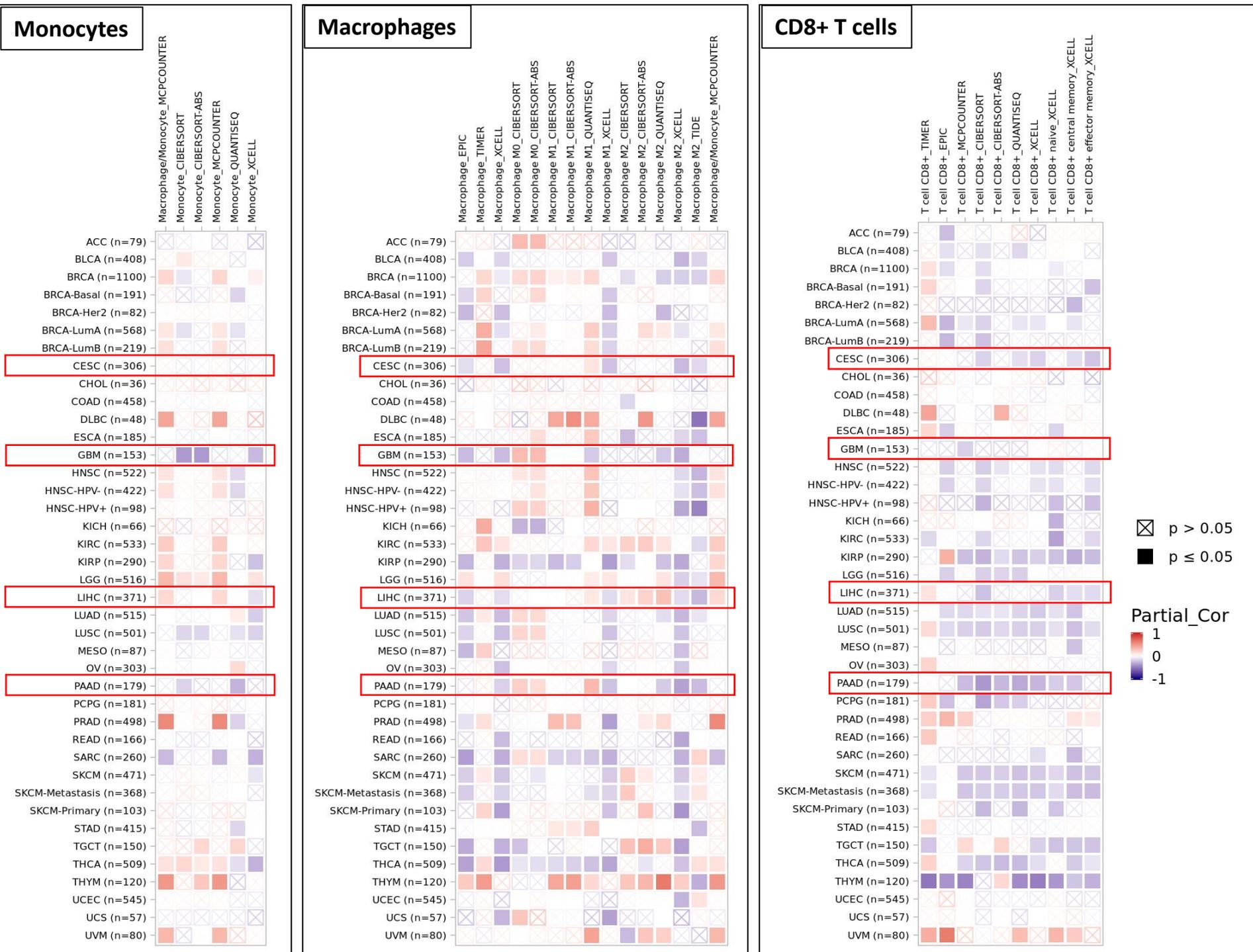


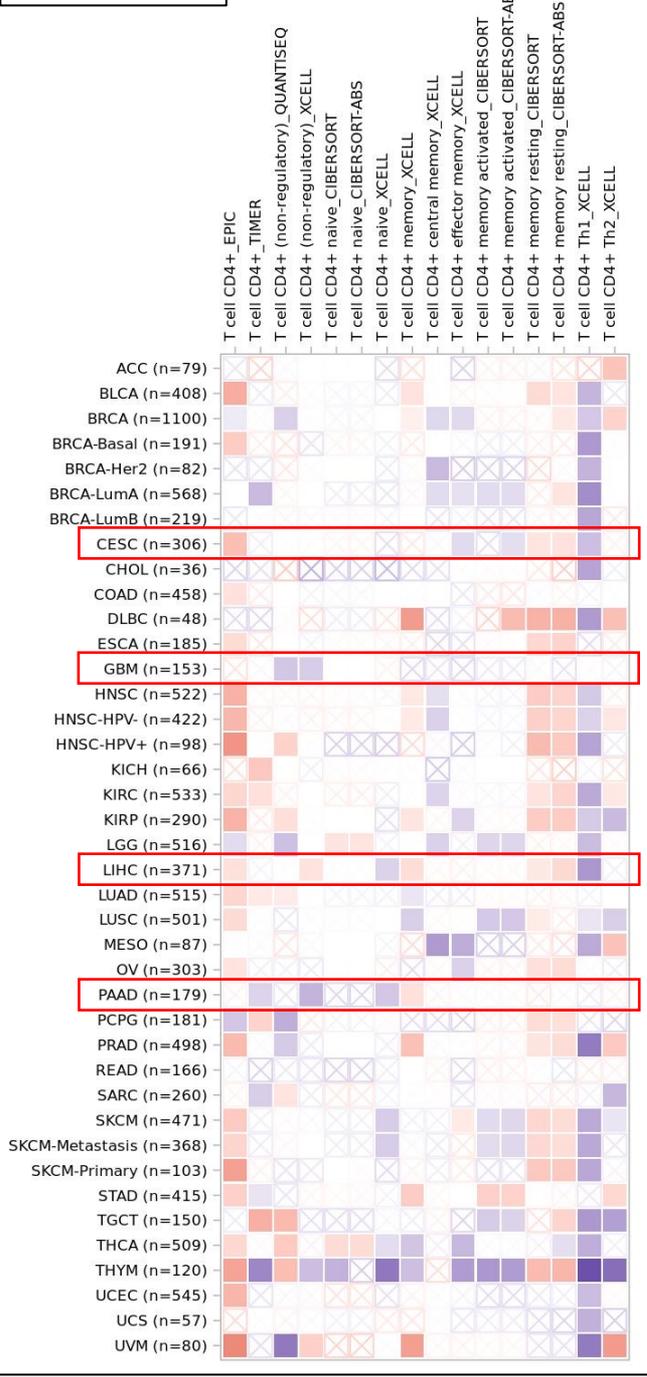
Figure S1(a)



