

Evaluating the functionality of expert-assessed wildlife corridors with genetic data: setting priorities for management measures in roe deer (*Capreolus capreolus*)

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1 **Evaluating the functionality of expert-assessed wildlife corridors with genetic**
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11 **Running title:** Genetic structure supports the functionality of wildlife corridors

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15 **Abstract**

16 Transport infrastructure such as fenced motorways may cause the loss of functional connectivity
17 in landscapes by impeding the passage of individuals and thus reducing gene flow. This may result
18 in increased genetic differentiation and possibly inbreeding, eventually leading to reduced genetic
19 diversity of wildlife populations owing to genetic drift. Landscape managers and conservation
20 agencies apply a range of measures to mitigate such adverse effects for wildlife in intensively
21 managed landscapes. Among these, expert-assessed wildlife corridors are used to evaluate the
22 permeability of a landscape for wildlife. The corridors are qualitatively categorized into intact or
23 interrupted. Here, we used landscape genetics to test whether functional connectivity among roe-
24 deer populations, inferred from spatial genetic structure, supports the expert-assessed categorization
25 of wildlife corridors in the Swiss Plateau and the northern Prealps. Though the genetic structure of
26 roe deer is not very pronounced at the landscape scale, we observed distinct local genetic structure.
27 Overall, wildlife corridors formerly identified as intact are supported by showing low genetic
28 differentiation between roe-deer populations (average $F_{ST} = 0.008$), whereas interrupted corridors
29 exhibited higher genetic differentiation (average $F_{ST} = 0.022$). This study serves as reference for
30 assessing the need to take management measures and setting priorities for reconnecting or
31 maintaining functional wildlife corridors.

32 **Keywords:** classification uncertainty; fragmentation; functional connectivity; genetic structure;
33 landscape genetics; landscape permeability; nuclear microsatellites

34 **Introduction**

35 Transport infrastructure and urban sprawl are major factors of habitat fragmentation in highly
36 populated regions (Forman, Sperling, Bissonette, Clevenger, Cutshall et al. 2002). Consequences of
37 such fragmentation include increasingly impermeable landscapes for wildlife movement (Frantz,
38 Bertouille, Eloy, Licoppe, Chaumont et al. 2012), which ultimately leads to a loss of functional
39 connectivity (Tischendorf & Fahring 2000; Epps, Palsboll, Wehausen, Roderick, Ramey et al.
40 2005). Barrier effects of roads, for example, may cause an increase in genetic differentiation of
41 populations, reduced genetic diversity (Kuehn, Hindenlang, Holzgang, Senn, Stoeckl et al. 2007;
42 Holderegger & Di Giulio 2010) or promote inbreeding (Corlatti, Hacklander & Frey-Roos 2009).
43 This indicates that habitat fragmentation caused by roads may constitute an important topic,
44 particularly in densely populated areas such as the Swiss Plateau where high road densities of six to
45 seven km road per km² are common (Klaus 2012).

46 The construction of motorways and the spread of settled area has impaired or blocked many
47 regionally important wildlife corridors in Switzerland since 1950 (BUWAL, SGW & Vogelwarte
48 2001). Wildlife corridors are expert-assessed axes of animal movement which are laterally
49 restricted by natural and anthropogenic structures or intensively used areas (BUWAL et al. 2001).
50 In Switzerland, only about a third (85 out of 303) of the wildlife corridors identified are considered
51 intact (BUWAL et al. 2001). To date, 40 regionally important wildlife corridors classified as
52 interrupted by motorways are already or will soon be restored through expensive mitigation
53 measures such as wildlife passages (Caron 2012; Klaus 2012).

54 It has been shown that fenced motorways are impossible to pass for some wildlife such as
55 ungulates whereas for other groups such as carnivores permeability may be reduced (BUWAL et al.
56 2001; Hepenstrick, Thiel, Holderegger & Gugerli 2012). Until now, there are a few, spatially
57 restricted studies about the effects of roads on the genetic structure of wild ungulates (but see

58 Coulon, Cosson, Angibault, Cargnelutti, Galan et al. 2004; Epps et al. 2005; Coulon, Guillot,
59 Cosson, Angibault, Aulagnier et al. 2006; Kuehn et al. 2007; Hepenstrick et al. 2012). As a
60 common and widespread species of relatively large body size the roe deer (*Capreolus capreolus*) is
61 a suitable model species for studying population genetic structure in response to landscape structure
62 and potential barrier effects of linear landscape elements (Hepenstrick et al. 2012).

63 This large-scale study identifies the genetic structure of roe deer in four regions of Switzerland to
64 evaluate whether the genetic structure reflects the expert-assessed categorization of wildlife
65 corridors into intact and interrupted. We expect to find low levels of genetic differentiation of roe
66 deer across the landscape due to potential bottleneck effects and/or founder events, but distinct
67 genetic structure at the local scale – if landscape elements indeed act as barriers to gene flow. The
68 local genetic structure can then be related to landscape elements which may act as potential barriers
69 and to wildlife corridors categorized into intact or interrupted.

70 A previous study of Hepenstrick et al. (2012) showed that linear landscape elements such as
71 fenced roads induced genetic differentiation of roe deer in a nationally important wildlife corridor.
72 However, the spatial genetic structure and the effect of multiple wildlife corridors have not been
73 investigated in a larger spatial context. Here, we present a reference study with a set of corridors for
74 assessing the need to take management measures, setting priorities for building wildlife passages,
75 and for controlling the performance of defragmentation measures.

