

Supporting Information

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SI Methods

Preparation of Libraries for Multiplexed 16S Amplicon Sequencing.

Bacterial communities were analyzed by 16S amplicon pyrosequencing as follows. The V1–V2 regions of the 16S gene were amplified using primers 8f with 5' Roche FLX Amplicon Adapter B (underlined in primer sequence) and TC linker (denoted in lowercase), GCCTTGCCAGCCCGCTCAG-tc-AGR-GTTYGATYMTGGCTCAG, and 338r with 5' Roche FLX Amplicon Adapter A, an 8-bp barcode (denoted by "xxxxxxx") (1), and CA linker, GCCTCCCTCGCGCCATCAG-xxxxxxx-ca-TGCWGCCWCCCGTAGGWT. For the 16S amplicon library of samples from the laboratory experiment, the 8-basepair barcode was incorporated into the forward primer. Each 25-μL PCR assay consisted of 1.25 units of DNA polymerase (5PRIME) in proprietary buffer, 200 μmol·L⁻¹ each dNTP, 2 mmol·L⁻¹ MgCl₂, 5% acetamide, 200 nmol·L⁻¹ each primer, and 1 μL of DNA template. PCR conditions were 94 °C for 120 s, followed by 35 cycles of 94 °C for 30, 58 °C for 45 s, 72 °C for 60 s, and a final extension (72 °C for 300 s). A subset of samples and all negative controls were visualized by electrophoresis in a 1% agarose gel stained with ethidium bromide and further quantified using PicoGreen fluorescence on a Qubit fluorometer (Invitrogen). All PCR products were pooled in equimolar quantities for sequencing on one-half picotiter plate on a Roche/454 GS FLX instrument using Titanium chemistry (laboratory of Stefan Schuster, Pennsylvania State University, University Park, PA). Samples generated in the experiment (168 frog swabs, 12 water samples) and field survey (99 frog swabs, seven water samples) were analyzed on separate pyrosequencing runs.

Bioinformatic Processing. The program mothur (version 1.30) (2) was used to quality-filter and align sequences, cluster into OTUs, classify OTUs, and calculate per-sample diversity measures and among-sample distance measures as follows. Pyrosequence flowgrams were first quality-filtered using PyroNoise (3). Sequence reads were then screened to remove reads with any ambiguous base call, any barcode mismatch, more than 1 primer mismatch, homopolymers greater than eight bases, or read length <200 bases. Sequences identified as chimeric PCR products were removed using Perseus (4). Sequences were aligned to a nonredundant representative subset of ~50,000 template sequences (5) of the SILVA version 111 SSU Ref 16S curated alignment database (6); sequences beginning after or ending before 95% of sequences, or with fewer than 200 bases, were considered potential sequencing artifacts and removed from the dataset. To minimize further the generation of spurious OTUs due to PCR or sequencing error, sequences differing by <1% were grouped using average-neighbor single-linkage preclustering (7). Sequences were then assigned to OTUs by average-neighbor hierarchical clustering at the 95% identity level [95% identity across the sequenced V1–V2 region of the 16S gene best approximates 97% identity across the entire 16S gene, a standard benchmark for assigning bacterial taxa (8)]. OTU relative abundances were used to calculate pairwise among-sample phylogenetic distances [weighted UniFrac (9)]. Sequences were classified using the Bayesian classifier of Wang et al. (10) with minimum 70% confidence, and each OTU was assigned consensus taxonomy from SILVA version 111. Sample-based richness and diversity measures [observed OTU richness, Chao's richness estimate (11), Shannon diversity, and Shannon evenness] were calculated after randomly subsampling to 500 sequences per sample. Eleven field and two experiment samples

had fewer than 500 sequences and were excluded from diversity analyses. Across the 106 field-collected samples, 159,126 sequences passed the quality control pipeline, with a median sequence length of 323 bp and a mean of 1,508 sequences per sample. From the 180 experimental samples analyzed here (experiment details are provided below), 393,119 sequences passed quality control, with a median sequence length of 323 bp and a mean of 2,184 sequences per sample.

Analysis of Temporal Change in OTU Relative Abundances. We conducted analyses to examine whether patterns of change in bacterial OTU relative abundances over time are consistent with Bd driving temporal change in the outbreak population; these analyses are intended to be exploratory rather than conclusive because analyses of OTU relative abundances may be sensitive to specifics of community composition, which may be particularly important when incorporating data from multiple host populations and survey dates into the analysis. Unlike the time-independent analyses (within-population visit analyses and experimental study), it is critical to consider not only the direction of OTU change but also the magnitude of change in the temporal analysis. This is because a given OTU may be affected by both Bd and baseline seasonal change; in such case, it would change with time in both the epizootic population (where temporal change potentially includes effects of both Bd and seasonal variation) and reference populations (where only seasonal variation is relevant). Therefore, it is not informative simply to compare lists of OTUs that change with time in each frog population. Instead, we accounted for baseline seasonal change in the outbreak population and then conducted statistical analyses to ask if, across all OTUs that changed with time in the outbreak population, the magnitude and/or direction of change in time is predicted by patterns of Bd–OTU correlations that were calculated in the absence of temporal or geographic confounding (e.g., Fig. 2). To do this, we first used *t* tests (with false discovery rate correction for multiple tests as described in *Methods, Statistical Analyses*) to identify OTUs that had significant differences in relative abundance between the early and late sampling dates in the outbreak population. Only common OTUs were tested, with "common" defined as the 60 OTUs that were present in at least 25% of samples across the three populations, as described in *Methods, Statistical Analyses*. For each OTU that showed significant temporal change, we calculated an estimate of the magnitude and direction of temporal change in the outbreak population after accounting for baseline seasonal variation, which we refer to as the reference-adjusted effect of time, $D_{\text{reference-adjusted}}$:

