Supplemental Information

Proteomics and Molecular Network Analyses Reveal that the Interaction between the TAT-DCF1 Peptide and TAF6 Induces an Antitumor Effect in Glioma Cells

Jiao Wang[a], Fushuai Wang[a] , Qian Li[a], Qian Wang[a], Jie Li[a], Yajiang Wang [a], Jiamin Sun[b], Dongfang Lu [b], Hong Zhou[a], Shiman Li[a], Sujuan Ma[c], Jiang Xie [b,*] , Tieqiao Wen[a, *]

Table S1

Project	Contents
Data Acquisition Software	Thermo Xcalibur 4.0 (Thermo, USA)
Reversed phase column information	C18 column (75μm x 25cm, Thermo, USA)
Chromatography instrument	EASY-nLC 1200
Mass Spectrometer	Q-Exactive (Thermo, USA)
Chromatographic separation time	90min A : 2% ACNwith 0.1% formic acid B: 80% ACN with 0.1% formic acid
Flow rate	300nL/min
Gradient [Time(min)/B(%)]	0/2,70/40,70.1/90,75/90,75.1/2,90/2
MS scan range (m/z)	350-1300
Acquisition mode	DDA
First-order mass spectrometry resolution	7000
Fragmentation mode	HCD
Secondary resolution	17500

Dynamic exclusion time(s)	18

Table S1. Liquid chromatography tandem mass spectrometry parameters

Table S2

Gene name	Primer sequence (5' to 3')
DCF1	Upstream : CCTACCCCTTGCACACCTAC Downstream : GGGACATGAGTTGTTCTTGTCTC
TAF6	Upstream : GCACATGGGGAAACGACAGAA Downstream : CTTCAAGGCGTAGTCAATGTCA
RPS27A	Upstream : CTCGAGGTTGAACCCTCGGA Downstream : CTGATCAGGAGGAATTCCTTCC
TRAF6	Upstream : CATAGCCCTGGATTCTACAC Downstream : TCTCCTTGCATTGTGTGGAC
HMGB1	Upstream : AAGAAGTGCTCAGAGAGGTGGAAG Downstream : GAAGAAGGCCGAAGGAGGCCTCTT
HMGB2	Upstream : CGGGGCAAAATGTCCTCGTA Downstream : GCAGACATGGTCTTCCATCTCTC
TOP2	Upstream : TGGCTGTGGTATTGTAGAAAGC Downstream : TTGGCATCATCGAGTTTGGGA
GAPDH	Upstream : TCACCACCATGGAGAAGGC Downstream : GCTAAGCAGTTGGTGGTGCA

Table S2.List of the primers used for qPCR

Table S3

Function	*P*-value	Genes in the predicted signaling network
SRP-dependent cotranslational protein targeting to membrane	8.89×10^{-40}	*RPL18, RPL17, RPL14, RPL15, RPS15A, RPLP2, RPL36, RPS2, RPS3, RPS25, RPL30, RPL7, RPL32, RPL31, RPS3A, RPLP0, RPL34, RPL8, FAU, RPL10A, RPL7A, RPS20, RPL12, RPS21, RPS24, RPSA, RPL24, RPL23A, RPS8, RPL29, RPS18, RPS19, RPS16, RPL18A, RPL22, RPL13A, RPS14, RPS10, UBA52*
translational initiation	1.34×10^{-36}	*RPL18, RPL17, RPL14, RPL15, RPS15A, RPLP2, RPL36, RPS2, RPS3, RPS25, RPL30, RPL7, RPL32, RPS3A, RPL31, RPLP0, RPL34, EIF1AY, RPL8, FAU, RPL10A, RPL7A, RPS20, RPL12, RPS21, RPS24, RPSA, RPL24, RPL23A, RPS8, RPL29, RPS18, RPS19, RPS16, RPL18A, RPL22, RPL13A, RPS14, EIF2S1, EIF4A1, RPS10, UBA52*
viral transcription	2.49×10^{-36}	*RPL18, RPL17, RPL14, RPL15, RPS15A, RPLP2, RPL36, RPS2, RPS3, RPS25, RPL30, RPL7, RPL32, RPL31, RPS3A, RPLP0, RPL34, RPL8, FAU, RPL10A, RPL7A, RPS20, RPL12, RPS21, RPS24, RPSA, RPL24, RPL23A, RPS8, RPL29, RPS18, RPS19, RPS16, RPL18A, RPL22, RPL13A, RPS14, RPS10, UBA52*
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	3.52×10^{-35}	*RPL18, RPL17, RPL14, RPL15, RPS15A, RPLP2, RPL36, RPS2, RPS3, RPS25, RPL30, RPL7, RPL32, RPL31, RPS3A, RPLP0, RPL34, RPL8, FAU, RPL10A, RPL7A, RPS20, RPL12, RPS21, RPS24, RPSA, RPL24, RPL23A, RPS8, RPL29, RPS18, RPS19, RPS16, RPL18A, RPL22, RPL13A, RPS14, RPS10, UBA52*

translation	3.23×10^{-26}	*RPL18, RPL17, RPL14, RPL15, RPS15A, RPLP2, RPL36, RPS2, RPS3, RPS25, RPL30, RPL7, RPL32, RPL31, RPS3A, RPLP0, RPL34, RPL8, SLC25A3, FAU, RPL10A, RPL7A, RPS20, RPL12, RPS21, RPS24, RPSA, SLC25A5, RRBP1, SLC25A6, RPL24, RPL23A, RPS8, RPL29, RPS18, RPS19, RPS16, RPL18A, RPL22, RPL13A, RPS14, RPS10, UBA52*
rRNA processing	5.80×10^{-26}	*RPL18, RPL17, RPL14, RPL15, RPS15A, RPLP2, RPL36, RPS2, RPS3, RPS25, RPL30, RPL7, RPL32, RPL31, RPS3A, RPLP0, RPL34, RPL8, FAU, RPL10A, RPL7A, RPS20, RPL12, RPS21, RPS24, RPSA, RPL24, RPL23A, RPS8, RPL29, RPS18, PA2G4, RPS19, RPS16, RPL18A, RPL22, RPL13A, RPS14, RPS10, UBA52*
cell-cell adhesion	5.23×10^{-24}	*HSP90AB1, RPL14, CHMP4B, RPL15, CAPZA1, H1FX, RDX, RPS2, CAPZB, PRDX1, PKM, RACK1, CTTN, HNRNPK, MACF1, RPL34, LRRC59, RANBP1, HSPA5, RPL7A, HSPA8, AHNAK, ENO1, BSG, RAN, FSCN1, RPL24, RPL23A, EEF2, FLNB, YWHAE, ANXA2, RPL29, EVPL, SERBP1, SPTBN2, TMOD3, EEF1G, SPTBN1, DBN1, PUF60, SPTAN1*
movement of cell or subcellular component	1.79×10^{-11}	*ACTB, CAPZA1, VIM, TPM1, CAPZB, TPM4, ACTG1, ACTR3, ARPC1B, ACTR2, TUBB, ARPC3, ARPC2, TXN, RAC1, MSN, TUBB4B*
mitochondrial ATP synthesis coupled proton transport	1.36×10^{-10}	*ATP5B, ATP5F1, ATP5C1, STOML2, ATP5O, ATP5A1, ATP5I, COX5B, ATP5H, ATP5J*
cytoplasmic translation	2.28×10^{-8}	*RPL7, RPL22, RPL31, RPLP0, RPL15, RPL8, RPL36, RPLP2, RPL29*

