

Figure S1. Expression of the 5 long non-coding RNAs in tumor and non-tumor tissues. Differential expression of (A) PRKG1-AS1, (B) ITGB1-DT, (C) NPSR1-AS1, (D) LMO7DN and (E) OGFRP1 between tumor and non-tumor tissues. The P-value are derived from the differential expression analysis, and $P < 0.05$ was considered to indicate a statistically significant difference. *** $P < 0.001$ vs. non-tumor tissues. OGFRP1, opioid growth factor receptor pseudogene 1; ITGB1-DT, integrin subunit beta 1 divergent transcript; LMO7DN, LIM domain 7 downstream neighbor; NPSR1-AS1, neuropeptide S receptor 1-antisense RNA 1; PRKG1-AS1, protein kinase cyclic GMP-dependent 1-antisense RNA 1.

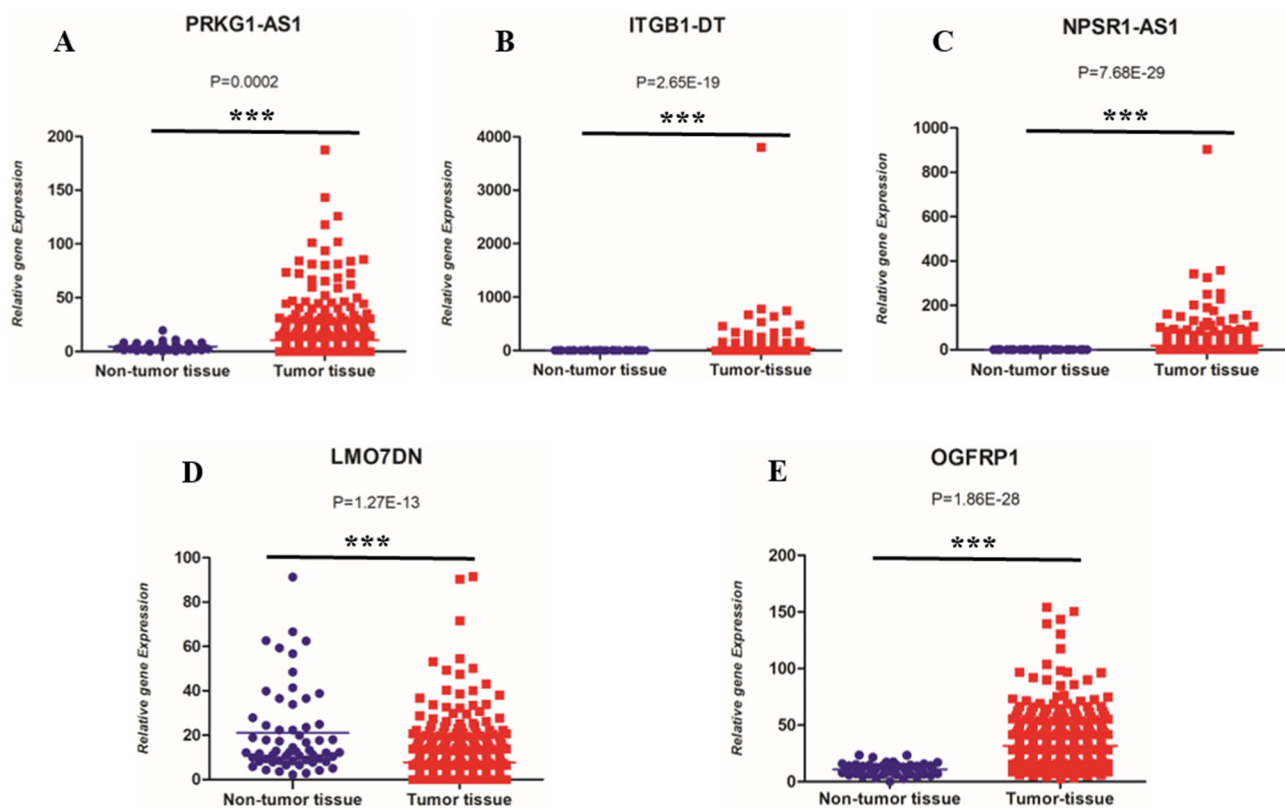


Figure S2. Results of the analysis of differentially expressed mRNAs using the same data and methods as for long non-coding RNA. (A) Forest Plot of the 5-mRNA signature. (B) Kaplan-Meier survival curves for high- and low-risk groups, and the '+' on the survival curves represents the censored data-points. (C) ROC curve of the 5-mRNA signature in predicting the 5-year survival rate. ROC, receiver operating characteristic; AUC, area under ROC curve; FAM189A2, family with sequence similarity 189 member A2; C1QTNF6, C1q and tumor necrosis factor related 6; COL22A1, collagen type XXII alpha 1 chain; NTSR1, neurotensin receptor 1; CIDEC, cell death inducing DNA fragmentation factor subunit alpha like effector c.

