

Sampling methods

Location information

Spp	Source_St	Source_County	n
LABO DE			3
LABO IL			8
LABO IN			30
LABO MD	Allegany		14
LABO MD	Carroll		2
LABO MD	Garrett		13
LABO MD	Washington		3
LABO MD			4
LABO NY	–		1
LABO OH	Paulding		1
LABO OH	Van Wert		1
LABO WV	Greenbrier and Nicholas Counties		9
LABO WV			6
LACI CA	Contra Costa		1
LACI IL			11
LACI IN			23
LACI MD	Garrett		1
LACI MD			2
LACI NV	White Pine Co.		1
LACI NY			16
LACI OH	Van Wert		5
LACI PA			9
LACI WV	Greenbrier and Nicholas Counties		2
LACI WV			4
LANO ID			54
LANO IL			1
LANO IN			21
LANO MD	Allegany		2
LANO NY			11
LANO OH	Paulding		1
LANO OH	Van Wert		2
LANO RI	Providence		2
LANO WV	Greenbrier and Nicholas Counties		8

Data from Table 1: Individuals of each species sampled by state and range of years and month of year sampled.

Spp **Source_St** **range_year** **range_month** **n_indiv**

Spp	Source_St	range_year	range_month	n_indiv
LABO	DE	2015	7	3
LABO	IL	2015	7 - 8	8
LABO	IN	2009 - 2014	7 - 10	30
LABO	MD	2011 - 2017	6 - 10	36
LABO	NY	2010	Inf	1
LABO	OH	2014 - 2016	5 - 6	2
LABO	WV	2011 - 2015	9 - 10	15
LACI	CA	2016	6	1
LACI	IL	2015 - 2018	8	11
LACI	IN	2009 - 2014	4 - 10	23
LACI	MD	2003 - 2017	7 - 10	3
LACI	NV	2013	10	1
LACI	NY	2008 - 2009	8	16
LACI	OH	2014	6 - 8	5
LACI	PA	2013	6 - 9	9
LACI	WV	2011 - 2016	5 - 10	6
LANO	ID	2012 - 2015	6 - 10	54
LANO	IL	2018	8	1
LANO	IN	2009 - 2014	4 - 10	21
LANO	MD	2015	5	2
LANO	NY	2009 - 2010	6 - 8	11
LANO	OH	2014 - 2016	6 - 8	3
LANO	RI	2014 - 2018	8	2
LANO	WV	2015	9 - 10	8

