

Figure S1. circMVP expression in CRC

(A) Heatmap plot of differentially expressed circRNAs from transcriptome analysis of colorectal cancer tissues (3) and paired adjacent normal tissues. **(B)** Information and molecular predictions of CircMVP (hsa_circ_0000688) included in CSCD (Cancer-Specific CircRNA Database). **(C)** Combining PCR with an electrophoresis assay indicated the presence of circMVP using divergent and convergent primers from cDNA or genomic DNA (gDNA) in DLD1, HCT8 and HCT116 cells. **(D)** The expression level of circMVP in CRC cell line (DLD1, HCT8, HCT116, RKO) and 293T were detected by separation of nucleus and cytoplasm and qRT-PCR. **(E)** Expression of circMVP was examined by ISH in normal epithelial tissues (n=46) and CRC tissues (n=46), (Student's t-test; log-rank test). **(F)** Features plot showed distribution and expression levels of circMVP and its hostgene: MVP. **(G)** CircMVP knockdown and overexpression cell models were constructed in DLD-1 and HCT8 cells, respectively, and transfection effect was verified by qRT-PCR. Data were presented as mean±SD. *p<0.05; **p<0.01; ***p<0.001(Student's t-test; log-rank test). CRC, colorectal cancer; ISH, *in situ* hybridization.

Figure S2. CircMVP facilitates CRC growth

(A) The effects of circMVP on cell proliferation in HCT116 and RKO. **(B and C)** Transwell-matrigel was used to detect the effect of circMVP on the invasion ability of cancer cells. Scale bars, 300 µm. **(D and E)** Transwell was used to detect the effect of circMVP on the migration ability of cancer cells. Scale bars, 300 µm. **(F)** The expression of circMVP in mouse cell lines (B16, BMDM, MC38, 4T1 and CT26) was detected by PCR and analyzed by gel electrophoresis. **(G)** The effects of circMVP on cell proliferation in MC38. **(H and I)** Transwell-matrigel and transwell were used to detect the effect of circMVP on the invasion and migration ability of MC38. Scale bars, 300 µm. **(J)** Pathological section and Spatial transcriptome MVP in the CRC samples from PRJNA942633. Each dot was a cell colored by its analyzed cell types. Data are presented as mean±SD. *p<0.05; **p<0.01; ***p<0.001(Student's t-test; log-rank test). CRC, colorectal cancer.

Figure S3. CircMVP interacts with METTL3

(A) The proteins enriched by circMVP RNA pull-down were obtained with 40kDa-72kDa specific

differential expression bands, and the METTL3 protein was found by MS analysis, peak map and proteins abundance table were displayed. **(B)** RNA-EMSA was used to detect the binding between circMVP and METTL3 protein. **(C)** CircMVP expression inhibited the ubiquitin modification of METTL1. HCT8 cells were transfected with circMVP or METTL3 and treated with MG132 (20 mmol/mL) for 3 hours, the binding ubiquitin level was detected. **(D, E, F and G)** The combination of METTL3 and circMVP was detected by RIP, and the fluorescence signal of RNA was obtained by PCR amplification and then gel electrophoresis to identify the specificity of circMVP, respectively in DLD1, 293T, HCT8 and MC38. **(H)** The protein levels of METTL1 were measured in si-circMVP DLD1 cells by Western blot. Cells were treated with CHX (50 µg/mL) for 3 hours. MS, Mass spectrum.

Figure S4. CircMVP/METTL3/β-catenin regulates B7-H3 expression

(A) Transcriptome analysis differentially expressed genes in HCT8-circMVP compared with HCT8-NC in scatter plot. **(B)** KEGG demonstrated the β-catenin signaling pathway (<https://www.kegg.jp/pathway/map04310>). **(C)** GSEA plot demonstrated the Wnt/β-catenin signaling pathway in HCT8-circMVP and HCT8-NC. **(D and E)** SRAMP predicted the sites and confidence intervals of Homo sapiens (CTNNB1) and mouse (Ctnnb1) mRNA modified by m6A, respectively (<http://www.cuilab.cn/sramp>). **(F)** Transcriptome of RNAseq analysis of basic expression levels of Ctnnb1 in mouse cell lines (GEO: GSE18398) and expression of β-catenin protein in mouse cell lines (B16, BMDM, MC38, 4T1 and CT26) was detected by PCR. **(G and H)** Transcriptome and qRT-PCT were used to analyze the effect of circMVP on downstream regulatory gene expression of β-catenin signaling pathway. **(I)** The effect of circMVP/METTL3 regulation on CTNNB1 transcription level was detected by qRT-PCR. KEGG, Kyoto Encyclopedia of Genes and Genomes; GSEA, Gene Set EnrichmentAnalysis; SRAMP, sequence-based RNA adenosine methylation site predictor.

Figure S5. Single cell sequencing of CircMVP MC38 mouse tumor model

(A) UMAP plot showed the clusters of scRNA-seq in tumor tissue of MC38 cells (NC vs. circMVP). Each dot is a cell colored by its analyzed cell types. **(B)** Feature plots showed tumor Epithelial cell signatures (Grb2 and Krt14) transcript levels in MC38-NC and MC38-circMVP. **(C)**

and D) Violin plots showed tumor Immune checkpoint signatures transcript levels in MC38-NC and MC38-circMVP. **(E)** GO pathway enrichment terms of the differentially expressed genes in CD8+ T cells of MC38-circMVP compared with CD8+ T cells of MC38-NC. **(F)** scRNA sequencing analysis. The expression levels of NK cells function markers Klrd1, Gzmb and Tigit infiltrated by MC38-circMVP were compared with those of MC38-NC. **(G)** The expression levels of CD276 in MC38-circMVP was compared with those of MC38-NC. **(H)** scRNA sequencing analysis. The expression levels of Mettl3 and Tthdf1 by MC38-circMVP were compared with those of MC38-NC. UMAP, Uniform Manifold Approximation and Projection; TAM,Tumor-associated macrophages; GO, Gene ontology.

Figure S6. β -catenin expression, METTL3 and B7-H3 survival analysis

(A) qRT-PCT were used to analyze the effect of circMVP on downstream regulatory gene expression of CD276; ChIP-seq analysis of β -catenin acts on heat maps of CD276 chromatin Peak distribution upstream and downstream of TSS. **(B)** Expression of circMVP in in vivo tumorigenic tissue detected by ISH. **(C)** IGV tracks showing m6A peaks distribution on CD276 transcript from MeRIP-seq data in PRJNA927821. **(D)** Expression of β -catenin proteins detected by IHC in CRC tissue. Scale bar, 60 μ m. **(E)** Kaplan-Meier survival plots for the correlation between the expression of METTL3, high= 50 and low = 112 with the overall survival (OS) in patients. **(F)** Kaplan-Meier survival plots for the correlation between the expression of B7-H3, high= 82 and low = 80 with the overall survival (OS) in patients. ChIP, Chromatin immunoprecipitation; TSS, Transcription start site.

