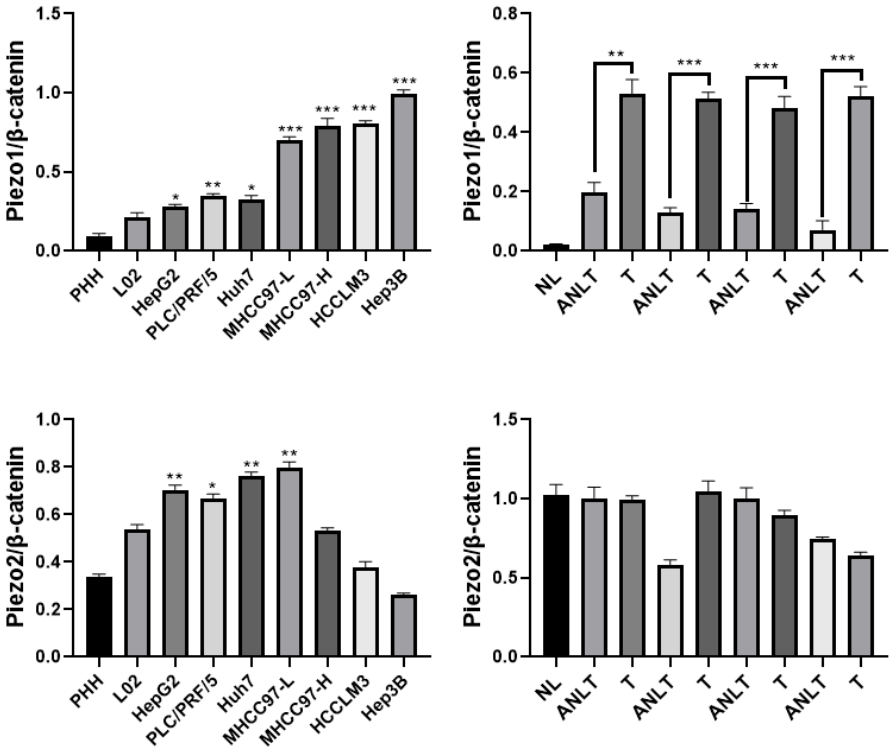
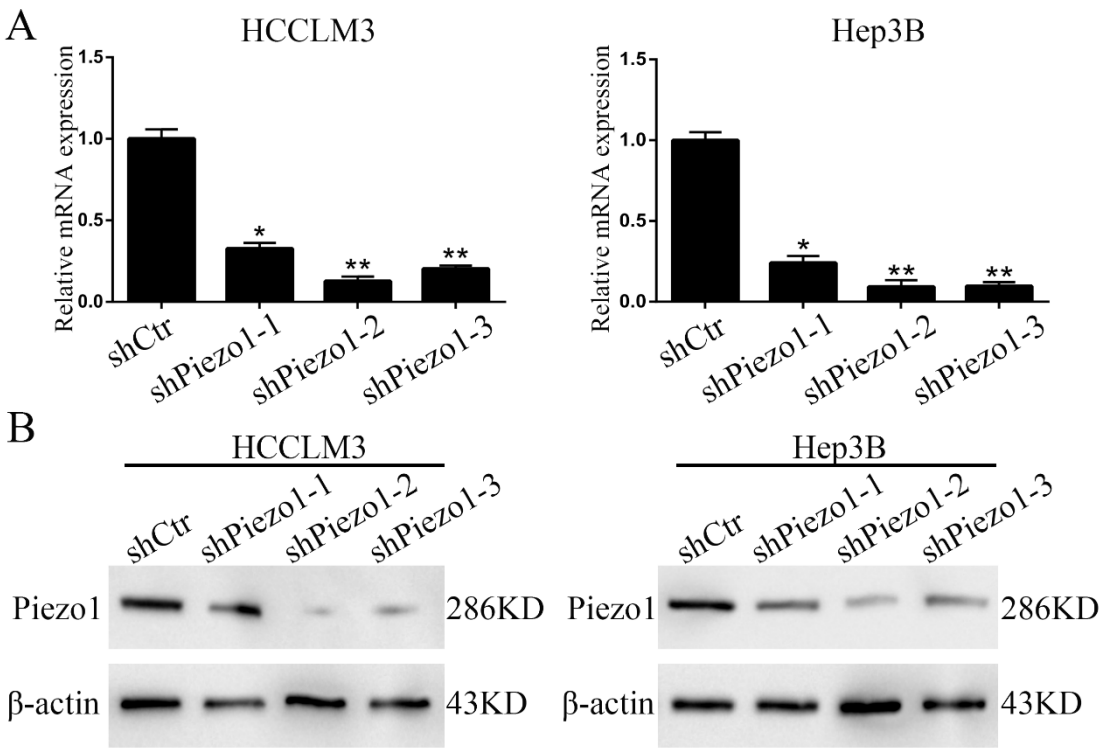
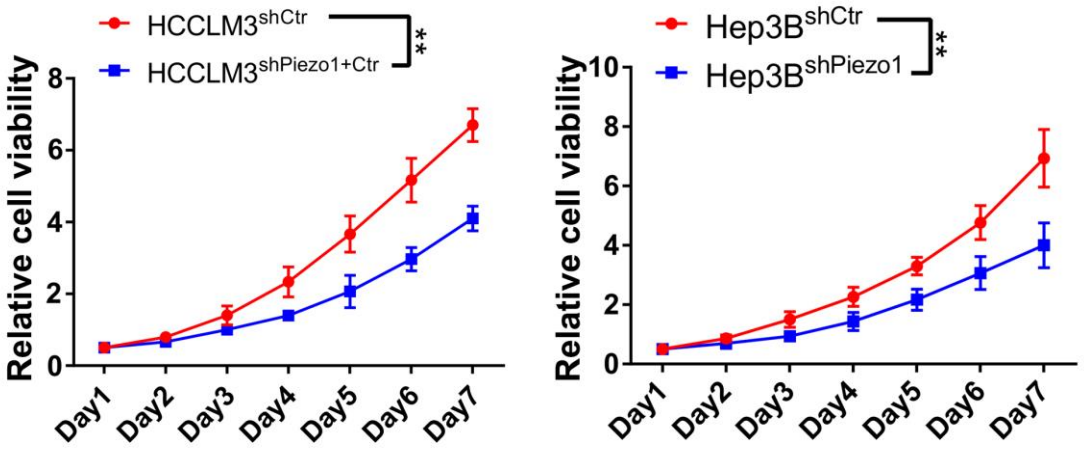
Supplementary Figures