76 **Materials and Methods**

77 **Study area**

78 The four regional study areas were located in the Swiss Plateau and the northern Prealps, and
79 ranged between 500 and 4,000 km² in size (Fig. 1; Table 1). The Swiss Plateau ranges from the lake
80 of Geneva in the southwest to the Lake Constance in the northeast with a mean altitude of 580 m

81 a.s.l., and the area is bordered by the mountain ranges of Jura and the Alps (Präsenz Schweiz 2013).
82 This part of the country is the most densely populated area and also harbours intensively managed
83 agriculture (BAFU 2010; Klaus 2012).

84 Selection criteria for the four study areas were the presence of national motorways as main
85 landscape elements. In Switzerland, national motorways are fenced, comprise four or more lanes,
86 are at least 25 m wide and were mainly constructed in the sixties and seventies (ASTRA 2001,
87 2007). The lengths of the motorways within the four study areas ranged between 25 and 156 km
88 (Table 1). The four areas are described as follows: Study area I was characterized by the national
89 motorway A6, which passes from north (Bern) to south (Thun). Study area II contained the national
90 motorways A1 (Aarburg–Aarau) and A2 (Aarburg–Lucerne). Study area III was located in the area
91 of the Y-junction of the motorways A7 (Winterthur–Frauenfeld) and A1 (Winterthur–Wil). Study
92 area IV was bordered by the motorway A4 (Schwyz–Sihlbrugg) in the west and the A13 (Sargans–
93 Altstätten) and the river Rhine in the east. Motorway A3 (Sargans–Freienbach) divided the whole
94 study area into a north-eastern and a south-western part (Fig. 1).

95

96 **Study species**

97 The roe deer (*Capreolus capreolus*) is the smallest and most common native ungulate in
98 Switzerland. Its home range size in the Swiss Plateau varies between 5 and 40 ha (Kurt 1991). In
99 general, roe deer are quite stationary (Müri 1999). Roe deer occur from the lowlands (400 m a.s.l.)
100 up to the tree line (1800-2200 m a.s.l.; Kurt 1991).

101

102 **Genetic data**

103 The genetic data relied on heart-tissue samples of 1,102 roe-deer individuals from regular
104 hunting and traffic casualties, collected between December 2004 and December 2005. The
105 coordinates of the location of each individual were assessed with a GPS or printed maps with a

106 scale of 1:25'000. The sample comprised 704 males, 389 females, and 9 individuals with unknown
107 sex. The number of roe-deer individuals per region ranges between 65 and 560 (Table 1).

108 The samples were genotyped at 12 nuclear microsatellite loci. The data set was processed as
109 described in Kuehn et al. (2007).

110

111 **Wildlife corridors**

112 A wildlife corridor is a linear range in a landscape which is laterally restricted by natural and/or
113 artificial obstacles and therefore represents a compulsory passage for wildlife (UVEK 2001).

114 Wildlife corridors across Switzerland were expert-assessed: 21 cantonal hunting authorities, hunters
115 and wildlife guards were asked to delineate areas where wildlife predominantly crossed the
116 landscape (BUWAL et al. 2001). The information obtained was related to the surrounding
117 landscape, with larger settlements and motorways classified as impassable. Reduced permeability
118 was assigned to rocks, lakes and areas around settlements (BUWAL et al. 2001). Open agricultural
119 land was identified as moderately permeable, whereas forests and conservation areas were
120 considered fully permeable (BUWAL et al. 2001). Based on this scheme, wildlife corridors were
121 identified and categorized into intact, hampered or interrupted. For the sake of convenience,
122 categories hampered and interrupted were combined into one category interrupted in this study.

123 The four study areas considered in this analysis contained between eight and 32 wildlife
124 corridors (Table 1). In study areas II and III almost all corridors were interrupted. However, in
125 regional study areas I and IV, about half and a third were indicated as interrupted, respectively.

126

127 **Genetic structure**

128 The genetic structure of roe deer was identified using GENELAND 4.0.2 (Guillot, Santos &
129 Estoup 2008), which uses spatially explicit information on multilocus genotypes to define genetic
130 clusters and to assign individuals to their most likely cluster (Blair, Weigel, Balazik, Keeley,

131 Walker et al. 2012). GENELAND groups individuals into populations of randomly mating
132 individuals with maximized Hardy-Weinberg equilibrium (HWE) and minimized linkage
133 disequilibrium (LD). Departure from HWE and LD causes the splitting of a population into
134 subpopulations (Guillot et al. 2008).

135 GENELAND was parameterized as follows: number of populations ranged between 1 and 10
136 with a number of iterations of one million, thinning was chosen at 1,000 and the uncertainty on
137 coordinates was zero. We used the correlated allele frequency model. The spatial model and the null
138 allele model were assumed to be true. Because the number of pixels in the spatial domain should be
139 chosen so that there is only one individual per pixel, pixel size varied among regional samples
140 between 11 and 40 m; burnin was chosen at 500. Thus, the parameterization largely conformed to
141 standard settings. GENELAND calculated the number of populations and the average posterior
142 probability. Furthermore, the program generated memberships for all genetic clusters for each roe-
143 deer individual and a spatial extrapolation of the cluster memberships for all four study regions. We
144 conducted several runs for the entire data set and several for each regional sample separately. While
145 the results of the runs showed good consistency, for each data set the run with the highest posterior
146 probability was considered for further analysis (Coulon et al. 2006; Chen, Durand, Forbes &
147 Francois 2007; Coulon, Fitzpatrick, Bowman, Stith, Makarewich et al. 2008; Frantz, Cellina, Krier,
148 Schley & Burke 2009). To reduce the amount of data for visualization, we converted the maps with
149 the genetic clusters into a 100 m grid.

