MOLECULAR ECOLOGY

Supplemental Information for:

Encouraging news for in situ conservation: translocation of salamander larvae has limited impacts on their skin microbiota

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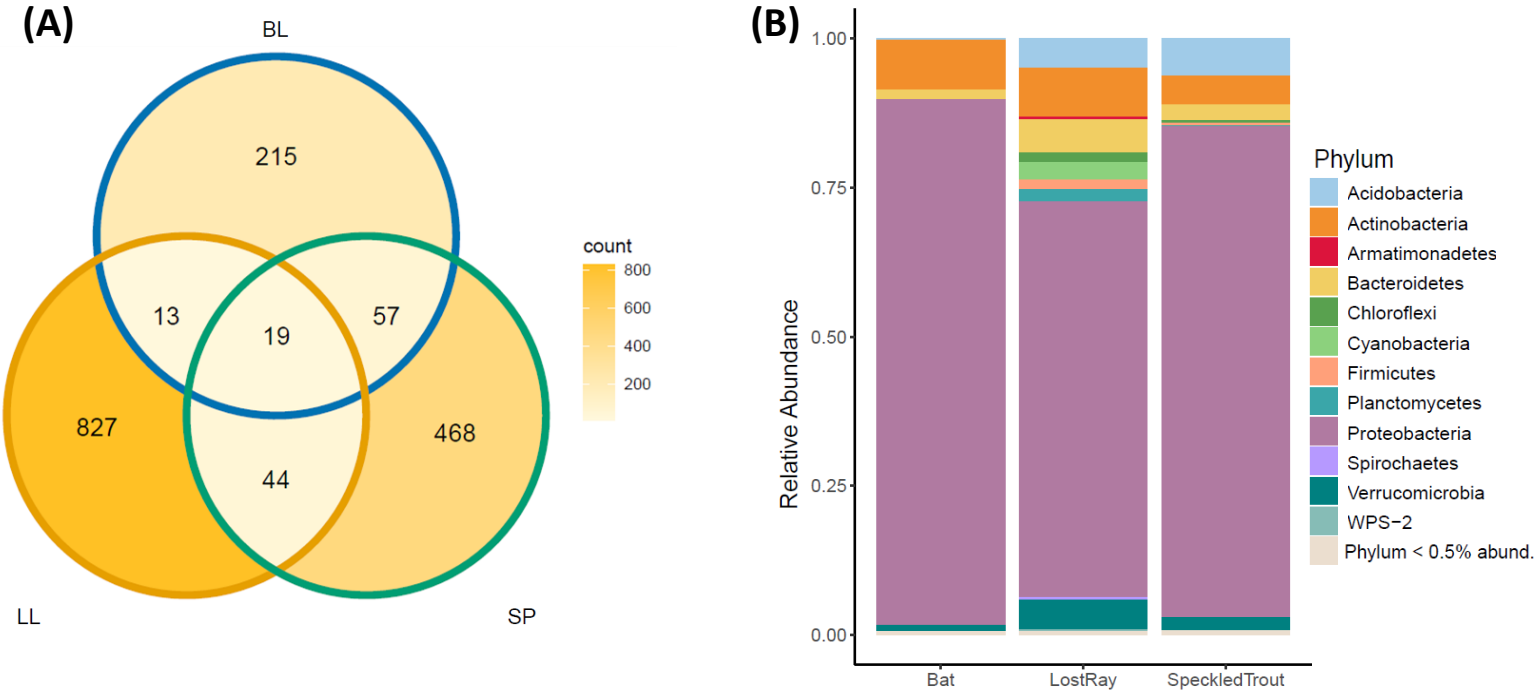
Table of Contents:

MOLECULAR ECOLOGY

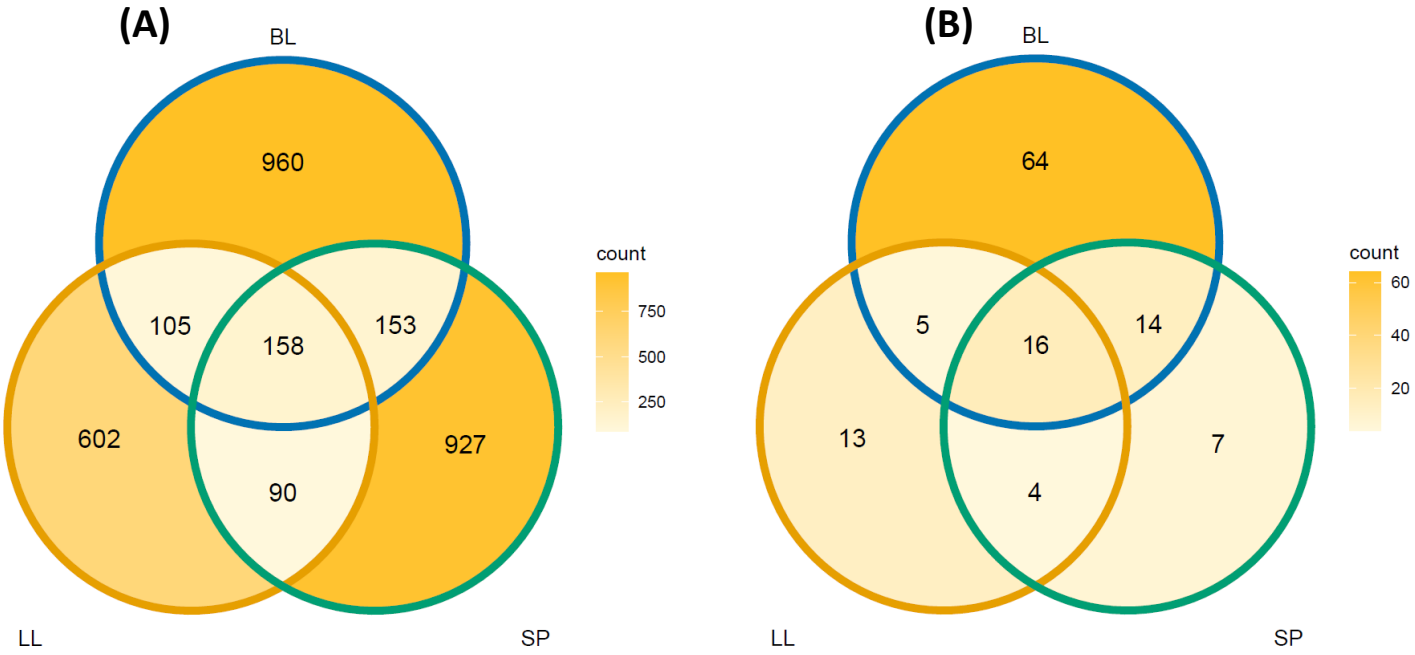


(C)

Contrast	Phylum	Order	Family	Genus	Log2 fold difference	SE	*p*-value
LL vs. BL	Proteobacteria	Rhizobiales	Rhodomicrobiaceae	Rhodomicrobium	26.05	3.91	2.95E-08
LL vs. SP	Proteobacteria	Rhizobiales	Rhodomicrobiaceae	Rhodomicrobium	27.04	3.91	6.05E-09
SP vs. BL	Proteobacteria	Betaproteobacteriales	Burkholderiaceae		-22.53	3.91	4.81E-06
SP vs. BL	Proteobacteria	Enterobacteriales	Enterobacteriaceae	Serratia	-22.25	3.91	4.81E-06
SP vs. BL	Proteobacteria	Betaproteobacteriales	Chromobacteriaceae	Aquitalea	-13.81	3.33	0.009

