## **Supplementary Figures**

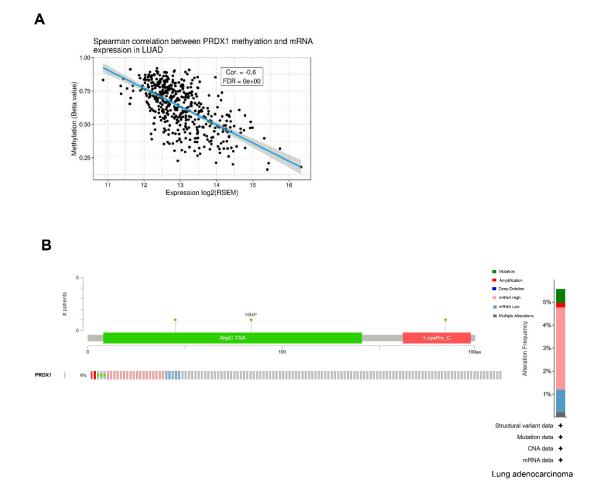
Characteristics Total	(N) OR (95% CI)	P value	Characteristics	Total (N	I) OR (95% CI)	P value
Pathologic T stage (T2&T3&T4 vs. T1) 53		0.038	Pathologic T stage (T2&T3&T4 vs.	,		0.098
Pathologic M stage (M1 vs. M0) 39		0.273	Pathologic M stage (M1 vs. M0	<u>^</u>	1.085 (0.480 - 2.455)	- 0.844
athologic N stage (N1&N2&N3 vs. N0)52		0.007	Pathologic N stage (N1&N2&N3 vs.		1.536 (1.064 - 2.218)	→ 0.022
Gender (Male vs. Female) 53		0.243	Gender (Male vs. Female)	539	1.119 (0.798 – 1.570)	0.515
Age (> 65 vs. <= 65) 52	0 0.898 (0.637 – 1.267)	0.542	Age (> 65 vs. <= 65)	520	0.831 (0.589 – 1.173)	0.293
Smoker (Yes vs. No) 52	25 0.957 (0.590 – 1.552)	0.859	Smoker (Yes vs. No)	525	0.548 (0.333 - 0.900)	0.018
, ,						
Association between PRDX3 expres ogistic regression in the TCGA data		in LUAD by	Association between PRDX4 e logistic regression in the TCG/			n LUAD
Characteristics Total		P value	Characteristics	Total (N		P valu
athologic T stage (T2&T3&T4 vs. T1) 53		0.003	Pathologic T stage (T2&T3&T4 vs.	T1) 536	2.031 (1.405 - 2.934)	-< 0.00
Pathologic M stage (M1 vs. M0) 39		- 0.086	Pathologic M stage (M1 vs. M0	390	0.934 (0.415 – 2.102)	0.86
athologic N stage (N1&N2&N3 vs. N0)52		0.239	Pathologic N stage (N1&N2&N3 vs.	N0)523	1.351 (0.937 – 1.947)	0.10
Gender (Male vs. Female) 53	· · · ·	0.042	Gender (Male vs. Female)	539	1.510 (1.075 – 2.123)	0.01
Age (> 65 vs. <= 65) 52	0 1.132 (0.802 – 1.596)	0.481	Age (> 65 vs. <= 65)	520	0.912 (0.646 – 1.286)	0.598
Smoker (Yes vs. No) 52	25 1.255 (0.772 – 2.039)	0.359	Smoker (Yes vs. No)	525	1.017 (0.627 – 1.650) 🛏 🛏	0.94
	1 2 3 4	5	F			
<ul> <li>Association between PRDX5 expres</li> </ul>		in LUAD by	<ul> <li>Association between PRDX6 logistic regression in the TCG</li> </ul>			in LUAD
<ul> <li>Association between PRDX5 expres</li> </ul>	abase.	s in LUAD by	<ul> <li>Association between PRDX6</li> </ul>		ise.	in LUAD P valu
Association between PRDX5 expree ogistic regression in the TCGA data Characteristics Tota	abase. I (N) OR (95% CI)		Association between PRDX6	A databa Total (N	ase. I) OR (95% CI)	
Association between PRDX5 expre- ogistic regression in the TCGA data Characteristics Tota	abase. (N) OR (95% Cl) 66 1.011 (0.705 – 1.450)	P value	Association between PRDX6 logistic regression in the TCG Characteristics	A databa Total (N T1) 536	ase. I) OR (95% CI)	P valu
Association between PRDX5 expre: ogistic regression in the TCGA data Characteristics Tota athologic T stage (T2&T3&T4 vs. T1) 53 Pathologic M stage (M1 vs. M0) 35	abase. (N) OR (95% Cl) 16 1.011 (0.705 – 1.450) +1→ 10 1.807 (0.779 – 4.195)	P value 0.952	Association between PRDX6 logistic regression in the TCG Characteristics Pathologic T stage (T2&T3&T4 vs.	A databa Total (N T1) 536 ) 390	ase. I) OR (95% CI) 1.297 (0.903 – 1.862) ♥◄	P valu 0.15 0.024
Association between PRDX5 expre: ogistic regression in the TCGA data Characteristics Tota athologic T stage (T2&T3&T4 vs. T1) 53 Pathologic M stage (M1 vs. M0) 35	abase. (N) OR (95% Cl) 16 1.011 (0.705 – 1.450) H→ 1.807 (0.779 – 4.195) → 1.189 (0.825 – 1.712) →	P value 0.952 → 0.168	Association between PRDX6 logistic regression in the TCG Characteristics Pathologic T stage (T2&T3&T4 vs. Pathologic M stage (M1 vs. M0	A databa Total (N T1) 536 ) 390 N0)523	ase. I) OR (95% CI) 1.297 (0.903 – 1.862) • • • 2.949 (1.151 – 7.553)	P valu 0.15 
Pathologic T stage (T2&T3&T4 vs. T1) 53 Pathologic M stage (M1 vs. M0) 39 Pathologic N stage (N1&N2&N3 vs. N0)52	abase. (N) OR (95% Cl) 6 1.011 (0.705 − 1.450) + + + 0 1.807 (0.779 − 4.195) + - 3 1.189 (0.825 − 1.712) + - 9 0.782 (0.557 − 1.098) + +	P value 0.952 0.168 0.353	Association between PRDX6 - logistic regression in the TCG Characteristics Pathologic T stage (T2&T3&T4 vs. Pathologic M stage (M1 vs. M0 Pathologic N stage (N1&N2&N3 vs.	A databa Total (N T1) 536 ) 390 . N0)523 539	ISE. I) OR (95% CI) 1.297 (0.903 – 1.862) ■ → 2.949 (1.151 – 7.553) ↓ → → 1.189 (0.825 – 1.712) ↓ →	P valu 0.159

