

**Table S1** Thirty-three pyroptosis-related genes

Gene	ID
<i>AIM2</i>	9447
<i>CASP1</i>	834
<i>CASP3</i>	836
<i>CASP4</i>	837
<i>CASP6</i>	839
<i>CASP8</i>	841
<i>CASP9</i>	842
<i>GSDMA</i>	284110
<i>GSDMC</i>	56169
<i>GSDMD</i>	79792
<i>IL18</i>	3606
<i>IL6</i>	3569
<i>NLRC4</i>	58484
<i>NLRP1</i>	22861
<i>NLRP2</i>	55655
<i>NLRP3</i>	114548
<i>NLRP6</i>	171389
<i>NLRP7</i>	199713
<i>NOD1</i>	10392
<i>NOD2</i>	64127
<i>PJVK</i>	494513
<i>PLCG1</i>	5335
<i>PRKACA</i>	5566
<i>PYCARD</i>	29108
<i>SCAF11</i>	9169
<i>TIRAP</i>	114609
<i>TNF</i>	7124
<i>CASP5</i>	838
<i>ELANE</i>	1991
<i>GPX4</i>	2879
<i>GSDMB</i>	55876
<i>GSDME</i>	1687
<i>IL1B</i>	3553

**Table S2** The primers of qRT-PCR

Gene	Forward	Reverse
<i>GAPDH</i>	5'-CAGGAGGCATTGCTGATGAT-3'	5'-GAAGGCTGGGGCTCATT-3'
<i>CASP8</i>	5'-CAAAC TTCACAGCATTAGGGAC-3'	5'-ATGTTACTGTGGTCCATGAGTT-3'
<i>GSDMC</i>	5'-CATAATGGTGCTGAGTGACTTC-3'	5'-GTTATCCAGCTCCATCCTAAGG-3'
<i>NLRP6</i>	5'-CCGAGAAGGAACTGGAGCAACTG-3'	5'-CTGGAAGCTCTGGTCGATGAACTG-3'
<i>NOD2</i>	5'-GTCTGGAATAAGGGTACTTGGG-3'	5'-GGCAACCTGATTCATCACATT-3'
<i>PLCG1</i>	5'-ACCGTCATGACTTTGTTCTACT-3'	5'-AATTCACGAATGTCAATGGCC-3'

qRT-PCR, quantitative real-time PCR.

**Table S3** DEGs between the low- and high-risk groups in the TCGA cohort

Gene	LogFC	P value	FDR
<i>AFP</i>	1.09044	0.000342	0.000548
<i>F9</i>	-1.02753	1.52E-10	6.28E-10
<i>ASPDH</i>	-1.01379	1.93E-15	2.15E-14
<i>CFHR3</i>	-1.02585	1.35E-11	6.71E-11
<i>SPP1</i>	1.929189	6.32E-16	7.89E-15
<i>ANG</i>	-1.06635	3.77E-20	1.60E-18
<i>CYP2A6</i>	-1.65173	1.09E-11	5.47E-11
<i>APOA1</i>	-1.11224	3.54E-11	1.63E-10
<i>CD24</i>	1.087973	1.14E-10	4.84E-10
<i>CYP3A4</i>	-1.47793	5.55E-09	1.77E-08
<i>GLYAT</i>	-1.04015	1.22E-12	7.41E-12
<i>CYP2C8</i>	-1.31019	2.62E-16	3.58E-15
<i>HPD</i>	-1.27606	1.51E-09	5.32E-09
<i>APOA5</i>	-1.2028	1.07E-16	1.64E-15
<i>ALDOB</i>	-1.14992	1.54E-10	6.37E-10
<i>MYBL2</i>	1.087569	9.04E-21	4.69E-19
<i>HSD17B6</i>	-1.149	1.79E-17	3.36E-16
<i>SLC27A5</i>	-1.25115	1.93E-19	6.49E-18
<i>AFM</i>	-1.19978	1.28E-19	4.55E-18
<i>TTR</i>	-1.01994	8.87E-10	3.24E-09
<i>CYP4F2</i>	-1.06124	1.53E-16	2.22E-15
<i>SLC10A1</i>	-1.53609	9.13E-18	1.86E-16
<i>AKR7A3</i>	-1.05685	1.48E-14	1.36E-13
<i>CYP8B1</i>	-1.29992	1.00E-12	6.20E-12
<i>HRG</i>	-1.29935	3.47E-12	1.92E-11
<i>C6</i>	-1.10432	5.64E-18	1.22E-16
<i>HPX</i>	-1.09698	3.73E-19	1.14E-17
<i>TAT</i>	-1.39328	1.45E-11	7.17E-11
<i>AQP9</i>	-1.25752	4.89E-11	2.20E-10
<i>HSD17B13</i>	-1.22015	3.07E-09	1.02E-08
<i>SLC22A1</i>	-1.48603	8.27E-14	6.40E-13
<i>HP</i>	-1.19783	1.69E-12	9.86E-12
<i>HPR</i>	-1.28784	4.09E-17	7.03E-16
<i>CYP2C9</i>	-1.03819	3.54E-10	1.38E-09
<i>CFHR4</i>	-1.04032	9.91E-17	1.54E-15
<i>ADH4</i>	-1.03096	5.56E-07	1.29E-06
<i>CYP4A11</i>	-1.11204	4.27E-15	4.44E-14
<i>SERPINC1</i>	-1.41085	1.54E-19	5.32E-18
<i>ADH1C</i>	-1.40467	7.46E-13	4.73E-12
<i>ADH1B</i>	-1.24505	1.60E-12	9.39E-12
<i>TTC36</i>	-1.08952	5.06E-15	5.19E-14
<i>G6PD</i>	1.069211	4.61E-25	1.80E-22
<i>APOC3</i>	-1.30412	1.29E-18	3.31E-17

DEGs, differentially expressed genes; FC, fold change; FDR, false discovery rate; TCGA, The Cancer Genome Atlas.