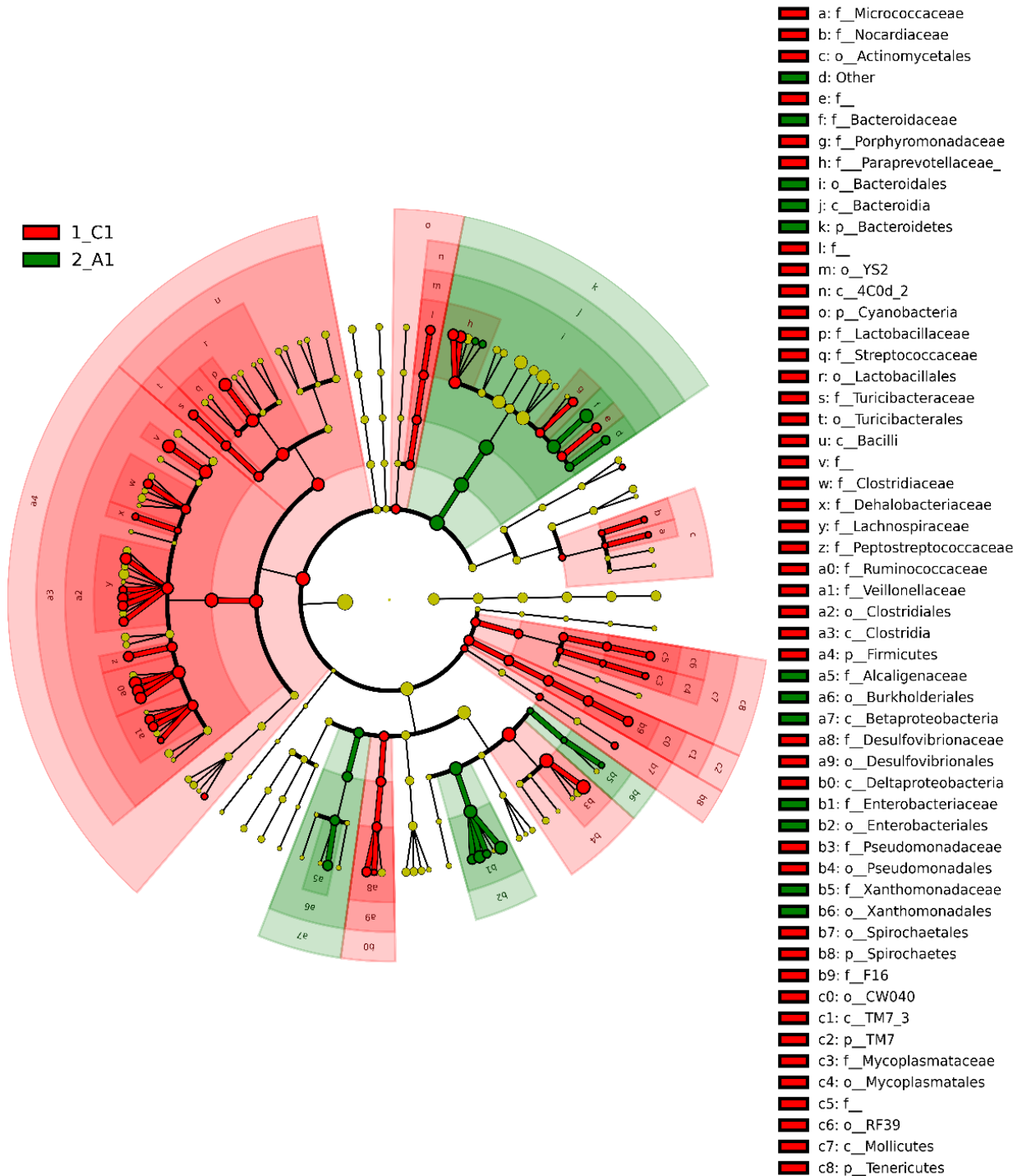