

Supporting Information

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SI Materials and Methods

Field Data. To test for a significant change in community-wide abundance in pre- versus postdecline periods, we ran a linear mixed-effects repeated-measures ANOVA on the 53 species with quantitative abundance data (Table S2), designating species as a random effect and survey date as a fixed effect variable. Analyses were conducted in the statistical environment R (1) using the function `lme` in the `nlme` package to account for nonindependence of observations. To individually test each of the 53 species for a change in abundance in predecline versus postdecline surveys, we applied a nonparametric Wilcoxon rank-sum test with continuity correction. We did not apply a Bonferroni correction for multiple tests as, with a sample size of six field seasons, adopting an α value of 0.001 would leave no power to reject the null hypothesis. These single-species tests serve to highlight taxa of interest, but the significance levels should be interpreted with caution.

Genetic Data. Most genetic samples were collected before the decline event (2), with some additional material collected from dead frogs in November 2004, most notably the samples of *Ateolopus zeteki*. Twenty samples came from toe clips and 280 samples came from vouchered specimens (Table S3). For three species (*Oedipina collaris*, *Oophaga vicente*, and *Ranitomeya minuta*), we used previously published data obtained from samples collected during our field surveys (Table S3). For another three species, we used samples collected elsewhere in Panama: *Bolitoglossa colonnea*, *Oedipina parvipes*, and *Dendrobates auratus*. These three substitutions should not affect our estimates of PD as long as intraspecific variation is low relative to interspecific divergence.

Genomic DNA was extracted with a standard phenol-chloroform protocol implemented with an AutoGenprep 965 (AutoGen) automated DNA isolation robot following digestion with proteinase K (0.4 mg/mL) at 55 °C. After a maximum of three attempts, the 16S primers yielded a failure rate of 1.3% and the degenerate COI primers failed in 7.7% of samples, which is lower than the failure rate reported previously in amphibian barcode surveys (3, 4). All COI and 16S sequences were deposited in BoLD (<http://www.barcodinglife.com>) and GenBank (Table S3). The concatenated two-gene DNA sequence alignment (including inferred gaps) was submitted to TreeBASE (www.treebase.org) under study accession number S2643.

The COI sequences were 648 bp long and showed no length variation. The 16S gene fragments were aligned with default parameters and multiple iterations in ClustalX 2.0 (5). All analyses of the 16S data excluded sites with gaps plus one additional base on either side of all gaps of length greater than 1 bp, resulting in 436 aligned bp included in phylogenetic and distance analyses.

Phylogenetic Analyses. We inferred an unconstrained molecular phylogeny by Metropolis coupled Markov chain Monte Carlo (MCMC) Bayesian analysis (6, 7) using a parallel version of MrBayes 3.1.2 (8, 9). Selection of appropriate models of nucleotide substitution used a Bayesian information criterion as implemented in DT-ModSel (10) and Modeltest 3.7 (11), which gave identical results. Four data partitions were created: 16S plus codon positions 1 through 3 in COI, with the following models applied to each GTR+I+ Γ , GTR+I, GTR+ Γ , and GTR+I+ Γ , respectively (12–14). Rates of evolution were allowed to vary across partitions using a rate multiplier (15). Each analysis consisted of three parallel MCMC runs with three Metropolis-coupled chains each. Two initial analyses of 2 million generations each were conducted, and prior distributions, the heating parameter, and

burn-in were adjusted according. Our final analysis consisted of 8 million generations with trees sampled every 2,000 generations, a burn-in period of 2 million generations (at which point the average SD of split frequencies had decreased to less than 0.032), heating parameter of 0.01 (resulting frequencies of chain swapping ranged from 0.07 to 0.73), a U(0.0001, 20.0) prior distribution on shape parameters, and an exponential(5.0) prior distribution of branch lengths. Bayesian consensus tree with nodal support and unmodified branch lengths is shown in Fig. S2.

We also inferred a molecular phylogeny constrained to match published higher level amphibian relationships using unpartitioned ML analysis (16) implemented in the software, GARLI, version 0.95 (17), run six times assuming a single GTR+I+ Γ model and default parameters except that the setting of generations without improving topology was increased to 50,000. The ML tree matched the Bayesian tree at all well-supported nodes. Both trees largely agreed with previously published higher level amphibian relationships, with five exceptions that were constrained in the GARLI analyses: monophyletic Bufonidae, monophyletic Hylidae, Lepidodactylidae + Leiuperidae (18), ((Strabomantidae) (Craugastoridae) Eleutherodactylidae (19), and within Bufonidae the clade ((*Rhinella*, *Incilius*) *Rhaebo*) (20). Because of the lack of resolution even with many more genes, no other relationships among families within Hyloidea were constrained in the GARLI analyses. The following relationships were also constrained in the GARLI analyses, yet were successfully recovered in the unconstrained Bayesian phylogenetic analyses (Fig. S2). Within *Craugastor*: the *C. fitzingeri* group, *C. gollmeri* group, and the *C. rugulosus* group + *C. biporcatus* group (21, 22); all genera monophyletic; within Phyllomedusinae, ((*Agalychnis*, *Hylomantis*) *Cruziohyla*) (23); the Central America Hylinae, *Ecnomiophyla* + *Smlisca* (24); the South American Hylinae, *Hyloscirtus* + *Hypsiboas* (25); monophyletic Hylinae (25); within Dendrobatidae, ((*Oophaga*, *Dendrobates*) (*Ranitomeya*) *Phyllobates*) and *Silverstoneia* + *Colostethus* (26); within Centrolenidae, *Hyalinobatrachium* sister to all other centrolenids sampled here (27); monophyletic Hemiphractidae (27); Microhylidae + Ranidae (18); Aromobatidae + Dendrobatidae (26); as well as a monophyletic Caudata, Anura, and Batrachia (Caudata + Anura).

Candidate Species. We emphasize that the candidate species designation is provisional, pending further systematic investigations (28), and that evolutionary processes such as introgression, retention of ancestral polymorphisms, and rapid speciation may cause incongruence between mitochondrial DNA gene trees and species boundaries (29). Although threshold values of more than 8% in COI and more than 2% at 16S (Fig. 1 in the main text) are lower than has been suggested previously in the literature (30), they were determined empirically for the present dataset via an analysis of a bivariate barcode gap (Fig. 1 in the main text). Divergence at 16S may have been underestimated if the same sites that contained informative point mutations distinguishing congeneric samples were the same sites inferred to contain gaps when we aligned families and orders of amphibians (as described earlier). Such sites could include the more variable loop regions of the 16S rRNA molecule (4).

