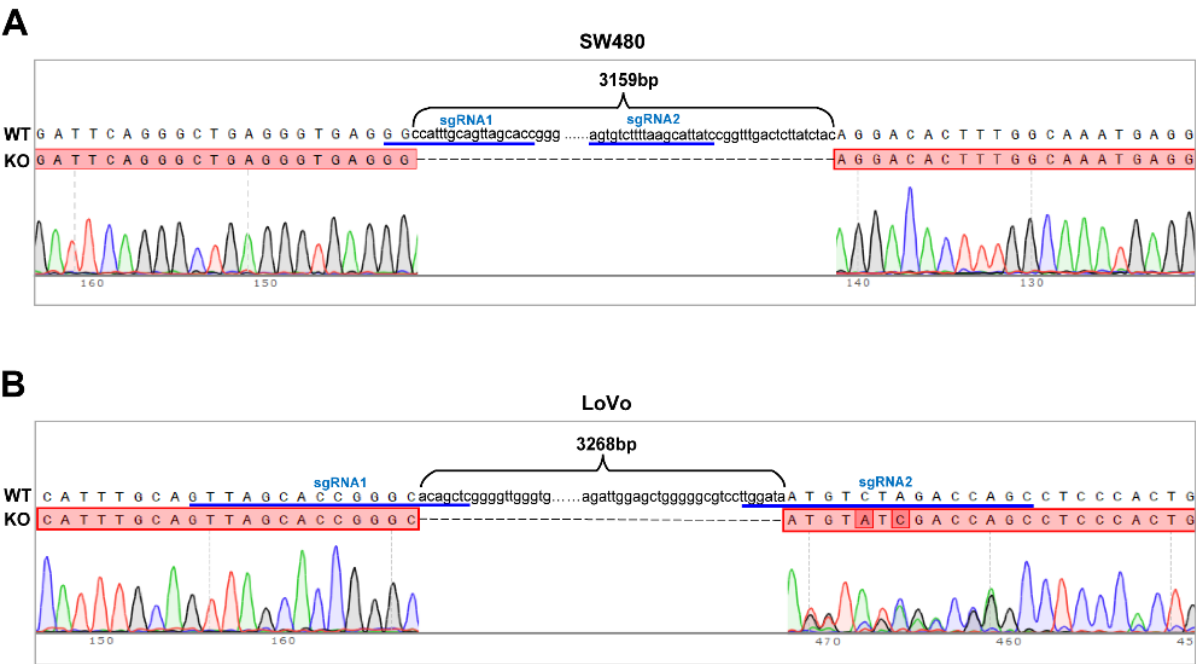
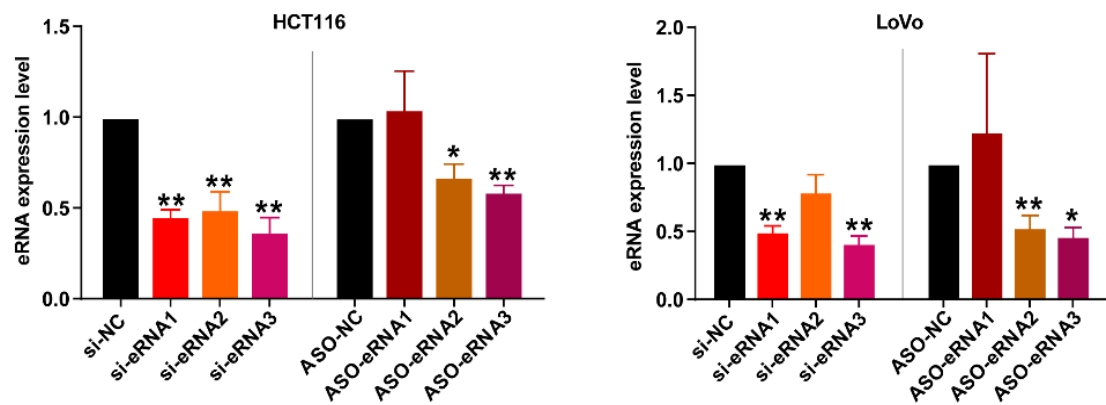


