

Table S1 Basic information of 32 genes associated with ICD

Genes	Function
<i>CALR</i>	Tumor cell uptake by DCs and chemotherapy-induced antitumoral immune response
<i>HMGB1</i>	Promotes the maturation and cross-presentation activity of APCs
<i>HMGN1</i>	Induces dendritic cell maturation, recruitment of APCs and antigen-specific immune responses
<i>IL1A</i>	Cell activation, cytokine release
<i>IL33</i>	Can bind ST2 on mast cells and TH2 cells and trigger secretion of pro-inflammatory and TH2 cytokines. The immunostimulatory activity of IL-33 might be inactivated during apoptosis
<i>ROCK1</i>	Release the find-me signals ATP and UTP
<i>PANX1</i>	Release the find-me signals ATP and UTP
<i>BCL2</i>	Reduces reperfusion injury of skeletal or cardiac muscle when injected extracellularly
<i>PPIA</i>	Initiate and perpetuate the inflammatory response
<i>HSPA4</i>	Protein folding, protein refolding, protein transport, and protein targeting
<i>HSP90AA1</i>	Provides chaperoning activity for client proteins
<i>TLR2</i>	Promotes the production of pro-inflammatory cytokines and chemokines
<i>TLR3</i>	Promotes the production of pro-inflammatory cytokines, chemokines and IFN-I
<i>TLR4</i>	Promotes the production of pro-inflammatory cytokines, chemokines and IFN-I
<i>TLR7</i>	Promotes the production of IFN α and other cytokines and chemokines
<i>TLR9</i>	Promotes the production of IFN α and other cytokines and chemokines
<i>CLEC4E</i>	Promotes the release of pro-inflammatory cytokines
<i>CLEC7A</i>	Initiating of intracellular signalling that produce pro-inflammatory cytokines
<i>NLRP3</i>	Promotes IL-1b and IL-18 secretion and initiates pyroptosis
<i>DDX58</i>	Trigger a transduction cascade which inducing the expression of antiviral cytokines
<i>IFIH1</i>	Promotes the production of IFN-I and other cytokines and chemokines
<i>CGAS</i>	Promotes the production of IFN-I and other cytokines and chemokines
<i>AIM2</i>	Promotes IL-1b and IL-18 secretion and initiates pyroptosis
<i>AGER</i>	Promotes the expression of pro-inflammatory genes, as well as cell migration, proliferation and apoptosis
<i>TREM1</i>	Promotes pro-inflammatory cytokine and chemokine secretion
<i>FPR1</i>	Promotes chemotaxis of neutrophils and monocytes/macrophages
<i>FPR2</i>	Promotes chemotaxis of neutrophils and monocytes/macrophages
<i>P2Y2R</i>	Promotes migration and activation of various immune cells
<i>P2Y6R</i>	Promotes proliferation and cytokine and chemokine production in stromal cells
<i>P2Y12R</i>	Promotes platelet activation and Th17 differentiation
<i>CASR</i>	Promotes monocyte/macrophage recruitment and NLRP3 activation
<i>P2RX7</i>	Promotes cytokine and chemokine production, NLRP3 inflammasome activation and T cell activation

ICD, immunogenic cell death.

Table S2 Nine lncRNAs primer sequence information

The name of the primer	The sequence (5' to 3')
h-AC116158.1-109-F	CCACCATTGTGCTTTCCTCT
h-AC116158.1-109-R	GTCCAGAGGATGGTGGATGT
h-AC048382.2-74-F	GCCTTCTCAAGTGGGAATCA
h-AC048382.2-74-R	ACTGCTTCAGCCCTACAGGA
h-AC068790.7-74-F	AAGAGAAGAGCTGCCAGTGC
h-AC068790.7-74-R	AGTACAGGAGCCAGGGGAAG
h-LINC00106-115-F	GGCTGGTCTCAAACCTCTGA
h-LINC00106-115-R	TCCCGTTAAAACACCTCTGC
h-AP002954.1-105-F	GCAAATCAGATGGCACCTTT
h-AP002954.1-105-R	CCTCGAAACTCTGTGGCTTC
h-AC144548.1-117-F	CAAACCTCATCGGAAACATGG
h-AC144548.1-117-R	TGCATGATACACCAAAAGCTG
h-AC116914.1-74-F	TTAAAAGGGCTTCGCTCTG
h-AC116914.1-74-R	GAGTGCTGTGGCGTGATCT
h-AL049838.1-139-F	TGGCCATGTAACACTCTGC
h-AL049838.1-139-R	CAATCCCCCATGGATACCTA
h-AP000695.1-119-F	TGGAAAGAGGGACAATTTGC
h-AP000695.1-119-R	ACATCGCTGTCAAGCAAGTG

lncRNA, long non-coding RNA.

