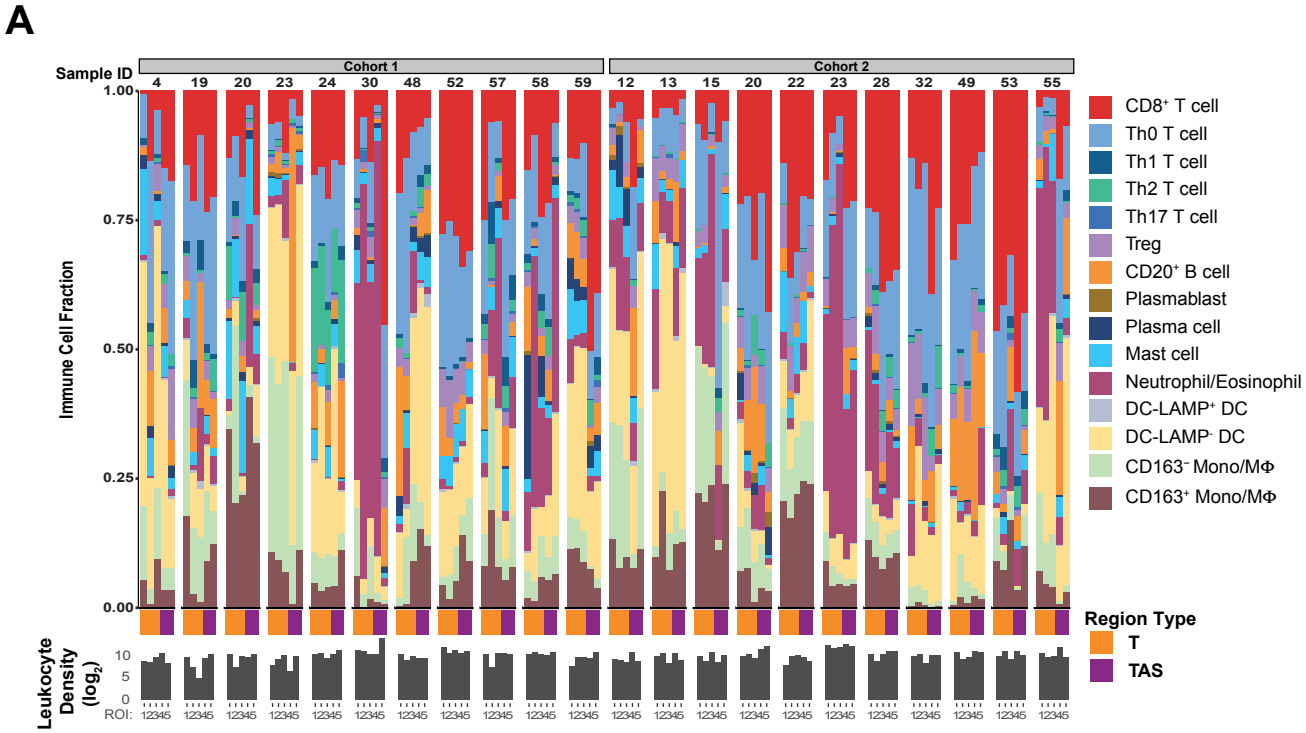
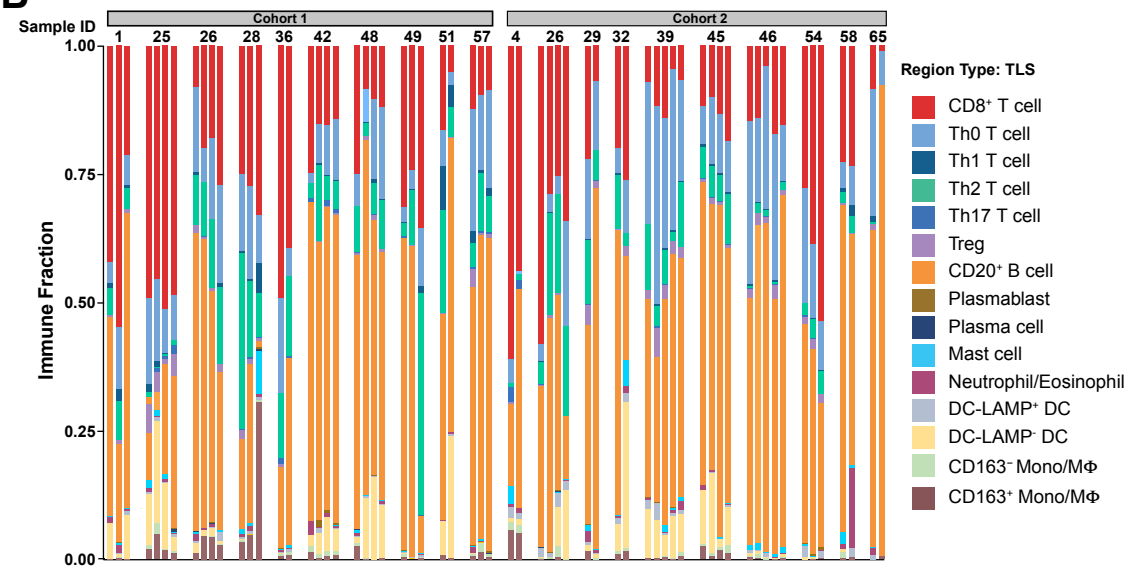