Figure S3

A



B

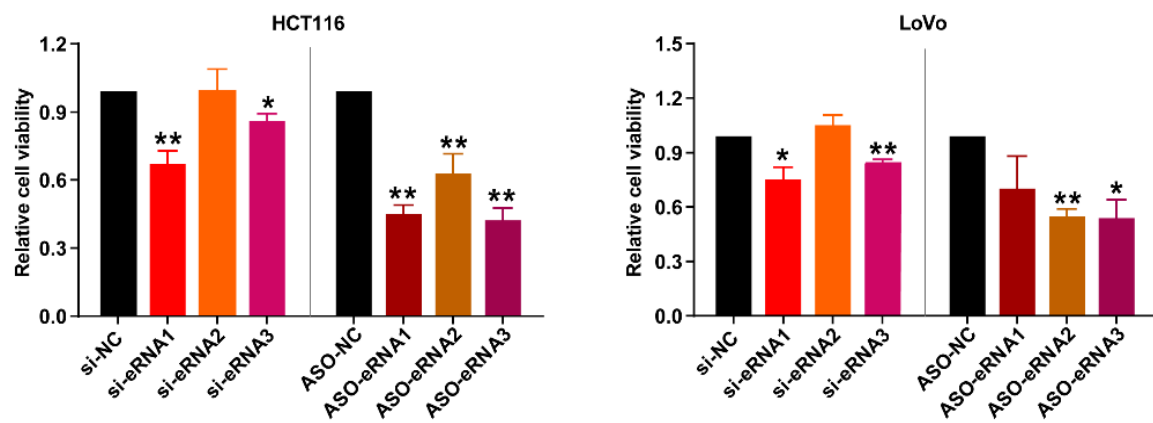


Figure S4

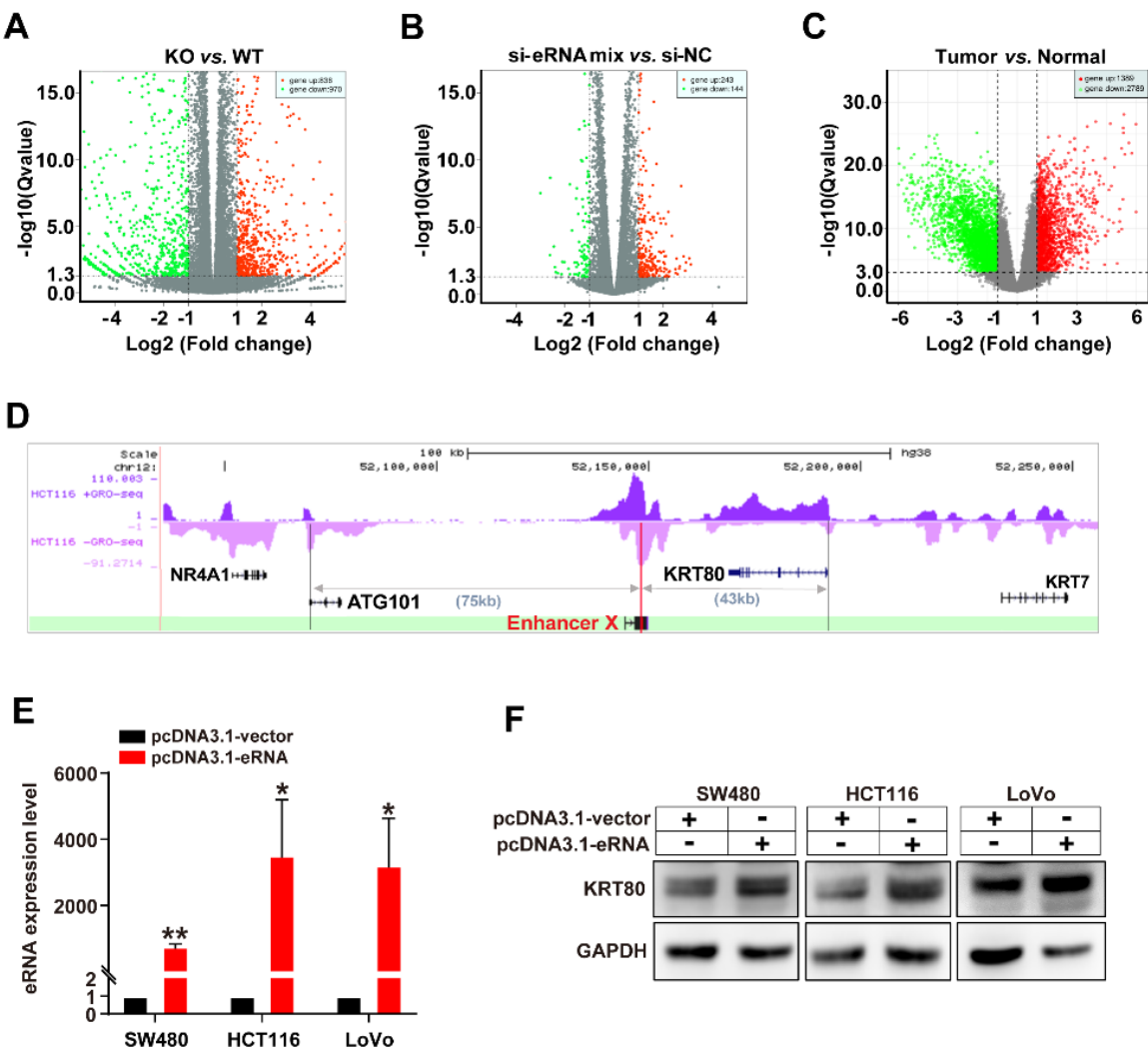


