

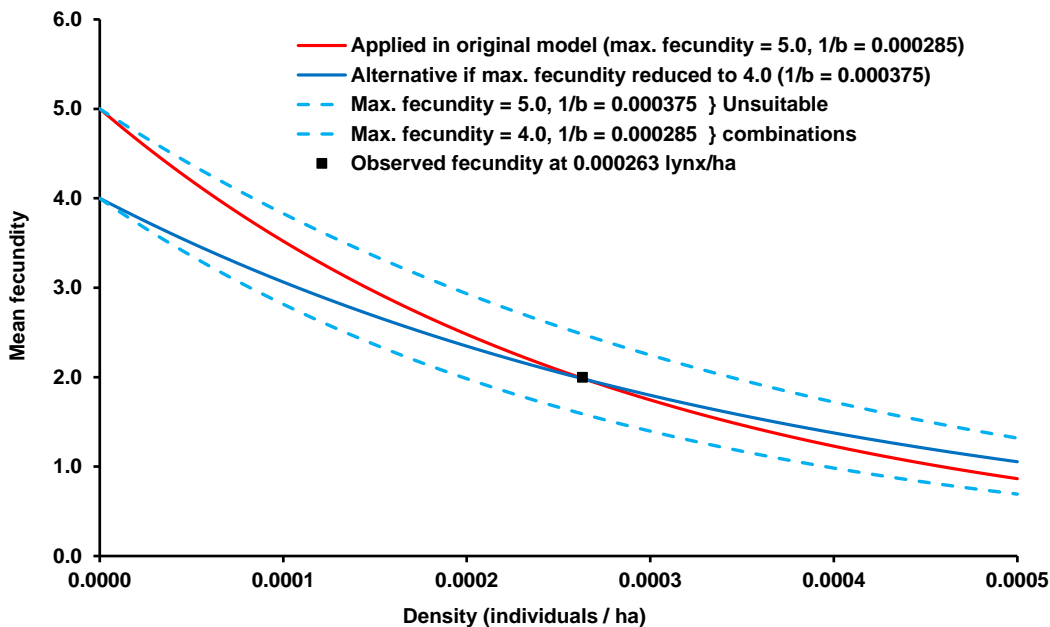
## Supplementary Material

### Methods

#### *Estimation of the parameter $1/b$*

The parameter  $1/b$  in RangeShifter is the exponential rate at which fecundity declines as local density increases (Bocedi et al., 2014). We estimated it in this study by fitting the relationship between mean fecundity and density through the average of 2 kittens per female (Breitenmoser-Würsten et al., 2007; Gaillard et al., 2014) at a density of 0.000263 lynx/ha proposed for Scotland (Hetherington and Gorman, 2007), given that we had assumed a maximum fecundity of 5 kittens per female at very low density (i.e. the unobtainable intercept density of 0 lynx/ha). Had we assumed a different intercept density, e.g. 4 kittens per female, then we would have required a higher value of  $1/b$  to match the observed point, as illustrated in Fig. S1.

**Figure S1.** Density dependence in fecundity as applied in the original model (solid red line), in an alternative demographic scenario (below) assuming reduced intercept fecundity (solid blue line) and two unsuitable relationships (broken lines) which would not match observed data.

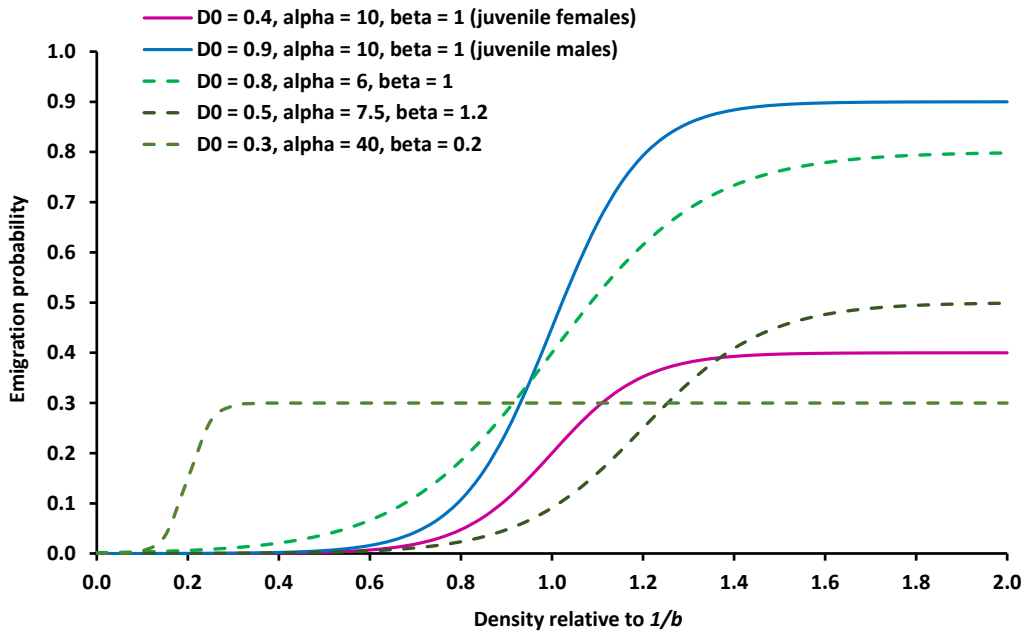


Ideally, we would require observed estimates of mean fecundity at two or more densities, in which case we would not need to assume the intercept density in order to estimate  $1/b$ , but we were unable to find any suitable estimate in this case. *It is possible that fecundity may not vary with density in lynx, however there are no Scotland-specific data and density-dependent fecundity has been used in the modelling of other lynx species Gaona et al (1998).*

#### *Density-dependent emigration*

An individual's density-dependent emigration probability in RangeShifter is determined by applying a logistic reaction norm as a function of density in the local patch, where density is expressed relative to the summed total of  $1/b$  for the whole patch. Note that the patch might comprise more than one type of suitable habitat class, which differ in their values of  $1/b$ , although that was not the case in the model applied here ( $1/b = 0.000285$  individuals/ha for high and low quality woodland). The reaction norm requires three parameters, all of which are dimensionless: the maximum emigration probability ( $D0$ ), the slope ( $alpha$ ) and the inflection point ( $beta$ ). We set these parameters such that emigration probability was negligible at low density and reached  $D0$  at high density, but was substantially higher for juvenile males than for juvenile females, as illustrated in Fig. S2.

