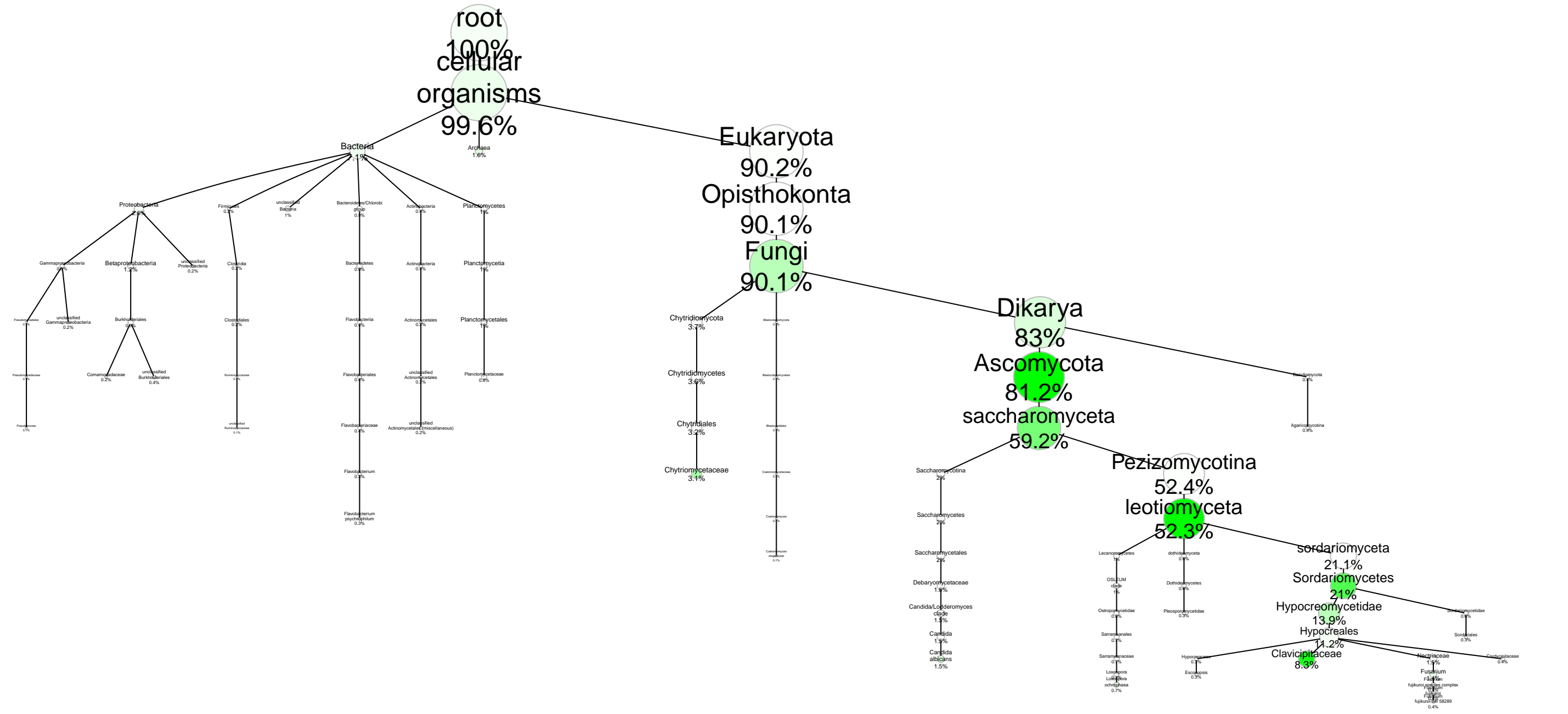


Diagram illustrating the overlap between root and cellular organisms:

- Intersection: 100% cellular organisms
- Root only: 99.6%



sample_SM12_norm2_sequence_fastq (total reads: 441892)

root
100%
cellular
organisms
99.5%

Eukaryota
84.1%
Opisthokonta
83.9%
Fungi
83.9%

Dikarya
77.1%
Ascomycota
75.2%
saccharomyceta
54.7%

Pezizomycotina
48.3%
leotiomyceta
48.2%

sordariomyceta
20.7%
Sordariomycetes
20.6%
Hypocreomycetidae
14%
Hypocreales
11.1%
Clavicipitaceae
8.4%