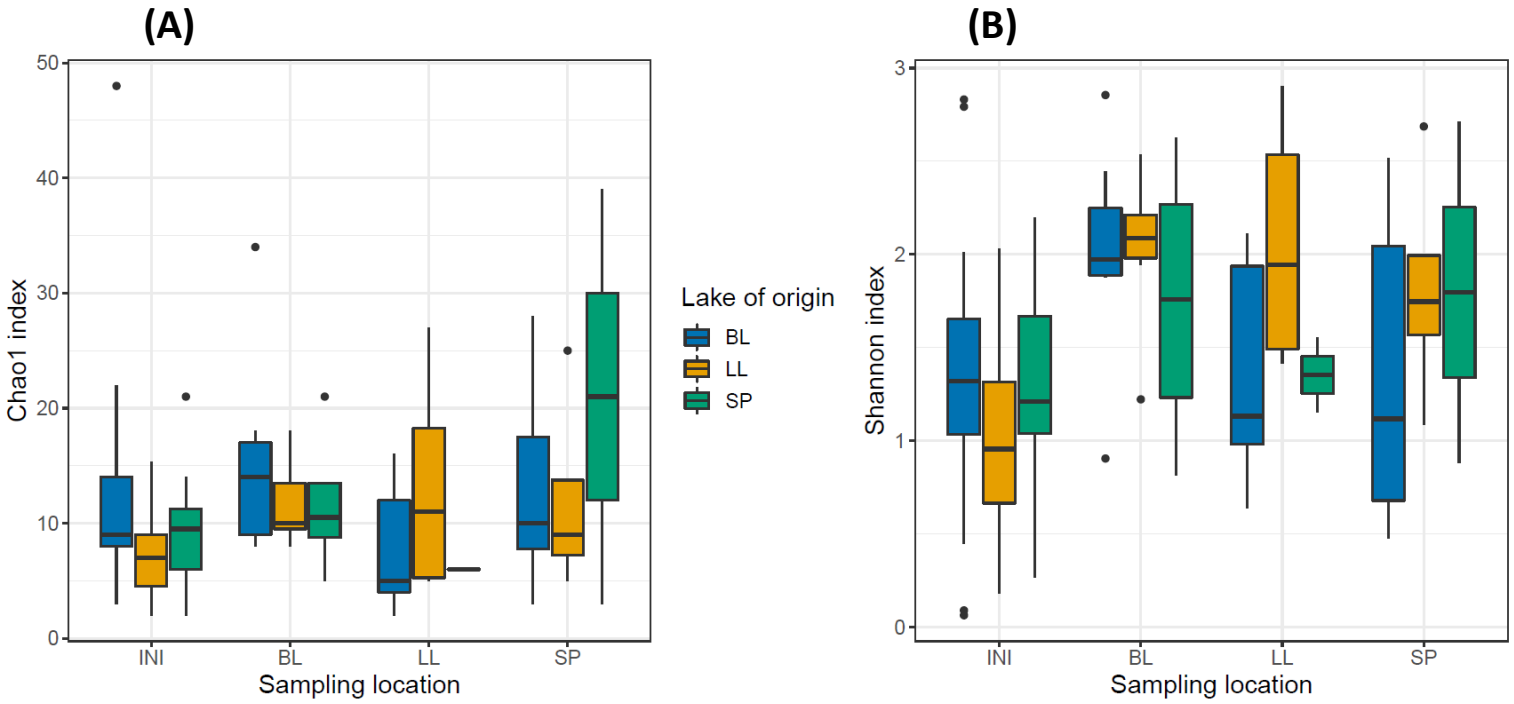
Appendix S1. Differences between environmental microbiota of the 3 lakes in the study. (A) Venn diagrams of the total number of phylotypes shared between lakes (BL = Bat Lake; LL = Lost Ray Lake; SP = Speckled Trout Lake). The intensity of the yellow color is proportional to the sum of ASVs in each group. (B) Relative abundance of the main phyla in each lake. (C) Significant log2 fold differences in abundance of bacterial phylotypes between lakes (Contrast). The direction of the difference in abundance is provided with its amplitude (Log2 fold change) and its standard error (SE). A blank space indicates unknown phylogenetic attribution according to SILVA.

MOLECULAR ECOLOGY



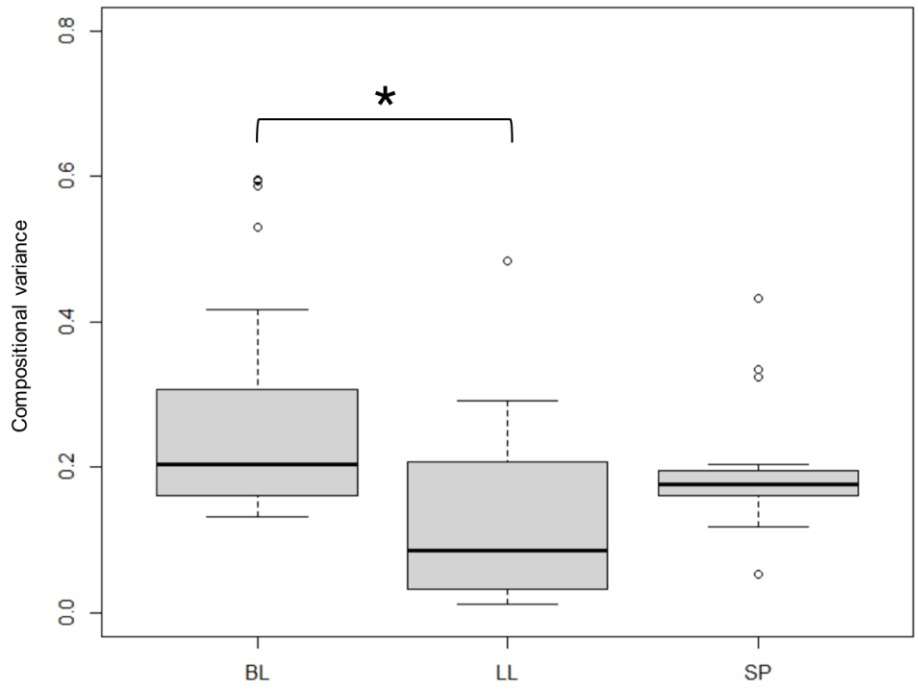
Appendix S2. Venn diagrams of the total number of phylotypes (A) or of *Bd*-inhibitory phylotypes (B) shared and unique between the three populations (BL = Bat Lake; LL = Lost Ray Lake; SP = Speckled Trout Lake) of yellow-spotted salamander at the initial sampling (D0). The intensity of the yellow color is proportional to the sum of ASVs in each group.

