

Supplementary Table A. Results from gene-specific methylation analyses.

Case	Mean gene specific promoter methylation (%)						
no.	APC	CDH1	DAPK1	DCR2	PTEN	RARB	TP73
<i>Malignant tumors</i>							
1	0.7	10.7	0.7	66.6	0.5	26.5	1.3
2	0.4	25.0	0.3	62.9	0.2	29.5	0.6
3	0.5	6.0	1.2	61.9	0.3	2.3	0.3
4	0.6	4.8	0.5	40.0	0.4	14.5	0.7
5	0.0	7.4	0.3	48.9	0.6	n/a	0.9
6	0.4	4.4	0.2	30.4	0.7	1.3	1.0
7	0.7	4.8	0.3	21.7	0.4	1.5	0.8
8	0.0	2.1	0.1	2.2	0.7	1.0	0.0
9	0.0	n/a	0.0	6.2	0.6	0.9	0.7
10	0.0	3.4	0.0	1.3	1.2	0.8	0.0
11	0.0	3.6	0.2	1.0	0.2	2.1	0.7
12	n/a	5.3	0.2	4.0	0.4	2.3	0.0
13	1.0	n/a	0.0	6.2	0.7	1.3	0.5
<i>Benign tumors</i>							
14	0.8	4.2	0.2	62.0	0.3	18.4	3.0
15	0.0	16.6	0.1	2.4	0.7	2.1	1.0
16	n/a	5.4	n/a	10.2	0.6	0.4	0.0
17	0.4	2.7	0.0	1.4	0.7	0.3	0.7
18	0.3	7.8	0.7	3.1	0.7	5.4	n/a
19	0.7	3.4	0.1	1.5	0.4	0.4	0.3
20	0.8	2.0	0.2	1.2	0.6	1.4	0.0
21	0.2	4.2	0.2	24.2	0.7	1.2	0.4
22	0.5	4.2	0.1	2.7	0.3	1.8	0.2
23	1.0	3.6	0.2	7.9	0.3	1.0	0.0
24	0.3	4.1	0.6	7.1	0.3	1.4	0.2
25	1.3	3.8	1.0	5.2	0.8	2.2	2.4
26	0.7	3.1	0.1	4.0	0.6	1.1	0.5
27	0.0	4.5	0.3	7.0	0.7	0.9	1.1
28	n/a	n/a	0.0	24.2	0.6	0.8	n/a
29	0.5	n/a	0.0	1.9	0.3	5.9	0.6
30	0.9	2.6	0.2	3.2	0.3	0.9	0.4
31	0.2	7.1	0.0	5.8	0.4	3.8	0.3
32	0.0	6.6	0.5	1.0	0.4	2.5	0.0
33	0.0	n/a	0.1	3.7	0.3	0.4	0.3
34	0.4	4.1	0.3	5.9	0.5	1.2	0.0
35	0.6	n/a	0.6	1.6	0.3	1.0	0.4
36	0.0	3.2	0.1	0.4	0.2	2.7	0.6
37	0.9	5.0	2.2	1.8	1.1	4.1	0.4
38	n/a	n/a	1.9	6.1	1.5	n/a	n/a
39	0.5	3.6	0.5	9.9	0.4	1.8	0.5
40	0.0	2.7	0.5	1.9	0.2	2.8	0.0
41	0.9	3.5	0.2	7.0	0.5	1.9	0.5
42	n/a	10.1	0.4	n/a	0.9	0.9	1.3
43	2.0	n/a	0.2	14.7	0.5	1.3	0.0
44	n/a	2.2	0.0	0.5	0.5	0.9	0.7
45	0.7	3.2	0.1	1.6	0.5	0.8	1.0
46	0.0	3.6	0.2	1.5	0.6	n/a	0.4
47	n/a	4.0	0.1	4.3	0.8	0.9	0.0
48	0.8	3.6	0.3	6.2	0.3	2.0	0.6
49	0.6	3.4	0.2	1.8	1.3	0.8	0.0
50	0.0	1.5	0.3	3.4	0.9	2.5	0.3
51	17.4	2.8	0.4	8.9	1.1	3.8	0.4
52	n/a	2.1	0.1	6.3	0.6	1.0	2.3
53	n/a	3.2	1.9	6.5	0.8	1.6	n/a
54	n/a	2.5	0.1	3.3	1.0	1.2	0.4
55	0.9	4.3	0.0	4.8	n/a	1.9	0.0

n/a = not analysed; values above the cut-off levels are indicated in bold

Supplementary Table B. Global methylation analyses of LINE-1 promoters.

