Supplemental Table S1. Point estimates for transmission probabilities based on experimental observations. These values correspond to coinfection reducing the probability of *Borrelia burgdorferi* (*Bb*) transmission from mouse to larva by a factor $\xi = 0.87$ and increasing the probability of *Babesia microti* (*Bm*) transmission from mouse to larva by a factor $\sigma = 1.54$.

Transmission Pathway	Parameter	Probability	Reference
Bb mouse to larva†	β_1^{ML}	0.83	Unpublished data MAD
Bb coinfected mouse to larva†	$\xi\beta_1^{ML}$	0.72	Unpublished data MAD
Bm mouse to larva†	β_2^{ML}	0.37	Dunn et al. 2014
Bm coinfected mouse to larva†	$\sigma\beta_2^{ML}$	0.57	Dunn et al. 2014
Bb nymph to mouse	β_1^{NM}	0.83	Dunn et al. 2013
Bm nymph to mouse	β_2^{NM}	0.90	Piesman 1982
Bm vertically to offspring	υ	0.74	Tufts & Diuk-Wasser 2020

†These values were from experiments that checked for infection after engorged larvae molted to simulate transmission changes that occur during the molt.

Supplemental Table S2. All model parameters and descriptions of parameters used in the mechanistic mathematical model, and prior distributions for stages 1 and 2 of the ABC algorithms. Parameters for uniform priors (*) are the interval bounds. Parameters for lognormal priors (#) are the mean and standard deviation on the log scale. In stage 2, lognormal priors were used where they give reasonable approximations to stage 1 posteriors. Distributions marked (†) are based on point estimates from experiments. For ABC algorithms we also specified the following parameter constraints: $r > \mu$, τ_N, $\tau_E < \tau_L$, $0 < \nu$, β_{ML}^1, β_{ML}^2, β_{NM}^1, $\beta_{ML}^2 < 1$.

Parameter	Description	Stage 1 prior	Stage 2 prior BI	Stage 2 prior CT
r	Mouse intrinsic growth rate/day	(0, 0.2)*	(0.07, 0.2)*	(0.07, 2)*
μ	Mouse death rate/day	(0, 0.05)*	(0, 0.05)*	(0, 0.05)*
K	Mouse reproduction carrying capacity/hectare	(10, 70)*	(3.79, 0.22)#	(3.4, 0.376)#
ω_M	Proportion of mice that survive winter	(0, 1)*	(0, 1)*	(0, 1)*
τ_E	Day unengorged larvae begin emergence from diapause	(90, 140)*	(90, 140)*	(90, 140)*
τ_L	Day larvae begin emergence from eggs	(170, 220)*	(5.3, 0.05)#	(5.31, 0.05)#
τ_N	Day nymphs begin to emerge from diapause	(90, 135)*	(4.69, 0.11)#	(4.69, 0.11)#
η_E	Emergence rate of unengorged diapaused larvae/day	(0.05, 2)*	(0.05, 2)*	(0.05, 0.2)*
η_L	Emergence rate of larvae from eggs/day	(0.05, 2)*	(0.05, 0.2)*	(0.05, 0.2)*
η_N	Emergence rate of nymphs/day	(0.05, 2)*	(0.05, 2)*	(0.05, 2)*
λ	Tick-host encounter rate/host/day	(le^{-4}, le^{-3})*	(-7.86, 0.56)#	(-7.84, 0.64)#
Ω	Density of eggs at beginning of each season/hectare	(le^{4}, le^{3})*	(10.43, 0.53)#	(9.97, 0.50)#
ω_L	Proportion of unengorged larvae that survive the winter	(0.2, 0.8)*	(-0.9, 0.38)#	(-0.96, 0.38)#
D	Density of non-competent hosts/hectare	(0, 100)*	(0, 100)*	(0, 100)*
δ	Engorged larva/nymph detachment rate/day	(0.2, 0.4)*	(0.2, 0.4)*	(0.2, 0.4)*
ν	Probability of vertical transmission of *Bm*	-	(-3, 0.2)#†	(-3, 0.2)#†
β_1^{ML}	Probability of *Bb* transmission from mouse to larva	-	(-0.19, 0.2)#†	(-0.19, 0.2)#†
β_1^{NM}	Probability of *Bb* transmission from nymph to mouse	-	(-0.19, 0.2)#†	(-0.19, 0.2)#†
γ	Rate of mouse recovery from *Bb*/day	-	(0, 0.05)*	(0, 0.05)*
β_2^{ML}	Probability of *Bm* transmission from mouse to larva	-	(-0.99, 0.2)#†	(-0.99, 0.2)#†
β_2^{NM}	Probability of *Bm* transmission from nymph to mouse	-	(-0.19, 0.2)#†	(-0.19, 0.2)#†
σ	Increase *Bm* transmission probability from coinfected mice	-	(0.43, 0.2)#†	(0.43, 0.2)#†
ξ	Decrease *Bb* transmission probability from coinfected mice	-	(-0.14, 0.2)#†	(-0.14, 0.2)#†
α	Increase *Bb* transmission probability to *Bm* infected mice	-	(0.5, 1.5)*	(0.5, 1.5)*

* uniform priors
# lognormal priors
† experimental point estimates given in Supplementary Table S1

Supplemental Table S3. Transmission probabilities in the epidemiological model used to predict pathogen transmission in *Peromyscus leucopus* mice and *Ixodes scapularis* ticks.

