

**SUPPLEMENTARY TABLES**

**Table S1:** qRT-PCR primer sequences.

ID (human)	Sequence (5'-3')
U6 F	CTCGCTTCGGCAGCACACA
U6 R	AACGCTTCACGAATTTGCGT
All R	CTCAACTGGTGTCTGTGGGA
Hsa-miR-630 RT	CTCAACTGGTGTCTGTGGAGTCGGCAATTCAGTTGAGACCTTCC
Hsa-miR-630 F	ACACTCCAGCTGGGAGTATTCTGTACCAGGGA
Hsa-miR-4286	ACCCCACTCCTGGTACC
Hsa-miR-4286 RT	CTCAACTGGTGTCTGTGGAGTCGGCAATTCAGTTGAGGGTACCA
Hsa-miR-4286 F	ACACTCCAGCTGGGACCCCACTCCTGG
Hsa-miR-5703 RT	CTCAACTGGTGTCTGTGGAGTCGGCAATTCAGTTGAGACCTTCC
Hsa-miR-5703 F	ACACTCCAGCTGGGAGGAGAAGTCGGGA
Hsa-miR-7641 RT	CTCAACTGGTGTCTGTGGAGTCGGCAATTCAGTTGAGGCTTAG
Hsa-miR-7641 F	ACACTCCAGCTGGGTTGATCTCGGAAGCT
Hsa-miR -6869 RT	CTCAACTGGTGTCTGTGGAGTCGGCAATTCAGTTGAGGCCGCCG
Hsa-miR-6869 F	ACACTCCAGCTGGGGTGTAGTAGTGGCGCGCGG
ING4 F	TCGTGCTCGTTCCAAAGG
ING4 R	GGCAATAGGTGGGTTTCGTT
GAPDH F	CATGAGAAGTATGACAACAGCCT
GAPDH R	AGTC CTTCCACGATACCAAAGT

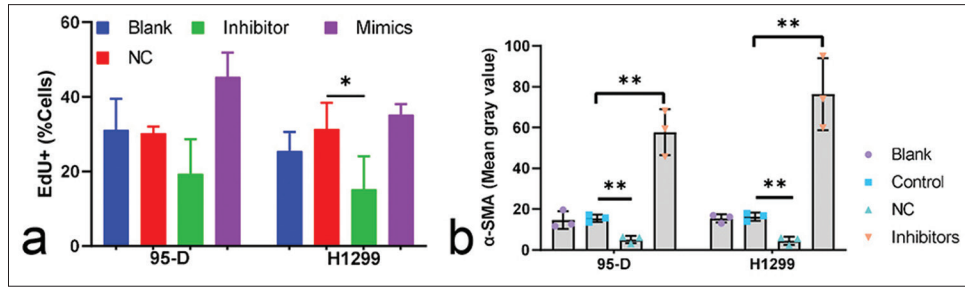
qRT-PCR: Quantitative reverse transcription polymerase chain reaction, Hsa-miR: Human microRNA, miR-5703: microRNA-5703, ING4: Inhibitor of growth family, member 4, GAPDH F: Glyceraldehyde-3-phosphate dehydrogenase Forward, GAPDH R: Glyceraldehyde-3-phosphate dehydrogenase Reverse.

