

Supplementary information

Supplementary Table 1.

Information about the samples included in the study. ID = individual identification number. NA = information missing.

ID	Population	Sample site	Tissue	Sample year	Sex
U1	Roslagen	Lötaholmen	Dried, whole specimen	NA	NA
U2	Roslagen	Lötaholmen	Dried, whole specimen	NA	NA
U3	Roslagen	Lötaholmen	Dried, whole specimen	NA	NA
U4	Roslagen	Lötaholmen	Dried, whole specimen	NA	NA
U5	Roslagen	Lötaholmen	Dried, whole specimen	NA	NA
U6	Roslagen	Brudskäret	Dried, whole specimen	NA	NA
U7	Roslagen	Brudskäret	Dried, whole specimen	NA	NA
U8	Roslagen	Brudskäret	Dried, whole specimen	NA	NA
U9	Roslagen	Brudskäret	Dried, whole specimen	NA	NA
NAU37	NordensArk	NA	Dried, whole specimen	2020	NA
B11	Blekinge	NA	Leg in EtOH	2015	NA
B14	Blekinge	NA	Leg in EtOH	2016	NA
B15	Blekinge	NA	Leg in EtOH	2016	NA
B16	Blekinge	NA	Leg in EtOH	2016	NA
B18	Blekinge	NA	Leg in EtOH	2016	NA
B20	Blekinge	NA	Leg in EtOH	2016	NA
B25	Blekinge	NA	Wing piece in EtOH	2017	NA
B26	Blekinge	NA	Wing piece in EtOH	2017	NA
B27	Blekinge	NA	Wing piece in EtOH	2017	NA
B28	Blekinge	NA	Wing piece in EtOH	2017	NA
NAB2	NordensArk	NA	Full specimen, frozen	2017	NA
NAB4	NordensArk	NA	Full specimen, frozen	2017	NA
NAB5	NordensArk	NA	Full specimen, frozen	2018	NA
NAB6	NordensArk	NA	Full specimen, frozen	2018	NA
NAB7	NordensArk	NA	Full specimen, frozen	2018	NA
NAB10	NordensArk	NA	Full specimen, frozen	2018	NA
NAB12	NordensArk	NA	Full specimen, frozen	2018	NA
NAB17	NordensArk	NA	Full specimen, frozen	2018	NA
NAB21	NordensArk	NA	Full specimen, frozen	2018	NA
NAB23	NordensArk	NA	Full specimen, frozen	2018	NA
VN2	Västernorrland	Tynderö	Wing in EtOH	2016	Male
VN4	Västernorrland	Tynderö	Wing in EtOH	2016	Male
VN10	Västernorrland	Alnö	Wing in EtOH	2016	Male
VN11	Västernorrland	Alnö	Wing in EtOH	2016	Male
VN12	Västernorrland	Alnö	Wing in EtOH	2016	Male
VN13	Västernorrland	Alnö	Wing in EtOH	2016	Male
VN14	Västernorrland	Alnö	Wing in EtOH	2016	Male
VN15	Västernorrland	Hässjö	Wing in EtOH	2016	Male
VN16	Västernorrland	Hässjö	Wing in EtOH	2016	Male
VN18	Västernorrland	Hässjö	Wing in EtOH	2016	Male

Supplementary Table 2.

Information about the yield (Mreads = millions of read-pairs) and percentage of bases with Phred score > 30 (Q30%) for the 40 specimens included in the sequencing effort. NGI ID = identification number from the sequencing facility, User ID = identification number from collectors, Mreads = antal sekvensläsningar (*10⁶), Q30(%) = proportion baser med Phred-score >30 (%).