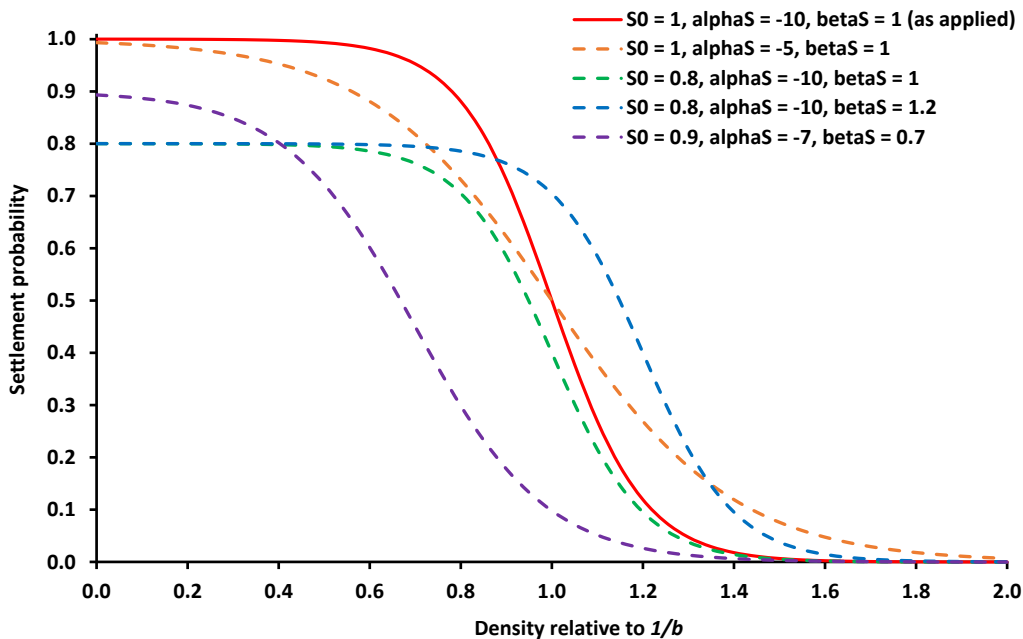
**Figure S2.** Emigration reaction norms applied in the model for juveniles of each sex (solid lines) and examples of three alternative relationships which could be applied by altering one or more of the three parameters



**Settlement**

A similar method was used to apply density-dependent settlement in the model, but based on the relative density of the patch that the disperser has reached after passing through the inter-patch matrix. The same relationship was applied to both sexes. As we have no observed data on settlement at the scale of the patches implemented in the model, we set the parameters so that settlement was certain at low local density, whilst at very high local density the disperser would reject the patch and continue on its dispersal trajectory. At a density of half the total  $1/b$  for the patch, there was a 50% chance that the disperser would settle (Fig. S3).

**Figure S3.** Settlement reaction norm applied in the model (solid line) and examples of four alternative relationships which could be applied by altering one or more of the three parameters



In our model, the settlement parameters for males and females differed. Both sexes required a suitable habitat patch to be located (“find a suitable patch”) and existing lynx densities within that patch to be low

enough to permit occupancy (“density dependence”). However, for males to settle, a female was also required to be in that patch (“mating requirements”).

### *SMS Parameters*

In the absence of any detailed movement data for lynx in Scotland, or comparable data from elsewhere, the setting of SMS parameters was unavoidably subjective, but based to some degree on experience we have gained in modelling other species for which data were available (Aben et al., 2016, 2014).

We set the perceptual range (PR) to 500 m (five cells). Whilst a large carnivore can presumably see much further than this if visibility permits, the PR should reflect the distance over which a disperser makes decisions based on local landscape composition, and we assumed 500 m to be a reasonable average across a range of landscapes likely to be encountered in rural Scotland. However, this is not likely to be a crucial parameter, as the ability of SMS to generate connectivity estimates closely correlated with genetic data was insensitive to PR when PR was three cells or more (Coulon et al., 2015). The PR method was set to 2, i.e. the harmonic mean method for averaging perceived costs within the PR. This method tends to weight effective costs towards the detection of low-cost habitat, whereas the arithmetic mean method tends to be influenced more strongly by high-cost habitat. We assumed that a dispersing large carnivore would be more strongly attracted to suitable breeding habitat than it would be repelled by partial barriers such as main roads, with lynx known to follow forested habitats during dispersal (Schmidt, 1998).

The directional persistence (DP) parameter is the one to which SMS is usually most sensitive (Coulon et al., 2015), and yet is the most difficult to estimate, as it is not directly estimable in the field, but can be derived from fitting simulated trajectory data to observed trajectories (Aben et al., 2014). Here, as we had no such observed data, we set DP subjectively by adjusting it so that simulated trajectories on the computer screen achieved a balance between some degree of response to variation in perceived landscape costs and a correlated pattern as is expected of naïve dispersers in a fragmented landscape (Zollner and Lima, 1999). Memory size (the number of previous steps over which the current direction is determined for the purpose of applying DP) was set to five cells, i.e. equal to the PR, and we applied no dispersal bias (goal type 0) in order to keep the SMS model as simple as possible.

