Figure S1. Map of the study system. A: Fennoscandian peninsula. B: Source population on Vega, and recipient population on Vikna. C: The recipient population on Vikna with subpopulations indicated as filled triangles.

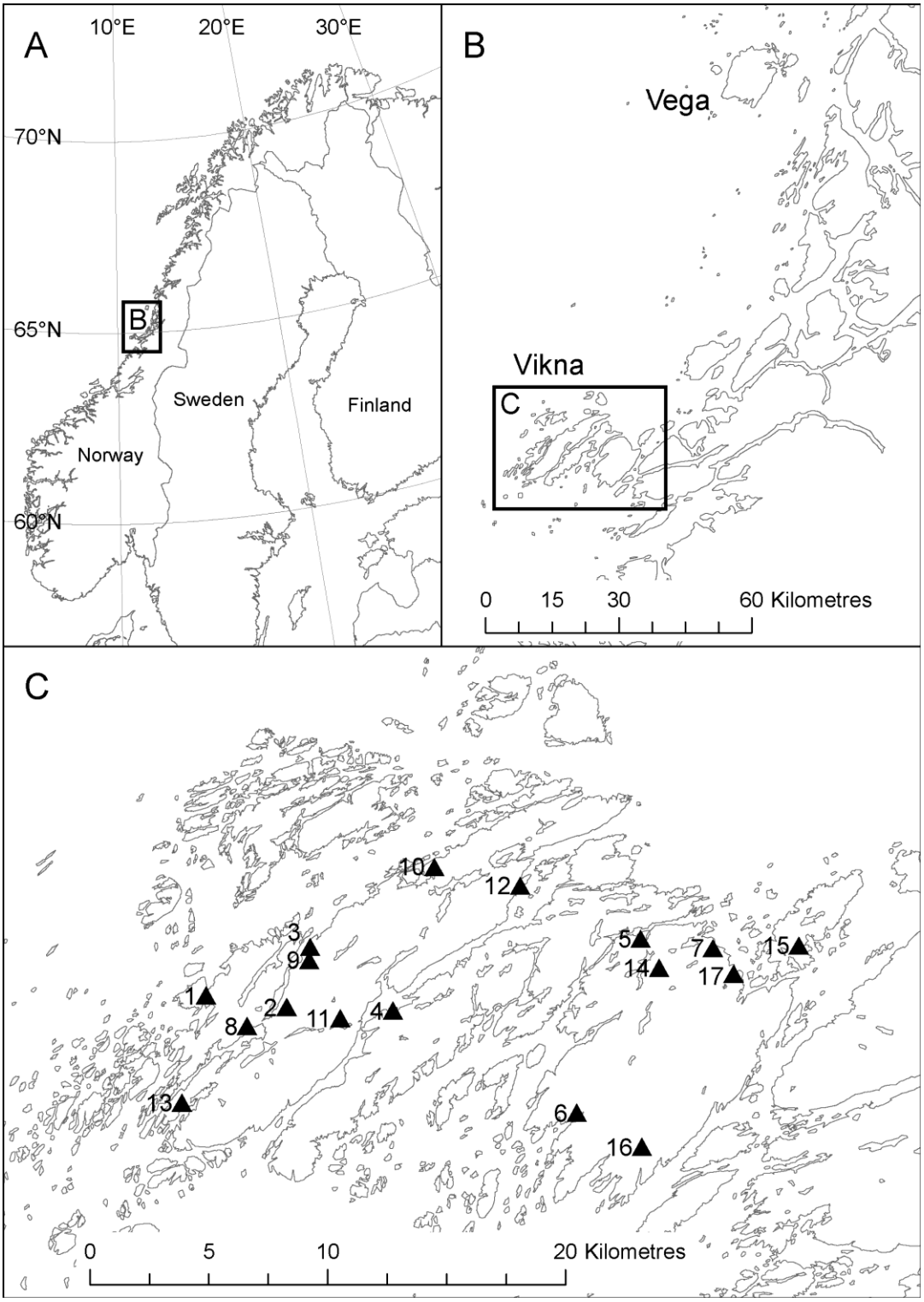

Figure S2. Comparing results using population samples constituting only recruits (similarly as in the main text; A; on the left hand side), and samples constituting the total population (recruits and older adults; B; on the right hand side). Comparisons were performed for mean number of alleles within loci (1), allelic richness (2), mean proportion of private alleles among loci (3), observed and expected heterozygosity (4) and genetic differentiation of the admixed population in terms of pairwise F_{ST} (5) with reference to (1) resident and (2) translocated individuals. All comparisons indicate that these population samples give very similar results. See main text for further details.