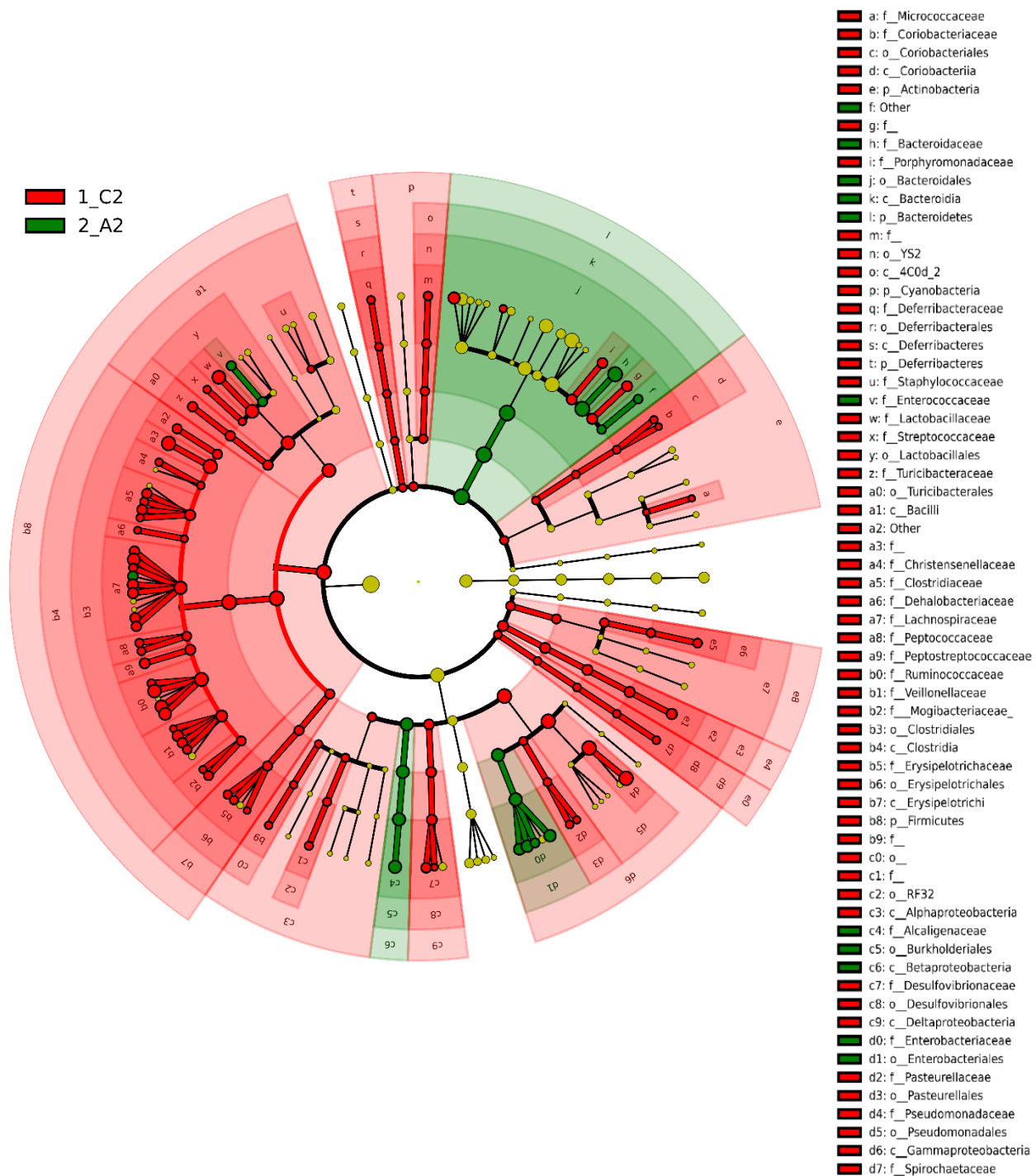# SUPPLEMENTAL MATERIAL