**Table S2:** Potential targets of miR-5703.

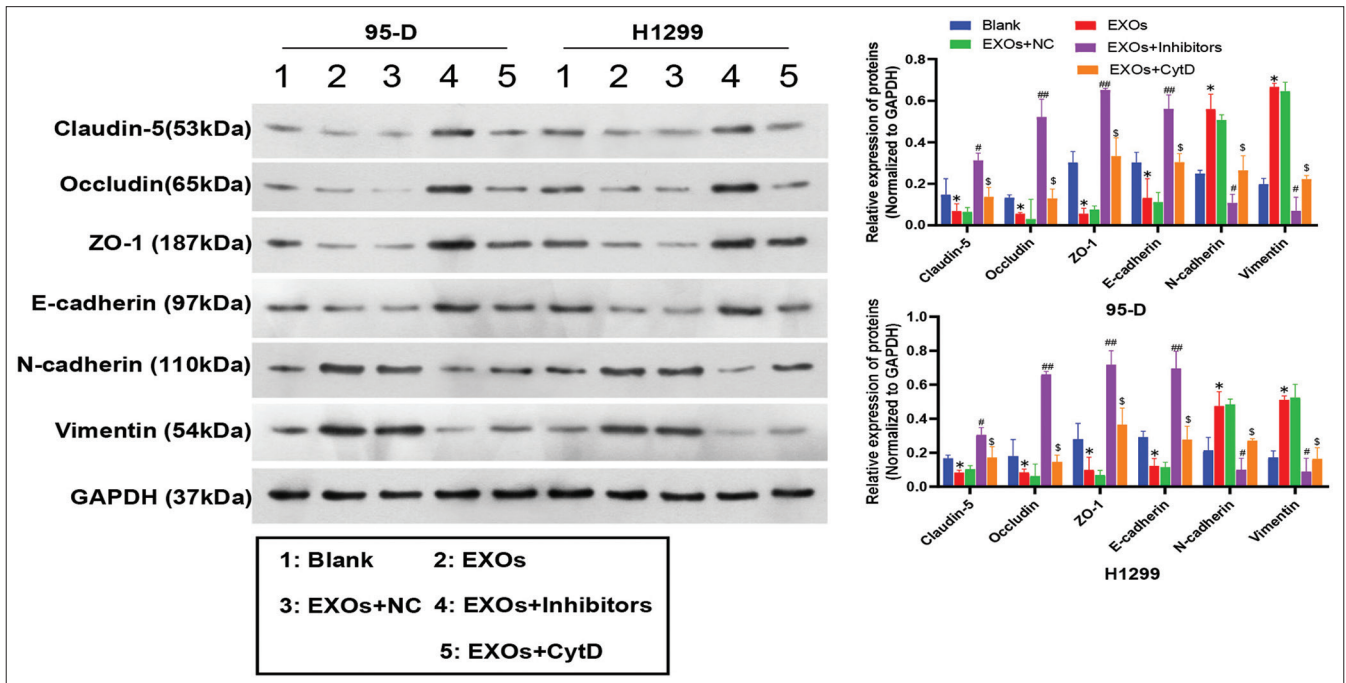
Target gene	Gene name	Cumulative weighted context++score	Total context++score
SPATA33	Spermatogenesis associated 33	-1.86	-2.26
WNT8B	Wingless-type MMTV integration site family, member 8B	-1.14	-1.17
SCN3B	Sodium channel, voltage-gated, type III, beta subunit	-0.96	-0.96
GRIK5	Glutamate receptor, ionotropic, kainate 5	-0.88	-0.88
GRIN2B	Glutamate receptor, ionotropic, N-methyl D-aspartate 2B	-0.88	-0.88
KSR2	Kinase suppressor of ras 2	-0.87	-0.87
CBL	Cbl proto-oncogene, E3 ubiquitin protein ligase	-0.83	-0.83
PIP	Prolactin-induced protein	-0.83	-0.83
RHO	Rhodopsin	-0.83	-0.83
ZNF133	Zinc finger protein 133	-0.81	-0.81
ING4	Inhibitor of growth family, member 4	-0.66	-0.85
ASXL2	Additional sex combs like 2 ( <i>Drosophila</i> )	-0.66	-1.03

