

Supplementary material:

Table 1: Characteristics of each sampling site (see Materials and Methods for details).

	Area (m ²)	Core Area (m ²)	Perimeter (Km)	Core Perimeter (Km)	%free perimeter	Permeability
KC1	161273.4	40280.71	2.05592	0.975391	39.44	2
KO1	23501.11	23501.11	0.88298	0.88298	63.76	2
KO2	235930.1	5624.91	2.12795	1.20835	66.92	2
KO3	22417.21	22417.21	0.876203	0.876203	60.85	1
KO4	33380.76	23827.15	1.39582	1.39416	55.87	1
KO5	60807.46	50605.04	1.11371	1.53509	80.07	3
KO6	3207.97	1812.15	0.248807	0.375192	100	3
FC1	69161.91	9164.87	1.11475	2.8017	66.45	2
FC2	117280.4	117280.4	1.25788	1.25788	100	3
FC3	297524.7	147141.3	2.2122	2.6113	38.07	2
FO1	82746.63	57196.52	1.57155	1.243	49.29	1
FO2	198243.2	0	1.81781	0	79.15	3
FO3	242127.2	0	2.1033	0	100	3

Table 3: Genetic differentiation across all populations. Pairwise F_{st} values are given for microsatellites below the diagonal and for cytochrome-b above the diagonal (pairs significant with $P < 0.05$ after sequential Bonferroni correction are shown in bold).

	KC1	KO1	KO2	KO3	KO4	KO5	KO6	FC1	FC2	FC3	FO1	FO2	FO3	TO1
KC1		0.038	0.015	-0.015	-0.016	-0.015	0.055	-0.016	0.009	0.042	0.502	0.564	0.136	0.073
KO1	0.025		0.01	0	0.054	0	0	0.054	0.04	0.087	0.574	0.664	0.227	-0.019
KO2	0.021	0.013		-0.038	-0.011	-0.038	0.023	-0.011	0.016	0.062	0.561	0.638	0.192	0.026
KO3	0.039	0.031	0.03		-0.031	0	0	-0.031	-0.014	0.032	0.481	0.539	0.132	-0.058
KO4	0.031	0.025	0.02	0.03		-0.031	0.089	-0.04	-0.015	0.021	0.452	0.506	0.102	0.077
KO5	0.034	0.036	0.03	0.049	0.049		0	-0.031	-0.014	0.032	0.481	0.539	0.132	-0.058
KO6	0.024	0.022	0.017	0.036	0.029	0.03		0.089	0.058	0.106	0.619	0.715	0.271	-0.012
FC1	0.047	0.068	0.059	0.074	0.068	0.072	0.058		-0.027	-0.027	0.417	0.473	0.055	0.077
FC2	0.018	0.023	0.023	0.038	0.035	0.027	0.019	0.056		0.026	0.482	0.548	0.116	0.076
FC3	0.016	0.021	0.018	0.037	0.031	0.029	0.021	0.049	0.012		0.403	0.461	0.027	0.139
FO1	0.016	0.022	0.021	0.038	0.031	0.04	0.024	0.053	0.018	0.015		-0.024	0.199	0.711
FO2	0.014	0.024	0.021	0.035	0.029	0.039	0.025	0.045	0.019	0.013	0.013		0.229	0.798
FO3	0.018	0.017	0.009	0.031	0.021	0.029	0.017	0.052	0.019	0.015	0.02	0.017		0.362
TO1	0.02	0.025	0.019	0.041	0.034	0.038	0.023	0.052	0.018	0.016	0.02	0.021	0.017	

Table 4: Results of the self-assignment test performed in GENECLASS (Piry et al., 2004). The number of individuals from each population that were assigned to the different populations (columns: origin, rows: assigned to) are shown. None = the number of individuals that were not assigned to any population. Correctly assigned (%) = the percentages of correctly assigned samples.

