Table S1: Nest and collection year of 33 osprey chicks collected from 13 nests located along the western coast of Corsica in the period 2006-2010 (translocation phase). The total number of chicks collected per year and per nest, as well as the total for the entire period (in square brackets) are reported. The asterisk indicates the two individuals who subsequently settled and reproduced in Italy (see main text). The individual ID is represented by the two-digit alphanumeric code of the PVC ring.

Nest/Year	2006	2007	2008	2009	2010	Tot per nest
Arangaggia	I1*		S3			2
Cala vecchia				S4		1
Cavallo_1	H1	I2	B3	D4	D5	5
Cavallo_2		A2	C3			2
Ciuttone	C1	D2	I3	A4	B5	5
Elpa nera	B1					1
Ficcaja		C2	D3			2
Ficcajola	D1					1
Gradelle	A1	B2	H3	T4	S5*	5
Orchinu artificiale					F5	1
Orchinu naturale					L5	1
Porto			A3	H4	C5	3
Senino		E2	E3	C4	K5	4
Tot per year	6	6	8	6	7	[33]

Table S2. Multiplex PCR primer sets used in this study.

MULTIPLEX	Locus1	Locus2	Locus3
MULTIPLEX1	PHA04	PHA11	
MULTIPLEX 2	PHA13	PHA29	
MULTIPLEX 3	PHA14	PHA16	PHA35
MULTIPLEX 4	PHA28	PHA27	
MULTIPLEX 5	PHA36	PHA37	
MULTIPLEX 6	Balbu18	Balbu23	Balbu17
SIMPLEX 7	Balbu40		
SIMPLEX 8	Balbu28		

Table S3. Details on the number of alleles (*Na*), allele richness (*Ar*) and private alleles (Pa) in the sampling periods. a) Number of alleles (*Na*), allele richness (*Ar*) in the 16 loci in the two sampling periods. b) Comparison between POP_1 and POP_2; private alleles distributed in the translocated (POP_1) and lacking in the POP_2 in which no private allele was found; c) Comparison between POP_1, POP_2 and the injured osprey (POP_N); alleles found in the injured osprey (POP_N) and not found either in POP_1 or in POP2. The allele 161, which was recorded as a private allele at the PHA4 locus in b) was no more scoring because it was retrieved also in the injured osprey.

a)

LOCUS	POP_1		POP_2	
	Na	Ar	*Na*	AR
BALBU17	3,0	3,0	3,0	3,0
BALBU18	2,0	2,0	2,0	2,0
BALBU23	3,0	3,0	2,0	2,0
BALBU28	2,0	2,0	1,0	1,0
BALBU40	2,0	2,0	2,0	2,0
PHA04	3,0	3,0	2,0	2,0
PHA11	5,0	5,0	5,0	4,7
PHA13	7,0	7,0	6,0	6,0
PHA14	4,0	4,0	4,0	3,9
PHA16	3,0	3,0	3,0	3,0
PHA27	5,0	5,0	5,0	4,7
PHA28	5,0	5,0	5,0	5,0
PHA29	2,0	2,0	2,0	2,0
PHA35	2,0	2,0	1,0	1,0
PHA36	4,0	4,0	3,0	3,0
PHA37	**2,0**	**2,0**	**2,0**	2,0

b)

POP	Locus	Allele	Frequency
POP_1	Balbu23	211	0,031
POP_1	Balbu28	77	0,030
POP_1	PHA04	161	0,030
POP_1	PHA13	184	0,030
POP_1	PHA36	170	0,015

c)

POP	Locus	Allele	Frequency
POP_N	PHA14	157	0,500
POP_N	PHA14	163	0,500
POP_N	PHA16	297	0,500
POP_N	PHA27	164	0,500
POP_N	PHA35	109	0,500
POP_N	PHA37	84	0,500
POP_1	Balbu23	211	0,031
POP_1	Balbu28	77	0,030
POP_1	PHA13	184	0,030
POP_1	PHA35	115	0,015