Figure S1. Cladogram generated from amoxicillin vs control treated rats microbiota at time point 1. (Expanded view of Figure 2c).

Legend:
- 1_C1 (red)
- 2_A1 (green)

- a: f__Micrococcaceae
- b: f__Nocardiaceae
- c: o__Actinomycetales
- d: Other
- e: f__
- f: f__Bacteroidaceae
- g: f__Porphyromonadaceae
- h: f___Paraprevotellaceae_
- i: o__Bacteroidales
- j: c__Bacteroidia
- k: p__Bacteroidetes
- l: f__
- m: o__YS2
- n: c__4C0d_2
- o: p__Cyanobacteria
- p: f__Lactobacillaceae
- q: f__Streptococcaceae
- r: o__Lactobacillales
- s: f__Turicibacteraceae
- t: o__Turicibacterales
- u: c__Bacilli
- v: f__
- w: f__Clostridiaceae
- x: f__Dehalobacteriaceae
- y: f__Lachnospiraceae
- z: f__Peptostreptococcaceae
- a0: f__Ruminococcaceae
- a1: f__Veillonellaceae
- a2: o__Clostridiales
- a3: c__Clostridia
- a4: p__Firmicutes
- a5: f__Alcaligenaceae
- a6: o__Burkholderiales
- a7: c__Betaproteobacteria
- a8: f__Desulfovibrionaceae
- a9: o__Desulfovibrionales
- b0: c__Deltaproteobacteria
- b1: f__Enterobacteriaceae
- b2: o__Enterobacteriales
- b3: f__Pseudomonadaceae
- b4: o__Pseudomonadales
- b5: f__Xanthomonadaceae
- b6: o__Xanthomonadales
- b7: o__Spirochaetales
- b8: p__Spirochaetes
- b9: f__F16
- c0: o__CW040
- c1: c__TM7_3
- c2: p__TM7
- c3: f__Mycoplasmataceae
- c4: o__Mycoplasmatales
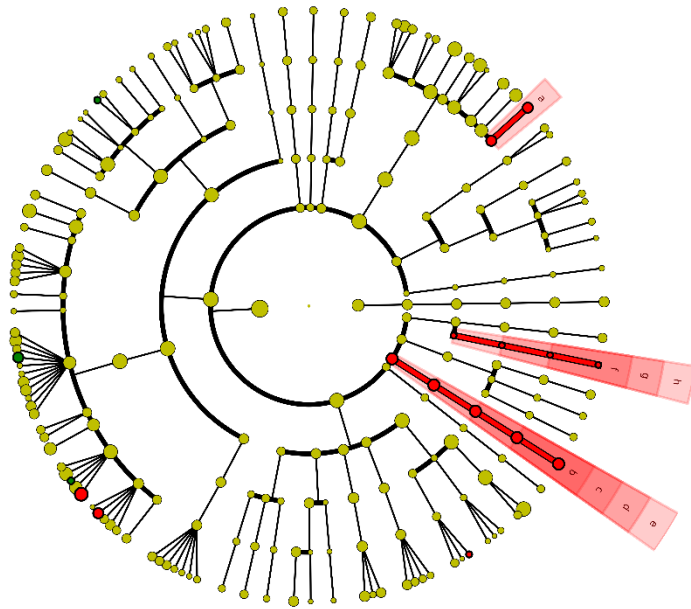- c5: f__
- c6: o__RF39
- c7: c__Mollicutes
- c8: p__Tenericutes

Figure S2. Cladogram generated from amoxicillin vs control treated rat's microbiota at time point 2. (Expanded view of Figure 2d).

