

Fig. S1

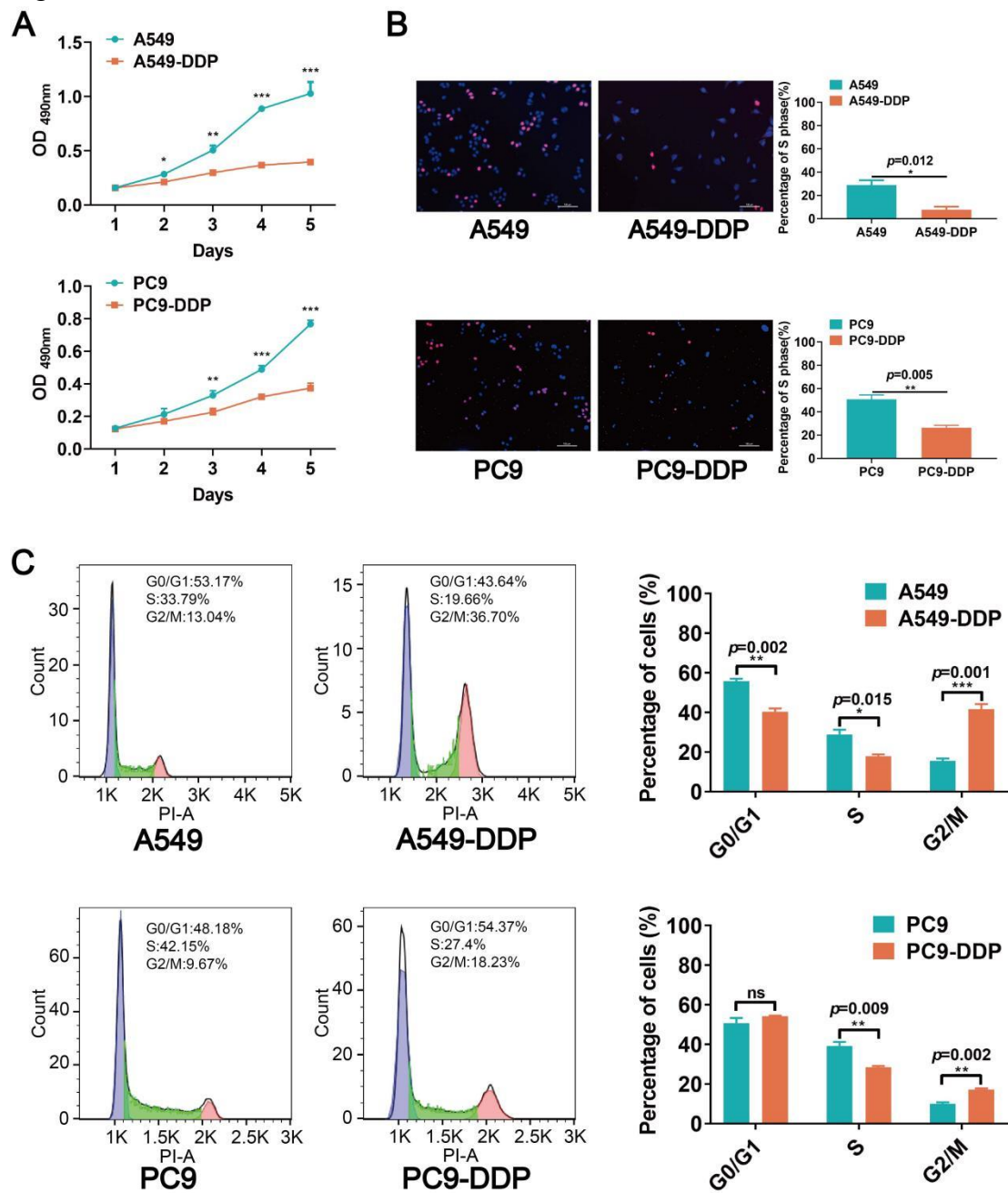


Fig. S1 The proliferative capacity of cisplatin-resistant LUAD cells. (A) The proliferation of cisplatin-resistant and parental cells was measured using Cell Counting Kit-8 (CCK8) assay. Error bars, mean±SEM. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. (B) EdU staining (EdU, red; DAPI, blue) of cisplatin-resistant and parental LUAD cells. Scar bars indicate 100µm. Error bars, mean±SEM. * $p < 0.05$, ** $p < 0.01$. (C) Flow cytometry was used to detect the cell cycle of A549-DDP, PC9-DDP and their corresponding parental cell lines. Error bars, mean±SEM. ns represents no significance. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