Figure S1

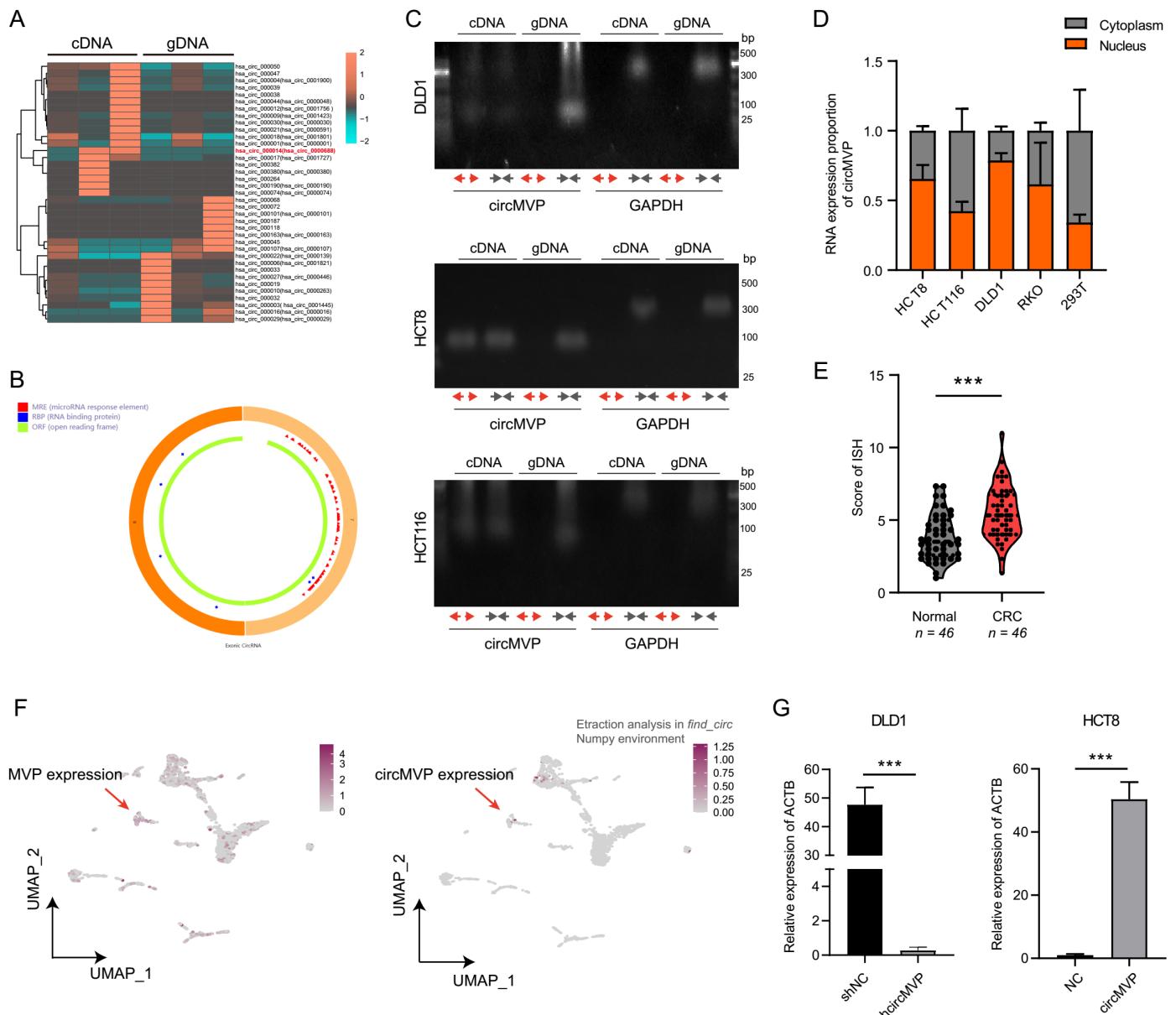


Figure S2

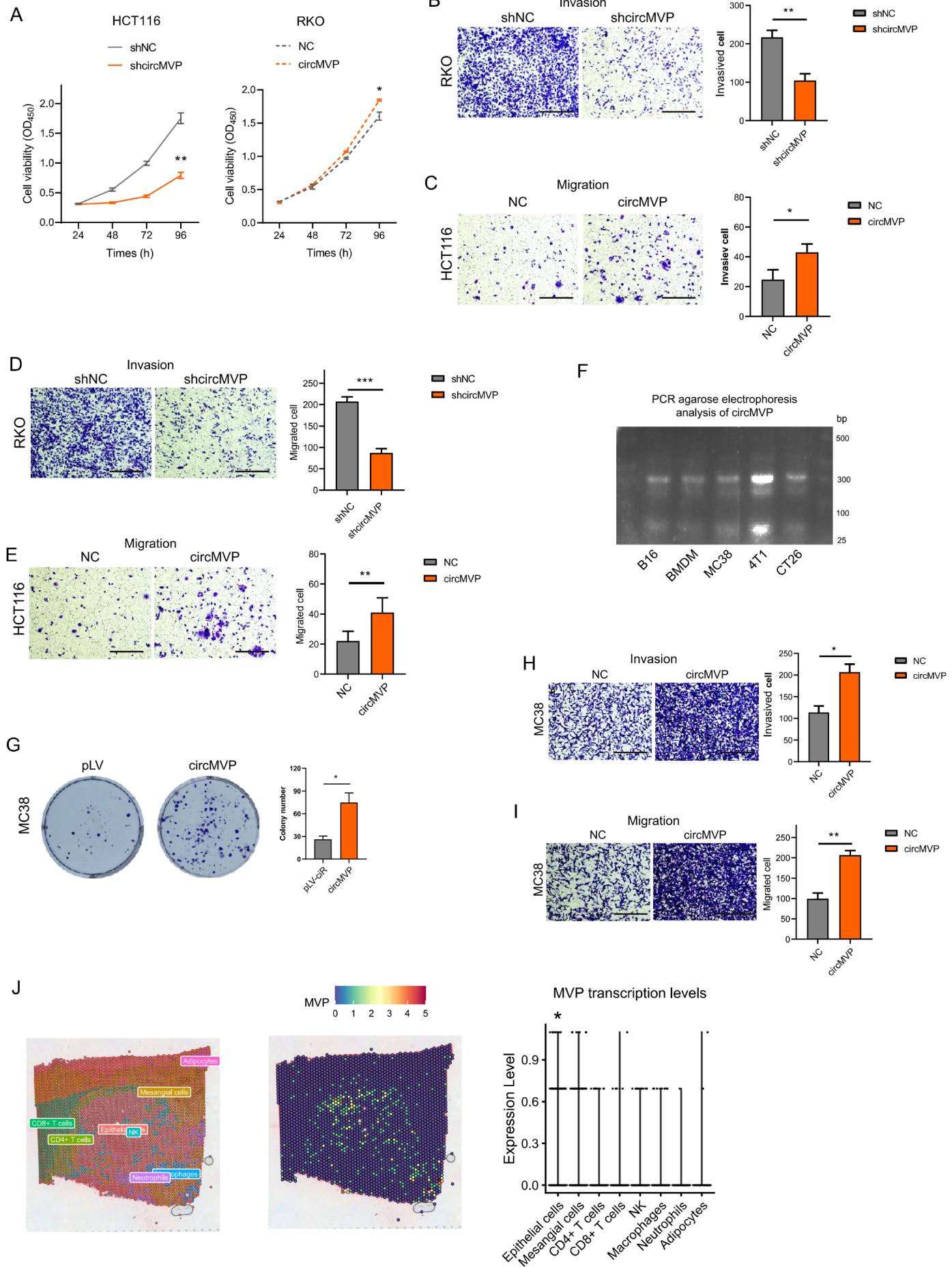
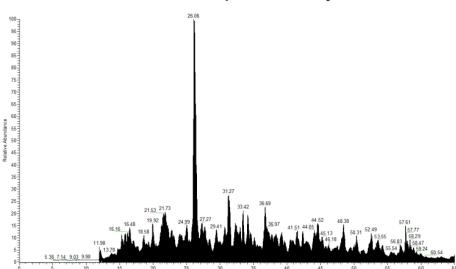


