

Tables

Table S1. The primers used for qPCR assays.

Gene	Forward primer (5'→3')	Reverse primer (5'→3')
HNRNPM	AGTATGGCTGGTGTGGTGGT	TTGCACAGCTTCATGGACT
PRPF4	GTTGTCGGTACTGATGCCCTG	GCAATCCATAGTCTGCCACC
PRPF4B	TGTCTTATGTACGTTACATG	GCCGTACCTAACACTTC
SCAF1	GGGGACCTGCCAACATGATAAA	CAGCATGTCCTCACTTCGC
SF3A1	AGGAAGTTGAGATGGAGGTG	CTTGCAGACAATGACTTGGTC
SF3A2	GTGTCTCCCAGTCTGCTAAA	AGGCAGAGTTGCATTCATAG
SF3B1	CACAGACCTCCAAAGATTGC	GCTGCTCCATTGACGACTT
SF3B2	TTACGAGCCAACTTTATCT	GTGAAGCGGTTCATTCGG
SF3B3	GGCGAGCCGTTATGATTAGT	AGGTCTAGCTCATAGAAAGTAAG
SRSF1	GCCGCATCTACGTGGTAAC	GAGGTCGATGTCGCGGATAG
SRSF3	GTGAGAGAGTTGGTGGTGGT	AAATGCGGCGGCTCAAATC
SRSF4	CTCGCACAGAGTACAGACTTAT	TTGCGTCCCTTGAGCATCT
SRSF5	TTGCGGATGCACACCGACCT	TCCGGCTCCTGCTCCTGCTT
SRSF6	CTTGCAGGCCGTTCGAC	GTATCCACCTCCACCACTGCGG
SRSF7	ACGCGACATGATGACAGAC	CGCATATATAAACGCGAAC
SRSF8	TCTGGGTCCCTCACTAGCTC	TCTTGGATCGCGACCTTGAC
SRSF9	CCTGCGTAAACTGGATGACACC	CCTGCTTGGTATGGAGAGTCAC
SRSF10	CCCCCAACACGTCTCTGTT	GGACGGCGAGTGTAGAAATCA
SRSF11	GGTCAAGAAGCAGATCGAGAC	AACGTCTGGCTGTGCTGTAAC
B7-H3	GGTCAGCTCTGTCCTCTG	GGAGTCCTGAGGGAGGAAC
CCDC50S	GCTGGCTATTGAGGCAGAG	TGGCTTCATTCCCTCCATCTT
TP53	CTCTGACTGTACCACCATCCACTA	GAGTTCCAAGGCCTCATTCACTC
GAPDH	TGCACCAACACTGCTTAGC	GGCATGGACTGTGGTCATGAG
β-actin	AGAAAATCTGGCACCAACACC	AGAGGCGTACAGGGATAGCA

Table S2. Correlation between the mRNA expression of B7-H3 and splicing factors in TCGA samples.

Splicing factor	R-value	P-value
SF3A1	0.3004	2.48×10 ⁻⁰⁸
SF3A2	0.3884	2.33×10 ⁻¹³
SF3A3	0.2857	1.22×10 ⁻⁰⁷
SF3B1	0.1150	3.65×10 ⁻⁰²
SF3B2	0.3815	6.57×10 ⁻¹³
SF3B3	0.4014	3.05×10 ⁻¹⁴
SF3B4	0.3757	1.54×10 ⁻¹²
SF3B5	0.0961	8.08×10 ⁻⁰²
SRSF1	0.2279	2.85×10 ⁻⁰⁵
SRSF2	0.2188	5.96×10 ⁻⁰⁵
SRSF3	0.3111	7.35×10 ⁻⁰⁹
SRSF4	0.3132	5.73×10 ⁻⁰⁹
SRSF5	-0.0693	2.09×10 ⁻⁰¹
SRSF6	0.0901	1.02×10 ⁻⁰¹
SRSF7	0.2915	6.64×10 ⁻⁰⁸
SRSF8	0.0600	2.76×10 ⁻⁰¹
SRSF9	0.3103	8.10×10 ⁻⁰⁹
SRSF10	0.1246	2.34×10 ⁻⁰²
SRSF11	0.2616	1.39×10 ⁻⁰⁶
SRSF12	-0.0401	4.67×10 ⁻⁰¹

Table S3. Correlation between cytoplasmic B7-H3 expression and clinicopathological features