Supplementary Fig. S1 Piezo1 and Piezo2 protein quantification in western blotting shown in Fig1. A (n=3,*P<0.05, **P<0.01,***P<0.001).

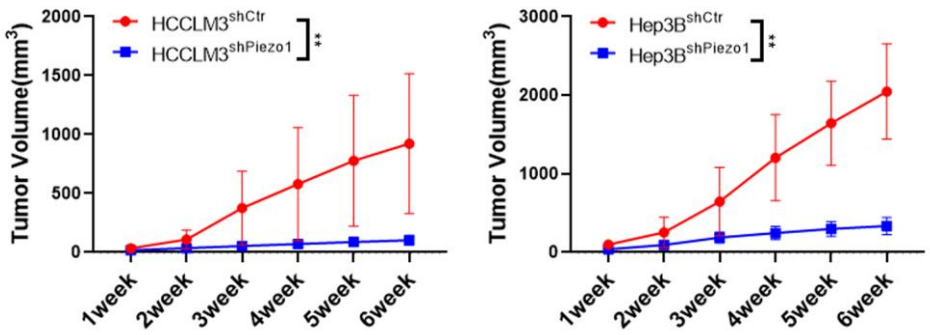


Supplementary Fig. S2 Interfered Piezo1 in HCCLM3 and Hep3B cells. (A-B) After interfered Piezo1 in HCCLM3 and Hep3B cells by three shRNAs separately, the expression level of Piezo1 was identified by real-time PCR(A) and western blotting(B).

