

Table S1 Fourteen NRGs were included in this study

NRGs

CASP8

BIRC2

BIRC3

CYLD

EZH2

HMGB1

MLKL

NDRG2

PGAM5

RIPK1

RIPK3

TRAF2

USP22

ZBP1

NRGs, necroptosis-related genes.

Table S2 Summary of the clinical characteristics of the patients in the training, testing, and entire sets

Characteristics	Entire set (n=504)		Testing set (n=252)		Training set (n=252)		P value
	Number	Percentage	Number	Percentage	Number	Percentage	
Age							0.4139
≤65 years	238	47.22	125	49.60	113	44.84	
>65 years	256	50.79	124	49.21	132	52.38	
Not available	10	1.98	3	1.19	7	2.78	
Sex							0.7887
Female	270	53.57	133	52.78	137	54.37	
Male	234	46.43	119	47.22	115	45.63	
Stage							0.729
Stage I	270	53.57	134	53.17	136	53.97	
Stage II	119	23.61	64	25.40	55	21.83	
Stage III	81	16.07	37	14.68	44	17.46	
Stage IV	26	5.16	13	5.16	13	5.16	
Not available	8	1.59	4	1.59	4	1.59	
T							0.1637
T1	168	33.33	83	32.94	85	33.73	
T2	269	53.37	141	55.95	128	50.79	
T3	45	8.93	21	8.33	24	9.52	
T4	19	3.77	5	1.98	14	5.56	
Not available	3	0.60	2	0.79	1	0.40	
M							0.8401
M0	335	66.47	160	63.49	175	69.44	
M1	25	4.96	13	5.16	12	4.76	
Not available	144	28.57	79	31.35	65	25.79	
N							0.375
N0	325	64.48	158	62.70	167	66.27	
N1	94	18.65	49	19.44	45	17.86	
N2	71	14.09	39	15.48	32	12.70	
N3	2	0.40	0	0	2	0.79	
Not available	12	2.38	6	2.38	6	2.38	

Table S3 Twenty-two necro-related lncs were screened by univariate Cox regression analysis

Necro-related lncs
AL606489.1
LINC02320
GSEC
AC080023.1
AC017033.1
AC087588.1
OGFRP1
LINC02323
LINC01352
AL513314.2
AC133785.1
AC004704.1
AC068228.1
LINC00941
AC018647.1
LINP1
AC099850.3
LINC00707
AP005137.2
FAM83A-AS1
LINC02178
AC090541.1

Necro-related lncs, necroptosis-related lncRNAs; lncRNA, long non-coding RNA.

Table S4 Univariate and multivariate Cox regression analyses of the NecroLncSig in the patients in the entire set

Variables	Univariate Cox regression analysis				Multivariate Cox regression analysis			
	HR	HR.95L	HR.95H	P value	HR	HR.95L	HR.95H	P value
Age	1.0078896	0.9926512	1.0233621	0.3120008	1.013737004	0.998533356	1.029172144	0.076794309
Gender	1.1021575	0.8207537	1.4800436	0.5178335	1.004666349	0.744179504	1.356331996	0.975746196
Stage	1.6318863	1.4198626	1.8755709	5.32E-12	1.631219956	1.411060003	1.88573026	3.72E-11
Risk score	1.9520372	1.652148	2.3063608	3.85E-15	1.944316922	1.631044914	2.317758549	1.19E-13

NecroLncSig, necroptosis-related long non-coding RNA signature; HR, hazard ratio; HR.95L, low 95% confidence interval of HR; HR.95H, high 95% confidence interval of HR.

