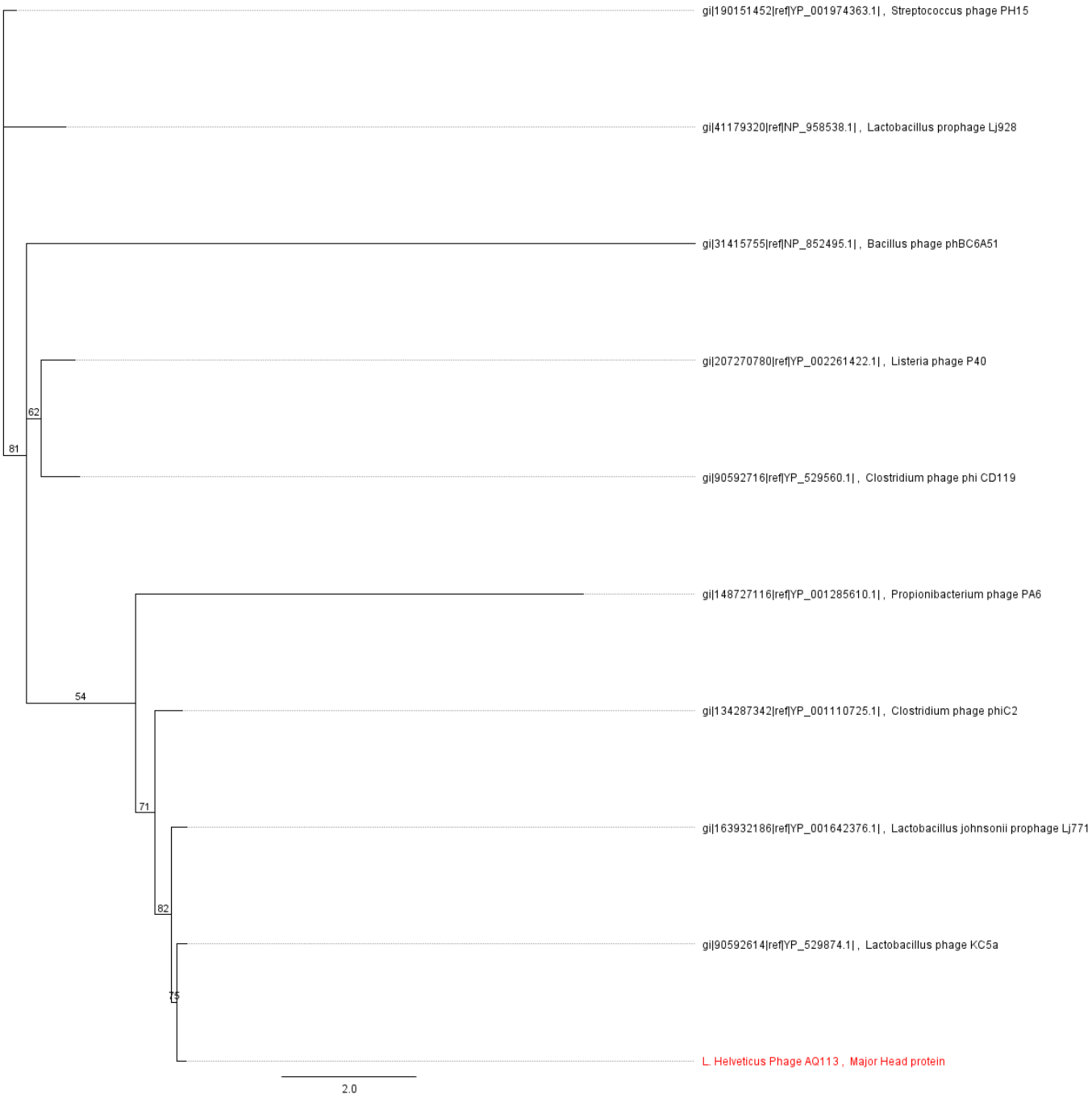
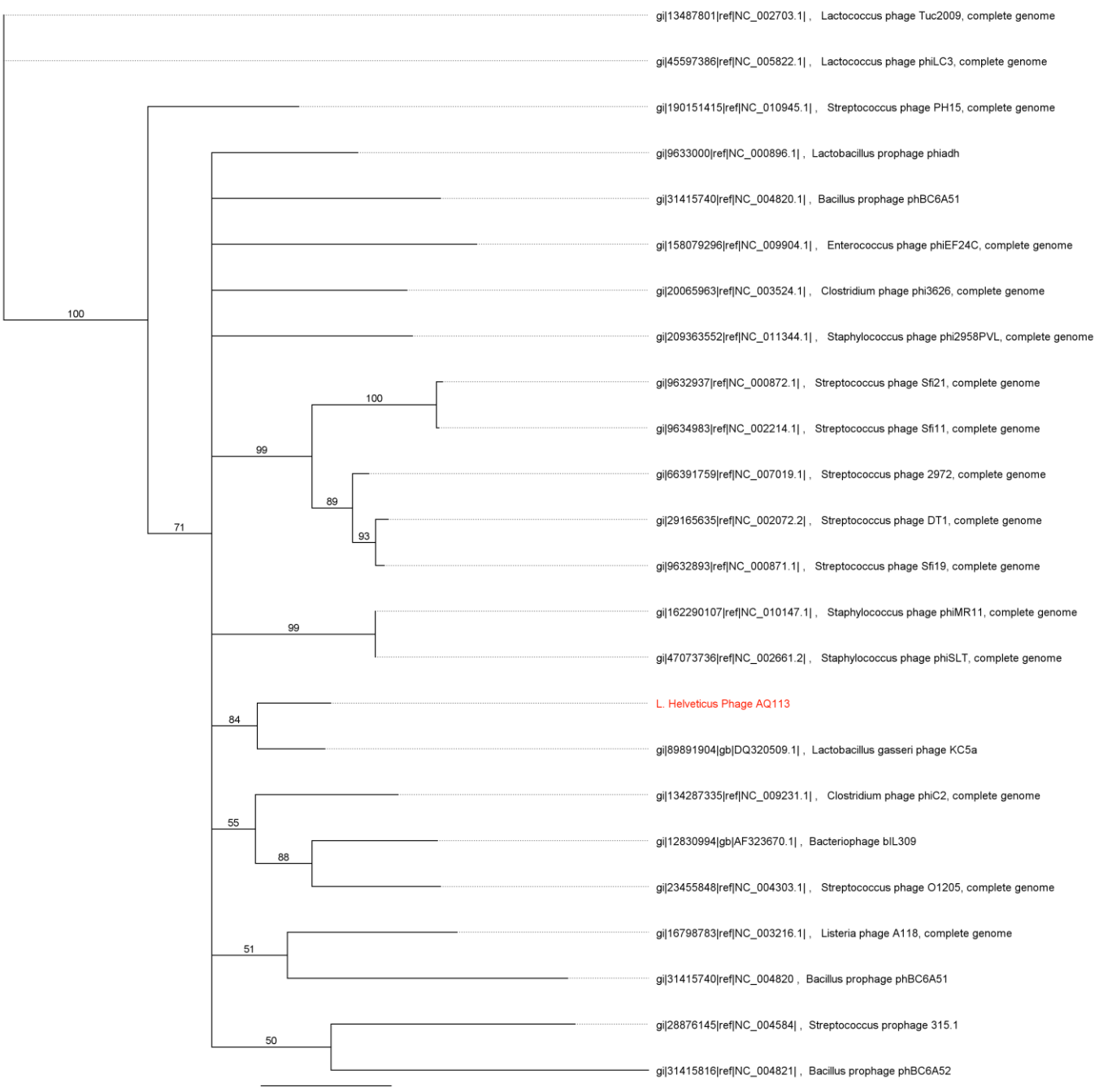

gi|190151452|ref|YP_001974363.1|, Streptococcus phage PH15
gi|41179320|ref|NP_958538.1|, Lactobacillus prophage Lj928
gi|31415755|ref|NP_852495.1|, Bacillus phage phBC6A51
gi|207270780|ref|YP_002261422.1|, Listeria phage P40
gi|90592716|ref|YP_529560.1|, Clostridium phage phi CD119
gi|148727116|ref|YP_001285610.1|, Propionibacterium phage PA6
gi|134287342|ref|YP_001110725.1|, Clostridium phage phiC2
gi|163932186|ref|YP_001642376.1|, Lactobacillus johnsonii prophage Lj771
gi|90592614|ref|YP_529874.1|, Lactobacillus phage KC5a
L. Helveticus Phage AQ113 , Major Head protein
62
81
54
71
82
75
2.0

A



B

FIG. S1. Dendrograms of bacteriophage proteins from NCBI database that showed significant similarity to the major head protein (A) and the trascriptional regulator protein (B) of the ΦAQ113. The phylogenetic trees were derived by alignment using Clustalw2 and were obtained using Jukes-Cantor algorithm for evaluating genetic distance and neighbour joining for clustering.