Figure S1. Immunohistochemical images of CDC45 expression across different cancers compared with control tissues; images were all downloaded from a public online website 'THE HUMAN PROTEIN ATLAS (https://www.proteinatlas.org/)'. CDC45, cell division cycle 45.

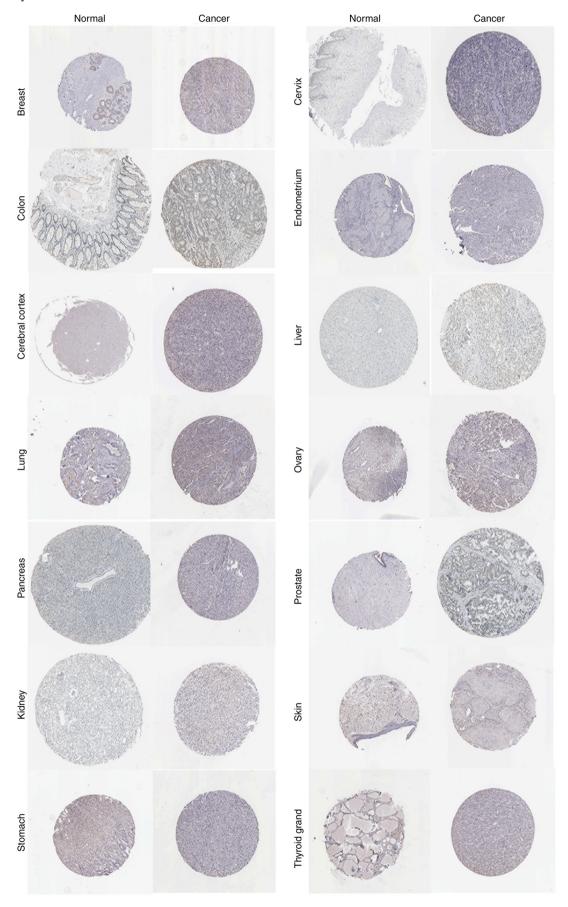


Figure S2. (A) Genomic alterations of CDC45 across different cancers according to cBioPortal. (B) Details of the CDC45 'mutation' diagram of RefSeq: NM-003504. (C) The 3D structure of R175 is shown in the 3D structure of the CDC45 protein (this image was downloaded from a public online website, cBioPortal). CDC45, cell division cycle 45.

