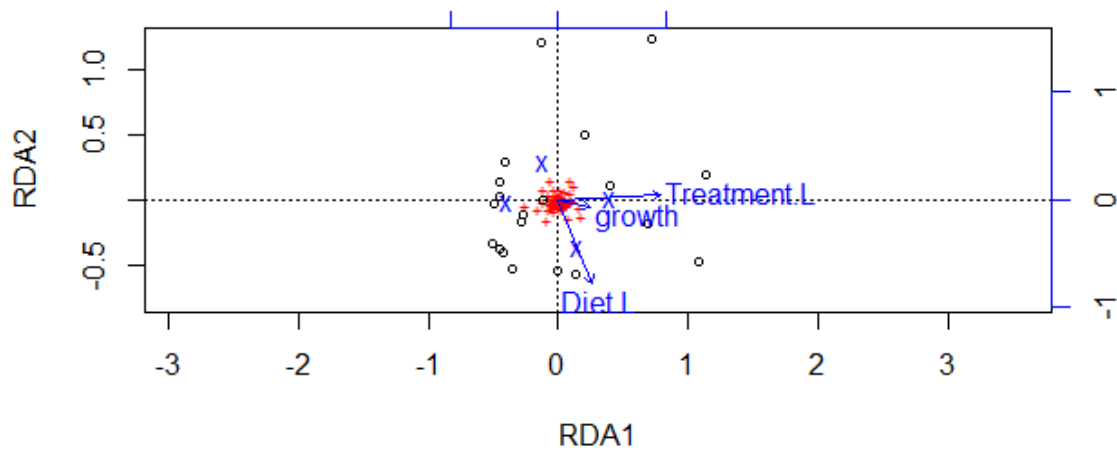


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2 Figure S1. Percent survival of spruce budworm larvae among treatment diets (spruce versus fir
3 foliage and synthetic diet) and antibiotic treatments (AB = antibiotic treatment).



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11 Figure S2. RDA biplot of foliage-associated communities with the growth rate of larvae feeding
 12 on foliage, diet, and treatment as explanatory variables. The first axis (constrained - 9.6%) and
 13 the second axis (unconstrained - 6.3%) account for 15.9 percent of the total variance.

