ONLINE SUPPLEMENTARY DATA

Prognostic phenotypes of early-stage lung adenocarcinoma

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Supplementary Table E1. Comparison of the patients selected for the present study with the originating cohort.

	All patient	s (<i>n</i> = 366)	Selected pa	tients (<i>n</i> = 200)	Probability		
	Patients	Percentage	Patients	Percentage	χ^2 test		
Smoking stat							
Never	75	20	43	21	0.0050		
Former	130	36	67	34			
Current	161 44 90		90	45			
Age							
< 45 years	11	3	7	3	0.0424		
45 – 65 years	160	44	88	44	0.9434		
> 65 years	195	53	105	53			
Sex	1			1			
Female	181	49	98	49	0.9301		
Male	185	51	102	51			
Tumor locati	on						
Right lung	163	45	45 98				
Left lung	133	36	76	38	0.1723		
Other	70	19	26	13			
pTNM7 stage	e						
Ia	78	21	42	21			
Ib	60	16	43	21			
IIa	54	15	25 13				
IIb	36	10	17	9	-0.4335		
IIIa	97	26	59 29		\neg		
IIIb	10	3	5	3	1		
IV	31	9	9 4				
Histology			·	1			
Lepidic	16	4	7	4			
Acinar	14	39	75	37	0.0941		
Papillary	70	19	39	19			
Solid	126	34	72 36				
Other	13	4	7	4			

Target	Host	Provider	RRID	Dilution	Conjugate	Incubation			
Primary									
Proliferating cell nuclear antigen, PCNA	Rabbit	Sigma- Aldrich, St. Louis, MO	AB_1855078	1:100	-	2h00 – 37°C			
Tumor protein 53, TP53	Mouse	Thermo Fisher, Waltham, MA	AB_10989883	1:100	-	overnight– 4°C			
Cluster of differentiation 45, CD45	Rabbit	Thermo Fisher, Waltham, MA	AB_2174009	1:250	-	overnight – 4°C			
Anti- hemophillic factor VIII, FVIII	Sheep	Thermo Fisher, Waltham, MA	AB_2262541	1:500	-	2h00 – 20°C			
Neurofibromin 1, NF1	Rabbit	Thermo Fisher, Waltham, MA	AB_2149657	1:500	-	overnight – 20°C			
Programmed cell death-1, PD-1	Mouse	Elabscience, Houston, TX	AB_2891227	1:100	-	overnight– 4°C			
Secondary		Γ	Γ	1	1				
Mouse IgG/IgM	Goat	Jackson, Cambridge, UK	AB_2338505	1:1000	horseradish peroxidase	1h30 – 20°C			
Rabbit IgG	Mouse	Abcam, London, UK	AB_2650595	1:5000	horseradish peroxidase	1h30 – 20°C			
Goat IgG with Sheep reactivity	Mouse	Santa Cruz Biotechnolo gy, Dallas, TX	AB_628490	1:50	horseradish peroxidase	1h00 – 20°C			

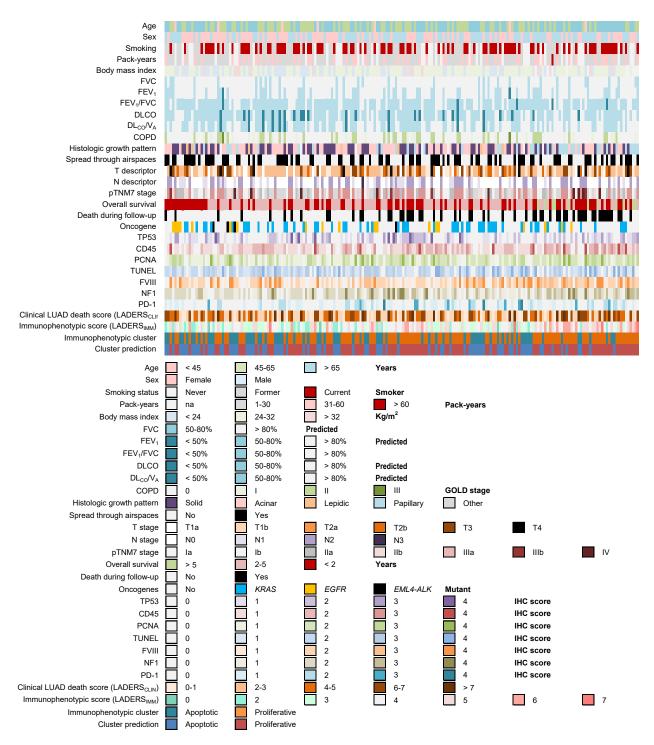
SupplementaryTable E2. Antibodies used in the present study.

RRID, research reagent identification.