$$D_{\text{reference-adjusted}} = D_{\text{outbreak}} - D_{\text{reference}},$$

where D_{outbreak} is the time parameter estimate for the effect of time on relative abundance of a given OTU in the one-way ANOVA (*t* test) for the outbreak population and $D_{\text{reference}}$ is the mean parameter estimate for time in the two reference (enzootic) populations. Only parameters from significant *t* tests are considered because parameters from nonsignificant *t* tests are not significantly different from zero. If Bd drives temporal change in OTU relative abundances, we expect those OTUs that were correlated with Bd in the within-date analyses (Fig. 2) to exhibit greater change through time, after accounting for seasonal variation, than OTUs that were not correlated with Bd load. To test this hypothesis statistically, we categorized each OTU as positively correlated, negatively correlated, or

uncorrelated with Bd based on within-date analyses (from Fig. 2) and conducted ANOVA (with Tukey HSD post hoc pairwise comparison of means) to test if the reference-adjusted time parameter ($D_{\text{reference-adjusted}}$) in the outbreak population differs across the three Bd correlation groups. For this analysis, we used the population-specific Bd correlations in Fig. 2 (i.e., Bd correlations from Marmot) because the objective is to predict change within the same population. However, we also conducted the same analysis using a less conservative definition to group OTUs into Bd correlation categories. Here, OTUs were categorized based on within-visit correlation in any population (any of the OTUs listed in Fig. 2). This did not change the qualitative outcome of the analyses.

SI Results

Overview of *R. sierrae* Microbiome and Aquatic Bacterial Communities.

We identified 5,188 bacterial OTUs (mean of 139 OTUs per sample) in the field-collected samples, representing 38 phyla and 998 phylotypes, 580 of which could be classified to the genus level. In the experiment, there were 1,162 OTUs (mean of 38 OTUs per sample), representing 26 phyla and 346 phylotypes, with 254 classified to genus. Bacterial communities differed between laboratory-reared and wild frogs. In particular, bacterial communities from laboratory-reared frogs had lower richness and diversity (observed OTU richness: $P < 0.0001$, Chao richness estimate: $P < 0.0001$, Shannon diversity: $P < 0.0001$, Shannon evenness: $P = 0.0006$). However, laboratory and field-collected microbiomes clustered together and were distinct from bacterial communities from ambient water in an ordination based on phylotypes of the combined laboratory and field data (Fig. S1), indicating that

community composition of laboratory-reared frogs was a reasonable representation of the *R. sierrae* microbiome.

No Effect of Life Stage on Microbiome Composition. Because our analysis included samples from both adult and subadult *R. sierrae*, we tested for effects of life stage on microbiome community composition. We used PERMANOVA to test for differences in the bacterial communities of adult vs. subadult frogs, based on the multivariate phylogenetic UniFrac distance and using data from the four focal surveys (i.e., visits with >10 frogs sampled; Table S1). The analyses were conducted separately for each population visit to avoid confounding with temporal or among-population variation. In three of the populations, Bd loads were higher in subadults than adults (t tests conducted separately within each population; $P < 0.0001$ for Mono, Unicorn, and Conness); therefore, we included $\log_{10}(\text{Bd load})$ as a covariate in the analysis. (In the Marmot population, Bd load did not differ significantly by life stage, probably because during epizootics, adult loads increase to levels similar to the levels generally seen in subadults. To ensure robust results, in Marmot, we conducted PERMANOVA tests for the effect of life stage on community composition both with and without Bd load in the model and obtained the same result: no significant effect of life stage.) Life stage had no significant effect on bacterial community composition in any of the four population visits (Marmot: $P_{\text{lifestage}} = 0.2840$, $P_{\text{BdLoad}} = 0.0007$; Mono: $P_{\text{lifestage}} = 0.6960$, $P_{\text{BdLoad}} = 0.0271$; Unicorn: $P_{\text{lifestage}} = 0.1034$, $P_{\text{BdLoad}} = 0.0008$; Conness: $P_{\text{lifestage}} = 0.8022$, $P_{\text{BdLoad}} = 0.0452$). This result is consistent with a previous study (12), which found that skin-associated bacterial communities did not differ between subadult and adult *Rana cascadae*.

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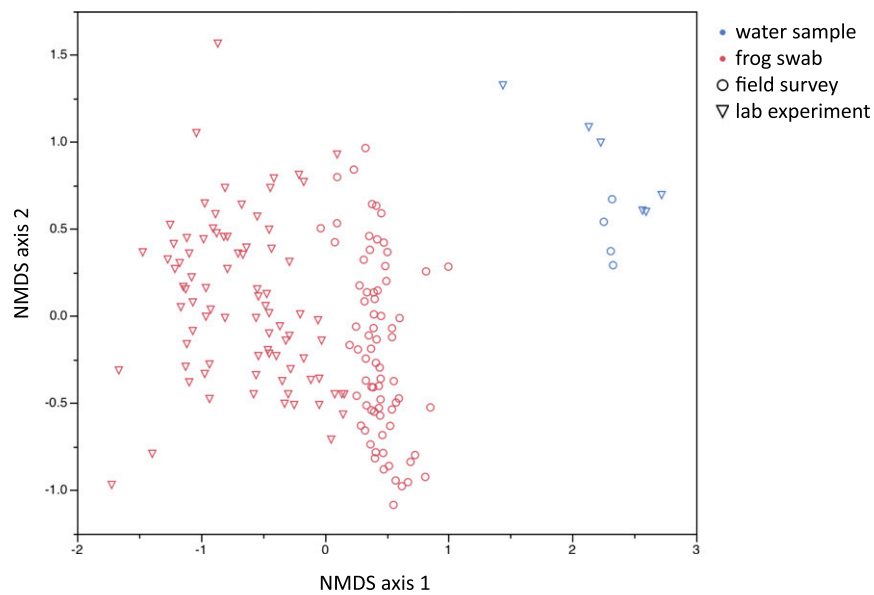


Fig. S1. NMDS ordination of microbial communities from frog skin and environmental water in the laboratory and field studies. Phylotype relative abundance data from the laboratory and field were combined, and Bray–Curtis distances were calculated based on relative abundances of all phylotypes. To avoid pseudoreplication, only one sampling date from the laboratory and field are shown, although results are qualitatively the same when all data are included. Ordination stress = 0.17.

