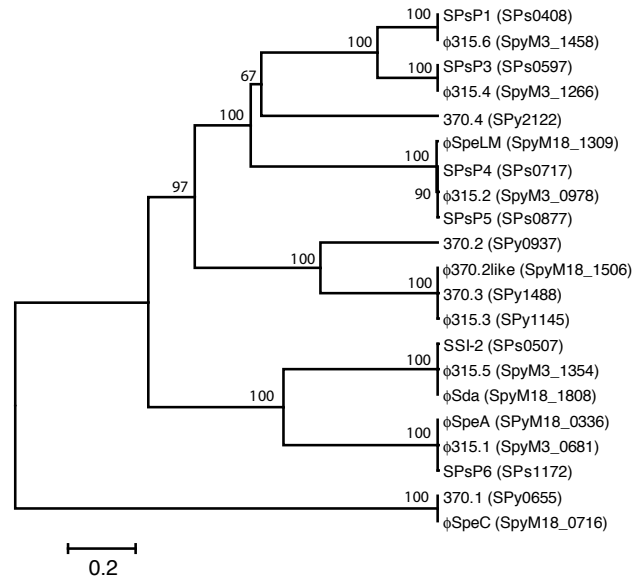
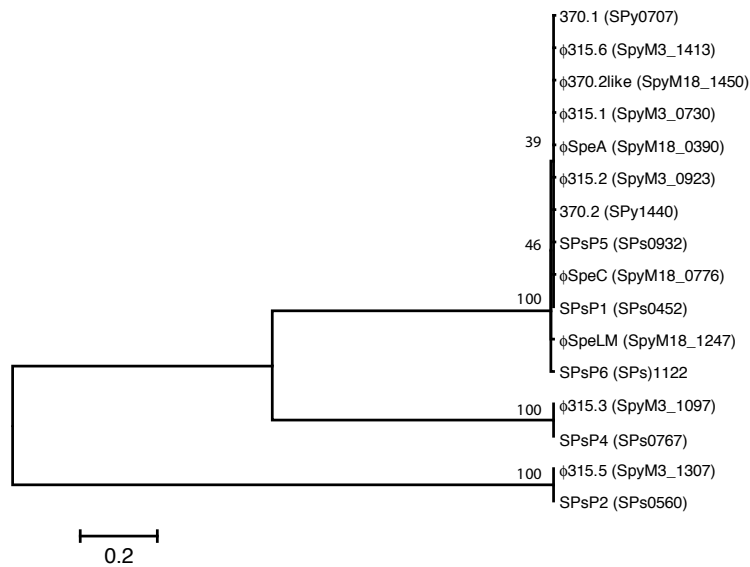


**A****B**

Supplemental Fig. B. Phylogenetic analysis of phage integrase (A) and holin (B). Predicted amino acids of each protein found in four GAS strains were compared with CLUSTAL W (DNA Data Bank of Japan) and construct the phylogenetic tree using NJ method (1) on MEGA2.1 software (<http://www.megasoftware.net/>, 2). Bootstrap values are indicated between the gene.

#### References.

1. Nei, M. & Kumar, S. 2000. *Molecular Evolution and Phylogenetics*. Oxford University Press, New York.
2. Kumar, S., Tamura K., Jakobsen, I. B. & Nei, M. 2001. *Bioinformatics* 17: 1244-1245.