

**Table S1** Highly expressed genes associated with LUAD metastasis

Gene	logFC	Gene	logFC	Gene	logFC
<i>LRRC38</i>	4.115872102	<i>GUCA2B</i>	2.276642003	<i>ABCC2</i>	1.374776363
<i>NNAT</i>	2.598832901	<i>TM4SF20</i>	2.67559724	<i>CHGB</i>	1.670343784
<i>S100A8</i>	2.03031514	<i>KRT20</i>	2.845900777	<i>NDP</i>	1.17157837
<i>MT1A</i>	1.876167804	<i>SPAG11B</i>	2.277371446	<i>NEUROD4</i>	1.175330904
<i>PI3</i>	2.408197028	<i>RSPO3</i>	1.257348989	<i>FAM228A</i>	1.021207733
<i>S100A12</i>	1.540121983	<i>GLP2R</i>	1.419295928	<i>ADH7</i>	1.401616715
<i>CYP2B6</i>	2.384631964	<i>KRT78</i>	1.242914841	<i>PAGE1</i>	1.839951996
<i>RHCG</i>	2.241716309	<i>RTP1</i>	1.268393463	<i>EPHA5</i>	1.130400739
<i>TAC1</i>	3.731489817	<i>SOST</i>	1.696655357	<i>KRT16</i>	1.071459263
<i>CALB1</i>	3.16661865	<i>CXorf67</i>	1.465135742	<i>KRTDAP</i>	1.159388837
<i>S100A9</i>	1.466930019	<i>GDPD2</i>	1.312368616	<i>SCG2</i>	1.144724598
<i>CGB5</i>	3.152939448	<i>ZACN</i>	1.177117745	<i>HTR3B</i>	1.123094007
<i>C1QTNF3</i>	1.124963406	<i>TRIM48</i>	2.697396009	<i>GUCA2A</i>	1.039662581
<i>STC1</i>	1.053503933	<i>BPIFB4</i>	1.681609102	<i>EIF4E1B</i>	1.133032617
<i>NKX2-3</i>	1.865700882	<i>AC187653.1</i>	1.378861741	<i>KHDC1L</i>	1.130389461
<i>COLEC10</i>	1.514190244	<i>PRH2</i>	1.347665707	<i>SPAG11A</i>	1.481473314
<i>SPX</i>	1.788358216	<i>DEFB1</i>	1.259832041	<i>SLC10A2</i>	1.408515173
<i>MUC2</i>	2.238366652	<i>NIPAL4</i>	1.123020494	<i>HHATL</i>	1.149929728
<i>VSX2</i>	1.572115559	<i>GSG1L2</i>	1.24992093	<i>TEX19</i>	1.015740755
<i>IL1A</i>	1.347787178	<i>A2ML1</i>	1.72894757	<i>NTS</i>	1.467268835
<i>PRB3</i>	1.499905792	<i>CRCT1</i>	1.564500616	<i>CRP</i>	1.056388369
<i>C8A</i>	1.775486777	<i>MYBPH</i>	1.268795033	<i>KRT13</i>	1.090032304
<i>MUCL1</i>	1.942169109	<i>ECEL1</i>	1.196685891	<i>NFE4</i>	1.004469025
<i>ACTL8</i>	2.033243312	<i>GCG</i>	2.47824742	<i>PRB1</i>	1.112467601
<i>RHOV</i>	1.106145485	<i>DAPL1</i>	1.175622384	<i>INSL4</i>	1.10861026

FC, fold change; LUAD, lung adenocarcinoma.

