**Figure 1**. **Phylogenetic tree reflecting the relationships of strains based on whole genome re-sequencing and analysis.**

Patient R14

Patient R15

Patient R12

Patient R10

Patient R8

HCW R6

Patient R5

HCW R4

Patient R1

Patient R2

HCW R9

Outpatient RC5

Patient R16

HCW R3

Patient R13

HCW R7

Outpatient RC2

Outpatient RC6

Outpatient RC4

Outpatient RC1

Patient R11

Outpatient RC7

Outpatient RC3

Outpatient RC8

5

89/88

100/99

89/89

100/99

89/86

68/78

100/99

The tree topology was obtained from a boot-strapped neighbor-joining analysis. Nodes for which bootstrap values equaled or exceed 70 % are indicated by a numerical value. The bootstrap values derived from maximum likelihood analysis is also indicated (NJ/ML). Polytomies indicate branching points that were not consistently supported by bootstrap analyses. Nodes supported by Bayesian analysis, with posterior probability values greater than 95 %, are indicated with black circles. The node indicated by the arrow represents 11 identical genomes based on mapping to the reference genome (GenBank AF013254.1).