

Prognostic role of pyroptosis-related genes in gastric cancer

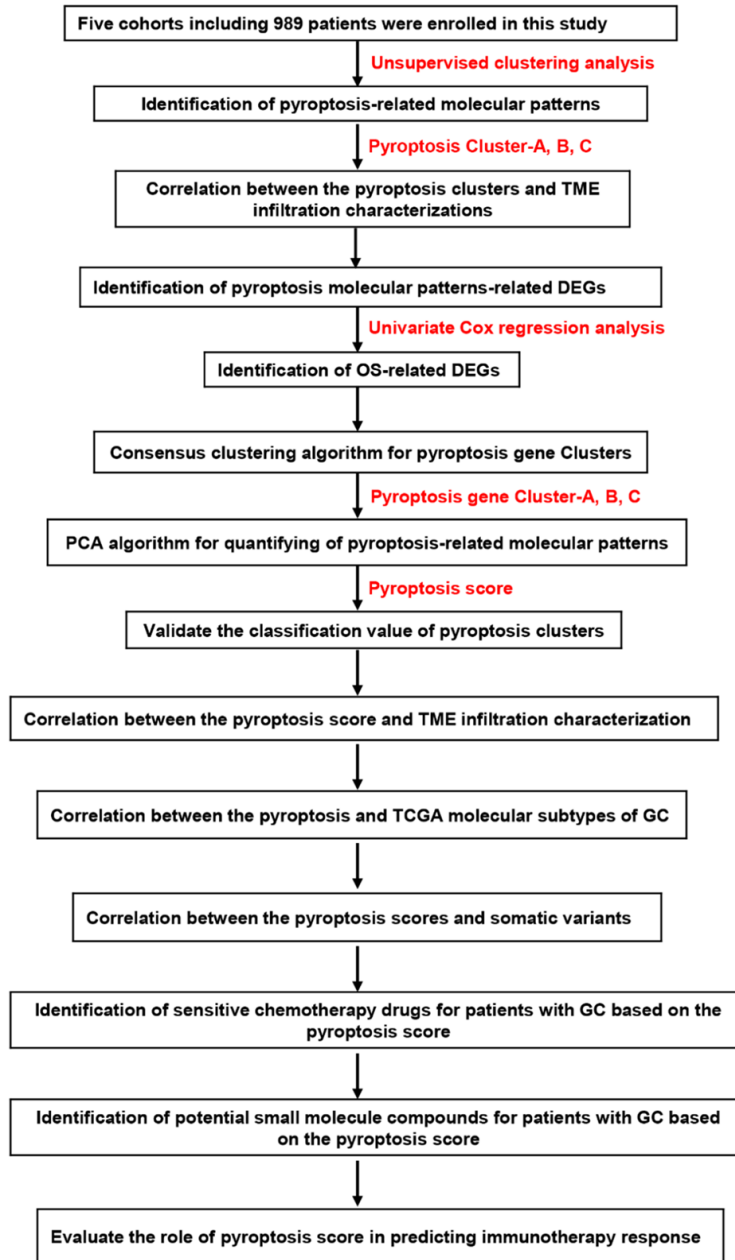


Figure S1. Workflow of the study design.

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Table S1. Datasets of GC patients

| Cohort | Platform | Number of patients | Survival data |
|-----------|---|--------------------|---------------|
| GSE15459 | Affymetrix Human Genome U133 Plus 2.0 Array | 192 | OS |
| GSE34942 | Affymetrix Human Genome U133 Plus 2.0 Array | 56 | OS |
| GSE57303 | Affymetrix Human Genome U133 Plus 2.0 Array | 70 | OS |
| GSE62254 | Affymetrix Human Genome U133 Plus 2.0 Array | 300 | OS |
| TCGA:STAD | Illumina RNAseq | 371 | OS |

Table S2. 33 acknowledged pyroptosis-related genes

| Gene | Full name |
|--------|--|
| AIM2 | Absent in melanoma 2 |
| CASP1 | cysteine-aspartic acid protease-1 |
| CASP3 | cysteine-aspartic acid protease-3 |
| CASP4 | cysteine-aspartic acid protease-4 |
| CASP5 | cysteine-aspartic acid protease-5 |
| CASP6 | cysteine-aspartic acid protease-6 |
| CASP8 | cysteine-aspartic acid protease-8 |
| CASP9 | cysteine-aspartic acid protease-9 |
| ELANE | elastase, neutrophil expressed |
| GPX4 | glutathione peroxidase 4 |
| GSDMA | gasdermin A |
| GSDMB | gasdermin B |
| GSDMC | gasdermin C |
| GSDMD | gasdermin D |
| GSDME | gasdermin E |
| IL18 | interleukin 18 |
| IL1B | interleukin 1 beta |
| IL6 | interleukin 6 |
| NLRC4 | NLR family CARD domain containing 4 |
| NLRP1 | NLR family pyrin domain containing 1 |
| NLRP2 | NLR family pyrin domain containing 2 |
| NLRP3 | NLR family pyrin domain containing 3 |
| NLRP6 | NLR family pyrin domain containing 6 |
| NLRP7 | NLR family pyrin domain containing 7 |
| NOD1 | nucleotide binding oligomerization domain containing 1 |
| NOD2 | nucleotide binding oligomerization domain containing 2 |
| PJVK | pejvakin/deafness, autosomal recessive 59 |
| PLCG1 | phospholipase C gamma 1 |
| PRKACA | protein kinase cAMP-activated catalytic subunit alpha |
| PYCARD | PYD and CARD domain containing |
| SCAF11 | SR-related CTD associated factor 11 |
| TIRAP | TIR domain containing adaptor protein |
| TNF | tumor necrosis factor |

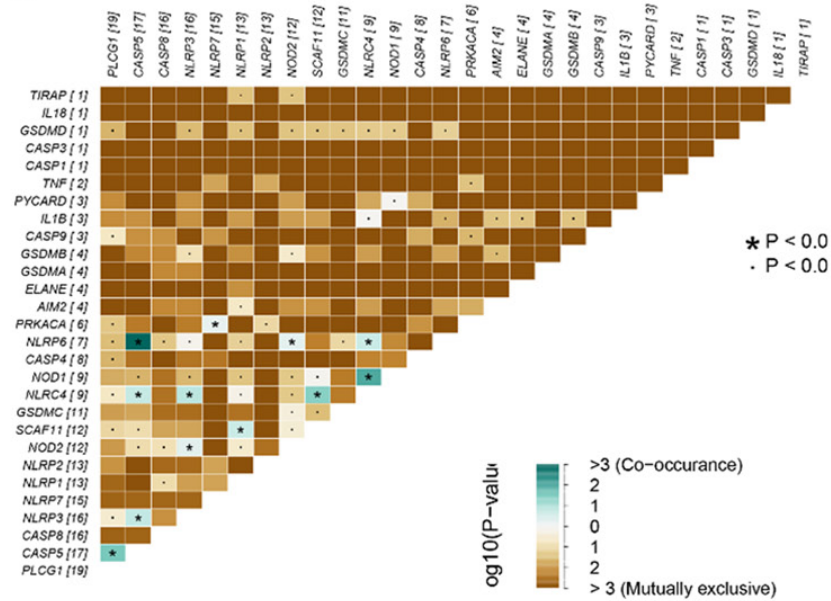
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Table S3. 30 overlapping pyroptosis-related genes

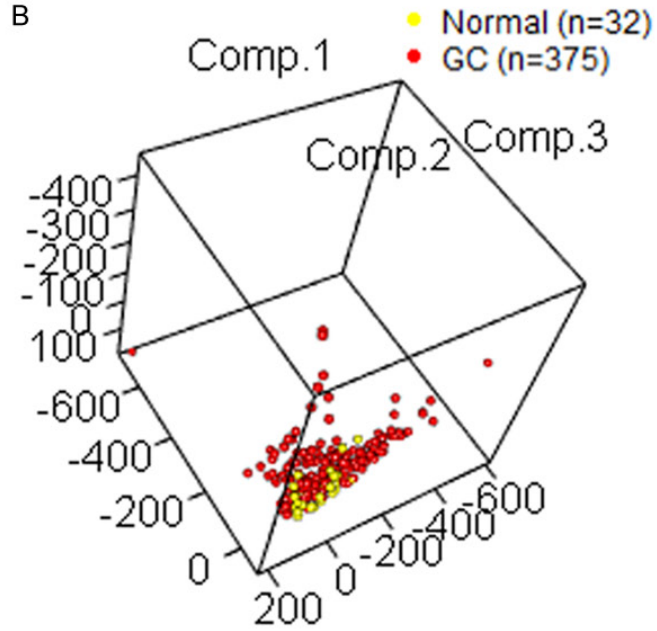
| Gene | Full name |
|--------|--|
| AIM2 | Absent in melanoma 2 |
| CASP1 | cysteine-aspartic acid protease-1 |
| CASP3 | cysteine-aspartic acid protease-3 |
| CASP4 | cysteine-aspartic acid protease-4 |
| CASP5 | cysteine-aspartic acid protease-5 |
| CASP6 | cysteine-aspartic acid protease-6 |
| CASP8 | cysteine-aspartic acid protease-8 |
| CASP9 | cysteine-aspartic acid protease-9 |
| ELANE | elastase, neutrophil expressed |
| GPX4 | glutathione peroxidase 4 |
| GSDMB | gasdermin B |
| GSDMC | gasdermin C |
| GSDMD | gasdermin D |
| IL18 | interleukin 18 |
| IL1B | interleukin 1 beta |
| IL6 | interleukin 6 |
| NLRC4 | NLR family CARD domain containing 4 |
| NLRP1 | NLR family pyrin domain containing 1 |
| NLRP2 | NLR family pyrin domain containing 2 |
| NLRP3 | NLR family pyrin domain containing 3 |
| NLRP6 | NLR family pyrin domain containing 6 |
| NLRP7 | NLR family pyrin domain containing 7 |
| NOD1 | nucleotide binding oligomerization domain containing 1 |
| NOD2 | nucleotide binding oligomerization domain containing 2 |
| PLCG1 | phospholipase C gamma 1 |
| PRKACA | protein kinase cAMP-activated catalytic subunit alpha |
| PYCARD | PYD and CARD domain containing |
| SCAF11 | SR-related CTD associated factor 11 |
| TIRAP | TIR domain containing adaptor protein |
| TNF | tumor necrosis factor |

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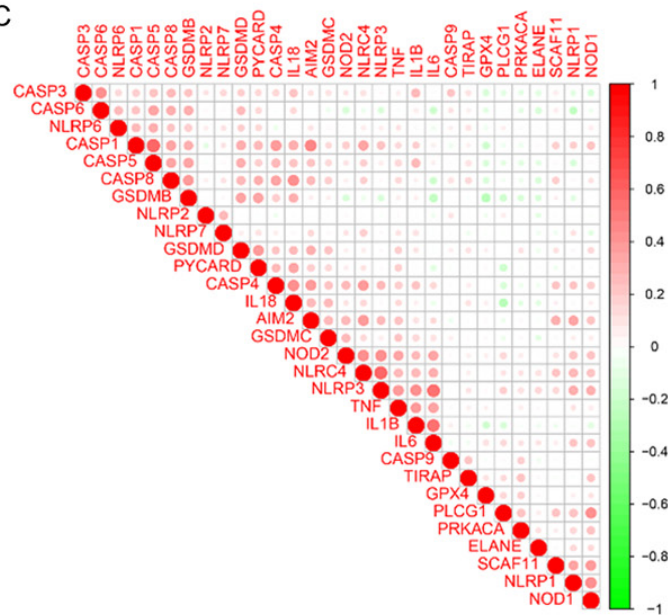
A



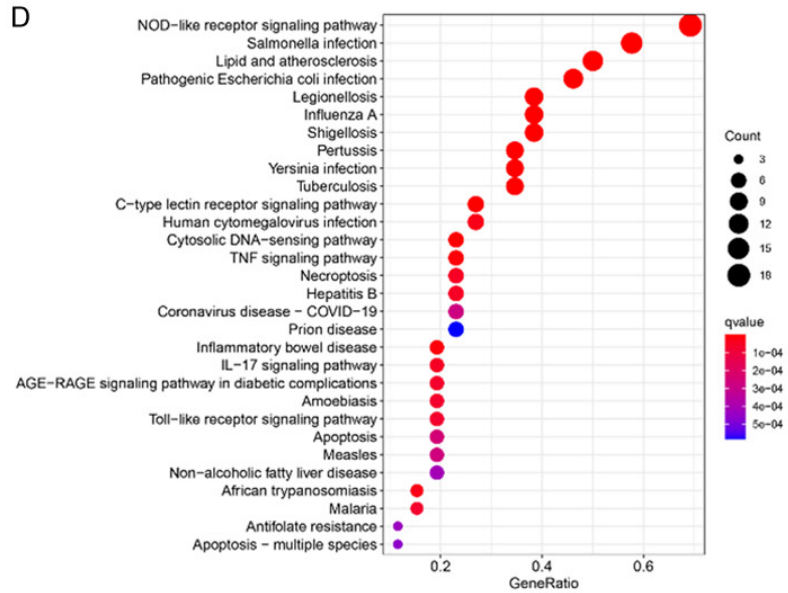
B



C



D



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Figure S2. Characteristics of PGRs in GC. A. The mutation co-occurrence and mutually exclusion analyses for PGRs. Co-occurrence, green; Mutually exclusion, brown. B. Three-dimensional principal component analysis (3D-PCA) of the mRNA expression profiles of PRGs to distinguish tumors from normal samples in TCGA-STAD cohort. C. The correlations between these PGRs were evaluated using the Spearman correlation analysis in GC. D. KEGG pathway enrichment analysis of the 33 PRGs.

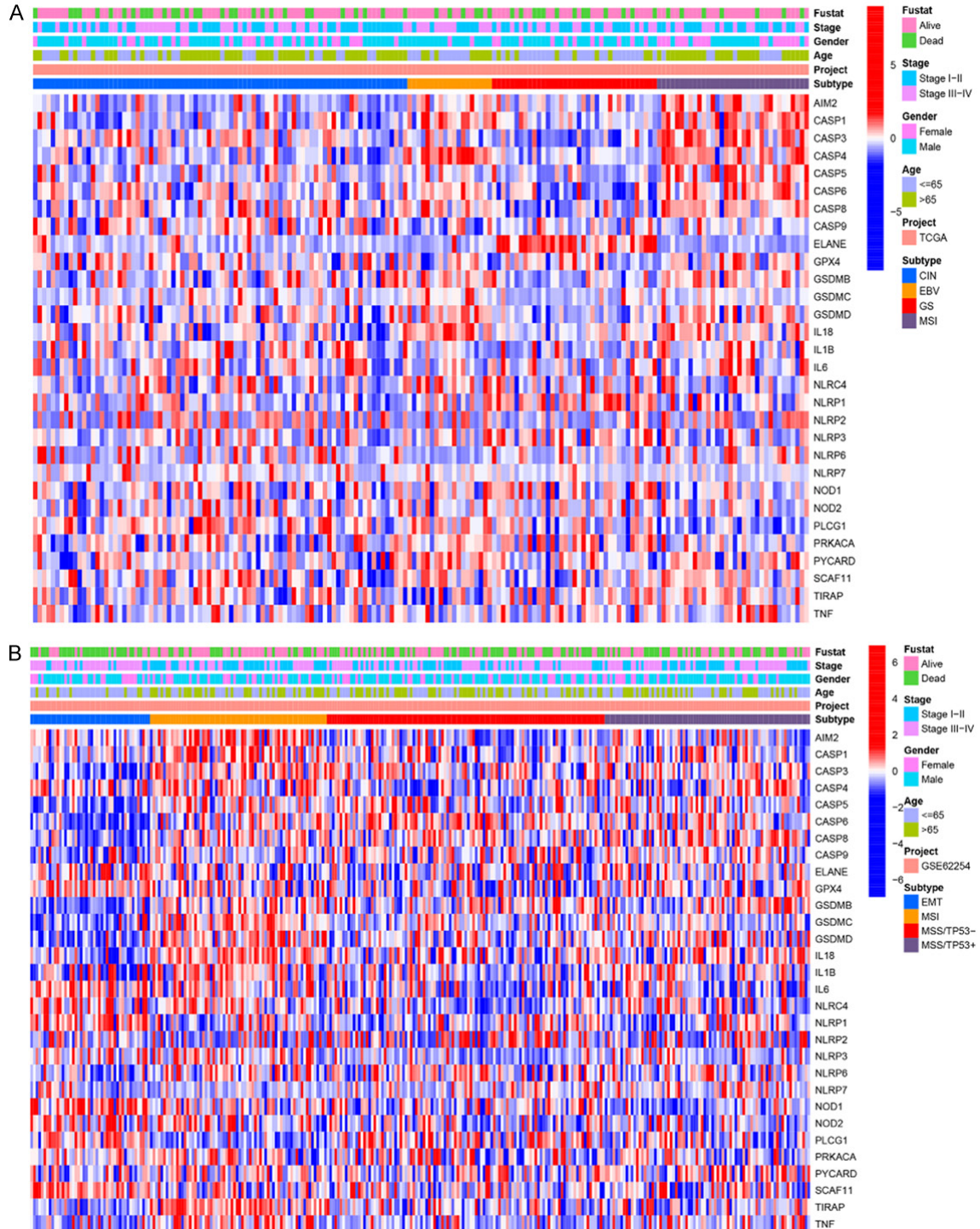


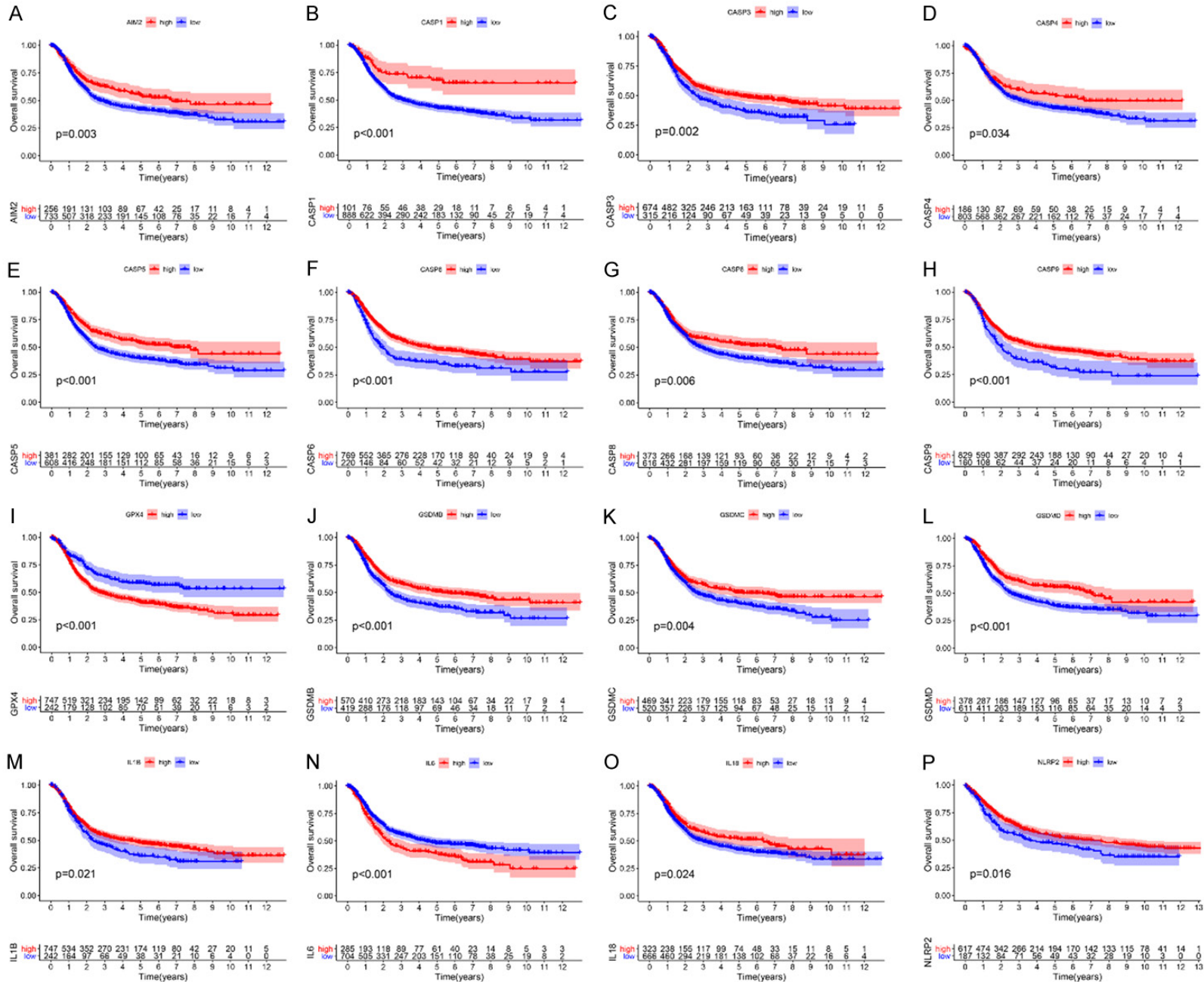
Figure S3. The expression of PGRs in TCGA molecular subtypes (A) and GSE62254 cohort subtypes (B).