Figure S3

A

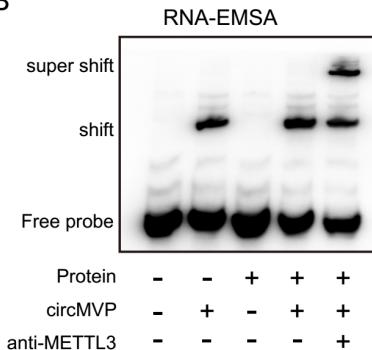
Proteins detected by circMVP Pull-down
Mass spectrometry



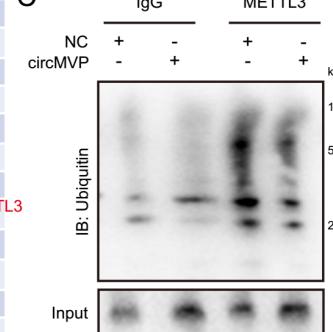
TOP15 proteins in MS

Protein FDR	Accession	Sum PEP Score	AAs	Molecular Function	Abundances
High	P35908	281.966	639	bone, tooth or skin structural activity;cytoskeletal activity	2571029694
High	P13645	279.866	584	bone, tooth or skin structural activity;other molecular function	4546927467
High	P68104	259.243	462	nucleic acid binding activity;other molecular function	9089267112
High	Q9UHB6	252.745	759	cytoskeletal activity;other molecular function	4591731775
High	P04264	247.527	644	bone, tooth or skin structural activity;other molecular function	6122395367
High	Q9Y5B9	235.682	1047	other molecular function	983139816.6
High	P19338	234.339	710	nucleic acid binding activity;other molecular function	15911389082
High	Q86U44	218.733	580	mRNA (2'-O-methyladenosine-N6)-methyltransferase activity; mRNA binding;other molecular function	356360533.1
High	P09429	213.081	215	signal transduction activity or receptor binding;nucleic acid binding activity;other molecular function	8005659883
High	P13639	209.514	858	translation activity;nucleic acid binding activity;other molecular function	812448307.4
High	Q9BUF5	205.62	446	cytoskeletal activity;other molecular function	101169641.3
High	P07355	197.655	339	transporter activity;enzyme regulator	1885017542
High	P35527	193.723	623	activity;cytoskeletal activity;other molecular function	1475197347
High	P14618	191.383	531	nucleic acid binding activity;kinase activity;other molecular function	726779818.3
High	P02545	179.879	664	cytoskeletal activity;other molecular function	792568860.1

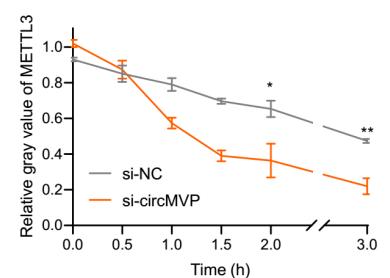
B



C

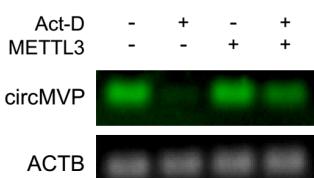


D

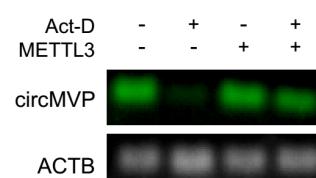


E

DLD1

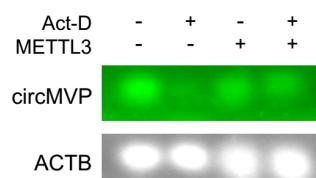


293T



G

HCT8



H

MC38

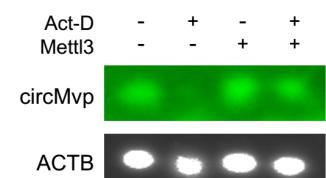


Figure S4

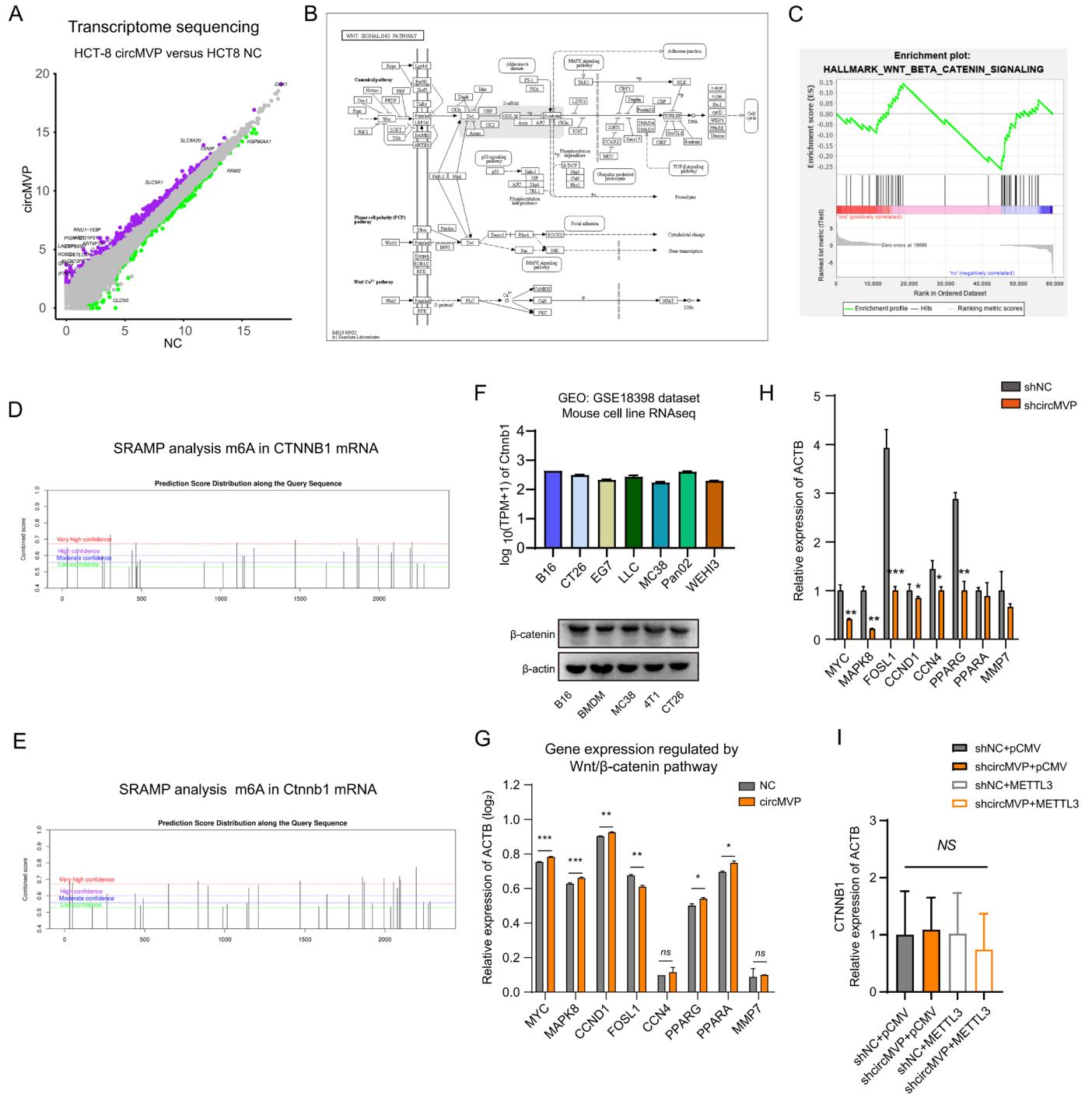
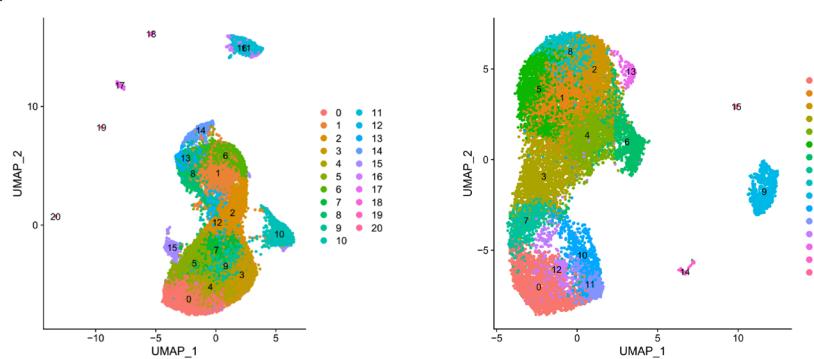
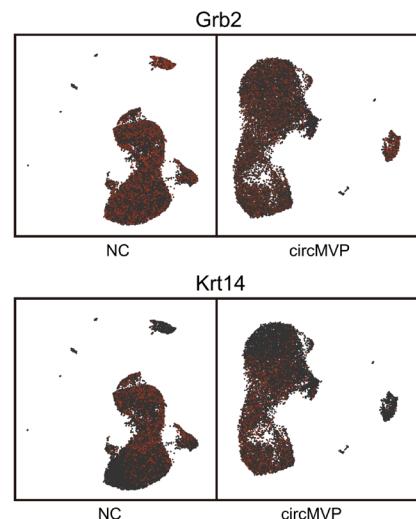