Fig. S2

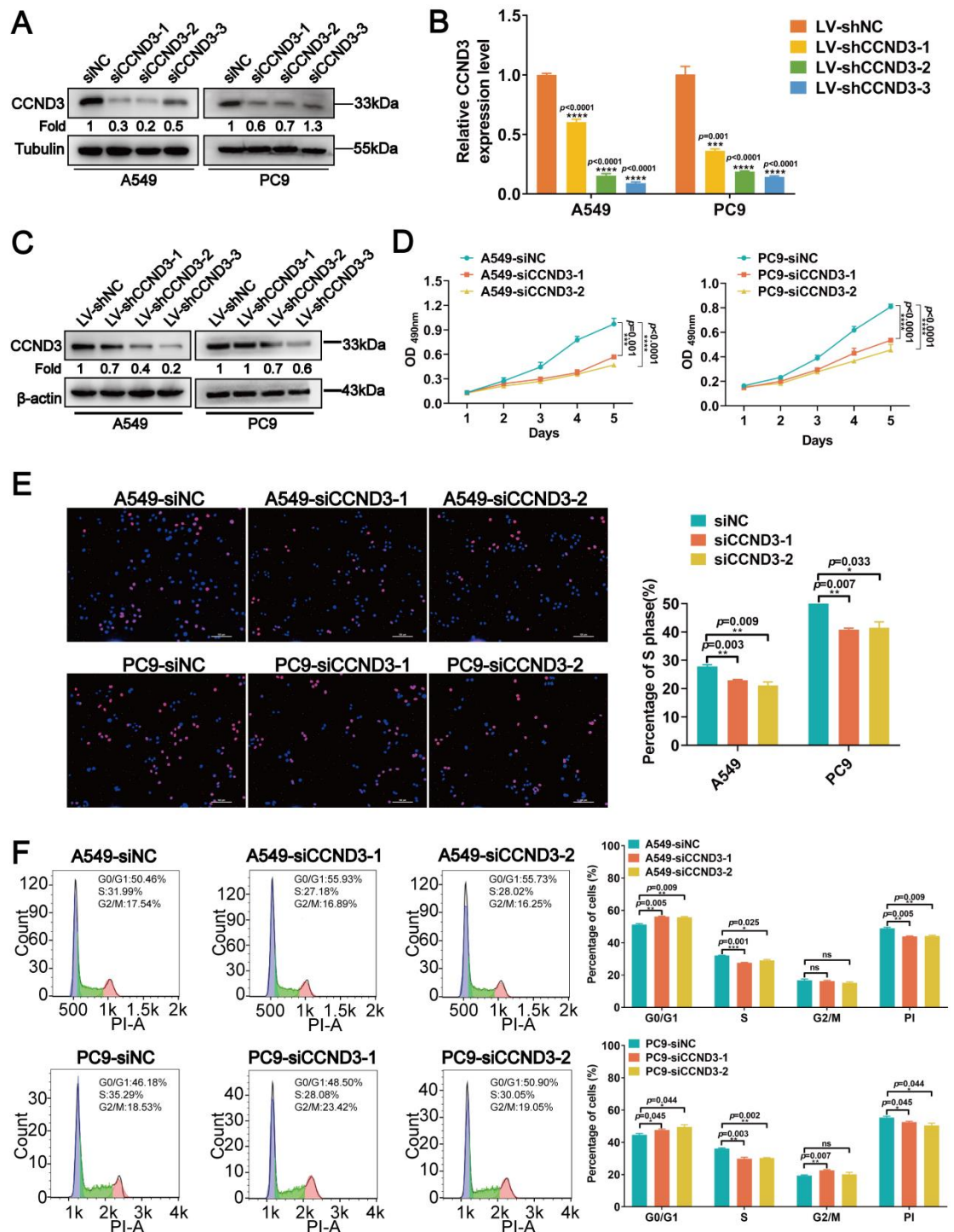


Fig. S2 The identification of CCND3 knockdown and the proliferation of CCND3-depleted LUAD cells. (A) The knockdown efficiency of three siRNAs targeting CCND3 in A549 and PC9 cells was evaluated by Western blot analysis. Tubulin was used as a loading control. (B, and C) The knockdown efficiency of lentivirus-mediated short hairpin RNAs targeting CCND3 in A549 and PC9 cells was evaluated by qRT-PCR (B) and Western blot analyses (C, β -actin was used as a loading control.). Error bars, mean \pm SEM. *** $p < 0.001$, **** $p < 0.0001$. (D, E, and F) The proliferation of CCND3-depleted A549 and PC9 cells was measured by CCK8

assay (D), EdU assay (E) and Cell cycle analysis (F). Scar bars indicate 100 μ m. Error bars, mean \pm SEM. ns represents no significance. * p <0.05, ** p <0.01, *** p <0.001, **** p <0.0001.

