Supporting Information

Table S1. Genomes used to design primers

Strain	GenBank assembly accession
Gilliamella apicola wkB7	GCA_001693435.1
Gilliamella apicola P54G	GCA_001690735.1
Gilliamella apicola wkB1	GCA_000599985.1
Gilliamella apicola I20	GCA_000725175.1
Gilliamella apicola P17	GCA_000725245.1
Gilliamella apicola M1_2G	GCA_001690775.1
Gilliamella apicola M6_3G	GCA_001723875.1
Gilliamella apicola P62G	GCA_001690755.1
Gilliamella apicola P83G	GCA_001690175.1
Snodgrassella alvi O02	GCA_000725195.1
Snodgrassella alvi PEB0178	MEIW00000000
Snodgrassella alvi O11	GCA_000725185.1
Snodgrassella alvi wkB2	GCA_000600005.1
Snodgrassella alvi J21	GCA_000722505.1
Snodgrassella alvi M1_3S	MEIX00000000

Table S2. Gene markers and primers used in this study.

Species	Locus Tag	Gene name	Annotation	Forward primer	Reverse Primer	Amplicon length (bp)
Gilliamella apicola	GAPWK_0415	*rimM*	16S rRNA processing protein RimM	GGCATTCGTGGWTGGCTCAG	ACGTTCTGTTGCTCCAAAYGC	393
	GAPWK_0528	*pflA*	Pyruvate formate-lyase activating enzyme	GMTTTAAAAGCWGGGCGWGAA	ACRTAGCGGATCCAAGTYCGT	379
Snodgrassella alvi	SALWKB2_1196	*guaA*	GMP synthase	GACATACACCAAGCTGTCCG	CATTTGCGCTTCYTGATARCG	346
	SALWKB2_0399	*gluS*	Glutaminyl-tRNA synthetase	GGATGARTATGTGCGCKCGAT	GCATCCGAAATCGCATGCGT	472

Table S3. Associations between allelic variation of *S. alvi* and *G. apicola* and the relative and absoulte frequencies of the different community members in the bee gut.

	Relative abundance							
	Snodgrassella				***Gilliamella***			
	guaA		***gluS***		***pflA***		***rimM***	
	Rho	*p*.value (adj)	Rho	*p*.value (adj)	Rho	*p*.value (adj)	Rho	*p*.value (adj)
Alpha2_1	–0.39	0.14	–0.21	1	0.05	1	0.11	1
Bartonella	**0.40**	**0.087**	0.39	0.18	**0.48**	**0.0008**	**0.48**	**0.0008**
Bifidobacterium	–0.10	1	–0.26	1	0.12	1	0.10	1
Firm_4	0.18	1	0.18	1	0.18	1	0.19	1
Firm_5	–0.05	1	–0.11	1	–0.13	1	0.03	1
Frischella	0.07	1	–0.06	1	–0.30	0.72	**–0.42**	**0.014**
Fructobacillus	0.14	1	0.19	1	0.28	1	0.36	0.13
Gluconobacter	0.18	1	0.13	1	0.17	1	0.15	1
Klebsiella	–0.15	1	–0.10	1	–0.10	1	–0.16	1
L_kunkeei	–0.34	0.58	–0.25	1	0.23	1	0.21	1
Serratia	0.03	1	0.11	1	0.16	1	0.25	1
Zymobacter	0.13	1	0.23	1	0.09	1	0.09	1
	Absolute abundance							
	Snodgrassella				***Gilliamella***			
	guaA		***gluS***		***pflA***		***rimM***	
	Rho	*p*.value (adj)	Rho	*p*.value (adj)	Rho	*p*.value (adj)	Rho	*p*.value (adj)
Alpha2_1	0.07	1	0.15	1	0.26	1	0.28	1
Bartonella	0.22	1	0.38	0.29	**0.49**	**0.0005**	**0.49**	**0.0004**
Bifidobacterium	0.10	1	0.25	1	**0.40**	**0.030**	**0.40**	**0.031**
Firm_4	0.10	1	0.27	1	**0.39**	**0.046**	0.31	0.65
Firm_5	0.06	1	0.20	1	0.23	1	0.29	1
Frischella	0.05	1	0.24	1	0.24	1	0.26	1
Fructobacillus	0.07	1	0.23	1	0.17	1	0.10	1
Gluconobacter	–0.10	1	–0.26	1	0.12	1	0.09	1
Klebsiella	–0.07	1	–0.02	1	0.01	1	0.18	1
L_kunkeei	–0.17	1	–0.08	1	–0.08	1	–0.11	1
Serratia	–0.22	1	–0.04	1	0.34	0.27	0.30	0.75
Zymobacter	–0.01	1	0.24	1	0.37	0.081	0.32	0.46