Infection	Transmitter	Recipient	Probability
B. burgdorferi	Mouse with single infection	Larva	β_1^{ML}
	Mouse with coinfection	Larva	$\xi\beta_1^{ML}(1-\sigma\beta_2^{ML})$
	Nymph with single infection	Mouse	β_1^{NM}
	Nymph with single infection	Mouse with *B. microti*	$\alpha\beta_1^{NM}$
	Nymph with coinfection	Mouse (uninfected)	$\beta_1^{NM}(1-\beta_2^{NM})$
	Nymph with coinfection	Mouse with *B. microti*	$\alpha\beta_1^{NM}$
	Nymph with coinfection	Mouse with *B. microti*	β_1^{NM}
B. microti	Mouse with single infection	Larva	β_2^{ML}
	Mouse with coinfection	Larva	$(1-\xi\beta_1^{ML})\sigma\beta_2^{ML}$
	Mouse with single infection	Mouse (vertical)	υ
	Mouse with coinfection	Mouse (vertical)	υ
	Nymph with single infection	Mouse (uninfected)	β_2^{NM}
	Nymph with coinfection	Mouse (uninfected)	$(1-\beta_1^{NM})\beta_2^{NM}$
Coinfection	Mouse with coinfection	Larva	$\xi\beta_1^{ML}\sigma\beta_2^{ML}$
	Nymph with coinfection	Mouse (uninfected)	$\beta_1^{NM}\beta_2^{NM}$

Supplemental Table S4. Sample size (*n*), *Borrelia burgdorferi*, *Babesia microti*, and coinfection infection prevalence and standard deviation (% ± SD) of *Peromyscus leucopus* mice and host-seeking nymphal *Ixodes scapularis* ticks from three years collected from Block Island, RI (BI) and Connecticut (CT).

Site	**Mice**				**Nymphs**			
	n	*B. burgdorferi*	*B. microti*	Coinfected	*n*	*B. burgdorferi*	*B. microti*	Coinfected
NI	80	15.00%	NA*	NA*	204	11.27%	1.47%	0.98%
EI	45	22.22%	NA*	NA*	220	11.82%	1.82%	0.91%
RH	70	22.86%	84.48%	28.00%	147	21.77%	1.36%	0.00%
2014 BI	**195**	**20.03% ±3.56**	**28.16% ±39.82**	**9.33% ±13.20**	**571**	**14.19% ±4.83**	**1.58% ±0.20**	**0.70% ±0.45**
HT	139	31.65%	80.58%	29.50%	163	3.07%	31.29%	1.84%
OL	132	21.97%	69.70%	19.70%	207	17.39%	28.50%	8.70%
LS	79	24.05%	81.01%	21.52%	190	43.16%	52.63%	28.95%
2014 CT	**350**	**25.89% ±4.16**	**77.10% ±5.23**	**23.57% ±4.26**	**560**	**21.96% ±16.59**	**37.50% ±10.78**	**13.57% ±11.51**
NI	94	72.34%	92.55%	71.28%	190	15.26%	3.68%	1.05%
EI	58	56.90%	60.34%	46.55%	190	21.05%	4.21%	2.63%
RH	132	65.91%	87.88%	63.64%	191	34.55%	4.71%	1.57%
2015 BI	**284**	**65.05% ±6.33**	**80.26% ±14.21**	**60.49% ±10.34**	**571**	**23.64% ±8.08**	**4.20% ±0.42**	**1.75% ±0.66**
HT	45	51.11%	75.56%	44.44%	74	20.27%	41.89%	12.16%
OL	77	42.86%	63.64%	36.36%	258	10.08%	51.55%	8.14%
LS	22	68.18%	81.82%	63.64%	237	27.85%	67.93%	19.83%
2015 CT	**144**	**54.05% ±10.54**	**73.67% ±7.54**	**48.15% ±11.44**	**569**	**18.80% ±7.28**	**57.12% ±10.75**	**13.53% ±4.85**
NI	139	10.79%	98.56%	10.07%	190	6.32%	8.95%	2.11%
EI	157	12.74%	99.36%	12.74%	182	6.04%	6.59%	1.65%
RH	249	14.46%	100.00%	14.46%	195	19.49%	55.38%	12.31%
2016 BI	**545**	**12.66% ±1.50**	**99.31% ±0.59**	**12.42% ±1.81**	**567**	**10.76% ±6.27**	**24.16% ±22.46**	**5.47% ±4.92**
HT	128	23.44%	97.66%	22.66%	190	26.32%	60.53%	18.42%
OL	201	17.41%	88.06%	17.41%	190	30.53%	61.05%	19.47%
LS	155	29.68%	97.42%	29.68%	190	40.53%	34.74%	31.58%
2016 CT	**484**	**23.51% ±5.01**	**94.38% ±4.47**	**23.25% ±5.03**	**570**	**32.46% ±5.96**	**52.11% ±12.28**	**23.16% ±5.97**

*****Blood samples were lost for these sites, therefore *B. microti* and coinfection prevalence could not be calculated.

Supplemental Table S5. All parameters used in the mechanistic model together with their meanings and estimated values for each field site. A total of 5 x 10^5 trials were computed for each field location. Trials for which the parameter combination resulted in *B. burgdorferi* (*Bb*), *B. microti* (*Bm*), or both being entirely absent were removed. Rejection sampling was applied to the remainder with an acceptance tolerance of 0.005. This table shows the 10%, 50% (median), and 90% quantiles (credible intervals) of the accepted parameter distributions.

