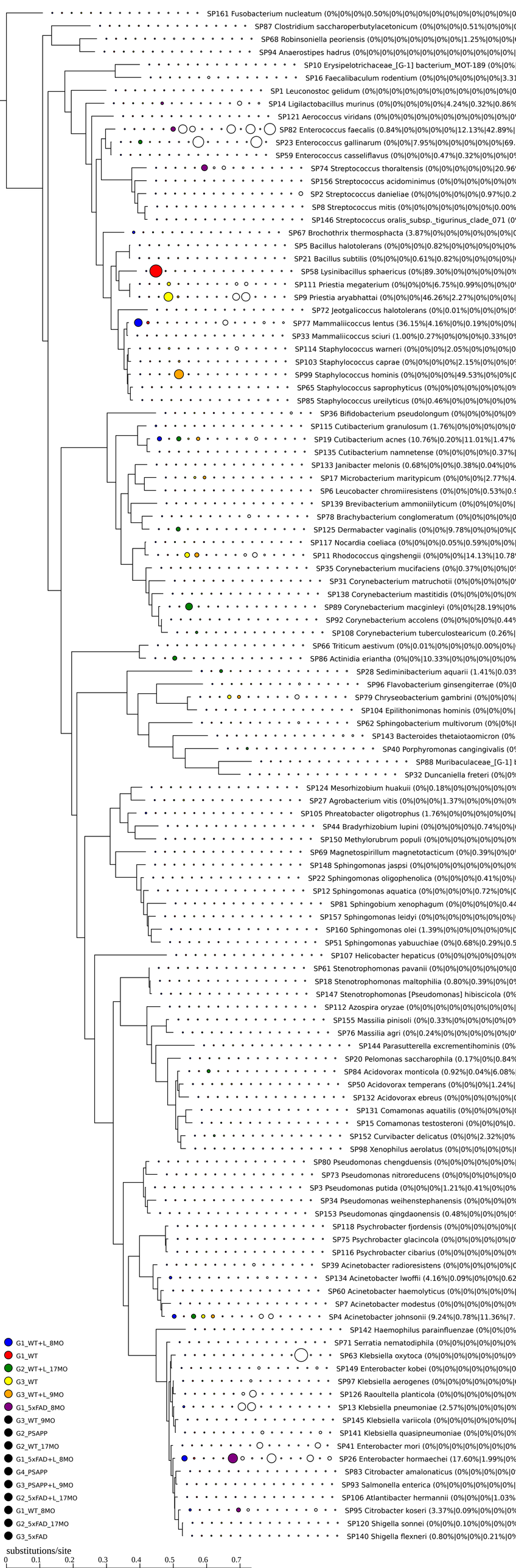
SP161 Fusobacterium nucleatum (0%|0%|0%|0.50%|0%|0%|0%|0%|0%|0%|0%|0%|0%|0%|0%|0
SP87 Clostridium saccharoperbutylacetonicum (0%|0%|0%|0.51%|0%|0%|0
SP68 Robinsoniella peoriensis (0%|0%|0%|0%|0%|0%|0%|0%|1.25%|0%|0%|
SP94 Anaerostipes hadrus (0%|0%|0%|0%|0%|0%|0%|0%|0%|0%|0%|0%|0%|
SP10 Erysipelotrichaceae_[G-1] bacterium_MOT-189 (0%|0%|
SP16 Faecalibaculum rodentium (0%|0%|0%|0%|0%|0%|3.31
SP1 Leuconostoc gelidum (0%|0%|0%|0%|0%|0%|0%|0%|0%|0%|0%|0%|0
SP14 Ligilactobacillus murinus (0%|0%|0%|0%|0%|4.24%|0.32%|0.86%
SP121 Aerococcus viridans (0%|0%|0%|0%|0%|0%|0%|0%|0%|0%|0%|0%|0
SP82 Enterococcus faecalis (0.84%|0%|0%|0%|0%|12.13%|42.89%|
SP23 Enterococcus gallinarum (0%|0%|7.95%|0%|0%|0%|0%|0%|69.