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Table S4. Univariate Cox regression analysis of 30 PRGs in GC patients

| Gene | HR | HR.95L | HR.95H | P-value | p-km |
|--------|----------|----------|----------|----------|----------|
| AIM2 | 0.9162 | 0.850929 | 0.986477 | 0.020285 | 0.002784 |
| CASP1 | 0.813646 | 0.738252 | 0.896739 | 3.23E-05 | 0.000138 |
| CASP3 | 0.791896 | 0.672539 | 0.932435 | 0.005122 | 0.002149 |
| CASP4 | 0.926298 | 0.779201 | 1.101162 | 0.385538 | 0.034045 |
| CASP5 | 0.826208 | 0.743883 | 0.917644 | 0.000364 | 6.20E-05 |
| CASP6 | 0.758625 | 0.643263 | 0.894675 | 0.001029 | 4.25E-05 |
| CASP8 | 0.766377 | 0.625849 | 0.938459 | 0.010038 | 0.005662 |
| CASP9 | 0.791276 | 0.612488 | 1.022252 | 0.073206 | 0.000452 |
| ELANE | 1.057157 | 0.928772 | 1.20329 | 0.40012 | 0.145916 |
| GPX4 | 1.29307 | 1.078449 | 1.550401 | 0.005511 | 1.97E-05 |
| GSDMB | 0.86055 | 0.784177 | 0.944361 | 0.001539 | 4.90E-05 |
| GSDMC | 0.848944 | 0.723394 | 0.996285 | 0.044904 | 0.003529 |
| GSDMD | 0.730325 | 0.60767 | 0.877739 | 0.000808 | 2.56E-05 |
| IL18 | 0.947813 | 0.858823 | 1.046024 | 0.286657 | 0.024476 |
| IL1B | 0.986575 | 0.918594 | 1.059588 | 0.710612 | 0.020541 |
| IL6 | 1.122685 | 1.052046 | 1.198068 | 0.000483 | 0.000552 |
| NLRC4 | 1.072602 | 0.913468 | 1.259458 | 0.392344 | 0.116657 |
| NLRP1 | 1.061701 | 0.914147 | 1.233072 | 0.432913 | 0.055706 |
| NLRP2 | 0.997506 | 0.941941 | 1.05635 | 0.93196 | 0.154515 |
| NLRP3 | 1.205337 | 1.065877 | 1.363046 | 0.002912 | 0.002096 |
| NLRP6 | 0.902724 | 0.818304 | 0.995854 | 0.041061 | 0.002225 |
| NLRP7 | 0.982512 | 0.881398 | 1.095225 | 0.750177 | 0.036066 |
| NOD1 | 1.087384 | 0.894139 | 1.322395 | 0.401384 | 0.042653 |
| NOD2 | 1.163598 | 1.021308 | 1.325712 | 0.022799 | 0.004966 |
| PLCG1 | 1.233606 | 1.048437 | 1.451479 | 0.011407 | 0.000288 |
| PRKACA | 0.985863 | 0.770836 | 1.260871 | 0.909696 | 0.266301 |
| PYCARD | 0.943283 | 0.827467 | 1.07531 | 0.382335 | 0.001941 |
| SCAF11 | 0.978412 | 0.773484 | 1.237634 | 0.855581 | 0.184893 |
| TIRAP | 0.689006 | 0.549698 | 0.863619 | 0.001228 | 1.25E-05 |
| TNF | 0.919229 | 0.818404 | 1.032475 | 0.155373 | 0.012761 |

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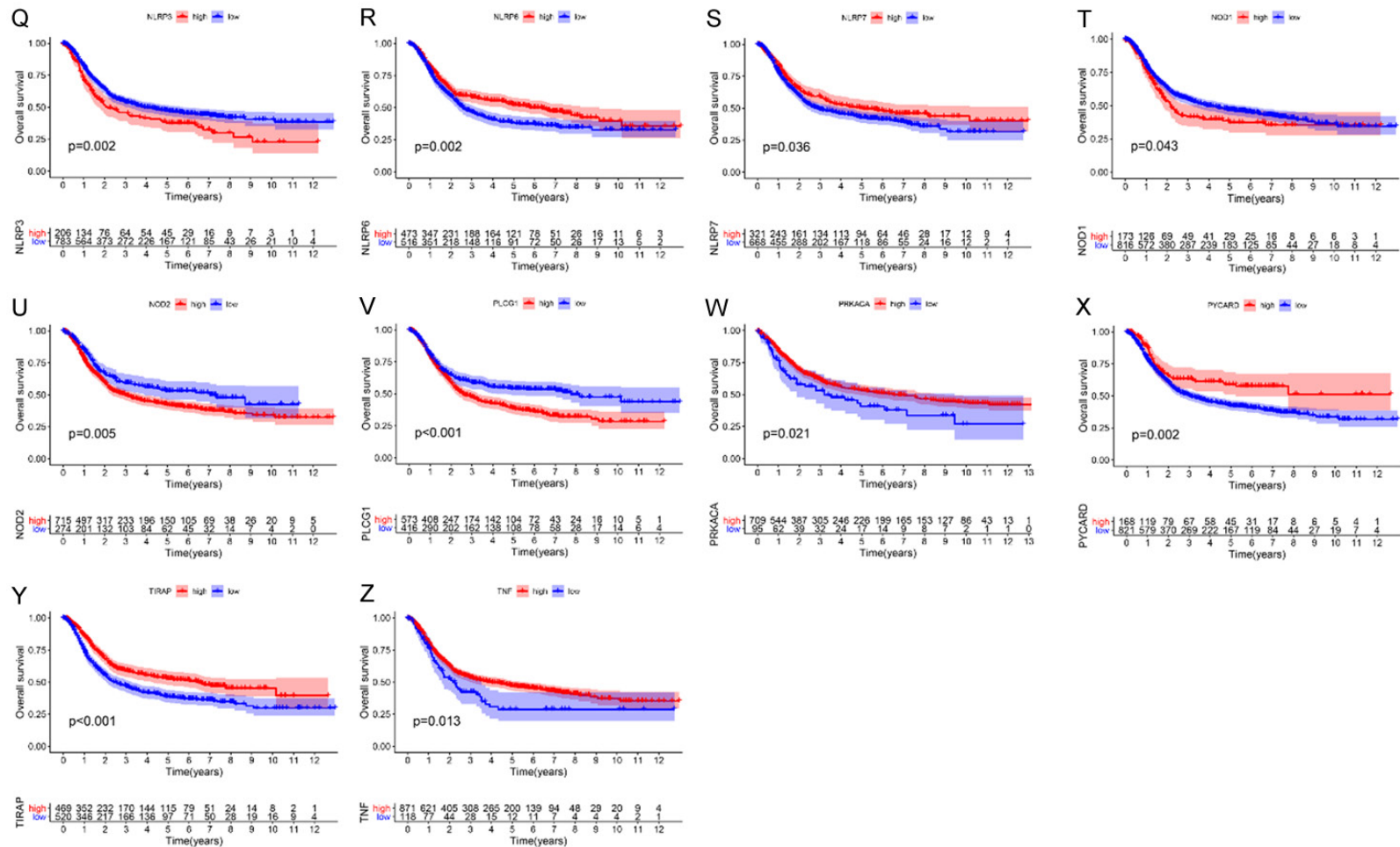


Figure S4. OS-related PRGs in gathered GC cohort. Kaplan-Meier curves for GC patients with high and low levels of AIM2 (A), CASP1 (B), CASP3 (C), CASP4 (D), CASP5 (E), CASP6 (F), CASP8 (G), CASP9 (H), GPX4 (I), GSDMB (J), GSDMC (K), GSDMD (L), IL1B (M), IL6 (N), IL18 (O), NLRP2 (P), NLRP3 (Q), NLRP6 (R), NLRP7 (S), NOD1 (T), NOD2 (U), PLCG1 (V), PRKACA (W), PYCARD (X), TIRAP (Y), TNF (Z) in gathered GC cohort.

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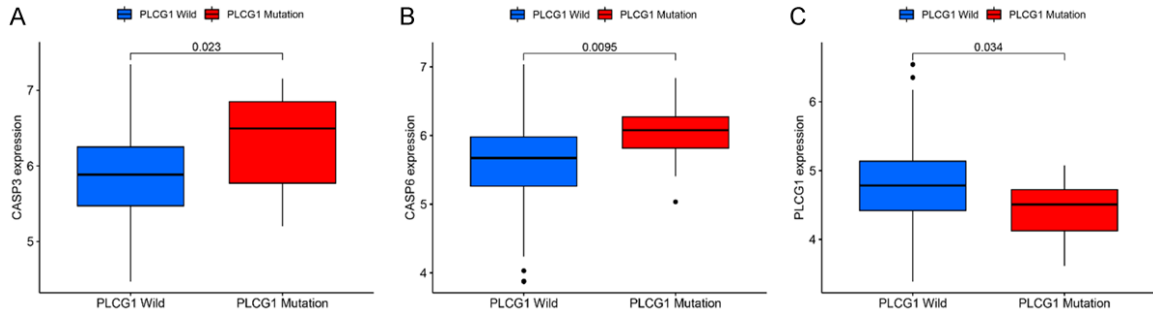


Figure S5. Difference in PRGs expression between PLCG1-mutant and wild types. (A-C) Expression levels of CASP3 (A), CASP6 (B), and PLCG1 (C) between PLCG1-mutant and wild types.

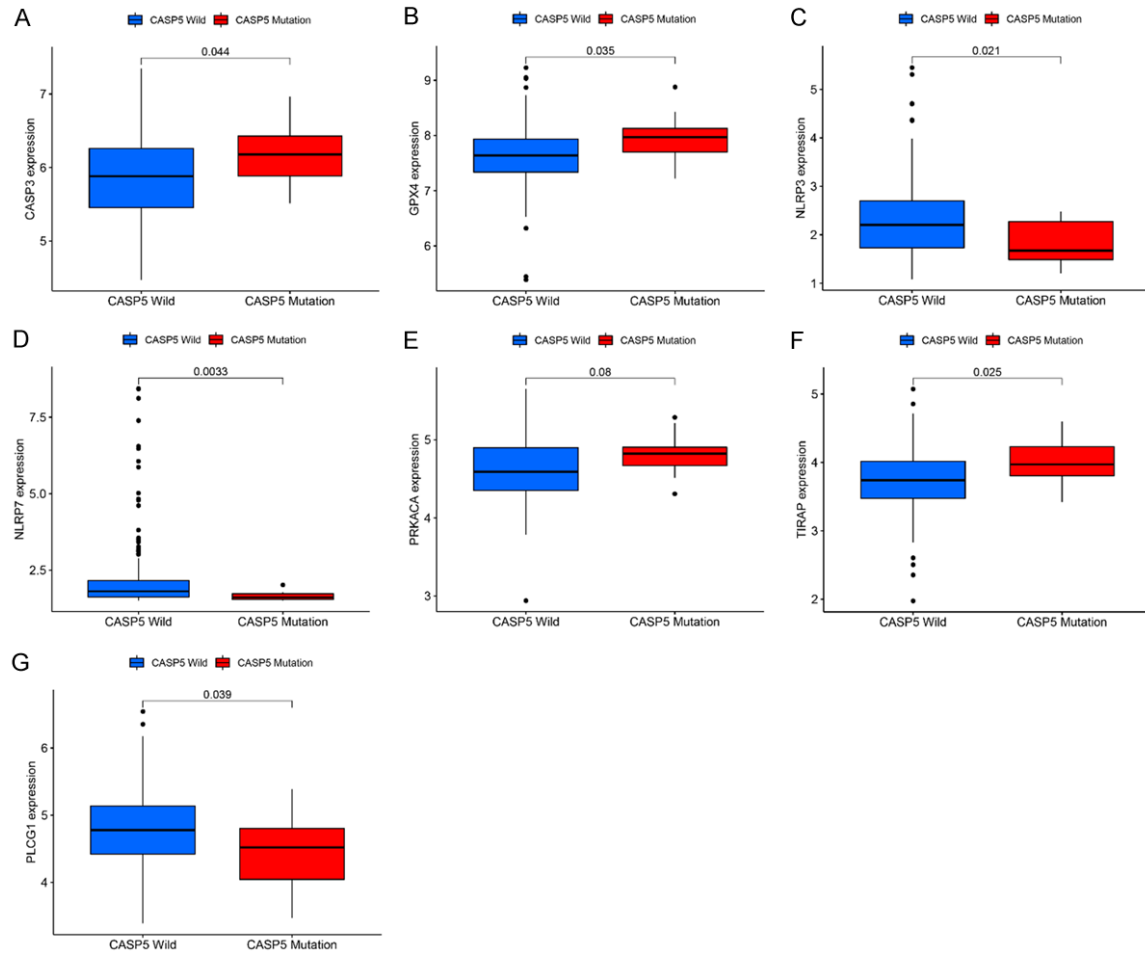


Figure S6. Difference in PRGs expression between CASP5-mutant and wild types. (A-G) Expression levels of CASP3 (A), GPX4 (B), NLRP3 (C), NLRP7 (D), PRKACA (E), TIRAP (F), and PLCG1 (G) between CASP5-mutant and wild types.

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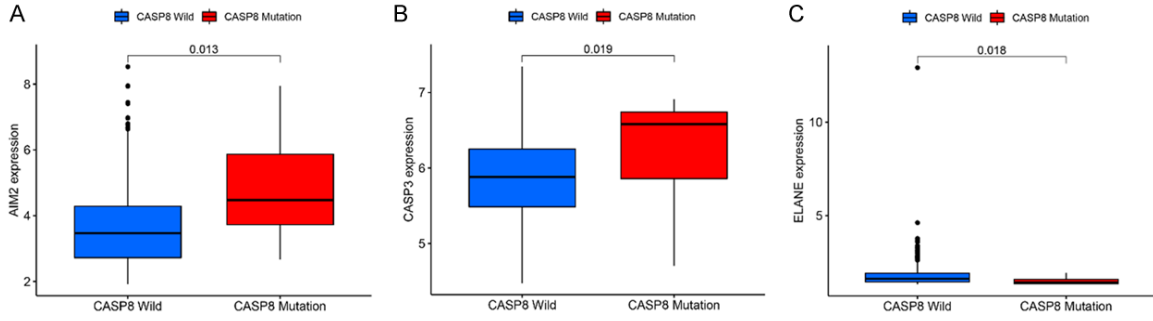


Figure S7. Difference in PRGs expression between CASP8-mutant and wild types. (A-C) Expression levels of AIM2 (A), CASP3 (B), and ELANE (C) between CASP8-mutant and wild types.

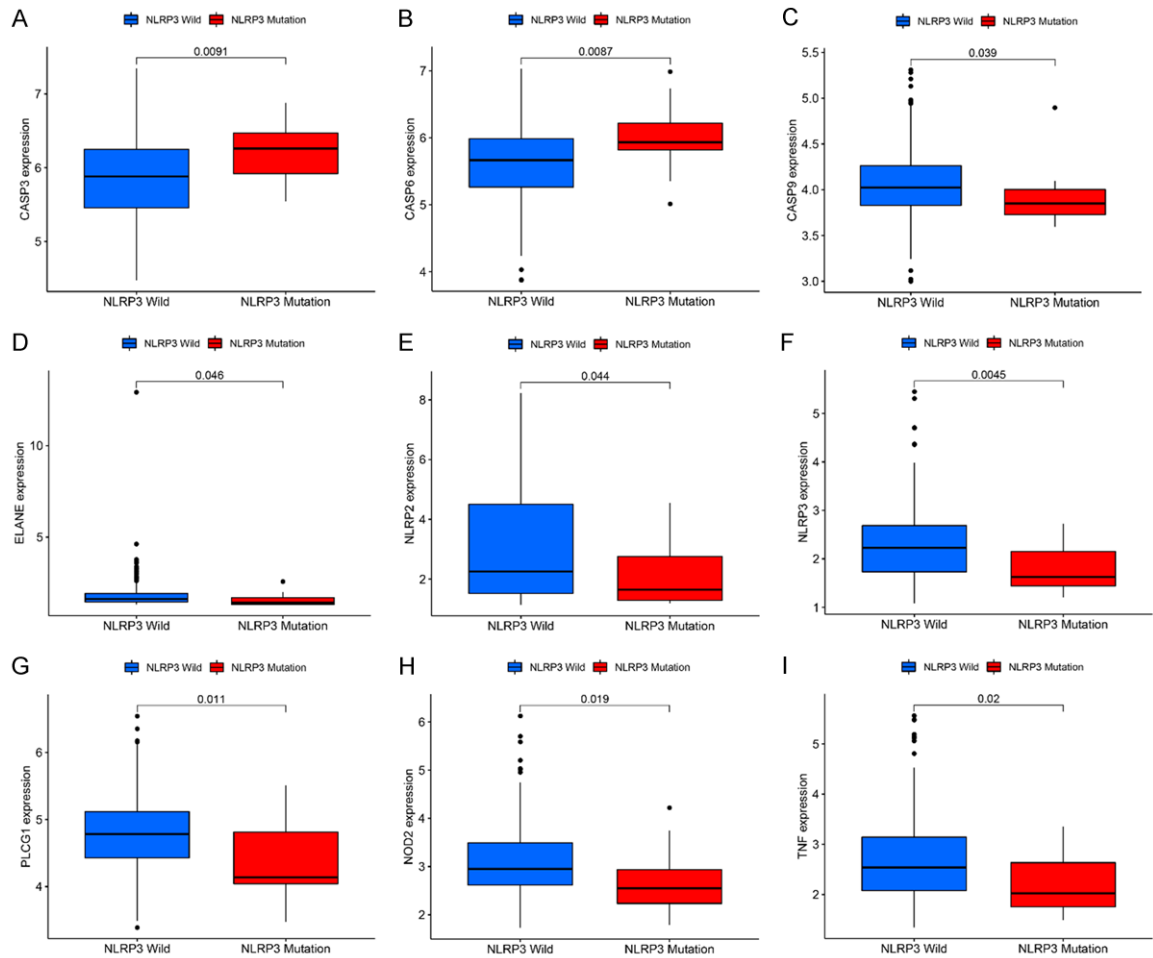


Figure S8. Difference in PRGs expression between NLRP3-mutant and wild types. (A-I) Expression levels of CASP3 (A), CASP6 (B), CASP9 (C), ELANE (D), NLRP2 (E), NLRP3 (F), PLCG1 (G), NOD2 (H), and TNF (I) between NLRP3-mutant and wild types.

