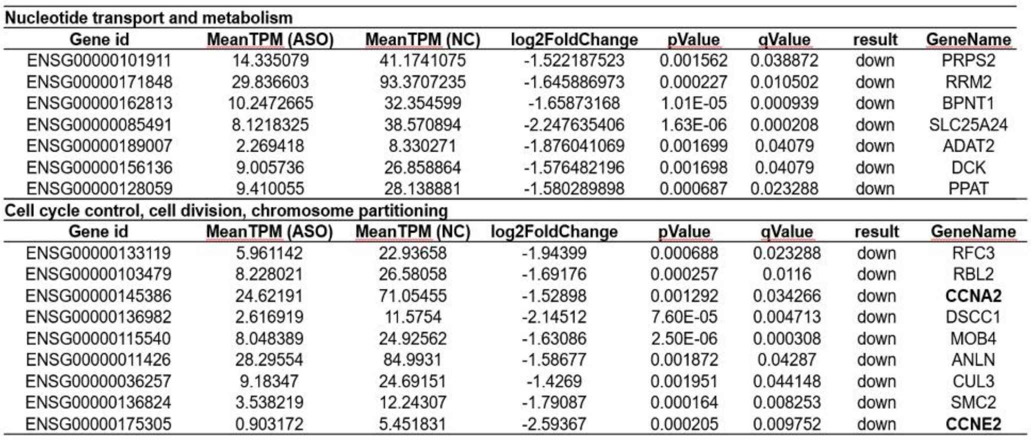
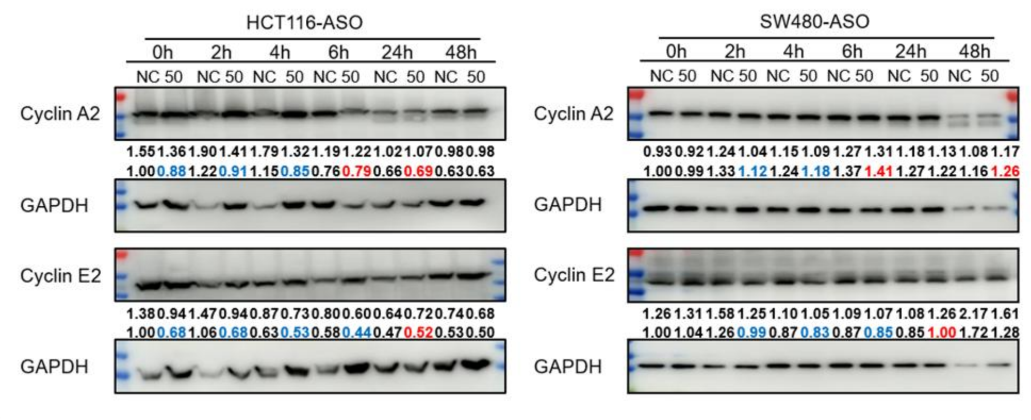
A

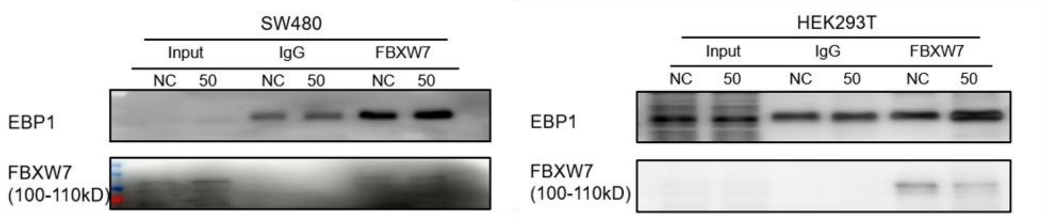


Gene id	MeanTPM (ASO)	MeanTPM (NC)	log2FoldChange	pValue	qValue	result	GeneName
Nucleotide transport and metabolism							
ENSG00000101911	14.335079	41.1741075	-1.522187523	0.001562	0.038872	down	PRPS2
ENSG00000171848	29.836603	93.3707235	-1.645886973	0.000227	0.010502	down	RRM2
ENSG00000162813	10.2472665	32.354599	-1.65873168	1.01E-05	0.000939	down	BPNT1
ENSG00000085491	8.1218325	38.570894	-2.247635406	1.63E-06	0.000208	down	SLC25A24
ENSG00000189007	2.269418	8.330271	-1.876041069	0.001699	0.04079	down	ADAT2
ENSG00000156136	9.005736	26.858864	-1.576482196	0.001698	0.04079	down	DCK
ENSG00000128059	9.410055	28.138881	-1.580289898	0.000687	0.023288	down	PPAT
Cell cycle control, cell division, chromosome partitioning							
Gene id	**MeanTPM (ASO)**	**MeanTPM (NC)**	**log2FoldChange**	**pValue**	**qValue**	**result**	**GeneName**
ENSG00000133119	5.961142	22.93658	-1.94399	0.000688	0.023288	down	RFC3
ENSG00000103479	8.228021	26.58058	-1.69176	0.000257	0.0116	down	RBL2
ENSG00000145386	24.62191	71.05455	-1.52898	0.001292	0.034266	down	**CCNA2**
ENSG00000136982	2.616919	11.5754	-2.14512	7.60E-05	0.004713	down	DSCC1
ENSG00000115540	8.048389	24.92562	-1.63086	2.50E-06	0.000308	down	MOB4
ENSG00000011426	28.29554	84.9931	-1.58677	0.001872	0.04287	down	ANLN
ENSG00000036257	9.18347	24.69151	-1.4269	0.001951	0.044148	down	CUL3
ENSG00000136824	3.538219	12.24307	-1.79087	0.000164	0.008253	down	SMC2
ENSG00000175305	0.903172	5.451831	-2.59367	0.000205	0.009752	down	**CCNE2**

B



C



Supplementary Figure S2. Down-regulated *circ86591* Regulated the Nucleotide Metabolism and Cell Cycle Pathways. (A) The lists showing the set of significantly DEG on the KOG enrichment pathway. (B) The western blot analysis to assess the time-dependent effects of MG132 treatment on intracellular CCNE2 and CCNA2 protein levels upon circ86591 knockdown. (C) The Co-IP analysis of the effect of *circ86591* downregulation on the interaction between EBP1 and FBXW7.