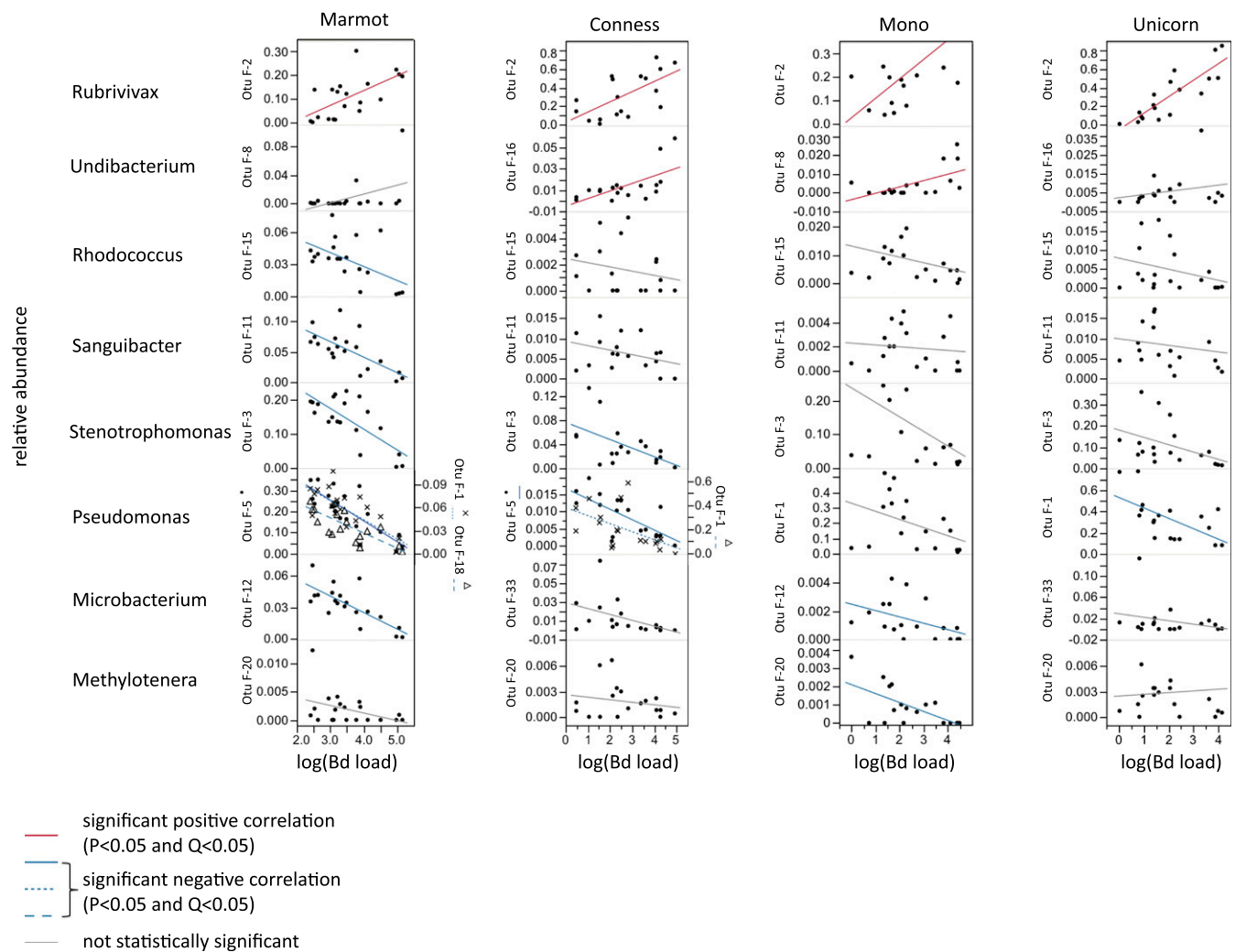


Fig. S2. OTUs classified to eight genera were associated with Bd infection in both the laboratory and field studies. Scatterplots show OTU relative abundances plotted against $\log_{10}(\text{Bd load})$. Data for the laboratory experiment and representative data for the Marmot field population on August 30 are shown in Fig. 3. Shown here are additional OTUs (genus *Pseudomonas*) correlated with Bd load in Marmot on August 30, as well as data for the remaining three frog population visits: Conness on August 18, Mono on September 16, and Unicorn on September 13. Blue lines indicate a significant negative correlation, red lines indicate a significant positive correlation, and gray lines indicate a relationship not statistically significant.

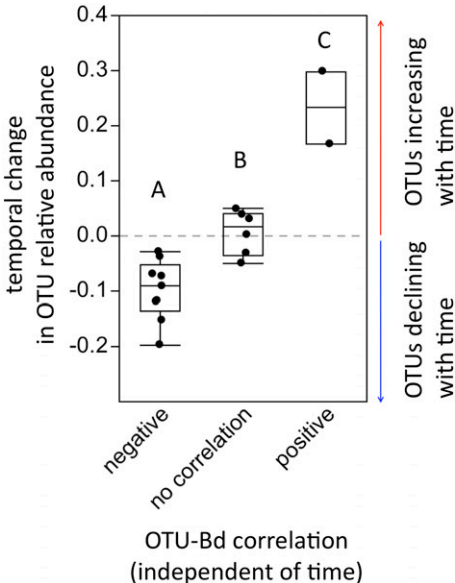


Fig. S3. Correlations between Bd and bacterial OTUs predict temporal change during a Bd outbreak. Shown are data from Marmot during a Bd epizootic that resulted in population collapse. OTUs that were positively correlated with Bd load increased with time, whereas OTUs that were negatively correlated with Bd load declined. The vertical axis shows the effect of time (parameter estimate for time) from one-way ANOVA in the outbreak population after accounting for baseline seasonal change as estimated from the two reference (enzootic) populations (details are provided in *SI Methods*). Only the 17 OTUs that changed significantly with time are included. OTUs are grouped based on their relationship to Bd (relative abundance positively correlated, negatively correlated, or uncorrelated with Bd load) based on analysis within a single survey date in the outbreak population, such that correlation results are not confounded with time. Groups annotated with different letters above the box plot are significantly different based on Tukey HSD post hoc comparison of means.

