

Supplement S2 (Figs S3–S5, Tables S2, S3) to: Natta G. et al. 2024: DNA metabarcoding of gut microbiota reveals considerable taxonomic differences among wild individuals of the dung beetle *Trypocopris pyrenaicus* (Coleoptera: Geotrupidae). — *Eur. J. Entomol.* **121**: 40–53.

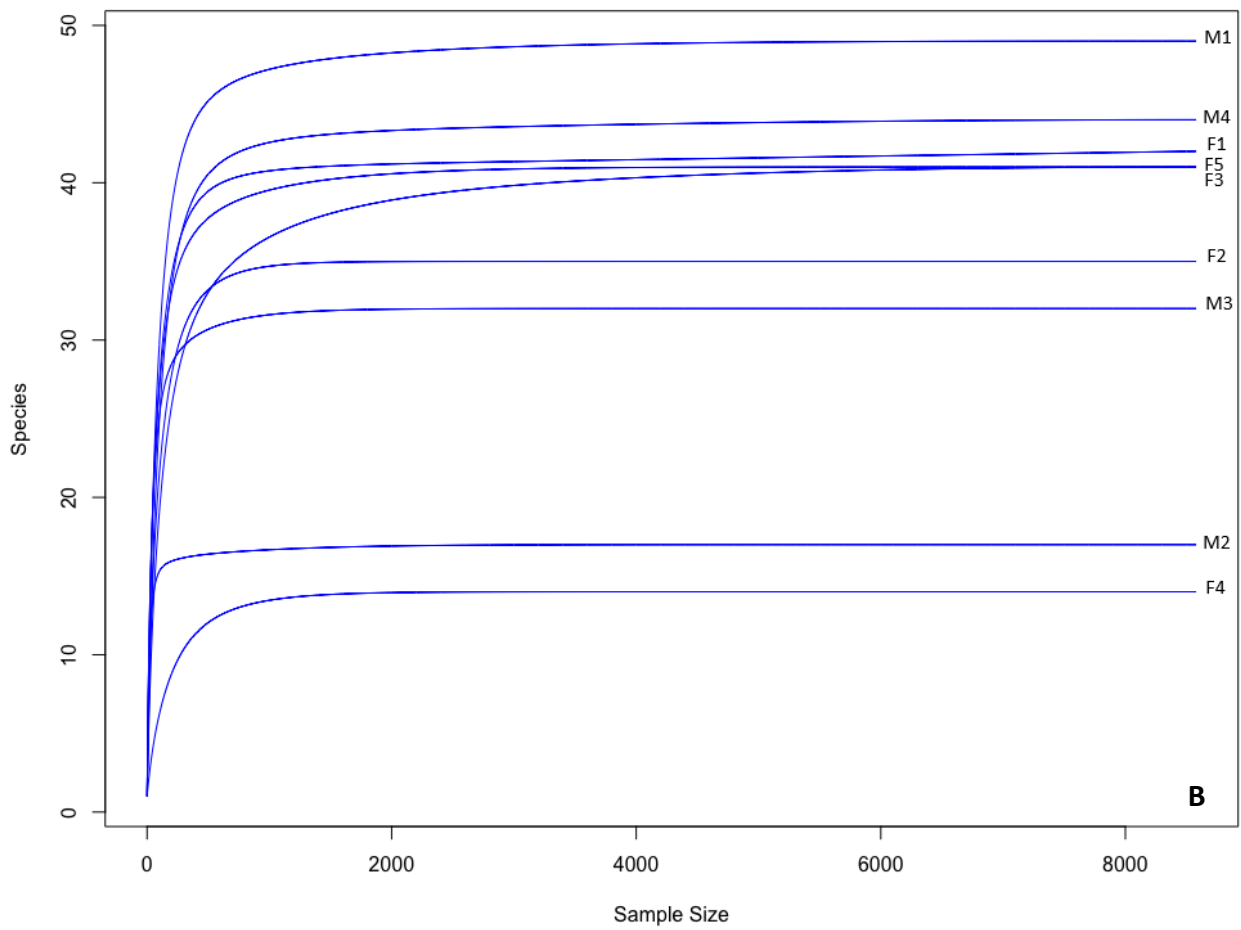
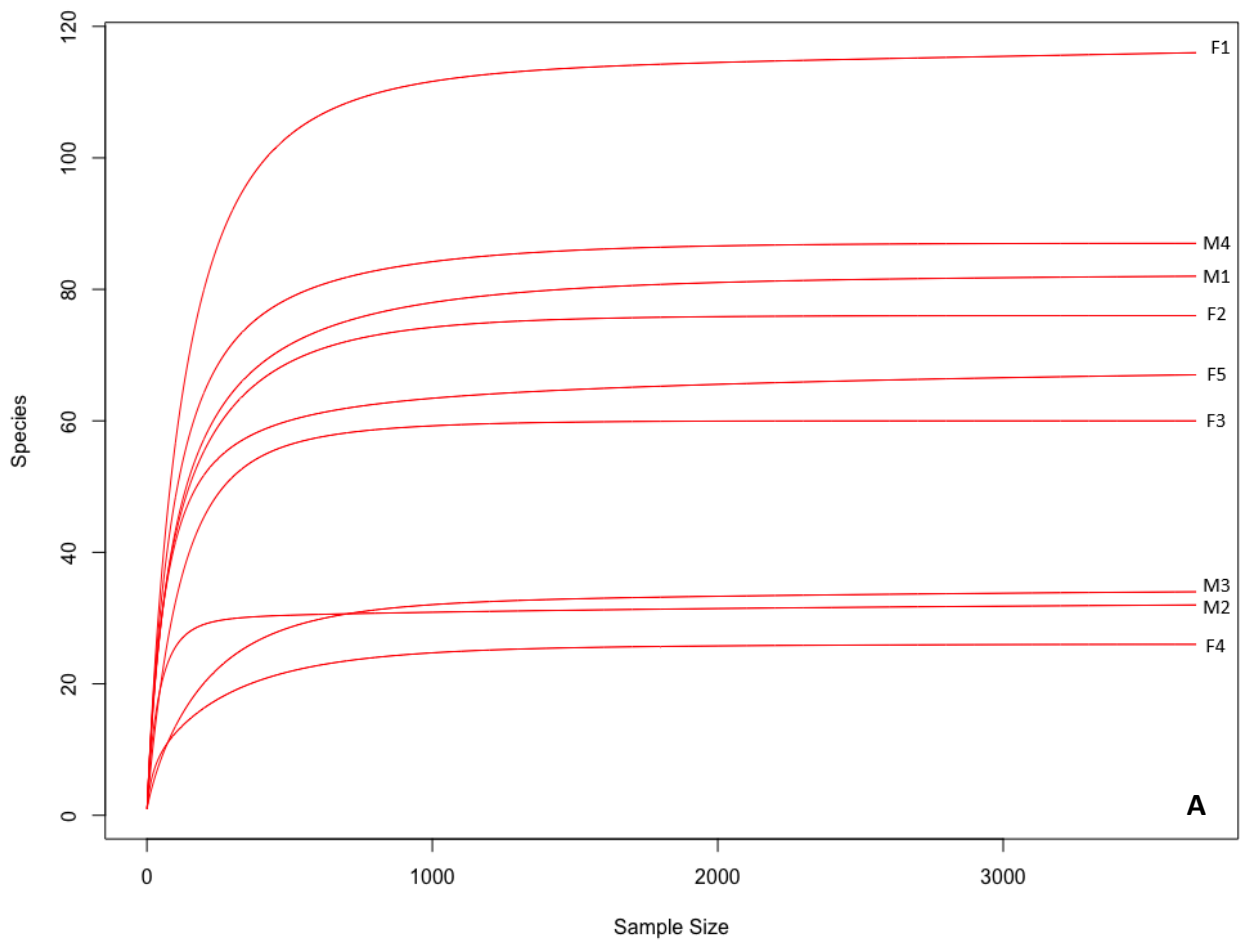


