Figure S1. Marginal effect of SERPINE1 on cell migration. (A) Relative mRNA expression of SERPINE1 in individual TD clones with the indicative shRNA clone. (B) Representative microscopic images (top) and time dependent cell migration ratio (bottom) of control (NC) and *SERPINE1* KD (KD#2 and KD#4) cells (magnification, x40; scale bar, 200 μm). (C) Relative mRNA expression of SERPINE1 in TD cells with siRNA clone. ****P<0.0001 (D) Enzymatic activity of MMP9 of control (Mock) and *SERPINE1* knockdown (siRNA) were determined via zymography. shNC, negative control shRNA; KD, knockdown; *SERPINE1*, serpin family E member 1; siRNA, small interfering RNA; shRNA, short hairpin RNA.

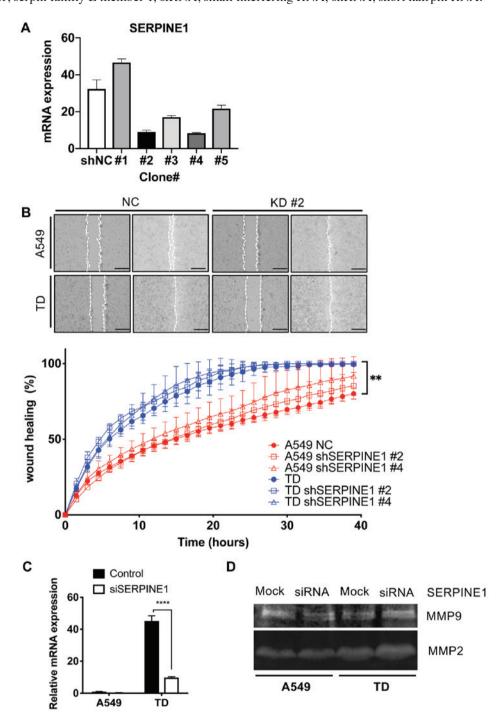


Figure S2. Marginal effect of SERPINE1 on epithelial mesenchymal transition marker status. (A) Immunofluorescence of YAP of A549 or TD cells grown at the indicated cell density (magnification, x100; scale bar, 80 μ m). Cell number of 100% confluence is ~3.0x10⁶. Indicative cell density was obtained via a serial dilution using normal culture media. (B) Immunoblotting for indicative proteins in A549 and TD cells, β -actin for equal protein loading (C) mRNA expression of *CDH1* and *CDH2* in A549 and TD cells at 24 h after 10 μ M Y27632 treatment. CDH, cadherin; YAP, yes-associated protein; TAZ, transcriptional co-activator with PDZ-binding motif; ns, not significant; *SERPINE1*, serpin family E member 1.

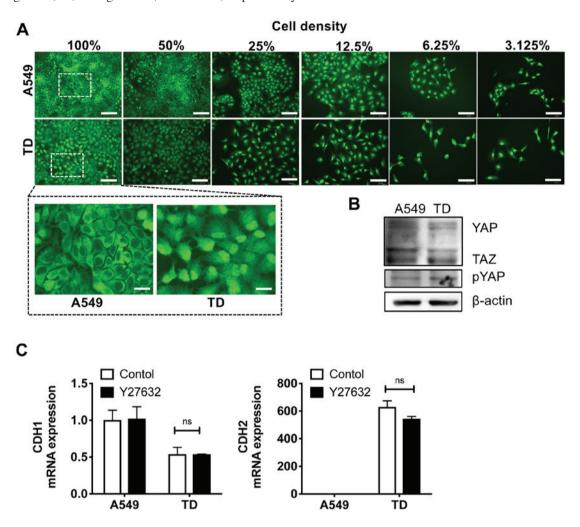


Figure S3. Knockdown of YAP/TAZ in A549 and TD cells. mRNA expression of (A) SMAD4, (B) YAP or (C) TAZ in A549 and TD cells at 24 h after siRNA for control, SMAD4, YAP or TAZ with (right) or without (left) TGF β treatment. *P<0.05, **P<0.01, ***P<0.001, ****P<0.001, ****P<0.0001. -T, without TGF β ; +T, with TGF β , siNC was used in the -/-TFG β experiment. SERPINEI, serpin family E member 1; YAP, yes-associated protein; TAZ, transcriptional co-activator with PDZ-binding motif; siRNA, small interfering RNA.

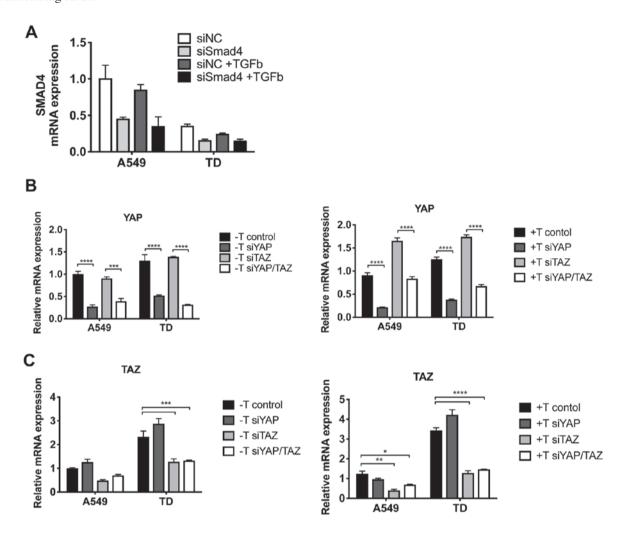


Table SI. List of ontology terms and corresponding genes associated to serpin family E member 1 expression.

Term	Overlap	P-value	Genes
Extracellular matrix organization (GO:0030198)	42/230	3.57x10 ⁻³⁸	ITGB1, SPARC, COL11A1, LAMA4, COL12A1, PDGFB, LAMC2,
			NID2, THBS1, LOXL2, ADAMTS4, HAS1, TIMP2, HAS2, POSTN, VCAM1, LUM, MMP2, FN1, BGN, LAMB1,
			COL1A1, ADAM19, GREM1, MMP14, COL3A1, VCAN, COL1A2,
			COL4A2, LOX, COL5A1, COL4A1, COL6A2, ADAM12, COL5A2,
			ITGA11, COL6A1, MMP19, COL6A3, TGFBI, ITGA5, FBN1
Regulation of cell migration	27/317	$6.34x10^{-16}$	CLIC4, SEMA7A, SERPINE2, PDGFB, STC1, NEXN, LAMC2,
(GO:0030334)			THY1, RND3, THBS1, MYLK, ADGRG3, HAS2, PDGFRB,
			PDGFRA, SPHK1, F2R, LAMB1, SULF1,
			COL1A1, MMP14, NAV3, SNAI1, MYADM, SNAI2, VCL, HBEGF
Collagen fibril organization	11/30	1.81×10^{-14}	COL1A1, GREM1, COL3A1, COL1A2, COL5A1,
(GO:0030199)			LOX, LUM, COL11A1, COL12A1, COL5A2, LOXL2