**Table S2** Lowly expressed genes associated with LUAD metastasis

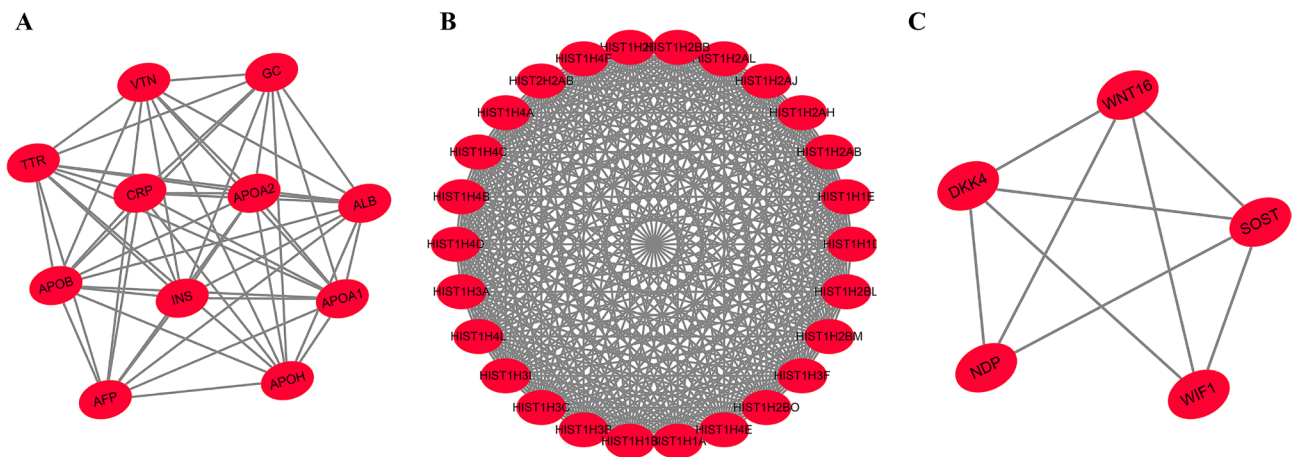
Gene	logFC	Gene	logFC	Gene	logFC
<i>ALB</i>	-5.079728232	<i>HIST2H2AB</i>	-1.95079741	<i>APOB</i>	-1.48668674
<i>NPY</i>	-4.660537685	<i>HIST1H2AH</i>	-1.945305733	<i>CYP1A1</i>	-1.479514228
<i>AFP</i>	-4.150027541	<i>FER1L6</i>	-1.930156354	<i>CPB1</i>	-1.446707372
<i>SPINK4</i>	-3.520266681	<i>HIST1H3C</i>	-1.927950184	<i>FGF3</i>	-1.44132808
<i>WFDC12</i>	-3.442749412	<i>HIST1H2BB</i>	-1.918138428	<i>TTR</i>	-1.431390359
<i>DKK4</i>	-3.426817639	<i>CRABP1</i>	-1.916379679	<i>LIPF</i>	-1.492784384
<i>WFDC5</i>	-3.421041261	<i>HIST1H2BI</i>	-1.88901368	<i>COX8C</i>	-1.413522106
<i>DLK1</i>	-3.309753519	<i>HIST1H3I</i>	-1.863873343	<i>ZFP42</i>	-1.400084091
<i>MSTN</i>	-3.192568886	<i>RERGL</i>	-1.834274109	<i>CYP2A6</i>	-1.387772556
<i>FABP7</i>	-3.084941905	<i>HIST1H3F</i>	-1.805336967	<i>PSG3</i>	-1.38172679
<i>GKN1</i>	-1.801620515	<i>HIST1H4E</i>	-1.787070398	<i>S100G</i>	-1.349125942
<i>BHMT</i>	-1.796430282	<i>UGT2B15</i>	-1.779261119	<i>TUBA3E</i>	-1.32599556
<i>GC</i>	-2.843840534	<i>HIST1H2AB</i>	-1.768817617	<i>PRSS33</i>	-1.312170884
<i>VTN</i>	-2.672501666	<i>HIST1H2AJ</i>	-1.646772648	<i>VCX</i>	-1.134784664
<i>FTHL17</i>	-2.536548085	<i>CYP11B1</i>	-1.626906727	<i>NPTX1</i>	-1.132641041
<i>MYBPC1</i>	-2.478767731	<i>HIST1H4C</i>	-2.861322629	<i>RBM46</i>	-1.135815572
<i>PSG4</i>	-2.390784252	<i>HIST1H1B</i>	-2.853524819	<i>ASGR2</i>	-1.109988044
<i>OLFM4</i>	-2.376884767	<i>HIST1H3B</i>	-2.295596172	<i>MAEL</i>	-1.303017648
<i>VGLL2</i>	-2.376288645	<i>HIST1H4L</i>	-2.267483191	<i>AKR1C4</i>	-1.30261952
<i>APOA1</i>	-2.365204735	<i>HIST1H4D</i>	-2.168005302	<i>NEUROG3</i>	-1.296631195
<i>KIR2DL1</i>	-2.312066188	<i>HIST1H4F</i>	-2.152486674	<i>LILRA2</i>	-1.295379798
<i>PSG5</i>	-2.311257398	<i>HIST1H1E</i>	-2.149380269	<i>CAPN6</i>	-1.294482763
