

Table 1. Methylation status of individual CpGs within analyzed *ALDH1L1* CpG island obtained by bisulfite genomic sequencing (see Materials and Methods for details). The regions analyzed correspond to those depicted in Fig. 1.

	A549	HCT116	HepG2	HEK293A	Liver	Spleen	Hemangioma	Hepatocellular carcinoma
Region: FDH I (-593 to -215) (17CpG)	Number of clones analyzed							
	(10)	(11)	(11)	(14)	(10)	(11)	(10)	(10)
CpG #	% of clones with methylated CpG							
1	100	100	100	50	0	100	0	0
2	100	100	100	50	0	100	0	0
3	100	100	100	50	0	100	0	0
4	100	100	100	50	0	100	0	0
5	100	100	100	50	0	100	0	0
6	100	100	100	50	0	0	0	0
7	100	100	100	50	0	100	0	0
8	100	100	100	50	0	100	0	0
9	100	100	100	50	0	0	0	0
10	100	100	100	50	0	0	0	0
11	100	100	100	50	0	100	0	0
12	100	100	100	50	0	0	0	0
13	100	100	100	0	0	100	0	0
14	100	100	100	0	0	100	0	0
15	100	100	0	0	0	0	0	0
16	100	100	100	0	0	0	0	0
17	100	100	100	0	0	0	0	0
Region: FDH II (-195 to +599) (46 CpG)	Number of clones analyzed							
	(10)	(11)	(14)	(11)	(10)	(11)	(11)	(11)
CpG #	% of clones with methylated CpG							
18	100	100	0	0	0	0	0	100
19	100	100	0	0	0	0	0	100
20	0	100	0	0	0	0	0	100
21	0	100	50	0	0	0	0	100
22	100	100	100	0	0	0	0	100
23	100	100	50	0	0	0	0	100
24	100	100	50	0	0	0	0	100
25	100	100	50	0	0	0	0	100
26	100	100	50	0	0	0	0	100
27	100	100	0	0	0	0	0	100
28	100	100	0	0	0	0	0	100
29	100	100	0	0	0	0	0	100
30	0	100	0	0	0	0	0	100
31	0	100	0	0	0	0	0	100
32	0	100	0	0	0	0	0	100
33	0	100	0	0	0	0	0	0
34	0	100	0	0	0	0	0	100
35	100	100	0	0	0	0	0	100
36	100	100	50	0	0	0	0	0
37	0	100	50	0	0	0	0	0
38	100	100	50	0	0	0	0	0
39	100	100	0	0	0	0	0	100
40	0	100	0	0	0	0	0	100
41	100	100	100	0	0	0	0	100
42	100	100	50	0	0	0	0	0
43	0	100	100	0	0	0	0	0
44	100	100	100	0	0	0	0	0
45	100	100	100	0	0	0	0	100
46	0	100	100	0	0	0	0	0
47	100	100	100	0	0	0	0	100

48	0	100	50	0	0	0	0	100
49	0	100	100	0	0	0	0	100
50	100	100	50	0	0	0	0	100
51	100	100	50	0	0	0	0	100
52	100	100	0	0	0	0	0	100
53	100	100	0	0	0	0	0	100
54	100	100	0	0	0	0	0	100
55	100	100	0	0	0	0	0	100
56	100	100	100	0	0	0	0	100
57	100	100	100	0	0	0	0	100
58	100	100	100	0	0	0	0	0
59	100	100	100	0	0	0	0	100
60	100	100	50	0	0	0	0	100
61	100	100	100	0	0	0	0	100
62	0	100	100	0	0	0	0	100
63	0	100	100	0	0	0	0	0

Number of clones analyzed

**Region: FDH III
(+574 to +1158)
(33 CpGs)**

(10) (11) (12) (10) (11) (11) (11) (11)

