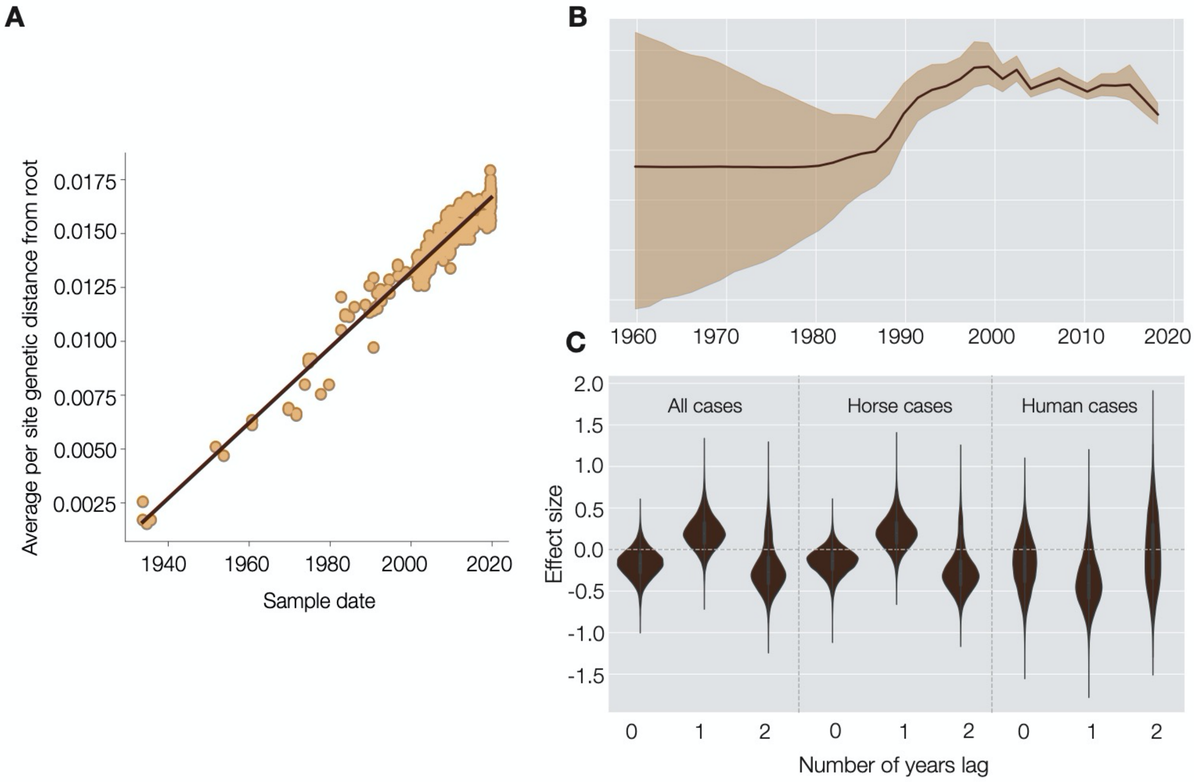


Figure S1 | Virus evolutionary characteristics, related to Figure 2 *A) Regression of EEEV sequence collection dates against genetic distance from the root of the phylogeny. Each dot represents a tip in the phylogeny, and the gradient of the line gives the rate of evolution of 1.74 x 10*$^{-4}$*. The low scatter of the dots around the line indicates a strong temporal signal. B) Change in viral effective population size over time as estimated by a non-parametric skygrid coalescent model. C) Kernel density estimates of the effect size of various case covariates on the historical change in population size of EEEV.*