Figure S3. Rarefaction curves for prokaryotes (A) and fungi (B). The y-axis shows the OTU number found in relation to the number of reads (x-axis) for each individual.

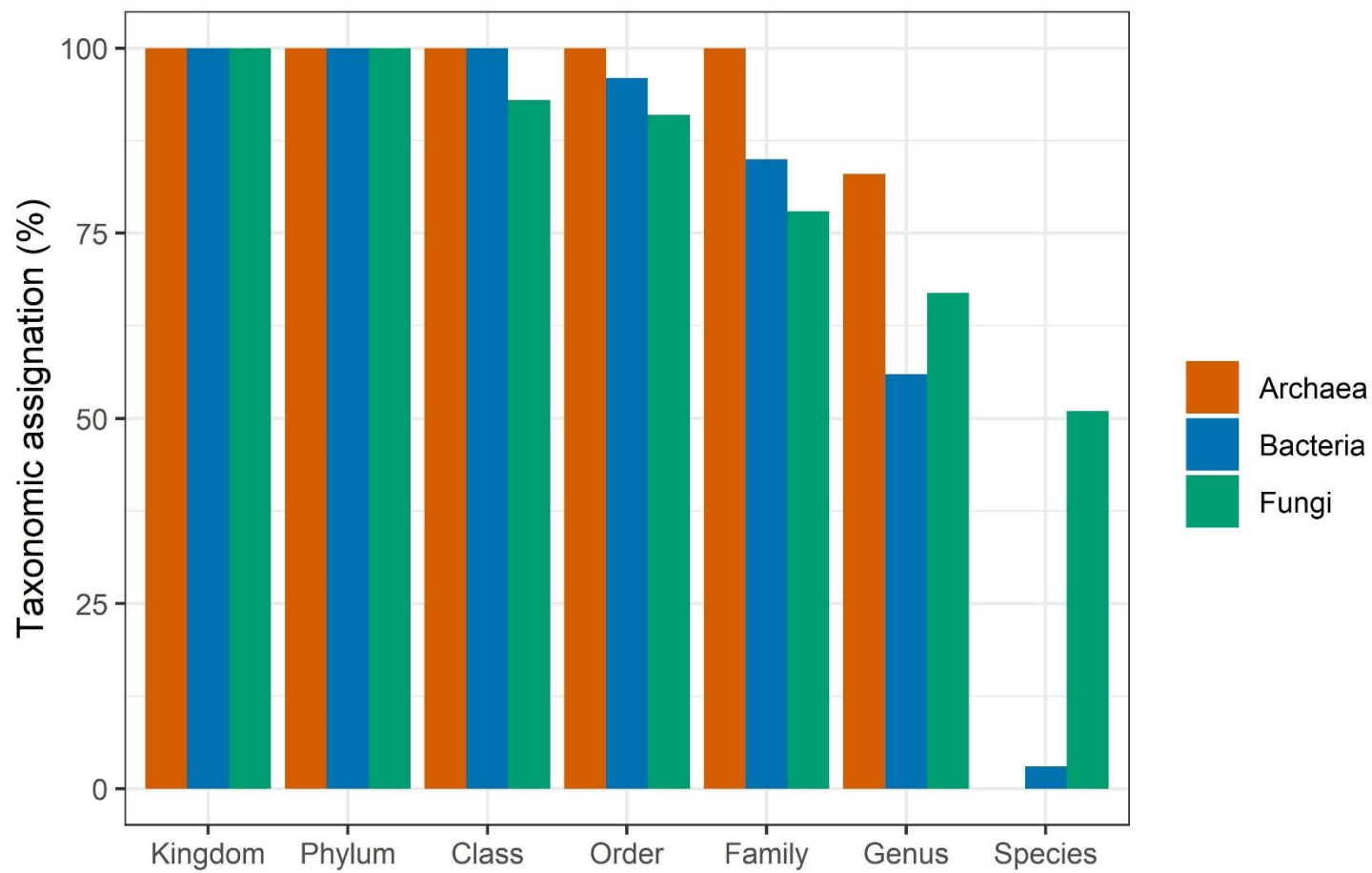


Figure S4. Taxonomic assignment percentages for OTUs of *T. pyrenaeus*. Percentages are calculated as the ratio of OTUs with a definite taxonomic assignment over the total number of OTUs (6 for archaea, 392 for bacteria, and 201 for fungi).