MOLECULAR ECOLOGY



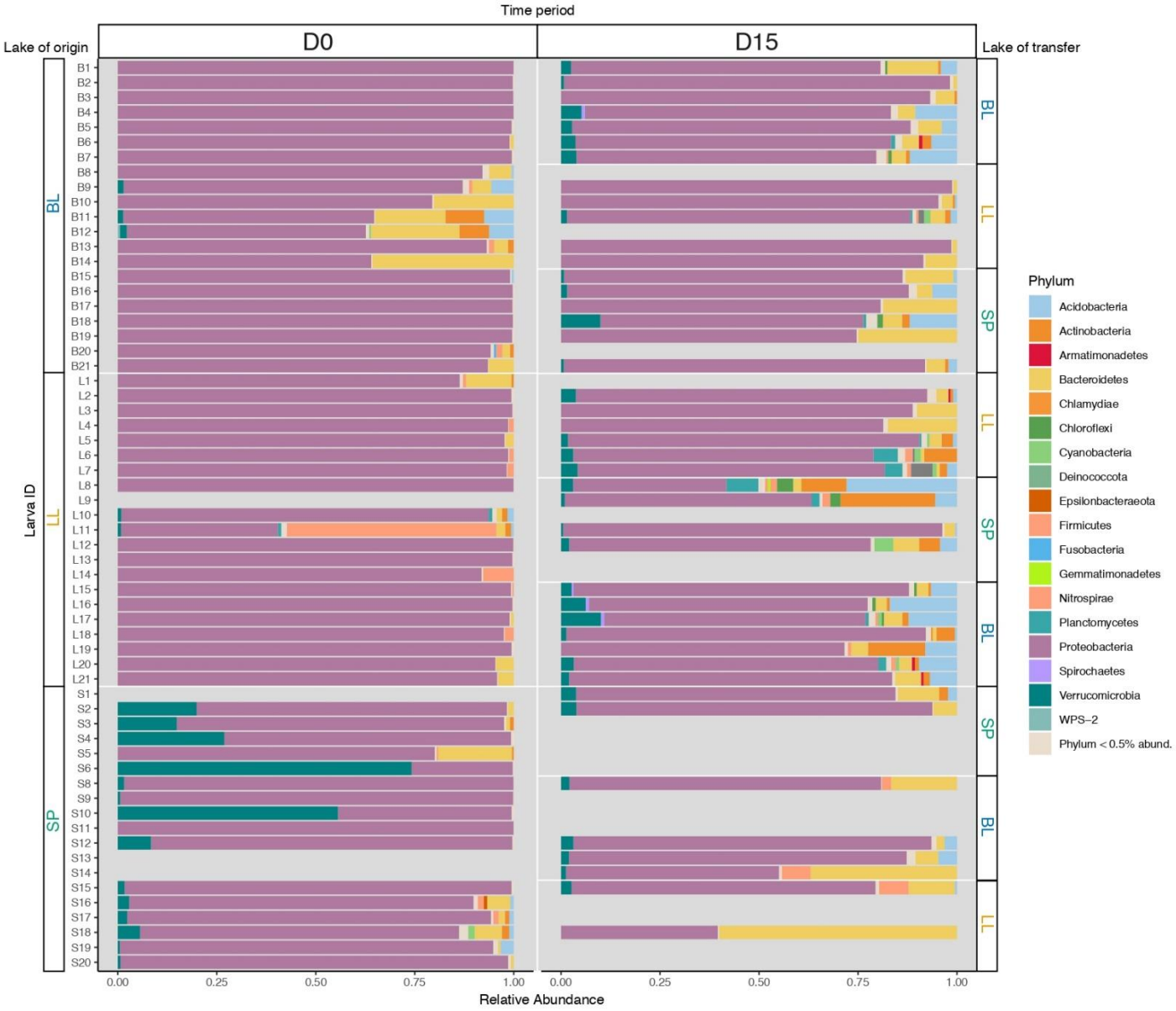
Appendix S3. Alpha diversity of the *Bd*-inhibitory bacterial communities of yellow-spotted salamander larvae at the beginning (at D0, "INI") and the end (at D15, by site: BL = Bat Lake; LL = Lost Ray Lake; SP = Speckled Trout Lake) of the experiment, measured as Chao1 (A) and Shannon (B) indexes. The color code indicates the initial site where the larvae were collected from, at D0.

