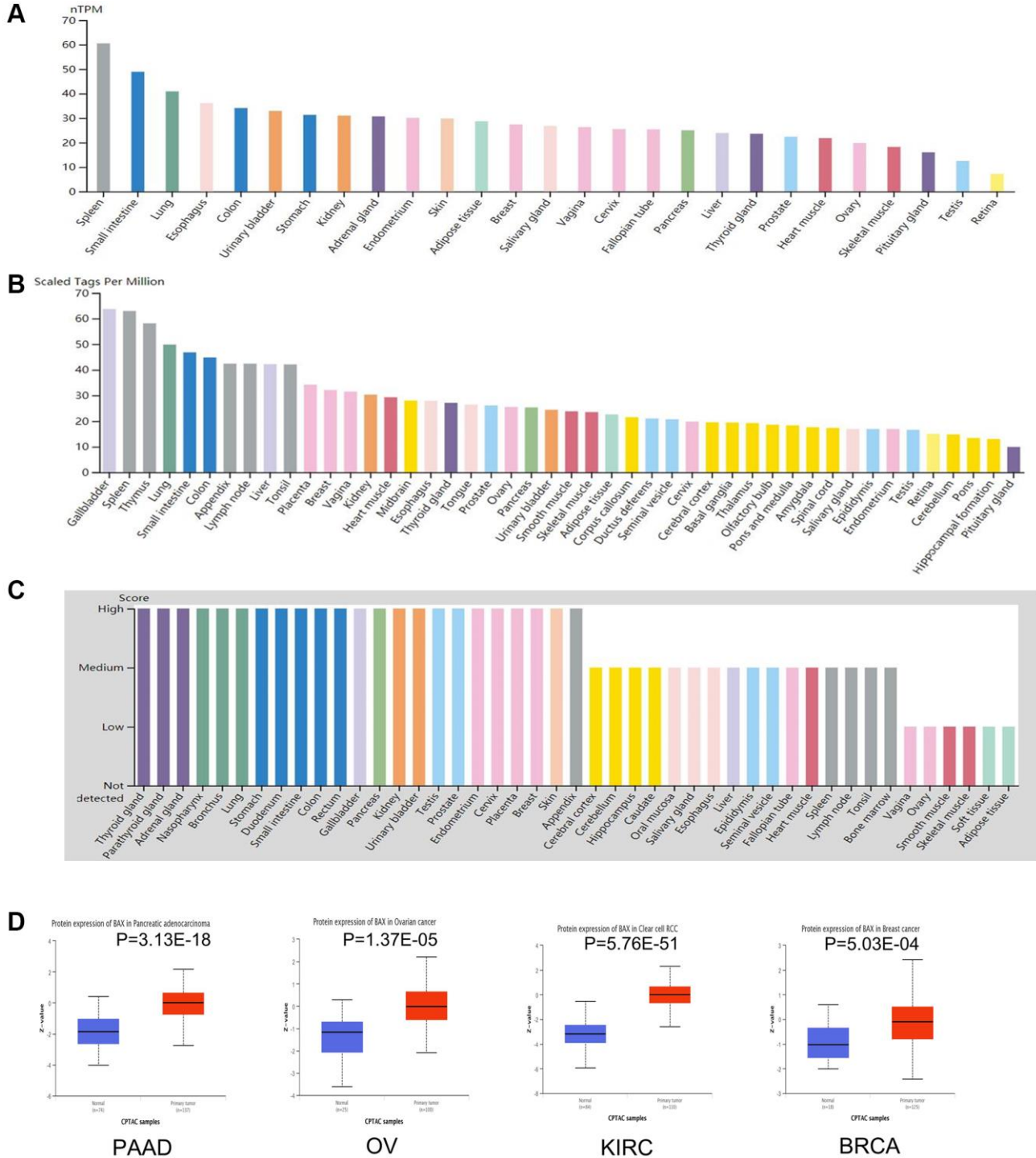
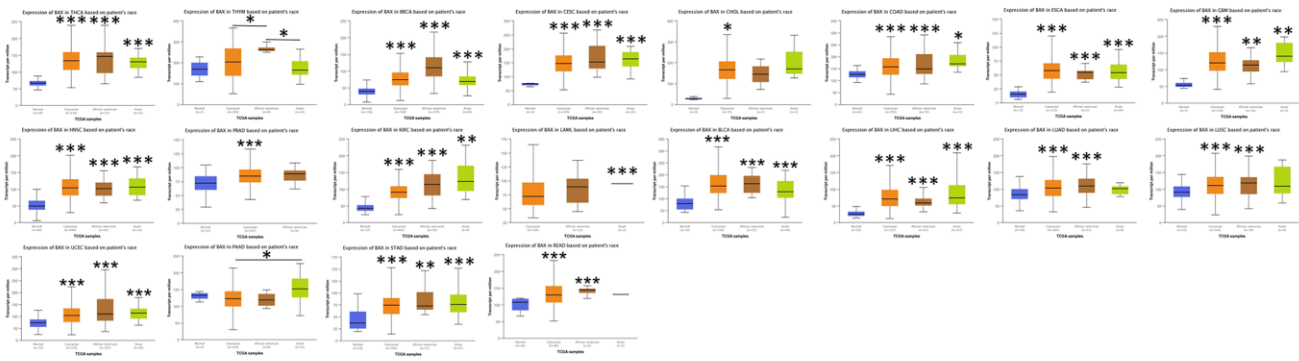


