

Supplemental Information

“Evolution of higher torque in *Campylobacter*-type bacterial flagellar motors”

Bonnie Chaban^{1†}, Izaak Coleman¹, Morgan Beeby^{1*}

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Supplementary Figures S1, S2, S3 and S4 (attached)

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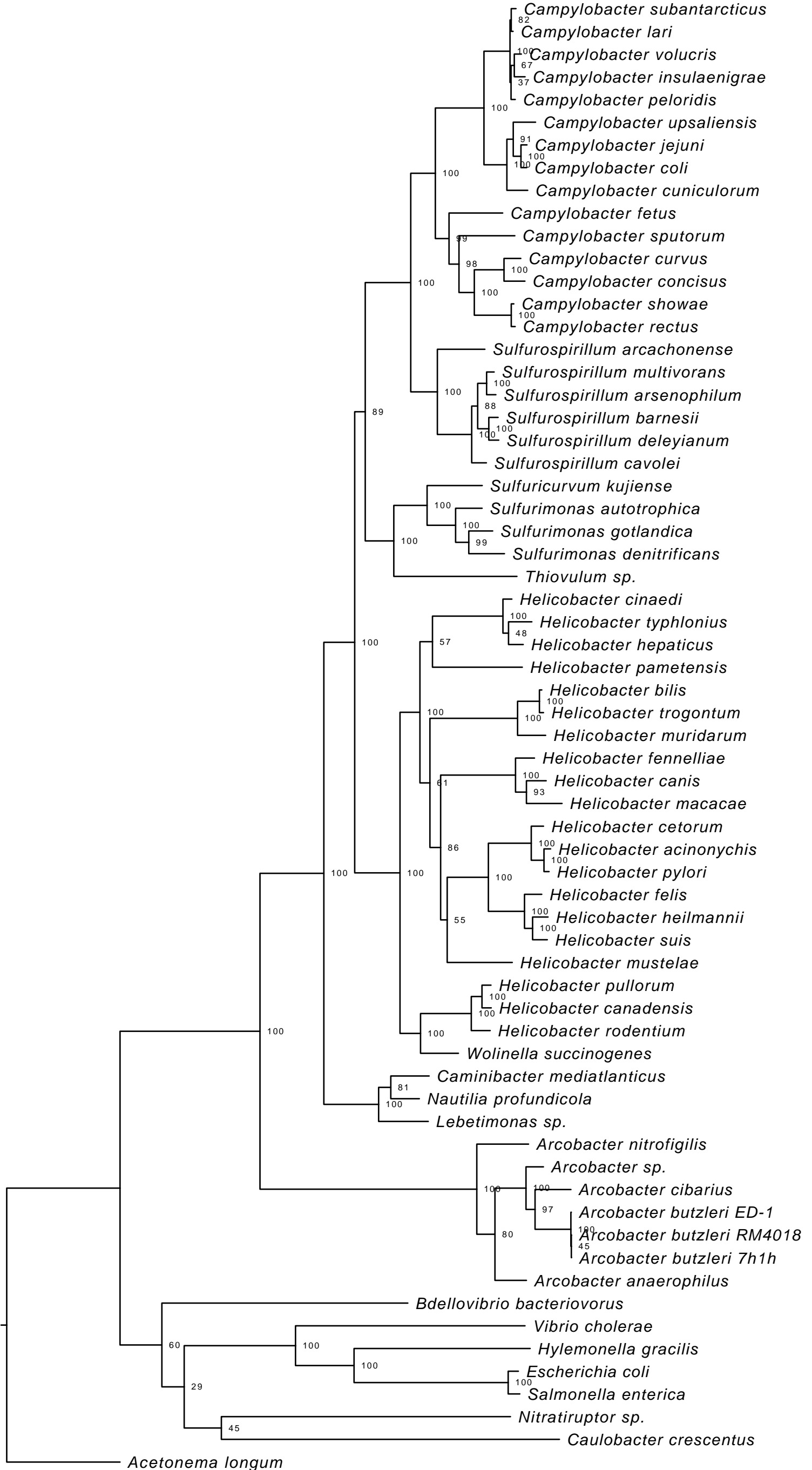
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Supplementary Figure S1: Flagellar motor phylogeny with a focus on ϵ -proteobacteria and related species. Phylogeny was determined using a concatenation of core flagellar motor proteins FlgB, FlgC, FlhB, FliE, FliF, FliG, FliI, FliM, FliN, FliP, FliR, bootstrapped 1000 times.



0.4

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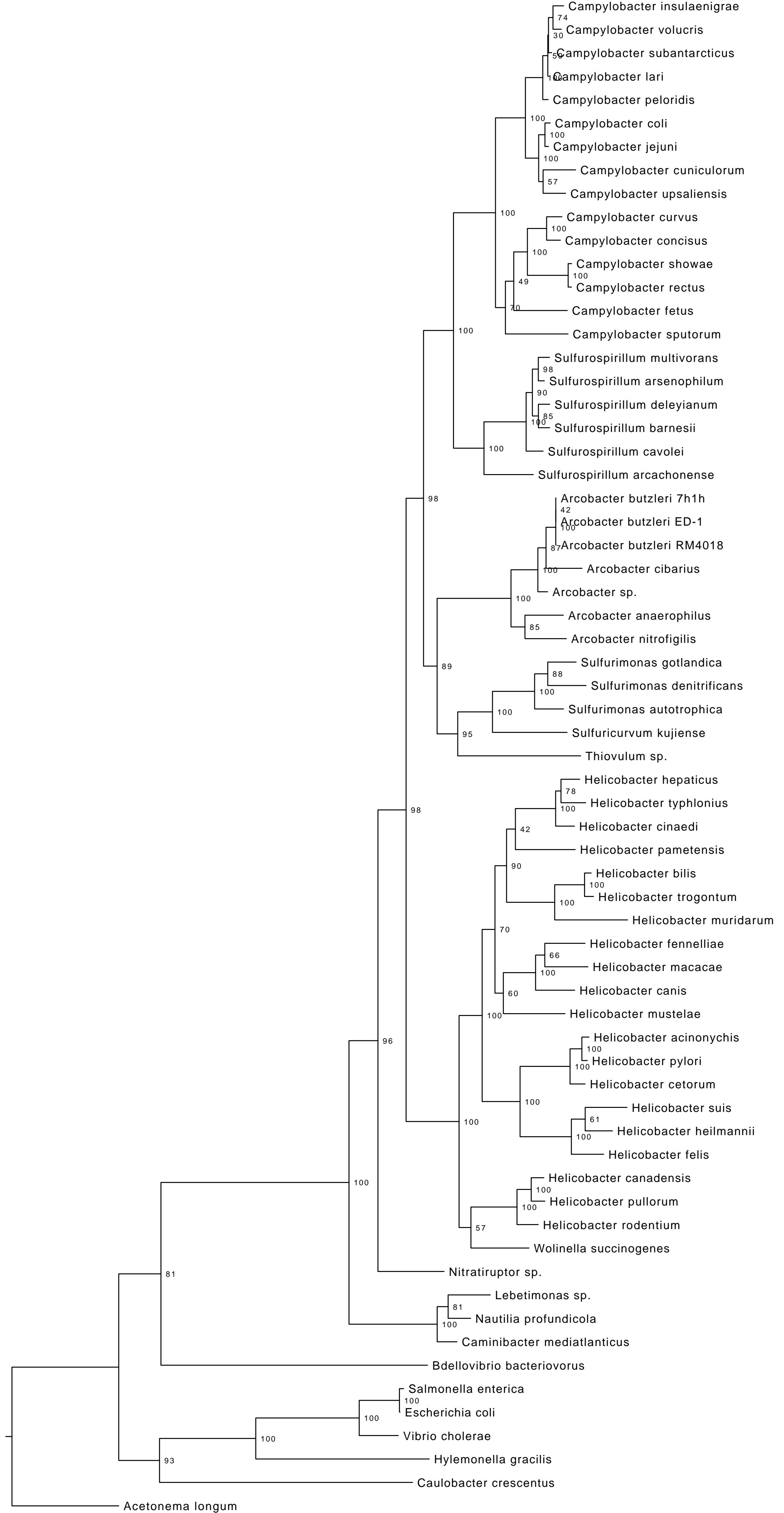
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Supplementary Figure S2: Organism phylogeny of organisms depicted in Figure S1.

Phylogeny was determined using a concatenation of ribosomal protein sequences L1, L2, L3, L4, L5, L9, L10, L11, L13, L14, L15, L16, L17, L18, bootstrapped 1000 times.