MOLECULAR ECOLOGY



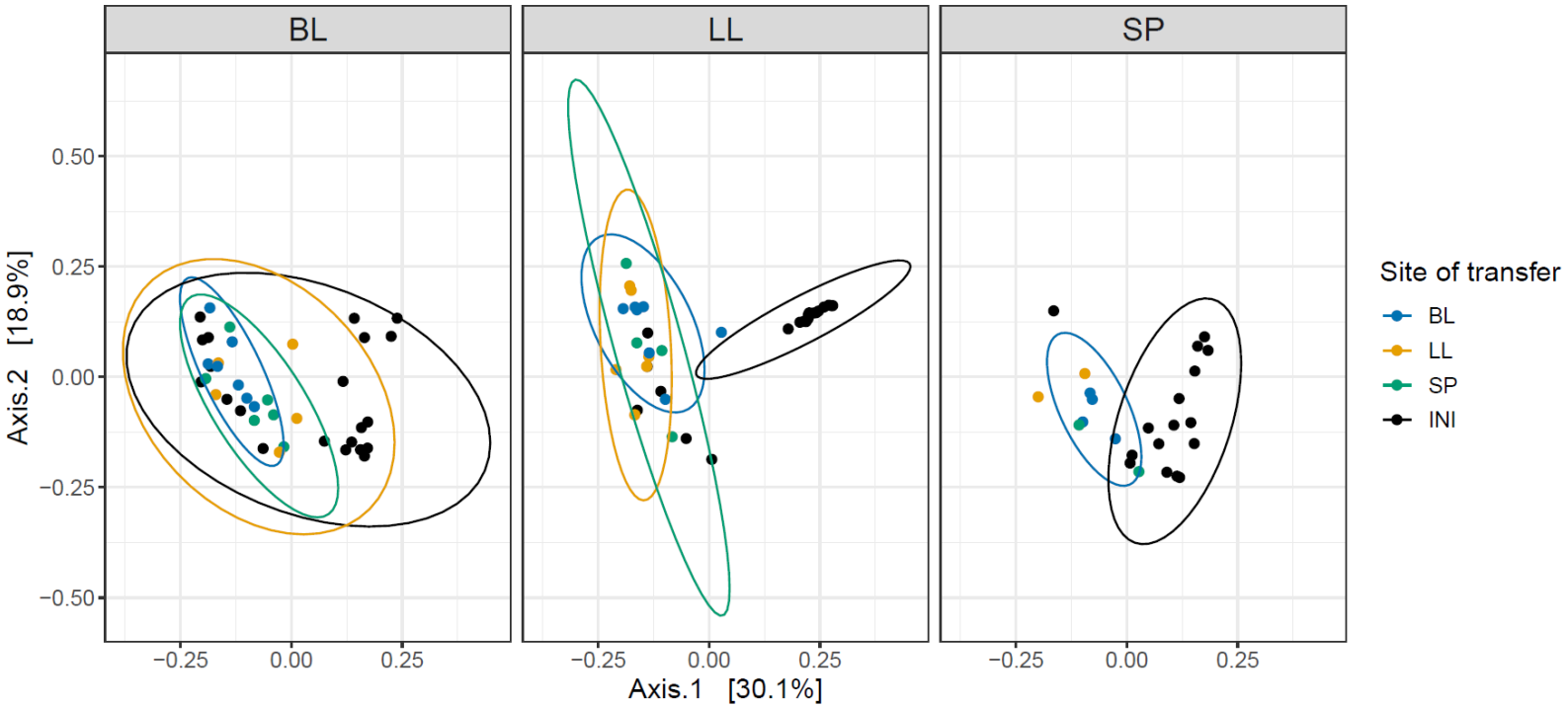
Appendix S4. Initial differences in compositional variance of *Bd*-inhibitory bacterial communities between populations (D0). The bracket and asterisk indicate a significant difference in compositional variance between *Bd*-inhibitory microbiota of samples from BL and LL.