Nectriaceae
1.1%
Fusarium
0.8%
fujikuro spores complex
0.5%
fujikuro
0.5%
fujikuro TM 58289
0.5%

Bacteria
13%
Proteobacteria
5.3%
Gammaproteobacteria
1.1%
Pseudomonadales
0.6%
Pseudomonadaceae
0.6%
Pseudomonas
0.4%
Betaproteobacteria
2.5%
Burkholderiales
1.6%
Comamonadaceae
0.3%
Burkholderiaceae
1%
unclassified
Proteobacteria
0.6%
Firmicutes
0.4%
Clostridia
0.3%
Clostridiales
0.3%
Ruminococcaceae
0.1%
unclassified
Firmicutes
0.1%

Bacteroidetes/Chlorobi
group
1.4%
Bacteroidetes
1.5%
Flavobacteria
0.9%
Flavobacteriales
0.9%
Flavobacteriaceae
0.9%
Flavobacterium
0.8%
Flavobacterium
psychrophilum
0.5%

Actinobacteria
0.1%
Actinobacteria
0.1%
Actinomycetales
0.1%
unclassified
Actinomycetales
0.1%
unclassified
Actinomycetales (miscellaneous)
0.1%

Planctomycetes
1.5%
Planctomycetia
1.5%
Planctomycetales
1.5%
Planctomycetaceae
1%

Chytridiomycota
3.6%
Chytridiomycetes
3.4%
Chytridiales
3%
Chytriomycetaceae
2.9%

Basidiomycota
0.1%
Basidiomycetes
0.1%
Basidiomycotina
0.1%
Colletotrichaceae
0.1%
Colletotrichum
0.1%
Colletotrichum
angulatum
0.1%

Saccharomycotina
2%
Saccharomycetes
2%
Saccharomycetales
2%
Debaryomycetaceae
1.5%
Candida/Lodderomyces
clade
1.5%
Candida
1.5%
Candida
albicans
1.4%

Lecanoromycetes
1.2%
OSLEUM
clade
1.2%
Ostropomycetidae
1%
Sarcomyces
1%
Sarcomycetaceae
1%
Lecanora
1%
Lecanora
ochroleuca
1%

Dothideomycota
0.1%
Dothideomycetes
0.1%
Dothideomycotina
0.1%
Pezizomycetidae
0.3%
Hypocreales
0.1%
Eschscholzia
0.1%