ATP biosynthetic process	8.43×10^{-8}	*PKM, ATP5B, ATP5F1, ATP5C1, ATP5O, ATP5A1, ATP5I, ATP5H, ATP5J*
protein folding	1.82×10^{-7}	*HSP90AB1, TMX1, HSP90AA1, GNAI3, GNAI2, PDIA3, PDIA6, LMAN1, CANX, TRAP1, HSP90B1, GNB2, PPIA, TXN, HSPE1, DNAJA3, HSPA8, HSPA9*
ATP synthesis coupled proton transport	1.86×10^{-7}	*ATP5B, ATP5F1, ATP5C1, ATP6V0A1, ATP5O, ATP5A1, ATP5H, ATP5J*
cytoskeleton organization	1.15×10^{-6}	*ACTB, CAPZB, TPM1, MAST3, KRT5, MACF1, KRT16, CFL1, AVIL, SPTBN2, SPTBN1, MSN, DST, TUBA1C, SPTAN1, TUBB4B*
ephrin receptor signaling pathway	1.41×10^{-6}	*ACTB, ACTR3, ACTG1, CDC42, ACTR2, ARPC1B, ARPC3, ARPC2, RAC1, RHOA, MYL12A, YES1*
Arp2/3 complex-mediated actin nucleation	4.00×10^{-6}	*ACTR3, ACTR2, ARPC1B, ARPC3, ARPC2, ARPC5L, ARPC4-TTLL3*
protein stabilization	4.48×10^{-6}	*HSP90AB1, HSP90AA1, ATP1B3, FLOT2, PHB, CLU, NAA16, HSPA1B, FLNA, PPIB, PHB2, HSPD1, GAPDH, DNAJA3*
leukocyte migration	7.78×10^{-6}	*CD47, SLC16A1, BSG, KRAS, ATP1B3, PROCR, PPIA, CD58, SHC1, MSN, MYH9, YES1, MIF*
Fc-gamma receptor signaling pathway involved in phagocytosis	1.18×10^{-5}	*ACTB, HSP90AB1, HSP90AA1, MYO1C, ACTG1, ACTR3, ACTR2, ARPC1B, CDC42, ARPC3, ARPC2, RAC1, YES1*
hydrogen ion transmembrane transport	3.27×10^{-5}	*COX7A2, UQCRC1, UQCRH, COX6B1, COX4I1, COX7A2L, COX5A, COX6C, UQCRB*
mitochondrial electron transport, cytochrome c to oxygen	4.22×10^{-5}	*COX6B1, COX4I1, COX7A2L, COX5A, COX5B, COX6C*

viral process	4.75×10^{-5}	*SLC25A5, RAN, VIM, HNRNPA1, YWHAE, VDAC1, RACK1, SET, HNRNPK, C1QBP, CENPA, NPM1, EIF4A1, RHOA, RANBP1, SHC1, HSPD1, RAB6A, HSPA8*
gene expression	5.09×10^{-5}	*HNRNPA3, HNRNPK, HNRNPA2B1, HNRNPD, HNRNPH1, RBMX, HNRNPA1, HNRNPU*
substantia nigra development	5.84×10^{-5}	*ACTB, CDC42, RHOA, ATP5F1, COX6B1, HSPA5, YWHAE, ATP5J*
actin filament capping	1.07×10^{-4}	*GSN, AVIL, SPTBN2, SPTBN1, SPTAN1*
oxidative phosphorylation	1.07×10^{-4}	*UQCRC2, UQCRC1, UQCRH, ATP5C1, UQCRB*
actin filament organization	1.09×10^{-4}	*INPPL1, FSCN1, TMOD3, ACTN1, TPM2, CTNNA1, TPM1, DBN1, TPM4*
muscle filament sliding	1.12×10^{-4}	*MYL6, ACTC1, NEB, VIM, TPM2, TPM1, TPM4*
membrane raft assembly	1.63×10^{-4}	*FLOT2, FLOT1, S100A10, ANXA2*
platelet aggregation	1.74×10^{-4}	*ACTB, ACTG1, ACTN1, MYL12A, MYH9, HBB, FLNA*
cell redox homeostasis	1.76×10^{-4}	*P4HB, TMX1, PDIA3, AIFM1, DLD, TXN, PDIA6, PRDX3, PRDX1*
translational elongation	4.22×10^{-4}	*TUFM, EEF1A1, EEF1G, RPLP2, EEF2*
positive regulation of substrate adhesion-dependent cell spreading	4.48×10^{-4}	*CDC42, C1QBP, ARPC2, RAC1, S100A10, FLNA*
ER to Golgi vesicle-mediated transport	4.67×10^{-4}	*CD55, CD59, ARF4, SPTBN2, TMED10, RAB1B, SPTBN1, LMAN1, NSF, GOLGB1, SPTAN1, BCAP31*
negative regulation of apoptotic process	4.83×10^{-4}	*ACTC1, NAA16, PRDX3, FLNA, MIF, ATAD3A, HSP90B1, PA2G4, HNRNPK, RPS3A, ALB, PHB2, CD59, CFL1, NPM1, ARF4, HSPA5, HSPD1, MYO18A,*