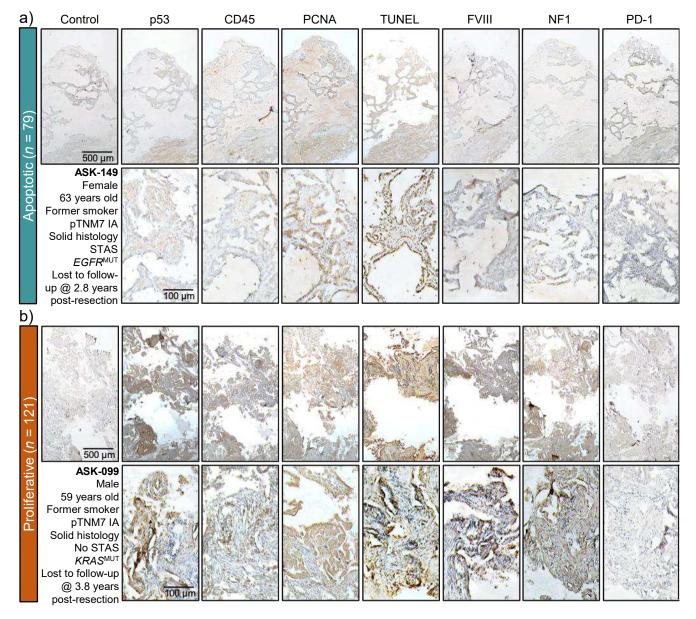
Ig, Immunoglobulin.

Supplementary Table E3. Raw data obtained from 200 resected lung adenocarcinoma donors.

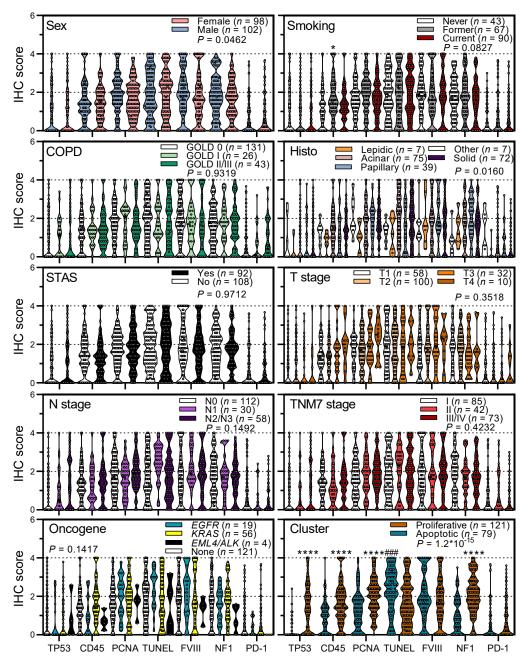
Provided as a separate *.xlsx file. Clinical and molecular variables (color-coded columns) of 200 lung adenocarcinoma donors where each row represents a patient. pTNM7, pathological tumor-node-metastasis staging system seventh edition; STAS, spread through the airspaces; TP53, tumor protein 53; CD45, cluster of differentiation 45; PCNA, proliferating cell nuclear antigen; TUNEL, terminal deoxynucleotidyl transferase dUTP nick-end labeling; FVIII, coagulation factor VIII; NF1, neurofibromatosis 1; PD-1, Programmed cell death protein 1; *KRAS*, KRAS proto-oncogene, GTPase; *EGFR*, epidermal growth factor receptor; numbers 0–4, semi-quantitative immunohistochemistry scores; LADERS_{CLIN}, clinical LUAD death score; LADERS_{IMM}, immunophenotypic score.



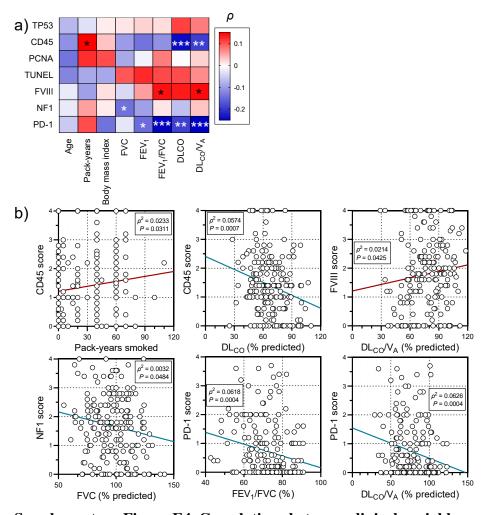
Supplementary Figure E1. Main findings of the study. Color-coded clinical and molecular variables (columns) of 200 lung adenocarcinoma donors where each column represents a patient. pTNM7, pathological tumour-node-metastasis staging system seventh edition; TP53, tumour protein 53; CD45, cluster of differentiation 45; PCNA, proliferating cell nuclear antigen; TUNEL, terminal deoxynucleotidyltransferase dUTP nick-end labelling; FVIII, coagulation factor VIII; NF1, neurofibromatosis 1; PD-1, Programmed cell death protein 1; *KRAS*, KRAS proto-oncogene, GTPase; *EGFR*, epidermal growth factor receptor; numbers 0–4, semi-quantitative immunohistochemistry scores; LADERS_{CLIN}, clinical LUAD death score; LADERS_{IMM}, immunophenotypic score.