Kalø	KC1	KO1	KO2	KO3	KO4	KO5	KO6
KC1	29	11	14	4	7	2	5
KO1	3	7	1	1	1	0	0
KO2	0	1	18	2	3	0	0
KO3	0	0	0	0	0	0	0
KO4	0	1	1	0	0	0	0
KO5	3	2	2	2	0	3	2
KO6	4	3	4	0	2	4	29
none	1	0	0	0	0	0	0
Correctly assigned (%)	72.5	28	45	0	0	33.3	80.6
Fussingø	FC1	FC2	FC3	FO1	FO2	FO3	
FC1	10	0	0	0	0	0	
FC2	4	35	15	10	6	12	
FC3	0	4	39	8	9	7	
FO1	0	0	0	13	0	2	
FO2	0	0	0	0	0	1	
FO3	0	0	0	3	4	5	
none	0	0	0	0	0	0	
Correctly assigned (%)	71.4	89.7	72.2	38.2	0	18.5	

Table 5: Estimated gene flow values for the last generation among Kalø (above) and Fussingø (below) sampling sites and number of first generation migrants (*italics*). Values for gene flow were estimated running BIMr (Faubet and Gaggiotti, 2008). Values for first generation migrants were estimated using GENECLASS (Piry et al., 2004).

Into/From	KC1	KO1	KO2	KO3	KO4	KO5	KO6	average
KC1		1.75E-10	3.08E-10	1.77E-10	1.82E-10	2.19E-10	2.05E-10	2.11E-10
		<i>3</i>	<i>4</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>1.17</i>
KO1	3.61E-10		4.15E-10	4.48E-10	3.66E-10	3.20E-10	3.33E-10	3.74E-10
	<i>2</i>		<i>2</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>0</i>	<i>0.67</i>
KO2	4.62E-09	7.40E-10		1.21E-09	1.35E-09	1.41E-09	1.24E-09	1.76E-09
	<i>4</i>	<i>1</i>		<i>0</i>	<i>1</i>	<i>1</i>	<i>0</i>	<i>1.17</i>
KO3	2.79E-10	4.56E-10	2.82E-10		3.66E-10	2.81E-10	3.57E-10	3.37E-10
	<i>1</i>	<i>1</i>	<i>2</i>		<i>0</i>	<i>0</i>	<i>0</i>	<i>0.67</i>
KO4	6.52E-10	1.07E-09	6.45E-10	9.79E-10		7.66E-10	7.76E-10	8.15E-10
	<i>1</i>	<i>2</i>	<i>2</i>	<i>1</i>		<i>0</i>	<i>0</i>	<i>1</i>
KO5	2.81E-10	3.26E-10	2.55E-10	3.65E-10	3.82E-10		2.84E-10	3.16E-10
	<i>1</i>	<i>0</i>	<i>2</i>	<i>1</i>	<i>0</i>		<i>0</i>	<i>0.67</i>
KO6	4.14E-10	4.61E-10	4.25E-10	4.92E-10	4.36E-10	3.41E-10		4.28E-10
	<i>2</i>	<i>2</i>	<i>1</i>	<i>0</i>	<i>1</i>	<i>1</i>		<i>1.17</i>
average	1.10E-09	5.38E-10	3.88E-10	6.12E-10	5.14E-10	5.56E-10	5.33E-10	
	<i>1.83</i>	<i>1.50</i>	<i>2.17</i>	<i>0.33</i>	<i>0.33</i>	<i>0.33</i>	<i>0</i>	
Into/From	FC2	FC3	FO1	FO2	FO3	average		
FC2		1.53E-09	2.90E-09	9.68E-10	1.84E-09	1.81E-09		
		<i>8</i>	<i>1</i>	<i>2</i>	<i>0</i>	<i>2.75</i>		
FC3	5.39E-09		4.16E-09	1.52E-09	3.41E-09	3.62E-09		
	<i>3</i>		<i>0</i>	<i>3</i>	<i>2</i>	<i>2</i>		
FO1	1.50E-08	4.90E-09		6.29E-09	8.19E-09	8.60E-09		
	<i>4</i>	<i>4</i>		<i>3</i>	<i>3</i>	<i>3.5</i>		
FO2	1.09E-08	2.40E-09	3.88E-09		3.31E-09	5.12E-09		
	<i>0</i>	<i>1</i>	<i>0</i>		<i>4</i>	<i>1.25</i>		
FO3	2.59E-09	1.32E-09	2.29E-09	2.15E-09		2.09E-09		
	<i>0</i>	<i>4</i>	<i>4</i>	<i>2</i>		<i>2.5</i>		
average	8.47E-09	2.54E-09	3.31E-09	2.73E-09	4.19E-09			
	<i>1.75</i>	<i>4.25</i>	<i>1.25</i>	<i>2.5</i>	<i>2.25</i>			