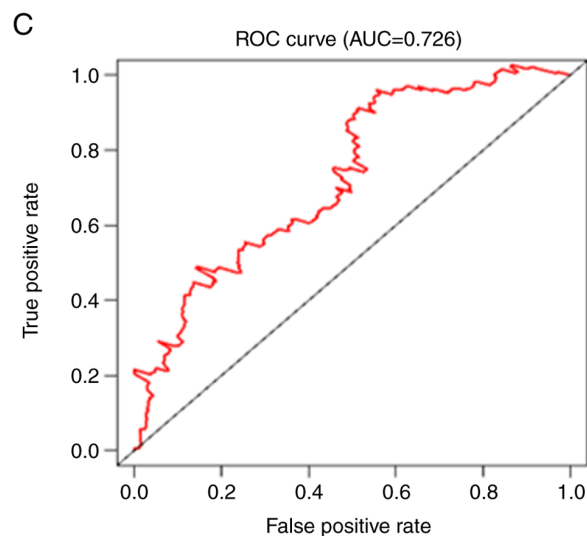
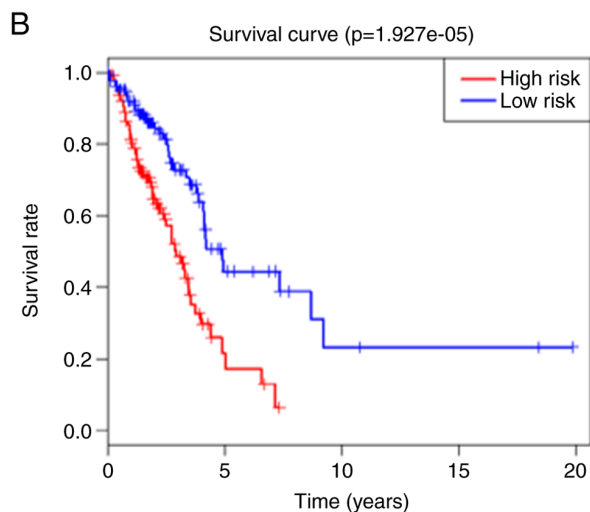
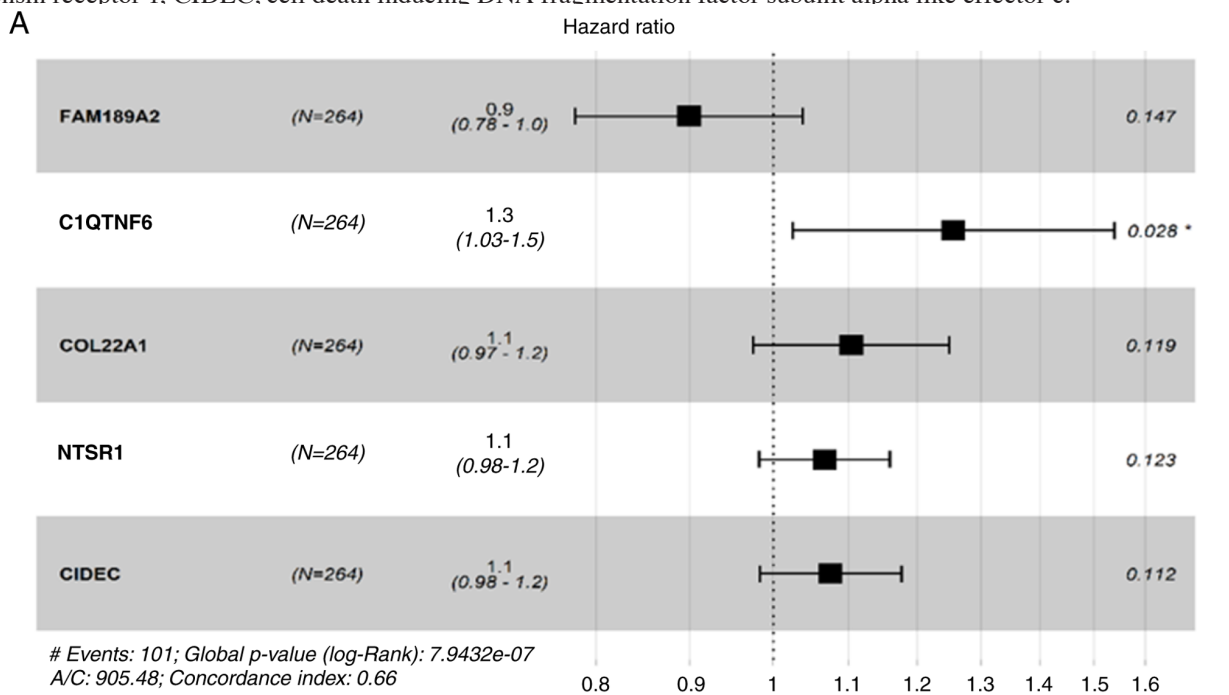