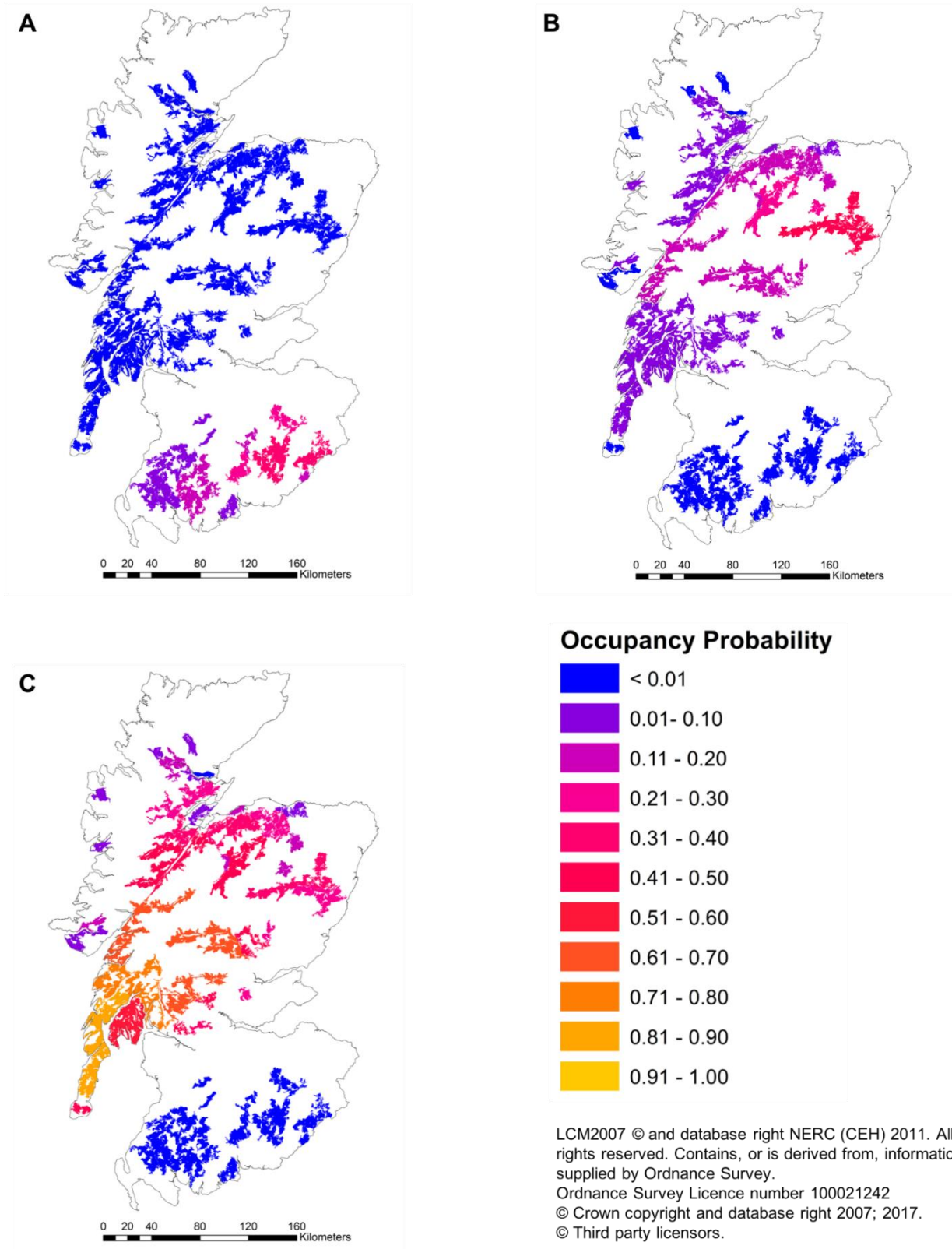
## Results

**Table S1.** RangeShifter model output for each of the 53 unique habitat patches. Reintroductions were modelled independently from Kielder Forest (Kield), Aberdeenshire (Aber) and the Kintyre Peninsula (Kint), averaged over 100 replicates.

Patch	Mean Probability of Patch Occupancy over 100 Years (%)			Occupancy Probability at Year 100 (%)			Mean Year of First Occupancy		
	Kield	Aber	Kint	Kield	Aber	Kint	Kield	Aber	Kint
1	0	0.69	48.86	0	3	44	-	84	2.67
2	0	3.05	40.44	0	10	60	-	66.44	24.93
3	0	0.82	5.62	0	3	13	-	78.43	59.07
4	0	2.44	13.99	0	6	34	-	73.57	52.24
5	0	1.28	6.88	0	5	24	-	76.88	69.76
6	9.48	0	0	16	0	0	28	-	-
7	32.19	0	0	21	0	0	3.02	-	-
8	6.91	0	0	11	0	0	31.47	-	-
9	21.56	0	0	19	0	0	12.89	-	-
10	19.59	0	0.01	19	0	0	12.2	-	64.33
11	3.92	0	0.06	9	0	0	38.85	-	59.2
12	0	2.19	20.17	0	5	37	-	65.85	38.58
13	0	13.85	25.84	0	19	42	-	12.13	45.31
14	0	21.82	15.81	0	21	59	-	11.15	67.46
15	0	17.48	14.5	0	21	54	-	14.88	71.01
16	0	0.64	5.03	0	4	20	-	81.13	74.29
17	0	0.36	3.7	0	4	14	-	83.78	80.47
18	0	0.12	0.64	0	1	2	-	88.67	83.27
19	10.03	0	0	18	0	0	32.38	-	-
20	11.99	0	0	20	0	0	29.94	-	-
21	0.34	2.79	33.41	0	10	47	45.56	68.56	32.36
22	0	8.85	69.55	0	21	83	-	54.89	15.37
23	0	4.02	58.35	0	15	82	-	67.53	19.16
24	0	15.88	49.17	0	24	79	-	20.47	35.3
25	0	16.66	63.64	0	31	83	-	25.3	18.43
26	0	4.98	77.21	0	16	83	-	63.5	6.91
27	0	13.1	63.68	0	31	83	-	45.33	18.12
28	0	10.89	19.53	0	23	56	-	37.8	54.61
29	0	18.84	34.37	0	31	81	-	35.86	50.9
30	0	7.05	8.22	0	17	30	-	43.65	76.68
31	0	7.77	12.37	0	19	43	-	55.84	70.97
32	0	9.08	45.01	0	25	82	-	61.52	40.48
33	0	1.03	7.01	0	3	28	-	72.36	74.09
34	0	1.53	9.41	0	7	38	-	79.33	77.47
35	0	0.2	1.23	0	1	7	-	86.75	86.43
36	0	1.61	11.1	0	8	47	-	78.17	76.97

