



HAL
open science

Strong genetic structure among populations of the tick *Ixodes ricinus* across its range

Pedro Poli, Jonathan Roger Michel Henri Lenoir, Olivier Plantard, Steffen Ehrmann, Knut Røed, Hans Petter Leinaas, Marcus Panning, Annie Guiller

► **To cite this version:**

Pedro Poli, Jonathan Roger Michel Henri Lenoir, Olivier Plantard, Steffen Ehrmann, Knut Røed, et al.. Strong genetic structure among populations of the tick *Ixodes ricinus* across its range. *Ticks and Tick-borne Diseases*, 2020, 11 (6), pp.101509. 10.1016/j.ttbdis.2020.101509 . hal-02917046

HAL Id: hal-02917046

<https://hal.inrae.fr/hal-02917046v1>

Submitted on 10 Nov 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

1 **Strong genetic structure among populations of the tick *Ixodes ricinus* across its**
2 **range**

3 Pedro Poli¹, Jonathan Lenoir¹, Olivier Plantard², Steffen Ehrmann³, Knut H. Røed⁴,
4 Hans Petter Leinaas⁵, Marcus Panning⁶, Annie Guiller¹

5 ¹Université de Picardie Jules Verne, UMR « Ecologie et Dynamique des Systèmes
6 Anthropisés » (EDYSAN, UMR 7058 CNRS), 33 Rue Saint Leu, 80000 Amiens CEDEX
7 1, France

8 ²BIOEPAR, INRAE, Oniris, 44307, Nantes, France

9 ³German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig,
10 Deutscher Platz 5e, 04103 Leipzig, Germany

11 ⁴Department of Basic Sciences and Aquatic Medicine, Norwegian University of Life
12 Sciences, N-0033, Oslo, Norway (knut.roed@nmbu.no)

13 ⁵Department of Biosciences, University of Oslo, Box 1066 Blindern, N-0316 Oslo,
14 Norway (h.p.leinaas@ibv.uio.no)

15 ⁶Institute of Virology, Medical Center - University of Freiburg, Faculty of Medicine,
16 University of Freiburg, Hermann-Herder-Str, 11 79104, Freiburg, Germany

17 **Corresponding author:** Pedro Poli, UMR « Ecologie et Dynamique des Systèmes
18 Anthropisés » (EDYSAN, UMR 7058 CNRS-UPJV), Université de Picardie Jules Verne,
19 33 Rue Saint Leu, 80000 Amiens CEDEX 1, France, pvpoli@gmail.com

20 **Abstract:** *Ixodes ricinus* is the most common and widely distributed tick species in
21 Europe, responsible for several zoonotic diseases, including Lyme borreliosis.
22 Population genetics of disease vectors is a useful tool for understanding the spread
23 of pathogens and infection risks. Despite the threat to the public health due to the
24 climate-driven distribution changes of *I. ricinus*, the genetic structure of tick
25 populations, though essential for understanding epidemiology, remains unclear.
26 Previous studies have demonstrated weak to no apparent spatial pattern of genetic
27 differentiation between European populations. Here, we analysed the population
28 genetic structure of 497 individuals from 28 tick populations sampled from 20
29 countries across Europe, the Middle-East, and northern Africa. We analysed 125
30 SNPs loci after quality control. We ran Bayesian and multivariate hierarchical
31 clustering analyses to identify and describe clusters of genetically related
32 individuals. Both clustering methods support the identification of three spatially-
33 structured clusters. Individuals from the south and north-western parts of Eurasia
34 form a separated cluster from northern European populations, while central
35 European populations are a mix between the two groups. Our findings have
36 important implications for understanding the dispersal processes that shape the
37 spread of zoonotic diseases under anthropogenic global changes.

38 **Keywords:** gene flow; infection risks; range shift

39 **Introduction**

40 *Ixodes ricinus* (Acari, Ixodidae) is the most widespread tick species occurring across
41 Europe and an important vector of multiple tick-borne diseases, both to humans
42 and livestock. Commonly reported pathogens transmitted by *I. ricinus* include: the
43 bacteria *Borrelia burgdorferi* sensu lato, responsible for the Lyme borreliosis, which
44 is the most prevalent tick-borne disease in temperate Europe (ECDC, 2015);
45 arboviruses (genus *Flavivirus*) causing tick-borne encephalitis (TBE) and louping-ill
46 (LI); the protozoan *Babesia microti*, responsible for the babesiosis; and the
47 bacterium *Candidatus Neoehrlichia mikurensis*, responsible for neoehrlichiosis, an
48 emerging tick-borne pathogen (Portillo et al., 2018; Welinder-Olsson et al., 2010).
49 The current climate-driven redistribution of hematophagous arthropods such as
50 ticks and mosquitoes may lead to severe challenges to public health and husbandry,
51 by carrying a wide range of vector-borne diseases to new areas (Dantas-Torres,
52 2015; Pecl et al., 2017). For instance, many studies have demonstrated that the
53 range of *I. ricinus* is already shifting northward and to higher elevations (e.g.
54 Hvidsten et al., 2020; Jore et al., 2011; Lindgren and Gustafson, 2001) and those
55 shifts are expected to continue in the future (Alkishe et al., 2017; Medlock et al.,
56 2013).

57 Despite the threats of emerging infectious diseases following the
58 redistribution of *I. ricinus*, little is known about the genetic structure of tick
59 populations across the entire species range. Population genetic differentiation and
60 spatial structuring can, however, impact the vector fitness and distribution, and
61 therefore disease transmission (Blanchong et al., 2016; Wonham et al., 2006).

62 Population genetics approaches such as individual genetic clustering and
63 assignment methods enable inference on migrants (exchange of genes between
64 populations) and the risk of pathogen spread between populations (Kozakiewicz et
65 al., 2018). For example, Lang and Blanchong (2012) applied clustering and distance-
66 based methods to assess gene flow and disease spread risk between populations
67 of white-tailed deer in the USA. Similarly, Van Zee et al. (2015) identified different
68 genetic clusters between the southern and northern range of the tick *Ixodes*
69 *scapularis* while the prevalence of borreliosis is known to be lower in the southern
70 range. The authors suggest that this pattern of spatial genetic structure might be
71 linked to differences in questing behaviour as ticks from the northern range would
72 be more likely to bite humans. Differences in several life history traits of *I. ricinus* –
73 such as the temperature at which nymphs begin to quest – have been reported
74 along a latitudinal gradient (Gilbert et al., 2014), suggesting a spatially explicit
75 phenotypic plasticity or adaptation. Yet, such basic knowledge about the
76 distribution of genetic variation in *I. ricinus* and the migration processes involved in
77 disease transmission remain largely unknown, albeit being essential to design
78 better vector control strategies (Araya-Anchetta et al., 2015; Gooding, 1996;
79 Tabachnick and Black, 1995).

80 The genetic structure of parasites' populations is known to be influenced
81 by the distribution of the hosts (Kempf et al., 2009; Wessels et al., 2019). In general,
82 it is assumed that generalist parasites relying on a wide range of hosts tend to show
83 weak or no genetic structure, as shown in many studies on various parasite species
84 (e.g. Archie and Ezenwa, 2011; Wessels et al., 2019). The tick species *I. ricinus* is a

85 generalist ectoparasite infesting a wide range of hosts, such as reptiles, mammals,
86 and birds (Casati et al., 2008; Norte et al., 2012). It has been proposed that tick
87 abundance and population genetic structure are dependent on the species' biology
88 (such as reproduction strategies and life cycle), but also on the host distribution
89 and behaviour (Kempf et al., 2011; McCoy et al., 2001; Rizzoli et al., 2009; Norte et
90 al., 2012). Large ungulates, such as deer, bovidae, and wild boar may be highly
91 efficient carriers of ticks for long distances, as long as there are no severe barriers
92 to their migration (Handeland et al., 2013; Kriz et al., 2014). By contrast,
93 transportation of ticks by migrating birds seems to be less efficient across
94 contiguous landmasses (Hasle et al., 2009; Røed et al., 2016). Based on these
95 findings, it is expected that *I. ricinus* populations should show a weak spatial genetic
96 structure.

97 Regarding previous works on population structure and dispersal of *I.*
98 *ricinus*, Nouredine et al. (2011) found a clear differentiation between European
99 and African populations using sequences from three nuclear and three
100 mitochondrial markers. Regarding the results from that study, it was later
101 suggested by Estrada-Peña et al. (2014) that those northern African samples could
102 correspond to *Ixodes inopinatus*, a sibling species of the *I. ricinus* complex within
103 the *Ixodes* subgenus. Considering only European populations, some studies showed
104 weak to no differentiation, but an extensive genetic diversity was observed within
105 each local population (Casati et al., 2008; Nouredine et al., 2011; Porreta et al.,
106 2013; Carpi, 2016). Other investigations analysing the frequency of mitochondrial
107 haplotypes showed a marked phylogeographical structure in northern Europe,

108 notably when considering populations from the north of the UK (Scotland) and
109 Scandinavia (Al Khafaji et al., 2019; Dinnis et al., 2014; Røed et al., 2016). Although
110 none of the mitochondrial haplotypes was exclusive to any of those populations,
111 their frequencies varied significantly between populations from different regions.
112 Interestingly, the British clade identified by Røed et al. (2016) coincides with the
113 occurrence of a particular subtype of the louping-ill virus, which is closely related
114 to other Irish and Spanish subtypes. Other studies focusing on the genetic structure
115 of *I. ricinus* populations were based on microsatellite loci (Kempf et al., 2009;
116 Kempf et al., 2011). Microsatellite variations have led to the identification of
117 significant levels of genetic structure at different spatial scales, deviation from
118 panmixia in *I. ricinus* populations likely due to assortative mating and patterns of
119 host use (see Araya-Anchetta et al., 2015 for a review). However, those studies have
120 also assessed patterns of genetic variation from localised samples that cover only a
121 subset of the species range and thus likely do not capture the entire species genetic
122 structure at the continental level.

123 Here, we aim to elucidate the population genetic structure of the tick *I.*
124 *ricinus* based on single nucleotide polymorphisms (SNPs). To the best of our
125 knowledge, no other study on the population genetic structure of *I.*
126 *ricinus* throughout the Eurasian continent was based on the variation detected by
127 this type of marker. Although generally having a weaker mutation rate than
128 microsatellites, SNPs offers the possibility of building a larger range of markers and
129 have been suggested to be more reliable markers for population genetic studies
130 (Helyar et al., 2011; Smouse, 2010). Our main objective is to describe the genetic

131 structure of *I. ricinus* populations to infer the geographical and environmental
132 factors shaping this structure. Particularly we hypothesized that (i) *I. ricinus* from
133 the western parts of Europe might have genetic similarities to the Great Britain
134 lineage (Røed et al., 2016) while (ii) there should be a pronounced genetic
135 differentiation between ticks south and north of the extensive mountain areas
136 covering central Europe (i.e., the Eastern Alps, the Western Alps, the Carpathian
137 Mountains, and the Balkan Mountains).

138

139 **Materials and Methods**

140 *Sampling*

141 A total of 28 tick populations from 20 countries were sampled covering most of the
142 species' range, including populations close to the northern (Norwegian, Sweden,
143 Ireland, and England) and southern (Iran, Spain, and northern Africa) range limit
144 of *I. ricinus* (Figure 1). Samples were collected by flagging inside or near forest
145 fragments from the ground vegetation and were preserved in alcohol. A significant
146 subset of the sampled populations we used, covering 8 regions across Europe
147 (southern and northern France; Belgium; western and eastern German; southern
148 and central Sweden; and northern Estonia), originated from a single project
149 (smallFOREST, BiodivERsA 2010-2011 Joint
150 call: <https://www.biodiversa.org/491/download>) and was sampled by the same
151 person during the same year 2013 (See Ehrmann et al., 2018 for details). The
152 remaining samples were collected for different projects (for details on those

153 projects see Røed et al., 2016 for the Norwegian samples and Nouredine et al.,
154 2011 for the remaining samples). The coordinates of the sampled populations are
155 provided in Table S1 (see Supporting Information). Aside from smallFOREST
156 samples, sampling dates varied among the sampled populations (Table S1).

157 Ticks sampled for those projects were identified at the laboratory using
158 standard morphological keys provided in Babos (1964), Hillyard (1996), or Perez-
159 Eid (2007). As most samples we used were identified before the description of *I.*
160 *inopinatus* (Estrada-Peña et al., 2014) and considering that it was impossible to re-
161 evaluate the identification of samples based on morphological features, we
162 conducted an *a posteriori* evaluation of the potential presence of *I.*
163 *inopinatus* among our samples. To fulfil this aim, northern African *I.*
164 *inopinatus* samples analysed by Nouredine et al. (2011) were included in the
165 present study.

166 *DNA extraction and SNP genotyping*

167 Since ticks and DNA samples analysed in this study had different origins and
168 therefore different storage methods, three different methods were used to ensure
169 DNA extraction. Ticks were either: (i) frozen and crushed with a pestle in individual
170 tubes before extracting DNA using DNeasy™ Tissue Kit (Qiagen); (ii) disrupted
171 using a Tissue Lyser (Qiagen) before DNA extraction using the Wizard Genomics
172 DNA Purification Kit (Promega, USA); or (iii) crushed with Lysing matrix H (MP
173 Biomedicals, Santa Ana, USA) before extracting DNA with MagNA Pure LC Total
174 Nucleic Acid Isolation Kit (Roche, Basel, Switzerland).

175 We genotyped 192 SNPs as described by Quillery et al. (2014). The list of
176 SNPs, variant basis, and primers are presented in Table S2. All samples were
177 amplified by whole genome amplification (WGA) before genotyping. The PEP-PCR
178 WGA kit (LGC-Biosearch Technologies) was used for whole genome amplification of
179 each sample. The WGA protocol associated with KASP genotyping has already been
180 tested by Quillery et al. (2014) and showed a reduced number of "no-call" data
181 (missing values) during genotyping. The WGA and genotyping steps were
182 subcontracted by the GENTYANE platform (INRA, Clermont-Ferrand, France:
183 <http://gentyane.clermont.inra.fr/>). The GENTYANE platform is an INRAE (French
184 National Research Institute for Agriculture, Food and Environment) research facility
185 located in Clermont-Ferrand (France) which offers sequencing and genotyping
186 services. Genotyping was conducted in a Biomark HD System (Fluidigm) and KASPar
187 assays. The KASPar method is a KBiosciences competitive allele-specific PCR
188 amplification. A PCR mix containing two allele-specific forward primers and one
189 common reverse primer was carried out. Each forward primer had a 5' tail sequence
190 homologous to universal secondary oligos labelled with a fluorophore (FAM or
191 HEX). If a particular locus is homozygous, only one fluorescent signal is generated.
192 Bi-allelic loci generate both fluorescent signals.

193 *Quality control*

194 Data was filtered after genotyping and before statistical analysis. First, all invariant
195 SNPs were removed. After this first filtering step, all individuals with more than 20%
196 of non-amplified sites (missing data) were removed. Finally, all remaining SNPs with
197 more than 20% missing data were also removed. The remaining dataset consisted

198 of both individuals and SNPs with less than 20% missing data. After quality control
199 steps, 125 SNP loci and 497 individuals were kept for further analyses.

200 *Cluster analysis and genetic structure*

201 Two complementary clustering methods were used to access the genetic structure
202 of *I. ricinus* populations. First, we investigated the genetic clustering by performing
203 a discriminant analysis of principal components (DAPC, Jombart et al., 2010) with
204 the package 'adegenet' (Jombart, 2008) in R (R Core Team, 2019). The
205 optimal k number of clusters was identified by the k -means algorithm using
206 the *find.cluster()* function based on BIC values. A maximum of 28 clusters was
207 allowed, i.e. the total number of sampled populations. Next we performed a
208 Bayesian analysis in STRUCTURE (Pritchard et al., 2000) with the parameter K , i.e.
209 the optimal number of clusters, varying from 1 to 10, according to the results from
210 the DAPC. We used a non-admixture model with the sampling locations as prior.
211 Twenty repetitions of 80,000 MCMC iterations with a burning length of 20,000
212 iterations were run for each value of K . The results were analysed with Structure
213 Harvester (Earl and vonHoldt, 2012). The best K value for the optimal number of
214 clusters was identified by comparing the estimates of log probabilities of the data
215 (i.e. $\ln[\Pr(X|K)]$) for each K value as well as Evanno's delta K method (Evanno et al.,
216 2005). Pritchard et al. (2007) suggested aiming for the smallest value of K that
217 captures most of the genetic structure in the data. Assigning probabilities for
218 individuals and populations across repetitions were then averaged in CLUMPP
219 (Jakobsson and Rosenberg, 2007). We applied a hierarchical clustering analysis (e.g.
220 Vähä et al., 2007) in each identified cluster to detect more refined patterns of

221 genetic structure. Hierarchical analysis in STRUCTURE was realised with ten
222 repetitions and the same other parameters as the first round of analysis. We
223 realised a similar analysis for each cluster identified by DAPC.

224 To test our data for isolation by distance (IBD), pairwise F_{ST} values were
225 estimated with the package 'hierfstat' (Goudet and Jombart, 2018) in R (R Core
226 Team, 2019) as Weir and Cockerham unbiased parameter θ (Weir and Cockerham,
227 1984). The IBD pattern was first tested across all pairs of Eurasian samples and
228 second only between pairs of samples collected during the same year to avoid
229 potential biases due to temporal variability in dispersal and genetic structure. Those
230 corresponded to samples from southern and northern France, Belgium, western
231 and eastern German, northern Estonia, southern and central Sweden, a total of 8
232 samples (28 pairs). Since the 25 Eurasian samples are distributed across a large
233 continental extent, pairwise geographical distances were calculated with the
234 'geosphere' package (Hijmans, 2017) in R (R Core Team, 2019) to account for the
235 curvature of the Earth. The strength of the IDB was evaluated as the relationship
236 between $\theta/(1 - \theta)$ and the natural logarithm of the geographic distance as
237 described by Rousset (1997). In a two dimensions population, the slope parameter
238 b of the linear regression $\theta/(1 - \theta) = a + bD_{Geo}$ is inversely proportional to the
239 average neighbourhood size $Nb = 1/b$, and $b = 1/(4D_e\pi\sigma^2)$, where D_e is the sub-
240 population density and σ^2 is the averaged square axial distances between adults
241 and their parents and σ is half the average adult-parent distance (Séré et al., 2017).
242 In this case, a proxy of dispersal can be calculated as $\delta \approx 2 * \sqrt{(4\pi Deb)}$
243 (Manangwa, 2018). The population density was calculated as $D_e = N_e/S\pi$, where

244 S is the smallest distance between sites considered and included in the IBD analysis.
245 We used NeEstimator version 2.1 to calculate effective population sizes (N_e) by
246 applying two different methods, one based on linkage disequilibrium and another
247 based on molecular co-ancestry (Do et al, 2014). We calculated the mean of N_e
248 estimated with these two methods after the exclusion of 'infinity' results. The
249 obtained mean value was weighted by the number of times one of the two methods
250 generated a non-infinity value. The significance of the IBD pattern was assessed by
251 Mantel tests as implemented in the 'vegan' package (Oksanen et al., 2019) in R (R
252 Core Team, 2019).