150 To relate the spatial genetic clusters derived from GENELAND to the underlying landscape, we
151 overlaid the extrapolated membership maps on landscape information provided by pixel maps
152 (1:500,000 or 1:1,000,000; pixmaps © 2013 Swisstopo).

153

154 **Assessing uncertainties in the genetic structure**

155 GENELAND outputs membership values for each individual, with the goal to identify spatial
156 genetic structure. However, as clustering results in an aggregation of spatial information, the
157 process also introduces a variety of uncertainties whose degree and extent may differ spatially.

158 Since results of clustering algorithms are widely applied in conservation management and
159 research, assessments of spatial classification uncertainties are mandatory. The membership
160 variation can be assessed spatially to identify areas of high or low agreement with respect to the
161 overall cluster definition or with regard to one particular cluster (Zhu 1997; Bolliger & Mladenoff
162 2005). Here we applied membership diffusion (Zhu 1997; Bolliger et al. 2005) as an overall
163 indicator for the degree of association of a particular location (cell) on the map with the set of
164 genetic clusters as assessed by GENELAND. The membership diffusion is a spatial extrapolation of
165 the degree of association of each pixel with the highest membership of the genetic clusters as
166 identified by GENELAND. Membership diffusion varies between 0 and 1, whereby 0 indicates no
167 association and 1 indicates a high association with the genetic clusters.

168 169 **Evaluating the functionality of wildlife corridors using genetic data**

170 We applied several criteria for selecting wildlife corridors within each region: At least ten roe-
171 deer specimen had to be sampled at each end of a corridor. Only the closest sampled individuals at
172 each end were taken (distance \leq 8 km). Furthermore, one individual could only belong to one
173 wildlife corridor and could not be allocated to another wildlife corridor nearby. Whether an
174 individual was still included also depended on the topography, i.e. individuals were not included if
175 sampled in an area that was topographically separated from the respective wildlife corridor.
176 Considering the above restrictions individuals on one side of a corridor were defined as a group. We
177 calculated pairwise genetic differentiation (F_{ST}) for the two groups of roe deer per wildlife corridor
178 with ARLEQUIN 3.5 (Excoffier & Lischer 2010). Overall, nine wildlife corridors were selected

179 from all four study areas for the evaluation of their functionality based on genetic data. Two
180 corridors were taken from regional sample II, two from regional sample III and five from regional
181 sample IV. No corridor from regional sample I fulfilled the criteria for being selected. Three of nine
182 wildlife corridors were considered intact and six were rated as interrupted (Table 2). Some corridors
183 located nearby were merged (Table 2).

184 **Results**

185 The twelve nuclear microsatellite loci showed 3-19 alleles (mean 9.58) per locus in the total sample.
186 For regional sample I, locus MM12 was monomorphic and therefore not further considered in the
187 analyses.

188

189 **Identification of the genetic structure and cluster uncertainty**

190 Results from GENELAND showed no distinct genetic structure in roe deer when considering all
191 four regional samples together. Genetic structure could only be delineated when looking at the four
192 regional study areas individually (Fig. 2A-D). The number of genetic clusters varied between the
193 four study regions. Regional samples I and III contained two genetic clusters each, whereas regional
194 sample IV delineated seven clusters and regional sample II nine genetic clusters (Fig. 2A-D).

195 Generally, genetic structure was stronger and cluster uncertainty was less pronounced with fewer
196 clusters (Fig. 2A, C). When overlaying the genetic structure with the landscape, motorways
197 appeared to influence the genetic structure in study region I (Fig. 2A) and partly in study area IV
198 (Fig. 2D). The majority of the clusters, however, seemed to be independent of the motorway
199 courses.

200

201 **Functionality of wildlife corridors**

202 The evaluation of expert-assessed wildlife corridors based on genetic data of roe deer indicates
203 that, overall, corridors identified as intact were confirmed by low F_{ST} values, whereas interrupted
204 corridors exhibited higher genetic differentiation (Table 2).

205 At the level of roe-deer individuals relating to wildlife corridors, the mean cluster uncertainties
206 between the two groups were similar (Table 2). The values were almost 1 for corridors no. 3 and 4,
207 indicating that cluster membership was very reliable. For the other corridors, mean uncertainty per
208 group ranged between 0.183 and 0.275.

209 As examples, two corridors are presented in more detail. Corridor no. 2 was located in regional
210 sample II between Sursee LU and Zofingen AG (Fig. 3A). Motorway A2 marks the boundary
211 between the two groups of roe deer (Fig. 3A; orange line). Group 'east' comprised 25 individuals
212 and group 'west' consisted of 31 roe deer (Table 2). Based on GENELAND results, individuals were
213 assigned to eight genetic clusters (Fig. 3A). Mean cluster uncertainties for both groups were almost
214 the same (Table 2). Genetic differentiation between the two groups was significant with $F_{ST} =$
215 0.0223 ($P \leq 0.05$; Table 2). Based on expert opinions, all three selected corridors were interrupted,
216 which is supported by the genetic differentiation observed.

217 Corridor no. 6 was located in regional sample IV between Pfäffikon SZ and Reichenburg SZ, to
218 the south of the lake of Zurich (Fig. 3B). We chose the intact corridor in the middle of this regional
219 sample, which crossed a low-elevation mountain pass with a highly frequented road (Fig. 3B;
220 orange line). Eleven individuals were sampled on the east side of the corridor, the western group
221 comprised 30 individuals. There were individuals assigned to two genetic clusters (Fig. 3B; blue
222 and yellow circles). Genetic differentiation, F_{ST} , was almost zero and not significant (Table 2).
223 Mean cluster uncertainty per group was nearly identical.