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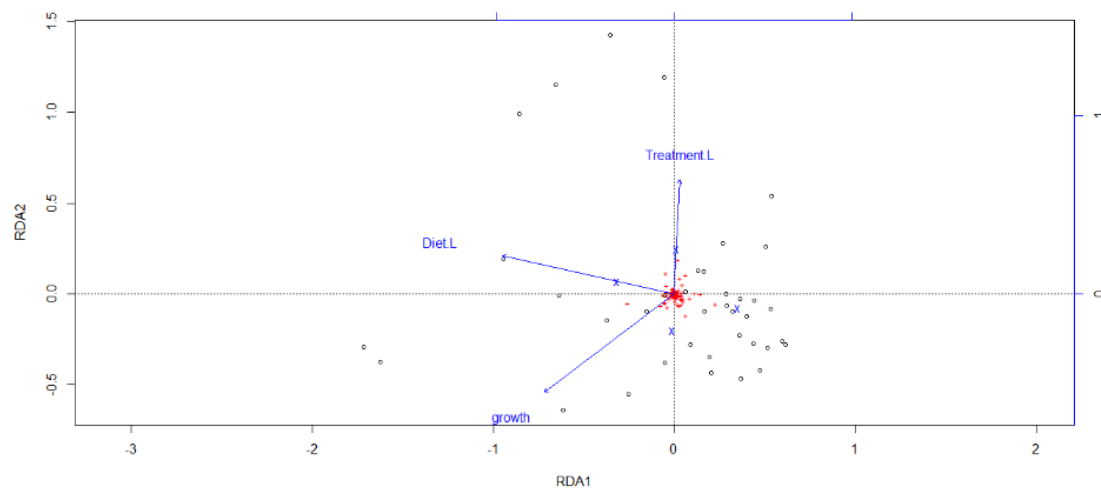
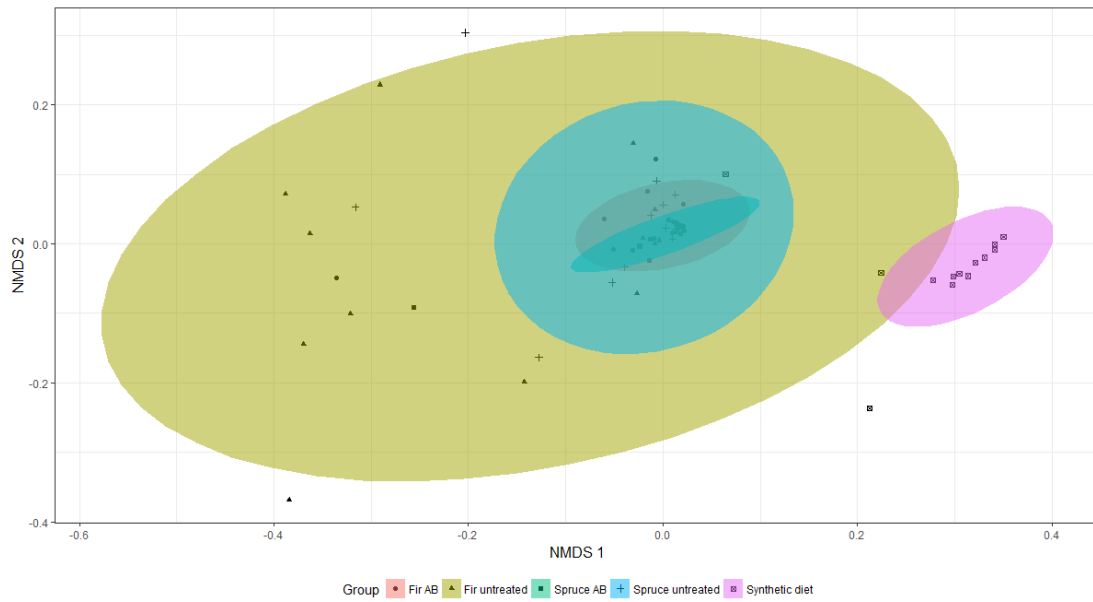
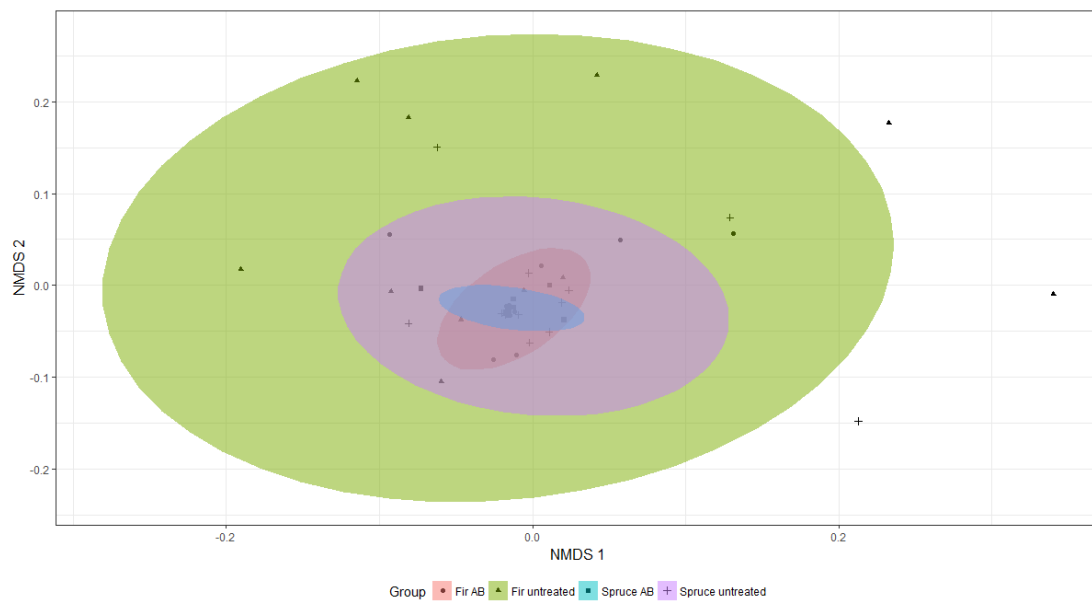


Figure S3. RDA biplot of spruce budworm larval gut communities of individuals that were fed foliage with growth rate, diet, and treatment as explanatory variables. The first axis (constrained - 4.9%) and the second axis (unconstrained - 3.0%) account for 7.98% of the total variance.

