Supporting materials

Diet and feeding selectivity of the Andean Flamingo *Phoenicoparrus andinus* and Chilean Flamingo *Phoenicopterus chilensis* in lowland wintering areas

Appendix S1. Detail of 16S rRNA gene sequencing for Bacterial and Archaea identification.

Molecular analyses. The Ribosomal Database Project (RDP) suggested universal primers (http://pyro.cme.msu.edu/pyro/help.jsp) that contain the Roche 454-sequencing A and B adaptors and a 10 nucleotide "multiple identifier" (MID). Five independent PCRs were performed to reduce bias. The PCR mixture (final volume 25 μl) contained 2.5 μL FastStart High Fidelity 10X Reaction Buffer (Roche Applied Science, Mannheim, Germany), 20 ng of template DNA, 0.4 μM of each primer, 1.25 U FastStart High Fidelity Enzyme Blend (Roche Applied Science), and 0.2 mM dNTPs. The PCR conditions were 95°C for 5 min for initial denaturation, followed by 95°C for 45 s, 57°C for 45 s, 72°C for 60 s in 30 cycles, and a final elongation step at 72 °C for 4 min. Two negative control reactions containing all components except for the template were performed. The five reactions products were pooled and purified using AMPure beads XP. Quantification of the purified PCR product was performed using the Quant-IT Pico Green dsDNA Kit (Invitrogen Molecular Probes Inc., Oregon, USA). Purified PCR product was sequenced on a Genome Sequencer FLX (Roche Applied Science) using Titanium Chemistry according to the manufacturer's instructions. 10,958 filtered sequences with an average length of 225 bp were obtained from samples. Filter parameters were set to reject reads that had a mean quality score of < 25, maximum homopolymer run of > 6, number of primer mismatches > 0, and read length < 200 bp or > 1,000 bp.

Table S1. Pianka's index showing the food-niche overlap.

	Observed	**Boot mean**	**Boot s.d.**	**Boot Cl21**	**Boot Cl2**
OTUs (16S rRNA sequencing)	0.928	0.910	0.084	0.668	0.998
Size categories	0.985	0.949	0.066	0.803	1.000

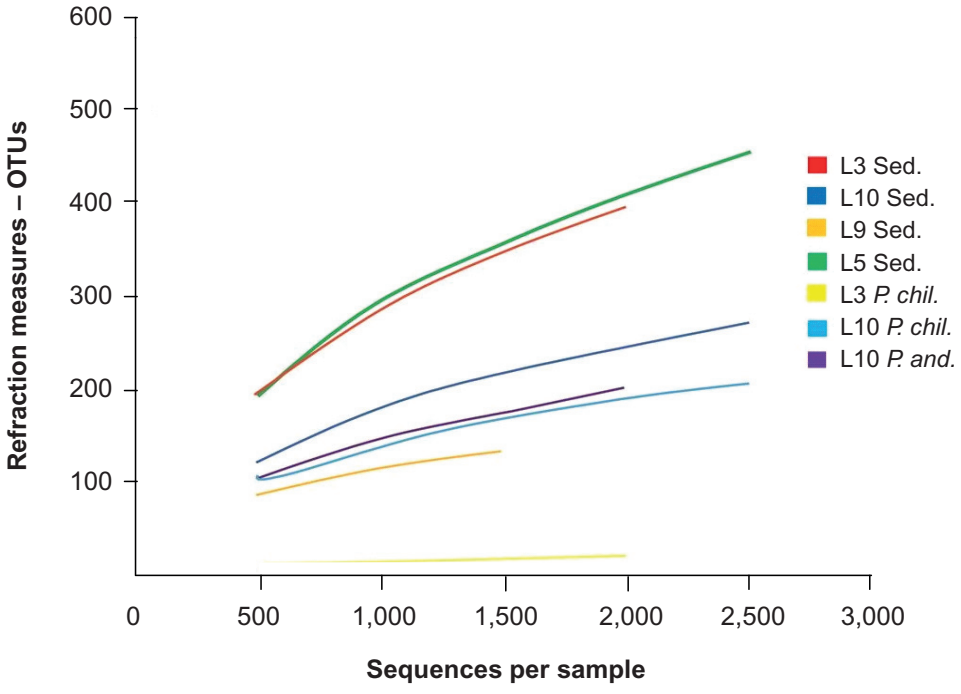

Figure S1. Rarefaction curves for the different samples collected for molecular analyses in each lake (L3 = La Badenia Lake, L10 = Bella Vista Lake, L9 = Melincué Lake, L5 = Muelle 1 Lake) and flamingo faeces (*P. chil.* = *Phoenicopterus chilensis* faeces; *P. and.* = *Phoenicoparrus andinus* faeces).