miR-5703: microRNA-5703

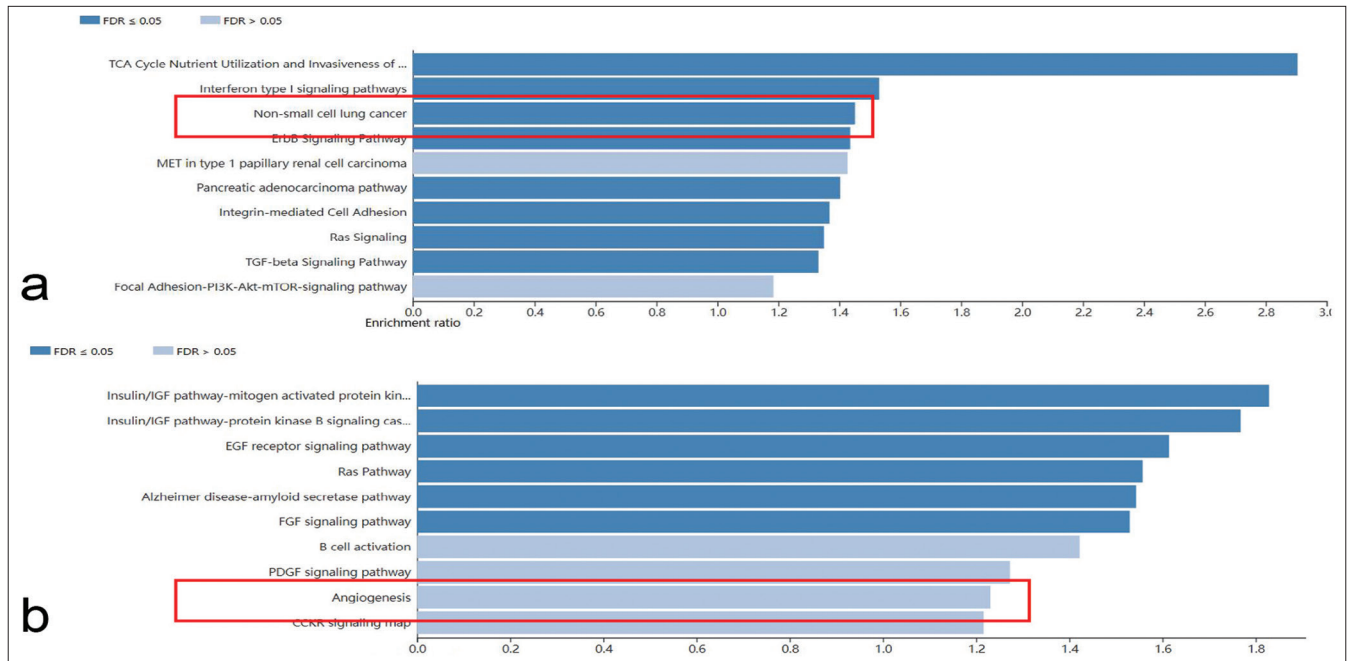
SUPPLEMENTARY FIGURES



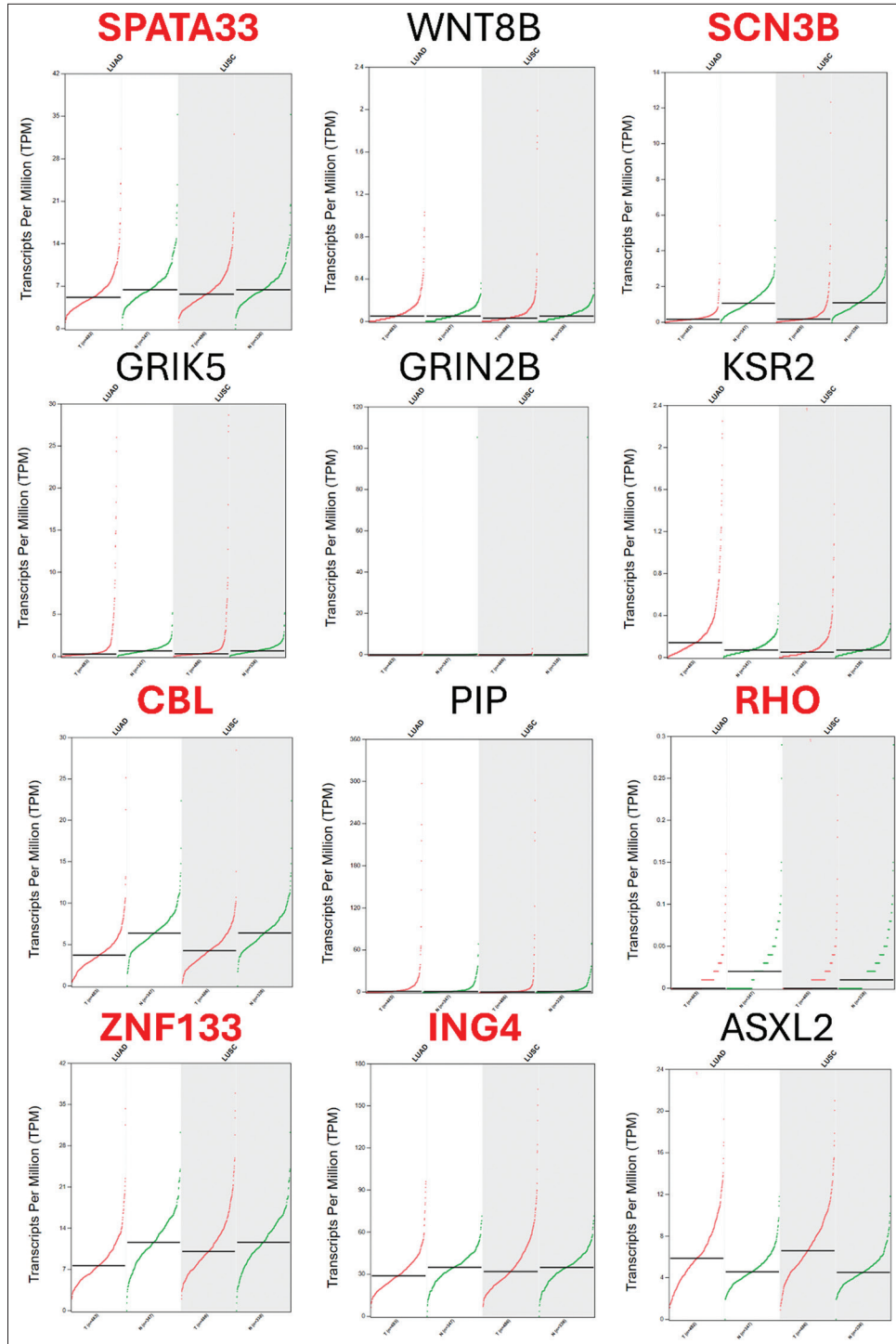
**Figure S1:** Statistical analysis diagram. (a) Figure 3e analysis diagram. (b) Figure 6d statistical analysis diagram. \* $P < 0.05$ , \*\* $P < 0.01$ . NC: Negative Control.



