

**SUPPLEMENTARY TABLES**

**Supplementary Table 1. Necroptosis-related genes.**

	Gene	Total
GeneCards	RIPK1,MLKL,RIPK3,ZBP1,CASP8,TNF,CYLD,ITPK1,IPMK,MAP3K7,TRPM7,FADD,PELI1,PGL YRP1,SPATA2,CASP6,TP53,TNFRSF1A,TNFAIP3,UCHL1,SIRT3,TNIP1,STING1,SERTAD1,TRA F2,CFLAR,MAPK14,HMGB1,FAS,BIRC2,AIFM1,KLHDC10,GSK3B,XIAP,MYC,TNIP3,GJB1,DN M1L,PTGES3,BRD4,RB1,SIRT2,DAPK1,FKBP1A,MIR425,EZH2,NFE2L2,CD274,CHMP4B,CXC L5,MIR29B1,BCL2,AXL,MERTK,TYRO3,SIRT6,NAT2,SLC39A7,USP22,SFTPA1,PANX1,FLOT1, FLOT2,PDCD6IP,DIABLO,FASN,CDK9,TIMM50,SLC25A37,PPP1R3G,MIR7- 1,NFKBIA,AURKC,NGFR,FMR1,GNLY,PARP1,HTRA2,HSPA5,PRKAA2,PRKAA1,PITPNA,TRA F5,METTL3,FNDC4,FNDC5,FASLG,TXN,RALBP1,TP53I3,PRKN,GSDMD,HSP90AA1,STUB1,T NFSF10,CDC37,NFKB1,RELA,TRPC6,SIRT5,MIR21,TNFRSF10B,AURKA,MYH9,CASP10,PLK1 ,SQSTM1,TNFRSF10A,SOAT1,HGF,SRC,ANXA1,FPR1,CASP2,MIF,KL,TNFRSF21,BCL2L1,BMI 1,BBC3,AVEN,ZNF7,PTEN,ESR2,GSK3A,C5,SP1,EGR1,C7,C9,C6,ATG5,CD74,NOX4,TNFSF12, MKRN1,RCN1,UHRF1,AIFM2,SGK1,PAK1,CDC7,CERK,CTSB,CD40LG,OGT,BID,IFNB1,ID1,M IR155,TLR3,KIAA1191,TRADD,TP63,IL1A,PADI4,MIR22,MIR221,MIR214,MIR101- 1,MIR485,MIR101- 2,CTSD,CLEC7A,OTULIN,STAT3,HPRT1,FAP,TRIM24,CHL1,PGAM5,TGFBR1,CDKN2A,ACVR 1B,PYGM,CCL2,MEFV,DPEP1,AIM2,UBR2,CHMP1A,GPX4,LAMP2,MPRIIP,MTOR,BRAF,AFP,A CHE,NFAT5,VIL1,CXCL1,SHARPIN,MAPK1,CBL,GSN,TBK1,MAPK8,RARG,CTSH,CTSL,CTSS ,TNFRSF25,DSTYK,RNF31,IKBKB,CHUK,BUB1B,IRAK1,MAPK3,TAB2,EIF2AK3,NQO1,HSPA 8,IKBKG,BDNF,BIRC3,XBP1,BECN1,TICAM1,SOX17,HSPA4,TAB1,BNIP3,RBCK1,UBC,TAB3, AGFG1,EIF2A,TNIP2,MIB2,H1- 5,DIRAS3,C20orf204,JAK1,EGFR,FLT3,IDH2,IDH1,HMOX1,MMP13,NPM1,G6PD,GJA1,TSC2,V IM,CASPI,CAD,DRD2,ATP2A1,KRT18,RPS19,TNNT2,TPM1,EPAS1,APC,AHR,ACTB,LRP1,VCP ,YWHAE,YWHAG,LEF1,NOD2,PIKFYVE,EEF2,BAX,MAPKAPK2,PRDX1,KIF11,SLC16A1,KR T8,KRT5,KRT1,KRT14,NLRP3,HIF1A,HSP90AB1,HSPD1,HSPA9,PINK1,RPL5,TNFRSF1B,TPM3 ,TRAF3,SLC25A13,BAP1,DDX3X,RANBP2,RPL11,PRPS1,SLC25A1,MYO6,FLNC,HNRNPA2B1, HNRNPA1,IKBKE,MYH14,IL4,NUP214,PFKL,RIPK2,UBE2D3,TPM2,UGDH,TUFM,TUBB4A,TR