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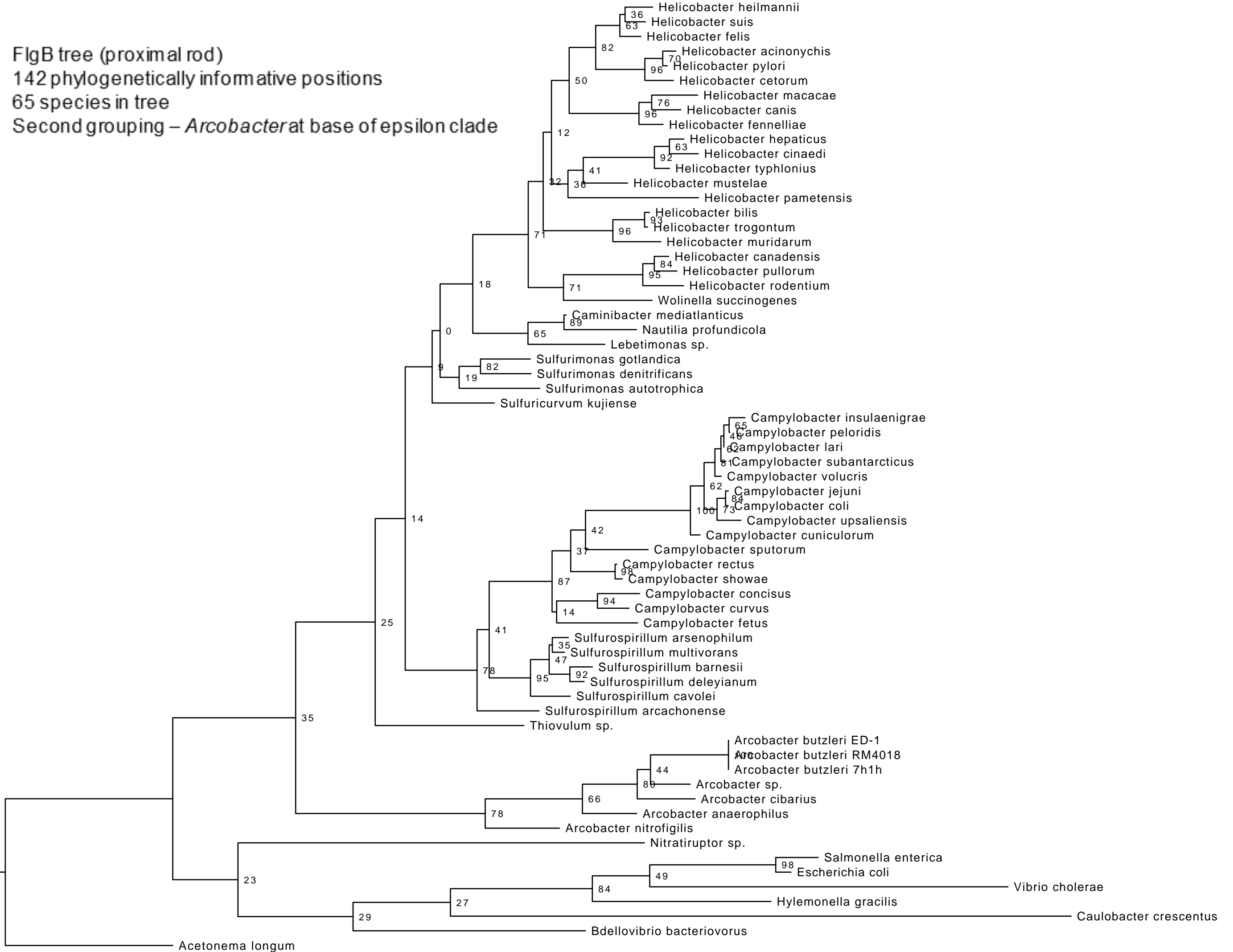
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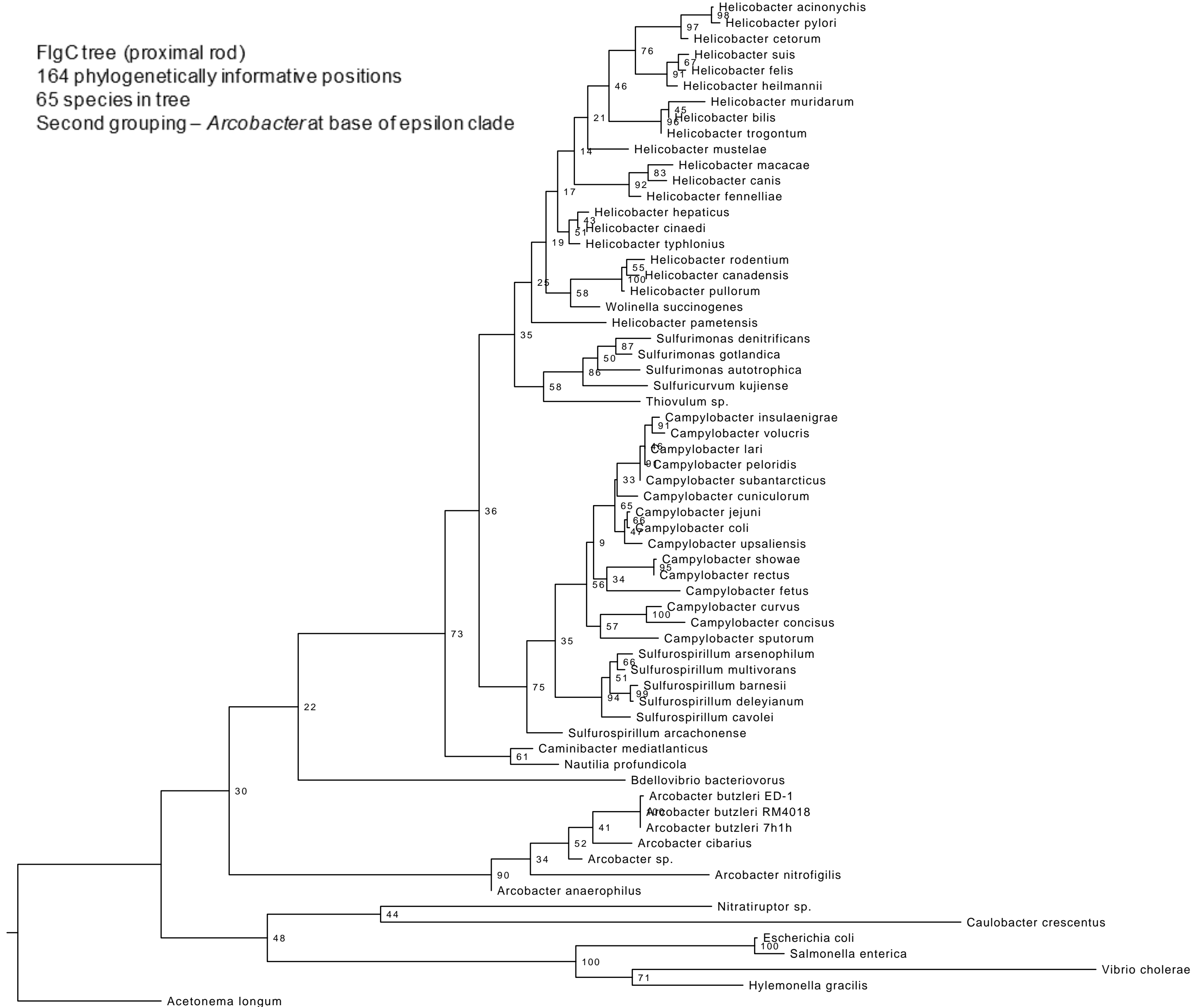
Supplementary Figure S3: Flagellar motor phylogeny of each flagellar motor protein separately, with a focus on ϵ -proteobacteria and related species. Phylogeny was determined for FlgB, FlgC, FlgH, FlgI, FlhA, FlhB, FliE, FliF, FliG, FliI, FliM, FliN, FliP, FliQ, FliR, individually, bootstrapped 100 times.