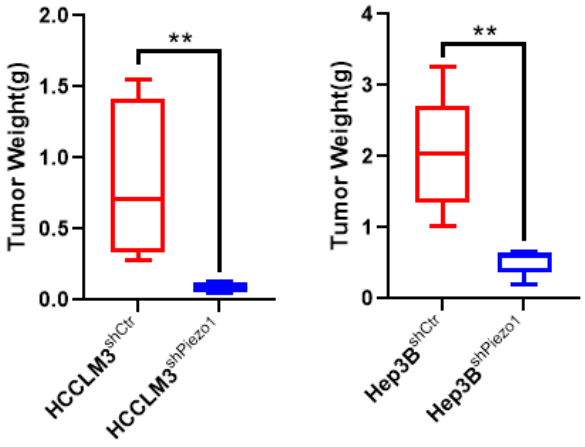


Supplementary Fig. S3 MTT assays was used to detect the proliferation of Hep3B^{shPiezo1}, HCCLM3^{shPiezo1} and the control HCC cells (n=6 for each

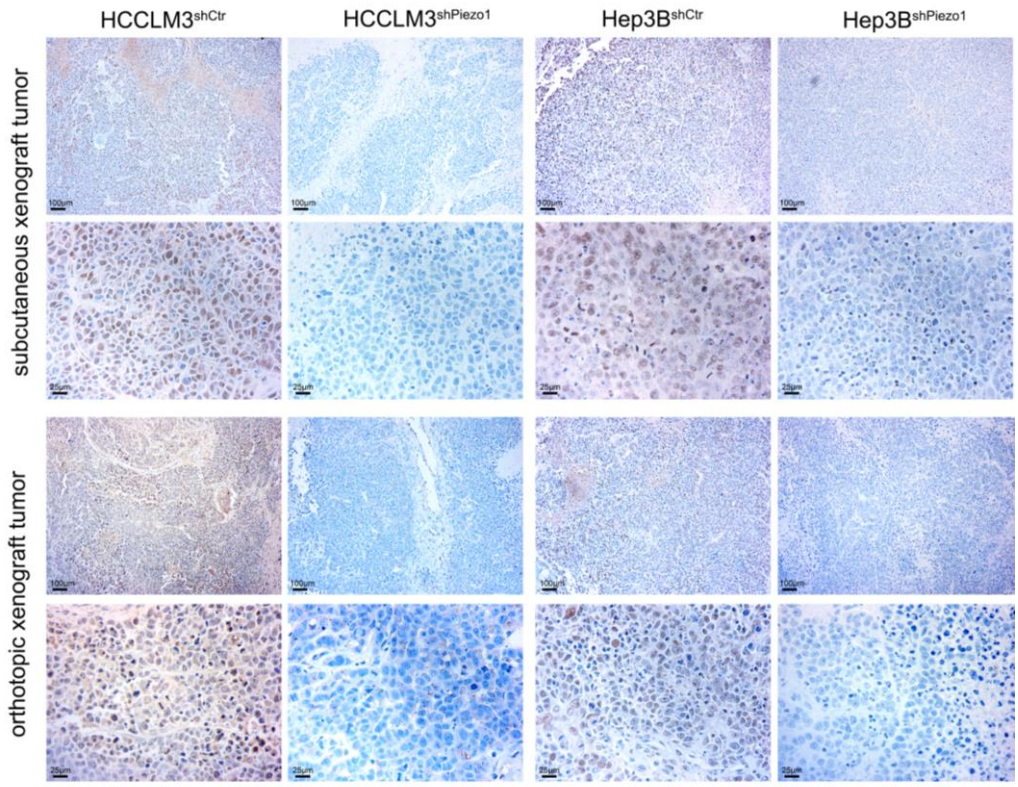
group).