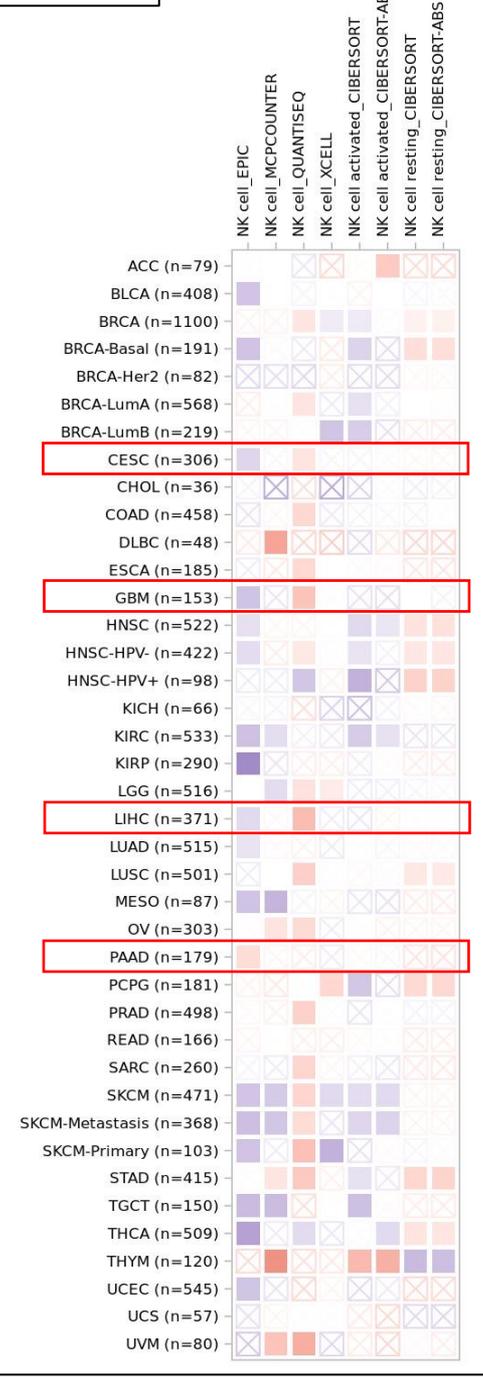
**Figure S1. (a-c)** Heat maps generated by TIMER2.0 depicting the correlation between FAT1 gene expression and infiltration levels of different types of immune cells in cancer cases from TCGA database. CESC (cervical and endocervical cancer), GBM (glioblastoma), LIHC (liver hepatocellular carcinoma) and PAAD (pancreatic adenocarcinoma) have been highlighted in the heat maps using red rectangles. Different algorithms such as xCell, MCP-counter, EPIC, quanTlseq, etc. are applied by TIMER2.0 web server to the expression profiles of TCGA tumors for immune infiltration estimation.

Figure S1(b)

