

Table S1. Number of ticks per host bird species.

Tick Species Bird Species	<i>I. ricinus</i>	<i>I. frontalis</i>	<i>I. arboricola</i>	<i>Ixodes spp.</i>	<i>H. concinna</i>	<i>H. punctata</i>	<i>Haemaphysalis spp.</i>	<i>Hyalomma spp.</i>	<i>Rhipicephalu s spp.</i>	Unidentifie d
<i>Acrocephalus arundinaceus</i>	1	0	0	0	0	0	0	0	0	0
<i>Acrocephalus palustris</i>	35	0	0	0	0	0	0	0	0	0
<i>Acrocephalus schoenobaenus</i>	6	0	0	0	0	0	0	0	0	1
<i>Acrocephalus scirpaceus</i>	19	0	0	0	0	0	0	5	0	3
<i>Aegithalos caudatus</i>	1	0	0	0	0	0	0	0	0	2
<i>Anthus trivialis</i>	40	0	0	0	0	0	1	0	0	3
<i>Aquila chrysaetos</i>	0	0	0	0	0	14	0	0	0	1
<i>Aquila fasciata</i>	0	0	0	0	0	0	0	0	2	0
<i>Athene noctua</i>	0	0	1	0	0	0	0	0	0	0
<i>Carduelis cannabina</i>	4	0	0	0	0	0	0	0	0	0
<i>Carduelis chloris</i>	1	0	0	0	0	0	0	0	0	0
<i>Cettia cetti</i>	3	0	0	0	0	0	0	0	0	1
<i>Coccothraustes coccothraustes</i>	28	0	0	0	2	0	1	0	0	2
<i>Cyanistes caeruleus</i>	16	1	1	2	5	0	1	0	0	9
<i>Emberiza cirrus</i>	0	0	0	0	2	0	0	0	0	1
<i>Emberiza schoeniclus</i>	3	0	0	0	0	0	0	0	0	0
<i>Erithacus rubecula</i>	444	4	0	0	0	0	0	0	0	33
<i>Fringilla coelebs</i>	54	1	0	0	0	0	0	0	0	3
<i>Garrulus glandarius</i>	116	3	0	0	0	0	0	0	0	26
<i>Hippolais polyglotta</i>	13	1	0	0	0	0	0	0	0	0
<i>Hirundo rustica</i>	0	0	0	0	0	0	0	0	0	2
<i>Lanius collurio</i>	11	0	0	0	0	0	0	0	0	1
<i>Leiothrix lutea</i>	0	1	0	0	0	0	0	0	0	0
<i>Limosa limosa</i>	0	0	0	0	0	2	0	0	0	0
<i>Lophophanes cristatus</i>	2	0	0	0	0	0	0	0	0	0
<i>Lullula arborea</i>	1	0	0	0	0	0	0	0	0	0
<i>Luscinia megarhynchos</i>	112	0	0	0	1	0	0	0	0	9

Table S2. Number of TBP-positive engorged tick larvae per pathogen and host bird species.

[illegible]

<i>Sylvia communis</i>	1	0	1	0	0	0	0	2	0	0	0	0	0	0	1	0	0
<i>Sylvia curruca</i>	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Sylvia undata</i>	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Troglodytes troglodytes</i>	1	0	0	8	0	0	1	0	0	0	0	0	0	0	2	0	1
<i>Turdus merula</i>	14	0	0	55	0	0	12	0	2	0	0	4	0	0	9	0	1
<i>Turdus philomelos</i>	4	0	0	15	1	3	6	3	2	0	0	0	0	0	3	0	3
<i>Turdus pilaris</i>	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total	63	2	2	100	1	4	20	11	22	3	1	9	5	4	45	10	23

A. pha = *A. phagocytophilum*, *B. afz* = *B. afzelii*, *Bbss* = *Borrelia burgdorferi* sensu stricto, *B. gar* = *B. garinii*, *Bor spp.* = *Borrelia spp.*, *B. tur* = *B. turdi*, *B. val* = *B. valaisiana*, *B. miy* = *B. miyamotoi*, *Bab spp.* = *Babesia spp.*, *B. ven* = *B. venatorum*, *E. can* = *E. canis*, *Ehr spp.* = *Ehrlichia spp.*, *Close to E. chaff* = *Close to E. chaffeensis*, *R. aes* = *R. aeschlimannii*, *R. hel* = *R. helvetica*, *R. slo* = *R. slovaca*, *Rick. spp.* = *Rickettsia spp.*

Table S3. Accession numbers of submitted sequences.

