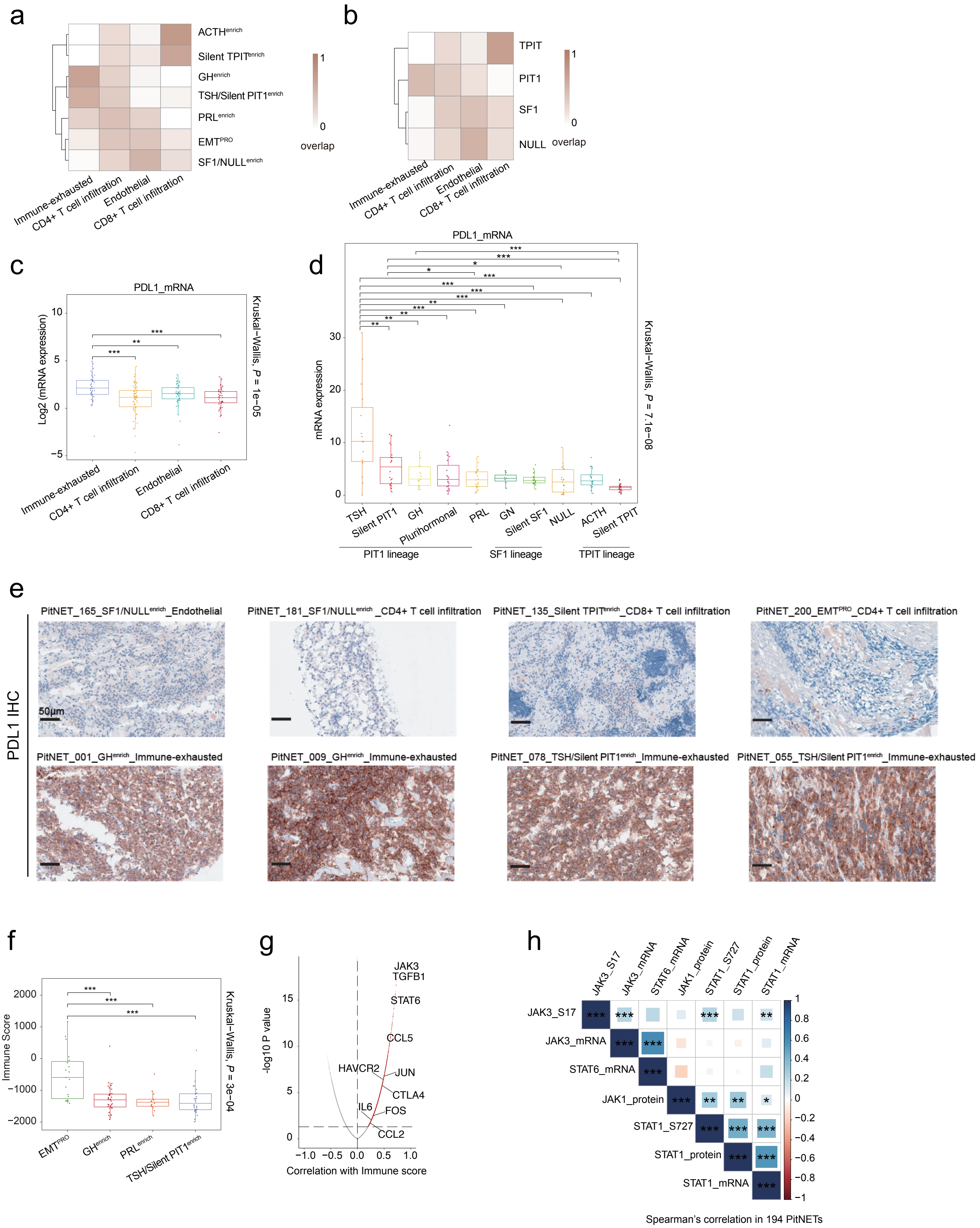
a
ACTHenrich
Silent TPITenrich
GHenrich
TSH/Silent PIT1enrich
PRLenrich
EMTPRO
SF1/NULLenrich
1
0
overlap
Immune-exhausted
CD4+ T cell infiltration
Endothelial
CD8+ T cell infiltration
b
TPIT
PIT1
SF1
NULL
1
0
overlap
Immune-exhausted
CD4+ T cell infiltration
Endothelial
CD8+ T cell infiltration
c
PDL1_mRNA
Log2 (mRNA expression)
10
5
0
−5
***
**
***
Kruskal−Wallis, P = 1e−05
Immune-exhausted
CD4+ T cell infiltration
Endothelial
CD8+ T cell infiltration
d
PDL1_mRNA
mRNA expression
30
20
10
0
***
*
**
Kruskal−Wallis, P = 7.1e−08
TSH
Silent PIT1
GH
Plurihormonal
PRL
GN
Silent SF1
NULL
ACTH
Silent TPIT
PIT1 lineage
SF1 lineage
TPIT lineage
e
PDL1 IHC
PitNET_165_SF1/NULLenrich_Endothelial
PitNET_181_SF1/NULLenrich_CD4+ T cell infiltration
PitNET_135_Silent TPITenrich_CD8+ T cell infiltration
PitNET_200_EMTPRO_CD4+ T cell infiltration
50μm
PitNET_001_GHenrich_Immune-exhausted
PitNET_009_GHenrich_Immune-exhausted
PitNET_078_TSH/Silent PIT1enrich_Immune-exhausted
PitNET_055_TSH/Silent PIT1enrich_Immune-exhausted
f
Immune Score
2000
1000
0
−1000
−2000
***
Kruskal−Wallis, P = 3e−04
EMTPRO
GHenrich
PRLenrich
TSH/Silent PIT1enrich
g
-log10 P value
15
10
5
0
JAK3
TGFB1
STAT6
CCL5
HAVCR2
JUN
CTLA4
IL6
FOS
CCL2
−1.0
−0.5
0.0
0.5
1.0
Correlation with Immune score
h
JAK3_S17
JAK3_mRNA
STAT6_mRNA
JAK1_protein
STAT1_S727
STAT1_protein
STAT1_mRNA
***
**
*
1
0.8
0.6
0.4
0.2
0
−0.2
−0.4
−0.6
−0.8
−1
Spearman's correlation in 194 PitNETs

