

SUPPLEMENTARY TABLES

Supplementary Table 1. Primer sequence of 6 genes for RT-qPCR.

Genes	Sequence (5'→3')	
	Forward Primer	Reverse Primer
VMP1	GGTAGCTGCAGCCAGTACAA	TGCAACAACAGCAAGGGTTG
LAMP5	CCCCTGATTTTGGGGCTCAT	TACTGGGATCTGTCCCGAGG
ARMC9	CCGGATGCTACCACTTCTCG	AAAATCTTTGCGGGAAGCAGC
CEBPB	TTTGTCCAAACCAACCGCAC	CCCCCAAAGGCTTTGTAACC
POC1A	GTGACAGCCTCTGACGACAA	AGAAAGTTGGGCATGGTGTG
PAOX	CTGCTTCGGGGCTATCAAGG	TCGTGGAGTAAACGTGCCA

Supplementary Table 2. Associations between POC1A mRNA levels and clinicopathological characteristics.

		Number	POC1A		p
			Low	High	
Gender	Female	25	17	8	0.205
	Male	76	61	15	
Age (Years)	<=65	67	51	16	0.709
	>65	34	27	7	
T stage	T1	11	6	5	0.085
	T2	6	4	2	
	T3	34	25	9	
	T4	50	43	7	
N stage	N0	27	21	6	0.001
	N1	9	2	7	
	N2	24	19	5	
	N3	31	36	5	
TNM stage	I	14	8	6	0.142
	II	22	17	5	
	III	65	53	12	
Tumor Location	Upper	37	27	10	0.486
	Middle	14	13	1	
	Lower	30	22	8	
	Diffuse	20	16	4	
Tumor Size (mm)	<50	13	6	7	0.043
	>=50	28	23	5	
Differentiation grade	G1	14	13	1	0.249
	G2	58	42	16	
	G3	29	23	6	

Supplementary Table 3. Associations between POC1A expression and clinicopathological characteristics in immunohistochemistry.

		Number	POC1A		p
			Low	High	
Gender					0.646
	Female	18	16	2	
	Male	73	59	14	
Age (Years)					0.368
	<=65	31	24	7	
	>65	60	51	9	
BMI (kg/m2)					0.646
	<=25	73	59	14	
	>25	18	16	2	
T stage					0.087
	T1	1	0	1	
	T2	10	7	3	
	T3	78	33	4	
	T4	2	35	8	
N stage					0.04
	N0	13	10	3	
	N1	16	14	2	
	N2	28	19	9	
	N3	34	32	2	
M stage					0.545
	M0	87	72	15	
	M1	4	3	1	
TNM stage					0.363
	I	4	3	1	
	II	23	17	6	
	III	60	52	8	
	IV	4	3	1	
Position					0.731
	Upper	31	25	6	
	Middle	17	14	3	
	Lower	36	31	5	
	Diffuse	7	5	2	
Tumor Size (mm)					0.05
	<50	48	36	12	
	>=50	43	39	4	
Differentiation grade					0.777
	Well-moderate	37	31	6	
	Poor-undifferentiation	54	44	10	
Lymphatic or nervous invasion					0.036
	Negative	59	45	14	
	Positive	32	30	2	
Borrmann					0.893
	Borrmann I-II	16	13	3	
	Borrmann III-IV	75	62	13	

Supplementary Table 4. Correlation between POC1A mRNA expression and clinical pathological features in GSE84433.

		Number	POC1A		p
			Low	High	
Gender	Female	115	76	39	0.996
	Male	242	160	82	
Age (Years)	<=65	241	158	83	0.836
	>65	116	78	38	
T stage	T1	11	5	6	0.002
	T2	35	16	19	
	T3	67	39	28	
	T4	244	176	68	
N stage	N0	71	35	36	0.008
	N1	155	107	48	
	N2	99	69	30	
	N3	32	25	7	

Supplementary Table 5. KEGG pathways of co-expression genes of POC1A.

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
hsa04110	Cell cycle	30/253	124/8016	6.54E-19	1.63E-16	1.45E-16	30
hsa03030	DNA replication	14/253	36/8016	1.39E-12	1.73E-10	1.54E-10	14
hsa04114	Oocyte meiosis	20/253	128/8016	2.59E-09	2.15E-07	1.91E-07	20
hsa04914	Progesterone-mediated oocyte maturation	17/253	99/8016	9.75E-09	6.07E-07	5.39E-07	17
hsa04022	cGMP-PKG signaling pathway	18/253	167/8016	4.83E-06	0.00024056	0.00021356	18
hsa03460	Fanconi anemia pathway	9/253	54/8016	4.14E-05	0.00171614	0.00152353	9
hsa05166	Human T-cell leukemia virus 1 infection	18/253	219/8016	0.00018402	0.00654571	0.00581103	18
hsa04115	p53 signaling pathway	9/253	72/8016	0.00040351	0.01175142	0.01043245	9
hsa04540	Gap junction	10/253	88/8016	0.00042475	0.01175142	0.01043245	10
hsa04218	Cellular senescence	14/253	160/8016	0.00051219	0.01275354	0.01132211	14
hsa03430	Mismatch repair	5/253	23/8016	0.00063523	0.01437923	0.01276532	5
hsa04270	Vascular smooth muscle contraction	12/253	132/8016	0.00091174	0.01891871	0.0167953	12
hsa04970	Salivary secretion	9/253	90/8016	0.00204635	0.03919542	0.03479619	9
hsa04730	Long-term depression	7/253	60/8016	0.00265927	0.04729696	0.04198842	7