Supplementary Figure 1: Association between PRDX1-6 expression and clinical characteristics in LUAD. (A-F) Correlation between PRDX1-6 expression and clinical characteristics in LUAD analyzed by logistic regression in the TCGA database.

Characteristics	Total(N)	HR(95% CI) Univariate analysis		P value Univariate analysis
Pathologic T stage	527			
T1	176	Reference	i	
T2	285	1.507 (1.059 - 2.146)	r	0.023
T3&T4	66	3.095 (1.967 - 4.868)		< 0.001
Pathologic N stage	514		I. I	
N0	345	Reference	1	
N1	96	2.293 (1.632 - 3.221)	<b></b>	< 0.001
N2&N3	73	2.993 (2.057 - 4.354)		< 0.001
Pathologic M stage	381		I	
MO	356	Reference	I	
M1	25	2.176 (1.272 - 3.722)	<b>ا</b>	0.005
Gender	530	. ,	I	
Female	283	Reference	I	
Male	247	1.087 (0.816 - 1.448)	4	0.569
Age	520		I	
<= 65	257	Reference	1	
> 65	263	1.216 (0.910 - 1.625)		0.186
Smoker	516			
No	74	Reference		
Yes	442	0.942 (0.625 - 1.420)	<b>⊷</b>	0.775
PRDX1	530	, , , , , , , , , , , , , , , , , , ,	1	
Low	266	Reference		
High	264	1.352 (1.009 - 1.812)	F•••	0.043
PRDX2	530		i	
Low	265	Reference	I	
High	265	1.170 (0.878 - 1.559)	<b>4</b> ∎	0.284
PRDX3	530		1	
Low	267	Reference	1	
High	263	1.463 (1.093 - 1.957)	k	0.01
PRDX4	530	,	I	
Low	264	Reference	I	
High	266	1.218 (0.912 - 1.625)	4 <b>-</b>	0.181
PRDX5	530		1	
Low	262	Reference	I	
High	268	1.093 (0.820 - 1.457)		0.543
PRDX6	530			0.010
Low	265	Reference	1	
High	265	1.604 (1.198 - 2.147)	↓ , <b>⊢</b> •	0.001
- ingri	200	1.004 (1.100 2.147)		0.001

**Supplementary Figure 2**: Independent prognostic risk factors for OS in patients with LUAD. (A) Independent prognostic risk factors for OS in patients with LUAD identified by univariate regression analysis of TCGA-LUAD dataset.

Α



Supplementary Figure 3: Methylation analysis and mutant landscape of PRDX1. (A)Correlation between PRDX1 expression and methylation analyzed in GSCA database.(B) Main mutation sites of PRDX1 genome alterations and mutant landscape ofPRDX1 identified in cBioportal website.