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2 **Climate-driven flyway changes and memory-based long-distance migration**

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44 **Millions of migratory birds occupy seasonally favourable breeding grounds in the Arctic<sup>1</sup>, but**  
45 **we know little about the formation, maintenance and future of Arctic bird migration routes**  
46 **and genetic determinants of migratory distance. Here, we established a continental-scale**  
47 **migration system, satellite tracking 56 peregrine falcons (*Falco peregrinus*) from six Eurasian**  
48 **Arctic breeding populations and resequencing 35 genomes from four of these. Different**  
49 **breeding populations used five migration routes across Eurasia, likely formed by longitude**  
50 **and latitude breeding ground shifts during the LGM-Holocene transition. Contemporary**  
51 **inter-route environmental divergence appears to maintain distinct migration routes. We**  
52 **found that the novel gene *ADCY8* was associated with population-level migratory distance**  
53 **differences. We elucidated its regulatory mechanism and found the most likely selective agent**  
54 **for this divergence was long-term memory. Global warming is predicted to influence**  
55 **migration strategies and diminish breeding ranges of Eurasian Arctic peregrines. Harnessing**  
56 **ecological interactions and evolutionary processes to study climate-driven changes in**  
57 **migration can facilitate the conservation of migratory birds.**

58 Global climate change and anthropogenic development are expected to affect the annual adaptive  
59 movements of migratory Arctic birds<sup>1-3</sup>, with potential fitness effects imposed by inhospitable  
60 routes and temporally mismatched breeding<sup>2,4</sup>. Next generation genome sequencing has facilitated  
61 studies of the interaction between genomic variation and environment in migratory birds<sup>5</sup>. However,  
62 to date there is no published research on the role of climate-driven genomic responses in shaping  
63 differences of migratory strategy among bird populations. Here, we combined satellite-tracking of  
64 56 peregrine falcons from migratory Arctic populations<sup>6</sup> (**Fig. 1a, Extended Data Fig. 1,**  
65 **Supplementary Table 1**) with genome data to explore their demographic history and the  
66 spatiotemporal dynamics of their migration.

### 67 **Migration patterns of Arctic peregrines**

68 From 41 individuals, we identified 150 completed migration paths (**Supplementary Table 2**).  
69 Peregrines initiated autumn migration in September, travelled 2,280-11,002 km, in *ca.* 27 days  
70 (95% confidence interval (CI): 14-46) covering 213 km/day (49-420), and arrived at their wintering  
71 areas in October. Peregrines migrate solitarily, with those departing from different breeding  
72 grounds, except Kola and Kolguev, using different routes and wintering at widely distributed sites  
73 across four distinct regions (**Fig. 1a, Extended Data Fig. 2**). Individuals tracked for more than one  
74 year exhibited strong path repeatability during migration ( $n = 26$ ;  $R_{pt} = 0.45$ ,  $P < 0.001$ ), complete  
75 fidelity to wintering locations and limited breeding dispersal (5.37 km on average; **Fig. 1b,**  
76 **Supplementary Table 3**). All populations demonstrated a high degree of migratory connectivity  
77 ( $R^2 = 0.86$ ,  $P < 0.001$ ; **Fig. 1c**), suggesting strong selection for long-term memory.

78 Principal component analysis (PCA) identified two main groups with migratory distance being the  
79 most significant differentiation (**Figs. 1d, e, Extended Data Fig. 3, Supplementary Table 4**). The  
80 Eastern birds flew significantly farther than Western birds (6,134 km *vs* 3,680 km;  $P < 1E-6$ ; **Fig.**  
81 **1e**). We therefore classified them as long-distance (LD; Kolyma-Lena-Popigai-Yamal) and short-  
82 distance (SD; Kolguev-Kola) migrants.

### 83 **Historical formation of migration routes**

84 We sequenced the genomes of 35 peregrines, obtaining 6,328,655 high-quality SNPs  
85 (**Supplementary Table 5**). Multiple analytical approaches consistently supported four distinct  
86 genetic clusters corresponding to the sequenced populations, with Yamal and Kolyma inferred to  
87 have diverged after the separation of their ancestors from that of Kola and Kolguev (**Fig. 2a**).  
88 Sequential Markovian Coalescent (SMC++) analysis revealed that the effective population size ( $N_e$ )  
89 of the ancestral lineage increased from ~100 thousands of years ago (kya) to a peak 20-30 kya (**Fig.**  
90 **2b**), around the Last Glacial Maximum (LGM)<sup>7</sup>. To resolve uncertainties in the recent demographic  
91 history (**Fig. 2a**), we developed a new Approximate Bayesian Computation (ABC) approach. The  
92 ABC-random forest model choice (**Fig. 2c, Supplementary Figs. 1-4, Supplementary Tables 6, 7**)  
93 confirmed the divergence pattern of four studied populations and ABC simulations further found  
94 that Eastern and Western populations started to separate during the LGM (23.03 kya; 95% CI:  
95 17.67-32.94), followed by an eastern split between Yamal and Kolyma 11.30 kya (9.14 -14.29), and  
96 between Kola and Kolguev 10.53 kya (9.18-12.90) (**Fig. 2d, Supplementary Table 8, Extended**  
97 **Data Fig. 4**).

98 Ecological Niche Modelling (ENM) based on present and paleo-climate datasets showed that  
99 potential breeding distribution range positively correlated with  $N_e$  fluctuations (**Supplementary**  
100 **Figs. 5, 6**). There was a much larger area suitable for breeding in Siberia during the LGM than the  
101 last interglacial period (LIG; 120-140 kya)<sup>8</sup> or Mid-Holocene, coinciding with the largest  $N_e$   
102 estimate (**Fig. 2e, f, Supplementary Fig. 5**). Arctic-dwelling peregrines mainly occupy tundra  
103 habitat<sup>9</sup>, and we found close coincidence between reconstructed tundra habitat and peregrine  
104 breeding distribution in the LGM (**Supplementary Fig. 7**), suggesting that enlargement of tundra  
105 habitat underpinned peregrine population expansion during the LGM. Conversely, population  
106 declines and gradual divergences after the LGM mirrored large-scale loss and northward  
107 contraction of tundra. Recent population declines after the Mid-Holocene (**Fig. 2b**) may have also

108 resulted from anthropogenic factors since habitat distributions have remained relatively stable (**Fig.**  
109 **2f, g**).