Three species (*O. collaris*, *Diasporus quidditus*, and *D. aff. diastema*) lacked COI data (Table S3). These lineages showed 5.4% to 7.7% mean K2P divergence from their nearest relative (Fig. 2) at the 16S gene, placing *D. aff. diastema* as well as *D. aff. quidditus* in the category of candidate species relative to *D. quidditus*. Recent studies have found that the DNA barcoding gap may not be significantly influenced by the number of individuals sequenced per

species (31). In this study, total sample size (N) for some pairs of named plus candidate species was low, yet these pairs showed high K2P percent divergence at COI: *Cruziophyla calcarifer* A+B ($n = 3$) showed 12.5% divergence, *Lithobates warszewitschii* + *L. aff. warszewitschii* ($n = 4$) showed 14.7%, *Pristimantis ridens* A+B ($n = 4$) showed 17.6%, and *P. caryophyllaceus* A+B+C ($n = 7$) 14.5%. These levels of mtDNA variation are higher than the maximum polymorphism observed for sympatric samples of conspecific amphibians (32, 33). Thus, sympatry provides additional evidence that these named taxa include candidate species (34).

Loss of Evolutionary History. Because we used relatively fast-evolving mitochondrial DNA markers to infer the history of an old group of vertebrates, the lengths of basal branches may be underestimated. To investigate the affect of basal branch length variation, we also estimated the loss of PD on a tree temporally calibrated (as well as topologically constrained; as detailed earlier) on the basis of a molecular analysis of lissamphibian evolutionary history (18). The divergence times assumed here may be too old (35), but any bias toward older ages should provide a sharper potential contrast in the loss of PD between trees with longer (time-calibrated) versus shorter (noncalibrated) basal branches. We imposed the following temporal constraints on our phylogeny using the MPL algorithm. We set the age of the most recent common ancestor (MRCA) of Lissamphibia at 332.6 million years ago (Ma), the minimum age of Batrachia (18). We constrained the minimum and maximum ages of three nested nodes, as follows: the MRCA of *Craugastor* + *Lithobates* (Phtanobatrachia) to the interval 143.3 to 179.9 Ma, the MRCA of *Lithobates* + *Nelsonophryne* (Ranoidea) to the interval 106.2 to 130.9 Ma, and the MRCA of *Craugastor* + *Rhinella* (Nobleobatrachia minus

Rhinoderma) to the interval 50.9 to 75.5 Ma (18). The resulting tree had much longer basal branch lengths, yet the resulting calculations of PD lost were very similar to those obtained for the MPL tree (Table 1), suggesting that our results were robust to substantial variation in branch lengths.

Trait Evolution. In testing for a phylogenetic correlation of percent decline in abundance among species, trait values were coded alternatively as percent change in abundance (Table S2) or as a percent decline (as a positive value) such that increases in abundance were coded as 0% decline. The GLS model describes the covariance of trait values and phylogeny, and assumes an evolutionary parameter, λ , for which a value of 0.0 indicates trait values are independent of shared history, whereas a value of 1.0 implies that trait evolution conforms to a random walk on the given phylogeny. Because abundance is a species-level trait, analyses were conducted on phylogenies containing one sample per each of the 74 named or candidate species. For Bayesian analyses, the 100 unconstrained trees were sampled at a rate of one tree per 10,000 generations from the final third of a Bayesian MCMC phylogenetic analysis run for 3 million generations in MrBayes. Conditions for 74-sample phylogenetic analyses were otherwise the same as for 300-sample analyses as described earlier. Time series plots of log-likelihood scores and SDs of among-chain split frequencies lower than 0.03 suggested convergence was reached by each independent chain. Using the software BayesTraits, the marginal likelihoods of λ under alternative models were approximated from a MCMC analysis run for 1 million generations preceding by a 50,000 generation burn-in period, with parameter values recorded once per 300 generations. At each generation, one of the 100 trees was selected at random and proposed λ values were evaluated.