MOLECULAR ECOLOGY



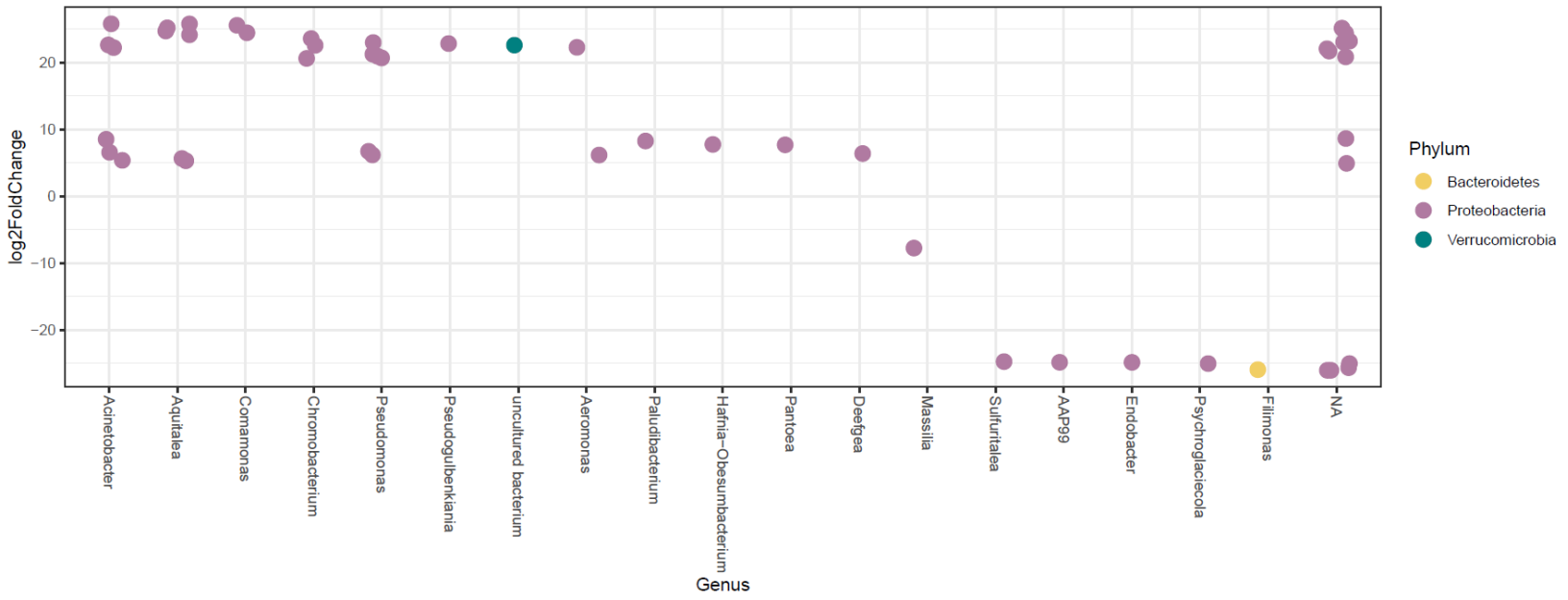
Appendix S5. Relative abundance of the most frequent bacterial phylotypes in the skin microbiota of yellow-spotted salamander larvae, at the phylum level. Each line represents the microbiota of an individual, at the initial sampling (D0) and at the end of the experiment (D15). Individuals are grouped by lake of origin (D0) and by final location (D15; BL = Bat Lake; LL = Lost Ray Lake; SP = Speckled Trout Lake). Blank lines correspond to missing samples (either because the samples were deleted after the rarefication process or because the larvae had deceased before D15). Dominant phyla are identified in the legend.