224 All three corridors considered intact had an F_{ST} value around zero (mean $F_{ST} = 0.008$), indicating
225 low genetic differentiation and, thus, high gene flow. The six interrupted corridors mostly possessed

226 significant F_{ST} values (mean $F_{ST} = 0.022$, $P \leq 0.05$), which indicates that these corridors had
227 restricted levels of gene flow, i.e. respective landscape elements impaired roe-deer movement to a
228 certain degree (Table 2).

229 **Discussion**

230 Landscape genetics is a helpful tool in combining the spatially explicit analysis of genetic
231 markers with methods of landscape ecology to identify barriers to wildlife movement restricting
232 gene flow (Storfer, Murphy, Evans, Goldberg, Robinson et al. 2007). On the basis of genetic data of
233 1,102 roe-deer individuals, our assessment on the evaluation of expert-derived wildlife corridors
234 indicates that in general, corridors identified as intact are confirmed by low genetic differentiation,
235 measured as F_{ST} , and interrupted corridors exhibited higher genetic differentiation.

236 Wildlife corridors formerly identified as intact (no. 5, 6, 9) were confirmed by exhibiting an
237 average F_{ST} value of 0.008, which indicates low genetic differentiation. These corridors were
238 supposed to be permeable to roe-deer movement, which seems intuitive when observing the
239 distribution of the genetic cluster memberships (e.g. corridor no. 6, Fig. 3B). In contrast, interrupted
240 corridors exhibited higher genetic differentiation (average $F_{ST} = 0.022$). The four corridors with
241 significant F_{ST} values (no. 2, 3, 7 and 8) were thus less permeable than intact corridors. For example
242 (Fig. 3A), motorway A2 acted as a barrier to gene flow between local roe-deer populations in the
243 area of the interrupted corridor 2. This supports the results of Kuehn et al. (2007) who came to the
244 same conclusion in a regional investigation closely located to our study region II. However, two
245 wildlife corridors (no. 1 and 4) categorized as interrupted did not exhibit statistically significant
246 genetic differentiation. Corridor no. 1 is located between Emmen LU and Sempach LU, crossing
247 motorway A2, and no. 4 is located between Winterthur ZH and Rickenbach ZH, crossing
248 motorways A1 and A7. Potential reasons for this outcome can be found in the local situations.

249 There were clearly more bridges or underpasses of small roads with limited traffic to make the
250 presumed barriers permeable to gene flow in roe deer, as compared to statistically significant
251 genetic differentiation in interrupted corridors (no. 2, 3, 7 and 8). Coulon et al. (2006) point out that
252 one barrier is rarely complete, but that the combination of several landscape elements with low
253 permeability may cause population differentiation. This demonstrates the importance of having a
254 comprehensive view and not only to consider the main obstacle (e.g. motorway) to understand the
255 local permeability of a landscape for a particular organism.

256 In 2003, 40 out of totally 303 regionally important wildlife corridors in Switzerland were
257 selected by the two federal offices FEDRO (Federal Roads Office) and FOEN (Federal Office for
258 the Environment) to be restored. Whereas corridor no. 4, intact from a roe-deer perspective, was
259 officially selected as one of the 40 regionally important wildlife corridors (Caron 2012; Klaus
260 2012), corridor no. 3 showed restricted permeability, yet was not selected for restoration. The fact
261 that wildlife corridors were not only evaluated for roe deer might explain such discrepancies
262 (BUWAL et al. 2001). This, however, also demonstrates the need for rigorous methods to test the
263 functionality of wildlife corridors.

264 We did not find any consistent genetic structure when considering all 1,102 roe-deer individuals
265 sampled in the four study areas. This indicates low genetic differentiation with up to now low
266 effects of landscape elements on the genetic structure at the large scale. Holderegger et al. (2010)
267 point out that a high-resolution power of genetic markers (e.g. 10-20 polymorphic microsatellite
268 loci) is recommended when only weak genetic effects are expected. With 12 nuclear microsatellite
269 loci, our genome sampling was within the suggested range, though some of the loci had limited
270 allelic diversity. Furthermore, the spatially explicit clustering algorithm implemented in the
271 program GENELAND has been shown to be suitable for populations exhibiting low genetic
272 differentiation (Coulon et al. 2006). Blair et al. (2012) emphasize in their study that GENELAND is
273 considered very powerful in reliably detecting linear barriers to gene flow within 20 generations or

274 less. All involved motorways are older than 20 roe-deer generations (ASTRA 2001). When
275 analysing the four regional study areas separately, we found genetic differentiation between the
276 encountered clusters within each regional sample ($F_{ST} \geq 0.018$), but landscape elements such as
277 motorways only partly supported the boundaries of the identified genetic clusters.

278 Our results are in line with the results of Wang and Schreiber (2001) who also found low levels
279 of genetic differentiation in roe deer across Central Europe. Many factors likely contribute to this
280 observation. Founder events and the chance for successive bottlenecks may have led to populations
281 with relatively small numbers of alleles owing to genetic drift. One hundred years ago, roe deer
282 were extinct in Switzerland due to widespread poaching. After the implementation of efficient
283 hunting laws at the end of the 19th century, roe deer originating from Germany and France
284 recolonized Switzerland along a broad front (Breitenmoser 1998). Thus, the shallow genetic
285 structure may be interpreted as reflecting the presence of one large, more or less panmictic
286 population of roe deer in the Swiss Plateau, while we may effectively measure a time lag that relates
287 to past recolonization rather than to effects of recent landscape permeability. Although there is
288 strong evidence that roads, and especially fenced motorways, promote genetic differentiation
289 between wildlife populations (Hepenstrick et al. 2012; Holderegger et al. 2010), their barrier effects
290 are rarely complete (Holderegger et al. 2010). In addition, the current road network was built over
291 the past 50 years (ASTRA 2001). Thus, response time of the genetic structure may not have been
292 long enough to be observed in synchrony with changes in the landscape, given a generation time of
293 roe deer of two years (Kurt 1991). There is a temporal lag of several generations between the
294 processes causing the formation of genetic structure due to responses to landscape changes and the
295 observed genetic structure itself (Anderson, Epperson, Fortin, Holderegger, James et al. 2010).