- R Development Core Team (2008) *R: A Language and Environment for Statistical Computing*. (R Foundation, Vienna).
- Lips KR, et al. (2006) Emerging infectious disease and the loss of biodiversity in a Neotropical amphibian community. *Proc Natl Acad Sci USA* 103:3165–3170.
- Smith MA, Poyarkov NA, Jr, Hebert PDN (2008) CO1 DNA barcoding amphibians: Take the chance, meet the challenge. *Mol Ecol Notes* 8:235–246.
- Vences M, Thomas M, van der Meijden A, Chiari Y, Vieites DR (2005) Comparative performance of the 16S rRNA gene in DNA barcoding of amphibians. *Front Zool* 2:5.
- Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG (1997) The CLUSTAL_X windows interface: Flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res* 25:4876–4882.
- Yang Z, Rannala B (1997) Bayesian phylogenetic inference using DNA sequences: A Markov Chain Monte Carlo Method. *Mol Biol Evol* 14:717–724.
- Rannala B, Yang Z (1996) Probability distribution of molecular evolutionary trees: a new method of phylogenetic inference. *J Mol Evol* 43:304–311.
- Altekar G, Dwarkadas S, Huelsenbeck JP, Ronquist F (2004) Parallel Metropolis coupled Markov chain Monte Carlo for Bayesian phylogenetic inference. *Bioinformatics* 20:407–415.
- Ronquist F, Huelsenbeck JP (2003) MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19:1572–1574.
- Minin V, Abdo Z, Joyce P, Sullivan J (2003) Performance-based selection of likelihood models for phylogeny estimation. *Syst Biol* 52:674–683.
- Posada D, Crandall KA (1998) MODELTEST: Testing the model of DNA substitution. *Bioinformatics* 14:817–818.
- Hasegawa M, Kishino H, Yano T (1987) Man's place in Hominoidea as inferred from molecular clocks of DNA. *J Mol Evol* 26:132–147.
- Yang Z (1994) Maximum likelihood phylogenetic estimation from DNA sequences with variable rates over sites: Approximate methods. *J Mol Evol* 39:306–314.
- Tavaré S (1986) Some probabilistic and statistical problems on the analysis of DNA sequences. *Lect Math Life Sci* 17:57–86.
- Marshall DC, Simon C, Buckley TR (2006) Accurate branch length estimation in partitioned Bayesian analyses requires accommodation of among-partition rate variation and attention to branch length priors. *Syst Biol* 55:993–1003.
- Felsenstein J (1981) Evolutionary trees from DNA sequences: A maximum likelihood approach. *J Mol Evol* 17:368–376.
- Zwickl DJ (2006) Genetic algorithm approaches for the phylogenetic analysis of large biological sequence datasets under the maximum likelihood criterion. PhD dissertation (Univ of Texas, Austin).
- Roelants K, et al. (2007) Global patterns of diversification in the history of modern amphibians. *Proc Natl Acad Sci USA* 104:887–892.
- Heinicke MP, et al. (2009) A new frog family (Anura: Terrarana) from South America and an expanded direct-developing clade revealed by molecular phylogeny. *Zootaxa* 2211:1–35.
- Van Bocxlaer I, Biju SD, Loader SP, Bossuyt F (2009) Toad radiation reveals into-India dispersal as a source of endemism in the Western Ghats-Sri Lanka biodiversity hotspot. *BMC Evol Biol* 9:131.
- Heinicke MP, Duellman WE, Hedges SB (2007) Major Caribbean and Central American frog faunas originated by ancient oceanic dispersal. *Proc Natl Acad Sci USA* 104:10092–10097.
- Crawford AJ, Smith EN (2005) Cenozoic biogeography and evolution in direct-developing frogs of Central America (Leptodactylidae: *Eleutherodactylus*) as inferred from a phylogenetic analysis of nuclear and mitochondrial genes. *Mol Phylogenet Evol* 35:536–555.
- Faivovich J, et al. (2009) The phylogenetic relationships of the charismatic poster frogs, Phyllomedusinae (Anura, Hylidae). *Cladistics* 26:227–261.
- Smith SA, de Oca AN, Reeder TW, Wiens JJ (2007) A phylogenetic perspective on elevational species richness patterns in Middle American treefrogs: Why so few species in lowland tropical rainforests? *Evolution* 61:1188–1207.
- Wiens JJ, Graham CH, Moen DS, Smith SA, Reeder TW (2006) Evolutionary and ecological causes of the latitudinal diversity gradient in hylid frogs: Treefrog trees unearth the roots of high tropical diversity. *Am Nat* 168:579–596.
- Santos JC, et al. (2009) Amazonian amphibian diversity is primarily derived from late Miocene Andean lineages. *PLoS Biol* 7:e56.
- Guayasamin JM, Castroviejo-Fisher S, Ayarzagüena J, Trueb L, Vilà C (2008) Phylogenetic relationships of glassfrogs (Centrolenidae) based on mitochondrial and nuclear genes. *Mol Phylogenet Evol* 48:574–595.
- Vieites DR, et al. (2009) Vast underestimation of Madagascar's biodiversity evidenced by an integrative amphibian inventory. *Proc Natl Acad Sci USA* 106:8267–8272.
- Moritz C, Cicero C (2004) DNA barcoding: Promise and pitfalls. *PLoS Biol* 2:e354.
- Fouquet A, et al. (2007) Underestimation of species richness in neotropical frogs revealed by mtDNA analyses. *PLoS ONE* 2:e1109.
- Aliabadian M, Kaboli M, Nijman V, Vences M (2009) Molecular identification of birds: Performance of distance-based DNA barcoding in three genes to delimit parapatric species. *PLoS ONE* 4:e4119.
- Crawford AJ (2003) Huge populations and old species of Costa Rican and Panamanian dirt frogs inferred from mitochondrial and nuclear gene sequences. *Mol Ecol* 12:2525–2540.
- Vences M, Thomas M, Bonett RM, Vieites DR (2005) Deciphering amphibian diversity through DNA barcoding: Chances and challenges. *Philos Trans R Soc Lond B Biol Sci* 360:1859–1868.
- Mallet J (2008) Hybridization, ecological races and the nature of species: Empirical evidence for the ease of speciation. *Philos Trans R Soc Lond B Biol Sci* 363:2971–2986.
- Marjanović D, Laurin M (2007) Fossils, molecules, divergence times, and the origin of lissamphibians. *Syst Biol* 56:369–388.
- Pounds JA, Fogden MPL, Campbell JH (1999) Biological response to climate change on a tropical mountain. *Nature* 398:611–615.
- Lips KR (1999) Mass mortality and population declines of anurans at an upland site in western Panama. *Conserv Biol* 13:117–125.
- Lips KR (1998) Decline of a tropical montane amphibian fauna. *Conserv Biol* 12:106–117.

Table S1. Field effort on standardized transects during each field season, plus predecline and postdecline totals, used to calculate relative abundances

Field effort on standardized transects during each field season, plus predecline and postdecline totals, used to calculate relative abundances (Table S2). Field effort is given as number of individual amphibians captured, number of surveys conducted, mean number of captures per survey, total number of hours invested, and total number of kilometers walked during a given interval. Number of species captured includes species found off of standardized transects.

[Table S1](#)

Table S2. Mean, SD, minimum, and maximum yearly abundance for predecline and postdecline periods, followed by percent change in abundance of each species and the resulting category of decline

Relative abundance was calculated as total number of captures per kilometer of survey during each field season, then averaged across seasons to give predecline and postdecline mean relative abundances. "Pond" refers to pond-breeding species that were abundant in local ponds that were not situated on standardized transects. "Rare" refers to additional species captured in the area but not during standardized surveys. "Candidate" refers to candidate species discovered by genetic analyses (4 candidate species were regarded as morphospecies in the field and abundance data were collected). Declines that were significant according to a nonparametric test ($\alpha = 0.05$, without Bonferroni correction) are indicated with an asterisk. See *Materials and Methods* for details.

[Table S2](#)

Table S3. Number of DNA sequences from COI and 16S genes obtained per named and candidate species, sample numbers, and corresponding GenBank numbers

Taxonomy follows recently suggested changes (ref. 27 and <http://research.amnh.org/herpetology/amphibia>). The two non-anuran families are indicated in bold. Within each species, sample numbers are given in the same order as their corresponding GenBank numbers, except sample numbers for single-gene data are in parentheses following the corresponding GenBank number. USNM, specimen voucher number in the National Museum of Natural History, Smithsonian Institution, Washington, DC; MVUP, specimen voucher number in the Museo de Vertebrados de la Universidad de Panamá, Republic of Panama; CH, specimen voucher number in the Círculo Herpetológico de Panamá, Republic of Panama; KRL and AJC, authors' field numbers for specimens awaiting accession numbers; toe, genetic data obtained from toe clip (no vouchered specimen). Specimens with underlined KRL numbers were used for histopathological study and are no longer available.

[Table S3](#)

Table S1. Field effort on standardized transects during each field season, plus predecline and postdecline totals, used to calculate relative abundances. Field effort on standardized transects during each field season, plus predecline and postdecline totals, used to calculate relative abundances (Table S2). Field effort is given as number of individual amphibians captured, number of surveys conducted, mean number of captures per survey, total number of hours invested, and total number of kilometers walked during a given interval. Number of species captured includes species found off of standardized transects.

