

Table 3. Hypermethylated regions on chromosome 8p in lung squamous cell carcinoma

Lung squamous cell carcinoma #1			
Stage I			
	Genome location	Gene symbol	CpG type / location
1	Chr8:4835989-4837638	CSMD1	CGI (promoter)
2	Chr8:11575055-11576776	GATA4	CGI (promoter)
3	Chr8:18288238-18289521	NAT2	CGI (promoter)
4	Chr8:21960744-21961726	FGF17	CGI (intragenic)
5	Chr8:22051937-22053186	REEP4	CGr (intragenic)
6	Chr8:22494950-22495299	PDLIM2	CGr (intragenic)
7	Chr8:24827148-24828797	NEFM	CGI (promoter)
8	Chr8:24868516-24869816	NEFL	CGI (promoter)
9	Chr8:25956098-25958848	EBF2	CGI (promoter)
10	Chr8:25960960-25962060	EBF2	CGI (promoter)
11	Chr8:26777671-26,779237	ADRA1	CGI (promoter)
12	Chr8:26192344-26193593	PPP2R2A	CGr (intragenic)
13	Chr8:35211737-35213286	UNC5D	CGI (promoter)
14	Chr8:36763459-36764208	BC0287701	CGr (intragenic)
15	Chr8:37677117-37678992	ZNF703	CGI (intragenic)
16	Chr8:41543396-41545120	N/A	CGI (Intergenic)

Lung squamous cell carcinoma #2			
Stage II			
	Genome location	Gene	CpG type / location
1	Chr8:615015-616864	ERICH1	CGI (promoter)
2	Chr8:4759834-4761320	CSMD1	CGr (intragenic)
3	Chr8:4836289-4840074	CSMD1	CGI (promoter)
4	Chr8:6217346-6219095	N/A	CGr (intergenic)
5	Chr8:9797852-9801858	N/A	CGI (intergenic)
6	Chr8:11574306-11576776	GATA4	CGI (promoter)
7	Chr8:13033732-13034981	DLC1	CGI (promoter)
8	Chr8:17702544-17703493	MTUS1	CGI (promoter)
9	Chr8:21599811-21601928	GFRA2	CGr (intragenic)
10	Chr8:23617955-23620733	N/A	CGI (intergenic)
11	Chr8:26777279-26779628	ADRA1	CGI (promoter)
12	Chr8:28613835-28615841	EXTL3	CGI (promoter)
13	Chr8:30787832-30790084	PPP2CB	CGI (promoter)
14	Chr8:35211937-35214616	UNC5D	CGI (promoter)
15	Chr8:37672180-37676766	ZNF703	CGI (intragenic)
16	Chr8:37875678-37876368	RAB11FIP1	CGI (promoter)
17	Chr8:38876610-38878801	AF286164	CGI (promoter)
18	Chr8:40873947-40874696	ZMAT4	CGI (promoter)
19	Chr8:43114818-43115585	FLJ3273	CGI (promoter)

Lung squamous cell carcinoma #3			
Stage III			
	Genome location	Gene	CpG type / location
1	Chr8:830303-831152	BC08783	CGr (intragenic)
2	Chr8:1832535-1834184	ARHGEF10	CGr (intragenic)
3	Chr8:4838851-4840074	CSMD1	CGI (promoter)
4	Chr8:6217446-6219095	N/A	CGr (intergenic)
5	Chr8:9799604-9800153	SWAW	CGI (promoter)
6	Chr8:11599647-11600696	GATA4	CGI (promoter)
7	Chr8:17148431-17149203	VPS37A	CGI (promoter)
8	Chr8:17445124-17445673	SLC7A2	CGI (intergenic)
9	Chr8:17702944-17703593	MTUS1	CGI (promoter)
10	Chr8:21701275-21702424	GFRA2	CGI (promoter)
11	Chr8:23617855-23620730	N/A	CGI (intergenic)
12	Chr8:25955098-25957047	EBF2	CGI (intragenic)
13	Chr8:26777379-26778628	ADRA1	CGI (promoter)
14	Chr8:40719785-40720934	ZMAT4	CGr (intragenic)
15	Chr8:41284732-41285332	SFRP1	CGI (promoter)
16	Chr8:41743716-41744508	ANK1	CGI (intragenic)
17	Chr8:43114818-43115685	FLJ32731	CGI (promoter)

The definition of a CpG island was according to the UCSC genome browser: GC content of 50% or greater, length more than 200 bp, and a ratio >0.6 of observed number of CpG dinucleotides to the expected number on the basis of the number of Gs and Cs in the segment. CpG-rich regions have a ratio of observed/expected CpGs of 0.3-0.6.
Promoter, overlapping any first exon/transcription start site (TSS) of a gene.
Intragenic, from TSS to the end of the gene boundary excluding those overlapping with first exon/TSS.
Intergenic; located between genes.
CGI, CpG island; CGr, CpG-rich region.