253 *Genetic diversity*

254 For each locus, we estimated the observed heterozygosity (H_o), the gene diversity
255 (H_s), and Wright's fixation indices F_{IS} , F_{ST} , and F_{IT} . Wright's statistics measure
256 inbreeding in three levels of population structure: F_{IS} is the inbreeding coefficient
257 of individuals relative to subpopulations; F_{ST} is the inbreeding coefficient of
258 subpopulations relative to populations; and F_{IT} is a measure of the inbreeding of
259 individuals relative to populations. All metrics were calculated with the package
260 'hierfstat' (Goudet and Jombart, 2018) in R (R Core Team, 2019). A Monte-Carlo
261 permutation test (999 replicates) was conducted to test for the significance of the
262 differences of mean gene diversity and F_{IS} values over loci between pairs of genetic
263 clusters identified. For each replicate, individuals were randomly assigned to one
264 genetic cluster and the simulated statistics were calculated. We ran
265 the *randtest()* function from the 'ade4' package (Dray and Dufour, 2007) to access
266 the significance of the observed differences.

267 To investigate null alleles and possible Wahlund effect on genotype
268 frequencies, we followed the procedure proposed by De Meeûs (2018). According
269 to that study, the presence of null alleles could be identified by a suit of
270 comparisons of F_{IS} , F_{ST} , and the number of missing data. In case of null alleles, we
271 would observe: (i) a high positive correlation between F_{IS} and F_{ST} ; (ii) high variation
272 of both F_{IS} and F_{ST} across loci; (iii) F_{IS} standard errors (StrdErrFIS) much bigger than
273 F_{ST} standard errors (StrdErrFst); and (iv) F_{IS} values mainly explained by the presence
274 of missing data. For the Wahlund effect, the correlation between F_{IS} and F_{ST} should
275 approximate zero, a small variation of F_{ST} and a moderate variation of F_{IS} should be
276 observed across loci, F_{IS} standard errors (StrdErrFIS) should be higher than F_{ST}
277 standard errors (StrdErrFst) and no or rare missing data should be obtained. To test
278 those relations, values of F_{IS} , F_{ST} , StrdErrFst, and StrdErrFIS were calculated in the
279 FSTAT software version 2.9.4 (Goudet, 2003), the latter values calculated by
280 Jackknife. The Spearman's rank correlation test was applied to test for correlations.
281 Finally, De Meeûs (2018) suggested a linear regression between F_{IS} and missing data
282 to quantify, using the R^2 value, the contribution of missing data in F_{IS} values.
283 Because the Wahlund effect can produce between-locus dependencies, we also
284 tested linkage disequilibrium for each pair of loci by using G-based tests
285 implemented in FSTAT 2.9.4. Since p -values from each test are not independent,
286 we applied the procedure described by Benjamini and Yekutieli (2001) to calculate
287 the false discovery rate (FDR) and correct p -values.

288

289 **Results**

290 *Clustering analysis, genetic differentiation and isolation by distance*

291 The DAPC analysis identified two possibilities for the number of clusters, one
292 suggesting three different genetic clusters and the other suggesting four genetic
293 clusters (the BIC difference is 0.842 between $K = 3$ and $K = 4$, Figure S1). Choosing K
294 = 4 clusters created two overlapping groups, while $K = 3$ grouped individuals into 3
295 well-separated clusters (Figure 2). Hence, we decided to set the number of clusters
296 to $K = 3$ with the DAPC approach. Bayesian analysis performed with STRUCTURE
297 also identified a $K = 3$ differentiated genetic clusters (Figure 2b and Figure S2)
298 whose compositions are very similar to the three clusters retained with the DAPC
299 approach. In both analyses, northern African (yellow colour in Figures 2 and 3) and
300 Eurasian populations (the other colours) were highly differentiated. Two main
301 groups were identified within Eurasia, one corresponding mainly to northern and
302 continental middle European populations (grey colour in Figures 2 and 3), the other
303 corresponding mainly to southern and western populations in Eurasia (blue colour
304 in Figures 2 and 3). The DAPC approach separated northern African populations
305 from Eurasian ones along the first axis, while Eurasian clusters were mostly
306 separated along the second axis (Figure 2a). Regarding clustering analyses with
307 STRUCTURE, individual probabilities of different K values ranging from 2 to 10,
308 excepted for $K = 3$ which is already depicted in Figure 2b, are presented in the
309 Supporting Information (see Figure S3).

310 Finer genetic structure was identified from our hierarchical analyses
311 (Figures S4 and S5). These analyses, either carried out with DAPC (Figure S4) or the
312 STRUCTURE approach (Figure S5), were able to isolate Iran and/or Turkey from the
313 other sampled sites within the southern Eurasian cluster. Atlantic sites (Spain,
314 southern and western France, Ireland, and England) were further isolated from the
315 remaining sites in this group (Italy, Romania, Hungary, and Slovakia). The northern
316 European sites showed a more admixture structure, and separation in further
317 clusters varied between the DAPC and STRUCTURE approaches (see the
318 'Hierarchical analysis' section in the Supplementary Information for more details).

319 A pattern of isolation by distance (IBD) was observed across all sampled
320 populations (Mantel $r = 0.726$, $p < 0.001$). Restricting the IBD analysis to the set of
321 sites sampled during the same year, we found an even stronger pattern of IBD
322 (Mantel $r = 0.870$, $p < 0.0001$, Figure 4). In the latter case, the coefficient estimate
323 of the slope parameter (b) in the regression was $b = 0.01$ with a 95% confidence
324 interval (CI) ranging from 0.007 to 0.013. Neighbourhood size (Nb) reached $Nb = 99$
325 individuals, on average (95% CI = [71-140]), and immigration rate ($N_e m$) was
326 estimated to reach $N_e m = 16$ (95% CI = [11-22]) individuals per generation and
327 subpopulation.

328 We found a mean effective population size of 62 individuals. The closest
329 sampled sites were North France and Belgium, separated 119 km from one another.
330 We found surface and population densities to reach, on average, $S^2 = 11.3 \text{ km}^2$ and

331 $De = 5.4$ individuals/m², respectively. We found the dispersal rate to reach, on
332 average, $\delta \approx 76$ km/generation (95% CI = [65-90]).

333 *Genetic diversity*

334 The observed heterozygosity (H_o), gene diversity (H_s), and F_{IS} were highly variable
335 across loci (Table S3). The observed F_{ST} values were, however, more constant than
336 F_{IS} ones. For most loci, gene diversity was higher than the observed heterozygosity.
337 Consequently, the overall gene diversity across all loci was significantly higher than
338 the observed heterozygosity (Wilcox Signed-Rank Test, $V = 6959$, $p < 0.0001$). The
339 mean gene diversity per sampled population was still higher than the observed
340 heterozygosity (Wilcox Signed-Rank Test, $V = 406$, $p < 0.0001$) and mean F_{IS} was
341 always positive. Mean values of observed heterozygosity, gene diversity, and F_{IS} for
342 each population are shown in Figure S6 (Supporting Information). The highest mean
343 gene diversity and F_{IS} values over loci were identified in the southern Eurasian
344 cluster ($H_s = 0.355$, $F_{IS} = 0.275$), followed by the northern European cluster ($H_s =$
345 0.340 , $F_{IS} = 0.2708$) and the cluster from northern Africa ($H_s = 0.171$, $F_{IS} = 0.191$)
346 (Figure 5). The Monte-Carlo test showed a significant difference in gene diversity
347 values for all pairs of clusters ($p = 0.001$ for all three comparisons), but none for F_{IS}
348 values ($p = 0.199$ and 0.239 when comparing northern Africa to the northern
349 European cluster and northern Africa to the southern Eurasian cluster, respectively;
350 while $p = 0.644$ when comparing the southern Eurasian cluster to the northern
351 European cluster). Populations from northern Africa showed a high deficit in
352 heterozygosity, of which 71 out of 125 loci with H_s values of zero.

353 After p -value correction (Benjamini and Yekutieli, 2001), no pair of locus
354 showed significance values of linkage disequilibrium. No correlation was found
355 between F_{IS} and F_{ST} ($\rho = -0.0206$, $p = 0.8198$) and missing data were positively
356 correlated to F_{IS} values ($\rho = 0.5804$, $p < 0.001$). The linear regression of F_{IS} against
357 the number of missing data estimated an adjusted R^2 of 0.19, suggesting that
358 around one-fifth of F_{IS} variance is explained by the number of missing data. Finally,
359 $StrdErrFIS$ was around 4 times bigger than $StrdErrFst$ (0.033 and 0.008,
360 respectively).

361 **Discussion**

362 We investigated the genetic structure of populations from the tick *I. ricinus* in much
363 of its range, *i.e.* in Eurasia and in northern Africa. In addition to a strong and
364 expected divergence between northern African and Eurasian populations, the two
365 Eurasian genetic clusters described here showed clear spatial patterns. The
366 isolation by distance patterns we found, either throughout the entire dataset or
367 restricted to samples from the same period, suggest an association between the
368 genetic structure of *I. ricinus* populations and the geographical location of these
369 populations. Hierarchical analyses confirmed the genetic affinity between western
370 European populations, from the UK and Ireland in the north to Spain in the south,
371 supporting our first hypothesis regarding genetic similarities in western continental
372 Europe and the British Isles. Also consistent with our second hypothesis stating a
373 genetic signature of central European mountains, we found a clear differentiation
374 between populations from southern Eurasia and populations from northern

375 Europe. Indication of migration of individuals between the two clusters is suggested
376 by the different degrees of affinity from central Europe with one cluster or another
377 (e.g. in Romania, Hungary, Slovakia, and Moldova).

378 *Ixodes ricinus* and *I. inopinatus* have recently been suggested to be
379 sympatric both in northern Africa (Younsi et al., 2020) and in Europe (Estrada-Peña
380 et al., 2014; Chitimia-Dobler et al., 2018). Our results are clear concerning the
381 genetic identity of northern African samples. According to the results from both the
382 DAPC and STRUCTURE analysis, there is no possibility of any individuals from those
383 populations to belong to any other genetic clusters. Also, no individual from Eurasia
384 had any probability of identity with the northern African cluster. Converging results
385 of both analyses indicate with a great deal of certitude that: (i) all samples from
386 northern Africa belong to the same species and have the same ancestry; (ii) no
387 sample in Eurasia share ancestry with northern African ones. Northern African
388 samples were also a particular case as more than half loci were monomorphic
389 across all three populations, which was not found in Eurasian populations. Again, it
390 is important to note that individuals from the three northern African populations
391 analysed here were identified before the description of *I. inopinatus* (Estrada-Peña
392 et al., 2014). If *I. inopinatus* was present in the Eurasian samples, we would expect
393 at least small probabilities of identity of Eurasian samples with the northern African
394 cluster, which was not the case. The clear-cut genetic differentiation we obtained
395 between Eurasian and northern African populations strongly suggests that all the
396 individuals from the three northern African populations analysed here correspond

397 to *I. inopinatus*. Those results also illustrate the potential of using some of the SNPs
398 analysed here to differentiate at a molecular level the two *Ixodes* species.

399 Two previous studies covering a large spatial extent of *I. ricinus*' range
400 (Nouredine et al., 2011; Porreta et al., 2013) did not find such a clear geographical
401 structure between Eurasian populations. Several reasons may explain this
402 difference. First, a somewhat reduced number of individuals per population
403 (sometimes a single individual per population in Nouredine et al., 2011) may
404 explain a lack of spatially structured signal in former studies. Second, those former
405 studies were based on mitochondrial and nuclear sequences. This said, a marked
406 genetic differentiation into two distinctive clades has already been reported (Dinnis
407 et al., 2014; Røed et al., 2016), suggesting a split in *I. ricinus* populations between
408 northern continental Europe and Great Britain. Our results confirm and extend this
409 pattern to most of the Eurasian range of the species by suggesting that
410 Scandinavian populations are genetically closer to the populations from the north-
411 eastern continental parts of Europe. Although there is a certain degree of gene flow
412 between the two clusters, the north vs. south-eastern exchange may be hampered
413 by mountain areas in central Europe. This reinforces the argument that large
414 animals efficiently maintain high gene flow between tick populations across
415 contiguous and permeable landscapes, while intense transportation by birds,
416 during spring and autumn migration across sea or mountains (Hasle et al., 2009;
417 Røed et al., 2016), may not be as sufficient to break down boundaries between
418 established genetic entities.

419 Surprisingly, we found a close genetic affinity between all Atlantic samples
420 (i.e. Ireland, England, western and southern France, and Spain) and the
421 geographically separated populations from Turkey and Iran. This genetic affinity
422 among distant populations in Eurasia was supported by the two different clustering
423 methods we used (DAPC and STRUCTURE). Besides these results, the refined
424 hierarchical analyses isolated Iran and Turkey in their particular clusters in the first
425 (DAPC) and second (STRUCTURE) round of hierarchical clustering analyses. This
426 suggests that an east-west transport of ticks across southern Eurasia must be
427 sufficient to maintain a genetically identifiable cluster across this extensive area.
428 Interestingly, louping-ill like viruses are also known from Greece and Turkey (Gao
429 et al., 1993; Marin et al., 1995), which might further support our findings and a link
430 between tick lineages and *Flavivirus*, although the causation is not known.

431 Since migratory birds carry *I. ricinus* across long distances, different
432 migratory routes could also contribute to the north-south genetic differentiation
433 we observed (Hasle et al., 2009; Røed et al., 2016). However, birds mainly carry
434 larvae and nymphs. Since surviving rates between development states are low, the
435 overall reproductive success of tick transported by birds is likely smaller than that
436 of adult ticks carried by large mammals. This may explain the maintenance of
437 genetic differentiation e.g. between the UK and Norway despite massive transport
438 of ticks' larvae in both directions (Røed et al., 2016).

439 Regarding the population structure observed within samples, the deviation
440 from Hardy-Weinberg equilibrium we found is in agreements with previous studies
441 on population genetics of *I. ricinus* based on SNPs (Quillery et al., 2014) and

442 microsatellites (Kempf et al., 2009; Kempf et al., 2011; Røed et al., 2006), as well as
443 other tick species (Dharmarajan et al., 2011). Possible causes of the observed
444 deviation from the Hardy-Weinberg equilibrium are assortative mating (or
445 assortative pairing), Wahlund effect, or errors in the genotyping. A tendency of
446 mating between phenotypically or genetically similar individuals may effectively
447 increase the inbreeding and thus heterozygote deficiency within populations (Jiang
448 et al., 2013). Kempf et al. (2009) suggested that assortative mating might occur in
449 *I. ricinus*, mostly via host selection (Kempf et al., 2011). Inbreeding in ticks could be
450 a result of host infestation by related individuals, which leads to high breeding
451 success of sibling groups (Araya-Ancheta et al., 2015). The highly aggregated egg
452 masses in *I. ricinus* (1000 to 3000 eggs) and the limited active dispersal of larvae
453 and nymphs may lead to a high likelihood of mating between related individuals
454 and thus inbreeding. Finally, the parasite-host relationship specificities could also
455 play an important role in establishing or maintaining population structure in *I.*
456 *ricinus*. If different host populations are present locally and exhibit behaviours
457 favouring mating within (and not between) each host population, this may induce
458 a Wahlund effect and explains the heterozygote deficiency observed. The existence
459 of such a host population behaviour has been characterized in *I. uriae*, a tick
460 associated with sea birds (Mc Coy et al., 2001) but also suggested in *I. ricinus* (Kempf
461 et al., 2009, 2011). Even though we did not conceive this study to test for such a
462 hypothesis, our results support at least partially non-random mating in *I. ricinus*
463 populations and the consequent Wahlund effect. Dharmarajan et al. (2011) facing
464 a similar result for the American species *I. texanus* showed that subdivided

465 breeding groups and high variance in individual reproductive success can correctly
466 explain Hardy-Weinberg equilibrium deviation.

467 It is widely acknowledged that more or less isolated populations could
468 develop particular adaptations in response to environmental differences between
469 habitats. Nonetheless, very few studies to date have clearly observed phenotypic
470 variations among *I. ricinus* populations from different geographical origins. In
471 Estrada-Peña et al. (1996 and 1998), differences in cuticular hydrocarbon
472 composition among European populations of *I. ricinus* were observed according to
473 the geographical origin of those populations. Interestingly, the multivariate
474 phenotypic analysis presented in those studies showed a somewhat similar pattern
475 to our hierarchical genetic clustering analysis, notably concerning what the authors
476 call 'peripheral populations'. Aside from chemical differentiation, behavioural
477 differences between ticks' populations have also been documented, such as
478 mismatches in questing peaks (Schulz et al., 2014) and questing responses to
479 temperature (Gilbert et al., 2014; Tomkins et al., 2014). In controlled conditions,
480 Gilbert et al. (2014) and Tomkins et al. (2014) showed that *I. ricinus* nymphs from
481 cooler climates begin questing at lower temperatures than nymphs from warmer
482 climates. They also start questing sooner when the temperature was kept constant.
483 In any case, local adaptations could impact the spatial redistribution of the species
484 range in response to changes in abiotic conditions. In a global changing context,
485 such consequences could be explored by environmental niche modelling to identify
486 areas of potential future expansion. It remains to be investigated if the different

487 clusters we identified here could pose different threats for human health and the
488 potential risk of tick-borne disease transmission to humans.

489 Our findings on isolation by distance suggest small population densities and
490 large dispersal distances among the sampled populations. The large dispersal
491 distance is not a surprising result since ticks can parasitize highly mobile species. In
492 a changing climate context, this result indicates that ticks could easily colonize new
493 suitable habitats outside the current limits of the species geographical range in a
494 few generations.

495 Despite being a generalist ectoparasite, our results highlight geographically
496 distinct and genetically structured populations in *I. ricinus*. More research on host
497 preference and dispersal capacity is needed to better understand those patterns.
498 The differentiation of Eurasian populations into two geographically distinct clusters
499 (northern Europe vs. southern Eurasia) could have important implications for the
500 redistribution of *I. ricinus* in response to anthropogenic climate change. Ticks from
501 a given genetic cluster could be more or less prone to increase in abundance in
502 some regions. Combining tick and pathogen population genetics with knowledge
503 on host distribution could help in the early detection of the spread of tick-borne
504 diseases and thus improve the responsiveness of public authorities to limit major
505 public health concerns.

506 **Acknowledgements**

507 We thank all the invaluable contribution of Dr. Brigitte Degeilh (Laboratory of
508 Parasitology and Mycology, Rennes University Hospital, France), Dr. Francesco

509 Nazi (Università Degli Studi di Udine), Dr. Mohammad Abdigoudarzi (Razi Institute,
510 Iran), Dr Ali Bouattour (Institut Pasteur de Tunis, Tunisia), Dr Loubna Dib (Institut
511 Vétérinaire, Centre Universitaire El Tarf, Algeria), M'hammed Sarih (Institut Pasteur
512 du Maroc, Morocco), Dr. Irina Golovljova (National Institute for Health
513 Development, Estonia), Nicole Voss (University of Erlangen-Nürnberg, Germany),
514 Dr. Zati Vatansever (Kafkas University, Turkey), Dr. Eoin Healy (University College,
515 Ireland), Dr. Davide Sassera (University of Pavia, Italy), Dr. Albert Agoulon (Oniris,
516 France), Dr. Ionut Pavel (Regional Institute of Oncology, Romania), Dr. György Csóka
517 (Hungary Forest Research Institut, Hungary), Dr. Elena Kocianová (Slovak Academy
518 of Sciences, Slovakia), Dr. Alexandru Movila (Academy of Sciences of Moldova,
519 Moldavia) for sharing some of the samples used in this study. We thank Dr. Michael
520 Scherer-Lorenzen (Freiburg University, German) for the general smallFOREST study
521 design, from which many samples were made available. The smallFOREST project
522 was funded by the ERA-Net BiodivERsA, via the national funders ANR (France),
523 FORMAS (Sweden), ETAG (Estonia), DFG (Germany), BELSPO (Belgium) and the
524 European Union through the European Regional Development Fund (the
525 EcolChange Centre of Excellence). We thank the Centre de Ressources Régionales
526 en Biologie Moléculaire (CRRBM) from the Université de Picardie Jules Verne. This
527 work was also supported by the Région Hauts-de-France, the Centre National de la
528 Recherche Scientifique (CNRS, INEE) and the European Regional Development
529 Fund.