Year	no.		no. surveys	mean no.		
	captures	no. species		captures / survey	no. hours	no. km
2000	2,155	49	82	26.28	153.9	23.43
2001	3,523	54	92	38.29	180.5	25.13
2002	8,726	45	115	75.87	229.1	31.74
2003	6,763	52	112	60.38	198.8	32.48
pre-decline totals	23,322	63	401		762.3	112.78
2006-2007	951	48	289	3.29	211.4	66.4
2008	95	29	9	10.55	10.3	2.7
post-decline totals	1,046	48	298		221.7	69.1

Table S2. Mean, SD, minimum, and maximum yearly abundance for predecline and postdecline periods, followed by percent change in abundance of each species and the resulting category of decline. Relative abundance was calculated as total number of captures per kilometer of survey during each field season, then averaged across seasons to give predecline and postdecline mean relative abundances. “Pond” refers to pond-breeding species that were abundant in local ponds that were not situated on standardized transects. “Rare” refers to additional species captured in the area but not during standardized surveys. “Candidate” refers to candidate species discovered by genetic analyses (4 candidate species were regarded as morphospecies in the field and abundance data were collected). Declines that were significant according to a nonparametric test ($\alpha = 0.05$, without Bonferroni correction) are indicated with an asterisk. See Materials and Methods for details.

Family	Taxon	PRE-DECLINE			POST-DECLINE			% Change abundance	Decline category
		Mean abundance	Standard deviation of abundance	Minimum-Maximum abundance	Mean abundance	Standard deviation of abundance	Minimum-Maximum abundance		
Aromobatidae	<i>Allobates talamancae</i>	0.0029	0.0037	0 - 0.0082	0.0000	0	0 - 0	-100	Extirpated
Bufo	<i>Atelopus zeteki</i>	0.1879	0.2918	0.0362 - 0.6255	0.0218	0.0309	0 - 0.0437	-88.38	Critical
Bufo	<i>Incilius coniferus</i>	0.0366	0.0689	0.0016 - 0.1399	0.0428	0.0077	0.0373- 0.0482	16.86	LC
Bufo	<i>Rhaebo haematiticus</i>	0.0230	0.0286	0.0068 - 0.0658	0.0023	0.0032	0 - 0.0045	-90.17*	Critical
Bufo	<i>Rhinella marina</i>							0	DD-LC
Caeciliidae	<i>Caecilia volceni</i>							0	DD-LC
Centrolenidae	<i>Cochranella euknemos</i>	0.0069	0.0070	0 - 0.0166	0.0000	0	0 - 0	-100	Extirpated
Centrolenidae	<i>Cochranella granulosa</i>	0.0021	0.0042	0 - 0.0083	0.0000	0	0 - 0	-100	Extirpated
Centrolenidae	<i>Espadarana prosoblepon</i>	0.2801	0.2719	0.1225- 0.6872	0.2758	0.2431	0.1039 - 0.4478	-1.53	Declined
Centrolendidae	<i>Hyalinobatrachium colymbiphyllum</i>	0.1344	0.0947	0.0791 - 0.2757	0.0699	0.0460	0.0373 - 0.1024	-48.02	Declined
Centrolendidae	<i>Hyalinobatrachium talamancae</i>	0.0033	0.0033	0 - 0.0072	0.0388	0.0506	0.0030 - 0.0746	1061.71	LC
Centrolenidae	<i>Sachatamia ilex</i>	0.0209	0.0245	0.0065 - 0.0576	0.0435	0.0088	0.0373 - 0.0497	108.30	LC
Centrolenidae	<i>Sachatamia albomaculata</i>	0.0620	0.0740	0.0221 - 0.1728	0.0045	0.0064	0 - 0.0090	-92.71*	Critical
Centrolenidae	<i>Teratohyla spinosa</i>	0.0004	0.0008	0 - 0.0015	0.0000	0	0 - 0	-100	Extirpated
Craugastoridae	<i>Craugastor bransfordii</i>	0.0203	0.0386	0 - 0.0782	0.0008	0.0011	0 - 0.0015	-96.29	Critical
Craugastoridae	<i>Craugastor cf. azueroensis</i>	0.0018	0.0035	0 - 0.0071	0.0000	0	0 - 0	-100	Extirpated
Craugastoridae	<i>Craugastor crassidigitus</i>	0.1698	0.1797	0.0438 - 0.4362	0.0120	0.0170	0 - 0.0241	-92.90*	Critical
Craugastoridae	<i>Craugastor fitzingeri</i>	0.0032	0.0061	0 - 0.0123	0.0075	0.0106	0 - 0.0151	132.26	LC

Craugastoridae	<i>Craugastor gollmeri</i>	0.0405	0.0390	0.0175 - 0.0988	0.0247	0.0179	0.0120 - 0.0373	-39.10	Declined
Craugastoridae	<i>Craugastor megacephalus</i>	0.0152	0.0094	0.0041 - 0.0268	0.0000	0	0 - 0	-100*	Extirpated
Craugastoridae	<i>Craugastor noblei</i>			rare				-100	DD-Extirpated
Craugastoridae	<i>Craugastor punctariolus</i>	0.1488	0.1242	0.0637 - 0.3333	0.0000	0	0 - 0	-100*	Extirpated
Craugastoridae	<i>Craugastor aff. longirostris</i>	0.0385	0.0569	0.0044 - 0.1235	0.0000	0	0 - 0	-100*	Extirpated
Craugastoridae	<i>Craugastor tabasarae</i>			rare				-100	DD-Extirpated
Craugastoridae	<i>Craugastor talamancae</i>	0.1095	0.1171	0.0330 - 0.2840	0.1978	0.0369	0.1717 - 0.2239	80.62	LC
Dendrobatidae	<i>Colostethus panamansis</i>	0.0445	0.0476	0.0163 - 0.1152	0.0008	0.0011	0 - 0.0015	-98.31*	Critical
Dendrobatidae	<i>Colostethus pratti</i>	0.0005	0.0011	0 - 0.0022	0.0000	0	0 - 0	-100	Extirpated
Dendrobatidae	<i>Dendrobates auratus</i>	0.0051	0.0076	0 - 0.0165	0.0008	0.0011	0 - 0.0015	-85.25	Critical
Dendrobatidae	<i>Oophaga vicentei</i>	0.0041	0.0080	0 - 0.0161	0.0933	0.1319	0 - 0.1866	2166.1	LC
Dendrobatidae	<i>Phyllobates lugubris</i>			rare				-100	DD-Extirpated
Dendrobatidae	<i>Ranitomeya minuta</i>	0.0045	0.0053	0.0009 - 0.0123	0.0000	0	0 - 0	-100*	Extirpated
Dendrobatidae	<i>Silverstoneia flotator</i>	0.0476	0.0373	0.0211 - 0.1029	0.0301	0.0426	0 - 0.0602	-36.79	Declined
Dendrobatidae	<i>Silverstoneia nubicola A</i>	0.0125	0.0112	0.0036 - 0.0288	0.0000	0	0 - 0	-100*	Extirpated
Dendrobatidae	<i>Silverstoneia nubicola B</i>			candidate				-100	Extirpated
Eleutherodactylidae	<i>Diasporus aff. diastema</i>	0.0037	0.0074	0 - 0.0148	0.1306	0.1847	0 - 0.2612	3434.83	LC
Eleutherodactylidae	<i>Diasporus quidditus</i>	0.0094	0.0059	0.0020 - 0.0165	0.0746	0.1055	0 - 0.1493	690.35	LC
Eleutherodactylidae	<i>Diasporus aff. quidditus</i>	0.0148	0.0231	0.0015 - 0.0494	0.0211	0.0298	0 - 0.0422	41.99	LC
Hemiphractidae	<i>Gastrotheca cornuta</i>	0.0172	0.0092	0.0048 - 0.0265	0.0000	0	0 - 0	-100*	Extirpated
Hemiphractidae	<i>Hemiphractus fasciatus</i>			rare				-100	DD-Extirpated
Hylidae	<i>Agalychnis callidryas</i>			pond				0	DD-LC
Hylidae	<i>Cruziohyla calcarifer A</i>			rare				0	DD-LC
Hylidae	<i>Cruziohyla calcarifer B</i>			candidate, rare				0	DD-LC
Hylidae	<i>Ecnomiohyla miliaria</i>			rare				-100	DD-Extirpated
Hylidae	<i>Hylomantis lemur</i>	0.0382	0.0514	0.0103 - 0.1152	0.0000	0	0 - 0	-100*	Extirpated
Hylidae	<i>Hyloscirtus colymba</i>	0.0457	0.0492	0.0170 - 0.1193	0.0038	0.0053	0 - 0.0075	-91.76*	Critical
Hylidae	<i>Hyloscirtus palmeri</i>	0.0540	0.0491	0.0259 - 0.1276	0.0403	0.0485	0.0060 - 0.0746	-25.35	Declined
Hylidae	<i>Hypsiboas rufitelus</i>			pond				0	DD-LC
Hylidae	<i>Smilisca phaeota</i>	0.0074	0.0143	0 - 0.0288	0.0166	0.0234	0 - 0.0331	125.11	LC
Hylidae	<i>Smilisca sila</i>			pond				-100	DD-Extirpated
Leiuperidae	<i>Engystomops</i>			pond				0	DD-LC

