González-Díaz P, Cavers S, Iason G, Booth A, Russell J, Jump A (2018).
Weak isolation by distance and geographic diversity gradients persist in Scottish relict pine forest, linked to flowering asynchrony and effective gene flow
iForest – Biogeosciences and Forestry – doi: 10.3832/ifor2454-011

Supplementary Material

Tab. S1 - Pairwise population differentiation (F_{ST}) (below diagonal) and differentiation index Jost´s *D* (above diagonal). Numbers in bold indicate significant *P*-values P<0.05. For the Differentiation index Jost´s *D*, numbers in bold indicate significant *P*-values P<0.05 after Bonferroni correction, and number in italics indicate significant *P*-values P<0.05 without Bonferroni correction. P-values for the differentiation index Jost´s *D* were obtained by bootstrapping 10,000 times.

	COG	GLL	CRA	CCC	MEG	BWR	ABE	ROT	ALT	GLT	GLA	AMA	LOC	SHI	BEE	GLE	STO	RHI
COG	-	***0.096***	*0.048*	*0.052*	*0.076*	*0.058*	*0.063*	0.019	*0.074*	0.029	0.021	*0.039*	-0.008	*0.043*	*0.053*	*0.040*	0.024	*0.064*
GLL	**0.034**	-	*0.050*	*0.055*	0.028	*0.049*	0.005	*0.057*	*0.059*	0.020	*0.040*	0.015	*0.079*	***0.085***	*0.041*	*0.066*	*0.063*	*0.071*
CRA	**0.019**	**0.014**	-	0.031	0.021	*0.058*	*0.042*	*0.047*	***0.092***	*0.038*	0.028	0.020	0.037	***0.121***	0.025	*0.051*	*0.073*	*0.087*
CCC	**0.025**	**0.013**	0.007	-	0.026	*0.057*	*0.068*	*0.081*	***0.126***	***0.085***	*0.040*	*0.054*	*0.066*	***0.116***	*0.038*	***0.093***	***0.123***	***0.026***
MEG	**0.035**	**0.016**	0.006	0.013	-	*0.043*	0.014	*0.045*	*0.060*	*0.044*	0.025	*0.045*	*0.077*	***0.127***	0.037	*0.078*	*0.074*	*0.068*
BWR	**0.023**	**0.021**	**0.023**	**0.018**	**0.016**	-	*0.043*	*0.041*	*0.031*	*0.037*	0.023	*0.048*	*0.065*	*0.055*	*0.084*	***0.092***	*0.033*	***0.116***
ABE	**0.022**	0.005	0.012	**0.019**	0.002	**0.015**	-	0.027	*0.039*	0.000	0.014	-0.003	*0.057*	***0.096***	0.029	0.013	0.015	0.019
ROT	0.007	**0.021**	**0.022**	**0.028**	**0.019**	**0.011**	0.009	-	0.012	-0.012	0.010	0.015	0.014	*0.062*	***0.085***	0.033	*0.012*	*0.052*
ALT	**0.029**	**0.026**	**0.044**	**0.045**	**0.029**	**0.013**	**0.018**	0.006	-	0.018	0.020	0.035	***0.074***	*0.070*	***0.123***	***0.090***	*0.030*	***0.091***
GLT	0.009	0.005	**0.014**	**0.025**	**0.017**	**0.012**	0.002	-0.005	0.008	-	0.007	0.003	0.021	*0.064*	*0.053*	0.010	-0.001	0.034
GLA	0.006	0.010	**0.015**	0.011	**0.017**	0.009	0.008	0.007	0.010	0.003	-	0.011	*0.040*	*0.048*	*0.059*	0.021	0.022	*0.061*
AMA	**0.015**	0.005	0.012	**0.015**	**0.018**	**0.013**	-0.001	0.005	**0.013**	0.004	0.002	-	0.023	*0.069*	0.040	0.016	0.033	0.024
LOC	-0.001	**0.022**	0.010	**0.023**	**0.026**	**0.024**	**0.014**	0.003	**0.032**	0.005	**0.016**	0.007	-	*0.064*	0.029	0.029	0.026	*0.056*
SHI	**0.023**	**0.036**	**0.053**	**0.046**	**0.065**	**0.028**	**0.046**	**0.031**	**0.038**	**0.032**	**0.019**	**0.029**	**0.035**	-	***0.132***	***0.095***	*0.049*	***0.135***
BEE	**0.025**	**0.014**	0.012	**0.021**	**0.020**	**0.040**	0.009	**0.033**	**0.050**	**0.020**	**0.026**	**0.017**	**0.012**	**0.067**	-	*0.042*	*0.077*	*0.061*
GLE	**0.018**	**0.019**	**0.017**	**0.031**	**0.031**	**0.041**	0.004	**0.020**	**0.046**	0.009	**0.013**	0.006	0.009	**0.048**	0.010	-	0.021	*0.047*
STO	0.009	**0.022**	**0.024**	**0.042**	**0.026**	**0.014**	0.001	0.004	**0.017**	0.001	0.011	0.008	0.006	**0.027**	**0.024**	0.007	-	*0.064*
RHI	**0.027**	**0.023**	**0.029**	**0.033**	**0.028**	**0.041**	0.007	**0.020**	**0.036**	**0.015**	**0.025**	0.008	**0.017**	**0.057**	**0.013**	**0.016**	**0.019**	-

