



Correction: CpG island hypermethylation-associated silencing of non-coding RNAs transcribed from ultraconserved regions in human cancer

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Correction to: *Oncogene*; <https://doi.org/10.1038/onc.2010.361>; published online 30 August 2010

In the original article the authors have noted that the wrong image was used to illustrate the Uc.346 + Lu1-Lu2-Lu3 subpanel of Figure 5a. The correct image is now provided as Figure 1 in this article. This change does not affect the legend of the figure, the results, or conclusions reported in the manuscript. The authors apologize for the error, and regret any inconvenience this may have caused.

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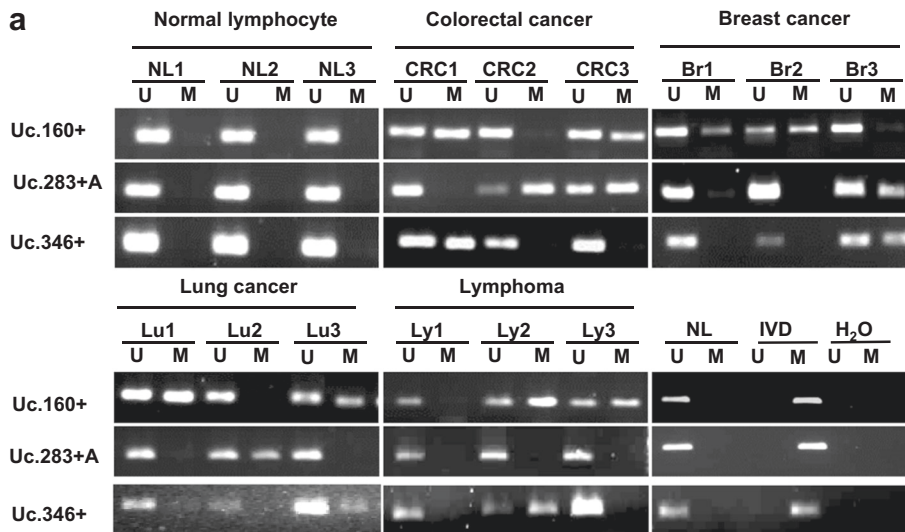
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b

Tumor type	Uc.160+	Uc.283+A	Uc.346+
Colon	60/83 (72.29%)	54/82 (65.85%)	38/81 (46.91%)
Breast	20/30 (66.67%)	14/28 (50%)	14/29 (48.3%)
Lung	23/42 (54.76%)	15/27 (55.56%)	15/41 (36%)
Melanoma	17/25 (68%)	42/53 (79.25%)	3/48 (6.25%)
Leukemia	12/64 (18.75%)	6/35 (17%)	6/35 (17%)
Lymphoma	6/9 (66.67%)	0/8 (0%)	2/11 (18.2%)
Normal Tissues			
Normal *	0/25	0/25	0/25
CRC			
Adenoma	9/19 (47.37%)	8/18 (44.44%)	5/17 (29.41%)

* 3 Normal lymphocyte; 5 normal colon, 2 normal breast and 15 normal lung were analyzed.

c

Uc.160+	Metastatic	Non metastatic
Methylated cases	30 of 42 (71.43%)	30 of 55 (54.54%)
P (Fisher's test)	0.009322377	
Uc.283+A	Metastatic	Non metastatic
Methylated cases	22 of 31 (70.97%)	49 of 77 (63.63%)
P (Fisher's test)	1.366E-07	
Uc.346+	Metastatic	Non metastatic
Methylated cases	18 of 41 (43.90%)	14 of 77 (18.18%)
P (Fisher's test)	2.582E-07	

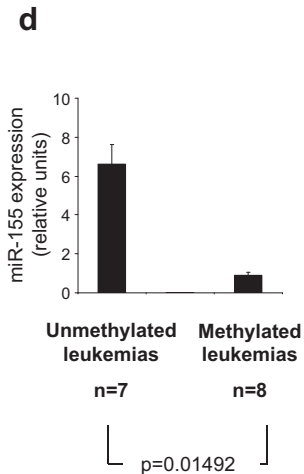


Fig. 1