SUPPLEMENTARY INFORMATION

We combined random sampling from fitted distributions and bootstrapping from empirical data to generate distributions for the expected proportions of larvae on Block Island feeding on white-footed mice, the seven avian hosts, and white-tailed deer (hereafter deer) in 2014. These estimates were back calculated using the observed value of NIP for 2015, which was directly calculated from field-collected samples as the proportion of infected nymphs over the total number of nymphs tested. We took into account the uncertainty in the estimates of population density, larval burden, realized reservoir competence, and nymphal infection prevalence derived from field data and of molting success percentage estimated in (LoGiudice et al. 2003).

We started with the competent host species (*Peromyscus leucopus*) and uniformly sampled between the lowest and highest values for density of mouse/ha to generate a mean value for a Poisson distribution of the per hectare density of mice on Block Island in 2014 (d_{mice}). This approach takes into account all of the uncertainty associated with the mark-recapture data on white-footed mice collected over three sites (NP, SP, ML). Similarly, we sampled from a log-normal density distributions for each of the seven avian species, as estimated from observational data collected in 2014. We next sampled from the distributions for the species-specific average tick burdens which were generated by bootstrapping the individual counts of larval ticks for each species.

The generated values of density of species s (d_s) (one value per species) and mean body burden of species s ($\bar{b}_s$) for white-footed mice and the seven avian reservoir host species (again, one value for each species) were then used to distribute a sample of 100,000 fed larval ticks across these hosts (Figure 1). The number 100,000 is arbitrary, but chosen to be large enough such that minor stochastic effects arising from distributing a finite number of ticks are negligible. The total number of larvae feeding on species *s* is

$$L_s = 100{,}000 \times \frac{d_s \bar{b}_s}{\sum_{i \in C} d_i \bar{b}_i} \tag{1}$$

where C is the set of competent host species, (white-footed mice, American Robin, Carolina Wren, Common Yellowthroat, Eastern Towhee, Gray Catbird, Song Sparrow, and Yellow Warbler).

The simulated population of engorged larvae was assumed to acquire and maintain the infection transstadially with a probability q_s sampled by bootstrapping the individual realized reservoir competence and survive the molt with a fixed probability m_s, derived from LoGiudice et al. (2003), with both probabilities dependent on s, the species they fed on. This gives $N_s^i \approx q_s m_s L_s$ as the number of infected nymphs that fed on species s as larvae, and $N_s^u \approx (1 - q_s) m_s L_s$ as the number of uninfected nymphs that fed on species s as larvae. The total number of nymphs that fed on species s is denoted $N_s = N_s^i + N_s^u$.

Using this notation, an equation for the nymphal infection prevalence (NIP) can be formulated, where N_{deer} is the number of nymphs that fed as larvae on white-tailed deer,

$$NIP = \frac{\sum_{s \in C} N_s^i}{\sum_{s \in C} N_s + N_{deer}}, \tag{2}$$

Note that the numerator of this expression does not include a term representing infected nymphs that fed as larvae on deer. This is because white-tailed deer are not competent reservoir hosts for *B. burgdorferi* (Telford et al. 1988, Luttrell et al. 1994).

The equation for NIP has only one unknown on the right-hand side, which is N_{deer} in the denominator. The observed NIP on Block Island in 2015 was 30% and to generate a value for N_{deer} we used bootstrapping from our field data to determine NIP on the left-hand side of the equation and solved for N_{deer}. To generate distributions for N_{deer} we repeated the back calculation 10,000 times, each time creating a different simulated population of engorged larvae by sampling from the distributions for host densities and burdens, different transmission probability from the distributions for host realized reservoir competence, and different NIP from the distribution of questing nymphs collected by dragging.

With a calculated value for N_{deer}, for each simulated population we worked backwards to calculate

$$L_{deer} = \frac{N_{deer}}{m_{deer}}, \quad (3)$$

where m_{deer} is the molting success of larvae that feed on deer from LoGiudice et al. (2003). For each simulation, the number of larvae feeding on deer (L_{deer}) was added to the sampled 100,000 engorged larvae restricted to feed on mice or one of the avian species. We then calculated the proportion of larvae feeding on all the different host species in the simplified Block Island community,

$$p_s = \frac{L_s}{\sum_{i \epsilon \mathrm{H}} L_i}, \quad (4)$$

where H =(white-footed mice, American robin, Carolina wren, Common yellowthroat, Eastern towhee, Gray catbird, Song sparrow, and Yellow warbler and white-tailed deer).

Finally, with a given estimate of deer density from a uniform distribution for 2014 (d_{deer}), we calculated the average larval burden on deer as

$$\bar{b}_{deer} = \frac{L_{deer}}{d_{deer}A} \quad (5)$$

where A is the theoretical number of hectares that would contain 100,000 engorged larvae that fed on mice and the seven avian species, calculated as

$$A = 100{,}000 / \sum_{s \in C} d_s \bar{b}_s \tag{6}$$

where $\sum_{s \in C} d_s \bar{b}_s$ is the total number of larvae feeding on mice and birds per hectare.

Supplementary Table 1. Capture and survey data of avian species collected from Block Island 2014, including the seven species with complete larval burden, realized reservoir competence, and density data that were used in this study.

