**FIGURE LEGENDS**

**FIGURE 1** Representative results of the PCR-based detection of MCPyV and HPV. A. Fragments were amplified from MCPyV DNA isolated from matched samples of lung cancer (lane 1, KL17; lane 3, BL17; lane 5, JL124) and normal tumor adjacent (lane 2, KC17; lane 4, BC17; lane 6, JC124) tissues. B. Fragments were amplified from HPV DNA of Korean patients with MCPyV-positivity in lung cancer tissues. Lane 1, KL17; lane 2, BL17; lane 3, JL124. ID KL, BL, and JL; the Biobank of Korea University Guro Hospital, Pusan National University Hospital, Jeonbuk National University Hospital. The arrow bar indicates the expected size of the target band. Lane M: molecular weight markers. Lane N: distilled water as a negative control.

**FIGURE 2** Mutations of full-length LT-ag of MCPyV. A. Structures of six MCPyV strains: MCC350 (GenBank, accession no. EU375803.1); MCC 339 (GenBank, accession no. EU375804.1); MKL–1 (GenBank, accession no. FJ173815); HB039C (GenBank, accession no. KC571692.1); TKS (GenBank, accession no. FJ464337); and KIB (GenBank, accession no. MK561422). B. Two of 9 DNA sequences of lung cancers showed a single-nucleotide substitution (JL93, JL95) (see Figure S1). Korean strains were compared with six full-length sequences. Open ovals, common sequences in all six strains (North American/European/Northeast Asia). Filled ovals, mutations in MCPyV specific to Korean strains.

**FIGURE 3** Mutation alterations of full-length VP1 of MCPyV. A. Structures of six MCPyV strains: MCC350 (GenBank, accession no. EU375803.1); MCC 339 (GenBank, accession no. EU375804.1); MKL–1 (GenBank, accession no. FJ173815); HB039C (GenBank, accession no. KC571692.1); TKS (GenBank, accession no. FJ464337); and KIB (GenBank, accession no. MK561422). B. Eight of 34 DNA sequences of lung cancers showed a single-nucleotide substitution: specifically, three samples, BL1, BL4, and BL28, show mutations in MCPyV specific to Korean strains (at positions 4,152 and 4,153 in BL1-filled ovals). In the case of positions 4,362 and 4,368, they existed in a mixed form (open ovals and filled ovals) (see Figure S2).

**FIGURE 4** Analysis of amplified MCPyV NCCR. As amplified with ORIF2/ORIR2 primers, PCR products were visualized after staining with ethidium bromide and photographed with UV light. Lane M: molecular weight markers. Lane N: distilled water as a negative control. Only two subtypes of the MCPyV NCCR were identified, lane 1 (236 bp) and lane 2 (229 bp).

**FIGURE 5** Analysis of the NCCR organization of MCPyV. **(A)** The NCCR is classified into two main subtypes: with a 25-bp insertion (subtype I) and without a 25-bp insertion (subtype II). Subtype II is further divided into four subgroups, IIa-1, IIa-2, IIb, and IIc, based on incidences of insertion and deletion of nucleotides. **(B, C)** Alignments and sequences of the NCCR were identified in 3 lung cancer tissue samples from Korean patients (BL13, BL28, and JL150). The nucleotide substitutions in the NCCR are numbered and marked in gray boxes and filled triangles: BL13, C > T at position 5,153, G > A at position 5,168; BL28, C > T at position 5,190, G > A at position 5,203, C > T at position 5,238; JL150, A > G at position 5,239. BL13\*; full-length MCPyV genome identified in this study.