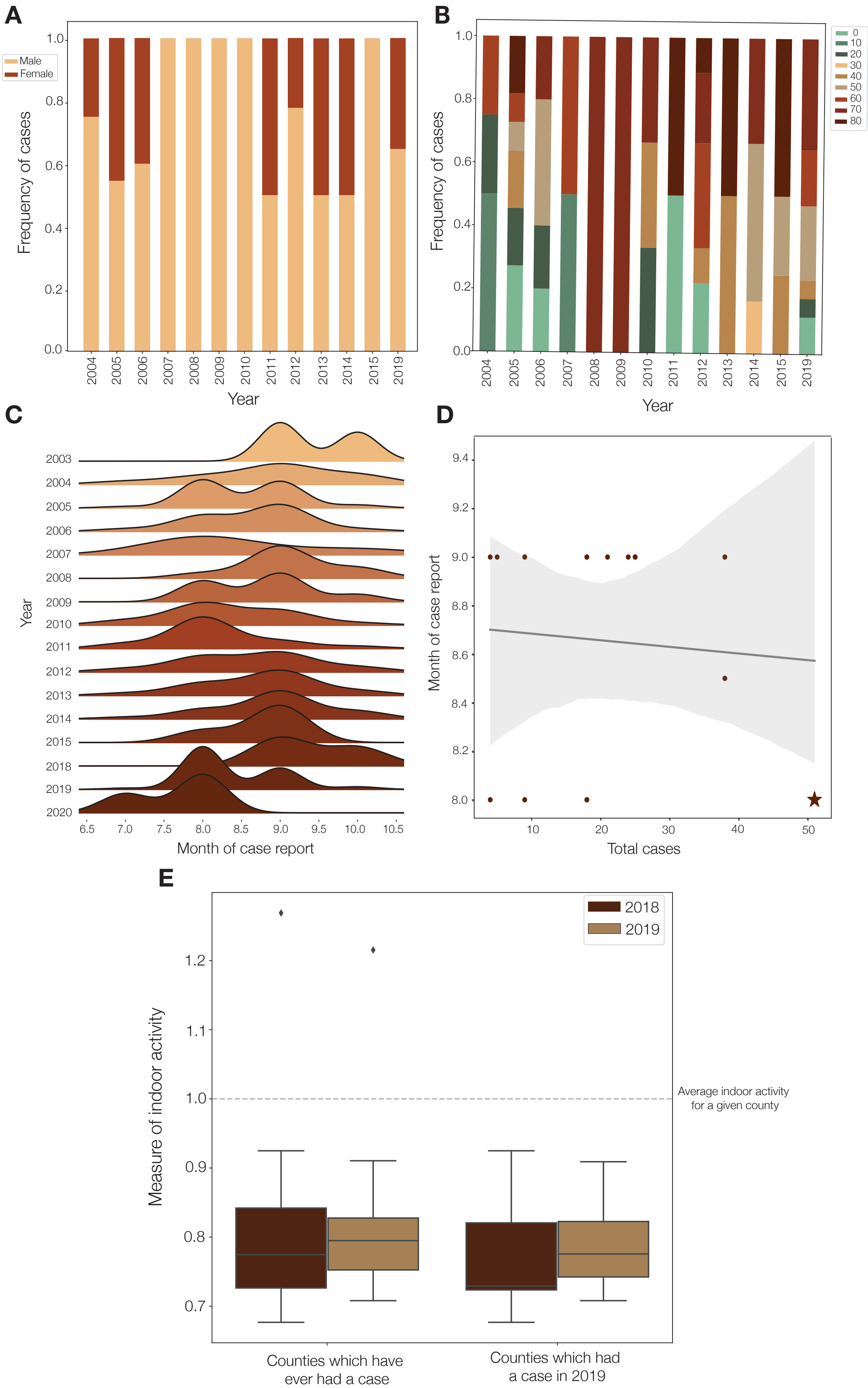

A
Male
Female
Frequency of cases
Year
B
Frequency of cases
Year
0
10
20
30
40
50
60
70
80
C
Year
Month of case report
D
Month of case report
Total cases
E
2018
2019
Measure of indoor activity
Average indoor activity
for a given county
Counties which have
ever had a case
Counties which had
a case in 2019