530 **Conflict of Interest**

531 The authors declare that they have no conflict of interest.

532 **References**

- 533 Al-Khafaji, A.M., Clegg, S.R., Pinder, A.C., Luu, L., Hansford, K.M., Seelig, F., Dinnis,
534 R.E., Margos, G., Medlock, J.M., Feil, E.J., Darby, A.C., McGarry, J.W., Gilbert,
535 L., Plantard, O., Sasser, D., Makepeace, B.L., 2019. Multi-locus sequence
536 typing of *Ixodes ricinus* and its symbiont *Candidatus* Midichloria mitochondrii
537 across Europe reveals evidence of local co-cladogenesis in Scotland. Ticks Tick-
538 Borne Dis. 10, 52–62. <https://doi.org/10.1016/j.ttbdis.2018.08.016>
- 539 Alkhishe, A.A., Peterson, A.T., Samy, A.M., 2017. Climate change influences on the
540 potential geographic distribution of the disease vector tick *Ixodes ricinus*. PLOS
541 ONE 12, e0189092. <https://doi.org/10.1371/journal.pone.0189092>
- 542 Araya-Anchetta, A., Busch, J.D., Scoles, G.A., Wagner, D.M., 2015. Thirty years of
543 tick population genetics: A comprehensive review. Infect. Genet. Evol. 29,
544 164–179. <https://doi.org/10.1016/j.meegid.2014.11.008>
- 545 Archie, E.A., Ezenwa, V.O., 2011. Population genetic structure and history of a
546 generalist parasite infecting multiple sympatric host species. Int. J. Parasitol.
547 41, 89–98. <https://doi.org/10.1016/j.ijpara.2010.07.014>
- 548 Babos S. 1964. Die Zeckenfauna Mitteleuropas. Budapest: Akadémiai Kiadó.
- 549 Benjamini, Y., Yekutieli, D., 2001. The control of the false discovery rate in multiple
550 testing under dependency. Ann. Stat. 29(4), 1165–1188.
551 www.jstor.org/stable/2674075
- 552 Blanchong, J.A., Robinson, S.J., Samuel, M.D., Foster, J.T., 2016. Application of
553 genetics and genomics to wildlife epidemiology: Genetics and Wildlife
554 Epidemiology. J. Wildl. Manag. 80, 593–608.
555 <https://doi.org/10.1002/jwmg.1064>
- 556 Carpi, G., Kitchen, A., Kim, H.L., Ratan, A., Drautz-Moses, D.I., McGraw, J.J.,
557 Kazimirova, M., Rizzoli, A., Schuster, S.C., 2016. Mitogenomes reveal diversity
558 of the European Lyme borreliosis vector *Ixodes ricinus* in Italy. Mol.
559 Phylogenet. Evol. 101, 194–202.
560 <https://doi.org/10.1016/j.ympev.2016.05.009>
- 561 Casati, S., Bernasconi, M.V., Gern, L., Piffaretti, J.-C., 2008. Assessment of
562 intraspecific mtDNA variability of European *Ixodes ricinus* sensu stricto (Acari:
563 Ixodidae). Infect. Genet. Evol. 8, 152–158.
564 <https://doi.org/10.1016/j.meegid.2007.11.007>
- 565 Chitimia-Dobler, L., Rieß, R., Kahl, O., Wölfel, S., Dobler, G., Nava, S., Estrada-Peña,
566 A., 2018. *Ixodes inopinatus* – Occurring also outside the Mediterranean
567 region. Ticks Tick-Borne Dis. 9, 196–200.
568 <https://doi.org/10.1016/j.ttbdis.2017.09.004>
- 569 Dantas-Torres, F., 2015. Climate change, biodiversity, ticks and tick-borne diseases:
570 The butterfly effect. Int. J. Parasitol. Parasites Wildl. 4, 452–461.
571 <https://doi.org/10.1016/j.ijppaw.2015.07.001>

572 De Meeûs, T., 2018. Revisiting FIS, FST, Wahlund Effects, and Null Alleles. *J. Hered.*
573 109, 446–456. <https://doi.org/10.1093/jhered/esx106>

574 Dharmarajan, G., Beasley, J.C., Rhodes, O.E., 2011. Heterozygote deficiencies in
575 parasite populations: an evaluation of interrelated hypotheses in the raccoon
576 tick, *Ixodes texanus*. *Heredity* 106, 253–260.
577 <https://doi.org/10.1038/hdy.2010.84>

578 Dinnis, R.E., Seelig, F., Bormane, A., Donaghy, M., Vollmer, S.A., Feil, E.J.,
579 Kurtenbach, K., Margos, G., 2014. Multilocus sequence typing using
580 mitochondrial genes (mtMLST) reveals geographic population structure of
581 *Ixodes ricinus* ticks. *Ticks Tick-Borne Dis.* 5, 152–160.
582 <https://doi.org/10.1016/j.ttbdis.2013.10.001>

583 Do, C., Waples, R.S., Peel, D., Macbeth, G.M., Tillett, B.J., Ovenden, J.R., 2014.
584 NEESTIMATOR v2: re-implementation of software for the estimation of
585 contemporary effective population size (N_e) from genetic data. *Mol. Ecol.*
586 *Resour.* 14, 209–214. <https://doi.org/10.1111/1755-0998.12157>

587 Dray, S., Dufour, A.-B., 2007. The ade4 Package: Implementing the Duality Diagram
588 for Ecologists. *J. Stat. Softw.* 22. <https://doi.org/10.18637/jss.v022.i04>

589 Earl, D.A., vonHoldt, B.M., 2012. STRUCTURE HARVESTER: a website and program
590 for visualizing STRUCTURE output and implementing the Evanno method.
591 *Conserv. Genet. Resour.* 4, 359–361. <https://doi.org/10.1007/s12686-011-9548-7>

592

593 Ehrmann, S., Liira, J., Gärtner, S., Hansen, K., Brunet, J., Cousins, S.A.O., Deconchat,
594 M., Decocq, G., De Frenne, P., De Smedt, P., Diekmann, M., Gallet-Moron, E.,
595 Kolb, A., Lenoir, J., Lindgren, J., Naaf, T., Paal, T., Valdés, A., Verheyen, K., Wulf,
596 M., Scherer-Lorenzen, M., 2017. Environmental drivers of *Ixodes ricinus*
597 abundance in forest fragments of rural European landscapes. *BMC Ecol.* 17.
598 <https://doi.org/10.1186/s12898-017-0141-0>

599 Estrada-Peña, A., Gray, J.S. & Kahl, O. 1996. Variability in cuticular hydrocarbons
600 and phenotypic discrimination of *Ixodes ricinus* populations (Acarina: Ixodidae)
601 from Europe. *Exp Appl Acarol* 20, 457–466.
602 <https://doi.org/10.1007/BF00053309>

603 Estrada-Peña, A., Daniel, M., Frandsen, F., Gern, L., Gettinby, G., Gray, J.S., Jaenson,
604 T.G.T., Jongejan, F., Kahl, O., Korenberg, E., Mehl, R., Nuttall, P.A., 1998. *Ixodes*
605 *ricinus* Strains in Europe. *Zentralblatt für Bakteriologie* 287, 185–189.
606 [https://doi.org/10.1016/S0934-8840\(98\)80119-9](https://doi.org/10.1016/S0934-8840(98)80119-9)

607 Estrada-Peña, A., Nava, S., Petney, T., 2014. Description of all the stages of *Ixodes*
608 *inopinatus* n. sp. (Acari: Ixodidae). *Ticks Tick-Borne Dis.* 5, 734–743.
609 <https://doi.org/10.1016/j.ttbdis.2014.05.003>

610 European Centre for Disease Prevention and Control and European Food Safety
611 Authority. Tick maps 2019. [https://ecdc.europa.eu/en/disease-](https://ecdc.europa.eu/en/disease-vectors/surveillance-and-disease-data/tick-maps)
612 [vectors/surveillance-and-disease-data/tick-maps](https://ecdc.europa.eu/en/disease-vectors/surveillance-and-disease-data/tick-maps) (accessed 12 January 2020).

613 Evanno, G., Regnaut, S., Goudet, J., 2005. Detecting the number of clusters of
614 individuals using the software structure: a simulation study. *Mol. Ecol.* 14,
615 2611–2620. <https://doi.org/10.1111/j.1365-294X.2005.02553.x>

616 Gao, G.F., Hussain, M.H., Reid, H.W., Gould, E.A., 1993. Classification of a new
617 member of the TBE *Flavivirus* subgroup by its immunological, pathogenetic
618 and molecular characteristics: identification of subgroup-specific
619 pentapeptides. *Virus Res.* 30, 129–144. [https://doi.org/10.1016/0168-
620 1702\(93\)90002-5](https://doi.org/10.1016/0168-1702(93)90002-5)

621 Gilbert, L., Aungier, J., Tomkins, J.L., 2014. Climate of origin affects tick (*Ixodes*
622 *ricinus*) host-seeking behavior in response to temperature: implications for
623 resilience to climate change? *Ecol. Evol.* 4, 1186–1198.
624 <https://doi.org/10.1002/ece3.1014>

625 Gooding, R.H., 1996. Genetic Variation in Arthropod Vectors of Disease-Causing
626 Organisms: Obstacles and Opportunities. *Clin. Microbiol. Rev.* 9, 301-320.

627 Goudet, J. (2003). FSTAT (version 2.9.4), a program to estimate and test population
628 genetics parameters. Available from:
629 <https://www2.unil.ch/popgen/softwares/fstat.htm>

630 Goudet, J. & Jombart, T. (2018). hierfstat: Estimation and Tests of Hierarchical F-
631 Statistics. <http://www.r-project.org>, <http://github.com/jg65/hierfstat>

632 Handeland, K., Qviller, L., Vikøren, T., Viljugrein, H., Lillehaug, A., Davidson, R.K.,
633 2013. *Ixodes ricinus* infestation in free-ranging cervids in Norway—A study
634 based upon ear examinations of hunted animals. *Vet. Parasitol.* 195, 142–149.
635 <https://doi.org/10.1016/j.vetpar.2013.02.012>

636 Hasle, G., Bjune, G., Edvardsen, E., Jakobsen, C., Linnehol, B., Røer, J.E., Mehl, R.,
637 Røed, K.H., Pedersen, J., Leinaas, H.P., 2009. Transport of ticks by migratory
638 passerine birds to Norway. *J. Parasitol.* 95, 1342–1351.
639 <https://doi.org/10.1645/GE-2146.1>

640 Helyar, S.J., Hemmer-Hansen, J., Bekkevold, D., Taylor, M.I., Ogden, R., Limborg,
641 M.T., Cariani, A., Maes, G.E., Diopere, E., Carvalho, G.R., Nielsen, E.E., 2011.
642 Application of SNPs for population genetics of nonmodel organisms: new
643 opportunities and challenges. *Mol. Ecol. Resour.* 11, 123–136.
644 <https://doi.org/10.1111/j.1755-0998.2010.02943.x>

645 Hijmans, R. J. (2017). geosphere: Spherical Trigonometry. R package version 1.5-7.
646 <https://CRAN.R-project.org/package=geosphere>

647 Hillyard PD. 1996. Ticks of North-West Europe. In: Barnes RSK, Crothers JH, editors.
648 Synopses of the British Fauna (New Series).

649 Hvidsten, D., Frafjord, K., Gray, J.S., Henningsson, A.J., Jenkins, A., Kristiansen, B.E.,
650 Lager, M., Rognerud, B., Slåtsve, A.M., Stordal, F., Stuen, S., Wilhelmsson, P.,
651 2020. The distribution limit of the common tick, *Ixodes ricinus*, and some
652 associated pathogens in north-western Europe. *Ticks Tick-Borne Dis.* 11,
653 101388. <https://doi.org/10.1016/j.ttbdis.2020.101388>

654 Jakobsson, M., Rosenberg, N.A., 2007. CLUMPP: a cluster matching and
655 permutation program for dealing with label switching and multimodality in

656 analysis of population structure. *Bioinformatics* 23, 1801–1806.
657 <https://doi.org/10.1093/bioinformatics/btm233>

658 Jiang, Y., Bolnick, D.I., Kirkpatrick, M., 2013. Assortative Mating in Animals. *Am. Nat.*
659 181, E125–E138. <https://doi.org/10.1086/670160>

660 Jombart, T., 2008. adegenet: a R package for the multivariate analysis of genetic
661 markers. *Bioinformatics* 24, 1403–1405.
662 <https://doi.org/10.1093/bioinformatics/btn129>

663 Jombart, T., Devillard, S., Balloux, F., 2010. Discriminant analysis of principal
664 components: a new method for the analysis of genetically structured
665 populations. *BMC Genet.* 11, 94. <https://doi.org/10.1186/1471-2156-11-94>

666 Jore, S., Viljugrein, H., Hofshagen, M., Brun-Hansen, H., Kristoffersen, A.B., Nygård,
667 K., Brun, E., Ottesen, P., Sævik, B.K., Ytrehus, B., 2011. Multi-source analysis
668 reveals latitudinal and altitudinal shifts in range of *Ixodes ricinus* at its northern
669 distribution limit. *Parasit. Vectors* 4. <https://doi.org/10.1186/1756-3305-4-84>

670 Kempf, F., de Meeûs, T., Arnathau, C., Degeilh, B., McCoy, K.D., 2009. Assortative
671 Pairing in *Ixodes ricinus* (Acari: Ixodidae), the European Vector of Lyme
672 Borreliosis. *J. Med. Entomol.* 46, 471–474.
673 <https://doi.org/10.1603/033.046.0309>

674 Kempf, F., De Meeûs, T., Vaumourin, E., Noel, V., Taragel'ová, V., Plantard, O.,
675 Heylen, D.J.A., Eraud, C., Chevillon, C., McCoy, K.D., 2011. Host races in *Ixodes*
676 *ricinus*, the European vector of Lyme borreliosis. *Infect. Genet. Evol.* 11, 2043–
677 2048. <https://doi.org/10.1016/j.meegid.2011.09.016>

678 Kriz, B., Daniel, M., Benes, C., Maly, M., 2014. The Role of Game (Wild Boar and
679 Roe Deer) in the Spread of Tick-Borne Encephalitis in the Czech Republic.
680 *Vector-Borne Zoonotic Dis.* 14, 801–807.
681 <https://doi.org/10.1089/vbz.2013.1569>

682 Kozakiewicz, C.P., Burrige, C.P., Funk, W.C., VandeWoude, S., Craft, M.E., Crooks,
683 K.R., Ernest, H.B., Fountain-Jones, N.M., Carver, S., 2018. Pathogens in space:
684 Advancing understanding of pathogen dynamics and disease ecology through
685 landscape genetics. *Evol. Appl.* 11, 1763–1778.
686 <https://doi.org/10.1111/eva.12678>

687 Lang, K.R., Blanchong, J.A., 2012. Population genetic structure of white-tailed deer:
688 Understanding risk of chronic wasting disease spread. *J. Wildl. Manag.* 76,
689 832–840. <https://doi.org/10.1002/jwmg.292>

690 Lindgren, E., Gustafson, R., 2001. Tick-borne encephalitis in Sweden and climate
691 change. *The Lancet* 358, 16–18. [https://doi.org/10.1016/S0140-6736\(00\)05250-8](https://doi.org/10.1016/S0140-6736(00)05250-8)

692
693 Manangwa, O., De Meeûs, T., Grébaud, P., Ségard, A., Byamungu, M., Ravel, S.,
694 2019. Detecting Wahlund effects together with amplification problems:
695 Cryptic species, null alleles and short allele dominance in *Glossina pallidipes*
696 populations from Tanzania. *Mol. Ecol. Resour.* 19, 757–772.
697 <https://doi.org/10.1111/1755-0998.12989>

698 Marin, M.S., McKenzie, J., Gao, G.F., Reid, H.W., Antoniadis, A., Gould, E.A., 1995.
699 The virus causing encephalomyelitis in sheep in Spain: a new member of the
700 tick-borne encephalitis group. Res. Vet. Sci. 58, 11–13.
701 [https://doi.org/10.1016/0034-5288\(95\)90081-0](https://doi.org/10.1016/0034-5288(95)90081-0)

702 Mccoy, K.D., Bouludier, T., Tirard, C., Michalakis, Y., 2001. Host specificity of a
703 generalist parasite: genetic evidence of sympatric host races in the seabird tick
704 *Ixodes uriae*. J. Evol. Biol. 14, 395-405. [https://doi.org/10.1046/j.1420-](https://doi.org/10.1046/j.1420-9101.2001.00290.x)
705 [9101.2001.00290.x](https://doi.org/10.1046/j.1420-9101.2001.00290.x)

706 Medlock, J.M., Hansford, K.M., Bormane, A., Derdakova, M., Estrada-Peña, A.,
707 George, J.-C., Golovljova, I., Jaenson, T.G., Jensen, J.-K., Jensen, P.M., 2013.
708 Driving forces for changes in geographical distribution of *Ixodes ricinus* ticks in
709 Europe. Parasit. Vectors 6, 1. <https://doi.org/10.1186/1756-3305-6-1>

710 Norte, A.C., de Carvalho, I.L., Ramos, J.A., Gonçalves, M., Gern, L., Núncio, M.S.,
711 2012. Diversity and seasonal patterns of ticks parasitizing wild birds in western
712 Portugal. Exp. Appl. Acarol. 58, 327–339. [https://doi.org/10.1007/s10493-012-](https://doi.org/10.1007/s10493-012-9583-4)
713 [9583-4](https://doi.org/10.1007/s10493-012-9583-4)

714 Nouredine, R., Chauvin, A., Plantard, O., 2011. Lack of genetic structure among
715 Eurasian populations of the tick *Ixodes ricinus* contrasts with marked
716 divergence from north-African populations. Int. J. Parasitol. 41, 183–192.
717 <https://doi.org/10.1016/j.ijpara.2010.08.010>

718 Oksanen, F., Blanchet, F. G., Friendly, M., Kindt, R., Legendre, P., McGlinn, D.,
719 Minchin, F., O’Hara, R. B., Simpson, G. L., Solymos, P., Stevens, H., Szoecs, E.,
720 Wagner, H., 2019. vegan: Community Ecology Package. R package version 2.5-
721 5. <https://CRAN.R-project.org/package=vegan>