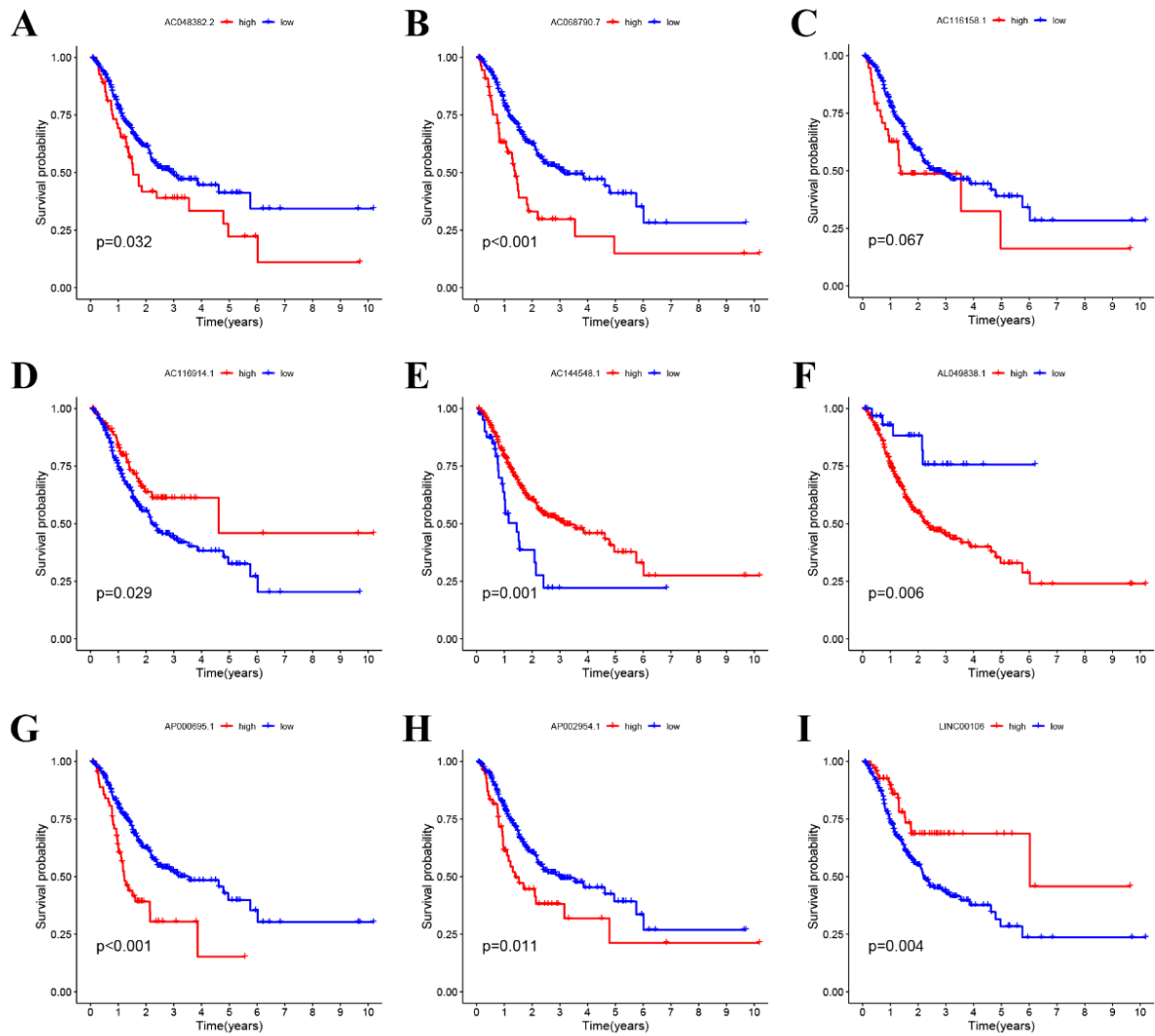


Figure S1 Kaplan-Meier curves of nine ICD-related lncRNAs in GC. ICD, immunogenic cell death; GC, gastric cancer.