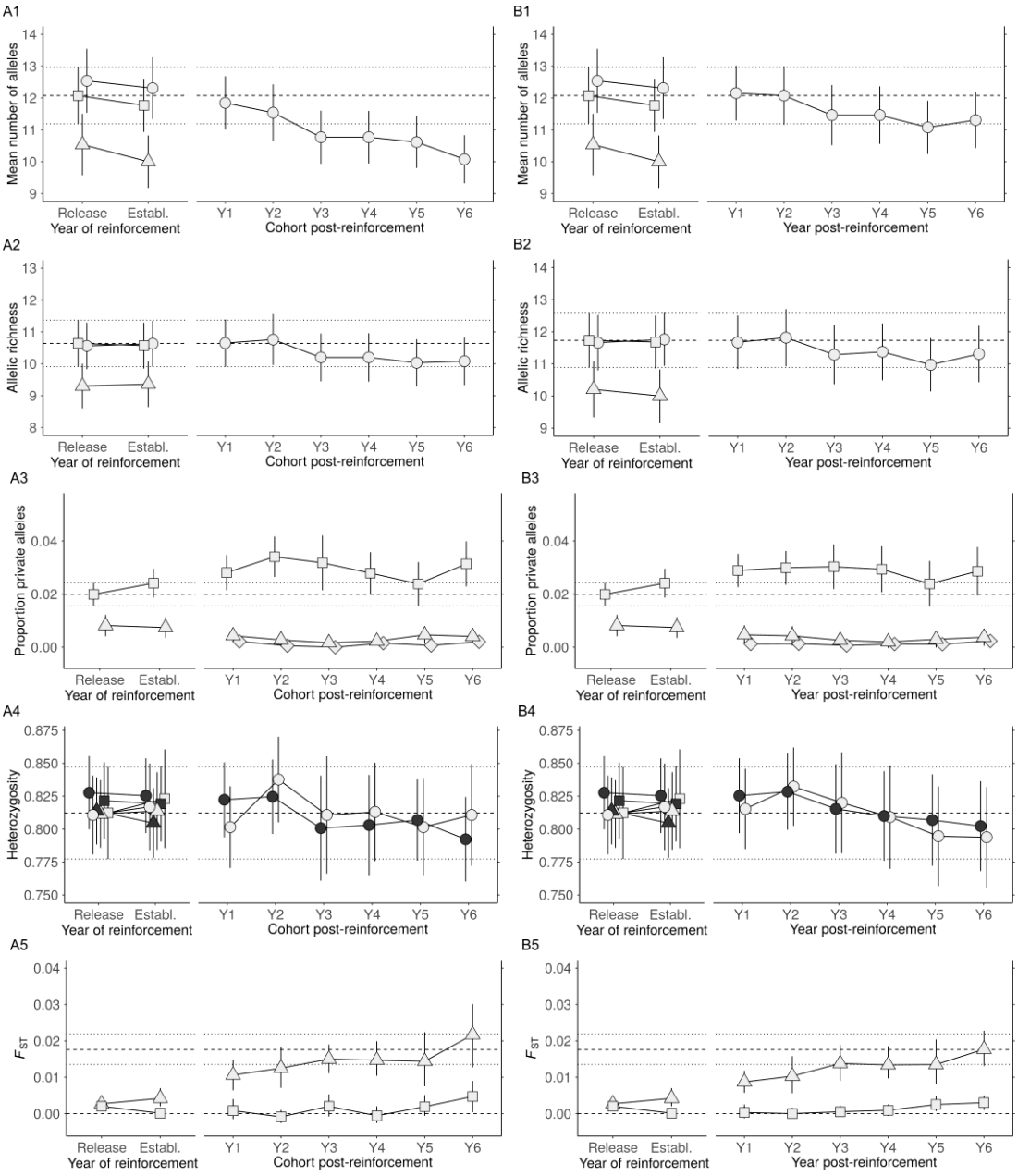

Table S1. Genetic differentiation measured as pairwise F_{ST} between the 7 largest house sparrow subpopulations at Vikna (N≥8 adult individuals) prior to the experiment in 2002. Pairwise F_{ST} were estimated using the R-package HIERFSTAT (Goudet 2005). Numbers refer to subpopulation numbers in Table S2. Estimates significantly different from zero are depicted in bold.