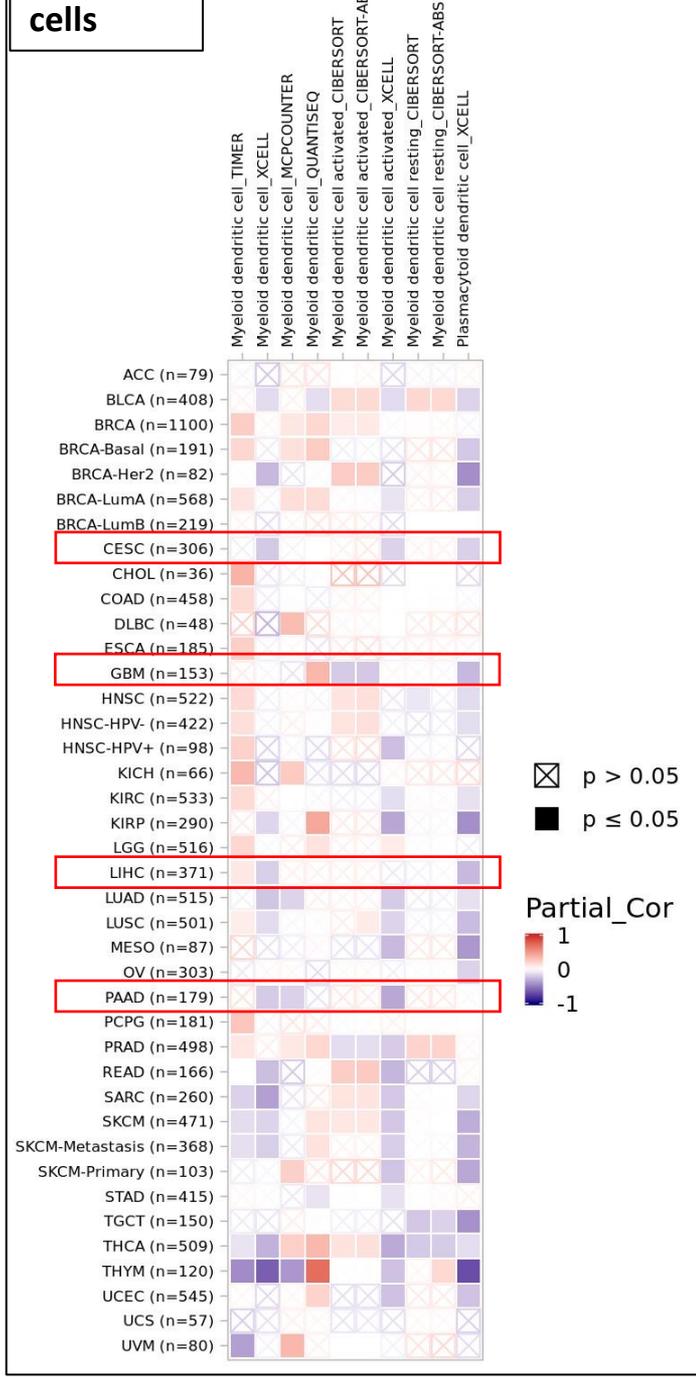
**CD4+ T cells**



**NK cells**



**Dendritic cells**



X  $p > 0.05$   
  $p \leq 0.05$   
 Partial\_Cor  
 1  
 0  
 -1

Figure S1(c)

