

Supplementary Figure S3. Correlations between the expression levels of *PKHD1L1* and lymphocytes. **(A)** *PKHD1L1* expression levels in common immune cell types were retrieved from RNA-seq-based expression quantitative trait loci (eQTLs) and epigenomics (DICE) database (<https://dice-database.org/landing>). *PKHD1L1* expression levels (x-axis) were represented as the number of transcripts per million transcripts (TPM). Common immune cell types (y-axis) are arranged based on the median expression level within the cohort from highest to lowest. Box plots indicate 25-75% ranges, and whiskers indicate minimum to maximum. **(B)** Common immune cell types (y-axis) are separated in detail by female-male. **(C)** Single cell analysis of melanoma intra-tumor heterogeneity, using the Single Cell Portal (https://singlecell.broadinstitute.org/single_cell), enriched for population cell subtypes, represented as violin plots. **(D)** t-Distributed Stochastic Neighbor Embedding (tSNE) visualization of immune cell populations identified through unsupervised cluster analysis of *PKHD1L1* expression from melanoma intra-tumor heterogeneity. Seven clusters including B cell (red), CAF (light blue), endothelial cluster (green), macrophage (purple), NK cell (orange), T cell (brown), and undefined (pink) were colorfully visualized.

