

**Supplementary**

**Table S1** Clinical information of patients enrolled in this study

Patient No.	Sex	Age	Smoking history (pack year)	Histologic subtype	Pathological stage
1	Male	51	Current smoker (20)	Adenocarcinoma	IV
2	Male	58	Current smoker (30)	Adenocarcinoma	IV
3	Male	44	Former smoker (10)	Adenocarcinoma	IV
4	Female	43	Never smoker	Adenocarcinoma	IV
5	Male	63	Current smoker (40)	Unspecified	IV
6	Male	40	Never smoker	Adenocarcinoma	IV
7	Female	66	Current smoker (50)	Adenocarcinoma	IV
8	Male	53	Current smoker (30)	Adenocarcinoma	IV
9	Male	31	Never smoker	Adenocarcinoma	IV
10	Female	60	Never smoker	Adenocarcinoma	IV
11	Male	68	Current smoker (87.5)	Adenocarcinoma	IV
12	Female	58	Never smoker	Adenocarcinoma	IV
13	Female	51	Never smoker	Adenocarcinoma	IV
14	Male	65	Current smoker (20)	Adenocarcinoma	IV
15	Male	58	Current smoker (2.5)	Adenocarcinoma	IV
16	Male	72	Current smoker (30)	Adenocarcinoma	IV
17	Male	73	Former smoker (20)	Adenocarcinoma	IV
18	Female	49	Never smoker	Adenocarcinoma	IV
19	Female	57	Never smoker	Adenocarcinoma	IV
20	Male	58	Current smoker (2.5)	Adenocarcinoma	IV
21	Female	77	Never smoker	Adenocarcinoma	IV
22	Male	44	Never smoker	Adenocarcinoma	IV
23	Female	77	Never smoker	Adenocarcinoma	IV
24	Female	70	Never smoker	Adenocarcinoma	IV
25	Male	53	Never smoker	Adenocarcinoma	IV
26	Male	65	Current smoker (60)	Adenocarcinoma	IV
27	Male	57	Current smoker (30)	Adenocarcinoma	IV
28	Male	63	Current smoker (45)	Adenocarcinoma	IV
29	Female	66	Never smoker	Adenocarcinoma	IV
30	Male	54	Never smoker	Adenocarcinoma	IV
31	Male	50	Former smoker (3.5)	Adenocarcinoma	IV
32	Male	42	Current smoker (2.5)	Adenocarcinoma	IV

**Table S2** Key quality control indices of whole-exome sequencing (WES) and panel-based sequencing conducted in this study

Patient No.	wesTMB	psTMB				
		Panel A	Panel B	Panel C	Panel D	Panel E
1	1.97	4.38	5	2.14	4.76	3.8
2	1.16	4.38	6	1.42	2.38	3.1
3	1.16	2.63	2	1.42	7.94	1.5
4	0.14	1.75	1	2.14	0.00	0.8
5	5.00	15.76	12	8.57	13.49	15.4
6	3.94	4.38	7	5.00	5.56	6.2
7	0.78	3.50	2	0.00	0.00	0.7
8	0.20	10.51	9	5.71	9.52	6.2
9	0.03	0.00	0	2.14	0.00	0.0
10	2.45	5.25	4	7.14	5.56	6.9
11	1.26	1.75	1	2.14	0.79	0.0
12	0.27	8.76	13	19.20	9.52	8.5
13	0.48	4.38	4	1.43	3.17	2.3
14	1.73	4.38	5	5.71	3.97	3.1
15	1.02	2.63	1	0.71	0.79	0.0
16	2.55	8.76	6	3.57	4.76	5.4
17	0.07	5.25	1	0.71	0.00	0.8
18	2.45	2.63	5	4.28	3.97	3.8
19	1.50	2.63	4	5.00	3.17	1.5
20	11.69	18.39	21	19.28	23.02	16.9
21	0.99	2.63	3	2.85	2.38	2.3
22	0.24	6.99	4	0.71	3.17	3.0
23	0.10	2.63	3	0.71	0.79	0.0
24	0.07	2.63	2	0.71	0.00	0.8
25	1.50	5.25	5	2.85	3.97	3.8
26	2.04	7.01	5	5.71	6.35	5.4
27	1.26	4.38	3	4.28	3.17	2.3
28	9.35	14.89	15	14.29	13.49	13.1
29	0.61	4.38	5	4.28	2.38	3.1
30	0.85	6.13	5	2.86	3.97	3.1
31	1.60	12.26	11	9.29	11.11	10.8
32	2.31	3.50	4	4.28	4.76	6.2

**Table S3** Maximum allelic frequencies (MAFs) based on mutations located within the coding region shared by all five gene panels

Panel A	Panel B	Panel C	Panel D	Panel E
0.056	0.599	0.453	0.447	0.836
0.968	0.970	0.949	0.968	0.967
0.977	0.959	0.947	0.959	0.943
0.927	0.885	0.851	0.877	0.829
0.088	0.123	0.493	0.127	0.093
0.050	0.091	0.031	0.150	0.082
0.079	0.061	0.081	0.121	0.030
0.844	0.776	0.647	0.772	0.725
0.877	0.868	0.865	0.861	0.858
0.413	0.464	0.462	0.512	0.428
0.421	0.498	0.231	0.460	0.536
0.193	0.220	0.178	0.324	0.166
0.554	0.657	0.676	0.660	0.636
0.353	0.359	0.332	0.341	0.351
0.085	0.085	0.102	0.150	0.341
0.520	0.543	0.530	0.518	0.793
0.561	0.407	0.254	0.380	0.339
0.471	0.632	0.599	0.650	0.268
0.038	0.048	0.037	0.048	0.038
0.064	0.056	0.051	0.080	0.059
0.114	0.096	0.133	0.100	0.115
0.352	0.384	0.337	0.387	0.244
0.133	0.191	0.186	0.181	0.163
0.161	0.149	0.162	0.151	0.145
0.023	0.010	0.012	0.032	0.003
0.016	0.022	0.009	0.030	0.009
0.327	0.338	0.369	0.341	0.311
0.099	0.279	0.010	0.096	0.143
0.000	0.010	0.035	0.022	0.000
0.019	0.020	0.032	0.017	0.017
0.014	0.014	0.027	0.020	0.026
0.013	0.011	0.005	0.000	0.011

**Table S4** Tumor mutation burden (TMB) levels determined by whole exome sequencing and by targeted sequencing

Panel	Median fragment length (bp)	Median sequencing depth (x)
Whole exome sequencing	178.5	523
A	174	2,496
B	187.5	1,883
C	202	3,776
D	175.5	3,171
E	402.5	2,386