	<i>pustulosus</i>										
Leptodactylidae	<i>Leptodactylus fragilis</i>								pond	0	DD-LC
Leptodactylidae	<i>Leptodactylus insularum</i>								pond	0	DD-LC
Leptodactylidae	<i>Leptodactylus savagei</i>								pond	-100	DD- Extirpated
Leptodactylidae	<i>Leptodactylus poecilochilus</i>								pond	0	DD-LC
Microhylidae	<i>Elachistocleis ovalis</i>								rare	-100	DD- Extirpated
Microhylidae	<i>Nelsonophryne aterrima</i>								rare	-100	DD- Extirpated
Plethodontidae	<i>Bolitoglossa colonnea</i>	0.0193	0.0257	0.0024 - 0.0576	0.0023	0.0032	0 - 0.0045	-88.29			Critical
Plethodontidae	<i>Bolitoglossa schizodactyla</i>	0.0377	0.0204	0.0175 - 0.0658	0.0315	0.0083	0-0.0256 - 0.0373	-16.49			Declined
Plethodontidae	<i>Oedipina collaris</i>	0.0026	0.0038	0.0003 - 0.0082	0.0030	0.0043	0 - 0.0060	17.3714			LC
Plethodontidae	<i>Oedipina parvipes</i>	0.0015	0.0017	0.0006 - 0.0041	0.0000	0	0 - 0	-100*			Extirpated
Ranidae	<i>Lithobates warszewitschii</i>	0.0065	0.0048	0.0006 - 0.0123	0.0000	0	0 - 0	-100*			Extirpated
Ranidae	<i>Lithobates aff. warszewitschii</i>								candidate	-100	Extirpated
Strabomantidae	<i>Pristimantis caryophyllaceus A</i>	0.0593	0.0788	0.0135 - 0.1770	0.1430	0.0616	0.0994 - 0.1866	140.94			LC
Strabomantidae	<i>Pristimantis caryophyllaceus B</i>								candidate	140.94	LC
Strabomantidae	<i>Pristimantis caryophyllaceus C</i>								candidate	140.94	LC
Strabomantidae	<i>Pristimantis cruentus</i>	1.0337	1.0182	0.4735 - 2.5597	0.6794	0.6222	0.2395 - 1.1194	-34.27			Declined
Strabomantidae	<i>Pristimantis cerasinus</i>	0.0257	0.0380	0.0022 - 0.0823	0.0120	0.0170	0 - 0.0241	-53.15*			Declined
Strabomantidae	<i>Pristimantis gaigeae</i>	0.0010	0.0012	0 - 0.0022	0.0000	0	0 - 0	-100			Extirpated
Strabomantidae	<i>Pristimantis museosus</i>	0.0206	0.0168	0.0080 - 0.0453	0.0226	0.0319	0 - 0.0452	9.85			LC
Strabomantidae	<i>Pristimantis aff. museosus</i>								candidate	9.85	LC
Strabomantidae	<i>Pristimantis pardalis</i>	0.0142	0.0157	0.0037 - 0.0370	0.0307	0.0093	0.0241 - 0.0373	116.36			LC
Strabomantidae	<i>Pristimantis ridens A</i>	0.0055	0.0073	0.0016 - 0.0165	0.0000	0	0 - 0	-100*			Extirpated
Strabomantidae	<i>Pristimantis ridens B</i>								candidate	-100	Extirpated
Strabomantidae	<i>Strabomantis bufoniformis</i>	0.0510	0.0513	0.0191 - 0.1276	0.0000	0	0 - 0	-100*			Extirpated

Table S3. Number of DNA sequences from COI and 16S genes obtained per named and candidate species, sample numbers, and corresponding GenBank numbers. Taxonomy follows recently suggested changes (ref. 27 and <http://research.amnh.org/herpetology/amphibia>). The two non-anuran families are indicated in bold. Within each species, sample numbers are given in the same order as their corresponding GenBank numbers, except sample numbers for single-gene data are in parentheses following the corresponding GenBank number. USNM, specimen voucher number in the National Museum of Natural History, Smithsonian Institution, Washington, DC; MVUP, specimen voucher number in the Museo de Vertebrados de la Universidad de Panamá, Republic of Panama; CH, specimen voucher number in the Círculo Herpetológico de Panamá, Republic of Panama; KRL and AJC, authors' field numbers for specimens awaiting accession numbers; toe, genetic data obtained from toe clip (no vouchered specimen). Specimens with underlined KRL numbers were used for histopathological study and are no longer available.

