Fig S6

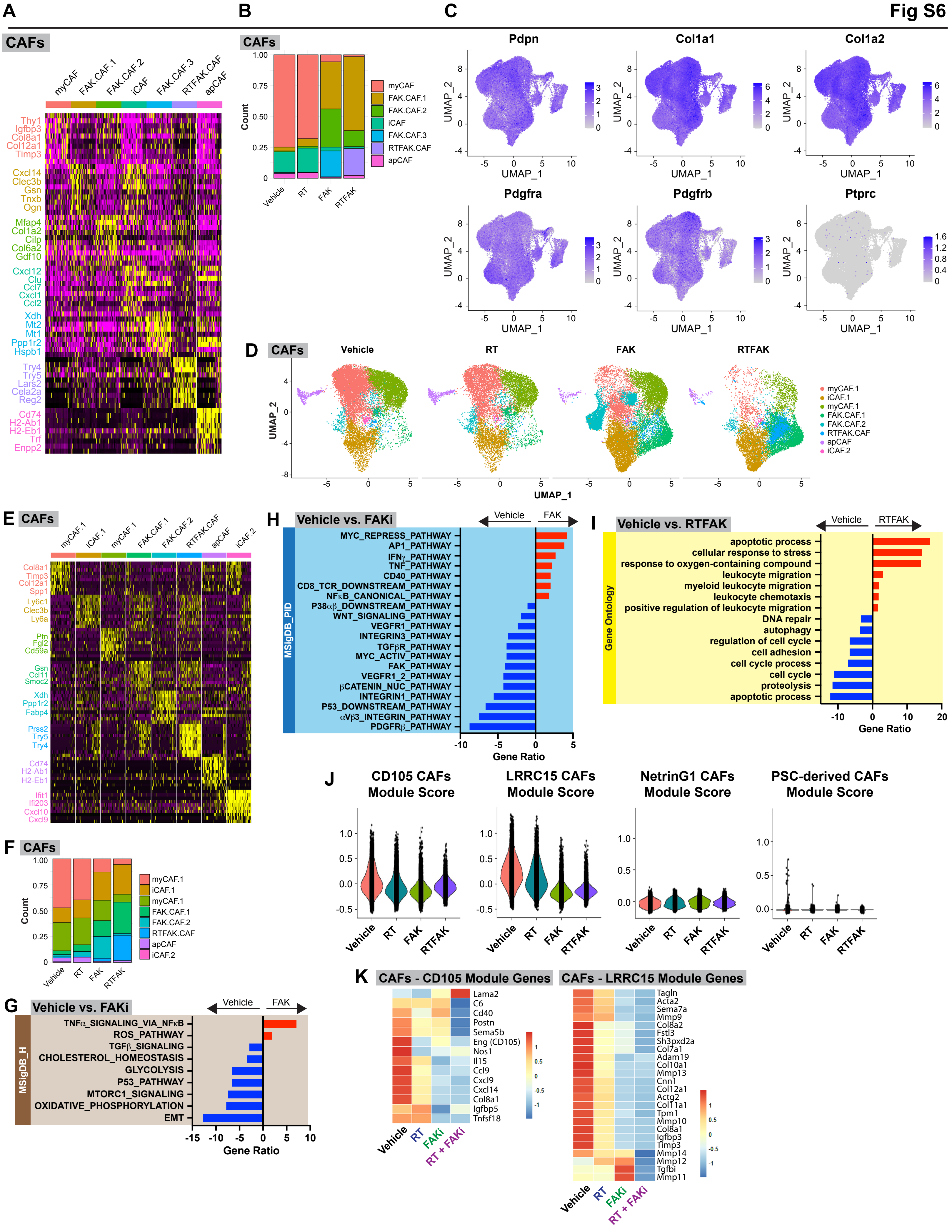
A
CAFs
myCAF
FAK.CAF.1
FAK.CAF.2
iCAF
FAK.CAF.3
RTFAK.CAF
apCAF
Thy1
Igfbp3
Col8a1
Col12a1
Timp3
Cxcl14
Clec3b
Gsn
Tnxb
Ogn
Mfap4
Col1a2
Cilp
Col6a2
Gdf10
Cxcl12
Clu
Ccl7
Cxcl1
Ccl2
Xdh
Mt2
Mt1
Ppp1r2
Hspb1
Try4
Try5
Lars2
Cela2a
Reg2
Cd74
H2-Ab1
H2-Eb1
Trf
Enpp2
B
CAFs
Count
1.00
0.75
0.50
0.25
0
Vehicle
RT
FAK
RTFAK
myCAF
FAK.CAF.1
FAK.CAF.2
iCAF
FAK.CAF.3
RTFAK.CAF
apCAF
C
Pdpn
Col1a1
Col1a2
Pdgfra
Pdgfrb
Ptprc
UMAP_1
UMAP_2
-5
0
5
10
-4
0
4
8
1.6
1.2
0.8
0.4
D
CAFs
Vehicle
RT
FAK
RTFAK
UMAP_1
UMAP_2
-8
-4
0
4
-5
0
5
myCAF.1
iCAF.1
myCAF.1
FAK.CAF.1
FAK.CAF.2
RTFAK.CAF
apCAF
iCAF.2
E
CAFs
myCAF.1
iCAF.1
myCAF.1
FAK.CAF.1
FAK.CAF.2
RTFAK.CAF
apCAF
iCAF.2
Col8a1
Timp3
Col12a1
Spp1
Ly6c1
Clec3b
Ly6a
Ptn
Fgl2
Cd59a
Gsn
Ccl11
Smoc2
Xdh
Ppp1r2
Fabp4
Prss2
Try5
Try4
Cd74
H2-Ab1
H2-Eb1
Ifit1
Ifi203
Cxcl10
Cxcl9
F
CAFs
Count
1.00
0.75
0.50
0.25
0
Vehicle
RT
FAK
RTFAK
myCAF.1
iCAF.1
myCAF.1
FAK.CAF.1
FAK.CAF.2
RTFAK.CAF
apCAF
iCAF.2
G
Vehicle vs. FAKi
Vehicle
FAK
MSigDB_H
TNFα_SIGNALING_VIA_NFκB
ROS_PATHWAY
TGFβ_SIGNALING
CHOLESTEROL_HOMEOSTASIS
GLYCOLYSIS
P53_PATHWAY
MTORC1_SIGNALING
OXIDATIVE_PHOSPHORYLATION
EMT
-15
-10
-5
0
5
10
Gene Ratio
H
Vehicle vs. FAKi
Vehicle
FAK
MSigDB_PID
MYC_REPRESS_PATHWAY
AP1_PATHWAY
IFNγ_PATHWAY
TNF_PATHWAY
CD40_PATHWAY
CD8_TCR_DOWNSTREAM_PATHWAY
NFκB_CANONICAL_PATHWAY
P38αβ_DOWNSTREAM_PATHWAY
WNT_SIGNALING_PATHWAY
VEGFR1_PATHWAY
INTEGRIN3_PATHWAY
TGFβR_PATHWAY
MYC_ACTIV_PATHWAY
FAK_PATHWAY
VEGFR1_2_PATHWAY
βCATENIN_NUC_PATHWAY
INTEGRIN1_PATHWAY
P53_DOWNSTREAM_PATHWAY
αVβ3_INTEGRIN_PATHWAY
PDGFRβ_PATHWAY
-10
-5
0
5
Gene Ratio
I
Vehicle vs. RTFAK
Vehicle
RTFAK
Gene Ontology
apoptotic process
cellular response to stress
response to oxygen-containing compound
leukocyte migration
myeloid leukocyte migration
leukocyte chemotaxis
positive regulation of leukocyte migration
DNA repair
autophagy
regulation of cell cycle
cell adhesion
cell cycle process
cell cycle
proteolysis
apoptotic process
-10
0
10
20
Gene Ratio
J
CD105 CAFs Module Score
LRRC15 CAFs Module Score
NetrinG1 CAFs Module Score
PSC-derived CAFs Module Score
1.0
0.5
0.0
-0.5
Vehicle
RT
FAK
RTFAK
K
CAFs - CD105 Module Genes
Lama2
C6
Cd40
Postn
Sema5b
Eng (CD105)
Nos1
Il15
Ccl9
Cxcl9
Cxcl14
Col8a1
Igfbp5
Tnfsf18
1
0.5
0
-0.5
-1
Vehicle
RT
FAKi
RT + FAKi
CAFs - LRRC15 Module Genes
Tagln
Acta2
Sema7a
Mmp9
Col8a2
Fstl3
Sh3pxd2a
Col7a1
Adam19
Col10a1
Mmp13
Cnn1
Col12a1
Actg2
Col11a1
Tpm1
Mmp10
Col8a1
Igfbp3
Timp3
Mmp14
Mmp12
Tgfbi
Mmp11
1
0.5
0
-0.5
-1
Vehicle
RT
FAKi
RT + FAKi