	2	3	4	11	16	13
6	**0.0125**	0.0022	**0.0225**	**0.0167**	**0.0200**	**0.0219**
2		0.0000*	**0.0255**	0.0144	0.0049	**0.0266**
3			**0.0169**	0.0000*	0.0000*	**0.0208**
4				**0.0257**	**0.0360**	**0.0555**
11					0.0084	**0.0134**
16						**0.0211**

*Negative F_{ST} values set to 0.0000.

References

Goudet J (2005) HIERFSTAT, a package for R to compute and test hierarchical *F*-statistics. Mol Ecol Notes 5:184-186

Table S2. An overview of sample sizes prior to reinforcement, translocated and resident individuals, and the experimentally admixed population. Each subpopulation (Id) is presented with information on the number of males (M), females (F) and total population size (N), for pre-reinforcement (pre), translocated (tra), resident (res) and admixed (adm; translocated and resident pooled) individuals, depicted in subscript. Each subpopulation can be found on the map of the study area (Figure S1). The column to the right (I) represents the experimental increase of each subpopulation in the number of individuals.

	Recipient			**Translocated**			**Resident**			**Admixed**	
Id	$\mathbf{M_{pre}}$	$\mathbf{F_{pre}}$	$\mathbf{N_{pre}}$	$\mathbf{M_{tra}}$	$\mathbf{F_{tra}}$	$\mathbf{N_{tra}}$	$\mathbf{M_{res}}$	$\mathbf{F_{res}}$	$\mathbf{N_{res}}$	$\mathbf{N_{adm}}$	**I**
1	4	5	9	3	3	6	3	3	6	12	3
2	8	10	18	5	5	10	5	5	10	20	2
3	7	6	13	4	4	8	4	4	8	16	3
4	12	17	29	8	8	16	8	9	17	33	4
5	3	5	8	3	3	6	3	3	6	12	4
6	8	6	14	5	5	10	5	5	10	20	6
7	2	6	8	3	3	6	2	3	5	11	3
8	5	2	7	3	3	6	2	2	4	10	3
9	1	3	4	2	2	4	1	2	3	7	3
10	2	5	7	2	2	4	2	2	4	8	1
11	12	5	17	5	5	10	6	4	10	20	3
12	3	5	8	3	3	6	3	3	6	12	4
13	14	7	21	6	6	12	8	6	14	26	5
14	3	5	8	2	2	4	2	2	4	8	0
15	0	1	1	2	2	4	0	1	1	5	4
16	6	9	15	4	4	8	4	4	8	16	1
17	1	4	5	3	3	6	1	3	4	10	5
Tot	91	101	192	63	63	126	59	61	120	246	54

Table S3. Overview of genome positions obtained from Basic Local Alignment Search Tool (BLAST)-analysis (NCBI) against the house sparrow reference genome (Elgvin et al. 2017). The BLAST-analysis was applied to identify the location of the different microsatellite loci on the house sparrow genome. From the chromosomal position of BLAST hits, these results show that the microsatellites are either on different chromosomes, or more than 3.7 million base pairs apart on the same chromosome. Because linkage disequilibrium (LD) drops to background levels at <100 000 base pair distance in house sparrows (Lundregan et al. 2018), this means that none of the microsatellite loci are in LD because of linkage.