Fig. S3

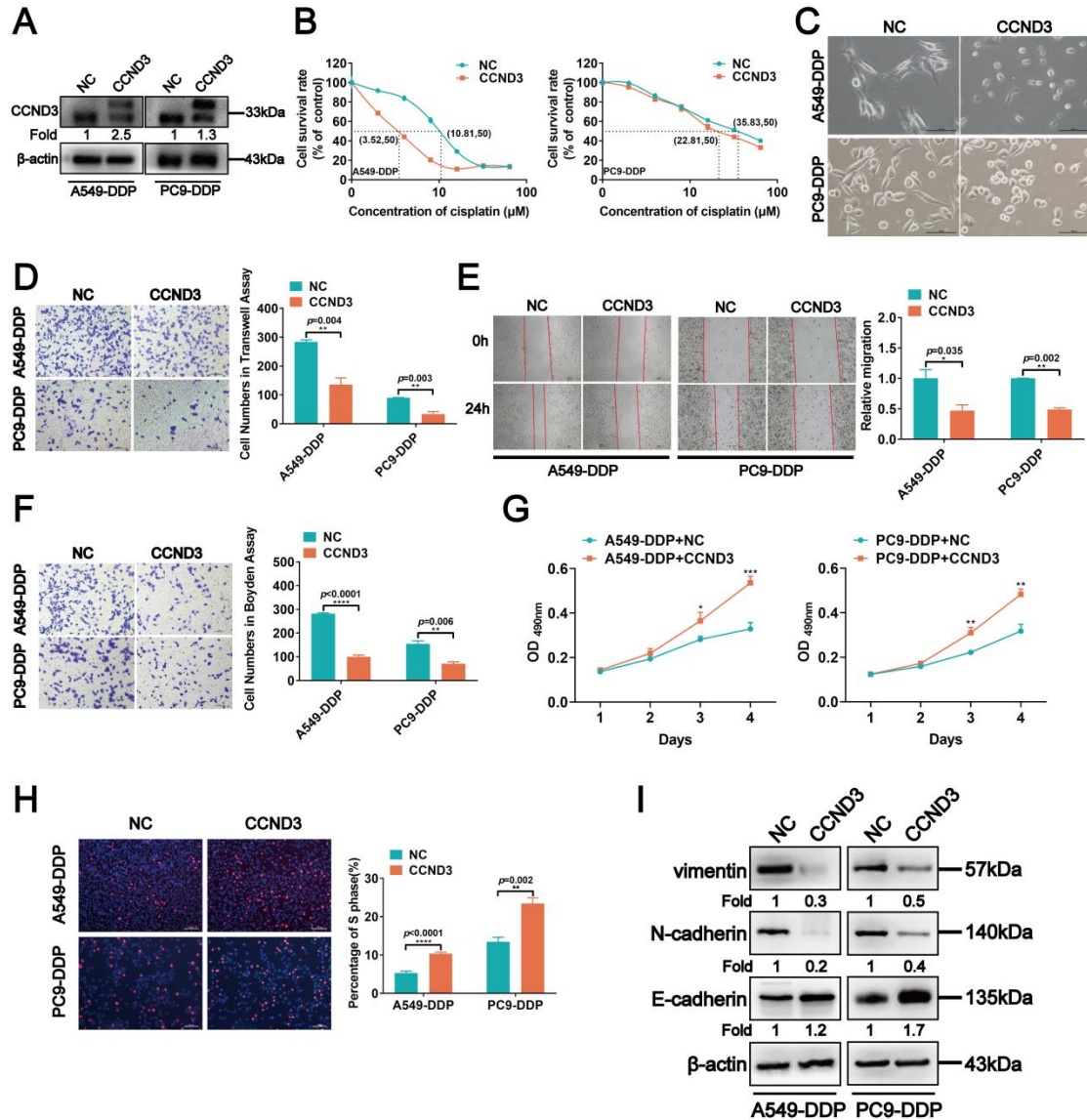


Fig. S3 The phenotypes of CCND3-overexpressed A549-DDP and PC9-DDP cells. (A) The efficiency of CCND3 overexpression in cisplatin-resistant LUAD cells was evaluated by Western blot analysis. β -actin was used as a loading control. (B) The IC₅₀ value of cisplatin was measured in CCND3-overexpressed A549-DDP and PC9-DDP cells. Error bars, mean \pm SEM. (C) The morphology of cisplatin-resistant LUAD cells after CCND3 overexpression. Scar bars indicate 100 μ m. (D, E, and F) Transwell chamber assay (D), wound-healing assay (E) and Boyden chamber assay (F) in CCND3-overexpressed A549-DDP and PC9-DDP cells. Scar bars indicate 100 μ m. Error bars, mean \pm SEM. * p <0.05, ** p <0.01, **** p <0.0001. (G, and H) CCK8 (G) and EdU assay (H) in CCND3-overexpressed A549-DDP and PC9-DDP cells. Scar

bars indicate 100 μ m. Error bars, mean \pm SEM. * p <0.05, ** p <0.01, *** p <0.001, **** p <0.0001. (I) Protein levels of vimentin, N-cadherin, and E-cadherin in CCND3-overexpressed A549-DDP and PC9-DDP cells were detected by Western blot analysis. β -actin was used as a loading control.