110 Interestingly, our ENM simulations suggest that peregrines had less potential western wintering  
111 area during the LGM, while eastern wintering areas remained stable (**Fig. 2e, Supplementary Fig.**  
112 **5**). Thus, during the LGM peregrines likely migrated to a wintering area across India and Southeast  
113 Asia, a striking south-eastward migration (**Fig. 2e**), distinct from the current south-westerly  
114 migration route formed during the Mid-Holocene (**Fig. 2f, g**). Furthermore, since the Mid-Holocene  
115 breeding areas are inferred to have shifted northward compared with the LGM, resulting in a longer  
116 migratory route (**Fig. 2e, f**), we conclude that glacial cycles can regulate both migratory orientation  
117 and distance.

#### 118 **Present migration route separation**

119 We used the Hausdorff distance ( $Hd$ )<sup>10</sup> to quantify the distance between individual migration paths  
120 (**Methods and Supplementary Information**). Mean  $Hd$  within populations ( $17.05 \pm 7.20$ ) was  
121 significantly lower than that between neighbouring populations ( $35.83 \pm 14.24$ ,  $P < 0.01$ ). Cluster  
122 analysis largely supported five migratory routes with Kola and Kolguev using the same route and  
123 very few individuals interchanging between populations (**Extended Data Fig. 5a**).

124 The proposition that migration routes are genetically determined, is mostly based on migratory  
125 restlessness<sup>11</sup>, displacement experiments<sup>12</sup> and correlations between genetic background and  
126 migration route<sup>13</sup>. We addressed this fundamental question by randomly selecting 93 putatively  
127 neutrally-evolved SNP loci and 75 loci under positive selection (**Methods**). With these markers, we  
128 genotyped nine and six individuals respectively for the Popigai and Lena populations, where we  
129 obtained insufficient DNA from shed feathers for genome resequencing. Combining the genotypes  
130 with those from the population genomic data, we measured genetic differentiation ( $F_{ST}$ ) among five  
131 peregrine populations and tested their relationship with the mean  $Hd$  for each migration route. We  
132 found a non-significant correlation between route  $Hd$  and  $F_{ST}$  ( $R^2 = 0.02$ ,  $P = 0.69$ ) based on neutral

133 loci, suggesting that demographic isolation is not the major factor in isolating migration routes. In  
134 contrast, we found a significant relationship for loci under selection ( $R^2 = 0.42$ ,  $P = 0.03$ ),  
135 suggesting a role for adaptive genomic regions in the maintenance of separated migration routes  
136 (**Fig. 2h**).

137 Environmental divergence was evident among the migration routes, with Köppen-Geiger climate  
138 zones being significantly different between adjacent routes ( $P < 0.01$ ,  $\chi^2$  test; **Fig. 2i**, **Extended**  
139 **Data Fig. 5b**) and during most breeding and wintering periods (**Supplementary Fig. 8**). We found  
140 a coincidence between abrupt changes of climate zone and population route boundaries (**Extended**  
141 **Data Fig. 5c, d**). Migration cost based on least-cost paths was significantly lower for birds  
142 following their population-specific route ( $P = 0.01$ , effective size = 0.45; **Extended Data Fig. 5e**,  
143 **f**). We conclude that current migration routes are mainly maintained by environmental constraints,  
144 with synergistic contribution from local adaptation.

#### 145 **Genes for migratory distance differences**

146 We used window-based  $F_{ST}$  and extended haplotype homozygosity (XP-EHH) to detect selection  
147 signals across the genomes of SD and LD peregrines. The methods combined identified 149  
148 selection sweeps (37 genes) between the two groups (**Supplementary Table 9**), and found the most  
149 significant outlier occurred at the *ADCY8* locus (**Fig. 2j**). We narrowed the signal down to a 1.8 kb  
150 region, containing 14 linked SNPs in the second intron of the gene (**Fig. 2k**). Haplotype frequency  
151 analysis demonstrated a positive selection signature of *ADCY8* in the LD group (**Fig. 2l**). The  
152 dominant haplotype (Hap2) was at a high frequency (34/38) in the LD group, whereas the SD group  
153 had six haplotypes with varying frequencies (Hap2 11/26, Hap1 6/26, with the other four haplotypes  
154 occurring 4, 2, 2, 1 times; **Fig. 2l**). We investigated the potential functional significance of Hap2 in  
155 LD peregrines and a randomly selected Hap1 sequence from SD peregrines by designing a dual  
156 luciferase reporter assay for functional analysis in our cultured chicken hippocampus primary cells  
157 (**Methods**). In contrast to Hap2 insert cells, the Hap1 insert cells showed a significantly lower

158 luciferase activity ( $P < 0.001$ ; **Fig. 2m, Supplementary Fig. 9**), suggesting that the peregrine Hap1  
159 sequence has a suppressing effect.

160 Of the 14 loci identified within the *ADCY8* locus, the SNP (*C/T*) in the position 5,170,169 of  
161 peregrine chromosome 3 produced the largest XP-EHH value (**Fig. 2n**) and the allele *T* was 100%  
162 fixed in the LD group, suggesting that this standing variation is under strongest selection and may  
163 have a major role in functional differentiation. A search of the focal fragment against the motif  
164 database found that the ancestral SD group had a 5'-*CGTCA*-3' motif, a canonical half-site cAMP-  
165 responsive element (CRE) that is a binding site for the transcription factor CREB<sup>14,15</sup>, while the  
166 fixed chr3-5170169\**T* changes the first nucleotide of the motif. We used ATAC-seq<sup>16</sup> to sequence  
167 both hippocampus and cerebral cortex tissues from a SD peregrine. Our ATAC-seq analysis  
168 detected a significant peak coinciding with the position of this motif (**Fig. 2n**), experimentally  
169 supporting its existence as a functional element.

170 Previous studies suggest that CREB can regulate gene expression by binding to the CRE element  
171 through CREB basic region/leucine zipper domain (bZIP), which can be regulated by its DNA  
172 methylation level<sup>17,18</sup>. In peregrines, the identified substitution from *C* to *T* in *ADCY8* gene creates a  
173 novel transcriptional binding site, 5'-*TGTCA*-3', which potentially disrupts the DNA methylated  
174 site, CpG island, on the canonical motif. Moreover, we found that, *CREB1*, the transcription  
175 activator, expressed the bZIP domain in the peregrine brain, but the conditional repressor *CREB2*<sup>19</sup>  
176 did not (**Supplementary Fig. 10**). Our results suggest that the new CRE motif may be free from  
177 DNA methylation and facilitate the binding of CREB1 on *ADCY8*, and will consequently maintain a  
178 higher activity of *ADCY8* in LD peregrines. Supporting evidence came from our comparison of  
179 expression levels of *ADCY8* in the peregrine brain with two genotypes of the focal SNP ( $RPKM =$   
180  $81.11$  in *CT* vs  $73.96$  in *CC*;  $P = 3.73E-5$ , hypergeometric test).

