

Parasites and the eukaryotic biome - diversity is associated with social rank in spotted hyena

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Context, Predictions, Aims

In the spotted hyena (*Crocuta crocuta*), a highly social, female-dominated carnivore, social status determines access to resources.



Hyenas interacting at a den.

Predictions:

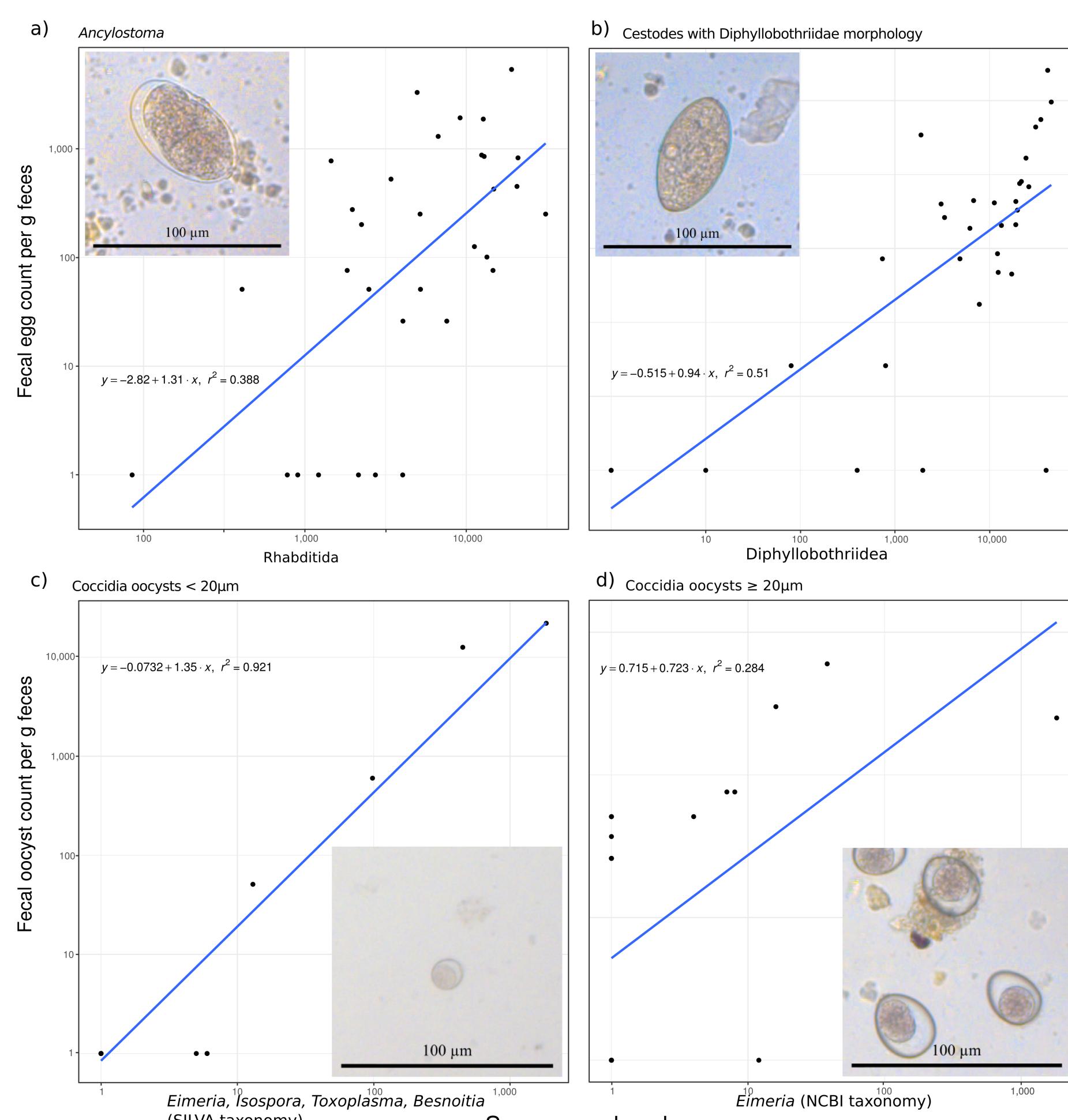
- High species diversity is an index of ecosystem health, the intestinal biome of healthier, socially dominant animals should be more diverse than that of subordinates.
- Gradual colonization of the juvenile intestine after birth predicts lower intestinal biome diversity in juveniles than adults.