Figure S5

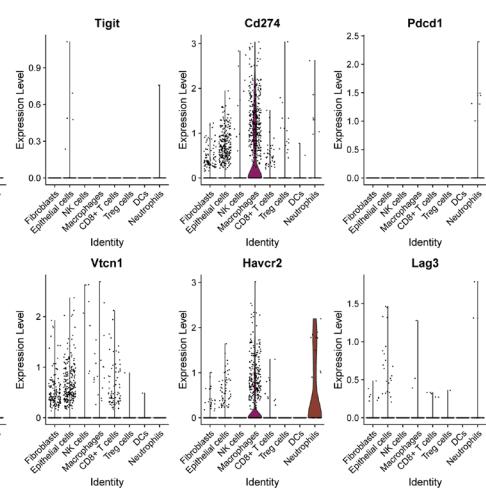
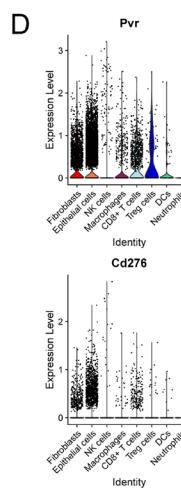
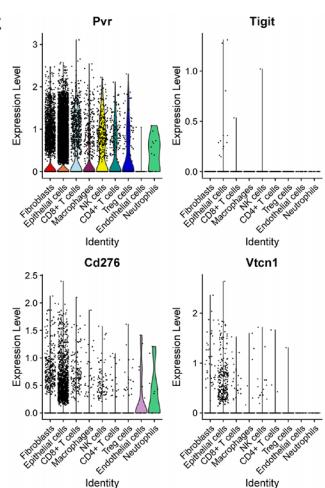
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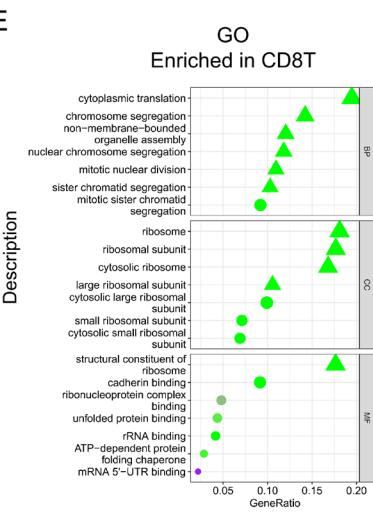
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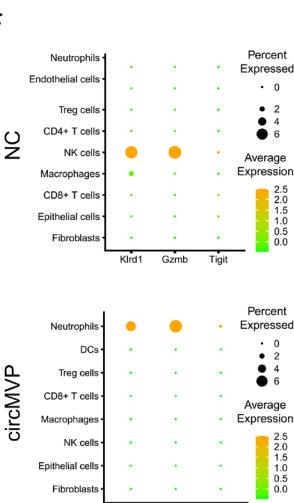
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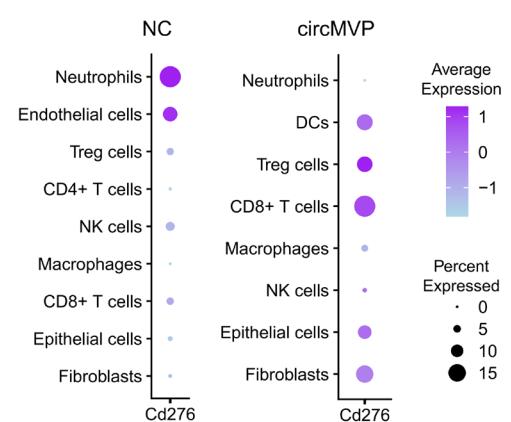
E