Supplementary information, Fig. S8 Immune landscape in PitNETs, related to Fig. 5.

a Heatmap showing the comparison between immune clusters (columns) with proteomic clusters (rows). Each row sums to one, with different entries showing the proportion of tumors allocated to different immune clusters.

b Heatmap showing the comparison between immune clusters (columns) with TF lineages (rows). Each row sums to one, with different entries showing the proportion of tumors allocated to different immune clusters.

c Boxplot showing the mRNA expression of *PDL1* among the four immune clusters. Kruskal-Wallis test was used to test if any of the differences among the subgroups were statistically significant. Wilcoxon rank-sum test was used to estimate the significance of two subgroups, $^{**}P < 0.01$, $^{***}P < 0.001$.

d Boxplot showing the mRNA expression of PDL1 among the ten clinicopathological subtypes. Kruskal-Wallis test was used to test if any of the differences among the subgroups were statistically significant. Wilcoxon rank-sum test was used to estimate the significance of two subgroups, $^{**}P < 0.01$, $^{***}P < 0.001$.

e Representative graphs of PDL1 staining in SF1/NULL$^{\text{enrich}}$, silent TPIT$^{\text{enrich}}$, EMT$^{\text{PRO}}$, GH$^{\text{enrich}}$, and TSH/silent PIT1$^{\text{enrich}}$ clusters. Scale bar is 50 μm.

f Boxplot showing the immune score among four proteomic clusters within PIT1 lineage. Kruskal-Wallis test was used to test if any of the differences among the subgroups were statistically significant. Wilcoxon rank-sum test was used to estimate the significance of two subgroups, $^{***}P < 0.001$.

g Volcano plot showing the Spearman's correlation (*x*-axis) versus *P* value (*y*-axis) between immune score and genes at the mRNA level.

h Spearman's correlation among JAK1, JAK3, STAT1 and STAT6 at the mRNA, protein and phosphorylation levels in 194 PitNETs ($^{*}P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$).