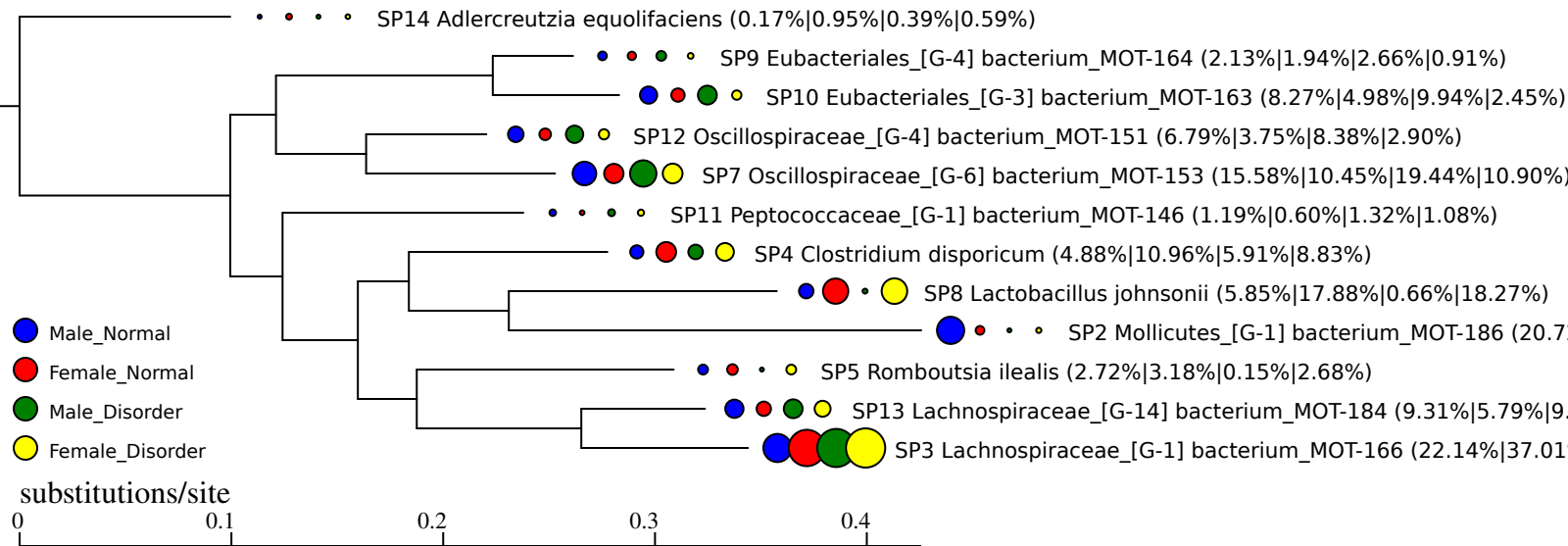
SP14 Adlercreutzia equolifaciens (0.17%|0.95%|0.39%|0.59%)
SP9 Eubacteriales_[G-4] bacterium_MOT-164 (2.13%|1.94%|2.66%|0.91%)
SP10 Eubacteriales_[G-3] bacterium_MOT-163 (8.27%|4.98%|9.94%|2.45%)
SP12 Oscillospiraceae_[G-4] bacterium_MOT-151 (6.79%|3.75%|8.38%|2.90%)
SP7 Oscillospiraceae_[G-6] bacterium_MOT-153 (15.58%|10.45%|19.44%|10.90%)
SP11 Peptococcaceae_[G-1] bacterium_MOT-146 (1.19%|0.60%|1.32%|1.08%)
SP4 Clostridium disporicum (4.88%|10.96%|5.91%|8.83%)
SP8 Lactobacillus johnsonii (5.85%|17.88%|0.66%|18.27%)
SP2 Mollicutes_[G-1] bacterium_MOT-186 (20.7
SP5 Romboutsia ilealis (2.72%|3.18%|0.15%|2.68%)
SP13 Lachnospiraceae_[G-14] bacterium_MOT-184 (9.31%|5.79%|9.
SP3 Lachnospiraceae_[G-1] bacterium_MOT-166 (22.14%|37.01
Male_Normal
Female_Normal
Male_Disorder
Female_Disorder
substitutions/site
0
0.1
0.2
0.3
0.4