Parameter	Description	Block Island			Connecticut		
		10%	50%	90%	10%	50%	90%
r	Mouse intrinsic growth rate/day	0.084	0.133	0.185	0.082	0.133	0.186
μ	Mouse death rate/day	0.009	0.023	0.041	0.010	0.028	0.045
K	Mouse reproduction carrying capacity/hectare	34.7	41.6	50.4	20.5	29.5	41.3
ω_M	Proportion of mice that survive winter	0.063	0.434	0.875	0.042	0.366	0.835
τ_E	Day diapaused unengorged larvae begin to emerge	95.9	116.2	135.0	95.9	115.9	135.0
τ_L	Day larvae begin to emerge from eggs	188.9	198.7	209.8	190.2	203.6	219.7
τ_N	Day nymphs begin to emerge from diapause	97.8	113.1	125.2	98.8	117.0	131.3
η_E	Emergence rate of diapaused larvae/day	0.063	0.123	0.185	0.065	0.123	0.183
η_L	Emergence rate of larvae from eggs/day	0.065	0.126	0.184	0.065	0.123	0.183
η_N	Emergence rate of nymphs/day	0.060	0.112	0.181	0.060	0.110	0.181
λ	Tick-host encounter rate, per host/day	$1.31e^{-4}$	$2.07e^{-4}$	$3.25e^{-4}$	$1.20e^{-4}$	$2.16e^{-4}$	$3.81e^{-4}$
Ω	Density of eggs at beginning of each season/hectare	19811	33043	56204	9316	16248	28765
ω_L	Proportion of larvae/nymphs that survive winter	0.236	0.347	0.510	0.209	0.312	0.460
D	Density of non-competent hosts/hectare	26.30	57.20	88.30	1.25	6.72	20.60
δ	Engorged larva/nymph detachment rate/day	0.217	0.290	0.376	0.228	0.315	0.385
ν	Probability of vertical transmission of *Bm*	0.598	0.745	0.862	0.542	0.673	0.793
β_1^{ML}	Probability of *Bb* transmission from mouse to larva	0.646	0.803	0.952	0.662	0.811	0.956
β_1^{NM}	Probability of *Bb* transmission from nymph to mouse	0.644	0.792	0.945	0.653	0.814	0.951
γ	Rate of mouse recovery from *Bb*/day	0.007	0.025	0.044	0.004	0.020	0.042
β_2^{ML}	Probability of *Bm* transmission from mouse to larva	0.272	0.342	0.446	0.315	0.394	0.502
β_2^{NM}	Probability of *Bm* transmission from nymph to mouse	0.614	0.778	0.938	0.610	0.760	0.921
σ	Increase *Bm* transmission probability from coinfected mice	1.15	1.48	1.88	1.24	1.59	2.00
ξ	Decrease *Bb* transmission probability from coinfected mice	0.687	0.884	1.140	0.712	0.892	1.142
α	Increase *Bb* transmission probability to *Bm* infected mice	0.600	1.000	1.400	0.659	1.090	1.410

Supplemental Table S6. Total number of observed state transitions for the Block Island (BI, top) and Connecticut (CT, bottom) field locations from 2014-2016.

		to state (BI)			
		Uninfected (0)	***Bb*-infected (1)**	***Bm*-infected (2)**	**Coinfected (12)**
from state	**Uninfected (0)**	5	0	1	4
	***Bb*-infected (1)**	0	1	1	0
	***Bm*-infected (2)**	1	0	204	53
	Coinfected (12)	0	1	36	88

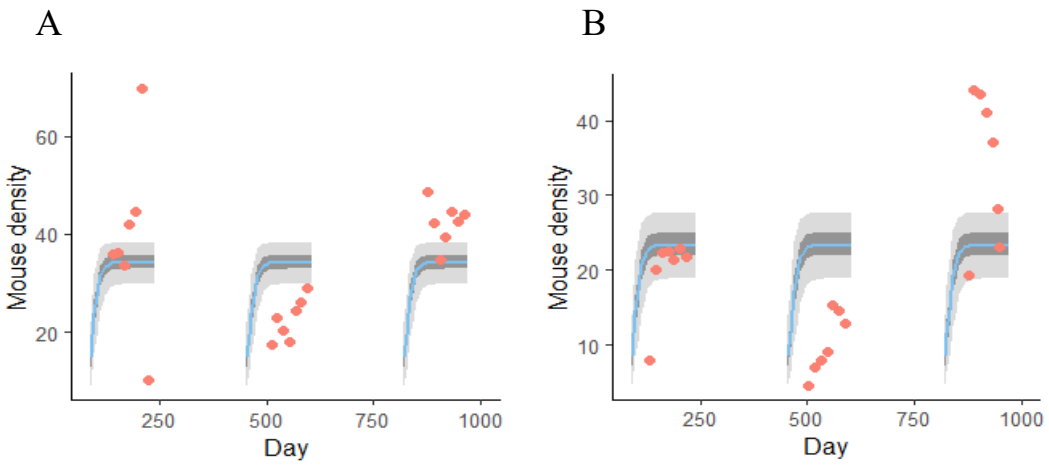
		to state (CT)			
		Uninfected (0)	***Bb*-infected (1)**	***Bm*-infected (2)**	**Coinfected (12)**
from state	**Uninfected (0)**	18	1	26	11
	***Bb*-infected (1)**	1	1	1	3
	***Bm*-infected (2)**	12	2	145	73
	Coinfected (12)	1	1	48	51

Supplemental Table S7. Maximum likelihood estimates, and 95% confidence intervals (using Mark) for state transition probabilities between two field sessions (2 weeks) for Block Island (BI, top) and Connecticut (CT, bottom). Most zero entries correspond to very small positive values and rows may not always sum to 1 due to rounding error. Note the very broad confidence intervals for most transitions involving the uninfected or *Borrelia burgdorferi* (*Bb*)-infected states. This uncertainty is due to the very small number of animals observed in these states.