Family	Taxon	Total	COI data	16S data	Samples with Both Genes	COI GenBank nos.	16S GenBank nos.
Aromobatidae	<i>Allobates talamancae</i>	2	2	2	USNM 572527, MVUP 1850.	FJ766610, FJ766609.	FJ784370, FJ784428.
Bufonidae	<i>Atelopus zeteki</i>	6	6	6	CH 5859, CH 5860, CH 5862, CH 5886, CH 5864, CH 5871.	FJ766577, FJ766576, FJ766575, FJ766574, FJ766573, FJ766572.	FJ784541, FJ784543, FJ784545, FJ784551, FJ784553, FJ784581.
Bufonidae	<i>Incilius coniferus</i>	8	8	8	MVUP 1820, USNM 572086, USNM 572087, USNM 572092, toe 140, toe 141 Ocon, toe 144 Ocon, toe 151 Ocon.	FJ766768, FJ766767, FJ766766, FJ766765, FJ766764, FJ766732, FJ766762, FJ766761.	FJ784379, FJ784382, FJ784444, FJ784586, FJ784595, FJ784597, FJ784599, FJ784601.
Bufonidae	<i>Rhaebo haematiticus</i>	7	7	7	USNM 572094, USNM 572095, MVUP 1842, USNM 572096, USNM 57209, USNM 572098, toe 120.	FJ766818, FJ766817, FJ766816, FJ766815, FJ766814, FJ766813, FJ766812.	FJ784404, FJ784426, FJ784439, FJ784452, FJ784546, FJ784560, FJ784593.
Bufonidae	<i>Rhinella marina</i>	1	1	1	MVUP 1802.	FJ766819.	FJ784357.
Caeciliidae	<i>Caecilia volcani</i>	1	1	1	CH 5777.	FJ766580.	FJ784371.
Centrolenidae	<i>Cochranella euknemos</i>	5	4	5	USNM 572158, USNM 572159, KRL 1054, USNM 572160.	FJ766603, FJ766602, FJ766601, FJ766600.	FJ784396, FJ784443, FJ784458, FJ784459, FJ784377 (MVUP 1817).
Centrolenidae	<i>Cochranella granulosa</i>	1	1	1	USNM 572166.	FJ766604.	FJ784455.
Centrolenidae	<i>Espadarana prosoblepon</i>	6	5	6	USNM 572195, MVUP 1807, MVUP 1834, toe 2253, toe 2301.	FJ766593, FJ766592, FJ766591, FJ766590, FJ766589.	FJ784362, FJ784363, FJ784419, FJ784604, FJ784605, FJ784606 (toe 2333).
Centrolendidae	<i>Hyalinobatrachium colymbiphyllum</i>	10	10	10	USNM 572111, USNM 572112, USNM 572115, USNM 572116, USNM 572121, USNM 572123,	FJ766709, FJ766708, FJ766716, FJ766715, FJ766713, FJ766712, FJ766711, FJ766710,	FJ784359, FJ784366, FJ784345, FJ784346, FJ784475, FJ784527, FJ784561, FJ784562,

					USNM 572125, KRL 1557, USNM 572113, USNM 572114.	FJ766714, FJ766717.	FJ784402, FJ784471.
Centrolenidae	<i>Hyalinobatrachium talamancae</i>	1	1	1	USNM 572134.	FJ766718.	FJ784480.
Centrolenidae	<i>Sachatamia ilex</i>	8	8	8	USNM USNM 572176, USN 572181, USNM 572184, USNM 572187, USNM 572189, toe 10.	FJ766585, FJ766582, FJ766588, FJ766587, FJ766586, FJ766584, FJ766583, FJ766581.	FJ784582, FJ784588, FJ784403, FJ784574, FJ784580, FJ784583, FJ784584, FJ784591. FJ784392, FJ784441, FJ784449, FJ784468, FJ784474, FJ784550, FJ784463 (USNM 572172), FJ784466 (USNM 572173)
Centrolenidae	<i>Sachatamia albomaculata</i>	8	6	8	MVUP 1827, USNM 572141, USNM 572142, USNM 572174, USNM 572144, USNM 572151.	FJ766599, FJ766598, FJ766597, FJ766596, FJ766595, FJ766594.	
Centrolenidae	<i>Teratohyla spinosa</i>	4	4	4	USNM 572169, USNM 52710, MVUP 1806, MVUP 1926.	FJ766608, FJ766607, FJ766606, FJ766605.	FJ784330, FJ784348, FJ784361, FJ784479.
Craugastoridae	<i>Craugastor bransfordii</i>	6	6	6	USNM 572220, MVUP 1803, USNM 572221, MVUP 1841, USNM 572222, USNM 572223.	FJ766631, FJ766630, FJ766629, FJ766628, FJ766627, FJ766626.	FJ784339, FJ784358, FJ784376, FJ784427, FJ784481, FJ784496.
Craugastoridae	<i>Craugastor cf. azueroensis</i>	4	4	4	<u>KRL 0680</u> , USNM 572219, USNM 572278, USNM 572279.	FJ766637, FJ766636, FJ766675, FJ766674.	FJ784332, FJ784393, FJ784324, FJ784325.
Craugastoridae	<i>Craugastor crassidigitus</i>	7	7	5	USNM 572229, USNM 572230, KRL 0129, MVUP 1831, MVUP 1778.	FJ766643, FJ766641, FJ766644, FJ766639, FJ766642, FJ766640 (USNM 572232), FJ766638 (USNM 572233)	FJ784327, FJ784329, FJ784322, FJ784407, FJ784328.
Craugastoridae	<i>Craugastor fitzingeri</i>	4	4	4	KRL 0693, USNM 572256, MVUP 1798, KRL 1548.	FJ766648, FJ766647, FJ766646, FJ766645.	FJ784337, FJ784344, FJ784356, FJ784555.
Craugastoridae	<i>Craugastor gollmeri</i>	8	8	8	USNM 572259, MVUP 1795, USNM 572260, USNM 572261, USNM 572262, MVUP 1844, USNM 572264, USNM 572275.	FJ766656, FJ766655, FJ766654, FJ766653, FJ766652, FJ766651, FJ766650, FJ766649.	FJ784341, FJ784353, FJ784364, FJ784408, FJ784432, FJ784442, FJ784489, FJ784492.
Craugastoridae	<i>Craugastor megacephalus</i>	7	7	7	<u>KRL 0618</u> , KRL 0686, USNM 572267, USNM 572268, MVUP 1840, USNM 572269, USNM 572270.	FJ766663, FJ766662, FJ766661, FJ766660, FJ766659, FJ766658, FJ766657.	FJ784323, FJ784335, FJ784347, FJ784378, FJ784431, FJ784456, FJ784472.