Table S5 GO enrichment analysis of the 269 DEGs

Ontology	ID	Description	Gene ratio	Bg ratio	P value	P adjust	q value	Gene ID	Count
BP	GO:0019730	Antimicrobial humoral response	12/207	122/18,723	1.08E-08	0.0000253	0.0000237	<i>SFTPD/KRT6A/PI3/CXCL11/H2BC7/PRSS3/KLK7/PGC/S100A7/SLPI/WFDC12/WFDC5</i>	12
	GO:0008544	Epidermis development	17/207	324/18,723	1.27E-07	0.0001487	0.0001393	<i>ALOX15B/CD109/KRT17/LAMC2/KLK7/SPRR3/GJB5/SOSTDC1/KRT16/S100A7/COL7A1/EREG/LAMA3/USH1C/SPRR1B/COL17A1/KRT14</i>	17
	GO:0010466	Negative regulation of peptidase activity	15/207	262/18,723	2.36E-07	0.0001778	0.0001666	<i>SERPINB4/SERPINB3/CD109/PI3/CST4/VIL1/SERPINB5/COL7A1/SERPINA5/SLPI/WFDC12/SERPIND1/SERPINA4/GPC3/WFDC5</i>	15
	GO:0019731	Antibacterial humoral response	8/207	60/18,723	3.05E-07	0.0001778	0.0001666	<i>SFTPD/PI3/H2BC7/KLK7/PGC/SLPI/WFDC12/WFDC5</i>	8
	GO:0010951	Negative regulation of endopeptidase activity	14/207	252/18,723	8.64E-07	0.0004033	0.0003778	<i>SERPINB4/SERPINB3/CD109/PI3/CST4/VIL1/SERPINB5/COL7A1/SERPINA5/SLPI/WFDC12/SERPIND1/SERPINA4/WFDC5</i>	14
	GO:0045861	Negative regulation of proteolysis	16/207	351/18,723	1.94E-06	0.0007549	0.0007071	<i>SERPINB4/SERPINB3/CD109/PI3/CST4/VIL1/SERPINB5/COL7A1/SERPINA5/SLPI/IL1R2/WFDC12/SERPIND1/SERPINA4/GPC3/WFDC5</i>	16
	GO:0045109	Intermediate filament organization	5/207	25/18,723	6.98E-06	0.0023287	0.0021813	<i>PKP2/KRT17/KRT20/DES/KRT14</i>	5
	GO:0042182	Ketone catabolic process	4/207	15/18,723	0.000018	0.0044028	0.0041242	<i>HSD17B6/CYP4F11/CYP4F3/KYNU</i>	4
	GO:0045104	Intermediate filament cytoskeleton organization	6/207	51/18,723	0.0000202	0.0044028	0.0041242	<i>PKP2/KRT17/KRT20/DES/KRT16/KRT14</i>	6
	GO:0007586	Digestion	9/207	137/18,723	0.0000219	0.0044028	0.0041242	<i>CHIA/PRSS3/VIL1/TFE1/TFE2/GCNT3/PRSS1/PGC/UCN3</i>	9
	GO:0051346	Negative regulation of hydrolase activity	15/207	379/18,723	0.000022	0.0044028	0.0041242	<i>SERPINB4/SERPINB3/CD109/PI3/CST4/VIL1/SERPINB5/COL7A1/SERPINA5/SLPI/WFDC12/SERPIND1/SERPINA4/GPC3/WFDC5</i>	15
	GO:0045103	Intermediate filament-based process	6/207	52/18,723	0.0000226	0.0044028	0.0041242	<i>PKP2/KRT17/KRT20/DES/KRT16/KRT14</i>	6
	GO:0051384	Response to glucocorticoid	9/207	148/18,723	0.0000404	0.0072494	0.0067907	<i>FOSL1/AGTR2/FOSB/SCGB1A1/ABCC2/MSTN/BCHE/FAM107A/UCN3</i>	9
	GO:0006959	Humoral immune response	13/207	317/18,723	0.0000546	0.0088699	0.0083087	<i>SFTPD/KRT6A/PI3/CXCL11/H2BC7/PRSS3/KLK7/PGC/S100A7/C7/SLPI/WFDC12/WFDC5</i>	13
	GO:0052547	Regulation of peptidase activity	16/207	461/18,723	0.000057	0.0088699	0.0083087	<i>SERPINB4/SERPINB3/CD109/PI3/CST4/VIL1/SERPINB5/COL7A1/SERPINA5/AGER/SLPI/WFDC12/SERPIND1/SERPINA4/GPC3/WFDC5</i>	16