Features	Variables	B7-H3 expression		Total	χ^2	P-value
		Low	High			
Expression	Normal	87	0	87	57.115	0.000
	Carcinoma	44	43	87		
Age (year)	≤ 68	29	19	48	4.76	0.029
	> 68	17	28	45		
T stage	T2	3	2	5	0.238	0.625
	T3/T4	39	41	80		
TNM stage	I/II	21	24	45	0.178	0.673
	III/IV	20	19	39		
N stage	N0	24	27	51	0.022	0.883
	N1/N2	18	19	37		
M stage	M0	43	46	89	1.09	0.296
	M1	3	1	4		
Sex	Female	18	23	41	0.907	0.341
	Male	28	24	52		
Grade	I/II	41	35	76	3.34	0.067
	III	5	12	17		
P53	negative	19	26	45	1.82	0.176
	positive	27	21	48		
MSH6	negative	28	33	61	0.899	0.343
	positive	18	14	32		
MSH2	negative	16	22	38	1.39	0.238
	positive	30	25	55		
KI67	negative	23	29	52	1.32	0.250
	positive	22	17	39		

Table S4. Correlation between cytoplasmic SFRS3 expression and clinicopathological features.

variables	SFRS3 expression		total	χ^2	<i>P</i> -value
	low	High			
Tissue	Normal	87	0	87	74.164
	Carcinoma	35	52	87	
Age (year)	≤ 68	18	30	48	0.464
	> 68	20	25	45	
T stage	T2	4	1	5	3.54
	T3/T4	30	50	80	
TNM stage	I/II	23	22	45	5.68
	III/IV	10	29	39	
N stage	N0	27	24	51	7.26
	N1/N2	9	28	37	
M stage	M0	37	52	89	0.435
	M1	1	3	4	
Sex	Female	15	26	41	0.555
	Male	23	29	52	
grade	I/II	32	44	76	0.267
	III	6	11	17	
B7-H3	negative	26	17	43	0.001
	positive	12	38	50	
p53	negative	24	21	45	5.61
	positive	14	34	48	
Ki67	negative	30	22	52	14.5
	positive	7	32	39	
MSH2	negative	13	25	38	1.17
	positive	25	30	55	
MSH6	negative	23	38	61	0.73
	positive	15	17	32	

Table S5. Correlation between nuclear SFRS3 expression and clinicopathological features

variables		SFRS3 expression		total	χ^2	P-value
		low	High			
Tissue	Normal	79	8	87	67.463	0.000
	Carcinoma	26	67	93		
Age (year)	≤ 68	10	38	48	2.49	0.114
	> 68	16	29	45		
T stage	T2	3	2	5	2.64	0.104
	T3/T4	21	59	80		
TNM stage	I/II	20	25	45	16.7	0.000
	III/IV	2	37	39		
N stage	N0	22	29	51	15.3	0.000
	N1/N2	2	35	37		
M stage	M0	26	63	89	1.62	0.203
	M1	0	4	4		
Sex	Female	11	30	41	0.046	0.830
	Male	15	37	52		
grade	I/II	23	53	76	1.09	0.295
	III	3	14	17		
p53	negative	16	29	45	2.49	0.114
	positive	10	38	48		
Ki67	negative	21	31	52	8.29	0.004
	positive	5	34	39		
MSH2	negative	8	30	38	1.52	0.218
	positive	18	37	55		
MSH6	negative	16	45	61	0.263	0.608
	positive	10	22	32		

Figures

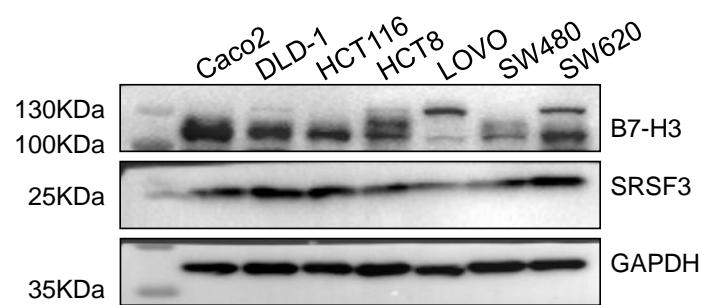


Figure S1. The expression of B7-H3 and SRSF3 proteins in CRC cells.