Figure S2 | Human case characteristics and behavior, related to Figure 1. *A) Frequency of sex of human cases by year. We found 62% of cases were male in 2019, following earlier patterns, and this proportion did not vary across years (Fisher's exact test, p=0.838) B) Frequency of human cases in each age category by year. This did vary across years (p=0.047) but years with large outbreaks (5 or more human cases) did not have significantly different age distributions (Fisher's exact test, p=0.322). C) Kernels of human and horse case counts over time per year. The median month of symptom onset in all years was either August or September, with earliest cases in July and latest in October. D) Regression of total cases against median month of symptom onset of human and horse cases; there is no relationship between the two (Pearson's correlation, p=0.777. E) Measure of indoor activity for counties in Massachusetts, Connecticut, and New York which have ever had a case or only had a case in 2019, colored by year. The dotted line at 1.0 indicates the average indoorness of a county, and values less than 1.0 indicate more indoor activity than average.*

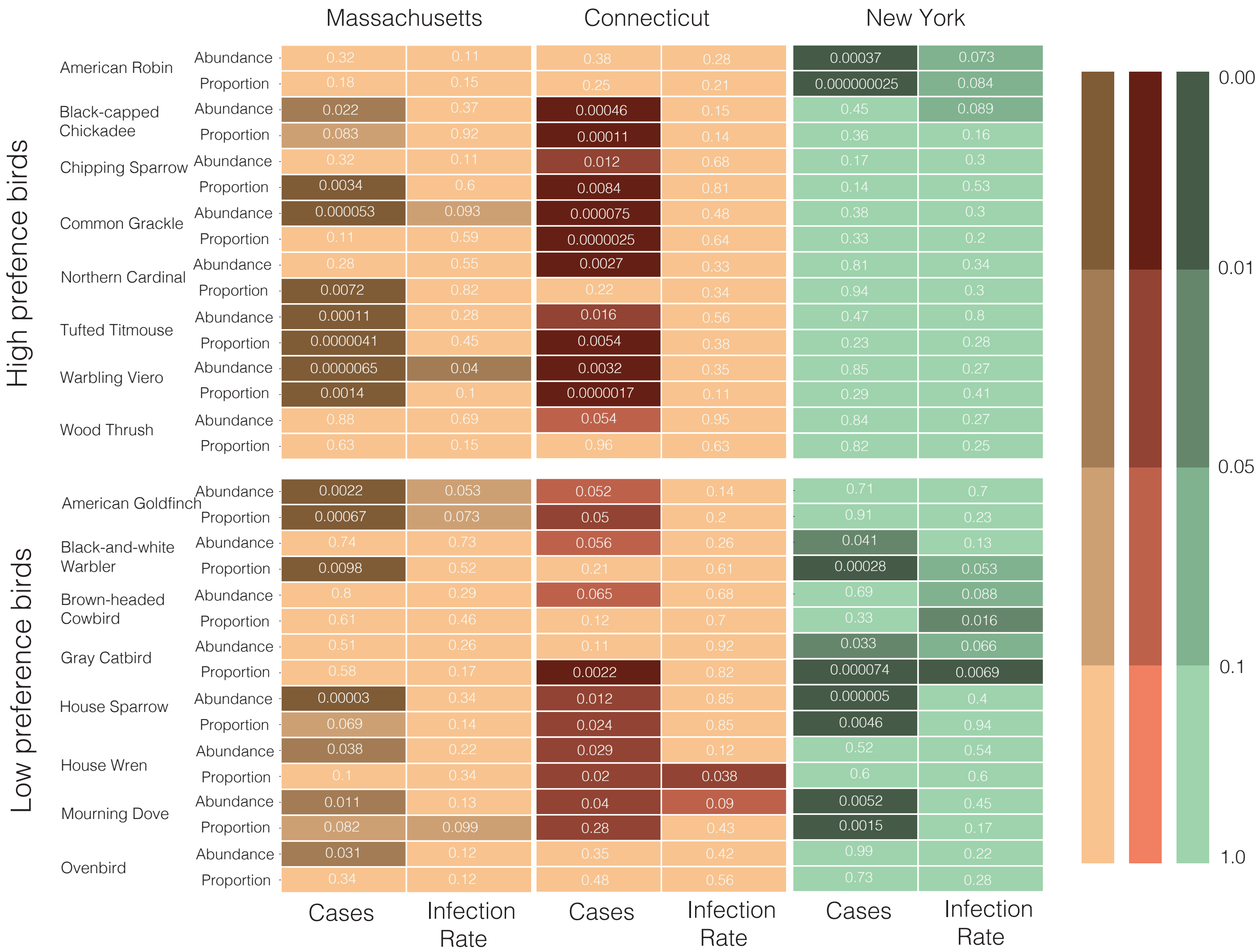
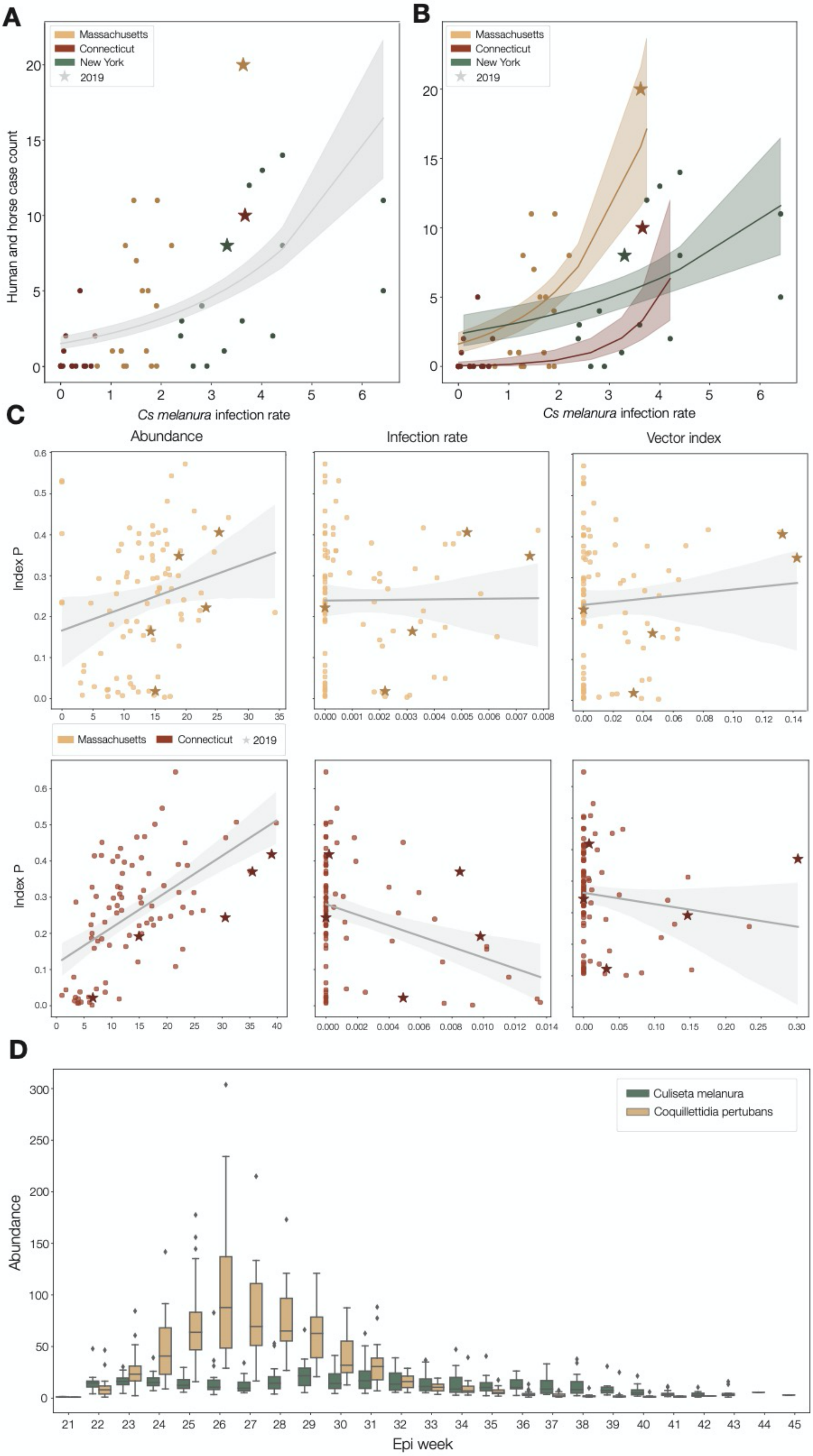
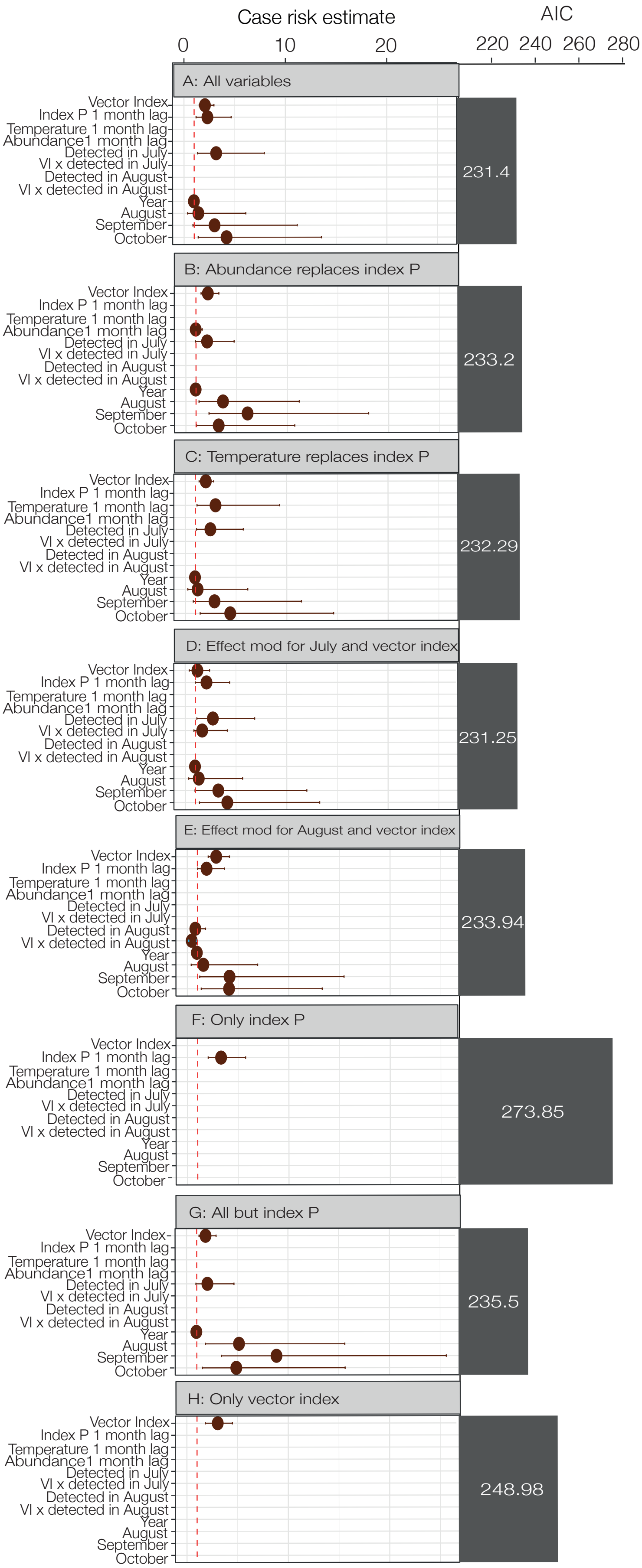


