

Figure S1. Stepwise selection processes for candidate genes. Methylated DNA was separately enriched for DNA from 13 primary lung tumors and paired adjacent non-tumor tissues. Methylated DNA (Cy5) was individually compared with amplified common reference DNA (Cy3) without methylation enrichment. Statistical and fold-change analyses (mean value  $\geq 4.0$ ) identified 10 genes as candidate genes that were significantly hypermethylated in primary lung tumors compared with adjacent non-tumor tissues.