<i>FOXI1</i>	-1.788148655	<i>HIST1H1D</i>	-2.08342783	<i>BMX</i>	-1.043823741
<i>GNRH2</i>	-1.557652305	<i>SPRR2G</i>	-2.01057535	<i>CA6</i>	-1.25855064
<i>G6PC</i>	-2.190878152	<i>HIST1H4B</i>	-1.991030038	<i>DPPA5</i>	-1.249194272
<i>SPIC</i>	-1.606336263	<i>HSD3B2</i>	-1.554002906	<i>B3GALT5</i>	-1.248282703
<i>STAR</i>	-1.58316233	<i>HIST1H2AL</i>	-1.427435476	<i>SLC7A3</i>	-1.245150828
<i>TFAP2B</i>	-1.568999384	<i>PLA2G2A</i>	-1.410032331	<i>DHRS2</i>	-1.226463753
<i>INS</i>	-2.095832241	<i>HIST1H4A</i>	-1.403263725	<i>CPN1</i>	-1.222939832
<i>MUC6</i>	-1.743521454	<i>TMEM229A</i>	-1.35988277	<i>PCK1</i>	-1.217873797
<i>PGC</i>	-2.057997158	<i>HIST1H3A</i>	-1.308476052	<i>PI15</i>	-1.214958866
<i>TAC3</i>	-2.03204835	<i>HIST1H2BM</i>	-1.282864769	<i>COL11A2</i>	-1.208569681
<i>ZP2</i>	-1.611639323	<i>HIST1H1A</i>	-1.175265584	<i>TAC4</i>	-1.199695777
<i>WIF1</i>	-1.637147552	<i>SERPINA6</i>	-1.159766806	<i>CDH16</i>	-1.197352159
<i>XAGE3</i>	-1.545787281	<i>HIST1H2BO</i>	-1.15219093	<i>FXYP4</i>	-1.082317459
<i>CRHR2</i>	-1.197145579	<i>APOA2</i>	-1.517103224	<i>SLC5A8</i>	-1.071277875
<i>CBLN1</i>	-1.194660601	<i>TUBA3C</i>	-1.489488203	<i>SCGB1A1</i>	-1.056351964
<i>WNT16</i>	-1.190775724	<i>CYP17A1</i>	-1.958874326	<i>SPRR2B</i>	-1.05593709
<i>OTX2</i>	-1.189934074	<i>PIK3C2G</i>	-1.03113146	<i>CD177</i>	-1.05557762
<i>CREB3L3</i>	-1.509649185	<i>SPANXD</i>	-1.108219388	<i>NOTUM</i>	-1.049113799
<i>CDH22</i>	-1.168108863	<i>CDC20B</i>	-1.105517671	<i>PRAC1</i>	-1.048660802
<i>PAGE2</i>	-1.539126019	<i>NELL1</i>	-1.104602759	<i>CYP4B1</i>	-1.04420733
<i>A4GNT</i>	-1.528089966	<i>UGT1A8</i>	-1.102632454	<i>FOXH1</i>	-1.043004968
<i>SPRR2E</i>	-1.52807188	<i>CELF3</i>	-1.087787494	<i>KRT33A</i>	-1.142192724
<i>REG1A</i>	-1.526407309	<i>AGTR2</i>	-1.020513278	<i>HIST1H2BL</i>	-1.136379748
<i>SLC14A2</i>	-1.00392211	<i>APOH</i>	-1.015314806	<i>GDF6</i>	-1.021729806

