

Supplementary Table 2. Frequency of CpG hypermethylation in lung tumours

Gene	Hypermethylated tumour samples*, (%)	Methylation level cut-off
<i>CDH1</i>	1.2	15.3
<i>GSTP1</i>	0.6	4.2
<i>CDKN2A</i>	91.5	9.2
<i>RASSF1A</i>	36.0	4
<i>MTHFR</i>	39.4	75.6

*Samples with methylation levels above the quantile representing the upper 95% of methylation in blood samples