Tick and Tick-Borne Pathogen Species	Accession Number	Percent Identity to GenBank Sequence	Comment
<i>I. ricinus</i>	ON387755	100%	Compared to the sequence KF197132.1 in GenBank that came from a host-seeking female collected in Italy
<i>I. frontalis</i>	ON387754	99.8%	Compared to the sequence KU170492.1 in GenBank that came from a tick collected in Hungary
<i>H. concinna</i>	ON303650	100%	Compared to the sequence KY364906.1 in GenBank that came from a tick collected in China
<i>H. punctata</i>	ON387756	100%	Compared to the sequence NC_062064.1 in GenBank that came from an adult tick collected on cattle in China
<i>B. venatorum</i>	ON171470	99.6%	Compared to the sequence MG344777.1 in GenBank that came from the blood of <i>Capreolus capreolus</i> in Czech Republic
<i>B. afzelii</i>	ON310820)	100%	Compared to the sequence MT007941.1 in GenBank that came from a host-seeking tick collected in Russia
<i>Borrelia burgdorferi sensu stricto</i>	ON310821	100%	Compared to the sequence MF150052.1 in GenBank that came from a host seeking <i>I. ricinus</i> collected in Poland
<i>B. garinii</i>	ON310822	99.5%	Compared to the sequence KU672556.1 in GenBank that came from a host-seeking <i>I. persulcatus</i> collected in Russia
<i>B. turdi</i>	ON310824	98.9%	Compared to the sequence D85071.1 in GenBank
<i>B. valaisiana</i>	ON310823	99.3%	Compared to the sequence MF150077.1 in GenBank that came from a host-seeking <i>I. ricinus</i> collected in Poland
<i>B. miyamotoi</i>	ON398526	100%	Compared to the sequence LC540659.1 in GenBank that came from an <i>I. ricinus</i> collected in Russia
<i>E. canis</i>	-	100%	Compared to the sequence MT066094.1 in GenBank that came from a <i>Rhipicephalus sanguineus</i> collected on a <i>Canis lupus familiaris</i> in Egypt
Close to <i>E. chaffeensis</i>	ON390894	99.2%	Compared to the sequence NR_074500.2 in GenBank
<i>R. aeschlimannii</i>	ON310825	100%	Compared to the sequence KU961544.1 in GenBank that came from a host-seeking <i>H. marginatum</i>

Note: *E. canis* sequence was too small to be submitted on GenBank. Here is the sequence:

CCACCTACGTGCCCTTTACGCCCAATAATTCCGAACAACGCTTGCCCCCTCCGTATTACCGCGGCTGCTGGCACAGAGTT
TGCCGGGACTTCTTCTATAGGTACCGTCATTATCTTCCCT

Table S4. Percentage of co-infected larvae (calculated on the total of engorged larvae, n = 1,106).

Pathogen Species	Percentage of Infected Larvae (n)
<i>Anaplasma</i> spp. + <i>Bbsl</i>	1% (11)
<i>A. phagocytophilum</i> + <i>B. garinii</i>	0.7% (8)
<i>A. phagocytophilum</i> + <i>B. valaisiana</i>	0.3% (3)
<i>Rickettsia</i> spp. + <i>Bbsl</i>	0.9% (10)
<i>B. garinii</i> + <i>R. helvetica</i>	0.5% (6)
<i>B. garinii</i> + <i>R. slovaca</i>	0.1% (1)
<i>B. valaisiana</i> + <i>R. helvetica</i>	0.1% (1)
<i>B. garinii</i> + <i>Rickettsia</i> spp.	0.1% (1)
<i>B. turdi</i> + <i>Rickettsia</i> spp.	0.1% (1)
<i>Anaplasma</i> spp. + <i>Rickettsia</i> spp.	0.4% (4)
<i>A. phagocytophilum</i> + <i>R. helvetica</i>	0.3% (3)
<i>A. phagocytophilum</i> + <i>R. aeschlimannii</i>	0.1% (1)
<i>Babesia</i> spp. + <i>Rickettsia</i> spp.	0.3% (3)
<i>B. venatorum</i> + <i>Rickettsia</i> spp.	0.1% (1)
<i>Babesia</i> spp. + <i>R. aeschlimannii</i>	0.1% (1)
<i>Babesia</i> spp. + <i>Rickettsia</i> spp.	0.1% (1)
<i>B. miyamotoi</i> + <i>Bbsl</i>	0.2% (2)
<i>B. miyamotoi</i> + <i>B. garinii</i>	0.2% (2)
<i>Anaplasma</i> spp. + <i>Ehrlichia</i> spp.	0.1% (1)
<i>A. phagocytophilum</i> + <i>Ehrlichia</i> spp.	0.1% (1)
<i>Babesia</i> spp. + <i>Bbsl</i>	0.1% (1)
<i>Babesia</i> spp. + <i>B. garinii</i>	0.1% (1)
<i>Anaplasma</i> spp. + <i>Babesia</i> spp. + <i>Rickettsia</i> spp	0.2% (2)
<i>A. phagocytophilum</i> + <i>Babesia</i> spp. + <i>Rickettsia</i> spp.	0.1% (1)
<i>A. phagocytophilum</i> + <i>Babesia</i> spp. + <i>R. aeschlimannii</i>	0.1% (1)
<i>Anaplasma</i> spp.+ <i>Ehrlichia</i> spp. + <i>Bbsl</i>	0.1% (1)
<i>A. phagocytophilum</i> + <i>B. valaisiana</i> + <i>Ehrlichia</i> spp.	0.1% (1)
<i>Anaplasma</i> spp.+ <i>Rickettsia</i> spp. + <i>Bbsl</i>	0.1% (1)
<i>A. phagocytophilum</i> + <i>B. garinii</i> + <i>R. helvetica</i>	0.1% (1)