Craugastoridae	<i>Craugastor noblei</i>	3	3	3	MVUP 1948, USNM 572273, MVUP 1814.	FJ766665, FJ766664, FJ766666.	FJ784513, FJ784523, FJ784367.
Craugastoridae	<i>Craugastor punctariolus</i>	7	7	7	MVUP 1784, USNM 572281, USNM 572282, KRL 572283, MVUP 1845, USNM 572285, USNM 572286.	FJ766673, FJ766672, FJ766671, FJ766670, FJ766669, FJ766668, FJ766667.	FJ784333, FJ784411, FJ784417, FJ784418, FJ784448, FJ784483, FJ784488.
Craugastoridae	<i>Craugastor</i> aff. <i>longirostris</i>	7	6	7	MVUP 1696, USNM 572231, KRL 1399, KRL 1417, KRL 1473, KRL 1549.	FJ766681, FJ766680, FJ766679, FJ766678, FJ766677, FJ766676.	FJ784343, FJ784349, FJ784518, FJ784524, FJ784537, FJ784556, FJ784539 (KRL 1480).
Craugastoridae	<i>Craugastor tabasarae</i>	3	3	3	USNM 572294, USNM 572295, USNM 572296.	FJ766684, FJ766683, FJ766682.	FJ784342, FJ784512, FJ784515.
Craugastoridae	<i>Craugastor talamancae</i>	12	12	12	USNM 572477, KRL 1342, KRL 1360, USNM 572307, USNM 572478, USNM 572309, USNM 572310, USNM 572311, USNM 572312, USNM 572313, KRL 572314, USNM 572316.	FJ766696, FJ766695, FJ766694, FJ766693, FJ766692, FJ766691, FJ766690, FJ766689, FJ766688, FJ766687, FJ766686, FJ766685.	FJ784462, FJ784506, FJ784510, FJ784511, FJ784517, FJ784521, FJ784530, FJ784533, FJ784536, FJ784542, FJ784549, FJ784572.
Dendrobatidae	<i>Colostethus panamansis</i>	10	9	10	MVUP 1849, USNM 572498, USNM 572499, USNM 572501, USNM 572502, USNM 572503, USNM 572508, USNM 572510, USNM 572511.	FJ766619, FJ766618, FJ766617, FJ766616, FJ766615, FJ766614, FJ766613, FJ766612, FJ766611.	FJ784447, FJ784504, FJ784505, FJ784507, FJ784508, FJ784509, FJ784516, FJ784526, FJ784529, FJ784501 (USNM 572497).
Dendrobatidae	<i>Colostethus pratti</i>	6	6	6	USNM 572523, USNM 572524, MVUP 1913, USNM 572525, USNM 572521, MVUP 1799.	FJ766623, FJ766622, FJ766621, FJ766620, FJ766625, FJ766624	FJ784429, FJ784438, FJ784464, FJ784494, FJ784350, FJ784351.
Dendrobatidae	<i>Dendrobates auratus</i>	2	2	2	AJC 1999, CH 6605.	FJ766698, FJ766697.	FJ784317, FJ784319.
Dendrobatidae	<i>Oophaga vicentei</i>	1	1	1	KRL 0789.	DQ502869.	DQ502167.
Dendrobatidae	<i>Phyllobates lugubris</i>	1	1	1	KRL 1735.	FJ766769.	FJ784587.
Dendrobatidae	<i>Ranitomeya minuta</i>	1	1	1	KRL 0790.	DQ502870.	DQ502168.
Dendrobatidae	<i>Silverstoneia flotator</i>	3	3	3	USNM 572530, USNM 572531, USNM 572532.	FJ766822, FJ766821, FJ766820.	FJ784352, FJ784400, FJ784450.
Dendrobatidae	<i>Silverstoneia nubicola</i> A	3	3	3	USNM 572590, USNM 572591, USNM 572592.	FJ766831, FJ766824, FJ766823.	FJ784420, FJ784563, FJ784564.

Dendrobatidae	<i>Silverstoneia nubicola</i> B	8	8	8	MVUP 1823, USNM 572593, MVUP 1847, USNM 572594, USNM 572595, USNM 572596, USNM 572597, USNM 572598.	FJ766833, FJ766832, FJ766830, FJ766829, FJ766828, FJ766827, FJ766826, FJ766825.	FJ784383, FJ784401, FJ784446, FJ784465, FJ784514, FJ784532, FJ784534, FJ784544.
Eleutherodactylidae	<i>Diasporus</i> aff. <i>diastema</i>	6	0	6			FJ784338 (MVUP 1783), FJ784425 (USNM 572442), FJ784395 (MVUP 1830), FJ784423 (USNM 572454), FJ784424 (USNM 572455), FJ784484 (USNM 572443).
Eleutherodactylidae	<i>Diasporus quidditus</i>	2	0	2			FJ784326 (USNM 572444), FJ784405 (MVUP 1832).
Eleutherodactylidae	<i>Diasporus</i> aff. <i>quidditus</i>	2	2	2	USNM 572546, MVUP 1826.	FJ766810, FJ766809.	FJ784369, FJ784390.
Hemiphractidae	<i>Gastrotheca cornuta</i>	3	3	3	USNM 572472, USNM 572473, USNM 572474.	FJ766706, FJ766705, FJ766704.	FJ784373, FJ784477, FJ784528.
Hemiphractidae	<i>Hemiphractus fasciatus</i>	1	1	1	MVUP 1927.	FJ766707.	FJ784476.
Hylidae	<i>Agalychnis callidryas</i>	5	5	4	MVUP 1835, toe 11, toe 2, toe 4.	FJ766570, FJ766569 (toe 1), FJ766568, FJ766567, FJ766566.	FJ784436, FJ784592, FJ784603, FJ784608.
Hylidae	<i>Cruziohyla calcarifer</i> A	1	1	1	USNM 572742.	FJ766571.	FJ784368.
Hylidae	<i>Cruziohyla calcarifer</i> B	2	2	2	USNM 572743, USNM 572744.	FJ766565, FJ766564.	FJ784374, FJ784495.
Hylidae	<i>Ecnomiohyla miliaria</i>	1	1	1	KRL 0758.	FJ766699.	FJ784360.
Hylidae	<i>Hylomantis lemur</i>	7	3	7	MVUP 1801, USNM 572750, USNM 572751.	FJ766721, FJ766720, FJ766719.	FJ784355, FJ784440, FJ784445, FJ784594 (toe 134), FJ784598 (toe 142), FJ784600 (toe 151), FJ784602 (toe 153).
Hylidae	<i>Hyloscirtus colymba</i>	10	10	10	USNM 572618, USNM 572621, USNM 572629, USNM 572630, USNM 572632, USNM 572634, USNM 572635, USNM 572636, USNM 572647, toe 3.	FJ766731, FJ766730, FJ766729, FJ766728, FJ766727, FJ766726, FJ766725, FJ766724, FJ766723, FJ766722.	FJ784381, FJ784500, FJ784540, FJ784554, FJ784566, FJ784571, FJ784575, FJ784576, FJ784585, FJ784607.
Hylidae	<i>Hyloscirtus palmeri</i>	7	7	7	USNM 572670, USNM 572671, KRL 1336, USNM 572673, USNM 572674, USNM 572675, toe 141.	FJ766738, FJ766737, FJ766736, FJ766735, FJ766734, FJ766733, FJ766732.	FJ784457, FJ784493, FJ784503, FJ784568, FJ784573, FJ784577, FJ784596.
Hylidae	<i>Hypsiboas rufitelus</i>	2	2	2	USNM 572699, USNM 572700.	FJ766740, FJ766739.	FJ784372, FJ784486.