Population	NGI ID	User ID	Mreads	Q30(%)
Roslagen	P21213_101	U1	106.60	92.63
Roslagen	P21213_102	U2	68.44	92.76
Roslagen	P21213_103	U3	74.11	92.42
Roslagen	P21213_104	U4	74.84	92.57
Roslagen	P21213_105	U5	96.29	92.56
Roslagen	P21213_106	U6	92.34	92.64
Roslagen	P21213_107	U7	85.61	92.52
Roslagen	P21213_108	U8	86.65	92.60
Roslagen	P21213_109	U9	104.05	93.07
Roslagen	P21213_110	NAU37	84.53	93.04
Blekinge	P21213_111	B11	60.43	93.02
Blekinge	P21213_112	B14	47.68	92.95
Blekinge	P21213_113	B15	60.71	92.86
Blekinge	P21213_114	B16	65.52	92.86
Blekinge	P21213_115	B18	58.07	92.85
Blekinge	P21213_116	B20	61.44	92.68
Blekinge	P21213_117	B25	64.41	93.56
Blekinge	P21213_118	B26	63.63	93.24
Blekinge	P21213_119	B27	66.07	93.15
Blekinge	P21213_120	B28	54.62	93.32
Nordens Ark	P21213_121	NAB2	73.88	93.31
Nordens Ark	P21213_122	NAB4	85.28	93.31
Nordens Ark	P21213_123	NAB5	73.87	93.12
Nordens Ark	P21213_124	NAB6	97.58	93.27
Nordens Ark	P21213_125	NAB7	79.13	92.95
Nordens Ark	P21213_126	NAB10	69.33	93.24
Nordens Ark	P21213_127	NAB12	63.39	93.39
Nordens Ark	P21213_128	NAB17	82.24	93.01
Nordens Ark	P21213_129	NAB21	92.62	92.71
Nordens Ark	P21213_130	NAB23	95.23	93.28
Västernorrland	P21213_131	VN2	82.01	93.14
Västernorrland	P21213_132	VN4	86.08	93.27
Västernorrland	P21213_133	VN10	106.32	93.25
Västernorrland	P21213_134	VN11	86.59	93.21
Västernorrland	P21213_135	VN12	75.22	93.40
Västernorrland	P21213_136	VN13	79.85	93.05
Västernorrland	P21213_137	VN14	95.80	93.28
Västernorrland	P21213_138	VN15	96.82	93.12
Västernorrland	P21213_139	VN16	88.76	93.34
Västernorrland	P21213_140	VN18	87.90	93.34

Supplementary Table 3.

Information about sample origin for the previously sequenced and publicly available individuals included in the mtDNA-analysis (Gratton *et al.* 2008).

Origin	NCBI Accessionsnummer
Italy	EU836664
Greece	EU836670
Czech Rep.	EU836680
Austria	EU836664, EU836673
Åland, Fin.	EU092977
Finland	EU836676, EU093006
Lithuania	EU836676, EU836677, EU836678, EU836679
Macedonia	EU836666, EU836667, EU836668
Russia	EU836681, EU836682

Supplementary Table 4.