Table S1. Field surveys conducted in the study populations, 2010–2011

| Population nickname | Survey date | No. of frog swabs analyzed for Bd load: Total (adults, subadults) | No. of frog swabs analyzed for bacterial communities | Bd infection status | Bd load (log ₁₀) for adult frogs: Mean (SD) | Bd disease dynamics |
|------------------------|--------------------------|-------------------------------------------------------------------------|------------------------------------------------------------|---------------------|---------------------------------------------------------------|------------------------|
| Marmot | 16 July 2010 | 30 (30, 0) | | Uninfected | 0.00 (0.00) | Epizootic |
| | 8 August 2010 | 30 (27, 3) | | Uninfected | 0.06 (0.24) | |
| | 30 August 2010 | 30 (22, 8) | 20 | Infected | 3.18 (0.88) | |
| | 14 September 2010 | 14 (9, 5) | 10 | Infected | 4.58 (0.37) | |
| | 15 September 2010 | 29 (27, 2) | | Infected | 4.38 (0.38) | |
| | 6 September 2011 | Population crashed; no frogs encountered | | Infected* | N/A | |
| Mono | 7 July 2010 | 6 (6, 0) | | Infected | 0.63 (0.60) | Enzootic |
| | 11 August 2010 | 20 (17, 3) | | Infected | 1.5 (0.77) | |
| | 1 September 2010 | 33 (26, 7) | 8 | Infected | 1.49 (0.85) | |
| | 16 September 2010 | 40 (31, 9) | 18 | Infected | 1.58 (0.80) | |
| | 21 July 2011 | 28 (27, 1) | | Infected | 1.58 (0.83) | |
| Unicorn | 28 July 2010 | 19 (19, 0) | | Infected | 0.45 (0.65) | Enzootic |
| | 29 August 2010 | 31 (22, 9) | 7 | Infected | 1.74 (0.80) | |
| | 13 September 2010 | 37 (24, 13) | 18 | Infected | 1.47 (0.71) | |
| | 5 August 2011 | 31 (28, 3) | | Infected | 1.08 (0.98) | |
| Conness | 9 July 2010 | 27 (20, 7) | | Infected | 1.31 (0.88) | Enzootic |
| | 18 August 2010 | 30 (18, 12) | 18 | Infected | 1.85 (0.75) | |
| | 10 September 2010 | 30 (19, 11) | | Infected | 2.08 (0.63) | |
| | 17 July 2011 | 14 (13, 1) | | Infected | 1.58 (0.96) | |

Bd infection status was determined by qPCR. Disease dynamics (enzootic, epizootic) were determined by historical data (1, 2), together with data presented here on Bd load trajectories and *R. sierrae* population stability (current table and *Results*). Population visits analyzed individually for a within-population visit association between Bd and bacterial communities are shown in bold text. N/A, not applicable (no adult frogs available for collection of Bd load data).

*In the Marmot population, no postmetamorphic frogs were found in the 2011 census due to Bd-induced population crash, but the presence of Bd at the site could be determined based on swab samples of *R. sierrae* tadpoles. (Tadpoles can persist after extinction of postmetamorphic *R. sierrae* because Bd does not cause lethal disease in tadpoles of this species.)

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Table S2. Bacterial OTUs significantly affected by Bd infection in the laboratory experiment

| Bacterial OTU | Group with higher relative abundance | Least squares mean | |
|-----------------------------------------------------------------------|--------------------------------------|--------------------|-----------------|
| | | Bd ⁻ | Bd ⁺ |
| Actinobacteria-Nocardiaceae- <i>Rhodococcus</i> (E-24) | Uninfected | 0.0650 | 0.0297 |
| Actinobacteria-Cellulomonadaceae-uncultured (E-47) | Uninfected | 0.0123 | 0.0052 |
| Actinobacteria-Microbacteriaceae- <i>Microbacterium</i> (E-26) | Uninfected | 0.0400 | 0.0179 |
| Actinobacteria-Sanguibacteraceae- <i>Sanguibacter</i> (E-9) | Uninfected | 0.1205 | 0.0576 |
| Sphingobacteriia-Chitinophagaceae- <i>Filimonas</i> (E-55) | Uninfected | 0.0202 | 0.0075 |
| Alphaproteobacteria-Brucellaceae- <i>Ochrobactrum</i> (E-41) | Uninfected | 0.0362 | 0.0178 |
| Alphaproteobacteria-Rhizobiaceae- <i>Rhizobium</i> (E-49) | Infected | 0.0153 | 0.0345 |
| Gammaproteobacteria-Enterobacteriaceae- <i>Pantoea</i> (E-20) | Uninfected | 0.0739 | 0.0335 |
| Gammaproteobacteria-Pseudomonadaceae- <i>Pseudomonas</i> (E-2) | Uninfected | 0.3078 | 0.1595 |
| Gammaproteobacteria-Xanthomonadaceae- <i>Stenotrophomonas</i> (E-7) | Uninfected | 0.1650 | 0.0954 |
| Gammaproteobacteria-Xanthomonadaceae- <i>Stenotrophomonas</i> (E-105) | Uninfected | 0.0096 | 0.0035 |
| Betaproteobacteria-Methylophilaceae- <i>Methylothera</i> (E-57) | Uninfected | 0.0131 | 0.0071 |
| Betaproteobacteria-Neisseriaceae- <i>Aquitalea</i> (E-6) | Uninfected | 0.2609 | 0.0801 |
| Betaproteobacteria-Comamonadaceae- <i>Acidovorax</i> (E-11) | Infected | 0.0546 | 0.1980 |
| Betaproteobacteria-Comamonadaceae- <i>Curvibacter</i> (E-5) | Infected | 0.1701 | 0.3246 |
| Betaproteobacteria-Comamonadaceae- <i>Rhodoferrax</i> (E-25) | Infected | 0.0159 | 0.0540 |
| Betaproteobacteria-Comamonadaceae- <i>Rubrivivax</i> (E-4) | Infected | 0.3203 | 0.4033 |
| Betaproteobacteria-Oxalobacteraceae- <i>Janthinobacterium</i> (E-34) | Infected | 0.0129 | 0.0247 |
| Betaproteobacteria-Oxalobacteraceae- <i>Undibacterium</i> (E-1) | Infected | 0.3605 | 0.4719 |