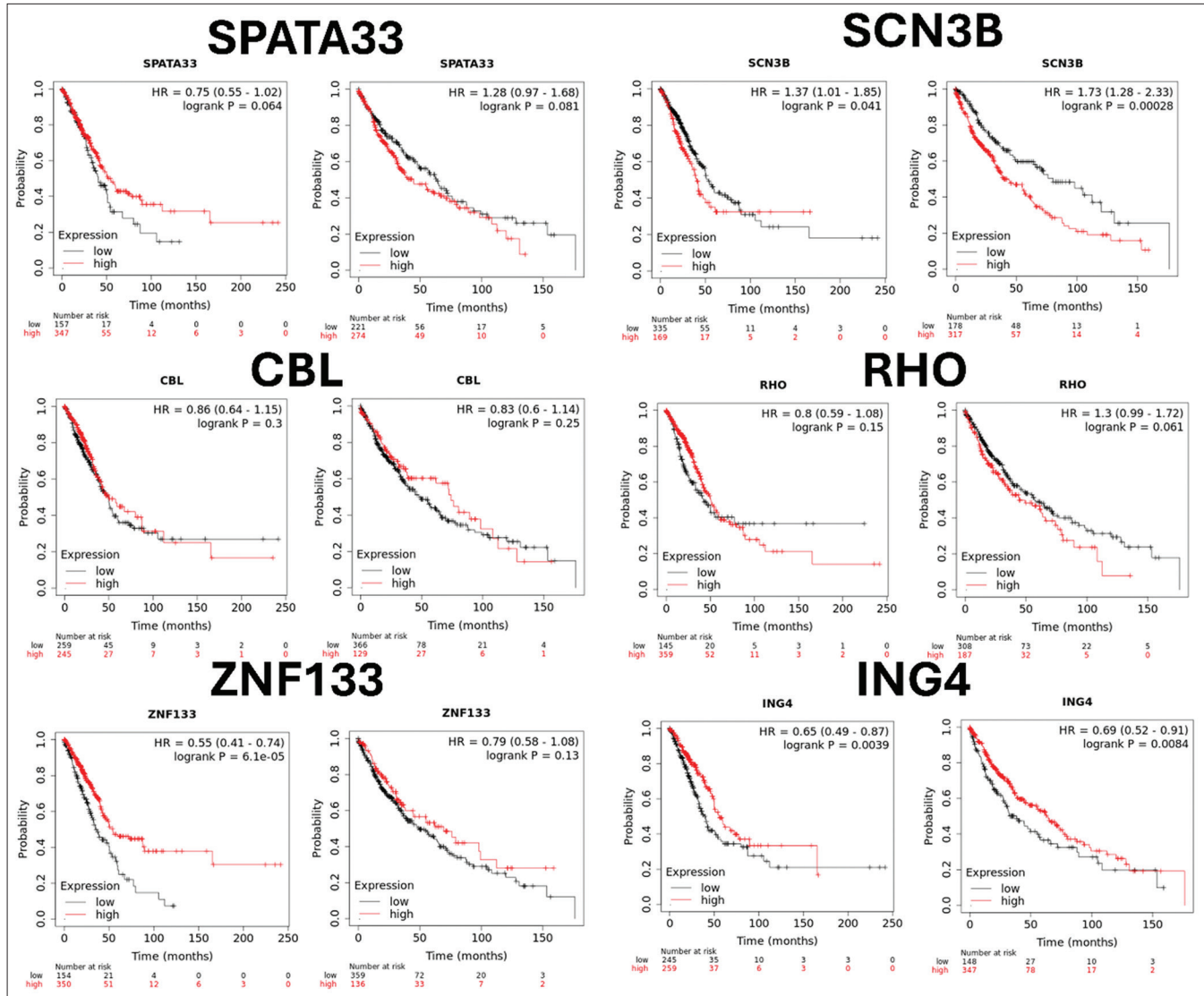
**Figure S2:** Western blot analysis showed the altered expression of endothelial–mesenchymal transition-associated proteins (E-cadherin, N-cadherin, and vimentin) and tight junction proteins (claudin-5, occludin, and ZO-1) in tumor-associated endothelial cells on exosome treatment.  $n = 3$ , \* $P < 0.05$ ,  $P < 0.01$ . ZO-1: Zonula Occludens-1; NC: Negative Control; EXOs: Exosomes; GAPDH: glyceraldehyde-3-phosphate dehydrogenase.



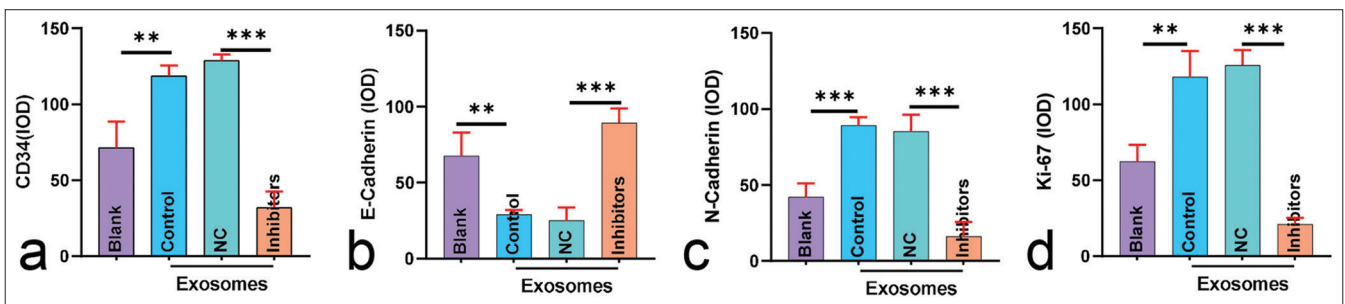
**Figure S3:** Identification and functional annotation of microRNA-5703 targets in lung cancer. (a) Association analysis using KEGG Online Analysis and Visualization System (KOBAS) database based on TargetScan (v8.0) targets. (b) Functional enrichment analysis of the predicted target genes with KOBAS. FDR: False Discovery Rate; TCA: Tricarboxylic Acid cycle; MET: Metalloproteinase; TGF: Transforming Growth Factor; mTOR: Mammalian Target of Rapamycin; IGF: Insulin-like Growth Factor; EGF: Epidermal Growth Factor; Ras: Ras GTPase; PDGF: Platelet-Derived Growth Factor; CCKR: Cholecystokinin Receptor.