CC	GO:0000786	Nucleosome	10/218	109/19,550	3.94E-07	0.000095	0.0000819	<i>H2BC9/H2BC7/H2AC7/H4C4/H1-3/H2BC17/H1-4/H2AC13/H4C5/H1-5</i>	10
	GO:0044815	DNA packaging complex	10/218	117/19,550	7.63E-07	0.000095	0.0000819	<i>H2BC9/H2BC7/H2AC7/H4C4/H1-3/H2BC17/H1-4/H2AC13/H4C5/H1-5</i>	10
	GO:0032993	Protein-DNA complex	11/218	199/19,550	0.0000151	0.0012551	0.0010824	<i>H2BC9/H2BC7/H2AC7/H4C4/H1-3/H2BC17/H1-4/H2AC13/H4C5/H1-5/HMGA2</i>	11
	GO:0031225	Anchored component of membrane	10/218	170/19,550	0.0000217	0.0013532	0.001167	<i>CD109/ITLN1/LY6D/CA4/LYPD3/GPIHBP1/MELTF/CPM/PSCA/GPC3</i>	10
	GO:0042599	Lamellar body	4/218	17/19,550	0.0000319	0.0015907	0.0013718	<i>KLK7/SFTPB/SFTPC/SFTPA1</i>	4
	GO:0005903	Brush border	7/218	106/19,550	0.0001864	0.0077355	0.0066711	<i>ITLN1/CA4/VIL1/ABCC2/CDHR5/USH1C/SLC15A1</i>	7
	GO:0016324	Apical plasma membrane	13/218	367/19,550	0.0002566	0.0091261	0.0078703	<i>ECRG4/SLC26A9/CA4/PTPRH/UPK1B/CLIC5/SLC2A1/GPIHBP1/ZMYND10/ABCC2/CDHR5/AGER/SLC15A1</i>	13
MF	GO:0004867	Serine-type endopeptidase inhibitor activity	12/208	98/18,368	1.12E-09	4.39E-07	3.82E-07	<i>SERPINB4/SERPINB3/CD109/PI3/SERPINB5/COL7A1/SERPINA5/SLPI/WFDC12/SERPIND1/SERPINA4/WFDC5</i>	12
	GO:0030414	Peptidase inhibitor activity	15/208	187/18,368	3.61E-09	7.08E-07	6.16E-07	<i>SERPINB4/SERPINB3/CD109/PI3/CST4/VIL1/SERPINB5/COL7A1/SERPINA5/SLPI/WFDC12/SERPIND1/SERPINA4/GPC3/WFDC5</i>	15
	GO:0004866	Endopeptidase inhibitor activity	14/208	180/18,368	1.81E-08	2.36E-06	2.06E-06	<i>SERPINB4/SERPINB3/CD109/PI3/CST4/VIL1/SERPINB5/COL7A1/SERPINA5/SLPI/WFDC12/SERPIND1/SERPINA4/WFDC5</i>	14
	GO:0061135	Endopeptidase regulator activity	14/208	194/18,368	4.67E-08	4.57E-06	3.98E-06	<i>SERPINB4/SERPINB3/CD109/PI3/CST4/VIL1/SERPINB5/COL7A1/SERPINA5/SLPI/WFDC12/SERPIND1/SERPINA4/WFDC5</i>	14
	GO:0061134	Peptidase regulator activity	15/208	230/18,368	5.87E-08	0.0000046	4.01E-06	<i>SERPINB4/SERPINB3/CD109/PI3/CST4/VIL1/SERPINB5/COL7A1/SERPINA5/SLPI/WFDC12/SERPIND1/SERPINA4/GPC3/WFDC5</i>	15
	GO:0008201	Heparin binding	9/208	166/18,368	0.0001177	0.0076885	0.0066892	<i>LPL/LAMC2/CXCL11/REG4/SERPINA5/MSTN/SERPIND1/RSPO3/ADAMTS8</i>	9
	GO:0071723	Lipopeptide binding	3/208	10/18,368	0.000162	0.0082167	0.0071488	<i>CD1E/CD1A/CD1C</i>	3
	GO:0070330	Aromatase activity	4/208	25/18,368	0.0001677	0.0082167	0.0071488	<i>CYP3A5/CYP4F11/CYP4F3/CYP4B1</i>	4

GO, Gene Ontology; DEGs, differentially expressed genes; BP, biological progress; CC, cellular component; MF, molecular function.