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**Figure S1.** Intergroup prognostic analysis of three immune subtypes. **(A)** Comparison between C1 and C2 (*p*=0.00094). **(B)** Comparison between C2 and C3 (*p*=0.038). **(C)** Comparison between C1 and C3 (*p*=0.24).



**Figure S2.** Prognostic analysis of B cells, CD8+ T cells, NK cells, mast cells, monocytes, DCs, eosinophils, basophils and neutrophils.



**Figure S3.** DEGs and correlation analysis in GEO database (GSE28735 and GSE62452) led to gene TGM2. **(A)** Normalization of gene profiles in GSE28735. **(B)** DEGs in GSE28735. **(C)** Cluster heat map of the top 100 DEGs in GSE28735. **(D)** Cluster heat map of the top 100 DEGs in GSE62452. **(E)** Normalization of gene profiles in GSE62452. **(F)** DEGs in GSE62452. **(G)** Heat map of partial DEGs in GSE28735 and GSE62452. **(H)** Prognostic analysis of TGM2 by GEPIA online tool (<http://gepia.cancer-pku.cn/>). **(I)** Correlation analysis of TGM2 and GM-CSF (gene: CSF2) by TIMER online tool (<https://cistrome.shinyapps.io/timer/>).



**Figure S4.** Prognostic analysis of TGM2 in TCGA-ICGC-GEO cohort (*p*=0.0012).