		UBA52, DNAJA3, HSPA9
small GTPase mediated signal transduction	5.73×10^{-4}	*RAB7A, HACD3, RAN, RAB5C, RAB1B, CDC42, KRAS, ARF4, RAC1, RHOA, RAB11A, RAP1A, RAB6B, RAB6A, DNAJA3*
mRNA splicing, via spliceosome	6.86×10^{-4}	*FUS, HNRNPA2B1, RBMX, HNRNPA1, HNRNPU, PNN, SRSF3, NONO, HNRNPA3, HNRNPK, DHX38, HNRNPD, HNRNPH1, HSPA8*
nucleosome assembly	7.67×10^{-4}	*H1F0, HIST1H1E, HIST1H2BN, HIST1H1D, SET, HIST1H4A, HIST1H1C, CENPA, NPM1, H1FX*
response to endoplasmic reticulum stress	8.57×10^{-4}	*P4HB, TMX1, HSP90B1, PDIA3, EIF2S1, FLOT1, PDIA6, EEF2*
mitochondrion organization	1.00×10^{-3}	*SSBP1, PHB2, ATP5B, PHB, STOML2, PRDX3, PARP1, DNAJA3*
positive regulation of gene expression	1.06×10^{-3}	*ACTC1, PHB, VIM, RDX, HSPA1B, HNRNPU, RPS3, CDC42, KRAS, EZR, RPS6KA2, GSN, HNRNPD, MSN, ZPR1*
actin cytoskeleton organization	1.44×10^{-3}	*CDC42, KRAS, RAN, FSCN1, CFL1, RAC1, RHOA, TMOD3, FLNB, CAPZB*
retrograde vesicle-mediated transport, Golgi to ER	1.45×10^{-3}	*ARF4, SURF4, TMED10, RAB1B, RAB6B, RAB6A, BICD2, NSF*
establishment of protein localization to plasma membrane	1.60×10^{-3}	*JUP, EZR, FLOT2, FLOT1, S100A10, RDX*
canonical glycolysis	1.81×10^{-3}	*PKM, TPI1, HK1, GAPDH, ENO1*
protein folding in endoplasmic reticulum	2.09×10^{-3}	*HSP90B1, PDIA3, HSPA5, CANX*

actomyosin structure organization	2.09×10^{-3}	*EPB41L2, ACTC1, MYH9, MYO18A, MYH10*
adenine transport	2.44×10^{-3}	*SLC25A5, SLC25A6, VDAC3*
regulation of organelle assembly	2.44×10^{-3}	*EZR, RDX, MSN*
barbed-end actin filament capping	2.62×10^{-3}	*GSN, CAPZA1, RDX, CAPZB*
actin cytoskeleton reorganization	2.65×10^{-3}	*CTTN, EZR, RHOA, SHC1, MYH9, FLNA*
actin filament bundle assembly	3.11×10^{-3}	*CDC42, EZR, ACTN4, FSCN1, ACTN1*
regulation of complement activation	3.11×10^{-3}	*CD55, C1QBP, C4A, PHB2, CD59*
protein refolding	3.23×10^{-3}	*HSP90AA1, HSPA1B, HSPD1, HSPA8*
mitochondrial electron transport, ubiquinol to cytochrome c	3.23×10^{-3}	*UQCRC2, UQCRC1, UQCRH, UQCRB*
positive regulation of lamellipodium assembly	3.91×10^{-3}	*HSP90AA1, ARPC2, FSCN1, RAC1*
establishment of endothelial barrier	3.91×10^{-3}	*EZR, RAP1A, RDX, MSN*
ATP hydrolysis coupled proton transport	3.96×10^{-3}	*ATP6AP1, ATP5B, ATP6V0A1, ATP1A1, ATP5A1*
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	3.96×10^{-3}	*RPS19, RPS16, RPS14, RPS8, RPS24*
positive regulation of protein localization to early endosome	4.02×10^{-3}	*EZR, RDX, MSN*
aerobic respiration	4.43×10^{-3}	*UQCRC2, UQCRC1, UQCRH, NDUFV1, UQCRB*

Table S3. The top 61 most-enriched functions of the genes that have a *P*-value less than 0.05 in the predicted signaling network regulated by DCF1 in HEK293T-blank, where the

biological process from Gene Ontology was considered.

Table S4

Function	*P*-value	Genes in the predicted signaling network
epidermis development	4.75×10^{-7}	*KRT9, KRT17, KRT5, KRT16, CASP14, KRT14, KRT2, DSP*
intermediate filament organization	1.59×10^{-6}	*KRT9, KRT17, VIM, KRT2, DSP*
establishment of skin barrier	2.65×10^{-6}	*HRNR, FLG, KRT16, KRT1, FLG2*
keratinization	6.99×10^{-6}	*HRNR, KRT17, KRT16, CASP14, KRT2, TGM3*
cytoskeleton organization	3.33×10^{-5}	*ACTB, TUBA8, KRT6B, KRT5, APOE, KRT16, MSN, DST*
keratinocyte differentiation	6.67×10^{-5}	*FLG, KRT16, DSP, TGM3, KRT10, CSTA*
intermediate filament cytoskeleton organization	7.36×10^{-5}	*KRT6C, KRT6A, KRT16, DST*
cellular oxidant detoxification	6.37×10^{-4}	*APOE, ALB, TXN, HBA1, HBB*
mitochondrion organization	9.12×10^{-4}	*SSBP1, PHB2, ATP5B, PHB, PARP1*
protein stabilization	9.98×10^{-4}	*LAMP1, PHB2, PHB, DSG1, HSPD1, GAPDH*
movement of cell or subcellular component	1.38×10^{-3}	*ACTB, TUBB, VIM, TXN, MSN*
retina homeostasis	1.44×10^{-3}	*ACTB, AZGP1, ALB, KRT1*

SRP-dependent cotranslational protein targeting to membrane	1.91×10^{-3}	*RPL7, RPL15, FAU, RPS2, RPL29*
hemidesmosome assembly	1.97×10^{-3}	*KRT5, KRT14, DST*
single organismal cell-cell adhesion	2.48×10^{-3}	*JUP, DSG1, DSP, SHC1, CSTA*
anion transport	2.70×10^{-3}	*VDAC2, VDAC3, VDAC1*
translation	2.97×10^{-3}	*RPL7, SLC25A5, RPL15, SLC25A3, FAU, RPS2, RPL29*
viral transcription	3.61×10^{-3}	*RPL7, RPL15, FAU, RPS2, RPL29*
regulation of anion transmembrane transport	3.99×10^{-3}	*VDAC2, VDAC3, VDAC1*
cell-cell adhesion	4.16×10^{-3}	*BSG, FSCN1, RPL15, RPS2, DBN1, ANXA2, RPL29*
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	4.48×10^{-3}	*RPL7, RPL15, FAU, RPS2, RPL29*
translational initiation	7.34×10^{-3}	*RPL7, RPL15, FAU, RPS2, RPL29*
cytoplasmic translation	8.55×10^{-3}	*RPL7, RPL15, RPL29*
positive regulation of cell death	1.14×10^{-2}	*PHB, HBA1, HBB*
ATP biosynthetic process	1.14×10^{-2}	*LDHC, ATP5B, ATP5A1*
positive regulation of gene expression	1.59×10^{-2}	*APOB, ACTA1, PHB, VIM, ZPR1, MSN*
regulation of heart rate by cardiac conduction	1.64×10^{-2}	*JUP, DSP, AKAP9*
cell envelope organization	1.67×10^{-2}	*HRNR, TGM3*
muscle filament sliding	1.91×10^{-2}	*MYL6, ACTA1, VIM*
lipoprotein metabolic process	1.91×10^{-2}	*APOB, APOE, ALB*

