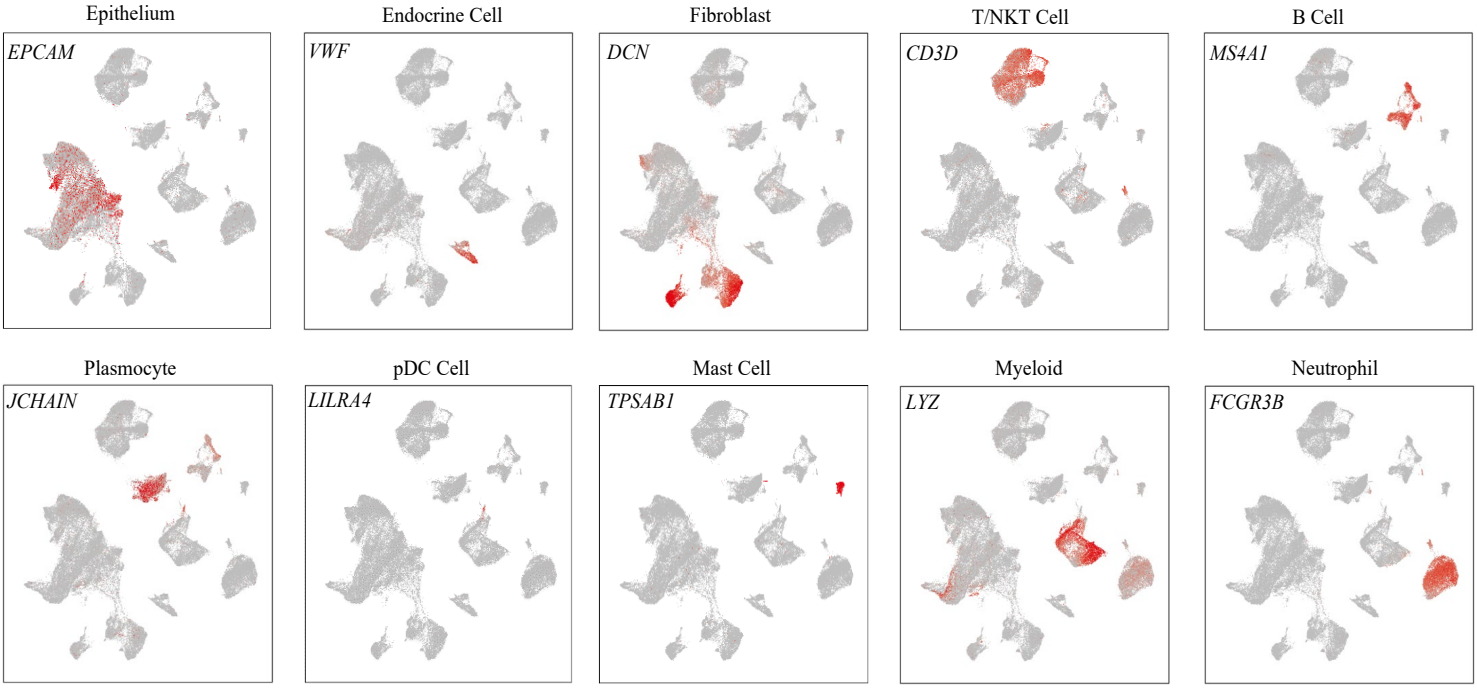
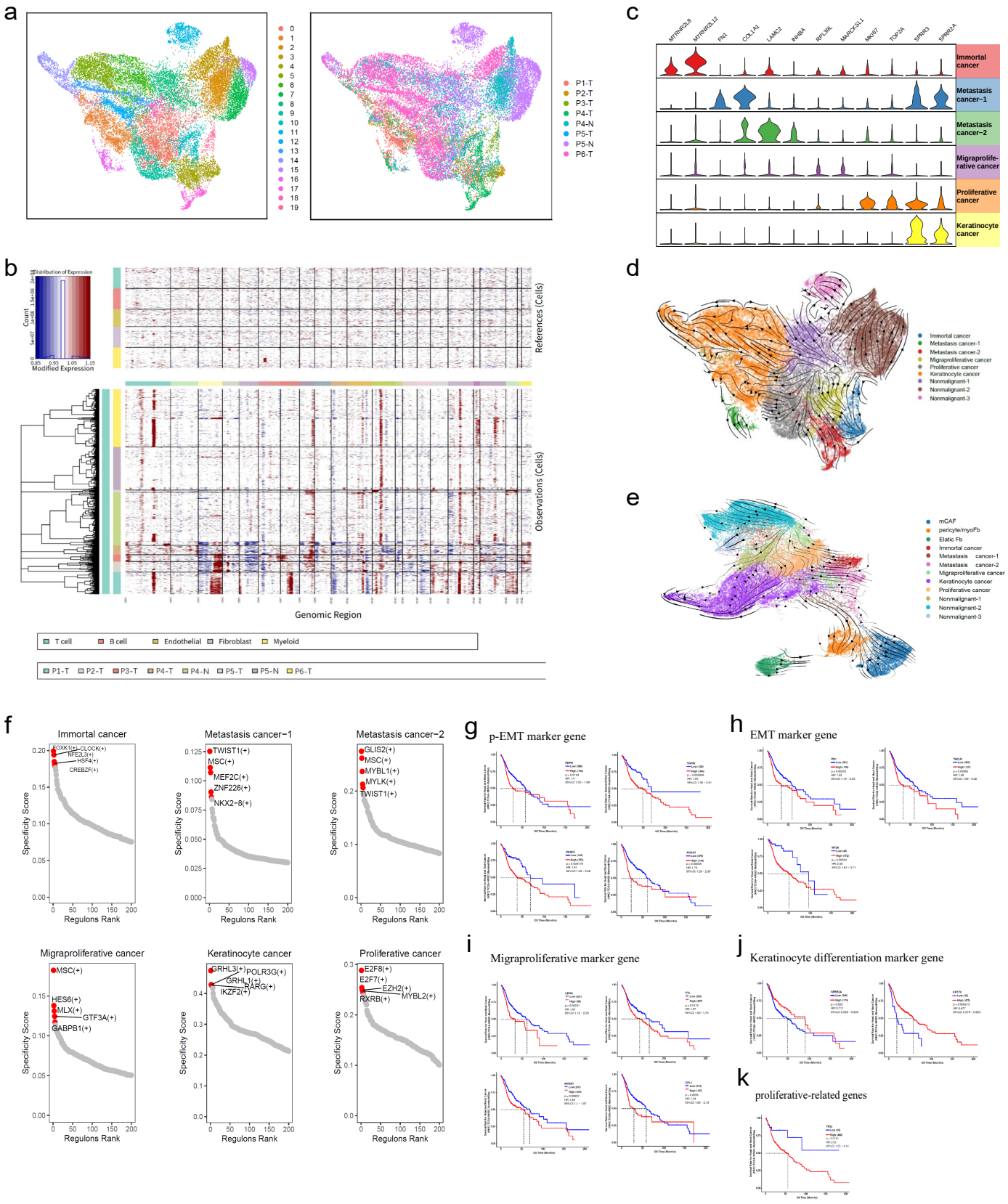
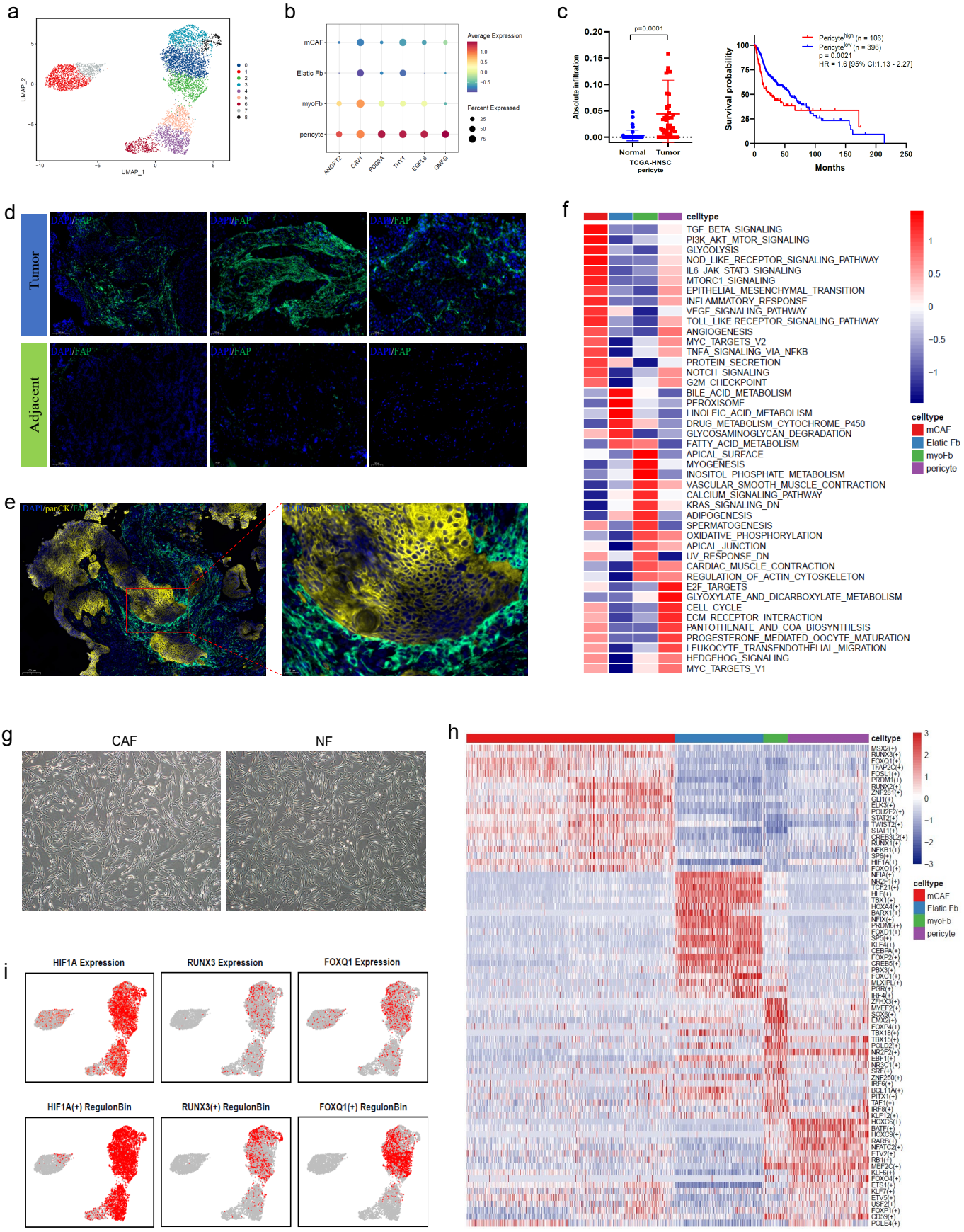
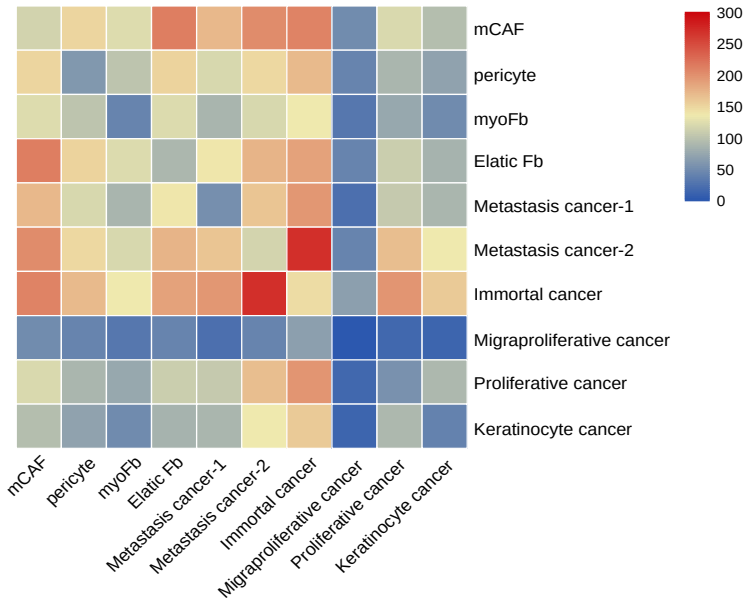
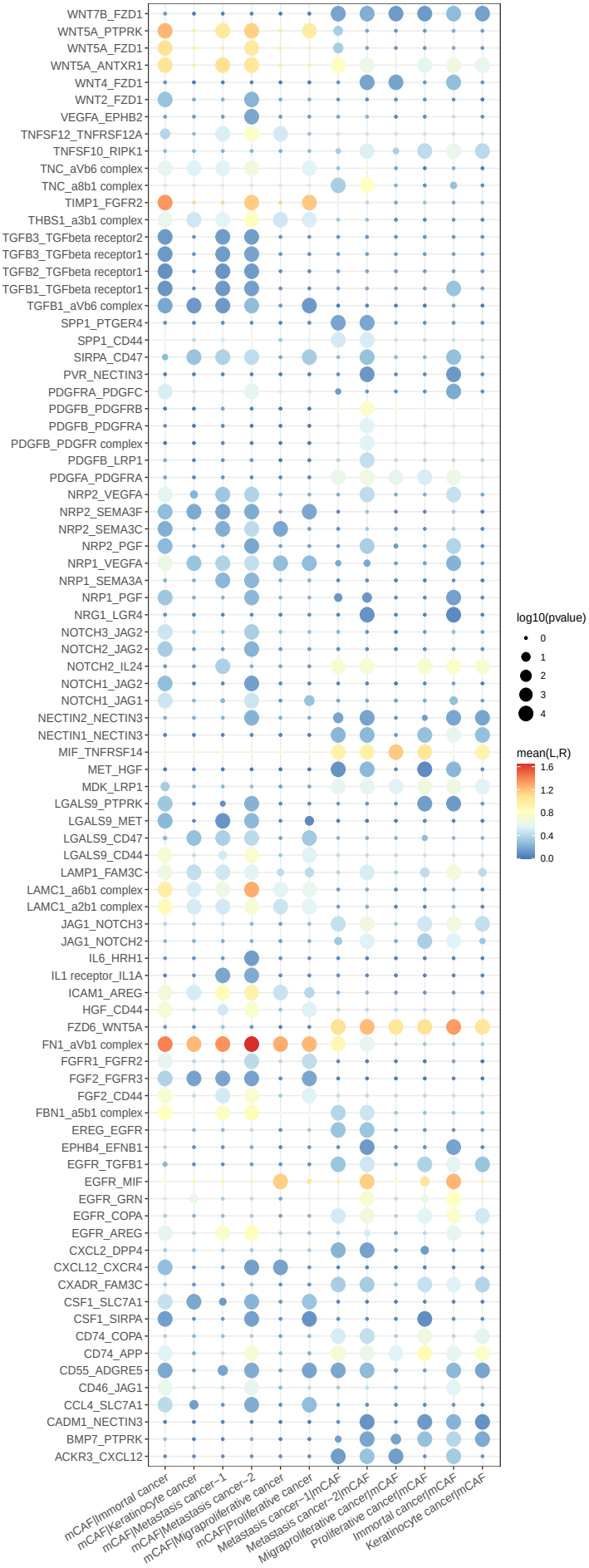
Expression of marker genes

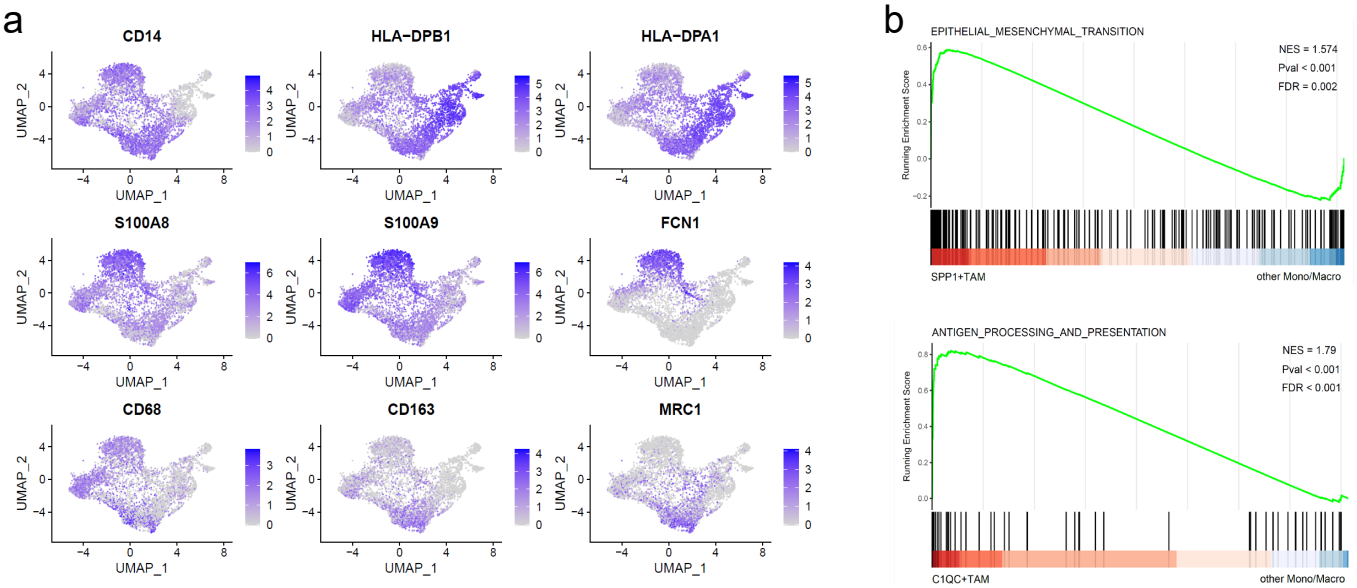


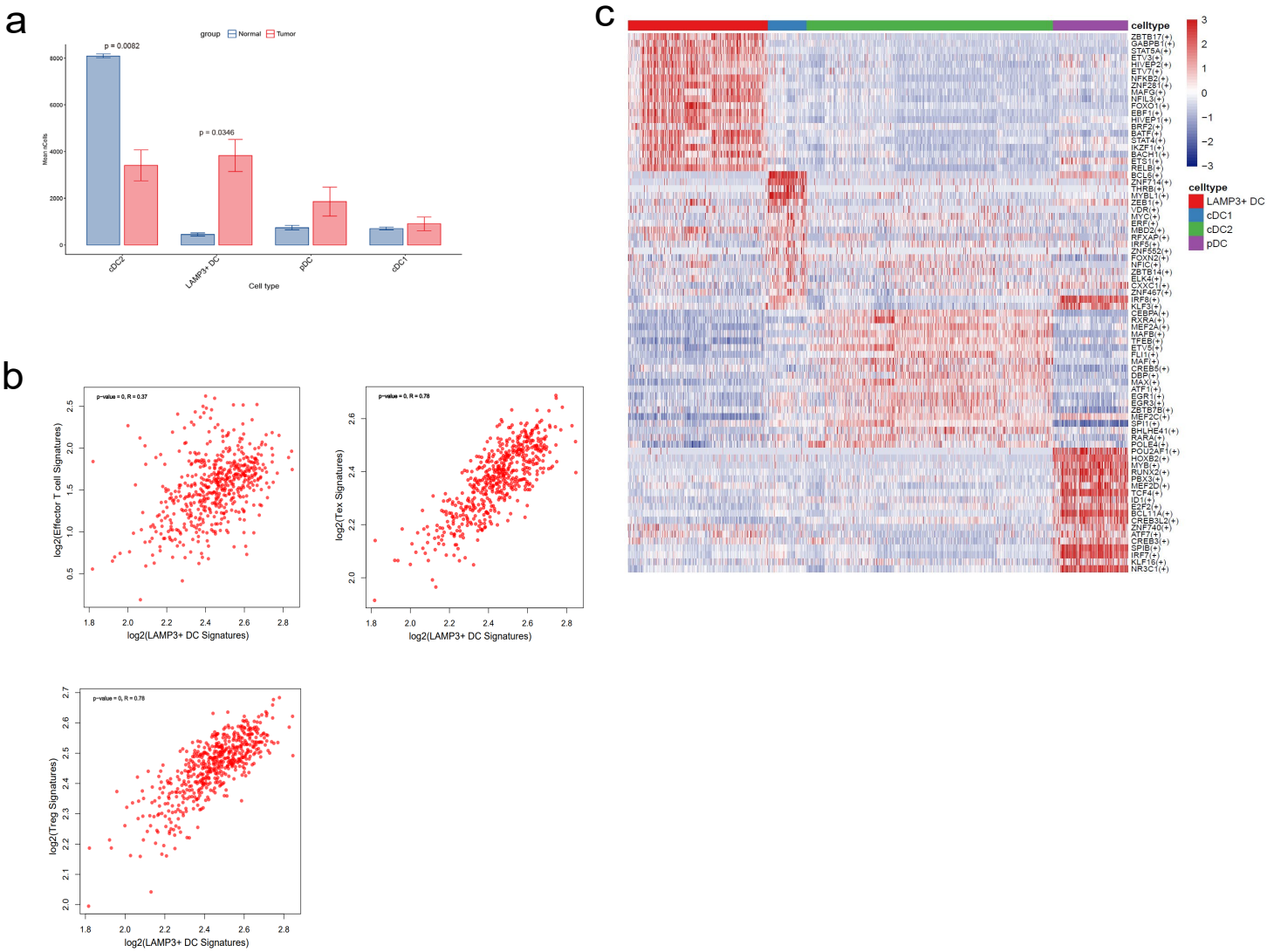

a
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
P1-T
P2-T
P3-T
P4-T
P4-N
P5-T
P5-N
P6-T
c
MTRNR2L8
MTRNR2L12
FN1
COL1A1
LAMC2
INHBA
RPL39L
MARCKSL1
MKI67
TOP2A
SPRR3
SPRR2A
Immortal cancer
Metastasis cancer−1
Metastasis cancer−2
Migraprolife-rative cancer
Proliferative cancer
Keratinocyte cancer
b
Distribution of Expression
Count
Modified Expression
References (Cells)
Observations (Cells)