Taxonomic information listed on left, with OTU identifiers in parentheses. Experimental group (Bd-infected or uninfected) in which relative abundance of each OTU was higher is indicated. Least squares means are based on arcsine square-root-transformed data. Criteria for statistical significance: $P < 0.05$ and $Q < 0.05$.

Table S3. Bacterial OTUs that changed in relative abundance between the early and late sampling points in the outbreak population

| Bacterial OTU | Time parameter | Change with time | Relationship with Bd |
|----------------------------------------------------------------------|----------------|------------------|-----------------------|
| | | | (independent of time) |
| Betaproteobacteria-Comamonadaceae- <i>Rubrivivax</i> (F-2) | 0.1668 | Increase | Positive |
| Flavobacteria-Flavobacteriaceae- <i>Soona</i> (F-4) | 0.2986 | Increase | Positive |
| Actinobacteria-Microbacteriaceae- <i>Microbacterium</i> (F-12) | -0.0909 | Decline | Negative |
| Actinobacteria-Microbacteriaceae- <i>Microbacterium</i> (F-30) | -0.0730 | Decline | Negative |
| Actinobacteria-Nocardiaceae- <i>Rhodococcus</i> (F-15) | -0.0691 | Decline | Negative |
| Actinobacteria-Sanguibacteraceae- <i>Sanguibacter</i> (F-11) | -0.1521 | Decline | Negative |
| Actinobacteria-Sporichthyaceae-hgcl_clade (F-13) | -0.0285 | Decline | Negative |
| Betaproteobacteria-Comamonadaceae- <i>Variovorax</i> (F-36) | -0.0376 | Decline | Negative |
| Gammaproteobacteria-Pseudomonadaceae- <i>Pseudomonas</i> (F-1) | -0.1172 | Decline | Negative |
| Gammaproteobacteria-Pseudomonadaceae- <i>Pseudomonas</i> (F-18) | -0.1188 | Decline | Negative |
| Gammaproteobacteria-Pseudomonadaceae- <i>Pseudomonas</i> (F-5) | -0.1967 | Decline | Negative |
| Actinobacteria-Cellulomonadaceae-uncultured (F-35) | -0.0495 | Decline | No correlation |
| Betaproteobacteria-Burkholderiaceae- <i>Polynucleobacter</i> (F-6) | -0.0312 | Decline | No correlation |
| Flavobacteria-Flavobacteriaceae- <i>Flavobacterium</i> (F-26) | 0.0490 | Increase | No correlation |
| Gammaproteobacteria-Aeromonadaceae- <i>Aeromonas</i> (F-57) | 0.0308 | Increase | No correlation |
| Gammaproteobacteria-Enterobacteriaceae- <i>Enterobacter</i> (F-98) | 0.0022 | Increase | No correlation |
| SubsectionIII-Pseudanabaena-unclassified <i>Pseudanabaena</i> (F-79) | 0.0389 | Increase | No correlation |

Of 17 OTUs that changed with time, 11 were also correlated with Bd load in the same population in previous analyses (shown in Fig. 2). Taxonomic information and OTU identifiers (in parentheses) are listed (left). OTUs are grouped by relationship with Bd (independent of time), corresponding to groups in ANOVA (Fig. S3), and are sorted taxonomically within groups. "Time parameter" is the parameter estimate for the effect of time (comparing early and late time points in one-way ANOVA, where the response variable is relative abundance of a given OTU, arcsine square-root-transformed) in the outbreak population after subtracting the corresponding time effect in the reference populations (details are provided in *SI Methods*). "Change with time" denotes the qualitative direction of the time parameter. "Relationship with Bd" refers to the OTU-Bd correlations, calculated on a single sampling date to avoid confounding with time, for each OTU in the outbreak population (as shown in Fig. 2).

Table S4. National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA) accession numbers and primer barcodes for 16S sequence data from the field survey