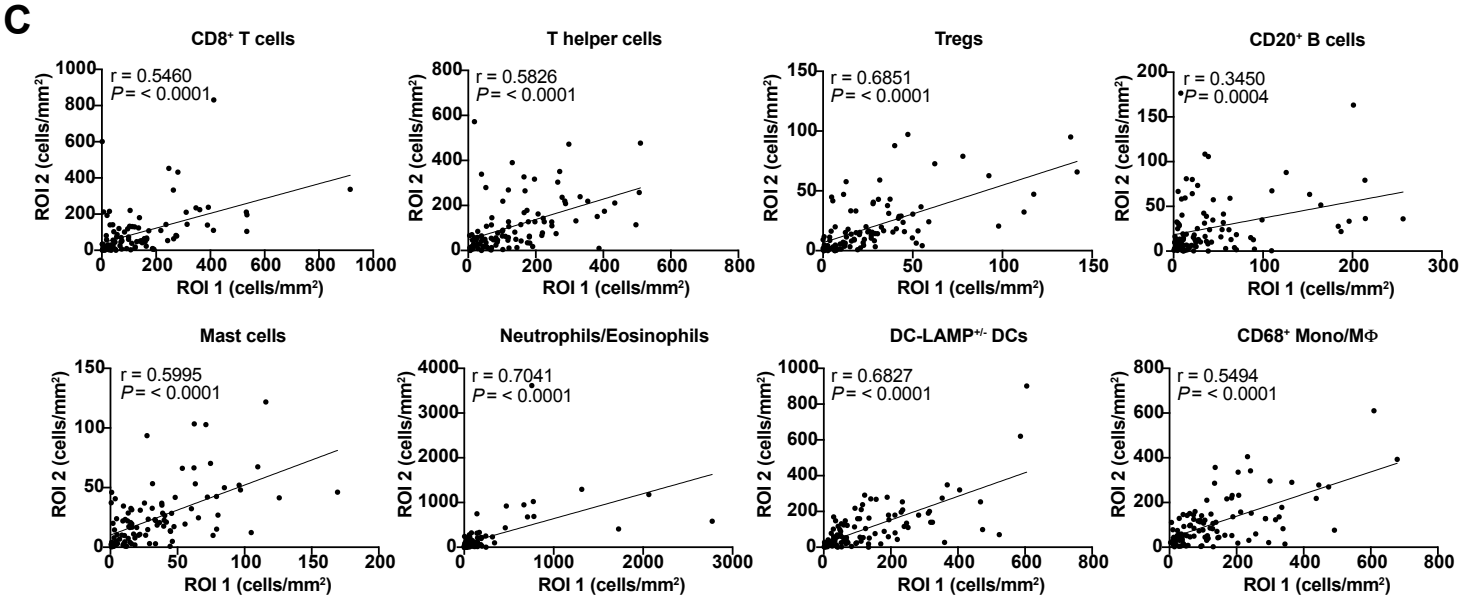