CpG#	% of clones with methylated CpG								
64	100	0	100	0	0	0	0	0	0
65	100	100	100	100	0	0	0	0	0
66	100	0	0	0	0	0	0	0	0
67	100	100	100	0	0	0	0	0	0
68	0	100	0	0	0	0	0	0	0
69	100	100	50	0	0	0	0	0	0
70	0	100	50	0	0	0	0	0	0
71	0	100	50	0	0	0	0	0	0
72	0	100	100	0	0	0	0	0	0
73	100	100	100	0	0	0	0	0	0
74	100	100	100	0	0	0	0	0	0
75	100	100	100	0	0	0	0	0	0
76	100	100	100	0	0	0	0	0	0
77	0	0	100	0	0	0	0	0	0
78	0	0	100	0	0	0	0	0	0
79	0	0	100	0	0	0	0	0	0
80	100	100	0	0	0	0	0	0	0
81	100	100	0	0	0	0	0	0	0
82	100	100	50	0	0	0	0	0	0
83	100	100	100	0	0	0	0	0	0
84	100	100	100	0	0	0	100	0	0
85	100	100	100	0	0	0	100	0	0
86	100	100	100	100	0	0	0	0	0
87	100	100	100	100	0	0	0	0	0
88	100	100	100	100	0	0	0	0	0
89	100	100	100	100	0	0	100	0	0
90	100	100	100	0	0	0	0	0	0
91	100	100	100	0	0	0	0	0	0
92	100	100	100	0	0	0	0	0	0
93	100	100	100	0	0	0	0	0	0
94	100	100	100	0	0	0	0	0	0
95	100	100	100	0	0	0	0	0	0
96	100	100	100	0	0	0	0	0	0

Table 2. Summary of data from Table 1.

Region within <i>ALDH1L1</i> CpG island	Total methylation, %							
	A549	HCT116	HepG2	HEK293A	Liver	Spleen	Hemangioma	Hepatocellular carcinoma
FDH I, (17CpGs)	100	100	94.1	38.23	0	58.8	0	0
FDH II, 46 CpGs)	67.4	100	46.7	0	0	0	0	78.3
FDH III, (33 CpGs)	78.8	84.9	77.3	18.2	0	0	9.1	0
Entire CpG island (FDH I +FDH II+FDH III), (96 CpGs)	77.1	94.8	67.2	13.02	0	10.4	3.1	37.5

Table 3. Methylation status of individual CpGs within analyzed *ALDH1L1* CpG island in matched pairs (normal lung tissues and lung adenocarcinomas from the same individuals) obtained by bisulfite genomic sequencing (see Materials and Methods for details). The regions analyzed correspond to those depicted in Fig. 1.