1_C2
2_A2

a: f__Micrococcaceae
b: f__Coriobacteriaceae
c: o__Coriobacteriales
d: c__Coriobacteriia
e: p__Actinobacteria
f: Other
g: f__
h: f__Bacteroidaceae
i: f__Porphyromonadaceae
j: o__Bacteroidales
k: c__Bacteroidia
l: p__Bacteroidetes
m: f__
n: o__YS2
o: c__4C0d_2
p: p__Cyanobacteria
q: f__Deferribacteraceae
r: o__Deferribacterales
s: c__Deferribacteres
t: p__Deferribacteres
u: f__Staphylococcaceae
v: f__Enterococcaceae
w: f__Lactobacillaceae
x: f__Streptococcaceae
y: o__Lactobacillales
z: f__Turicibacteraceae
a0: o__Turicibacterales
a1: c__Bacilli
a2: Other
a3: f__
a4: f__Christensenellaceae
a5: f__Clostridiaceae
a6: f__Dehalobacteriaceae
a7: f__Lachnospiraceae
a8: f__Peptococcaceae
a9: f__Peptostreptococcaceae
b0: f__Ruminococcaceae
b1: f__Veillonellaceae
b2: f__Mogibacteriaceae_
b3: o__Clostridiales
b4: c__Clostridia
b5: f__Erysipelotrichaceae
b6: o__Erysipelotrichales
b7: c__Erysipelotrichi
b8: p__Firmicutes
b9: f__
c0: o__
c1: f__
c2: o__RF32
c3: c__Alphaproteobacteria
c4: f__Alcaligenaceae
c5: o__Burkholderiales
c6: c__Betaproteobacteria
c7: f__Desulfovibrionaceae
c8: o__Desulfovibrionales
c9: c__Deltaproteobacteria
d0: f__Enterobacteriaceae
d1: o__Enterobacteriales
d2: f__Pasteurellaceae
d3: o__Pasteurellales
d4: f__Pseudomonadaceae
d5: o__Pseudomonadales
d6: c__Gammaproteobacteria
d7: f__Spirochaetaceae

Figure S3. Cladogram generated from amoxicillin vs control treated rat's microbiota at time point 3. (Expanded view of Figure 2e).

Figure S4. Cladogram generated from the microbiota of offspring of amoxicillin vs control treated dams. (Expanded view of Figure 7c).

Legend:
- 1_male-ctl-t2 (red)
- 2_male-ab-t2 (green)

- a: Other
- b: Other
- c: Other
- d: Other
- e: f__
- f: f__Porphyromonadaceae
- g: f__Deferribacteraceae
- h: o__Deferribacterales
- i: c__Deferribacteres
- j: p__Deferribacteres
- k: f__Gemellaceae
- l: o__Gemellales
- m: f__Mogibacteriaceae
- n: f__Desulfovibrionaceae
- o: o__Desulfovibrionales
- p: c__Deltaproteobacteria
- q: f__Enterobacteriaceae
- r: o__Enterobacteriales
- s: c__Gammaproteobacteria
- t: p__Proteobacteria
- u: f__Spirochaetaceae
- v: o__Spirochaetales
- w: c__Spirochaetes
- x: p__Spirochaetes
- y: f__F16
- z: o__CW040
- a0: c__TM7_3
- a1: p__TM7
- a2: f__Cerasicoccaceae_
- a3: o__Cerasicoccales_
- a4: c__Opitutae
- a5: p__Verrucomicrobia