Figure S5

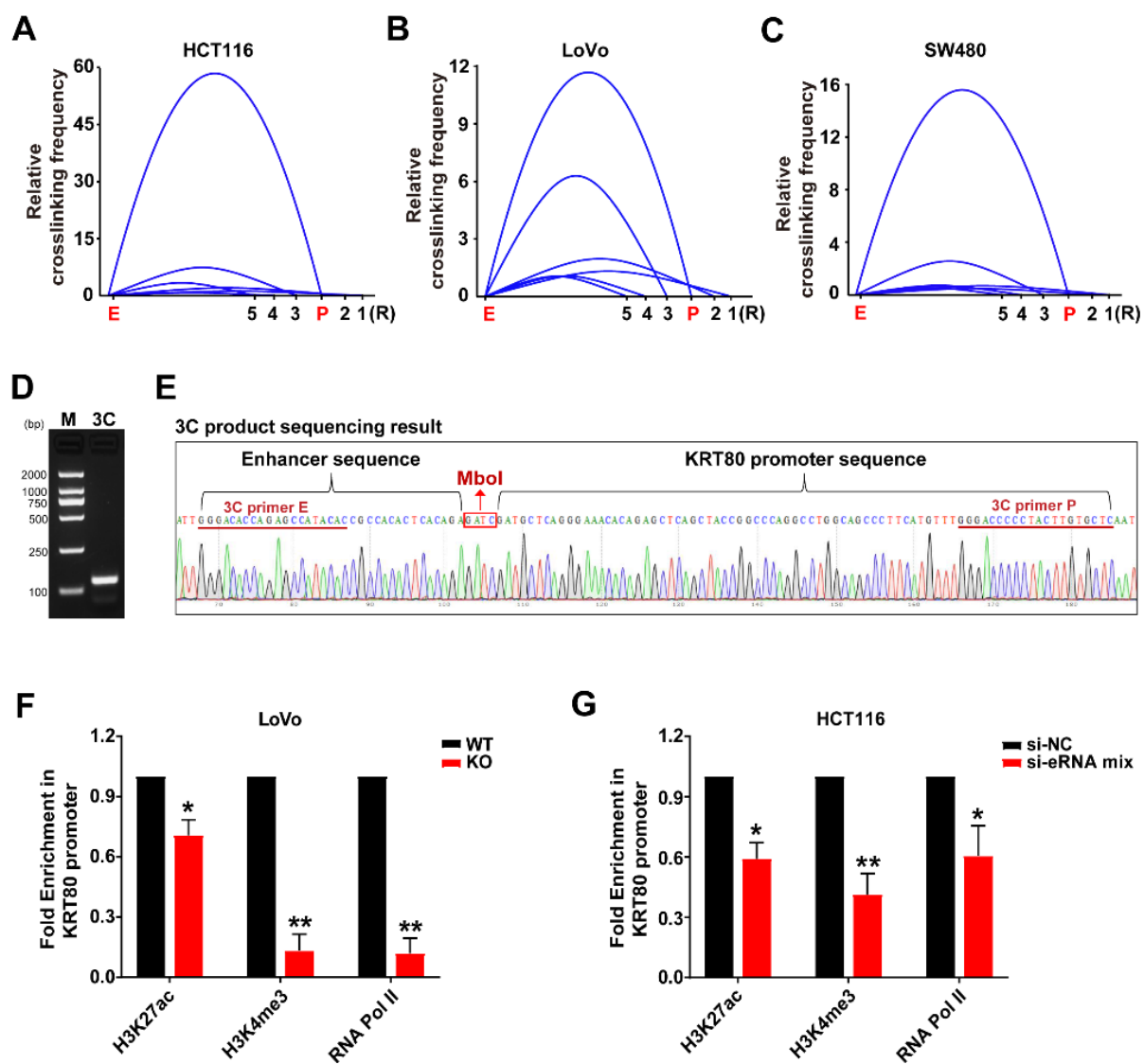
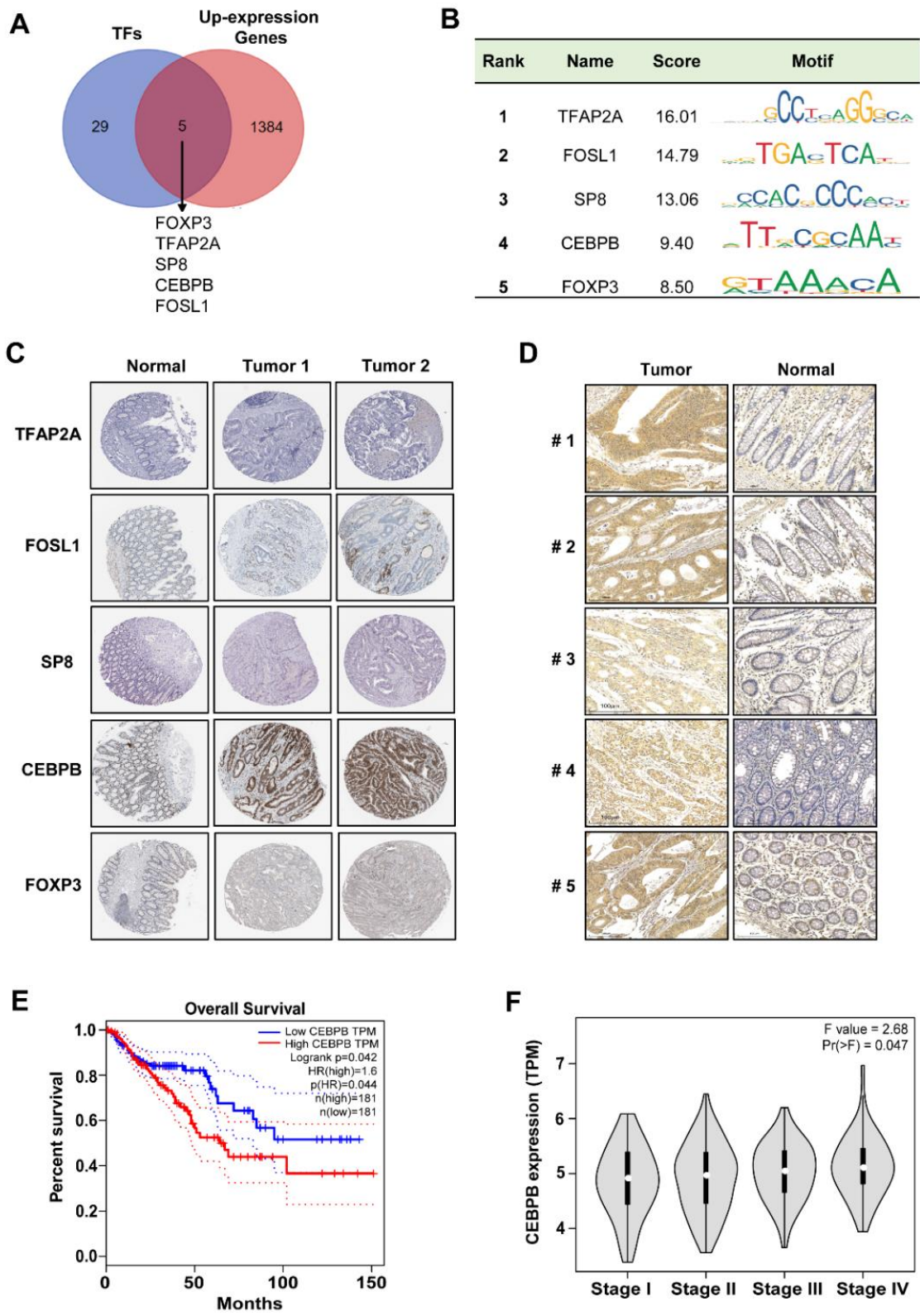


Figure S6



Supplementary tables

Table S1. Data for ChIP-seq downloaded from the GEO datasets.