MOLECULAR ECOLOGY



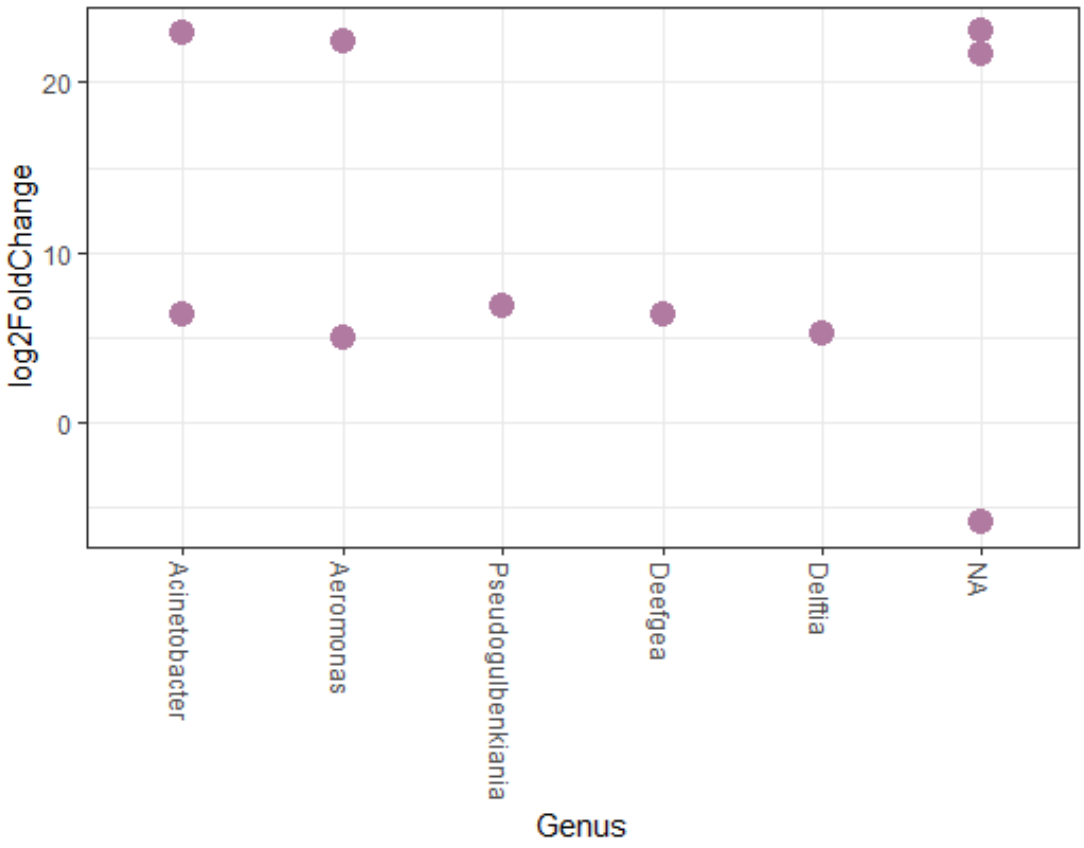
Appendix S6. PCoA representing the beta diversity (calculated as the weighted Unifrac distance) of the skin microbiota of yellow-spotted salamander larvae. Results are plotted separately in three blocks to gather larvae initially coming from the same location (D0). The color of the datapoints and ellipses indicate whether they correspond to microbiota of larvae at the beginning (D0, INI) or at the end of the experiment (D15); in that latter case, the color indicates the final location of the larvae at D15 (BL = Bat Lake; LL = Lost Ray Lake; SP = Speckled Trout Lake).