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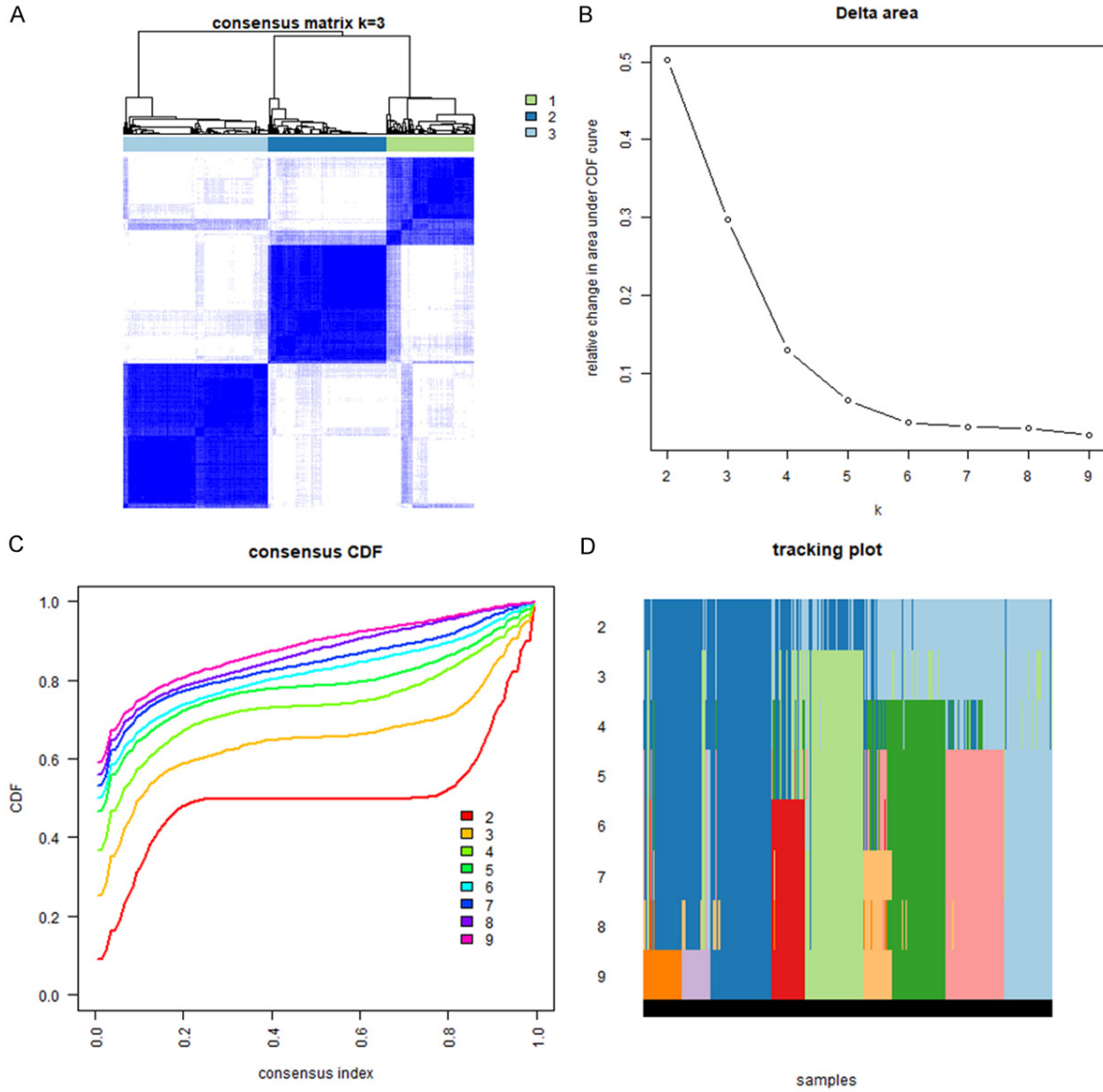
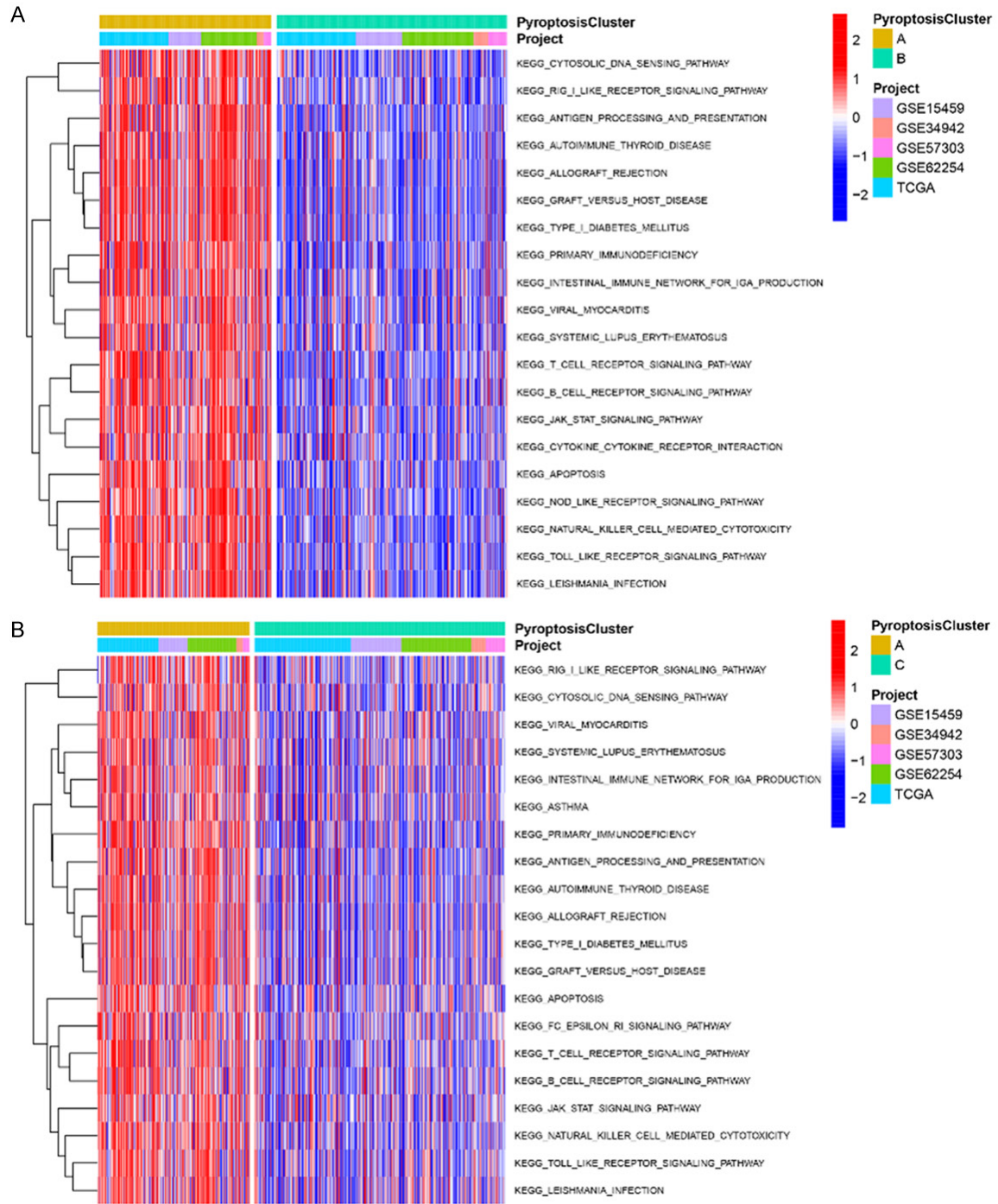


Figure S9. Unsupervised clustering analysis for identifying pyroptosis-related molecular patterns. A. Consensus clustering matrix for k=3. B. Relative change in area under CDF curve for k=2-9. C. Consensus clustering cumulative distribution function (CDF) for k=2-9. D. The tracking plot for k=2-9.

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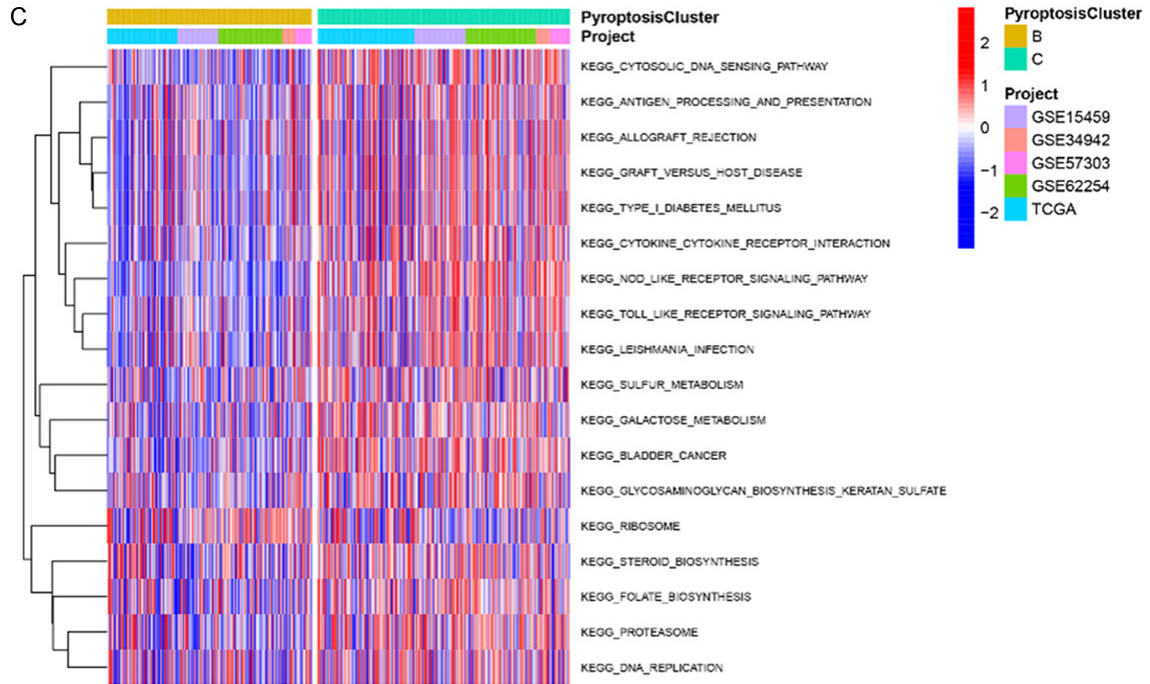


Figure S10. Identification of biological pathways by GSVA enrichment analysis in distinct pyroptosis-related molecular patterns. The heatmap was used to show the activation states of biological pathways. Red represents the activated pathways, while blue represents the inhibited pathways. The GC cohorts were used as sample annotations. A. Pyroptosis Cluster A vs pyroptosis Cluster B; B. Pyroptosis Cluster A vs pyroptosis Cluster C; C. Pyroptosis Cluster B vs pyroptosis Cluster C.

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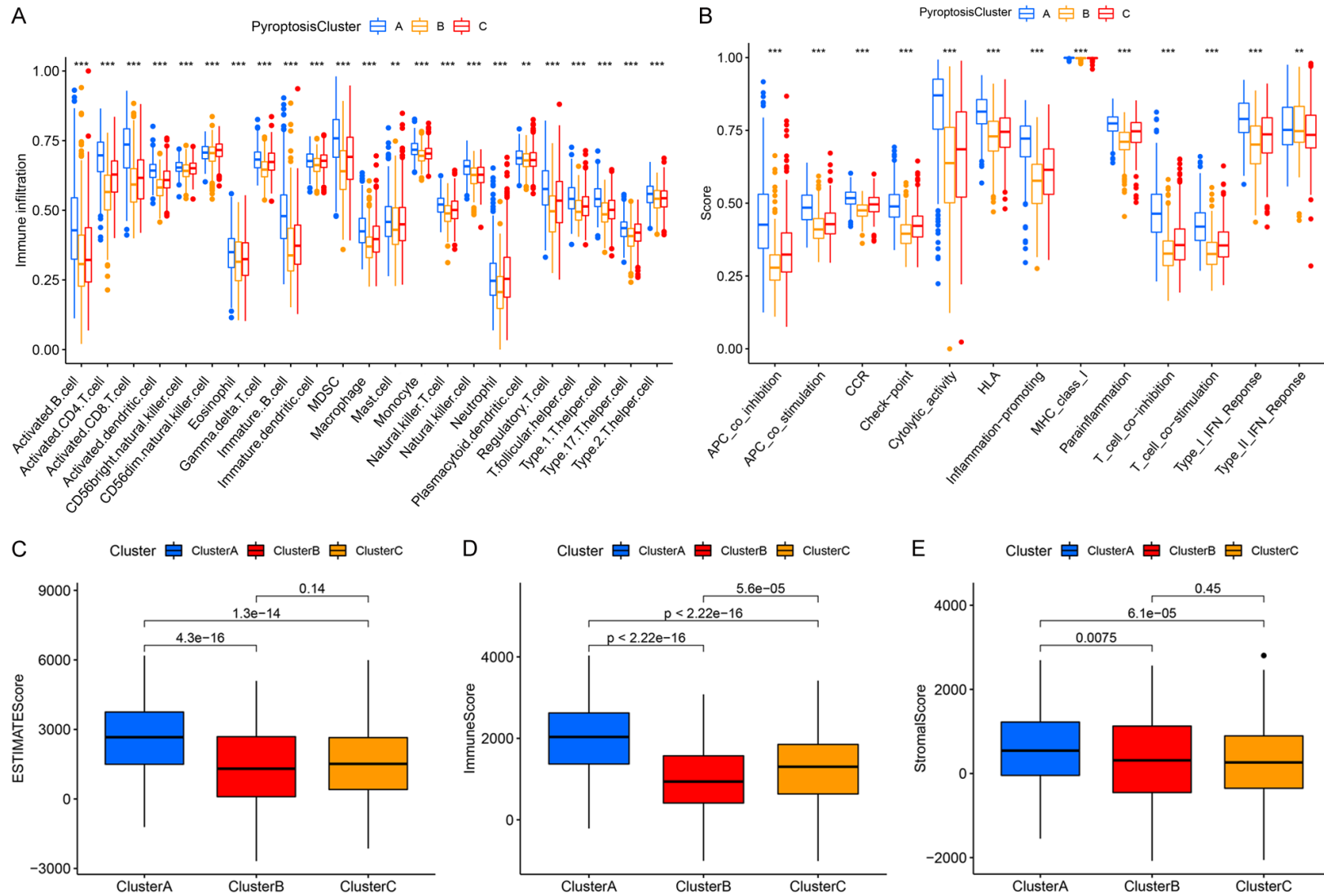
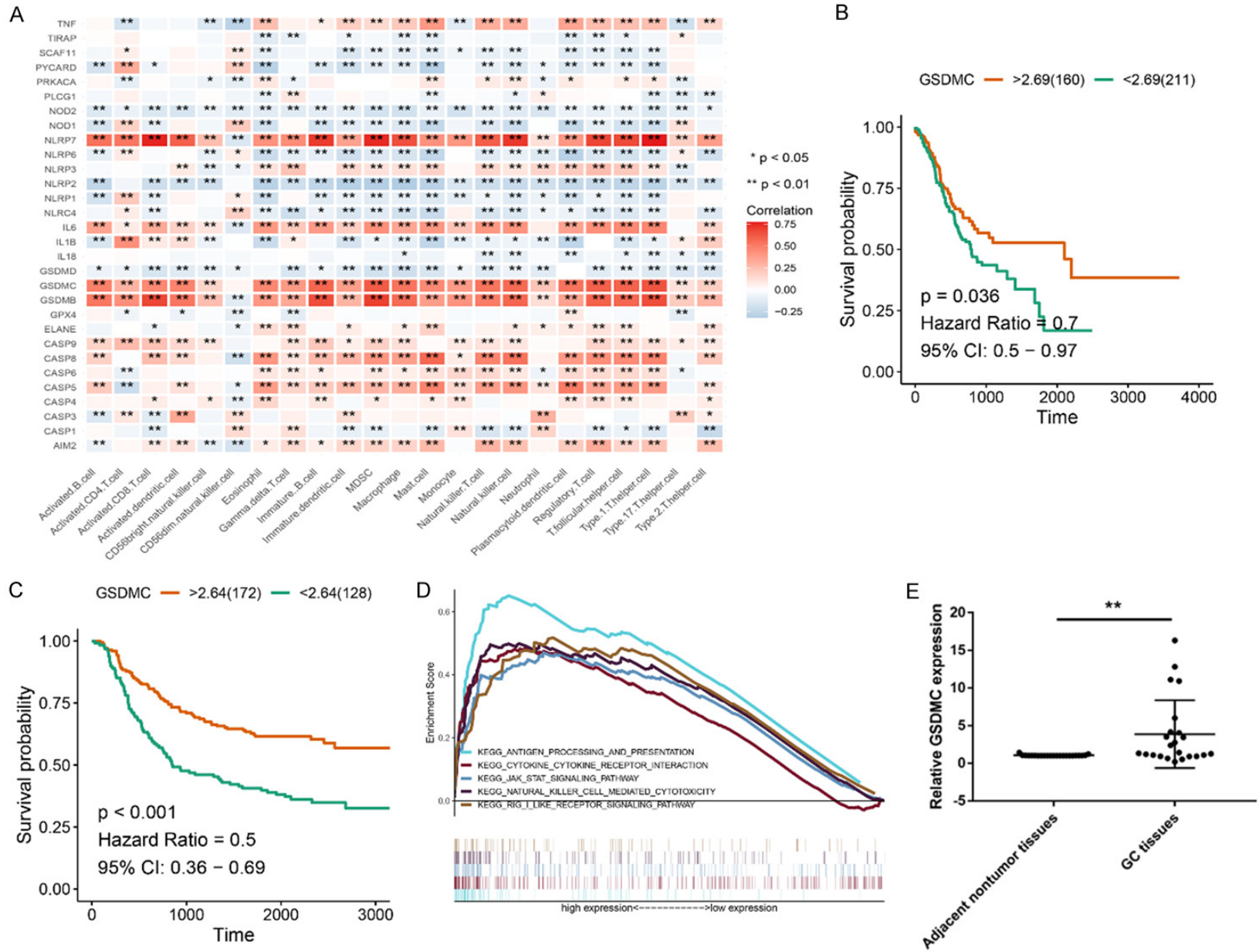


Figure S11. Correlation between the characteristics of tumor immune microenvironment (TIME) and pyroptosis clusters. (A) Box plots depicts the scores of immune infiltrations among the three pyroptosis clusters. (B) Box plots presents the scores of immune functions among the three pyroptosis clusters. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$. (C-E) Box plots shows the differences in (C) ESTIMATE score, (D) immune score, and (E) stromal score among the three pyroptosis clusters.

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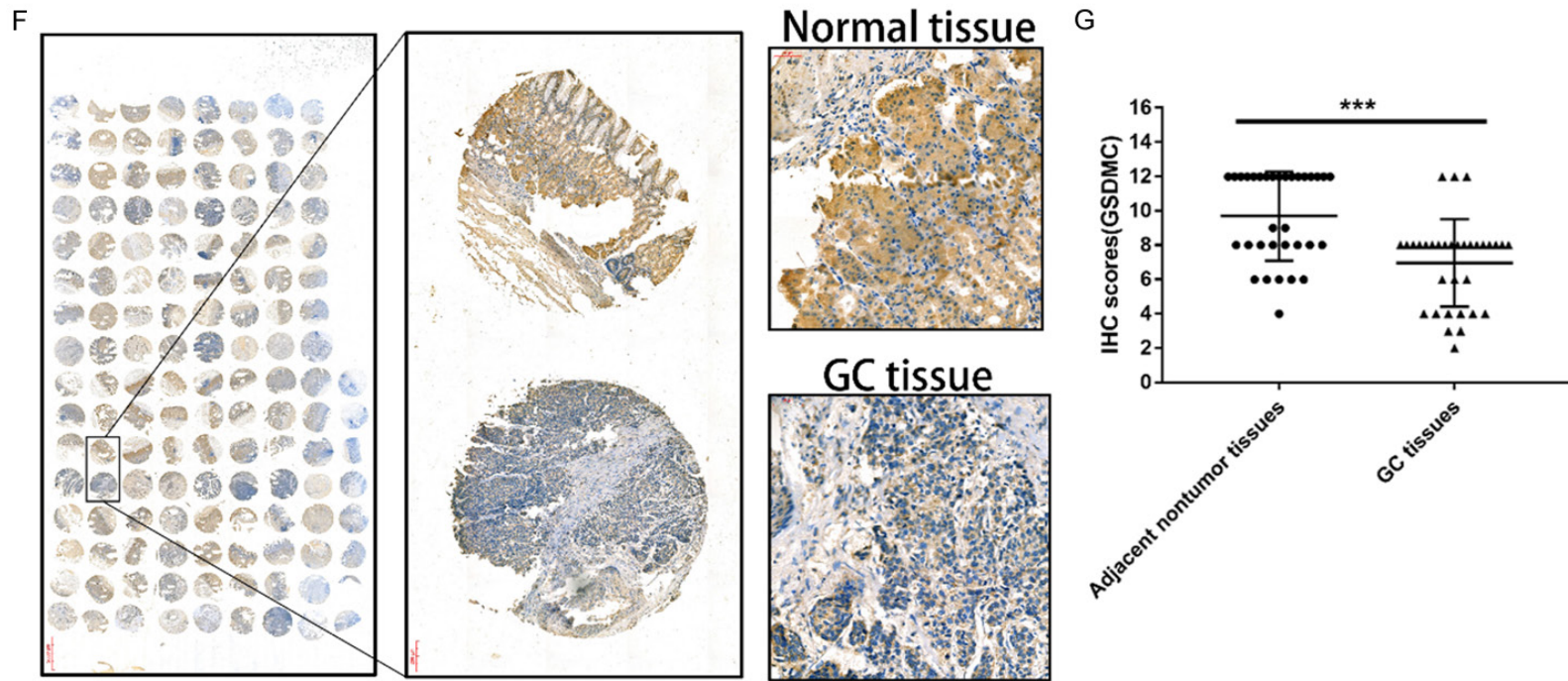


Figure S12. Correlation between GSDMC expression and TME infiltration as well as the prognostic role of GSDMC in GC. (A) The correlation between each PRGs and each TME infiltration cell type using spearman analysis. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$. (B, C) Survival analyses for patients with low or high GSDMC expression in the TCGA-STAD (B) and GSE62254 (C) cohorts using Kaplan-Meier curves. (D) GSEA analysis indicated that five immune or inflammation-related pathways were enriched in the GSDMC high expression group in the gathered GC cohort. (E) RT-qPCR results showed that the mRNA expression level of GSDMC was higher expressed in GC tissues than adjacent non-tumor tissues. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$. (F) GSDMC expression in GC tumor tissues and the paired adjacent non-tumor tissues was evaluated by immunohistochemical staining with tissue microarray. (G) IHC scores of GSDMC staining in GC tissues and adjacent non-tumor tissues. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.