SUPPLEMENTARY FIGURES

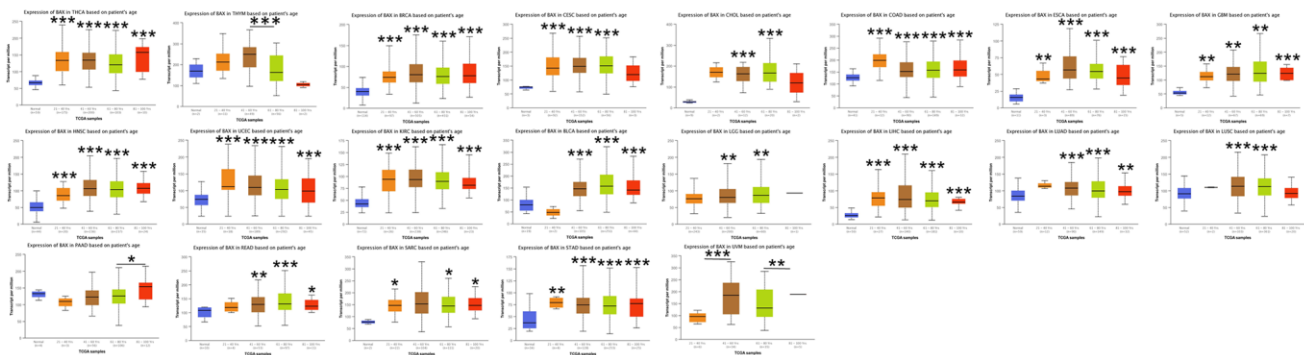


Supplementary Figure 1. (A–D) Expression level of BAX in different tissues and the protein expression of BAX were greater in some other tumor tissues than in adjacent normal tissues, such as PAAD, OV, KIRC and BRCA.

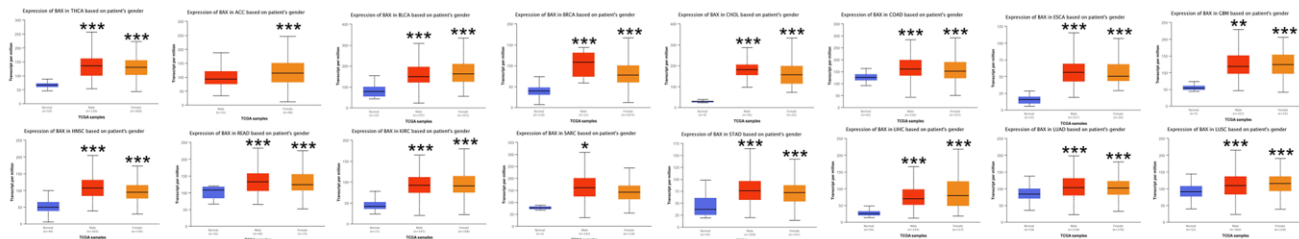
Race:



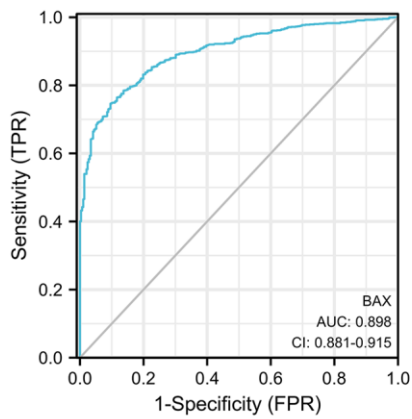
Age:



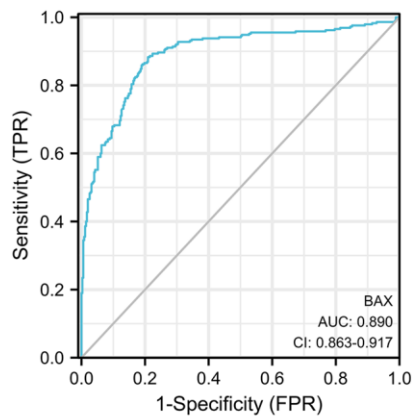
Gender:



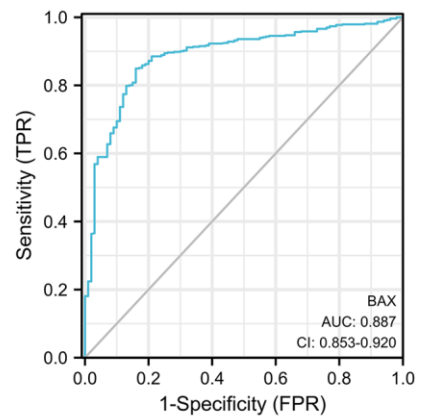
Supplementary Figure 2. BAX expression was significantly associated with age, gender and race in great majority of tumors. (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$).