722 Pecl, G.T., Araújo, M.B., Bell, J.D., Blanchard, J., Bonebrake, T.C., Chen, I.-C., Clark,
723 T.D., Colwell, R.K., Danielsen, F., Evengård, B., Falconi, L., Ferrier, S., Frusher,
724 S., Garcia, R.A., Griffis, R.B., Hobday, A.J., Janion-Scheepers, C., Jarzyna, M.A.,
725 Jennings, S., Lenoir, J., Linnetved, H.I., Martin, V.Y., McCormack, P.C.,
726 McDonald, J., Mitchell, N.J., Mustonen, T., Pandolfi, J.M., Pettorelli, N.,
727 Popova, E., Robinson, S.A., Scheffers, B.R., Shaw, J.D., Sorte, C.J.B., Strugnell,
728 J.M., Sunday, J.M., Tuanmu, M.-N., Vergés, A., Villanueva, C., Wernberg, T.,
729 Wapstra, E., Williams, S.E., 2017. Biodiversity redistribution under climate
730 change: Impacts on ecosystems and human well-being. Science 355, eaai9214.
731 <https://doi.org/10.1126/science.aai9214>

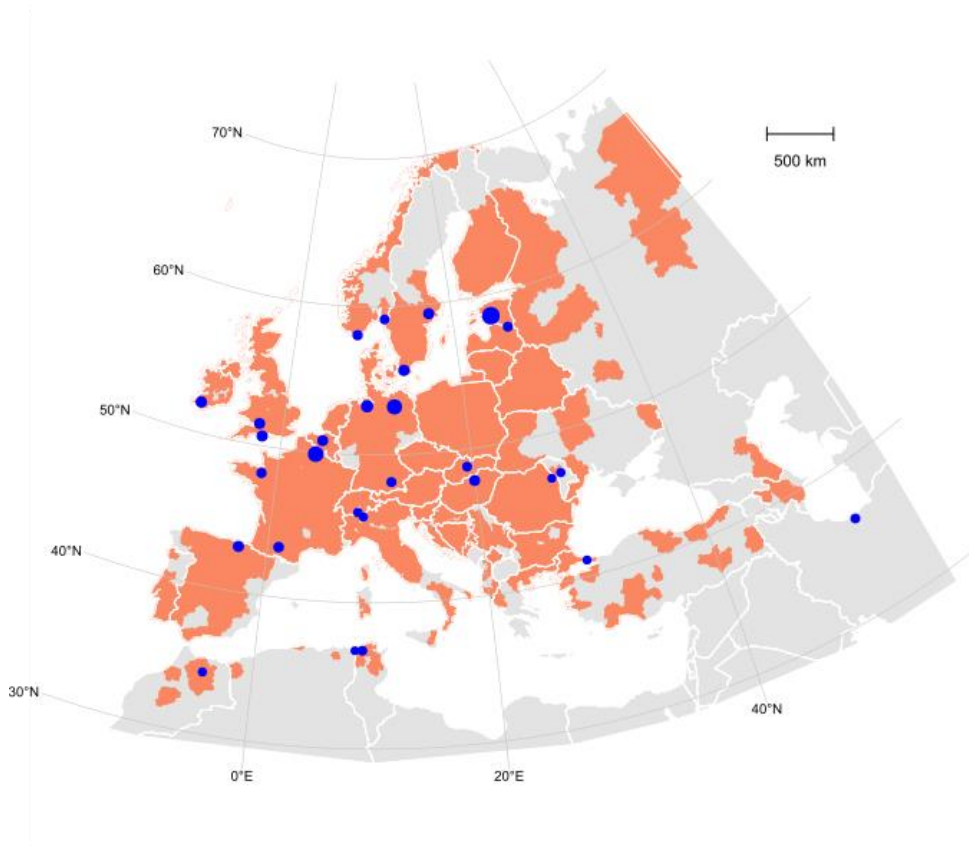
732 Pérez-Eid, C., 2007. Les tiques - Identification, biologie, importance médicale et
733 vétérinaire. Lavoisier, Provigny.

734 Portillo, A., Santibáñez, P., Palomar, A.M., Santibáñez, S., Oteo, J.A., 2018.
735 ‘*Candidatus* Neoehrlichia mikurensis’ in Europe. New Microbes New Infect. 22,
736 30–36. <https://doi.org/10.1016/j.nmni.2017.12.011>

737 Pritchard, J.K., Stephens, M., Donnelly, P., 2000. Inference of population structure
738 using multilocus genotype data. Genetics. 155, 945-959.
739 <https://www.genetics.org/content/155/2/945>

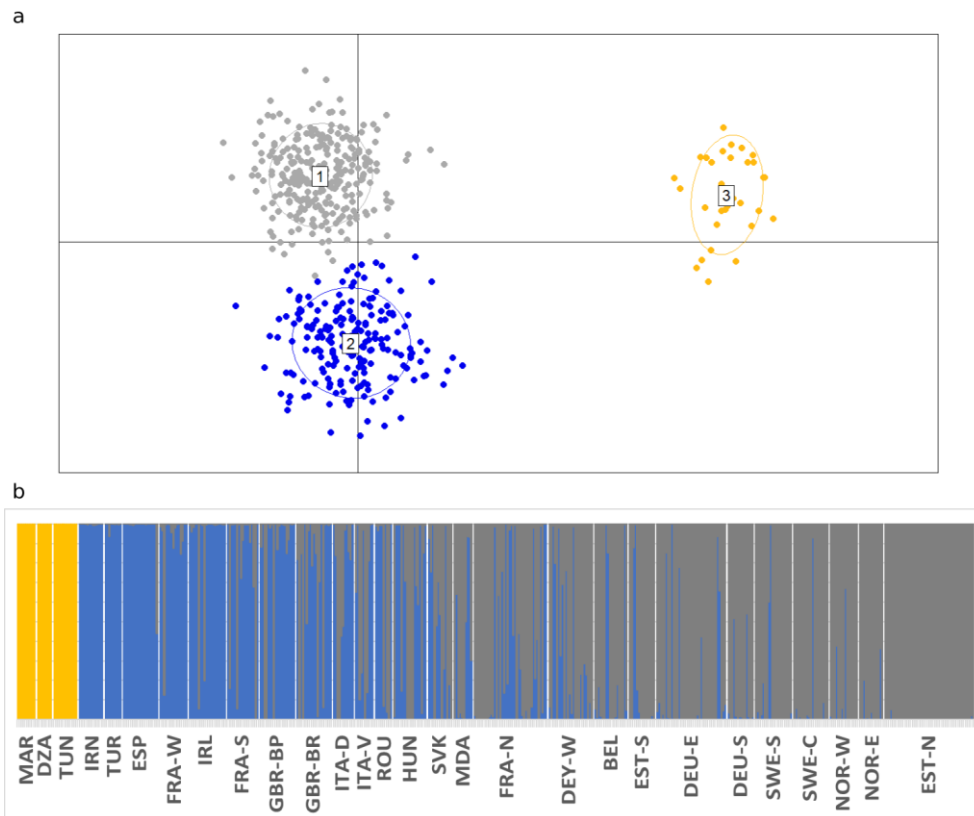
740 Pritchard, J.K., Wen., X., Falush, D. 2007. Documentation for structure software:
741 version 2.2.
742 [https://web.stanford.edu/group/pritchardlab/software/structure22/readme.](https://web.stanford.edu/group/pritchardlab/software/structure22/readme.pdf)
743 [pdf](https://web.stanford.edu/group/pritchardlab/software/structure22/readme.pdf) (accessed 20 November 2019)
744 Quillery, E., Quenez, O., Peterlongo, P., Plantard, O., 2014. Development of
745 genomic resources for the tick *Ixodes ricinus*: isolation and characterization of
746 single nucleotide polymorphisms. Mol. Ecol. Resour. 14, 393–400.
747 <https://doi.org/10.1111/1755-0998.12179>
748 R Core Team (2019). R: A language and environment for statistical computing. R
749 Foundation for Statistical Computing, Vienna, Austria. URL [https://www.R-](https://www.R-project.org/)
750 [project.org/](https://www.R-project.org/)
751 Rizzoli, A., Hauffe, H.C., Tagliapietra, V., Neteler, M., Rosà, R., 2009. Forest Structure
752 and Roe Deer Abundance Predict Tick-Borne Encephalitis Risk in Italy. PLoS
753 ONE 4, e4336. <https://doi.org/10.1371/journal.pone.0004336>
754 Røed, K.H., Hasle, G., Midthjell, V., Skretting, G., Leinaas, H.P., 2006. Identification
755 and characterization of 17 microsatellite primers for the tick, *Ixodes ricinus*,
756 using enriched genomic libraries: PRIMER NOTE. Mol. Ecol. Notes 6, 1165–
757 1167. <https://doi.org/10.1111/j.1471-8286.2006.01475.x>
758 Røed, K.H., Kvie, K.S., Hasle, G., Gilbert, L., Leinaas, H.P., 2016. Phylogenetic
759 Lineages and Postglacial Dispersal Dynamics Characterize the Genetic
760 Structure of the Tick, *Ixodes ricinus*, in Northwest Europe. PLOS ONE 11,
761 e0167450. <https://doi.org/10.1371/journal.pone.0167450>
762 Rousset, F., 1997. Genetic Differentiation and Estimation of Gene Flow from
763 FStatistics Under Isolation by Distance. Genetics 145, 1219–1228.
764 <https://www.genetics.org/content/145/4/1219>
765 Séré, M., Thévenon, S., Belem, A.M.G., De Meeûs, T., 2017. Comparison of different
766 genetic distances to test isolation by distance between populations. Heredity
767 119, 55–63. <https://doi.org/10.1038/hdy.2017.26>
768 Schulz, M., Mahling, M., Pfister, K., 2014. Abundance and seasonal activity of
769 questing *Ixodes ricinus* ticks in their natural habitats in southern Germany in
770 2011. J. Vector Ecol. 39, 56–65. [https://doi.org/10.1111/j.1948-](https://doi.org/10.1111/j.1948-7134.2014.12070.x)
771 [7134.2014.12070.x](https://doi.org/10.1111/j.1948-7134.2014.12070.x)
772 Smouse, P.E., 2010. How many SNPs are enough? Mol. Ecol. 19, 1265–1266.
773 <https://doi.org/10.1111/j.1365-294X.2010.04555.x>
774 Tabachnick, W.J., Black, W.C., 1995. Making a case for molecular population genetic
775 studies of arthropod vectors. Parasitol. Today 11, 27–30.
776 [https://doi.org/10.1016/0169-4758\(95\)80105-7](https://doi.org/10.1016/0169-4758(95)80105-7)
777 Tomkins, J.L., Aungier, J., Hazel, W., Gilbert, L., 2014. Towards an Evolutionary
778 Understanding of Questing Behaviour in the Tick *Ixodes ricinus*. PLoS ONE 9,
779 e110028. <https://doi.org/10.1371/journal.pone.0110028>

- 780 Vähä, J.-P., Erkinaro, J., Niemelä, E., Primmer, C.R., 2007. Life-history and habitat
781 features influence the within-river genetic structure of Atlantic salmon. *Mol.*
782 *Ecol.* 16, 2638–2654. <https://doi.org/10.1111/j.1365-294X.2007.03329.x>
- 783 Van Zee, J., Piesman, J.F., Hojgaard, A., Black IV, W.C., 2015. Nuclear Markers Reveal
784 Predominantly North to South Gene Flow in *Ixodes scapularis*, the Tick Vector
785 of the Lyme Disease Spirochete. *PLOS ONE* 10, e0139630.
786 <https://doi.org/10.1371/journal.pone.0139630>
- 787 Weir, B.S., Cockerham, C.C., 1984. Estimating F-Statistics for the Analysis of
788 Population Structure. *Evolution* 38, 1358-1370. [https://doi:10.1111/j.1558-
789 5646.1984.tb05657.x](https://doi:10.1111/j.1558-5646.1984.tb05657.x)
- 790 Younsi, H., Fares, W., Cherni, S., Dachraoui, K., Barhoumi, W., Najjar, C., Zhioua, E.,
791 2020. *Ixodes inopinatus* and *Ixodes ricinus* (Acari: Ixodidae) Are Sympatric Ticks
792 in North Africa. *J. Med. Entomol.* 57, 952–956.
793 <https://doi.org/10.1093/jme/tjz216>
- 794 Welinder-Olsson, C., Kjellin, E., Vaht, K., Jacobsson, S., Wenneras, C., 2010. First
795 Case of Human “*Candidatus* Neohrlichia mikurensis” Infection in a Febrile
796 Patient with Chronic Lymphocytic Leukemia. *J. Clin. Microbiol.* 48, 1956–1959.
797 <https://doi.org/10.1128/JCM.02423-09>
- 798 Wessels, C., Matthee, S., Espinaze, M.P.A., Matthee, C.A., 2019. Comparative
799 mtDNA phylogeographic patterns reveal marked differences in population
800 genetic structure between generalist and specialist ectoparasites of the
801 African penguin (*Spheniscus demersus*). *Parasitol. Res.* 118, 667–672.
802 <https://doi.org/10.1007/s00436-018-6150-x>
- 803 Wonham, M.J., Lewis, M.A., Renclawowicz, J., van den Driessche, P., 2006.
804 Transmission assumptions generate conflicting predictions in host-vector
805 disease models: a case study in West Nile virus. *Ecol. Lett.* 9, 706–725.
806 <https://doi.org/10.1111/j.1461-0248.2006.00912.x>



807

808 **Figure 1.** Distribution of the sampled populations of *Ixodes ricinus* across its
 809 putative range. The range of *I. ricinus* is displayed in dark orange on the map and
 810 was adapted from the European Centre for Disease Prevention and Control – ECDC
 811 (January 2019). The size of each blue dot on the map is proportional to the sample
 812 size of each sampled population.



813

814 **Figure 2.** Cluster assignment analysis results based on either the DAPC scatter plot

815 of individual memberships for $K = 3$ (a) or the STRUCTURE individual membership

816 probabilities for $K = 3$ as described by Evanno et al. (2005) (b). The sampled

817 populations are coded as follows: MAR: Morocco; DZA: Algeria; TUN: Tunisia; ESP:

818 Spain; IRN: Iran; TUR: Turkey; FRA-W: West France; IRL: Ireland; FRA-S: South

819 France; GBR-BP: England Blue Pool; GBR-BR: England Bristol; ITA-D: Italy

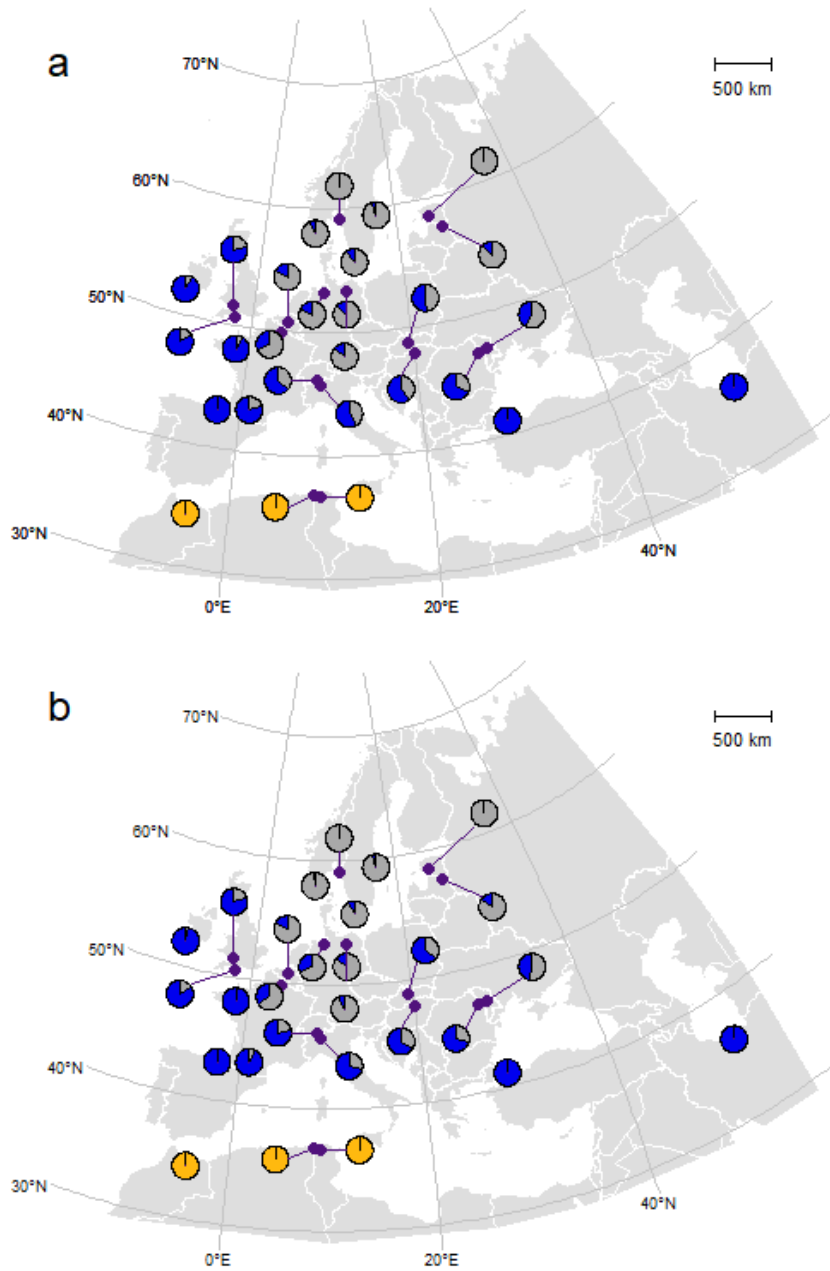
820 Domodossola; ITA-V: Italy Varese; ROU: Romania; HUN: Hungary; SVK: Slovakia;

821 MDA: Moldavia; FRA-N: North France; DEU-W: West Germany; BEL: Belgium; EST-

822 S: South Estonia; DEU-E: East Germany; DEU-S: South Germany; SWE-S: South

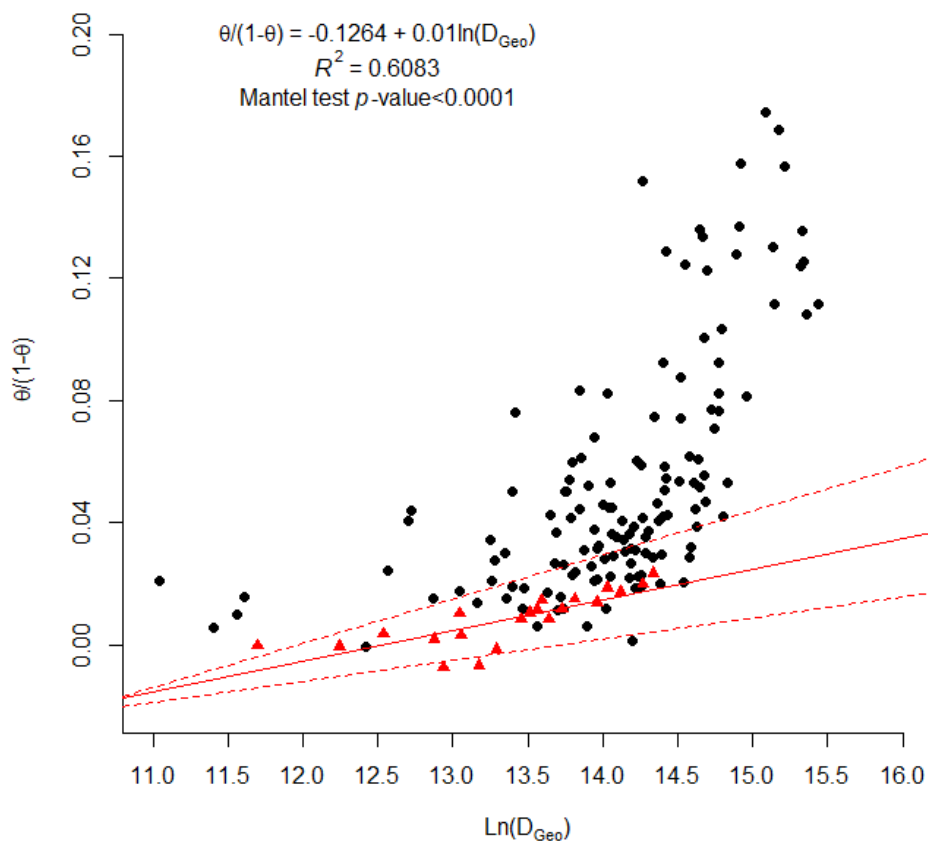
823 Sweden; SWE-C: Central Sweden; NOR-So: Norway Søgne; NOR-Gr: Norway