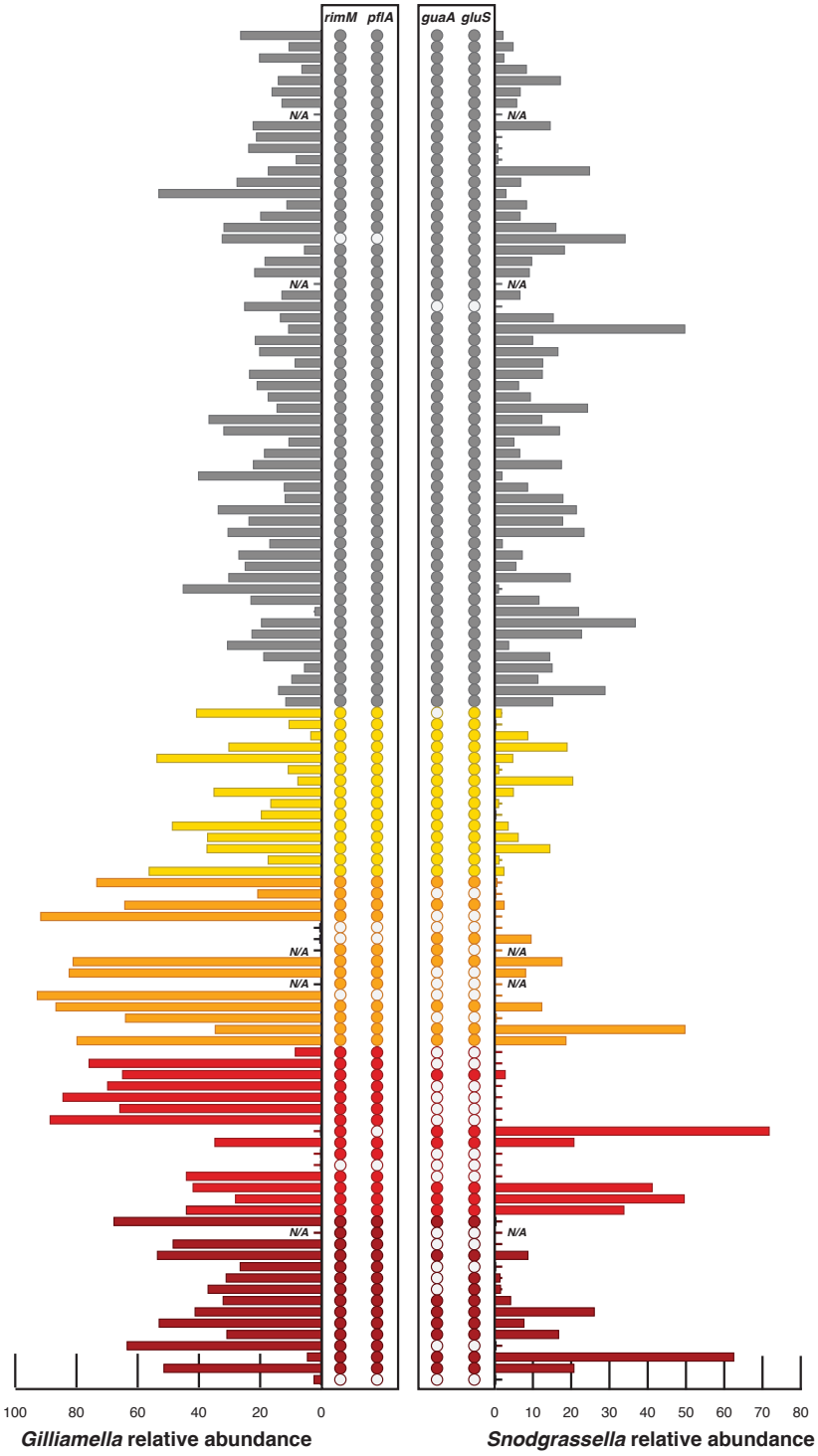

Figure S1. Honeybee samples amplified in this study. Bar graphs show the relative abundance of *G. apicola* (left) and *S. alvi* (right) reported by Raymann et al. 2017 (based on 16S rRNA gene sequencing). Samples that did not have relative abundance information are marked by *N/A*. Filled circles represent samples that we successfully amplified using our designed primers for RimM, PflA, GMP, and GluS. All control bees are shown in gray bars and circles. Treated bees are colored by day (Day 0= yellow, Day 3= orange, Day 5= light red, Day 7= dark red). Samples for which no relative abundance data was available are marked by N/A.