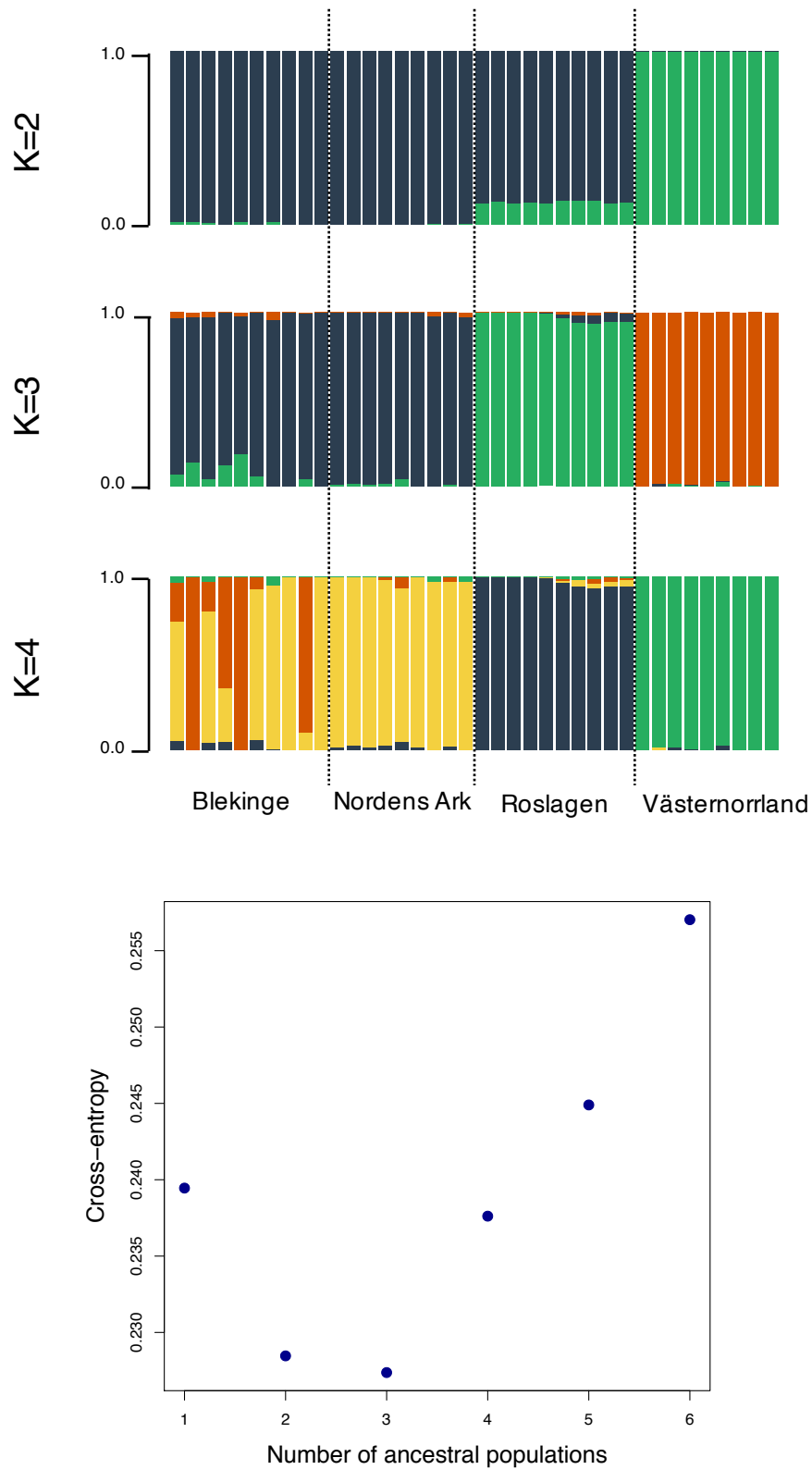
Summary of estimated levels (median +/- standard deviation) of genetic diversity (θ_π , θ_W , *10⁻³) and Tajima's D (Taj. D) in the two subpopulations in Roslagen (Lötaholmen och Brudskäret). All estimates are based on autosomal 4D-sites estimated in 100 kb windows. CP = codon position. 4D = 4D-sites.

Population	Position	θ_π	θ_W	T_D
Brudskäret	4D	5.3 ± 13.7	5.5 ± 10.6	0.12 ± 1.05
Lötaholmen	4D	4.6 ± 13.5	4.8 ± 10.4	0.06 ± 1.10
Brudskäret	CP3	4.7 ± 12.2	4.9 ± 9.4	0.10 ± 1.06
Lötaholmen	CP3	4.2 ± 12.1	4.4 ± 9.3	0.02 ± 1.11
Brudskäret	CP2	3.4 ± 9.9	3.6 ± 7.7	0.06 ± 1.04
Lötaholmen	CP2	3.0 ± 9.9	3.2 ± 7.6	0.03 ± 1.08
Brudskäret	CP1	3.5 ± 10.2	3.6 ± 7.9	0.07 ± 1.04
Lötaholmen	CP1	3.0 ± 10.2	3.2 ± 7.8	0.02 ± 1.08

Supplementary Table 5.