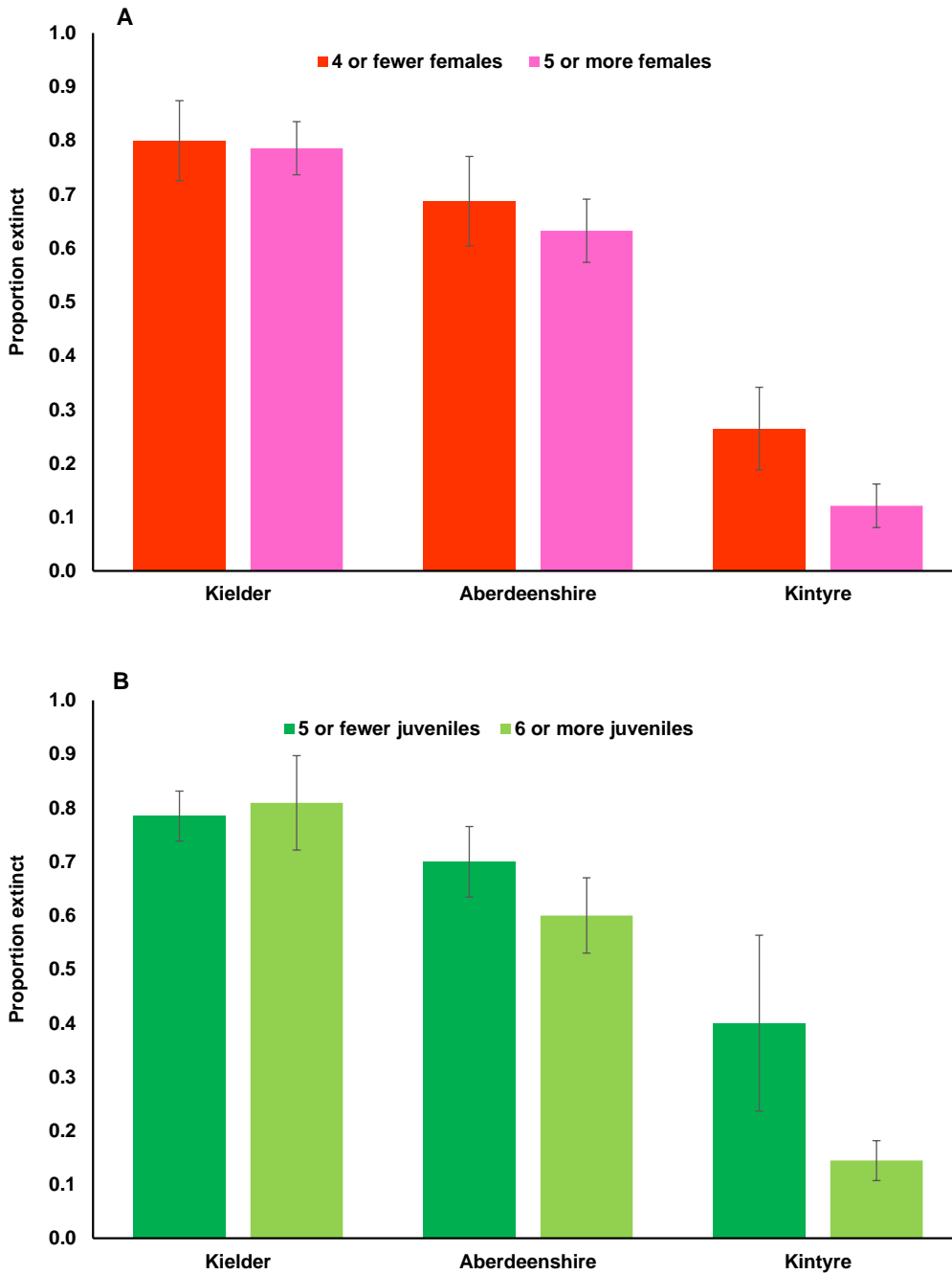
Patch	Mean Probability of Patch Occupancy over 100 Years (%)			Occupancy Probability at Year 100 (%)			Mean Year of First Occupancy		
	Kield	Aber	Kint	Kield	Aber	Kint	Kield	Aber	Kint
37	0	6.39	6.57	0	16	27	-	36.82	78.07
38	17.03	0	0	9	0	0	3.95	-	-
39	35.87	0	0	17	0	0	0	-	-
40	25.52	0	0.14	17	0	0	4.46	-	66.5
41	0	4.26	46.59	0	12	71	-	63.53	26.61
42	0	46.31	35.31	0	33	81	-	1.72	46.13
43	7.82	0	0	19	0	0	58.45	-	-
44	8.19	0	0	19	0	0	51.56	-	-
45	0	46.95	21.79	0	31	67	-	0	63.17
46	0	1.71	82.46	0	10	79	-	81.91	0
47	0	4.48	84.45	0	16	83	-	67.47	1.46
48	0	8.63	78.02	0	22	83	-	58.48	6.01
49	0	13.77	47.45	0	32	83	-	44.7	37.98
50	0	4.39	25.57	0	17	77	-	71.15	63.24
51	0	8.09	34.61	0	23	80	-	64.34	53.89
52	0	29.43	43.7	0	33	83	-	13.37	39.17
53	0	19.23	24.52	0	31	79	-	29.6	64.12

**Figure S4.** Predicted mean probability of patch occupancy across mainland Scotland averaged from year 0-100 following reintroduction from (A) Kielder Forest, (B) Aberdeenshire and (C) the Kintyre Peninsula.

