Figure S1. Analyzation of B cell subsets and IL-10 expression in HCC PBMC with public scRNA-seq data. (A) tSNE ploting showed the B cell clusters in Normal and HCC PBMC. (B) The expression of markers in B cell subsets. (C) ssGSEA analyzation on different B cells in different histology, B cell related hallmark biological functions and GO_BP are obviously repressed in HCC B cells globally. (D) Biological process of target B subclasses (B10/MZB/FoB) were also analyzed by ssGSEA. (E-F) The landscape of interaction of B cell in both health and HCC PB. (G) Expression of IL-10 in B10 cell and other B cell subtypes at single-cell mRNA level. (H) Survival analysis in TCGA LIHC project, total 364 patients with clinical information, and figure KM-curve, dividing the cohort into IL10-high and IL10-low groups.

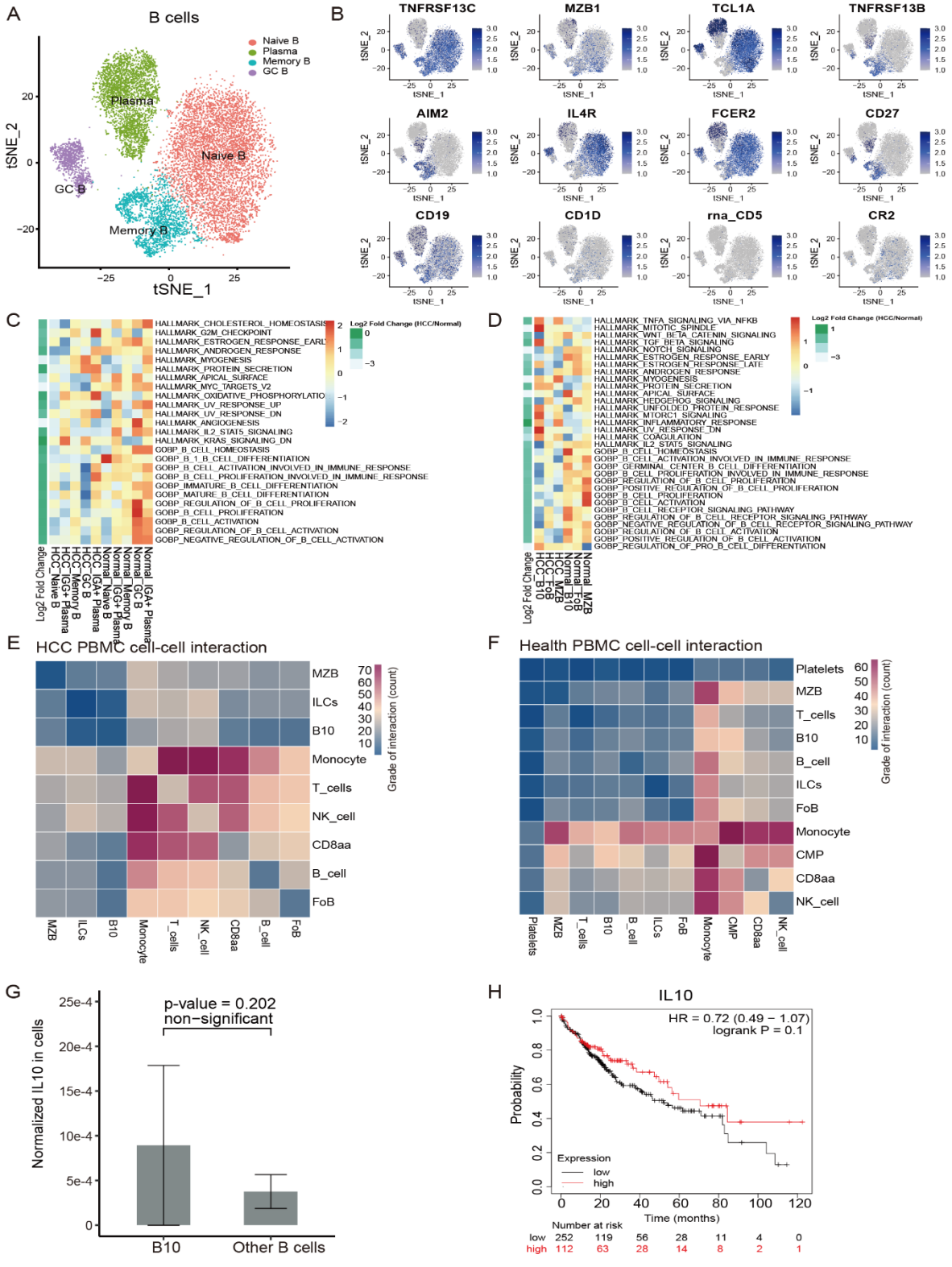
A
B cells
Naive B
Plasma
Memory B
GC B
tSNE_1
tSNE_2
B
TNFRSF13C
MZB1
TCL1A
TNFRSF13B
AIM2
IL4R
FCER2
CD27
CD19
CD1D
rna_CD5
CR2
C
Log2 Fold Change (HCC/Normal)
HALLMARK_CHOLESTEROL_HOMEOSTASIS
HALLMARK_G2M_CHECKPOINT
HALLMARK_ESTROGEN_RESPONSE_EARL
HALLMARK_ANDROGEN_RESPONSE
HALLMARK_MYOGENESIS
HALLMARK_PROTEIN_SECRETION
HALLMARK_APICAL_SURFACE
HALLMARK_MYC_TARGETS_V2
HALLMARK_OXIDATIVE_PHOSPHORYLATIO
HALLMARK_UV_RESPONSE_UP
HALLMARK_UV_RESPONSE_DN
HALLMARK_ANGIOGENESIS
HALLMARK_IL2_STAT5_SIGNALING
HALLMARK_KRAS_SIGNALING_DN
GOBP_B_CELL_HOMEOSTASIS
GOBP_B_1_B_CELL_DIFFERENTIATION
GOBP_B_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE
GOBP_B_CELL_PROLIFERATION_INVOLVED_IN_IMMUNE_RESPONSE
GOBP_IMMATURE_B_CELL_DIFFERENTIATION
GOBP_MATURE_B_CELL_DIFFERENTIATION
GOBP_REGULATION_OF_B_CELL_PROLIFERATION
GOBP_B_CELL_PROLIFERATION
GOBP_B_CELL_ACTIVATION
GOBP_REGULATION_OF_B_CELL_ACTIVATION
GOBP_NEGATIVE_REGULATION_OF_B_CELL_ACTIVATION
Log2 Fold Change
HCC_Naive B
HCC_IGG+ Plasma
HCC_Memory B
HCC_GC B
HCC_IGA+ Plasma
Normal_Naive B
Normal_IGG+ Plasma
Normal_Memory B
Normal_GC B
Normal_IGA+ Plasma
D
Log2 Fold Change (HCC/Normal)
HALLMARK_TNFA_SIGNALING_VIA_NFKB
HALLMARK_MITOTIC_SPINDLE
HALLMARK_WNT_BETA_CATENIN_SIGNALING
HALLMARK_TGF_BETA_SIGNALING
HALLMARK_NOTCH_SIGNALING
