

Stock structure of Atlantic herring *Clupea harengus* in the Norwegian Sea and adjacent waters

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Table S1. Characteristics of multiplexes for 24 microsatellite loci of Atlantic herring *Clupea harengus*. Tm stands for annealing temperature and μ l for micro-litres of primer used. Genotyping quality reports the percentage of individuals which were correctly genotyped at a specific microsatellite locus. The forward primers were labelled with dye colors: 6-FAM (blue dye), NED (yellow dye), PET (red dye) and VIC (green dye).

Multiplex	Loci	μ l	Tm	Dye	Allele range	Genotyping quality
SildPrint2	Cha113	0.10	58	PET	104-156	97
	Cha17	0.18	58	6-FAM	85-189	99
	Cha1059	0.03	58	NED	63-127	98
	Cha1020	0.14	58	VIC	153-245	90
	Cpa111	0.16	58	VIC	256-295	91
SildPrint4	Cpa113	0.06	57	PET	118-230	93
	Cha1017	0.15	57	VIC	161-213	98
	Cpa103	0.13	57	6-FAM	163-263	93
	Cpa112	0.14	57	VIC	232-416	92
	Cpa108	0.10	57	NED	233-275	96
SildPrint6	msild12	0.03	58	VIC	73-139	97
	Cha1027	0.10	58	PET	113-213	100
	Cha63	0.10	58	NED	137-181	100
	Cpa101	0.06	58	VIC	169-321	98
SildPrint7	Cpa104	0.08	60	NED	180-506	97
	Cpa114	0.08	60	VIC	178-282	98
	Cha1202	0.10	60	6-FAM	97-173	100
SildPrint9	Cha4	0.07	58	VIC	106-194	99
	Cpa102	0.06	58	NED	128-420	99
	msild13	0.16	58	6-FAM	176-251	99
SildPrint13	msild17	0.10	58	VIC	336-420	95
	msild24	0.15	58	PET	165-351	96
	msild27	0.06	58	6-FAM	185-233	99
	msild32	0.10	58	VIC	172-272	99

Table S2. Genetic diversity of the 24 microsatellite loci. Expected heterozygosity (H_e) and deviation from the Hardy-Weinberg equilibrium (HWE) (F_{IS}) for 24 microsatellite loci in 14 samples of Atlantic herring *Clupea harengus*. See Table 1 in the main text for sample codes.