Figure S3. Results of the analysis of the differentially expressed long non-coding RNAs and mRNAs using the same data and methods as above. (A) Forest Plot of the 4-gene signature. (B) Kaplan-Meier survival curves for high- and low-risk groups, and the '+' on the survival curves represents the censored data-points. (C) ROC curve of the 4-gene signature in predicting the 5-year survival rate. COL22A1, collagen type XXII alpha 1 chain; NTSR1, neurotensin receptor 1; OGFRP1, opioid growth factor receptor pseudogene 1; LINC01322, long intergenic non-protein coding RNA 1322; ROC, receiver operating characteristic; AUC, area under ROC curve.

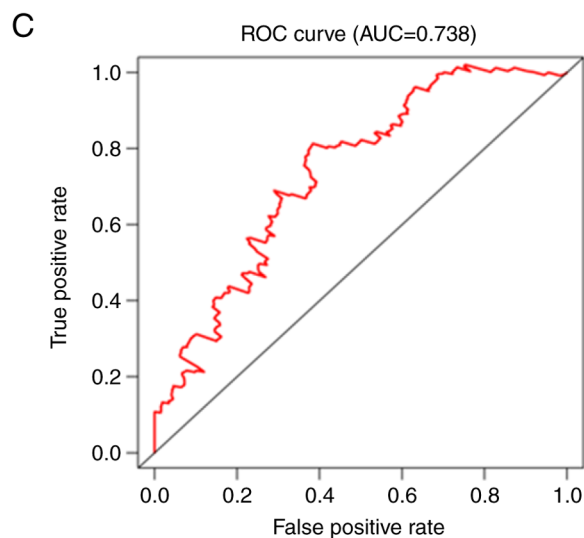
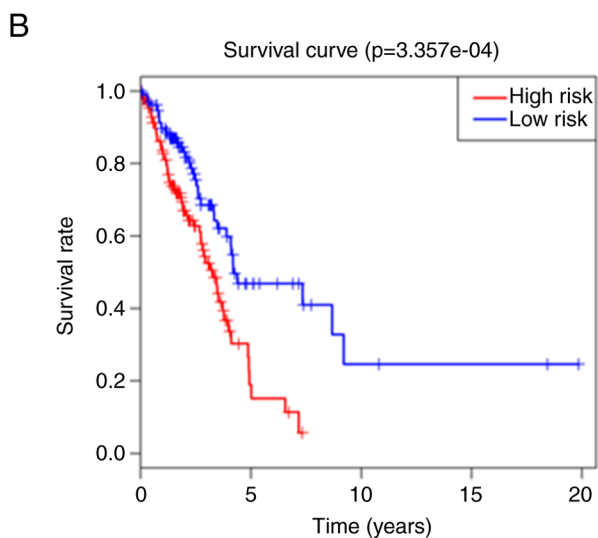
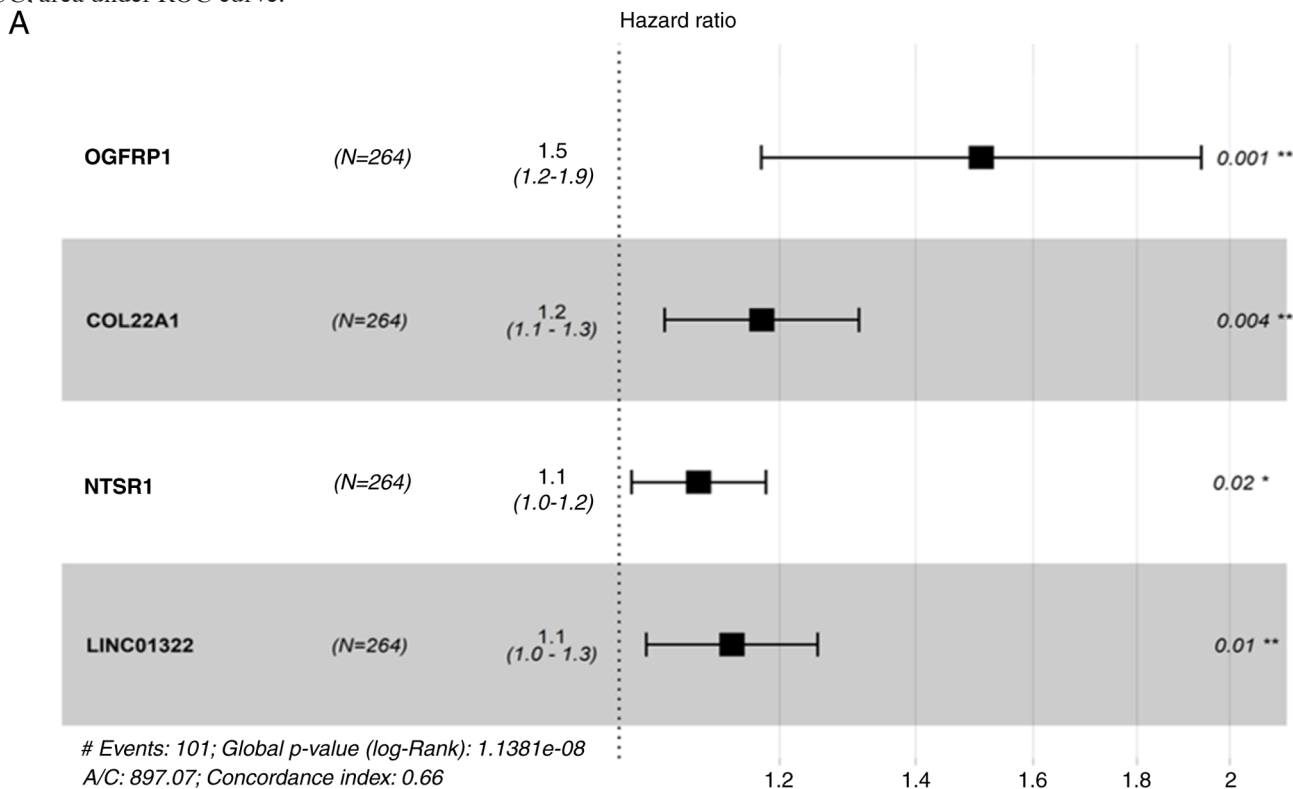