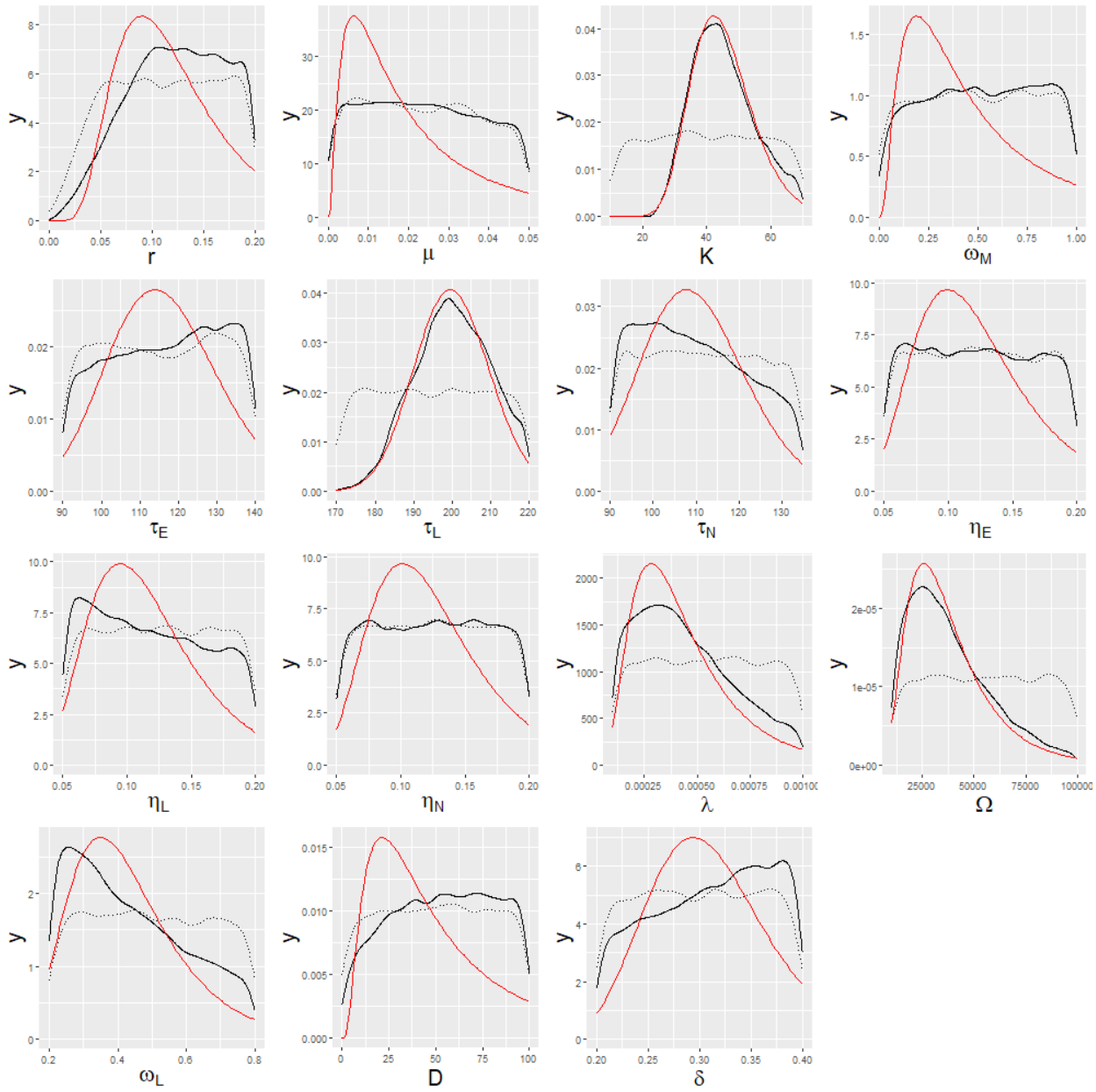
		to state (BI)			
		Uninfected (0)	***Bb*-infected (1)**	***Bm*-infected (2)**	**Coinfected (12)**
from state	**Uninfected (0)**	0.57 (0.28 – 0.81)	0 (0 – 1)	0.10 (0.01 – 0.50)	0.32 (0.12 – 0.63)
	***Bb*-infected (1)**	0 (0 – 1)	0.57 (0.08 – 0.94)	0.43 (0.05 – 0.92)	0 (0 – 1)
	***Bm*-infected (2)**	0 (0 – 0.02)	0 (0 – 1)	0.81 (0.77 – 0.86)	0.18 (0.14 – 0.23)
	Coinfected (12)	0 (0 – 1)	0 (0 – 0.04)	0.25 (0.19 – 0.34)	0.74 (0.66 – 0.81)

		to state (CT)			
		Uninfected (0)	***Bb*-infected (1)**	***Bm*-infected (2)**	**Coinfected (12)**
from state	**Uninfected (0)**	0.34 (0.23 – 0.48)	0.02 (0 – 0.12)	0.46 (0.33 – 0.59)	0.18 (0.10 – 0.30)
	***Bb*-infected (1)**	0.14 (0.01 – 0.67)	0.25 (0.04 – 0.70)	0.18 (0.02 – 0.68)	0.43 (0.12 – 0.81)
	***Bm*-infected (2)**	0.05 (0.03 – 0.09)	0 (0 – 0.04)	0.63 (0.57 – 0.70)	0.31 (0.26 – 0.38)
	Coinfected (12)	0.01 (0 – 0.08)	0.01 (0 – 0.08)	0.46 (0.36 – 0.56)	0.52 (0.41 – 0.62)