Genomic Region
T cell
B cell
Endothelial
Fibroblast
Myeloid
P1-T
P2-T
P3-T
P4-T
P4-N
P5-T
P5-N
P6-T
d
Immortal cancer
Metastasis cancer-1
Metastasis cancer-2
Migraproliferative cancer
Proliferative cancer
Keratinocyte cancer
Nonmalignant-1
Nonmalignant-2
Nonmalignant-3
e
mCAF
pericyte/myoFb
Elatic Fb
Immortal cancer
Metastasis cancer-1
Metastasis cancer-2
Migraproliferative cancer
Keratinocyte cancer
Proliferative cancer
Nonmalignant-1
Nonmalignant-2
Nonmalignant-3
f
Immortal cancer
FOXK1(+)
CLOCK(+)
NFE2L3(+)
HSF4(+)
CREBZF(+)
Metastasis cancer−1
TWIST1(+)
MSC(+)
MEF2C(+)
ZNF226(+)
NKX2−8(+)
Metastasis cancer−2
GLIS2(+)
MSC(+)
MYBL1(+)
MYLK(+)
TWIST1(+)
Migraproliferative cancer
MSC(+)
HES6(+)
MLX(+)
GTF3A(+)
GABPB1(+)
Keratinocyte cancer
GRHL3(+)
POLR3G(+)
GRHL1(+)
PARG(+)
IKZF2(+)
Proliferative cancer
E2F8(+)
E2F7(+)
EZH2(+)
MYBL2(+)
RXRB(+)
Specificity Score
Regulons Rank
g
p-EMT marker gene
h
EMT marker gene
i
Migraproliferative marker gene
j
Keratinocyte differentiation marker gene
k
proliferative-related genes


a
UMAP_1
UMAP_2
b
mCAF
Elatic Fb
myoFb
pericyte
ANGPT2
CAV1
PDGFA
TH1
EGFL6
GMFG
Average Expression
Percent Expressed
c
p=0.0001
Absolute infiltration
Normal
Tumor
TCGA-HNSC
pericyte
Pericyte^high (n = 106)
Pericyte^low (n = 396)
p = 0.0021
HR = 1.6 [95% CI:1.13 - 2.27]
Survival probability
Months
d
Tumor
Adjacent
DAPI/FAP
e
DAPI/panCK/FAP
f
celltype
TGF_BETA_SIGNALING