Table S3 KEGG pathway enrichment analysis explained

ID	Description	Gene ratio	Bg ratio	P value	p.adjust	qvalue	geneID	Count
hsa05414	Dilated cardiomyopathy	13/130	96/8142	3.14E-09	6.15E-07	5.45E-07	LAMA2/ITGA9/ITGA7/ SGCA/TPM2/ITGA8/ CACNA2D1/DMD/ADCY5/ CACNA1C/DES/PLN/SGCD	13
hsa04270	Vascular smooth muscle contraction	14/130	134/8142	2.33E-08	2.28E-06	2.02E-06	ACTA2/MYL9/IRAG1/MYLK/ KCNMA1/KCNMB1/ACTG2/ GUCY1A1/PPP1R14A/ CALD1/ADCY5/CACNA1C/ MYH11/PPP1R12B	14
hsa05410	Hypertrophic cardiomyopathy	11/130	90/8142	1.60E-07	1.05E-05	9.28E-06	LAMA2/ITGA9/ITGA7/ SGCA/TPM2/ITGA8/ CACNA2D1/DMD/ CACNA1C/DES/SGCD	11
hsa05412	Arrhythmogenic right ventricular cardiomyopathy	10/130	77/8142	3.37E-07	1.65E-05	1.46E-05	LAMA2/ITGA9/ITGA7/ SGCA/ITGA8/CACNA2D1/ DMD/CACNA1C/DES/SGCD	10
hsa04510	Focal adhesion	14/130	201/8142	3.50E-06	0.0001372	0.0001215	MYL9/LAMA2/ITGA9/MYLK/ ITGA7/FLNA/TNC/ITGA8/ THBS4/ERBB2/FLNC/ PPP1R12B/TNXB/CAV1	14
hsa04310	Wnt signaling pathway	12/130	167/8142	1.32E-05	0.0004323	0.0003831	ROR2/BAMBI/SERPINF1/ PRICKLE2/SFRP4/RSP03/ NOTUM/WNT9A/SFRP2/ FRZB/DAAM2/SFRP1	12

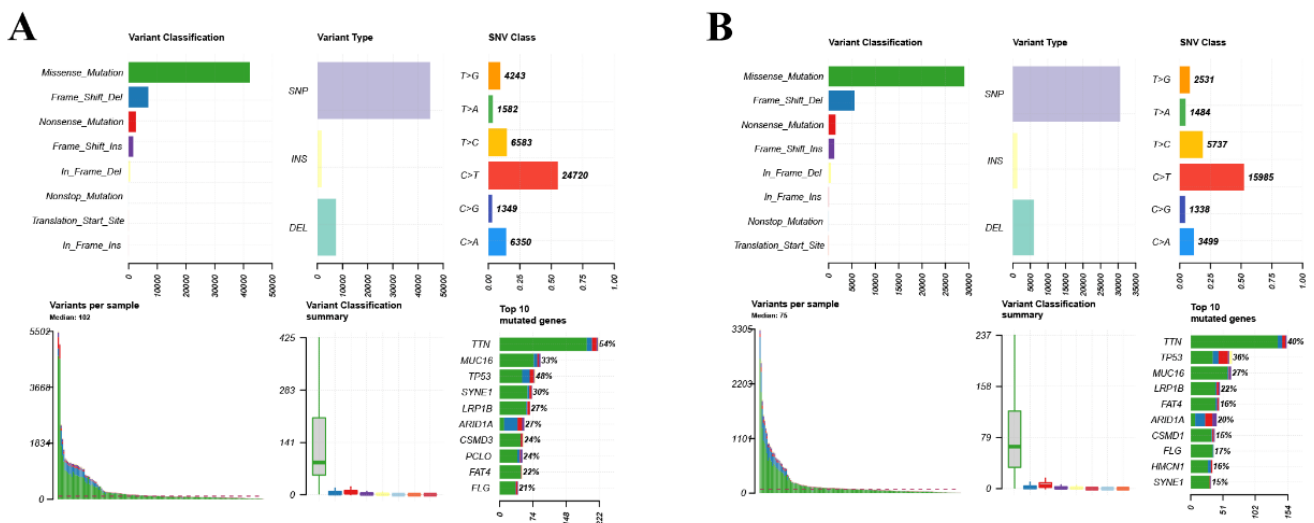


Figure S2 Distribution of somatic genomic mutations between ICDIncSig high-risk and low-risk groups in the entire cohort.