HALLMARK_ESTROGEN_RESPONSE_EARLY
HALLMARK_ESTROGEN_RESPONSE_LATE
HALLMARK_ANDROGEN_RESPONSE
HALLMARK_MYOGENESIS
HALLMARK_PROTEIN_SECRETION
HALLMARK_APICAL_SURFACE
HALLMARK_HEDGEHOG_SIGNALING
HALLMARK_UNFOLDED_PROTEIN_RESPONSE
HALLMARK_MTORC1_SIGNALING
HALLMARK_INFLAMMATORY_RESPONSE
HALLMARK_UV_RESPONSE_DN
HALLMARK_COAGULATION
HALLMARK_IL2_STAT5_SIGNALING
GOBP_B_CELL_HOMEOSTASIS
GOBP_B_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE
GOBP_GERMINAL_CENTER_B_CELL_DIFFERENTIATION
GOBP_B_CELL_PROLIFERATION_INVOLVED_IN_IMMUNE_RESPONSE
GOBP_REGULATION_OF_B_CELL_PROLIFERATION
GOBP_POSITIVE_REGULATION_OF_B_CELL_PROLIFERATION
GOBP_B_CELL_PROLIFERATION
GOBP_B_CELL_ACTIVATION
GOBP_B_CELL_RECEPTOR_SIGNALING_PATHWAY
GOBP_REGULATION_OF_B_CELL_RECEPTOR_SIGNALING_PATHWAY
GOBP_NEGATIVE_REGULATION_OF_B_CELL_RECEPTOR_SIGNALING_PATHWAY
GOBP_REGULATION_OF_B_CELL_ACTIVATION
GOBP_POSITIVE_REGULATION_OF_B_CELL_ACTIVATION
GOBP_REGULATION_OF_PRO_B_CELL_DIFFERENTIATION
Log2 Fold Change
HCC_B10
HCC_FoB
HCC_MZB
Normal_B10
Normal_FoB
Normal_MZB
E
HCC PBMC cell-cell interaction
MZB
ILCs
B10
Monocyte
T_cells
NK_cell
CD8aa
B_cell
FoB
Grade of interaction (count)
F
Health PBMC cell-cell interaction
Platelets
MZB
T_cells
B10
B_cell
ILCs
FoB
Monocyte
CMP
CD8aa
NK_cell
Grade of interaction (count)
G
p-value = 0.202
non−significant
Normalized IL10 in cells
B10
Other B cells
H
IL10
HR = 0.72 (0.49 − 1.07)
logrank P = 0.1
Probability
Expression
low
high
Time (months)
Number at risk
low 252 119 56 28 11 4 0
high 112 63 28 14 8 2 1

Figure S1

Table S1. Marker Genes by Cell.

Marker genes of lymphocyte subsets in the three datasets.

Table S2. DEG_10x_vs_zhang's data.

Differentially expressed genes (DEGs) of PBMC between HCC and healthy donors are analyzed by R packages DESeq2 (v1.16.1). DESeq2 provides an acceptable strategy to determine the differences in single-cell datasets. We use p adjust < 0.01 and log2fold-change > 0.3 (or < -0.3) as a cutoff to interpret significant differentially expressed genes to plot heatmap.

Table S3. Cell interaction.

Cell-cell interactions are operated by CellPhoneDB, and ggplot2 was used for drawing dot diagrams.