receptor-mediated endocytosis	2.05×10^{-2}	*APOB, APOE, ALB, HBA1, HBB*
lipoprotein catabolic process	2.22×10^{-2}	*APOB, APOE*
adenine transport	2.22×10^{-2}	*SLC25A5, VDAC3*
keratinocyte migration	2.77×10^{-2}	*KRT16, KRT2*
leukocyte migration	3.11×10^{-2}	*APOB, BSG, SHC1, MSN*
peptide cross-linking	3.19×10^{-2}	*DSP, TGM3, CSTA*
rRNA processing	3.22×10^{-2}	*RPL7, RPL15, FAU, RPS2, RPL29*
response to hydrogen peroxide	3.31×10^{-2}	*HSPD1, HBA1, HBB*
bundle of His cell-Purkinje myocyte adhesion involved in cell communication	3.31×10^{-2}	*JUP, DSP*
lipoprotein biosynthetic process	4.93×10^{-2}	*APOB, APOE*

Table S4. The top 40 most-enriched functions of the genes that have a *P*-value less than 0.05 in the predicted signaling network regulated by DCF1 in HEK293T-TAT-DCF1, where the biological process from Gene Ontology was considered.

Table S5

Function	*P*-value	Genes in the predicted signaling network
intermediate filament organization	1.02×10^{-3}	*KRT9, VIM, KRT2*
viral process	1.90×10^{-3}	*SLC25A5, KRT8, VIM, SHC1, HSPD1, VDAC1*

epidermis development	2.07×10^{-3}	*KRT9, KRT5, KRT16, KRT2*
SRP-dependent cotranslational protein targeting to membrane	2.75×10^{-3}	*RPL18, RPL14, RPL15, RPL29*
viral transcription	4.51×10^{-3}	*RPL18, RPL14, RPL15, RPL29*
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	5.34×10^{-3}	*RPL18, RPL14, RPL15, RPL29*
retina homeostasis	6.31×10^{-3}	*ACTG1, ALB, KRT1*
translation	6.73×10^{-3}	*RPL18, RPL14, SLC25A5, RPL15, RPL29*
protein stabilization	7.72×10^{-3}	*PPIB, NAA16, HSPD1, GAPDH*
translational initiation	7.87×10^{-3}	*RPL18, RPL14, RPL15, RPL29*
keratinocyte migration	1.48×10^{-2}	*KRT16, KRT2*
membrane raft assembly	1.77×10^{-2}	*FLOT1, ANXA2*
rRNA processing	2.58×10^{-2}	*RPL18, RPL14, RPL15, RPL29*
chaperone mediated protein folding requiring cofactor	2.94×10^{-2}	*HSPE1, HSPD1*
hemidesmosome assembly	3.52×10^{-2}	*KRT5, DST*
anion transport	4.09×10^{-2}	*VDAC2, VDAC1*
intermediate filament cytoskeleton organization	4.38×10^{-2}	*KRT16, DST*
cell-cell adhesion	4.68×10^{-2}	*RPL14, RPL15, RPL29, ANXA2*
regulation of anion transmembrane transport	4.95×10^{-2}	*VDAC2, VDAC1*

Table S5. The top 19 most-enriched functions of the genes that have a *P*-value less than 0.05 in the predicted signaling network regulated by DCF1 in U251-blank, where the biological

process from Gene Ontology was considered.

Table S6

Function	*P*-value	Genes in the predicted signaling network
SRP-dependent cotranslational protein targeting to membrane	3.89×10^{-5}	*RPL23, RPL14, RPL4, RPL28, RPS27A, RPS8, RPL29*
viral transcription	1.04×10^{-4}	*RPL23, RPL14, RPL4, RPL28, RPS27A, RPS8, RPL29*
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	1.45×10^{-4}	*RPL23, RPL14, RPL4, RPL28, RPS27A, RPS8, RPL29*
translation	2.93×10^{-4}	*SLC25A31, RPL23, RPL14, RRBP1, RPL4, RPL28, RPS27A, RPS8, RPL29*
translational initiation	3.11×10^{-4}	*RPL23, RPL14, RPL4, RPL28, RPS27A, RPS8, RPL29*
rRNA processing	5.79×10^{-4}	*RPL23, RPL14, RIOK3, RPL4, RPL28, RPS27A, RPS8, RPL29*
DNA topological change	1.54×10^{-3}	*HMGB1, HMGB2, TOP2A*
V(D)J recombination	1.92×10^{-3}	*HMGB1, HMGB2, LIG1*
DNA ligation involved in DNA repair	1.92×10^{-3}	*HMGB1, HMGB2, LIG1*
establishment of protein localization to plasma membrane	2.74×10^{-3}	*ROCK1, FLOT2, SPTBN4, FLOT1*

apoptotic DNA fragmentation	4.37×10^{-3}	*HMGB1, HMGB2, KPNB1*
intermediate filament organization	4.98×10^{-3}	*KRT9, VIM, KRT2*
microtubule cytoskeleton organization	1.19×10^{-2}	*SON, MAPT, PAFAH1B1, GAPDH*
positive regulation of interferon-beta production	1.39×10^{-2}	*HMGB1, HMGB2, FLOT1*
adult walking behavior	1.81×10^{-2}	*EFNB3, MAPT, SPTBN4*
DNA geometric change	2.64×10^{-2}	*HMGB1, HMGB2*
negative regulation of cholesterol biosynthetic process	3.29×10^{-2}	*ERLIN1, SCAP*
neuron migration	3.32×10^{-2}	*NDE1, MAPT, DNER, PAFAH1B1*
membrane raft assembly	3.94×10^{-2}	*FLOT2, FLOT1*
regulation of circadian rhythm	4.23×10^{-2}	*MAPK10, TOP2A, FBXL3*
SREBP signaling pathway	4.58×10^{-2}	*ERLIN1, SCAP*
regulation of microtubule motor activity	4.58×10^{-2}	*NDE1, PAFAH1B1*

Table S6. The top 22 most-enriched functions of the genes that have a *P*-value less than 0.05 in the predicted signaling network regulated by DCF1 in U251-TAT-DCF1, where the biological process from Gene Ontology was considered.