Figure S3 | Bird abundance and proportion in the Northeast, related to Figure 5. *Heatmap showing p-values of Poisson regressions by state of the proportion and abundance of birds for which Cs. melanura has a high or low preference against the human and horse cases or infection rate. Light colors indicate a lower p-value, and boxes are annotated with the p-value. Notable significant relationships for Connecticut and Massachusetts are the common grackle (abundance only; p<0.001 for both states), chipping sparrow (proportion only; p<0.01 for both states), tufted titmouse (proportion only; p<0.01 for both states), and warbling vireo (abundance and proportion; p<0.01 for both states).*



A
B
Massachusetts
Connecticut
New York
2019
Human and horse case count
Cs melanura infection rate
C
Abundance
Infection rate
Vector index
Index P
Massachusetts
Connecticut
2019
D
Culiseta melanura
Coquillettidia pertubans
Abundance
Epi week

Figure S4 | Mosquito infection rate and abundance data compared to index P and case counts, related to Figure 5. *Poisson regression of Cs. melanura infection rate against human and horse case count A) overall and B) by state. In both, data from 2019 are shown as stars. C) Linear regressions of index P against abundance, IR and VI for Connecticut and Massachusetts. Index P and Abundance have the strongest correlation. D) Abundance of Cs. melanura and Cq. perturbans from 2003-2019 across the year from week 21 (approximately mid-May depending on year) to week 45 (approximately the end of October, depending on year). Populations mostly peak in mid-June.*



Case risk estimate
0
10
20
AIC
220
240
260
280
A: All variables
231.4
B: Abundance replaces index P
233.2
C: Temperature replaces index P
232.29
D: Effect mod for July and vector index
231.25
E: Effect mod for August and vector index
233.94
F: Only index P
273.85
G: All but index P
235.5
H: Only vector index
248.98
Vector Index
Index P 1 month lag
Temperature 1 month lag
Abundance1 month lag
Detected in July
VI x detected in July
Detected in August
VI x detected in August
Year
August
September
October

Figure S5 | Results of different negative binomial models to explain cases, related to Figure 5.
Brief description of each model above the relevant panel. Akaike information criteria (AIC) results shown above. The best fitting models here using this criterion is model D or model A, as they have the lowest AIC value. Results can be found in Table S4. Model A is the same as that shown in Figure 5C and its results are in Table S3. State (i.e. risk of being in Massachusetts compared to Connecticut) is not shown for scale.

Prior	Mean	Standard deviation
Bird lifespan	12	2
Bird to Mosquito Transmission Probability	0.5	0.01
Bird Infectious Period	6	1
Bird Incubation Period	1.5	1
Mosquito Lifespan	10	2
Mosquito Extrinsic incubation period	4	1
Mosquito Biting rate	0.14	0.02

Table S2 | Priors for the Mosquito-borne Viral Suitability Estimator adapted from [28] for index P estimates in Figure 5.

Term	Estimate	Std. Error	Conf. Low	Conf. High
Vector Index	2.069	0.16	1.501	2.956
Month Detected	3.17	0.445	1.337	7.924
Year	0.967	0.034	0.906	1.03
August	1.408	0.729	0.342	6.089
September	3.003	0.665	0.871	11.158
October	4.184	0.569	1.39	13.551
Index P 1 month lag	2.312	0.33	1.193	4.654
Massachusetts	11.948	0.623	3.879	43.699

Table S3 | Results from the negative binomial regression model in Figure 5.

Model	Term	Estimate	Std.Error	Conf. Low	Conf. High
B: Abundance replaces index P	Vector Index	2.176	0.179	1.507	3.261
B: Abundance replaces index P	Detected in July	2.094	0.413	0.94	4.763
B: Abundance replaces index P	Year	0.96	0.038	0.892	1.032
B: Abundance replaces index P	August	3.659	0.552	1.292	11.183
B: Abundance replaces index P	September	6.078	0.532	2.277	18.024
B: Abundance replaces index P	October	3.228	0.578	1.041	10.735
B: Abundance replaces index P	Abundance 1 Month Lag	0.972	0.246	0.573	1.621
B: Abundance replaces index P	Massachusetts	14.295	0.626	4.719	52.542
C: Temperature replaces index P	Vector Index	2.025	0.16	1.465	2.908
C: Temperature replaces index P	Detected in July	2.473	0.419	1.103	5.722
C: Temperature replaces index P	Year	0.948	0.035	0.888	1.011
C: Temperature replaces index P	August	1.207	0.814	0.24	6.153
C: Temperature replaces index P	September	2.87	0.694	0.774	11.446
C: Temperature replaces index P	October	4.42	0.574	1.453	14.621
C: Temperature replaces index P	Temperature 1 Month Lag	2.982	0.512	1.156	9.313
C: Temperature replaces index P	Massachusetts	14.612	0.605	4.99	51.143
D: Effect modifier for July and Vector index	Vector Index	1.395	0.316	0.588	2.595
D: Effect modifier for July and Vector index	Detected in July	2.72	0.463	1.142	6.842
D: Effect modifier for July and Vector index	Year	0.95	0.037	0.887	1.016
D: Effect modifier for July and Vector index	August	1.321	0.724	0.325	5.647

