

Title: Supplementary Data 1.

- Composition of the 2 superclusters and 2 orphan clusters of HUH endonucleases;
- Accession numbers for the HUH endonucleases depicted in the network shown in Figure 1;
- Composition of the 9 groups of bacterial viral-like Repts;
- Genomic neighborhoods of the integrated plasmids.

Title: Supplementary Data 2.

- Sequence alignment used to generate the tree shown in Figure 2A.

Title: Supplementary Data 3.

- Sequence alignment used to generate the tree shown in Figure 5.

Title: Supplementary Data 4.

- Maximum likelihood tree shown in Figure 2A in newick format.

Title: Supplementary Data 5.

- Maximum likelihood tree shown in Figure 5 in newick format.

Title: Supplementary Data 6.

- Constrained tree shown in Supplementary figure S5A in newick format.

Title: Supplementary Data 7.

- Constrained tree shown in Supplementary figure S5B in newick format.

Title: Supplementary Data 8.

- Constrained tree shown in Supplementary figure S5C in newick format.

Title: Supplementary Data 9.

- Maximum likelihood tree shown in Supplementary figure S6A in newick format.

Title: Supplementary Data 10.

- Maximum likelihood tree shown in Supplementary figure S6B in newick format.