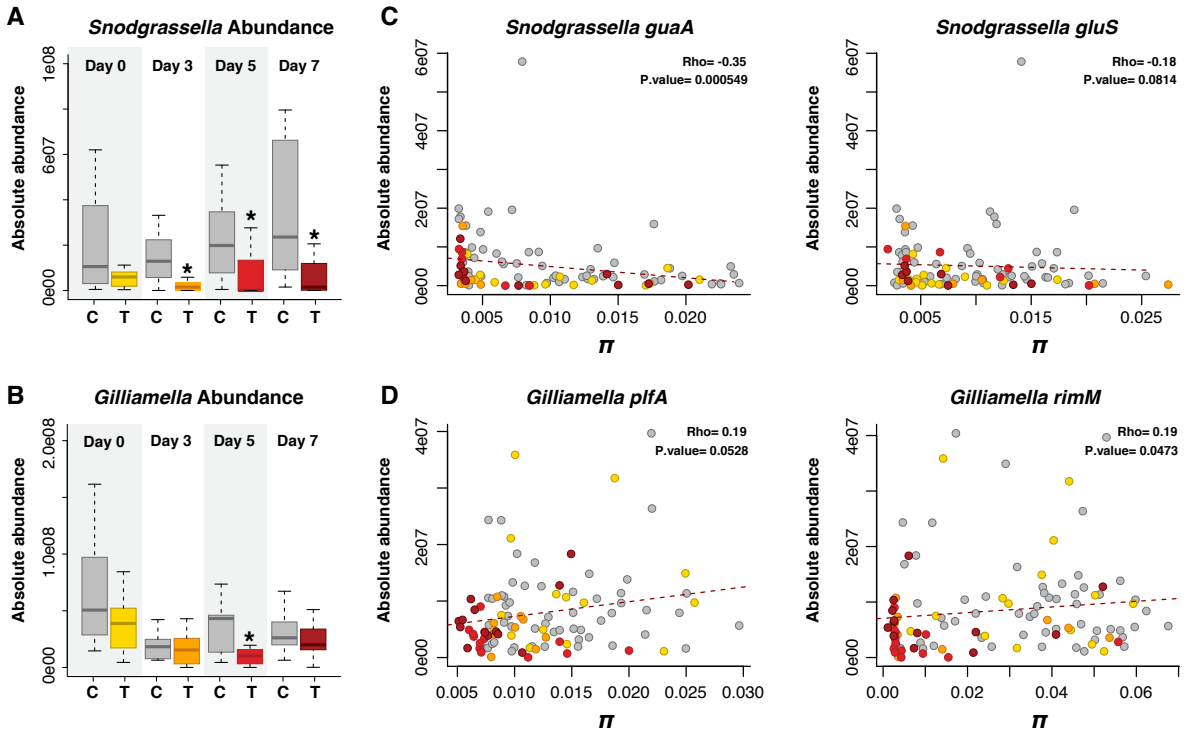

Figure S2. Correlation between allelic diversity and absolute abundance. Absolute abundance of *S. alvi* (**a**) and *G. apicola* (**b**) in control (C) and treatment (T) bees at Days 0, 3, 5, and 7 post-treatment taken from Raymann et al. 2017. Box-and-whisker plots show high, low, and median values, with lower and upper edges of each box denoting first and third quartiles, respectively. The central vertical lines represent the data range, with a maximal distance of 1.5 interquartile ranges. * = $P < 0.05$, Wilcoxon test. Spearman Correlation between absolute abundance and π (**c**-**d**). All control bees are shown in gray dots. Treated bees are colored by day as in **a**-**b**.