Summary

	Bacterial microbiome	Eukaryome
Adults vs. Cubs	More diversity Higher evenness	More diversity Higher evenness
High vs. low social rank	More diversity Higher evenness	More diversity Higher evenness

Green circles = Results matching predictions Red cubes = No confirmatory results

Results: Validation



Ribosomal sequence variants (RSVs) predict fecal egg or oocyst counts for (a) *Ancylostoma* (Rhabditida), (b) *Diphyllobothriidae* and (c and d) small and a large size classes of *Coccidia* (*Eimeria*, *Isospora*, *Besnoitia*, and *Toxoplasma*).

⇒ Quantitative assessment of eukaryotes with high sensitivity.

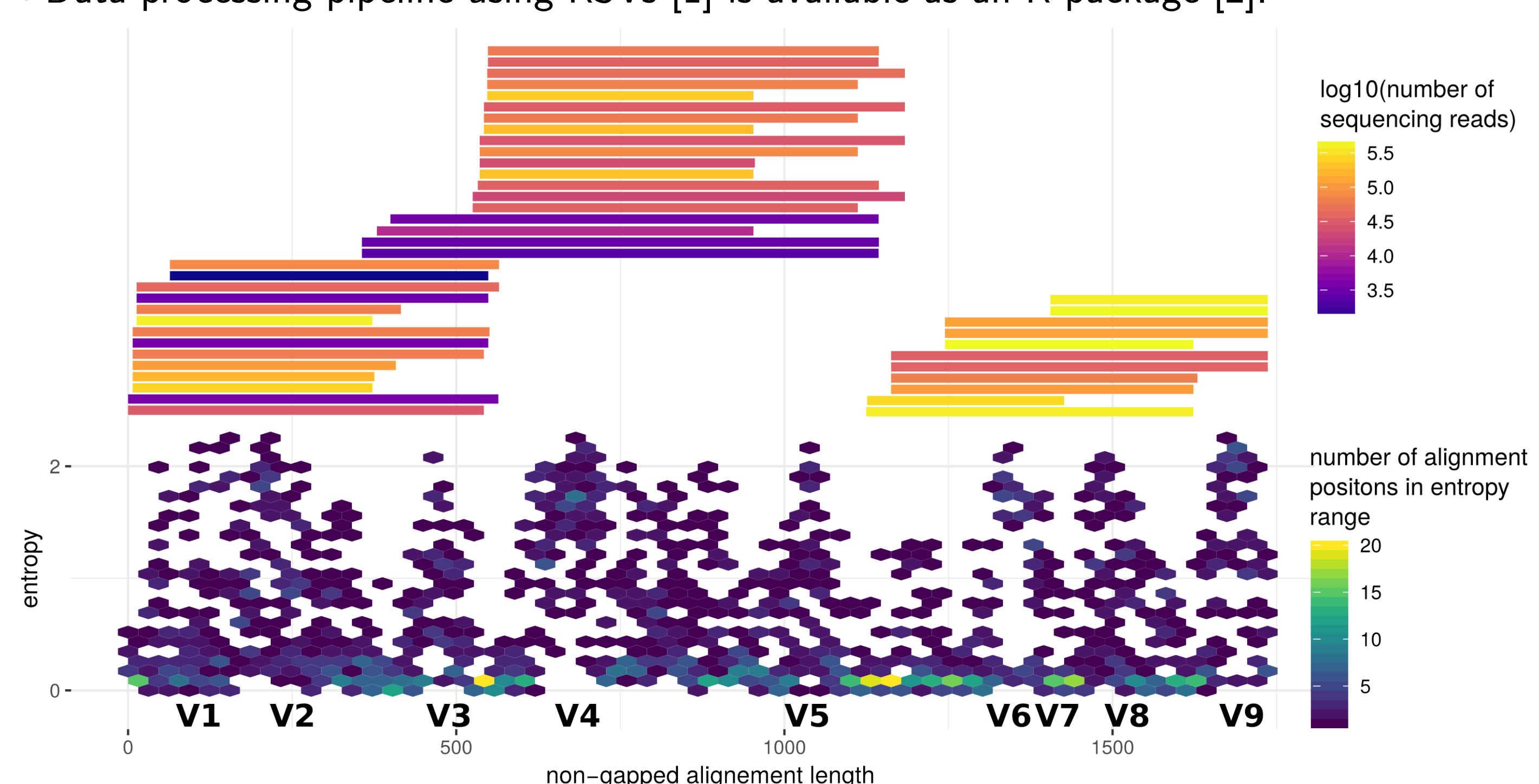
Methods

Study animals:

- 35 individually known adult females and 7 juveniles (< 24 months) for three clans in the Serengeti ecosystem.
- Social status categorized as above/below the median rank.
- Parasite eggs or oocysts counted for 32 individuals.