FlgB tree (proximal rod)
 142 phylogenetically informative positions
 65 species in tree
 Second grouping – *Arcobacter* at base of epsilon clade



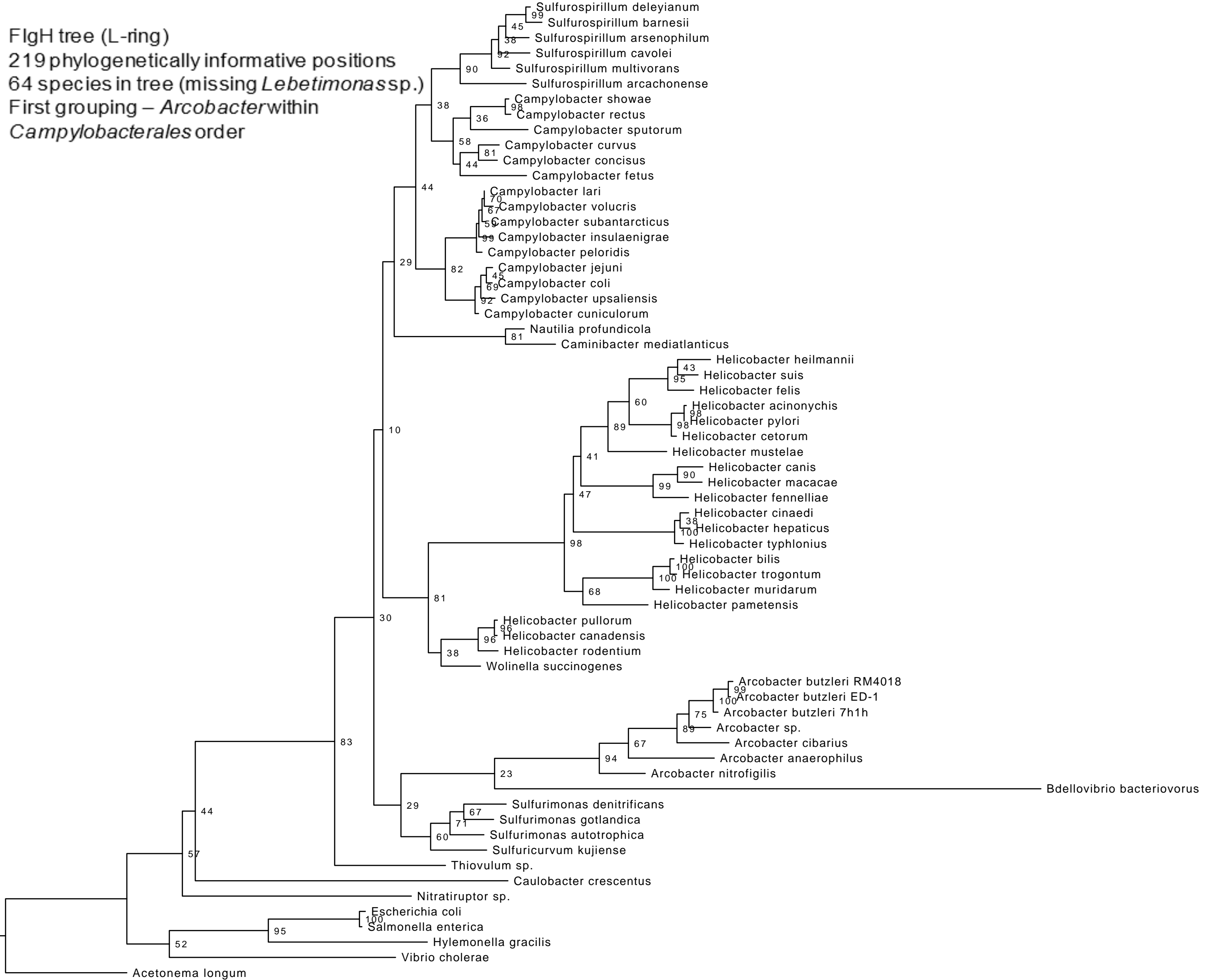
0.6

FlgC tree (proximal rod)
 164 phylogenetically informative positions
 65 species in tree
 Second grouping – *Arcobacter* at base of epsilon clade



0.5

FlgH tree (L-ring)
 219 phylogenetically informative positions
 64 species in tree (missing *Lebetimonas* sp.)
 First grouping – *Arcobacter* within
Campylobacterales order



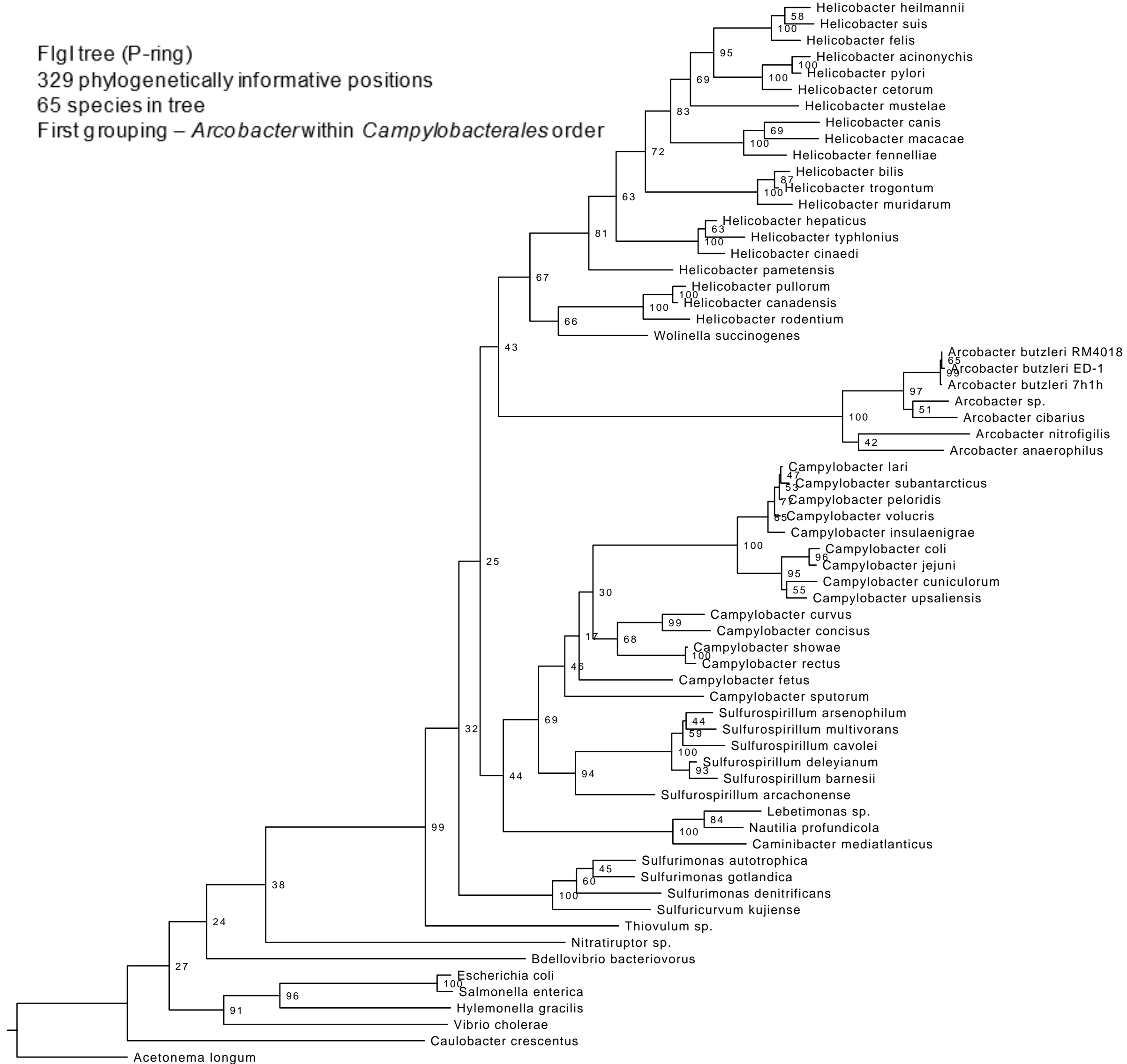
0.4

FlgI tree (P-ring)