Sordariomycetes
0.1%
Sordariomycetidae
0.1%
Sordariales
0.3%

Clavicipitaceae
8.4%

Nectriaceae
1.1%

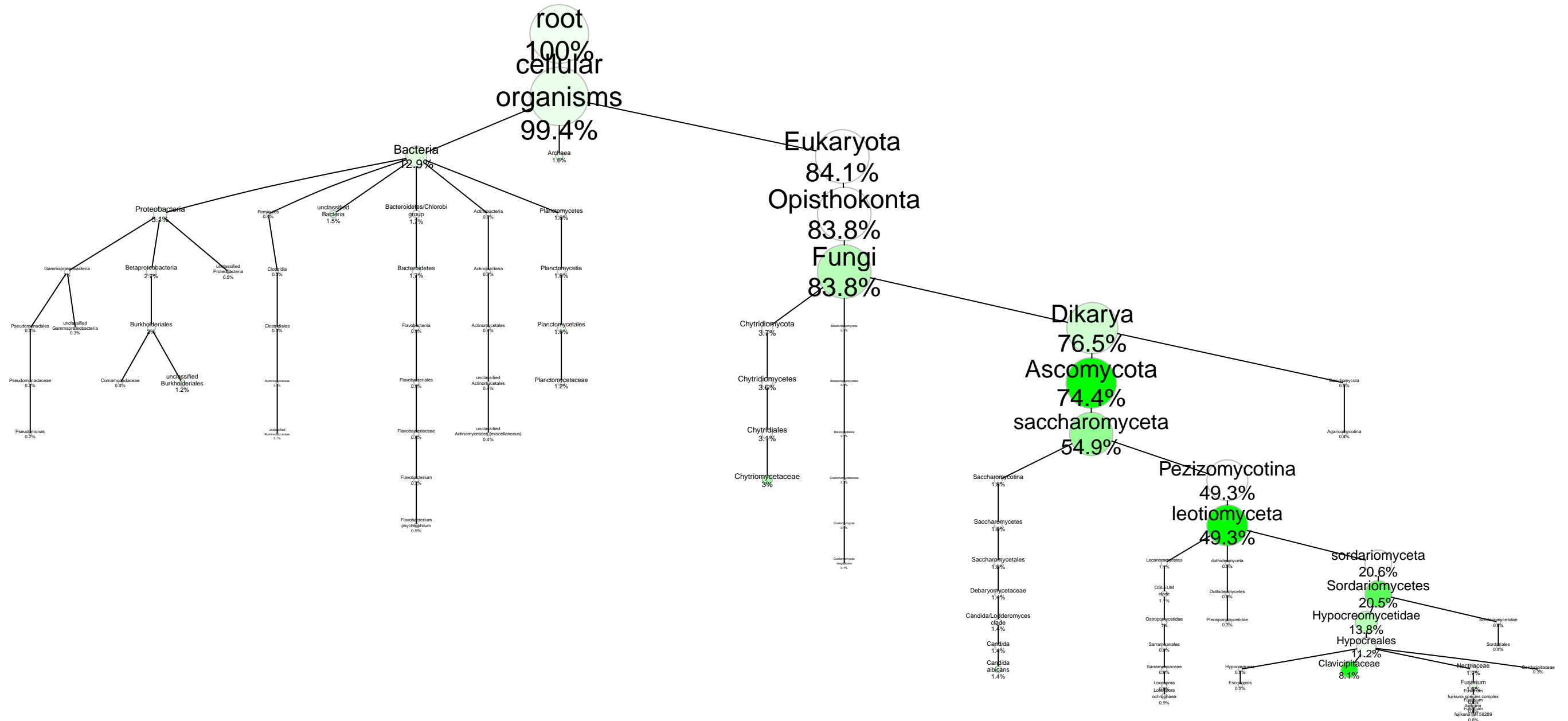
Fusarium
0.8%

fujikuro spores complex