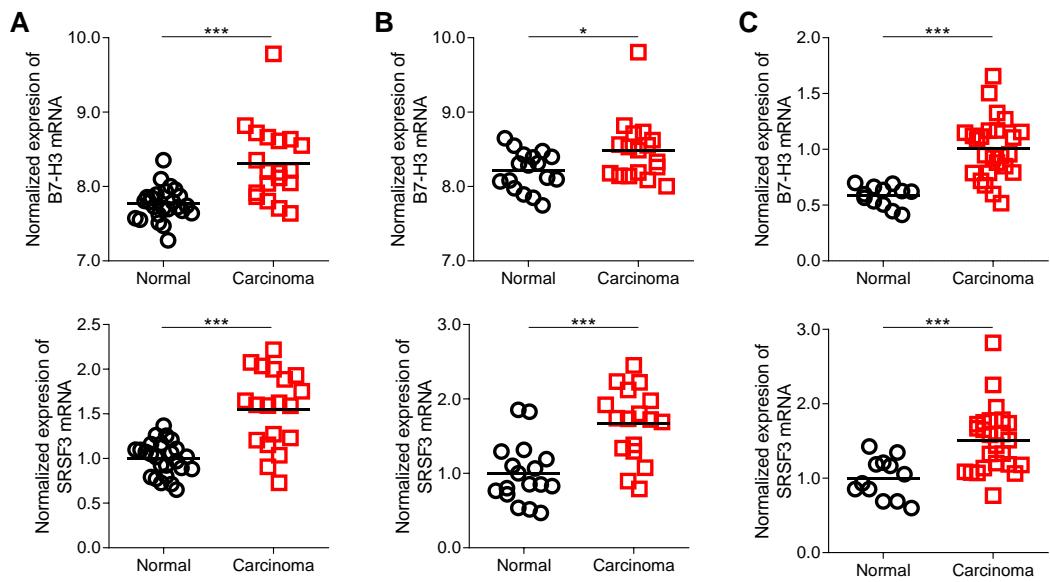


Figure S2. The upregulation of B7-H3 and SRSF3 mRNA in CRC tissues. **(A-C)** The gene microarray data were collected from GEO Datasets of GDS4718, GDS4382, and GSE41657, respectively. Significance was assessed by *t*-test. *** $P<0.001$; * $P<0.05$.

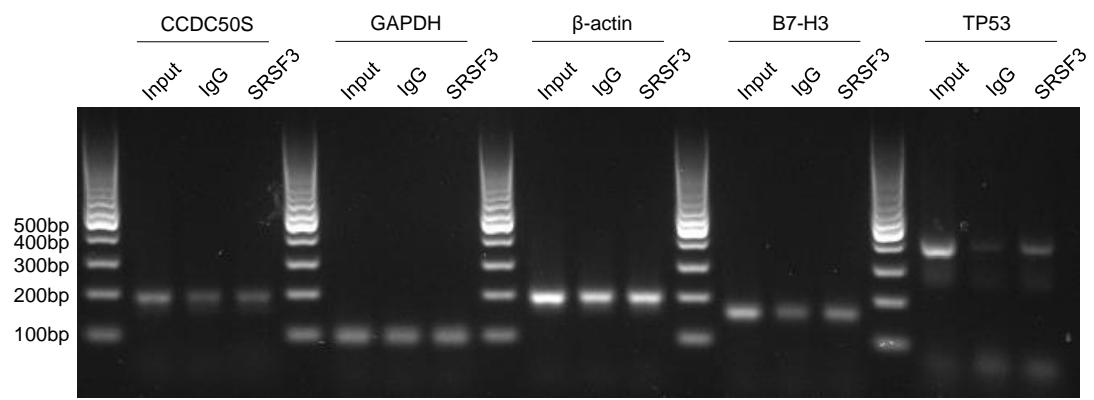


Figure S3. The gel image of qPCR products of B7-H3 or, TP53, CCDC50S, GAPDH, and β -actin.

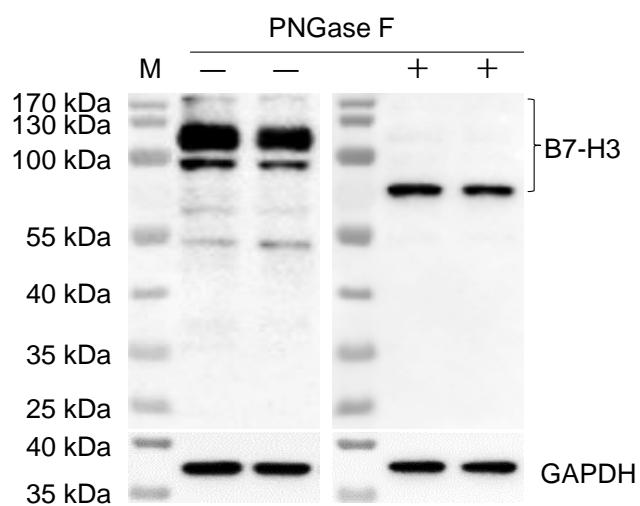


Figure S4. Multiple glycoforms of B7-H3. WB results of the total proteins of HCT-116 cells before (left) and after (right) digestion by PNGase F.