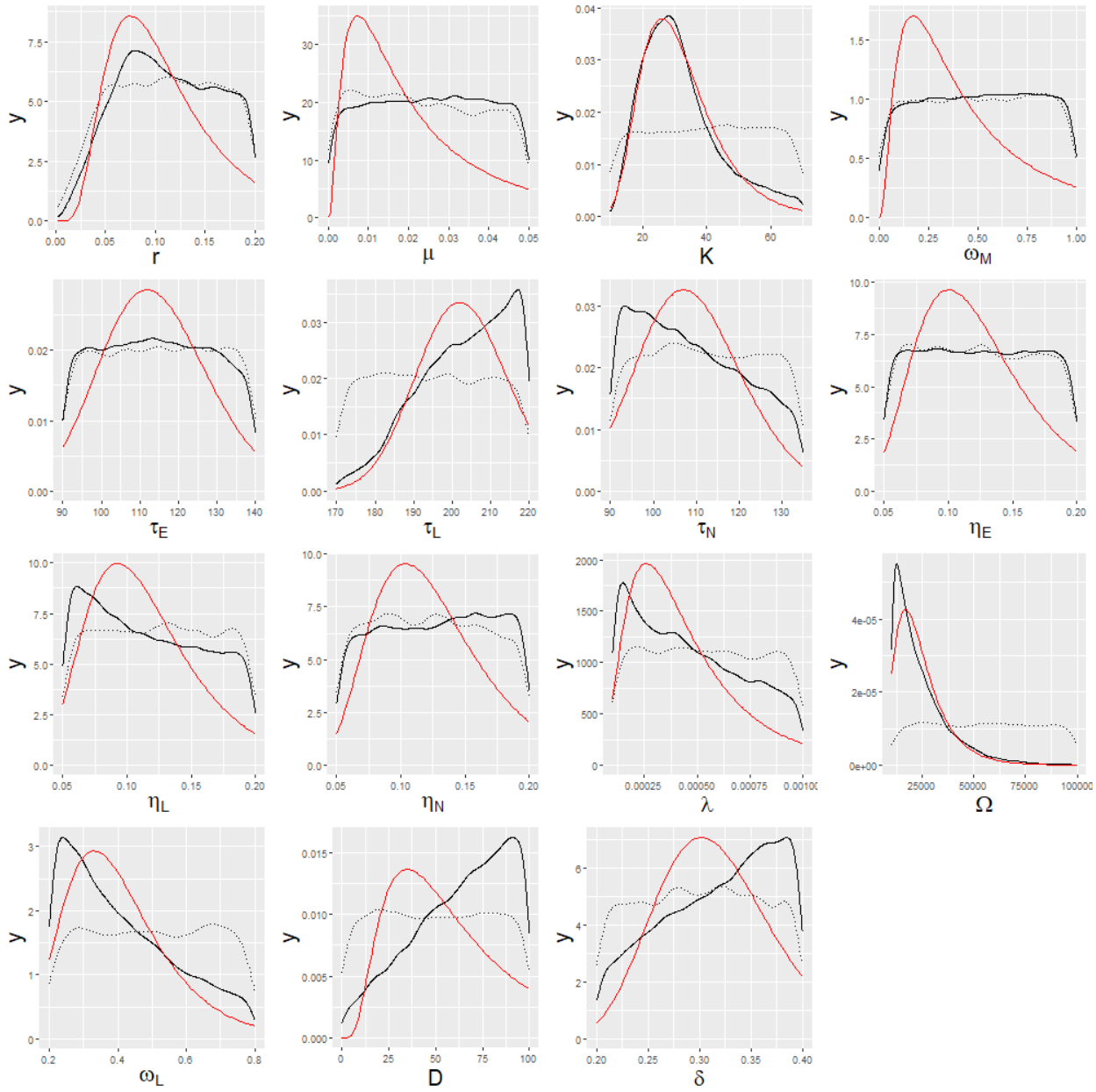
Figures



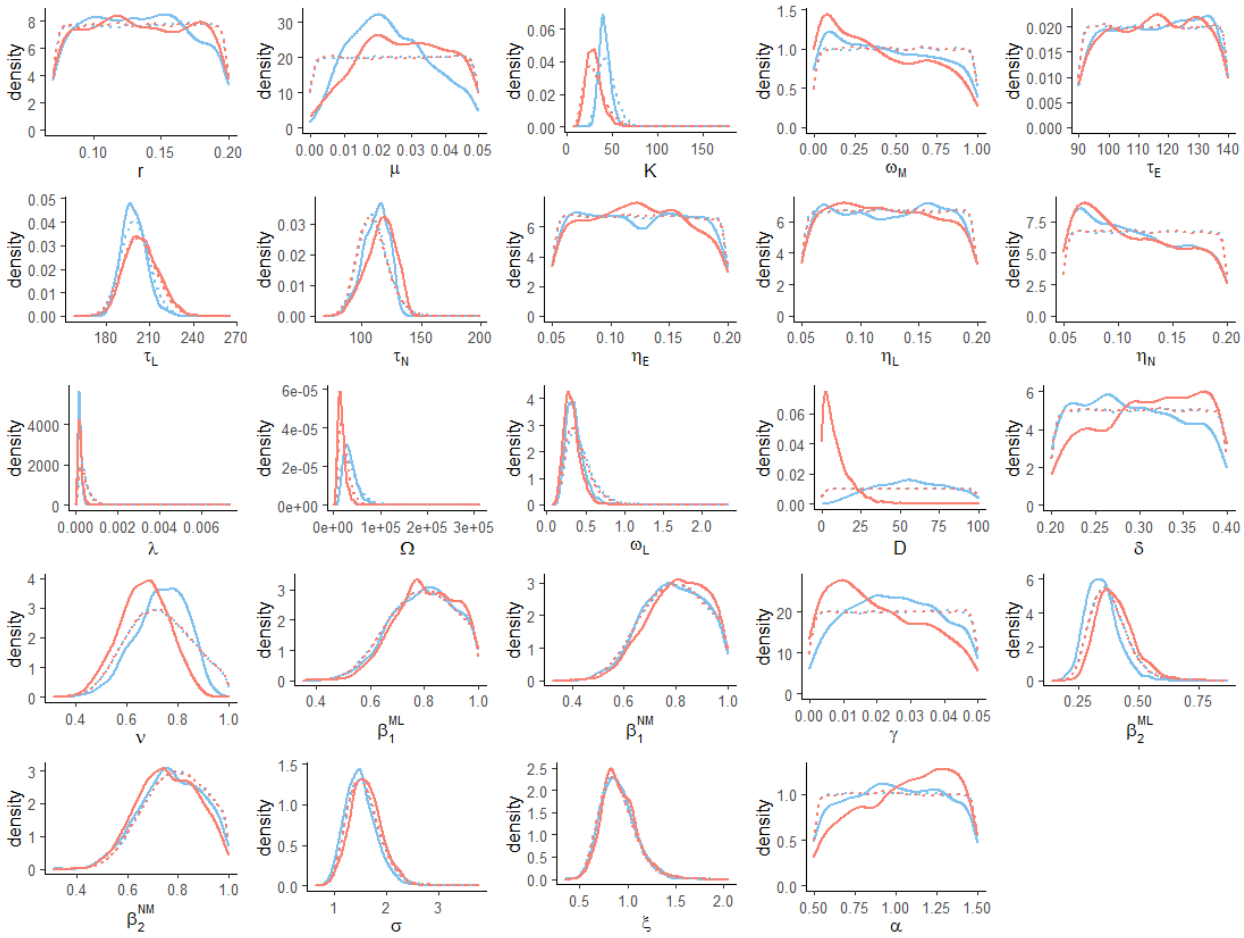
Supplemental Figure S1. Mouse density (per hectare) on BI (A) and CT (B). Blue lines denote the model with posterior median values for each parameter. Dark grey and pale grey areas are the minimal envelope containing 1000 model trajectories with parameter values sampled from the 10% and 30% credible intervals of the posteriors, respectively. Red circles represent field data. Each year is depicted with a new segment in the figure, 2014 (90-240 days), 2015 (455-605 days), 2016 (820-970 days).



