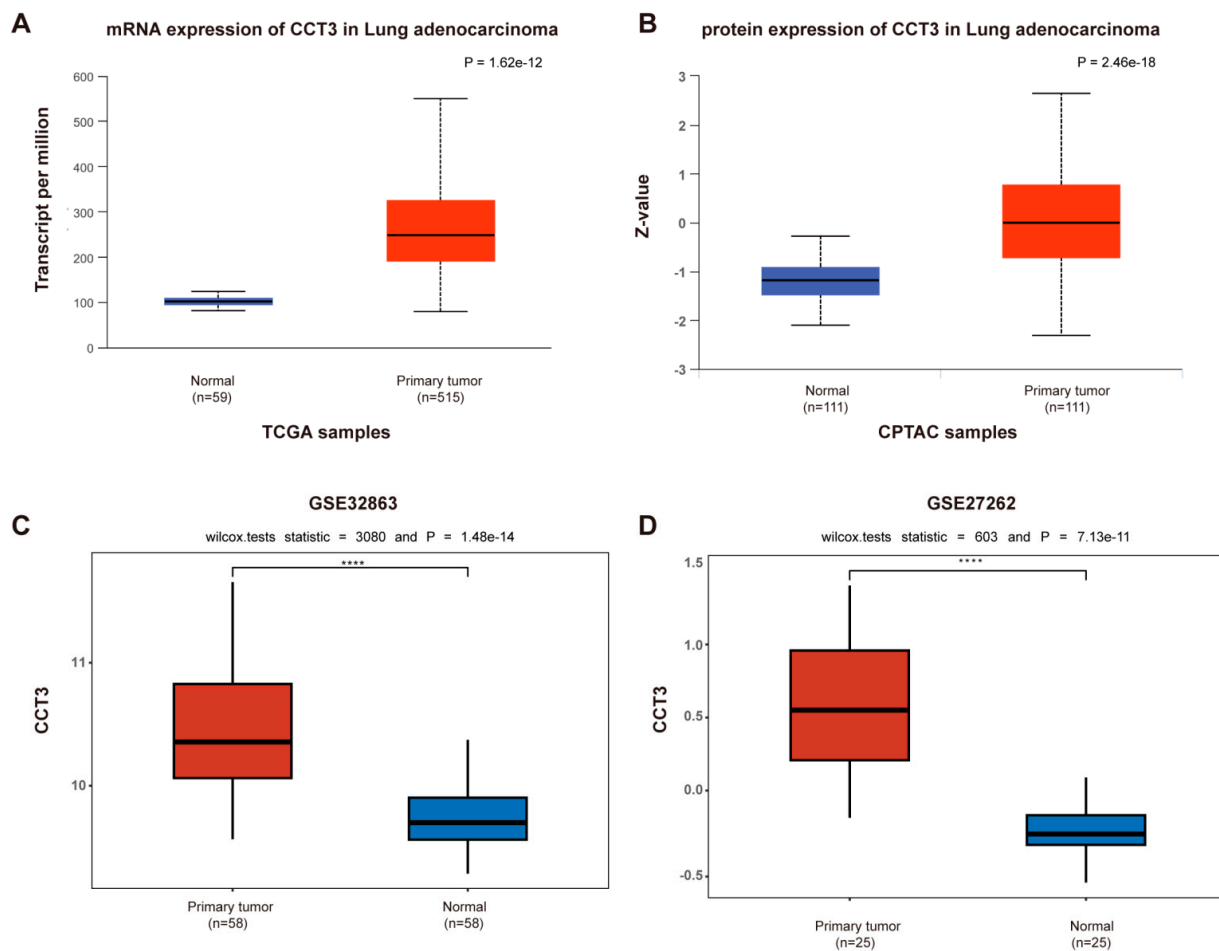




Supplementary Figure S1. Independent validation of CCT3 expression in lung adenocarcinoma.

(A) CCT3 mRNA expression in normal lung and primary LUAD tissues from the TCGA-LUAD cohort analyzed using UALCAN. (B) CCT3 protein abundance in normal lung and LUAD tissues from the CPTAC cohort analyzed using UALCAN. (C) CCT3 expression in 58 paired LUAD and adjacent non-tumor lung tissues from GSE32863. (D) CCT3 expression in 25 paired LUAD and adjacent non-tumor tissues from GSE27262. Statistical significance was evaluated using a two-sided Wilcoxon matched-pairs signed-rank test. Exact P values are indicated in the corresponding panels.

Supplementary Table S1. Clinicopathological characteristics of the NSCLC cohort

Characteristic	Category	n	Percentage (%)
Total cohort		90	100.0
	Median (range)	62	
Age, years	<65	48	53.3
	≥65	42	46.7
Sex	Male	53	58.9
	Female	37	41.1
Histological subtype	Lung adenocarcinoma	90	100.0
	I	39	43.3
TNM stage	II	28	31.1
	III	18	20.0
	IV	5	5.6
	Never smoker	37	41.1
Smoking history	Former smoker	31	34.4
	Current smoker	22	24.4
	Mutant	35	38.9
EGFR status	Wild type	43	47.8
	Not tested/unknown	12	13.3
	Mutant	39	43.3
TP53 status	Wild type	35	38.9
	Not tested/unknown	16	17.8
	Low expression	42	46.7
CCT3 IHC expression	High expression	48	53.3