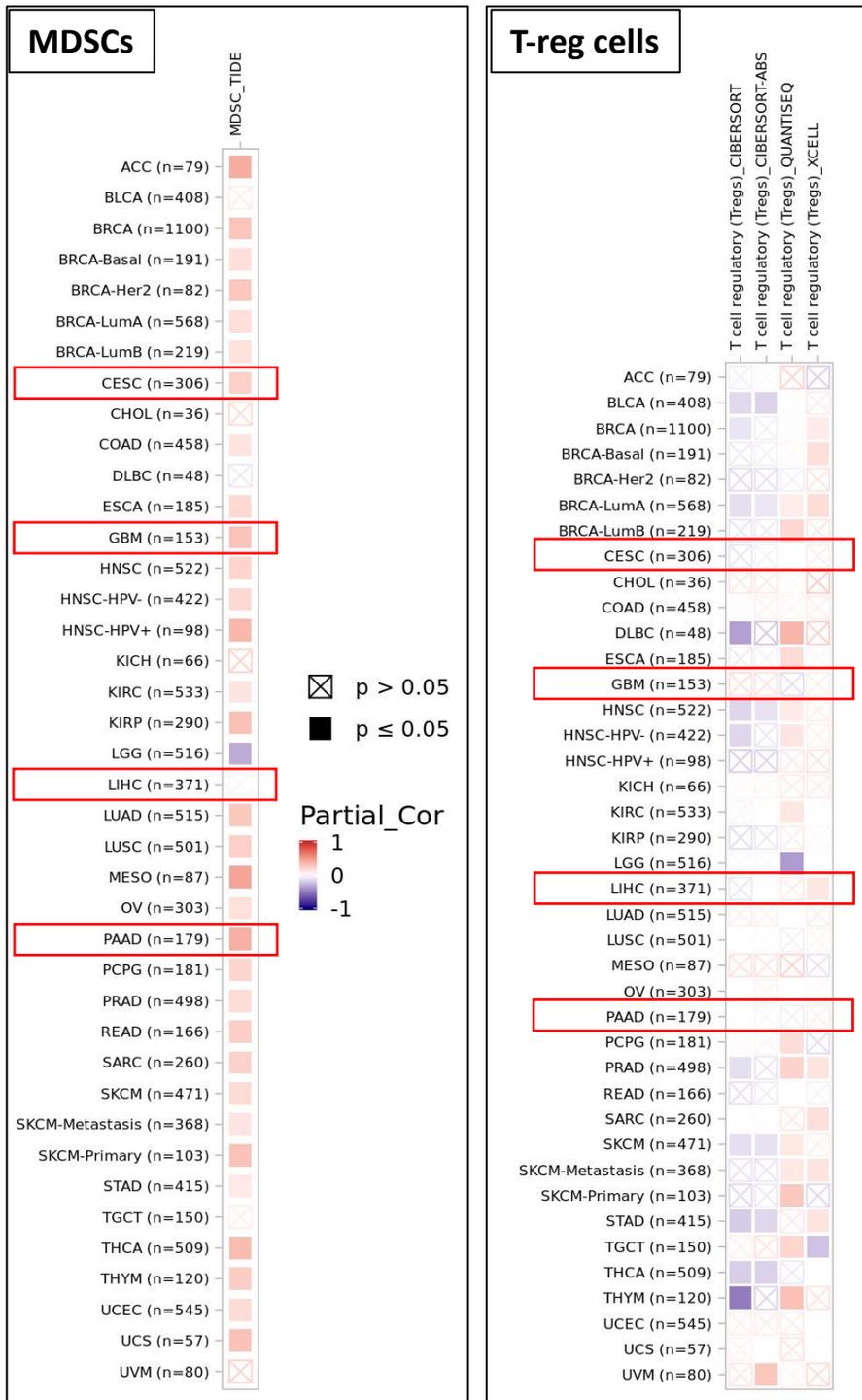
