Adaptation of tree shown, noting root positions discussed here

```
                Hadobacteria            Gracilicutes            Actinobacteria    Eukaryota
                |                       | Eurybacteria          |                 |
Chlorobacteria  |       Cyanobacteria   |   |||   Endobacteria  |     Archaebacteria |
  __|___________|___________|___________|___|||_______|___________|____________|_______|
  |                                                   | |                 |
  |                                                   | |                 |
  New                                               Alternates          Paralog
```

Character evolution under alternate roots (within Endobacteria or between Endobacteria & Actinobacteria)

```
                Hadobacteria            Gracilicutes            Actinobacteria    Eukaryota
                |                       |  Eurybacteria         |                 |
Chlorobacteria  |       Cyanobacteria   |   |||   Endobacteria  |     Archaebacteria |
    |___________|___________|___________|____|||_____|___________|____________|_______|
        ^           ^         ^ ^            ^      |    |    ^ ^
        |           |         | |            |      |    |    | |
    Omp85 loss   LPS loss     | HslVU loss   |      |    |    | Phosphatidylinositol gain
                 Flagella loss    OM gain     |      | 20S proteasome gain/HslVU loss
                                              |      |
                                          Alternate roots
                                      (Flagella & HslVU present)
```