Sample	1		2		3		4		5		6		7		8		9		10		11		12		13		14	
	H_e	F_{IS}	H_e	F_{IS}	H_e	F_{IS}	H_e	F_{IS}	H_e	F_{IS}	H_e	F_{IS}	H_e	F_{IS}	H_e	F_{IS}	H_e	F_{IS}	H_e	F_{IS}	H_e	F_{IS}	H_e	F_{IS}	H_e	F_{IS}	H_e	F_{IS}
Cha4	0.874	0.091	0.884	-0.031	0.862	0.098	0.856	0.037	0.889	0.076	0.875	-0.025	0.853	0.020	0.858	0.020	0.865	0.058	0.868	0.074	0.884	0.034	0.852	0.012	0.854	0.060	0.882	0.020
Cha17	0.941	0.025	0.937	0.002	0.929	0.025	0.944	0.010	0.941	0.023	0.944	0.026	0.943	0.019	0.949	0.036*	0.945	0.024	0.941	0.015	0.942	0.006	0.928	0.007	0.941	-0.055	0.940	0.025
Cha63	0.862	0.010	0.878	0.136	0.862	0.019	0.868	0.005	0.860	-0.054	0.858	0.005	0.851	0.044	0.855	-0.060	0.847	-0.024	0.841	0.014	0.846	0.021	0.816	-0.083	0.859	-0.022	0.863	0.053
Cha113	0.891	-0.003	0.875	0.016	0.893	0.026	0.884	-0.017	0.883	0.039	0.872	-0.005	0.877	0.091	0.866	-0.036	0.863	-0.003	0.889	0.010	0.881	0.036	0.861	0.023	0.905	0.010	0.881	-0.014
Cha1017	0.793	0.018	0.788	0.054	0.839	0.066	0.834	0.095	0.843	0.051	0.798	0.134	0.825	0.008	0.797	0.098	0.833	0.124	0.815	0.047	0.802	0.050	0.778	-0.015	0.762	0.084	0.812	0.035
Cha1020	0.926	0.008	0.931	-0.003	0.920	-0.004	0.918	-0.042	0.923	0.028	0.923	-0.017	0.914	0.026	0.915	0.013	0.921	0.004	0.920	0.036	0.917	-0.036	0.881	-0.055	0.871	-0.073	0.901	-0.044
Cha1027	0.934	-0.012	0.923	0.096	0.907	-0.022	0.936	0.052	0.923	0.032	0.930	0.058	0.939	-0.023	0.938	0.139	0.929	-0.022	0.930	0.061	0.922	0.028	0.917	0.023	0.908	0.033	0.914	0.008
Cha1059	0.670	0.035	0.695	0.257	0.708	0.132	0.674	0.065	0.666	0.020	0.663	0.061	0.660	0.130*	0.679	0.059	0.663	-0.043	0.729	0.091	0.693	0.123	0.668	0.035	0.787	0.080	0.680	0.143
Cha1202	0.701	0.057	0.744	0.082	0.676	-0.007	0.709	-0.048	0.763	-0.056	0.722	0.023	0.750	0.060	0.761	0.097	0.761	0.009	0.750	-0.085	0.753	0.002	0.704	-0.008	0.760	0.027	0.752	0.065
Cpa101	0.919	0.000	0.916	0.006	0.909	0.033	0.915	0.047	0.910	0.119	0.915	0.028	0.913	-0.039	0.914	-0.036	0.912	0.044	0.926	-0.006	0.918	-0.011	0.900	0.054	0.912	0.040	0.916	0.032
Cpa102	0.923	-0.024	0.927	-0.038	0.912	0.034	0.929	-0.031	0.922	0.050	0.924	0.028	0.927	0.062	0.928	-0.001	0.923	0.048	0.930	0.002	0.939	-0.007	0.913	-0.003	0.913	-0.053	0.919	0.060
Cpa103	0.874	0.045	0.880	0.162	0.878	0.085	0.891	0.086	0.878	0.034	0.885	0.130	0.884	0.025	0.883	0.096	0.870	0.047	0.874	0.144	0.874	-0.018	0.884	0.077	0.865	0.039	0.839	0.045
Cpa104	0.836	0.022	0.840	0.120	0.823	0.049	0.870	0.041	0.834	0.073	0.878	0.040	0.823	0.155	0.810	0.0182	0.847	0.101	0.832	0.024	0.739	0.071	0.830	0.067	0.719	-0.023	0.699	0.057
Cpa108	0.481	0.070	0.535	0.103	0.492	0.121	0.540	0.135	0.447	0.024	0.461	-0.043	0.424	-0.093	0.543	0.072	0.448	0.059	0.457	0.025	0.627	-0.018	0.396	-0.083	0.533	0.020	0.576	0.082
Cpa111	0.434	-0.003	0.389	-0.028	0.331	0.003	0.372	-0.001	0.397	0.021	0.402	0.033	0.502	0.009	0.464	0.014	0.402	0.140	0.349	0.041	0.447	-0.085	0.468	-0.010	0.600	0.019	0.541	-0.065
Cpa112	0.904	-0.027	0.882	0.066	0.879	-0.078	0.889	0.003	0.886	0.033	0.887	-0.020	0.860	0.038	0.904	-0.092	0.878	0.085	0.885	-0.017	0.901	-0.019	0.791	-0.065	0.872	-0.050	0.880	-0.017
Cpa113	0.937	0.030	0.921	-0.044	0.919	-0.025	0.935	-0.025	0.925	0.035	0.929	0.016	0.928	0.010	0.919	0.035	0.926	0.030	0.929	0.011	0.935	0.010	0.886	0.022	0.930	0.035	0.924	-0.020
Cpa114	0.917	0.043	0.903	-0.038	0.902	0.087	0.905	0.049	0.905	0.111	0.908	0.013	0.913	0.089	0.918	0.038	0.910	-0.013	0.905	0.016	0.912	-0.010	0.908	0.044	0.903	0.048	0.909	0.008
msild12	0.883	0.042	0.849	-0.075	0.892	0.036	0.873	-0.040	0.874	0.004	0.877	0.016	0.876	-0.007	0.893	-0.032	0.883	0.011	0.881	0.005	0.881	0.086	0.860	0.044	0.873	0.015	0.879	0.025
msild13	0.898	0.012	0.898	0.011	0.899	0.014	0.884	-0.004	0.898	-0.026	0.901	-0.057	0.894	0.005	0.881	0.051	0.907	0.021	0.895	0.028	0.865	0.003	0.845	-0.006	0.838	-0.003	0.851	0.012
msild17	0.895	0.055	0.898	0.042	0.881	-0.045	0.887	0.024	0.884	0.030	0.888	0.056	0.878	0.002	0.878	0.023	0.894	0.057	0.896	0.058	0.857	-0.034	0.811	0.005	0.847	0.123	0.821	-0.029
msild24	0.957	0.023	0.943	-0.021	0.943	0.039	0.956	0.053	0.951	0.062	0.951	0.034	0.953	0.041	0.955	-0.006	0.951	-0.016	0.961	0.004	0.949	-0.014	0.925	-0.018	0.945	-0.048	0.952	0.030
msild27	0.816	0.013	0.790	0.007	0.811	0.040	0.786	0.033	0.791	-0.015	0.823	0.054	0.801	-0.013	0.787	-0.039	0.753	0.020	0.806	0.032	0.816	0.067	0.782	-0.015	0.808	0.010	0.811	0.004
msild32	0.910	-0.028	0.899	0.178	0.904	-0.025	0.905	0.047	0.891	0.022	0.907	-0.026	0.902	-0.053	0.904	0.056	0.903	0.041	0.908	0.061	0.893	-0.020	0.897	0.040	0.890	-0.037	0.913	-0.028
Overall all loci	0.844	0.020	0.850	0.042	0.841	0.028	0.845	0.022	0.843	0.032	0.843	0.024	0.841	0.025*	0.847	0.031	0.842	0.032	0.842	0.028	0.845	0.012	0.813	0.007	0.838	0.010	0.836	0.019