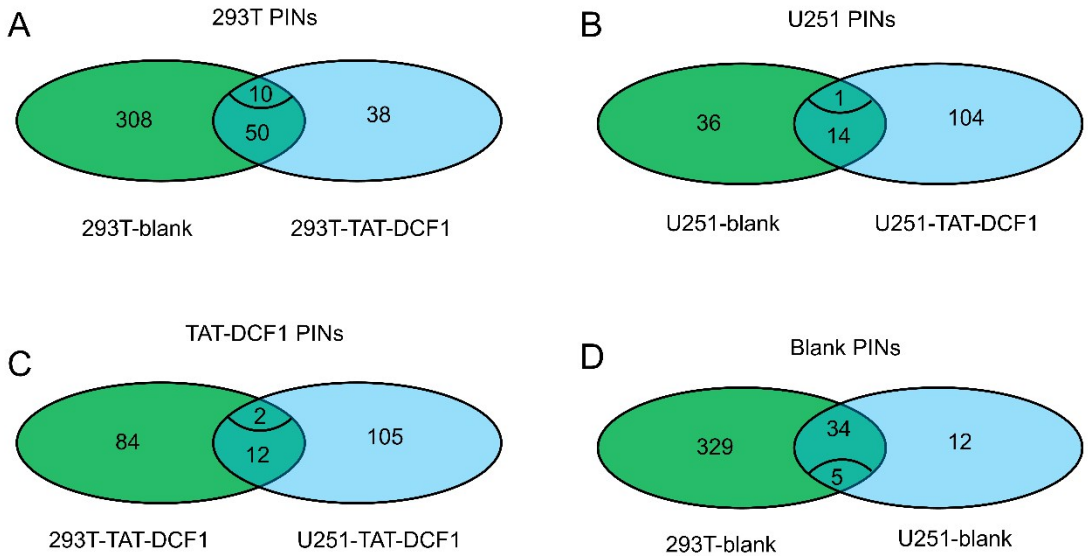


Figure S1. Protein numbers in PINs. The connected PINs were constructed based on the STRING database. HEK293T-blank, HEK293T-TAT-DCF1, U251-blank, and U251-TAT-DCF1 involved 368, 98, 51, and 119 proteins, respectively, among which the D values greater than 0.4 were selected and recognized as proteins with significant changes, which were 10, 1, 2, and 34, respectively.

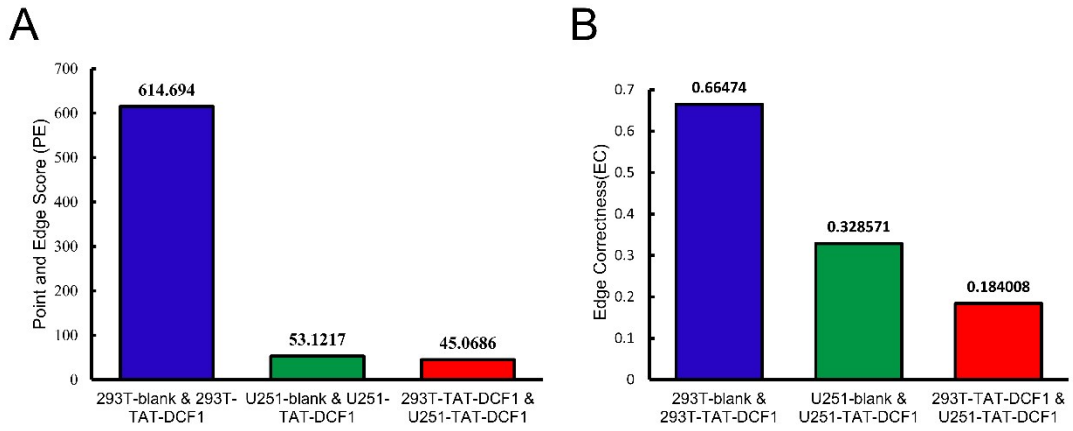
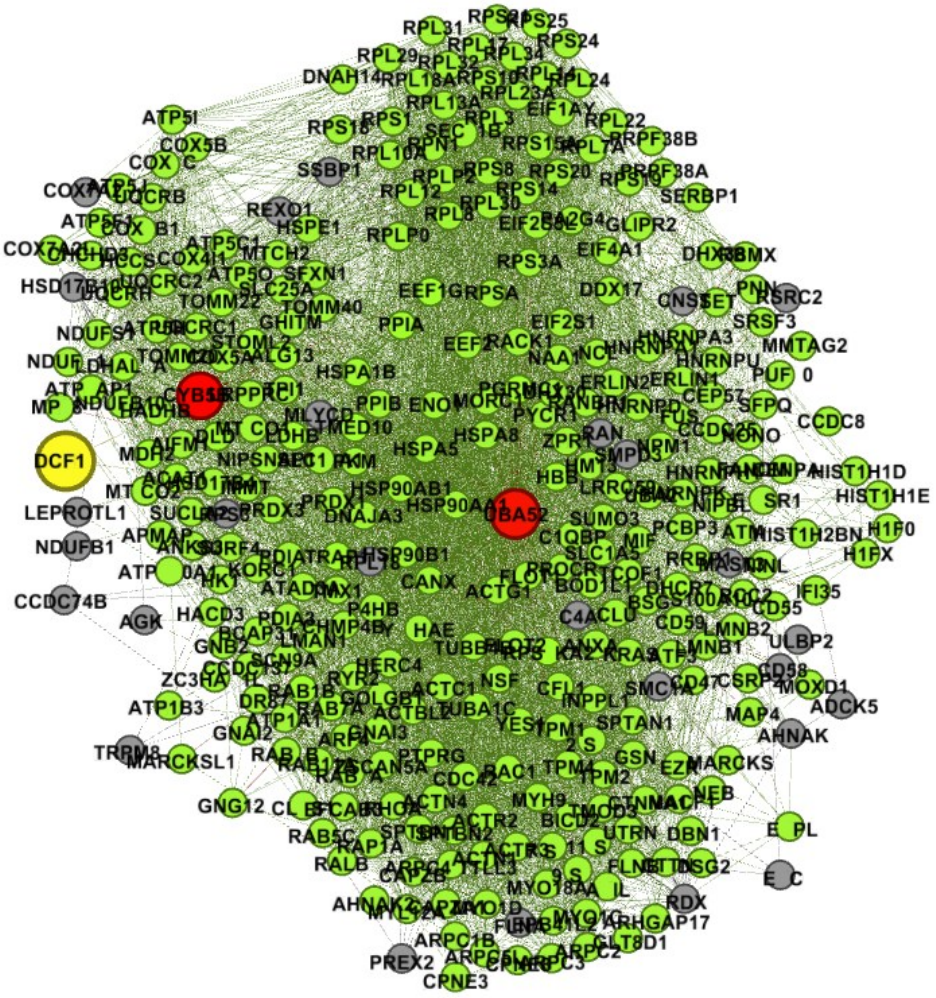