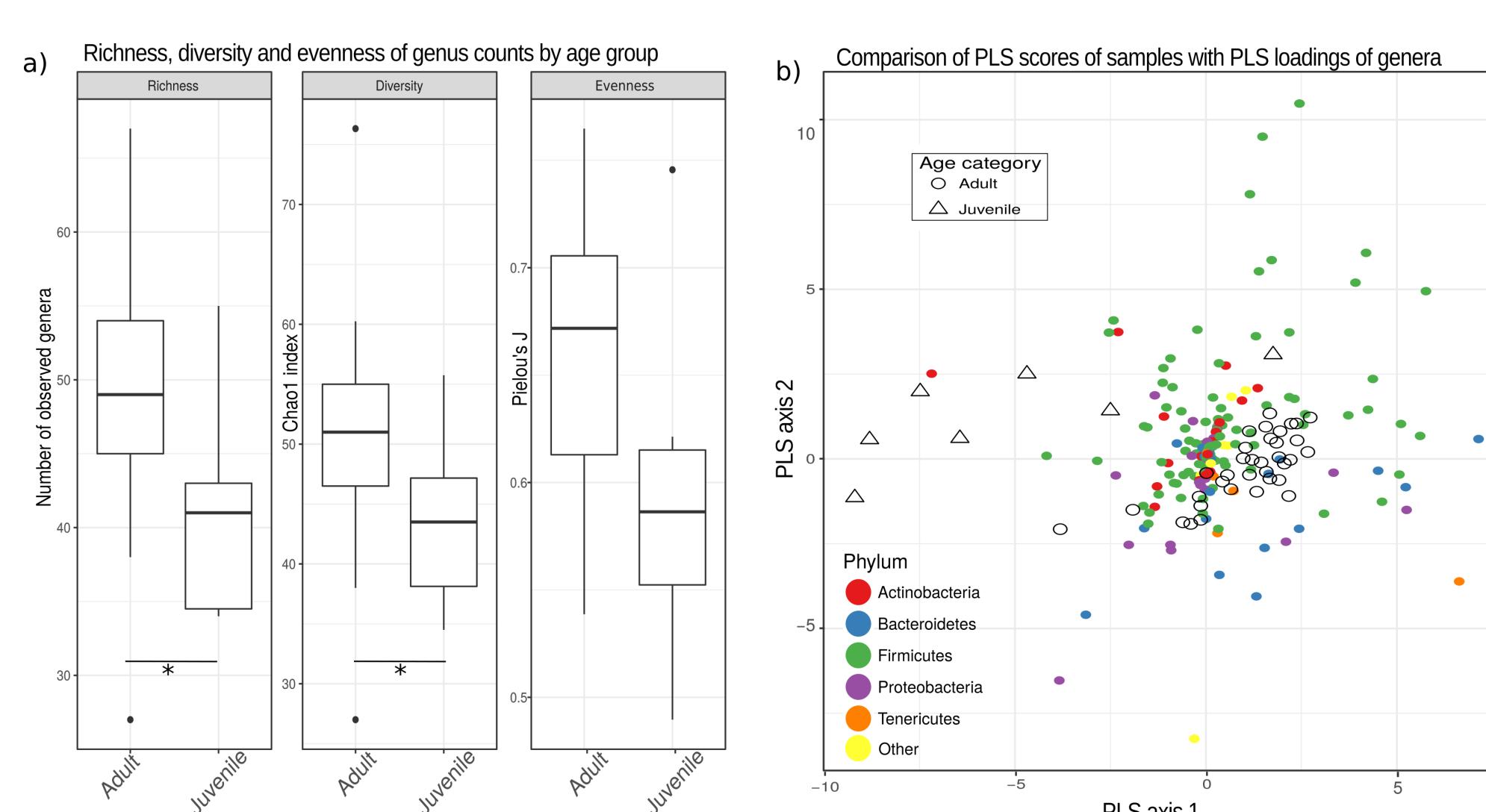
AmpliSeq sequencing:

- 48 different amplicons (4 for bacterial 16S, 44 for eukaryotic 18S) in a multi-amplicon sequencing approach.
- Processed on a microfluidics PCR system (Fluidigm Access Array®).
- Data processing pipeline using RSVs [1] is available as an R package [2].



