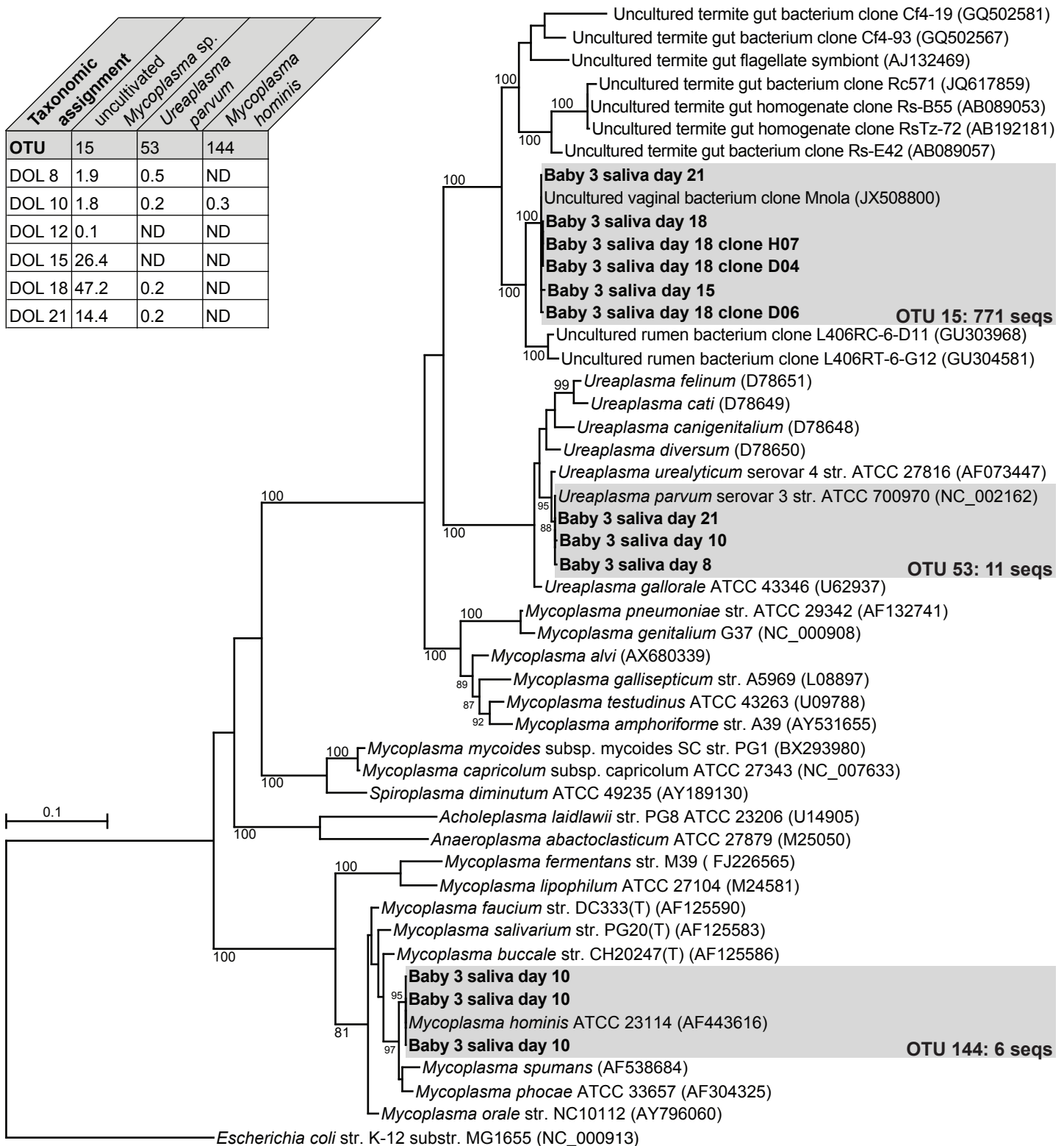


| OTU    | 15   | 53  | 144 |
|--------|------|-----|-----|
| DOL 8  | 1.9  | 0.5 | ND  |
| DOL 10 | 1.8  | 0.2 | 0.3 |
| DOL 12 | 0.1  | ND  | ND  |
| DOL 15 | 26.4 | ND  | ND  |
| DOL 18 | 47.2 | 0.2 | ND  |
| DOL 21 | 14.4 | 0.2 | ND  |



**Supplemental Figure S4.** Phylogenetic relationships among 3 Tenericutes OTUs (gray boxes) and close relatives, inferred using a maximum likelihood approach. Node support was assessed using 100 bootstrap replicates; values >80% are shown. The scale bar represents 0.1 substitutions per site. The phylogeny was inferred using RAxML version 7.2.8 and the GTRCAT model. The near-full length alignment contained 620 distinct alignment positions (columns). The alignment also included nine shorter pyrosequencing reads. ‘Clone’ indicates near-full length cloned sequence. Upper left, OTU proportional abundances in baby 3’s saliva; ND, not detected