181 Empirical evidence indicates that *ADCY8* is involved in long term memory<sup>20,21</sup>. *ADCY8* encodes  
182 Adenylyl Cyclase type 8 that catalyses the conversion of ATP to cAMP, which acts as a secondary

183 messenger and regulates downstream memory-related genes<sup>22,23</sup>. We found LD peregrines had a  
184 significantly higher mean migration path fidelity than SD peregrines ( $P < 0.001$ ; **Supplementary**  
185 **Fig. 11**), requiring strong long-term memory. Together with numerical evidence that *CREB* genes  
186 determine the development of long-term memory<sup>24</sup>, our work suggests that the *ADCY8* and *CREB*  
187 genes play a key role in influencing migratory flight distance via co-regulating the capacity of long  
188 term memory. For the *T* allele that is positively selected in the LD populations, the selection time  
189 was estimated to be 18.87 kya (**Supplementary Information**), after the separation of two  
190 migratory groups, strengthening our conclusion that the regulation of migratory distances is the  
191 result of natural selection.

### 192 **Predicted effect of global warming**

193 We used ENM simulations to project future (2070) breeding and wintering distributions for each  
194 Arctic peregrine population under Representative Concentration Pathway (RCP) 8.5. The breeding  
195 and wintering distributions of all populations would shift poleward by 2.08° (95% CI: 0.31-3.44)  
196 and 1.47° (0.11-11.06) latitude, respectively (**Extended Data Fig. 6, Supplementary Fig. 12**),  
197 which is consistent with observations for most Arctic shorebirds<sup>25</sup> and congruent with the climatic  
198 envelope corresponding to tundra habitats. Greatest reduction is predicted to occur in Kolguev and  
199 Kola, losing 100% and 93% of their suitable breeding habitats, respectively (**Fig. 3a**). We also  
200 found Western peregrines may have a much shorter migration route (655 km; 442-868), while  
201 Eastern peregrines may have a longer route (286 km; 56-515) (**Fig. 3a, Supplementary Fig. 13**). If  
202 the climate warms at the same rate as over recent decades, peregrines in Western Eurasia may stop  
203 migrating altogether, while Eastern peregrines may face greater risks since mortality is positively  
204 associated with migratory distance<sup>26</sup>.

205 Recent population declines in migratory Arctic birds have been attributed to the amplification of  
206 global warming in the High Arctic<sup>1,4,25</sup>. Climate change may have already impacted peregrine  
207 populations, so we compared  $N_e$  changes of each population with local temperature during breeding

208 periods (May-July) since 1840. Our *SNeP* analysis showed that each population has undergone  
209 declines during the past 25 generations (*ca.* 150 years). However, *Ne* slope (*NeS*) analysis further  
210 revealed some variation, with recovery detected during relatively cooler summers (**Fig. 3b**), and  
211 four populations showed the largest negative *NeS* 8~9 generations ago (1960s), coinciding  
212 widespread use of organochlorine pesticides<sup>27</sup>. Importantly our generalized linear modelling (GLM)  
213 analysis found that *Ne* change was negatively correlated with mean breeding season temperature in  
214 Kola ( $R^2 = 0.46$ ,  $P = 0.03$ ) and Yamal ( $R^2 = 0.39$ ,  $P = 0.02$ ), with mean breeding season temperature  
215 and duration of extreme warm days in Kolguev ( $R^2 = 0.61$ ,  $P = 0.01$ ), and with duration of extreme  
216 cold/warm days in Kolyma ( $R^2 = 0.68$ ,  $P = 0.02$ ; **Fig. 3c**, **Supplementary Table 10**). Our predicted  
217 *NeS* in the future (i.e. from 2020 to 2100) showed a continuing decrease trend, but the SD migrants  
218 in Kola and Kolguev will suffer the highest probability of population decline (**Fig. 3d**,  
219 **Supplementary Fig. 14**).

## 220 Discussion

221 Spatiotemporal changes in animal migration behaviour are thought to be related to climatic changes,  
222 anthropogenic impacts<sup>28</sup> and evolutionary responses of migrants. Since these dynamic processes can  
223 leave a footprint on the genome, by combining animal movement and population genomic data, we  
224 were able to identify a major role of climate in the formation and maintenance of peregrine  
225 migration patterns (**Fig. 2**, **Extended Data Fig. 5**).

226 Previous studies have identified several candidate genes that may regulate migration<sup>29,30</sup>. The higher  
227 activity of ADCY8 we identified in LD peregrine migrants (**Fig. 2**) may increase their long-term  
228 memory. Our analysis reveals a unique mutation that facilitates the binding of its transcription  
229 factor CREB1, and fixation of this variation happened after the divergence of LD and SD  
230 populations. Our work thus not only reveals a novel causative gene to explain migratory  
231 differences, but also provides a mechanistic basis.

232 In a changing global climate, peregrines may move to new wintering areas and adjust their  
233 migration routes. However, our prediction of dramatic shrinkage in Arctic breeding areas, together  
234 with a predicted population collapse in the European Arctic, represents a clear threat to peregrines  
235 and possibly many other migratory Arctic species. Our study demonstrates the value of an  
236 integrated approach, combining satellite telemetry, population and functional genomics and  
237 modelling, to untangle intriguing scientific questions related to migration, laying a cornerstone for  
238 conserving migratory species in conjunction with ecological interactions and evolutionary  
239 processes.

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308 **Figure Legends**

309 **Figure 1. Migration system.** **a**, Five migration routes for 56 satellite tracked peregrine falcons in  
310 Old World. Only complete migration path is shown ( $n = 41$ ). **b**, Individual migration path fidelity of  
311 one representative individual (Lena Delta) tracked for four years (2010-2014). **c**, Migration  
312 connectivity at the population level as shown in a linear regression analysis. Significance was  
313 calculated using  $F$ -test ( $P = 2.2E-16$ ). **d**, PCA analysis of migratory strategy. Small and large dots  
314 represent individuals ( $n = 41$ ) and centroids of the minimum convex polygon for each population ( $n$   
315  $= 6$ ). PC1 is the mix of autumn departure and arrival dates and PC2 is the migration distance. **e**,  
316 Migratory distance comparison ( $P < 1E-6$ , two-sided  $t$ -tests, effect size = 1.43) between short-  
317 distance (SD) ( $n = 12$  individuals; 3,680 km: 95% CI: 2,443-5,018) and long-distance (LD) groups  
318 ( $n = 32$  individuals; 6,134 km: 95% CI: 3,282-8,828). In the box plots, the center line represents the  
319 median, whiskers represent maximum and minimum values, and box boundaries represent 75th and  
320 25th percentiles. The  $P$  values for the comparisons for any two populations within SD and LD were  
321 not significant (ns;  $P > 0.05$ , two-sided  $t$ -tests). The tracking data of three additional Kola  
322 peregrines from a previous study (**Methods**) were also used for this analysis.