Figure S6: FAKi reshapes CAFs to participate in tumor immunity

(A) Heatmap displaying top 10 genes of CAFs in **Fig. 6A**. **(B)** Count ratio of the CAF clusters from **Fig. 6A-B**. **(C)** Feature plots of known CAF marker genes superimposed onto UMAP in **Fig. 6A**. **(D)** UMAP dimensionality reduction plot of scRNA-seq data on the same cells in **Fig. 6A** when Harmony integration was included in analysis. Annotation shows different cell types. **(E)** Heatmap displaying top 10 genes of the CAFs in (D). **(F)** Count ratio of the CAF clusters in (D). **(G-H)** Bar graphs displaying over-representation analysis of DEGs on CAFs in **Fig. 6A** to known biological functions in MSigDB_Hallmark (G) and MSigDB_PID (H) databases. All graphs display comparisons of CAFs from vehicle to FAKi-treated mice. All pathways were filtered with p.adj value < 0.05. **(I)** Bar graph displaying over-representation analysis from GO database. All graphs display comparisons of CAFs from vehicle to RT+FAKi-treated mice. All pathways were filtered with p.adj value < 0.05. **(J)** Gene signature module scores for CD105$^+$ CAFs, LRRC15$^+$ CAFs, NetrinG1$^+$ CAFs, and PSC-derived CAFs from CAFs in **Fig. 6A** split by treatment. **(K)** Heatmap of CD105$^+$ CAFs and LRRC15$^+$ CAFs module genes signatures for the CAFs in **Fig. 6A** split by treatment.