F



G



H

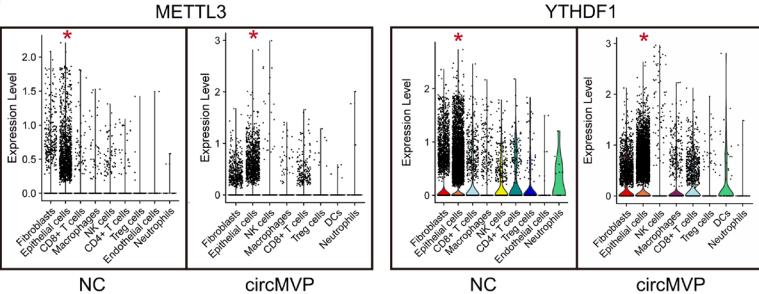


Figure S6

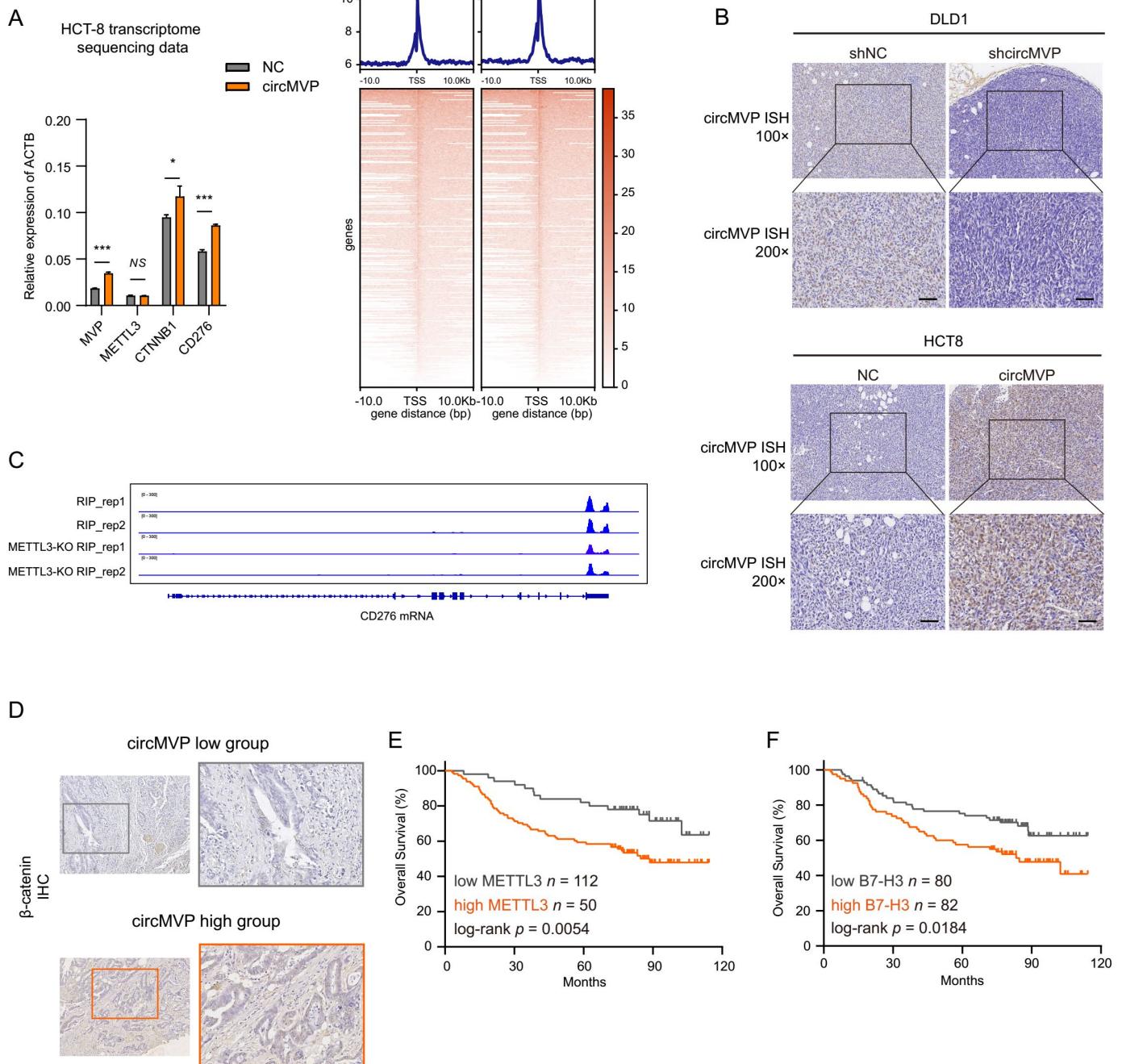


Table S1. Colorectal cancer pathological characteristics table of circMVP in Cohort of affiliated hospital of Jiangnan University.

Clinical parameters	ISH of circMVP		χ^2	<i>P value</i>
	Low	High		
	(n=92)	(n=70)		
Gender			0.096	0.756
Female	43(46.7%)	31(44.3%)		
Male	49(53.3%)	39(55.7%)		
Age			2.127	0.145
<60	42(45.7%)	24(34.3%)		
≥ 60	50(54.3%)	46(65.7%)		
Location			5.535	0.019*
Colon	28(30.4%)	34(48.6%)		
Rectum	64(69.6%)	36(51.4%)		
T stage			4.017	0.045*
T1-T2	30(32.6%)	13(18.6%)		
T3-T4	62(67.4%)	57(81.4%)		
N stage			7.685	0.006**
N0	57(62.0%)	28(40.0%)		
N1-N4	35(38.0%)	42(60.0%)		
M stage			13.285	<0.001***
M0	89(96.7%)	55(78.6%)		
M1	3(3.3%)	15(21.4%)		
METTL3			3.704	0.054
IHC score ≤ 3	34(37.0%)	16(22.9%)		
IHC score > 3	58(63.0%)	54(77.1%)		
B7-H3			8.953	0.004**
IHC score ≤ 4	56(60.9%)	26(37.1%)		
IHC score > 4	36(39.1%)	44(62.9%)		

Pearson χ^2 test or Fisher exact test. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

Table S2. Primer and sequences.

Primers for PCR and real time PCR		
Primers	Sequences-F	Sequences-R
circMVP#1	5'-CCCGAAAGATCCATGGAGAGA-3'	5'-GGCTGGGTGGTAATGTAGA-3'
circMVP#2	5'-AAGTGGAGGTCGTGGAGATC-3'	5'-CCACCACCTTGTCTCCATCT-3'
circMVP-co nvergent	5'-CTGTCACCCCTCTCCTGCC-3'	5'-ATGAGTGGCTTTCGAGGGA-3'
MVP	5'-ATCGAAACGGCGGATCATGCCA-3'	5'-GGCATCACCTACAAAGTCTGGC-3'
β -actin (ACTB) for human	5'-AACTCCATCATGAAGTGTGACG-3'	5'-GATCCACATCTGCTGGAAGG-3'
β -actin (ACTB) for mouse	5'-CATTGCTGACAGGATGCAGAAGG- 3'	5'-TGCTGGAAGGTGGACAGTGAGG- 3'
GAPDH for human	5'-GTCTCCTCTGACTTCAACAGCG-3'	5'-ACCACCTGTTGCTGTAGCAA-3'
Gapdh for mouse	5'-CATCACTGCCACCCAGAACAGTG- 3'	5'-ATGCCAGTGAGCTTCCGTTCAAG- 3'
U6	5'-CTCGCTCGGCAGCACA-3'	5'-AACGCTTCACGAATTGCGT-3'
CTNNB1 for human	5'-CACAAAGCAGAGTGCTGAAGGTG-3'	5'-GATTCTGAGAGTCCAAAGACAG -3'
Ctnnb1 for mouse	5'-GTTCGCCTTCATTATGGACTGCC-3'	5'-ATAGCACCCCTGTTCCCGCAAAG-3'
CD276 for human	5'-CTGGCTTCTCGTGTGCTGGAGAA-3'	5'-GCTGTCAGAGTGTTCAGAGGC-3 ,
Cd276 for mouse	5'-AGCATCCAGGACTTGACAGCG-3'	5'-CGTGATGGTCACCATGTTCCCT-3'

CD276 for ChIP	5'-CTGGGAGCACTGTGGTTCT-3'	5'-TTGGTATCTGTCAGCTGCCA-3'
METTL3 for human	5'-CTATCTCCTGGCACTCGCAAGA-3'	5'-GCTTGAACCGTGCAACCACATC-3' ,
Mettl3 for mouse	5'-CAGTGCTACAGGATGACGGCTT-3'	5'-CCGTCCTAATGATGCGCTGCAG-3'
CTNNB1 for RIP	5'-CTCCTAGTGTGTTGGCCTGGA-3'	5'-CGGTTCCATGCATAACACAGG-3'
MYC	5'-CCTGGTGCTCCATGAGGAGAC-3'	5'-CAGACTCTGACCTTTGCCAGG-3'
MAPK8	5'-GACGCCTTATGTAGTGACTCGC-3'	5'-TCCTGGAAAGAGGAGTTGTGGC-3'
FOSL1	5'-GGAGGAAGGAACTGACCGACTT-3'	5'-CTCTAGGCGCTCCTCTGCTTC-3'
CCND1	5'-TCTACACCGACAACCTCCATCCG-3'	5'-TCTGGCATTTGGAGAGGAAGTG-3'
CCN4	5'-AAGAGAGCCGCCTCTGCAACTT-3'	5'-TCATGGATGCCTCTGGCTGGTA-3'
PPARG	5'-AGCCTGCGAAAGCCTTTGGT-3'	5'-GGCTTCACATTCAAGCAAACCTGG-3'
PPARA	5'-TCGGCGAGGATAGTTCTGGAAG-3'	5'-GACCACAGGATAAGTCACCGAG-3'
MMP7	5'-TCGGAGGAGATGCTCACTCGA-3'	5'-GGATCAGAGGAATGTCCCATAAC-3'
Sequences for gene knockdown		
Si-circMVP #1	GGAUAAAAGAUGGAGACAAG	CUUGUCUCCAUCUUUAUCC
Si-circMVP #2	GGAGAGGGUGACAGGACAU	AUGUCCUGUCACCCUCUCC
sh-circMVP #1	GGATAAAAGATGGAGACAAG	CTTGTCTCCATCTTATCC
sh-circMVP	GGAGAGGGTGACAGGACAT	ATGTCCTGTCACCCCTCTCC