824 Grønnsundfjellet; EST-N: North Estonia. Coordinates of sampled populations are
825 presented in Table S1.



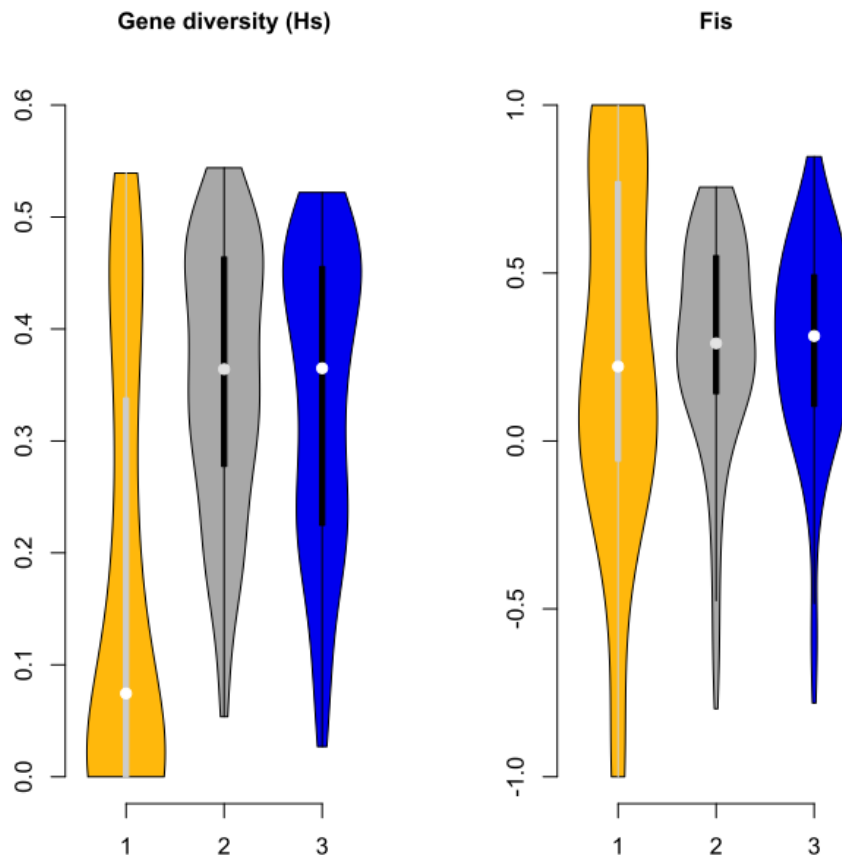
826

827 **Figure 3.** Distribution of the relative importance of each cluster on each sampled
828 population (see Figure 2 for the groups which colors are matching). Results are
829 provided for both the DAPC (a) and the STRUCTURE (b) analysis.



830
831 **Figure 4.** Isolation by distance between all Eurasian samples. Red triangles
832 represent the pair of samples from the same year: South and North France,
833 Belgium, West and East German, North Estonia, South and Central Sweden. The
834 regression line (plain line), 95% confidence interval (CI) calculated by bootstrap
835 (dashed lines), Mantel test significance and regression equation corresponds only

836 to red triangles pairs of samples are also shown. Black points correspond to all other
837 pairs of samples not used for further IBD analysis.



838

839 **Figure 5.** Values of gene diversity (a) and F_{IS} (b) for each of the three genetic clusters
840 identified by DAPC. Yellow: northern Africa cluster; Blue: southern Eurasia; Grey:
841 northern Europe. Permutation test (Monte-Carlo test, 999 replicates) between all
842 pairs of clusters was significant for gene diversity ($p = 0.001$) but no significance was
843 identified for F_{IS} . Eurasian clusters show a more pronounced heterozygote excess
844 than the northern African one. A variation of F_{IS} values across loci was observed in

845 the three clusters, even though this variation was much larger in the northern

846 African cluster.

847

Supporting Information for:

Strong genetic structure among populations of the tick *Ixodes ricinus* across its range: insights from population genetics

Pedro Poli, Jonathan Lenoir, Olivier Dr. Plantard, Steffen Ehrmann, Knut H. Røed, Hans Petter Leinaas, Marcus Panning, Annie Guiller

Table of Contents:

Table S1	Page 2
Table S2	Page 4
Table S3	Page 11
Figure S1	Page 16
Figure S2	Page 17
Figure S3	Page 18
Hierarchical analysis	Page 19
Figure S4	Page 21
Figure S5	Page 22
Figure S6	Page 23

Materials and Methods

Table S1. Sample coordinates. The Reference column indicates from which source samples were made available. PC = Personal collection.

Sample locality	Code	Longitude	Latitude	Number of samples	Sample Date	Reference
Morocco	MAR	4221933.21	1519759.51	10	Before 2010	Dr. Plantard, PC
Algeria	DZA	4165854.78	1520079.18	8	Before 2010	Dr. Plantard, PC
Tunisia	TUN	4287083.09	1370080.62	13	Before 2010	Dr. Plantard, PC
Spain	ESP	3292343.37	2302053.84	19	Before 2010	Dr. Plantard, PC
Iran	IRA	7920535.19	2511813.36	13	Before 2010	Dr. Plantard, PC
Turkey Istanbul	TUR	5907775.11	2200447.26	9	Before 2010	Dr. Plantard, PC
North France	FRA-N	3872010.67	2994279.45	40	2013	Erhmann et al., 2018
West France	FRA-W	3465235.38	2853298.78	15	2016	Dr. Degeilh, PC
South France	FRA-S	3593881.21	2296634.56	17	2013	Erhmann et al., 2018
Ireland	IRL	3013710.61	3385835.15	20	Before 2010	Dr. Plantard, PC
England Blue Pool	GBR-BP	3470079.25	3130233.33	19	Before 2010	Dr. Plantard, PC
England Bristol	GBR-BR	3450947.31	3224484.53	19	Before 2010	Dr. Plantard, PC
Italy Domodossola	ITA-D	4188665.99	2556599.15	11	Before 2010	Dr. Plantard, PC
Italy Varese	ITA-V	4229419.76	2523525.45	10	Before 2010	Dr. Plantard, PC
Romania	ROU	5643875.12	2813096.13	9	Before 2010	Dr. Plantard, PC
Hungary	HUN	5064737.95	2796444.23	18	Before 2010	Dr. Plantard, PC
Slovakia	SVK	5008087.64	2900574.08	13	Before 2010	Dr. Plantard, PC
Moldavia	MDA	5711169.6	2856440.17	10	Before 2010	Dr. Plantard, PC

Sample locality	Code	Longitude	Latitude	Number of samples	Sample Date	Reference
West Germany	DEU-W	4257417.83	3352915.67	24	2013	Erhmann et al., 2018
East Germany	DEU-E	4462732.5	3348531.08	38	2013	Erhmann et al., 2018
South Gemany	DEU-S	4440340.3	2784710.43	14	2013	Dr. Plantard, PC
Belgium	BEL	3924610.12	3095109.35	18	2013	Erhmann et al., 2018
North Estonia	EST-N	5186688.83	4032319.73	49	2013	Erhmann et al., 2018
South Estonia	EST-S	5313297.86	3950296.69	14	Before 2010	Dr. Plantard, PC
South Swqeen	SWE-S	4533959.53	3622513.31	20	2013	Erhmann et al., 2018
Central Sweden	SWE-C	4720133.45	4047795.89	19	2013	Erhmann et al., 2018
Norway West	NOR-W	4186225.49	3886420.36	15	2006	Dr. Leinaas, PC
Norway East	NOR-E	4389275.28	4003811.98	13	2006	Dr. Leinaas, PC

Table S2. List of SNPs, variant basis and primers used in the study (from Quillery et al., 2014)

locus	variant	Primer1-specific to allele1	Primer2-specific to allele2	Primer3-common to both alleles
1133	T/C	GCTTGGCCACTTCCACTGCTTT	GCTTGGCCACTTCCACTGCTTC	ACAACAGAGAAGGCAGCCCACA
3705	A/C	AGCATGGCGCACTGTGAAAGCTC	AGCATGGCGCACTGTGAAAGCTA	TCCTAGTCGGCTGGCTGGAG
6283	T/C	AATGAGGCGTCAGTGACAGCATAAC	AATGAGGCGTCAGTGACAGCATAAT	CGTGACGTCAAGGCAGAATGCTAT
6363	A/G	TCGTCCTCCGTCACGTAGCCG	TCGTCCTCCGTCACGTAGCCA	CCATTGAACCCTGGTGGGTCATCA
10041	A/G	GTTGTTCCCTTGGCAGACG	GTTGTTCCCTTGGCAGACA	AACATACCCGAGACTGTCAAC
19998	A/G	CAGAAGTGGAGATTGTTGCGTGTA	CAGAAGTGGAGATTGTTGCGTGTA	TACATACATTGAGCATCGACCAA AGGCACGTAGATCACGAGAATTATT TC
21130	C/T	GCTGCTGCAACCGGTTTATCTTC	GCTGCTGCAACCGGTTTATCTTT	TC
30736	C/G	GCTAGGTGACGAGGACTGGACG	GCTAGGTGACGAGGACTGGACC	GTTGTTCCACCTTTCGCAGGAGAT
31200	A/G	CGTTCAGGTTGACCGAGAAGTAA GACTAATCACCAGGAAATCCATTCTG	GTTTCAGGTTGACCGAGAAGTAG GACTAATCACCAGGAAATCCATTCTG	GCCTCTCGTTACTGTTCGTATC
32114	C/T	C	T	GGCTATACTCGGACGTATGTTGA
32551	T/C	TTCGGTGGCAACAGCTCGTCCATC	TTCGGTGGCAACAGCTCGTCCATT	CCAGCCTCATAGCCGAGCACCA
34502	G/A	CGGATTCGAACCAGTTATCAATGGG	CGGATTCGAACCAGTTATCAATGGA	GCCTCTCTAGAAAACAGTTGCTCTC
42351	A/G	CTTGTAGGAATGGAGGTCATCTTCG	CTTGTAGGAATGGAGGTCATCTTCA	CTTCTGTGTCGCAGGTGGCATCAT ACGTGACAACACTTACACGGCATT TC
57206	C/G	GCACTATGAGCCATCGAAGCCAAG	GCACTATGAGCCATCGAAGCCAAC	C
60684	C/T	TGCACATAGTCGCGCAATACGTTT	TGCACATAGTCGCGCAATACGTTT	CGAGCCGTTGCAACCGATCCG
61606	G/A	ACATAGGACATCTCAAGGTCATTTCG	ACATAGGACATCTCAAGGTCATTCA	GAAGAAACCGAGGATGAGTGTCATG
66390	C/T	GCCGAACAGCCGTGCAACCC	GCCGAACAGCCGTGCAACCT	TCGCTGCTGTATACCCATTG TAGAGGTTTCCAAGTATTTATCGT A
68328	G/C	CAGGCAGTTTGCGGTTACAG	CAGGCAGTTTGCGGTTACAC	A
68391	A/G	CAGCGTCAAGTTGTGGTGTT	CAGCGTCAAGTTGTGGTGTC	GCATCGCGTGACATTAGTTACA
72226	G/A	GAGGTTCTGACATGCAGGAAACG	GAGGTTCTGACATGCAGGAAACA	GCTCTGCAGATGCAAGTTCCAA
77668	G/A	GGAACGTCGTGACAGCCGTAG	GGAACGTCGTGACAGCCGTAA	GGATGGCTTCGAGTTGGACTACTA
78934	G/C	AAAGAAGCGTTTCCCGGTTCG	AAAGAAGCGTTTCCCGGTCC	TCTGGCAAAGCAAGCACTCACC
81501	T/C	GTCCTTTCGAAGGTGTATGCATTC	GTCCTTTCGAAGGTGTATGCATTT	ACGATGCTAGTTTGTCAAATAGTG

locus	variant	Primer1-specific to allele1	Primer2-specific to allele2	Primer3-common to both alleles
81758	G/A	ACAAATCTGAAGCAGGCGCGAAAG	ACAAATCTGAAGCAGGCGCGAAAA	AGGACGTCGCCGAGTCGTAGAT
87199	T/C	GCTGGATTGCGTCGTTCGCCT	GCTGGATTGCGTCGTTCGCC	CGGCTCTGGCCAGGACCTGATG
93695	G/A	GTCCTAGCCGCTGTCCCGTG GCATAAGCAAACCTTCAAAGCTTCCAC	GTCCTAGCCGCTGTCCCGTA GCATAAGCAAACCTTCAAAGCTTCCAC	CTGGGACAAACTCTTTCTCGAAGTG
96296	G/A	G	A	ACGAGGCGGCTCTCATGTACCA
105385	T/G	CCGCGAGCATTTTTGCCACATG	CCGCGAGCATTTTTGCCACATT	TTGACGTCACGACCTATTTGACGAA
113142	A/T	GAGCTCATAGTCCTGAAGACCACA	GAGCTCATAGTCCTGAAGACCACT	TTACGTTGGTCACTATGGGAACGCT
114791	G/C	CGCTGCTAGCAGACGGGAGG	CGCTGCTAGCAGACGGGAGC	GAGAGCGTACACGATTTGCCACGA
116335	A/C	GTGCGTCGAATGTCCAGGTTTATCC	GTGCGTCGAATGTCCAGGTTTATCA	CAAGTTGCGCAAGAGGTGGCAA
125671	C/T	GTCTGCTTCTGCTATGCTCTGTTTC	GTCTGCTTCTGCTATGCTCTGTTTT	AGCGTCTGCTGCGGAACATCGTA
129322	T/A	CAAGGCAGCGCAGTTCTGACACT	CAAGGCAGCGCAGTTCTGACACA	ATCTGCGTAGCATAAGCCGTGCC
133049	G/A	ACGGGTCGTACAGCGACAAGAG	ACGGGTCGTACAGCGACAAGAA	CGAACATTACAAACGCCGCAAGAGG
137096	T/G	GTGAATGGCAATGCCAGAGTGTAT	GTGAATGGCAATGCCAGAGTGTAG	CTCGGTATTCTGCGGAGCACAA
143089	G/A	GGCACAGGATTTGCTGGTTATAGAGG	GGCACAGGATTTGCTGGTTATAGAGA	GGTGCTATGTGTACCTCACGCC
144259	C/T	GTTGAGTGTCTGCTCCTTCGCC	GTTGAGTGTCTGCTCCTTCGCT	AACAGCTCCTCGTAGACTGCGTAC
145634	C/T	CGGACGCGTGGACGTGACTC	CGGACGCGTGGACGTGACTT	TGGTGACCGTGTGTTGCGCAG
150669	T/C	TGTGCACAAGATGATTCCATAATT GAATGTGATCGTGGGAGAAGATATAG	TGTGCACAAGATGATTCCATAATC GAATGTGATCGTGGGAGAAGATATAG	GTCATCGGTGATTGTGTCAGTTTAT
155043	G/A	G	A	GCTGTGGAAGCTAAGTGCTCGTTG
159151	C/G	AGACAACGTACGCGGATTTTAC	AGACAACGTACGCGGATTTTACG	TGCTAACTGCCAGCGCGTGG
166766	A/G	ATCGACCGGCTGGCTGGCTA	ATCGACCGGCTGGCTGGCTG	GCCTGTTCTTCTGTAAGTCGCTCTA
167418	T/A	TGTCCGATACCTGCCTCCAATTTGTT	TGTCCGATACCTGCCTCCAATTTGTA	TTACCTCCACCGGGTGTCCCAT
175115	T/C	ATGGCAGTGTCAAGAAGGCCAAGT	ATGGCAGTGTCAAGAAGGCCAAGC	CAATGGCAGTGTCAAGGTCGATCTC
176991	C/A	AGAAGCTAGACGCAGAGTTAGGGC	AGAAGCTAGACGCAGAGTTAGGGA	AGGAAGAGTCCAATGTGTGCGCAA
180239	G/T	GTCCGTGTGCTGTTGCCGCCG	GTCCGTGTGCTGTTGCCGCCT	TGTTCCCTGGACGCAAGTCACG TCTAAGGCTCCTGGTGTAAAGCACAC
189207	T/A	TGGGCGTTGCAGTAATGCAACAGTT	TGGGCGTTGCAGTAATGCAACAGTA	G
197784	C/T	GTTTCATTAGAAGCTGTCAGTTGACTC	GTTTCATTAGAAGCTGTCAGTTGACTT	CAGTGGCGTAACACGAGAACTAG
198227	C/T	GACAACATCCAGGGCGAGTTCTAC	GACAACATCCAGGGCGAGTTCTAT	TTGCTATAACCAGTCTTCGACGC

