IDO1 in cancer: a Gemini of immune checkpoints

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Supplementary Material and Methods

The cancer genome atlas (TCGA) sample description

The TCGA data for all cancer types analyzed were accessed from the UCSC Xena browser (http://xena.ucsc.edu/). mRNA expression data represented by RNASeq (Illumina Hi-seq platform) includes RSEM normalized level 3 data present in TCGA as of April 13th, 2017.

Statistical analysis

The cutoff value for each gene expression level was determined with Cutoff Finder software (http://molpath.charite.de/cutoff/) using significance as the cutoff optimization method (25). Kaplan-Meier (KM) survival analysis was performed to estimate the survival distribution, while the log-rank test was used to assess the statistical significance of differences between the stratified survival groups using GraphPad Prism (version 6, GraphPad Software, Inc., La Jolla, CA). Renyi family of test statistics was computed via SAS software (version9.4, SAS Institute Inc.,Cary, NC) to determine the survival difference between two groups given the presence of crossing hazard rates. The correlation between *IDO1* mRNA levels and CD8+ T cells ($CD3^+CD8^+$) were examined by Canonical Correlation analysis, where each cell type was defined by a linear combination of the corresponding signature marker genes. Differences were considered to be statistically significant when $P < 0.05$.