#2		
Si-METTL3	CAGUGGAUCUGUUGUGAUUAUC	UAUCACAAACAGAUCCACUGAG
Gene sequences		
circMVP	GACATCACACCCCTGCAGGTGGTTCTGCCAACACTGCCCTCCATCTAAAGG CGCTGCTTGATTTGAGGATAAAGATGGAGACAAGGTGGTGGCAGGAGATGA GTGGCTTCGAGGGACCTGGCACGTACATCCCCCGGAAGGAAGTGGAGGTC GTGGAGATCATTCAAGGCCACCACATCAGGCAGAACCAAGGCTCTGCGGCTCA GGGCCCGCAAGGAGTGCTGGGACCGGGACGGCAAGGAGAGGGTGACAG	
circMVP Probe	5'-Cy3/Biotin-TGTGATGTCCTGTCACCCTCT-3'	

Table S3. The detailed antibody information used in this study.

Antibodies	Source	Cat#
Anti-β-actin	Cell Signaling Technology	Cat#3700
Anti-METTL3 (Rabbit)	Cell Signaling Technology	Cat#86132
Anti-METTL3 (Mouse)	Proteintech	Cat#67733-1-Ig
Anti-YTHDF1	Cell Signaling Technology	Cat#57530
Anti-B7-H3	Cell Signaling Technology	Cat#14058
Anti-β-catenin (Rabbit)	Cell Signaling Technology	Cat#8480
Anti-β-catenin (Mouse)	Proteintech	Cat#66379-1-Ig
Anti-m6A	Cell Signaling Technology	Cat#56593
Anti-Histone 3	Cell Signaling Technology	Cat#4499
Methylene blue	Sigma-Aldrich	Cat#M9140
Phalloidin	Beyotime	Cat#25682-1-AP
Omburtama	Selleck	Cat#1895083-75-6
Mouse IgG1	Selleck	Cat#MOPC-21
Anti-Mouse CD16/CD32, APC	MultiScience	Cat#F210163203
FoxP3/Transcription Factor Staining Buffer Kit	MultiScience	Cat#IC001
Anti-CD326 (EpCAM) Monoclonal, PE, eBioscience™	Invitrogen	Cat#12-9326-42
Anti-Mouse CD45, FITC	MultiScience	Cat#F2104501
Anti-Mouse CD3ε, PE	MultiScience	Cat#F2100302
Anti-Mouse CD4, APC	MultiScience	Cat#F2100403
Anti-Mouse CD8α, FITC	MultiScience	Cat#F2100801
Anti-Mouse NK1.1(CD161), PE-Cy7	MultiScience	Cat#F2116105
Anti-Human/Mouse CD11b, PerCP-Cy5.5	MultiScience	Cat#F41011b04
Anti-Mouse F4/80, APC	MultiScience	Cat#F21480A03
Anti-CD206/MRC1 Rabbit mAb (Alexa Fluor® 594)	MultiScience	Cat#59414

eBioscience™ Fixable Viability Dye	Invitrogen	Cat#65-2860-40
Anti-mouse-IgG-HRP for WB	Promega	Cat#W4021
Anti-rabbit-IgG-HRP for WB	Promega	Cat#W4011
Cy3-labeled Goat Anti-Mouse IgG (H+L)	Beyotime	Cat#A0521
Cy3-labeled Goat Anti-Rabbit IgG (H+L)	Beyotime	Cat#A0516
FITC-labeled Goat Anti-Mouse IgG (H+L)	Beyotime	Cat#A0568
FITC-labeled Goat Anti-Rabbit IgG (H+L)	Beyotime	Cat#A0562
Anti-mouse-IgG-HRP for IHC	Beyotime	Cat#A0216
Anti-rabbit-IgG-HRP for IHC	Beyotime	Cat#A0208
Multiplex Fluorescence IF Staining Kit	ABSIN	Cat#abs50013
DAB detection kit	ABSIN	Cat#abs9210
ChIP or CUT&RUN Assay Kit	Vazyme	Cat#HD101

Table S4. Differentially expressed circRNAs in Colorectal cancer.

circBASE ID	circBANK ID	logFC	P.Value	Regulation
hsa_circ_000014		1.271174896	0.038990425	UP
hsa_circ_000050		0.754344802	0.045015071	UP
hsa_circ_000017		1.123316537	0.089556881	UP
hsa_circ_000018		0.526715161	0.129154697	UP
hsa_circ_000047		0.74216951	0.137060076	UP
hsa_circ_000030	hsa_circ_0000030	1.135330787	0.209592288	UP
hsa_circ_000004		0.602451641	0.219659551	UP
hsa_circ_000021		0.744220252	0.222333938	UP
hsa_circ_000009		0.528320834	0.226712002	UP
hsa_circ_000380	hsa_circ_0000380	1.092661582	0.236663442	UP
hsa_circ_000044		0.754344802	0.241032831	UP
hsa_circ_000001	hsa_circ_0000001	0.62917509	0.242771623	UP
hsa_circ_000012		0.654491375	0.24374094	UP
hsa_circ_000039		0.356796443	0.244314542	UP

hsa_circ_000038		0.528320834	0.24951087	UP
hsa_circ_000264		0.459503874	0.254739529	UP
hsa_circ_000382		0.356796443	0.268399785	UP
hsa_circ_000190	hsa_circ_0000190	0.255178249	0.298624688	UP
hsa_circ_000074	hsa_circ_0000074	0.255178249	0.298624688	UP
hsa_circ_000022		-0.635630199	0.060452328	DOWN
hsa_circ_000016	hsa_circ_0000016	-0.868023775	0.061351332	DOWN
hsa_circ_000029	hsa_circ_0000029	-1.101016695	0.066824723	DOWN
hsa_circ_000010	hsa_circ_0000263	-0.816300317	0.087858824	DOWN
hsa_circ_000003		-0.489828428	0.095842268	DOWN
hsa_circ_000032		-1.137593842	0.099286803	DOWN
hsa_circ_000068		-0.836987306	0.21413584	DOWN
hsa_circ_000027		-0.615998969	0.218970453	DOWN
hsa_circ_000045		-0.512017633	0.232109455	DOWN
hsa_circ_000019		-0.40054462	0.237044391	DOWN
hsa_circ_000006	hsa_circ_0001821	-0.712501175	0.242032814	DOWN
hsa_circ_000033		-0.477653136	0.253149432	DOWN
hsa_circ_000072		-0.379167841	0.264530021	DOWN
hsa_circ_000107	hsa_circ_0000107	-0.421011469	0.266238623	DOWN
hsa_circ_000118		-0.308666473	0.27944487	DOWN
hsa_circ_000163	hsa_circ_0000163	-0.308666473	0.27944487	DOWN
hsa_circ_000187		-0.282665636	0.287588805	DOWN
hsa_circ_000101	hsa_circ_0000101	-0.282665636	0.287588805	DOWN

Table S5.TOP100 protein detected by circRNA Pull-down Mass spectrometry.