locus	variant	Primer1-specific to allele1	Primer2-specific to allele2	Primer3-common to both alleles
205578	G/A	GATGTAGCCCCAGATATACTCAAAG CGAGGTAAGATTGCCACTTATCTTTC	GATGTAGCCCCAGATATACTCAAAA CGAGGTAAGATTGCCACTTATCTTTC	ACAGGTACTAAACCAATTTTCGGC
207995	A/C	C	A	ACCACCTGCCAGTGTTTCGACGAT
208593	C/G	GGTCTGGTGCCTGGAAAGTGC	GGTCTGGTGCCTGGAAAGTGG	GGACGCAGTAAACAGAGCAGTCATA
209761	C/T	ACATCATAAGTCACGTGGCCTGAC GTGATTCTGCTGGTGTCTTTGTGAT	ACATCATAAGTCACGTGGCCTGAT GTGATTCTGCTGGTGTCTTTGTGAT	ACGCCGTGACGTCTCCTGAT
210654	T/C	C	T	AGCACGCCCAACAAGATCAACGG
212829	C/G	GGCATCTGAACGACATCGTCCACC	GGCATCTGAACGACATCGTCCACG	CGTGTGTCAGGAATGAGAGATAATC
214684	T/C	GTAACGCCGTACACGGTAAGAC	GTAACGCCGTACACGGTAAGAT	CTGTCTGATCCAGGCTTTACGCAA
221603	T/C	AGTCGATCATACTTACTGCTGTGT	AGTCGATCATACTTACTGCTGTGC	TTCGCGAGTCCGAGTTGCACAGA CTATTCCCCTTTTCGATCGAACATCG
224277	C/A	ACAGCTAGGAGCAAAGTCCAGTTCCC	ACAGCTAGGAGCAAAGTCCAGTTCCA	G
225377	G/A	TAAAGAGTCGCCTTGGGGAATCTGG	TAAAGAGTCGCCTTGGGGAATCTGA	CACGGACAACAACATTGAACGAG
230247	T/G	GTTTCCAGCTCGCGGTTCGATT	GTTTCCAGCTCGCGGTTCGATG	GACTGCGTAGAGTGCCTTTTCAA
233961	A/C	GTCATGCATTTGACAAACTTTGTTA	GTCATGCATTTGACAAACTTTGTTC	GACACTACTAGGGCCTCAATCAA
234508	C/T	TGCTGTGCTACGCTCGACC	TGCTGTGCTACGCTCGACT	GAGAGCAGCTCCTGGGAGTCCTTG
236290	T/C	GATGCAATATGTTTACTGGATTTCG	GATGCAATATGTTTACTGGATTTCGT	TAGAAATCGGGGCCCAACGG
243436	T/C	CTTGTGCCTGGCGTCATCTGT	CTTGTGCCTGGCGTCATCTGC	AGGCCCGTGCTCGCTCG
251320	T/A	AGGATCACGTTATACGAAGGCAAGT	AGGATCACGTTATACGAAGGCAAGA	CAAGGATGACAGCACCGGTACGA
255757	T/G	TTCATCGGCGTATCCTTTGAGCGAT	TTCATCGGCGTATCCTTTGAGCGAG	ATGATGGCGACGTAGAGGTAGTTCA
259770	C/G	ACCCTTTTTGAAAGATGAACGTTGTC GACACTACTAGGGCCTCAATCAAGCA	ACCCTTTTTGAAAGATGAACGTTGTG GACACTACTAGGGCCTCAATCAAGCA	CGTTGCTCAAAGTCAAATGCCAGTG
281206	T/G	T	G	CAGTCATGCATTTGACAAACTTTG
283680	T/A	GGCGAAACCTTTGAAGCGTTCTTCAT	GGCGAAACCTTTGAAGCGTTCTTCAA	GACAGCGTGATGACTGTTCTTGTG
287805	T/G	CTGCCGCCTGTAATTTCCCGACT	CTGCCGCCTGTAATTTCCCGACG	TAGGTTACAGACACGAGGTTGATTC
292025	C/T	AACGCCGTGAAAGCCGCGAAC	AACGCCGTGAAAGCCGCGAAT	GCACACCGTACATACCCGAAGCC
296275	C/A	CTGCGTAGAGTGCCTTTTCAAGGTC TTTGTTCAGTTGTCAGAGGTGGCAGT	CTGCGTAGAGTGCCTTTTCAAGGTA TTTGTTCAGTTGTCAGAGGTGGCAGT	TCGTTTGGTTTCCAGCTCGCGGT
298125	A/G	A	G	CCTTGTGGCATGCTCCAGTGATTC

locus	variant	Primer1-specific to allele1	Primer2-specific to allele2	Primer3-common to both alleles
299627	C/T	GGTATCCGCTCGCTCGATATGTATAT C	GGTATCCGCTCGCTCGATATGTATAT T	CGTGTGCAGCTATCCAAAGACTCG
300752	T/G	AGATGCTGAACTGTCAGATGACGAAT	AGATGCTGAACTGTCAGATGACGAAG	ACCACTGTAGTTGTGTCTCGCTCTG CTTGGTTAGTTTCTGCTGGCGTTTT
303781	C/G	CTCCAATTAGCTTCAAATGAATGTTT	CTCCAATTAGCTTCAAATGAATGTTG	C
305888	C/A	GTTTCCTCCACGCAGAGCGAAAGA	GTTTCCTCCACGCAGAGCGAAAGC	CATGCGCTTCGCACTGTCTG
307361	T/C	GCGGTATTTTCGGTCAGGC	GCGGTATTTTCGGTCAGGT	GACAAATGTTTCGTCTTCTCAACAG
313057	A/C	AATAGCGGCCAGCAGTTCCTCATA CAAATTTTCGTGTTTCGTCCATGGCGTG	AATAGCGGCCAGCAGTTCCTCATA CAAATTTTCGTGTTTCGTCCATGGCGTG	CGAATCCGATAGTGCCGTGAGAGA
320000	A/C	A	C	CGTGACTTGACGTGACGTGCCA CTTTCCCAGTTCAAGCACTCTTTTA G
329834	T/G	TAGAAAGCCGGCCCGGATCTT GCTCCTCCATGTCTTGTCGTCGTTTC	TAGAAAGCCGGCCCGGATCTG GCTCCTCCATGTCTTGTCGTCGTTTC	
333882	T/C	T	C	CACGGTGGCAGCGGGAA
336267	G/T	GCGTTGTCTGTACATCCGCCAT	GCGTTGTCTGTACATCCGCCAG	GAGCGCAGCGGATACTCTGTTCA
339272	A/G	CCGCACCGGCTTTTACGACA	CCGCACCGGCTTTTACGACG	TCTCGTCGCTGGAGGCGTCAT ACTGAGTGGTTCTAGTAACGATGGC T
340581	C/T	CTGAACCCAACGTTGGCTGAACT	CTGAACCCAACGTTGGCTGAACC	
356074	G/A	AAGTATGGGGGAACCCGTGTGA CATTTGCGATAGGTCGATCACGATAT	AAGTATGGGGGAACCCGTGTGG CATTTGCGATAGGTCGATCACGATAT	TAGGAGTTGGAACACTGCGACG
356395	G/A	G	A	CCGACTTCCGACGCATGTAAAATG
371093	A/G	AGCGATGGCGTCTACCAGCGGA	AGCGATGGCGTCTACCAGCGGG	TTCTGGACTAGCAGCGAGCGAC
374382	T/C	CATGCTTTGTCAACTTTTCGAGAT	CATGCTTTGTCAACTTTTCGAGAC	TTATGCTGTCAGCTGAGTCCCG TGTAGAGTGTAGATGCCAGCTTCCT C
376474	T/C	AGGTGGCCACTCTGACATGGATC	AGGTGGCCACTCTGACATGGATT	
380487	C/T	CAGCCGTTTCGACGGGATC CTGCATGTCTTGGCGTCTGATGTCTT	CAGCCGTTTCGACGGGATT CTGCATGTCTTGGCGTCTGATGTCTT	TCGCTCGTGTCCCTCGTGT GGTTCACTGGCCAAACGCTCCTCTA C
393248	T/G	CT	CG	
399212	A/G	GTTCAATGGGGCTTCTGCTATCA	GTTCAATGGGGCTTCTGCTATCG	GCGTGAATTCAACGTTTCGCTAAG
411541	G/A	AGTCGTTGTGGGCGCGCATGGG	AGTCGTTGTGGGCGCGCATGGA	GTCAGGCTGTTTCGGCTTGACGTATG

locus	variant	Primer1-specific to allele1	Primer2-specific to allele2	Primer3-common to both alleles
419658	T/G	TGTCCTCGTACGTGCTCGTTGTGACT	TGTCCTCGTACGTGCTCGTTGTGACG	AGCAGATGGCCTGGTAGCGGTCC
428503	G/A	CATGCAGGATACCGTGTGAGTTCAG GCACTGCAAACACCTCTGCTCAAGTA	CATGCAGGATACCGTGTGAGTTCAA GCACTGCAAACACCTCTGCTCAAGTA	GATGCTGTGCGCGTTGGACTG CTATGAATGCTCTTGCTAGCAGGCT
438644	A/G	TG GAATTCCAAACGCGGTTTCATAAACCA	TA GAATTCCAAACGCGGTTTCATAAACCA	TTA TCGAAGATAGTGTGCTCAATGGCGG
441042	A/G	CG TTGTTGCGAACATAGAGTACAGAGGA	CA TTGTTGCGAACATAGAGTACAGAGGA	TTA
446758	T/A	GCA	GCT	GCTACAACGTGGGAATTGCCGAGGA
450975	T/G	TGCGGTTACGCAGTCGAAGCTATT	TGCGGTTACGCAGTCGAAGCTATG	ATGGGCACTCAAGGTGCGCACG
465604	A/T	CCTAAACGTCTCGGCGCTAATA	CCTAAACGTCTCGGCGCTAATT	AACTAAGACCACATTCCCGACATTG CATGCTCTTTCTGTTGTCCGGTTC
465892	G/A	CCCCTGACGAGCGTGCTGAAGA CATAACGCTGAATTATCTTCGCCGAC	CCCCTGACGAGCGTGCTGAAGG CATAACGCTGAATTATCTTCGCCGAC	A
468480	A/G	TA	TG	GTAAGGGGCCCACAAGCCTGG
480915	A/G	CTAATTCTCGTTCTACTGCCGCATG	CTAATTCTCGTTCTACTGCCGCATA	GGACACATCTCAGAACCAGATTG
487540	T/C	CACGGGAACGACGGGCACT TAGTGGGTTTCGCTGAAGAACTACAAG	CACGGGAACGACGGGCAACC TAGTGGGTTTCGCTGAAGAACTACAAG	GGCACGTGAAGCTCCGAGATTTTCAT
493429	A/G	AA	AG	CGCGCAGCTTTCTGAAGTAGTTGT GTTCTGGACTAAGTATGATTCGCTC
552113	T/A	TCATAGTTGGTTCACAGGCGACCT	TCATAGTTGGTTCACAGGCGACCA	CA
558063	A/G	CAGCTCCTGGGAGTCCTTGAGA	CAGCTCCTGGGAGTCCTTGAGG	AGTGGCTGCTGTCGCTACGCT
561492	T/C	ATCTTGCGACTGCTCGAT	ATCTTGCGACTGCTCGAC	TTCTCGCCCAGGAATGCCAT
580716	T/C	TCGGCGTTCAGCAGGCTTGAC	TCGGCGTTCAGCAGGCTTGAT	GCACCAGACCGCCGGCGA
583125	T/G	TGTTCTGAGGAAATGAGATGACTGTT	TGTTCTGAGGAAATGAGATGACTGTG	CAACACACGTCAACAGCAACAT
585284	T/A	GCTTCAGTTATCAGCTGTAAACCTA	GCTTCAGTTATCAGCTGTAAACCTT	TTCGGTAATGCGTGTATTACTCA
585318	A/G	GTACATCACCGAAGCCGAACAG	GTACATCACCGAAGCCGAACAA	TTAGCCGCAACGCCGTGAAA CAAGAAACGGCAACAGCGGACAATG
589219	C/T	ATGCCGCACGTGCTTGAGGTC	ATGCCGCACGTGCTTGAGGTT	AAC
627150	A/C	CAATACAGCGGTATTTGCACTA	CAATACAGCGGTATTTGCACTC	CAATGGAGCAGACGCATCT
751708	G/A	TTGAAGCACAGCTCTTAGAGAAGG	TTGAAGCACAGCTCTTAGAGAAGA	GACTCCGTCAGCTGGTTTATG

locus	variant	Primer1-specific to allele1	Primer2-specific to allele2	Primer3-common to both alleles
754496	C/G	GCCTCGGCGTCGGAAGCTCG	GCCTCGGCGTCGGAAGCTCC	TGGCTGAAACCAGGGACCTCAA
761047	G/A	CAACATGGACGTTTTCAAGATTGCCA	CAACATGGACGTTTTCAAGATTGCCG	GAGCCTCGCTCAGCACGGAA
763022	T/C	CACAAAGGGCAGGATTTCTCT	CACAAAGGGCAGGATTTCTCTCC	AGATGAGTCTGCCATCGTGTCT
764527	T/A	GGGCGTTGCAGTAATGCAACAGTA	GGGCGTTGCAGTAATGCAACAGTT	AAGGCTCCTGGTGTAAGCACACG
767569	A/G	AAACACACCTTGAAGTCAGCCTCA GAACAATTCAAACCATGATTGAAAC	AAACACACCTTGAAGTCAGCCTCG GAACAATTCAAACCATGATTGAAAC	GGACGACAGCTATCAACATTAGCC
768618	C/G	AC	AG	TACTACTCCCAAGTGAGTTGATGC
771828	T/C	GATCCAAAGTGATCATGCCGATAGT	GATCCAAAGTGATCATGCCGATAGC	ATATCACAGTATCACGTCACGG
775381	A/G	TGTGCAGCTATCCAAAGACTCGG	TGTGCAGCTATCCAAAGACTCGA	ATGGTATCCGCTCGCTCGATATGT
777961	C/G	CTCAGCACAAGTGAATGTCAAG GGCTCTATGTAGAACCAAAGATAAGT	CTCAGCACAAGTGAATGTCAAC GGCTCTATGTAGAACCAAAGATAAGT	GGCATTGTGTAAGCATCTTATCGC
781023	G/T	GAG	GAT	ATTCTGCGGCTTCAACGAATCA
783090	G/A	ACCCGTACAGCAAACCACTACG	ACCCGTACAGCAAACCACTACA	CGACTGATTTCTCGCAACCCA
792422	T/C	TGCCACGGTAGTTTTGCTTAGT	TGCCACGGTAGTTTTGCTTAGC	ATGTTCCACGAGGCCCGTTG
43247	C/T	AGTAGACTTAAAGGCCACGCTCGAC CAATCGAAATCGTGACCAATGGGATT	AGTAGACTTAAAGGCCACGCTCGAT CAATCGAAATCGTGACCAATGGGATT	CCTTATATTCTCTGTGTCAGCGTAAG
84140	T/C	C	T	ACCAAGTGCCGCGCAAAGCAT
117944	C/T	CGAATTCTGAAGGCGGAGATCCTC	CGAATTCTGAAGGCGGAGATCCTT	CGGCTTGGCGAAGCGACG
316915	T/G	CGCTTCGCCGAGCACTCG	CGCTTCGCCGAGCACTCT	ACCGGTTGTGCTACGCGTAGGT
197588	T/G	CAAGCGCATCCCCATTCTGATCTT	CAAGCGCATCCCCATTCTGATCTG	CTTAGAAAGGCAAGACCTCCTTCA
2932	C/T	CTCCTACGAGGGGTGCCTGT	CTCCTACGAGGGGTGCCTGC	TTGTGACGTTCCCTCGTGCTCCCT
112567	C/T	GCTCATGCGCATTGGAAGC	GCTCATGCGCATTGGAAGT	TTGCACGTACTACGTGCCCTCTG
207179	T/C	CGCACGGAGATGGCATTCCCTC	CGCACGGAGATGGCATTCCCTT	ACACGATCTTCGGCGAGAACGTCA
165428	G/C	GTCCGCCACGTCCGTTCCAGAG	GTCCGCCACGTCCGTTCCAGAC	AAGCGGGGCTCTGCTTCCGCT
109194	C/T	AGGCCACAACCTCCACTCTTC	AGGCCACAACCTCCACTCTTT	TACGGTAGCTATGTAACAGACACTA
139650	C/T	TACGACGGCACCAGATC	TACGACGGCACCAGATT	ATCTCCGGCGAGGCGTACA
56083	T/C	CCAGGCGCTCCTCCTCGGTC	CCAGGCGCTCCTCCTCGGTT	CGCCGGAGTTGGCCCAGGA
143860	A/G	ACAGGTACACGAACGATCGCAGAA	ACAGGTACACGAACGATCGCAGAG	TGCGTTCGTGCTTGTGTCATGT
152555	A/G	GCTCCAGGACAACCGTTTACCTCA	GCTCCAGGACAACCGTTTACCTCG	ATGGAAACATCGCTACACATGG

locus	variant	Primer1-specific to allele1	Primer2-specific to allele2	Primer3-common to both alleles
51899	A/G	GAGGTGTACGAGTGTCACTCGAAG	GAGGTGTACGAGTGTCACTCGAAA	GTATCTAGGAGGCTCGGGCGAAA
225801	C/T	GACTTCTGACATTTGATAGAATGCTC	GACTTCTGACATTTGATAGAATGCTT	TGCGGGTCAGCCATCTTACAAGTA
190468	G/A	TGAACGAAGCTGAGAGGCGCTATGA	TGAACGAAGCTGAGAGGCGCTATGG	TACGCCAGACACTCTTGTTCAGT
31277	C/G	ATCATAGACCAACTCGCCTGCATC	ATCATAGACCAACTCGCCTGCATG	GATTCTGGAAGACAGCTTTTTTCGC GGATTTCCGAGAGAAGCCATTTTCA G
455987	G/C	AATGTACGCGACGTACGCACAAG	AATGTACGCGACGTACGCACAAC	G
27147	T/G	CGCAATTGTGACACCACTAG CCGCATTTCTTCACTGCTGTTTGAAA G	GCGCAATTGTGACACCACTAT CCGCATTTCTTCACTGCTGTTTGAAA T	CGGCTTTTGATACTCCCATCA
751588	G/T	G	T	TCGCAAATCCTGGCGCGGTAA
313642	T/A	GTGCAGTTGGCAATGGAGGTGA	GTGCAGTTGGCAATGGAGGTGT	CCGGACAACCTGAAGGTGGTGC
182969	G/A	AAGACGCACTTGCCCTGGAAACATG	AAGACGCACTTGCCCTGGAAACATA	GGTCTGAGTCTTGGTTGTGTGCAT
186625	A/G	GAGGAGCTGCGATGCAGAAGTGGTA	GAGGAGCTGCGATGCAGAAGTGGTG	ATGCTGATGACGCAACGCTGACTTC
191703	A/G	CCGCCGTCTTTGCAGCCTCA	CCGCCGTCTTTGCAGCCTCG	GGGGCCCCGATTTCTAGAAC
438440	A/G	GTTGAGCGCATGCGCAGGGAA	GTTGAGCGCATGCGCAGGGAG	ACTCCCTGACGTAGCCTTCGTAGGA
82163	T/C	TAAGGCTTCCAGGTGACTTC	CTAAGGCTTCCAGGTGACTTT	GGTGTGTTGCTTCTATATTG
788521	C/T	ACCCGAACCTTTCAGGCCAT	ACCCGAACCTTTCAGGCCAC	AATGAACGACCGAGCGAATCCAGA
233756	C/G	TCTACAAACCAGGCGGTTGTAAGC	TCTACAAACCAGGCGGTTGTAAGG	TCTGTTTGGGACTCCTTCCACCG
201653	G/A	GCAGTCATCAAACGTGATTTTCGTCCG	GCAGTCATCAAACGTGATTTTCGTCCA	AAATTGGAGAGATCACTTGACCCGC
259800	C/G	CGTGTGCCTCGCTGGCATC GACACCCTAGCAAAGCAAAGCGTTCT C	CGTGTGCCTCGCTGGCATG GACACCCTAGCAAAGCAAAGCGTTCT T	GCGCATTCCAGAGGCTTCC TTTCGTTACGGCTCCCGCAA
370147	C/T	C	T	T
153000	G/A	CCTACCTGCTTCCAACATTCTTTAGG	CCTACCTGCTTCCAACATTCTTTAGA	TGCACATTAGGTCAGAGATGCGGA AGACGATTATTCGGCTGTGACACAT T
500950	A/T	CCACAACCTCATCGCACCGAAGACT	CCACAACCTCATCGCACCGAAGACA	T
170547	C/G	GGTGAATACGCGTCGCGTGAGTC GAATATTTATGATGTGACCACGGCAA AC	GGTGAATACGCGTCGCGTGAGTG GAATATTTATGATGTGACCACGGCAA AG	GTGACCTTTGGTAGGACGGCAGC AACGCCCTGCCGCATAGTCC
466967	C/G	AC	AG	AACGCCCTGCCGCATAGTCC
246408	T/C	GGAAACAGTTATAACTATCTAGAACT	GGAAACAGTTATAACTATCTAGAACC	CACACCGAGAAATCAGACGTACC
5630	G/A	CAGCAAGCAGAGAACGTCGTCGATG	CAGCAAGCAGAGAACGTCGTCGATA	TTCAGGGTGAGACCGTCGGC
561563	A/G	TGAAGGATCTCGTACACAATACACAG	TGAAGGATCTCGTACACAATACACAA	CGAGTACTTCACGACCACGCA