| SRA accession no. | Barcode | Sample type | Population nickname | Date collected |
|-------------------|----------|-----------------------------|---------------------|-------------------|
| SRR1598941 | AACCGCTA | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | AACCGGAA | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | AACGCCAT | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | AACGCCTA | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | AACGCGAA | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | AAGCATCC | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | AAGCATGG | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | AAGCCGAA | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | AAGGAACC | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | AAGGAAGG | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | AATACCGC | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | AATACGCC | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | ACACAGAG | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | ACACAGTC | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | ACACTGAC | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | ACACTGTG | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | ACAGGTCT | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | ACAGGTGA | <i>R. sierrae</i> skin swab | Conness | 18 August 2010 |
| SRR1598941 | AACCTTGG | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598941 | AACGTAGG | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598941 | AAGCGGTA | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598941 | AAGGCGAT | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598941 | AAGGCGTA | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598941 | AATTGCGC | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598941 | AATTGCCG | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598941 | ACACGACT | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598941 | ACACGAGA | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598941 | ACAGCACT | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598941 | ACAGCAGA | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598941 | ACCAACCA | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598942 | AACCAACC | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598942 | AACGAACG | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598942 | AAGTTTCG | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598942 | AAGCTACC | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598942 | AAGGTACG | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598942 | AATTGCGC | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598942 | ACACGTCA | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598942 | ACAGCTCA | <i>R. sierrae</i> skin swab | Marmot | 30 August 2010 |
| SRR1598942 | AACCTAGC | <i>R. sierrae</i> skin swab | Marmot | 14 September 2010 |
| SRR1598942 | AACGGCTT | <i>R. sierrae</i> skin swab | Marmot | 14 September 2010 |
| SRR1598942 | AAGCGCTT | <i>R. sierrae</i> skin swab | Marmot | 14 September 2010 |
| SRR1598942 | AAGGCCTT | <i>R. sierrae</i> skin swab | Marmot | 14 September 2010 |
| SRR1598942 | AATTCCGG | <i>R. sierrae</i> skin swab | Marmot | 14 September 2010 |
| SRR1598942 | AATTGCGG | <i>R. sierrae</i> skin swab | Marmot | 14 September 2010 |
| SRR1598942 | ACACCTCT | <i>R. sierrae</i> skin swab | Marmot | 14 September 2010 |
| SRR1598942 | ACACCTGA | <i>R. sierrae</i> skin swab | Marmot | 14 September 2010 |
| SRR1598942 | ACAGAGAC | <i>R. sierrae</i> skin swab | Marmot | 14 September 2010 |
| SRR1598942 | ACAGTGAG | <i>R. sierrae</i> skin swab | Marmot | 14 September 2010 |
| SRR1598942 | AACCATCG | <i>R. sierrae</i> skin swab | Mono | 1 September 2010 |
| SRR1598942 | AACGATCC | <i>R. sierrae</i> skin swab | Mono | 1 September 2010 |
| SRR1598942 | AAGCAACG | <i>R. sierrae</i> skin swab | Mono | 1 September 2010 |
| SRR1598942 | AAGTTTCG | <i>R. sierrae</i> skin swab | Mono | 1 September 2010 |
| SRR1598942 | AAGTTTCC | <i>R. sierrae</i> skin swab | Mono | 1 September 2010 |
| SRR1598942 | ACACACAC | <i>R. sierrae</i> skin swab | Mono | 1 September 2010 |
| SRR1598942 | ACACTCAG | <i>R. sierrae</i> skin swab | Mono | 1 September 2010 |
| SRR1598942 | ACAGGACA | <i>R. sierrae</i> skin swab | Mono | 1 September 2010 |
| SRR1598942 | AACCTTCC | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598942 | AACCTTGG | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598942 | AACGTACC | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598942 | AACGTAGG | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598942 | AAGCGGAT | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598942 | AAGCGGTA | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |

Table S4. Cont.

| SRA accession no. | Barcode | Sample type | Population nickname | Date collected |
|-------------------|----------|-----------------------------|---------------------|-------------------|
| SRR1598942 | AAGGCGAT | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598942 | AAGGCGTA | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598942 | AATTCGGC | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598942 | AATTGCCG | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598942 | ACACGACT | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598942 | ACACGAGA | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598942 | ACAGAGTG | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598942 | ACAGCACT | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598942 | ACAGCAGA | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598942 | ACAGTGTC | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598942 | ACCAACCA | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598942 | ACCAACGT | <i>R. sierrae</i> skin swab | Mono | 16 September 2010 |
| SRR1598941 | AACCTTCC | <i>R. sierrae</i> skin swab | Unicorn | 29 August 2010 |
| SRR1598941 | AAGCGGAT | <i>R. sierrae</i> skin swab | Unicorn | 29 August 2010 |
| SRR1598941 | AAGGCCTT | <i>R. sierrae</i> skin swab | Unicorn | 29 August 2010 |
| SRR1598941 | AATTCGGC | <i>R. sierrae</i> skin swab | Unicorn | 29 August 2010 |
| SRR1598941 | ACACCTGA | <i>R. sierrae</i> skin swab | Unicorn | 29 August 2010 |
| SRR1598941 | ACAGAGTG | <i>R. sierrae</i> skin swab | Unicorn | 29 August 2010 |
| SRR1598941 | ACAGTGTC | <i>R. sierrae</i> skin swab | Unicorn | 29 August 2010 |
| SRR1598942 | AACCGGTT | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | AACCTACG | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | AACGCGTT | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | AACGGCAA | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | AAGCCGAA | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | AAGCCGTT | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | AAGCGCAA | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | AAGGATCG | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | AAGGATGC | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | AAGGCCAA | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | AATAGCGG | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | AATAGGCG | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | ACACCACA | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | ACACCAGT | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | ACAGACAG | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | ACAGACTC | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | ACAGTCAC | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598942 | ACAGTCTG | <i>R. sierrae</i> skin swab | Unicorn | 13 September 2010 |
| SRR1598941 | AACGTTCG | Water sample | Conness | 18 August 2010 |
| SRR1598941 | ACAGCTCA | Water sample | Marmot | 30 August 2010 |
| SRR1598941 | ACACGTGT | Water sample | Marmot | 14 September 2010 |
| SRR1598941 | AACGAAGC | Water sample | Mono | 1 September 2010 |
| SRR1598941 | ACAGCTGT | Water sample | Mono | 16 September 2010 |
| SRR1598941 | ACACGTCA | Water sample | Unicorn | 29 August 2010 |
| SRR1598941 | AATTGGCC | Water sample | Unicorn | 13 September 2010 |

Detailed sampling design and sequencing and bioinformatics protocols are provided in *Methods* and *SI Methods*.