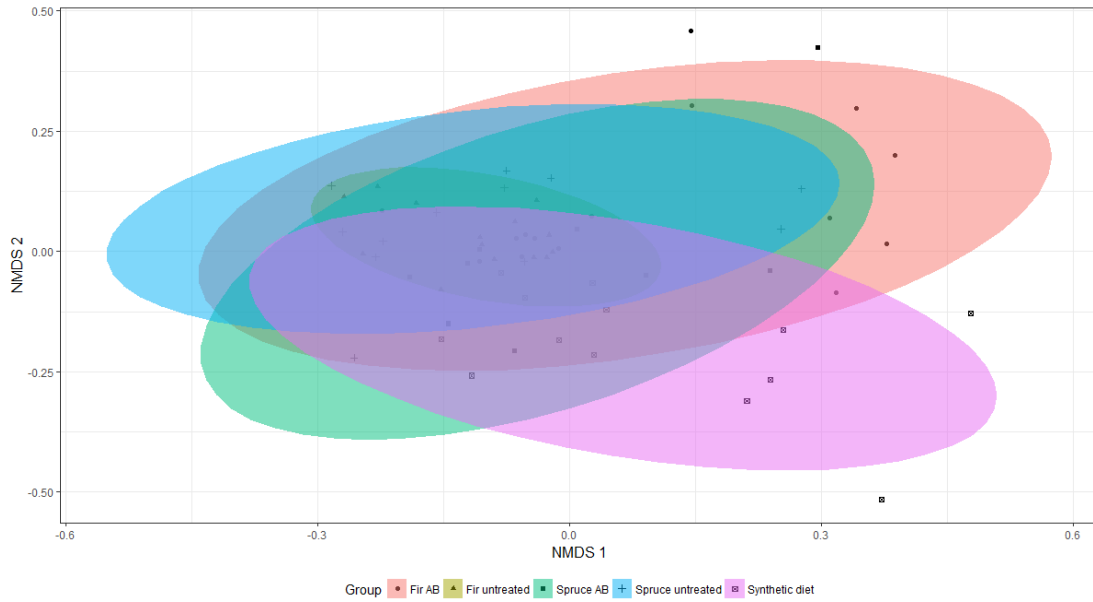


24 A)

25 B)

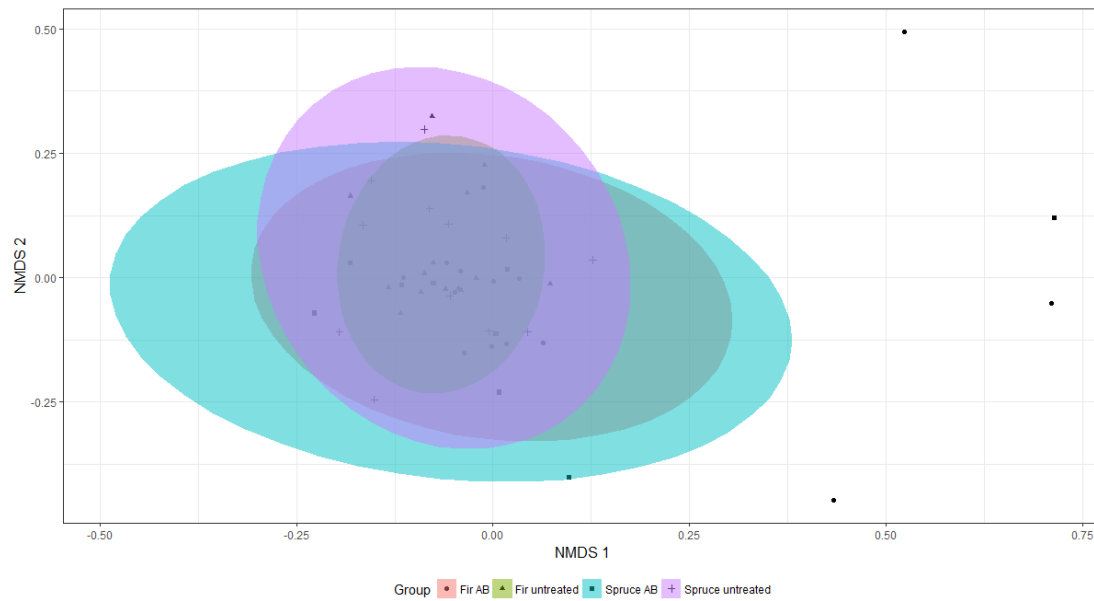


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27 C)

28 D)



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30 Figure S4. NMDS ordinations of diet-associated microbial communities based on weighted and
 31 unweighted UniFrac distances. (A: all diets weighted UniFrac stress =0.13, B: All diets
 32 unweighted UniFrac stress =0.18, C: only foliage weighted UniFrac stress =0.10, D: only foliage

33 unweighted UniFrac stress =0.20). Ellipses represent 95% confidence intervals around samples
34 from different treatments (Fir.AB = antibiotic treated fir, Spruce.AB = antibiotic spruce,
35 Fir.untreated = untreated fir, and Spruce.untreated = untreated spruce)