FC, fold change; LUAD, lung adenocarcinoma.

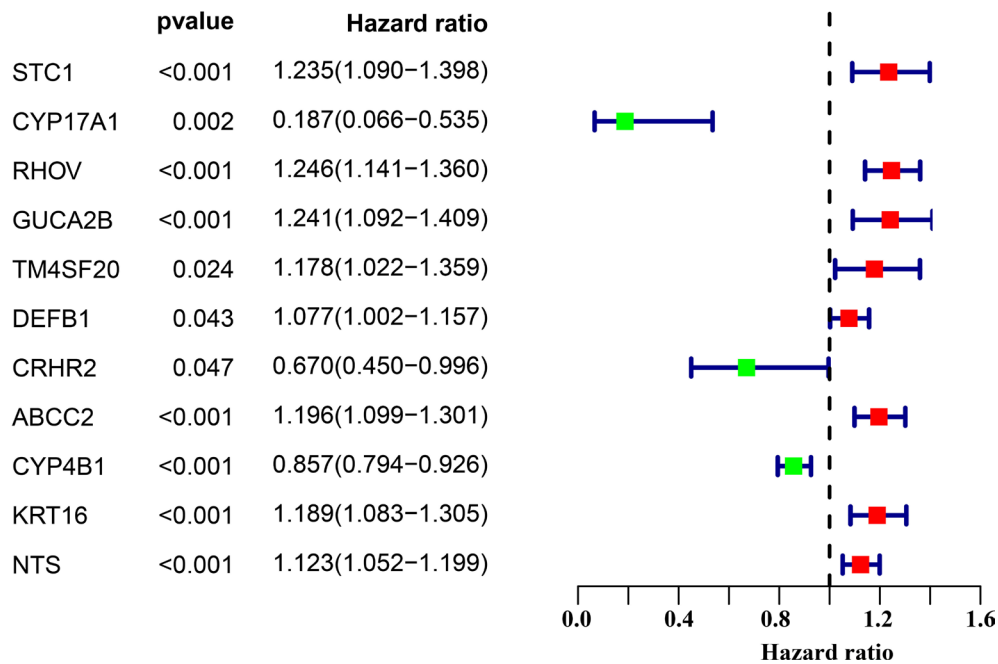
**Table S3** Functions of LUAD metastasis-related DEGs using GO analysis