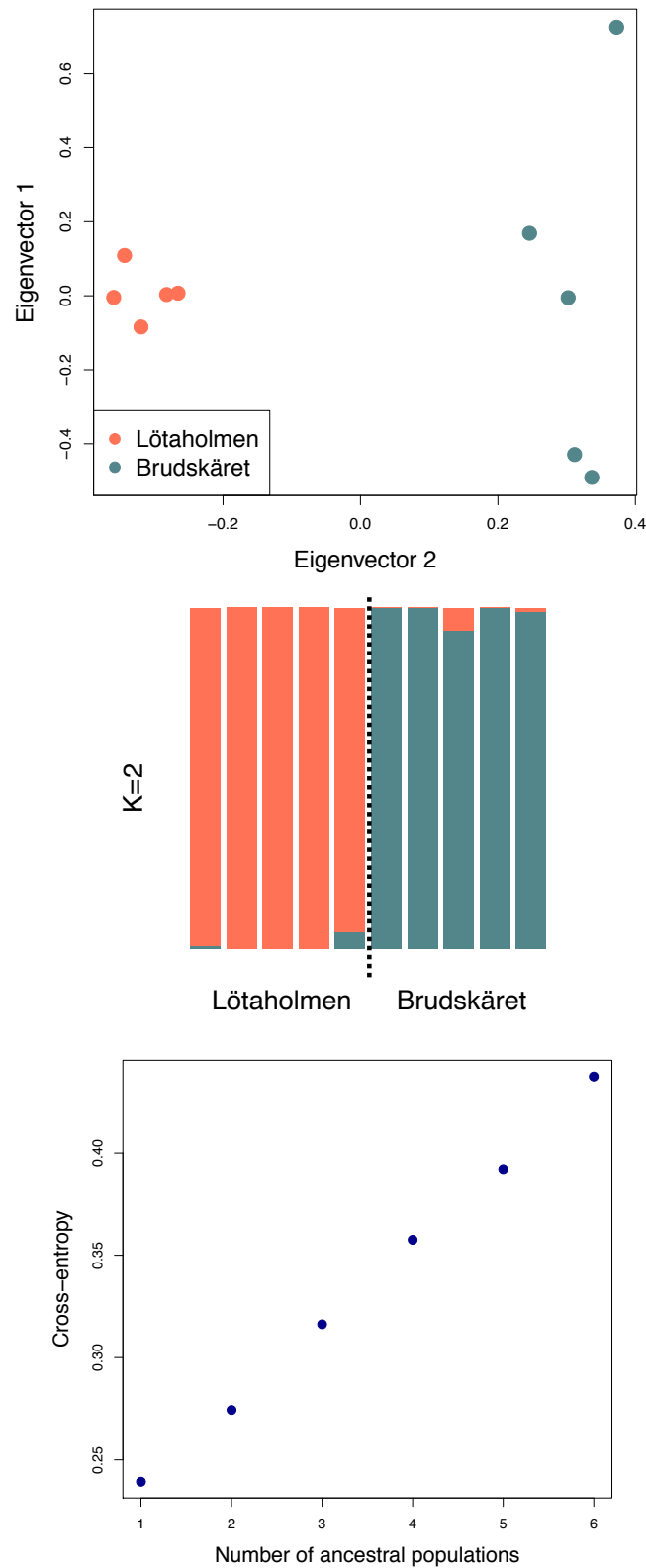
Summary of the counts of fixed, shared and private alleles for autosomal 4D-sites in the comparison of the two subpopulations in Roslagen (Lötaholmen och Brudskäret).

Population A	Population B	Fixed	Shared	Private A	Private B	Total
Brudskäret	Lötaholmen	76	43,841	19,871	15,295	79,083