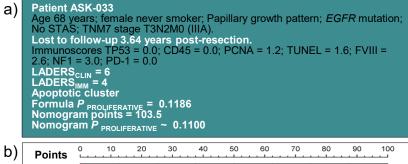
Supplementary Figure E2. Representative patients' immunoreactivity. Shown are representative immunohistochemistry microphotographs of one patient from each immunophenotype.



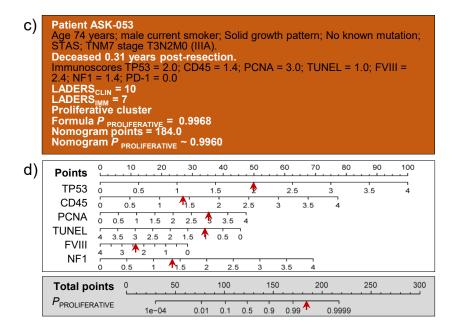
Supplementary Figure E3. Immunoreactivity of early-stage LUAD for seven cancer hallmarks. Immunoreactivity scores of tumour tissues of n = 200patients with LUAD for seven cancer hallmarks stratified by clinicopathologic features shows phenotypic cluster to be the main defining factor of hallmark expression. Data are shown as patient numbers (*n*), raw data points (circles), rotated kernel density distributions (violins), medians (dashed lines), quartiles (dotted lines), and *P*, 2-way ANOVA probability values (*P*). *, P < 0.05 for comparison between former and never-smokers; ****, P < 0.0001 for comparison between proliferative over apoptotic patients; ^{###}, P < 0.001 for comparison between apoptotic over proliferative patients; Sidak's post-test. TP53, tumour protein 53; CD45, cluster of differentiation 45; PCNA, proliferating cell nuclear antigen; TUNEL, terminal deoxynucleotidyl nick-end labelling; FVIII, anti-hemophilic factor; NF1, neurofibromatosis 1; PD-1, programmed cell death-1.



Supplementary Figure E4. Correlations between clinical variables and immunoreactivity of early-stage LUAD for seven cancer hallmarks. Immunoreactivity scores of tumor tissues of n = 200 patients with LUAD for seven cancer hallmarks were determined and were correlated with clinical and laboratory features. Data in **a**) are shown as heatmap of Spearman's correlation coefficients (ρ). *, **, and ***, P < 0.05, P < 0.01, and P < 0.001, respectively, Spearman's correlation. Data in **b**) are shown as raw data points (circles), linear regression lines (coloured lines), and squared Spearman's correlation coefficients (ρ^2) and probabilities (P) of some representative correlations. TP53, tumour protein 53; CD45, cluster of differentiation 45; PCNA, proliferating cell nuclear antigen; TUNEL, terminal deoxynucleotidyl nick-end labelling; FVIII, anti-hemophilic factor; NF1, neurofibromatosis 1; PD-1, programmed cell death-1.



<i>」</i>	Points	<u> </u>											
	TP53	♦	0.5		1	1.5	2		2.5		3	3.5	4
	CD45	♦	0.5	1	1.5	2	2.5	3	3	3.5	4		
	PCNA	6	0.5 1	1.5	2 2.5	3 3.5	4						
	TUNEL	4	3.5 3	2.5 2	2 1.5	1 0.5	0						
	FVIII	4	3				0						
	NF1	0	0.5	1	1.5	2 2	5	<u>}</u>	3.5	4			
L r		-					-						
	Total po	ints	°	!	50	100		150		200		250	300
	P _{PROLIFER}	ATIVE	Ξ	1e-04	0.	01 0.1	0.5	0.9	0.99		0.9999		



Supplementary Figure E5. Exemplary patient cluster prediction using the formula and nomogram provided. a, c) Clinical and immunoreactivity features, clinical (LADERS_{CLN}) and immunoreactivity (LADERS $_{IMM}$) risk scores and probability of belonging to the proliferative phenotype $(P_{\text{PROLIFERATIVE}})$ of two representative patients, as derived from the formula and the nomogram using a cut-off of $P_{\text{PROLIFERATIVE}}$ > 0.538. **b**, **d**) Exemplary uses of the nomogram with red arrows in white boxes indicating individual hallmark scores corresponding to points and red arrows in grey boxes indicating total hallmark scores corresponding to $P_{\text{PROLIFERATIVE}}$. TP53, tumour protein 53; CD45, cluster of differentiation 45; PCNA, proliferating cell nuclear antigen; TUNEL, terminal deoxynucleotidyl nick-end labelling; FVIII, anti-hemophilic factor; NF1, neurofibromatosis 1; PD-1, programmed cell death-1; LADERS_{CLIN}, clinical LUAD death score; LADERS_{IMM}, immunophenotypic score..