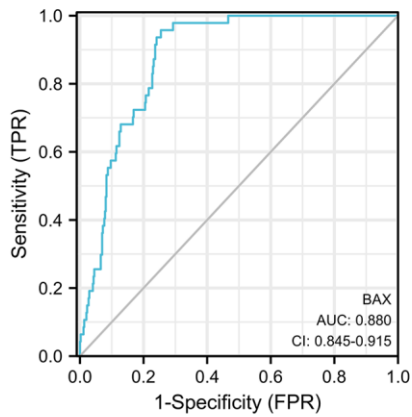
BRCA 0.898



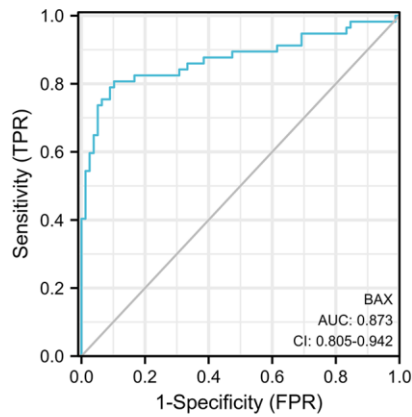
COAD 0.890



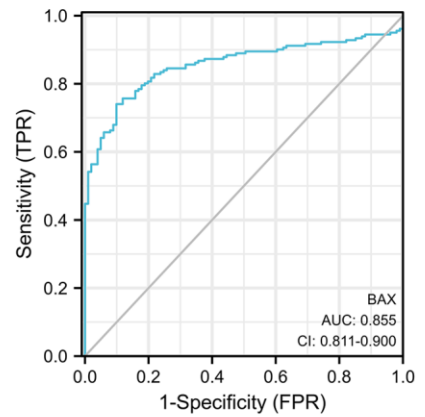
COAD 0.887



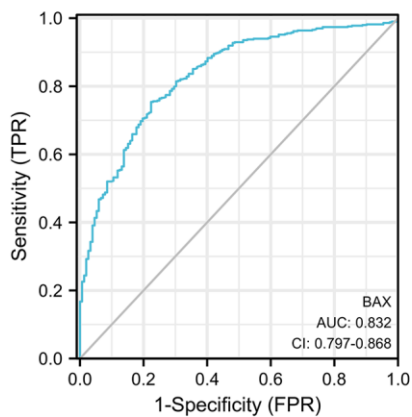
DLBC 0.880



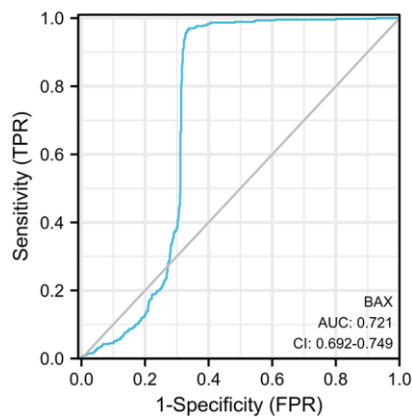
UCS 0.873



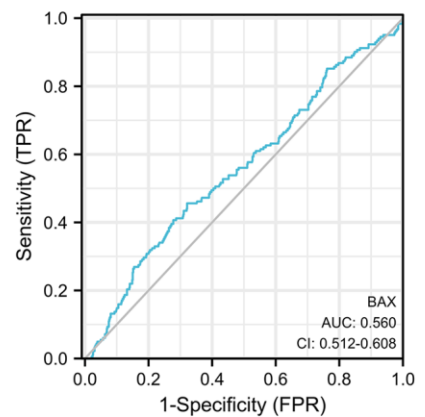
UCEC 0.855



PRAD 0.832



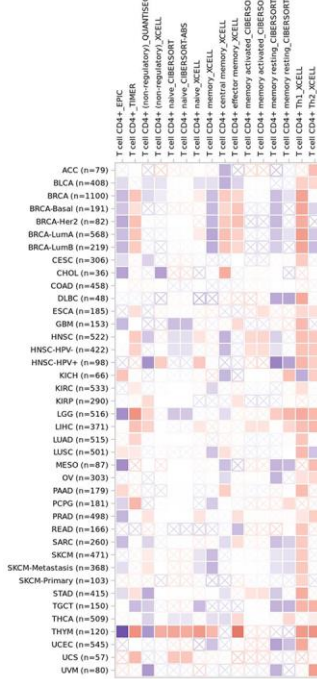
SKCM 0.721



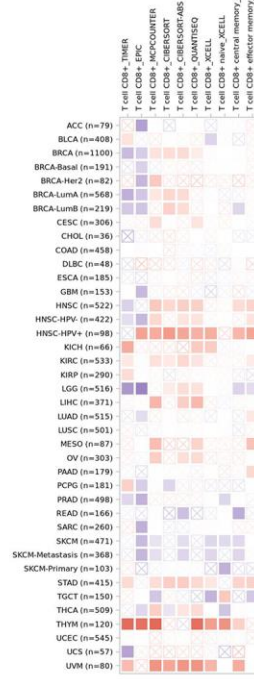
ESCA 0.560

Supplementary Figure 3. The AUC value of ROC curve of BAX from 0.5 to 0.9 for many cancer types.

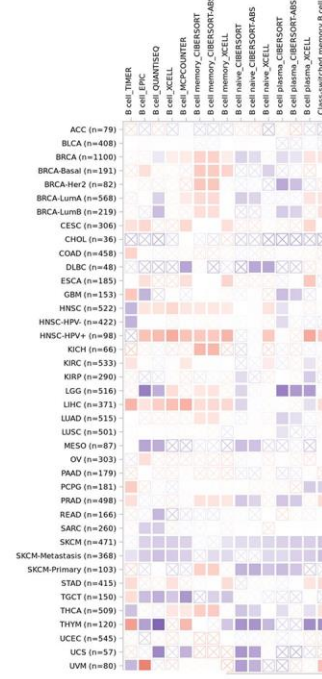
CD4+ T cell:



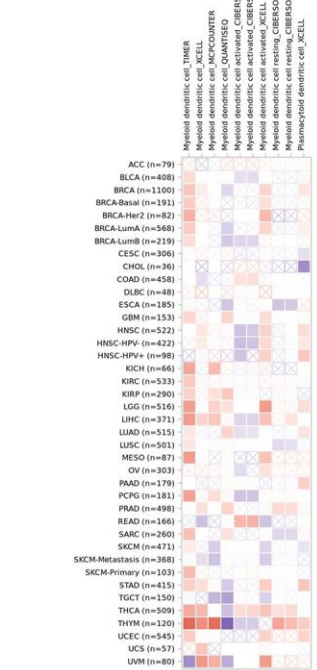
CD8+ T cell:



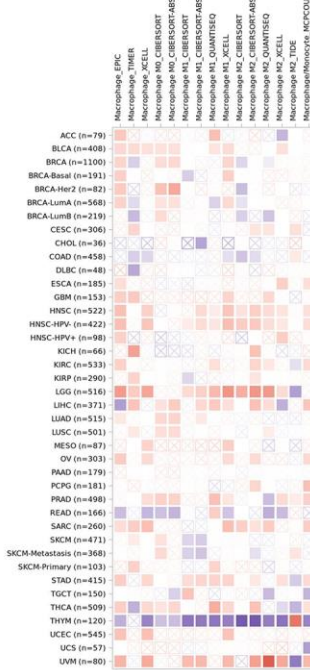
B cell:



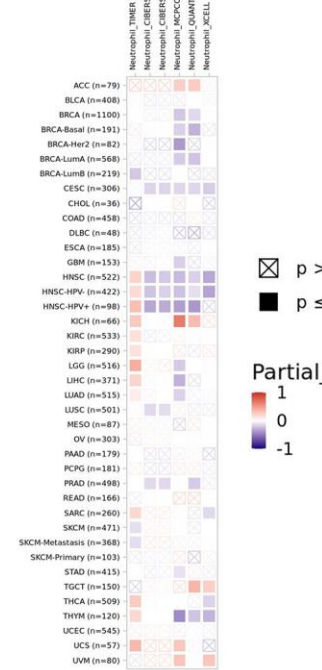
Dendritic cell:



Macrophage:

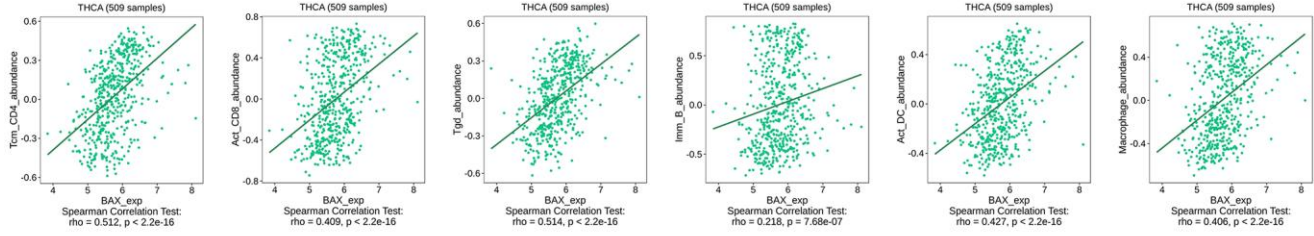


Neutrophil:

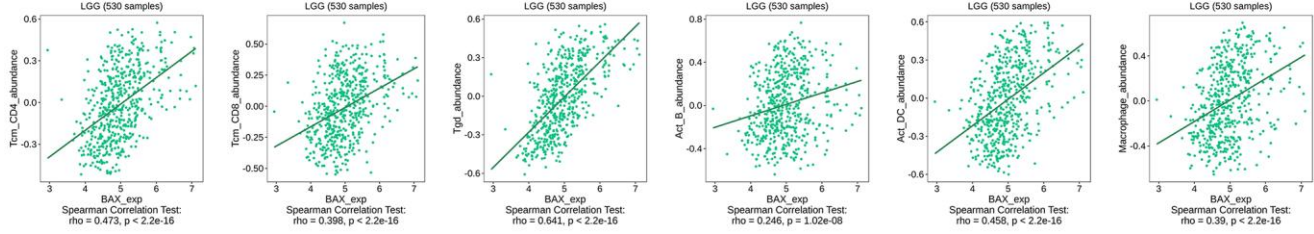


Supplementary Figure 4. The six algorithms suggested that BAX was closely related to immune infiltration of various cancers. ($P < 0.05$).

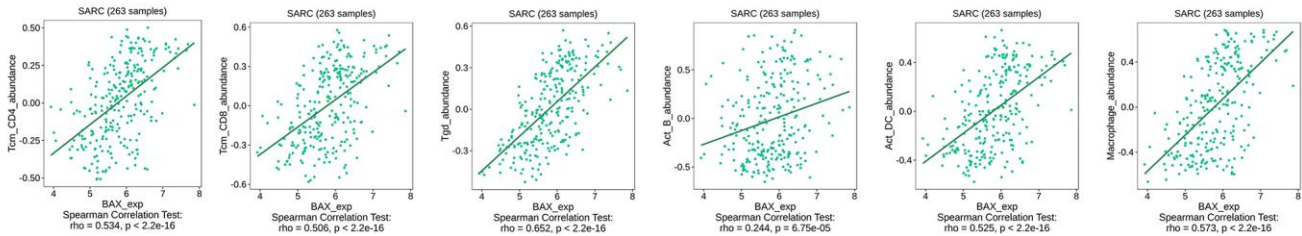
THCA



LGG



SARC



Supplementary Figure 5. The scatter plots of THCA, LGG and SARC were positively correlated with almost all TILs. ($P < 0.05$).