329 phylogenetically informative positions

65 species in tree

First grouping – *Arcobacter* within *Campylobacterales* order



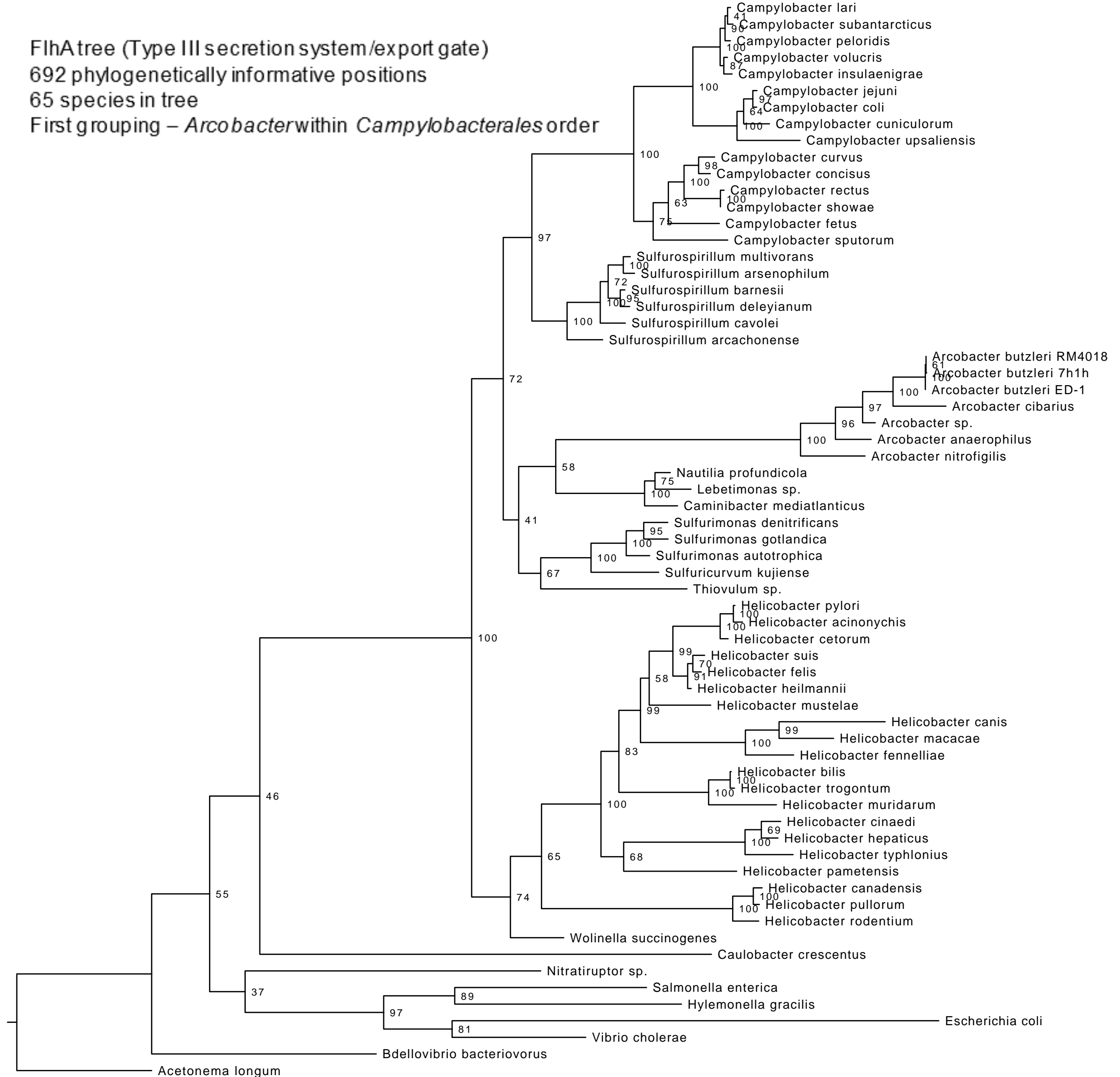
0.3

FliA tree (Type III secretion system/export gate)

692 phylogenetically informative positions

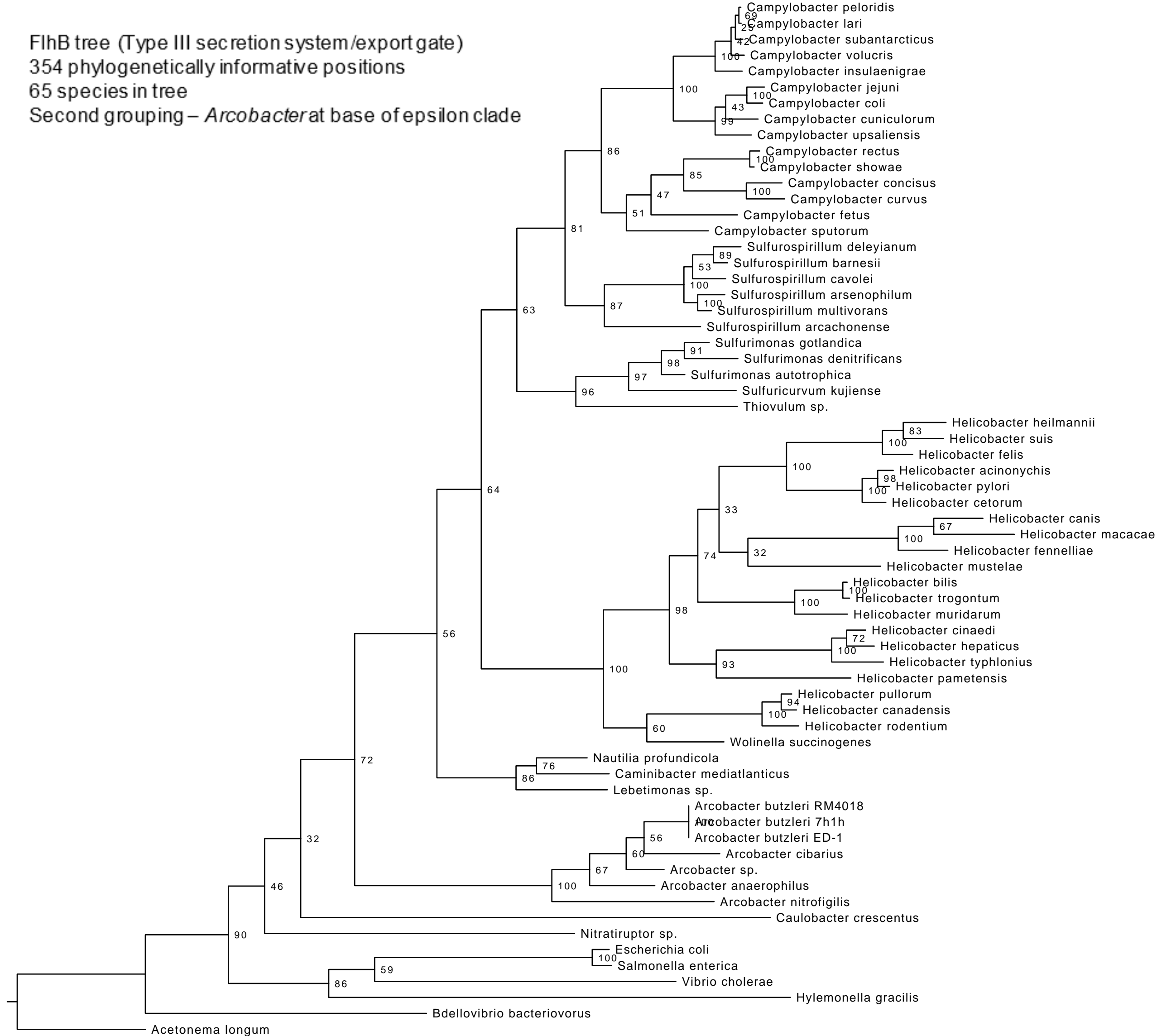
65 species in tree

First grouping – *Arcobacter* within *Campylobacterales* order



0.3

FlhB tree (Type III secretion system/export gate)
 354 phylogenetically informative positions
 65 species in tree
 Second grouping – *Arcobacter* at base of epsilon clade



0.4

FliE tree (Proximal rod)

76 phylogenetically informative positions

64 species in tree (missing *Campylobacter rectus*)