No.	Dataset	Antibody	Sample type
1	GSM2698631	H3K27ac	Colon tissue
2	GSM883681	H3K27ac	Colon cancer tissue
3	GSM2532777	H3K27ac	SW480
4	GSM1224664	H3K27ac	HCT116
5	GSM2700616	H3K4me1	Colon tissue
6	GSM883659	H3K4me1	Colon cancer tissue
7	GSM2746535	H3K4me1	SW480
8	GSM2809622	H3K4me1	HCT116
9	GSM2701778	H3K4me3	Colon tissue
10	GSM883688	H3K4me3	Colon cancer tissue
11	GSM621673	H3K27me3	Colon tissue
12	GSM2459947	H3K27me3	Colon cancer tissue
13	GSM1010852	CEBPB	HCT116
14	GSM1208598	CEBPB	LoVo

Table S2. Primer and probe sequences used in real-time RT-PCR, si-RNA(ASO), ChIP, RACE, CRISPR/Cas9, 3C, and ChIRP.

Assay	Primer Sequence (sense 5' - 3')	Primer Sequence (antisense 5' - 3')
Real time RT-PCR		
β-actin	CTGGAACGGTGAAGGTGACA	AAGGGACTTCCTGTAACAATGCA
eRNA-primer1	TGACAGCAATAGCGGTCTGG	TCCATCCCTGGAGAGTCTGG
eRNA-primer2	ATGTGCCATCTGTCCAAACTG	GTGTCCGCATCTGTAAAGTGG
eRNA-primer3	CTCCAAGGGCGTAGTCTCAG	TGCTTCCCTGGAACAGAGAT
KRT80	CCTCCCTAATTGGCAAGGTG	AGATGCCCCGAGGTCTGAAGAT
ATG101	TTCATCGACTTCACTTATGTGCG	GATGCACTCGTCTGAGAATGG
CEBPB	CTTCAGCCCGTACCTGGAG	GGAGAGGAAGTCGTGGTGC
GAPDH	GCTCTCTGCTCCTCCTGTTC	ACGACCAAATCCGTTGACTC
U3 snoRNA	CCACGAGGAAGAGAGGTAGC	CACTCAGACCGCGTTCTCTC
si-RNA (ASO)		
eRNA ASO1	GAGACATTCCCAAGAAGCTC	
ASO2	CTTCCTAAGCCTGAACCTTC	
ASO3	GTCCCTCCACTTACAAACAC	
siRNA1	TGTGAGACATTCCCAAGAA	
siRNA2	GCACCTTATTAGGTAAGAA	
siRNA3	GCCTGAACCTTCTCTTCTA	
CEBPB siRNA1	CCATGGAAGTGGCCAACCT	
siRNA2	CACAGCGACGAGTACAAGA	
siRNA3	TGCGGAACCTGTTCAAGCA	
ChIP-qPCR		
Enhancer	TCAACCCAGACTGAGCCA	CCACAGTGAGGAAACCGA
Enhancer-NC	AAAATGCAGGAGTGGTGGTC	AGCATGGCAGTTGCAATTGC
KRT80	ACGTCAGCCTTCAAGTATGC	AAAGGAAGGCCATTCAAGGG
CEBPB-site1	GACGCTCCCCTTGTAGGAAA	AGACCGCTATTGCTGTCTAGG
CEBPB-site2	CCACTTCAGTCCAGCTCACC	CCCAGAGAAAGCAGGTCAGG
CEBPB-NC1	GTTACCCTGAAGGGTTGGGG	CTTCCACCAGTCCAGACACC
CEBPB-NC2	ACCCCTACAAGTCTTGCCA	CCCACTTGTGCTCAGACTGC
RACE		
3'-RACE F1	CCTTGCTCCAAACCCAGAGCTTGCC	
3'-RACE F2	CCAGGGCAGGTCAGTCAGTTTCCAGG	
5'-RACE R1	GTCTCTACAAGGCCCATTTGCTGTA	
5'-RACE R2	CCTGGAAACTGACTGACCTGCCCTGG	
CRISPR/Cas9 for Enhancer X KO		
SW480 sgRNA1	GGCCATTTGCAGTTAGCACC	
sgRNA2	GATAATGCTTAAAAGACACT	
genotyping	AGGGTCAGAGCTGGGGTTT	GGCAGGATCCTGGGCTCTAG
LoVo sgRNA1	GTTAGCACCGGGCACAGCTC	
sgRNA2	GCTGGTCTAGACATTATCCA	
genotyping	GGGTCAGAGCTGGGGTTTAG	GATACTGGGGGATTCCCTGAGC
CRISPR/Cas9 for CEBPB mut		
sgRNA1	TGGGGCCAGATCTTCCCATGGGG	
sgRNA2	GTTGTGTCAGTGTCCCTCCCAGG	
Genotyping	GGGACACCAGAGCCATACAC	CCAACACCCGGTATAAGCCA
3C-qPCR		
E	GGGACACCAGAGCCATACAC	
P	GAGCACAAGTAGGGGGTCC	
F1	AACTTGTCACTGGAATTAGGTCC	
F2	GTTTTTTTTGTGGAGCGGAGCC	