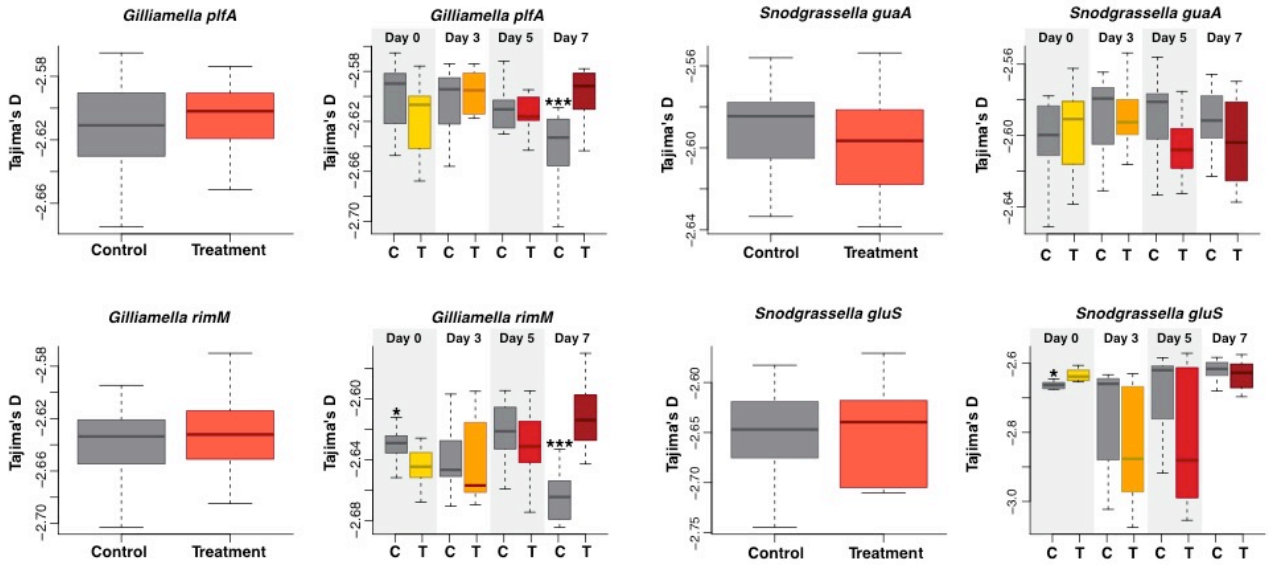

Figure S3. Impact of antibiotic treatment on allele frequency. Tajima's *D* for each gene marker for all control and treated bees as well as for control and treated bees at each day post-treatment (Days 0, 3, 5, and 7). Box-and-whisker plots show high, low, and median values, with lower and upper edges of each box denoting first and third quartiles, respectively. The central vertical lines represent the data range, with a maximal distance of 1.5 interquartile ranges. * = $P < 0.05$, *** = $P < 0.0001$, Wilcoxon test.