Protein	FDACcession	Description	Sum PEP	#Covers	#Pepti	#PSMs	#Uniq	#AAs	Biological	Cellular	C	Molecular	Abundances
High	P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens OX=9606 GN=KRT2 PE=1 SV=2	281.966	67	38	91	29	639	cell cycle plasma me bone, tooth	2571029694			
High	P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6	279.866	61	33	102	31	584	cell organi plasma me bone, tooth	4546927467			
High	P68104	Elongation factor 1-alpha 1 OS=Homo sapiens OX=9606 GN=EEF1A1 PE=1 SV=1	259.243	54	20	139	7	462	protein me non-struct nucleic aci	9089267112			
High	Q9UHB6	LIM domain and actin-binding protein 1 OS=Homo sapiens OX=9606 GN=LIMA1 PE=1 SV=1	252.745	60	38	76	38	759	cell organi plasma me cytoskeleti	4591731775			
High	P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6	247.527	48	39	122	32	644	cell organi non-struct bone, tooth	6122395367			
High	Q9Y5B9	FACT complex subunit SPT16 OS=Homo sapiens OX=9606 GN=SUPT16H PE=1 SV=1	235.682	39	40	79	40	1047	cell organi nucleus other mole	983139817			
High	P19338	Nucleolar OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=3	234.339	44	38	251	38	710	developme plasma me nucleic aci	1.5911E+10			
High	Q86U44	Methyltransferase-like protein 3 OS=Homo sapiens OX=9606 GN=METTL3 PE=1 SV=2	218.733	65	24	240	7	580	N6-adenos cytosol; R mRNA (2)	356360533			
High	P09429	High mobility group protein B1 OS=Homo sapiens OX=9606 GN=HMGB1 PE=1 SV=3	213.081	54	20	135	18	215	cell organi non-struct signal tran	8005659883			
High	P13639	Elongation factor 2 OS=Homo sapiens OX=9606 GN=EEF2 PE=1 SV=4	209.514	40	35	65	34	858	protein me non-struct translation	812448307			
High	Q9BUF5	Tubulin beta-6 chain OS=Homo sapiens OX=9606 GN=TUBB6 PE=1 SV=1	205.62	65	22	179	9	446	cell cycle cytoskelet cytoskeleti	101169641			
High	P07355	Annexin A2 OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=2	197.655	65	28	71	28	339	cell organi non-struct transporter	1885017542			
High	P25527	Keratin, type I cytoskeletal 9 OS=Homo sapiens OX=9606 GN=KRT9 PE=1 SV=3	193.723	53	27	61	27	623	cell organi cytosol;cy cytoskeleti	1475197347			
High	P14618	Pyruvate kinase PKM OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=4	191.383	63	29	53	29	531	cell organi non-struct nucleic aci	7267797818			
High	P02545	Prelinam A/C OS=Homo sapiens OX=9606 GN=LMNA PE=1 SV=1	179.879	56	36	53	35	664	cell cycle cytosol;cy cytoskeleti	792568860			
High	Q15417	Calponin-3 OS=Homo sapiens OX=9606 GN=CNNS3 PE=1 SV=1	178.878	60	16	85	14	329	cell organi cytosol;cy cytoskeleti	2964544631			
High	Q8WV93	Palladin OS=Homo sapiens OX=9606 GN=PALLD PE=1 SV=3	177.516	31	33	48	33	1383	cell adhes plasma me cytoskeleti	738178205			
High	P29401	Transketolase OS=Homo sapiens OX=9606 GN=TKT PE=1 SV=3	161.438	47	27	43	27	623	other met other mem other mole	633271782			
High	P06748	Nucleophosmin OS=Homo sapiens OX=9606 GN=NPM1 PE=1 SV=2	155.886	39	11	41	11	294	cell cycle cytosol;cy enzyme re	2539798252			
High	P161978	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens OX=9606 GN=HNRNPK PE=1 SV=1	154.238	44	18	66	18	463	RNA meta cytoskelet nucleic aci	1877975233			
High	Q05636	Elongation factor 1-alpha 2 OS=Homo sapiens OX=9606 GN=EEF1A2 PE=1 SV=1	150.27	44	17	96	4	463	protein me other mem nucleic aci	36099612.9			
High	Q9Y450	HBS1-like protein OS=Homo sapiens OX=9606 GN=HBS1L PE=1 SV=1	139.637	50	26	36	26	684	cell organi cytosol;tra nucleic aci	2197196413			
High	P15311	Ezrin OS=Homo sapiens OX=9606 GN=EZR PE=1 SV=4	139.575	48	32	66	32	586	cell adhes plasma me cytoskeleti	1273894929			
High	Q08945	FACT complex subunit SSRP1 OS=Homo sapiens OX=9606 GN=SSRP1 PE=1 SV=1	139.288	39	22	43	22	709	cell organi nucleus nucleic aci	740463986			
High	P05787	Keratin, type II cytoskeletal 8 OS=Homo sapiens OX=9606 GN=KRT8 PE=1 SV=7	137.844	60	32	57	25	483	cell organi plasma me other mole	666200698			
High	Q14247	Src substrate cortactin OS=Homo sapiens OX=9606 GN=CTTN PE=1 SV=2	136.688	39	25	50	25	550	cell adhes plasma me other mole	1572022288			
High	Q86XP3	ATP-dependent RNA helicase DDX42 OS=Homo sapiens OX=9606 GN=DDX42 PE=1 SV=1	135.741	38	27	36	27	938	cell organi cytosol;nu nucleic aci	303427832			
High	Q9Y2W1	Thyroid hormone receptor-associated protein 3 OS=Homo sapiens OX=9606 GN=THRA3 PE=1 SV=2	127.264	25	23	38	22	955	RNA meta nucleus nucleic aci	423692042			
High	P25269	General transcription factor IIII subunit I OS=Homo sapiens OX=9606 GN=GTF2F1 PE=1 SV=2	126.119	41	20	36	20	517	RNA meta nucleus;ot enzyme re	388612085			
High	P06733	Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=2	124.3	55	20	41	20	434	other met plasma me nucleic aci	539707896			
High	Q9Y4X5	E1 ubiquitin-protein ligase ARHI OS=Homo sapiens OX=9606 GN=ARHI1 PE=1 SV=2	121.625	36	18	30	18	557	protein me cytosol;nu other mole	325086831			
High	P63244	Small ribosomal subunit protein RACK1 OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=3	119.035	75	17	25	17	317	cell cycle plasma me signal tran	347634207			
High	O15371	Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens OX=9606 GN=EIF3D PE=1 SV=1	116.775	47	17	30	17	548	cell organi cytosol;ot nucleic aci	320462533			
High	P60842	Eukaryotic initiation factor 4A-1 OS=Homo sapiens OX=9606 GN=EIF4A1 PE=1 SV=1	114.677	58	22	39	20	406	protein me cytosol;tra nucleic aci	441200283			
High	P23588	Eukaryotic translation initiation factor 4B OS=Homo sapiens OX=9606 GN=EIF4B PE=1 SV=2	113.187	38	24	54	24	611	protein me cytosol;tra nucleic aci	1457444917			
High	P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 SV=3	107.727	46	13	34	13	335	cell organi plasma me enzyme re	718986362			
High	P13647	Keratin, type II cytoskeletal 5 OS=Homo sapiens OX=9606 GN=KRT5 PE=1 SV=3	105.589	45	30	54	15	590	cell organi cytosol;cy bone, tooth	339783592			
