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**Supplementary Figure S1**: **The Cladogram for DENV1-serotypes based on CprM sequences.** The phylogenetic tree constructed for DENV-1 serotypes with Maximum Likelihood method and Tamura-Nei model using 1000 bootstrap value. The sequences from this study were highlighted with the red circle. Evolutionary analyses were conducted in MEGA X.



**Supplementary Figure S2:** : **The Cladogram for DENV2-serotypes based on CprM sequences.** The phylogenetic tree constructed for DENV-2 serotypes with Maximum Likelihood method and Tamura-Nei model using 1000 bootstrap value. The sequences from this study were highlighted with the red circle. Evolutionary analyses were conducted in MEGA X.



**Supplementary Figure S3:** : **The Cladogram for DENV3-serotypes based on CprM sequences.** The phylogenetic tree constructed for DENV-3 serotypes with Maximum Likelihood method and Tamura-Nei model using 1000 bootstrap value. The sequences from this study were highlighted with the red circle. Evolutionary analyses were conducted in MEGA X.



**Supplementary Figure S4:** : **The Cladogram for DENV4-serotypes based on CprM sequences.** The phylogenetic tree constructed for DENV-4 serotypes with Maximum Likelihood method and Tamura-Nei model using 1000 bootstrap value. The sequences from this study were highlighted with the red circle. Evolutionary analyses were conducted in MEGA X.