SP59 Enterococcus casseliflavus (0%|0%|0%|0.47%|0.32%|0%|0%|0
SP74 Streptococcus thoraltensis (0%|0%|0%|0%|0%|20.96
SP156 Streptococcus acidominimus (0%|0%|0%|0%|0%|0%
SP2 Streptococcus danieliae (0%|0%|0%|0%|0%|0.97%|0.2
SP8 Streptococcus mitis (0%|0%|0%|0%|0%|0%|0%|0.00%
SP146 Streptococcus oralis_subsp._tigurinus_clade_071 (0
SP67 Brochothrix thermosphacta (3.87%|0%|0%|0%|0%|0%|0%|0
SP5 Bacillus halotolerans (0%|0%|0%|0.82%|0%|0%|0%|0%|0%
SP21 Bacillus subtilis (0%|0%|0%|0.61%|0.82%|0%|0%|0%|0%|
SP58 Lysinibacillus sphaericus (0%|89.30%|0%|0%|0%|0%|0%
SP111 Priestia megaterium (0%|0%|0%|6.75%|0.99%|0%|0%|0
SP9 Priestia aryabhattai (0%|0%|0%|46.26%|2.27%|0%|0%|0%|
SP72 Jeotgalicoccus halotolerans (0%|0.01%|0%|0%|0%|0
SP77 Mammaliicoccus lentus (36.15%|4.16%|0%|0.19%|0%|0%|
SP33 Mammaliicoccus sciuri (1.00%|0.27%|0%|0%|0%|0.33%|0
SP114 Staphylococcus warneri (0%|0%|0%|2.05%|0%|0%|0%|0
SP103 Staphylococcus caprae (0%|0%|0%|0%|2.15%|0%|0%|0
SP99 Staphylococcus hominis (0%|0%|0%|0%|49.53%|0%|0%|0
SP65 Staphylococcus saprophyticus (0%|0%|0%|0%|0%|0%|0%
SP85 Staphylococcus ureilyticus (0%|0.46%|0%|0%|0%|0%|0%
SP36 Bifidobacterium pseudolongum (0%|0%|0%|0%|0%|0%
SP115 Cutibacterium granulosum (1.76%|0%|0%|0%|0%|0
SP19 Cutibacterium acnes (10.76%|0.20%|11.01%|1.47%
SP135 Cutibacterium namnetense (0%|0%|0%|0%|0.37%|
SP133 Janibacter melonis (0.68%|0%|0%|0.38%|0.04%|0%
SP17 Microbacterium maritypicum (0%|0%|0%|2.77%|4.
SP6 Leucobacter chromiiresistens (0%|0%|0%|0.53%|0.9
SP139 Brevibacterium ammoniilyticum (0%|0%|0%|0%|
SP78 Brachybacterium conglomeratum (0%|0%|0%|0%|0
SP125 Dermabacter vaginalis (0%|0%|9.78%|0%|0%|0%|0
SP117 Nocardia coeliaca (0%|0%|0%|0.05%|0.59%|0%|0%|
SP11 Rhodococcus qingshengii (0%|0%|0%|14.13%|10.78
SP35 Corynebacterium mucifaciens (0%|0.37%|0%|0%|0
SP31 Corynebacterium matruchotii (0%|0%|0%|0%|0
SP138 Corynebacterium mastitidis (0%|0%|0%|0%|0%
SP89 Corynebacterium macginleyi (0%|0%|28.19%|0%
SP92 Corynebacterium accolens (0%|0%|0%|0%|0.44%
SP108 Corynebacterium tuberculostearicum (0.26%|
SP66 Triticum aestivum (0%|0.01%|0%|0%|0%|0.00%|0%|
SP86 Actinidia eriantha (0%|0%|10.33%|0%|0%|0%|0%|0%
SP28 Sediminibacterium aquarii (1.41%|0.03%
SP96 Flavobacterium ginsengiterrae (0%|0
SP79 Chryseobacterium gambrini (0%|0%|0%|
SP104 Epilithonimonas hominis (0%|0%|0%|
SP62 Sphingobacterium multivorum (0%|0%|0
SP143 Bacteroides thetaiotaomicron (0%
SP40 Porphyromonas cangingivalis (0
SP88 Muribaculaceae_[G-1] b
SP32 Duncaniella freteri (0%|0%
SP124 Mesorhizobium huakuii (0%|0.18%|0%|0%|0%|0%|0%
SP27 Agrobacterium vitis (0%|0%|0%|1.37%|0%|0%|0%|0%
SP105 Phreatobacter oligotrophus (1.76%|0%|0%|0%|0%|0%|
SP44 Bradyrhizobium lupini (0%|0%|0%|0%|0.74%|0%|
SP150 Methylorubrum populi (0%|0%|0%|0%|0%|0%|0%|0%
