Supplementary Methods

DeepTrio use a Siamese structure with the multiple parallel convolution module to extract various protein features from multiscale windows. Each protein was embedded as a 2D matrix and inputted into the multiscale convolution neural network which generated a group of feature maps using corresponding convolution filters. The filter outputs were activated by the rectified linear unit and yielded a set of nonlinear feature maps. The feature maps were flattened, concatenatedand passed though the dense layers to get the probability vector for prediction.

Supplementary Table 1. Primers used for qPCR analyzes

Gene	Forward Primers	Reverse primers
CDKN1A	5′ -tgtccgtcagaacccatgc-3′	5′ -aaagtcgaagttccatcgctc-3′
BAX	5′ -cccgagaggtctttttccgag-3′	5′ -ccagcccatgatggttctgat-3′
BIX	5′ -cctgcacctgct gctcaag-3′	5′ -ctccagggcagtggtcatg-3′
PTEN	5′ -tttgaagaccataacccaccac-3′	5′ -attacaccagttcgtccctttc-3′
CDH1	5′ -aaaggcccatttcctaaaaacct-3′	5′ -tgcgttctctatccagaggct-3′
CDKN2C	5′ -ggggacctagagcaacttact-3′	5′ -cagcgcagtccttccaaat-3′
ADI1	5′ -ggcctggtatatggacgacg-3′	5′ -gtcagcatccagcttccagta-3′

Supplementary Table 2. Primers used for ChIP qRT-PCR analyzes

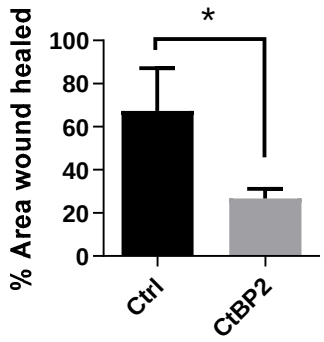
Promoter	Forward Primers	Reverse primers
CDH1	5’- GTGAACCCTCAGCCAATCAG -3’	5’-TCACAGGTGCTTTGCAGTTC -3’
PTEN	5’-GGCTCAGGCGAGGGAGAT-3’	5’-GAAGAGGCTGCACGGTTAGA-3’
p21	5’-GTGGCTCTGATTGGCTTTCTG-3’	5’-CTGAAAACAGGCAGCCCAAG -3’
Bax	5’- CCTGCCCGAAACTTCTAAAAATGG -3’	5’-CCAATGAGCATCTCCCGATAAG-3’

Supplementary Table 3.Protein-protein interaction prediction results for ALDOB by Deeptrio.

Gene symbol	Description	Binding probability
CTBP2	C-terminal-binding protein 2	0.885
CTBP1	C-terminal-binding protein 1	0.326
APC	Adenomatous polyposis coli protein	0.236
HIF1A	Hypoxia-inducible factor 1-alpha	0.102
HRAS	GTPase HRas	0.085
KRAS	GTPase KRas	0.120
MYB	Transcriptional activator Myb	0.027
TP53	Cellular tumor antigen p53	0.120
VHL	von Hippel-Lindau disease tumor suppressor	0.071
BCL2	Apoptosis regulator Bcl-2	0.082

