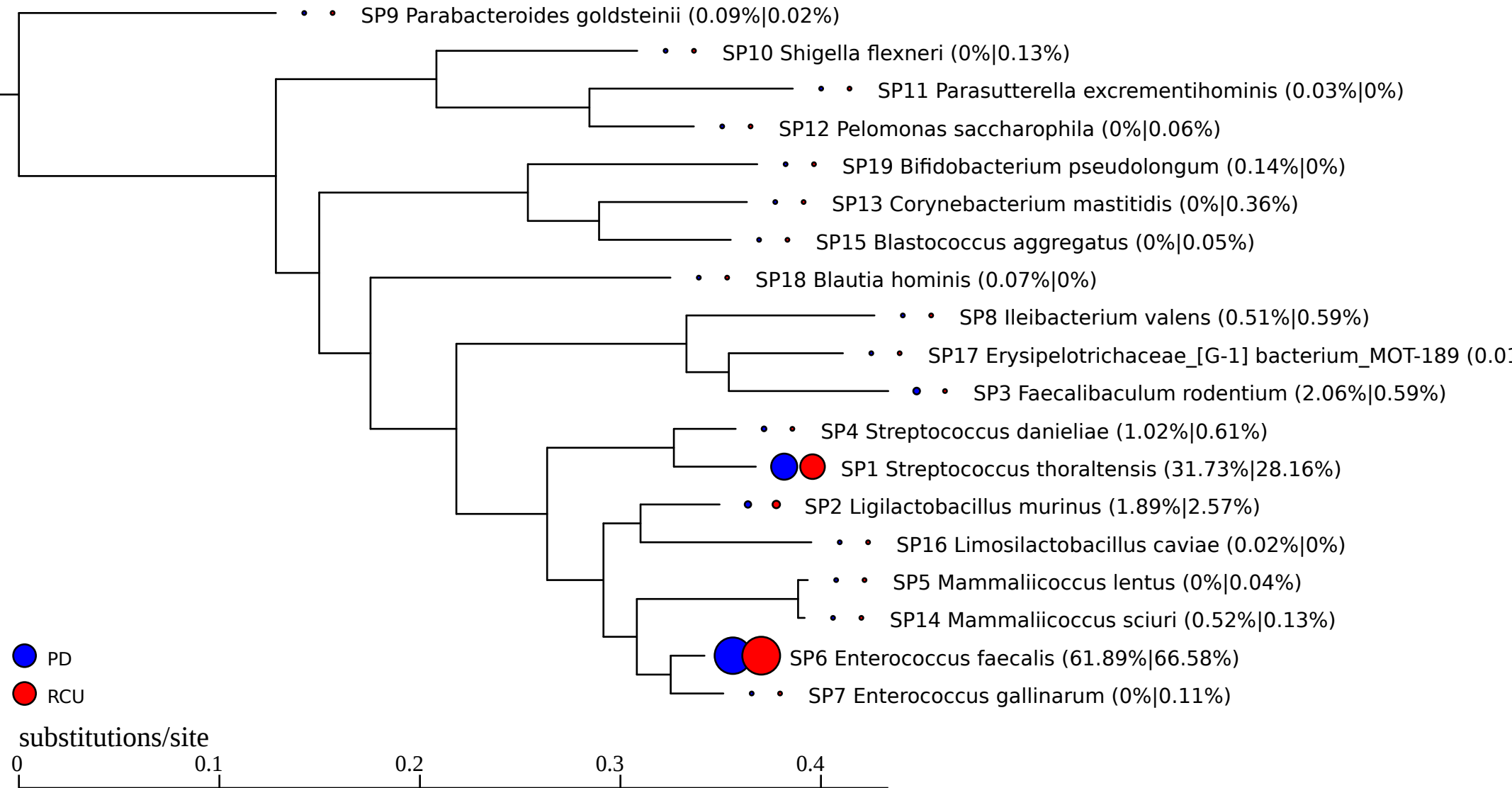
SP9 Parabacteroides goldsteinii (0.09%|0.02%)
SP10 Shigella flexneri (0%|0.13%)
SP11 Parasutterella excrementihominis (0.03%|0%)
SP12 Pelomonas saccharophila (0%|0.06%)
SP19 Bifidobacterium pseudolongum (0.14%|0%)
SP13 Corynebacterium mastitidis (0%|0.36%)
SP15 Blastococcus aggregatus (0%|0.05%)
SP18 Blautia hominis (0.07%|0%)
SP8 Ileibacterium valens (0.51%|0.59%)
SP17 Erysipelotrichaceae_[G-1] bacterium_MOT-189 (0.01
SP3 Faecalibaculum rodentium (2.06%|0.59%)
SP4 Streptococcus danieliae (1.02%|0.61%)
SP1 Streptococcus thoraltensis (31.73%|28.16%)
SP2 Ligilactobacillus murinus (1.89%|2.57%)
SP16 Limosilactobacillus caviae (0.02%|0%)
SP5 Mammaliicoccus lentus (0%|0.04%)
SP14 Mammaliicoccus sciuri (0.52%|0.13%)
SP6 Enterococcus faecalis (61.89%|66.58%)
SP7 Enterococcus gallinarum (0%|0.11%)
PD
RCU
substitutions/site
0
0.1
0.2
0.3
0.4