Fig. S4

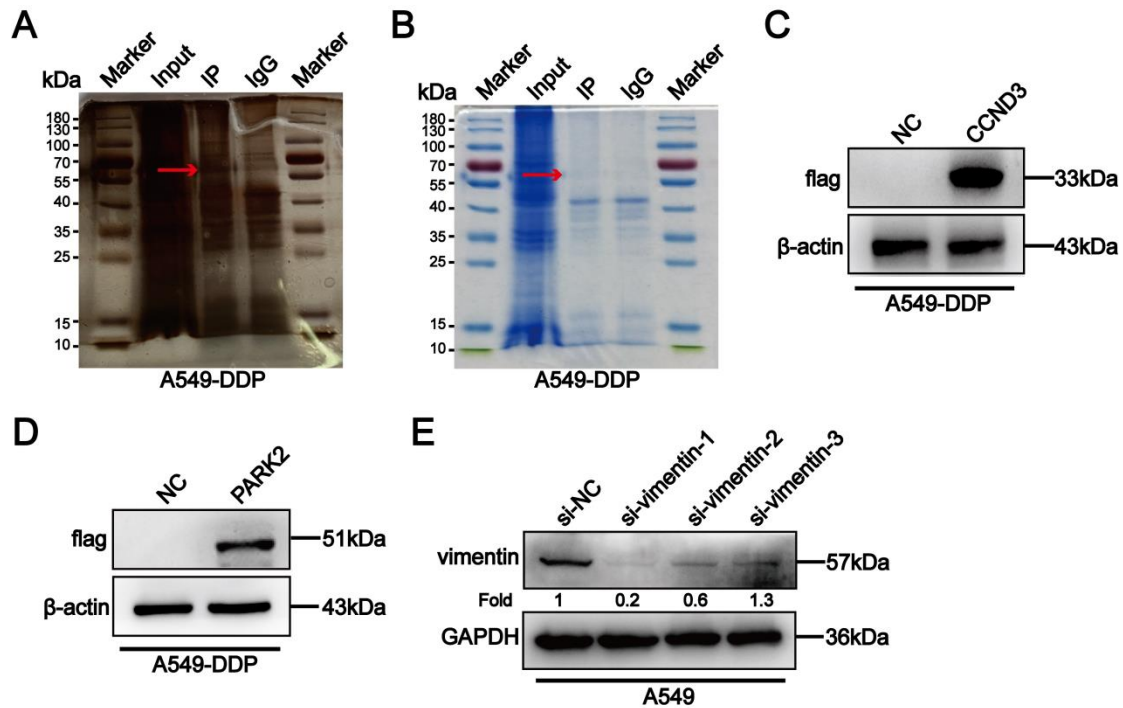


Fig. S4 Plasmids, siRNAs efficiency detection and protein staining. (A, and B) Silver staining (A) and Coomassie Brilliant Blue staining (B) on polyacrylamide gels following co-immunoprecipitation displayed the interacting protein bands of CCND3. Input served as a positive control. Red arrows represent the location of stained vimentin protein. (C) The overexpression of CCND3 in A549-DDP cells after transfection of the Flag-tagged CCND3 plasmids was evaluated by Western blot analysis. β -actin was used as a loading control. (D) The overexpression of PARK2 in A549-DDP cells after transfection of the Flag-tagged PARK2 plasmids was evaluated by Western blot analysis. β -actin was used as a loading control. (E) The knockdown efficiency of three siRNAs targeting vimentin in A549 cells was evaluated by Western blot analysis. GAPDH was used as a loading control.

