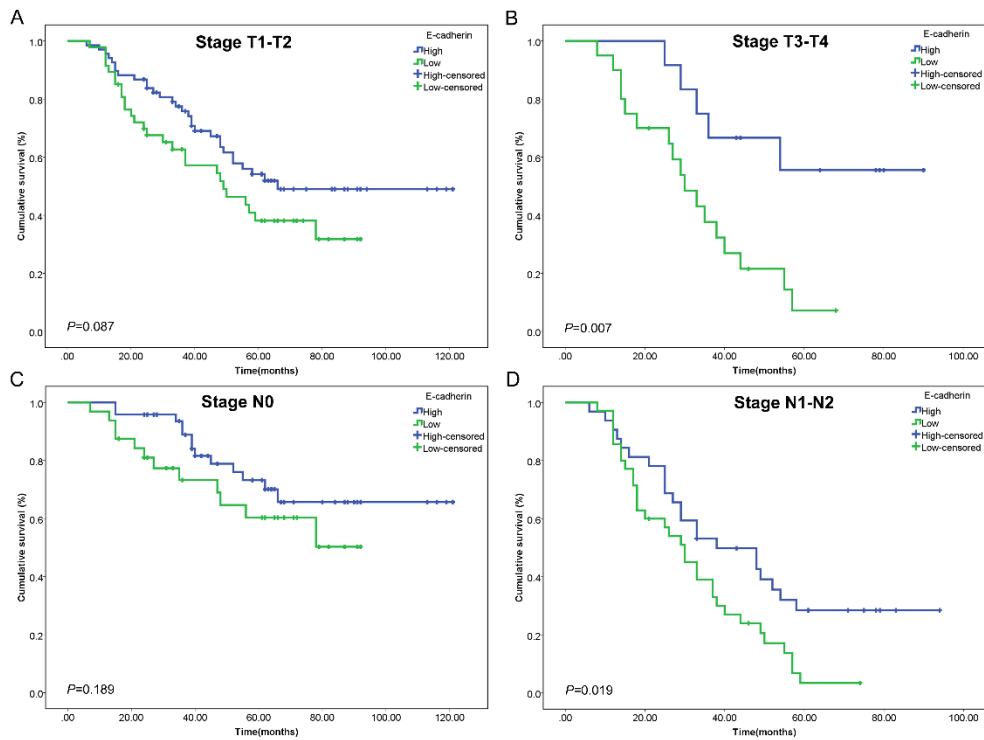
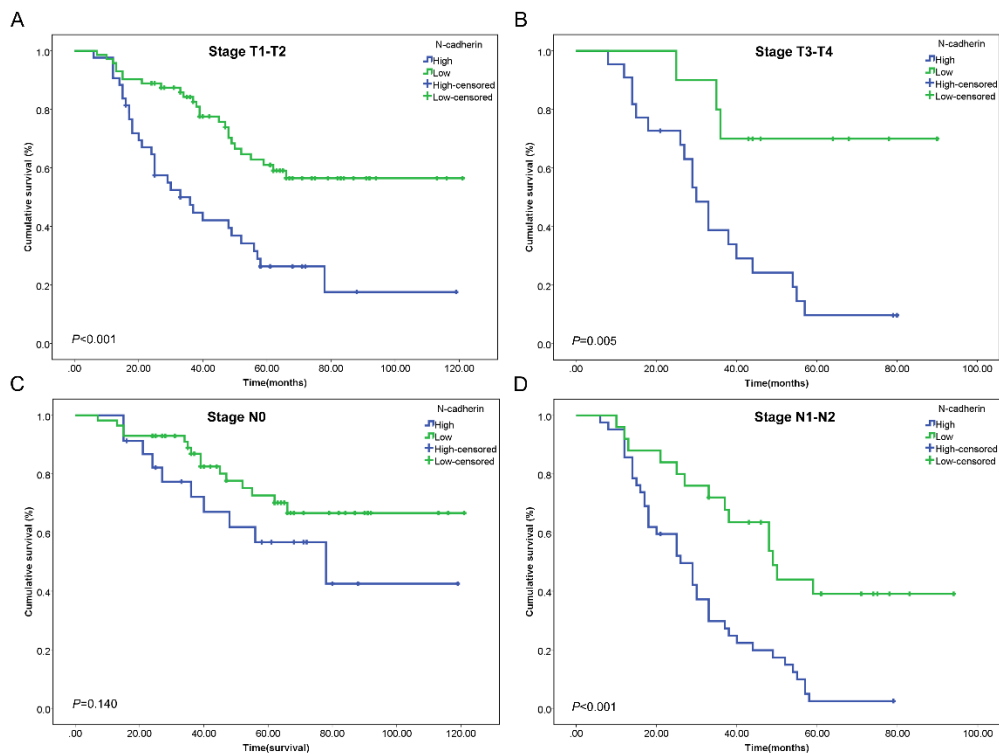