323 **Figure 2. Past formation, present maintenance of migration routes and genetic basis for**  
324 **migration distance differences.** **a**, PCA, Neighbor-Joining tree and *frappe* showing the  
325 evolutionary relationship of the four genome-enabled populations. **b**, Demographic history  
326 reconstruction for each population using SMC++. **c**, Four candidate models for model choice in  
327 ABC. 84% of the total of 313 chunks (**Methods**) support Model 1.  $T_1$ ,  $T_2$ ,  $T_3$  are divergence times.  
328 **d**, Posterior distribution of divergence time estimates for the Model-1 in ABC. **e-g**, Species  
329 distributions predicted during the LGM, Mid-Holocene and present. **h**, The relationship between the  
330 route distance,  $Hd$ , and neutral genetic distance (Left),  $F_{ST}/(1-F_{ST})$ , and genetic distance based on  
331 selected loci (Right). The dashed line is the linear regression line. Significance levels were  
332 calculated using  $F$ -test. **i**, Proportion of grids ( $0.083^\circ \times 0.083^\circ$ ) with different Köppen-Geiger  
333 climate zones within each migration route. Full names of climate zones can be seen in

334 **Supplementary Information. j**, Spline-window based  $F_{ST}$  and XP-EHH to detect selective sweeps.  
335 Red points indicate windows containing selected genes. **k**, *ADCY8* haplotype heatmap. The dashed  
336 rectangle marks the focal 1.8kb fragment in *ADCY8*. Red and light blue squares symbol different  
337 alleles in each column (SNP). **l**, Haplotype frequency in the identified segment. **m**, Results of dual-  
338 luciferase reporter assay in chicken hippocampus primary cells. Data are mean  $\pm$  s.e.m. Significance  
339 levels were calculated using two-sided  $t$ -test ( $n = 14$  replicates for each of the first three groups and  
340  $n = 6$  for the *pGL3*-basic group). **n**, XP-EHH results for every selected SNPs within 1.8 kb flanking  
341 regions (Upper) and ATAC-seq results confirming the existence of CRE-motif (Lower).

342 **Figure 3. Shortened migration route and population decline in Europe populations due to**  
343 **global warming. a**, Area changes in breeding and wintering areas (Upper) between present and  
344 future (2070; RCP 8.5) and migratory distance comparisons (Lower) in the six peregrine  
345 populations. N/A: no predicted future breeding areas.  $\Delta d$  is the mean change of migration  
346 distances. In the box plots, the center line represents the median, whiskers represent maximum and  
347 minimum values, and box boundaries represent 75th and 25th percentiles.  $n = 200$  for each  
348 comparison. Significance and effect size were calculated using two-sided  $t$ -tests and Cohen's  $d$ ,  
349 respectively (Kola:  $P = 3.4E-9$ , effect size = 0.580; Yamal:  $P = 0.090$ , effect size = 0.170; Popigai:  
350  $P = 0.676$ , effect size = 0.042; Lena:  $P = 0.868$ , effect size = 0.017; Kolyma:  $P = 0.015$ , effect size  
351 = 0.243). **b**,  $LD_{Ne}$  and  $NeS$  estimates in recent 25 generations. **c**, The linear regression between  $NeS$   
352 and the most significant environmental variable identified in the GLM analysis. Data are median  $\pm$   
353 95% CI. Dashed lines represent the linear regression lines. **d**,  $NeS$  changes of each population  
354 predicted in the future. Data are median  $\pm$  95% CI.

## 355 **Methods**

### 356 **Tracking peregrine migration**

357 We used satellite-received Argos Platform Transmitter Terminals (PTTs) and GSM-received GPS  
358 transmitters to track 56 peregrines from six breeding regions in Arctic Eurasia (**Supplementary**  
359 **Table 1**). From which, we obtained the data of at least one full migration for 41 peregrines: Kola  
360 Peninsula ( $n = 1$  autumn/0 spring migration), Kolguev Island ( $n = 8/4$ ), Yamal Peninsula ( $n = 9/5$ ),  
361 Popigai River ( $n = 10/9$ ), Lena Delta ( $n = 6/6$ ) and Lower Kolyma River ( $n = 7/5$ ) (**Supplementary**  
362 **Information**). Permits to trap, collect blood samples and deploy satellite transmitters on peregrines  
363 were provided by the relevant authorities in Russia. All lab experiment procedures were under the  
364 guidance of the Ethics Committee of the Institute of Zoology, Chinese Academy of Sciences (IoZ,  
365 CAS). Studies in this manuscript involving peregrine brain tissue collection and analyses were in  
366 full compliance with the Institutional Animal Care and Use Committee at the IoZ, CAS.

367 For tracking data processed by the Argos system, we removed duplicate timestamps and used the  
368 Douglas Argos Filter algorithm designed to retains points (**Supplementary Fig. 15**), which  
369 correspond to a realistic rate of movement ( $\leq 100$  km/h) and which do not form tight angles  
370 between successive locations ( $\leq 15^\circ$ )<sup>31</sup>. Migration strategy<sup>32,33</sup> was quantified using  
371 departure/arrival date, duration and migratory distance (migration path distance) for all individuals,  
372 where possible (**Supplementary Fig. 16**). We defined the start and end of migration as the day that  
373 birds moved more than 40 km from their breeding (natal) range, or arrived at wintering range.

### 374 **Population migration connectivity and wintering distribution pattern**

375 To quantify the degree of migratory connectivity<sup>34</sup>, we extracted the longitudes of breeding and  
376 wintering sites for each tracked individual and used a linear regression to explore the correlation  
377 between breeding sites and wintering sites as used in a previous study<sup>33</sup>. The coefficient of  
378 determination ( $R^2$ ) was used to proxy the migratory connectivity. For the spatial distribution pattern

379 of wintering sites, we obtained the minimum convex polygon (MCP) of wintering sites and used a  
380  $G$ -function from  $R$  package *spatstat*<sup>35</sup> to conduct a point pattern analysis. A greater empirical  $\hat{G}(x)$   
381 than the theoretical function suggests that the sites tend to be closer than expected, in contrast with a  
382 dispersed pattern. More details please see **Supplementary Information**.