Table S1.**Supplementary Table 1 The antibodies used in this study.**

| Antibody name | Brand name | Cat: | Dilution |
|--|-------------------|-------------|------------------------|
| β -actin | Fudebio-tech | FD0060 | WB: 1:1000 |
| β -Tubulin | CST | 2128 | WB: 1:1000 |
| GAPDH | Proteintech Group | 60004-1-AP | WB: 1:1000 |
| CCND3 | Proteintech Group | 26755-1-AP | WB: 1:1000; IF: 1:50 |
| CCND3 | CST | 2936 | IHC: 1: 200 |
| N-cadherin | CST | 13116 | WB: 1:1000 |
| vimentin | CST | 5741 | WB: 1:1000 |
| vimentin | Santa Cruz | sc-6260 | IF: 1:50; IP: 1:70 |
| snail | CST | 3879 | WB: 1:1000 |
| E-cadherin | CST | 3195 | WB: 1:1000 |
| p21 | CST | 2947 | WB: 1:1000 |
| p27 | CST | 3686 | WB: 1:1000 |
| CCND1 | CST | 2978 | WB: 1:1000 |
| CDK4 | CST | 12790 | WB: 1:1000 |
| NANOG | Proteintech Group | 14295-1-AP | WB: 1:1000 |
| Oct4 | Proteintech Group | 11263-1-AP | WB: 1:1000 |
| PARK2 | Santa Cruz | sc-32282 | WB: 1:200; IF: 1:50 |
| Ubiquitin | Proteintech Group | 10201-2-AP | WB: 1:1000 |
| c-Jun | CST | 9165 | WB: 1:1000; ChIP: 1:50 |
| phospho-AKT | CST | 4060 | WB: 1:1000 |
| phospho-PI3K | CST | 17366 | WB: 1:1000 |
| flag | Sigma-Aldrich | F1804 | WB: 1:1000; IP: 1:70 |
| 6 \times His | Proteintech Group | 10001-0-AP | WB: 1:1000; IP: 1:70 |
| HRP-conjugated Affinipure Goat Anti-Rabbit IgG (H+L) | Proteintech Group | SA00001-2 | WB: 1:5000 |
| HRP-conjugated Affinipure Goat Anti-Mouse IgG (H+L) | Proteintech Group | SA00001-1 | WB: 1:5000 |
| Goat anti-Mouse IgG (H+L) | | | |
| Cross-Adsorbed Secondary Antibody, Alexa Fluor™ 594 | Invitrogen | A11005 | IF: 1:200 |
| Goat anti-Rabbit IgG (H+L) | | | |
| Cross-Adsorbed Secondary Antibody, Alexa Fluor™ 488 | Invitrogen | A11008 | IF: 1:500 |
| Mouse IgG | CST | 3420 | IP: 1:70 |
| Rabbit IgG | CST | 2729 | ChIP: 1:50 |

Table S2.**Supplementary Table 2 The target sequences of siRNAs used in this study.**

| mRNA name | NO. | Target Sequence |
|-----------------|-----|---------------------|
| <i>CCND3</i> | 1 | ATCGCTACCTGTCTTGCGT |
| | 2 | AGATCGAAGCTGCACTCAG |
| | 3 | CTACAGATGTCACAGCCAT |
| <i>vimentin</i> | 1 | GCAGAAGAATGGTACAAAT |
| | 2 | CAACGAAACTTCTCAGCAT |
| | 3 | GGATGTTGACAATGCGTCT |

Table S3.**Supplementary Table 3 The target sequences of shRNAs from the CCND3 mRNA sequence [GenBank: NM_001760].**

| NO. | Accession | Target Sequence | CDS | GC% |
|-----------------------|---|-----------------------|-----------|--------|
| CCND3-RNAi (85145-3) | NM_001760 | GCTGGTCCTAGGGAAGCTCAA | 200..1078 | 57.14% |
| CCND3-RNAi (85146-11) | NM_001760 | CTGCTGTGATTGCACATGATT | 200..1078 | 42.86% |
| CCND3-RNAi (85147-1) | NM_001760 | ATGGGACAGAATTGGATACAT | 200..1078 | 38.10% |
| Description | Homo sapiens Cyclin D3 (CCND3), transcript variant 2, mRNA. | | | |

Table S4.**Supplementary Table 4 The primers used in this study.**

| Primers name | | Sequence (5'-3') |
|--------------------------|---------|-----------------------|
| GAPDH | Forward | GAACGGGAAGCTCACTGG |
| | Reverse | GCCTGCTTCACCACCTTCT |
| CCND3 | Forward | ACCTGGCTGCTGTGATTGC |
| | Reverse | GATCATGGATGGCGGGTAC |
| c-Jun | Forward | AACTCGGACCTCCTCACCTC |
| | Reverse | TCATCTGTACGTTCTTGGGG |
| promoter of CCND3 site 1 | Forward | TCAGGTCAGGAGTTCGAGAC |
| | Reverse | GCCTCCCGGATTCAAGCTAT |
| promoter of CCND3 site 2 | Forward | ATGGTACTTCGGGCACTTGA |
| | Reverse | ACTCTTACTACACGTCAGGCA |

Table S5.