Figure S5. Heatmap representing in amoxicillin fed and control dams bacterial communities. Groups of pregnant S rats (n=3/group) in Study 2 were maintained with (columns 1-3) or without (columns 4-6) amoxicillin. Fecal pellets were analyzed for microbiota and the abundance of various bacterial taxa were hierarchically clustered. Blu: Low abundance, Maroon: High abundance.
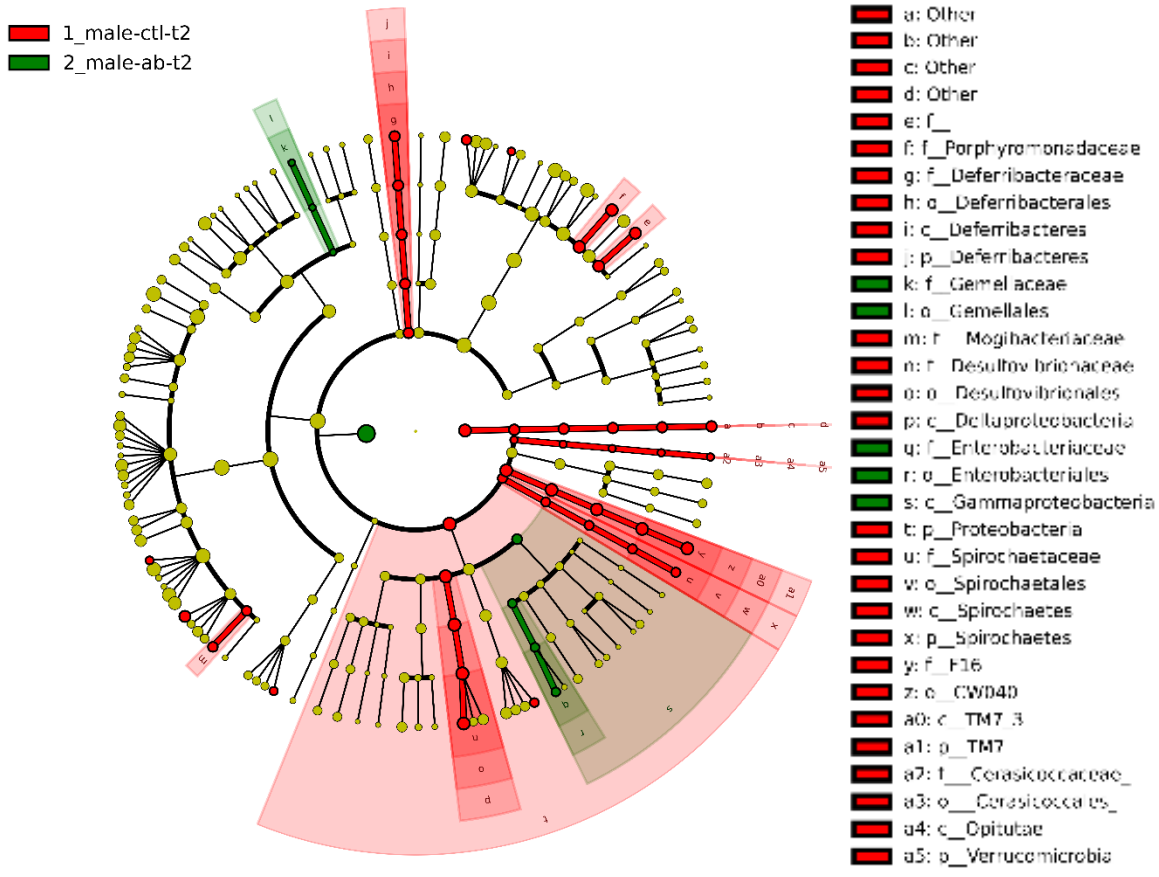
Figure S6. Cladogram generated from the microbiota of amoxicillin vs control treated dams.

mom-ab
mom-ctl

a: f__Coriobacteriaceae
b: o__Coriobacteriales
c: c__Coriobacteriia
d: Other
e: f__
f: f__Bacteroidaceae
g: f___Paraprevotellaceae_
h: o__Bacteroidales
i: c__Bacteroidia
j: p__Bacteroidetes
k: f__
l: o__YS2
m: c__4C0d_2
n: p__Cyanobacteria
o: f__Deferribacteraceae
p: o__Deferribacterales
q: c__Deferribacteres
r: p__Deferribacteres
s: f__Elusimicrobiaceae
t: o__Elusimicrobiales
u: c__Elusimicrobia
v: p__Elusimicrobia
w: f__Enterococcaceae
x: f__Lactobacillaceae
y: f__Streptococcaceae
z: o__Lactobacillales
a0: c__Bacilli
a1: f__
a2: f__Clostridiaceae
a3: f__Peptococcaceae
a4: f__Peptostreptococcaceae
a5: f__Ruminococcaceae
a6: f__Veillonellaceae
a7: f___Mogibacteriaceae_
a8: o__Clostridiales
a9: c__Clostridia
b0: p__Firmicutes
b1: f__
b2: o__
b3: o__RF32
b4: c__Alphaproteobacteria
b5: f__Alcaligenaceae
b6: o__Burkholderiales
b7: c__Betaproteobacteria
b8: f__Desulfovibrionaceae
b9: o__Desulfovibrionales
c0: c__Deltaproteobacteria
c1: f__Enterobacteriaceae
c2: o__Enterobacteriales
c3: c__Gammaproteobacteria
c4: p__Proteobacteria
c5: f__Spirochaetaceae
c6: o__Spirochaetales
c7: c__Spirochaetes
c8: p__Spirochaetes
c9: f__F16
d0: o__CW040
d1: c__TM7_3
d2: p__TM7
d3: f__
d4: o__RF39
d5: c__Mollicutes
d6: p__Tenericutes