Case No	Methylation at CpG sites (%)				Mean
	CpG 1	CpG 2	CpG 3	CpG 4	
<i>Malignant tumors</i>					
1	64.1	64.7	56.9	67.7	63.4
2	67.3	64.9	57.9	67.9	64.5
3	60.5	66.5	58.4	69.1	63.6
4	56.0	60.6	48.6	62.6	57.0
5	62.8	64.5	57.7	65.9	62.7
6	66.2	63.5	56.8	65.5	63.0
7	60.7	64.2	54.1	66.9	61.5
8	69.1	68.9	60.2	58.6	64.2
9	72.0	67.5	60.8	68.6	67.2
10	65.8	65.2	54.4	67.1	63.1
11	54.4	56.1	45.6	61.7	54.5
12	68.4	62.5	57.5	65.2	63.4
13	53.8	52.3	41.2	58.4	51.4
<i>Benign tumors</i>					
14	69.0	66.2	60.1	68.2	65.9
15	72.1	68.1	59.9	69.3	67.4
16	68.6	62.5	57.9	65.4	63.6
17	42.4	45.4	32.8	53.9	43.6
18	69.6	63.6	59.3	67.0	64.9
19	63.2	59.6	52.3	63.3	59.6
20	72.2	64.0	57.6	66.5	65.1
21	75.7	70.4	62.3	69.7	69.5
22	59.4	59.5	48.1	64.2	57.8
23	68.2	66.3	57.8	68.3	65.2
24	75.4	68.3	61.7	69.4	68.7
25	70.2	65.9	56.4	67.9	65.1
26	65.5	63.1	52.7	66.1	61.9
27	72.7	68.1	60.0	69.8	67.7
28	68.9	63.9	56.2	65.6	63.7
29	66.5	63.5	55.7	66.6	63.1
30	65.2	64.5	54.1	66.3	62.5
31	54.1	57.0	45.4	62.8	54.8
32	59.1	57.3	48.0	62.1	56.6
33	65.0	63.9	53.6	66.6	62.3
34	74.5	66.0	59.5	72.1	68.0
35	61.3	61.0	45.7	65.1	58.3
36	74.0	68.9	61.6	70.2	68.7
37	66.9	62.9	55.4	64.8	62.5
38	n/a	n/a	n/a	n/a	n/a
39	65.9	63.9	53.6	67.2	62.7
40	68.4	67.2	55.1	66.7	64.4
41	65.0	62.7	54.8	65.2	61.9
42	70.1	66.9	58.3	68.5	66.0
43	67.9	65.9	56.6	66.9	64.3
44	69.5	68.8	57.1	70.5	66.5
45	54.3	54.5	41.0	60.6	52.6
46	57.3	57.6	47.2	64.2	56.6
47	58.9	55.5	45.6	60.5	55.1
48	69.5	63.5	55.8	65.5	63.5
49	60.1	59.1	46.6	62.7	57.1
50	60.5	56.1	44.1	60.5	55.3
51	74.9	69.4	62.5	70.1	69.2
52	63.7	63.2	50.7	65.7	60.8
53	70.2	64.9	57.7	66.7	64.9
54	56.7	58.3	44.0	64.6	55.9
55	72.2	67.5	60.3	69.9	67.5
<i>Normal</i>	(63.5-75.0)	(53.5-70.5)	(52.1-62.3)	(59.1-73.4)	

n/a = not analysed