Avian species	No. Birds	Mean larval burden (SE)	No. Larva	Larva tested	Larva infected	Density	Std error	95% CI
American Robin (*Turdus migratorius*)	12	8.50 ± 7.07	102	16	10	0.71	0.32	0.29, 1.78
Carolina Wren (*Thryothorus ludovicianus*)	7	31.71 ± 13.67	222	50	35	5.61	2.58	2.29, 13.76
Common Yellowthroat (*Geothlypis trichas*)	14	9.53 ± 2.72	139	46	20	1.56	1.87	0.13, 19.29
Eastern Towhee (*Pipilo erythrophthalmus*)	6	2.33 ± 1.02	14	6	2	4.14	1.60	1.92, 8.94
Gray Catbird (*Dumetella carolinensis*)	45	3.91 ± 0.81	176	25	2	11.60	4.63	5.31, 25.35
Song Sparrow (*Melospiza melodia*)	15	4.87 ± 1.69	73	26	8	1.70	0.61	0.83, 3.50
Yellow Warbler (*Setophaga petechia*)	9	0.33 ± 0.17	3	7	1	0.59	0.50	0.09, 4.11
Total	126		738	176	78			

Supplementary Table 2. Estimated models for white-footed mouse density per site including the Akaike information criterion with a correction for finite sample sizes (AICc) implemented in SECR. Model parameters include: density (D), magnitude (intercept) of detection function (g0), and spatial scale of detection function (sigma). Effects on parameters (denoted with a ~ symbol after the respective parameter) include: learned response (b), session factor which has one level for each session (session), and session trend with a linear trend on link scale (Session). Examples of models: g0~1 means g0 is constant across occasions (capture histories) and detectors (traps); g0~b means learned response effects g0; and g0~b + Session means learned response in g0 combined with trend over sessions. Standard error (SE), the lower (LCL) and upper (UCL) confidence limits for each density model type are also included.

Site	Model	AICc	Density (ha^{-1})	SE	LCL (ha^{-1})	UCL (ha^{-1})
NP	D~1, g0~b, sigma~b	1084.02	14.74	5.47	7.28	29.80
	D~1, g0~1, sigma~1	1084.47	13.89	2.31	10.06	19.20
	D~1, g0~b, sigma~1	1084.48	18.75	6.67	9.53	36.89
	D~1, g0~b + Session, sigma~b	1086.26	14.64	5.44	7.24	29.62
	D~1, g0~b + session, sigma~b	1094.70	13.81	4.66	7.26	26.29
SE	D~1, g0~b, sigma~b	1061.94	7.99	1.95	4.99	12.80
	D~1, g0~b + Session, sigma~b	1062.89	7.63	1.62	5.06	11.52
	D~1, g0~b + Session, sigma~1	1086.50	8.84	1.83	5.92	13.21
	D~1, g0~b + session, sigma~1	1086.52	10.78	2.31	7.11	16.34
	D~1, g0~b, sigma~1	1086.58	10.16	2.57	6.24	16.55
	D~1, g0~1, sigma~1	1087.02	8.17	1.15	6.21	10.76
ML	D~1, g0~1, sigma~1	557.68	11.99	3.36	7.00	20.54
	D~1, g0~b + Session, sigma~1	558.51	9.50	3.39	4.82	18.71
	D~1, g0~b + session, sigma~1	559.32	15.52	8.57	5.65	42.67
	D~1, g0~b, sigma~1	559.87	14.58	10.26	4.21	50.53
	D~1, g0~b, sigma~b	561.88	19.81	17.48	4.48	87.65

NP = North Plot; SP = South Plot; ML = Midland Plot

Supplementary Table 3. Parameter estimates and standard errors (SE) of the best fit models for mouse and seven avian species densities from SECR and DISTANCE, respectively. SECR model parameters include density (D), intercept (g0), and spatial scale (sigma) of the detection function. DISTANCE model parameters include A(i), which represents the i-th parameter in the estimated probability density function, h(0) = $2*p_i/v$ where p_i is probability of observing the i-th animal in a defined area and v is the effective detection area for point transects, and EDR, which denotes the effective detection radius for point transects.

Mouse trapping site	**Model**	**Density (SE)**	**g0 (SE)**	**sigma (SE)**
North Plot	D~1, g0~b, sigma~b	14.73 (5.47)	0.03 (0.02)	19.20 (3.27)
South Plot	D~1, g0~b, sigma~b	7.99 (1.95)	0.03 (0.01)	19.77 (1.99)
Middle Plot	D~1, g0~1, sigma~1	11.99 (3.36)	0.04 (0.01)	15.08 (2.92)

Avian species	**Detection function (Adjustments)**	**Density (SE)**	**A(1) (SE)**	**A(2) (SE)**	**h(0) (SE)**	***p* (SE)**	**EDR (SE)**
American Robin (*Turdus migratorius*)	Half-normal	0.71 (0.32)	27.59 (5.98)	NA	0.001 (0)	0.26 (0.10)	38.53 (7.56)
Carolina Wren (*Thryothorus ludovicianus*)	Negative Exponential	5.61 (2.58)	13.96 (2.91)	NA	0.005 (0.002)	0.07 (0.03)	19.45 (3.77)
Common Yellowthroat (*Geothlypis trichas*)	Negative Exponential	1.56 (1.87)	10.13 (4.97)	NA	0.010 (0.010)	0.04 (0.04)	14.29 (6.89)
Eastern Towhee (*Pipilo erythrophthalmus*)	Half-normal (Cosine)	4.14 (1.60)	24.79 (2.60)	0.71 (0.23)	0.004 (0.001)	0.10 (0.03)	23.74 (3.18)
Gray Catbird (*Dumetella carolinensis*)	Negative Exponential	11.60 (4.63)	10.73 (1.84)	NA	0.009 (0.003)	0.04 (0.01)	15.12 (2.53)
Song Sparrow (*Melospiza melodia*)	Half-normal	1.70 (0.61)	23.76 (3.41)	NA	0.002 (0)	0.20 (0.06)	33.49 (4.64)
Yellow Warbler (*Setophaga petechia*)	Half-normal	0.59 (0.50)	16.38 (5.52)	NA	0.004 (0.003)	0.10 (0.06)	23.17 (7.81)