296 To conclude, our study demonstrates that landscape genetics may be a useful approach to
297 identify the need for management measures and setting priorities for reactivating dysfunctional
298 wildlife corridors in intensely managed landscapes. Moreover, our study may later serve for

299 monitoring the performance of mitigation measures to restore gene flow within wildlife
300 metapopulations (Epps et al. 2005).

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389 **Table 1.** Characterization of the regional study areas I to IV (cf. Fig. 1) with totally 1,102 sampled
 390 individuals of roe deer *Capreolus capreolus* located in the Swiss Plateau and the northern Prealps.
 391 Genetic sample size, area size, elevation range, length of motorways and the number of intact and
 392 interrupted wildlife corridors are listed for each regional sample.

Regional sample	Genetic sample [N]	Area [km ²]	Elevation range [m a.s.l.]	Motorways (length) [km]	Number of wildlife corridor	
					No. of intact	No. of interrupted
I	65	1,241	500-1,200	25.4	4	4
II	302	1,669	400-700	64.5	0	21
III	175	534	400-900	45.3	1	8
IV	560	4,032	400-1,300	156.2	11	21

393

394 **Table 2.** Characterization of the nine selected wildlife corridors in the Swiss Plateau and the
 395 northern Prealps (cf. Fig. 1). The table contains information about the location of the corridors
 396 concerning the regional study areas and the number of individuals (N) per group. The subscripts (N,
 397 S, E, W) indicate the geographic direction of each group based on the presumed boundary
 398 separating the two groups of roe-deer individuals on either side. Furthermore, the number of genetic
 399 clusters, F_{ST} values, the mean membership diffusion (U) per group and the condition of the corridor
 400 is listed for each of the nine corridors are given.

Corridor	Regional study area	No. of individuals per group	No. of genetic clusters represented	F_{ST}	Mean membership diffusion per group	Condition of the corridor
1	II	$N_N = 20$ $N_S = 14$	6	-0.0014	$U_N = 0.223$ $U_S = 0.224$	interrupted
2	II	$N_E = 25$ $N_W = 31$	8	0.0223*	$U_E = 0.219$ $U_W = 0.210$	3x interrupted
3	III	$N_N = 37$ $N_S = 8$	2	0.0506*	$U_N = 0.985$ $U_S = 0.968$	interrupted
4	III	$N_N = 14$ $N_S = 13$	2	0.0135	$U_N = 0.981$ $U_S = 0.999$	interrupted
5	IV	$N_W = 35$ $N_E = 32$	3	0.0111	$U_W = 0.196$ $U_E = 0.240$	intact
6	IV	$N_E = 11$ $N_W = 30$	2	0.0081	$U_W = 0.273$ $U_E = 0.275$	intact
7	IV	$N_N = 32$ $N_S = 36$	4	0.0220*	$U_N = 0.202$ $U_S = 0.275$	interrupted
8	IV	$N_E = 77$ $N_W = 29$	4	0.0236*	$U_W = 0.203$ $U_E = 0.225$	4x interrupted
9	IV	$N_N = 16$ $N_S = 25$	3	0.0056	$U_N = 0.230$ $U_S = 0.183$	2x intact

401 * denotes significant F_{ST} values ($P \leq 0.05$).

402 **Figure legends**

403

404 **Fig. 1.** Location of study area in the Swiss Plateau and the northern Prealps (inset) and regional
405 study areas I to IV (I: red circles, II: blue stars, III: orange squares and IV: green triangles) of
406 sampled roe deer *Capreolus capreolus*, located between the Jura mountains and the Alps, to assess
407 the effect of landscape elements on gene flow in roe deer.

408

409 **Fig. 2.** Genetic cluster memberships (colour) and membership diffusion (grey shades) for the four
410 regional samples I to IV (A-D) of roe deer *Capreolus capreolus* in the Swiss Plateau and the
411 northern Prealps (cf. Fig. 1). The larger the coloured symbol, the higher the probability for a
412 particular cluster. The darker the grey shades, the stronger the degree of association of a location on
413 the map with the respective genetic clusters. Both cluster membership and membership diffusion
414 range between 0 and 1.

415

416 **Fig. 3.** Examples of (A) an interrupted wildlife corridor located between Sursee LU and Zofingen
417 AG in regional sample II and (B) an intact wildlife corridor located in regional sample IV between
418 Pfäffikon SZ and Reichenburg SZ, illustrated using genetic clustering of roe deer *Capreolus*
419 *capreolus*. Membership diffusion (grey shades) and cluster assignment (dot colours) of sampled roe
420 deer are given (cf. Fig. 2). The black dots are roe-deer individuals which were not considered in the
421 analyses. The potential barriers are indicated by an orange line, the barrier for (A) is motorway A2
422 and for (B) a low-elevation mountain pass. Interrupted wildlife corridors are shown in red, intact in
423 green.