AF6,TET2,COPB2,ARHGEF2,ATF4,EIF4EBP1,CLTC,CALM2,LTBP1,DDX5,PPP1CB,PRSS1,TUB A4A,KRT19,KRT6A,LGALS3,FUS,EMD,HSPA1A,GBE1,MYO5A,PARK7,RPS10,RPL35,S100A10 ,S100A4,CALM1,CCT5,AFG3L2,AHSG,MAP1B,PPM1B,PKM,PABPN1,PKP2,ULK1,XRCC6,XRC C5,UBE2L3,NDUFA4,NRIP1,NSUN2,OPTN,RPS20,STK38,SFPQ,TUBB4B,SLC25A5,LITAF,RPL1 5,KRT10,LGALS1,KLF6,KRT16,KRT7,MYO1C,EEF1A1,HNRNPU,FLII,ACTC1,KHDRBS1,PNK D,PSMA3,RPL7A,RPS14,RPS17,RPS24,RPS27,RPS3,RPS6,RPL13A,RPL13,TANK,TCOF1,TNFRS F8,TRIM28,TUBA1C,S100A6,TCP1,SLC30A9,CALM3,ASIC1,CADM1,CALU,RBMX,RPL22,RPL 27,PCMI,PABPC1,COPA,PLEC,TUBA1B,XRN2,VDAC2,KRT2,KRT9,NCL,ELAVL1,IGF2BP3,AP 2S1,PAWR,RPL26,RPL9,RPL4,RPL7,PSMC4,RPS13,RPS23,RPS26,RPS29,RPL10A,RPS12,RPL12, SVIL,SLC25A6,SNRPE,CAPZA1,EIF4B,CUL4A,CNBP,BANF1,AP2B1,MAP1LC3A,RNGTT,RPL3 ,PCBP1,PRPF8,PYCARD,SLC25A10,TUBB6,IGF2BP1,HNRNPF,HSPA1B,IQSEC1,IL24,MPP1,M YL6,IVNS1ABP,MVP,PDIA4,PDLIM7,RPL2,RPS16,RPL1,TPM4,SRSF9,SRSF1,CCNT1,DYNL L1,DNAJA1,DDX17,CCT3,BCLAF1,AGO2,RPL23A,KRT86,NME8,HNRNPH1,HNRNPL,HOK1, HNRNPH3,FIP1L1,PDIA6,RPL6,RIOK1,RPL23,RPL28,RPL29,SSBP1,SF1,TRA2B,TRA2A,SYNC RIP,SRSF7,CCT8,ADAMTSL4,CCT6A,DNAJA2,BAG2,ATAD3A,RCC2,RFWD3,WDR77,LARP1, MYL12A,MYO1D,MYO1B,MYCBP,HNRNPM,MYL6B,GOSR1,MRPS12,RPS18,RPS8,RPS4X,RP L34,SCYL2,THRAP3,TRIP6,TMOD3,SNRPF,SRSF6,SRSF4,SRSF3,CLINT1,CEP170,AMBRA1,CP SF6,COPS2,CARD6,CAPN7,ATXN2L,ADRM1,LRRFIP2,PREB,PKP3,ZNF24,ZFP36,YBX1,ZNF21 7,ZC3HAV1,GCC2,FAF2,HELQ,GTFC3,CDC42BPG,RPL17,RPS25,RPS27,TNRC6B,TWF1,TA NC2,ALYREF,CPSF2,CPSF3,DCD,MGA,RAI14,RPL38,OTUD4,PLEKHA5,TXNIP,WRNIP1,ZNF1 46,LIMCH1,LACTB,G3BP2,FAM83D,HEMGN,HSPBAP1,GOLGA3,HRNR,GLTP,NUDT21,SERB P1,SEC16A,SRRM2,SRP14,SRSF10,ESYT2,ERH,MLF2,RBM14,PRPF40A,POF1B,VBP1,YTHDC 1,AKAP8L,AKNA,TRAFFD1,CALML5,PNN,ELP1,KCTD5,RBM25,UBL4A,APOOL,CRTAM,CTA G2,LRRC59,PPP1R12C,PALMD,TLE6,ZSCAN20,ZKSCAN4,H1- 2,RPL39,SP6,CHTOP,UBAP2,ZAN,GSDME,TMEM44,CEP44,ATP5F1C,LZTS3,RHOXF2,TMEM2 63,ZNF391,H1-10,UTP11,H2BC12,H2AC12,OBI1,MAIP1,RBM14-RBM4,MIR137,MIR148A	601
MSigDB	FADD,FAS,FASLG,MLKL,RIPK1,RIPK3,TLR3,TNF	8

