

Figure S1. TP53 genotyping in HCT116 TP53-WT and HCT116 TP53-KO cell lines. (A) Scheme of genotyping primers for CTCF exon 12 and TP53 exon 2 regions. (B) PCR showing 519 bp amplicon for CTCF exon 12 detected in both TP53-WT and TP53-KO cells, while 220 bp amplicon for TP53 exon 2 detected only in TP53-WT cells.

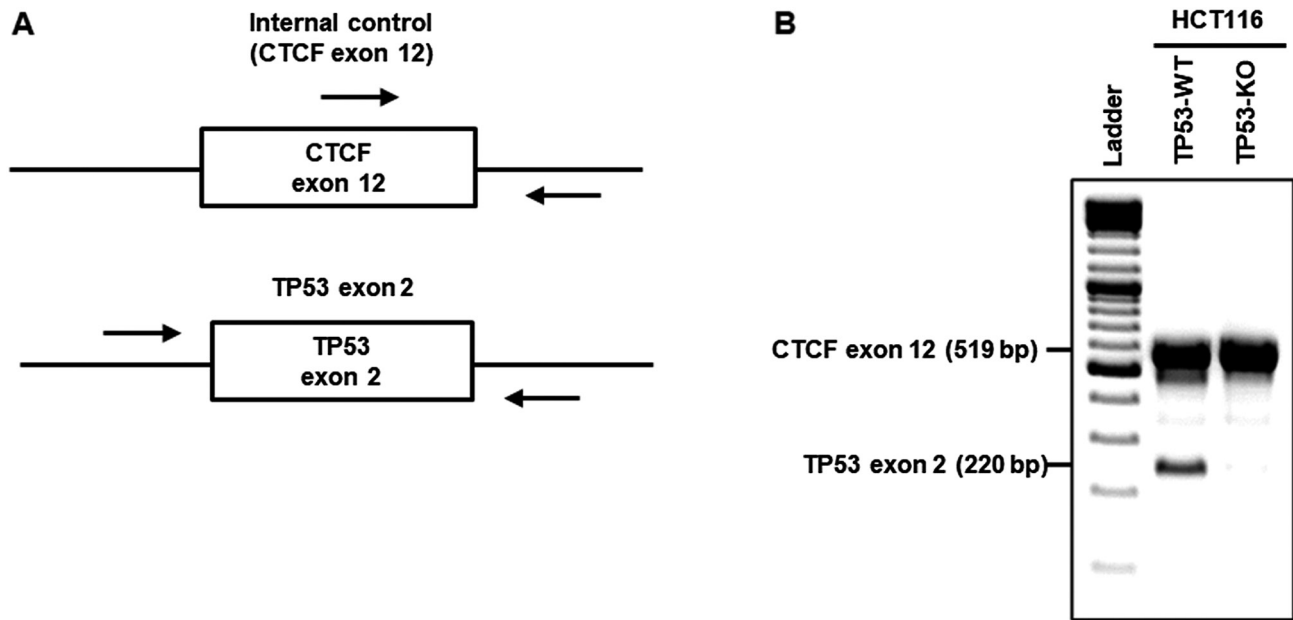


Figure S2. Gene Ontology analysis of 135 genes overlapped among the genes whose expressions and chromatin accessibilities were changed after 5-FU treatment in both TP53-WT and TP53-KO cells.

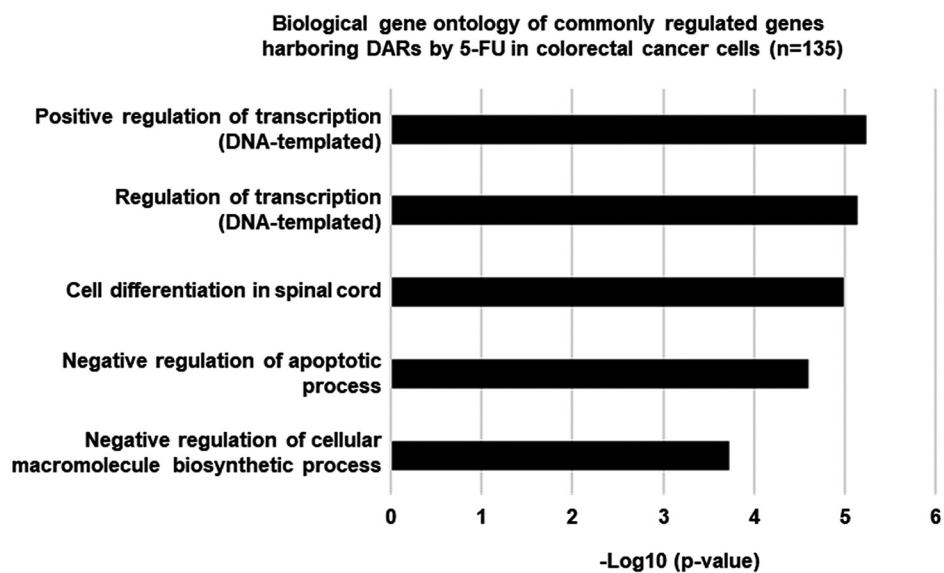


Table SI. List of primers for PCR genotyping.

Target gene	Primers	Sequence
CTCF	CTCF Forward	5'-ACTAGTCTAAAAGACCCTTGTGATTCTTGG-3'
	CTCF Reverse	5'-GGTACCCACTGTCCTCAGCACTTCAC-3'
TP53	TP53 Forward	5'-TTGGAAGTGTCTCATGC-3'
	TP53 Reverse	5'-TCCCACAGGTCTCTGCTAGG-3'

Table SII. List of specifically up-regulated 95 genes in TP53-WT (Adjusted P-value <0.001).