Table SI. Clinical information of 14 patients with lung adenocarcinoma.

Patient number	Gender	Age (year)	Histology
1	Female	57	Lung adenocarcinoma
2	Female	49	Lung adenocarcinoma
3	Male	61	Lung adenocarcinoma
4	Male	76	Lung adenocarcinoma
5	Female	55	Lung adenocarcinoma
6	Male	69	Lung adenocarcinoma
7	Male	66	Lung adenocarcinoma
8	Male	47	Lung adenocarcinoma
9	Female	40	Lung adenocarcinoma
10	Female	43	Lung adenocarcinoma
11	Female	64	Lung adenocarcinoma
12	Male	62	Lung adenocarcinoma
13	Male	70	Lung adenocarcinoma
14	Male	53	Lung adenocarcinoma

Table SII. Primer sequences.

Gene	Forward sequence (5'-3')	Reverse sequence (5'-3')
PRKG1-AS1	CTACCAGCGAGCGTTATAGCAGAC	TGCACAGTCAGCGAGTATTGGC
ITGB1-DT	CCATTAGGAAGACGGTGCAGTGTG	GTGCCTCCTCCACCACCTACTC
NPSR1-AS1	GGAGTTCAAGTCCAACCTGGCAAC	ACTCTGGCTCTAGTGCAGTGGTG
LMO7DN	TGTATCTGGTGGAGGAGGCTTGG	TCGGTTGTGACAATGAGGACTGT
OGFRP1	GCGTGGATTGATTGAGGAGACTGG	GCTGGCAAGTGAGGAAGGACATC

OGFRP1, opioid growth factor receptor pseudogene 1; ITGB1-DT, integrin subunit beta 1 divergent transcript; LMO7DN, LIM domain 7 downstream neighbor; NPSR1-AS1, neuropeptide S receptor 1-antisense RNA 1; PRKG1-AS1, protein kinase cyclic GMP-dependent 1-antisense RNA 1; chr, chromatin.