GO	SLC25A4,BIRC2,BIRC3,BOK,CASP8,CAV1,CYLD,FZD9,YBX3,RIPK1,FADD,CFLAR,ARHGEF2,SPATA2,RBCK1,RIPK3,PELI1,ZBP1,MIR101-1,MIR101-2,MIR103A1,MIR103A2,MIR107,MIR214,MIR22,MIR221,MIR485,FAS,FASLG,CD14,ITPK1,PYGL,TLR3,TLR4,TNF,TP53,DNM1L,PPIF,LY96,TRPM7,TICAM1,PGAM5,MLKL,IPMK,TICAM2,TNF,TNFRSF1A,TRADD,TRAF2,TRAF5,RIPK1,BIRC2,BIRC3,XIAP,RBCK1,RNF31,SHARPIN,SPATA2L,SPATA2,CYLD,FADD,CASP8,CFLAR,RIPK3,CYBB,CAMK2A,CAMK2D,CAMK2B,CAMK2G,SLC25A4,SLC25A5,SLC25A6,SLC25A31,PPID,VDAC1,VDAC2,VDAC3,GLUD2,GLUD1,GLUL,PYGL,PYGM,PYGB,MAPK8,MAPK10,MAPK9,FTH1,FTL,PLA2G4E,PLA2G4A,JMJD7-PLA2G4B,PLA2G4B,PLA2G4C,PLA2G4D,PLA2G4F,ALOX15,CAPN1,CAPN2,SMPD1,MLKL,PGAM5,DNM1L,NLRP3,PYCARD,CASP1,IL1B,CHMP2A,CHMP2B,CHMP3,RNF103-CHMP3,CHMP4B,CHMP4A,CHMP4C,CHMP6,VPS4B,VPS4A,CHMP1B,CHMP1A,CHMP5,CHMP7,TRPM7,IL1A,IL33,HMGB1,TNFSF10,TNFRSF10A,TNFRSF10B,FASLG,FAS,FAF1,IFNA1,IFNA2,IFNA4,IFNA5,IFNA6,IFNA7,IFNA8,IFNA10,IFNA13,IFNA14,IFNA16,IFNA17,IFNA21,IFNB1,IFNG,IFNAR1,IFNAR2,IFNGR1,IFNGR2,JAK1,JAK2,JAK3,TYK2,STAT1,STAT2,STAT3,STAT4,STAT5A,STAT5B,STAT6,IRF9,EIF2AK2,TLR4,TICAM2,TICAM1,TLR3,ZBP1,USP21,SQSTM1,HSP90AA1,HSP90AB1,TNFAIP3,PARP1,BID,BAX,AIFM1,H2AX,H2AC20,H2AC12,H2AC1,H2AW,H2AB3,H2AC8,H2AC4,MACROH2A2,MACROH2A1,H2AC19,H2AJ,H2AB1,H2AC17,H2AC18,H2AC11,H2AC21,H2AZ2,H2AC7,H2AZ1,H2AC15,H2AC6,H2AC13,H2AC14,H2AC16,H2AB2,PPIA,BCL2	45
KEGG		159

**Supplementary Table 2. Sequences of primers and siRNA.**

	Names	Sequences
Sequences of primers (5'-3')	SNHG6(Forward)	ACGCGGCATGTATTGAGCATATAGG
	SNHG6(Reverse)	TGCCACACTTGAGGTAACGAAGC
	AXL(Forward)	TGTGCTGTCTCAGACGATGGGATG
	AXL(Reverse)	CGGATGCTTGCGAGGTGAGG
	GAPDH(Forward)	ACACCCACTCCTCCACCTTTG
	GAPDH(Reverse)	TCCACCACCCTGTTGCTGTAG
Target sequences of siRNA (5'-3')	si-SNHG6-1	ACGCGGCATGTATTGAGGTTGCTGT
	si-SNHG6-2	TGAGGTGAAGGTGTATGAAAGTCAT
	si-SNHG6-3	TCACGCGGCATGTATTGAGCATATA