Gene name	Log2 fold change	Adjusted P-value
TIMP3	7.23	2.61x10 ⁻⁵
NID1	5.73	1.39x10 ⁻²
KLHDC7A	5.65	2.47x10 ⁻⁵
ABCA1	5.56	7.66x10 ⁻²
SORCS2	5.33	2.37x10 ⁻¹¹
ICAM1	4.57	2.75x10 ⁻¹⁷
MAST4	4.47	8.64x10 ⁻¹¹
SLC1A3	4.35	2.54x10 ⁻⁸
SH3TC1	4.22	3.22x10 ⁻¹¹
SLC5A5	4.21	1.27x10 ⁻⁸
SYT8	4.19	1.39x10 ⁻³
SULF2	4.10	2.24x10 ⁻²³
KLHL30	3.98	6.03x10 ⁻⁴
KCNB1	3.97	2.99x10 ⁻³
GRIN2C	3.55	7.94x10 ⁻⁸
GDF15	3.53	6.79x10 ⁻³⁰
PXDN	3.48	5.58x10 ⁻¹⁰
PRODH	3.26	4.33x10 ⁻⁶
SUSD2	3.20	2.34x10 ⁻¹⁰
DRAXIN	2.99	6.31x10 ⁻¹¹
RNF152	2.79	2.05x10 ⁻³
FDXR	2.73	2.12x10 ⁻¹⁶
LAMP3	2.72	5.97x10 ⁻⁶
CACNA1A	2.62	1.10x10 ⁻³
NTF4	2.55	3.24x10 ⁻²
CD82	2.51	1.88x10 ⁻⁸
BIRC3	2.49	3.19x10 ⁻⁵
ENC1	2.46	9.54x10 ⁻⁸
PHLDA3	2.39	2.70x10 ⁻⁸
PLPP3	2.33	1.60x10 ⁻²
SLC26A1	2.33	3.14x10 ⁻³
IKBIP	2.28	3.74x10 ⁻⁴
CDKN1A	2.28	4.66x10 ⁻¹⁴
PAG1	2.21	1.82x10 ⁻²
OASL	2.16	6.55x10 ⁻⁴
SEMA3B	2.16	3.19x10 ⁻⁵
NUAK2	2.15	1.10x10 ⁻⁴
GRIN2B	2.14	8.52x10 ⁻⁵
ADGRG1	2.09	6.23x10 ⁻⁹
SLC22A17	2.08	1.92x10 ⁻³
STON2	2.05	2.35x10 ⁻³
NINJ1	2.04	5.97x10 ⁻⁶
SULT1A1	2.00	1.07x10 ⁻²
ABCG4	2.00	2.00x10 ⁻³
BBC3	1.98	2.69x10 ⁻⁴
RIN1	1.95	1.28x10 ⁻⁵
CES3	1.93	2.34x10 ⁻²
ATF3	1.83	1.42x10 ⁻⁵
PTPRU	1.81	4.25x10 ⁻⁶
PGF	1.80	5.47x10 ⁻³
PLXNB1	1.77	9.62x10 ⁻⁵
TMEM92	1.76	4.08x10 ⁻²
NTPCR	1.74	2.08x10 ⁻³
AQP3	1.73	2.82x10 ⁻³
TMEM173	1.70	5.22x10 ⁻³
SERPINE1	1.67	1.56x10 ⁻⁴
P2RY2	1.67	4.66x10 ⁻²

Table SII. Continued.

Gene name	Log2 fold change	Adjusted P-value
ARAF	1.65	2.58x10 ⁻²
PTPRE	1.64	4.57x10 ⁻⁴
CCN1	1.63	2.36x10 ⁻³
HSPG2	1.63	6.36x10 ⁻⁴
CASKIN1	1.57	3.15x10 ⁻²
IRF1	1.57	6.21x10 ⁻³
SLC46A1	1.54	5.22x10 ⁻³
ICOSLG	1.52	1.90x10 ⁻³
SSTR5	1.52	2.83x10 ⁻²
TNS2	1.42	9.44x10 ⁻³
TGFBR2	1.42	3.51x10 ⁻²
SLC4A11	1.41	2.32x10 ⁻²
SLC30A1	1.35	5.22x10 ⁻³
CCDC9B	1.35	3.98x10 ⁻²
ABCB9	1.35	2.01x10 ⁻²
TNFRSF6B	1.33	4.90x10 ⁻²
ESPN	1.33	3.51x10 ⁻²
KDM4B	1.32	2.87x10 ⁻²
NECTIN1	1.31	3.44x10 ⁻³
CYP4F11	1.30	1.09x10 ⁻²
CASZ1	1.29	2.82x10 ⁻²
FADS3	1.29	5.71x10 ⁻³
MINK1	1.27	1.58x10 ⁻²
TNRC18	1.26	1.50x10 ⁻³
LIF	1.22	1.45x10 ⁻²
STARD9	1.21	2.53x10 ⁻²
NRBP2	1.18	3.69x10 ⁻²
CELSR1	1.17	2.66x10 ⁻²
ISYNA1	1.17	1.69x10 ⁻²
CST3	1.13	2.83x10 ⁻²
RHOB	1.12	2.36x10 ⁻²
MICALL2	1.12	2.36x10 ⁻²
PDLIM5	1.12	3.39x10 ⁻²
ABCC2	1.11	1.65x10 ⁻²
SLC12A4	1.10	3.71x10 ⁻²
TRAK1	1.06	3.82x10 ⁻²
AHNAK2	1.03	2.03x10 ⁻²
CTSD	0.98	2.95x10 ⁻²