A
Sample ID
Cohort 1
Cohort 2
4 19 20 23 24 30 48 52 57 58 59
12 13 15 20 22 23 28 32 49 53 55
Immune Cell Fraction
1.00
0.75
0.50
0.25
0.00
CD8+ T cell
Th0 T cell
Th1 T cell
Th2 T cell
Th17 T cell
Treg
CD20+ B cell
Plasmablast
Plasma cell
Mast cell
Neutrophil/Eosinophil
DC-LAMP+ DC
DC-LAMP- DC
CD163- Mono/MΦ
CD163+ Mono/MΦ
Region Type
T
TAS
Leukocyte Density (log2)
10
5
0
ROI: 12345


B
Sample ID
Cohort 1
Cohort 2
1 25 26 28 36 42 48 49 51 57
4 26 29 32 39 45 46 54 58 65
Immune Fraction
1.00
0.75
0.50
0.25
0.00
Region Type: TLS
CD8+ T cell
Th0 T cell
Th1 T cell
Th2 T cell
Th17 T cell
Treg
CD20+ B cell
Plasmablast
Plasma cell
Mast cell
Neutrophil/Eosinophil
DC-LAMP+ DC
DC-LAMP- DC
CD163- Mono/MΦ
CD163+ Mono/MΦ


C
CD8+ T cells
r = 0.5460
P = < 0.0001
T helper cells
r = 0.5826
P = < 0.0001
Tregs
r = 0.6851
P = < 0.0001
CD20+ B cells
r = 0.3450
P = 0.0004
Mast cells
r = 0.5995
P = < 0.0001
Neutrophils/Eosinophils
r = 0.7041
P = < 0.0001
DC-LAMP+/- DCs
r = 0.6827
P = < 0.0001
CD68+ Mono/MΦ
r = 0.5494
P = < 0.0001
ROI 1 (cells/mm2)
ROI 2 (cells/mm2)