Microsatellite	**Chromosome**	**Hit start**	**Hit end**
Ase18	3	32472127	32472009
Pdoμ1	1A	31818206	31818395
Pdoμ3	8	24307901	24308036
Pdoμ5	4	48033172	48032773
Pdo10	1	53802831	53802585
Pdo16	2	56782128	56782413
Pdo17	1	50052912	50052699
Pdo19	2	95523770	95523428
Pdo22	4	10469269	10469424
Pdo27	6	18882189	18882635
Pdo40	7	20931780	20931414
Pdo44	1A	14412439	14412133
Pdo47	5	57610302	57610579

References

Elgvin TO, Trier CN, Tørresen OK, Hagen IJ, Lien S, Nederbragt AJ, Ravinet M, Jensen H, Sætre G-P (2017) The genomic mosaicism of hybrid speciation. Sci Adv 3:e1602996

Lundregan SL, Hagen IJ, Gohli J, Niskanen AK, Kemppainen P, Ringsby TH, Kvalnes T, Pärn H, Rønning B, Holand H, Ranke PS, Båtnes AS, Selvik L-K, Lien S, Sæther B-E, Husby A, Jensen H (2018) Inferences of genetic architecture of bill morphology in house sparrow using a high density SNP array point to a polygenic basis. Mol Ecol 27:3498-3514

Table S4. Wilcoxon sign-rank tests for deviation of observed heterozygosity compared to expected heterozygosity (e.g. due to heterozygosity excess). Estimates of heterozygosity are reported from 12 population samples of house sparrow *Passer domesticus*. Individuals were sampled (Sample) at time of release (Release), time of establishment (Establ.) and for each subsequent cohort (Y1-Y6). Translocated (tra), resident (res) or admixed (adm; translocated and resident individuals pooled) are depicted in subscript. The other columns represents the number of individuals sampled (N), observed heterozygosity (H_o), expected heterozygosity (H_e) in Hardy-Weinberg equilibrium, Wilcoxon's sum of signed ranks (*W*), the z-score (*z*) calculated from *W* and the probability of no deviation in heterozygosity from expected (*P*).

Sample	**N**	**H_o ± SE**	**H_e ± SE**	***W***	***z***	***P***	
$Release_{tra}$	125	0.812 ± 0.026	0.814 ± 0.025	29.0	-0.31	0.754	
$Release_{res}$	134	0.811 ± 0.035	0.822 ± 0.029	21.5	-1.00	0.319	
$Release_{adm}$	259	0.811 ± 0.030	0.828 ± 0.028	3.00	-2.81	0.005	**
$Establ._{tra}$	64	0.814 ± 0.029	0.805 ± 0.027	37.0	0.92	0.357	
$Establ._{res}$	97	0.823 ± 0.038	0.819 ± 0.029	52.0	0.99	0.325	
$Establ._{adm}$	161	0.817 ± 0.033	0.825 ± 0.028	29.0	-0.75	0.451	
Y1	89	0.802 ± 0.031	0.822 ± 0.028	13.0	-2.01	0.045	*
Y2	68	0.838 ±0.033	0.825 ± 0.028	33.5	1.25	0.210	
Y3	69	0.811 ± 0.045	0.801 ± 0.040	59.0	0.91	0.363	
Y4	51	0.813 ± 0.037	0.803 ± 0.038	48.5	0.71	0.479	
Y5	59	0.802 ± 0.037	0.807 ± 0.031	42.0	-0.21	0.834	
Y6	38	0.811 ± 0.039	0.792 ± 0.032	60.5	1.02	0.309	

* $P < 0.05$, ** $P < 0.01$

Table S5. The number of different alleles on each of the 13 microsatellite markers present in the translocated individuals from Vega, the resident individuals from Vikna, and pooled in the admixed population (Total), at the time of release.

Microsatellite	**Translocated**	**Resident**	**Total**
Ase18	10	11	11
Pdoμ1	10	11	11
Pdo10	9	12	13
Pdo16	10	12	12
Pdo17	17	17	18
Pdo19	3	4	4
Pdo22	9	12	12
Pdo27	7	9	9
Pdoμ3	14	15	16
Pdo40	14	15	16
Pdo44	12	13	13
Pdo47	12	14	16
Pdoμ5	10	12	12
Total	**137**	**157**	**163**

Table S6. Overview of annual known immigrants from ringing records and annual new unique alleles that appeared in the admixed population. The recorded immigrants indicate some annual immigration from neighbouring populations and some immigrants originating from further away (>20 km). The majority of the novel alleles found was most likely introduced by immigrants from local neighbouring populations where at least four of the respective alleles were present.

Year	**>20 km**	**<5 km**	**Novel alleles**
2003	0	0	3
2004	1	0	0
2005	2	1	0
2006	0	4	1
2007	1	2	1
2008	1	3	1