### 383 **Individual migration path fidelity**

384 We estimated the path fidelity of each bird by assessing individual repeatability<sup>36</sup> of migration paths  
385 across multiple years ( $n \geq 2$ ). To quantify the consistency of these migratory paths, we first  
386 calculated the track deviation from the great circle distance for each path in each year and then  
387 evaluated the repeatability of deviation after standardized measurement based on latitude.  
388 Specifically, we measured the total migratory distance (sum of all distances between successive  
389 positions along a migration path). Then, the straightness was calculated as the distance between the  
390 start and end locations of the path divided by total migratory distance<sup>37</sup>. The repeatability of path  
391 straightness was calculated using a linear mixed model implemented in the  $R$  package *rptR*<sup>38</sup>,  
392 followed by a significance testing through a permutation test.

393 To compare the path fidelity between SD and LD migratory groups, we considered the latitudes and  
394 longitudes of all sites along each migration path as response and independent variables respectively,  
395 and conducted a linear regression analysis to estimate the regression coefficient  $\alpha$  of an individual  
396 in different migration periods. We calculated the standard variation of  $\alpha$  ( $\alpha_{sd}$ ), as a proxy of  
397 individual path fidelity, that is, a lower  $\alpha_{sd}$  indicates that an individual uses a more similar path  
398 across migration periods. We compared differences in the mean  $\alpha_{sd}$  estimates between SD and LD  
399 groups using a  $t$ -test.

### 400 **Migratory strategy comparison**

401 Principal component analysis was used to cluster individuals based on their migratory strategy (i.e.  
402 migratory distance, duration and departure/arrival date during autumn migration). Noted that we did

403 not use the spring departure/arrival date because we did not obtain these data for the Kola  
404 population. In our study, only individuals that completed at least one migration route were included,  
405 and for individuals that were tracked for multiple years, we used mean migratory values to control  
406 pseudo-replication. We removed one of the variables if they were highly related ( $|r| > 0.75$ ). For the  
407 comparison of migratory strategy between SD and LD groups, we used a random forest model in *R*  
408 and *t*-test to detect the most significantly different strategy parameter. We calculated the effect size  
409 (Cohen's  $d^{39}$ ) for the *t*-test. In the comparisons, as we obtained the data of only one complete  
410 autumn migration in the Kola population (**Supplementary Table 2**), we also used the tracking data  
411 of three Kola peregrines from a previous study<sup>40</sup>.

## 412 **Sample collection and genomic DNA extraction and sequencing**

413 Blood samples were collected for the genome resequencing of 35 peregrines across the Eurasian  
414 Arctic (10 from Kola, 5 from Kolguev, 11 from Yamal and 9 from Kolyma). We also obtained nine  
415 and six feather samples from Popigai and Lena, respectively. Genomic DNA was extracted from  
416 blood and feather samples using the Blood & Cell Culture DNA Midi Kit and Blood & Tissue  
417 Extraction Kit (Qiagen), respectively. Paired-end libraries with insert size of 170 bp for blood DNA  
418 were constructed and subjected to sequencing on an Illumina HiSeq 2000 platform in BGI,  
419 Shenzhen and Novogene, Beijing. The feather DNA was used for the following PCR experiments.

## 420 **Sequencing data filtering and SNP calling**

421 An average of 68.75 Gb clean data (55.79×) were generated for 35 individuals. We used FASTQC  
422 and trimmomatic<sup>41</sup> to remove reads with low quality as previously described<sup>42</sup>. We used the  
423 chromosome-level peregrine genome assembly<sup>43</sup> as the reference genome, where our original  
424 assembly<sup>44</sup> was upgraded to chromosomal fragments. We then used the Burrows-Wheeler  
425 Alignment<sup>45</sup> to map the filtered reads from each individual onto the autosomal reference genome  
426 with Z-chromosome fragments excluded (**Supplementary Information**). Finally, we used the  
427 pipeline in Genome Analysis Toolkit<sup>46</sup> (version 3.5) to call SNPs.

## 428 **Population genomic analysis**

429 Since close relatedness can bias population assignment<sup>47</sup>, pairwise Identity-By-State scores among  
430 all individuals were estimated using PLINK<sup>48</sup> (version 1.9) and a threshold of 0.1 was applied,  
431 resulting in the removal of three closely related individuals for the following analysis  
432 (**Supplementary Fig. 17**). PCA was conducted on the autosomal biallelic SNPs for the remaining  
433 32 individuals using our in-house scripts. To reconstruct the phylogenetic tree, we used PLINK to  
434 calculate genetic distances among the studied peregrines based on the identified SNPs with default  
435 settings. A neighbor joining unrooted tree was then obtained using the *R* package ‘*phangorn*’ with  
436 *upgma* function<sup>49</sup>. Analysis of genetic structure was implemented in *frappe*<sup>50</sup> which employs an  
437 expectation maximization algorithm. The number of genetic clusters *K* was set to range from 2 to 5.

## 438 **Demographic history reconstruction**

439 We used SMC++ (version 1.10.0)<sup>51</sup> to model historical effective population sizes for each peregrine  
440 population with the mutation rate and generation time derived from our previous estimates<sup>44</sup>. To  
441 date the divergence among the peregrine populations, we developed a new ABC approach (details  
442 in **Supplementary Information**). Briefly, we established four candidate historical demographic  
443 models for model choice according to our phylogenetic results. The prior *Ne* distributions and  
444 divergence time parameters were set from a range of 1,000 to 100,000 and 1,000 to 10,000  
445 generations ago, respectively, according to the SMC++ results. The peregrine genome was divided  
446 into chunks with a size of 2 Mb and gene number in each chunk was counted and ranked. We  
447 conducted 100,000 simulations for each candidate model using the rapid coalescent *scrm*  
448 simulator<sup>52</sup> and summarized them using 95 different summary statistics (e.g. the total number of  
449 segregating sites, summarized site frequency spectrum). A machine learning tool, ABC random  
450 forest<sup>53</sup> was employed to conduct model choice. For the selected model with the highest  
451 approximated posterior probability (Model-1), we further simulated 1,000,000 datasets for  
452 parameter inferences. The neural network methods were applied for the inference in *R* package

453 *abc*<sup>54</sup>. To evaluate the ABC performance, we applied the cross validation on model choice and  
454 parameter inference.