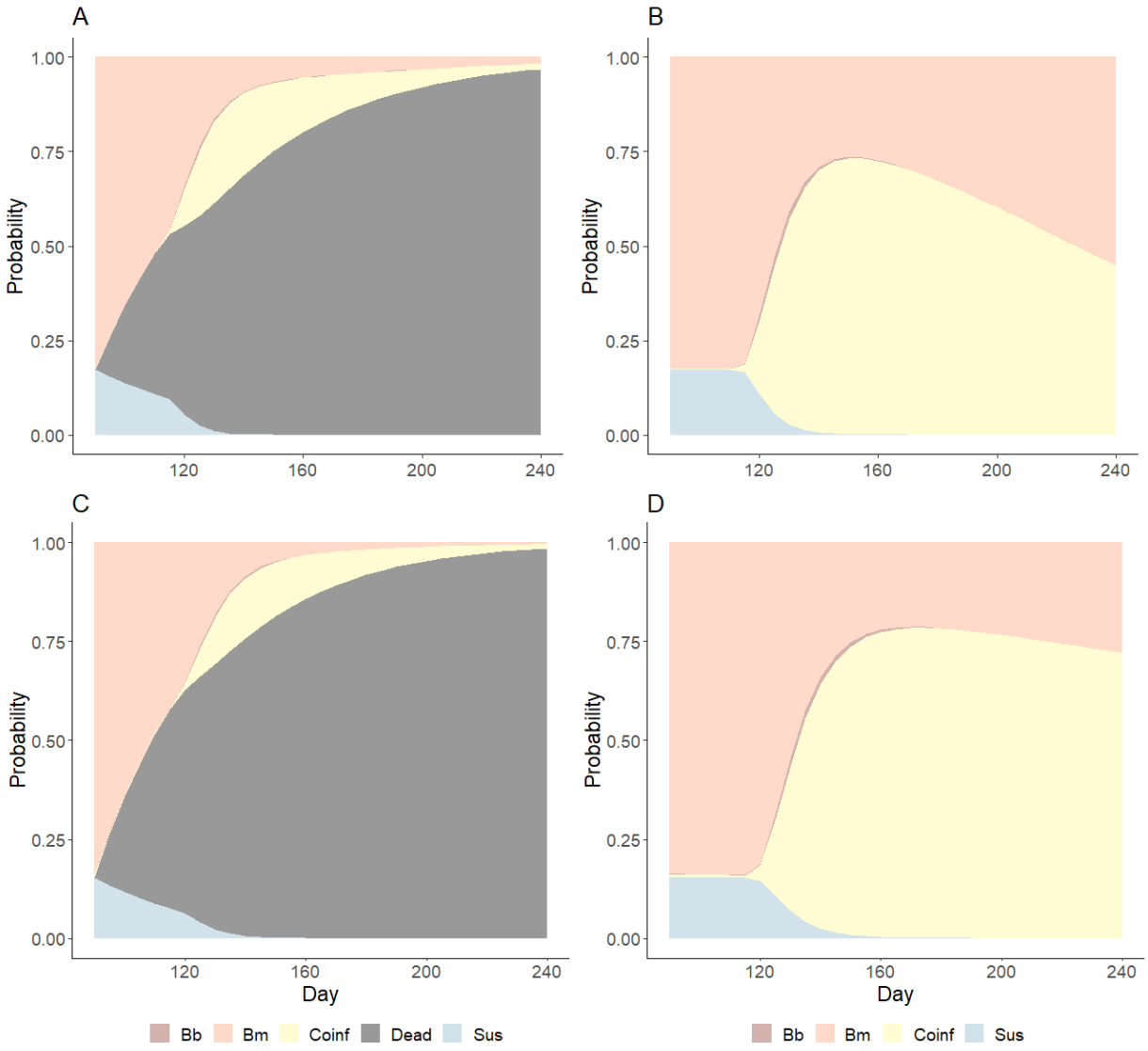
Supplemental Figure S2. Prior and posterior distributions for all parameters of the model with mouse and tick demography but no infection dynamics, observed data from BI (stage 1 of the estimation process). A total of 5 x 10^5 trials were computed and rejection sampling was applied with an acceptance tolerance of 0.05. Solid black: posterior distribution. Red: best fit lognormal distribution to posterior. Dotted: prior distribution.



