Phylogenetic studies were performed on E6 nucleotide sequence alignment of 477 positions from each case, which was constructed by the neighbor joining method and the Kimura 2-Parameter model by MEGA 6 package. Bootstrap proportions were calculated with 1000 replicates. Study sequences are labeled in KT GenBank accession numbers, others are reference GenBank sequences. E, European variant; Ep, European prototype; As, Asia lineage; AA, Asian American lineage; Af, African lineage.

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Figure S2 Phylogenetic studies were performed on E7 nucleotide sequence alignment of 297 positions from each case, which was constructed by the neighbor joining method and the Kimura 2-Parameter model by MEGA 6 package. Bootstrap proportions were calculated with 1000 replicates. Study sequences are labeled in KT GenBank accession numbers, others are reference GenBank sequences. E, European variant; Ep, European prototype; As, Asia lineage; AA, Asian American lineage; Af, African lineage.
Figure S3 Phylogenetic studies were performed on partial L1 nucleotide sequence alignment of 369 positions from each case, which was constructed by the neighbor joining method and the Kimura 2-Parameter model by MEGA 6 package. Bootstrap proportions were calculated with 1000 replicates. Study sequences are labeled in KT GenBank accession numbers, others are reference GenBank sequences. E, European variant; Ep, European prototype; As, Asia lineage; AA, Asian American lineage; Af, African lineage.