

Table SI. Expression of differentiation antagonizing non-protein coding RNA between cancer and normal tissues in different cancer types

Cancer type	Patient samples, n	P-value
Bladder urothelial carcinoma	T=411; N=19	<0.05
Breast invasive carcinoma	T=1,104; N=113	<0.0001
Cervical squamous cell carcinoma and endocervical adenocarcinoma	T=306; N=3	ns
Cholangiocarcinoma	T=36; N=9	<0.0001
Colon adenocarcinoma	T=471; N=41	<0.0001
Esophageal carcinoma	T=162; N=11	ns
Liver hepatocellular carcinoma	T=374; N=50	<0.0001
Lung adenocarcinoma	T=526; N=59	<0.0001
Lung squamous cell carcinoma	T=501; N=49	<0.0001
Pancreatic adenocarcinoma	T=178; N=4	ns
Prostate adenocarcinoma	T=499; N=52	<0.0001
Rectum adenocarcinoma	T=167; N=10	<0.05
Skin cutaneous melanoma	T=471; N=1	^a
Stomach adenocarcinoma	T=375; N=32	ns
Thymoma	T=119; N=2	ns
Uterine corpus endometrial carcinoma	T=548; N=35	<0.0001
Pan-cancer	T=9,807; N=727	<0.0001

^aOnly 1 normal sample was available for statistical analysis.

Table SII. Demographic features of the patients.

Cancer subtype	Age, years	T	N	M	TNM	ER	PR	HER2	Ki-67
TNBC	71	3	2	0	IIIA	-	-	-	90
TNBC	63	2	2	0	IIIA	-	-	-	60
HER2	45	2	0	0	IIIA	-	-	3+	9
Luminal	66	2	2	0	IIIA	+	+	-	18
TNBC	58	1	3	0	IIIC	-	-	-	80

TNBC, triple-negative breast cancer; HER2, human epidermal growth factor receptor 2; T, tumor stage; N, lymph node stage; M; metastasis stage; ER, estrogen receptor; PR, progesterone receptor; +, positive; -, negative.

Table SIII. Methylation of the differentiation antagonizing non-protein coding RNA locus between cancer and normal tissues in different cancer types

Cancer type	Patient samples, n	P-value
A, cg12634276		
BLCA	T=416; N=21	<0.0001
CHOL	T=36; N=9	<0.0001
COAD	T=309; N=38	<0.001
ESCA	T=186; N=16	<0.0001
LUAD	T=471; N=32	<0.0001
LUSC	T=370; N=42	<0.0001
PAAD	T=185; N=10	<0.05
PRAD	T=503; N=50	<0.0001
READ	T=99; N=7	<0.0001
STAD	T=395; N=2	<0.001
UCEC	T=436; N=46	<0.0001
HNSC	T=530; N=50	<0.05
KIRC	T=323; N=16	<0.05
KIRP	T=276; N=45	<0.0001
B, cg02016130		
CHOL	T=36; N=9	<0.01
ESCA	T=186; N=16	<0.05
LUAD	T=471; N=32	<0.0001
LUSC	T=370; N=42	<0.0001
PRAD	T=503; N=50	<0.0001
READ	T=99; N=7	<0.0001
UCEC	T=436; N=46	<0.001
HNSC	T=530; N=50	<0.0001
C, cg23387220		
Cancer type	Patient samples, n	P-value
BLCA	T=416; N=21	<0.0001
PRAD	T=503; N=50	<0.01
READ	T=99; N=7	<0.0001
D, cg07005843		
Cancer type	Patient samples, n	P-value
BRCA	T=794; N=96	<0.05
BLCA	T=416; N=21	<0.05
PRAD	T=503; N=50	<0.0001
HNSC	T=530; N=50	<0.01
E, cg06634961		
BRCA	T=793; N=96	<0.0001
BLCA	T=416; N=21	<0.001
LIHC	T=380; N=50	<0.0001
LUAD	T=471; N=32	<0.05
LUSC	T=370; N=42	<0.0001
PAAD	T=185; N=10	<0.01
PRAD	T=503; N=50	<0.0001
F, cg14966236		
BRCA	T=794; N=96	Ns
BLCA	T=416; N=21	<0.0001
COAD	T=309; N=38	<0.01
ESCA	T=186; N=16	<0.05
LIHC	T=380; N=50	<0.0001
LUAD	T=471; N=32	<0.01
LUSC	T=370; N=42	<0.0001
PAAD	T=185; N=10	<0.05
PRAD	T=503; N=50	<0.0001
READ	T=99; N=7	<0.05
HNSC	T=530; N=50	<0.0001

KIRC	T=323; N=160	<0.05
KIRP	T=276; N=45	<0.0001

T, tumor tissues; N, normal tissues; BLCA, bladder urothelial carcinoma; BRCA, breast invasive carcinoma; CESC, cervical squamous cell carcinoma and endocervical adenocarcinoma; CHOL, cholangiocarcinoma; COAD, colon adenocarcinoma; ESCA, esophageal carcinoma; LIHC, liver hepatocellular carcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; PAAD, pancreatic adenocarcinoma; PRAD, prostate adenocarcinoma; READ, rectum adenocarcinoma; SKCM, skin cutaneous melanoma; STAD, stomach adenocarcinoma; THYM, thymoma; UCEC, uterine corpus endometrial carcinoma; HNSC, head and neck squamous cell carcinoma; KIRC, kidney renal clear cell carcinoma; KIRP, kidney renal papillary cell carcinoma.

Table SIV. Methylation of differentiation antagonizing non-protein coding RNA locus between cancer and normal tissues in pan-cancer.

CG site	Patient samples, n	P-value
cg12634276	T=8,990; N=746	<0.0001
cg06634961	T=8,989; N=746	<0.0001
cg14966236	T=8,986; N=746	<0.0001

T, tumor tissues; N, normal tissues.