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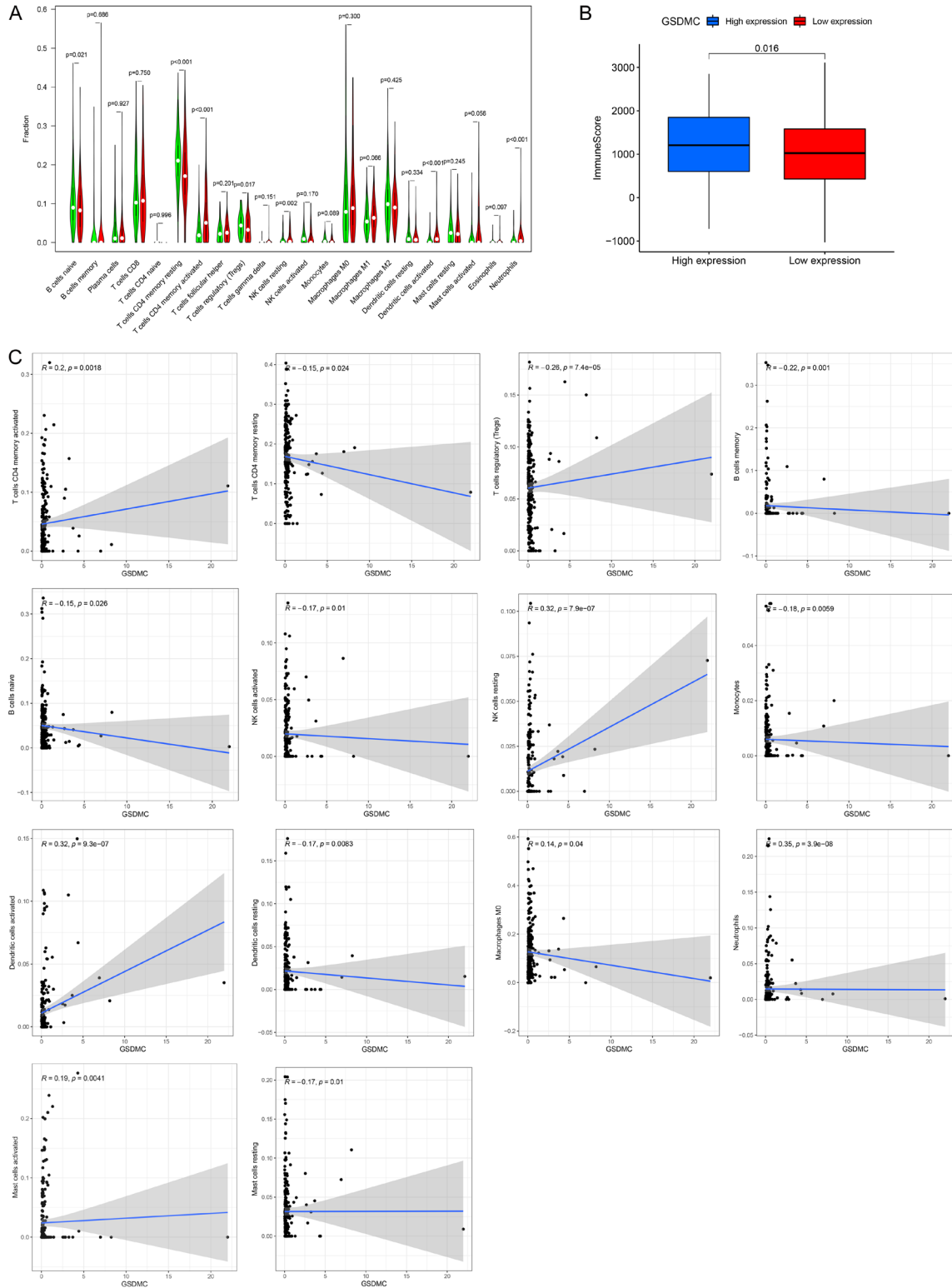


Figure S13. Correlation between GSDMC expression and immune cells infiltration. A. Difference in the abundance of each TME infiltrating cell between GSDMC high expression (Red) and low expression (Green) groups. B. Box plots shows the differences in immune score between GSDMC high expression and low expression groups. C. Correlation between GSDMC expression and immune cells infiltration.

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Table S5. 346 overlapping DEGs

| Gene |
|---|
| IRF1 IDO1 CASP1 GBP5 GBP1 CD274 APOL6 IL12RB1 TAP1 TYMP TAP2 IFNG TNFRSF9 PSMB9 RNF213 IL2RB TNFSF13B CARD16 ICOS UBE2L6 IL32 SAMD9L IL2RA ETV7 BATF2 GZMB SLAMF8 SNX20 CXCL11 STAT1 LCP2 CD80 LAMP3 BIRC3 CD300LF IFIH1 CCL4 HAVCR2 IFIT3 ICAM1 SIGLEC10 CXCL10 SNX10 PRF1 PSMB8 TRAFD1 PLEK KLRD1 ZBP1 NCF1 CYBB CD300A ADAMDEC1 RNF19B LAG3 PLA2G7 CD53 IFI35 FLVCR2 CD86 ACP5 LYN IGSF6 NMI IL15RA SAMSN1 KMO OAS2 BCL2A1 CD38 SLAMF1 CLEC7A TFEC SLAMF7 LCP1 LILRB4 HK3 DAPP1 IL18RAP KLHL6 GPR65 TLR8 LILRB1 OAS3 IL4I1 NFAM1 STX11 RAC2 ST8SIA4 CLEC4E CCR1 ITGB2 PARP12 ITGAX MICB CLEC4A TAGAP GNLY FGR CTLA4 DOK3 SLC2A5 PDCD1LG2 LAPT5 KIR2DL4 STAT4 LAIR1 HCK SIGLEC7 PIK3R5 JAK3 CYTH4 RHOH PTAFR CASP5 HPS5 NCF2 PIK3AP1 LST1 MNDA TRAF1 APOL1 USP18 FCER1G GCH1 PILRA NLRC4 PMAIP1 KLHDC7B ALOX5AP LACTB CASP4 SOCS1 TNFAIP3 CSF3R FPR3 OASL CASP10 FCGR1B TNFRSF1B LILRB2 SERPINB9 SLC31A2 ZNF267 MOV10 MMP25 LAIR2 APOBR OSCAR CCR8 CD40 CMPK2 HLA-C PLSCR1 DENND2D MTURN CD69 CD83 SH2D2A SRGN CD7 SELL THEMIS2 LINC01094 CSF2RB LILRB3 RIPK2 LILRA6 ISG20 NFE2L3 CCL18 TNF PRDM1 PREX1 RSAD2 ITGA4 SECTM1 MYD88 HPSE NPL KIF2A LMNB1 GSTO1 TNFRSF4 MLKL SIGLEC9 SPI1 GCA RELT NOS2 FBXO6 TYROBP CYTIP GSDMB CKB RASGRP3 FCGR2A SH2B3 HMOX1 SERTAD4 ITGAM PIM2 CCRL2 TMSB10 CCL22 ADPGK BAK1 RNF149 CDCP1 NFKBIE CNDP2 MCM5 IL12RB2 DNMT1 OAS1 FCGR2C MEI1 UBE2D1 TNIP3 ADAM10 BATF SIGLEC5 ADA KYNU CASS4 NOD2 PBX1 HELZ2 ISG15 WFS1 CD300C EXOSC9 C15orf48 NECAP2 DRAM1 PSMA4 REEP1 IGHG1 TNFRSF18 ACOT7 MYO7A TCEAL4 KCNH2 UHRF1 NCEH1 CASP7 TMPO IKBKE COL4A5 IL17RA HELLS SIRPB1 EZH2 BRIP1 PPP1R14A NUP50 CENPK PTBP3 CEACAM4 ALAS1 DYNC1I1 RHEBL1 DDX60L CD14 SDS ACP2 CAPG OLR1 RAB39A IRF7 CAPZA1 TRIM15 SIRPB2 CENPH NAV2 WLS TPM3 GTF2B HLA-G KNTC1 TRPV2 PRKAB2 EAF2 RGS19 IL7R MCM6 DENND1A CHST11 PRELID1 APBB1IP BATF3 CXCL16 SLC25A22 E2F7 VLDLR TTLL7 DEPDC1B BMPR1B PTGES3L LINC01278 ENAH HNRNPF MREG SLC41A3 PDZRN3 CYP39A1 SLC16A6 PDZK1IP1 GNAZ VNN2 C3orf70 CTSZ MALT1 CDCA2 CDV3 POLD1 MYEF2 GINS3 RAB42 COQ2 PCP4 GPD2 ALOX5 PARP8 M6PR VAMP8 NUP62 SLC15A4 MZB1 ATOX1 RP2 ZNF827 MFSD5 AK2 IL1B CELF2 TK2 RBM43 PROK2 PIK3IP1 NLRP2 ACSM5 BCL2 MBNL1 LNPEP RASD1 |

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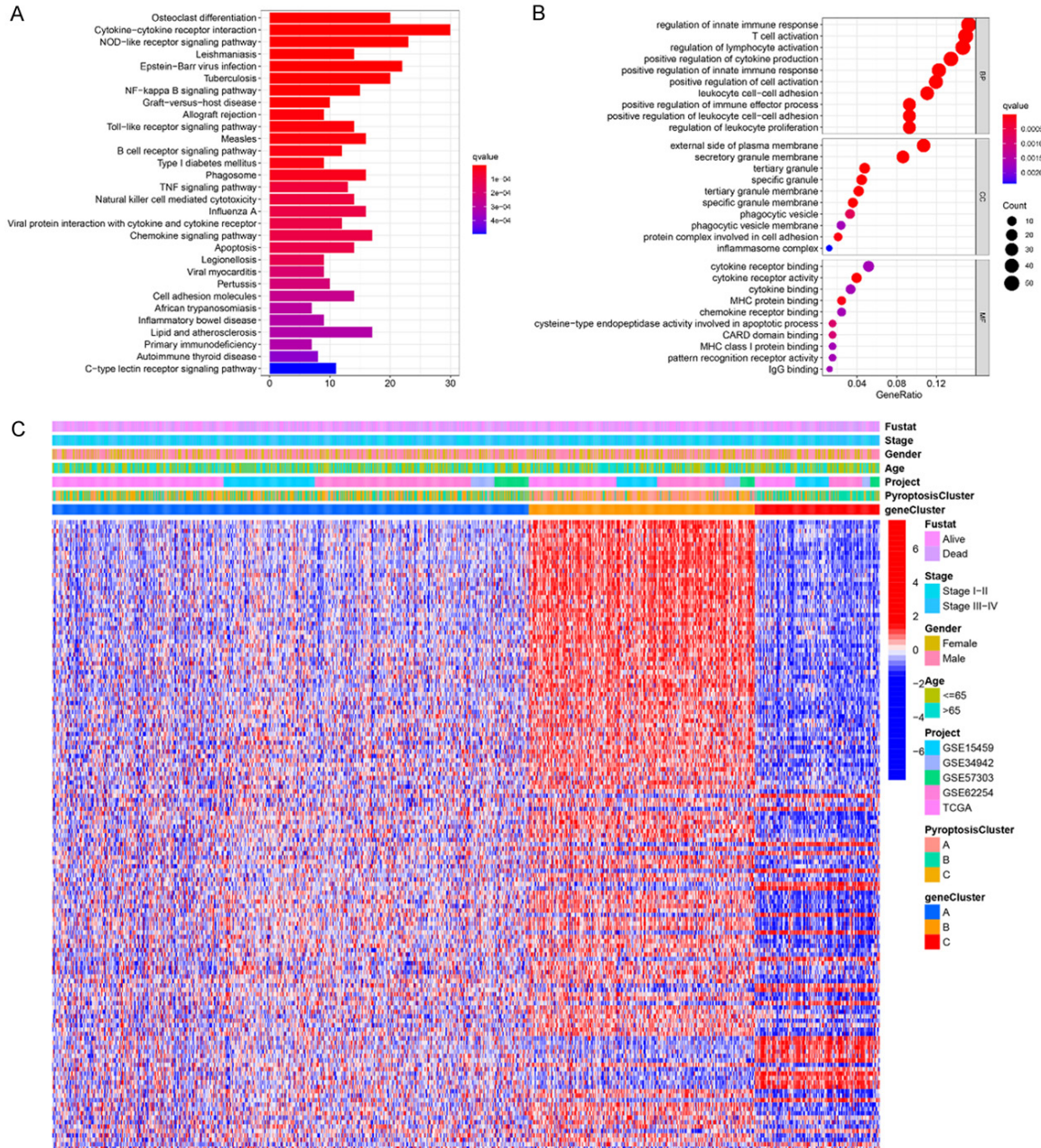


Figure S14. Identification of pyroptosis gene clusters. A. KEGG pathway enrichment analysis presents the enriched pathways of 346 overlapping DEGs. B. GO enrichment analysis of biological process (BP), cellular component (CC) and molecular function (MF) terms of 346 overlapping DEGs ranked by adjusted p -value. C. Heatmap presents the correlation between the three gene clusters and clinicopathological characteristics of GC patients.

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Table S6. 143 OS-related DEGs

| Gene | HR | HR.95L | HR.95H | P value |
|---------|----------|----------|----------|----------|
| IRF1 | 0.807396 | 0.715696 | 0.910845 | 0.000505 |
| IDO1 | 0.913376 | 0.863272 | 0.966388 | 0.001646 |
| CASP1 | 0.813646 | 0.738252 | 0.896739 | 3.23E-05 |
| GBP5 | 0.925065 | 0.857991 | 0.997382 | 0.042537 |
| CD274 | 0.859674 | 0.76913 | 0.960876 | 0.007749 |
| APOL6 | 0.73715 | 0.642404 | 0.845871 | 1.39E-05 |
| IL12RB1 | 0.804104 | 0.692594 | 0.933568 | 0.004204 |
| TAP1 | 0.796753 | 0.717163 | 0.885175 | 2.32E-05 |
| TAP2 | 0.748394 | 0.64462 | 0.868875 | 0.000142 |
| IFNG | 0.876235 | 0.793202 | 0.967961 | 0.009294 |
| PSMB9 | 0.825908 | 0.744501 | 0.916216 | 0.000303 |
| RNF213 | 0.847019 | 0.735574 | 0.97535 | 0.02107 |
| CARD16 | 0.817257 | 0.709925 | 0.940817 | 0.004966 |
| UBE2L6 | 0.850847 | 0.75684 | 0.956531 | 0.006852 |
| ETV7 | 0.78489 | 0.704059 | 0.875 | 1.25E-05 |
| BATF2 | 0.819535 | 0.746162 | 0.900123 | 3.20E-05 |
| GZMB | 0.870201 | 0.80528 | 0.940356 | 0.000441 |
| LAMP3 | 0.898799 | 0.820095 | 0.985056 | 0.02249 |
| BIRC3 | 0.906458 | 0.827936 | 0.992427 | 0.033636 |
| IFIH1 | 0.787342 | 0.680068 | 0.911538 | 0.001377 |
| PRF1 | 0.884607 | 0.79423 | 0.985267 | 0.025754 |
| PSMB8 | 0.761764 | 0.670688 | 0.865209 | 2.81E-05 |
| TRAFD1 | 0.718729 | 0.582103 | 0.887422 | 0.002139 |
| KLRD1 | 0.8558 | 0.738816 | 0.991306 | 0.037857 |
| ZBP1 | 0.864853 | 0.77625 | 0.963569 | 0.008465 |
| RNF19B | 0.830844 | 0.71336 | 0.967676 | 0.017201 |
| LAG3 | 0.86336 | 0.783926 | 0.950843 | 0.002849 |
| IFI35 | 0.844633 | 0.735133 | 0.970443 | 0.017151 |
| LYN | 0.838348 | 0.720759 | 0.975122 | 0.022215 |
| NMI | 0.765955 | 0.651375 | 0.90069 | 0.001259 |
| IL15RA | 0.842184 | 0.718375 | 0.987331 | 0.03425 |
| OAS2 | 0.904819 | 0.820738 | 0.997514 | 0.044433 |
| DAPP1 | 0.869986 | 0.766543 | 0.987389 | 0.031047 |
| OAS3 | 0.865288 | 0.773493 | 0.967976 | 0.011445 |
| NFAM1 | 0.829233 | 0.711609 | 0.9663 | 0.016432 |
| PARP12 | 0.807629 | 0.694691 | 0.938928 | 0.005438 |
| MICB | 0.848303 | 0.761751 | 0.944689 | 0.002733 |
| GNLY | 0.898997 | 0.825789 | 0.978696 | 0.014016 |
| CTLA4 | 0.837573 | 0.735601 | 0.953681 | 0.007451 |
| KIR2DL4 | 0.700891 | 0.593537 | 0.827663 | 2.79E-05 |
| CASP5 | 0.826208 | 0.743883 | 0.917644 | 0.000364 |
| USP18 | 0.853709 | 0.76377 | 0.954239 | 0.005359 |
| GCH1 | 0.730314 | 0.629373 | 0.847445 | 3.46E-05 |
| OASL | 0.911778 | 0.83342 | 0.997503 | 0.043957 |
| CASP10 | 0.672346 | 0.580646 | 0.778529 | 1.12E-07 |
| MOV10 | 0.784419 | 0.651599 | 0.944313 | 0.010308 |
| MMP25 | 0.719693 | 0.614968 | 0.842253 | 4.14E-05 |

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|-----------|----------|----------|----------|----------|
| LAIR2 | 0.793559 | 0.706695 | 0.891099 | 9.26E-05 |
| CMPK2 | 0.891545 | 0.808428 | 0.983207 | 0.021497 |
| DENND2D | 0.747292 | 0.641983 | 0.869875 | 0.000171 |
| LINC01094 | 1.186739 | 1.038648 | 1.355946 | 0.011817 |
| ISG20 | 0.887751 | 0.799108 | 0.986227 | 0.02653 |
| NFE2L3 | 0.840868 | 0.755551 | 0.935819 | 0.001498 |
| SECTM1 | 0.867966 | 0.783065 | 0.962072 | 0.007014 |
| MYD88 | 0.804417 | 0.656286 | 0.985984 | 0.036091 |
| LMNB1 | 0.827362 | 0.744515 | 0.919428 | 0.000431 |
| MLKL | 0.835612 | 0.701855 | 0.994858 | 0.043603 |
| GCA | 0.735403 | 0.607031 | 0.890921 | 0.00169 |
| NOS2 | 0.885801 | 0.827356 | 0.948374 | 0.000498 |
| FBXO6 | 0.830328 | 0.73806 | 0.93413 | 0.001977 |
| TYROBP | 1.150582 | 1.04052 | 1.272285 | 0.006252 |
| GSDMB | 0.86055 | 0.784177 | 0.944361 | 0.001539 |
| CKB | 1.094855 | 1.020508 | 1.174618 | 0.011544 |
| FCGR2A | 1.171335 | 1.051725 | 1.304548 | 0.004007 |
| HMOX1 | 1.132562 | 1.013423 | 1.265708 | 0.028158 |
| SERTAD4 | 1.177681 | 1.071471 | 1.294417 | 0.000695 |
| BAK1 | 0.778463 | 0.665738 | 0.910275 | 0.001702 |
| CDCP1 | 0.882331 | 0.794858 | 0.979429 | 0.018765 |
| CNDP2 | 0.672423 | 0.567409 | 0.796873 | 4.63E-06 |
| DNMT1 | 0.774564 | 0.652206 | 0.919876 | 0.003591 |
| OAS1 | 0.889679 | 0.804738 | 0.983586 | 0.022417 |
| ADAM10 | 0.836061 | 0.699363 | 0.999478 | 0.049333 |
| NOD2 | 1.163598 | 1.021308 | 1.325712 | 0.022799 |
| PBX1 | 1.16536 | 1.048668 | 1.295037 | 0.004473 |
| HELZ2 | 0.811761 | 0.705668 | 0.933803 | 0.003518 |
| WFS1 | 1.14481 | 1.016241 | 1.289645 | 0.02608 |
| EXOSC9 | 0.69493 | 0.564794 | 0.855053 | 0.000581 |
| C15orf48 | 0.926584 | 0.873933 | 0.982408 | 0.010631 |
| PSMA4 | 0.781498 | 0.621595 | 0.982535 | 0.034789 |
| REEP1 | 1.186947 | 1.103541 | 1.276657 | 4.02E-06 |
| TNFRSF18 | 0.830752 | 0.723653 | 0.953701 | 0.00846 |
| ACOT7 | 0.797017 | 0.690832 | 0.919523 | 0.00187 |
| TCEAL4 | 1.495561 | 1.308147 | 1.709825 | 3.81E-09 |
| KCNH2 | 1.179119 | 1.093046 | 1.271971 | 2.04E-05 |
| UHRF1 | 0.833989 | 0.755463 | 0.920677 | 0.000321 |
| NCEH1 | 0.869246 | 0.782718 | 0.965339 | 0.00881 |
| CASP7 | 0.6674 | 0.572033 | 0.778668 | 2.75E-07 |
| TMPO | 0.761282 | 0.652237 | 0.888558 | 0.000544 |
| IKBKE | 0.706057 | 0.598759 | 0.832583 | 3.50E-05 |
| COL4A5 | 1.180412 | 1.085782 | 1.283289 | 0.0001 |
| HELLS | 0.798777 | 0.702036 | 0.908849 | 0.000647 |
| EZH2 | 0.774796 | 0.688768 | 0.871569 | 2.15E-05 |
| BRIP1 | 0.796093 | 0.692997 | 0.914527 | 0.00127 |
| PPP1R14A | 1.202651 | 1.131172 | 1.278646 | 3.58E-09 |
| NUP50 | 0.669595 | 0.544852 | 0.822898 | 0.000137 |
| CENPK | 0.865314 | 0.767958 | 0.975011 | 0.017524 |