Figure 1: mtDNA diversity indices for all sampling sites as calculated with ARLEQUIN v3.1 (Excoffier et al., 2005).

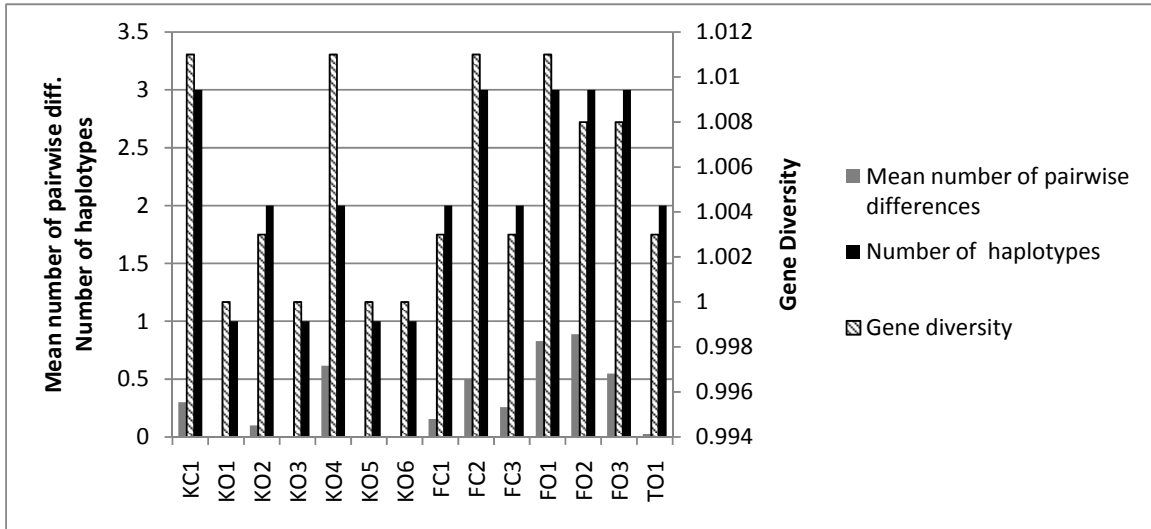
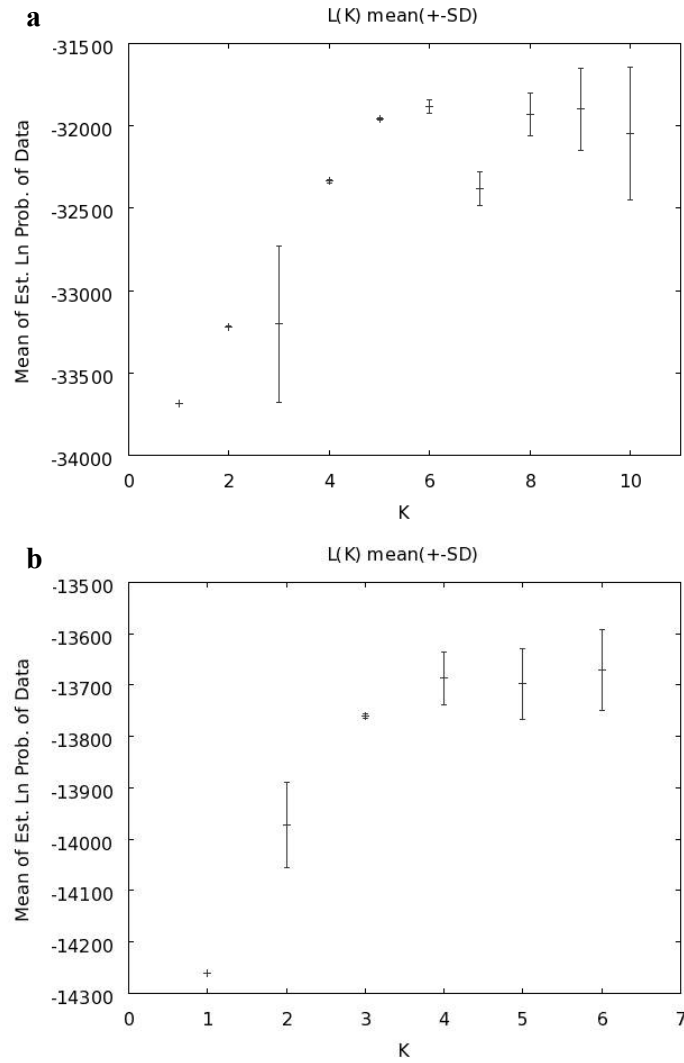