Table S4. Results from Bottleneck test using both the Infinite Allele Model (IAM) and the Two-Phase Model (TMP). 1 and 2 tail Wilcoxon tests were checked for significance. TMP (a) and (b) refer to different computation parameters: 70% Stepwise Mutation Model (SMM) and 30% TMP in (a) and 0.00% SMM and 35% TMP variance in (b).

| Population	mean_N	mean_k	mean_He	IAM_1t_W	IAM_2t_W	TPM_1t_W (a)	TPM_2t_W (a)	TPM_1t_W (b)	TPM_2t_W (b)
POP_1	65.88	3.38	0.45086	0.028839	0.057678	0.046722	0.093445	0.041626	0.083252
POP_2	97.88	3.00	0.43713	*0.000092*	*0.000183*	*0.000305*	*0.000610*	*0.000153*	*0.000305*

Table S5. Family relationships among translocated, adult and newborn individuals. In grey and bold are reported the misassignment of individuals with respect to the knowledge reported in Figure 2. Numbers preceded by an asterisk or by a pound sign identify unsampled ospreys. Identical genotypes in the hypothetical breeding pair share the same number.

| Offspring	Father	Mother	Offspring	Father	Mother
1-B7-E3270	1-I1-L7-E4647	#1	3-IAM-E1063	*3	3-IAC-E4741
1-IAP-E1055	1-I1-L7-E4647	#1	3-IBE-E1058	*3	3-IAC-E4741
1-IAT-E1056	1-I1-L7-E4647	#1	3-IBH-E2424	*3	3-IAC-E4741
1-IAZ-E1057	1-I1-L7-E4647	#1	3-IBI-E1059	*3	3-IAC-E4741
1-IBA-E1066	1-I1-L7-E4647	#1	3-IBK-E2425	*3	3-IAC-E4741
1-IAA-E1150	1-I1-L7-E4647	#1	3-IDA-E4745	*3	3-IAC-E4741
1-IBM-E2427	*1	**Pha12-translocated**	3-IDB-E4746	*3	3-IAC-E4741
1-IBS-E2428	*1	**Pha12-translocated**	3-IFA-E2431	*3	3-IAC-E4741
2-A7-E4736	2-IAA-E1150	2-S5-E1146	3-IFB-E2432	*3	3-IAC-E4741
2-E4737	2-IAA-E1150	2-S5-E1146	4-IBV-E2429	*4	#4
2-E4738	2-IAA-E1150	2-S5-E1146	4-ICE-E4742	*4	#4
2-IAD-E1051	2-IAA-E1150	2-S5-E1146	4-ICI-E4744	*4	#4
2-IAK-E1060	2-IAA-E1150	2-S5-E1146	4-ICT-E4748	*4	#4
2-IAS-E1065	2-IAA-E1150	2-S5-E1146	4-ICV-E4743	*4	#4
2-IAU-E4747	2-IAA-E1150	2-S5-E1146	4-ICZ-E4749	*4	#4
2-IAV-E1061	2-IAA-E1150	2-S5-E1146	4-IFC-E2434	*4	#4
2-IBZ-E2426	2-IAA-E1150	2-S5-E1146	4-IFD-E2436	*4	#4
2-IAO-E1064	**Pha32-translocated**	**#3**	4-IFF-E2437	*4	#4
3-E4739	*3	3-IAC-E4741	5-IBB-E4750	*5	3-IAE-E1053
3-E4740	*3	3-IAC-E4741	5-IBC-E2421	*5	3-IAE-E1053
3-IAB-E1062	*3	3-IAC-E4741	5-IBD-E2422	*5	3-IAE-E1053
3-IAE-E1053	*3	3-IAC-E4741	5-IFH-E2438	*5	3-IAE-E1053
3-IAH-E1054	*3	3-IAC-E4741	**5-IFJ-E2439**	**Pha31-translocated**	**#5**