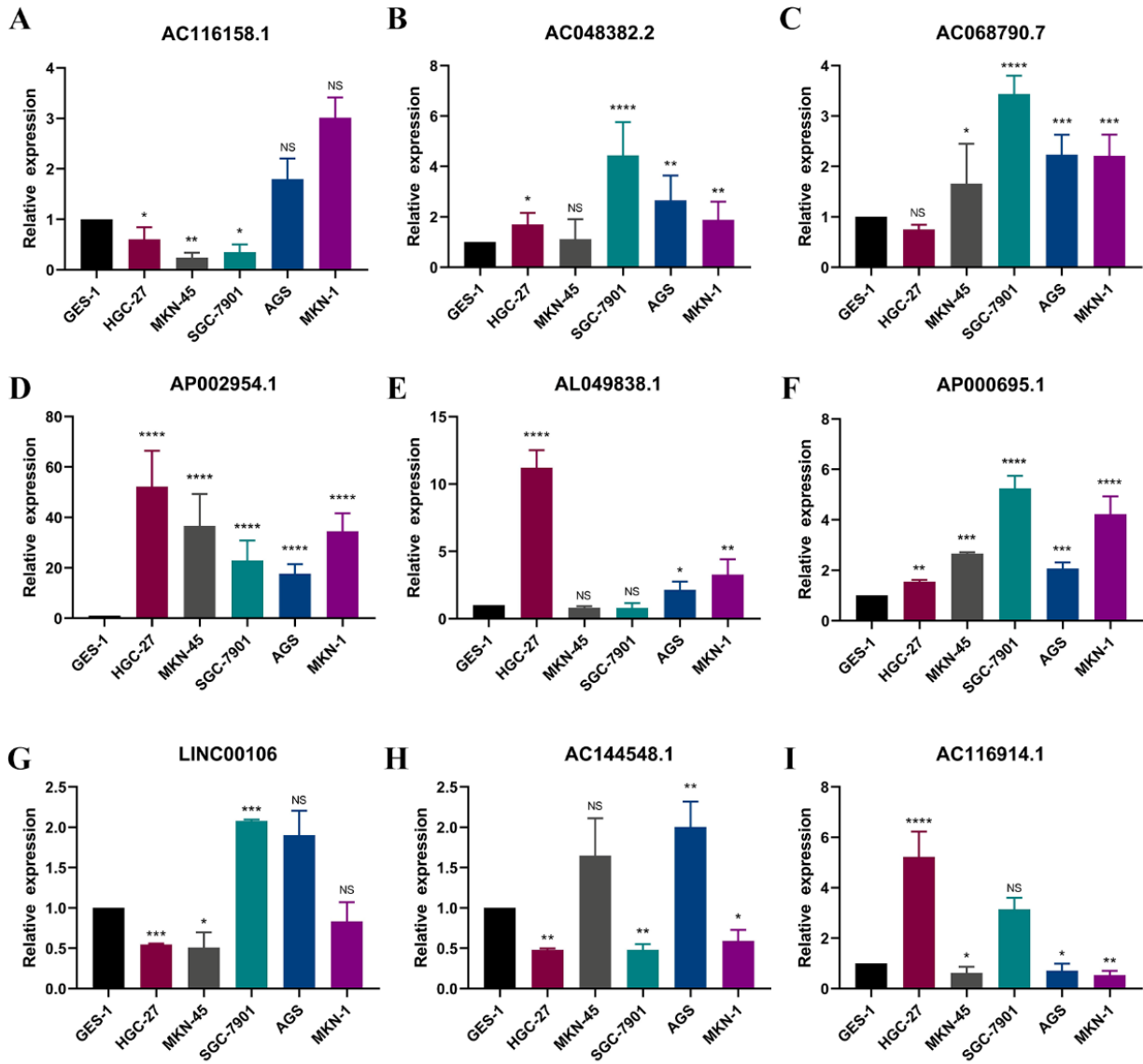


Figure S3 Validation of the expression of nine lncRNAs. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$. lncRNAs, long non-coding RNAs.