**Supplementary Table 3. GO and KEGG enrichment of necroptosis-related mRNAs.**

	<b>ID</b>	<b>Description</b>	<b>p-value</b>	
Top 5 results for GO enrichment of necroptosis-related mRNAs	GO:0042110	T cell activation	0.000	
	GO:0007159	leukocyte cell-cell adhesion	0.000	
	GO:0032944	regulation of mononuclear cell proliferation	0.000	
	GO:0050863	regulation of T cell activation	0.000	
	GO:0070663	regulation of leukocyte proliferation	0.000	
	GO:0009897	external side of plasma membrane	0.000	
	GO:0000775	chromosome, centromeric region	0.000	
	GO:0030667	secretory granule membrane	0.000	
	GO:0042613	MHC class II protein complex	0.000	
	GO:0000776	kinetochore	0.000	
	GO:0140375	immune receptor activity	0.000	
	GO:0023023	MHC protein complex binding	0.000	
	GO:0004896	cytokine receptor activity	0.000	
	GO:0019955	cytokine binding	0.000	
	GO:0019864	IgG binding	0.000	
	Top 20 results for KEGG enrichment of necroptosis-related mRNAs	hsa04060	Cytokine-cytokine receptor interaction	0.000
		hsa04640	Hematopoietic cell lineage	0.000
		hsa05152	Tuberculosis	0.000
		hsa04650	Natural killer cell mediated cytotoxicity	0.000
		hsa04514	Cell adhesion molecules	0.000
hsa05150		Staphylococcus aureus infection	0.000	
hsa04145		Phagosome	0.000	
hsa04380		Osteoclast differentiation	0.000	
hsa05140		Leishmaniasis	0.000	
hsa04658		Th1 and Th2 cell differentiation	0.000	
hsa04659		Th17 cell differentiation	0.000	
hsa05323		Rheumatoid arthritis	0.000	
hsa04660		T cell receptor signaling pathway	0.000	
hsa05416		Viral myocarditis	0.000	
hsa05330		Allograft rejection	0.000	
hsa05320		Autoimmune thyroid disease	0.000	
hsa05321		Inflammatory bowel disease	0.000	
hsa05340		Primary immunodeficiency	0.000	
hsa05332		Graft-versus-host disease	0.000	
hsa04940		Type I diabetes mellitus	0.000	

**Supplementary Table 4. Cox regression analyses on various clinical characteristics and risk scores.**

<b>Characteristic</b>	<b>Univariate analysis</b>				<b>Multivariate analysis</b>			
	<b>p-value</b>	<b>HR</b>	<b>lower .95</b>	<b>upper .95</b>	<b>p-value</b>	<b>HR</b>	<b>lower .95</b>	<b>upper .95</b>
RiskScore	0	7.966	3.345	18.97	0	18.755	6.435	54.668
Age	0.004	1.023	1.007	1.04	0.856	0.96	0.62	1.486
Gender	0.438	0.853	0.571	1.275	0.001	1.029	1.012	1.047
Lipomatous Neoplasms	0.125	1.718	0.861	3.427	0.022	2.298	1.129	4.677
Myomatous Neoplasms	0.258	1.451	0.762	2.763	0.111	1.707	0.884	3.296
Nerve Sheath Tumors	0.535	1.494	0.421	5.3	0.346	1.857	0.513	6.726
Soft Tissue Tumors and Sarcomas (NOS)	0.063	2.131	0.96	4.729	0.228	1.635	0.735	3.633
Synovial-like Neoplasms	0.565	1.395	0.449	4.33	0.877	0.906	0.261	3.15