0.5%

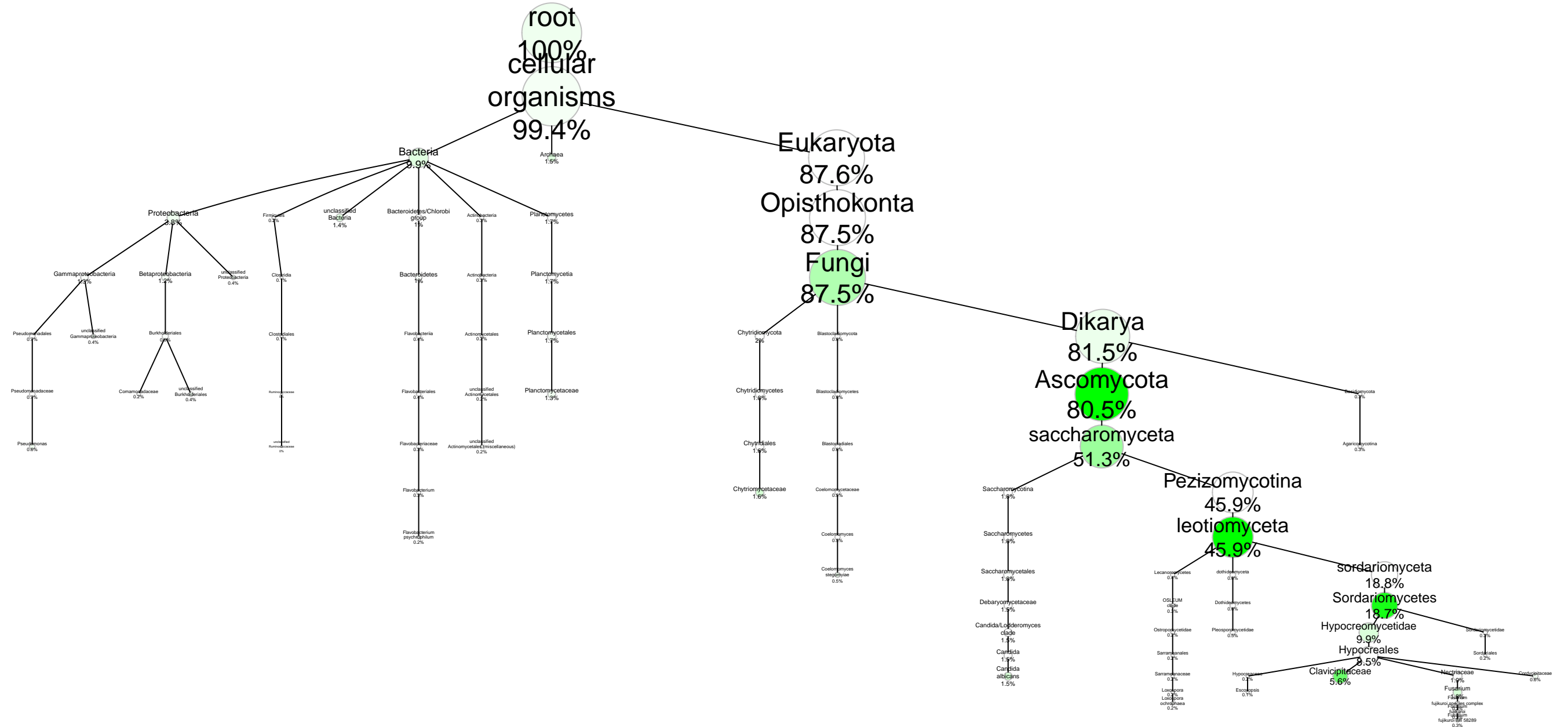
fujikuro
0.5%

fujikuro TM 58289
0.5%

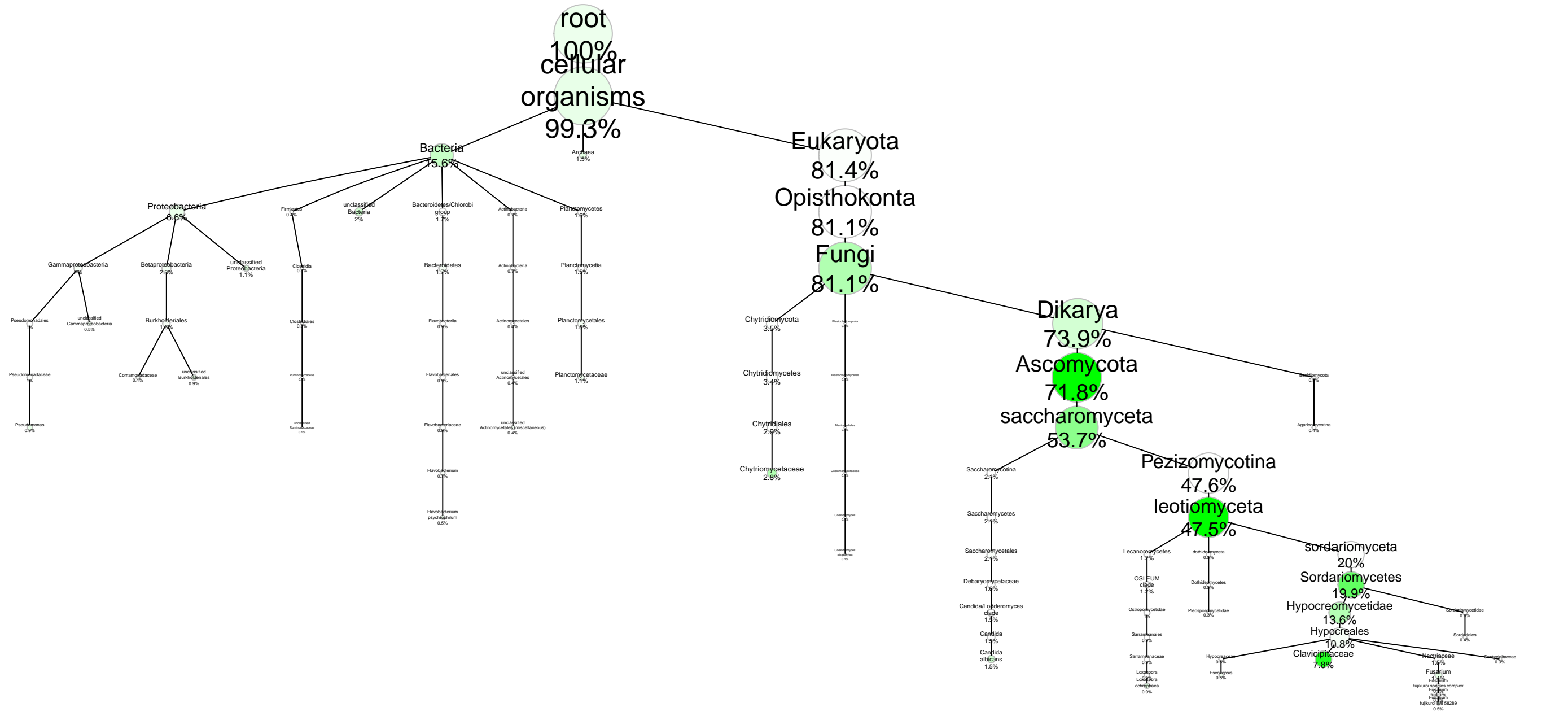
sample_SM13_norm3_sequence_fastq (total reads: 426473)