PI3K_AKT_MTOR_SIGNALING
GLYCOLYSIS
NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY
IL6_JAK_STAT3_SIGNALING
MTORC1_SIGNALING
EPITHELIAL_MESENCHYMAL_TRANSITION
INFLAMMATORY_RESPONSE
VEGF_SIGNALING_PATHWAY
TOLL_LIKE RECEPTOR_SIGNALING_PATHWAY
ANGIOGENESIS
MYC_TARGETS_V2
TNFA_SIGNALING_VIA_NFKB
PROTEIN_SECRETION
NOTCH_SIGNALING
G2M_CHECKPOINT
BILE_ACID_METABOLISM
PEROXISOME
LINOLEIC_ACID_METABOLISM
DRUG_METABOLISM_CYTOCHROME_P450
GLYCOSAMINOGLYCAN_DEGRADATION
FATTY_ACID_METABOLISM
APICAL_SURFACE
MYOGENESIS
INOSITOL_PHOSPHATE_METABOLISM
VASCULAR_SMOOTH_MUSCLE_CONTRACTION
CALCIUM_SIGNALING_PATHWAY
KRAS_SIGNALING_DN
ADIPOGENESIS
SPERMATOGENESIS
OXIDATIVE_PHOSPHORYLATION
APICAL_JUNCTION
UV_RESPONSE_DN