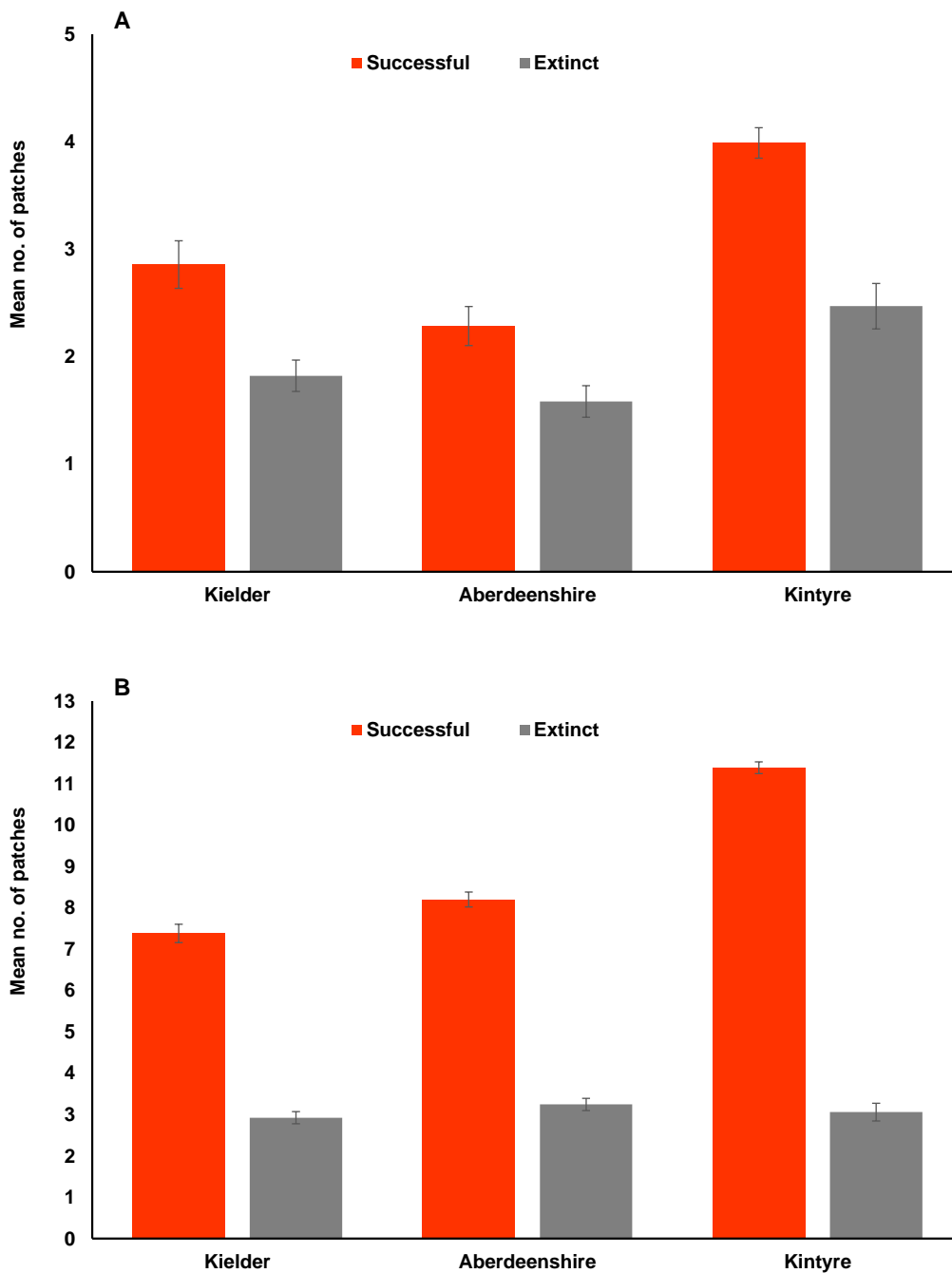


**Factors affecting extinction/establishment of released population**

**Figure S5.** Effect on population extinction probability by year 100 of (A) the number of females in the initial population of 10 individuals and (B) the number of juveniles born in the first breeding year after release. Error bars show 1 standard error.

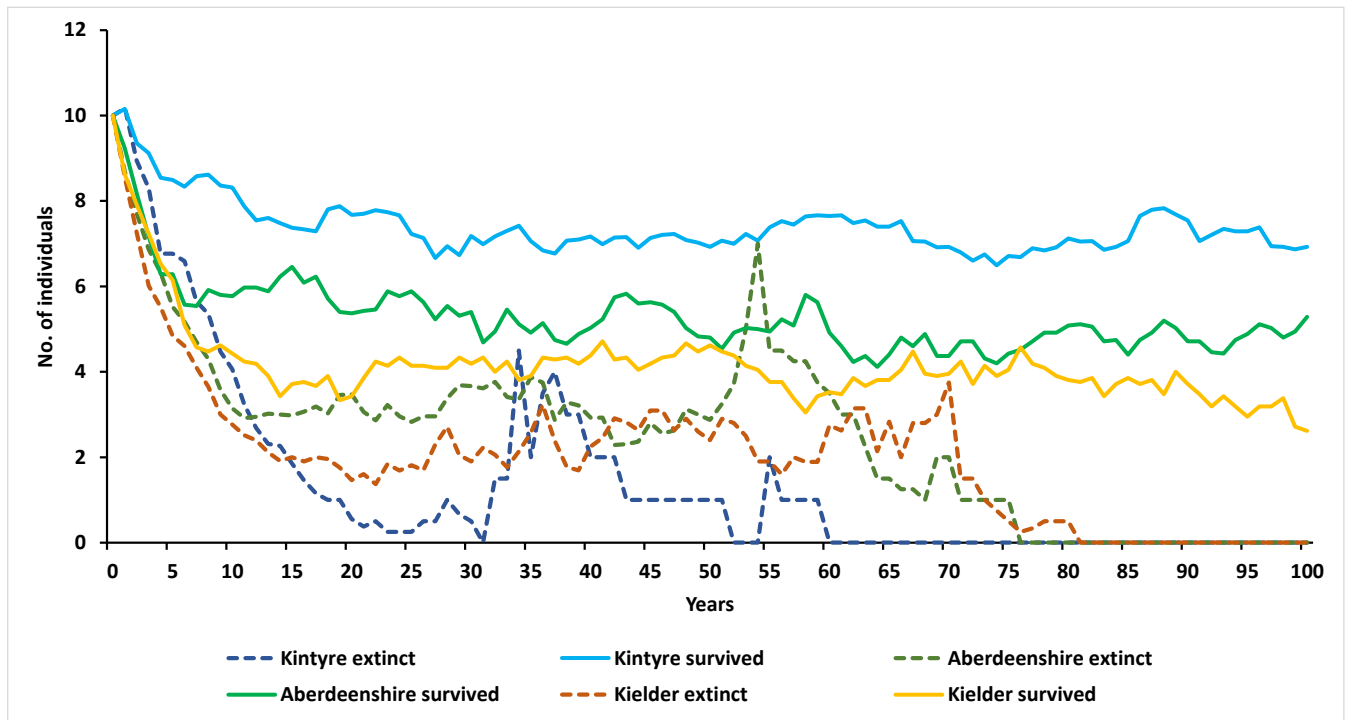


**Figure S6.** Number of different patches colonised by successful dispersers (here defined as those which survived their first winter) in (A) the first 10 years and (B) the first 30 years after release. Error bars show 1 standard error.