GO	Category	Count	P
CC	Nucleosome	26	7.61E-28
CC	Extracellular region	70	8.70E-24
BP	Nucleosome assembly	21	4.67E-18
BP	Telomere organization	12	3.59E-15
BP	DNA replication-dependent nucleosome assembly	12	3.43E-14
BP	Chromatin silencing at rDNA	12	2.16E-13
BP	Protein heterotetramerization	12	1.03E-12
BP	Negative regulation of gene expression, epigenetic	12	8.30E-12
CC	Nuclear chromosome	12	1.33E-11
CC	Extracellular space	46	2.23E-11
MF	Protein heterodimerization activity	26	6.45E-11
BP	Cellular protein metabolic process	15	7.48E-11
BP	Positive regulation of gene expression, epigenetic	12	1.00E-10
CC	Nuclear nucleosome	10	1.17E-09
BP	Gene silencing by RNA	13	5.20E-09
CC	Nuclear chromosome, telomeric region	13	2.54E-08
BP	Negative regulation of megakaryocyte differentiation	7	3.42E-08
MF	Histone binding	12	1.11E-07
CC	Extracellular exosome	62	1.15E-07
BP	Telomere capping	7	1.77E-07
BP	DNA replication-independent nucleosome assembly	7	3.93E-07
BP	Steroid metabolic process	8	5.21E-07
BP	DNA-templated transcription, initiation	7	3.03E-06
BP	Regulation of gene silencing	5	5.13E-06
BP	Beta-catenin-TCF complex assembly	7	8.86E-06
BP	CENP-A containing nucleosome assembly	7	8.86E-06
CC	Protein complex	16	6.53E-05
BP	Double-strand break repair via nonhomologous end joining	7	8.17E-05
MF	Hormone activity	8	8.31E-05
CC	Extracellular matrix	13	1.32E-04
CC	Chylomicron	4	4.59E-04
MF	Cholesterol transporter activity	4	5.52E-04
BP	Retinoid metabolic process	6	6.57E-04
BP	Triglyceride metabolic process	5	6.57E-04
BP	Glucocorticoid metabolic process	3	7.69E-04
MF	Vitamin D binding	3	0.001194091
CC	Very-low-density lipoprotein particle	4	0.001369119
CC	Secretory granule	6	0.001441816
CC	Nuclear chromatin	9	0.001519683
MF	Nucleosomal DNA binding	5	0.00165476
BP	Chromatin silencing	5	0.001711258
BP	Keratinocyte differentiation	6	0.001777404
MF	Oxygen binding	5	0.00179322
BP	Coumarin metabolic process	3	0.001892821
MF	Protein domain specific binding	9	0.002258561
BP	Negative regulation of endopeptidase activity	7	0.002678439
BP	Positive regulation of cytokine secretion	4	0.002812071
BP	Defense response to Gram-positive bacterium	6	0.00290604
BP	Tachykinin receptor signaling pathway	3	0.003480372
BP	Drug metabolic process	4	0.003516806
BP	Female pregnancy	6	0.003545304
MF	Chromatin DNA binding	5	0.003881638
BP	Negative regulation of heart rate	3	0.00444119
BP	Glucocorticoid biosynthetic process	3	0.00444119
BP	Lipoprotein biosynthetic process	3	0.00444119
MF	Serine-type endopeptidase inhibitor activity	6	0.004479843
CC	Golgi lumen	6	0.004491116
MF	RAGE receptor binding	3	0.006286122
BP	Regulation of blood pressure	5	0.006515875
BP	Response to estrogen	5	0.006515875
BP	Low-density lipoprotein particle remodeling	3	0.006683856
MF	Iron ion binding	7	0.007220785
BP	Cholesterol metabolic process	5	0.007633451
CC	Secretory granule lumen	3	0.007644016
BP	Exogenous drug catabolic process	3	0.007960614
BP	Lipoprotein metabolic process	4	0.009253098
BP	Acute inflammatory response	3	0.009337671
MF	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	3	0.011657032
BP	Antibacterial humoral response	4	0.0138206
CC	Cornified envelope	4	0.014739111
MF	Phospholipid binding	5	0.015309052
CC	Organelle membrane	5	0.016493902
BP	Keratinization	4	0.017460907
BP	Epoxygenase P450 pathway	3	0.017643624
MF	Heme binding	6	0.01827361
BP	Transport	10	0.018975122
BP	Peptide cross-linking	4	0.019462409
BP	Regulation of cytoskeleton organization	3	0.019572763
MF	Structural molecule activity	8	0.020333057
BP	WNT signaling pathway	7	0.020713935
BP	Insecticide metabolic process	2	0.022737969
BP	Neutrophil aggregation	2	0.022737969
CC	High-density lipoprotein particle	3	0.024865479
BP	Defense response to Gram-negative bacterium	4	0.024998124
MF	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	4	0.025282421
MF	Monoxygenase activity	4	0.026449736
MF	Retinoic acid binding	3	0.026510249
MF	Lipid binding	6	0.026517937
CC	Blood microparticle	6	0.02841997
BP	Glucose homeostasis	5	0.028683462
BP	Inflammatory response	10	0.030153755
BP	O-glycan processing	4	0.031292909
BP	Triglyceride catabolic process	3	0.03283976
BP	Cholesterol efflux	3	0.03283976
MF	Apolipoprotein receptor binding	2	0.032867777
MF	High-density lipoprotein particle receptor binding	2	0.032867777
MF	Heparin binding	6	0.032881847
MF	Steroid hydroxylase activity	3	0.033328039
BP	Protein oxidation	2	0.03391333
BP	Positive regulation of saliva secretion	2	0.03391333
BP	Biphenyl metabolic process	2	0.03391333
BP	Chemokine production	2	0.03391333
BP	Negative regulation of very-low-density lipoprotein particle remodeling	2	0.03391333
MF	Aromatase activity	3	0.035736913
BP	Cholesterol homeostasis	4	0.036870385
BP	Bile acid and bile salt transport	3	0.037857464
BP	Defense response to fungus	3	0.037857464
BP	Response to lipopolysaccharide	6	0.04031827
BP	Defense response	4	0.041365056
BP	Cellular response to dexamethasone stimulus	3	0.043146799
MF	Receptor binding	9	0.043246864
MF	Neuropeptide hormone activity	3	0.043347817
MF	Toll-like receptor 4 binding	2	0.04358313
BP	Positive regulation of peptide secretion	2	0.044961554
BP	Sequestering of zinc ion	2	0.044961554
BP	Negative regulation of lipase activity	2	0.044961554

