Figure S1 Flow chart of the NETs score model construction and validation.
Figure S2 The disease specific survival (DSS) of the 32 tumor patients in TCGA training set.
Figure S3 The overall survival (OS) of the 32 types of tumor patients in TCGA training set.
Figure S4 The progression-free interval (PFI) of the 32 types of tumor patients in TCGA
Figure S5 The correlation between the NETs z-score and Cell-Cycle z-score in the 32 types of tumors arranged by their locations.
**Figure S6** Representative results of GO enrichment analyses of DEGs. The significant and shared GO enrichment pathways in the TCGA cohorts of LUAD (A), COAD (B), KIRC (C), and TNBC (D) are displayed.

**Figure S7** Comparison of the MPO scores between the tumor and corresponding normal tissues. IHC statistical analyses for MPO expression between tumor tissues and adjacent normal tissues, including COAD (A), KIRC (B), LUAD (C), and TNBC (D).
Figure S8 IHC validation of IL17 staining in stroma cells of tumor in our clinical cohorts. (A) and (B) The forest plots representing the prognostic values of IL17 in stroma cells and other clinical features of patients with COAD and KIRC. (C) and (D) The comparison of OS of patients with COAD and KIRC, who were stratified by their IL17 scores in stroma cells. MAC, mucinous colorectal adenocarcinoma; CRC, colorectal carcinomas; MSI, microsatellite instability; MSS, microsatellite stable.