

Supplementary Table S1. Fold change and p value for AKAP12

Gene symbol	logFC	P-value
ONECUT1	12.71223	5.49E-17
TERT	13.03691	1.15E-20
C11orf86	13.29445	1.98E-16
LHFPL5	13.32436	8.42E-18
CST4	13.63425	3.02E-19
DMBX1	13.93465	2.45E-19
DLL3	14.11936	5.72E-27
PITX2	14.29935	2.59E-20
ARSH	14.40587	1.08E-25
AKAP12	16.27319	1.97E-34
MOGAT1	-13.30962878	1.28E-24
CYP1A2	-13.26869722	4.69E-21
LY6G6F	-13.02899273	1.24E-21
ADCY8	-12.8506146	1.85E-18
KISS1R	-12.5192951	3.83E-21
ITLN2	-12.36028491	1.09E-18
CELA2B	-12.22593814	4.35E-16
HELT	-12.17242195	3.57E-17
CHRM2	-12.13483173	1.51E-18
OTC	-12.09905464	5.55E-19

Supplementary Table SII. Selected miRs from miRanda and TargetScan

Score	hsa-miR-107	hsa-miR-613	hsa-miR-206	hsa-miR-338-3p
mirSVR score	-0.2484	-0.4849	-0.4917	-0.8009
PhastCons score	0.5604	0.5675	0.5675	0.5673
Context++ score percentile	90	92	91	94

MirSVR score and PhastCons score were obtained from miRanda. MirSVR revealed thermodynamic stability, and a lower score indicated a stronger combination of miRNA-mRNA. PhastCons revealed conservatism among different species, and a higher score indicated better conservatism. The context++ score percentile was obtained from TargetScan, and the higher the score, the greater the conservation and the greater the mRNA destabilization expected.

Supplementary Table SIII. Average immunochemical staining positive score

Number	Adjacent	Tumor
1	0.64	1.91
2	0.58	1.84
3	0.72	1.23
4	0.59	1.57
5	0.66	1.83
6	0.56	1.66
7	0.57	1.73
8	0.61	1.83
9	0.59	2.08
10	0.59	2.00
11	0.53	2.17
12	0.60	1.93
13	0.65	2.00
14	0.51	2.20
15	0.59	1.96
16	0.65	1.93
17	0.64	2.09
18	0.61	1.55
19	0.55	1.70
20	0.54	1.58