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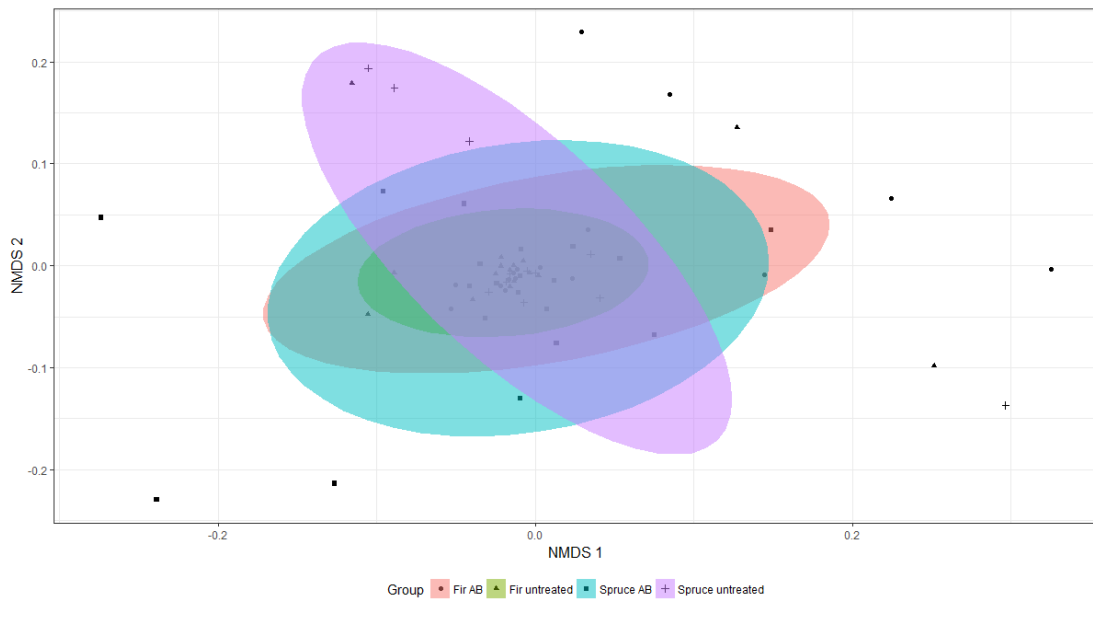
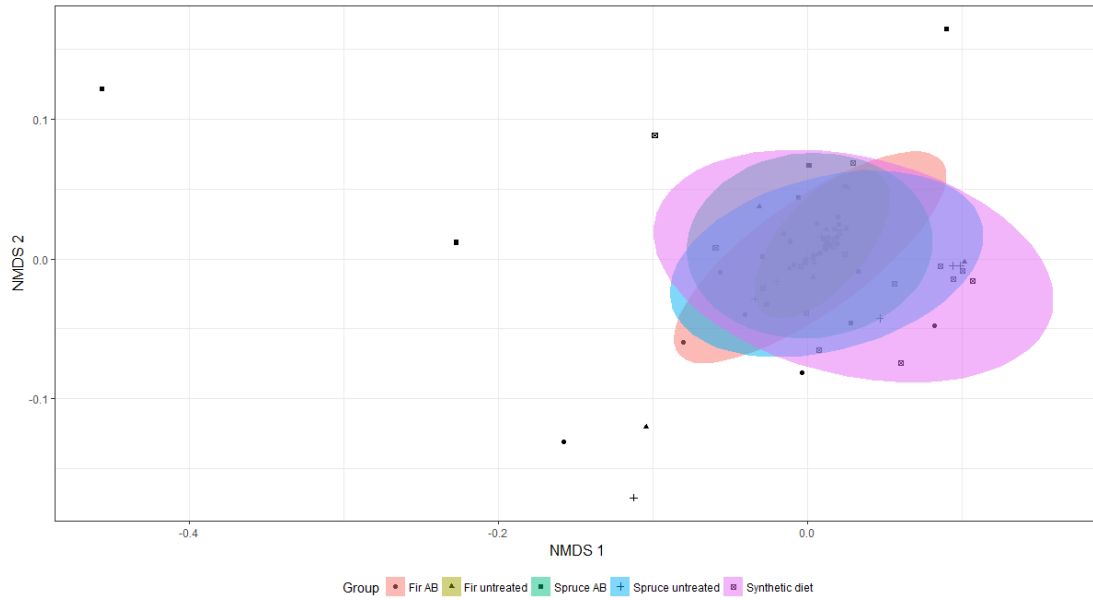
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