**Figure S4:** Expression characteristics of candidate genes in lung cancer in the Gene Expression Profiling Interactive Analysis (GEPIA) database. SPATA33: Short Spine-associated Protein, alpha-33; WNT8B: Wnt family member 8B; SCN3B: Sodium channel, voltage-gated, type III, beta subunit; GRIK5: Glutamate receptor-like kinase 5; GRIN2B: Glutamate receptor ionotropic NMDA subunit 2B; KSR2: KSR family member 2; CBL: Casitas B-lineage lymphoma; PIP: Phosphoinositide-3-kinase regulatory subunit 1; RHO: Rho family GTPase; ZNF133: Zinc finger protein 133; ING4: Inhibitor of Growth 4; ASXL2: ATX-like 2.

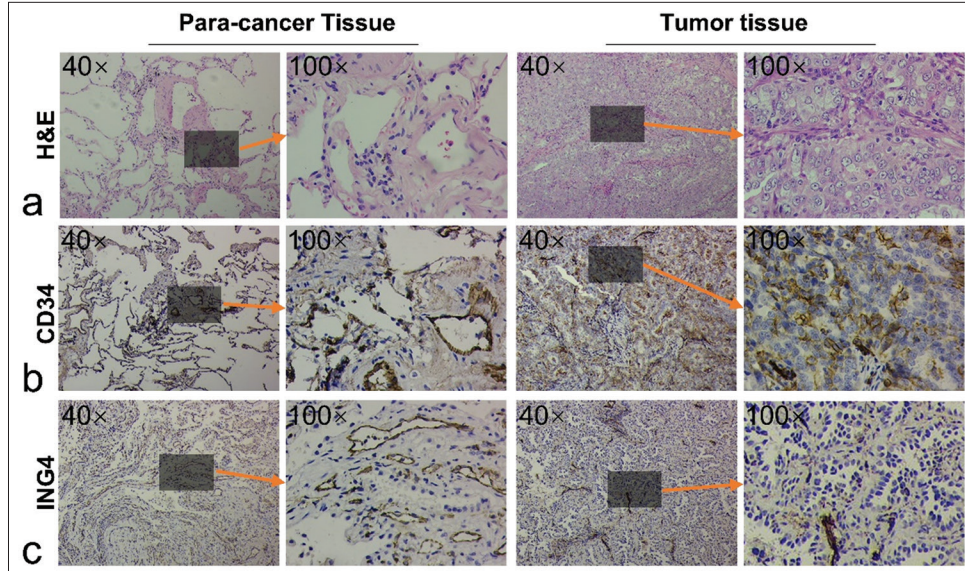


**Figure S5:** Association of SPATA33, SCN3B, CBL, RHO, ZNF133, and inhibitor of growth family, member 4 expression on the prognoses of patients with lung cancer. SPATA33: Short Spine-associated Protein, alpha-33; SCN3B: Sodium channel, voltage-gated, type III, beta subunit; CBL: Casitas B-lineage lymphoma; RHO: Rho family GTPase; ZNF133: Zinc Finger Protein 133; HR: Hazard Ratio; ING4: Inhibitor of Growth 4.



**Figure S6:** Statistical analysis diagram. (a) Figure 10f statistical analysis diagram. (b) Figure 10g statistical analysis diagram. (c) Figure 10h statistical analysis diagram. (d) Figure 10i statistical analysis diagram. \*\* $P < 0.01$ , \*\*\* $P < 0.001$ .





**Figure S7:** Hematoxylin and eosin (H&E) staining, CD34, and Inhibitor of growth family, member 4 (ING4) expression in clinical tissues. (a) The pathological examination of lung cancer tissues was performed using H&E staining. (b and c) Immunohistochemical detection of CD34 and ING4 expression levels in clinical tissues was performed. Scale: 50  $\mu\text{m}$ ,  $n = 3$ .