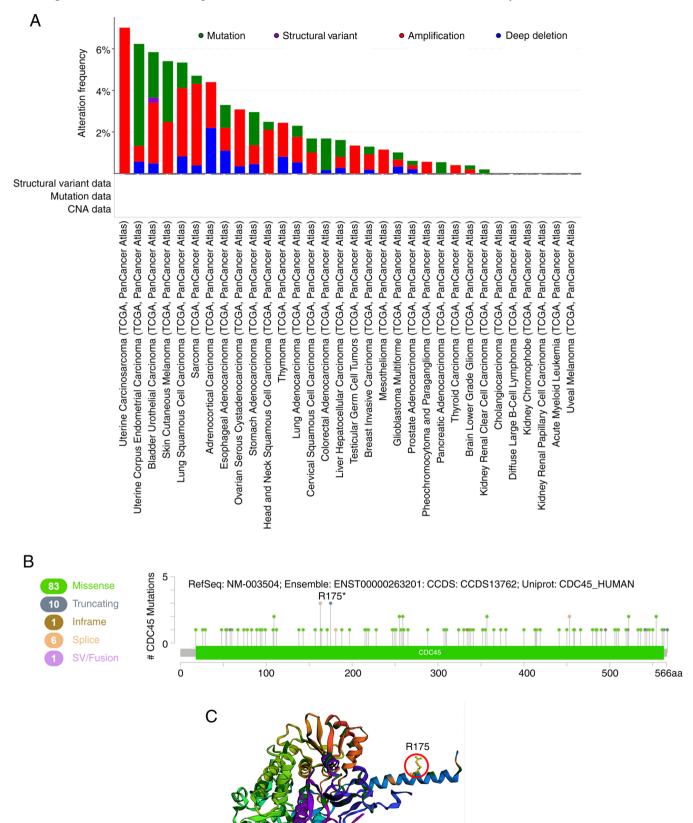


Figure S3. Association between CDC45 and (A) immune checkpoints, (B) immune cells and (C) ESTIMATE in various cancers. *P<0.05, **P<0.01 and ***P<0.001. CDC45, cell division cycle 45; ESTMATE, Estimation of stromal and immune cells in malignant tumor tissues using expression data; GBM gliosblastoma; OV, ovarian serous cystadenocarcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; PRAD, prostate adenocarcinoma; UCEC, uterine corpus endometrial carcinoma; BLCA, bladder urothelial carcinoma; TGCT, testicular germ cell tumors; ESCA, esophageal carcinoma; PAAD, pancreatic adenocarcinoma; KIRP, kidney renal papillary cell carcinoma; LIHC, liver hepatocellular carcinoma; CESC, cervical squamous cell carcinoma and endocervical adenocarcinoma; SARC, sarcoma; BRCA, breast invasive carcinoma; MESO, mesothelioma; COAD, colon adenocarcinoma; STAD, stomach adenocarcinoma; SKCM, skin cutaneous melanoma; CHOL, cholangiocarcinoma; KIRC, kidney renal clear cell carcinoma; THCA, thyroid carcinoma; HNSC, head and neck squamous cell carcinoma; LAML, acute myeloid leukemia; READ, rectum adenocarcinoma; LGG, brain lower grade glioma; DLBC, diffuse large B-cell lymphoma; KICH, kidney chromophobe; UCS, uterine carcinosarcoma; ACC, adrenocortical carcinoma; PCPG, pheochromocytoma and paraganglioma; UVM, uveal melanoma.

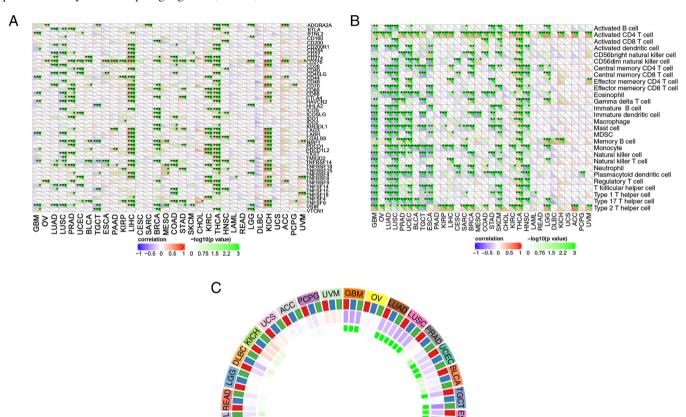


Figure S4. Association between CDC45 and m⁶A posttranslational modification determined using REPIC. CDC45, cell division cycle 45; m⁶A, N⁶-methyladenosine; REPIC, RNA Epitranscriptome Collection.

REPIC | RNA epitranscriptome collection

Gene ID	Gene Name	Gene Type	Cell/ Tissue	exomePeak Sites	MACS2 Sites	MeTPeak Sites	Supported Samples
ENSG00000093009.9	CDC45	protein_coding	A549	1	4	3	5
ENSG00000093009.9	CDC45	protein_coding	H1299	0	1	0	1
ENSG00000093009.9	CDC45	protein_coding	293T	5	18	1	8
ENSG00000093009.9	CDC45	protein_coding	HepG2	0	0	3	1
ENSG00000093009.9	CDC45	protein_coding	Huh7	0	6	1	6
ENSG00000093009.9	CDC45	protein_coding	NOMO-1	0	11	0	2
ENSG00000093009.9	CDC45	protein_coding	U2OS	3	21	0	10
ENSG00000093009.9	CDC45	protein_coding	Jurkat	0	9	0	4
ENSG00000093009.9	CDC45	protein_coding	MA9.3ITD	3	38	3	6
ENSG00000093009.9	CDC45	protein_coding	MA9.3RAS	0	6	0	2
ENSG00000093009.9	CDC45	protein_coding	MOLM13	0	2	1	2
ENSG00000093009.9	CDC45	protein_coding	MT4	0	12	0	4

Figure S5. Results of gene co-expression analysis with CDC45 in different cancers determined using LinkedOmics database. CDC45, cell division cycle 45; ACC, adrenocortical carcinoma; CESC, cervical squamous cell carcinoma and endocervical adenocarcinoma; KICH, kidney chromophobe; KIRP, kidney renal papillary cell carcinoma; LAML, acute myeloid leukemia; LIHC, liver hepatocellular carcinoma; LUAD, lung adenocarcinoma; MESO, mesothelioma; PAAD, pancreatic adenocarcinoma; SARC, sarcoma; SKCM, skin cutaneous melanoma.