SP69 Magnetospirillum magnetotacticum (0%|0.39%|0%|0
SP148 Sphingomonas jaspsi (0%|0%|0%|0%|0%|0%|0%|0%
SP22 Sphingomonas oligophenolica (0%|0%|0%|0.41%|0%|
SP12 Sphingomonas aquatica (0%|0%|0%|0%|0.72%|0%|0
SP81 Sphingobium xenophagum (0%|0%|0%|0%|0.44
SP157 Sphingomonas leidyi (0%|0%|0%|0%|0%|0%|0%|
SP160 Sphingomonas olei (1.39%|0%|0%|0%|0%|0%|0
SP51 Sphingomonas yabuuchiae (0%|0.68%|0.29%|0.5
SP107 Helicobacter hepaticus (0%|0%|0%|0%|0%|0%
SP61 Stenotrophomonas pavanii (0%|0%|0%|0%|0%|0%|0
SP18 Stenotrophomonas maltophilia (0.80%|0.39%|0%|0
SP147 Stenotrophomonas [Pseudomonas] hibiscicola (0%
SP112 Azospira oryzae (0%|0%|0%|0%|0%|0%|0%|
SP155 Massilia pinisoli (0%|0.33%|0%|0%|0%|0%|0%
SP76 Massilia agri (0%|0.24%|0%|0%|0%|0%|0%|0
SP144 Parasutterella excrementihominis (0%
SP20 Pelomonas saccharophila (0.17%|0%|0.84%
SP84 Acidovorax monticola (0.92%|0.04%|6.08%|
SP50 Acidovorax temperans (0%|0%|0%|1.24%|
SP132 Acidovorax ebreus (0%|0%|0%|0%|0%|0
SP131 Comamonas aquatilis (0%|0%|0%|0%|0
SP15 Comamonas testosteroni (0%|0%|0%|0.
SP152 Curvibacter delicatus (0%|0%|2.32%|0%
SP98 Xenophilus aerolatus (0%|0%|0%|0%|0%|0
SP80 Pseudomonas chengduensis (0%|0%|0%|0%|0%|0%|
SP73 Pseudomonas nitroreducens (0%|0%|0%|0%|0%|0
SP3 Pseudomonas putida (0%|0%|0%|1.21%|0.41%|0%|0%
SP34 Pseudomonas weihenstephanensis (0%|0%|0%|0%
SP153 Pseudomonas qingdaonensis (0.48%|0%|0%|0%|0
SP118 Psychrobacter fjordensis (0%|0%|0%|0%|0%|0
SP75 Psychrobacter glacincola (0%|0%|0%|0%|0%|0
SP116 Psychrobacter cibarius (0%|0%|0%|0%|0%|0%
SP39 Acinetobacter radioresistens (0%|0%|0%|0%|0
SP134 Acinetobacter lwoffii (4.16%|0.09%|0%|0%|0.62
SP60 Acinetobacter haemolyticus (0%|0%|0%|0%|0%|
SP7 Acinetobacter modestus (0%|0%|0%|0%|0%|0%
SP4 Acinetobacter johnsonii (9.24%|0.78%|11.36%|7.
SP142 Haemophilus parainfluenzae (0%|0%|0%
SP71 Serratia nematodiphila (0%|0%|0%|0%|0%|0%
SP63 Klebsiella oxytoca (0%|0%|0%|0%|0%|0%|0%
SP149 Enterobacter kobei (0%|0%|0%|0%|0%|0%|0
SP97 Klebsiella aerogenes (0%|0%|0%|0%|0%|0%|
SP126 Raoultella planticola (0%|0%|0%|0%|0%|0%
SP13 Klebsiella pneumoniae (2.57%|0%|0%|0%|0%
SP145 Klebsiella variicola (0%|0%|0%|0%|0%|0%|
SP141 Klebsiella quasipneumoniae (0%|0%|0%|0%
SP41 Enterobacter mori (0%|0%|0%|0%|0%|0%|0%
SP26 Enterobacter hormaechei (17.60%|1.99%|0%
SP83 Citrobacter amalonaticus (0%|0%|0%|0%|0
SP93 Salmonella enterica (0%|0%|0%|0%|0%|
SP106 Atlantibacter hermannii (0%|0%|0%|1.03%
SP95 Citrobacter koseri (3.37%|0.09%|0%|0%|0%
SP120 Shigella sonnei (0%|0%|0.10%|0%|0%|0%
SP140 Shigella flexneri (0.80%|0%|0%|0.21%|0%
G1_WT+L_8MO
G1_WT
G2_WT+L_17MO
G3_WT
G3_WT+L_9MO
G1_5xFAD_8MO
G3_WT_9MO
G2_PSAPP
G2_WT_17MO
G1_5xFAD+L_8MO
G4_PSAPP
G3_PSAPP+L_9MO
G2_5xFAD+L_17MO
G1_WT_8MO
G2_5xFAD_17MO
G3_5xFAD
substitutions/site
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7