Figure 2: log likelihood graphs for the clustering analysis performed in structure 2.3.3 (Pritchard et al., 2000) for all populations (a) and for Kalø (b) and Fusingø (c) areas separately. See Materials and Methods section for details.



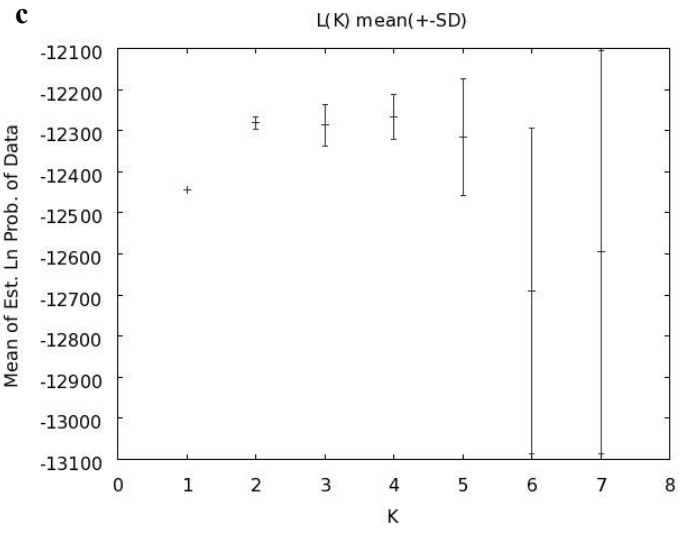
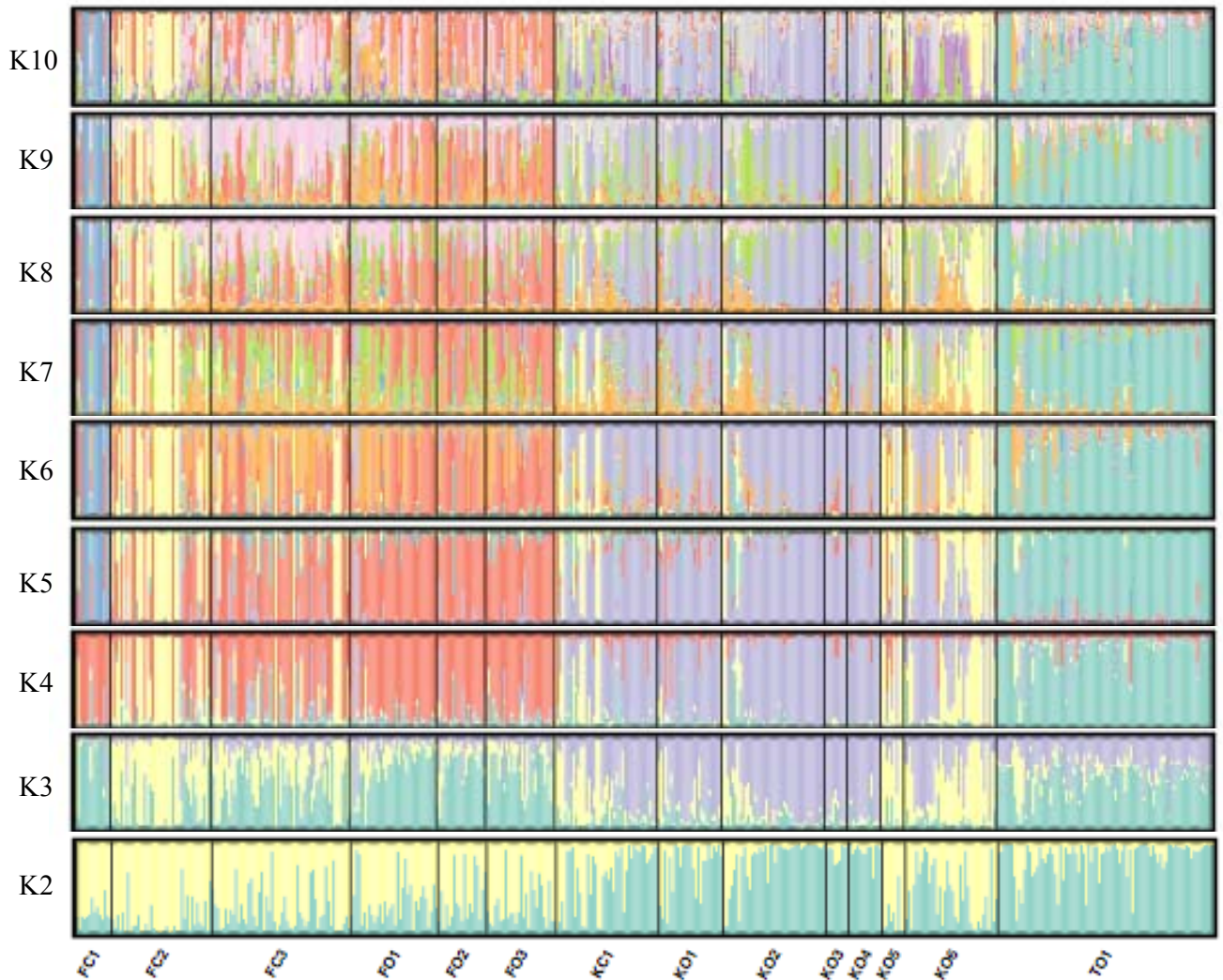


Figure 3: barplots for the clustering analysis performed in structure 2.3.3 (Pritchard et al., 2000) for all populations and for Kalø and Fussingø areas separately. The figures show the individuals' assignment probabilities for different K values (K = number of clusters). See Materials and Methods section for details.