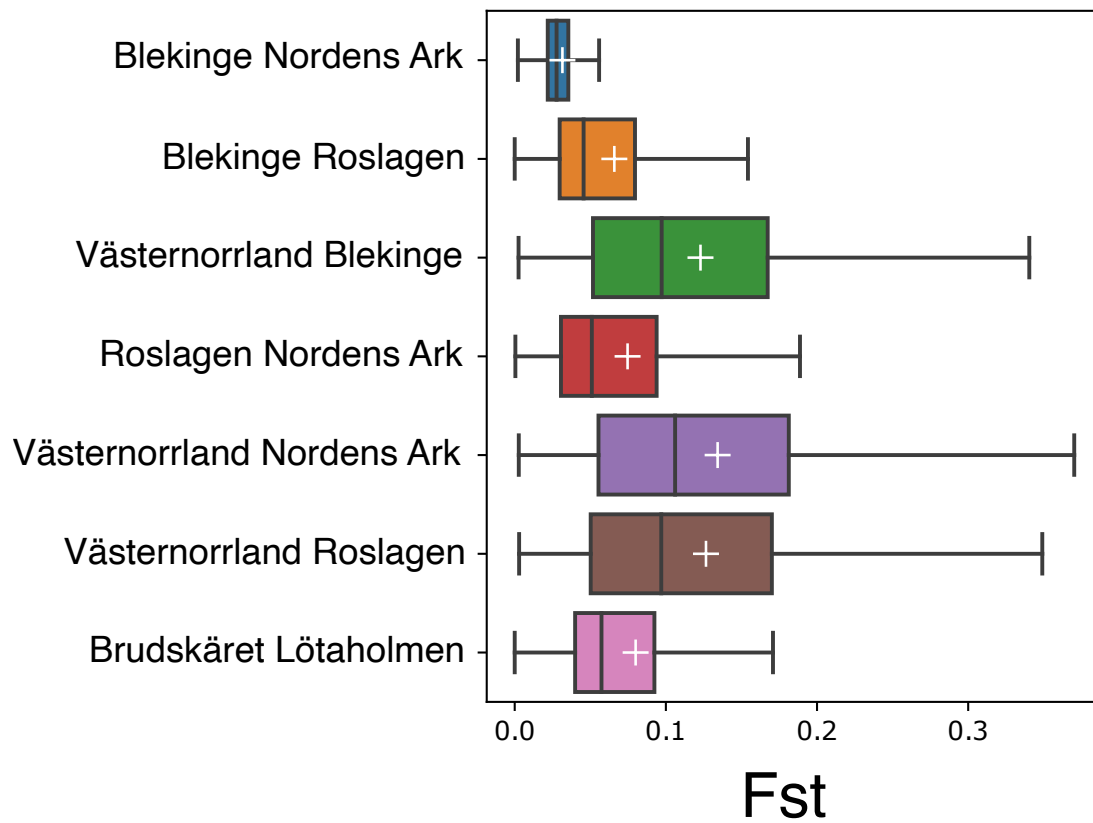
Supplementary Figure 1.

Top three panels illustrate the results from the Admixture analysis of SNPs at 4D-sites for the clouded apollo in Sweden for $K = 2 - 4$, respectively. At the bottom the cross-entropy scores for different K values are given.



