

## SUPPLEMENTAL FIGURE LEGENDS

**Supplemental Figure 1.**  $p16^{INK4\alpha}$  methylation status in controls (A) and PAHs-exposed workers (B) by bisulfite sequencing on CpG island (+150 bp to +538 bp) of the  $p16^{INK4\alpha}$  gene. For each human sample, 8 clones were selected for sequencing. The CpG position relative to transcription start site was shown at top of each CpG site. At each CpG site, the area filled with black represents the average percentage of methylation across all CpG sites tested in subjects indicated. The value of average percentage was shown at the end of each row.

**Supplemental Figure 2.** p16 expression, methylation status at the promoter of  $p16^{INK4\alpha}$  gene in BaP-treated peripheral blood mononuclear cells (PBMC). A, time course of mRNA levels (upper panel) of and protein expression (lower panel) of p16 in PBMCs with 10  $\mu$ m BaP treatment. B, bisulfite sequencing on CpG island (+150 bp to +538 bp) of  $p16^{INK4\alpha}$  gene. For each cell line, 10 clones were selected for sequencing. The area filled with black represents the average percentage of methylation across all CpG sites tested in cells indicated. The value of average percentage was shown at the end of each row.