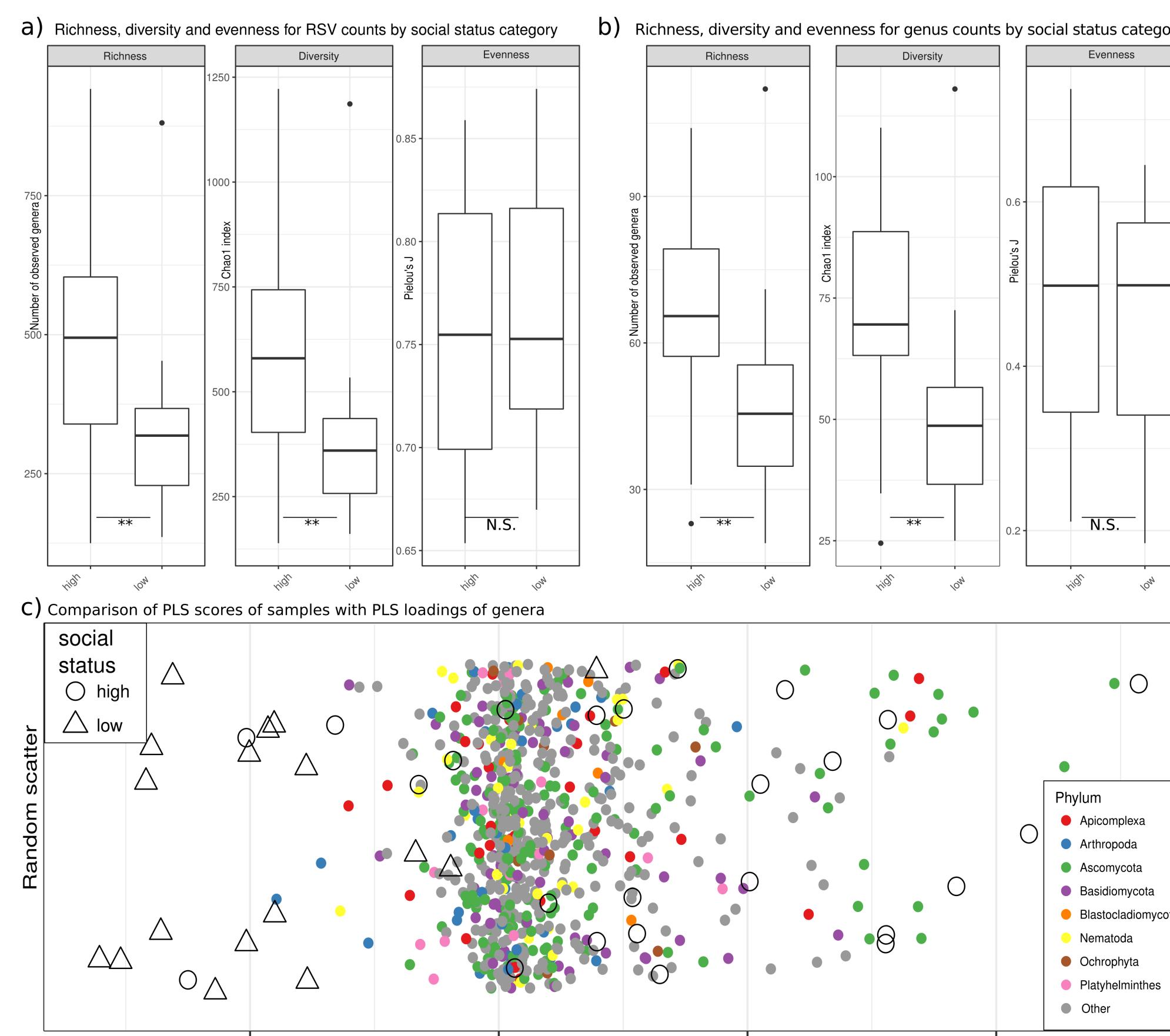
AmpliSeq used in this study are visualized in the context of entropy (evolutionary conservation and information content) of the eukaryotic 18S gene. Shannon entropy is displayed for the Silva reference alignment [3] of all eukaryotes. Primers were mapped against the same alignment. Positions along the gene are expressed as mean length of sequences (excluding gaps) for each column in the alignment.

Results: Bacterial microbiome



⇒ Adult female hyenas have a bacterial microbiome which is more diverse and differs in composition from that of juveniles.

Results: Eukaryome



⇒ A more diverse eukaryome in high-ranking than low-ranking hyenas.

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References

- [1] Callahan et al. (2016) DADA2: High-resolution sample inference from Illumina amplicon data. *Nature Methods* 13, 581–583
- [2] Heitlinger (2017). MultiAmplicon version 0.01 [R - package]. Zenodo; Development version at <https://github.com/derele/MultiAmplicon>
- [3] Pruesse et al. (2007) SILVA: a comprehensive online resource for quality checked and aligned ribosomal RNA sequence data compatible with ARB. *Nucleic Acids Research* 35:7188–7196