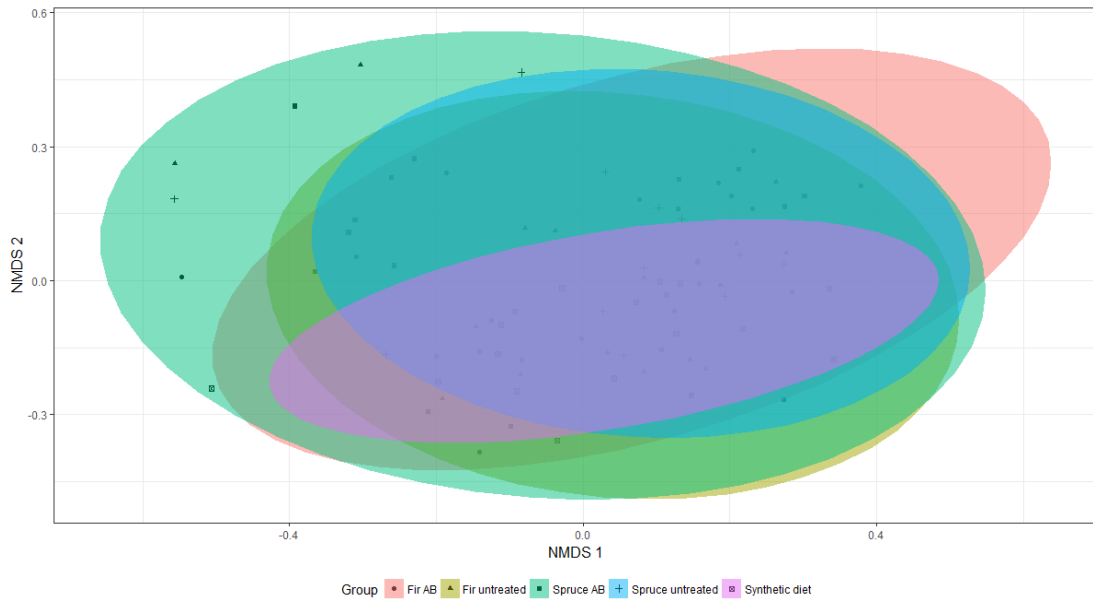
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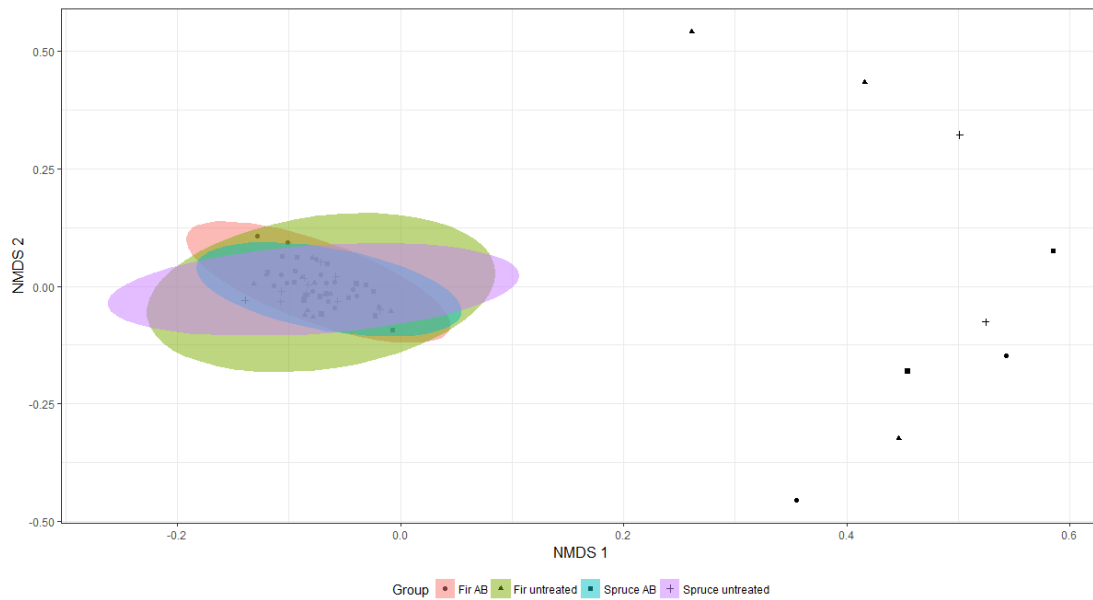
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49 C)