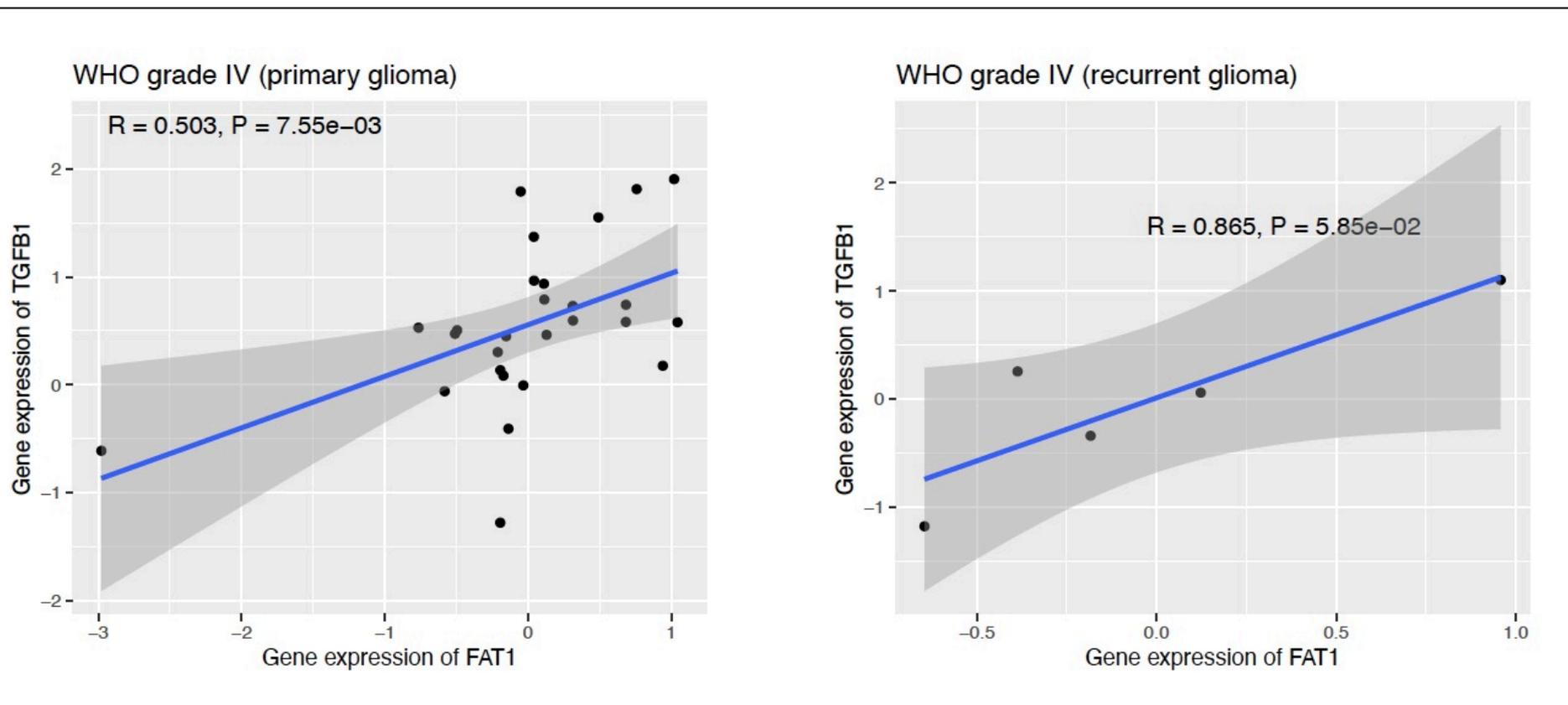