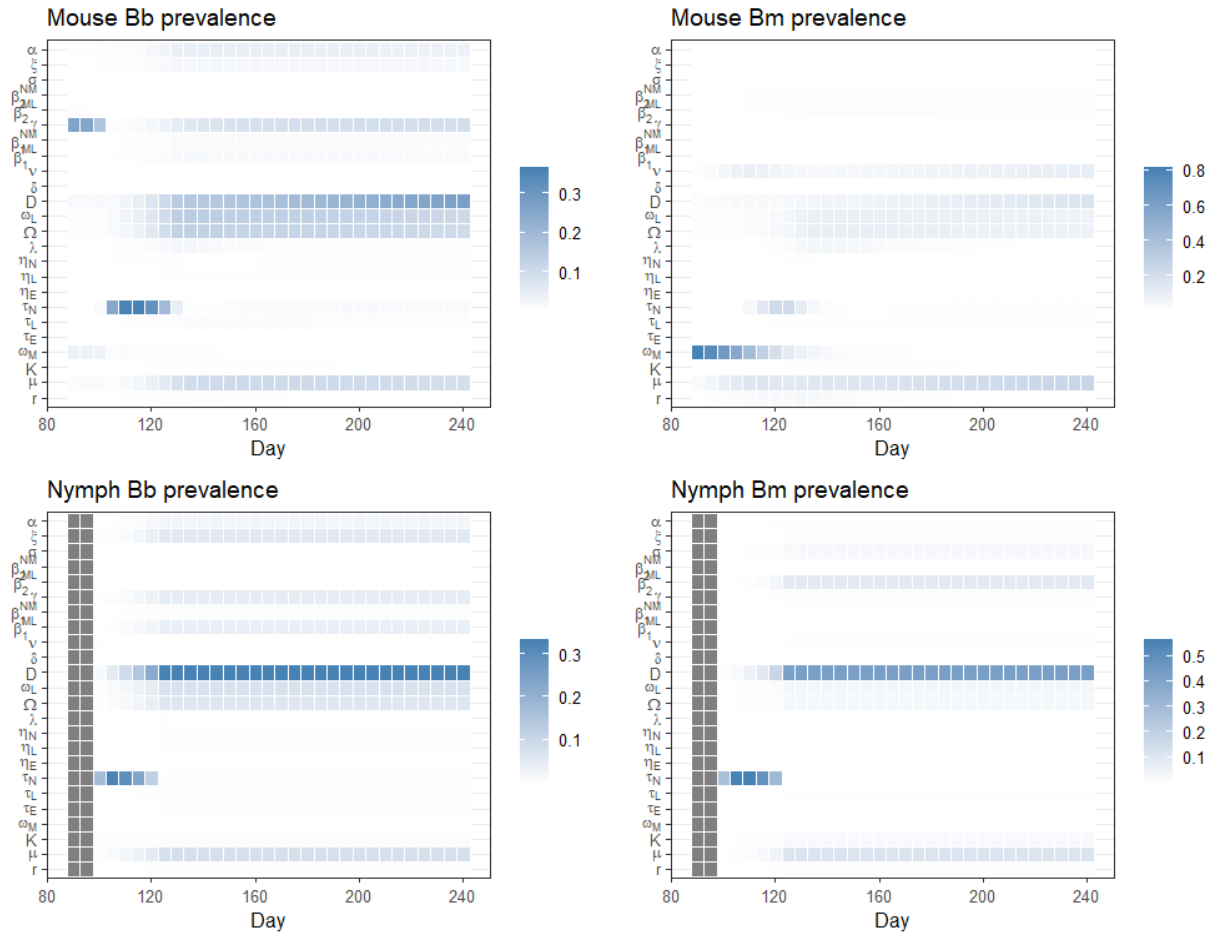
Supplemental Figure S3. Prior and posterior distributions for all parameters of the model with mouse and tick demography but no infection dynamics, observed data from CT (stage 1 of the estimation process). A total of 5 x 10^5 trials were computed and rejection sampling was applied with an acceptance tolerance of 0.05. Solid black: posterior distribution. Red: best fit lognormal distribution to posterior. Dotted: prior distribution.



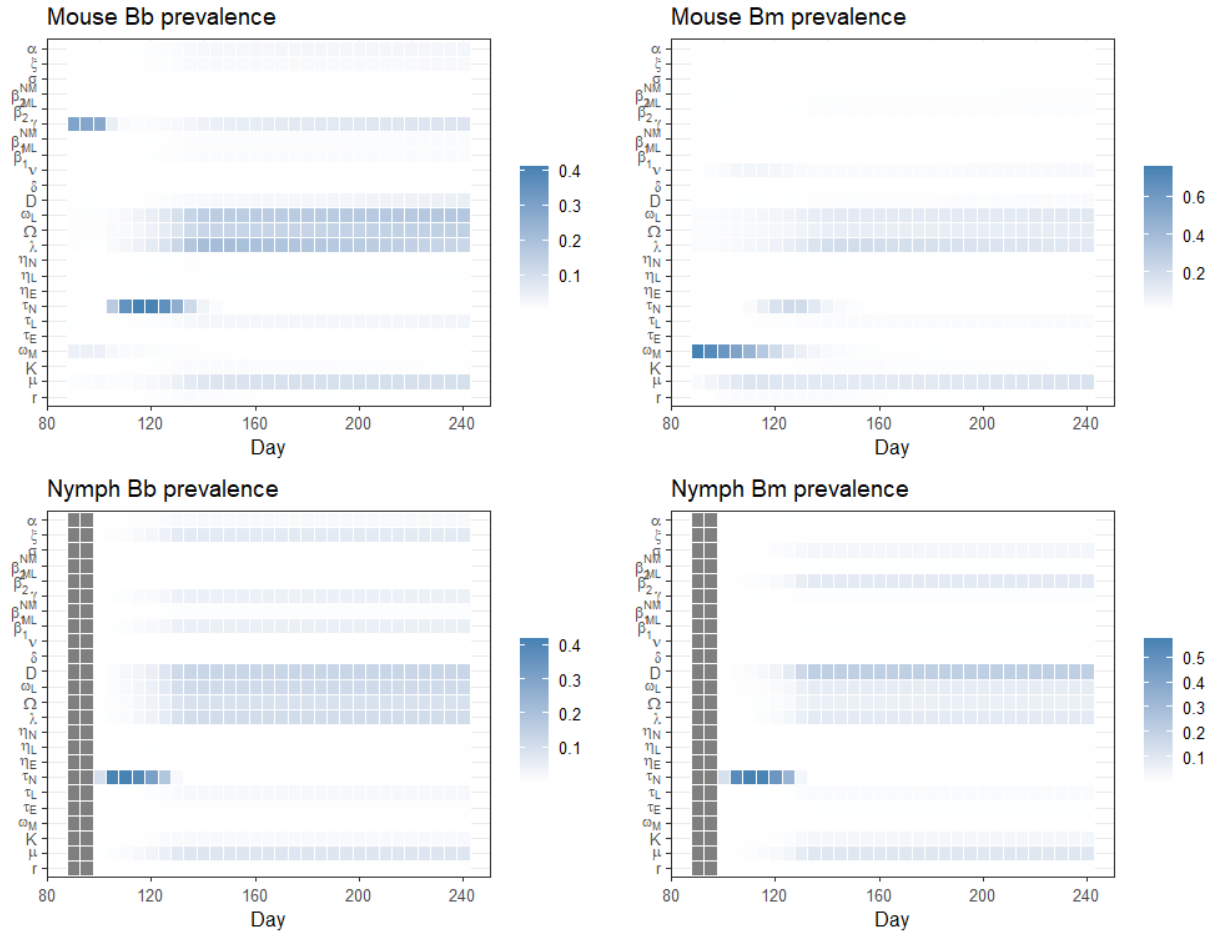
Supplemental Figure S4. Distributions for all parameters estimated by ABC rejection with BI and CT field observations (stage 2 of the estimation process). A total of 5 x 10^5 trials were computed for each field site. Trials for which the parameter combination resulted in *B. burgdorferi*, *B. microti*, or both being entirely absent were removed. Rejection sampling was applied to the remainder with an acceptance tolerance of 0.005. Solid lines signify the posterior estimate; dashed lines signify the prior; blue lines are BI; red lines are CT.