MOLECULAR ECOLOGY



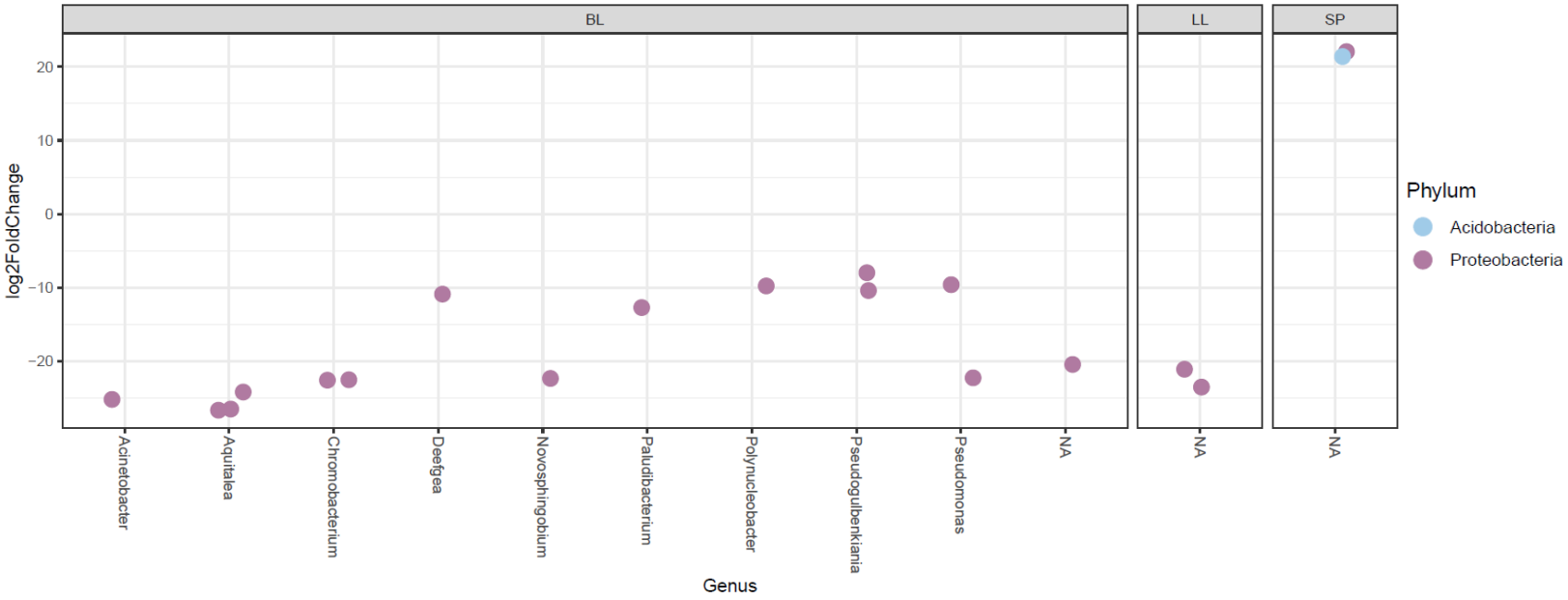
Appendix S7. Significant log2 fold changes in abundance of bacterial phylotypes between microbiota of control larvae at the initial (D0) and last (D15) times of sampling. Each point represents a phylotype differentially abundant between D0 and D15. The color code and the columns respectively indicate the phylum and the genus to which belongs each of these phylotypes. Genera that could not be identified are indicated as NA.

MOLECULAR ECOLOGY



Appendix S8. Significant log2 fold changes in abundance of *Bd*-inhibitory bacterial phylotypes between the microbiota of control larvae at the initial (D0) and last (D15) times of sampling. Each point represents a phylotype differentially abundant between D0 and D15. Here, all differentially abundant phylotypes belonged to Proteobacteria. Columns indicate the genus to which belongs each of these phylotypes. Genera that could not be identified are indicated as NA.

MOLECULAR ECOLOGY



Appendix S9. Significant log2 fold differences in abundance of bacterial genera between the initial microbiota (D0) of larvae that eventually died compared to that of larvae that survived at the end of the experiment (D15), per lake of origin (BL = Bat Lake; LL = Lost Ray Lake; SP = Speckled Trout Lake). Each point represents a phylotype differentially abundant between dead and surviving larvae. The color code and the columns respectively indicate the phylum and the genus to which belongs each of these phylotypes. Genera that could not be identified are indicated as NA.

MOLECULAR ECOLOGY

Phylum	Order	Family	Genus	Log2 fold difference	SE	*p*-value
Proteobacteria	Betaproteobacteriales	Chitinibacteraceae	Deefgea	-11.92	2.53	6.00E-05
Proteobacteria	Betaproteobacteriales	Chromobacteriaceae	Pseudogulbenkiania	-8.67	2.31	0.002

Appendix S10. Significant log2 fold differences in abundance of *Bd*-inhibitory phylotypes between the initial microbiota (D0) of individuals that eventually died compared to that of individuals that survived at the end of the experiment (D15), in larvae initially collected in Bat Lake (D0). The direction of the difference in abundance is provided with its amplitude (Log2 fold change) and its standard error (SE).