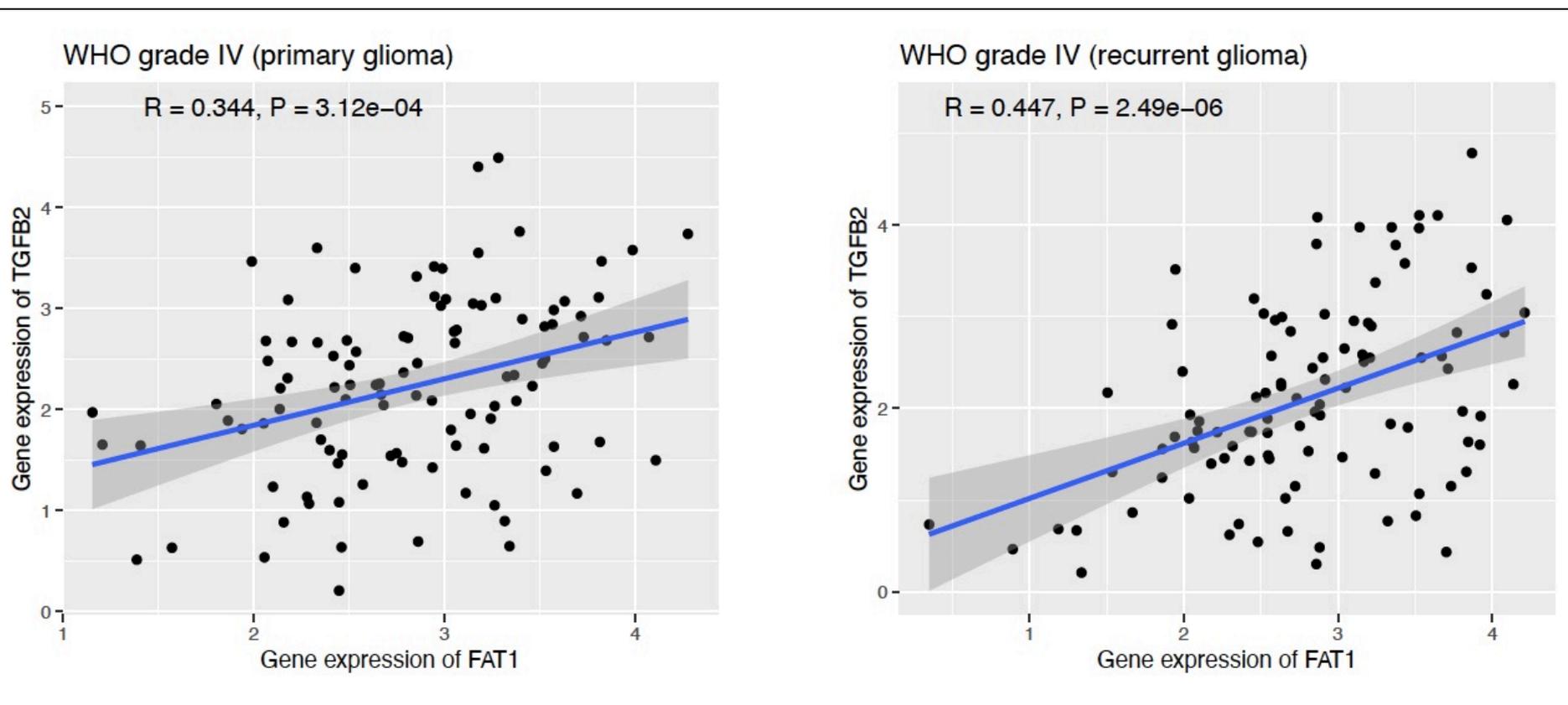