Supplementary Figure 1. Kaplan-Meier curves of E-cadherin stratified by T stage and N stage. The prognostic value of E-cadherin in (A) stage T1-T2 patients ($P=0.087$), (B) stage T3-T4 patients ($P=0.007$), (C) stage N0 patients ($P=0.189$), and (D) stage N1-N2 patients ($P=0.019$).



Supplementary Figure 2. Kaplan-Meier curves of N-cadherin stratified by T stage and N stage. The prognostic value of N-cadherin in (A) stage T1-T2 patients ($P<0.001$), (B) stage T3-T4 patients ($P=0.005$), (C) stage N0 patients ($P=0.140$), and (D) stage N1-N2 patients ($P<0.001$).



Supplementary Table 1. The association between Wnt3a, EMT-related markers and clinical characteristics and lymph node metastasis in lung adenocarcinoma patients.

Factor	Category	Total (N)	Lymph node metastasis (n)	n/N	χ^2	P-value
Wnt3a(C)	low	109	45	41.28%	3.134	0.077
	high	38	22	57.89%		
E-cadherin(C)	low	67	35	52.24%	2.202	0.138
	high	80	32	40.00%		
N-cadherin(C)	low	82	25	30.49%	17.025	<0.001
	high	65	42	64.62%		
Smoke	N	82	36	43.90%	0.21	0.647
	Y	65	31	47.69%		
Gender	F	68	30	44.12%	0.109	0.741
	M	79	37	46.84%		
Age	<70	113	49	43.36%	0.967	0.326
	\geq 70	34	18	52.94%		
Pathological differentiation	poor	46	23	50.00%	0.528	0.468
	moderate and well	101	44	43.56%		
T stage	T1	32	5	15.63%	22.744	<0.001
	T2	83	38	45.78%		
	T3-4	32	24	75.00%		

P-value was tested by Pearson Chi-square analysis

Supplementary Code. The detailed code for building a nomogram.

##Related Computerized Programs for Nomogram With R

```
library(rms)
```

##For Cox Proportional Hazards Model

```
f<-cph(Surv(Time,Survival)~Wnt3a+Ecadherin+Ncadherin+Age+T+N, x=T, y=T, surv=T,
data=bc,Time.inc=1)
```

##For Nomogram

```
surv <- Survival(f)
```

```
nom <- nomogram(f, fun=list (function(x) surv(36, x)), lp=F, funlabel=c("3-year survival"),
maxscale=10, fun.at=c(0,0.05,seq(0,1,by = 0.1),0.95,1))
```

```
plot(nom)
```

##For Resampling Validation of Nomogram

```
validate(f, method = "boot," B = 1000, dxy = T)
```

##For Computing the C-Index and 95% CI

```
rcorrceis(Surv(Time,Survival)~predict(f)) 95%CI, data=bc, 1.96 * se; se = S.D./2
```

##For the Comparison of C-Index in Different Models

```
y <- Surv(bc$Time,bc$Survival)
```

```
rcorrr.cens(x1, x2, y)
```

##For Calibration Curve

```
f3<-cph(Surv(Time,Survival)~Wnt3a+Ecadherin+Ncadherin+Age+T+N, x=T, y=T, surv=T,
data=bc,Time.inc=36)
cal3 <- calibrate(f3, cmethod = "KM", method="boot", u=36, m=35, B=1000)
plot(cal3,lwd=2,lty=1,
      errbar.col=c(rgb(0,118,192,maxColorValue=255)),
      xlim=c(0,1),ylim=c(0,1),
      xlab="Nomogram-Predicted Probability of 3-Year survival",
      ylab="Actual 3-Year survival (proportion)",
      col=c(rgb(192,98,83,maxColorValue=255))
)
```