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|-----------|----------|----------|----------|----------|
| PTBP3 | 0.835305 | 0.703892 | 0.991253 | 0.039345 |
| CEACAM4 | 0.8132 | 0.673753 | 0.981508 | 0.031206 |
| ALAS1 | 0.734179 | 0.61261 | 0.879874 | 0.000821 |
| DYNC111 | 1.385781 | 1.241473 | 1.546863 | 6.06E-09 |
| CD14 | 1.185833 | 1.069669 | 1.314612 | 0.001194 |
| SDS | 1.130917 | 1.012385 | 1.263327 | 0.029417 |
| OLR1 | 1.186747 | 1.097358 | 1.283418 | 1.83E-05 |
| CAPZA1 | 0.698459 | 0.546468 | 0.892725 | 0.004153 |
| TRIM15 | 0.866508 | 0.796407 | 0.94278 | 0.000872 |
| NAV2 | 1.198031 | 1.04816 | 1.369331 | 0.008054 |
| WLS | 1.308671 | 1.172479 | 1.460683 | 1.60E-06 |
| TPM3 | 0.721183 | 0.584335 | 0.890081 | 0.00233 |
| KNTC1 | 0.80263 | 0.693607 | 0.92879 | 0.00316 |
| PRKAB2 | 1.248247 | 1.086094 | 1.434609 | 0.001789 |
| MCM6 | 0.80674 | 0.680872 | 0.955875 | 0.013087 |
| DENND1A | 0.725169 | 0.603349 | 0.871585 | 0.000615 |
| CHST11 | 1.227235 | 1.085619 | 1.387323 | 0.001064 |
| PRELID1 | 0.816181 | 0.668596 | 0.996345 | 0.045939 |
| BATF3 | 1.226234 | 1.023152 | 1.469627 | 0.027264 |
| SLC25A22 | 0.758829 | 0.649719 | 0.886263 | 0.000493 |
| E2F7 | 0.82213 | 0.726085 | 0.930879 | 0.002002 |
| VLDLR | 1.242559 | 1.134498 | 1.360912 | 2.89E-06 |
| TLL7 | 1.174714 | 1.08259 | 1.274677 | 0.000111 |
| BMPR1B | 1.249103 | 1.140952 | 1.367507 | 1.48E-06 |
| PTGES3L | 1.23219 | 1.107465 | 1.370962 | 0.000126 |
| LINC01278 | 1.210759 | 1.065914 | 1.375286 | 0.003262 |
| ENAH | 1.291734 | 1.13575 | 1.469141 | 9.67E-05 |
| MREG | 0.742326 | 0.645139 | 0.854154 | 3.16E-05 |
| SLC41A3 | 1.288212 | 1.030903 | 1.609744 | 0.025902 |
| PDZRN3 | 1.205114 | 1.112511 | 1.305425 | 4.79E-06 |
| CYP39A1 | 1.154878 | 1.03603 | 1.28736 | 0.009355 |
| GNAZ | 1.157637 | 1.044683 | 1.282804 | 0.005198 |
| C3orf70 | 1.141964 | 1.059314 | 1.231062 | 0.000534 |
| CDCA2 | 0.815699 | 0.73714 | 0.902631 | 8.06E-05 |
| POLD1 | 0.81475 | 0.705986 | 0.94027 | 0.005072 |
| MYEF2 | 1.220187 | 1.101455 | 1.351717 | 0.000139 |
| GINS3 | 0.721311 | 0.60262 | 0.863379 | 0.000369 |
| COQ2 | 0.708387 | 0.577748 | 0.868566 | 0.000917 |
| GPD2 | 0.762171 | 0.651281 | 0.891941 | 0.000711 |
| SLC15A4 | 1.338972 | 1.048805 | 1.709417 | 0.019163 |
| MZB1 | 0.935363 | 0.878006 | 0.996467 | 0.038491 |
| RP2 | 0.751701 | 0.61416 | 0.920043 | 0.005636 |
| ZNF827 | 1.272892 | 1.091552 | 1.484359 | 0.00209 |
| MFSD5 | 0.760984 | 0.596689 | 0.970516 | 0.027727 |
| AK2 | 0.750842 | 0.59152 | 0.953077 | 0.018527 |
| ACSM5 | 1.321234 | 1.055818 | 1.653372 | 0.014905 |
| RASD1 | 1.084967 | 1.010045 | 1.165447 | 0.025501 |

Prognostic role of pyroptosis-related genes in gastric cancer

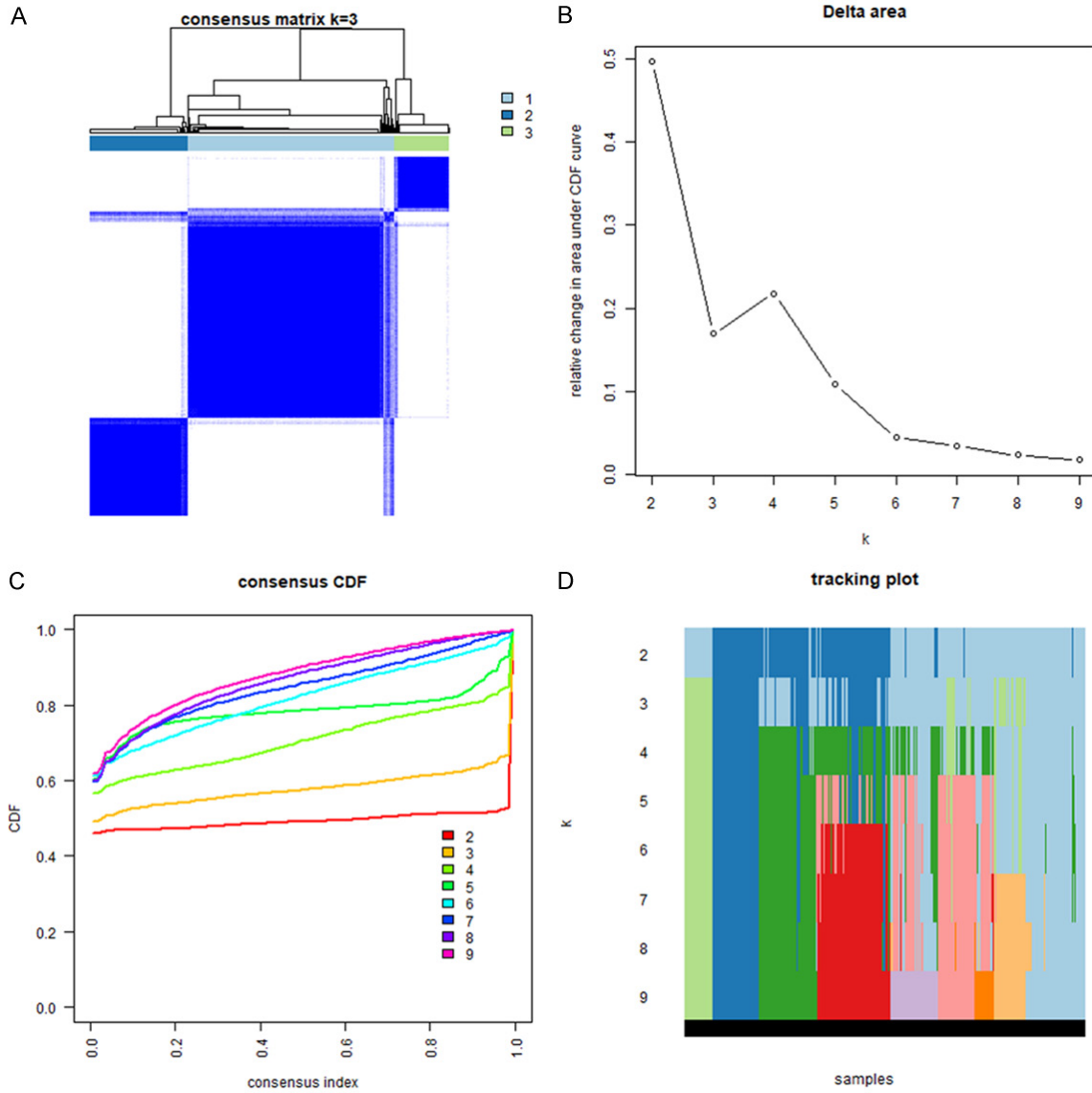


Figure S15. Unsupervised clustering analysis for identifying pyroptosis gene Clusters. A. Consensus clustering matrix for k=3. B. Relative change in area under CDF curve for k=2-9. C. Consensus clustering cumulative distribution function (CDF) for k=2-9. D. The tracking plot for k=2-9.

Prognostic role of pyroptosis-related genes in gastric cancer

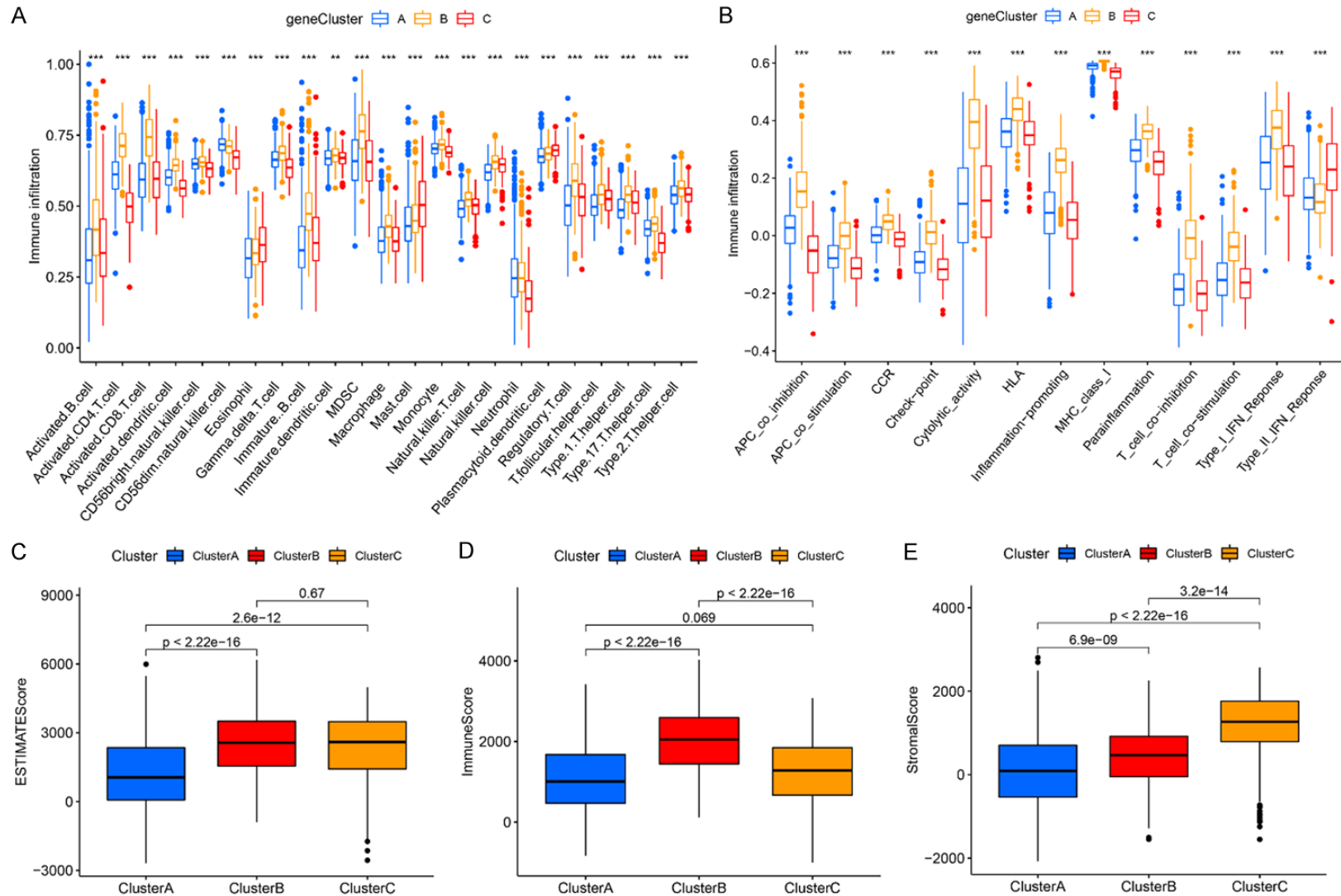


Figure S16. Correlation between the characteristics of TIME and pyroptosis gene clusters. (A) Box plots depicts the scores of immune infiltrations among the three pyroptosis gene clusters. (B) Box plots presents the scores of immune functions among the three pyroptosis gene clusters. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$. (C-E) Box plots shows the differences in (C) ESTIMATE score, (D) immune score, and (E) stromal score among the three pyroptosis gene clusters.

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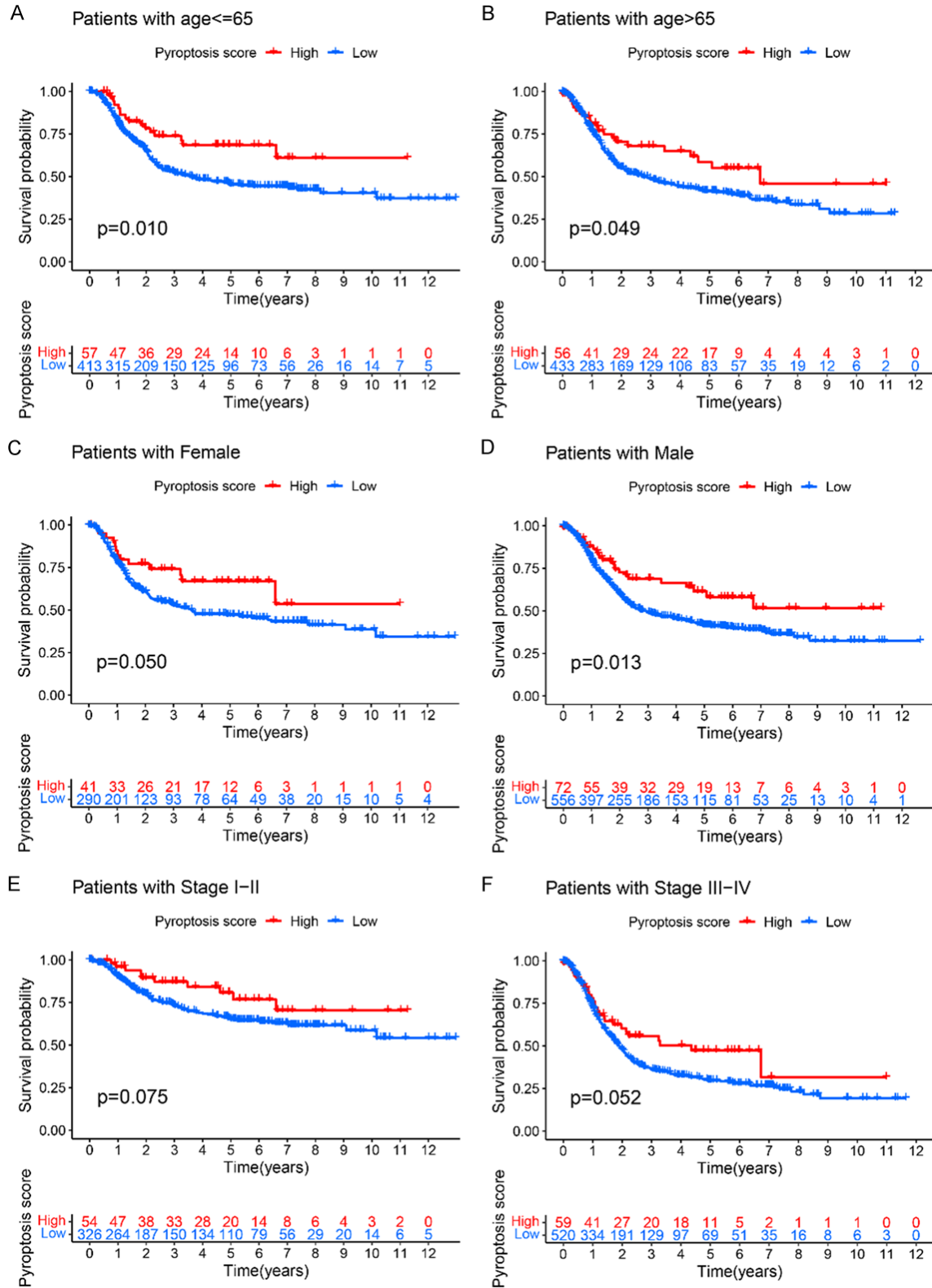


Figure S17. Subgroup analysis of the prognostic role of pyroptosis score in GC patients. A, B. Subgroup analysis of the prognostic role of pyroptosis score in GC patients stratified by age. C, D. Subgroup analysis of the prognostic role of pyroptosis score in GC patients stratified by gender. E, F. Subgroup analysis of the prognostic role of pyroptosis score in GC patients stratified by stage.

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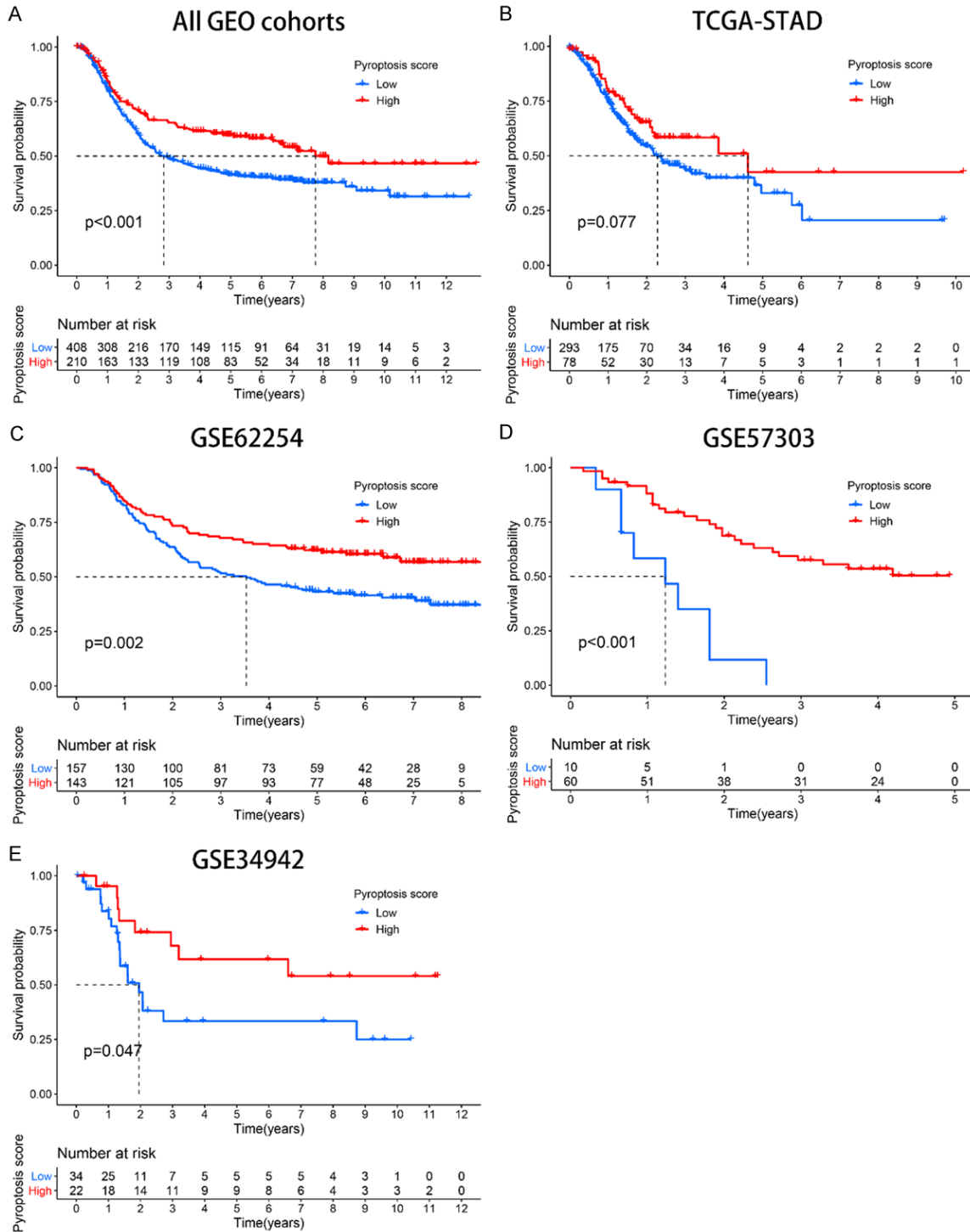


Figure S18. Survival analysis of the prognostic role of pyroptosis score in different GC cohort. (A-E) Survival analysis of the prognostic role of pyroptosis score in meta-GEO cohort (A, n=618, including GSE15459, GSE34942, GSE57303, and GSE62254 cohorts), TCGA-STAD cohort (B, n=371), GSE62254 cohort (C, n=300), GSE57303 cohort (D, n=70), and GSE34942 cohort (E, n=56).