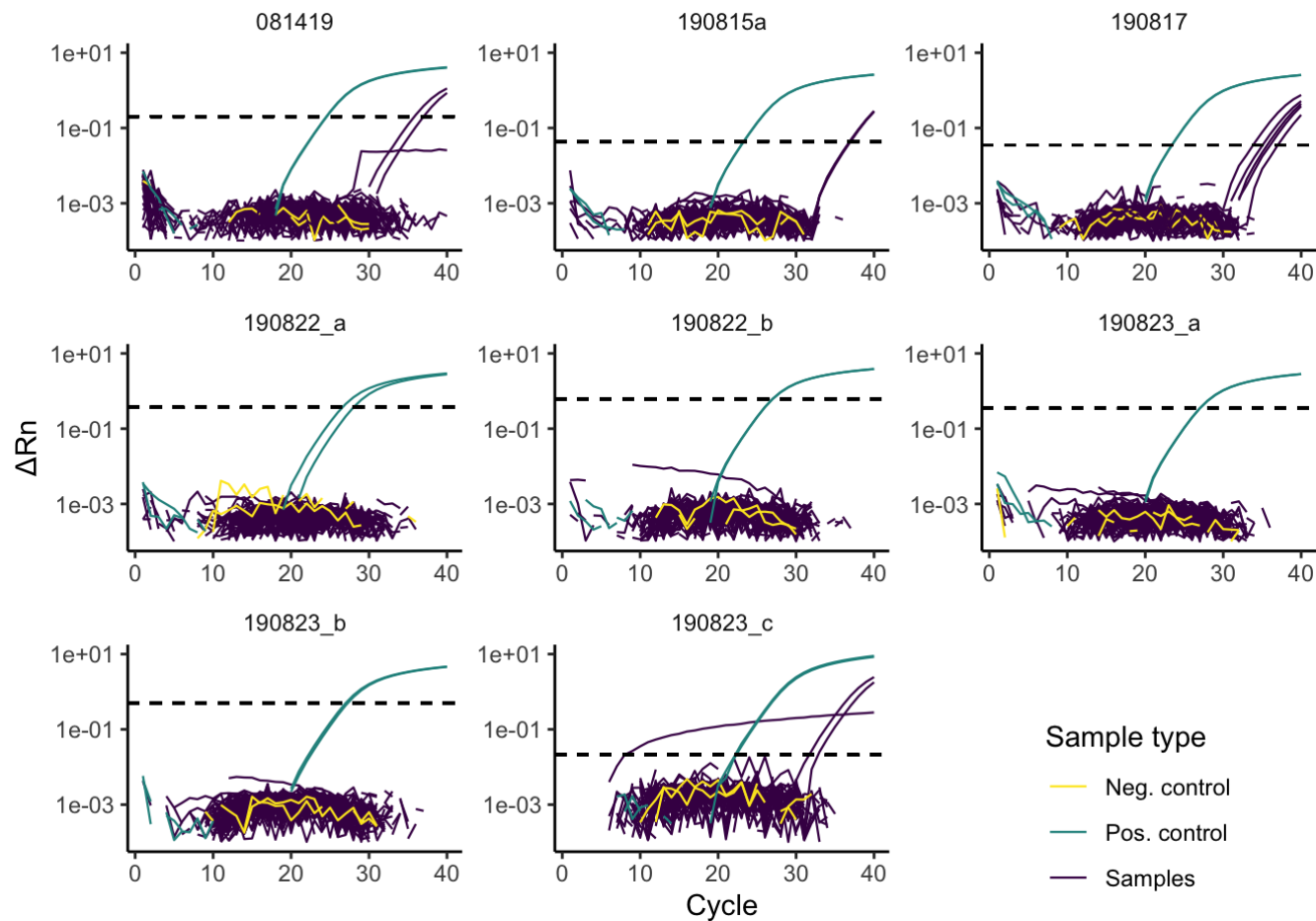
We conducted qPCR on a total of 322 samples representing 272 individuals (76 samples from 75 individual hoary bats, 119 samples from 95 individual eastern red bats, and 127 samples from 102 individual silver-haired bats; Table 2).

Data included in Table 2: Number of individuals sampled by each sampling method. Note that individuals sampled by multiple methods (e.g., “tissue and skin swab”) correspond with multiple samples.

Spp	samplingMethod	Tissue only	Fur swab only	Skin and fur swabs	Skin swab only	Tissue and skin swab
LABO	carcass	60				
LABO	live		3	24	8	
LACI	carcass	74				
LACI	live			1		
LANO	carcass	77				23
LANO	live			2		

Data from table 3: Sampling details for Pd-positive individuals. One individual represented here was discarded due to irregular curve results (i.e., Ct very low).

Species	State	Year	Month	Day	Sample type	Ct results
Lasiurus borealis	IL	2015	8	11	Extracted DNA	36.91, NA, NA, NA
Lasiurus borealis	IL	2015	8	14	Extracted DNA	37.01, 36.08, NA, NA
Lasiurus borealis	MD	2017	6	8	Fur swab	8.22, NA
Lasiurus borealis	MD	2017	6	8	Skin swab	NA, NA
Lasiurus borealis	OH	2014	6	30	Extracted DNA	37.04, 36.9, 35.09, NA
Lasiurus cinereus	NY	2009	8	22	Extracted DNA	36.96, 35.81, 32.89, 31.72
Lasionycteris noctivagans	WV	2015	9	16	Extracted DNA	35.67, 33.86, NA, NA



SI Figure 1: Response curves from qPCR analyses. Each panel represents a distinct plate run, with the date and sequence of each run identified in the panel title. Dotted lines indicate run-specific thresholds. Control positives (teal) and negatives (yellow) all performed as expected. The spurious positive result (discarded) is visible in the last plate, 190823_c.