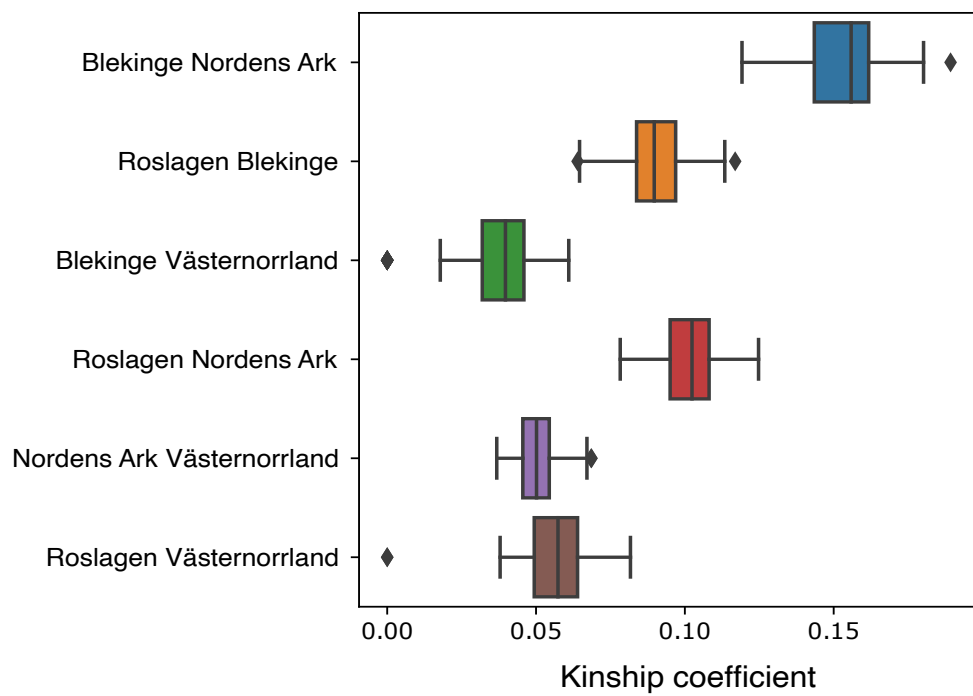
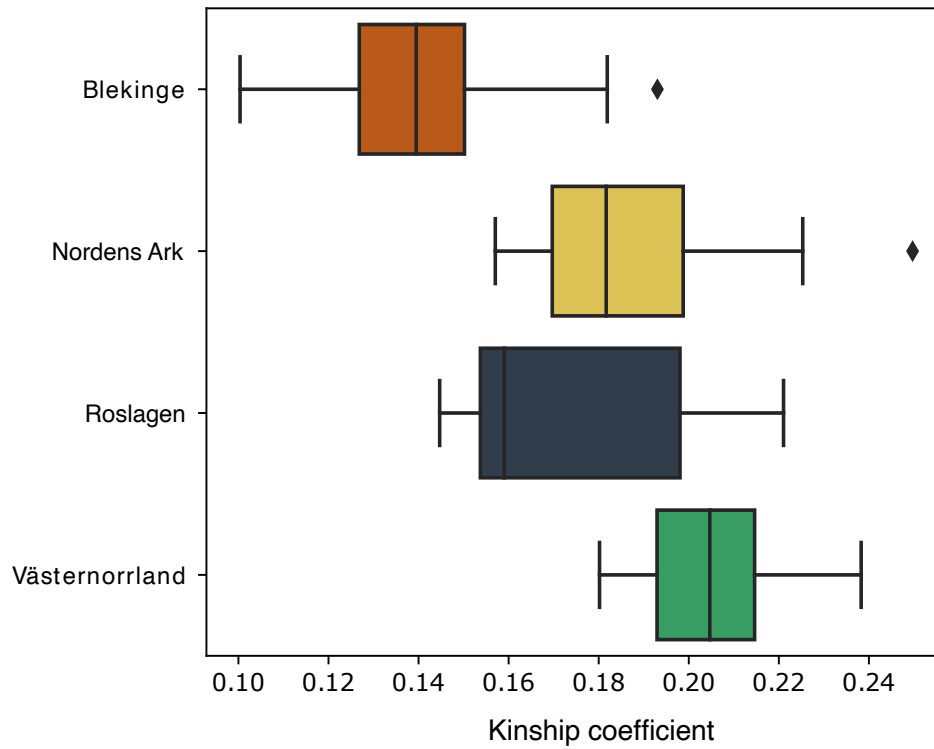
Supplementary Figure 2.

Results from a principal component analysis (PCA, top) and Admixture-analysis (middle) of the genetic variation at autosomal 4D-sites in clouded apollo individuals from two sampling sites in Roslagen. The X-axis (PCA1) explained 14% and the Y-axis (PCA2) 12% of the total variation. The two sub-populations came out as distinct clusters in the Admixture analysis but the cross-entropy scores showed that the data were best explained by a single population.