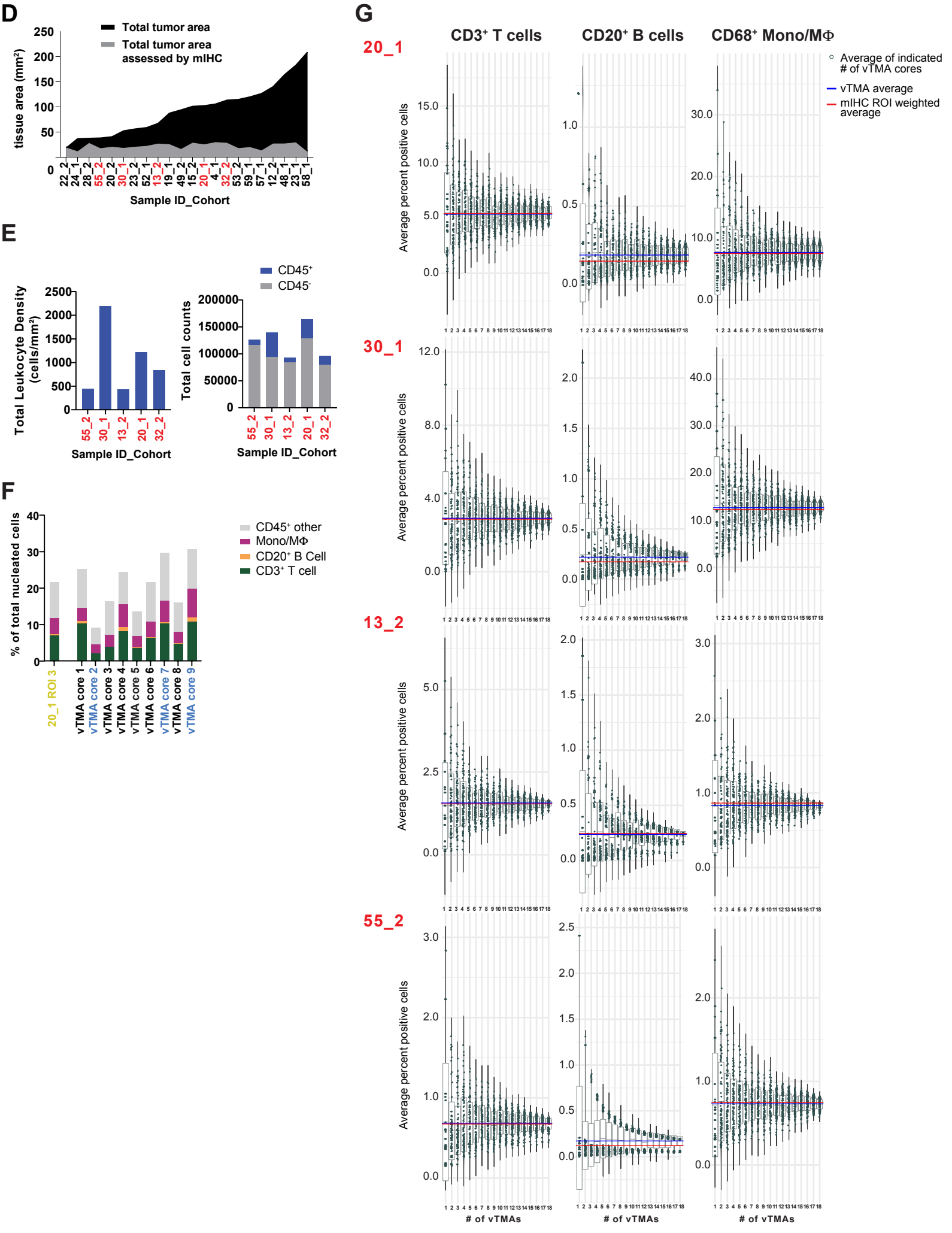

D
Total tumor area
Total tumor area assessed by mIHC
tissue area (mm²)
Sample ID_Cohort
E
CD45⁺
CD45⁻
Total Leukocyte Density (cells/mm²)
Total cell counts
Sample ID_Cohort
F
CD45⁺ other
Mono/MΦ
CD20⁺ B Cell
CD3⁺ T cell
% of total nucleated cells
20_1 ROI 3
vTMA core 1
vTMA core 2
vTMA core 3
vTMA core 4
vTMA core 5
vTMA core 6
vTMA core 7
vTMA core 8
vTMA core 9
G
CD3⁺ T cells
CD20⁺ B cells
CD68⁺ Mono/MΦ
Average of indicated # of vTMA cores
vTMA average
mIHC ROI weighted average
20_1
30_1
13_2
55_2
Average percent positive cells
# of vTMAs

Figure S5, related to Figure 5. Intrapatient heterogeneity based on size and histopathology of assessed tissue

(A) Leukocyte composition of individual regions of interest (ROIs) from a subsample of specimens from Cohorts 1 and 2 (n = 22) illustrating relative abundance of cell populations in three 'T' (orange) and two 'TAS' (purple) regions from each patient. Dark gray bars (bottom) indicate total leukocyte density in log2 scale for each ROI. **(B)** Leukocyte composition of 2 to 5 individual 'TLS' ROIs from a subsample of specimens from Cohorts 1 and 2 (n = 20). **(C)** Spearman correlation coefficients were calculated between two 'T' mIHC ROIs per PDAC for the indicated leukocyte populations (n = 208 ROIs from 104 treatment-naïve tumors). **(D)** Measurement of histopathologically-annotated invasive tumor areas for 22 representative PDAC specimens from Cohorts 1 and 2 (X-axis, sample ID is followed by underscore and cohort number). Black curve indicates total tumor area identified by a pathologist on one FFPE tissue section and gray curve indicates total tumor area included in T ROIs for mIHC analysis. Red text indicates samples used for subsequent vTMA analysis. **(E)** Total leukocyte density (left) and cell counts (right) for the 5 cases selected for vTMA analysis. Data displayed are averages of all T ROIs per sample. **(F)** Abundance of indicated cell populations in the entirety of T ROI3 of Sample 20_1 (leftmost bar) as compared to nine individual vTMA cores placed within the ROI. **(G)** $CD3^+$ T cell (left), $CD20^+$ B cell (middle), and $CD68^+$ monocyte/macrophage (right) cell frequencies calculated from the average of 1-18 vTMA cores (x-axis) for 100 sample iterations. The vTMA average (blue line, sample reference) and mIHC ROI weighted averages (red line) are shown as solid lines.