Figure S2. The PES and EC of the protein-protein interaction network.

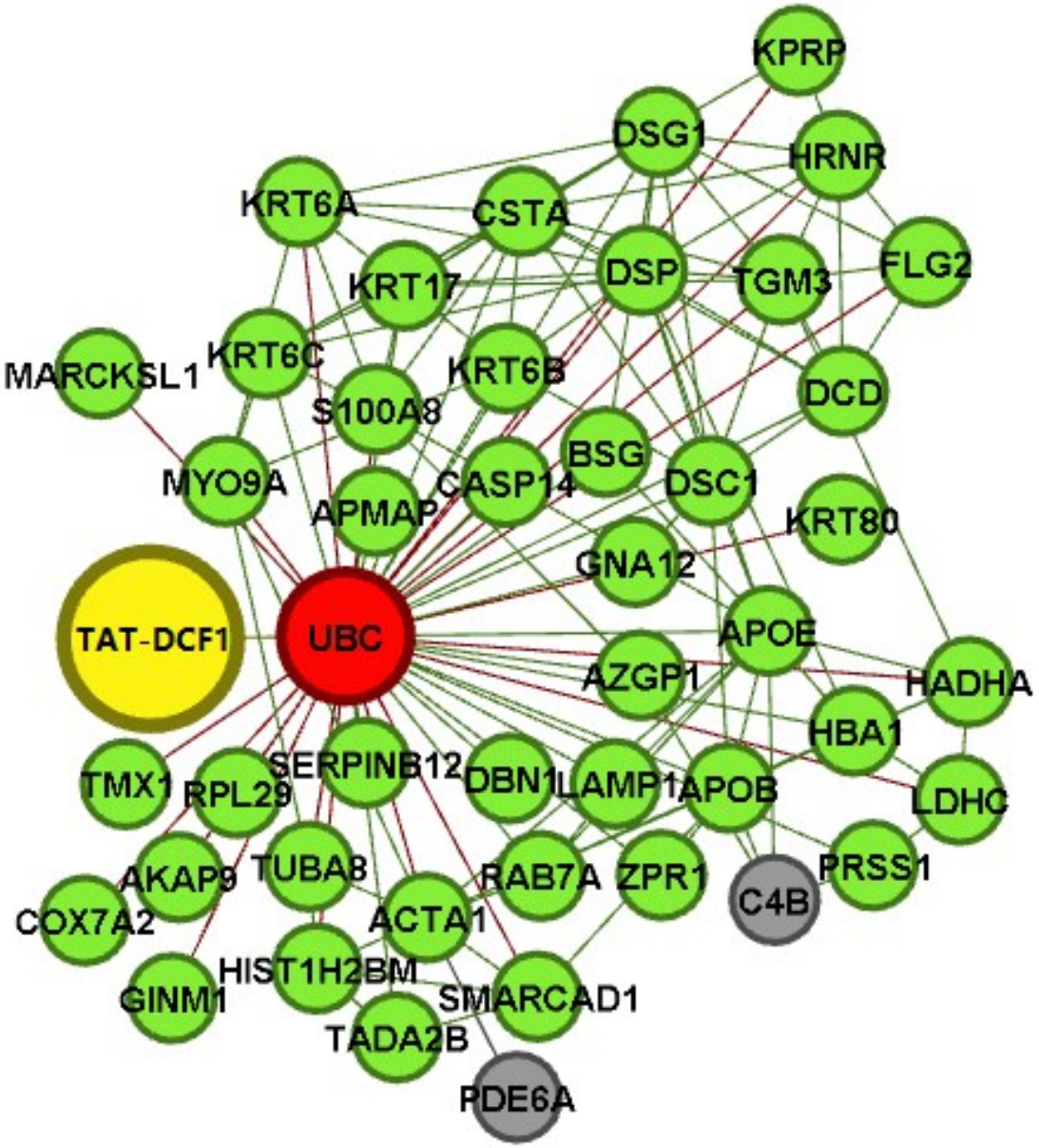
Figure S3

A



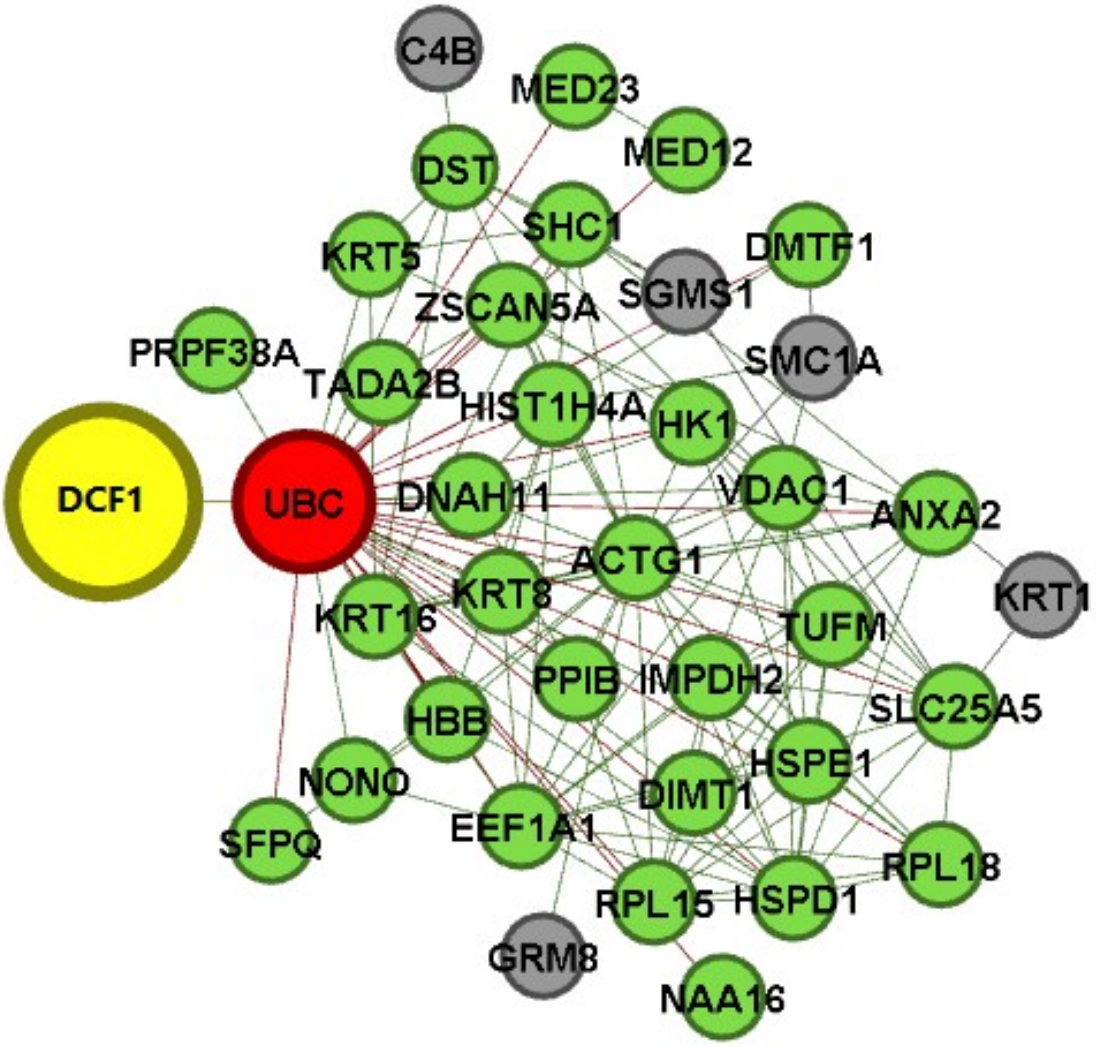
HEK293T-blank (318)