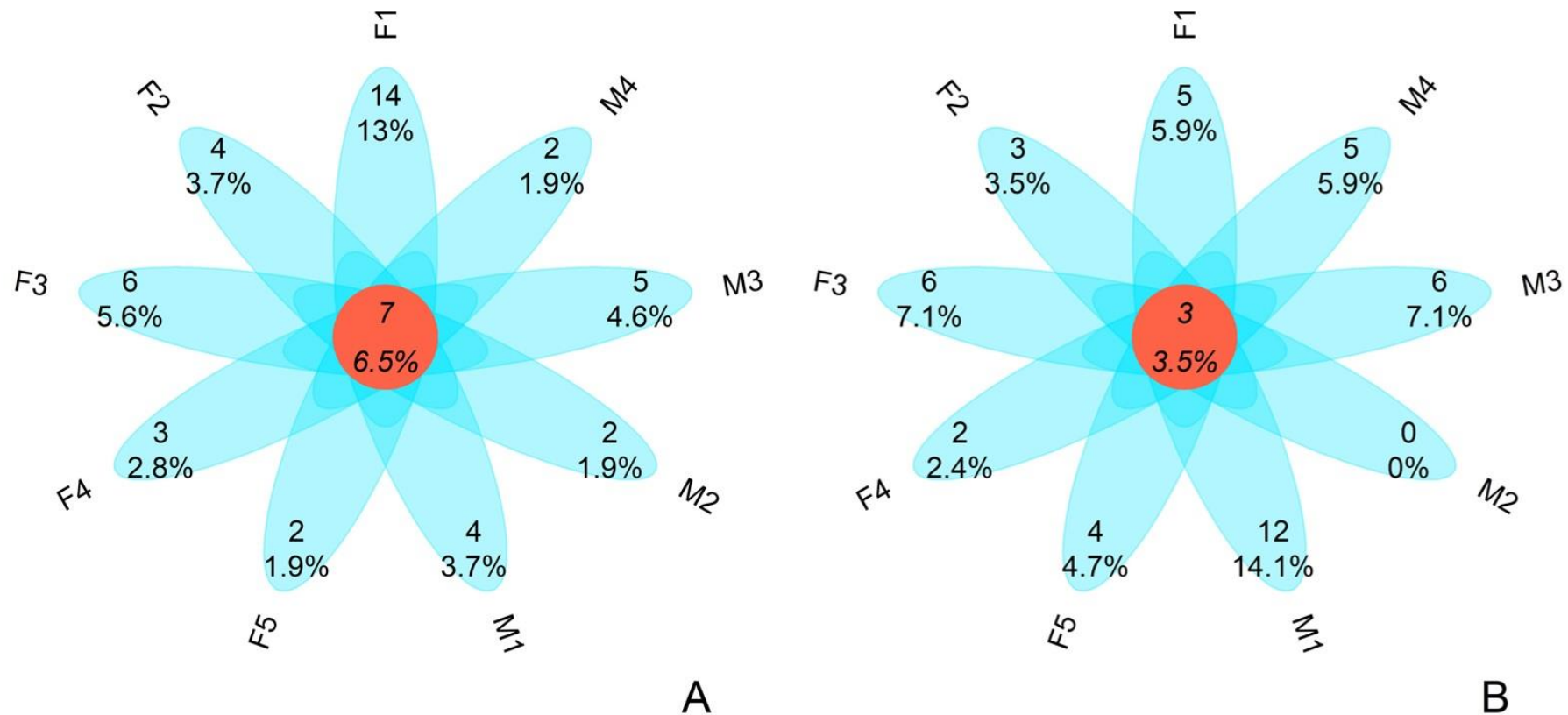


Figure S5. Flower plots show the number of core and exclusive bacterial (A) and fungal (B) families among the individuals of *T. pyrenaeus*. Bacterial core families account for 49.5% of the total abundance of retrieved sequences. These shared families are Comamonadaceae, Enterobacteriaceae, Enterococcaceae, Flavobacteriaceae, Pseudomonadaceae, Sphingobacteriaceae and Yersiniaceae. Fungal core families account for 45.6% of the total abundance of retrieved sequences. These shared families are Helotiaceae, Mycosphaerellaceae and Nectriaceae.

Kingdom	Family	F1	F2	F3	F4	F5	M1	M2	M3	M4	total	freq_core
Bacteria	Comamonadaceae	0.11	0.38	0.42	0.00	0.96	0.00	0.47	0.05	0.29	2.68	7
	Enterobacteriaceae	0.84	0.18	0.20	0.52	0.41	0.32	0.00	0.00	0.97	3.44	7
	Enterococcaceae	0.50	0.60	5.67	6.50	0.79	1.77	0.58	8.80	0.43	25.64	9
	Flavobacteriaceae	0.08	0.08	0.29	0.00	0.20	0.00	3.09	0.13	0.17	4.04	7
	Pseudomonadaceae	0.18	0.78	0.00	0.02	0.62	0.00	0.58	0.08	0.20	2.45	7
	Sphingobacteriaceae	0.08	0.48	0.00	0.02	0.55	0.02	0.74	0.02	0.88	2.79	8
	Yersiniaceae	0.00	0.30	0.00	0.49	0.15	0.13	1.50	0.25	0.10	2.93	7
Fungi	Helotiaceae	0.12	0.11	0.08	0.08	0.00	0.00	1.25	0.50	0.04	2.17	7
	Mycosphaerellaceae	0.16	0.56	0.01	10.21	0.42	0.89	2.11	1.52	0.18	16.05	9
	Nectriaceae	0.34	0.19	8.16	0.03	0.16	5.23	0.40	0.64	7.15	22.31	9

Table S2. Percentage of relative reads of each core family within each individual and over the total number of individuals. The 'freq\_core' column represents the number of individuals in which the family considered is found, i.e. from a minimum of 7 to a maximum of 9, as these are the requirements for a family to be part of the core.

<b>Kingdom</b>	<b>Index</b>	<b><i>t</i>_value</b>	<b>DF</b>	<b><i>p</i>_value</b>
Prokaryotes	Observed OTUs	0.493	6.79	n.s.
	Family	1.578	6.17	n.s.
	Phyla	1.503	6.92	n.s.
	Chao1	0.517	6.86	n.s.
	Simpson	0.334	4.5	n.s.
	Shannon	0.329	5.95	n.s.
Fungi	Observed OTUs	-0.101	5.89	n.s.
	Family	-0.33	6.34	n.s.
	Phyla	-1.76	4.42	n.s.
	Chao1	-0.101	5.89	n.s.
	Simpson	-0.994	5.31	n.s.
	Shannon	-0.966	5.05	n.s.

Table S3. The table shows the results of *t*-tests carried out to investigate any significant differences in the alpha diversity indices between the two sexes. All the results are not significant (n.s. = not significant).