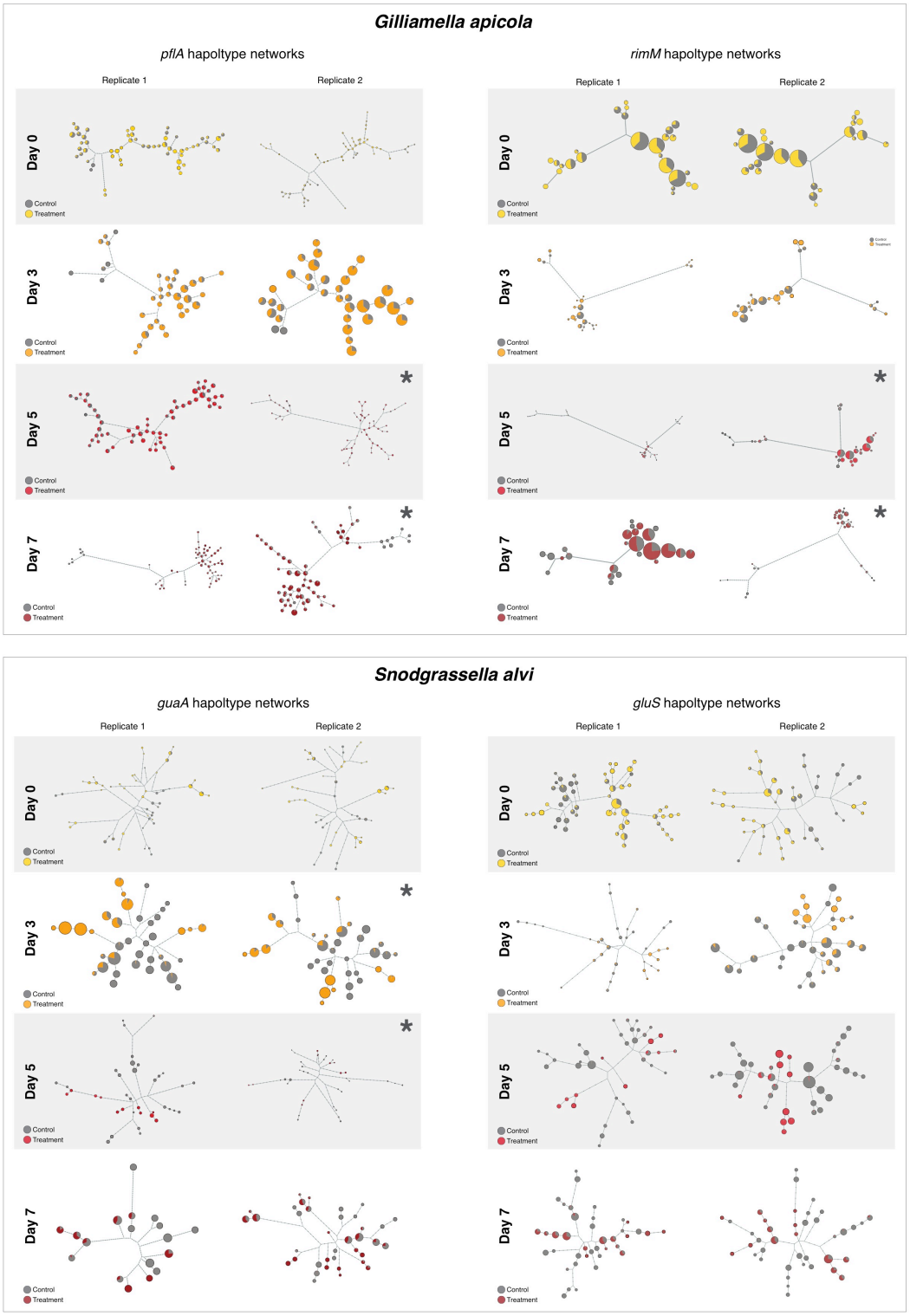

Figure S4. Haplotype networks of *G. apicola* and *S. alvi* based on the four marker genes. Haplotype networks were built for each marker gene and for each day independently. For each graph, 100 reads were randomly sampled per bee twice (i.e. sampling Replicates 1 and 2). Circles represent haplotypes and circle size is proportional to the number of reads. Haplotypes supported by fewer than 10 reads were collapsed into small light gray circles. Within circles, dark gray areas indicate haplotypes found in control bees and colored areas represent haplotypes found in treated bees. Edges between haplotypes indicate substitutions (unit= 1 substitution). Asterisks indicate significant differences observed based on nucleotide diversity in Figure 1.