Table S5. NCBI SRA accession numbers and primer barcodes for 16S sequence data from the laboratory experiment

| SRA accession no. | Barcode | Sample type | Time point | Bd treatment | Frog population source | Water source |
|-------------------|----------|-----------------------------|--------------|-----------------|------------------------|--------------|
| SRR1598944 | CCTTGCTA | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | A |
| SRR1598944 | AAGCCGTT | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | A |
| SRR1598944 | CCTTGGAA | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | A |
| SRR1598944 | TTGGAAGG | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | A |
| SRR1598944 | ATCCGGAT | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | A |
| SRR1598944 | GCTTGGAT | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | A |
| SRR1598944 | CCATGGAT | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | B |
| SRR1598944 | GCGCATAT | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | B |
| SRR1598944 | CGTTGCAA | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | B |
| SRR1598944 | CGAAGGTA | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | B |
| SRR1598944 | ATGCATGC | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | B |
| SRR1598944 | TACCATGG | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | B |
| SRR1598944 | TTCGCGTT | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | C |
| SRR1598944 | TAGGCCAT | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | C |
| SRR1598944 | AAGGCGTA | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | C |
| SRR1598944 | GCATCCTT | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | C |
| SRR1598944 | CGAAGGAT | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | C |
| SRR1598944 | GCATCGTA | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | C |
| SRR1598944 | TATAGCCG | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | D |
| SRR1598944 | ATGCCGTA | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | D |
| SRR1598944 | CGTACCAA | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | D |
| SRR1598944 | ATCCTAGG | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | D |
| SRR1598944 | AACCATCG | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | D |
| SRR1598944 | ATATCGCG | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | D |
| SRR1598944 | GCGGAATA | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | E |
| SRR1598944 | TTGCAACG | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | E |
| SRR1598944 | TACGATGC | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | E |
| SRR1598944 | TAGCATCG | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | E |
| SRR1598944 | CGTAATGC | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | E |
| SRR1598944 | CGCCTTAT | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | E |
| SRR1598944 | CGTTAACG | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | F |
| SRR1598944 | TATACCGG | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | F |
| SRR1598944 | TACGTACG | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | F |
| SRR1598944 | CCTTCGAT | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | F |
| SRR1598944 | TTGCGCAA | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | F |
| SRR1598944 | GCTTAAGC | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | F |
| SRR1598944 | CGATTAGC | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | G |
| SRR1598944 | TTGGCCTT | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | G |
| SRR1598944 | TAGGCGAA | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | A | G |
| SRR1598944 | AACGCGTT | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | G |
| SRR1598944 | CCAAGGTT | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | G |
| SRR1598944 | TAGGATGG | <i>R. sierrae</i> skin swab | Preinfection | Bd challenge | B | G |
| SRR1598944 | GCAATAGG | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | A |
| SRR1598944 | TACCAACG | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | A |
| SRR1598944 | ATCCTTGC | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | A |
| SRR1598944 | CGAAGCTT | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | A |
| SRR1598944 | CCAAGCAT | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | A |
| SRR1598944 | AAGGATCG | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | A |
| SRR1598944 | TAGCATGC | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | B |
| SRR1598944 | CGAACCTA | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | B |
| SRR1598944 | TACGCCAA | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | B |
| SRR1598944 | AACGTTGC | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | B |
| SRR1598944 | GCTTCGAA | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | B |
| SRR1598944 | ATCGCCTT | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | B |
| SRR1598944 | GCAACGAA | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | C |
| SRR1598944 | TACCGGAT | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | C |
| SRR1598944 | ATATCCGG | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | C |
| SRR1598944 | TTCGCGAA | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | C |
| SRR1598944 | ATCGTAGC | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | C |
| SRR1598944 | ATGCCGAT | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | C |
| SRR1598944 | ATCGGCAT | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | D |
| SRR1598944 | GCATCCAA | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | D |
| SRR1598944 | ATCGCCAA | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | D |

Table S5. Cont.

| SRA accession no. | Barcode | Sample type | Time point | Bd treatment | Frog population source | Water source |
|-------------------|----------|-----------------------------|---------------|-----------------|------------------------|--------------|
| SRR1598944 | TTCCGCAT | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | D |
| SRR1598944 | ATCCTTCG | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | D |
| SRR1598944 | CGTAGGTT | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | D |
| SRR1598944 | TAATGCGC | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | E |
| SRR1598944 | AAGCATGG | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | E |
| SRR1598944 | GCATTACG | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | E |
| SRR1598944 | ATGCGCAT | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | E |
| SRR1598944 | ATGCAAGG | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | E |
| SRR1598944 | CCGCATAA | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | E |
| SRR1598944 | CGAATTCG | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | F |
| SRR1598944 | AATTCCGG | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | F |
| SRR1598944 | GCTATTGG | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | F |
| SRR1598944 | CCGGTTAA | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | F |
| SRR1598944 | CGTAGCTA | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | F |
| SRR1598944 | TTCGTAGG | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | F |
| SRR1598944 | TATTGCGG | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | G |
| SRR1598944 | CGCCATAA | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | A | G |
| SRR1598944 | ATATGCGC | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | G |
| SRR1598944 | ATCGTACG | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | G |
| SRR1598944 | AACGCCTA | <i>R. sierrae</i> skin swab | Preinfection | No Bd (control) | B | G |
| SRR1598944 | ATCGGCTA | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | A |
| SRR1598944 | TTGCGCTT | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | A |
| SRR1598944 | GCTTATGG | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | A |
| SRR1598944 | CCAAGCTA | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | A |
| SRR1598944 | ATTAGCGC | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | A |
| SRR1598944 | TTAACGGC | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | A |
| SRR1598944 | GCAACCAT | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | B |
| SRR1598944 | TATACGGC | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | B |
| SRR1598944 | CCATAAGC | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | B |
| SRR1598944 | TACGCCTT | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | B |
| SRR1598944 | TACCTTCG | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | B |
| SRR1598944 | CCATCCTA | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | B |
| SRR1598944 | ATGGAAGC | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | C |
| SRR1598944 | TAGGCGTT | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | C |
| SRR1598944 | TACGGCAT | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | C |
| SRR1598944 | ATATGCCG | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | C |
| SRR1598944 | TTAACCGG | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | C |
| SRR1598944 | GCATGGAA | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | C |
| SRR1598944 | CCATCGAA | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | D |
| SRR1598944 | GCTTGCAA | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | D |
| SRR1598944 | CGGCATTA | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | D |
| SRR1598944 | TTGGCGTA | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | D |
| SRR1598944 | GCGGTTAA | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | D |
| SRR1598944 | CCATTAGG | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | D |
| SRR1598944 | ATCGATGC | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | E |
| SRR1598944 | CCGGATAT | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | E |
| SRR1598944 | CGTTGGAT | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | E |
| SRR1598944 | AAGCGGTA | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | E |
| SRR1598944 | TTCCGGTT | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | E |
| SRR1598944 | AACCATGC | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | E |
| SRR1598944 | ATCCGGTA | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | F |
| SRR1598944 | TATACCGG | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | F |
| SRR1598944 | CCGCTTAT | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | F |
| SRR1598944 | TAGCCGAT | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | F |
| SRR1598944 | TTGCCGAA | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | F |
| SRR1598944 | GCTACGAT | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | F |
| SRR1598944 | AACCTTGG | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | G |
| SRR1598944 | GCTAATGC | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | G |
| SRR1598944 | CGTAGCAT | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | A | G |
| SRR1598944 | CCATAACG | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | G |
| SRR1598944 | TTCCATGC | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | G |
| SRR1598944 | GCTAGGAA | <i>R. sierrae</i> skin swab | Postinfection | Bd challenge | B | G |