Second grouping – *Arcobacter* at base of epsilon clade



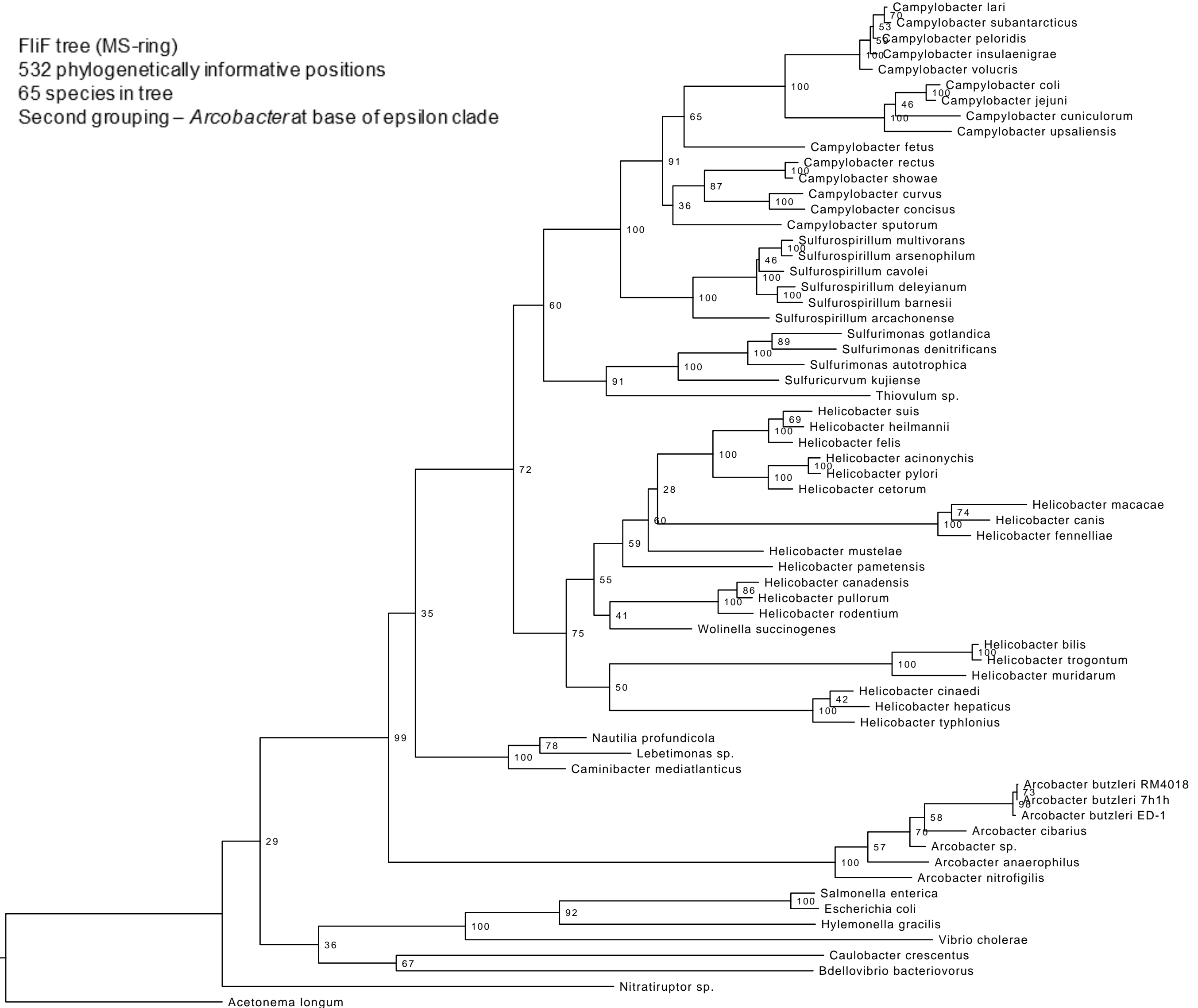
0.5

FliF tree (MS-ring)

532 phylogenetically informative positions

65 species in tree

Second grouping – *Arcobacter* at base of epsilon clade



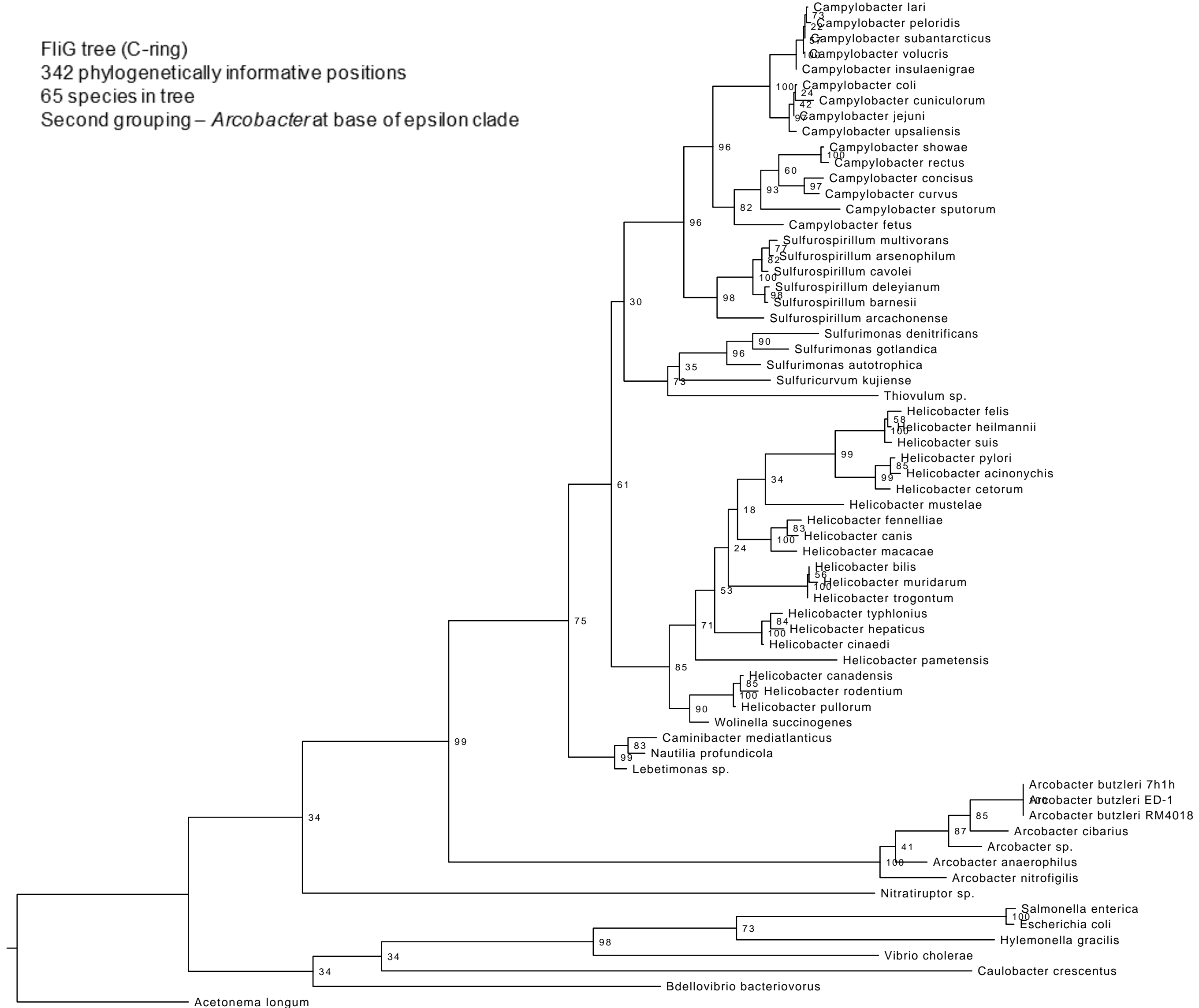
0.3

FliG tree (C-ring)