Prognostic role of pyroptosis-related genes in gastric cancer

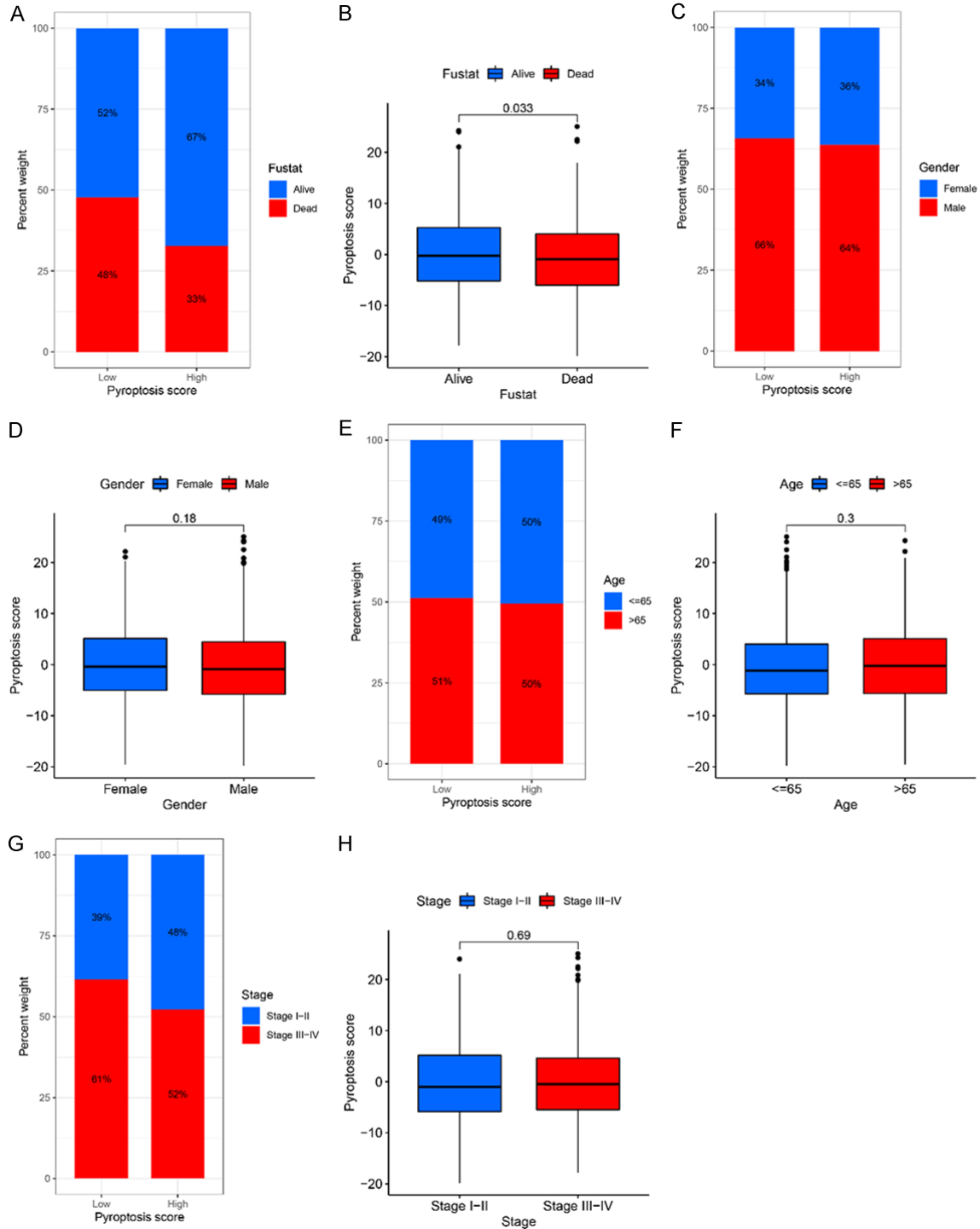


Figure S19. Correlation between the pyroptosis score and clinicopathologic features. A, B. Differences in pyroptosis score between patients with different survival state. C, D. Differences in pyroptosis score between patients with different gender. E, F. Differences in pyroptosis score between patients with different age distribution. G, H. Differences in pyroptosis score between patients with different stage.

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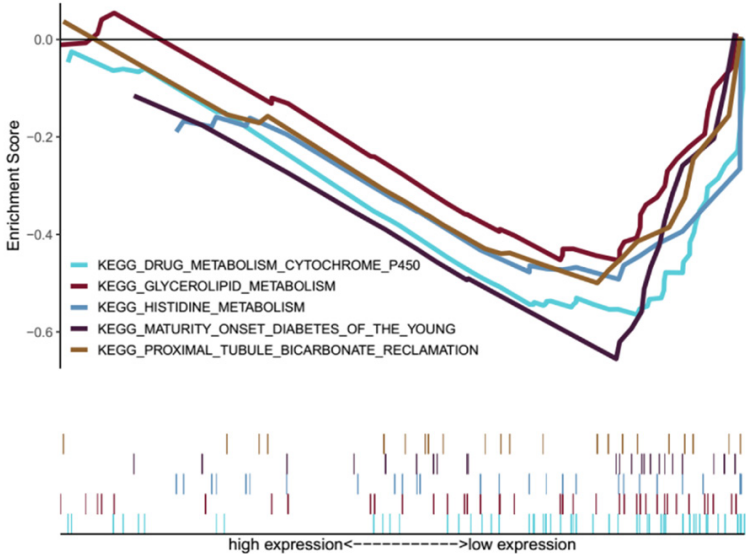


Figure S20. GSEA identified the pathways enriched in the low pyroptosis score group.

Prognostic role of pyroptosis-related genes in gastric cancer

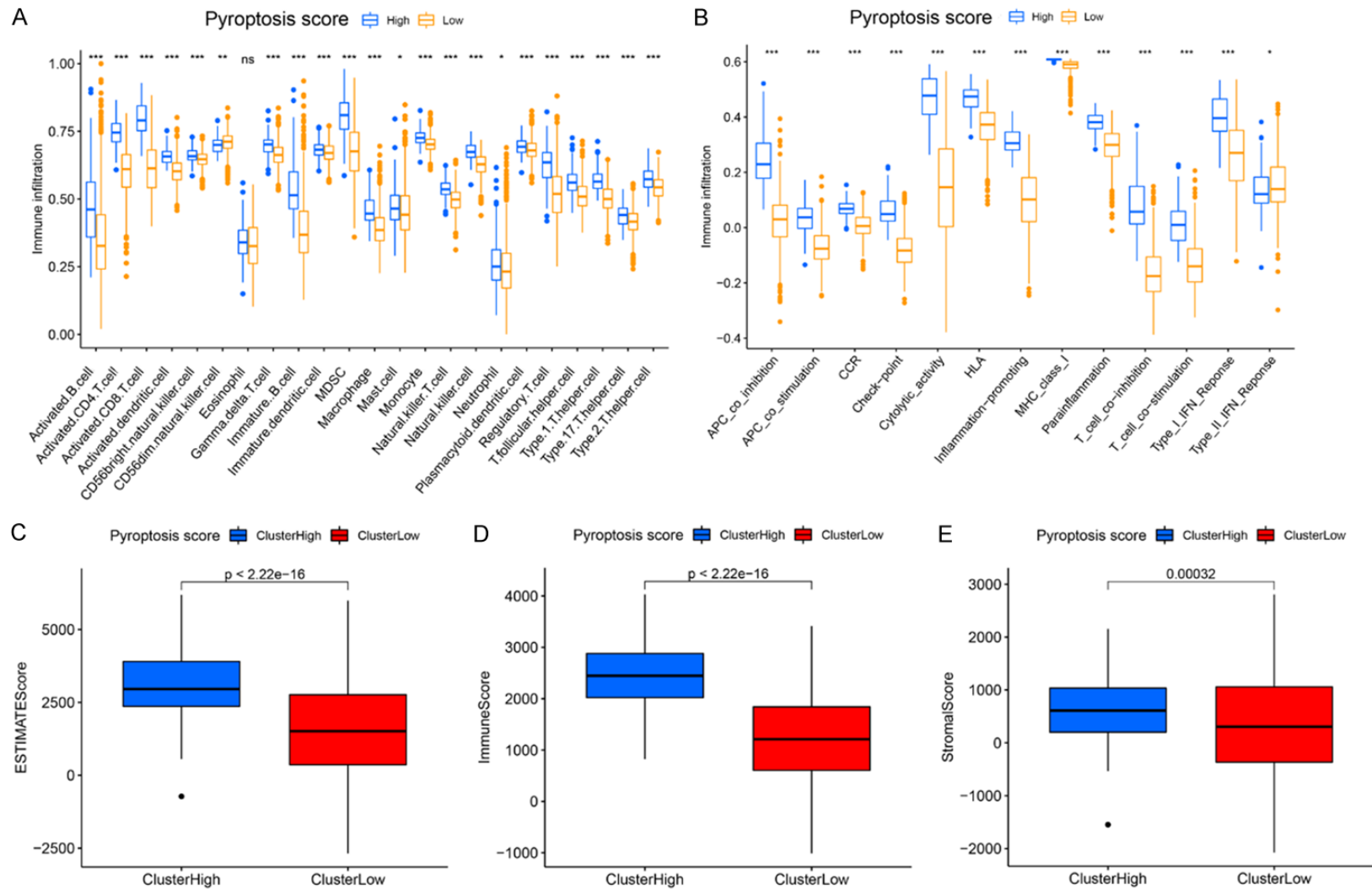
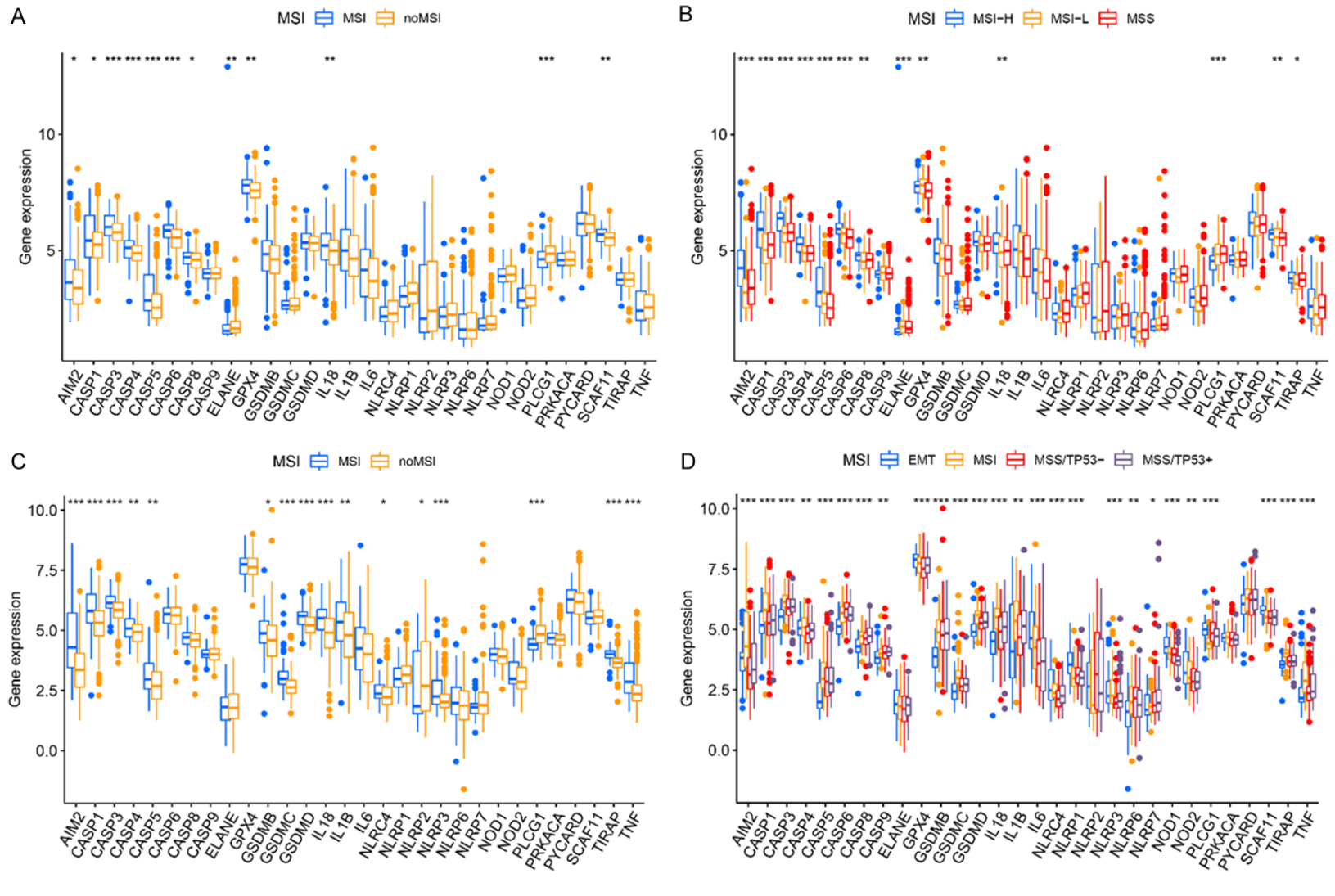


Figure 21. Correlation between the characteristics of TIME and pyroptosis score. (A) Box plots depicts the scores of immune infiltrations between the high and low pyroptosis score groups. (B) Box plots presents the scores of immune functions between the high and low pyroptosis score groups. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$. (C-E) Box plots shows the differences in (C) ESTIMATE score, (D) immune score, and (E) stromal score between the high and low pyroptosis score groups.

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Prognostic role of pyroptosis-related genes in gastric cancer

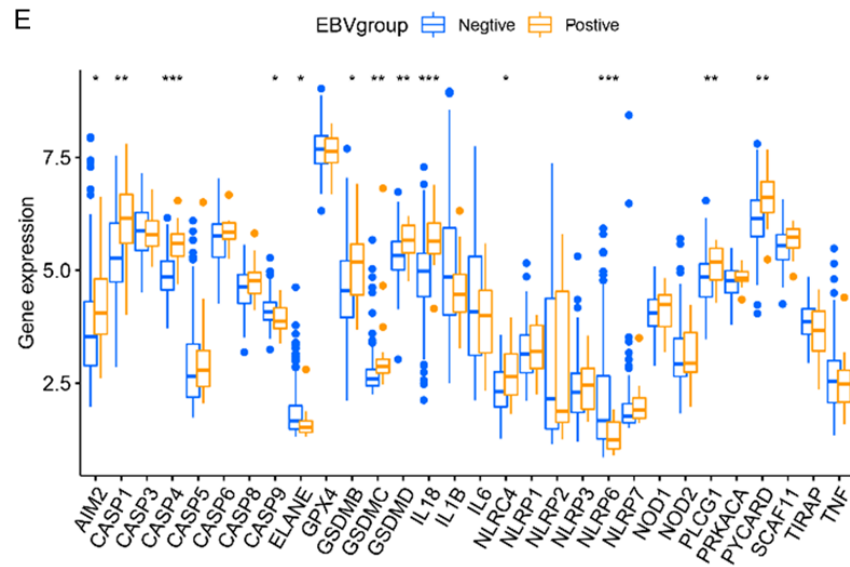
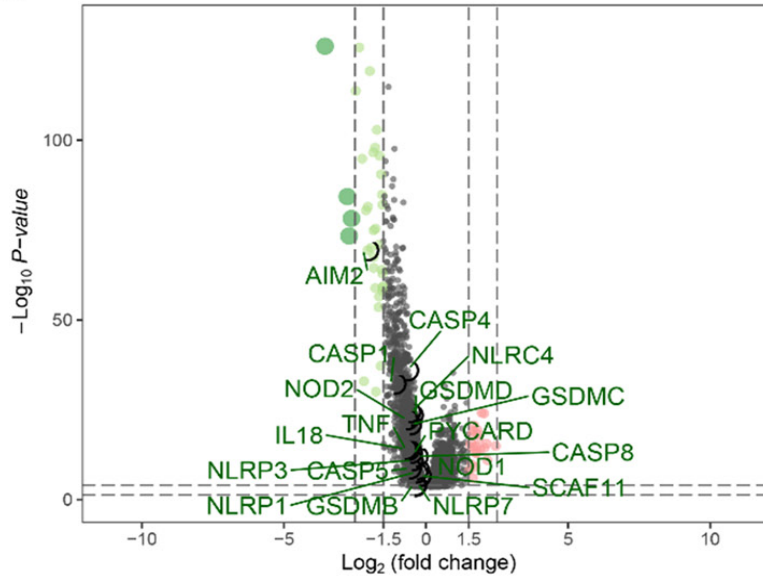


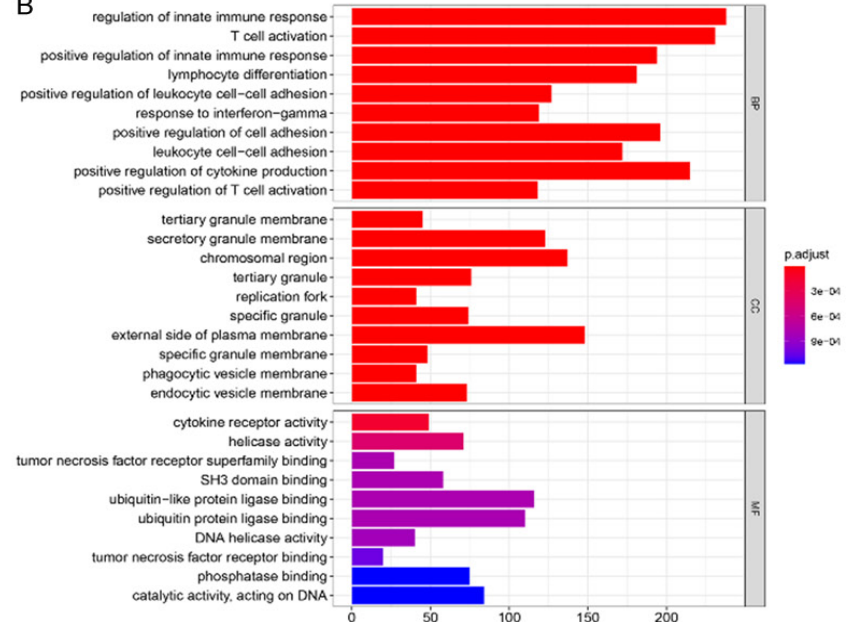
Figure S22. The expression levels of PRGs in different subgroups of GC. A. The expression levels of PRGs between the MSI and no MSI groups in TCGA-STAD cohort. B. The expression levels of PRGs among the MSI-High, MSI-Low, and MSS groups in TCGA-STAD cohort. C. The expression levels of PRGs between the MSI and no MSI groups in GSE62254 cohort. D. The expression levels of PRGs among the EMT, MSI, MSI/TP53- and MSI/TP53+ groups in GSE62254 cohort. E. The expression levels of PRGs between the EBV negative and EBV positive groups in TCGA-STAD cohort. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.

Prognostic role of pyroptosis-related genes in gastric cancer

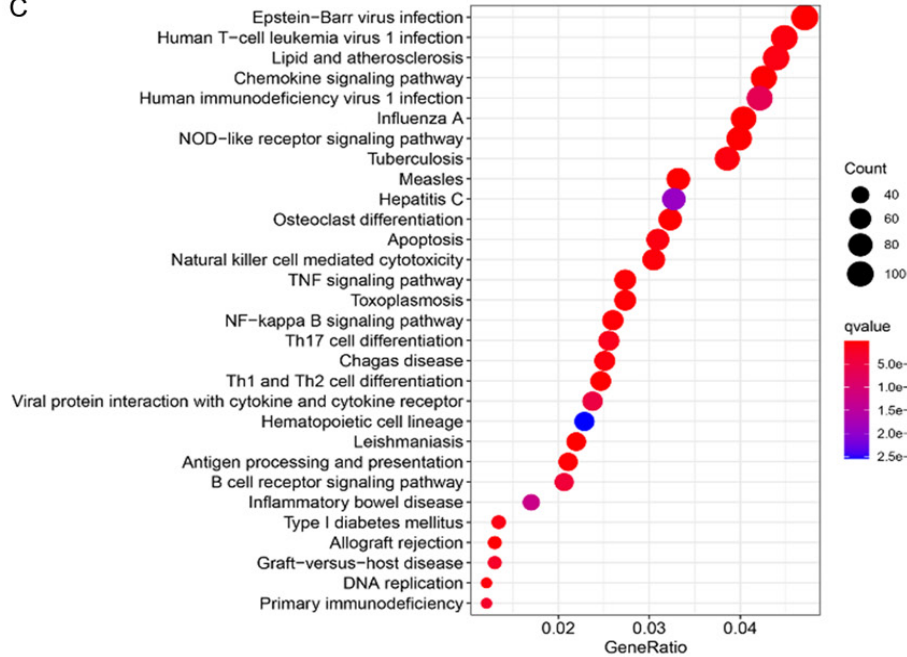
A



B



C



Prognostic role of pyroptosis-related genes in gastric cancer

D












| rank | cmap name | mean | n | enrichment | p | specificity | % non-null | |
|------|----------------------|--------|---|------------|---------|-------------|------------|---|
| 1 | caffeic acid | 0.451 | 3 | 0.873 | 0.00373 | 0.0000 | 66 |  |
| 2 | puromycin | -0.636 | 4 | -0.719 | 0.01255 | 0.0970 | 75 |  |
| 3 | alimemazine | -0.618 | 4 | -0.714 | 0.01355 | 0.0068 | 75 |  |
| 4 | memantine | 0.418 | 4 | 0.683 | 0.02166 | 0.0000 | 50 |  |
| 5 | piperlongumine | 0.379 | 2 | 0.887 | 0.02648 | 0.1364 | 50 |  |
| 6 | dorzolamide | 0.361 | 4 | 0.655 | 0.03284 | 0.0000 | 50 |  |
| 7 | bumetanide | -0.384 | 4 | -0.646 | 0.03744 | 0.1487 | 50 |  |
| 8 | 0198306-0000 | 0.422 | 4 | 0.643 | 0.03923 | 0.0073 | 50 |  |
| 9 | bacitracin | -0.495 | 3 | -0.728 | 0.04160 | 0.0424 | 66 |  |
| 10 | diprophylline | -0.281 | 5 | -0.569 | 0.04500 | 0.0397 | 60 |  |
| 11 | levothyroxine sodium | -0.213 | 4 | -0.630 | 0.04603 | 0.0848 | 50 |  |

Figure S23. Potential small molecule compounds for GC treatment based on the pyroptosis score. A. Volcano plot shows the downregulated genes (green dots) and upregulated genes (red dots) between the low and high pyroptosis score groups. B. GO enrichment analysis of biological process (BP), cellular component (CC) and molecular function (MF) terms ranked by adjusted *p*-value. C. KEGG pathway enrichment analysis presents the enriched pathways. D. Potential small molecule compounds obtains from the CMap database.