Table S5. Cont.

| SRA accession no. | Barcode | Sample type | Time point | Bd treatment | Frog population source | Water source |
|-------------------|-----------|-----------------------------|---------------|-----------------|------------------------|--------------|
| SRR1598944 | TAATCCGG | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | A |
| SRR1598944 | TAGCTTGG | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | A |
| SRR1598944 | TAGCGGAA | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | A |
| SRR1598944 | TTGGCCAA | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | A |
| SRR1598944 | GCTACGTA | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | A |
| SRR1598944 | GCAATTTCG | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | A |
| SRR1598944 | GCTTCGTT | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | B |
| SRR1598944 | TAATGCCG | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | B |
| SRR1598944 | CGTATACG | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | B |
| SRR1598944 | GCGGTATT | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | B |
| SRR1598944 | CCATGCAA | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | B |
| SRR1598944 | CCTACCAT | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | B |
| SRR1598944 | AACGCCAT | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | C |
| SRR1598944 | GCAAGGAT | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | C |
| SRR1598944 | CCAATTGG | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | C |
| SRR1598944 | CCGCAATA | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | C |
| SRR1598944 | CGATGCAT | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | C |
| SRR1598944 | TTCGCCAT | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | C |
| SRR1598944 | TTCGAAGC | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | D |
| SRR1598944 | CGATCCTT | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | D |
| SRR1598944 | TTAAGCGC | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | D |
| SRR1598944 | AACGTTGC | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | D |
| SRR1598944 | CCAATACG | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | D |
| SRR1598944 | TACCGCTT | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | D |
| SRR1598944 | CGCGTTAA | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | E |
| SRR1598944 | ATGCTTGG | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | E |
| SRR1598944 | ATGCGGAA | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | E |
| SRR1598944 | CGTACCTT | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | E |
| SRR1598944 | TTAAGCCG | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | E |
| SRR1598944 | GCGCAATT | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | E |
| SRR1598944 | GCTATAGC | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | F |
| SRR1598944 | AACGCGAA | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | F |
| SRR1598944 | GCGCATTA | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | F |
| SRR1598944 | CGCGATAT | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | F |
| SRR1598944 | TTATGCGG | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | F |
| SRR1598944 | GCTTAACG | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | F |
| SRR1598944 | TACGAAGG | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | G |
| SRR1598944 | TTCTTGG | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | A | G |
| SRR1598944 | TATAGCGC | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | G |
| SRR1598944 | ATTAGCCG | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | G |
| SRR1598944 | CGTATAGC | <i>R. sierrae</i> skin swab | Postinfection | No Bd (control) | B | G |
| SRR1598944 | GCTACCAA | Water sample | Preinfection | N/A | N/A | A |
| SRR1598944 | AAGGCCTT | Water sample | Preinfection | N/A | N/A | B |
| SRR1598944 | AACCTACG | Water sample | Preinfection | N/A | N/A | C |
| SRR1598944 | GCAAGCTT | Water sample | Preinfection | N/A | N/A | D |
| SRR1598944 | CGCGAATT | Water sample | Preinfection | N/A | N/A | E |
| SRR1598944 | CCGCTATT | Water sample | Preinfection | N/A | N/A | F |
| SRR1598944 | ATCCAAGC | Water sample | Postinfection | N/A | N/A | A |
| SRR1598944 | ATGCTACG | Water sample | Postinfection | N/A | N/A | B |
| SRR1598944 | GCTTGGTA | Water sample | Postinfection | N/A | N/A | C |
| SRR1598944 | CCGGTATA | Water sample | Postinfection | N/A | N/A | D |
| SRR1598944 | CGTTCCAT | Water sample | Postinfection | N/A | N/A | E |
| SRR1598944 | CCTACGAA | Water sample | Postinfection | N/A | N/A | F |

"Time point" is in reference to the timing of experimental inoculations, and all samples are labeled according to this scheme for the purpose of grouping together samples collected before and after the inoculation event, although Bd inoculation was not applied to frogs in the "No Bd (control)" treatment group or to water samples. Detailed experimental design and sequencing and bioinformatics protocols are provided in *Methods* and *SI Methods*.