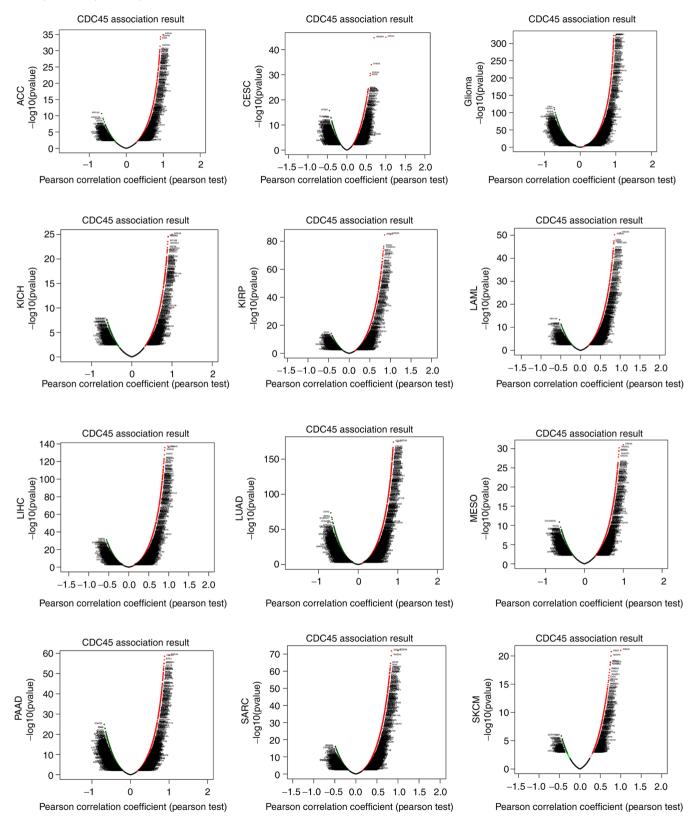


Figure S6. (A) PPI network of CDC45 according to BioGRID. (B) PPI network of CDC45 according to HIPPIE. (C) PPI network of CDC45 according to HitPredict. (D) Venn diagram of potential proteins predicted by BioGRID, HIPPIE and HitPredict databases. (E) GO and KEGG enrichment analysis of CDC45-binding proteins. PPI, protein-protein interaction; CDC45, cell division cycle 45; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

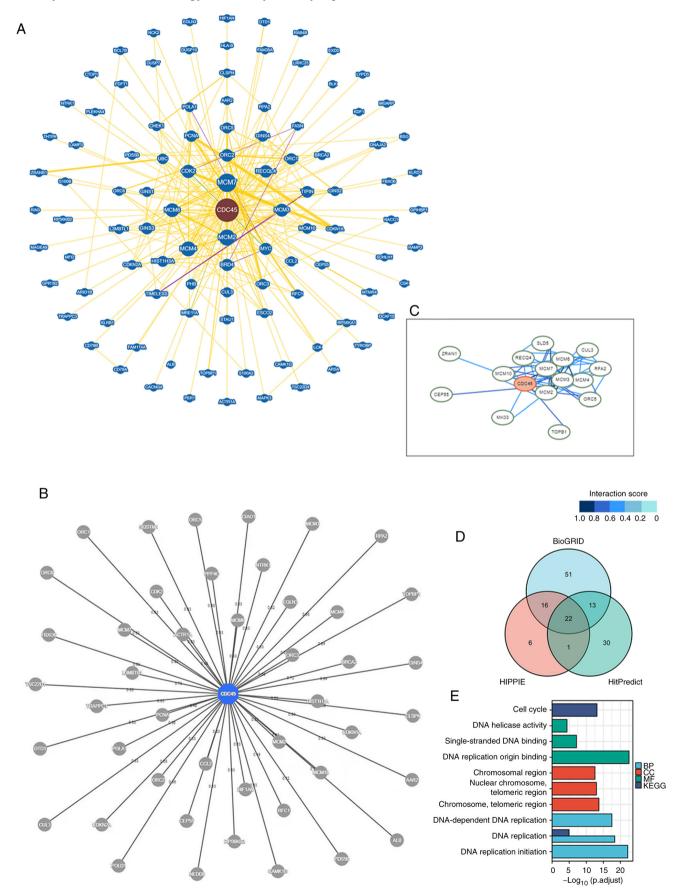


Figure S7. Graphical abstract of the present research. CDC45, cell division cycle 45; TIMER, Tumor Immune Estimation Resource; HPA, Human Protein Atlas; TCGA, The Cancer Genome Atlas; GTex, Genotype-Tissue Expression; TISIDB, tumor-immune system interactions database; GEPIA, Gene Expression Profiling Interactive Analysis; m⁶A, N⁶-methyladenosine; REPIC, RNA Epitranscriptome Collection; STRING, Search Tool for the Retrieval of Interacting Genes/Proteins; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; CCK-8, Cell Counting Kit-8; EdU, 5-ethynyl-2'-deoxyuridine.