342 phylogenetically informative positions

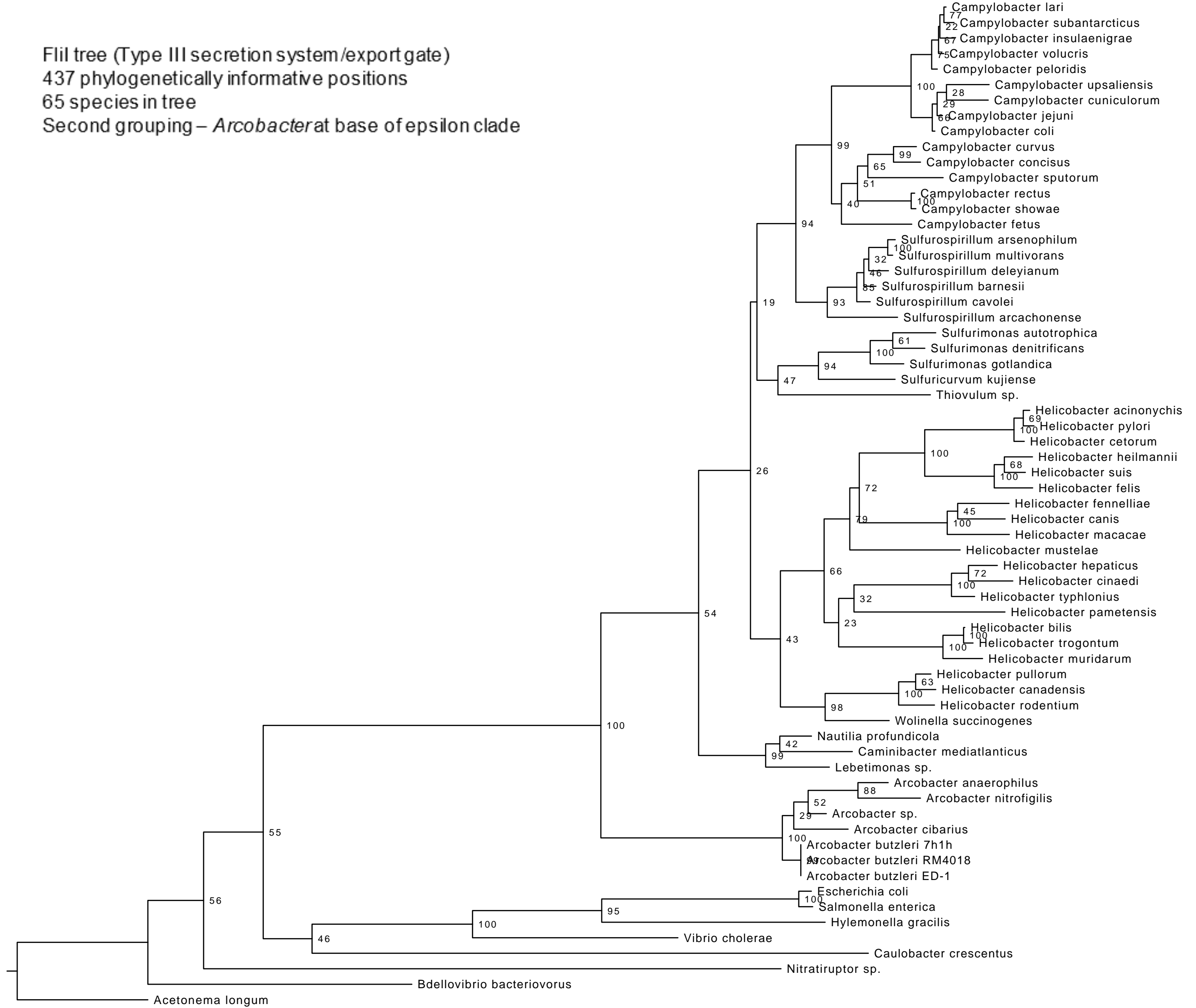
65 species in tree

Second grouping – *Arcobacter* at base of epsilon clade



0.3

Flil tree (Type III secretion system/export gate)
 437 phylogenetically informative positions
 65 species in tree
 Second grouping – *Arcobacter* at base of epsilon clade



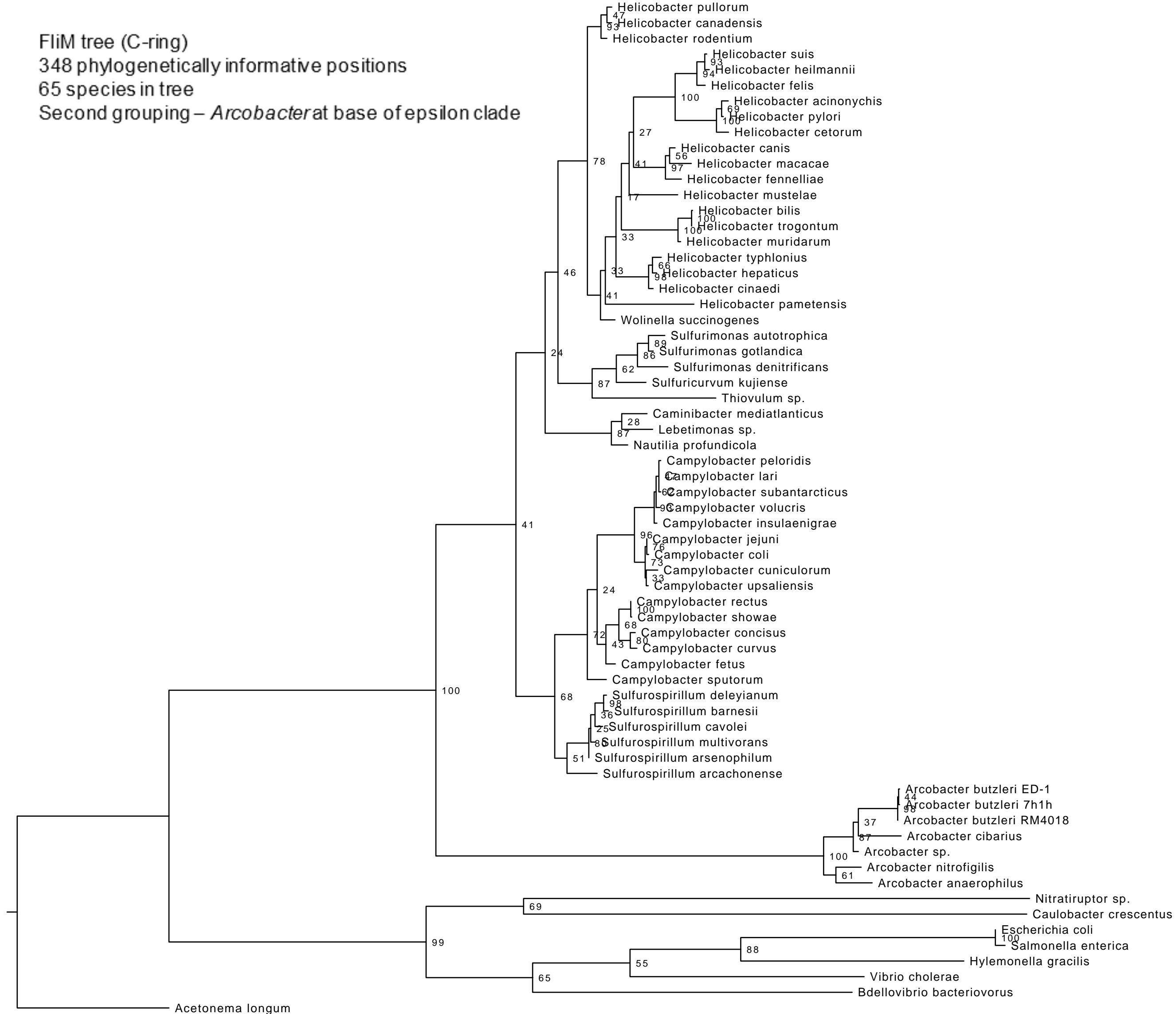
0.5

FlIM tree (C-ring)

348 phylogenetically informative positions

65 species in tree

Second grouping – *Arcobacter* at base of epsilon clade



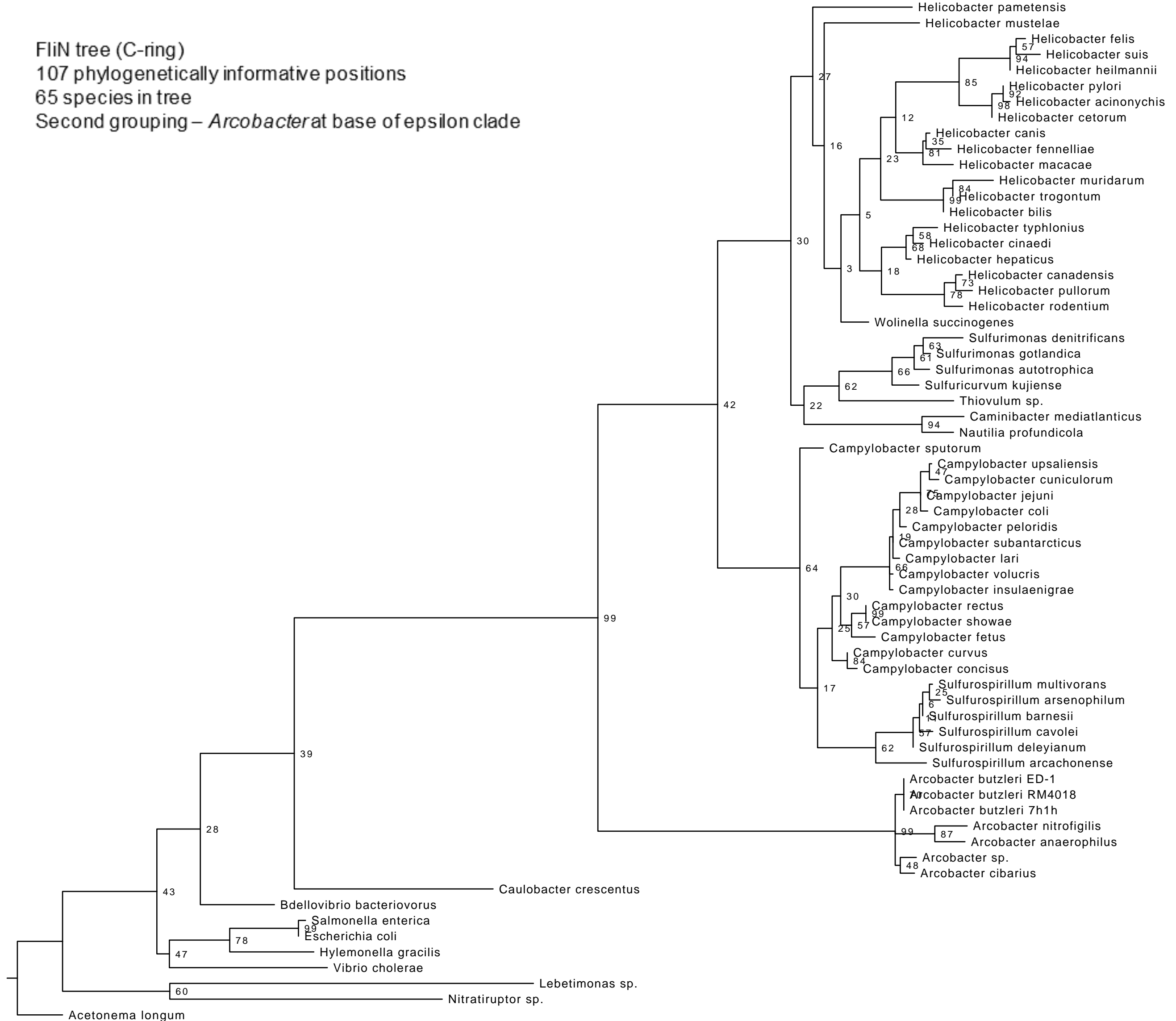
0.6

FliN tree (C-ring)

