

Additional file 1

Divergent and non-parallel evolution of MHC IIB in the Neotropical Midas cichlid species complex

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Figure S1. Alignment of 142 bp of exon 2 of 150 *Amphilophus* MHC class IIB alleles. Conserved sites are shaded in grey.

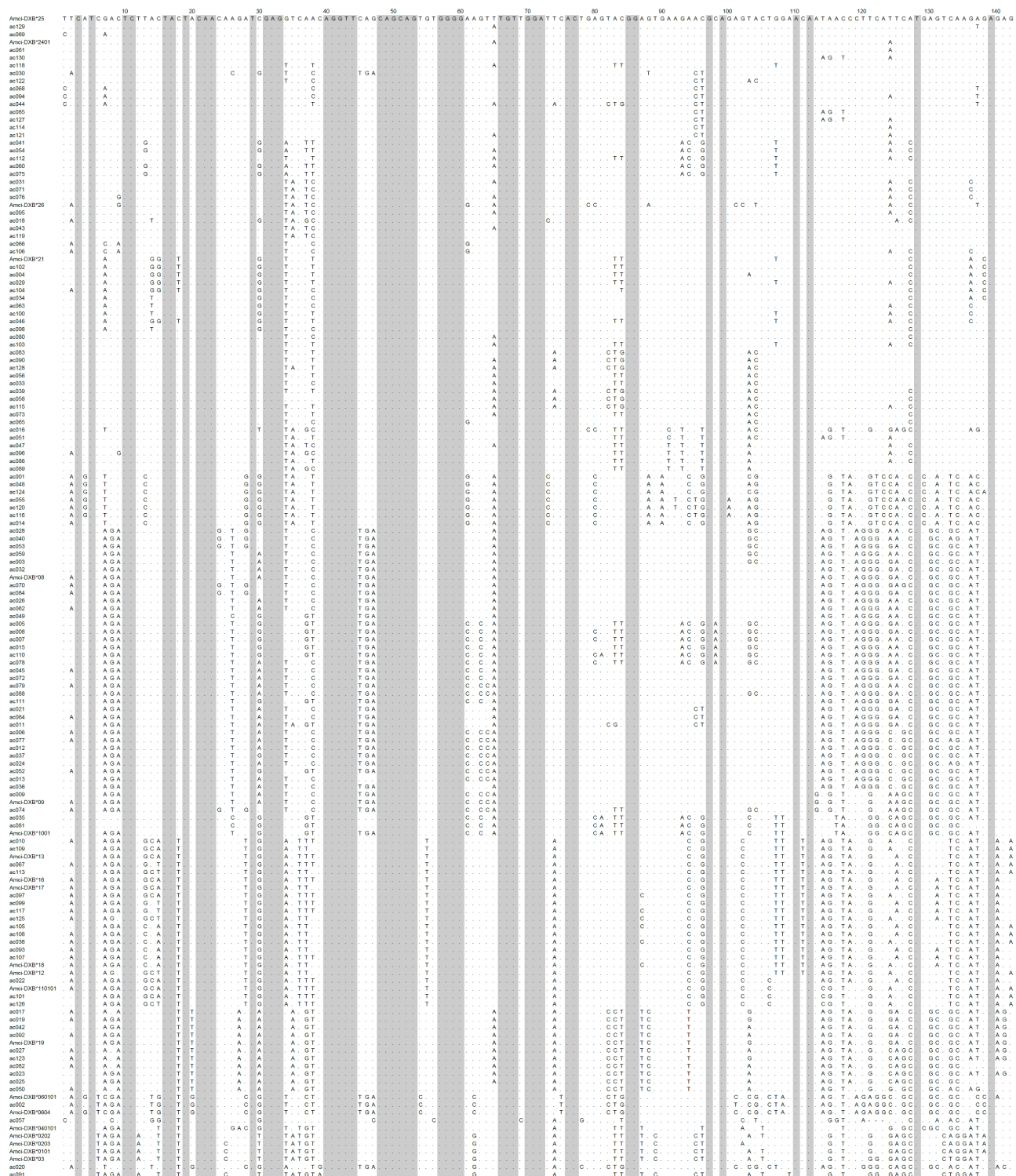
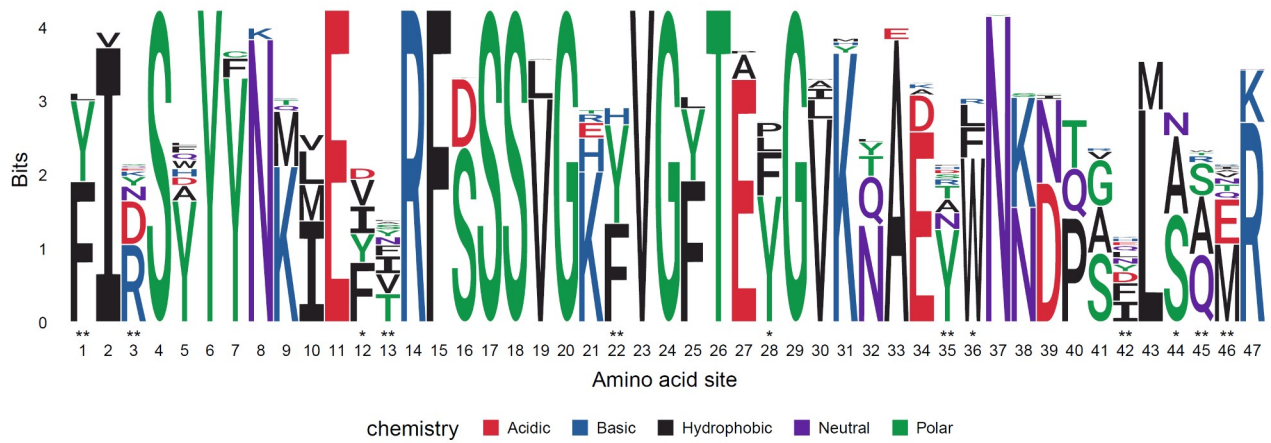