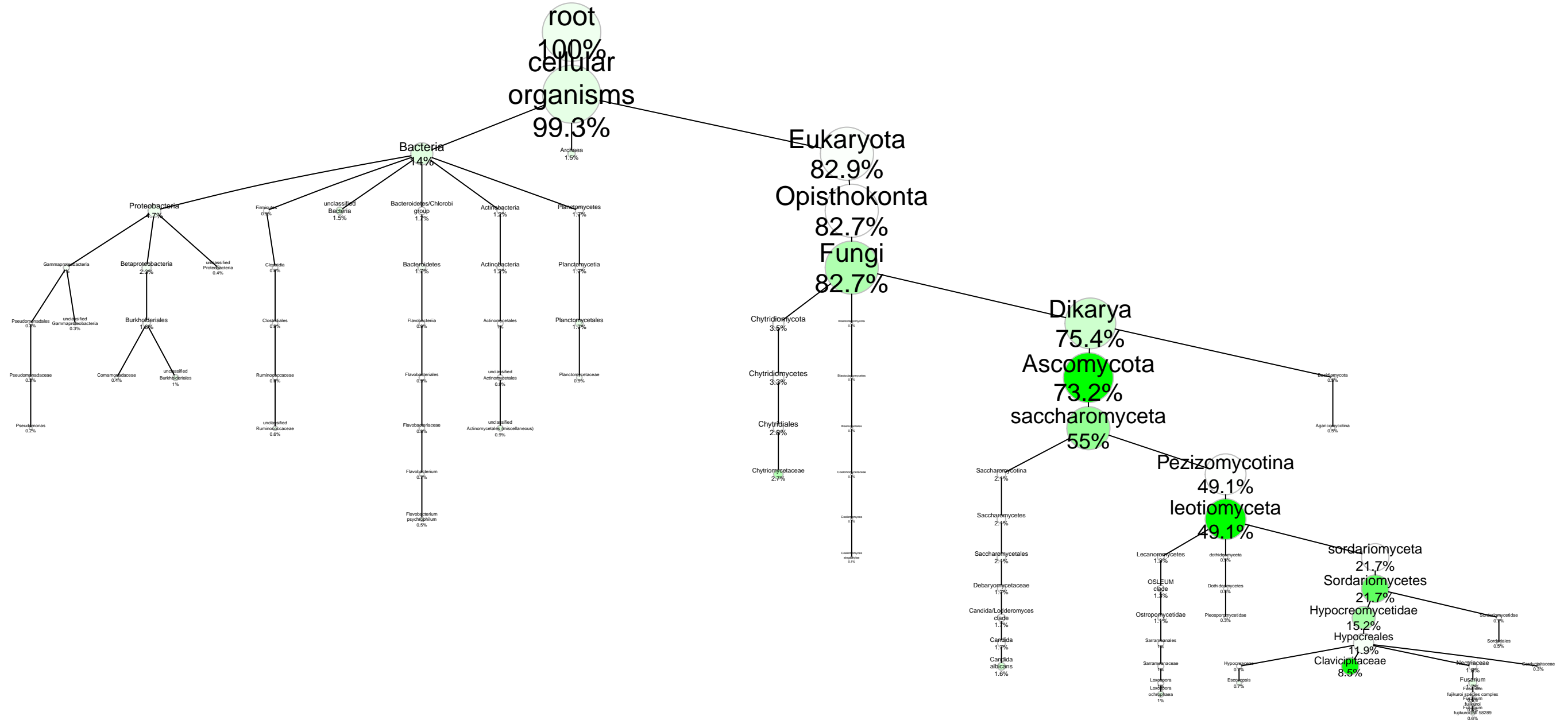
sample_SM1_crc1_sequence_fastq (total reads: 149978)