50 D)

51 Figure S5. NMDS ordinations of frass-associated microbial communities based on weighted and
 52 unweighted UniFrac distances. (A: all frass samples weighted unifrac stress =0.15, B: All frass
 53 samples UniFrac stress =0.13, C: frass of larvae feeding on foliage weighted UniFrac stress
 54 =0.10, D: frass of larvae feeding on foliage unweighted UniFrac stress =0.19). Ellipses represent

55 95% confidence intervals around samples from different treatments (Fir.AB = antibiotic treated
56 fir, Spruce.AB = antibiotic spruce, Fir.untreated = untreated fir, and Spruce.untreated = untreated
57 spruce).

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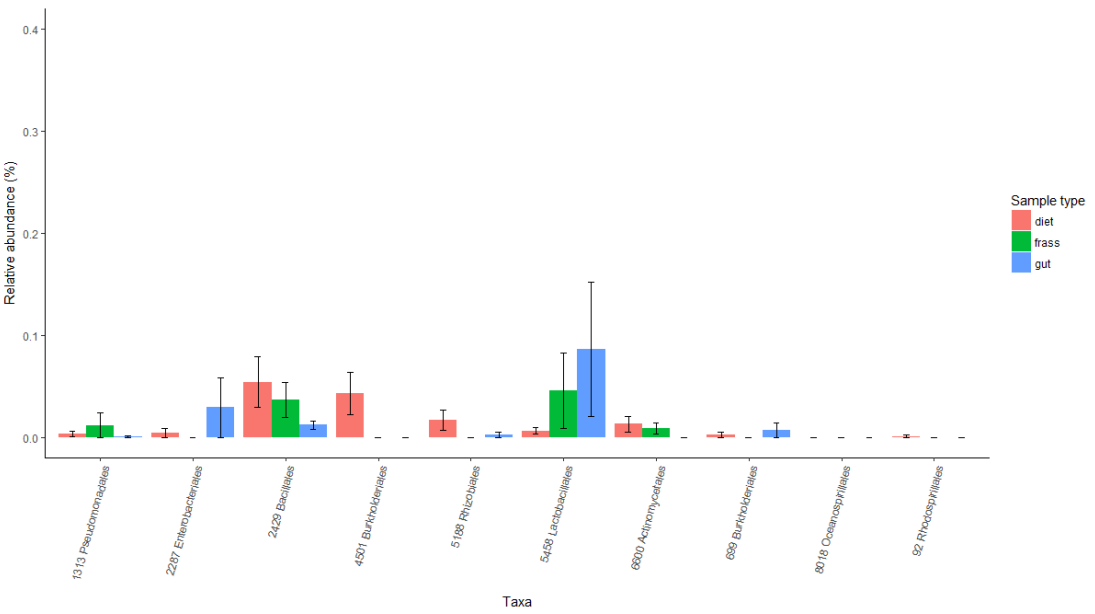
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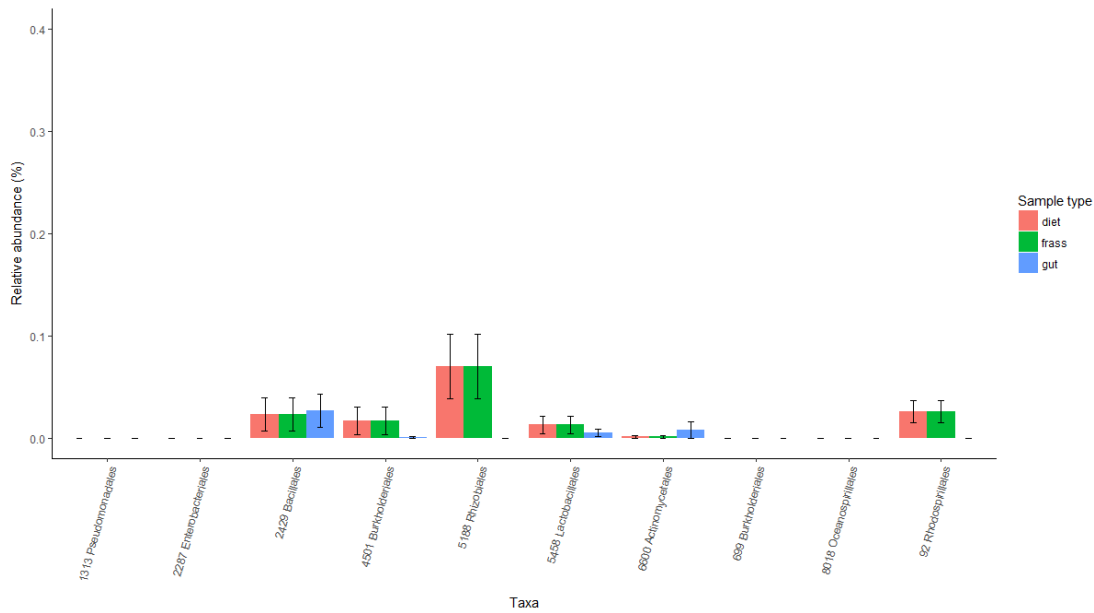
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70 A) (Fir AB)



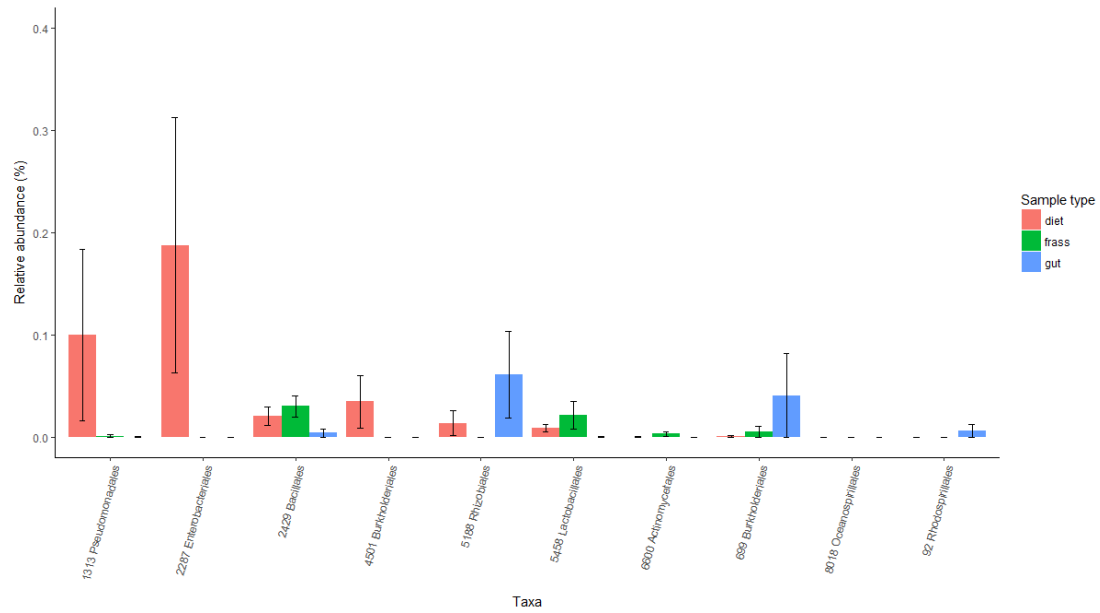
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72 B) (fir untreated)