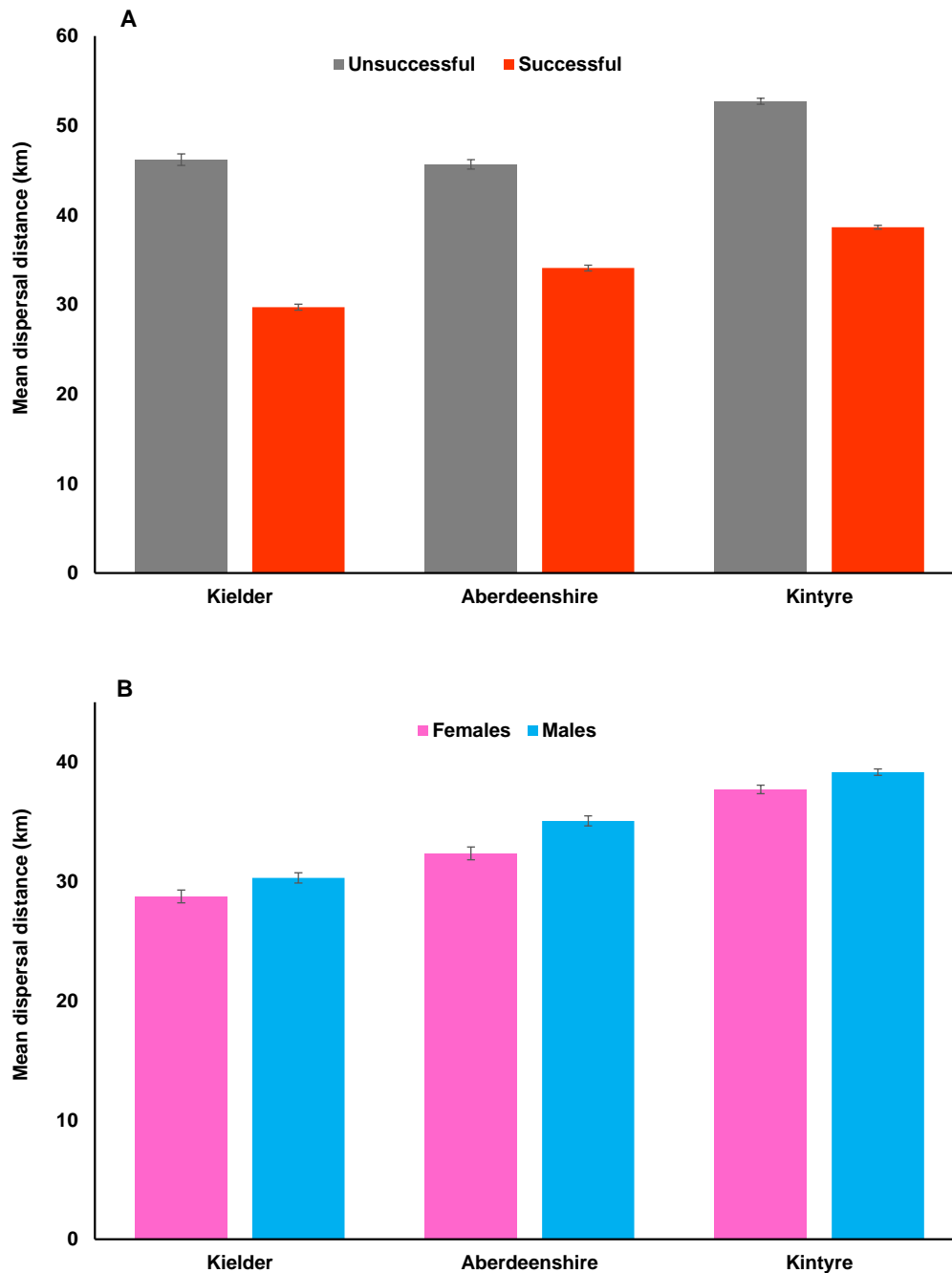
**Figure S7.** Pre-reproduction population size in the reintroduction patch for each reintroduction site over time for those replicates that survived and those replicates that went extinct.



### *Dispersal and survival at the individual level*

Across all release sites, the mean year in which the last founder died was 10.7 (s.e. 0.46, range across sites 10.4 - 11.0), and the mean year in which there remained alive at least one founder of each sex (i.e. the founding population remained viable even if all juveniles had died or dispersed) was 5.6 (s.e. 0.47, range across sites 5.3 - 6.3) (Fig. S8).

**Figure S8.** Mean dispersal distance of (A) all dispersers as a function of success and (B) successful dispersers by sex. Data were extracted from the individual-level output files of an additional 10 replicate simulations run for each release site, and error bars show 1 standard error.



## Sensitivity to Model Assumptions

### *Landscape configuration*

In a model such as this, the number of ways of representing the landscape, and in particular how discrete patches are delimited from continuous regions of suitable habitat, is potentially huge, and we cannot therefore evaluate the model's sensitivity to all possible landscape configurations. However, in our model there were 16 patches of area less than 100 km<sup>2</sup>, which might be regarded as being too small to contain a local sub-population of lynx, given that home ranges have been estimated to lie in the range of 45 - 210 km<sup>2</sup> (Breitenmoser-Würsten et al., 2001). We therefore constructed an alternative landscape configuration in which most of these small patches (except those that were too remote) were combined with an adjacent larger patch or with another small patch, thereby reducing the total number of patches from 53 to 42. In so doing, the Kintyre and Kielder release patches were increased in size, and their initial densities were therefore adjusted to retain initial population sizes of 10 individuals in each case. We ran 100 replicates for each release site as previously.

**Table S2.** Metrics of success for landscape in which some small patches were combined with other patches - original model predictions (Table 3) in brackets.

	<b>Kielder</b>	<b>Aberdeenshire</b>	<b>Kintyre</b>
No. of replicates reaching year 100	51 [21]	37 [35]	86 [83]
Mean no. of patches occupied at year 100	8.9 [10.2]	22.7 [18.9]	25.2 [27.1]
Mean no. of individuals at year 100	60.0 [55.0]	131 [97.8]	159 [150]

Combining some of the small patches with other patches had a limited effect on the outcome of the reintroduction, other than an increased number of replicates for Kielder surviving to 100 years, and a somewhat larger final population after release in Aberdeenshire (Table S2). In both cases, the combining of small patches likely to be reached by dispersers in the early years after reintroduction would reduce the chance of local extinction due to demographic stochasticity, whereas the nearest six patches to Kintyre (other than a small patch combined with the release patch) were all large anyway, and therefore there was no similar gain by combining small patches elsewhere in the country.

In many modelling studies, there is only one representation of the landscape applied, yet issues such as the choice of cell size (Bocedi et al., 2012) and how continuous tracts of suitable habitat are split into discrete patches, as is required for RangeShifter, can potentially be important. We would therefore advocate that, in the case of a reintroduction programme being in the planning stage (rather than simply speculative, as here), the sensitivity of model predictions to assumptions made in representing the landscape should be assessed.