B



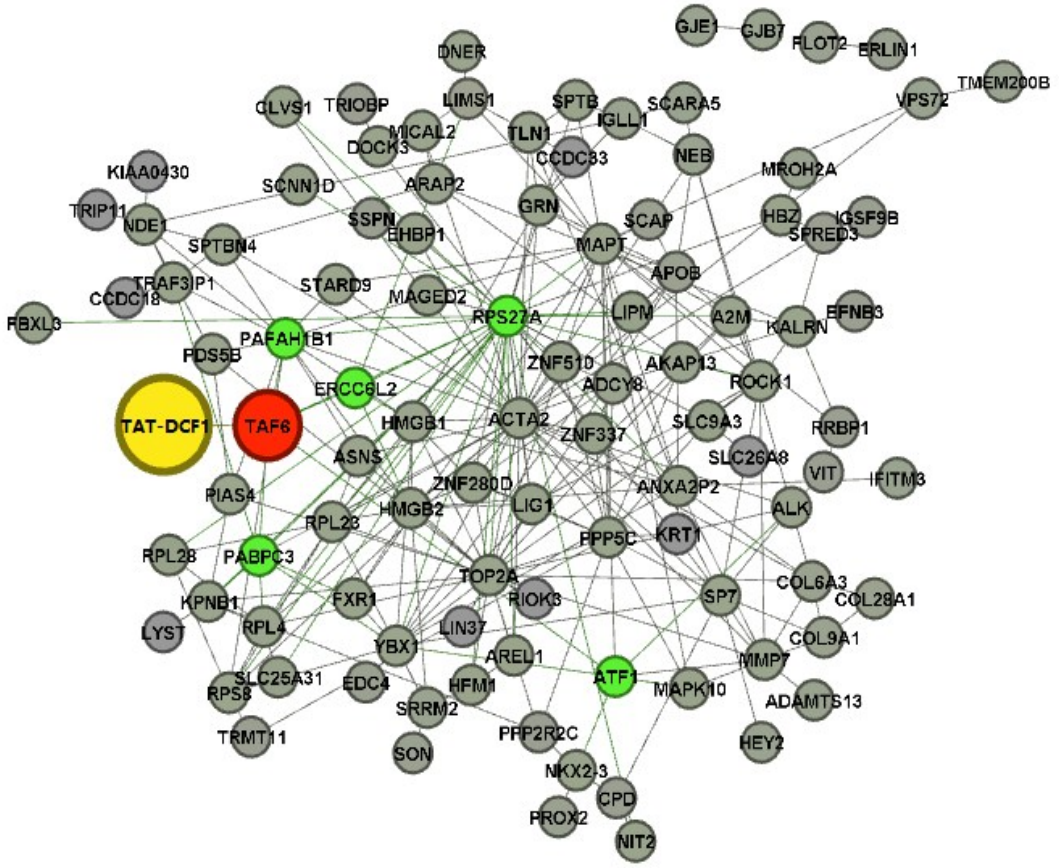
HEK293T-TAT-DCF1（48）

C



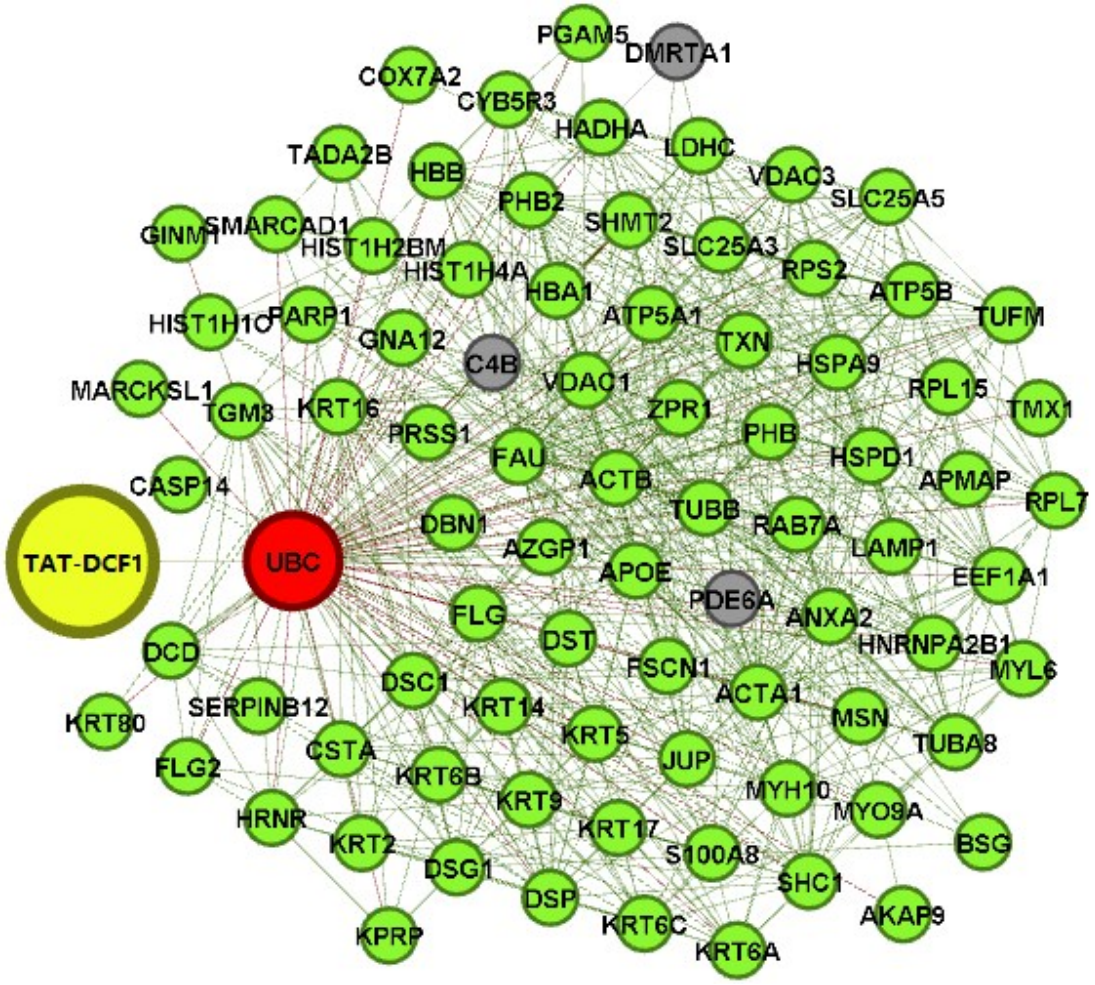
U251-blank (37)

D



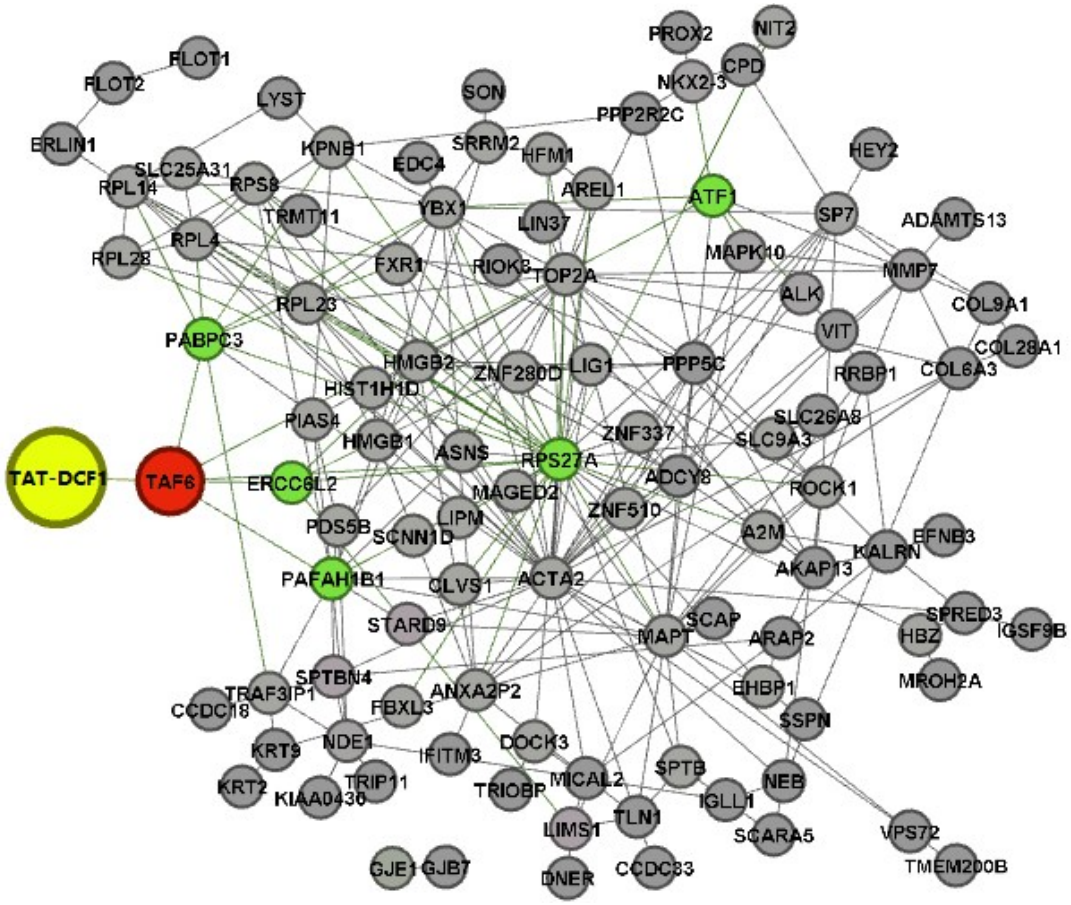
U251-TAT-DCF1 (105)

E



HEK293T-TAT-DCF1 (86)

F



U251-TAT-DCF1 (107)

Figure S3 Protein interaction networks induced by the TAT-DCF1 peptide in U251 and HEK293T cells. Networks were constructed through pairwise comparison between HEK293T-blank (318) (A) and HEK293T-TAT-DCF1 (48) (B) U251-blank (37) (C) and U251-TAT-DCF1 (105) (D), HEK293T-TAT-DCF1(86) (E) and U251-TAT-DCF1(107) (F). The red nodes denote the genes that directly interact with the yellow nodes, and the green nodes denote the genes that directly interact with the red nodes.