Hylidae	<i>Smilisca phaeota</i>	2	2	2	USNM 572702, USNM 572703.	FJ766835, FJ766834.	FJ784413, FJ784433.
Hylidae	<i>Smilisca sila</i>	3	3	3	USNM 572707, USNM 572708, toe 1000.	FJ766837, FJ766836, FJ766838.	FJ784578, FJ784579, FJ784320.
Leiuperidae	<i>Engystomops pustulosus</i>	5	4	5	USNM 572715, USNM 572716, MVUP 1837, USNM 572717.	FJ766703, FJ766702, FJ766701, FJ766700.	FJ784414, FJ784415, FJ784434, FJ784435, FJ784478 (USNM 572713).
Leptodactylidae	<i>Leptodactylus fragilis</i>	5	5	5	USNM 572722, USNM 572725, MVUP 1836, USNM 572727, KRL 572729.	FJ766745, FJ766744, FJ766743, FJ766742, FJ766741.	FJ784331, FJ784416, FJ784437, FJ784453, FJ784497.
Leptodactylidae	<i>Leptodactylus insularum</i>	1	1	1	USNM 572730.	FJ766746.	FJ784467.
Leptodactylidae	<i>Leptodactylus poecilochilus</i>	1	1	1	KRL 0118.	FJ766747.	FJ784321.
Leptodactylidae	<i>Leptodactylus savagei</i>	1	1	1	MVUP 1828.	FJ766748.	FJ784394.
Microhylidae	<i>Elachistocleis ovalis</i>	2	2	2	MVUP 1923, USNM 572735.	FJ766754, FJ766753.	FJ784469, FJ784470.
Microhylidae	<i>Nelsonophryne aterrima</i>	5	5	5	USNM 572736, USNM 572738, USNM 572740, KRL 1597, USNM 572741.	FJ766759, FJ766758, FJ766757, FJ766756, FJ766755.	FJ784519, FJ784547, FJ784567, FJ784569, FJ784570.
Plethodontidae	<i>Bolitoglossa colonnea</i>	1	1	1	CH 6526.	FJ766578.	FJ784318.
Plethodontidae	<i>Bolitoglossa schizodactyla</i>	1	1	1	USNM 572791.	FJ766579.	FJ784482.
Plethodontidae	<i>Oedipina collaris</i>	1	0	1			FJ196863 (SIUC H-08896).
Plethodontidae	<i>Oedipina parvipes</i>	1	1	1	AJC 1786.	FJ766760.	FJ784316.
Ranidae	<i>Lithobates warszewitschii</i>	3	3	3	USNM 572770, USNM 572779, USNM 572780.	FJ766752, FJ766751, FJ766750.	FJ784454, FJ784552, FJ784558.
Ranidae	<i>Lithobates aff. warszewitschii</i>	1	1	1	USNM 572787.	FJ766749.	FJ784384.
Strabomantidae	<i>Pristimantis caryophyllaceus A</i>	4	4	4	USNM 572329, USNM 572335, USNM 572330, USNM 572331.	FJ766771, FJ766770, FJ766774, FJ766773.	FJ784397, FJ784589, FJ784421, FJ784422.
Strabomantidae	<i>Pristimantis caryophyllaceus B</i>	1	1	1	USNM 572338.	FJ766775.	FJ784491.
Strabomantidae	<i>Pristimantis caryophyllaceus C</i>	2	2	2	MVUP 1925, USNM 572343.	FJ766776, FJ766772.	FJ784473, FJ784375.
Strabomantidae	<i>Pristimantis cerasinus</i>	3	2	3	USNM 572376, USNM 572377.	FJ766786, FJ766785.	FJ784387, FJ784391, FJ784498 (USNM 572378).
Strabomantidae	<i>Pristimantis cruentus</i>	9	9	9	USNM 572788, USNM 572361, USNM 572375, USNM 572362, USNM 572364, USNM 572365, USNM 572366, USNM 572367, USNM 572369.	FJ766787, FJ766784, FJ766783, FJ766782, FJ766781, FJ766780, FJ766779, FJ766778, FJ766777.	FJ784380, FJ784502, FJ784520, FJ784525, FJ784531, FJ784535, FJ784538, FJ784548, FJ784557.

Strabomantidae	<i>Pristimantis gaigeae</i>	5	5	5	USNM 572380, USNM 572381, MVUP 1910, USNM 572382, USNM 572383.	FJ766792, FJ766791, FJ766790, FJ766789, FJ766788.	FJ784385, FJ784412, FJ784461, FJ784487, FJ784490.
Strabomantidae	<i>Pristimantis museosus</i>	4	4	3	USNM 572389, MVUP 1839, USNM 572395.	FJ766798, FJ766795, FJ766793, FJ766794 (KRL 0983).	FJ784340, FJ784430, FJ784559.
Strabomantidae	<i>Pristimantis aff. museosus</i>	3	3	3	USNM 572404, USNM 572403, MVUP 1796.	FJ766796, FJ766799, FJ766797.	FJ784409, FJ784334, FJ784354.
Strabomantidae	<i>Pristimantis pardalis</i>	5	5	5	USNM 572405, USNM 572406, MVUP 1824, USNM 572407, USNM 572409.	FJ766804, FJ766803, FJ766802, FJ766801, FJ766800.	FJ784336, FJ784365, FJ784386, FJ784406, FJ784590.
Strabomantidae	<i>Pristimantis ridens A</i>	2	2	2	USNM 572416, USNM 572417.	FJ766808, FJ766807.	FJ784388, FJ784389.
Strabomantidae	<i>Pristimantis ridens B</i>	2	2	2	MVUP 1829, USNM 572415.	FJ766806, FJ766805.	FJ784398, FJ784399.
Strabomantidae	<i>Strabomantis bufoniformis</i>	7	4	7	USNM 57242, USNM 572427, USNM 572433, USNM 572534.	FJ766635, FJ766634, FJ766633, FJ766632.	FJ784410, FJ784451, FJ784522, FJ784565, FJ784460 (USNM 572478), FJ784485 (KRL 1186), FJ784499 (USNM 572430).
TOTALS		300	276	296			