424 Fig. 1

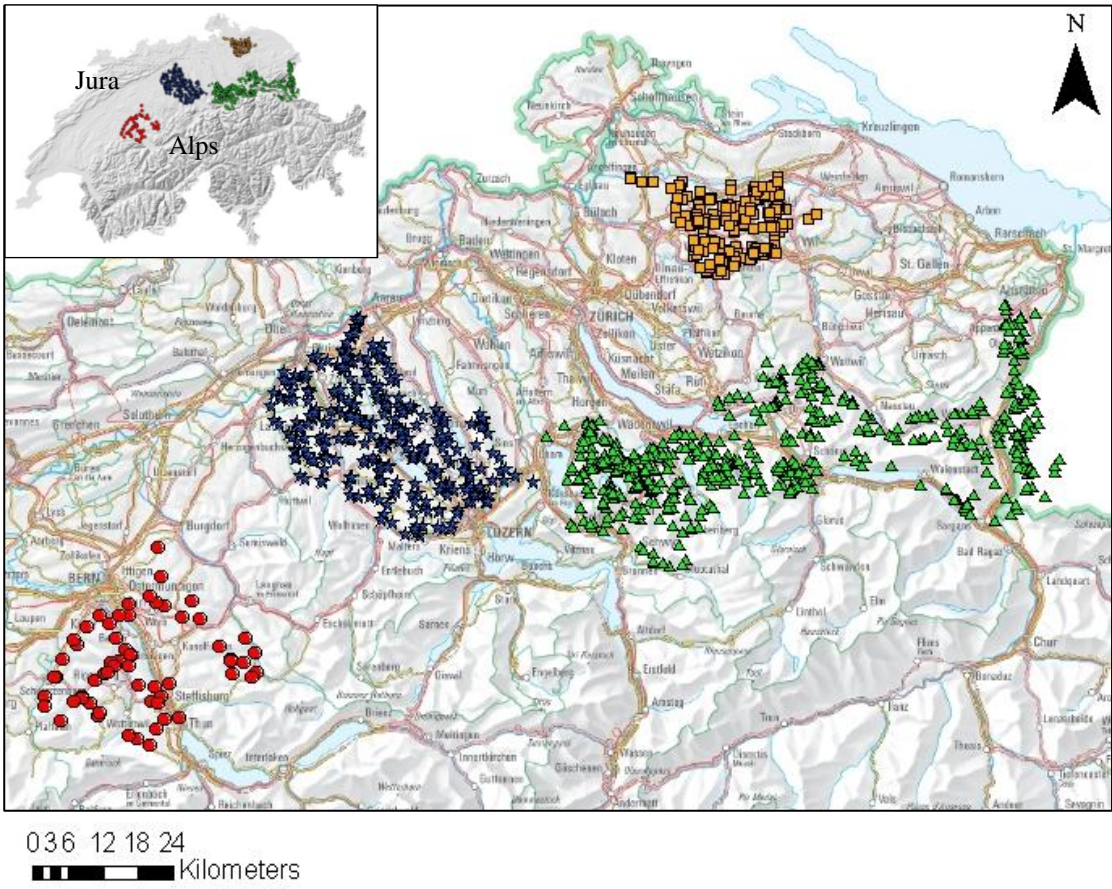
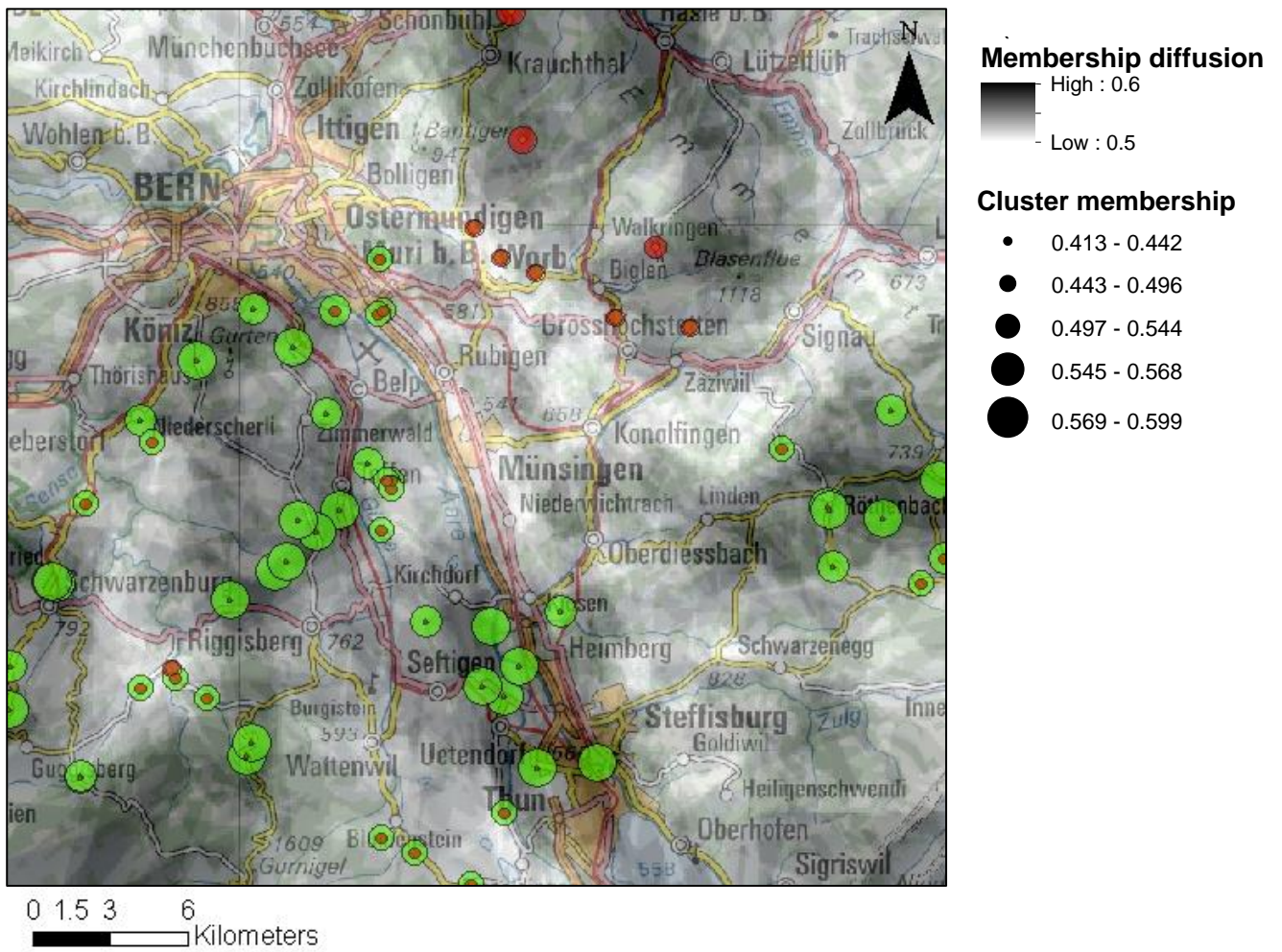
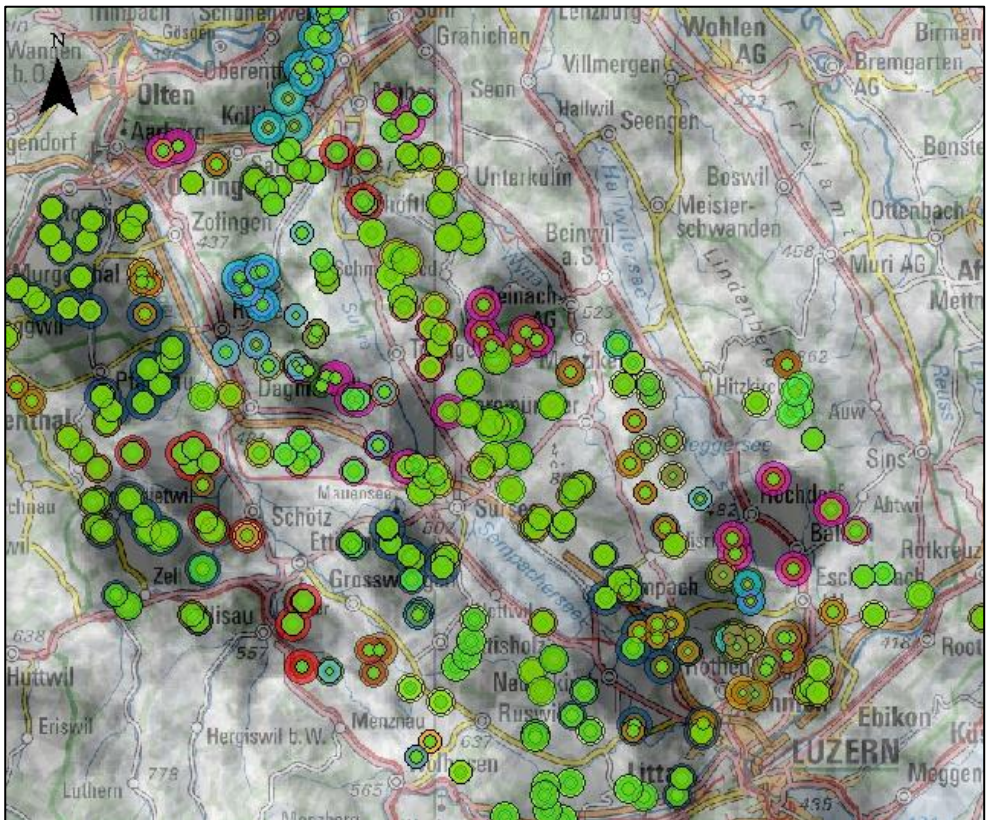