locus	variant	Primer1-specific to allele1	Primer2-specific to allele2	Primer3-common to both alleles
338495	T/C	GGTTCTCGAAGCCGCGTTTC	GGTTCTCGAAGCCGCGTTTT	TCTGCAGCTGCTGTAGAGTCCTG
166887	A/G	TCGGCCGCCAGCAGCGTCA	CGGCCGCCAGCAGCGTCC	CCCGTCGGGAGCAATGCAG
766292	T/C	TGCCGAAGCTGGGTTTCGT	TGCCGAAGCTGGGTTTCGC	CTGGGCTGCTCCGAGGACTA
176206	G/T	ACTGCGATTGAAGTGCGTCCCG	ACTGCGATTGAAGTGCGTCCCT	ATCCTCTTGAAATTTGCTGCGGGTG
245496	T/C	TTCCAGCGTGCACCGTACC	TTCCAGCGTGCACCGTACT	GAAAATGCAATTTTTGTGAGCCT
199727	T/A	GGCTTCTTGTCTCGTTATTATCGT	GGCTTCTTGTCTCGTTATTATCGA	CAGTGCCACTTTTATGTGAGTTG ACTAATTCATTGTAACCCATTTTAC GAT
524153	G/A	CTCTATCAAACGATGTGCTACTGTGA	CTCTATCAAACGATGTGCTACTGTGG	ATGACTGTTACAATCTTTTGAATGC
54140	A/G	GGTAGACACAATCTGCTCATAATGG	GGTAGACACAATCTGCTCATAATGA	GGCGCGTATCATCCCAGAGC
18708	A/G	CTCCGCGTGTATGCGAGTGAA	CTCCGCGTGTATGCGAGTGAG	TCAAGGCCAACGGCGCGCA
546612	G/C	TTTCCC GCGCAGGCCGCTAG	TTTCCC GCGCAGGCCGCTAC	GCTCAGGATGTCGTACGCGCGG
523859	C/A	CTGGACCTGTGCTACCGTGAGTCC	CTGGACCTGTGCTACCGTGAGTCA	CGTCGACGGGCGATCGTGA
160279	A/T	ATCAGCAGCGCACACGCTCA TATCAGCTAAAGCCTCCTTCTCAGTC	ATCAGCAGCGCACACGCTCT TATCAGCTAAAGCCTCCTTCTCAGTC	GAACTGAAGCACCAGCGCCT TAAGAAGGTTGGCCCGAATTTGTGA A
624322	A/G	A GTCAGAGTAAGGATCTGCTAGATACC	G GTCAGAGTAAGGATCTGCTAGATACC	A
410904	C/G	G	C	A
71660	C/A	GAAATTAGAATGGTACCTGGATTACC	GAAATTAGAATGGTACCTGGATTACA	CCTTTGGGGTGCGCTTATGTAAT GGTTGTATTTACAACCTGACTCCTCG G
87165	G/A	GAATCCACGTGTCAGAGCCCTGG	GAATCCACGTGTCAGAGCCCTGA	CGATCCTGAAATCGAGCAAAGCC
61479	A/G	GGCTAATCCTGCTTCTTGGCCTT	GGCTAATCCTGCTTCTTGGCCTC	GGATGGATGCAAAGTGATATTTTAG CCTTTTTACGGACACTCACTTTTCT G
571455	T/A	GTTCTGCCAGCAATTCTATCACT	GTTCTGCCAGCAATTCTATCACA	CGTTTTCAATGAGTCTTGATTCTCG
270863	C/T	GCAATTATAGGATCTCCGTAAACTCT	GCAATTATAGGATCTCCGTAAACTCC	GTTTACGCGCATACTATGACTGACAA
185472	C/G	ATTCGCCAGACCACTTGGATTCTC	ATTCGCCAGACCACTTGGATTCTG	GCAGCAACGTTTGTTCAGA
200386	T/C	GATGGAATTAGGTACGGTCATTTTAC	GATGGAATTAGGTACGGTCATTTTAC	TCCACAGGGTACGTCGACGCA
40367	A/G	CACATGTGGCAAGCATTCAA	CACATGTGGCAAGCATTCAA	ATTAGCCAAGCGCCCCG
494898	T/C	AGCGTTGCACGCCATACATTCTCT	AGCGTTGCACGCCATACATTCTCC	GCTCACATGCATTGAACTGATGTC
14134	C/T	CATACATTCCCTGAATACCTAGAGC	CATACATTCCCTGAATACCTAGAGT	
361495	T/G	ATAACACAGGCAGACATTGGAGGCAG	ATAACACAGGCAGACATTGGAGGCAT	

Results

Table S3. Basic statistics per locus.

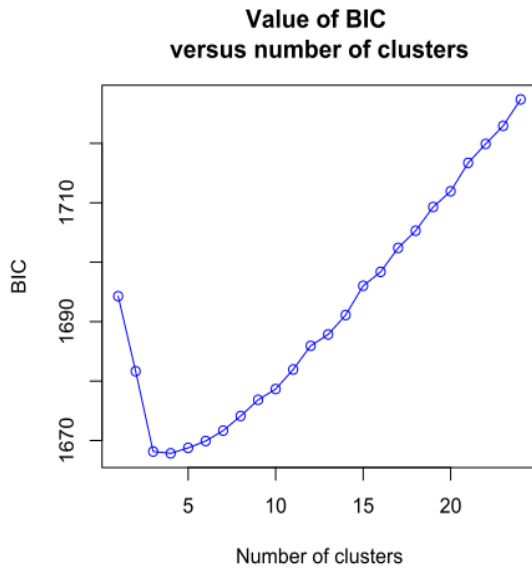
Locus	Observed heterozygosity	Gene diversity	Fst	Fis
1133	0.1101	0.2324	-0.0040	0.5262
31200	0.4319	0.467	0.0629	0.075
66390	0.1269	0.291	0.0539	0.5639
129322	0.0700	0.0873	0.0061	0.1974
159151	0.2649	0.3446	0.1504	0.2312
198227	0.5741	0.4987	-0.0093	-0.1512
221603	0.2760	0.3557	0.0932	0.2243
251320	0.1778	0.3271	0.1478	0.4564
298125	0.5543	0.4636	0.0127	-0.1956
329834	0.0918	0.2123	-0.0187	0.5675
374382	0.176	0.4705	0.0317	0.626
3705	0.1782	0.4146	0.0673	0.5704
32114	0.0759	0.1787	-0.0022	0.5753
68328	0.2477	0.3736	0.0396	0.3369
93695	0.2975	0.4519	0.0335	0.3418
133049	0.1991	0.3770	0.1375	0.4718
255757	0.2072	0.2468	0.2394	0.1604
299627	0.1109	0.2400	-0.0107	0.5381
376474	0.2141	0.3006	0.0491	0.288
6283	0.3140	0.4164	0.0634	0.2459
32551	0.262	0.343	0.0092	0.2361
96296	0.2678	0.3734	0.2144	0.2829
137096	0.5322	0.4652	0.0382	-0.1438
207995	0.8246	0.45	0.0726	-0.8323
225377	0.2191	0.3855	0.097	0.4316
259770	0.1676	0.2408	0.0235	0.3041
300752	0.4814	0.3724	0.1811	-0.2928
336267	0.2115	0.2254	0.0116	0.0618
380487	0.3168	0.4498	0.0807	0.2957
6363	0.3144	0.4011	0.1326	0.2162
34502	0.1219	0.3181	0.0031	0.6166
105385	0.3326	0.3783	0.0686	0.1208
143089	0.7837	0.4849	0.0132	-0.6163
208593	0.1799	0.2333	0.0843	0.2288
230247	0.2052	0.3581	0.223	0.427
281206	0.2277	0.3757	0.2359	0.394
303781	0.1121	0.2912	-0.027	0.6152

Locus	Observed heterozygosity	Gene diversity	Fst	Fis
339272	0.1745	0.1785	0.0237	0.0222
393248	0.0722	0.1882	-0.0019	0.6163
176991	0.1966	0.3406	0.029	0.4228
144259	0.1649	0.2687	0.0127	0.3863
113142	0.2391	0.3714	0.2421	0.3563
77668	0.4137	0.4424	0.0191	0.0648
42351	0.128	0.1783	0.439	0.2821
10041	0.1733	0.4534	0.0484	0.6178
399212	0.0839	0.3201	0.1127	0.7377
340581	0.0682	0.0911	0.0379	0.2513
305888	0.1105	0.1722	0.0151	0.3583
283680	0.6714	0.4485	0.0759	-0.497
233961	0.2212	0.3625	0.2481	0.3898
209761	0.0828	0.3481	0.0662	0.7621
180239	0.094	0.151	0.0109	0.3773
145634	0.3787	0.4585	0.018	0.1741
114791	0.2429	0.3708	0.0262	0.3449
57206	0.1859	0.3233	0.0253	0.425
19998	0.0914	0.1196	0.0199	0.2359
411541	0.227	0.3092	0.0348	0.2658
356074	0.2633	0.3343	0.0754	0.2123
307361	0.0887	0.1801	0.0333	0.5074
287805	0.0435	0.0744	0.0317	0.4154
234508	0.2516	0.3103	0.059	0.1891
210654	0.228	0.2674	0.4378	0.1475
189207	0.1252	0.3037	0.0042	0.5879
150669	0.2338	0.4764	0.0025	0.5092
116335	0.1823	0.3998	0.0415	0.544
81501	0.2806	0.4505	0.101	0.377
60684	0.2221	0.442	0.0547	0.4974
21130	0.1723	0.412	0.0976	0.5818
356395	0.3341	0.4604	0.0791	0.2745
313057	0.1085	0.388	0.0497	0.7203
292025	0.1001	0.1208	-0.0134	0.1714
236290	0.0798	0.1775	-0.0126	0.5505
212829	0.2648	0.4684	0.0637	0.4347
197784	0.3144	0.2259	0.1932	-0.392
155043	0.1033	0.1762	0.5208	0.4136
125671	0.3398	0.4652	0.0539	0.2695

Locus	Observed heterozygosity	Gene diversity	Fst	Fis
81758	0.1436	0.2886	0.1153	0.5023
61606	0.2479	0.3716	0.2166	0.3331
428503	0.3744	0.395	0.0206	0.0521
320000	0.2643	0.2579	0.1614	-0.0248
296275	0.1384	0.3744	0.2015	0.6303
243436	0.1853	0.2832	0.3311	0.3455
214684	0.2222	0.4963	-0.0018	0.5522
438644	0.1799	0.4129	0.149	0.5644
487540	0.0981	0.1404	0.288	0.3014
767569	0.1635	0.2148	0.0246	0.2389
165428	0.211	0.2398	0.0199	0.1199
191703	0.1966	0.3729	0.2489	0.4729
153000	0.0919	0.4793	0.0403	0.8082
166887	0.1921	0.3481	0.0653	0.4483
441042	0.3243	0.4491	0.0996	0.2777
84140	0.1825	0.3554	0.0587	0.4865
438440	0.0944	0.1089	0.1972	0.1325
766292	0.738	0.4745	0.0398	-0.5553
523859	0.3518	0.4397	0.1064	0.1999
270863	0.0571	0.23	0.0146	0.7516
446758	0.0327	0.1022	0.0336	0.6802
552113	0.144	0.219	0.0062	0.3423
627150	0.1918	0.4255	0.074	0.5491
117944	0.8044	0.4649	0.0642	-0.7304
139650	0.2503	0.2708	0.1388	0.0757
176206	0.3211	0.5036	-0.0175	0.3624
185472	0.1899	0.3965	0.0348	0.5211
450975	0.2154	0.3343	0.1091	0.3557
558063	0.2358	0.2929	0.0731	0.195
751708	0.0754	0.1006	-0.026	0.2506
775381	0.0911	0.2703	-0.0258	0.6629
27147	0.1022	0.3726	0.0636	0.7257
200386	0.1562	0.4361	0.1004	0.6418
777961	0.0977	0.3904	0.1195	0.7499
754496	0.3408	0.4748	0.051	0.2822
561492	0.0813	0.3268	0.0409	0.7512
465604	0.0536	0.2293	0.0085	0.7664
410904	0.1761	0.2763	-0.0034	0.3628
199727	0.1067	0.4443	-0.0179	0.7599

Locus	Observed heterozygosity	Gene diversity	Fst	Fis
751588	0.1149	0.3961	0.0719	0.7099
152555	0.1713	0.4355	0.058	0.6067
2932	0.0525	0.0604	0.0063	0.1315
781023	0.1682	0.4324	0.0954	0.6109
761047	0.1318	0.173	-0.0271	0.2378
580716	0.316	0.3822	0.0479	0.1731
465892	0.113	0.1621	-0.0162	0.3033
5630	0.7425	0.4783	0.0441	-0.5525
313642	0.1283	0.1442	0.0071	0.1102
783090	0.2976	0.3471	0.0268	0.1426
763022	0.1247	0.302	0.0606	0.5872
583125	0.534	0.4398	0.097	-0.2141
468480	0.3318	0.4527	0.0932	0.267
14134	0.1556	0.345	0.0144	0.549
259800	0.125	0.1671	0.0074	0.2517
182969	0.2349	0.2092	0.005	-0.1228
225801	0.1255	0.254	0.3865	0.5058
792422	0.402	0.4864	-0.0019	0.1736
764527	0.1107	0.2841	0.0287	0.6103
585284	0.1384	0.2335	-0.0063	0.4072
480915	0.0849	0.2483	0.032	0.6581
338495	0.2448	0.3455	0.0157	0.2915
186625	0.5284	0.4536	0.0852	-0.1649

A



B

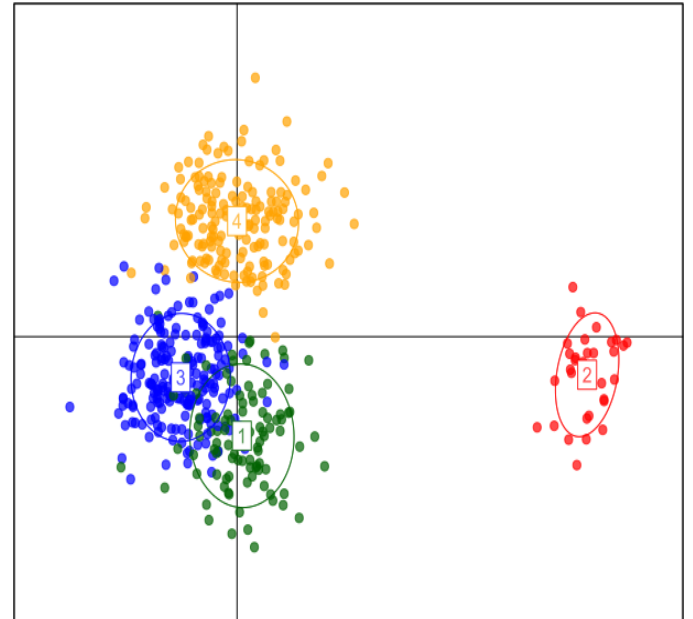


Figure S1. Discriminant analysis of principal component (DAPC) of *Ixodes ricinus* based on 497 individuals using 125 SNPs. A. BIC values as a function of the number of clusters k . The difference in BIC values between $k = 3$ and $k = 4$ is 0.842. B. Scatterplot of individuals on the two principal components of DAPC. The graph represents the individuals as dots and the groups as inertia ellipses. Two of the clusters overlap, while when $k = 3$ we identify 3 well separated groups (figure 3). Red : North African cluster; yellow : only individuals from southern Eurasian cluster; green : only individuals from the Northern European cluster; blue: admixture cluster with mainly individuals from the northern European cluster in figure 3.

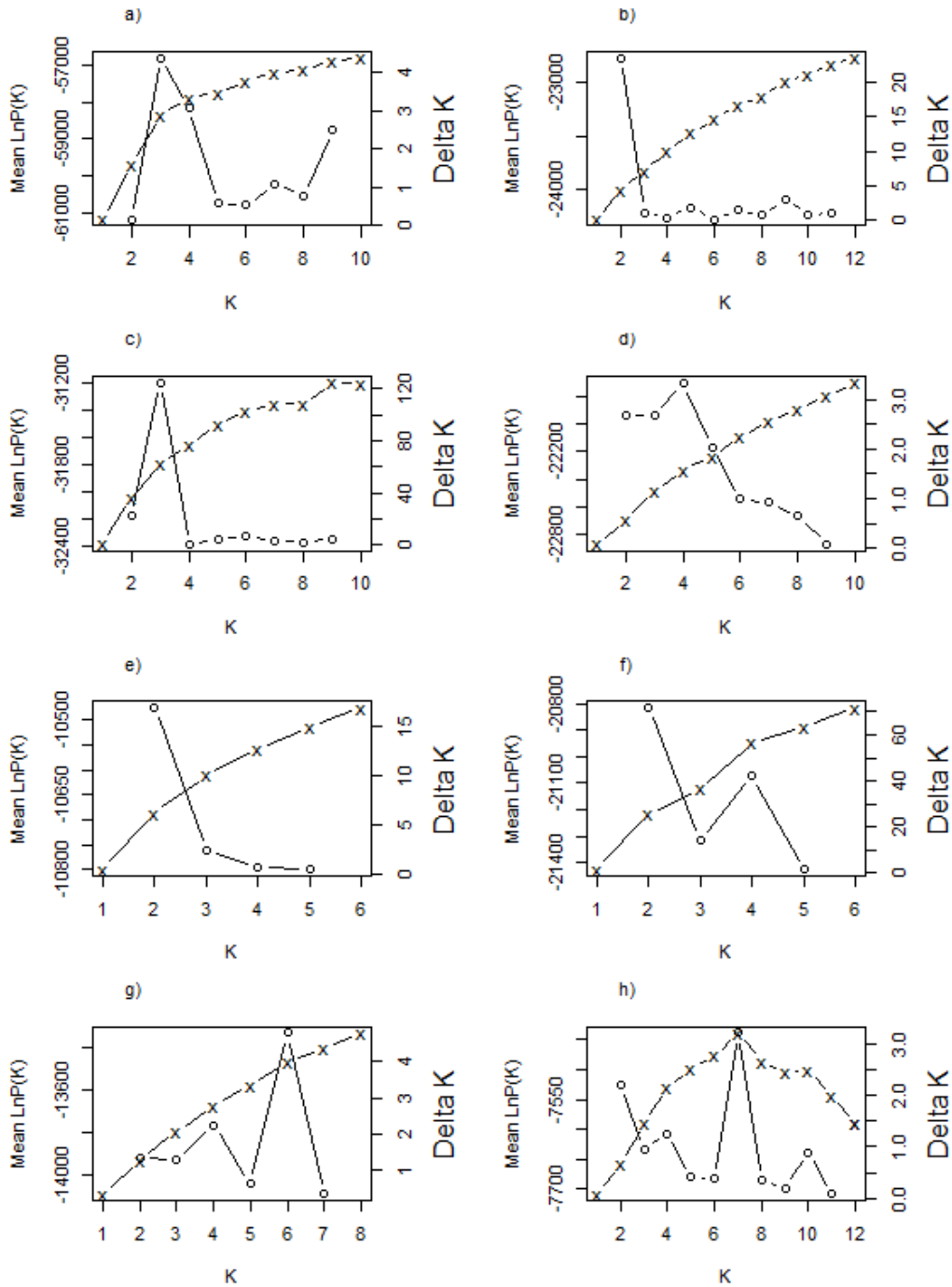


Figure S2. Probabilities $\ln P(X|K)$ for each level of hierarchical analysis. First round of analysis: a); Second round: b) southern Eurasian cluster and c) northern European clusters; Third round: d) Southern European cluster without Iran, e) Central Sweden, Norwegian West and East and North Estonia, f) Moldavia, North France, West German, Belgium, South Estonia, East German, South German and South Sweden; Forth round: g) Atlantic samples (Spain, South and West France, Ireland and England, h) South-west samples (Italy, Romania, Slovakia and Hungary), i) and i): fourth round of analysis. Details of each level of Hierarchical analysis are present in the corresponding session.