Figure S2

(a)

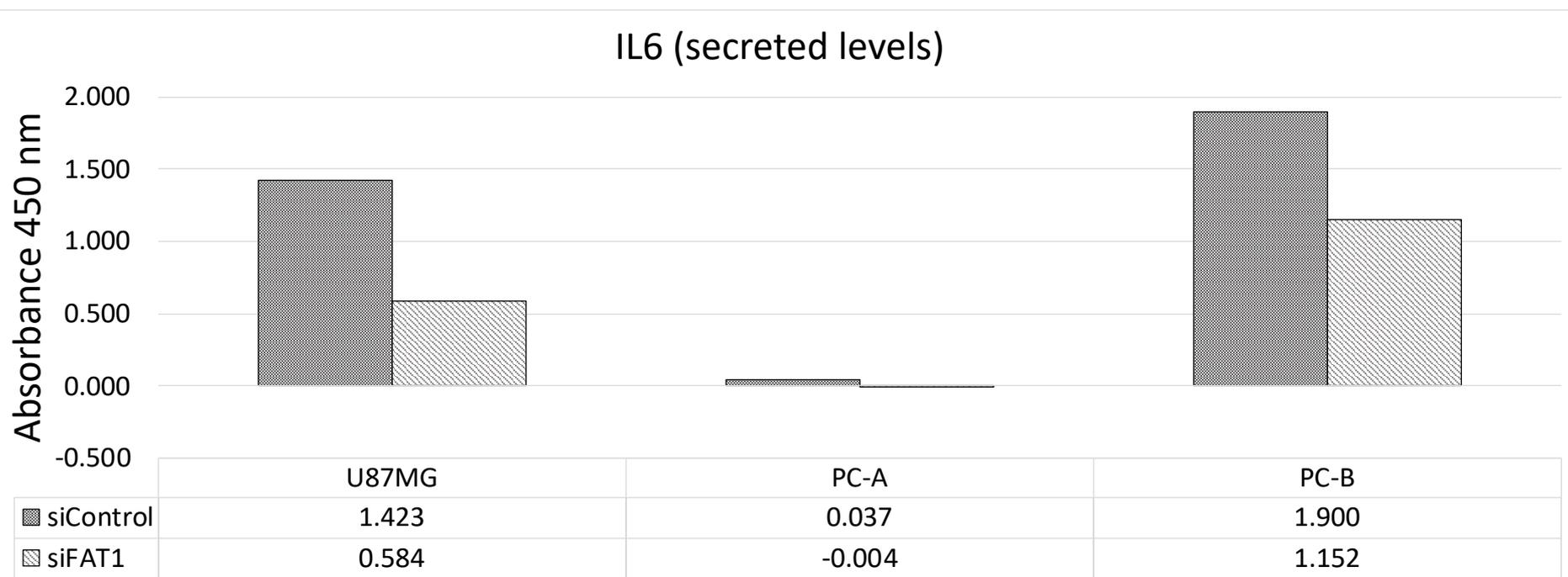


(b)