D: Effect modifier for July and Vector index	September	3.249	0.657	0.951	11.979
D: Effect modifier for July and Vector index	October	4.133	0.566	1.388	13.246
D: Effect modifier for July and Vector index	Vector index x Detected in July	1.666	0.347	0.849	4.147
D: Effect modifier for July and Vector index	Index P 1 Month Lag	2.29	0.324	1.191	4.574
D: Effect modifier for July and Vector index	Massachusetts	12.203	0.606	4.044	43.403
E: Effect modifier for August and Vector index	Vector Index	2.855	0.159	2.065	4.16
E: Effect modifier for August and Vector index	Detected in August	0.786	0.427	0.331	1.795
E: Effect modifier for August and Vector index	Year	0.932	0.035	0.872	0.994
E: Effect modifier for August and Vector index	August	1.574	0.735	0.376	6.929
E: Effect modifier for August and Vector index	September	4.155	0.663	1.214	15.45
E: Effect modifier for August and Vector index	October	4.106	0.575	1.364	13.298
E: Effect modifier for August and Vector index	Vector index x detected in August	0.428	0.4	0.141	0.892
E: Effect modifier for August and Vector index	Index P 1 Month Lag	1.9	0.304	1.012	3.68
E: Effect modifier for August and Vector index	Massachusetts	18.315	0.571	6.601	62.483
F: Just index P	Index P 1 Month Lag	3.315	0.224	2.046	5.735
F: Just index P	Massachusetts	4.896	0.426	2.141	11.639
G: No index P	Vector Index	2.264	0.164	1.621	3.305
G: No index P	Detected in July	2.05	0.413	0.919	4.672
G: No index P	Year	0.955	0.036	0.893	1.019
G: No index P	August	5.161	0.552	1.848	15.598
G: No index P	September	8.859	0.523	3.421	25.611
G: No index P	October	4.892	0.562	1.637	15.727

G: No index P	Massachusetts	16.038	0.638	5.204	59.747
H: Only Vector index	Vector Index	3.044	0.153	2.114	4.786
H: Only Vector index	Massachusetts	24.063	0.629	7.915	97.748

Table S4 | Results from the additional negative binomial regression model variations. The letter in the Model column relates to the panel in Figure S6, also related to Figure 5.

Name	Source	Sequence
EEEV primer 1 forward	IDT	ATAGGGTACGGTGTAGAGGCAACC
EEEV primer 1 reverse	IDT	TGGTCCGGCATCCCCTTTCTTTAC
EEEV primer 2 forward	IDT	CGTTAACGGAGGGGCACTGAAT
EEEV primer 2 reverse	IDT	GCGTAGATGCCGGTAGATAACAAC
EEEV primer 3 forward	IDT	AAAGCGCACCTCGTCAAGCATTCT
EEEV primer 3 reverse	IDT	GCGGTGAGTCTTATCGGGTTTGTC
EEEV primer 4 forward	IDT	CGAAACGGAATTGCAATGTCACTC
EEEV primer 4 reverse	IDT	CTGATCATAGGCTCGGCTGTCGTA
EEEV primer 5 forward	IDT	CCAAAAGGGGGTTACAGTCAAA
EEEV primer 5 reverse	IDT	TCGGTGTCGCAGAAGCAGTAGG
EEEV primer 6 forward	IDT	CAAAAGTGCCGTCTCCAGTAGTGA
EEEV primer 6 reverse	IDT	GAAATATTAAAAACAAAATAAAAACATAAAA

Table S5 | Primers designed for sequencing EEEV, related to STAR methods

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Table S6 \| Accession numbers for existing genomes used in this analysis, related to STAR Methods