High	Q07157	Tight junction protein ZO-1 OS=Homo sapiens OX=9606 GN=TJP1 PE=1 SV=3	103.984	16	24	32	24	1748	cell adhes plasma me other mole	155315115			
High	P02538	Keratin, type II cytoskeletal 6A OS=Homo sapiens OX=9606 GN=KRT6A PE=1 SV=3	100.006	44	27	56	1	564	cell organi cytosol;cy bone, tooth	79344694.3			
High	P00338	L-lactate dehydrogenase A chain OS=Homo sapiens OX=9606 GN=LDHA PE=1 SV=2	99.895	48	16	33	15	332	other met cytosol;mi other mole	465240273			
High	P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens OX=9606 GN=KRT6B PE=1 SV=5	99.021	43	25	54	0	564	cell organi cytosol;cy bone, tooth				
High	P25297	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens OX=9606 GN=HNRNPF PE=1 SV=3	98.557	41	12	36	10	415	RNA meta plasma me nucleic aci	625059444			
High	Q15691	Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens OX=9606 GN=MAPRE1 PE=1	97.551	59	14	28	14	268	cell cycle plasma me cytoskeleti	49278800			
High	P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens OX=9606 GN=KRT14 PE=1 SV=4	96.659	54	22	38	7	472	cell organi plasma me cytoskeleti	406322365			
High	Q9UHRS	SAP30-binding protein OS=Homo sapiens OX=9606 GN=SAP30BP PE=1 SV=1	95.766	55	16	30	16	308	other biolo cytoskeleti	412341574			
High	P60841	Eukaryotic translation initiation factor 5B OS=Homo sapiens OX=9606 GN=EIF5B PE=1 SV=4	95.45	20	19	29	19	1200	cell organi cytosol;ot nucleic aci	254084212			
High	P06744	Glucose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=4	94.316	36	17	29	17	558	other met non-struct signal tran	593606662			
High	P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSPB8 PE=1 SV=1	92.841	35	20	29	16	646	cell organi non-struct signal tran	157608036			
High	Q13428	Treacle protein OS=Homo sapiens OX=9606 GN=TCOF1 PE=1 SV=3	92.754	18	22	29	22	1488	RNA meta cytosol;mi other mole	298862655			
High	Q96KH4	PDZ2 and LIM domain protein 5 OS=Homo sapiens OX=9606 GN=PDLIM5 PE=1 SV=5	91.945	37	18	29	18	596	cell organi other mem cytosol	322802115			
High	Q06830	Peroxiredoxin-1 OS=Homo sapiens OX=9606 GN=PRDX1 PE=1 SV=1	90.008	75	15	33	14	199	cell cycle cytosol;nu other mole	1434007117			
High	O00267	Transcription elongation factor SPT5 OS=Homo sapiens OX=9606 GN=SUPT5H PE=1 SV=1	89.845	28	24	29	24	1087	cell organi nucleus nucleic aci	175880801			
High	P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens OX=9606 GN=ANP32	88.392	36	13	47	7	249	transports ER/Golgi; other mole	2548672617			
High	Q96CQ4	U3 small nucleolar RNA-associated protein 25 homolog OS=Homo sapiens OX=9606 GN=UTP25 PE=1 S	86.844	30	20	26	20	756	protein me nucleus;ot nucleic aci	171916957			
High	Q96KG9	N-terminal kinase-like protein OS=Homo sapiens OX=9606 GN=SCYL1 PE=1 SV=1	85.38	29	19	22	19	808	stress resp other mem nucleic aci	194941377			
High	P13984	General transcription factor IIII subunit 2 OS=Homo sapiens OX=9606 GN=GTF2F2 PE=1 SV=2	84.662	72	14	18	14	249	RNA meta cytoskelet nucleic aci	346716489			
High	Q9UJEM3	ERBB receptor feedback inhibitor 1 OS=Homo sapiens OX=9606 GN=ERRFI1 PE=1 SV=1	84.288	50	15	30	15	462	cell cycle plasma me enzyme re	240452491			
High	P50454	Serpin H1 OS=Homo sapiens OX=9606 GN=SERPINH1 PE=1 SV=2	81.91	44	13	23	13	418	cell organi non-struct enzyme re	204484572			
High	P26583	High mobility group protein B2 OS=Homo sapiens OX=9606 GN=HMG2B PE=1 SV=2	79.806	44	9	27	7	209	cell organi non-struct signal tran	289925517			
High	P23396	Small ribosomal subunit uS3 OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=2	79.305	71	17	33	17	243	cell cycle plasma me cytoskeleti	543712072			
High	O60716	Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNN1 PE=1 SV=1	79.059	25	18	23	18	968	cell adhes plasma me signal tran	103292612			
High	Q14978	Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens OX=9606 GN=NOLC1 PE=1 SV=2	78.88	25	17	40	17	699	cell cycle nucleus;ot other mole	1151006472			
High	Q92682	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens OX=9606 GN=ANP32	77.6	34	12	42	6	251	cell organi nucleus;ot other mole	1773656449			
High	Q9NYF8	Bcl-2-associated transcription factor 1 OS=Homo sapiens OX=9606 GN=BCLAF1 PE=1 SV=2	76.038	22	17	26	16	920	stress resp nucleus;ot nucleic aci	183377936			
High	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens OX=9606 GN=KRT19 PE=1 SV=4	75.677	52	20	27	13	400	cell organi plasma me cytoskeleti	262359097			
High	Q99613	Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens OX=9606 GN=EIF3C PE=1 SV=1	75.442	22	20	25	20	913	cell organi cytosol;tra translation	175940023			
High	P38919	Eukaryotic initiation factor 4A-III OS=Homo sapiens OX=9606 GN=EIF4A3 PE=1 SV=4	75.225	44	16	25	14	411	RNA meta cytosol;nu nucleic aci	169656420			
High	Q8IXT5	RNA-binding protein 12B OS=Homo sapiens OX=9606 GN=RBM12 PE=1 SV=2	74.021	30	25	32	25	1001	other biolo nucleus;ot	200639858			
High	P62424	Large ribosomal subunit protein eL8 OS=Homo sapiens OX=9606 GN=RPL7A PE=1 SV=2	73.314	45	16	23	16	266	protein me other mem other mole	28902734			
High	O00571	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=3	72.921	31	19	24	18	662	cell cell si non-struct enzyme re	151943115			
High	P08779	Keratin, type I cytoskeletal 16 OS=Homo sapiens OX=9606 GN=KRT16 PE=1 SV=4	72.882	39	17	27	6	473	cell organi plasma me cytoskeleti	27216555			
High	Q9NW82	WD repeat-containing protein 70 OS=Homo sapiens OX=9606 GN=WDR70 PE=1 SV=1	71.317	27	16	22	16	654	nucleus;ot other mole	113885017			
High	Q15185	Prostaglandin E synthase 3 OS=Homo sapiens OX=9606 GN=PTGES3 PE=1 SV=1	70.666	53	9	45	9	160	cell cycle cytosol;nu other mole	4580767025			
High	P11586	C-1-tetrahydrofol											