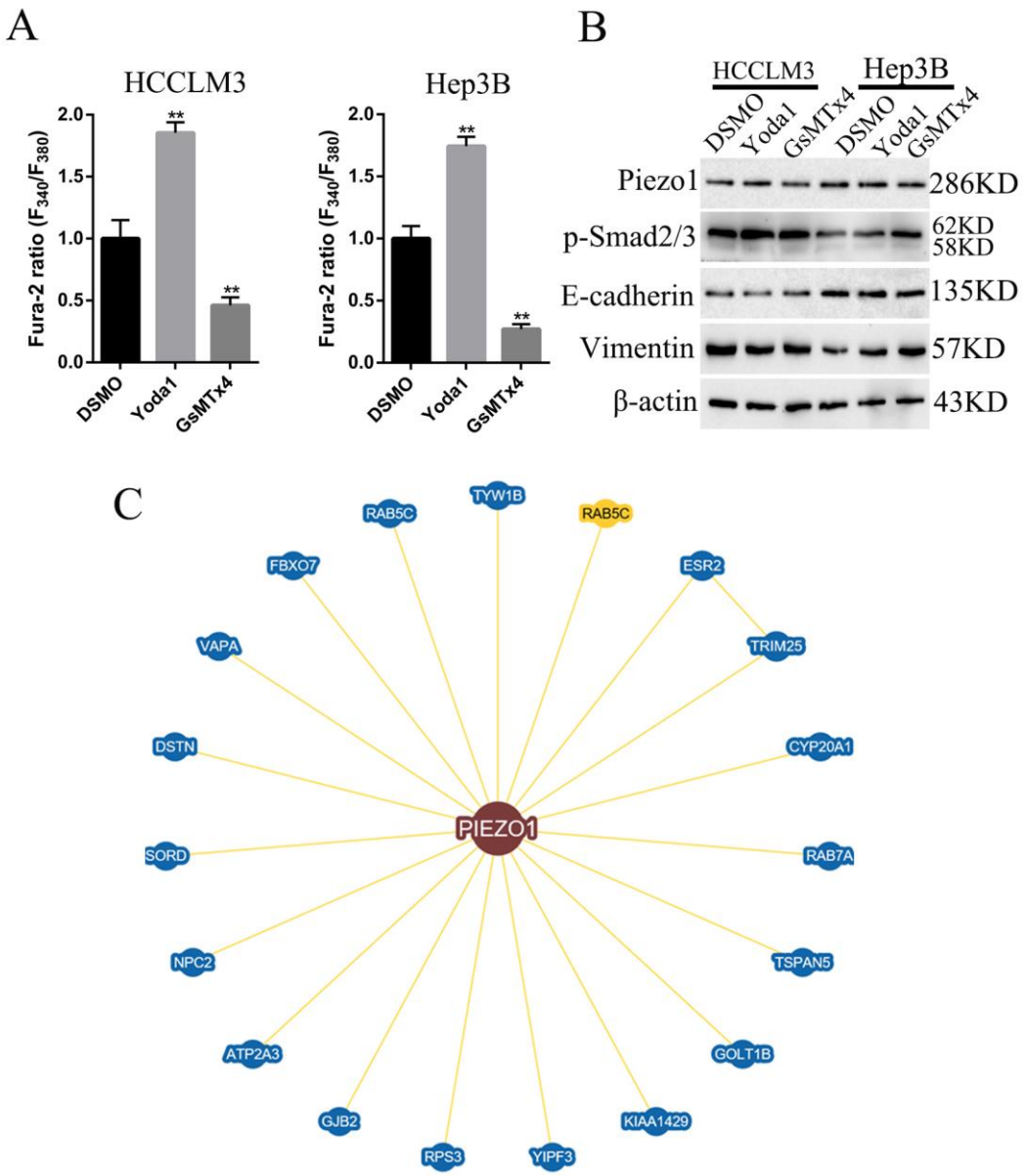
Supplementary Fig. S4 Growth curve of subcutaneous xenograft tumor derived Hep3B^{shPiezo1}, HCCLM3^{shPiezo1} and the control HCC cells (n=6 each group, **P<0.01).



Supplementary Fig. S5 Weight of subcutaneous xenograft tumors derived Hep3B^{shPiezo1}, HCCLM3^{shPiezo1} and the control HCC cells(n=6 each group, **P<0.01)



Supplementary Fig. S6 Ki67 for the subcutaneous xenograft tumors and orthotopic xenograft tumors was detected by IHC.



Supplementary Fig. S7 Ca^{2+} influx was not the dominant factor in Piezo1 activated TGF-β signaling. (A) Measurements of Ca^{2+} concentration after treated HCCLM3 and Hep3B cells with Yoda1(the activator of Piezo1, 20mM) and GsMTx4 (the inhibitor of Piezo1, 2.5μM). (B) Examination of p-Smad2/3 and marker of EMT by Western blot, the Ca^{2+} influx was not the dominant factor in Piezo1 activated TGF-β signaling and EMT. (C) BioGrid 4.4 database indicates that Piezo1 might interact with Rab5c.