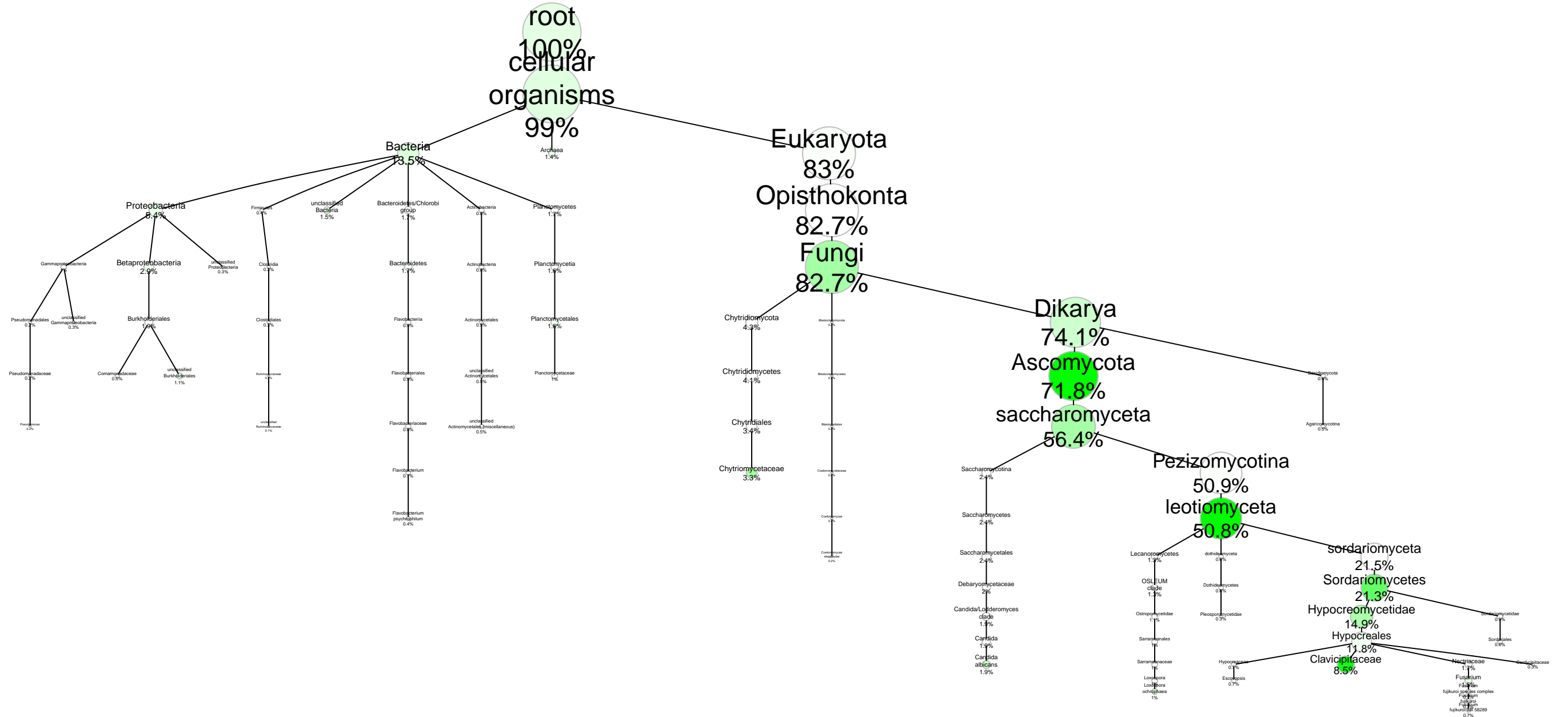
sample_SM2_crc2_sequence_fastq (total reads: 170695)