### *Differential age at maturity*

We used the 'complex sexual model' option of RangeShifter to run simulations in which males matured at three years rather than two years, which remained the age of first breeding for females. We set harem size to five to ensure that males were not locally limiting once they became mature. 100 replicates were run for each release site.

All three metrics of reintroduction success were reduced substantially for all release sites by delaying male maturity to three years (Table S3).

**Table S3.** Effect of increasing age of male maturity to three years on metrics of success - original model predictions (Table 3) in brackets.

	<b>Kielder</b>	<b>Aberdeenshire</b>	<b>Kintyre</b>
No. of replicates reaching year 100	5 [21]	6 [35]	45 [83]
Mean no. of patches occupied at year 100	5.4 [10.2]	11.5 [18.9]	15.8 [27.1]
Mean no. of individuals at year 100	21.6 [55.0]	54.2 [97.8]	82.4 [150]

Clearly the assumption of the age at which males first reproduce has a considerable quantitative effect on the model predictions, as sub-adult males must survive two years at a survival probability of 0.63 (~0.4 combined) compared to only one if they mature at two years. However, male lynx have been recorded as sexually mature at 1¾ years old (Kvam, 1991) so male maturity at three years in established populations in central Europe (von Arx et al., 2004) need not necessarily imply that they would not mate at two years in an expanding population where adult males are few, and their survival rate might be higher if they do not encounter adult males so frequently. Critically, the rank order of sites was maintained when assuming older male maturity. Although we acknowledge that this is an important issue, and data from other introduction schemes would be highly informative, we still consider that our original assumption was adequate for our principal aim of comparing the three proposed reintroduction sites.

#### **Demographic parameters**

Four demographic parameters were altered to reflect plausible alternatives: maximum fecundity was reduced to 4.0,  $1/b$  was increased accordingly to 0.000375 individuals/ha (see Fig. S1 illustrating the estimation of  $1/b$ ), reproduction probability was reduced to 0.875 and maximum age was increased to 20 years. We ran 100 replicates for each site.

**Table S4.** Effect of altering four demographic parameters on metrics of success - original model predictions (Table 3) in brackets:

	<b>Kielder</b>	<b>Aberdeenshire</b>	<b>Kintyre</b>
No. of replicates reaching year 100	25 [21]	17 [35]	64 [83]
Mean no. of patches occupied at year 100	6.0 [10.2]	7.0 [18.9]	13.1 [27.1]
Mean no. of individuals at year 100	28.2 [55.0]	36.4 [97.8]	87.2 [150]

Although all three metrics of reintroduction success were reduced relative to the original simulations (except for the number of replicates reaching year 100 for Kielder, which increased) by applying together the alternative demographic parameters, the rank order of release sites was maintained (Table S4). In relative terms, Aberdeenshire showed the greatest reduction in all metrics. Reducing the frequency of reproduction and the maximum fecundity would both serve to reduce the rate of population spread, whereas increasing the maximum age should serve to compensate (but apparently not enough). Increasing  $1/b$ , which was necessary to ensure that density dependence in fecundity would result in approximately the observed mean fecundity at the observed density, would also have the effect of increasing the threshold density at which emigration would occur, and therefore also slow the rate of expansion, since the population in a colonised patch would typically need longer to increase to the density at which further dispersal would occur. That effect could, however, be compensated by decreasing the emigration parameter  $\beta$ .

The interplay of demographic and dispersal parameters is complex, and even if we had good observed data on the rate of spread of an introduced population, there would remain some uncertainty in parameter values to be applied. It is highly encouraging, therefore, that the ranking of the three proposed reintroduction sites was robust to highly plausible alternative parameter values to those originally applied.

### ***Density-independent emigration***

Two simulations applying density-independent emigration were run for each release site (100 replicates each).

**Table S5.** *Metrics of success when applying density-independent emigration probability. The fixed emigration probability for the juveniles of each sex were (1) set equal to the maximum emigration probability (D0) in the original model and (2) set equal to D0 / 2 in order to try to reflect the overall emigration rate in the original model. Original model predictions (Table 3) are given in brackets.*

		<b>Kielder</b>	<b>Aberdeenshire</b>	<b>Kintyre</b>
(1)	No. of replicates reaching year 100	14 [21]	29 [35]	72 [83]
	Mean no. of patches occupied at year 100	8.1 [10.2]	18.7 [18.9]	27.3 [27.1]
	Mean no. of individuals at year 100	40.4 [55.0]	92.2 [97.8]	146 [150]
(2)	No. of replicates reaching year 100	14 [21]	32 [35]	81 [83]
	Mean no. of patches occupied at year 100	5.5 [10.2]	5.7 [18.9]	15.5 [27.1]
	Mean no. of individuals at year 100	25.7 [55.0]	32.3 [97.8]	108 [150]

Assuming a density-independent emigration probability for juveniles of each sex equal to the maximum emigration probability in the original model had only limited effect on reintroduction success, although halving those probabilities led to reduced final population sizes and patch occupancy (Table S5). Under density-independent emigration, some juveniles would disperse from a recently colonised patch sooner than they would have done under density-dependent emigration, thereby lengthening the time taken for the population in that patch to reach carrying capacity, but by way of compensation colonising patches further from the release site earlier. Therefore, the assumption of density-dependent emigration appears not to be critical in the case of this particular model.

### **Alternative Modelling Scenarios**

#### ***Choice of release sites***

In order to examine how critical was the choice of release patch to predicted reintroduction success, we ran a set of simulations in which we selected an alternative release site within each region as close as possible in size to the original sites: patch 53 in E Scotland (9% larger than Aberdeenshire), patch 44 in S Scotland (49% larger than Kielder) and patch 48 in W Scotland (5% larger than Kintyre) (see Fig. 1 in the main text). Initial densities were adjusted to ensure that the introduced populations comprised exactly 10 individuals in each case, and 100 replicates were run for each site.

**Table S6.** *Metrics of success for an alternative release patch within each region - original model predictions (Table 3) in brackets.*

	<b>South</b>	<b>East</b>	<b>West</b>
No. of replicates reaching year 100	75 [21]	31 [35]	75 [83]
Mean no. of patches occupied at year 100	10.7 [10.2]	22.3 [18.9]	26.9 [27.1]
Mean no. of individuals at year 100	58.9 [55.0]	117 [97.8]	150 [150]

The rank order of success across the three regions of Scotland was maintained, other than a substantial increase in the south over Kielder in the number of replicates reaching year 100 (Table S6). In all three regions, the final population sizes were very similar to those achieved following release from the three original sites. Therefore, it would seem that the likely success of reintroduction depends more on the regional characteristics of the landscape (such as density and spatial configuration of patches) rather than on the characteristics of the release patch itself, although if the release patch were very poorly connected to any other patches, we assume that success is likely to be very low.