CARDIAC_MUSCLE_CONTRACTION
REGULATION_OF_ACTIN_CYTOSKELETON
E2F_TARGETS
GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM
CELL_CYCLE
ECM_RECEPTOR_INTERACTION
PANTOTHENATE_AND_COA_BIOSYNTHESIS
PROGESTERONE_MEDIATED_OOCYTE_MATURATION
LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION
HEDGEHOG_SIGNALING
MYC_TARGETS_V1
mCAF
Elatic Fb
myoFb
pericyte
g
CAF
NF
h
celltype
i
HIF1A Expression
RUNX3 Expression
FOXQ1 Expression
HIF1A(+) RegulonBin
RUNX3(+) RegulonBin
FOXQ1(+) RegulonBin


mCAF
pericyte
myoFb
Elatic Fb
Metastasis cancer-1
Metastasis cancer-2
Immortal cancer
Migraproliferative cancer
Proliferative cancer
Keratinocyte cancer
300
250
200
150
100
50
0


WNT7B_FZD1
WNT5A_PTPRK
WNT5A_FZD1
WNT5A_ANTXR1
WNT4_FZD1
WNT2_FZD1
VEGFA_EPHB2
TNFSF12_TNFRSF12A
TNFSF10_RIPK1
TNC_aVb6 complex
TNC_a8b1 complex
TIMP1_FGFR2
THBS1_a3b1 complex
TGFB3_TGFbeta receptor2
TGFB3_TGFbeta receptor1
TGFB2_TGFbeta receptor1
TGFB1_TGFbeta receptor1
TGFB1_aVb6 complex
SPP1_PTGER4
SPP1_CD44
SIRPA_CD47
PVR_NECTIN3
PDGFRA_PDGFC
PDGFB_PDGFRB
PDGFB_PDGFRA
PDGFB_PDGFR complex
PDGFB_LRP1
PDGFA_PDGFRA
NRP2_VEGFA
NRP2_SEMA3F
NRP2_SEMA3C
NRP2_PGF
NRP1_VEGFA
NRP1_SEMA3A
NRP1_PGF
NRG1_LGR4
NOTCH3_JAG2
NOTCH2_JAG2
NOTCH2_IL24
NOTCH1_JAG2
NOTCH1_JAG1
NECTIN2_NECTIN3
NECTIN1_NECTIN3
MIF_TNFRSF14
MET_HGF
MDK_LRP1
LGALS9_PTPRK
LGALS9_MET
LGALS9_CD47
LGALS9_CD44
LAMP1_FAM3C
LAMC1_a6b1 complex
LAMC1_a2b1 complex
JAG1_NOTCH3
JAG1_NOTCH2
