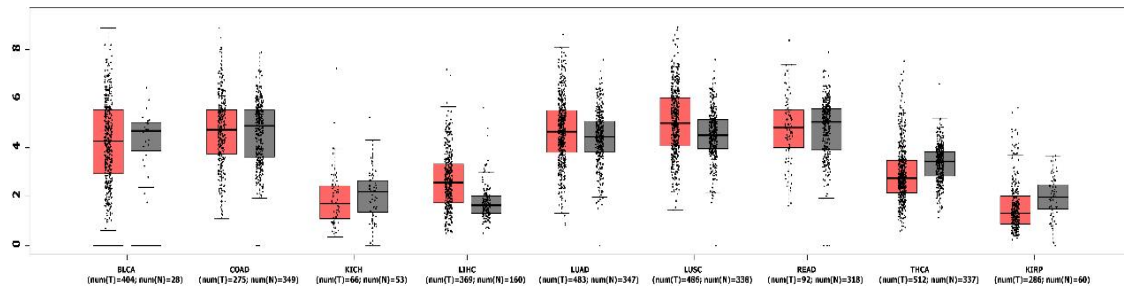
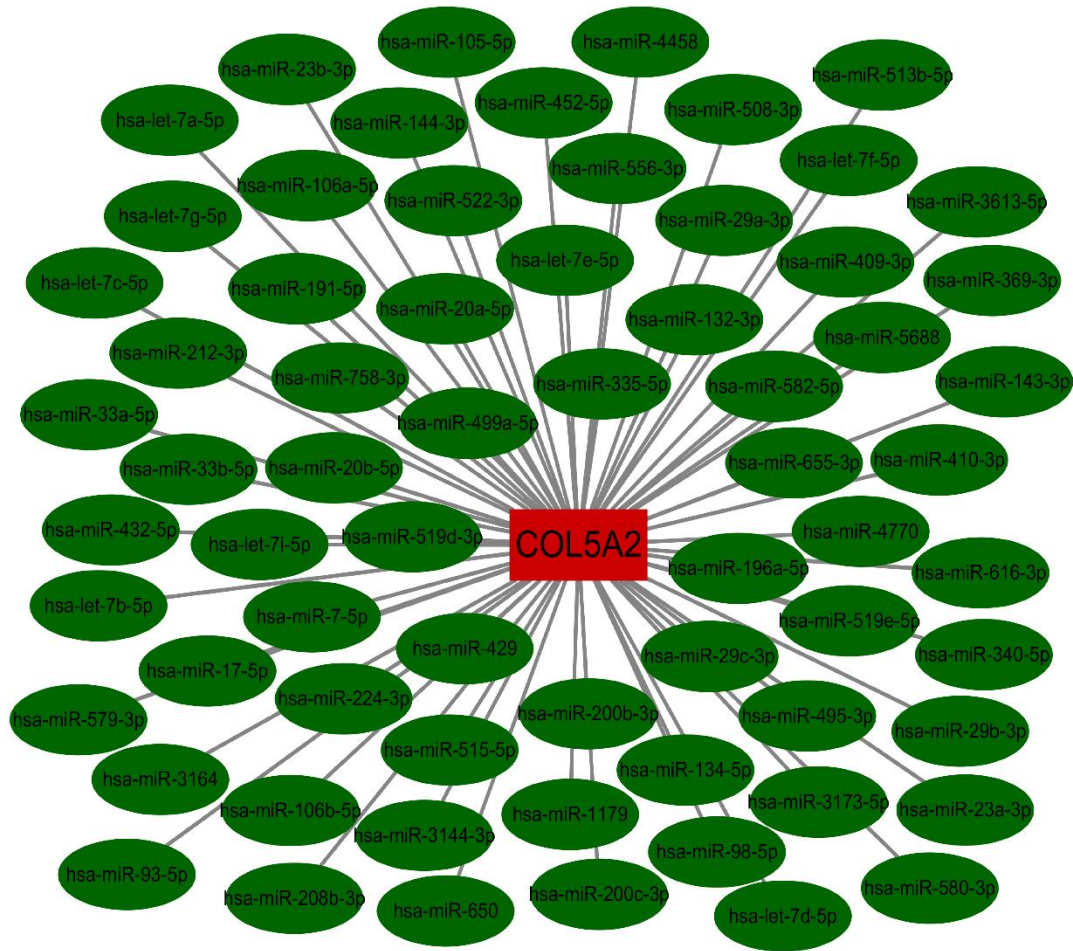


SUPPLEMENTAL FIGURE TITLES AND LEGENDS



Supplementary Figure 1 *COL5A2* expressions in 9 cancers were assessed by GEPIA database, related to Figure 1.



Supplementary Figure 2 predicted upstream miRNAs that could potentially bind to COL5A2 by starBase database, related to Figure 3. Cytoscape to visualize the miRNAs that could potentially bind to COL5A2.

Supplementary Table 1 Basic clinical information of TCGA data

Characteristics	Variable	Patients	Percentage (%)
Age	< 50 years	35	7.90
	≥ 50 years	403	90.97
	Unknow	5	1.13
Gender	Female	158	35.67
	male	285	64.33
Tumor grade	G1	12	2.71
	G2	159	35.89
	G3	263	59.37
	unknow	9	2.03
Pathological stage	I	59	13.32
	II	130	29.35
	III	183	41.31
	IV	44	9.93
	unknow	27	6.09
T	T1	23	5.19
	T2	93	20.99
	T3	198	44.70
	T4	119	26.86
	unknow	10	2.26
N	N0	132	29.80
	N1	119	26.86
	N2	85	19.19
	N3	88	19.86
	NX	17	3.84
	unknow	2	0.45
M	M0	391	88.26
	M1	30	6.77

	MX	22	4.97
Vital status	Alive	272	61.40
	Death	171	38.60

Supplementary Table 2 Gene set enrichment analyses

Gene Set Name	NES	NO	FDR
		M P	q-va
		valu	l
		e	
KEGG_FOCAL_ADHESION	2.65	0.000	0.00
	2		0
KEGG_PATHWAYS_IN_CANCER	2.60	0.000	0.00
	6		0
KEGG_TGF_BETA_SIGNALING_PATHWAY	2.52	0.000	<
	2		0.00
			1
KEGG_MAPK_SIGNALING_PATHWAY	2.49	0.000	<
	8		0.00
			1
KEGG_ECM_RECEPTOR_INTERACTION	2.44	0.000	<
	8		0.00
			1
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRA TION	2.44	0.000	<
	1		0.00
			1
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERAC TION	2.34	0.000	<
	1		0.00
			1
KEGG_WNT_SIGNALING_PATHWAY	2.26	0.000	<
	8		0.00
			1
KEGG_JAK_STAT_SIGNALING_PATHWAY	2.24	0.000	<
	0		0.00

			1
KEGG_MTOR_SIGNALING_PATHWAY	2.14	0.000	0.00
	8		2
