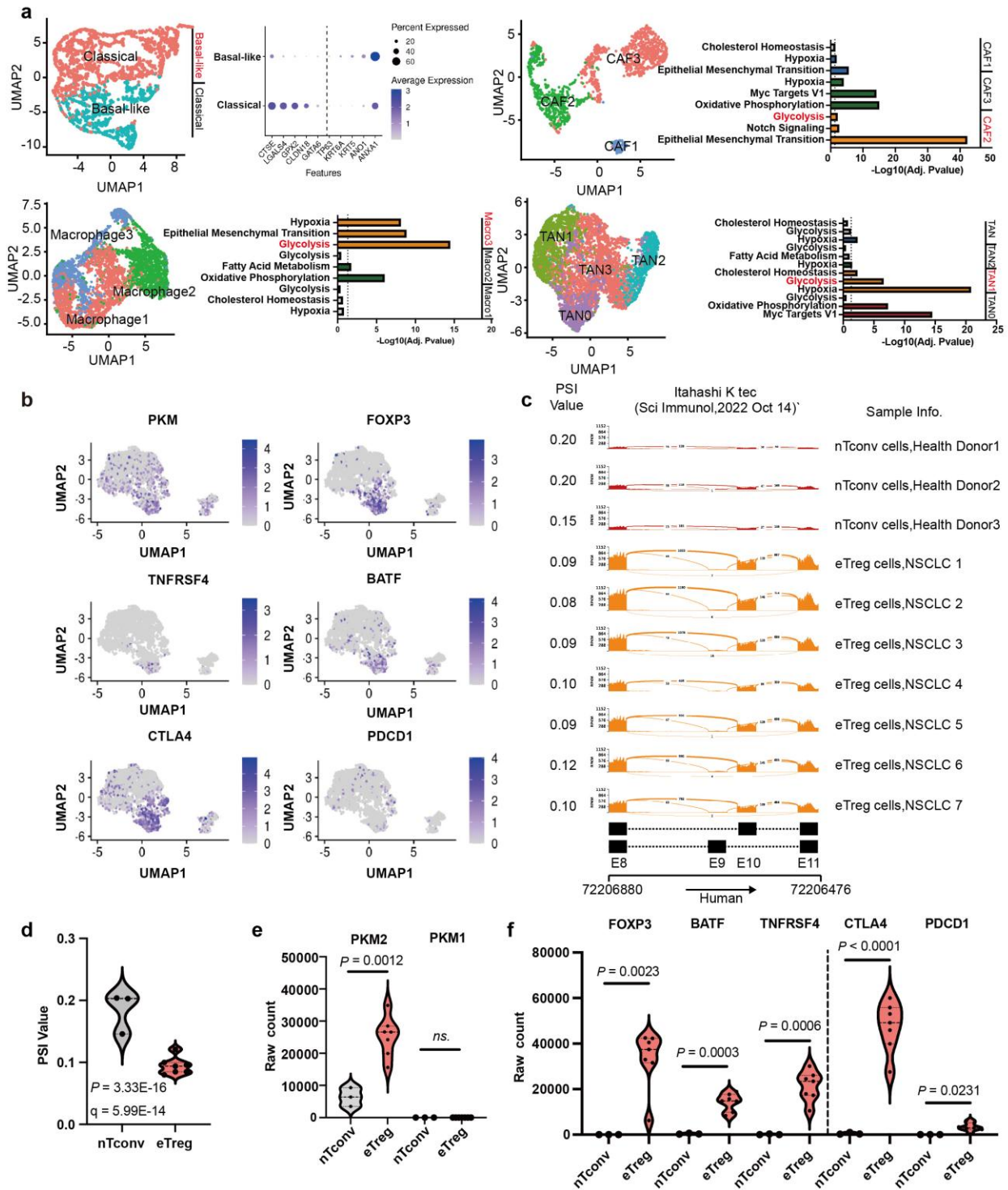




Supplementary Fig. S2 Broad screen for potential cells that can be targeted by PKM-ASO in the PDAC

TME. a, Subcluster of scRNAseq, and GO analysis. **b**, *PKM*, *FOXP3*, *TNFRSF4*, *BATF*, *CTLA4*, and *PDCD1* expression along T_{reg} differentiation. **c**, Re-analysis of bulk RNAseq data of nT_{conv} (CD4-CCR7) and eT_{reg} (CD4-FOXP3/BATF) from public dataset GSE211155. rMATS was used for PSI calculation and statistical analysis, and

JCEC value was input into rMATSSashimiplo for visualization. **d**, PSI value of exon 9 ($nT_{conv} = 3$, $eT_{reg} = 8$). **e**, PKM2 was more highly expressed than PKM1 in eT_{reg} . Statistical analysis: unpaired two-sided t-test. **f**, Three markers of CD4-FOXP3/BATF cells from scRNAseq were highly expressed in eT_{reg} , and two immune checkpoint markers are also shown. Statistical analysis: unpaired two-sided t-test (c, d, e); Benjamini-Hochberg method to correct for multiple hypotheses testing (a); Log-rank Mantel–Cox test (g).