IL6_HRH1
IL1 receptor_IL1A
ICAM1_AREG
HGF_CD44
FZD6_WNT5A
FN1_aVb1 complex
FGFR1_FGFR2
FGF2_FGFR3
FGF2_CD44
FBN1_a5b1 complex
EREG_EGFR
EPHB4_EFNB1
EGFR_TGFB1
EGFR_MIF
EGFR_GRN
EGFR_COPA
EGFR_AREG
CXCL2_DPP4
CXCL12_CXCR4
CXADR_FAM3C
CSF1_SLC7A1
CSF1_SIRPA
CD74_COPA
CD74_APP
CD55_ADGRE5
CD46_JAG1
CCL4_SLC7A1
CADM1_NECTIN3
BMP7_PTPRK
ACKR3_CXCL12
mCAF|Immortal cancer
mCAF|Keratinocyte cancer
mCAF|Metastasis cancer−1
mCAF|Metastasis cancer−2
mCAF|Migraproliferative cancer
mCAF|Proliferative cancer
Metastasis cancer−1|mCAF
Metastasis cancer−2|mCAF
Migraproliferative cancer|mCAF
Proliferative cancer|mCAF
Immortal cancer|mCAF
Keratinocyte cancer|mCAF
log10(pvalue)
0
1
2
3
4
mean(L,R)
1.6
1.2
0.8
0.4
0.0


a
CD14
HLA-DPB1
HLA-DPA1
S100A8
S100A9
FCN1
CD68
CD163
MRC1
UMAP_1
UMAP_2
b
EPITHELIAL_MESENCHYMAL_TRANSITION
NES = 1.574
Pval < 0.001
FDR = 0.002
Running Enrichment Score
SPP1+TAM
other Mono/Macro
ANTIGEN_PROCESSING_AND_PRESENTATION
NES = 1.79
Pval < 0.001
FDR < 0.001
Running Enrichment Score
C1QC+TAM
other Mono/Macro


a
group
Normal
Tumor
p = 0.0082
p = 0.0346
Mean nCells
8000
6000
4000
2000
0
cDC2
LAMP3+ DC
pDC
cDC1
Cell type
b
p-value = 0, R = 0.37
log2(Effector T cell Signatures)
log2(LAMP3+ DC Signatures)
p-value = 0, R = 0.78
log2(Tex Signatures)
log2(LAMP3+ DC Signatures)
p-value = 0, R = 0.78
log2(Treg Signatures)
log2(LAMP3+ DC Signatures)
c
celltype
LAMP3+ DC
cDC1
cDC2
pDC
3
2
1
0
−1
−2
−3