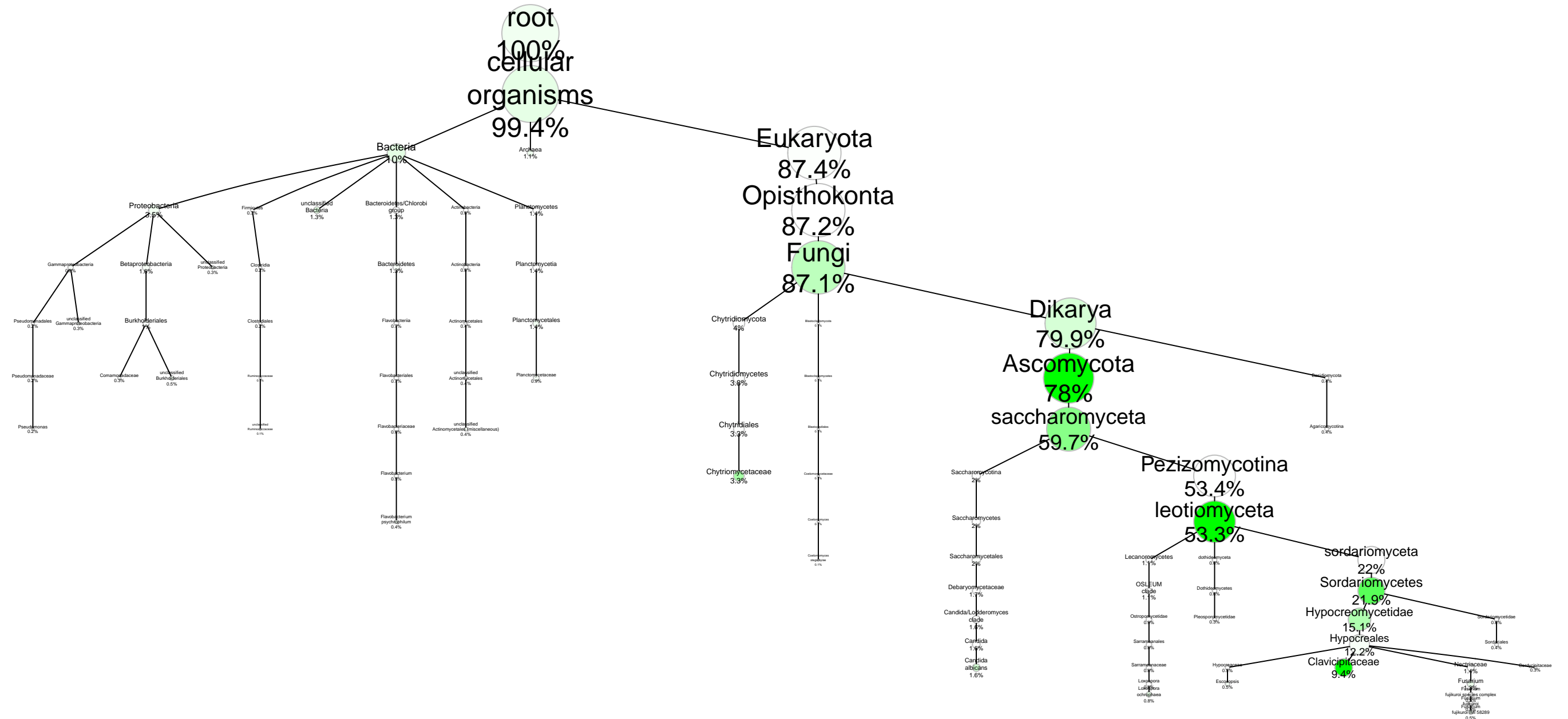
sample_SM3_crc3_sequence_fastq (total reads: 234597)



sample_SM6_uc1_sequence_fastq (total reads: 193029)



sample_SM7_uc2_sequence_fastq (total reads: 238275)



sample_SM8_uc3_sequence_fastq (total reads: 282740)