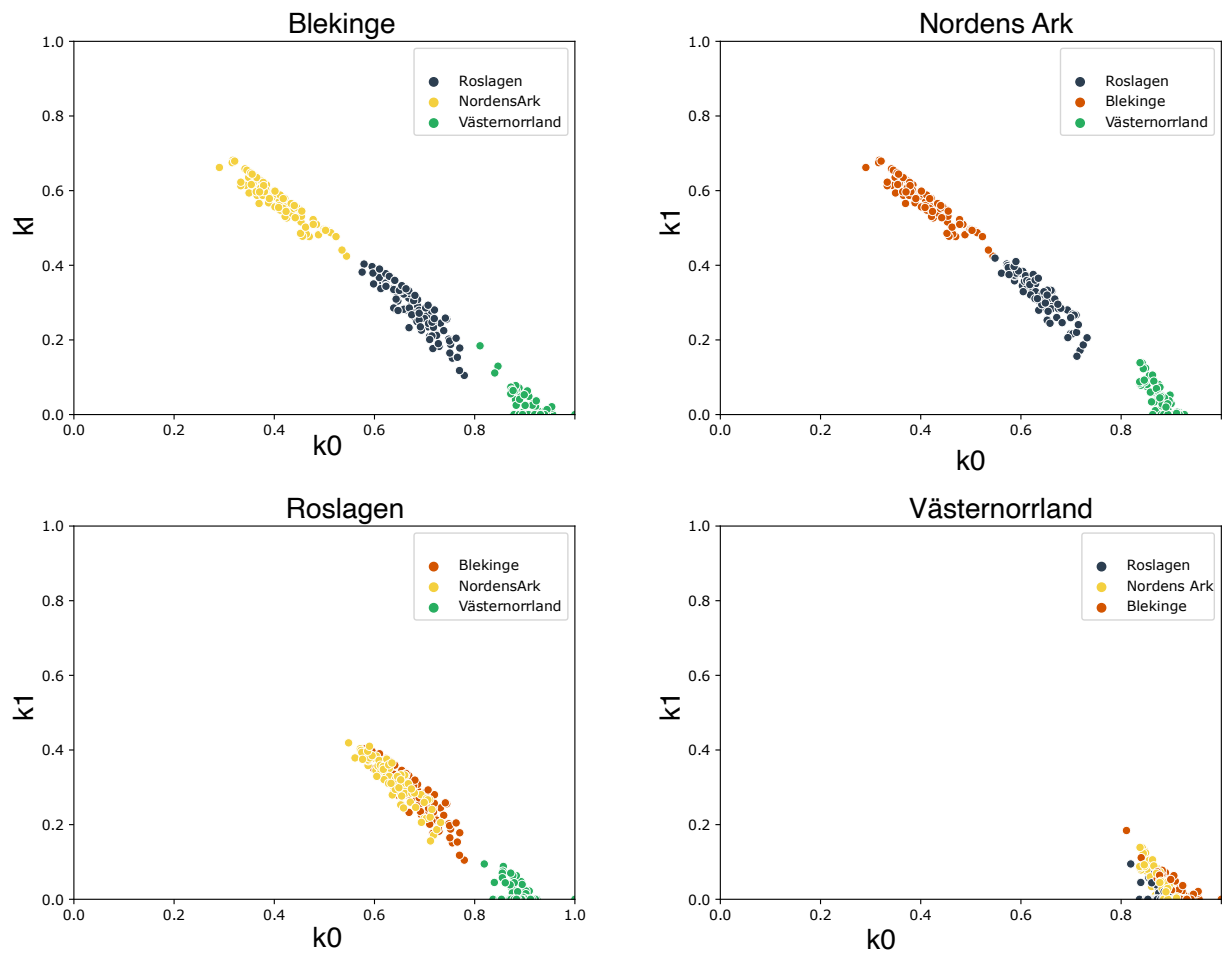


Supplementary Figure 3.

Box-plots illustrating the distribution of estimates of genetic differentiation (F_{ST}) in the comparison between the two sampling sites in Roslagen (bottom) in comparison to the estimates from all population comparisons (same data as in Table 3). F_{ST} was estimated based on genetic variation at autosomal 4D-sites as summarized in 100 kb non-overlapping windows. Boxes indicate the 25 - 75 percentiles, vertical bars within boxes show the median estimate and white + show the mean estimates. Whiskers delimit the total span of estimates over all 100 kb windows.



Supplementary Figure 4. Estimates of within (top) and between population (bottom) kinship coefficients (x-axis). The analysis was based on autosomal 4D-sites. Note that the scale of the X-axis differs between the panels.



Supplementary Figure 5. Estimates of probability of identity-by-descent (IBD) of two alleles in an individual, as compared to the probability of an allele in an individual having IBD with an allele from another individual. The analysis was based on autosomal 4D-sites and repeated for individuals in each subpopulation separately to give a clearer picture of the relationship between individuals in different populations. The analysis. The X-axis shows the probability that no allele in a pair is in IBD (k_0) and the Y-axis the probability that at least one allele in a pair is in IBD (k_1).