Prognostic role of pyroptosis-related genes in gastric cancer

Table S7. DEGs between the low and high pyroptosis score groups

| Gene | logFC | Average Expression | t | P-Value | Adjusted P-Value | B |
|-----------|----------|--------------------|----------|-----------|------------------|----------|
| IDO1 | -3.55431 | 4.838732 | -27.8995 | 6.69E-127 | 1.18E-122 | 278.8428 |
| GBP4 | -2.349 | 4.667764 | -27.8471 | 1.52E-126 | 1.34E-122 | 278.0286 |
| IFNG | -1.97693 | 2.58534 | -26.8786 | 5.58E-120 | 3.28E-116 | 262.9997 |
| FASLG | -1.31937 | 2.644864 | -26.2263 | 1.41E-115 | 6.21E-112 | 252.9223 |
| GBP5 | -2.4719 | 4.058779 | -26.0607 | 1.83E-114 | 6.47E-111 | 250.3708 |
| CD274 | -1.72634 | 3.513492 | -24.4395 | 1.26E-103 | 3.69E-100 | 225.5661 |
| GBP1 | -1.78767 | 5.78937 | -23.6833 | 1.25E-98 | 3.15E-95 | 214.1244 |
| TBX21 | -1.10858 | 2.774935 | -23.6407 | 2.38E-98 | 5.24E-95 | 213.4834 |
| LAG3 | -1.85205 | 3.377779 | -23.4894 | 2.35E-97 | 4.60E-94 | 211.2069 |
| PRF1 | -1.63103 | 4.379355 | -23.3453 | 2.07E-96 | 3.65E-93 | 209.0422 |
| GZMB | -2.24618 | 4.740927 | -23.2192 | 1.39E-95 | 2.22E-92 | 207.1524 |
| IRF1 | -1.42651 | 5.666289 | -23.1125 | 6.92E-95 | 1.02E-91 | 205.5539 |
| HAPLN3 | -1.41129 | 4.525962 | -22.575 | 2.19E-91 | 2.97E-88 | 197.5407 |
| TYMP | -1.58202 | 5.473206 | -22.5498 | 3.19E-91 | 4.02E-88 | 197.1668 |
| KLRD1 | -1.14652 | 2.880229 | -22.3416 | 7.11E-90 | 8.36E-87 | 194.0795 |
| LAP3 | -1.18876 | 7.021848 | -22.0442 | 5.90E-88 | 6.50E-85 | 189.6866 |
| GBP1P1 | -1.54847 | 2.716381 | -21.6716 | 1.46E-85 | 1.51E-82 | 184.2105 |
| CD96 | -1.45713 | 3.042683 | -21.6038 | 3.95E-85 | 3.87E-82 | 183.2182 |
| CXCL11 | -2.76598 | 4.432923 | -21.5883 | 4.96E-85 | 4.60E-82 | 182.9915 |
| TAP2 | -1.12166 | 4.58346 | -21.4417 | 4.28E-84 | 3.77E-81 | 180.8492 |
| USP30-AS1 | -1.46041 | 3.222933 | -21.3465 | 1.73E-83 | 1.45E-80 | 179.4613 |
| TAP1 | -1.53485 | 6.901162 | -21.2337 | 9.01E-83 | 6.91E-80 | 177.8192 |
| STAT1 | -1.37441 | 6.723666 | -21.1809 | 1.95E-82 | 1.43E-79 | 177.051 |
| GZMH | -2.04389 | 4.030525 | -21.1495 | 3.09E-82 | 2.18E-79 | 176.5946 |
| UBE2L6 | -1.33854 | 6.663227 | -21.0561 | 1.21E-81 | 8.19E-79 | 175.2394 |
| NKG7 | -2.10947 | 4.714764 | -20.9891 | 3.20E-81 | 2.09E-78 | 174.2695 |
| IL18BP | -1.16247 | 4.251962 | -20.6754 | 3.05E-79 | 1.92E-76 | 169.7397 |
| CXCL10 | -2.62148 | 6.017864 | -20.629 | 5.97E-79 | 3.63E-76 | 169.0722 |
| JAKMIP1 | -1.14945 | 2.271342 | -20.5908 | 1.04E-78 | 6.10E-76 | 168.5229 |
| SLA2 | -1.12374 | 3.334717 | -20.5796 | 1.22E-78 | 6.94E-76 | 168.3618 |
| CXCR6 | -1.41183 | 3.686143 | -20.5152 | 3.09E-78 | 1.70E-75 | 167.4373 |
| TIGIT | -1.387 | 3.102083 | -20.4872 | 4.63E-78 | 2.47E-75 | 167.0355 |
| IL21R | -1.24281 | 2.823282 | -20.2912 | 7.78E-77 | 4.04E-74 | 164.23 |
| CRTAM | -1.77706 | 2.507919 | -20.1785 | 3.93E-76 | 1.98E-73 | 162.6212 |
| GNLY | -1.84332 | 3.786585 | -20.0977 | 1.25E-75 | 6.12E-73 | 161.4711 |
| CXCL9 | -2.70501 | 5.879483 | -19.8492 | 4.34E-74 | 2.07E-71 | 157.9432 |
| ZNF683 | -1.49941 | 3.210272 | -19.6149 | 1.21E-72 | 5.62E-70 | 154.6355 |
| BATF2 | -1.66725 | 4.712729 | -19.4485 | 1.27E-71 | 5.76E-69 | 152.2963 |
| IL2RB | -1.48553 | 4.758879 | -19.3648 | 4.14E-71 | 1.83E-68 | 151.1233 |
| KLRC3 | -1.04734 | 1.911848 | -19.3608 | 4.39E-71 | 1.89E-68 | 151.067 |
| CCL5 | -1.92942 | 6.009196 | -19.3162 | 8.21E-71 | 3.37E-68 | 150.4433 |
| ICAM1 | -1.43026 | 5.295064 | -19.243 | 2.30E-70 | 9.02E-68 | 149.419 |
| AIM2 | -2.05065 | 3.717292 | -19.2081 | 3.76E-70 | 1.44E-67 | 148.9326 |
| IFIH1 | -1.0596 | 4.370766 | -19.1052 | 1.59E-69 | 5.97E-67 | 147.4982 |
| SIRPG | -1.39763 | 2.853407 | -19.0969 | 1.78E-69 | 6.56E-67 | 147.3832 |
| APOL3 | -1.25584 | 4.575031 | -19.0028 | 6.66E-69 | 2.40E-66 | 146.075 |
| APOL6 | -1.06443 | 5.153018 | -18.9589 | 1.23E-68 | 4.33E-66 | 145.4658 |

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|----------|----------|----------|----------|----------|----------|----------|
| GZMA | -1.84492 | 4.949727 | -18.8868 | 3.36E-68 | 1.16E-65 | 144.4665 |
| IL12RB1 | -1.00177 | 3.308407 | -18.7877 | 1.33E-67 | 4.52E-65 | 143.0962 |
| ETV7 | -1.36147 | 4.23029 | -18.669 | 6.92E-67 | 2.26E-64 | 141.4595 |
| RNF213 | -1.07039 | 5.05339 | -18.6644 | 7.37E-67 | 2.36E-64 | 141.3973 |
| PSMB9 | -1.3798 | 6.57102 | -18.6419 | 1.01E-66 | 3.17E-64 | 141.0869 |
| PTPN22 | -1.09793 | 3.200523 | -18.5563 | 3.29E-66 | 1.02E-63 | 139.9112 |
| APOBEC3G | -1.26387 | 4.206232 | -18.4628 | 1.19E-65 | 3.63E-63 | 138.6292 |
| PSMB10 | -1.11139 | 6.118016 | -18.4055 | 2.63E-65 | 7.85E-63 | 137.845 |
| CD8A | -1.84211 | 4.412119 | -18.385 | 3.48E-65 | 1.02E-62 | 137.565 |
| HLA-DOA | -1.5506 | 4.035924 | -18.2961 | 1.18E-64 | 3.36E-62 | 136.3505 |
| TNFSF13B | -1.39766 | 5.195762 | -18.282 | 1.43E-64 | 4.01E-62 | 136.1588 |
| KLHDC7B | -1.31388 | 3.11822 | -18.2359 | 2.70E-64 | 7.31E-62 | 135.5312 |
| NLR5 | -1.19484 | 5.043821 | -18.2256 | 3.10E-64 | 8.30E-62 | 135.3906 |
| SLAMF8 | -1.44643 | 4.348474 | -18.2102 | 3.83E-64 | 1.01E-61 | 135.1816 |
| SAMD9L | -1.53208 | 4.695359 | -18.1228 | 1.27E-63 | 3.28E-61 | 133.9945 |
| KLRC4 | -1.17385 | 1.577925 | -17.8906 | 2.98E-62 | 7.63E-60 | 130.8537 |
| ZBP1 | -1.35329 | 2.720734 | -17.8425 | 5.73E-62 | 1.44E-59 | 130.2054 |
| LILRB4 | -1.21939 | 3.165039 | -17.7503 | 2.00E-61 | 4.89E-59 | 128.9649 |
| THEMIS | -1.31427 | 2.756617 | -17.7282 | 2.69E-61 | 6.50E-59 | 128.6687 |
| SH2D1A | -1.29271 | 2.986779 | -17.565 | 2.42E-60 | 5.77E-58 | 126.4845 |
| IFIT3 | -1.51314 | 5.830556 | -17.513 | 4.87E-60 | 1.13E-57 | 125.7907 |
| CXCR3 | -1.24504 | 3.586424 | -17.4689 | 8.80E-60 | 2.02E-57 | 125.2029 |
| LAMP3 | -1.52723 | 4.752006 | -17.4494 | 1.14E-59 | 2.55E-57 | 124.9426 |
| PLA2G2D | -1.78298 | 2.619041 | -17.4332 | 1.42E-59 | 3.13E-57 | 124.7281 |
| HAVCR2 | -1.15342 | 3.775779 | -17.4262 | 1.56E-59 | 3.40E-57 | 124.6339 |
| IL2RA | -1.16975 | 3.369232 | -17.412 | 1.89E-59 | 4.01E-57 | 124.4456 |
| CD3G | -1.31208 | 3.751683 | -17.3951 | 2.36E-59 | 4.96E-57 | 124.2215 |
| PDCD1LG2 | -1.25256 | 2.459625 | -17.3669 | 3.45E-59 | 7.15E-57 | 123.8463 |
| GPR171 | -1.45689 | 3.594426 | -17.3135 | 7.03E-59 | 1.44E-56 | 123.1388 |
| ZBED2 | -1.52848 | 2.339475 | -17.2943 | 9.08E-59 | 1.84E-56 | 122.8842 |
| CCR5 | -1.34766 | 4.425179 | -17.2024 | 3.08E-58 | 6.18E-56 | 121.6691 |
| IFI35 | -1.02067 | 5.718356 | -17.1801 | 4.15E-58 | 8.13E-56 | 121.3745 |
| CD247 | -1.1519 | 3.651872 | -17.1423 | 6.85E-58 | 1.31E-55 | 120.8762 |
| ITGAL | -1.35197 | 4.10479 | -17.083 | 1.50E-57 | 2.82E-55 | 120.0944 |
| EPSTI1 | -1.35037 | 5.480953 | -17.0626 | 1.97E-57 | 3.64E-55 | 119.8263 |
| JAK2 | -1.20636 | 4.281729 | -17.0622 | 1.98E-57 | 3.64E-55 | 119.8205 |
| CD38 | -1.64728 | 3.864888 | -17.0249 | 3.25E-57 | 5.90E-55 | 119.3306 |
| TLR8 | -1.29719 | 3.144036 | -16.9794 | 5.92E-57 | 1.05E-54 | 118.7343 |
| IL32 | -1.3428 | 6.439153 | -16.9222 | 1.26E-56 | 2.22E-54 | 117.9848 |
| CLEC2D | -1.03037 | 2.750319 | -16.7064 | 2.14E-55 | 3.67E-53 | 115.1692 |
| OAS2 | -1.36606 | 5.098954 | -16.6002 | 8.57E-55 | 1.44E-52 | 113.7914 |
| PYHIN1 | -1.07541 | 2.758997 | -16.56 | 1.45E-54 | 2.40E-52 | 113.2719 |
| CD2 | -1.49103 | 5.174619 | -16.5402 | 1.87E-54 | 3.06E-52 | 113.0153 |
| SLAMF7 | -1.66653 | 4.210657 | -16.5037 | 3.01E-54 | 4.87E-52 | 112.5441 |
| CD300LF | -1.25538 | 3.703832 | -16.4993 | 3.19E-54 | 5.11E-52 | 112.4871 |
| ICOS | -1.42521 | 2.775487 | -16.2931 | 4.59E-53 | 7.17E-51 | 109.8361 |
| UBASH3A | -1.27128 | 2.530287 | -16.2522 | 7.78E-53 | 1.19E-50 | 109.3127 |
| SNX10 | -1.2003 | 5.184888 | -16.2376 | 9.40E-53 | 1.42E-50 | 109.1251 |
| STX11 | -1.04782 | 3.334425 | -16.1826 | 1.91E-52 | 2.80E-50 | 108.4232 |

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|----------|----------|----------|----------|----------|----------|----------|
| CD74 | -1.30425 | 8.058649 | -16.1321 | 3.65E-52 | 5.23E-50 | 107.7789 |
| SLC15A3 | -1.10948 | 4.826265 | -16.1194 | 4.29E-52 | 6.10E-50 | 107.617 |
| SIGLEC10 | -1.20916 | 3.706367 | -16.0145 | 1.64E-51 | 2.32E-49 | 106.2837 |
| IL4I1 | -1.42906 | 3.838432 | -15.9635 | 3.15E-51 | 4.41E-49 | 105.6372 |
| ZAP70 | -1.18635 | 3.236698 | -15.9006 | 7.01E-51 | 9.74E-49 | 104.8424 |
| CTLA4 | -1.06892 | 3.040391 | -15.8958 | 7.46E-51 | 1.03E-48 | 104.7813 |
| CMKLR1 | -1.08042 | 3.465696 | -15.8368 | 1.58E-50 | 2.14E-48 | 104.0366 |
| HLA-DMB | -1.36654 | 5.899453 | -15.7391 | 5.44E-50 | 7.21E-48 | 102.8075 |
| GBP2 | -1.12052 | 5.741394 | -15.6924 | 9.81E-50 | 1.29E-47 | 102.2221 |
| CD3D | -1.37019 | 5.244348 | -15.5937 | 3.40E-49 | 4.41E-47 | 100.9876 |
| FCGR1B | -1.08097 | 3.328647 | -15.5908 | 3.53E-49 | 4.54E-47 | 100.9513 |
| HK3 | -1.11209 | 2.776986 | -15.5062 | 1.02E-48 | 1.29E-46 | 99.89639 |
| LCP2 | -1.01079 | 4.096755 | -15.4985 | 1.12E-48 | 1.41E-46 | 99.80139 |
| TRAC | -1.37868 | 5.431936 | -15.4854 | 1.32E-48 | 1.66E-46 | 99.6379 |
| CD84 | -1.04861 | 3.534901 | -15.4412 | 2.30E-48 | 2.86E-46 | 99.08944 |
| DOK2 | -1.03446 | 4.068926 | -15.4261 | 2.78E-48 | 3.43E-46 | 98.9021 |
| CCL4 | -1.4232 | 5.066903 | -15.4134 | 3.26E-48 | 3.99E-46 | 98.74386 |
| CYBB | -1.27734 | 4.497968 | -15.3943 | 4.13E-48 | 5.02E-46 | 98.50815 |
| TRAT1 | -1.27845 | 2.727951 | -15.3477 | 7.39E-48 | 8.92E-46 | 97.93119 |
| HLA-DMA | -1.33004 | 6.639855 | -15.3179 | 1.07E-47 | 1.29E-45 | 97.56213 |
| SLAMF6 | -1.16313 | 3.664096 | -15.2152 | 3.83E-47 | 4.50E-45 | 96.29722 |
| TNFSF10 | -1.11654 | 6.358827 | -15.213 | 3.94E-47 | 4.60E-45 | 96.26956 |
| CX3CL1 | -1.34592 | 4.282181 | -15.0969 | 1.65E-46 | 1.89E-44 | 94.8457 |
| IGSF6 | -1.11907 | 4.130879 | -15.0781 | 2.08E-46 | 2.32E-44 | 94.61581 |
| APOL1 | -1.29514 | 6.285014 | -15.0058 | 5.07E-46 | 5.59E-44 | 93.73294 |
| CIITA | -1.08827 | 3.447376 | -14.9976 | 5.61E-46 | 6.14E-44 | 93.63248 |
| NCF1 | -1.12414 | 3.585945 | -14.9429 | 1.10E-45 | 1.19E-43 | 92.96622 |
| MAP4K1 | -1.08885 | 3.615022 | -14.9097 | 1.65E-45 | 1.76E-43 | 92.56325 |
| ITK | -1.16071 | 3.538305 | -14.8803 | 2.36E-45 | 2.49E-43 | 92.2058 |
| TFEC | -1.0093 | 2.852336 | -14.8109 | 5.50E-45 | 5.77E-43 | 91.36591 |
| LILRB1 | -1.1218 | 3.577598 | -14.7662 | 9.48E-45 | 9.89E-43 | 90.82556 |
| TRBC1 | -1.15323 | 4.324132 | -14.7539 | 1.10E-44 | 1.14E-42 | 90.67705 |
| TRIM22 | -1.21996 | 5.884855 | -14.7296 | 1.48E-44 | 1.52E-42 | 90.38481 |
| BIRC3 | -1.3359 | 5.67084 | -14.7056 | 1.98E-44 | 2.03E-42 | 90.09573 |
| C1QA | -1.41323 | 6.644572 | -14.6984 | 2.16E-44 | 2.20E-42 | 90.00893 |
| XAF1 | -1.064 | 4.574723 | -14.6928 | 2.31E-44 | 2.34E-42 | 89.94094 |
| HCST | -1.12102 | 4.906659 | -14.6739 | 2.90E-44 | 2.93E-42 | 89.71419 |
| PRKCQ | -1.01174 | 3.333984 | -14.6456 | 4.09E-44 | 4.10E-42 | 89.37383 |
| DHX58 | -1.00496 | 3.562542 | -14.615 | 5.93E-44 | 5.90E-42 | 89.00655 |
| ITGB7 | -1.09677 | 3.4338 | -14.6038 | 6.78E-44 | 6.68E-42 | 88.87282 |
| IKZF3 | -1.29399 | 3.540706 | -14.5683 | 1.04E-43 | 1.01E-41 | 88.4469 |
| PLEK | -1.26028 | 4.77013 | -14.4681 | 3.47E-43 | 3.35E-41 | 87.25112 |
| GFI1 | -1.0329 | 2.90409 | -14.3856 | 9.34E-43 | 8.90E-41 | 86.26976 |
| HLA-DPA1 | -1.48344 | 6.963538 | -14.3774 | 1.03E-42 | 9.76E-41 | 86.17338 |
| NLRC3 | -1.09113 | 3.450843 | -14.2959 | 2.72E-42 | 2.57E-40 | 85.20825 |
| MICB | -1.09486 | 4.543145 | -14.206 | 7.93E-42 | 7.40E-40 | 84.14704 |
| C1QB | -1.45876 | 6.975558 | -14.1872 | 9.91E-42 | 9.20E-40 | 83.92606 |
| EOMES | -1.1428 | 3.612076 | -14.153 | 1.48E-41 | 1.36E-39 | 83.52481 |
| DPYD | -1.05575 | 4.151208 | -14.0794 | 3.54E-41 | 3.19E-39 | 82.66165 |