### 455 **Ecological niche modeling**

456 We used MaxEnt (version 3.3.3k), in the *R* *dismo*<sup>55</sup> package, to predict breeding and wintering  
457 distributions under present environment conditions. Based on the satellite tracking data, we  
458 randomly selected presence data within the MCPs of individuals' summer (June to August) and  
459 wintering areas (December to January). The 90% MCP was calculated for each individual using the  
460 *MCP* function of the *adehabitatHR*<sup>56</sup> package in *R*. For climate data, we downloaded 19 present and  
461 paleo bioclimatic variables (**Supplementary Table 11**) from WorldClim<sup>57</sup>. To reconstruct breeding  
462 and wintering distributions in the past, we projected the ENMs built under present climate to  
463 paleoclimates during the Mid-Holocene (*ca.* 6 kya), LGM (22 kya) and LIG (120-140 kya),  
464 respectively.

### 465 **Paleo vegetation data analysis**

466 To examine whether the predicted LGM breeding areas mostly consisted of tundra biome, we  
467 obtained Eurasian paleo pollen data from a previous study<sup>58</sup>. Paleo pollen data classified as tundra  
468 biome by the *biome\_2000* model were extracted for LGM and then mapped to our predicted  
469 breeding areas to estimate the overlapping extent.

### 470 **Quantification of inter-route distances**

471 *Hausdorff distances* were used to quantify the dissimilarity between migratory paths of individual  
472 pairs of peregrines. The approach measures how far apart two subsets of a space metric are from  
473 each other<sup>10</sup>. In our study, a migratory path was treated as positional distribution of bird movement  
474 points in time and space and the distance between the migration path *A* and *B* was obtained using  
475 '*hausdorff\_dist*' function in *R* package *pracma*<sup>59</sup> (**Supplementary Information**). The mean *Hd*  
476 estimates were compared within and between neighboring populations using a *t*-test. The generated

477 *Hd* matrix was then used for the route clustering analysis using a ‘*hclust*’ method in *R* package  
478 ‘*heatmap*’. The inter-route distance was finally calculated as the mean *Hd* between pairs of  
479 individual paths from different migration routes.

#### 480 **Maintenance mechanisms of present migration routes**

481 To investigate maintenance mechanisms of present migration routes, we first checked the influence  
482 of neutral genetic and selective genetic distance on the route distances estimated above. For the  
483 estimation of genetic distance, we randomly selected 93 putatively neutrally-evolving and 75  
484 selected SNP loci based on the selection analysis of 32 resequenced peregrine genomes described  
485 below. Then, we genotyped nine and six individuals (shed feathers) sampled in Popigai and Lena,  
486 respectively. The detailed PCR amplifications and sequencing of these feather DNA extracts are  
487 described in **Supplementary Information**. With the combined genotypes from blood and feather  
488 samples, we calculated the  $F_{ST}$  for each locus among five populations (Kolguev, Yamal, Popigai,  
489 Lena and Kolyma) using *vcftools*<sup>60</sup>. The genetic distance was then calculated as  $F_{ST}/(1 - F_{ST})^5$ . We  
490 fitted the relationship between migration route separation (*Hd*) and neutral and selective genetic  
491 distance, respectively, using a linear regression model.

492 To investigate the environmental divergence among migration routes, we randomly sampled 200  
493 grids ( $0.083^\circ \times 0.083^\circ$ ) from the 90% MCP of each route and extracted the variable of climate  
494 zones referring to the Köppen-Geiger classification system<sup>61</sup> from each grid. Chi-squared tests were  
495 applied for the testing of differences in climate zones between adjacent migration routes (**Extended**  
496 **Data Fig. 5b**). To check the environmental boundaries, we further divided the Eurasian continent  
497 into geographic bands (width in  $2^\circ$  longitude based on the estimated migration distance per day in  
498 the studied peregrines) with direction parallel to the mean migration angle of all individuals and  
499 calculated the median value of climate zones of the grids ( $0.083^\circ \times 0.083^\circ$ ) at regular intervals ( $1^\circ$   
500 in latitude) from neighbouring bands for paired comparisons (illustrated in **Extended Data Fig. 5c**).  
501 Paired *t*-tests were used to check the abrupt change of climate zone (boundary) (**Extended Data**

502 **Fig. 5d)** between adjacent bands. It is noted that during comparison, we used the same latitude  
503 range between the pairwise routes.

504 To test whether there is more benefit from being a conventional migrator (migrating within a  
505 population route) or an unconventional migrator (migrating across routes), we first proved that the  
506 tracked peregrines migrated in a least-cost manner (**Supplementary Fig. 18**). We then simulated  
507 scenarios that peregrines depart from their actual breeding sites, fly along least-cost paths, but  
508 winter in the actual wintering sites of neighboring routes (illustrated in **Extended Data Fig. 5e**).  
509 Taking account for migration path length, we estimated the relative least cost of cross-route  
510 migration (**Supplementary Information**). A *t*-test was used to compare the difference in the  
511 relative least cost between the actual within-route and simulated cross-route migration. For the *t*-  
512 test, the effective size *d* was calculated.

### 513 **Identification of selective sweeps and detection of selected SNPs between SD and LD** 514 **peregrines**

515 We used two methods, a window-based  $F_{ST}$  and XP-EHH<sup>62</sup> to identify selective sweeps between the  
516 SD and LD groups. The  $F_{ST}$  of each locus was calculated using *vcftools*. A smoothed spline  
517 technique in *R* package *GenWin*<sup>63</sup> (version 1.0.1) was implemented to determine the window  
518 boundary and *w*-statistic was used as a proxy of windowed  $F_{ST}$ . The XP-EHH value of each locus  
519 was calculated using *selscan*<sup>64</sup> (version 1.1) with BEAGLE-phased<sup>65</sup> SNPs (*n iterations*=100).  
520 Outlier regions (top 1%) detected by both methods were considered as selective sweeps. For the  
521 sweeps identified on the focal gene, we calculated the nucleotide diversity ( $\theta_{\pi}$ ) of each locus using  
522 *vcftools* and narrowed the sweep down to a specific region. In addition, to verify the phased  
523 haplotype of *ADCY8* gene, we chose three individuals from each population for 10x genomics  
524 sequencing, followed by linked-reads phasing using the Long Ranger<sup>66</sup> (version 2.2.2)  
525 (**Supplementary Table 12**).