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74 C) Spruce AB



D) Spruce untreated

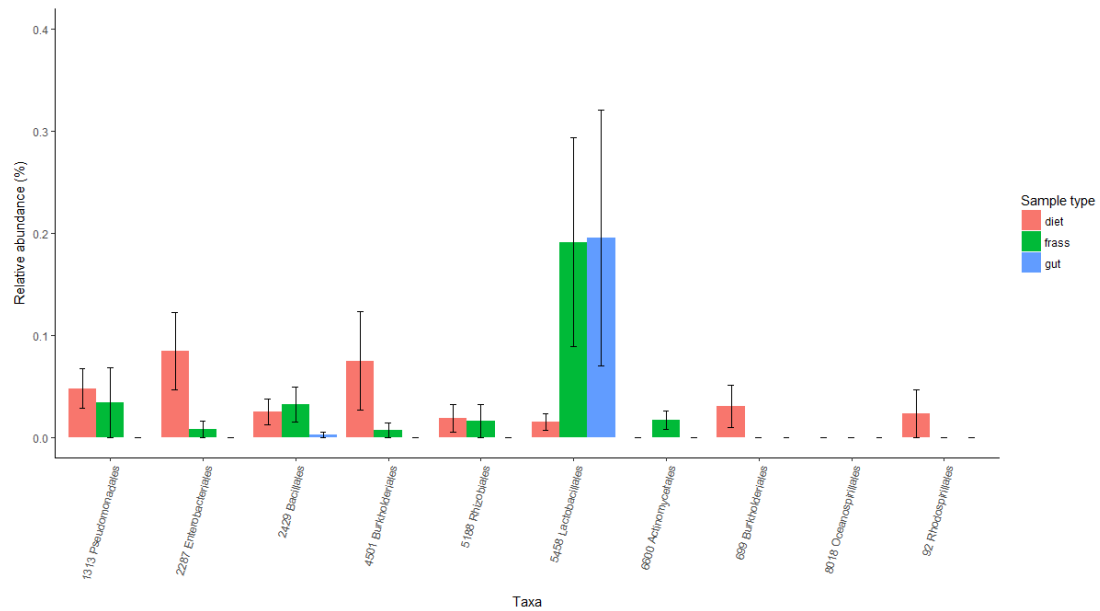
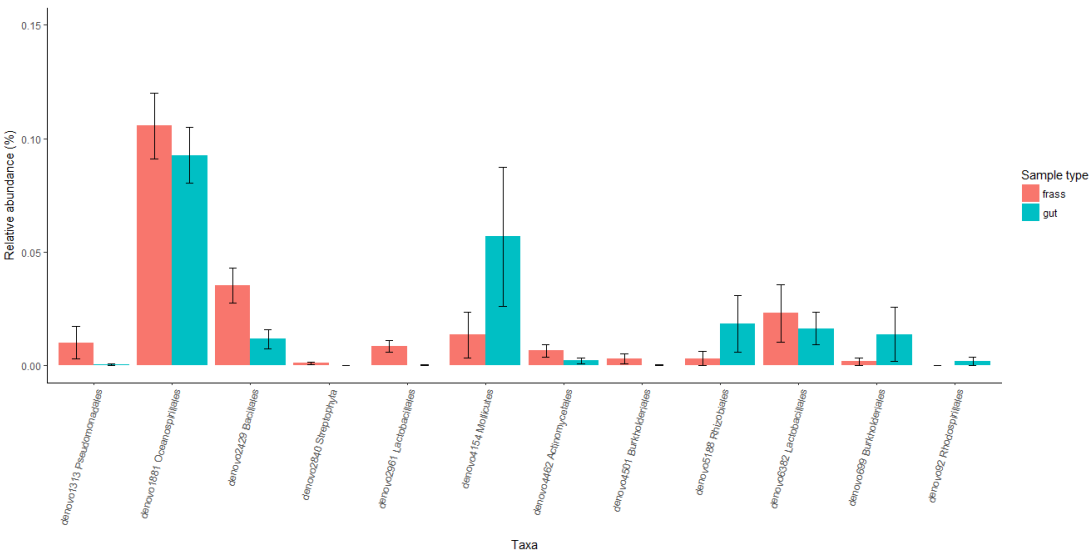


Figure S6. Mean relative abundance (\pm SE) of OTUs identified as being differentially abundant between comparisons of communities among sample types (diet, guts, and frass) within treatment combinations (fir versus spruce and antibiotic treated vs untreated) based on an ANCOM test (ANCOM; adjusted $p < 0.05$).

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84 Figure S7. Mean Relative abundance (\pm SE) of OTUs identified as being differentially abundant
85 between comparisons of all frass samples and all gut samples based on an ANCOM test
86 (ANCOM; adjusted $p < 0.05$). Blue bars represent gut samples and red bars represent frass
87 samples.

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Table S1: Total replicates sequenced across all sample types and the time in the experiment samples were collected and frozen.