Fig. 2

(A)

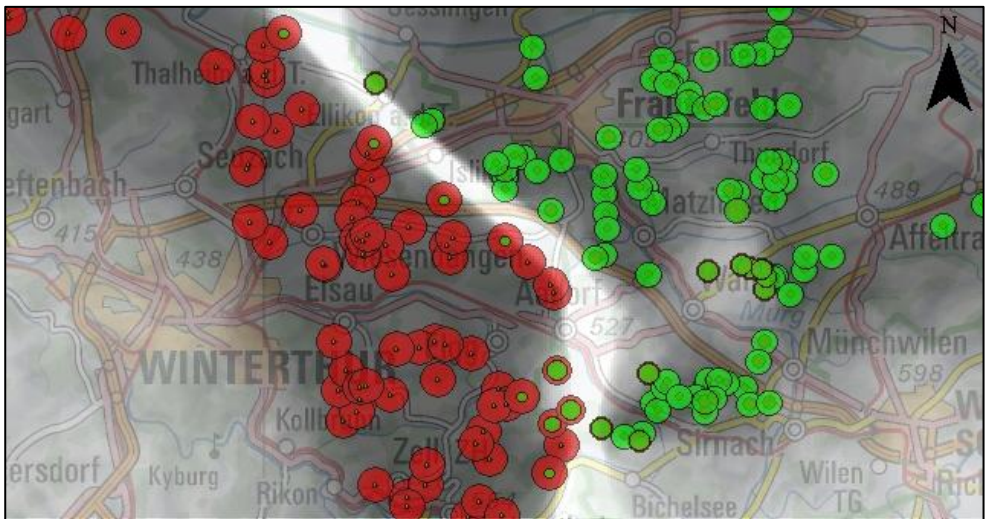


(B)