Supplementary Table 5 Correlation between CCND3 expression and the clinicopathological features of patients with lung adenocarcinomas (LUAD).

| Variables | N | CCND3 expression | | χ^2 | <i>p</i> * value |
|-----------------------|-----|------------------|------------|----------|------------------|
| | | low | high | | |
| Gender | | | | | |
| Male | 111 | 46(41.4%) | 65(58.6%) | 0.936 | 0.333 |
| Female | 102 | 49(48.0%) | 53(52.0%) | | |
| Age | | | | | |
| ≤50 | 41 | 21(51.2%) | 20(48.8%) | 0.900 | 0.343 |
| >50 | 172 | 74(43.0%) | 98(57.0%) | | |
| Clinical stage | | | | | |
| I-II | 154 | 51(33.1%) | 103(66.9%) | 29.675 | 0.000 |
| III-IV | 59 | 44(74.6%) | 15(25.4%) | | |
| T stage | | | | | |
| T1-T2 | 175 | 78(44.6%) | 97(55.4%) | 0.000 | 0.985 |
| T3-T4 | 38 | 17(44.7%) | 21(55.3%) | | |
| N stage | | | | | |
| N0 | 105 | 30(28.6%) | 75(71.4%) | 21.535 | 0.000 |
| N1-N3 | 108 | 65(60.2%) | 43(39.8%) | | |
| M stage | | | | | |
| M0 | 205 | 88(42.9%) | 117(57.1%) | 4.519 | 0.034 |
| M1 | 8 | 7(87.5%) | 1(12.5%) | | |

* Chi-square test was applied to assess the association between CCND3 expression and the clinicopathological parameters.

Table S6.**Supplementary Table 6 The expression levels of CCND3 protein in primary LUAD tissues and metastatic LUAD tissues of lymph node.**

| Classification | N | CCND3 expression | | <i>p</i> * value |
|--|-----|------------------|------------|------------------|
| | | low | high | |
| Primary LUAD tissues | 213 | 95(44.6%) | 118(55.4%) | |
| Metastatic LUAD tissues of lymph node | 12 | 12(100.0%) | 0(0.0%) | 0.000 |

* Fisher's exact test was applied to assess the expression of CCND3 in the primary LUAD group and the metastatic LUAD group.

Table S7.**Supplementary Table 7 CCND3-binding proteins from the approximate 55-70 kDa band screened by liquid chromatography-tandem mass spectrometry.**

| | Accession | Score | Coverage (%) [*] | pI | Protein description |
|---|------------|-------|---------------------------|------|--|
| 1 | ZZZ3_HUMAN | 3784 | 20.3 | 5.62 | ZZ-type zinc finger-containing protein 3 OS=Homo sapiens GN=ZZZ3 PE=1 SV=1 |
| 2 | ACTB_HUMAN | 1224 | 57.1 | 5.29 | Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 |
| 3 | ALBU_HUMAN | 973 | 19.2 | 5.92 | Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 |
| 4 | MYH9_HUMAN | 954 | 16.6 | 5.5 | Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 |
| 5 | ACTC_HUMAN | 575 | 30.2 | 5.23 | Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 |
| 6 | KPYM_HUMAN | 534 | 38 | 7.96 | Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 |

| | | | | | |
|----------|-------------------|------------|-------------|-------------|---|
| 7 | ACTN4_HUMAN | 530 | 24.9 | 5.27 | Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 |
| 8 | POTEE_HUMAN | 513 | 9.5 | 5.83 | POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 |
| 9 | VIME_HUMAN | 480 | 39.7 | 5.06 | Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 |
| 10 | CLH1_HUMAN | 452 | 15.3 | 5.48 | Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 |
| 11 | K2C1_HUMAN | 425 | 17.9 | 8.15 | Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 |
| 12 | CH60_HUMAN | 379 | 31.2 | 5.7 | 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 |
| 13 | ACTBL_HUMAN | 339 | 17.6 | 5.39 | Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 |
| 14 | AL1A1_HUMAN | 328 | 36.7 | 6.3 | Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2 |
| 15 | TKT_HUMAN | 256 | 25.8 | 7.58 | Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3 |
| 16 | CAPZB_HUMAN | 187 | 17.3 | 5.36 | F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4 |
| 17 | NUCL_HUMAN | 176 | 10.6 | 4.6 | Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3 |
| 18 | MYH14_HUMAN | 172 | 2 | 5.52 | Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 |

