Detailed 16S rRNA gene data processing methods

For the 16S amplicon data, overlapping forward and reverse paired reads were assembled with Fastq-join (https://code.google.com/p/ea-utils/wiki/FastqJoin) using default parameters and then processed with the Quantitative Insights Into Microbial Ecology (QIIME v. 1.7.0) pipeline [1]. Sequences were de-multiplexed and quality-filtered following methods similar to those in Bokulich *et al.* [2]. Specifically, sequences were discarded if there were any ambiguous base calls, errors in the barcode, less than 75% of read length had consecutive base calls with a phred quality score greater than 20, more than 10 consecutive low-quality base calls, or the read length was not between 252 and 255 bp. After quality filtering, the number of reads retained per sample ranged from 27,083 to 94,881. Quality-filtered sequences were then clustered into operational taxonomic units (OTUs, ~bacterial "species") at a sequence similarity threshold of 97% with the UCLUST method [3] and a minimum cluster size of 0.001% of the total reads [2]. Sequences were first clustered against the Greengenes database (May 2013 release) [4]. Sequences that did not match the database were then *de novo* clustered at a 97% sequence similarity threshold. The most abundant sequence for a given cluster was assigned as the representative sequence for that OTU. We assigned taxonomy for each OTU with RDP classifier [5] at an 80% confidence threshold and the Greengenes database. We aligned representative sequences to the Greengenes database with PyNAST [6] and constructed a phylogenetic tree with FastTree [7]. All samples were rarefied to 27,000 sequences to standardize sampling effort. We used a closed reference OTU picking approach to determine if any Illumina sequences matched the sequences of the four candidate probiotics at a 99% sequence similarity.

Table S1. Bacterial isolates chosen for probiotic treatments.

Isolate ID	Classification	Bd inhibition[a]	Frog species[b]	Prevalence[c]	# of species[d]
Pseudo1	*Pseudomonas sp.*	100	*Bufo typhonius*	20/67	7/11
Pseudo2	*Pseudomonas sp.*	100	*Craugastor crassidigitus*	10/67	5/11
Chryseo	*Chryseobacterium sp.*	100	*Craugastor crassidigitus*	2/67	2/11
Steno	*Stenotrophomonas sp.*	98	*Atelopus limosus*	3/67	3/11

[a]Percent inhibition calculated based on growth of Bd in the presence of the bacterial isolate's cell-free supernatant compared to Bd grown without cell-free supernatant [8].
[b]Species from which the bacterial isolate was collected.
[c]Prevalence of bacterial isolate among sampled amphibians.
[d]Number of amphibian species from which the isolate was collected.

Table S2. Sample sizes of treatment groups in relation to survival and infection outcome.

survival / infection outcome		treatment groups (n = x)					
		Bd	Pseudo1 +Bd	Pseudo2 +Bd	Chryseo +Bd	Steno +Bd	total
	died	4	5	5	2	7	**23**
survival / infection outcome	predicted to die	0	1	2	0	0	**3**
	cleared	4	0	0	1	0	**5**
	predicted to clear	0	1	0	4	1	**6**
	total	**8**	**7**	**7**	**7**	**8**	**37**

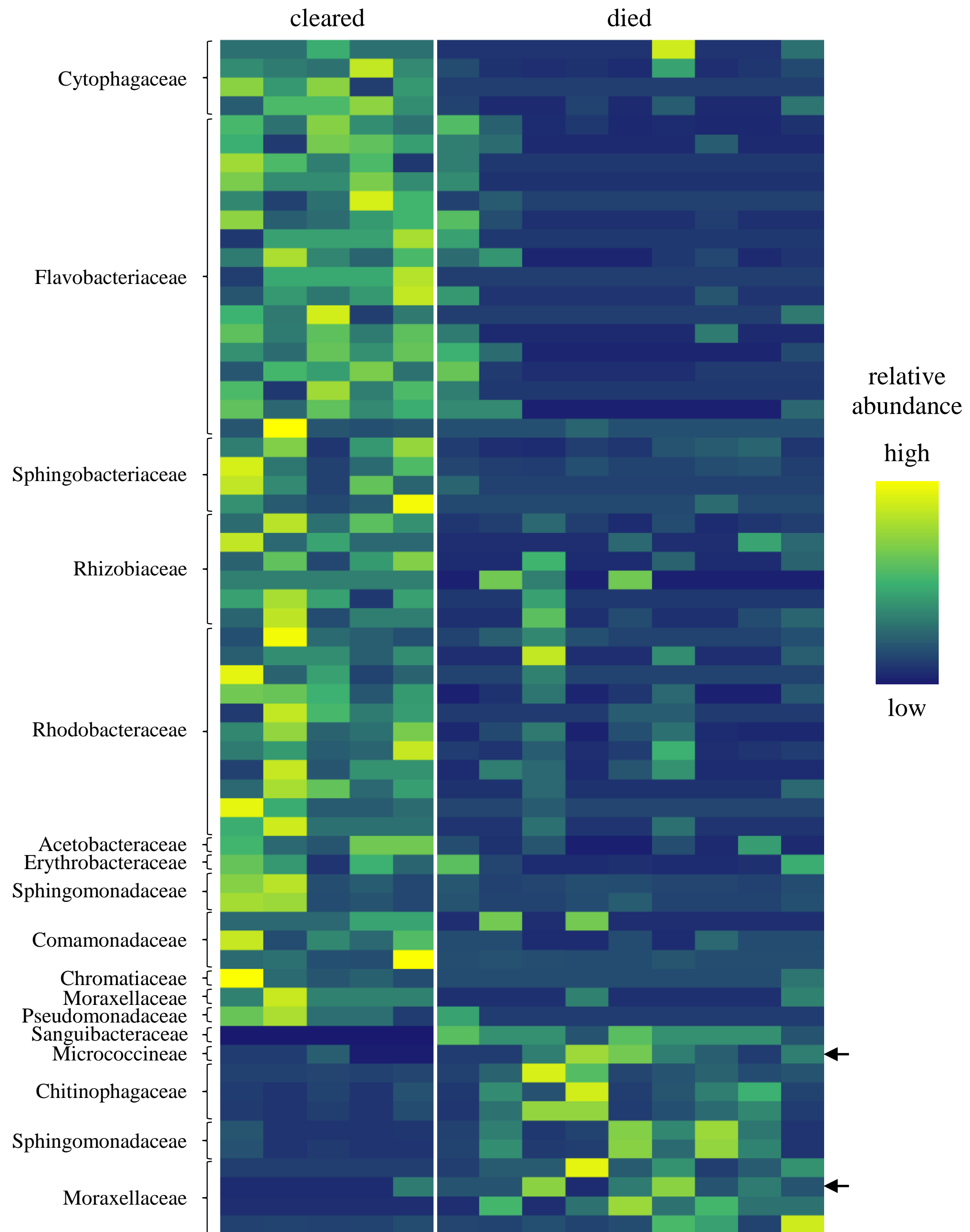

Figure S1. Heat map of the relative abundances of indicator OTUs from indicator species analysis associated with *Atelopus zeteki* 28 days after Bd exposure that cleared Bd infection or died of chytridiomycosis. Rows indicate unique OTUs and columns indicate individual frogs. Family level taxonomic classification is shown for each OTU. Arrows are indicator OTUs that were detected both three days prior to and 28 days after Bd exposure.

References

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