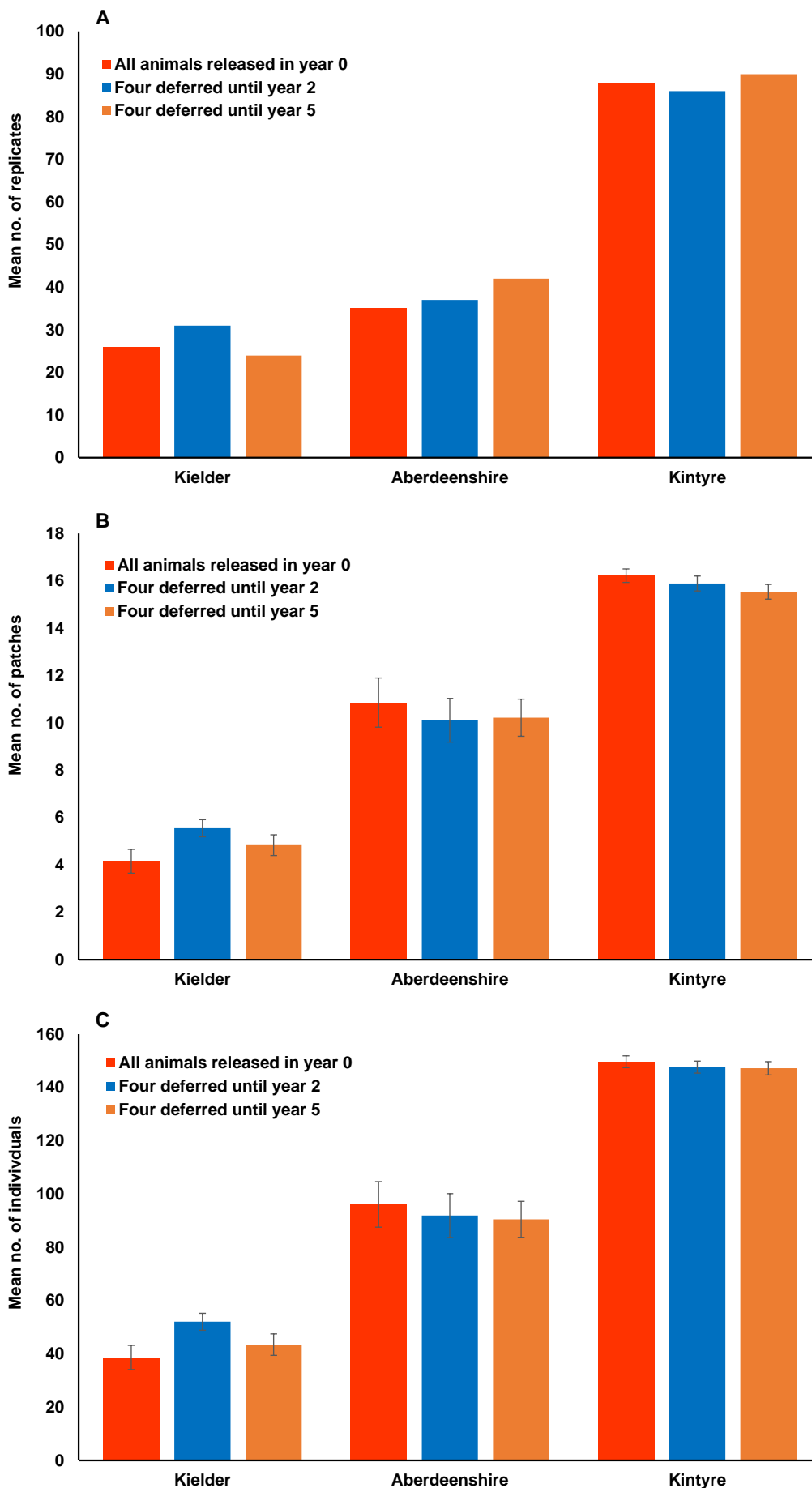
### *Phased release of initial individuals*

In the original simulations, all 10 individuals of the initial population were released at the start of the simulation (before reproduction in year 0), and the sex of each individual was determined independently and at random. In RangeShifter v1.1, there is no alternative mechanism by which to establish an initial population, and thus in some replicates the initial sex-ratio was skewed. However, since the original modelling for this study was completed, we have developed RangeShifter v2.0 (currently under test as at January 2019), in which the composition of the initial population may be specified from an input file, and individuals of specified sex, age and stage class may be introduced into specified patches at the start of any given year.

Release programmes for large predators may often be phased for reasons such as the logistics of capturing many individuals from a source population concurrently and avoiding excessive depletion of the source population(s). In order to assess how a phased release programme might compare with simultaneous release, we used RangeShifter v2.0 to run a set of additional simulations. However, the number of ways in which even as few as ten individuals might be released in phases is substantial, and we therefore limited this exercise to three simulations for each release site of 100 replicates in each case. In the first simulation, the initial population for every replicate comprised five adult females and five adult males, each sex was represented by two individuals of 2 years old, one of 3, one of 4 and one of 5, and all individuals were released in the first year (in effect a control scenario to match the original models, but with the characteristics of individuals fixed rather than determined at random as previously). In the second simulation, the release of one 2-year-old and one 5-year-old of each sex was deferred for 2 years, and in the third simulation, the release of the same four individuals was deferred for 5 years.

Deferring the release of four of the ten initial individuals had essentially a negligible influence on the outcome by any of the three metrics of success (Fig. S9). Of course, there might well be other patterns of phased release that would fare better on average, including varying the sex-ratio and age of released individuals, but the number of potential combinations is extremely large. The modelling approach would therefore be best suited to comparing feasible alternative phased-release scenarios (i.e. as determined by practical and ethical constraints), rather than being applied to search for some 'optimum' scenario.

**Figure S9.** Effect of phased release at a single site on (A) the survival of the population until year 100, (B) the number of occupied patches at year 100 and (C) the total population size at year 100. Error bars show 1 standard error.



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