| | | | | | |
|----|-------------|-----|------|------|---|
| 19 | TPM4_HUMAN | 168 | 26.6 | 4.67 | Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 |
| 20 | K1C10_HUMAN | 167 | 11.3 | 5.13 | Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 |
| 21 | ACTN2_HUMAN | 163 | 5.6 | 5.31 | Alpha-actinin-2 OS=Homo sapiens GN=ACTN2 PE=1 SV=1 |
| 22 | MYH11_HUMAN | 150 | 3.1 | 5.42 | Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3 |
| 23 | AL3A1_HUMAN | 149 | 10.8 | 6.11 | Aldehyde dehydrogenase, dimeric NADP-preferring OS=Homo sapiens GN=ALDH3A1 PE=1 SV=3 |
| 24 | K2C7_HUMAN | 133 | 14.3 | 5.4 | Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 |
| 25 | K1C9_HUMAN | 128 | 7.9 | 5.14 | Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 |
| 26 | K22E_HUMAN | 116 | 4.9 | 8.07 | Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 |
| 27 | HSP7C_HUMAN | 114 | 6.3 | 5.37 | Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 |
| 28 | MYL6_HUMAN | 109 | 30.5 | 4.56 | Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2 |
| 29 | CKAP4_HUMAN | 106 | 11.6 | 5.63 | Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2 |
| 30 | K2C5_HUMAN | 103 | 5.1 | 7.59 | Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 |

| | | | | | |
|----|-------------|-----|------|------|--|
| 31 | G6PI_HUMAN | 101 | 9.9 | 8.43 | Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4 |
| 32 | K2C1B_HUMAN | 98 | 5 | 5.73 | Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3 |
| 33 | LMNA_HUMAN | 97 | 7.5 | 6.57 | Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1 |
| 34 | K2C6B_HUMAN | 96 | 6.7 | 8.09 | Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 |
| 35 | ANXA2_HUMAN | 95 | 14.2 | 7.57 | Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2 |
| 36 | MYH10_HUMAN | 92 | 2.8 | 5.44 | Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3 |
| 37 | GRP75_HUMAN | 90 | 5.2 | 5.87 | Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 |
| 38 | TBB5_HUMAN | 86 | 4.7 | 4.78 | Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 |
| 39 | EF1A1_HUMAN | 84 | 6.7 | 9.1 | Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 |
| 40 | MYO1C_HUMAN | 80 | 5.3 | 9.46 | Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4 |
| 41 | GSTP1_HUMAN | 79 | 36.2 | 5.43 | Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 |
| 42 | TCPQ_HUMAN | 73 | 7.8 | 5.42 | T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 |

| | | | | | |
|----|-------------|----|-----|------|--|
| 43 | UGDH_HUMAN | 68 | 4.7 | 6.73 | UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1 |
| 44 | ATPA_HUMAN | 66 | 6.7 | 9.16 | ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 |
| 45 | K2C3_HUMAN | 61 | 3 | 6.12 | Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3 |
| 46 | MYL1_HUMAN | 61 | 8.2 | 4.97 | Myosin light chain 1/3, skeletal muscle isoform OS=Homo sapiens GN=MYL1 PE=1 SV=3 |
| 47 | AL1L1_HUMAN | 57 | 1.2 | 5.63 | Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 |
| 48 | K1C14_HUMAN | 56 | 8.3 | 5.09 | Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 |
| 49 | TCPH_HUMAN | 56 | 6.8 | 7.55 | T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 |
| 50 | PSMD3_HUMAN | 55 | 1.7 | 8.47 | 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2 |
| 51 | TCPZ_HUMAN | 55 | 6 | 6.23 | T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3 |
| 52 | ENOA_HUMAN | 55 | 7.8 | 7.01 | Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 |
| 53 | RO52_HUMAN | 54 | 1.9 | 5.98 | E3 ubiquitin-protein ligase TRIM21 OS=Homo sapiens GN=TRIM21 PE=1 SV=1 |

| | | | | | |
|----|-------------|----|------|------|---|
| 54 | TCPG_HUMAN | 53 | 4 | 6.1 | T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4 |
| 55 | TPM3_HUMAN | 52 | 17.5 | 4.68 | Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=2 |
| 56 | TBA1A_HUMAN | 51 | 8.6 | 4.94 | Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 |
| 57 | CLH2_HUMAN | 50 | 3.1 | 5.57 | Clathrin heavy chain 2 OS=Homo sapiens GN=CLTCL1 PE=1 SV=2 |
| 58 | PUF60_HUMAN | 47 | 7.5 | 5.19 | Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60 PE=1 SV=1 |
| 59 | TCPA_HUMAN | 46 | 3.2 | 5.8 | T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 |
| 60 | 1433B_HUMAN | 45 | 3.3 | 4.76 | 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 |
| 61 | WDR1_HUMAN | 44 | 5.1 | 6.17 | WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4 |
| 62 | MCLN2_HUMAN | 42 | 1.2 | 7.73 | Mucolipin-2 OS=Homo sapiens GN=MCOLN2 PE=2 SV=2 |
| 63 | RL12_HUMAN | 39 | 5.5 | 9.48 | 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 |
| 64 | AL8A1_HUMAN | 38 | 1.6 | 6.76 | Aldehyde dehydrogenase family 8 member A1 OS=Homo sapiens GN=ALDH8A1 PE=1 SV=1 |
| 65 | TPM1_HUMAN | 36 | 13.7 | 4.69 | Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2 |