Figure S1. Representation of the AMOVA pie graph after comparing POP_1 and POP_2. Almost the whole variance (in grey) is within individuals while a 2% of differentiation (in blue) has been recorded between the two populations.
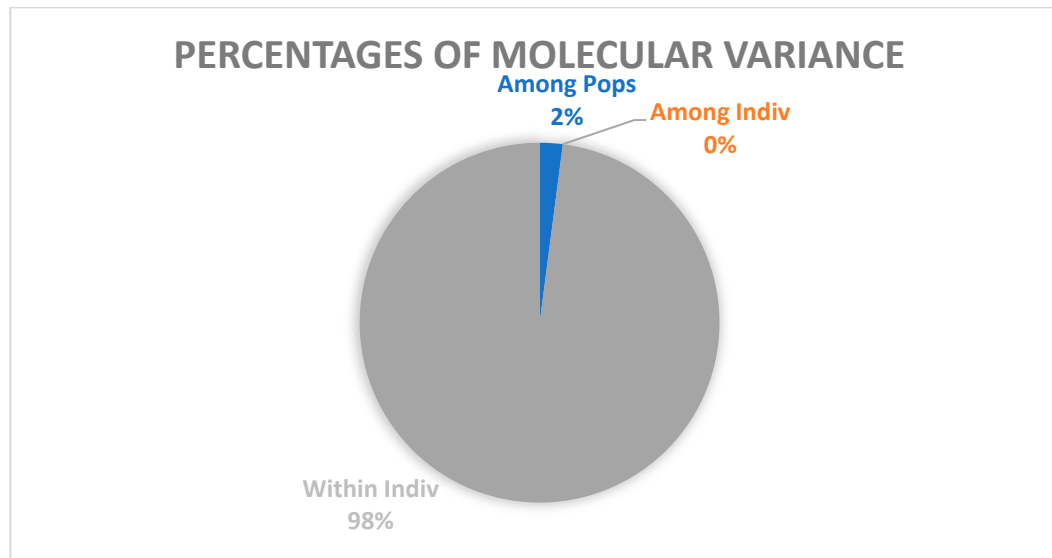
Figure S2. The plot of the Factorial Correspondence Analysis (FCA) that was carried out by comparing POP_1 and POP_2. The two populations partially overlap although the presence of a slight shift on axes 1 and 2.
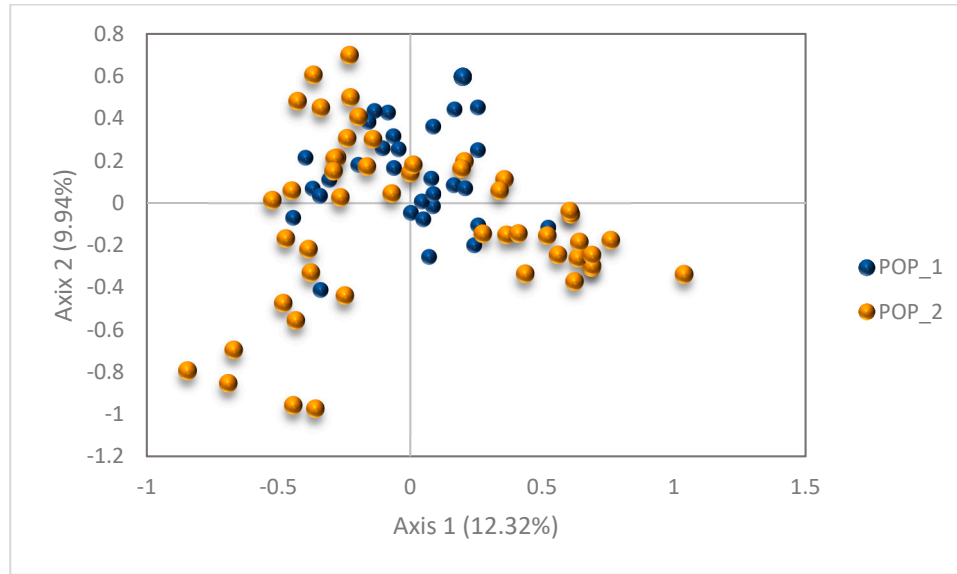