107 phylogenetically informative positions

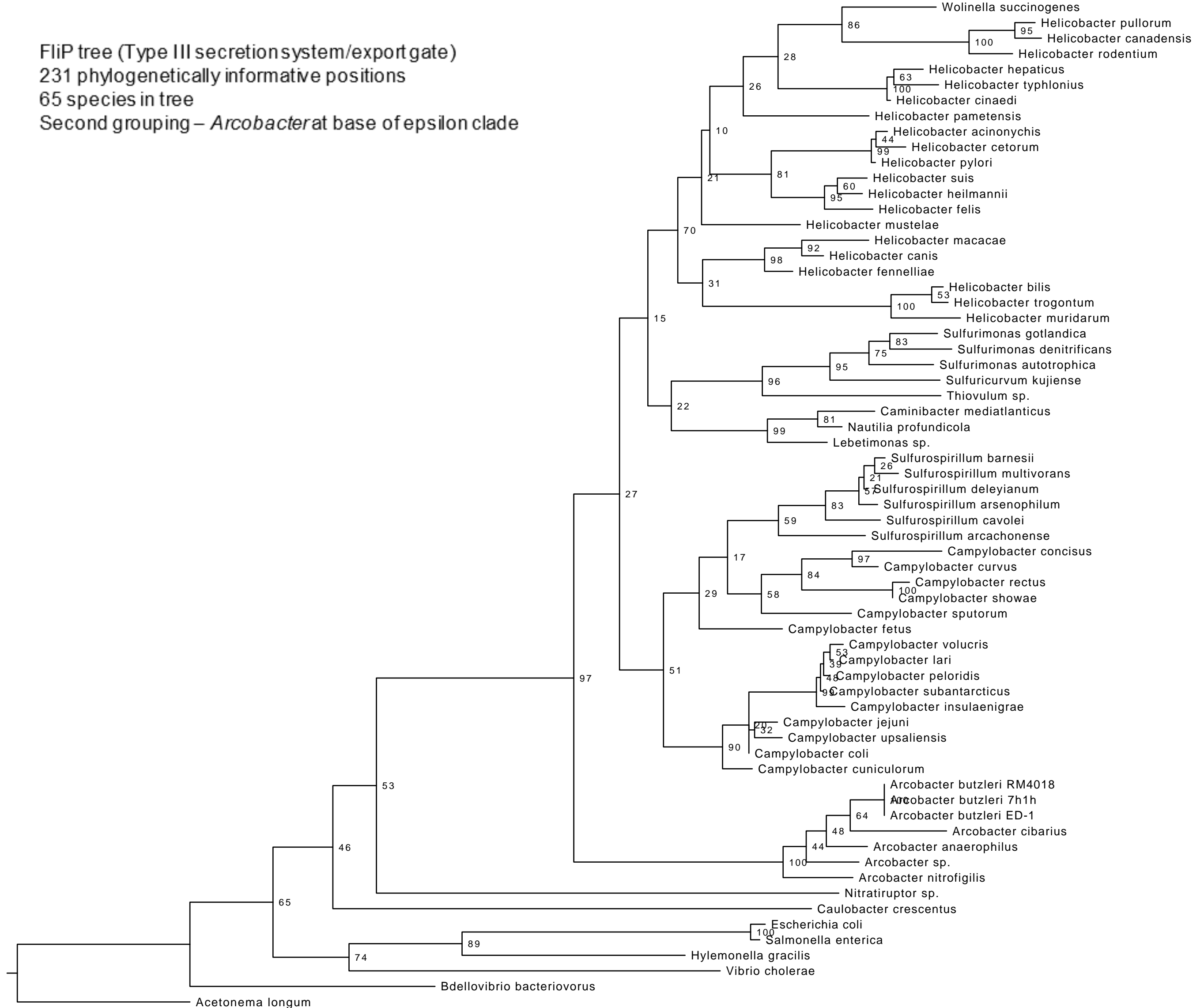
65 species in tree

Second grouping – *Arcobacter* at base of epsilon clade



0.7

Flp tree (Type III secretion system/export gate)
 231 phylogenetically informative positions
 65 species in tree
 Second grouping – *Arcobacter* at base of epsilon clade



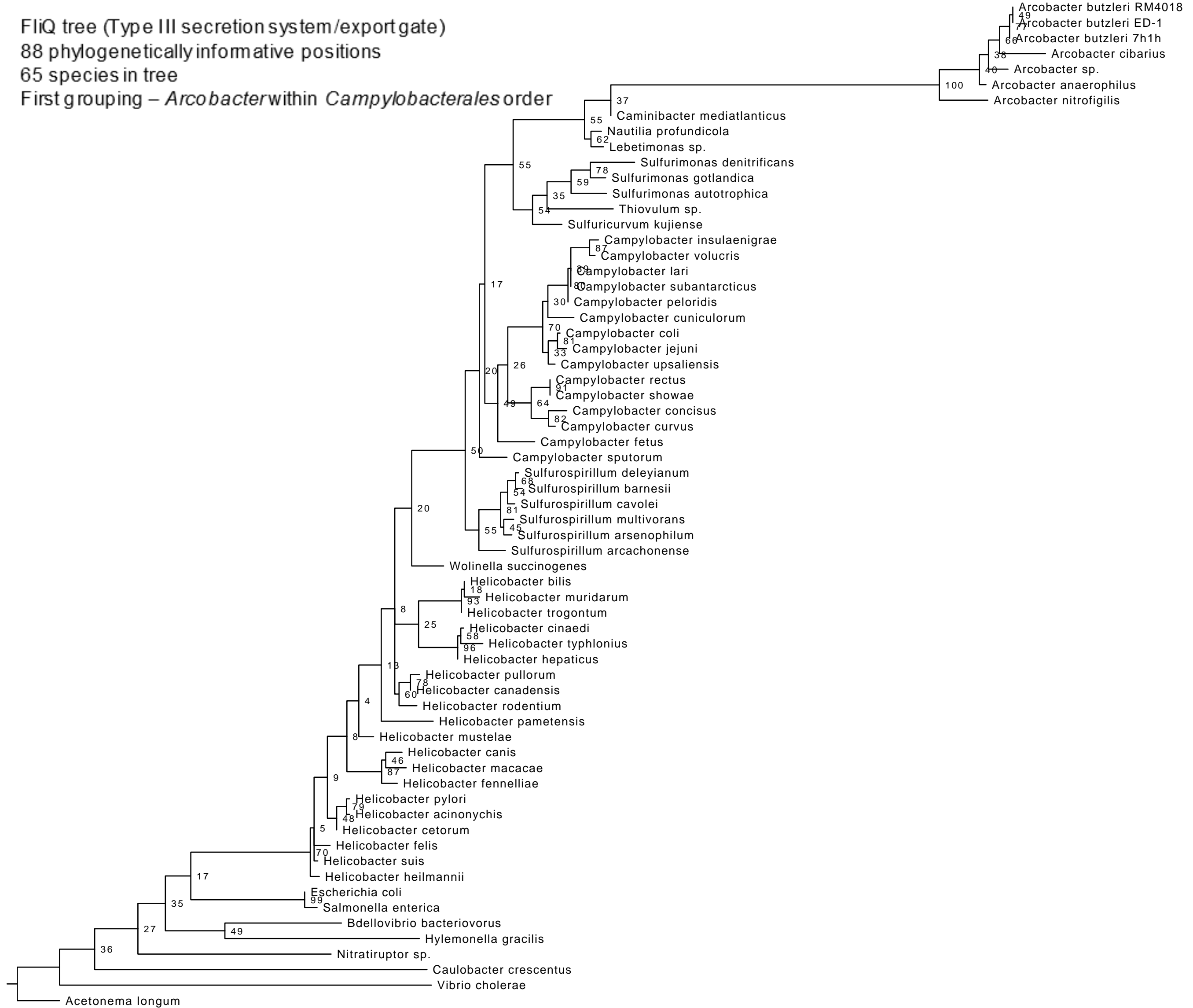
0.2

FliQ tree (Type III secretion system/export gate)