Fig. S1 - Percentage of differentiated sites within Scotland using nSSR.

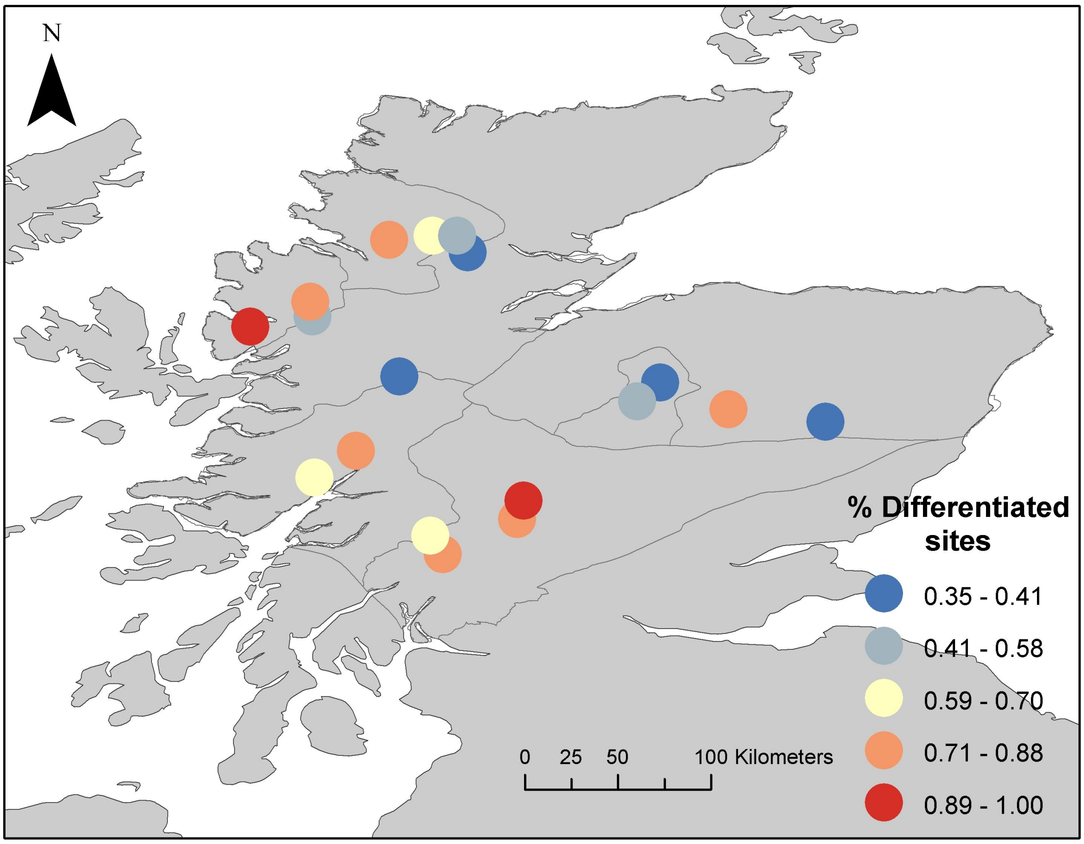
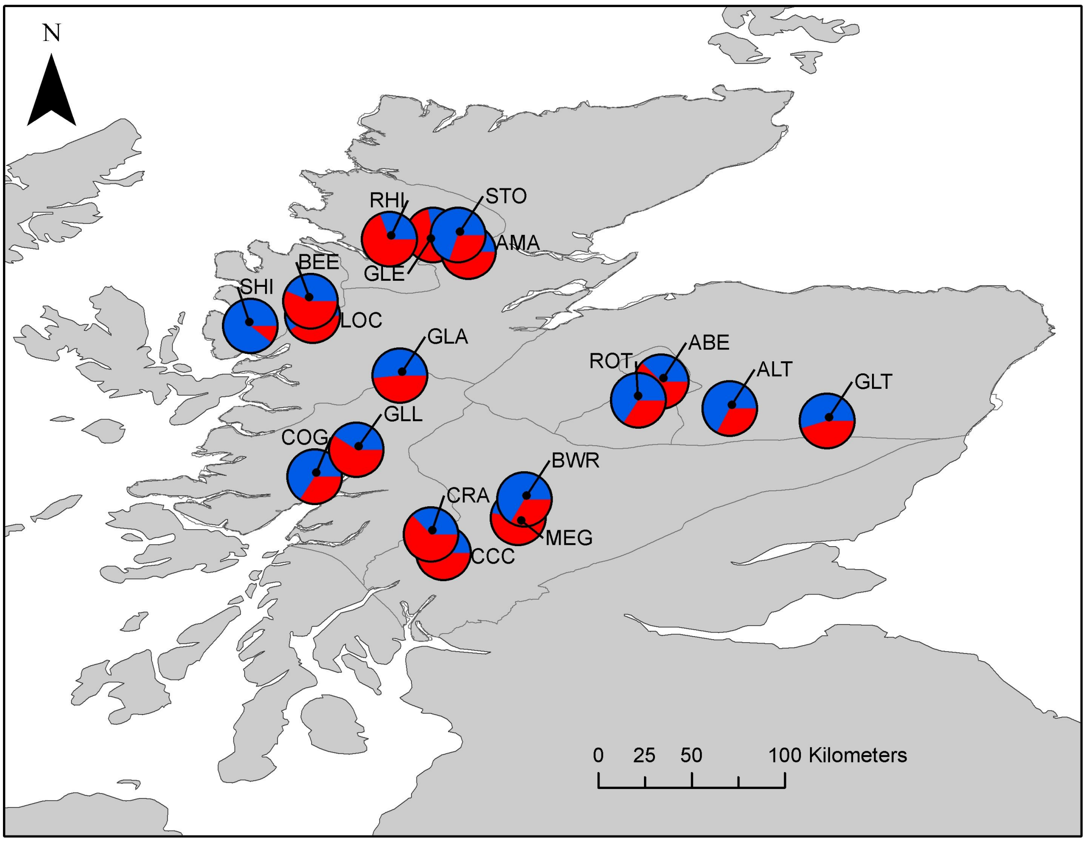


Figure S2 - Number of genetic clusters (K=2) identified by STRUCTURE for nSSR.



Fig, S3 - Relative migration networks for nSSR with populations sorted in seed groups. Seed group codes correspond to the following group of populations (see Tab. 2 for population details): NE= ALT, GLT; SC= CCC, MEG, BWR; EC= ABE, ROT; SW= COG, GLL, CRA; NC= GLA, AMA; NW= LOC, SHI, BEE; N= GLE, STO, RHI. (a) No using a threshold, (b) using a threshold of 0.5.