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|----------|----------|----------|----------|----------|----------|----------|
| OAS3 | -1.05063 | 5.337618 | -14.0731 | 3.81E-41 | 3.41E-39 | 82.58849 |
| CD3E | -1.13604 | 4.364999 | -14.0507 | 4.97E-41 | 4.38E-39 | 82.32584 |
| P2RY13 | -1.26058 | 3.187418 | -14.0465 | 5.22E-41 | 4.58E-39 | 82.27775 |
| SIGLEC1 | -1.164 | 3.79367 | -14.0415 | 5.53E-41 | 4.81E-39 | 82.21927 |
| CD86 | -1.04523 | 4.138302 | -14.0373 | 5.82E-41 | 5.03E-39 | 82.16927 |
| SIT1 | -1.26781 | 3.610463 | -14.0048 | 8.53E-41 | 7.23E-39 | 81.79033 |
| IFIT2 | -1.153 | 4.545695 | -13.9961 | 9.44E-41 | 7.97E-39 | 81.68904 |
| HLA-DPB1 | -1.24918 | 6.86552 | -13.8675 | 4.26E-40 | 3.54E-38 | 80.19446 |
| AOAH | -1.0955 | 3.770346 | -13.8234 | 7.12E-40 | 5.81E-38 | 79.68517 |
| CLEC4E | -1.01132 | 3.035083 | -13.8134 | 8.00E-40 | 6.47E-38 | 79.56907 |
| ITGB2 | -1.20878 | 4.930908 | -13.8074 | 8.58E-40 | 6.91E-38 | 79.49982 |
| TBC1D10C | -1.0571 | 3.748558 | -13.7511 | 1.65E-39 | 1.28E-37 | 78.85092 |
| ACP5 | -1.10619 | 5.737338 | -13.7237 | 2.27E-39 | 1.72E-37 | 78.53573 |
| CD40 | -1.03237 | 4.531851 | -13.674 | 4.03E-39 | 2.97E-37 | 77.96486 |
| CST7 | -1.25411 | 4.804418 | -13.6561 | 4.96E-39 | 3.63E-37 | 77.75864 |
| OASL | -1.25841 | 4.782212 | -13.593 | 1.03E-38 | 7.46E-37 | 77.03657 |
| HLA-DRA | -1.32331 | 8.887327 | -13.5849 | 1.13E-38 | 8.15E-37 | 76.94432 |
| BIN2 | -1.11549 | 3.799017 | -13.573 | 1.29E-38 | 9.27E-37 | 76.80911 |
| SLA | -1.01686 | 4.562465 | -13.5669 | 1.39E-38 | 9.87E-37 | 76.73867 |
| PTPRC | -1.25281 | 4.813935 | -13.5327 | 2.06E-38 | 1.44E-36 | 76.34878 |
| CD53 | -1.10205 | 5.209922 | -13.5141 | 2.54E-38 | 1.77E-36 | 76.13708 |
| SECTM1 | -1.14763 | 5.39264 | -13.5054 | 2.81E-38 | 1.94E-36 | 76.03845 |
| ADAMDEC1 | -1.5928 | 4.835004 | -13.4309 | 6.59E-38 | 4.54E-36 | 75.19282 |
| GZMM | -1.11075 | 2.899223 | -13.4248 | 7.07E-38 | 4.83E-36 | 75.12316 |
| RASGRP1 | -1.06847 | 4.045234 | -13.424 | 7.13E-38 | 4.86E-36 | 75.1146 |
| HCK | -1.01422 | 4.53857 | -13.339 | 1.88E-37 | 1.27E-35 | 74.15347 |
| CCR1 | -1.00579 | 4.570657 | -13.3118 | 2.56E-37 | 1.72E-35 | 73.84712 |
| PLA2G7 | -1.26829 | 5.001209 | -13.2754 | 3.87E-37 | 2.57E-35 | 73.43716 |
| SLC1A3 | -1.07067 | 3.316332 | -13.2538 | 4.94E-37 | 3.26E-35 | 73.19512 |
| C1QC | -1.26745 | 7.064372 | -13.223 | 7.00E-37 | 4.59E-35 | 72.84923 |
| LCP1 | -1.13223 | 5.967788 | -13.1612 | 1.41E-36 | 9.09E-35 | 72.15788 |
| IFITM1 | -1.20646 | 8.076191 | -13.1564 | 1.49E-36 | 9.56E-35 | 72.10357 |
| P2RY10 | -1.08626 | 3.05838 | -13.0133 | 7.40E-36 | 4.63E-34 | 70.51183 |
| BST2 | -1.30007 | 6.850634 | -12.9757 | 1.13E-35 | 6.95E-34 | 70.09505 |
| SASH3 | -1.07753 | 4.703293 | -12.9109 | 2.32E-35 | 1.42E-33 | 69.37921 |
| CORO1A | -1.09697 | 5.201756 | -12.823 | 6.15E-35 | 3.71E-33 | 68.41283 |
| CD7 | -1.05236 | 3.817542 | -12.7083 | 2.18E-34 | 1.28E-32 | 67.1584 |
| FCER1G | -1.12135 | 6.371534 | -12.6093 | 6.45E-34 | 3.70E-32 | 66.08295 |
| HLA-DOB | -1.06169 | 3.185148 | -12.5935 | 7.66E-34 | 4.37E-32 | 65.91163 |
| CXCL13 | -2.18367 | 5.296091 | -12.5497 | 1.24E-33 | 6.99E-32 | 65.43763 |
| TNFAIP2 | -1.03107 | 5.30466 | -12.4823 | 2.57E-33 | 1.43E-31 | 64.71153 |
| LCK | -1.09231 | 4.523586 | -12.4418 | 3.99E-33 | 2.20E-31 | 64.27617 |
| CASP1 | -1.0913 | 5.386825 | -12.4186 | 5.13E-33 | 2.79E-31 | 64.02712 |
| APOC1 | -1.37269 | 6.093299 | -12.2421 | 3.43E-32 | 1.79E-30 | 62.14581 |
| CTSW | -1.14301 | 3.436921 | -12.23 | 3.90E-32 | 2.02E-30 | 62.01783 |
| RSAD2 | -1.24958 | 4.529799 | -12.2186 | 4.41E-32 | 2.28E-30 | 61.89669 |
| LAPTM5 | -1.03957 | 7.050242 | -12.1701 | 7.39E-32 | 3.75E-30 | 61.38396 |
| FPR3 | -1.15369 | 4.638867 | -12.1659 | 7.73E-32 | 3.91E-30 | 61.33958 |
| IFI44 | -1.10063 | 5.035672 | -12.1522 | 8.94E-32 | 4.51E-30 | 61.19512 |

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|-----------|----------|----------|----------|----------|----------|----------|
| HLA-DQB2 | -1.19564 | 3.696556 | -12.1256 | 1.19E-31 | 5.92E-30 | 60.91407 |
| CMPK2 | -1.03886 | 5.313313 | -12.0827 | 1.87E-31 | 9.30E-30 | 60.46282 |
| IL10RA | -1.01365 | 4.733931 | -12.0713 | 2.11E-31 | 1.05E-29 | 60.34311 |
| CD48 | -1.04619 | 4.388943 | -11.9831 | 5.36E-31 | 2.60E-29 | 59.42041 |
| CCL18 | -1.76165 | 5.533357 | -11.9295 | 9.43E-31 | 4.54E-29 | 58.86193 |
| TGM2 | -1.02922 | 5.595118 | -11.8185 | 3.02E-30 | 1.42E-28 | 57.71029 |
| APOE | -1.28946 | 6.728426 | -11.7887 | 4.11E-30 | 1.93E-28 | 57.40278 |
| GZMK | -1.38006 | 3.9883 | -11.7173 | 8.63E-30 | 4.00E-28 | 56.66841 |
| MX1 | -1.09602 | 5.902376 | -11.7065 | 9.66E-30 | 4.45E-28 | 56.55726 |
| HLA-DRB6 | -1.32526 | 4.66653 | -11.6931 | 1.11E-29 | 5.08E-28 | 56.42054 |
| IFI44L | -1.36888 | 4.477214 | -11.6419 | 1.88E-29 | 8.56E-28 | 55.89647 |
| EVI2B | -1.06366 | 5.334309 | -11.3804 | 2.73E-28 | 1.20E-26 | 53.24767 |
| MNDA | -1.02138 | 4.627542 | -11.2768 | 7.79E-28 | 3.32E-26 | 52.21128 |
| SOWAHA | 1.428179 | 4.085916 | 11.23307 | 1.21E-27 | 5.12E-26 | 51.77619 |
| HLA-DQB1 | -1.25557 | 5.420894 | -11.2265 | 1.29E-27 | 5.45E-26 | 51.71059 |
| ISG15 | -1.05471 | 7.134546 | -11.2247 | 1.31E-27 | 5.52E-26 | 51.69299 |
| CCL8 | -1.26084 | 4.198086 | -11.184 | 1.98E-27 | 8.20E-26 | 51.28974 |
| TCEA3 | 1.012944 | 4.844596 | 11.03398 | 8.81E-27 | 3.47E-25 | 49.811 |
| BCL2A1 | -1.14247 | 4.837489 | -10.9986 | 1.25E-26 | 4.89E-25 | 49.46505 |
| CD27 | -1.11357 | 4.337048 | -10.9985 | 1.25E-26 | 4.89E-25 | 49.46415 |
| PMAIP1 | -1.00701 | 4.749237 | -10.9601 | 1.83E-26 | 7.07E-25 | 49.08853 |
| CD52 | -1.17849 | 5.816532 | -10.9146 | 2.86E-26 | 1.09E-24 | 48.64567 |
| FMO5 | 1.015765 | 3.722771 | 10.76843 | 1.19E-25 | 4.40E-24 | 47.23269 |
| MUC16 | -1.09618 | 1.747865 | -10.7164 | 1.98E-25 | 7.22E-24 | 46.73361 |
| FAM3B | 1.961208 | 4.921229 | 10.57783 | 7.52E-25 | 2.62E-23 | 45.41261 |
| IL2RG | -1.07946 | 5.919447 | -10.5497 | 9.84E-25 | 3.38E-23 | 45.14604 |
| HMGCS2 | 2.044358 | 4.938481 | 10.54024 | 1.08E-24 | 3.69E-23 | 45.05678 |
| CD163 | -1.03511 | 4.653017 | -10.4008 | 4.06E-24 | 1.33E-22 | 43.74501 |
| SUCNR1 | -1.10115 | 3.240811 | -10.2724 | 1.36E-23 | 4.33E-22 | 42.55002 |
| NEURL3 | -1.10558 | 3.270631 | -9.97601 | 2.12E-22 | 6.34E-21 | 39.83766 |
| GUCY2C | 1.688427 | 4.299357 | 9.720254 | 2.15E-21 | 6.02E-20 | 37.54908 |
| CHIT1 | -1.06803 | 2.348874 | -9.67109 | 3.34E-21 | 9.24E-20 | 37.11474 |
| SCNN1A | 1.2684 | 5.12814 | 9.507582 | 1.42E-20 | 3.82E-19 | 35.68346 |
| TFF3 | 1.808903 | 6.36527 | 9.38289 | 4.24E-20 | 1.09E-18 | 34.6056 |
| LINC00261 | 1.671566 | 3.850185 | 9.322564 | 7.16E-20 | 1.80E-18 | 34.0884 |
| IGHG1 | -1.12929 | 5.281731 | -9.24418 | 1.41E-19 | 3.48E-18 | 33.42053 |
| VSNL1 | -1.20523 | 3.767789 | -9.11632 | 4.21E-19 | 1.01E-17 | 32.34135 |
| TM4SF20 | 1.808621 | 4.250576 | 9.095341 | 5.03E-19 | 1.20E-17 | 32.16553 |
| PROM1 | 1.470239 | 5.761914 | 9.06579 | 6.47E-19 | 1.52E-17 | 31.91839 |
| SMIM24 | 1.635327 | 5.947574 | 9.041305 | 7.96E-19 | 1.86E-17 | 31.71414 |
| PLEKHS1 | -1.21704 | 4.017999 | -9.03826 | 8.16E-19 | 1.90E-17 | 31.68879 |
| REEP1 | 1.025573 | 3.668233 | 8.962791 | 1.54E-18 | 3.52E-17 | 31.06235 |
| CDH17 | 1.848436 | 6.130962 | 8.676104 | 1.66E-17 | 3.55E-16 | 28.72358 |
| MMP9 | -1.09152 | 5.631714 | -8.65634 | 1.94E-17 | 4.13E-16 | 28.56478 |
| NR1I2 | 1.056265 | 3.369352 | 8.539228 | 5.03E-17 | 1.03E-15 | 27.62998 |
| RBP4 | 1.387906 | 3.941766 | 8.435821 | 1.15E-16 | 2.34E-15 | 26.81372 |
| ZBTB7C | 1.047288 | 3.378303 | 8.413474 | 1.38E-16 | 2.77E-15 | 26.63846 |
| PRAP1 | 1.580725 | 4.853674 | 8.373743 | 1.89E-16 | 3.76E-15 | 26.32784 |
| CKB | 1.041133 | 5.799021 | 8.35812 | 2.14E-16 | 4.22E-15 | 26.20606 |

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|----------|----------|----------|----------|----------|----------|----------|
| REG4 | 2.131133 | 5.907702 | 8.322824 | 2.82E-16 | 5.52E-15 | 25.93163 |
| HLA-DQA1 | -1.48851 | 4.91039 | -8.31759 | 2.94E-16 | 5.74E-15 | 25.89105 |
| NROB2 | 1.181628 | 4.338953 | 8.305616 | 3.23E-16 | 6.27E-15 | 25.7982 |
| AOC1 | 1.282527 | 5.98737 | 8.296282 | 3.48E-16 | 6.71E-15 | 25.72593 |
| ERAP2 | -1.00117 | 4.286192 | -8.25253 | 4.91E-16 | 9.30E-15 | 25.38809 |
| REG1A | 2.45408 | 6.61988 | 8.133405 | 1.24E-15 | 2.29E-14 | 24.47619 |
| TM4SF5 | 1.125104 | 5.267303 | 8.104982 | 1.54E-15 | 2.82E-14 | 24.26032 |
| ITLN1 | 1.757415 | 4.203511 | 8.079021 | 1.89E-15 | 3.41E-14 | 24.06373 |
| GGT6 | 1.229835 | 4.126859 | 8.075182 | 1.94E-15 | 3.50E-14 | 24.0347 |
| CLDN3 | 1.553322 | 6.148682 | 8.058748 | 2.20E-15 | 3.95E-14 | 23.9106 |
| TM4SF4 | 1.663036 | 4.321273 | 8.054771 | 2.27E-15 | 4.06E-14 | 23.88059 |
| SLC01B3 | -1.26395 | 2.444378 | -8.03629 | 2.62E-15 | 4.65E-14 | 23.74136 |
| IGHM | -1.42255 | 6.427732 | -8.03362 | 2.67E-15 | 4.74E-14 | 23.72123 |
| MMP12 | -1.48014 | 5.93987 | -8.00706 | 3.27E-15 | 5.75E-14 | 23.52166 |
| REG3A | 2.064028 | 4.323832 | 7.978176 | 4.08E-15 | 7.08E-14 | 23.30532 |
| CHI3L1 | -1.10976 | 4.569415 | -7.94182 | 5.38E-15 | 9.24E-14 | 23.03393 |
| SPINK4 | 1.907325 | 4.637652 | 7.863413 | 9.72E-15 | 1.64E-13 | 22.45244 |
| MZB1 | -1.10917 | 4.621182 | -7.84148 | 1.15E-14 | 1.92E-13 | 22.2907 |
| IGHV1-69 | -1.10267 | 3.221195 | -7.76667 | 2.00E-14 | 3.29E-13 | 21.74195 |
| WFDC2 | 1.298359 | 4.466244 | 7.766705 | 2.00E-14 | 3.29E-13 | 21.74221 |
| VSIG2 | 1.323889 | 5.238353 | 7.761152 | 2.09E-14 | 3.43E-13 | 21.70165 |
| IGLL5 | -1.25481 | 5.886437 | -7.71162 | 3.01E-14 | 4.86E-13 | 21.34113 |
| PPP1R1B | 1.446869 | 5.513268 | 7.640876 | 5.08E-14 | 7.98E-13 | 20.82976 |
| FABP1 | 1.780536 | 3.796608 | 7.567355 | 8.68E-14 | 1.34E-12 | 20.30275 |
| CXCL14 | 1.225398 | 5.753145 | 7.550701 | 9.80E-14 | 1.50E-12 | 20.184 |
| SI | 1.753095 | 3.507331 | 7.520345 | 1.22E-13 | 1.86E-12 | 19.96816 |
| PCK1 | 1.2203 | 3.523833 | 7.490314 | 1.52E-13 | 2.29E-12 | 19.75538 |
| MUC20 | 1.029919 | 4.240138 | 7.476003 | 1.68E-13 | 2.51E-12 | 19.65425 |
| IGKC | -1.10027 | 7.627939 | -7.27102 | 7.23E-13 | 1.02E-11 | 18.22478 |
| SOSTDC1 | 1.293356 | 3.245767 | 7.20267 | 1.17E-12 | 1.62E-11 | 17.75604 |
| SLC44A4 | 1.000074 | 6.120378 | 7.163271 | 1.53E-12 | 2.10E-11 | 17.48767 |
| GSTA1 | 1.245838 | 4.737209 | 7.162771 | 1.54E-12 | 2.10E-11 | 17.48427 |
| HEPACAM2 | 1.270971 | 3.182235 | 7.127144 | 1.97E-12 | 2.66E-11 | 17.24275 |
| MEP1A | 1.437369 | 3.520276 | 7.120024 | 2.07E-12 | 2.79E-11 | 17.19461 |
| SLC39A5 | 1.014016 | 4.136339 | 7.113774 | 2.16E-12 | 2.90E-11 | 17.15239 |
| CHP2 | 1.251602 | 2.899363 | 7.032034 | 3.79E-12 | 4.95E-11 | 16.60331 |
| C9orf152 | 1.044916 | 5.221179 | 6.916676 | 8.28E-12 | 1.04E-10 | 15.83817 |
| SCGB2A1 | 1.246862 | 2.840178 | 6.883775 | 1.03E-11 | 1.28E-10 | 15.62206 |
| PGC | 2.158453 | 6.577776 | 6.880866 | 1.05E-11 | 1.31E-10 | 15.60299 |
| IGLV1-44 | -1.15993 | 6.268803 | -6.87654 | 1.08E-11 | 1.34E-10 | 15.57466 |
| CDX1 | 1.427475 | 4.623075 | 6.809218 | 1.70E-11 | 2.06E-10 | 15.13578 |
| ANXA13 | 1.114345 | 4.383017 | 6.731995 | 2.83E-11 | 3.33E-10 | 14.6372 |
| DUOX2 | 1.356959 | 4.514285 | 6.634826 | 5.34E-11 | 6.07E-10 | 14.01722 |
| CLRN3 | 1.127346 | 5.467898 | 6.559636 | 8.67E-11 | 9.64E-10 | 13.54314 |
| TFF1 | 1.599723 | 7.972554 | 6.48042 | 1.44E-10 | 1.54E-09 | 13.04902 |
| SERPINB2 | -1.01588 | 2.674147 | -6.24823 | 6.15E-10 | 6.10E-09 | 11.63259 |
| TFF2 | 1.733246 | 6.38321 | 6.186997 | 8.96E-10 | 8.66E-09 | 11.26699 |
| IGLV6-57 | -1.02998 | 4.487879 | -6.14619 | 1.15E-09 | 1.09E-08 | 11.02518 |
| FOLR1 | 1.00057 | 3.658 | 6.089129 | 1.62E-09 | 1.51E-08 | 10.68959 |

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|---------|----------|----------|----------|----------|----------|----------|
| SST | 1.230545 | 3.41636 | 6.03486 | 2.24E-09 | 2.05E-08 | 10.3731 |
| AKR1B10 | 1.429791 | 6.07492 | 5.876195 | 5.73E-09 | 4.86E-08 | 9.462895 |
| MUC6 | 1.325998 | 4.297497 | 5.873972 | 5.80E-09 | 4.91E-08 | 9.450306 |
| KRT20 | 1.52244 | 4.916111 | 5.795889 | 9.13E-09 | 7.50E-08 | 9.01083 |
| CHGA | 1.072955 | 3.729114 | 5.778185 | 1.01E-08 | 8.23E-08 | 8.911945 |
| SLC6A14 | -1.11978 | 4.735673 | -5.72461 | 1.37E-08 | 1.09E-07 | 8.614453 |
| PCSK1N | 1.03438 | 4.17106 | 5.708727 | 1.50E-08 | 1.19E-07 | 8.526745 |
| FAM3D | 1.030764 | 5.645195 | 5.640296 | 2.21E-08 | 1.70E-07 | 8.151506 |
| PSCA | 1.397946 | 5.06099 | 5.433306 | 6.96E-08 | 4.89E-07 | 7.042353 |
| AGR3 | 1.033655 | 6.608379 | 5.301997 | 1.41E-07 | 9.41E-07 | 6.358992 |
| GKN1 | 1.658028 | 4.561589 | 4.897706 | 1.13E-06 | 6.45E-06 | 4.354491 |
| GKN2 | 1.370019 | 4.169295 | 4.848052 | 1.45E-06 | 8.07E-06 | 4.118723 |
| ADH1C | 1.055051 | 5.590649 | 4.740801 | 2.44E-06 | 1.30E-05 | 3.617301 |
| MUC5AC | 1.119009 | 4.903346 | 4.660829 | 3.58E-06 | 1.85E-05 | 3.250387 |
| MAGEA6 | 1.193754 | 3.187223 | 4.57933 | 5.26E-06 | 2.61E-05 | 2.882621 |
| LIPF | 1.347958 | 4.557164 | 4.157699 | 3.49E-05 | 0.000146 | 1.079622 |
| OLFM4 | 1.249237 | 7.033496 | 3.86787 | 0.000117 | 0.000435 | -0.06224 |