88 phylogenetically informative positions

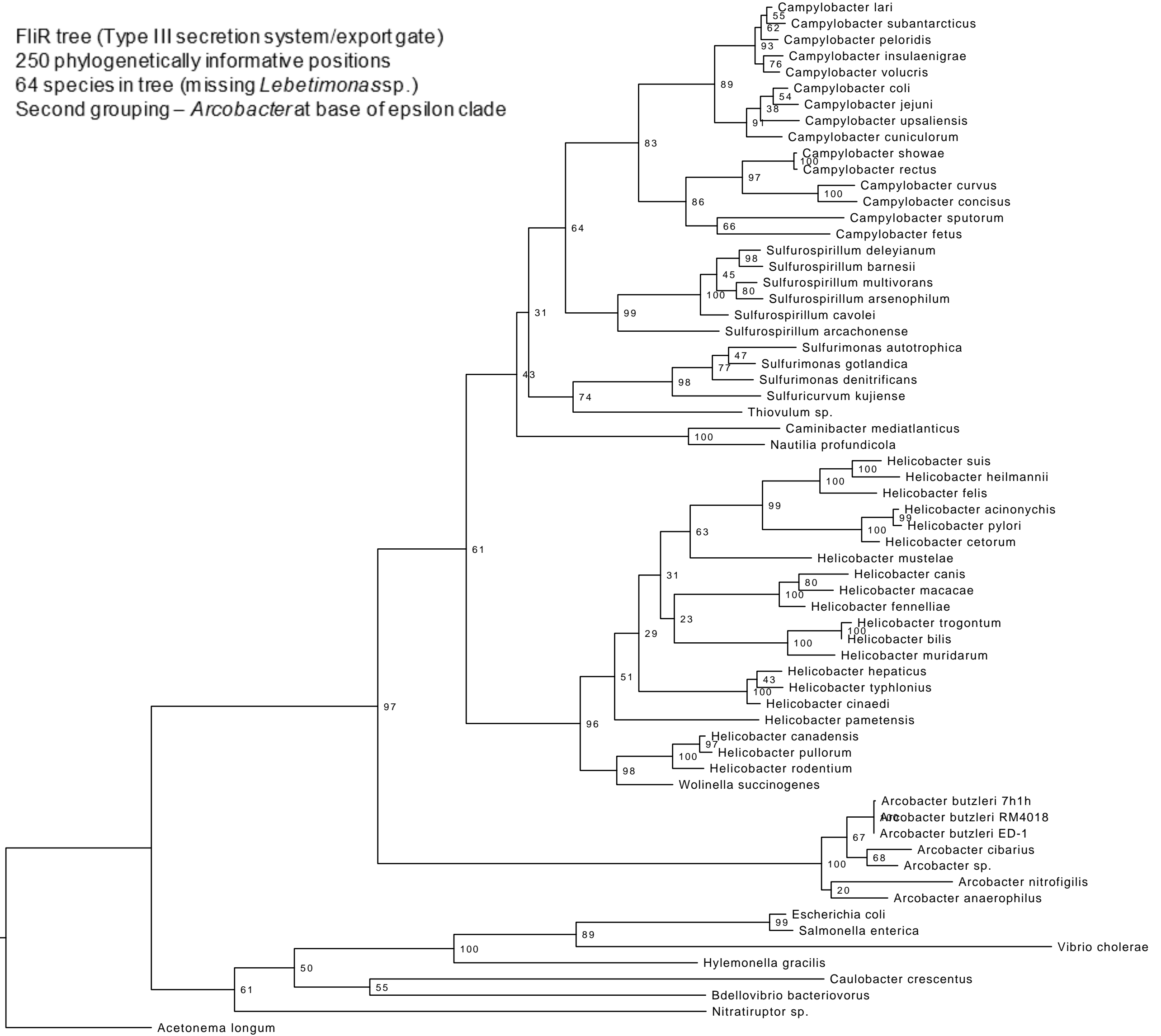
65 species in tree

First grouping – *Arcobacter* within *Campylobacterales* order



0.3

FliR tree (Type III secretion system/export gate)
 250 phylogenetically informative positions
 64 species in tree (missing *Lebetimonas* sp.)
 Second grouping – *Arcobacter* at base of epsilon clade



0.5

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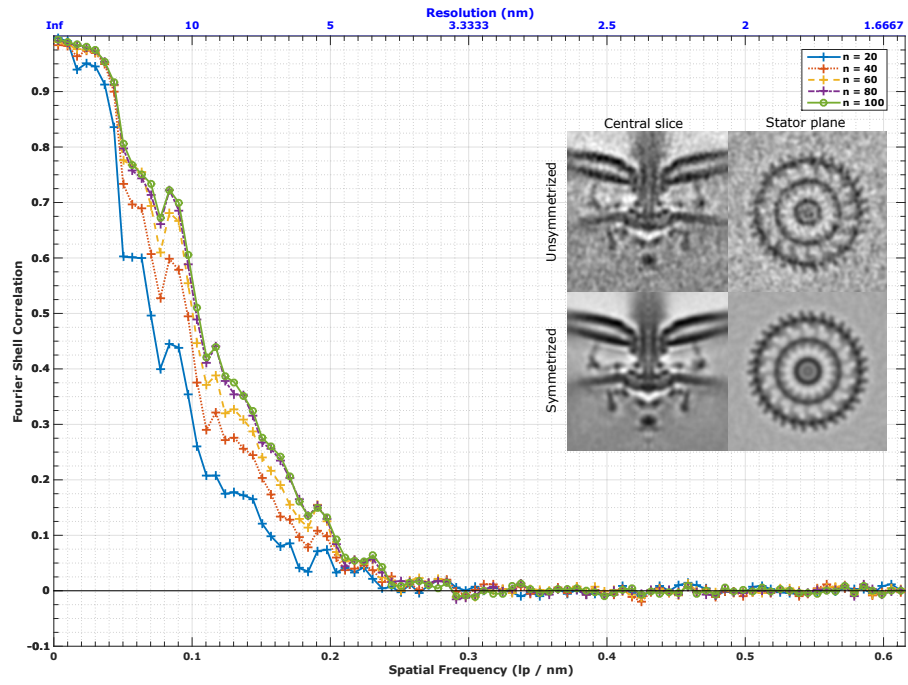
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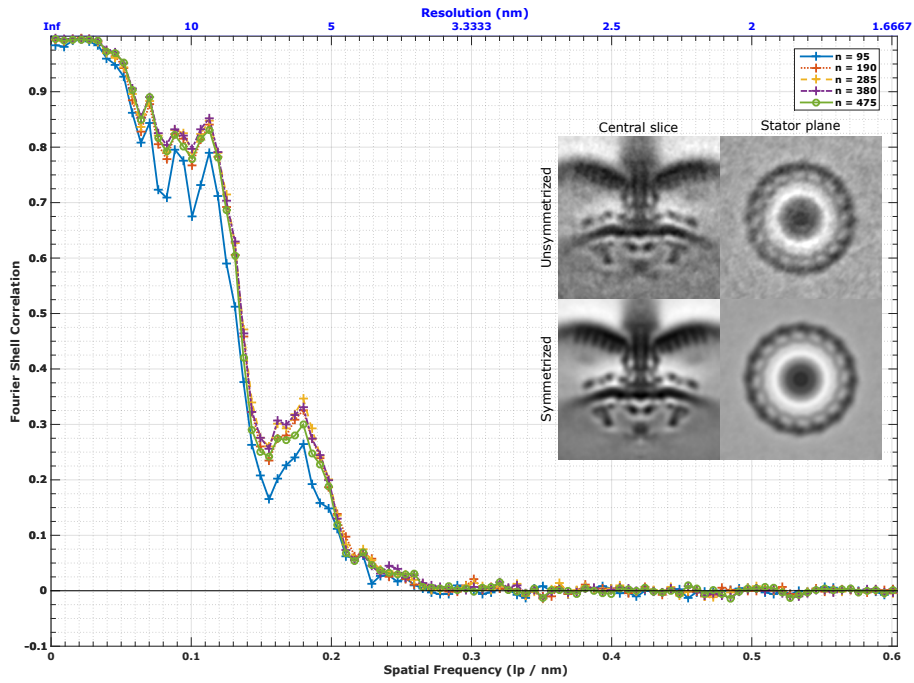
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Supplementary Figure S4: FSC curves of subtomogram averages, and side- and top-view slices through unsymmetrized and symmetrized structures. (Top to bottom): *Wolinella succinogenes*, *Arcobacter butzleri*, and *Bdellovibrio bacteriovorus*. FSC curves were determined using PEET's inbuilt *calcFSC* and *plotFSC* programs. Resolutions in Angstroms at a 0.5 threshold are 98 for *Wolinella succinogenes*, 82 for *Arcobacter butzleri*, and 80 for *Bdellovibrio bacteriovorus*.

Wolinella succinogenes



Arcobacter butzleri



Bdellovibrio bacteriovorus