F3	CTTCCCAGCCCCTTGGTC	
F4	ATCTGTTGAGAGAGTGATACCTGC	
F5	AGCATCTACTAAGTGCCAGGTC	
F6	TTACAGCACTCTGGGAGGC	
F7	ACAGACACCTGTTCTGCTTTG	
R1	AGCATATAGAAGGATGGGGAGGG	
R2	CGGGAAGCTGAAGCGGGA	
R3	TGGCCTCCATTGCCTCCT	
R4	CCTGGGGCTAAGACAAACAAATG	
R5	CAGGAGGCCCTGATACTCTAGT	
B2M	CTTGGGTCCCAGACTCTGC	TATTAAGACAGGGAAGTAGAGGAGG
ChIRP		
eRNA probe1	TCCCTGGTGAAATCTTGTCT	
eRNA probe2	ATAGCTGAGAGCAACCCACA	
eRNA probe3	AGACAAGGACCCAGAGTGAG	
eRNA probe4	TCCGTCACCTCTCAAATGTGG	
eRNA probe5	TCCGCATCTGTAAAGTGGGA	
eRNA probe6	CTCAAACAGCTTCTGACAAA	

Table S3. The amplify loci used in dual-luciferase reporter assay.

Plasmid	Inserted sequences	Inserted site
pGL4.1-basic vector		
pGL4.1-KRT80-promoter-Luc	chr12:52192015-52194014	XhoI-HindIII
pGL4.1-KRT80-promoter-Luc-Enhancer (+)	chr12:52146477-52149476(+)	BamHI-SalI
pGL4.1-KRT80 promoter-Luc-Enhancer (-)	chr12:52146477-52149476(-)	BamHI-SalI
pGL4.1-ATG101-promoter-Luc	chr12:52067974-52069973	XhoI-HindIII
pGL4.1-ATG101-promoter-Luc-Enhancer (+)	chr12:52146477-52149476(+)	BamHI-SalI
pGL4.1-ATG101-promoter-Luc-Enhancer (-)	chr12:52146477-52149476(-)	BamHI-SalI

Table S4. Correlation between the expression of EX-eRNA and clinicopathological features in CRC.

Variables	Categorization	eRNA expression		X^2	P value
		Low	High		
Age					
	≤60 years	13	10	0.751	0.386
	> 60 years	11	14		
Sex					
	Male	10	18	5.486	0.019
	Female	14	6		
Distant metastasis					
	M0	22	16	4.547	0.033
	M1	2	8		
Lymph node metastasis					
	N0	18	11	4.269	0.039
	N1	6	13		
Tumor invasion					
	T1-2	3	3	0	0.667
	T3-4	21	21		
Pathologic Stage					
	I-II	22	17	3.419	0.064
	III-IV	2	7		

Table S5. The potential transcription factors binding to the enhancer region were predicted using PROMO and UCSC database.

Database	Transcription factor					
PROMO	CEBPB	ESR1	PAX5	P53	NR3C1	TFAP2A
	GATA1	NR2B1	STAT4	FOXP3	SRY	SP1
	YY1	XBP1	ETS1	GTF2I	JUN	PGR
UCSC	KLF16	SP3	PBX3	GLI2	RELB	FOSL1
	FOSL2	JUNB	NEUROD1	KLF9	ESR2	
	RREB1	SP2	SP1	KLF5	ZFX	SP8