All



Fussingø

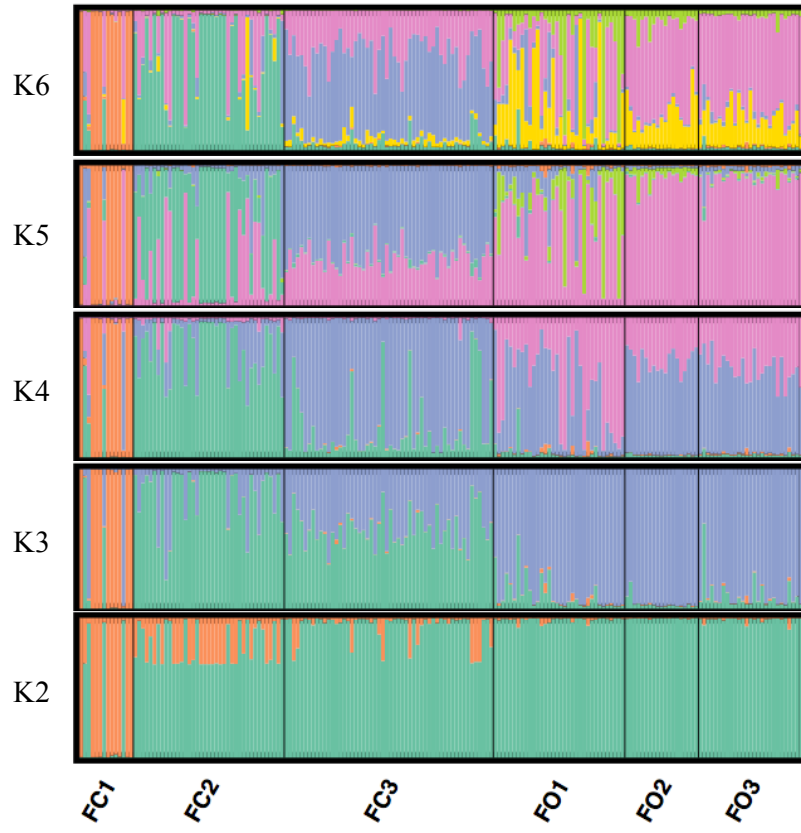


Figure 4: Position of individuals (grouped by transect location) and their cluster as recovered from GENELAND (Guillot et al., 2005) for the two areas (see Materials and Methods for details). Four clusters were found in Kalø area and five in Fusingø area. Different symbols represent different clusters.

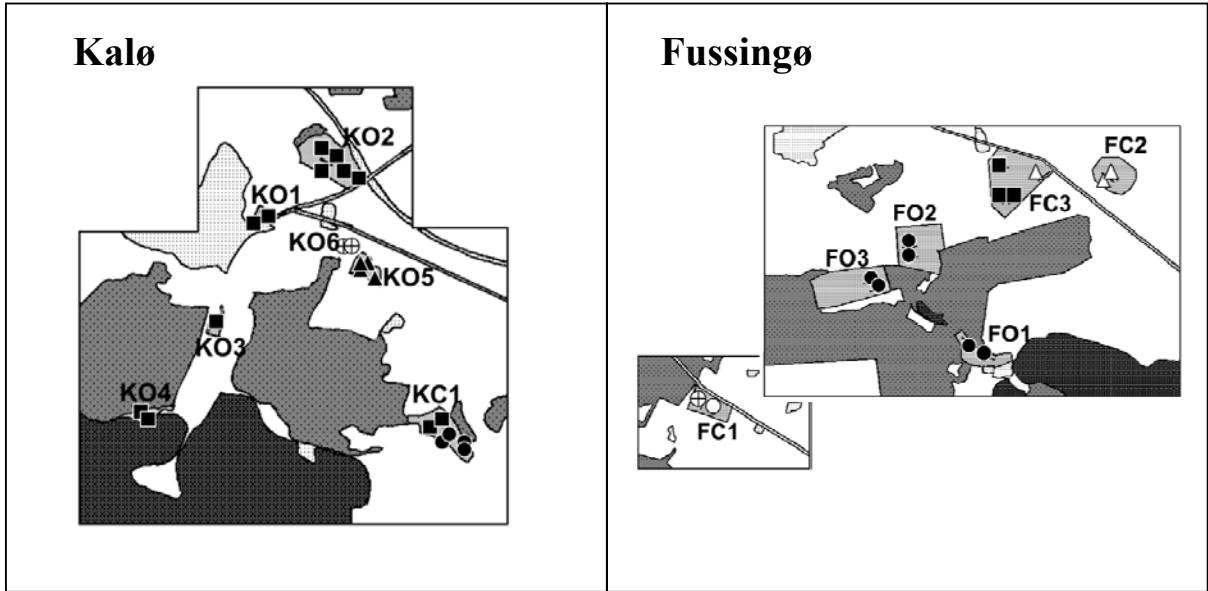


Figure 5: heatmap of the gene flow rates estimated by BIMr for Kalø and Fussingø.