0 1.5 3 6 Kilometers

(C)



0 1.5 3 6 Kilometers

(D)

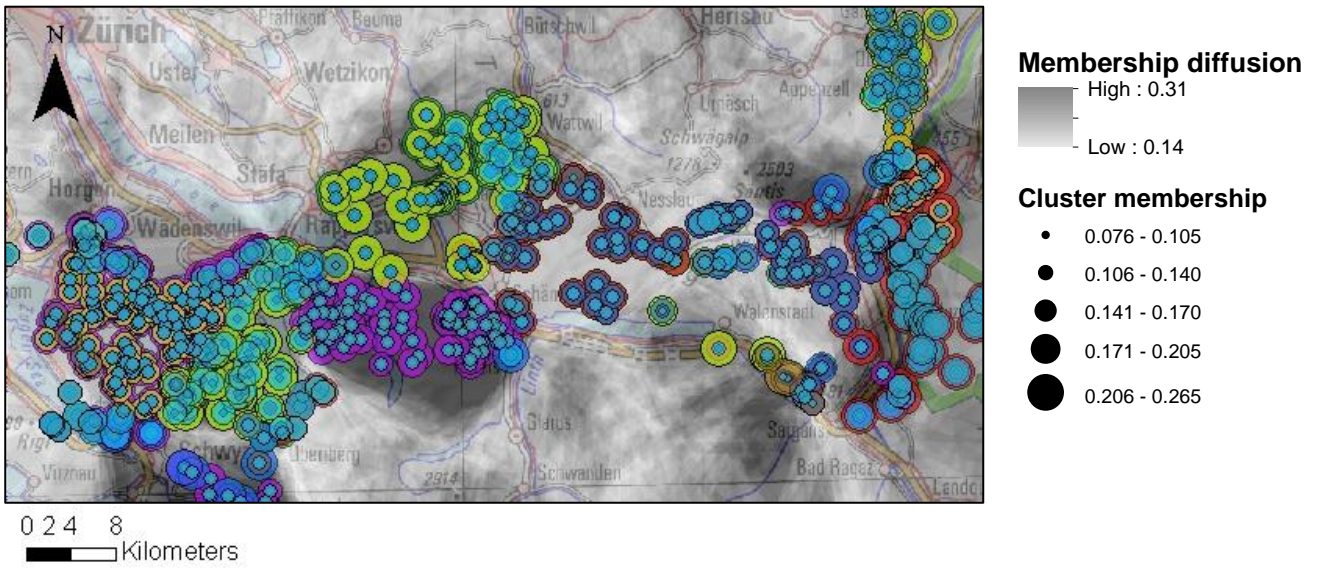
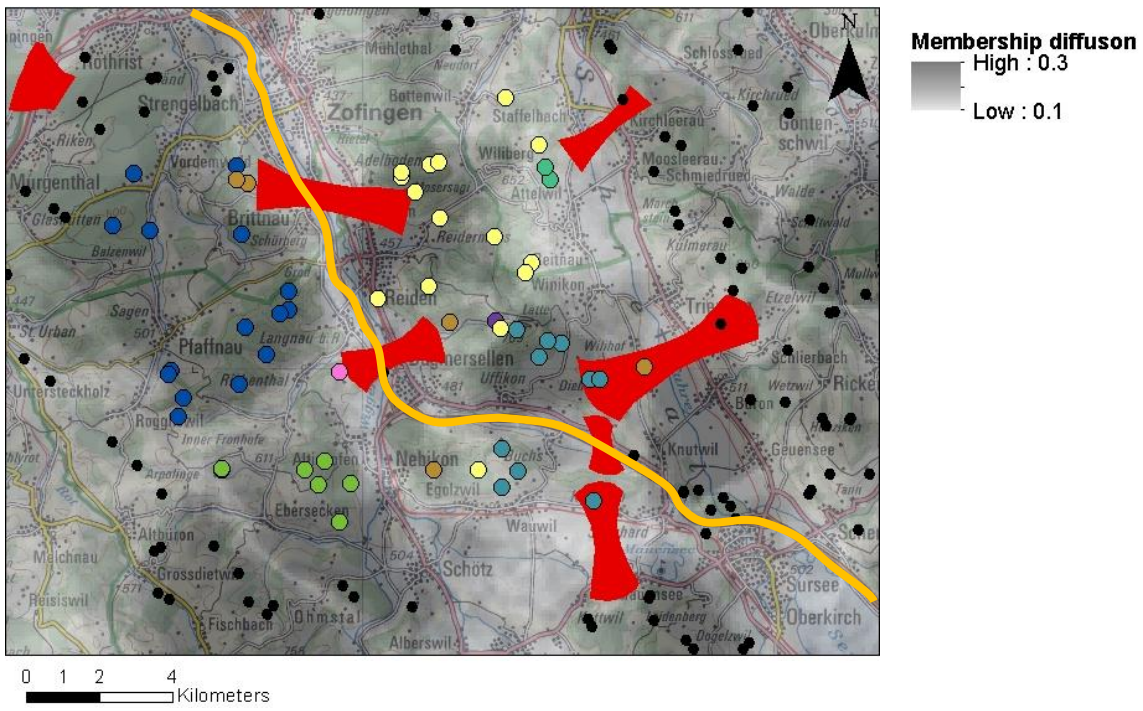


Fig. 3 (A)



(B)

