

1           Supplementary information for:  
2           Temperature dependence of parasitic  
3           infection and gut bacterial communities  
4           in bumble bees

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6           Running title: Temperature affects bee infection and microbiota

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16 **CONTENTS**

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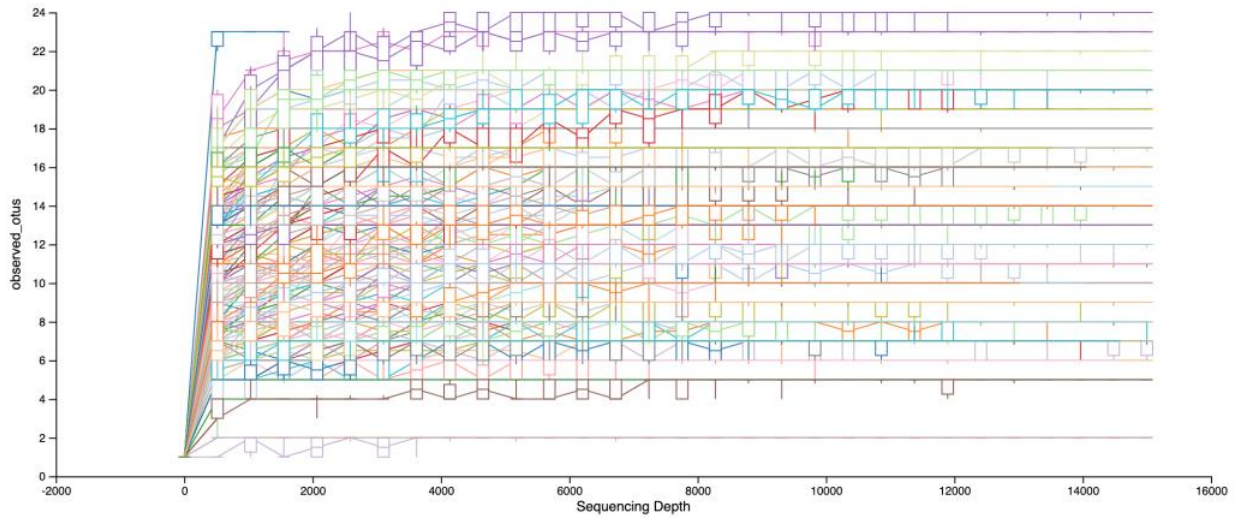
18       Supplementary tables ..... 4

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21 **SUPPLEMENTARY FIGURES**

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24 **Supplementary Figure 1. Rarefaction plot** of sequencing data. Lines show cumulative number of Exact  
25 Sequence Variants (y-axis) as a function of read depth (x-axis). Each line represents one sample.

26 **SUPPLEMENTARY TABLES**27 **Supplementary Table 1. Sample sizes** by infection treatment, temperature, and colony.

28 A. Infection treatment and temperature

Infection	Temperature	N
Parasite	21	67
Parasite	25	64
Parasite	29	64
Parasite	33	64
Parasite	37	63
Sham	21	43
Sham	25	42
Sham	29	40
Sham	33	39
Sham	37	39

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30 B. Colony

Colony	N
E08	90
E09	106
E10	129
E11	110
E12	90

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33 **Supplementary Table 2. Significance of terms in models of bacterial abundance by temperature.** A  
 34 separate model was fit for abundance of total bacteria and of each family (column “Family”). “Infection”  
 35 refers to infection treatment (parasite-inoculated or sham control). “Marginal.cell” refers to length of  
 36 the forewing marginal cell, an index of bee body size. “Significance” column indicates predictors with  $P <$   
 37  $0.05$  (\*),  $P < 0.01$  (\*\*), and  $P < 0.001$  (\*\*\*)).

Family	Predictor	$\chi^2$	df	P	Significance
Total	Temperature	0.004	1	0.95	
Total	Temperature <sup>2</sup>	20.486	1	< 0.001	***
Total	Infection	1.689	1	0.19	
Total	Colony	15.372	4	0.004	**
Total	Marginal.cell	28.749	1	< 0.001	***
Orbaceae	Temperature	3.425	1	0.064	.
Orbaceae	Infection	0.134	1	0.71	
Orbaceae	Colony	10.769	4	0.029	*
Orbaceae	Marginal.cell	14.151	1	< 0.001	***
Neisseriaceae	Temperature	5.405	1	0.02	*
Neisseriaceae	Infection	0.192	1	0.66	
Neisseriaceae	Colony	3.037	4	0.55	
Neisseriaceae	Marginal.cell	4.11	1	0.043	*
Lactobacillaceae	Temperature	25.15	1	< 0.001	***
Lactobacillaceae	Infection	0.049	1	0.82	
Lactobacillaceae	Temperature <sup>2</sup>	4.842	1	0.028	*
Lactobacillaceae	Colony	16.252	4	0.0027	**
Lactobacillaceae	Marginal.cell	10.469	1	0.0012	**
Bifidobacteriaceae	Temperature	6.254	1	0.012	*
Bifidobacteriaceae	Infection	0.0004	1	0.98	
Bifidobacteriaceae	Temperature <sup>2</sup>	6.188	1	0.013	*
Bifidobacteriaceae	Colony	25.952	4	< 0.001	***

Bifidobacteriaceae	Marginal.cell	6.225	1	0.013	*
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40 **Supplementary Table 3. Significance of terms in models of *C. bombi* infection intensity.** A separate  
 41 model was fit with abundance of total bacteria (Family = "Total") and abundance of each family as a  
 42 covariate, as indicated in the column "Family". "Marginal.cell" refers to length of the forewing marginal  
 43 cell, an index of bee body size. This predictor was significant only for models with Neisseriaceae.  
 44 "Significance" column indicates predictors with  $P < 0.05$  (\*),  $P < 0.01$  (\*\*), and  $P < 0.001$  (\*\*\*).

Family	Predictor	$\chi^2$	df	Pvalue	Significance
Total	Temperature	36	1	< 0.001	***
Total	Temperature <sup>2</sup>	4.89	1	0.027	*
Total	Colony	47.84	4	< 0.001	***
Total	log(abundance)	5.31	1	0.021	*
Orbaceae	Temperature	30.38	1	< 0.001	***
Orbaceae	Temperature <sup>2</sup>	4.4	1	0.036	*
Orbaceae	Colony	48.24	4	< 0.001	***
Orbaceae	log(abundance)	7.17	1	0.0074	**
Neisseriaceae	Temperature	39.73	1	< 0.001	***
Neisseriaceae	Temperature <sup>2</sup>	4.32	1	0.038	*
Neisseriaceae	Colony	48.26	4	< 0.001	***
Neisseriaceae	Marginal.cell	4.07	1	0.044	*
Neisseriaceae	log(abundance)	2.1	1	0.15	
Lactobacillaceae	Temperature	39.03	1	< 0.001	***
Lactobacillaceae	Temperature <sup>2</sup>	3.88	1	0.049	*
Lactobacillaceae	Colony	46.59	4	< 0.001	***
Lactobacillaceae	log(abundance)	0.76	1	0.38	
Bifidobacteriaceae	Temperature	36.86	1	< 0.001	***
Bifidobacteriaceae	Temperature <sup>2</sup>	3.93	1	0.047	*
Bifidobacteriaceae	Colony	45.96	4	< 0.001	***
Bifidobacteriaceae	log(abundance)	0.49	1	0.48	