

Figure S1 A heat map of the 12 immune genes in our model. H, high-risk patients; L, low-risk patients.

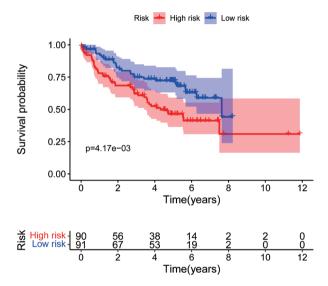


Figure S2 Independent validation of our model in the GEO dataset. GEO, Gene Expression Omnibus.

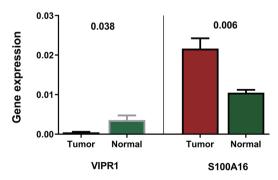


Figure S3 Representative genes expression in tumor and normal tissues.