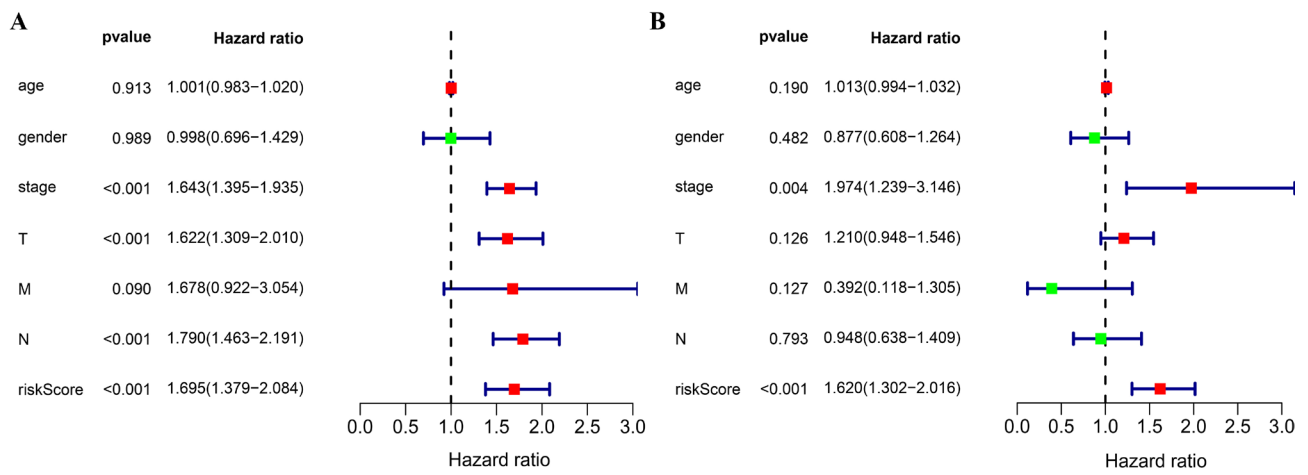
GO, Gene Ontology; MF, molecular function; BP: Biological processes; CC: Cellular components; DEGs, differentially expressed genes; LUAD, lung adenocarcinoma.



**Figure S1** PPI network of LUAD metastasis-related DEGs using MCODE method. LUAD, lung adenocarcinoma; DEGs, differentially expressed genes.



**Figure S2** Lymph node metastasis-related genes in prognosis of LUAD patients using univariate Cox analysis. LUAD, lung adenocarcinoma.



**Figure S3** Clinicopathological characteristic factors of prognosis in LUAD using Cox analysis. LUAD, lung adenocarcinoma.