526 We then used an integrative method<sup>67</sup> to detect the selected SNPs between the pairwise groups  
527 (Kolguev vs LD and Yamal vs Kolyma), which integrated the results obtained from three selection  
528 tests: the *FLK*<sup>68</sup> based on comparing different patterns of allele frequencies among populations to  
529 the values expected under a scenario of neutral evolution<sup>69</sup>, latent factor mixed models (LFMM) for  
530 which the environment is used as a fixed effect and latent factors used to infer environmental  
531 associations<sup>70</sup>, and *pcadapt* (version 3.03) analysis based on Bayesian factor model. Detailed  
532 settings were described in our previous work<sup>71</sup>. The adjusted  $z$ -scores were calculated for each of  
533 three above tests, and the calibrated  $P$  values were obtained as previously reported<sup>70</sup>. The candidate  
534 SNP loci were ultimately determined using Benjamini-Hochberg FDR (false discovery rate) control.  
535 The level of FDR was set to 0.05.

### 536 **Luciferase reporter assay for the focal *ADCY8* haplotype**

537 To investigate the potential functional significance of different *ADCY8* haplotypes, a randomly  
538 selected Hap1 in SD peregrines and the dominant Haplotype (Hap2) in LD peregrines (**Fig. 2l**) were  
539 fully synthesized in SinoGenoMax Co., Ltd and inserted into the *pGL3*-promoter backbone  
540 according to KpnI/XhoI restriction sites. Positive (*pGL3*-promoter) and negative (*pGL3*-basic)  
541 controls were also constructed. The activity of Hap1 or Hap2 was examined in primary cells  
542 cultured from chicken embryonic hippocampus tissues. We isolated and cultured neurons from  
543 fertilized chicken eggs (Boehringer Ingelheim; details in **Supplementary Information**) for  
544 lipofection and luciferase reporter assays referring to previous studies<sup>72</sup>. *pGL3*-Hap1 or *pGL3*-Hap2  
545 were co-transfected with pRL-TK into the neurons using Lipofectamine 2000 (Invitrogen). After 48  
546 h incubation, the dual-luciferase activity was measured using Dual-Glo<sup>®</sup> Luciferase Assay kit  
547 (Promega). A  $t$ -test was used to compare the fluorescence intensity among experimental groups. At  
548 least three independent experiments of each assay were performed with a minimum of six  
549 replicates. To predict the motif in this focal region, we extracted the sequences (10 bp) around each  
550 SNP and searched the sequences against the TFBS motif database<sup>73</sup>.

551 **ATAC-seq and RNA-seq analysis**

552 Hippocampus and cortex tissues were collected from a peregrine that died of natural causes in the  
553 Chongqing Zoo. For the ATAC experiment (**Supplementary Information**), the samples were  
554 prepared according to the manual<sup>74</sup> in Shanghai Jiayin Biotechnology Ltd, followed by library  
555 construction and subjected to sequencing on an Illumina NovaSeq 6000 (Novogene). The raw reads  
556 generated were further quality controlled. The clean reads were mapped to our reference peregrine  
557 genome and sequencing depth around the target region was evaluated.

558 For the RNA-seq, brain tissues were collected from two humanely euthanized peregrines from the  
559 Beijing Raptor Rescue Center. Total RNA was extracted from the samples of two peregrines (chr3-  
560 5170169SNP genotype *CC* and *CT*) using the TRIzol reagent according to the user guide  
561 (Invitrogen). For each brain RNA sample, library with insert-size of 350 bp was constructed and  
562 then sequenced on a HiSeq 2500 (Novogene). *Reads Per Kilobases per Million reads (RPKM)* of  
563 *ADCY8* with different genotypes were calculated by mapping RNA-seq reads to the peregrine gene  
564 set<sup>44</sup> using SOAP<sup>75</sup> (version 2.22). Expression difference between these genotypes was compared  
565 using a hypergeometric test.

566 Detailed descriptions of the ATAC-seq please see **Supplementary Information**.

567 **Global warming impacts and prediction of migratory distance in the future**

568 Based on the inferred present peregrine distribution, we predicted future (2070) potential breeding  
569 and wintering distributions under RCP 8.5, a scenario where emissions continue to rise through the  
570 21<sup>st</sup> century. Occurrence probabilities were transformed into binary maps using true skill statistic-  
571 maximizing values as thresholds. Differences between present and future distributions were  
572 investigated using two parameters: area change and latitude shift. We counted the grids ( $0.083^\circ \times$   
573  $0.083^\circ$ ) within the non-overlap regions between present and future, and the shifted latitude was  
574 represented as the ratio of area and longitude (per degree). To compare the migratory distance

575 between the present and future, we randomly selected 50 sites per population within breeding or  
576 wintering ranges and calculated great circle distances between corresponding sites. The confidential  
577 interval of these distance estimates were calculated as the minimum and maximum of great circle  
578 distances among all the sites in each of breeding and wintering ranges. For comparison, we  
579 conducted the same analyses under RCP 4.5, a mitigation scenario where emissions peak around  
580 2040 (**Supplementary Information**).

### 581 **Prediction of effective population size changes in the future**

582 To study how effective population size will change under future climate change, we initially  
583 investigated the association between most recent changes of  $N_e$  and climate variables since the  
584 industrial revolution (1840). We used a linkage disequilibrium based method  $SNeP$ <sup>76</sup> (version 1.11)  
585 to reconstruct recent  $N_e$  changes in generations for each population. For this analysis, we randomly  
586 selected 5,000 loci per chromosome and used a  $NeS$  to investigate the rate of  $N_e$  changes<sup>77</sup>. It is  
587 noted that  $SNeP$  could reliably examine the changes or trends of  $N_e$ , rather than the actual  $N_e$ <sup>76</sup>.

588 For the climate data, the monthly temperature of the Community Climate System Model (version 4)  
589 output was downloaded from Coupled Model Intercomparison Project 5. The yearly mean  
590 temperature was calculated as the average of monthly temperature in the breeding season (May to  
591 July), a vital period for the breeding success of peregrines<sup>78,79</sup>. To quantify the historical weather  
592 extremes, we downloaded the gridded daily minimum and maximum temperature data from  
593 Berkeley Earth Surface Temperature. The number of days exceeding the 95% upper threshold of  
594 average temperature was considered as extreme hot days and below the 5% lower threshold as  
595 extreme cold days. The simulated future daily temperature (2020 to 2100) was downloaded from  
596 the NASA Earth Exchange Global Daily Downscaled Projections. The inferring method for future  
597 weather extremes was the same as historical extremes.