**Supplementary Table 5. Baseline data chart of clinical characteristics.**

	<b>Alive (n=158)</b>	<b>Dead (n=98)</b>	<b>Total (n=256)</b>
<b>Gender</b>			
Female	82(51.9%)	57(58.2%)	139(54.3%)
Male	76(48.1%)	41(41.8%)	117(45.7%)
<b>Age</b>			
Mean	58.4	63.5	60.4
Median	60	66	60.5
Min	20	29	20
Max	87	89	89
<40	18(11.4%)	4(4.1%)	22(8.6%)
40-60	59(37.3%)	35(35.7%)	94(36.7%)
60-80	71(44.9%)	46(46.9%)	117(45.7%)
≥80	10(6.3%)	13(13.3%)	23(9.0%)
<b>Histologic Subtype</b>			
Conventional	42(26.6%)	22(22.4%)	64(25%)
Poorly differentiated	16(10.1%)	18(18.4%)	34(13.3%)
Well differentiated	3(1.9%)	1(1.0%)	4(1.6%)
Not reported	97(61.4%)	57(58.2%)	154(60.2%)
<b>Race</b>			
Asian	4(2.5%)	1(1.0%)	5(2.0%)
Black or African American	11(7.0%)	7(7.1%)	18(7.0%)
White	139(88.0%)	85(86.7%)	224(87.5%)
Not reported	4(2.5%)	5(5.1%)	9(3.5%)
<b>Metastatic</b>			
YES	19(17.3%)	37(57.8%)	56(32.2%)
NO	91(82.7%)	27(42.2%)	118(67.8%)
<b>Recurrence</b>			
YES	8(7.5%)	21(33.3%)	29(17.1%)
NO	99(92.5%)	42(66.7%)	141(82.9%)
<b>Disease Type</b>			
Fibromatous Neoplasms	28(17.7%)	12(12.2%)	40(15.6%)
Lipomatous Neoplasms	34(21.5%)	25(25.5%)	59(23.0%)
Myomatous Neoplasms	62(39.2%)	41(41.8%)	103(40.2%)
Nerve Sheath Tumors	6(3.8%)	3(3.1%)	9(3.5%)
Soft Tissue Tumors and Sarcomas, NOS	22(13.9%)	13(13.3%)	35(13.7%)
Synovial-like Neoplasms	6(3.8%)	4(4.1%)	10(3.9%)
<b>Treatment Outcome</b>			
Complete Response	119(78.8%)	6(13.6%)	125(64.1%)
Partial Response	0(0.0%)	2(4.5%)	2(1.0%)
Progressive Disease	25(16.6%)	33(75.0%)	58(29.7%)
Stable Disease	7(4.6%)	3(6.8%)	10(5.1%)

Supplementary Table 6. GSEA results of risk model.

	ID	Enrichment Score	p-value	
Top 10 GSEA results for KEGG	KEGG_ALLOGRAFT_REJECTION	-0.812	0	
	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	-0.751	0	
	KEGG_CHEMOKINE_SIGNALING_PATHWAY	-0.562	0	
	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	-0.627	0	
	High risk group	KEGG_GRAFT_VERSUS_HOST_DISEASE	-0.826	0
	KEGG_HEMATOPOIETIC_CELL_LINEAGE	-0.662	0	
	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	-0.787	0	
	KEGG_LEISHMANIA_INFECTION	-0.732	0	
	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	-0.624	0	
	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	-0.688	0	
Low risk group	KEGG_ALLOGRAFT_REJECTION	0.812	0	
	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	0.751	0	
	KEGG_CHEMOKINE_SIGNALING_PATHWAY	0.562	0	
	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0.627	0	
	KEGG_GRAFT_VERSUS_HOST_DISEASE	0.826	0	
	KEGG_HEMATOPOIETIC_CELL_LINEAGE	0.662	0	
	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	0.787	0	
	KEGG_LEISHMANIA_INFECTION	0.732	0	
	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	0.624	0	
	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.688	0	
High risk group	GOBP_ACTIVATION_OF_IMMUNE_RESPONSE	-0.781	0	
	GOBP_IMMUNE_RESPONSE_REGULATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY	-0.789	0	
	GOBP_IMMUNOGLOBULIN_PRODUCTION	-0.867	0	
	GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY	-0.779	0	
	High risk group	GOBP_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	-0.793	0
	GOCC_IMMUNOGLOBULIN_COMPLEX	-0.949	0	
	GOCC_IMMUNOGLOBULIN_COMPLEX_CIRCULATING	-0.942	0	
	GOCC_T_CELL_RECEPTOR_COMPLEX	-0.931	0	
	GOMF_ANTIGEN_BINDING	-0.901	0	
	GOMF_IMMUNOGLOBULIN_RECEPTOR_BINDING	-0.941	0	
Top 10 GSEA results for GO	GOBP_B_CELL_RECEPTOR_SIGNALING_PATHWAY	0.888	0	
	GOBP_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBULIN	0.863	0	
	GOBP_IMMUNOGLOBULIN_PRODUCTION	0.867	0	
	GOBP_LYMPHOCYTE_MEDIATED_IMMUNITY	0.779	0	
	Low risk group	GOBP_PHAGOCYTOSIS_RECOGNITION	0.876	0
	GOCC_IMMUNOGLOBULIN_COMPLEX	0.949	0	
	GOCC_IMMUNOGLOBULIN_COMPLEX_CIRCULATING	0.942	0	
	GOCC_T_CELL_RECEPTOR_COMPLEX	0.931	0	
	GOMF_ANTIGEN_BINDING	0.901	0	
	GOMF_IMMUNOGLOBULIN_RECEPTOR_BINDING	0.941	0	