Figure S3. Results from the Bayesian analysis conducted in the POP_1 and POP_2. Following the Delta K procedure and looking at the Mean Likelihood curve, the best clusters were described at K=4 and K=5. No structure was found between POP_1 and POP_2 although the bar plot colors evidence different frequencies of the genetic components in the two groups.
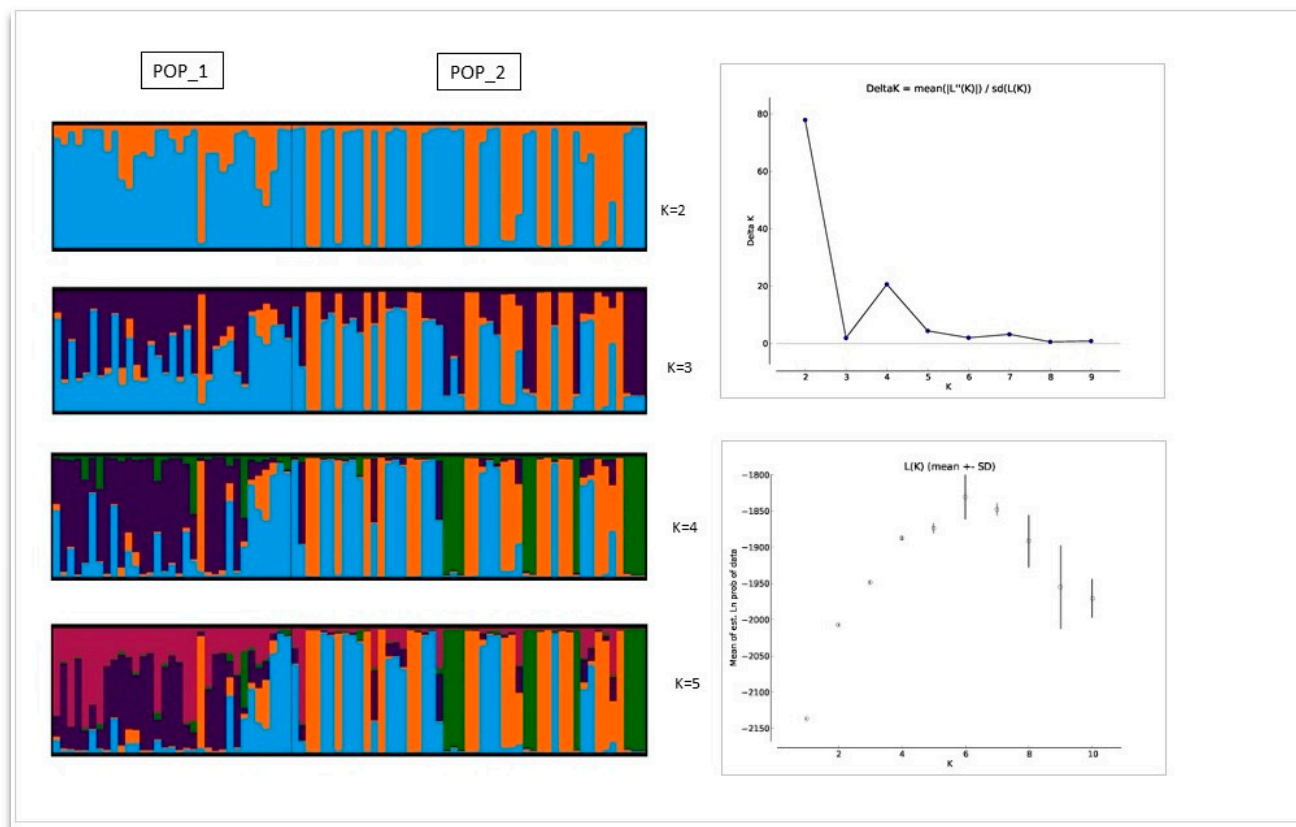
Figure S4. The plot of the Factorial Correspondence Analysis (FCA) of the comparison between the injured osprey individual from North Europe (POP_N) and the samples included in POP_1 and POP_2. All the variance from Axis 1 was recorded between this individual and the other samples.