Figure S2. Amino acid variability for 47 positions of 150 aligned Midas cichlid MHC class IIB alleles. Asterisks indicate positively selected sites (** = identified by all methods, * = identified by two methods). Colours indicate chemical properties of amino acids and bits are a measure of information content of each position.



Phylogenetic tree showing the relationships between various *Acinetobacter* strains. The tree is rooted at the bottom left and branches out to the right. Bootstrap values are indicated at the nodes. The strains are labeled with accession numbers (ac) and some are grouped into clusters (e.g., Amci-DXB*2401, Amci-DXB*26, Amci-DXB*21, Amci-DXB*18, Amci-DXB*12, Amci-DXB*17, Amci-DXB*16, Amci-DXB*13, Amci-DXB*110101, Amci-DXB*09, Amci-DXB*08, Amci-DXB*0604, Amci-DXB*060101, Amci-DXB*19, Amci-DXB*03, Amci-DXB*0203, Amci-DXB*0202, Amci-DXB*0101, Amci-DXB*040101).

Figure S4. Distribution of MHC IIB supertypes. A) number of individuals carrying a supertype. If multiple alleles of the same supertype occurred in an individual, they were only counted once. B) frequency of supertypes per population, C) per lake and D) per habitat. For supertypes occurring multiple times in an individual, each instance was counted for calculating frequencies in B), C) and D). Numbers in parentheses give the number of alleles per supertype. Asterisks (*) indicate that the supertype contributed to differences among groups. Bent = benthic, limn = limnetic.

