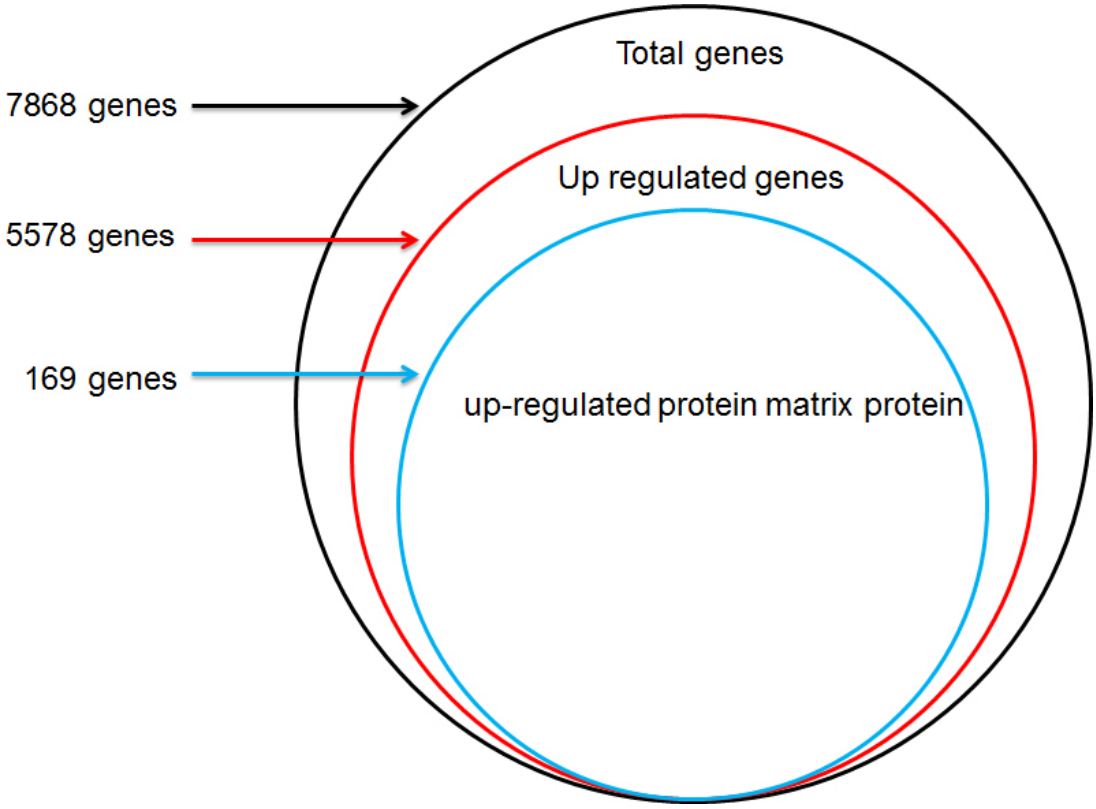
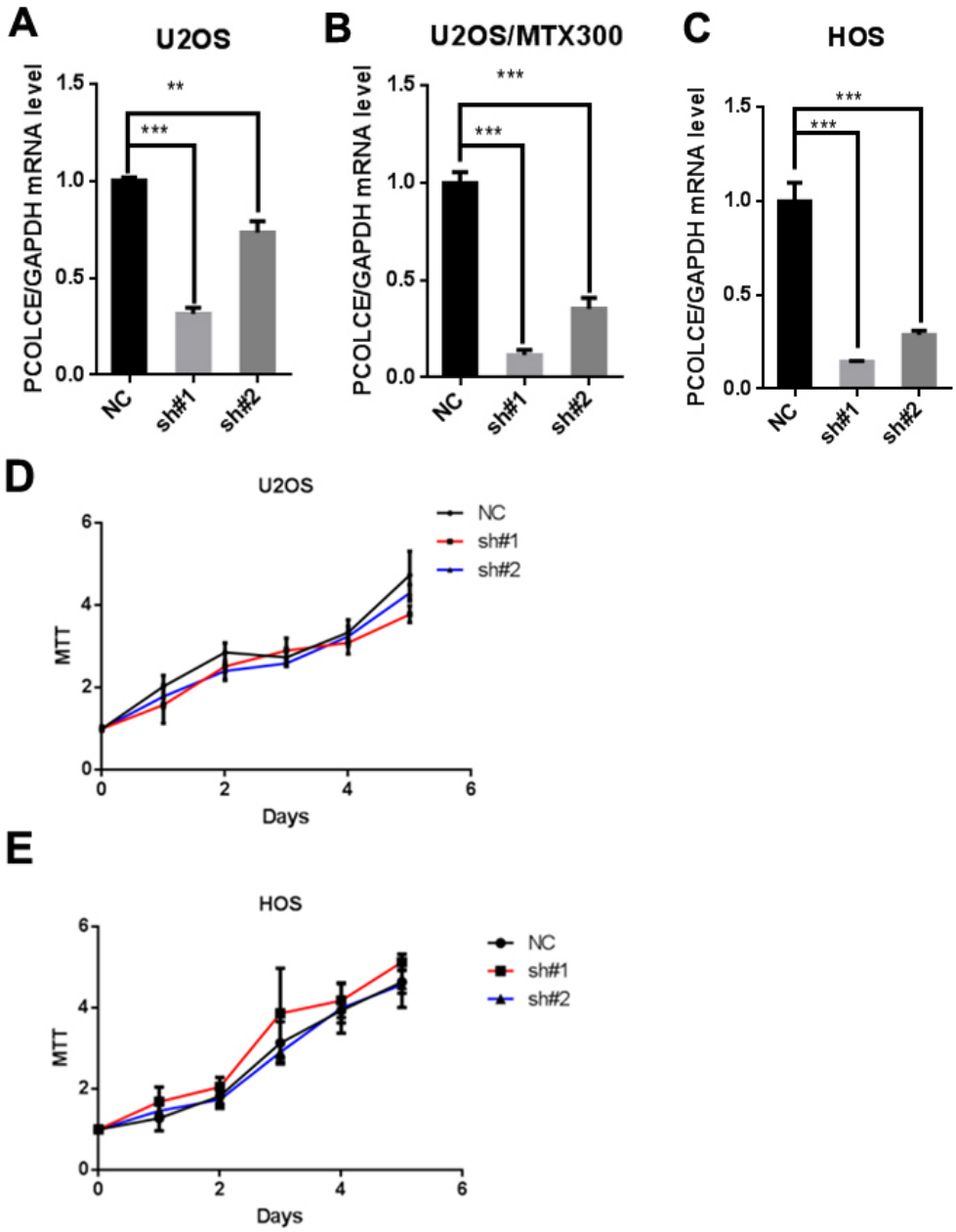
Supplementary Table 1. The correlations between *TWIST1* mRNA levels and *PCOLCE* mRNA levels in 18 different cancer types from the ChIPBase v2.0 database.

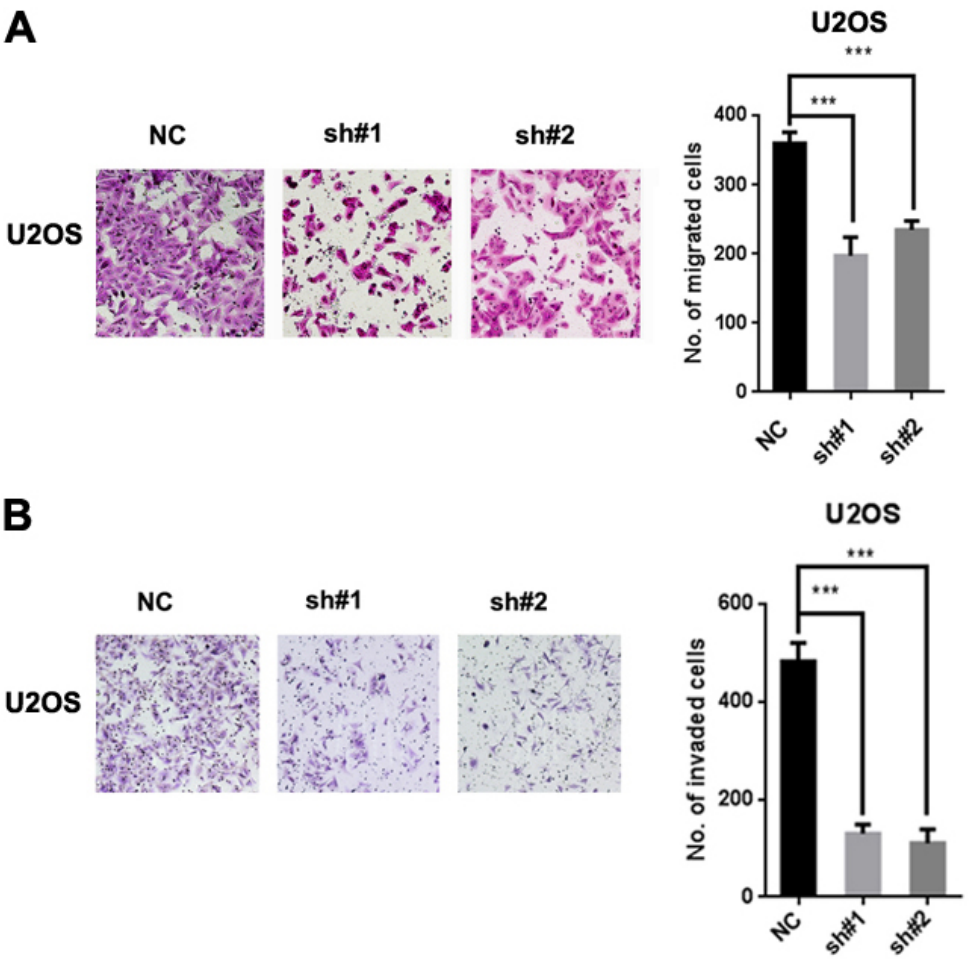
Diseases or Studies	Sample number	Pearson coefficient r	p-value(two tail, t-test)
thyroid carcinoma	571	0.8183	5.56E-139
glioblastoma multiforme	171	0.5292	9.96E-14
sarcoma	264	0.4724	4.46E-16
thymoma	121	0.6806	8.88E-18