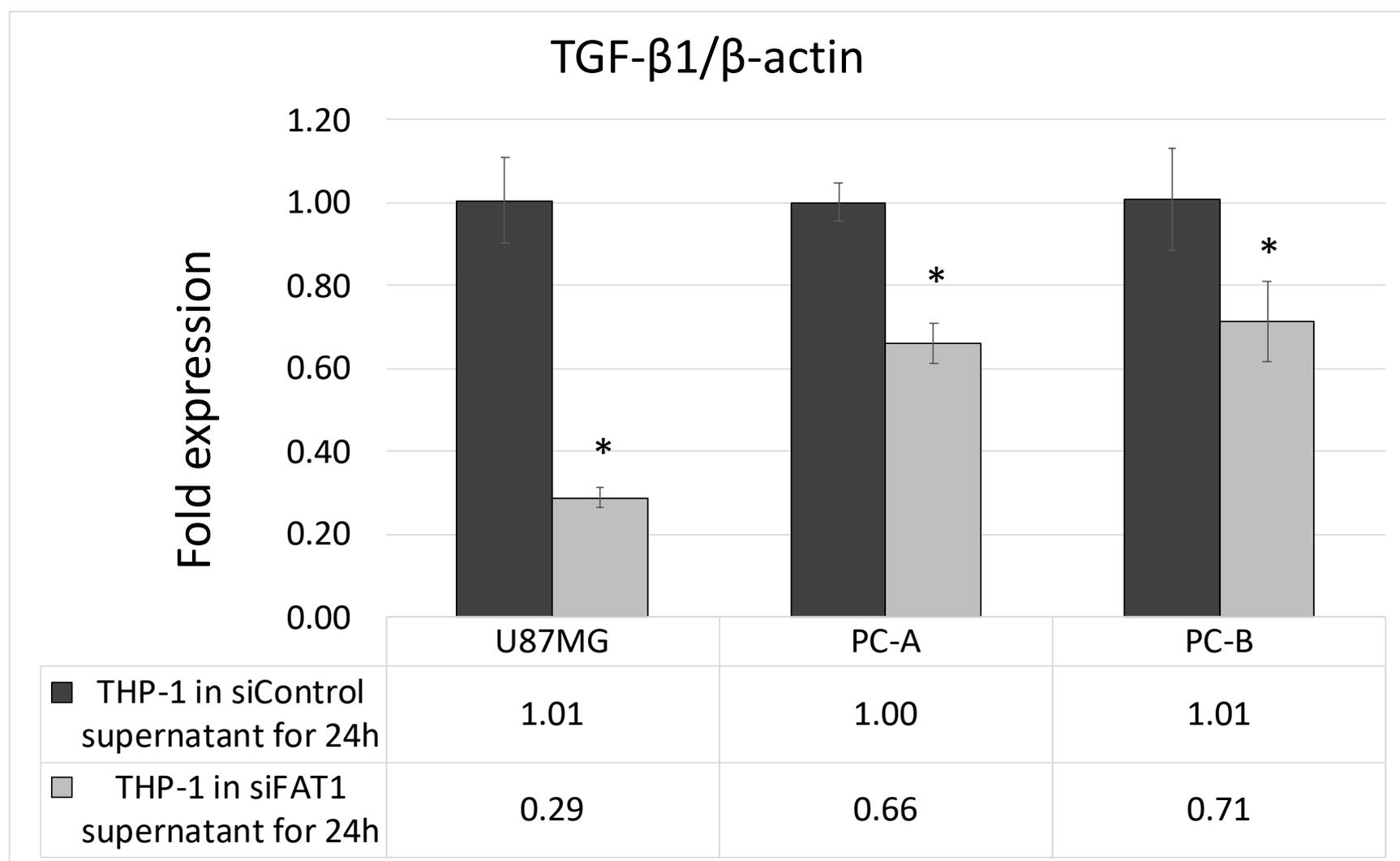
**Figure S2. (a-b)** Scatter plots showing correlation of FAT1 expression with expression of TGF- $\beta$ 1 (mRNA\_array\_301 dataset) and TGF- $\beta$ 2 (mRNAseq\_693 dataset) in primary and recurrent glioma cases belonging to CGGA database.

Figure S3



**Figure S3.** Graph showing optical densities of IL-6 cytokine secreted by siControl cells versus siFAT1 cells in U87MG, PC-A and PC-B culture supernatants depicting modulation of cytokine release by tumor cells upon *FAT1* knockdown.

Figure S4



**Figure S4.** Graph showing mRNA expression of TGF- $\beta$ 1 in THP-1 cells in response to 24-hour incubation in conditioned media from siFAT1/siControl-transfected U87MG, PC-A and PC-B glioma cells as analysed by q-PCR. (\*) indicates p-value  $\leq 0.05$ .