| | | | | | |
|----|-------------|----|-----|------|--|
| 66 | AMYP_HUMAN | 35 | 2 | 6.6 | Pancreatic alpha-amylase OS=Homo sapiens GN=AMY2A PE=1 SV=2 |
| 67 | HSP71_HUMAN | 33 | 4.4 | 5.48 | Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5 |
| 68 | PABP1_HUMAN | 33 | 1.3 | 9.52 | Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2 |
| 69 | UACA_HUMAN | 31 | 0.5 | 6.6 | Uveal autoantigen with coiled-coil domains and ankyrin repeats OS=Homo sapiens GN=UACA PE=1 SV=2 |
| 70 | DYH17_HUMAN | 31 | 0.2 | 5.56 | Dynein heavy chain 17, axonemal OS=Homo sapiens GN=DNAH17 PE=1 SV=2 |
| 71 | AP2B1_HUMAN | 31 | 1.1 | 5.22 | AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1 |
| 72 | IGHG1_HUMAN | 30 | 3.6 | 8.46 | Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1 |
| 73 | K2C71_HUMAN | 30 | 5.7 | 6.28 | Keratin, type II cytoskeletal 71 OS=Homo sapiens GN=KRT71 PE=1 SV=3 |
| 74 | KRT82_HUMAN | 30 | 1.4 | 6.4 | Keratin, type II cuticular Hb2 OS=Homo sapiens GN=KRT82 PE=1 SV=3 |
| 75 | ARP5_HUMAN | 30 | 1.5 | 5.17 | Actin-related protein 5 OS=Homo sapiens GN=ACTR5 PE=1 SV=2 |
| 76 | G3P_HUMAN | 29 | 7.8 | 8.57 | Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 |

| | | | | | |
|----|-------------|----|-----|------|---|
| 77 | COR1C_HUMAN | 29 | 5.3 | 6.65 | Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 |
| 78 | NFM_HUMAN | 28 | 3.2 | 4.9 | Neurofilament medium polypeptide OS=Homo sapiens GN=NEFM PE=1 SV=3 |
| 79 | XPP3_HUMAN | 28 | 1.4 | 6.37 | Probable Xaa-Pro aminopeptidase 3 OS=Homo sapiens GN=XPNPEP3 PE=1 SV=1 |
| 80 | HS90A_HUMAN | 28 | 1 | 4.94 | Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 |
| 81 | AXDN1_HUMAN | 27 | 1.5 | 5.49 | Axonemal dynein light chain domain-containing protein 1 OS=Homo sapiens GN=AXDND1 PE=2 SV=1 |
| 82 | RPN2_HUMAN | 27 | 1.4 | 5.44 | Dolichyl-diphosphooligosaccha ride--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=3 |
| 83 | STRN4_HUMAN | 26 | 1.2 | 5.21 | Striatin-4 OS=Homo sapiens GN=STRN4 PE=1 SV=2 |
| 84 | PCLO_HUMAN | 26 | 0.4 | 6.09 | Protein piccolo OS=Homo sapiens GN=PCLO PE=1 SV=4 |
| 85 | DYHC2_HUMAN | 25 | 0.1 | 6.13 | Cytoplasmic dynein 2 heavy chain 1 OS=Homo sapiens GN=DYNC2H1 PE=1 SV=4 |
| 86 | NONO_HUMAN | 25 | 2.5 | 9.01 | Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 |
| 87 | AP2A1_HUMAN | 24 | 2.6 | 6.63 | AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3 |

| | | | | | |
|----|-------------|----|------|------|--|
| 88 | UBB_HUMAN | 23 | 2.6 | 6.86 | Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 |
| 89 | PCL11_HUMAN | 22 | 2.8 | 6.53 | PTB-containing, cubilin and LRP1-interacting protein OS=Homo sapiens GN=PID1 PE=1 SV=1 |
| 90 | ZZEF1_HUMAN | 21 | 0.3 | 5.62 | Zinc finger ZZ-type and EF-hand domain-containing protein 1 OS=Homo sapiens GN=ZZEF1 PE=1 SV=6 |
| 91 | KV201_HUMAN | 21 | 11.3 | 5.28 | Ig kappa chain V-II region Cum OS=Homo sapiens PE=1 SV=1 |
| 92 | TIGAR_HUMAN | 20 | 2.6 | 7.6 | Fructose-2,6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1 |
| 93 | S12A7_HUMAN | 16 | 0.7 | 6.28 | Solute carrier family 12 member 7 OS=Homo sapiens GN=SLC12A7 PE=1 SV=3 |

* Percentage of the protein sequence covered by the matched peptides.