<i>Babesia</i> spp. + <i>Ehrlichia</i> spp. + <i>Bbsl</i>	0.1% (1)
<i>Babesia</i> spp. + <i>B. garinii</i> + <i>Ehrlichia</i> spp.	0.1% (1)
<i>Anaplasma</i> spp. + <i>B. miyamotoi</i> + <i>Bbsl</i>	0.1% (1)
<i>A. phagocytophilum</i> + <i>B. valaisiana</i> + <i>B. miyamotoi</i>	0.1% (1)
<hr/>	
<i>Bbsl</i> : <i>Borrelia burgdorferi</i> sensu lato	

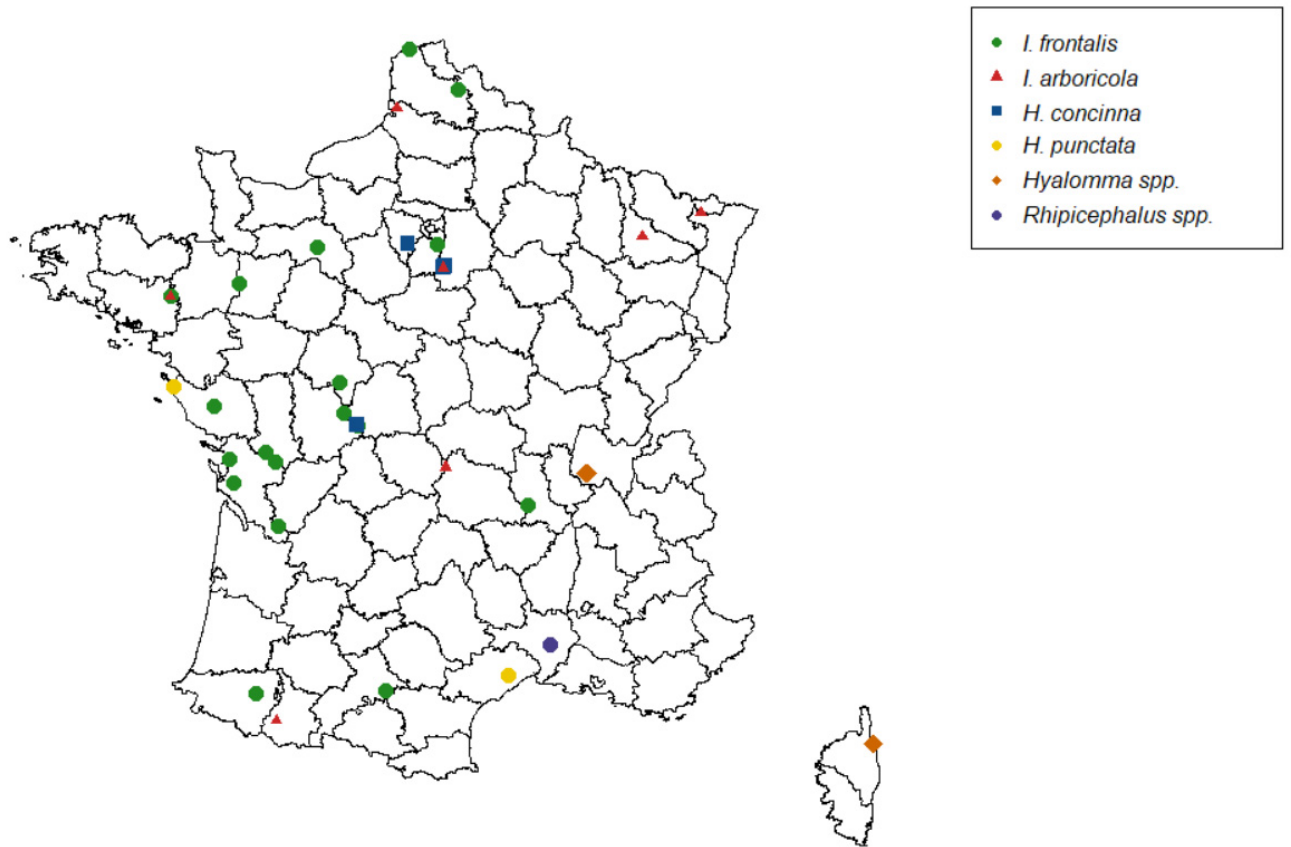


Figure S1. Geographical distribution of tick species other than *I. ricinus* (*I. frontalis*, *I. arboricola*, *H. concinna*, *H. punctata*, *Hyalomma* spp. and *Rhipicephalus* spp.) collected from breeding birds in 2019 and 2020. Green dots and red triangle represent the sites where *I. frontalis* and *I. arboricola* were collected respectively. Blue squares and yellow dots represent the sites where *H. concinna* and *H. punctata* ticks were collected respectively. Orange diamond represent the sites where *Hyalomma* spp. ticks were collected and purple dots represent the sites where *Rhipicephalus* spp. ticks were collected.

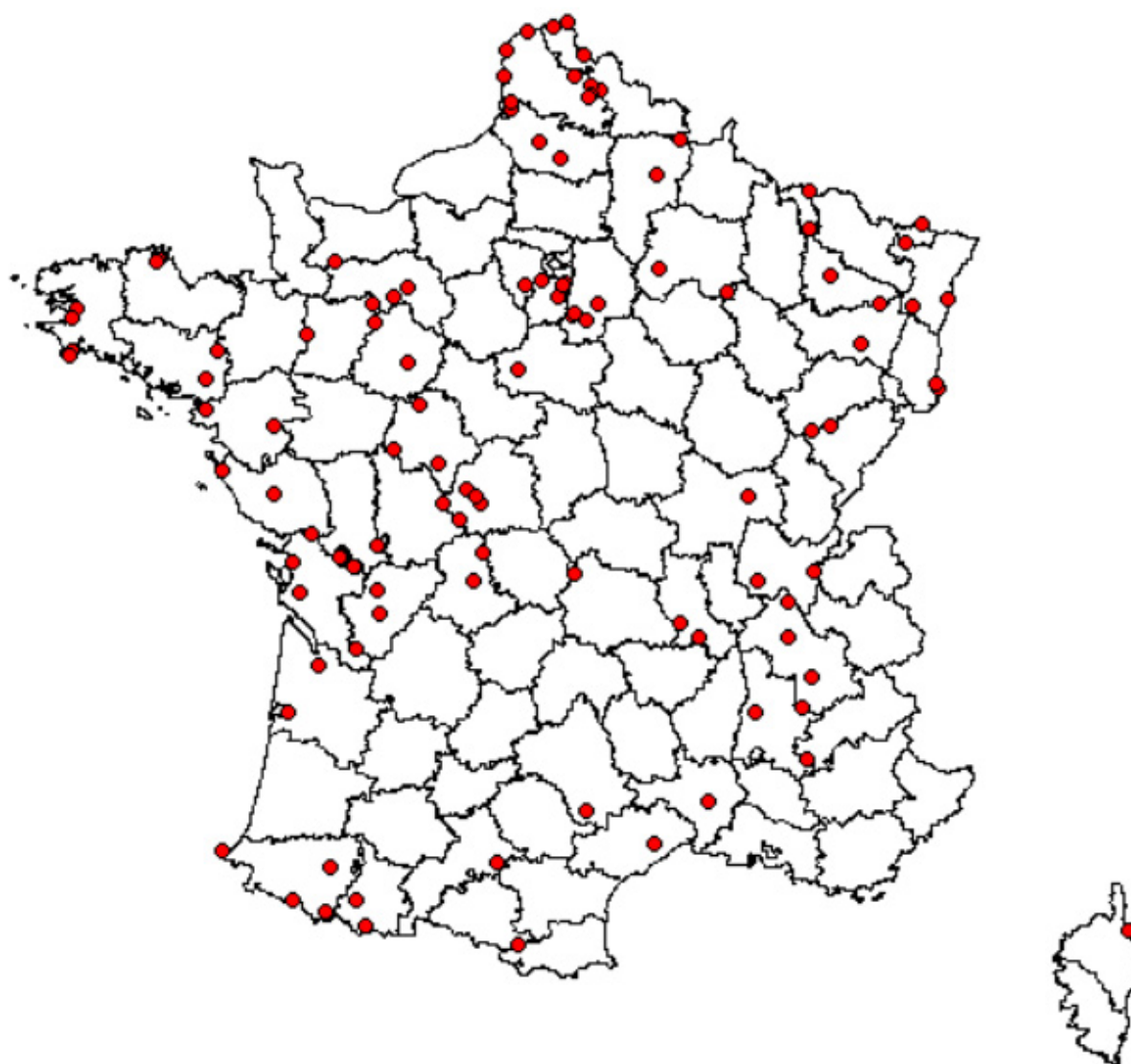


Figure S2. Capture sites for breeding birds in France in 2019-2020.