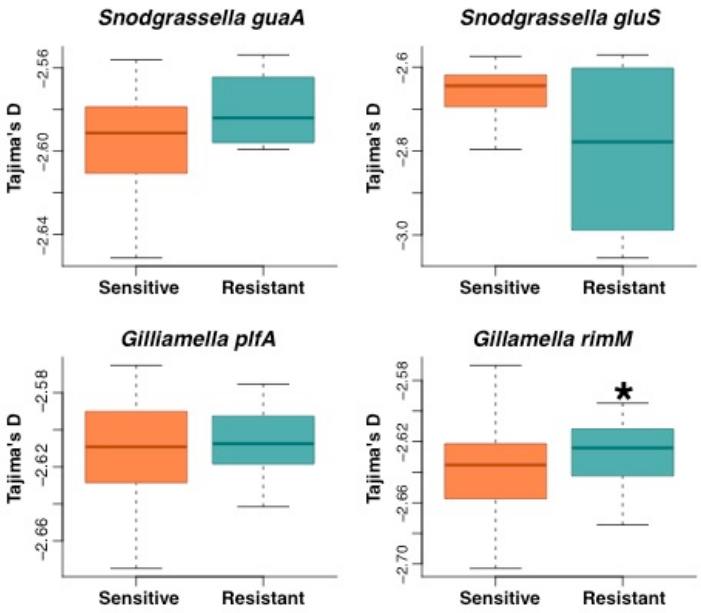

Figure S5. Impact of antibiotic treatment on allele frequency in "sensitive" versus "resistant" bees. Tajima's *D* for each gene marker for "sensitive" and "resistant" bees. Box-and-whisker plots show high, low, and median values, with lower and upper edges of each box denoting first and third quartiles, respectively. The central vertical lines represent the data range, with a maximal distance of 1.5 interquartile ranges. * = $P < 0.05$, Wilcoxon test.

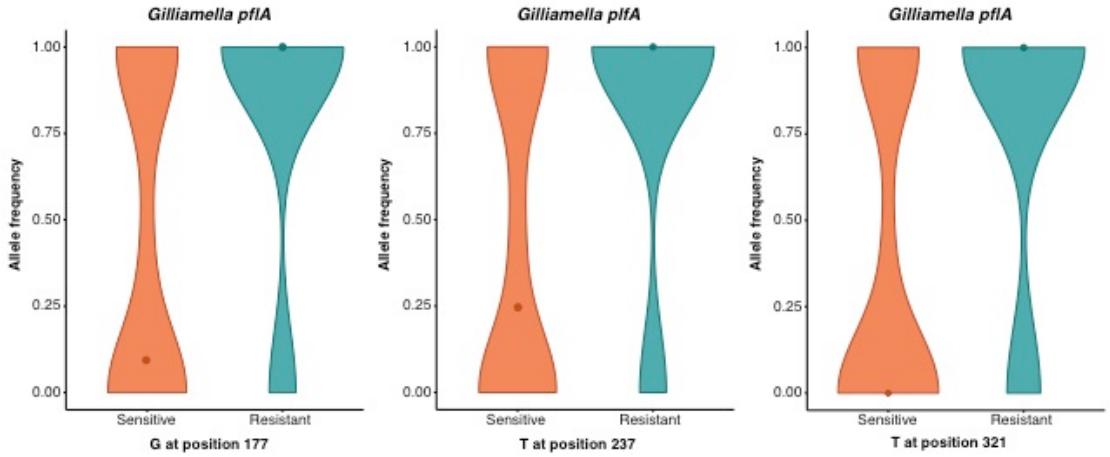

Figure S6. Shifts in individual allele frequencies in resistant populations relative to sensitive populations. Violin plots showing the three alleles that significantly ($P < 0.05$, Wilcoxon test and *t*-test with Bonferroni correction) increased in frequency in resistant bees.