uterine corpus endometrioid carcinoma	204	0.5825	6.31E-20
rectum adenocarcinoma	103	0.8425	6.96E-29
esophageal carcinoma	195	0.7032	2.07E-30
lung squamous cell carcinoma	548	0.4806	5.19E-33
skin cutaneous melanoma	470	0.5221	3.15E-34
ovarian serous cystadenocarcinoma	425	0.6148	1.57E-45
bladder urothelial carcinoma	426	0.625	1.53E-47
pancreatic adenocarcinoma	183	0.8456	3.26E-51
stomach adenocarcinoma	450	0.6373	1.19E-52
lung adenocarcinoma	574	0.5846	6.34E-54
colon adenocarcinoma	331	0.7708	2.17E-66
kidney clear cell carcinoma	603	0.6765	6.85E-82
head & neck squamous cell carcinoma	564	0.7383	3.3E-98
breast invasive carcinoma	1212	0.5644	6.6E-103



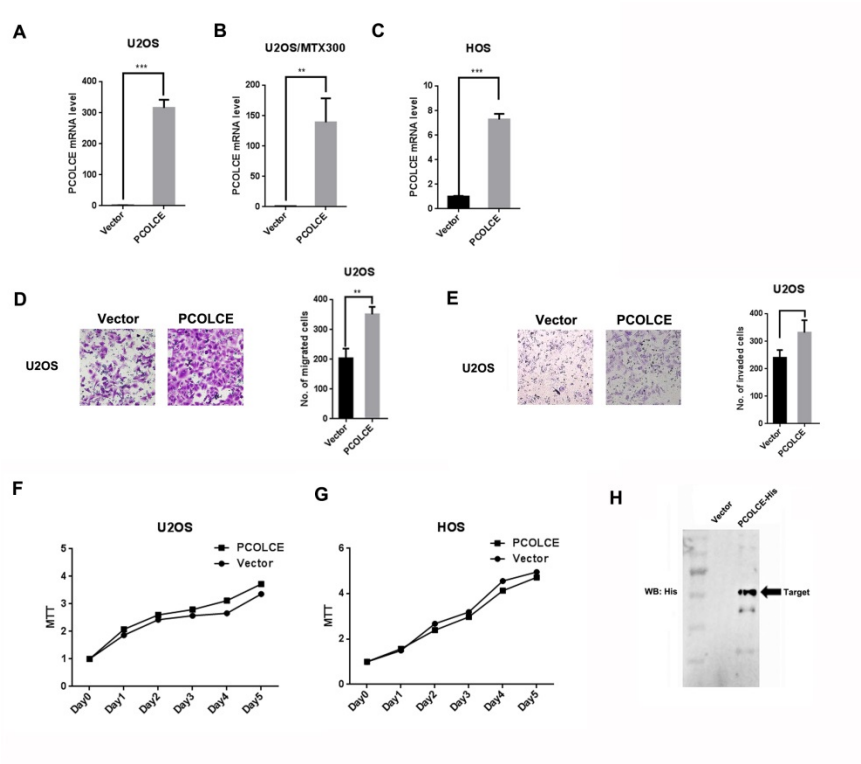
Supplementary Fig. S1. The analyses of RNA-seq data from 4 paracancerous tissues and 16 osteosarcoma tissues. 7868 genes were significantly changed, 5578 genes including 169 genes encoding extracellular matrix proteins were up-regulated, which were listed as Supplementary Table S1 (sheet 1-2).