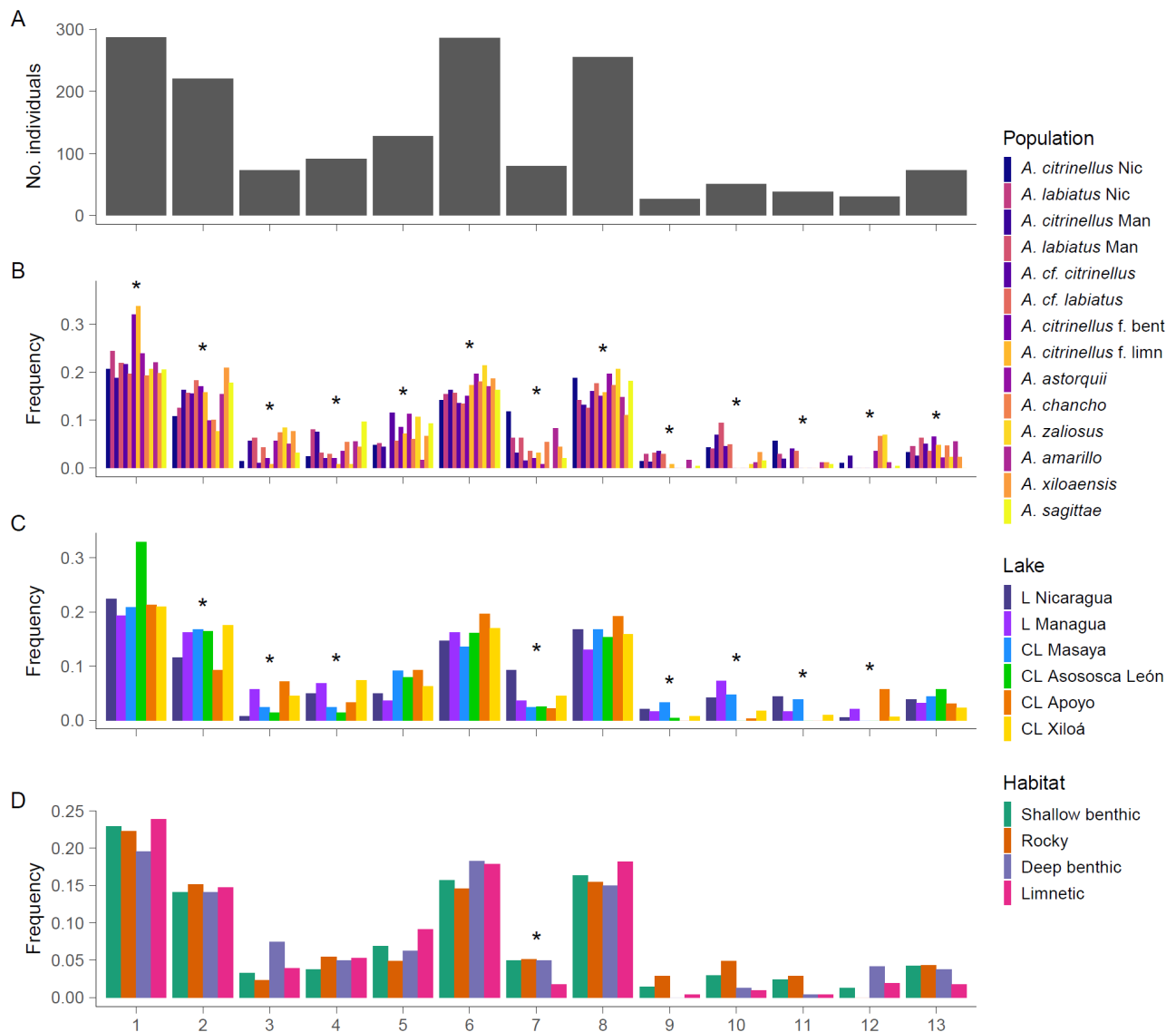


Figure S5. NMDS plot for all individuals grouped by lake showing the variation among individuals. MDS 1 and 2 are shown.

