

Table S1. The effects of propionate on the expression of 83 lncRNAs array in HCT116 cell.

lncRNA	fold change	lncRNA	fold change	lncRNA	fold change
21A	0.94	HOXA1AS AA489505	0.80	PCGEM1	3.50
AAA1	1.05	HOXA3AS BI823151	1.01	PR-AT2	2.34
aHIF	1.86	HOXA3AS BE873349	0.61	PRINS	0.98
AK023948	0.77	HOXA6AS AK092154	1.06	PSF inhibiting RNA	0.49
ANRIL	0.46	HOXA11AS	0.92	PTENP1	2.28
Anti-NOS2A	0.58	HULC	3.80	RMRP	1.22
BACE1AS	1.10	IPW	0.67	ROR	0.53
BC017743	0.90	IGF2AS	1.28	Saf	0.74
BC043430	0.92	KRAS P1	1.41	SCA8	0.75
BC200	1.25	l1pa16	0.75	SOX2OT	0.70
BCMS	1.15	LIT	2.61	SRA	1.10
BIC	1.32	LOC285194	0.86	ST7OT1	0.74
CCND1ANCR	1.05	LUST	1.05	ST7OT2	2.34
CMPD	0.59	LincRNA-VLDLR	1.09	ST7OT3	1.30
DD3	9.36	LincRNA-SFMBT2	0.57	ST7OT4	0.78
DGCR5	0.92	MALAT1	6.44	Telomerase RNA	1.09
DISC2	1.62	MEG3	20.06	TMEVPG1	0.67
DLG2AS	0.45	MER11C	0.95	TU_0017629	0.78
EGO	1.32	NEAT1	5.34	TUG	1.19
GAS5	1.52	NCRMS	62.96	UCA1	0.62
GOMAFU	1.24	NDM29	0.79	WT-1AS	0.59
H19	1.08	PANDA	1.00	Y1	1.64
H19-AS	0.74	PAR5	1.02	Y3	0.94
HAR1A	1.14	PCAT-1	0.71	Y4	1.17
HAR1B	3.31	PCAT-14	0.65	Y5	1.48
HOTAIR	0.56	PCAT-29	31.26	ZEB2NAT	0.61
HOTAIRM1	1.97	PCAT-32	0.96	7SK	1.64
HOTTIP	1.99	PCAT-43	0.56		

Table S2. Sequence of real-time PCR primers for mTOR regulator, and the effects of RMST on the expression of mTOR regulator.