598 We constructed a GLM to model the relationship between *NeS* and changes of climate variables  
599 (**Supplementary Information**) and finally predicted the future *NeS* under future climate using the  
600 fitted GLM model.

### 601 **Statistical analysis**

602 All reported *P* values were from student *t*-tests (two-sided) unless otherwise specified. All assays  
603 were performed in at least three independent experiments with a minimum of six replicates. In the  
604 analysis of individual route repeatability, *P* values were calculated using a permutation test. The  
605 comparisons of climate zones between migration routes were calculated using an  $\chi^2$  test. The *P*  
606 values of band comparisons of climate zones were calculated using a paired *t*-test with latitude  
607 differences controlled. For the *t*-test, Cohen's *d* is determined by calculating the mean difference  
608 between two groups, and then dividing the result by the pooled standard deviation. The expression  
609 difference between different alleles of the focal *ADCY8* SNP was compared using a hypergeometric  
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741 **Author contributions**

742 X.Z led the project. X.Z. and A.D. conceived and designed the study. A.D., S.G., V.S., A.S., I.P.,  
743 J.L. and Z.L. conducted the fieldwork and sample collection. X.Z. and A.D. examined migration  
744 paths, migration connectivity and genetic structure of peregrines across Eurasia. X.Z. and M.W.B.  
745 supervised the population genomic research. Z.G., S.P., L.H., J.C., and X.D. performed the data  
746 analyses. Z.L., Y.X., M.S., H.S. and F. J. conducted the molecular experiments. X.Z. and Z.G.  
747 wrote the manuscript with contributions from M.W.B., S.K. and A.D.

748 **Competing interests**

749 The authors declare no competing interests.

750 **Additional information**

751 **Supplementary Information** is available in the online version of the paper.

752 **Correspondence and requests for materials** should be addressed to X.Z.

753 **Reporting summary**

754 Further information on research design is available in the Nature Research Reporting Summary linked  
755 to this paper.

756 **Data availability**

757 All of the sequenced genome data have been deposited in the GenBank under accession number  
758 PRJNA686418. The tracking data are included in the Arctic Animal Movement Archive and in  
759 Movebank under ID numbers 103426553 and 934079034.

760 **Extended Data Figure Legends**

761 **Extended Data Fig. 1. Sampling sites for tracking peregrines in the Arctic.** The sample size,  
762 visit years for each places and the peregrines equipped with Argos satellite transmitters are shown.

763 **Extended Data Fig. 2. The broad-front migration pattern of peregrines. a,** Four main wintering  
764 regions identified in the cluster analysis. **b,** Migration paths with the centroids of breeding and  
765 wintering MCP for each bird and the MCP of wintering ranges for all birds (dashed line) are shown.  
766 **c,** *G*-function results in the point pattern analysis showing a broad-front wintering distribution. The  
767 solid and dashed line mean the observed and theoretical value of *G*, respectively. The 95% CI of  
768 theoretical *G* value is shadowed. The *P* value was calculated for the statistic of maximum absolute  
769 deviation using Monte Carlo simulations ( $n = 100$ ). **d,** The distance from each winter centroid to its  
770 nearest neighbour centroid (Nearest neighbour distance) is shown ( $n = 40$ ).

771 **Extended Data Fig. 3. The migration strategy comparisons between SD and LD. a,** Variable  
772 importance estimated by random forest modelling. **b,** Migratory strategy comparisons between the  
773 short-distance (SD) and long-distance (LD) peregrine groups. Significance was determined by a  
774 two-sided *t*-test and sample size ( $n$ ) for each comparison is shown. In the box plots, the center line  
775 represents the median, whiskers represent maximum and minimum values, and box boundaries  
776 represent 75th and 25th percentiles.

777 **Extended Data Fig. 4. ABC simulation and parameter inference. a,** Linear discriminant  
778 summary statistics values of the simulated datasets and the observations given four ABC candidate  
779 models. Based on the three statistics (LD1-3), Model-1 is best supported because the targets (dark)  
780 fit simulated data (shadow) well. **b,** Distribution of divergence times estimated using the chunks  
781 supporting the Model-1. One column represents one chunk and we only show 100 chunks. The  
782 density bar symbols posterior distribution of inferred divergence time in each chunk.

783 **Extended Data Fig. 5 Maintenance mechanisms of present migration routes. a,** Route cluster  
784 analysis based on *Hd*. **b,**  $\chi^2$  testing results of climate zones between adjacent migration routes at the  
785 whole route level. **c,** The schematic diagram of environment comparisons between neighboring  
786 geographic bands. Each route was divided into geographic bands parallel to the main migration  
787 direction. Grids at regular intervals were chosen from neighboring bands for comparisons. **d,**  
788 Environmental boundaries coinciding with migration route boundaries. The Eurasia continent was  
789 divided into geographic bands (at 2° longitude). The *P* values of paired *t*-tests between compared  
790 bands are shown and the dashed line equals to 0.05 (Upper). The bar is scaled as the number of  
791 space between two targeted bands in a paired comparison. The MCPs (90%) of five migration  
792 routes are shaded (Lower). Arrows point the coincidence between environmental and migration  
793 route boundaries. Noted that the distinct environment difference within the Popigai route may result  
794 from the inclusion of large “barrier islands” of unsuitable region in comparison. **e,** Illustration of the  
795 model simulating the least-cost migration path. For a typical migration route, we simulated the  
796 potential migration path (dashed lines) that a peregrine depart from its actual breeding site (e.g. B1  
797 in Route1), fly along a least-cost path, but winter in a wintering site of the neighboring route (e.g.  
798 W2 in Route2). B1-3 means breeding areas and W1-3 means wintering areas. Solid lines are the  
799 actual tracked migration path. **f,** Migration cost comparison between within-route and across-route  
800 paths ( $P = 0.01$ ,  $t = -2.58$ ,  $df = 101.68$ ), respectively. Significance was calculated using a two-sided  
801 *t*-test ( $n = 45$  and  $64$  for within- and cross-route, respectively). In the box plots, the center line  
802 represents the median, whiskers represent maximum and minimum values, and box boundaries  
803 represent 75th and 25th percentiles.

804 **Extended Data Fig. 6 Differences in breeding and wintering areas ( $\Delta_{\text{Future-Present}}$ ) between**  
805 **present and future (2070).** Predicted breeding (Upper) and wintering (Lower) area changes under  
806 RCP 8.5 scenario, and zoomed in Kola and Europe.