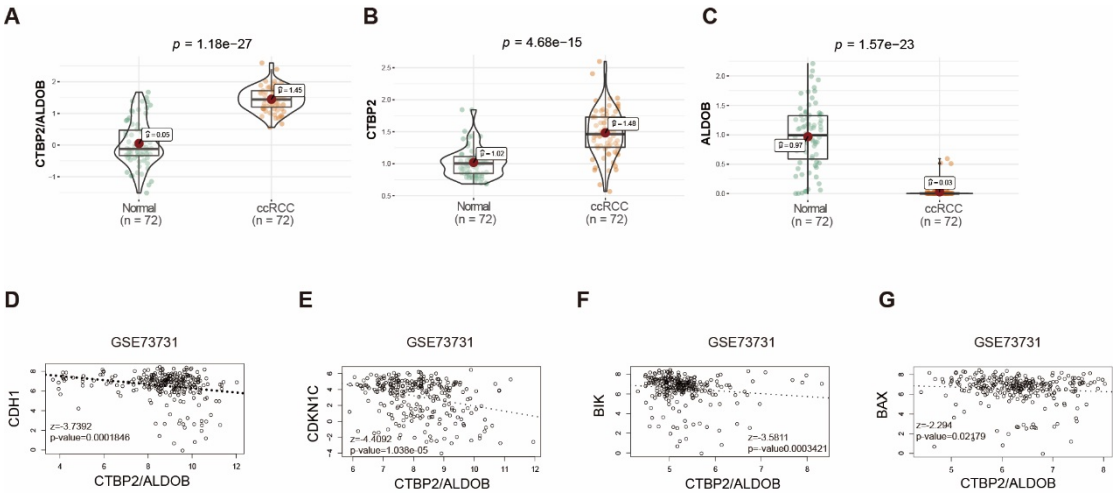
BRAF	Serine/threonine-protein kinase B-raf	0.048
EGFR	Epidermal growth factor receptor	0.188
ERBB2	Receptor tyrosine-protein kinase erbB-2	0.088
ETV1	ETS translocation variant 1	0.036
ETV4	ETS translocation variant 4	0.173
JUN	Transcription factor AP-1	0.068
PDGFB	Platelet-derived growth factor subunit B	0.049
RET	Proto-oncogene tyrosine-protein kinase receptor Ret	0.242
FGFR2	Fibroblast growth factor receptor 2	0.019
NFKB2	Nuclear factor NF-kappa-B p100 subunit	0.019
PAX8	Paired box protein Pax-8	0.020
PIK3CA	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform	0.054
MDM2	E3 ubiquitin-protein ligase Mdm2	0.092
JAK2	Tyrosine-protein kinase JAK2	0.045
BRCA2	Breast cancer type 2 susceptibility protein	0.014
BRCA1	Breast cancer type 1 susceptibility protein	0.004
TSC1	Hamartin	0.025
CDKN2C	Cyclin-dependent kinase 4 inhibitor C	0.058
WT1	Wilms tumor protein	0.046

Supplementary Fig. 1Knockdown of CtBP2 inhibits Caki-1 cell migration



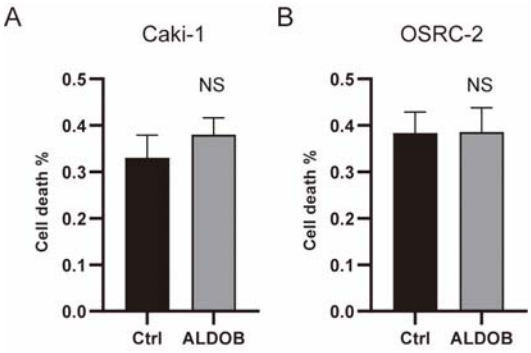
Statistical analysis of the wound healing assay using Caki-1 cells transiently transfected with siCtrl or siCtBP2#1.

Supplementary Fig.2The CtBP2-to-ALDOB expression ratio correlates with CtBP2 target gene expression and is associated with shorter survival



(A) Boxplot of the relative CTBP2-to-ALDOB expression ratio in normal kidneys and ccRCC tissues based on the GSE53757 dataset. (B-C) Boxplot of the relative CTBP2 (B) and ALDOB (C) expression in normal kidneys and ccRCC tissues based on the GSE53757 dataset. (D-G) A scatter plot was used to visualize the relationship between the CtBP2/ALDOB expression ratio and expression of target genes [CDH1 (D), CDKN2C (E), BIK (F), and BAX (G)] in the GSE73731 dataset.

Supplementary Fig. 3Overexpression of ALDOB does not sensitize ccRCC cells to paclitaxel



(A-B) The Caki-1 (A) and OSRC-2 (B) cells were treated with 8 nM paclitaxel for 10 and 12hrs.

Percentages of dead paclitaxel-treated Caki-1 (A) and OSRC-2 (B) cells expressing Ctrl or ALDOB according to the results of the trypan blue exclusion assay. ns indicates not significant.