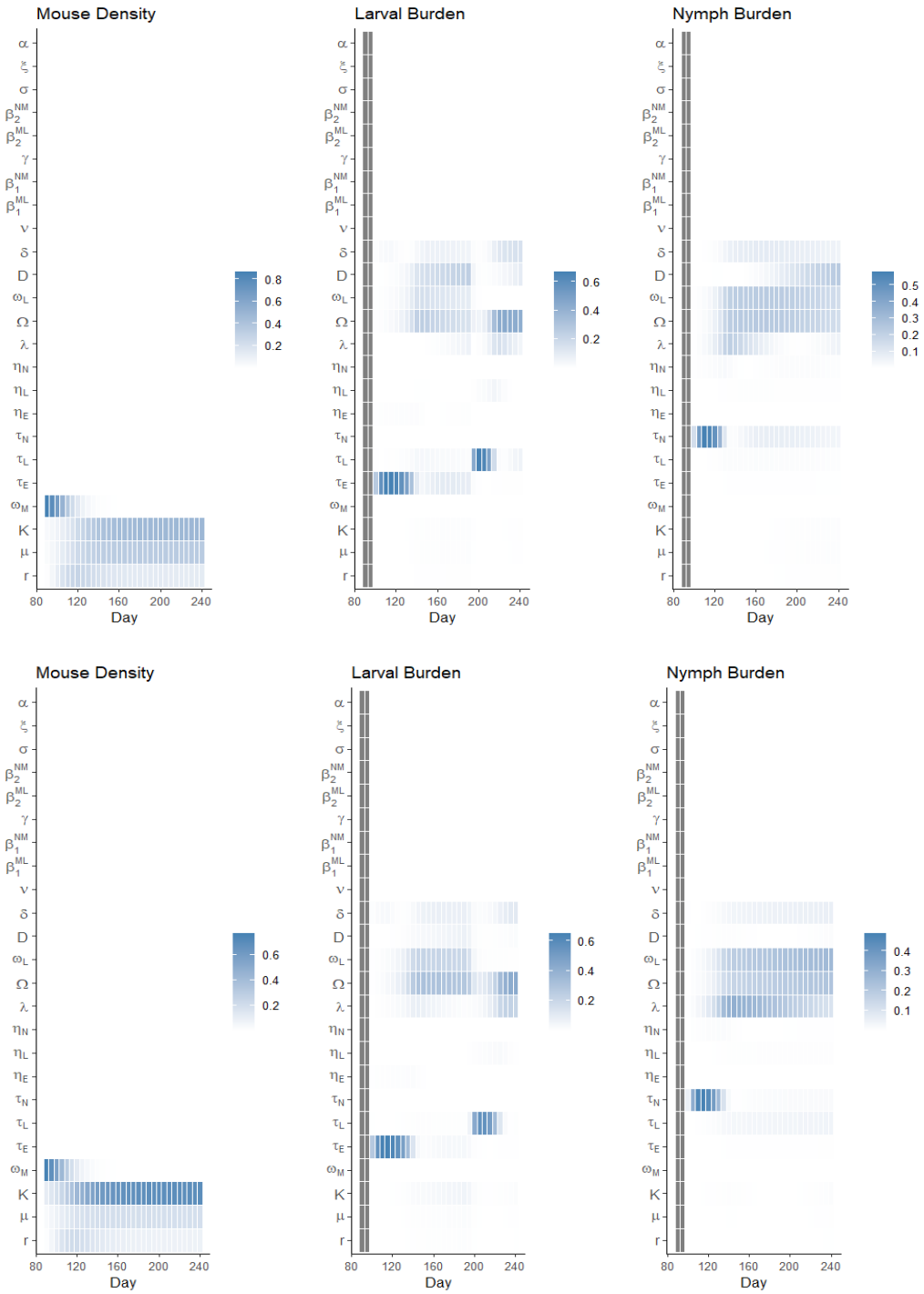
Supplemental Figure S5. State probability of a single mouse over one active season of the mechanistic model with the ecological and epidemiological dynamics at approximate steady state. The model was parameterized with the median values for BI (A, B) and CT (C, D) shown in Supp Table S5. Panels A and C include the probability that the mouse has died. Panels B and D show the infection state probability conditional on the mouse still being alive. Dark orange: infected with *Borrelia burgdorferi* (*Bb*) only (barely visible); pale orange: infected with *Babesia microti* (*Bm*) only; yellow: coinfected; black: dead; blue: susceptible.



Supplemental Figure S6. Fourier Amplitude Sensitivity Test (FAST) analysis of the sensitivity to the value of each parameter of model infection prevalence at 31 time points between days 90 and 240 for mice and nymphs. Baseline parameters are the median values for Block Island, *Borrelia burgdorferi* (*Bb*), *Babesia microti* (*Bm*), and darker shades indicate higher sensitivity.



Supplemental Figure S7. Fourier Amplitude Sensitivity Test (FAST) analysis of the sensitivity to the value of each parameter of model infection prevalence at 31 time points between days 90 and 240. Baseline parameters are the median values for Connecticut, *Borrelia burgdorferi* (*Bb*), *Babesia microti* (*Bm*), and darker shades indicate higher sensitivity.



Supplemental Figure S8. Fourier Amplitude Sensitivity Test (FAST) analysis of the sensitivity of model demographic variables at 31 time points between days 90 and 240 to the value of each parameter for mice and immature tick stages. Baseline parameters are the median values for Block Island (top panels) and Connecticut (bottom panels). Darker shades indicate higher sensitivity.