Sample type	Time after start of treatments	Replicates sequenced
Larval midguts	14 days	96
Foliage	7 days	50
Foliage	14 days	51
Frass	7 days	50
Frass	14 days	49

101 Table S2: Statistical tests used in this study along with the hypothesis tested, the variables used,
102 and the type of data used to

Test	Hypothesis tested	Variables	Type of data used
Mixed-effects model	Diet and antibiotic treatment will influence growth	Weight , Diet type, Antibiotic treatment, Time	Log transformed weight values of individual larvae recorded every two days for 2 weeks
Logistic regression	Diet and antibiotic treatment will affect larval survival	Mortality	Mortality- Binary response
Redundancy analysis (RDA)	Gut microbial communities are correlated with larval growth	Diet type, Antibiotic treatment, Gut community composition	Growth rates of each larva and relative abundances of OTUs detected in midgut samples.
Redundancy analysis (RDA)	Foliage-associated microbial communities are correlated with larval growth	Diet type, Antibiotic treatment, Foliage-associated community composition	Growth rates of each larva and relative abundances of OTUs detected in foliage samples.
Permutational multivariate ANOVA	Gut community composition is different among fast and slow growing larvae	Gut community composition Growth class(based on growth rate, defined as upper and lower quartiles)	Square root transformed UniFrac distance matrix (weighted by the relative abundance of taxa and unweighted)
ANOVA	Diet and antibiotic treatment will affect microbial alpha diversity	Diet type, Antibiotic treatment	Shannon diversity calculated using relative abundances of OTUs

Permutational multivariate ANOVA	Gut microbial community composition will differ among diets and	Diet type, Antibiotic treatment, Gut community composition	Square root transformed UniFrac distance matrix (weighted by the relative abundance of taxa and unweighted)
Analysis of the composition of microbiomes (ANCOM)	What sample type (guts, foliage, or frass) are individual OTUs associated with	Sample type	Relative abundance of OTUs

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112 Table S3. Estimates of the influence time, antibiotic treatment, and diet on the weight of spruce
 113 budworm larvae exposed to different diet and antibiotic treatments. Results represent ANOVA
 114 analysis of a mixed effect model with time, antibiotic treatment, and diet and their interactions as
 115 fixed factors and time nested within individual as random factors. In our model time as a fixed
 116 effect represents the growth rate of larvae and significant interactions between Time and other
 117 factors indicate that growth rates differed among treatment combinations.

Variable	F value	P value
Intercept	16637.5	<.0001
Time	751.8	<.0001
Treatment	5.78	0.018
Diet	3.2	0.076
Time:Treatment	3.0	0.081
Time:Diet	33.9	<.0001
Treatment:Diet	3.8	0.056
Time:Treatment:Diet	2.1	0.151

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Table S4. Pairwise comparisons of growth rate estimates for spruce budworm larvae within treatment groups as determined by a Tukey's Honest Significant Difference post-hoc test based on a mixed effect model with time, antibiotic treatment, and diet as fixed factors and time nested within individual as random factors.

Contrast	Estimate	Standard error	Degrees of freedom	T ratio	P value
Antibiotic fir versus antibiotic spruce	-0.0290	0.0054	483	-5.339	<.0001
Antibiotic fir versus untreated fir	-0.0012	0.0054	483	-0.232	0.9956
Antibiotic fir versus untreated spruce	-0.0184	0.0063	483	-2.92	0.0191
Antibiotic spruce versus untreated Fir	0.0278	0.0053	483	5.165	<.0001
Antibiotic spruce versus untreated spruce	0.0106	0.0062	483	1.693	0.3284
Untreated fir versus untreated spruce	-0.0171	0.0062	483	-2.744	0.0319

125 Table S5. OTUs identified as being differentially abundant between different comparisons. The
 126 first column represents the OTU number as determined during OTU picking (see methods for
 127 details). Taxonomic identification is presented for each taxa, if a taxon was not able to be
 128 identified to a certain taxonomic level, i.e species, that cell was left blank. Group represents
 129 which comparison group that taxon was more abundant in.

Differentially abundant OTUs							
	Phylum	Class	Order	Family	Genus	Species	group
Antibiotic treated fir: guts vs diet							
denovo8018	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	Halomonas		gut
Untreated fir: guts vs diet							
denovo5188	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae			diet
denovo92	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae			diet
Antibiotic treated spruce: guts vs diet							
denovo2429	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus		diet
denovo4501	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae			diet
denovo5458	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus		diet
Untreated spruce: guts vs diet							
denovo2287	Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae	Erwinia		diet
denovo1313	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas		diet
denovo699	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae			diet
Antibiotic treated fir: guts vs frass							
denovo8018	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	Halomonas		gut
denovo6600	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium		frass
Antibiotic treated fir: guts frass							
denovo2429	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus		frass
Untreated spruce: guts vs frass							
denovo2961	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus		gut
denovo2429	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus		frass
denovo4154	Tenericutes	Mollicutes					frass
All samples combined: guts vs foliage							
denovo5188	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae			diet
denovo2840	Cyanobacteria	Chloroplast	Streptophyta				diet
denovo6382	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus		diet
denovo1313	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas		diet
denovo2429	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus		diet
denovo4501	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae			diet
denovo699	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae			diet
All samples combined: guts vs frass							
denovo2961	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus		frass
denovo2429	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus		frass
denovo4154	Tenericutes	Mollicutes					gut
All samples combined: antibiotic treated vs untreated							
denovo92	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae			untreated
denovo4462	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria	palustris	untreated
All samples combined: spruce vs fir							
denovo1881	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	Halomonas		fir