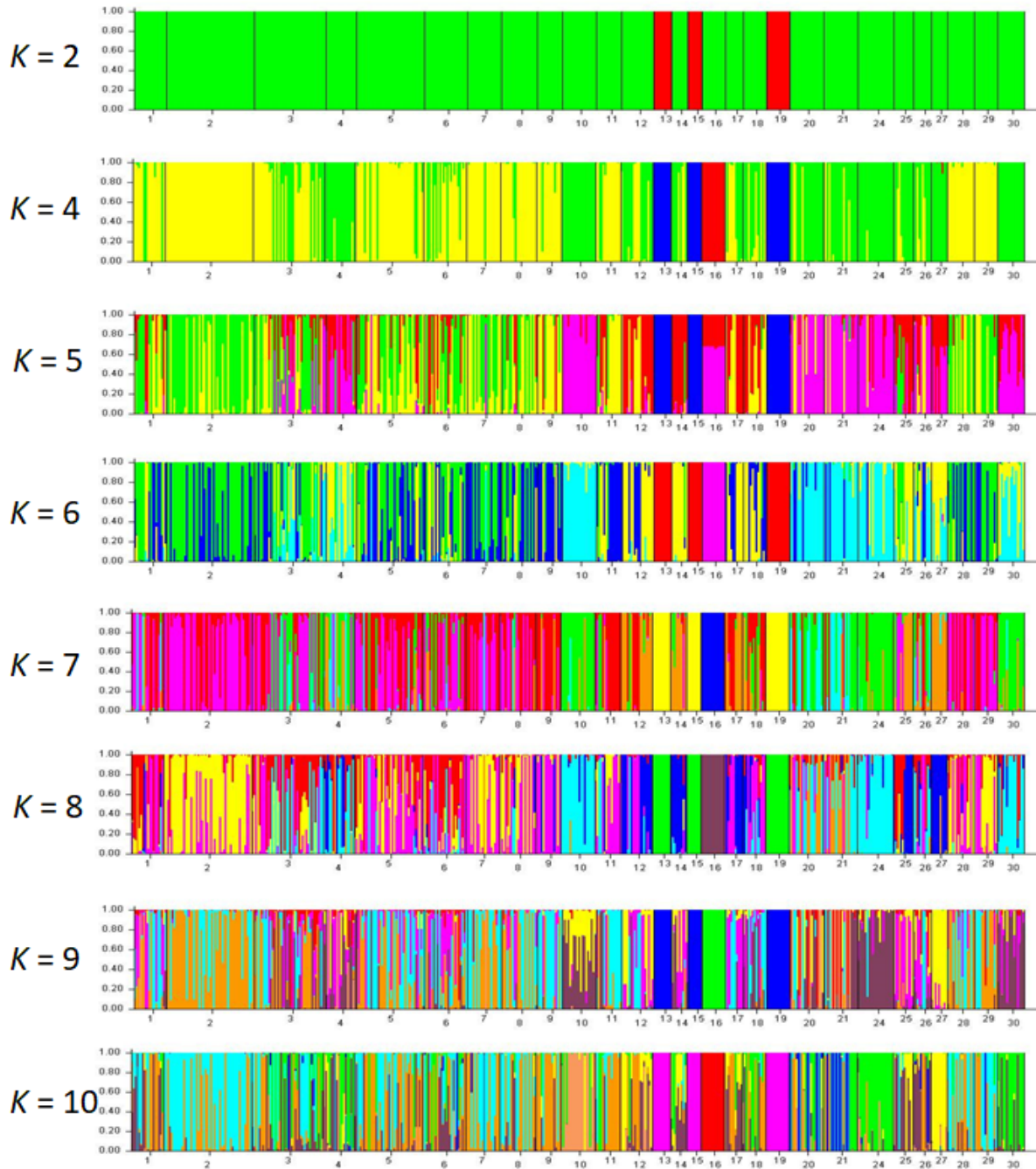


Figure S3. STRUCTURE Individual probabilities for each value of K from 2 to 10.

Hierarchical analysis

Finer genetic structure was identified from hierarchical analysis (Figure S6 and S7 for STRUCTURE and DAPC analysis, respectively). The southern Eurasian cluster was further separated into two differentiated clusters, irrespective of the approach used (STRUCTURE or DAPC). The STRUCTURE approach separated Iran from the remaining samples, while the DAPC approach assigned most individuals from both Iran and Turkey samples to the same cluster (violet). The northern European cluster was further separated into two to three clusters depending on the methods, DAPC and STRUCTURE, respectively. Clusters identified by the DAPC approach were distributed almost equally among the different sampled locations. Of the three clusters identified by STRUCTURE, the orange and green ones showed a clear affinity to certain sample locations, while the grey cluster was represented in all sampled locations. No further structure was identified for the African cluster in both methods.

The DAPC's third round of analysis was unable to identify further genetic structure in the northern European cluster. It did however identify two groups inside the southern Eurasian cluster (without Turkey and Iran as a result of previous analyse). It appears that individuals from Spain, Western France and Ireland were mainly assigned to one (light blue) cluster. No other cluster was identified by the DAPC approach regarding refined hierarchical analysis. The STRUCTURE's third round of analysis was able to identify a $K = 4$ in the southern European cluster. Individuals from Turkey were assigned to an exclusive cluster (grey). Individuals from southwestern Europe and from Italy were mainly assigned to one cluster (orange), while those from Spain, West France and Ireland were grouped in a different cluster (blue). The fourth cluster (green) was distributed across all sampling locations with few individuals (11 out of 179) exhibiting more than 50% of assigning probability. In the northern European cluster, for this third

round of hierarchical analysis, individuals were regrouped according to population probabilities *of the two almost exclusive clusters from last step, green and orange ones. From this third round until the last one, Evanno's method* (Evanno et al. 2005) always identified two clusters, but the analyses of $\ln[\text{Pr}(X|K)]$ was not clear in identifying those clusters (Figure SX). Also, individual probabilities of inside those $K = 2$ clusters show very mixed populations. The results for those subsequent rounds with a $K = 2$ are presented in Supplementary Information (figure SXX). We did a fourth and last round of hierarchical analysis for the two main southern Eurasian clusters identified in the previous round: (i) one cluster composed of Spain, West and South France, Ireland and England samples and (ii) the other cluster composed of Italy, Romania, Hungary and Slovakia. For the first one, Evanno's method identified $K = 6$, but the analysis of $\ln[\text{Pr}(X|K)]$ does not indicate any structure. For the later, both methods clearly identified a $K = 7$ structuring. In both cases, clusters are mainly distributed in all sample sites and very rarely a single individual had $\sim 100\%$ probability of being assigned to a particular cluster. The exceptions were individuals from West France and Ireland for which probability values to be assigned to the same cluster reached one.

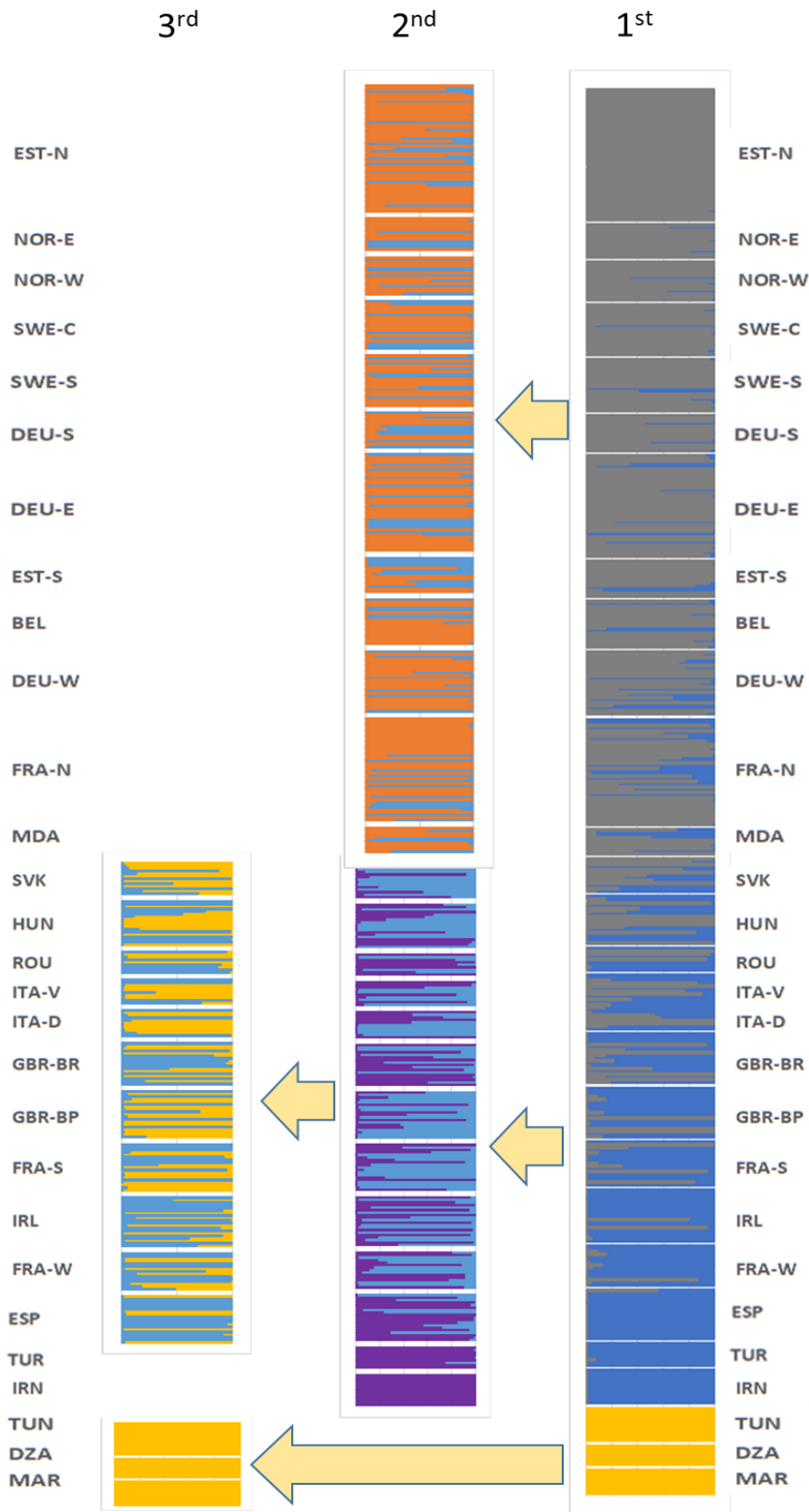


Figure S4. DAPC Hierarchical analysis. Each column corresponds to one level of analysis.

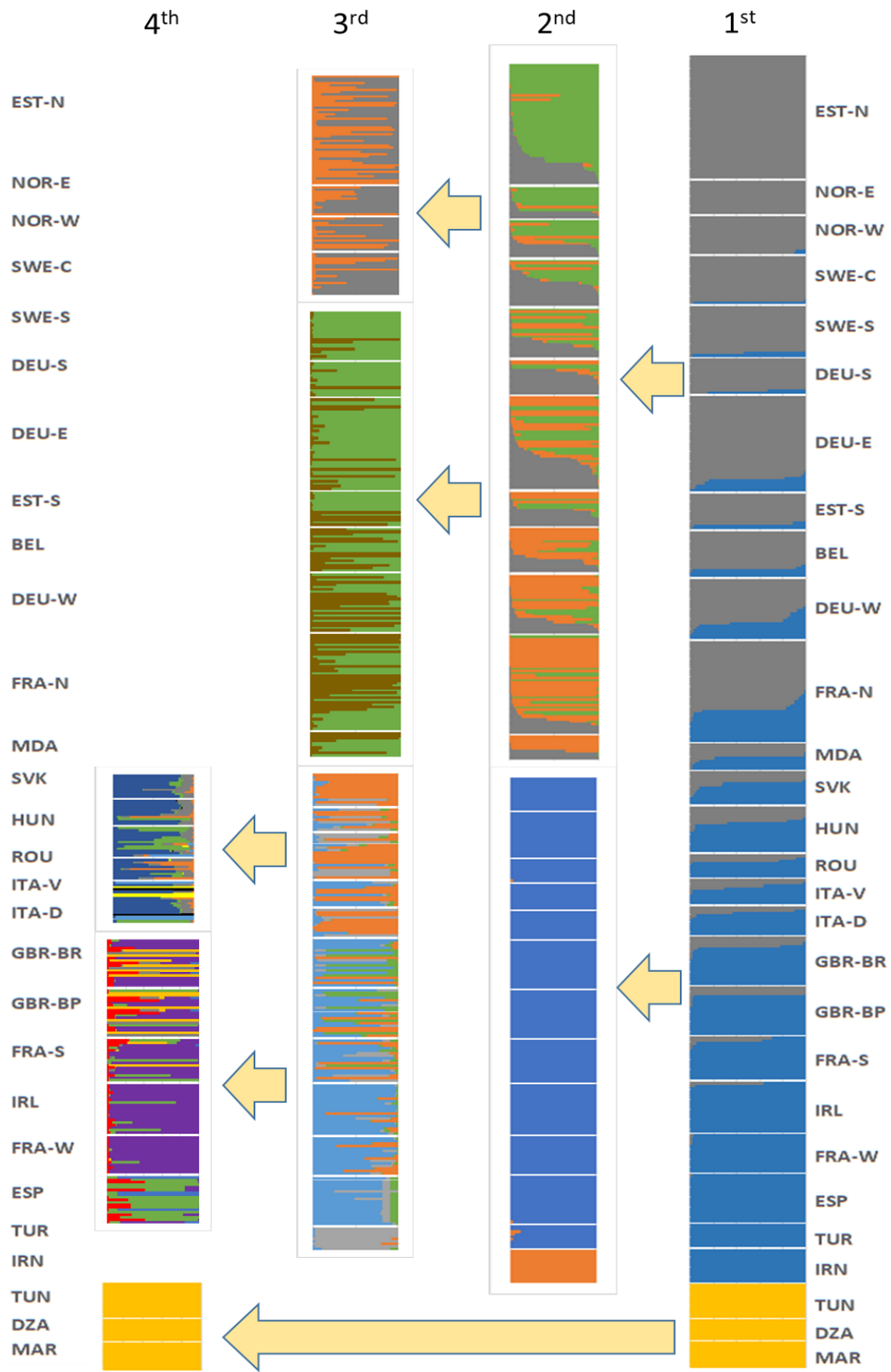


Figure S5. STRUCTURE Hierarchical analysis. Each column corresponds to one level of analysis.

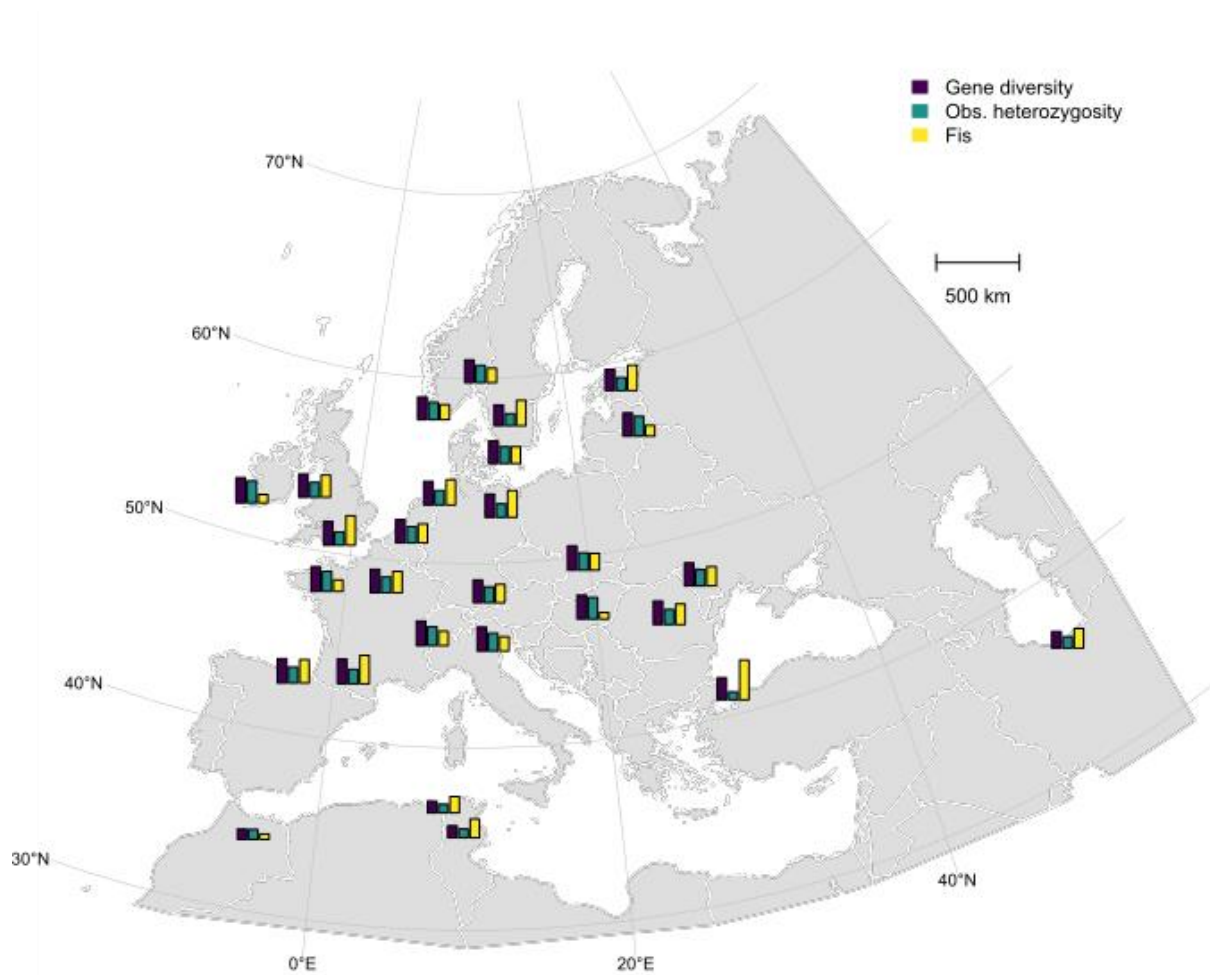


Figure S6. Mean gene diversity, observed heterozygosity, and *Fis* per population. Mean population gene diversity was always greater than the observed heterozygosity and *Fis* was always positive.