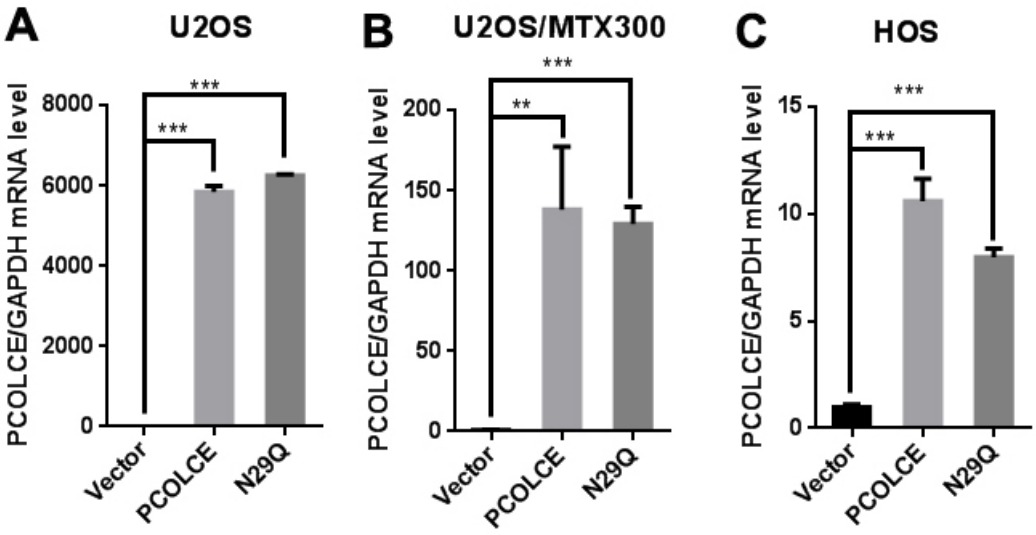
Supplementary Fig. S2. The knockdown efficiencies in shRNA#1 or shRNA#2 against *PCOLCE* in the indicated stable cell lines. The mRNA levels were measured by qRT-PCR in U2OS **(A)**, U2OS/MTX300 **(B)** and HOS **(C)**. The cell viability of U2OS **(D)** and HOS **(E)** was measured as described in "Materials and Methods". The representative images and quantification analyses were shown (mean ± SD , n=3, **p*<0.05, ***p*<0.01, ****p*<0.001)



Supplementary Fig. S3. The Migration **(A)** and invasion **(B)** assays were performed and quantified in U2OS as described in Materials and Methods. The representative images and quantification analyses were shown (mean ± SD , n=3, **p*<0.05, ***p*<0.01, ****p*<0.001).



Supplementary Fig. S4. The over-expression of PCOLCE in the indicated stable cell lines was confirmed at mRNA level by qRT-PCR in U2OS **(A)**, U2OS/MTX300 **(B)** and HOS **(C).** Migration **(D)** and invasion **(E)** assays were performed and quantified in U2OS as described in Materials and Methods. The representative images and quantification analyses were shown (mean ± SD , n=3, **p*<0.05, ***p*<0.01, ****p*<0.001), Cell viability of U2OS **(F)** and HOS **(G)** was measured as described in Materials and Methods. **(H)** The purified PCOLCE-His tag proteins from 293T cells transiently transfected with the indicated plasmids were subjected to Western blotting.



Supplementary Fig. S5. The relative mRNA levels of *PCOLCE* in the indicated cells stably overexpressing wild-type PCOLCE or N29Q-PCOLCE as indicated.