	3613 (N/T)	3673 (N/T)	1258 (N/T)	1245 (N/T)	1261 (N/T)	3549 (N/T)	1440 (N/T)	1262 (N/T)	3640 (N/T)	3905 (N/T)
Region: FDH I (-593 to -215) (17 CpGs)	Number of clones analyzed									
	(4/10)	(4/10)	(4/9)	(4/12)	(4/8)	(4/10)	(4/14)	(4/8)	(8/8)	(8/8)
CpG #	% of clones with methylated CpG									
1	0/0	25/0	0/0	0/0	0/0	0/0	0/0	0/0	25/100	0/0
2	0/0	0/0	0/0	0/0	0/0	0/0	0/50	0/0	0/0	0/0
3	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
4	0/0	0/0	0/0	0/0	0/0	0/0	0/0	25/0	0/0	0/100
5	0/0	0/0	0/0	0/0	0/0	0/0	0/50	0/0	12.5/100	0/0
6	0/0	0/0	0/11	0/0	0/0	0/0	0/0	0/0	0/0	0/0
7	0/0	0/0	0/22	0/0	0/0	0/0	0/50	0/0	12.5/0	0/100
8	0/0	0/0	0/11	0/0	0/0	0/0	0/50	0/0	0/100	0/100
9	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/100	0/0
10	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
11	0/0	0/0	0/0	0/0	0/0	0/0	0/50	0/0	0/0	0/0
12	0/0	0/0	0/11	0/0	0/0	0/0	0/0	0/0	0/0	0/100
13	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/100	0/0
14	0/0	0/0	0/11	0/0	0/0	0/0	0/0	0/0	0/0	0/0
15	0/0	0/0	0/11	0/0	0/0	0/0	0/100	0/0	12.5/0	0/0
16	0/0	0/0	0/0	0/42	0/50	0/0	0/0	0/0	0/0	0/100
17	0/0	0/0	0/0	0/67	0/50	0/0	0/0	0/0	12.5/0	0/0
Region: FDH II (-195 to +599) (46 CpGs)	Number of clones analyzed									
	(4/11)	(4/11)	(4/10)	(4/10)	(4/11)	(4/9)	(4/10)	(4/10)	(8/10)	(8/10)
CpG #	% of clones with methylated CpG									
18	0/0	0/0	0/60	0/60	0/55	0/56	0/0	0/0	0/0	0/0
19	0/0	0/0	0/60	0/60	0/55	0/56	0/0	0/0	0/0	0/0
20	0/0	0/0	0/60	0/60	0/55	0/0	0/0	0/0	0/0	0/0
21	0/0	0/0	0/100	0/100	0/9	0/0	0/100	0/0	0/0	0/0
22	0/0	0/0	0/90	0/100	0/55	0/0	0/0	0/0	0/0	0/0
23	0/0	0/0	0/60	0/60	0/9	0/0	0/0	0/0	0/100	0/100
24	0/0	0/0	0/60	0/60	0/55	0/0	0/0	0/0	0/0	0/0
25	0/0	0/0	0/60	0/60	0/55	0/0	0/0	0/0	0/0	0/0
26	0/0	0/0	0/90	0/60	0/9	0/56	25/0	0/0	0/0	12.5/0
27	0/0	0/0	25/60	0/60	0/55	25/0	0/0	0/0	12.5/0	0/100
28	0/0	0/0	0/60	0/60	0/55	0/0	0/0	0/0	0/100	0/100
29	0/0	0/0	0/60	0/60	0/55	0/0	0/0	0/0	0/0	0/0
30	0/0	0/0	0/60	0/0	0/55	0/0	0/0	0/0	0/0	0/0
31	0/0	0/0	0/60	0/60	0/9	0/0	0/0	0/0	0/0	0/100
32	0/0	0/0	0/60	0/100	0/9	0/0	0/0	0/0	0/0	0/0
33	0/0	0/0	0/0	0/100	0/9	0/0	0/0	0/0	0/0	0/100
34	0/0	0/0	0/60	0/60	0/9	0/0	0/0	0/0	0/100	0/100
35	0/0	0/0	0/60	0/100	0/55	0/0	0/0	0/0	0/0	0/100
36	25/0	0/0	0/90	0/60	0/9	0/0	0/0	0/0	0/0	12.5/0
37	0/0	0/0	0/60	0/60	0/55	0/0	0/0	0/0	0/0	0/100
38	0/0	0/0	0/60	0/100	0/55	0/0	0/0	0/0	0/0	0/0
39	0/0	0/0	0/100	0/100	0/55	0/56	0/100	0/0	0/0	0/100
40	0/0	0/0	0/90	0/100	0/55	0/0	0/100	0/0	0/0	0/100
41	0/0	0/0	0/90	0/100	0/55	0/0	0/100	0/0	0/0	0/0
42	0/0	0/0	0/90	0/100	0/55	0/0	0/0	0/0	0/0	0/0
43	0/0	0/0	0/90	0/60	0/55	0/0	0/0	0/0	0/0	0/0
44	0/0	0/0	0/90	0/60	0/55	0/0	0/0	0/0	0/0	0/0
45	0/0	0/0	0/90	0/60	0/55	0/0	0/100	0/0	0/0	0/0
46	0/0	0/0	0/90	0/60	0/55	0/0	0/0	0/0	0/0	0/0
47	0/0	0/0	0/60	0/60	0/55	0/0	0/0	0/0	0/0	0/0
48	0/0	0/0	0/60	0/60	0/55	0/0	0/0	0/0	0/0	0/0
49	0/0	0/0	0/60	0/60	0/9	0/0	0/0	0/0	0/0	0/100
50	0/0	0/0	0/60	0/60	0/9	0/0	0/100	0/0	12.5/0	0/0
51	0/0	0/0	0/60	0/0	0/9	0/0	0/0	0/0	0/100	0/0

Table 4. Summary of data from Table 3.

Region within <i>ALDH1L1</i> CpG island	Total methylation, %									
	3613 N/T	3673 N/T	1258 N/T	1245 N/T	1261 N/T	3549 N/T	1440 N/T	1262 N/T	3640 N/T	3905 N/T
FDH I, (17 CpGs)	0/0	0/0	0/5.8	0/11.8	0/5.9	0/2.9	0/20.5	0/0	0/29.4	0/29.4
FDH II, (46 CpGs)	0/5.4	0/1.1	0/67.4	0/57.6	0/27.2	0/3.3	0/16.3	0/0	0/8.7	0/37
FDHI II (33 CpGs)	0/12.1	0/22.7	0/1.5	0/0	0/0	0/0	0/22.7	0/1.4	0/0	0/0
Entire CpG island (FDH I+FDH II+ FDH III), (96 CpGs)	0/6.8	0/8.3	0/34.4	0/29.7	0/14.1	0/2.1	0/19.3	0/0.48	0/9.4	0/23