mTOR regulator	forward primer	reverse primer	fold change
AKT1	TCCTCCTCAAGAATGATGGCA	GTGCGTTCGATGACAGTGGT	1.23
AKT2	AGGCACGGGCTAAAGTGAC	CTGTGTGAGCGACTTCATCCT	2.12
AKT3	AATGGACAGAAGCTATCCAGGC	TGATGGGTGTGTAGAGGCATCC	1.10
HRAS	GACGTGCCTGTTGGACATC	CTTCACCCGTTTGATCTGCTC	1.39
IGF1	GCTCTTCAGTTCGTGTGTGGA	GCCTCCTTAGATCACAGCTCC	1.19
IKKB (IKK β)	GTCTTTGCACATCATTCGTGGG	GTGCCGAAGCTCCAGTAGTC	1.35
INS	GCAGCCTTTGTGAACCAACAC	CCCCGCACACTAGGTAGAGA	NA
INSR	AAAACGAGGCCCGAAGATTTC	GAGCCCATAGACCCGGAAG	1.55
IRS1	CCCAGGACCCGCATTCAAA	GGCGGTAGATACCAATCAGGT	1.94
MAPK1 (ERK2)	TCACACAGGGTTCCTGACAGA	ATGCAGCCTACAGACCAAATATC	1.26
MAPK3 (ERK1)	CTACACGCAGTTGCAGTACAT	CAGCAGGATCTGGATCTCCC	1.42
PDPK1	TTCCGAGCTGGAACGAGTAT	GGTCTCTTGCCTTAGGGAAGAA	1.14
PIK3C3 (Vps34)	GTCTGGCCTAATGTAGAAGCAG	GGCAAGACGGCTCATCTGAT	1.18
PIK3CA (p110-alpha)	CCACGACCATCATCAGGTGAA	CCTCACGGAGGCATTCTAAAGT	1.49
PIK3CB	CTGCCTGCGACAGATGAGTG	TCCGATTACCAAGTGCTCTTTC	1.34
PIK3CD	TCAACTCACAGATCAGCCTCC	CGCGAAAGTCGTTCACTTCT	1.41
PIK3CG	AACACCGACCTCACAGTTTTT	CTCAAGCCACACATTCCACAG	NA
PLD1	CCCAGCGATCCCAAGATACAA	GACAGCCGGAGAGATACGTCT	1.34
PLD2	ACTCACGGCGACTTTTCTCTG	AACGGCAAATCGAGCCAGA	1.22
RHEB	TTGTGGACTCCTACGATCCAA	GGCTGTGTCTACAAGTTGAAGAT	1.15
RPS6KA1	CAGTGGGCACCTGTATGCTAT	ACGAATGGGTGATTTACATCAGC	1.33
RPS6KA2	GCCACCCTAAAAGTTCGGGAC	TTTCTTCCGTCTGAAAGGCA	1.61
RPS6KA5	AGGCAGTCGCCATTTTTGGTA	TCTCCAACATAAATCTGCACCTC	1.39
RRAGA	ACACTCCCACGTCCGATTC	CTCTCCACGTCAAACACGTAA	1.14
RRAGB	GGTGGGCAAGACACCTTCAT	GCGGCTCTCCACATCAAAGA	0.94
RRAGC	AGGGCCAATGATGACCTTGC	GTGGAATGAGTTTCTGCACCA	1.32
RRAGD	CTAGCGGACTACGGAGACG	ATGAGCAGGATTCTCGGCTTC	1.22
TELO2	CCCGCAGAGATCGTGGATG	CATGTCTAGGGGACAACTC	1.17
AKT1S1 (PRAS40)	CCTCCACGACATCGCACTG	TCACAAAGAGCCCTCCATTATCA	1.88
CAB39	GCAGCCCATCCTAGACATCC	TCTTCTCGTCGTTAACTGCTC	1.14
CAB39L	GGCCTGCTAGTGACACTGATA	TACTCCACAGTAGGACTCCGA	1.18
DDIT4 (REDD1)	TGAGGATGAACACTTGTGTGC	CCAACTGGCTAGGCATCAGC	1.55
DDIT4L (REDD2)	TGTGGCTATCACCAGAGAG	TGCTTTGATTTGGACAGACAGT	1.35
DEPTOR (DEPDC6)	TTAGCAGACCGGGCATTATT	GAAGGTGCCGTCATCCTTTCT	0.96
DEPTOR (DEPDC6)	GCGGAGGCGAAGACTGATG	GGCTCACTGACATAAAGCTGGTA	0.89
FKBP1A (FKBP12)	CTCCAGATTATGCCTATGGTGC	AGCTCCACATCGAAGACGAGA	0.72
FKBP8	GACTTCGAGGTACTGGATGGG	CTTCTTCCTCAACAGCCCGTT	5.46
IGFBP3	AGAGCACAGATACCCAGAACT	GGTGATTCAGTGTGTCTTCCATT	1.10
PRKAA1 (AMPK)	TTGAAACCTGAAAATGTCCTGCT	GGTGAGCCACAACCTGTTCTT	1.27
PRKAA2	GTGAAGATCGGACACTACGTG	CTGCCACTTTATGGCCTGTTA	1.05
PRKAB1	CCTCACCAGAAGCCACAATAAC	CGTCCACTGACCATCCACA	1.09
PRKAB2	CAGTCAGCTTGGCACAATTAAC	TCCTCAGATCGAAACGCATACA	1.28
PRKAG1	CCACAAGCGCATTTCTGAAGTT	TGGTAGTGCGAACCATAGCAATA	1.24
PRKAG2	CCAGATGCAAGCCTCTTCGAT	GATAGGGTCAATAACGGGCAATC	1.09

PRKAG3	CCTGGGAGTGTGAGCTAGAAG	GTTTCCGCAGTTCGTCATCC	NA
PTEN	AGGGACGAACTGGTGTAATGA	CTGGTCCTTACTTCCCCATAGAA	1.35
STK11 (LKB1)	TCTACAACATCACCACGGGTC	TTCGTACTCAAGCATCCCTTTC	1.08
STRADB	GGTCACGTCCATCCACTAGAG	ACCAGTGTTCTGTGGGAGTA	1.15
TP53 (p53)	CAGCACATGACGGAGGTTGT	TCATCCAAATACTCCACACGC	1.19
TSC1	CCATGCTACCAATGATTCCACA	TGATGACAGACGGCCAAAAATG	1.28
TSC2	ATAGCTGTTACCTCGACGAGT	TGCAGGGAGACCTCTATGTCC	4.66
YWHAQ	AGGGTCATCTCTAGCATCGAG	CCACTTTCTCCCGATAGTCCTT	1.11