Values in bold indicate significant deviations from HWE (Exact tests, $p < 0.05$).

*Values remaining significant after Bonferroni correction ($\alpha = 0.05/168 = 0.0003$).

Table S3. Results from Lositan outlier tests for the 24 microsatellite loci in 14 samples of Atlantic herring *Clupea harengus*. Expected heterozygosity (H_e) and F_{ST} are given. The loci in bold were identified as 95% outliers, while one marked with an asterisk was identified as a significant outlier at a false discovery rate of 0.01.

Locus	Heterozygosity	F_{ST}	P (Simul $F_{ST} <$ Sample F_{ST})
Cha4	0.881	0.008	0.824
Cha17	0.948	0.002	0.113
Cha63	0.863	0.003	0.344
Cha113	0.889	0.003	0.358
Cha1017	0.816	0.003	0.389
Cha1020	0.927	0.008	0.882
Cha1027	0.935	0.004	0.480
Cha1059	0.695	0.004	0.471
Cha1202	0.742	0.001	0.293
Cpa101	0.922	0.002	0.236
Cpa102	0.935	0.006	0.706
Cpa103	0.885	0.004	0.483
Cpa104	0.824	0.007	0.691
Cpa108	0.504	0.005	0.547
Cpa111*	0.457	0.040	0.998
Cpa112	0.894	0.011	0.940
Cpa113	0.936	0.006	0.694
Cpa114	0.916	0.002	0.209
msild12	0.884	0.002	0.269
msild13	0.899	0.012	0.986
msild17	0.889	0.012	0.972
msild24	0.960	0.003	0.234
msild27	0.805	0.001	0.239
msild32	0.910	0.003	0.298

Table S4. Outlier tests performed in BAYESCAN for the 24 microsatellite loci in 14 samples of Atlantic herring *Clupea harengus*. The posterior probability for the model including selection (p), the log10 of the Posterior Odds for the model including selection (log10(PO)), and the estimated alpha coefficient indicating the strength and direction of selection (alpha; positive values indicate positive selection, while negative values indicate putative balancing selection) are given for each locus. It should be noted that the power to detect loci under putative balancing selection is low. The locus in bold was identified as a significant outlier under a false discovery rate of 0.05.

Locus	p	log10(PO)	alpha	F_{ST}
Cha4	1	1000	-1.40	0.006
Cha17	1	1000	-2.36	0.002
Cha63	1	1000	-2.19	0.003
Cha113	1	1000	-1.77	0.004
Cha1017	1	1000	-2.46	0.002
Cha1020	1	1000	-1.14	0.006
Cha1027	1	1000	-1.81	0.004
Cha1059	1	1000	-2.30	0.003
Cha1202	1	1000	-2.04	0.003
Cpa101	1	1000	-2.71	0.002
Cpa102	1	1000	-1.60	0.005
Cpa103	1	1000	-1.48	0.006
Cpa104	1	1000	-2.03	0.003
Cpa108	1	1000	-1.65	0.005
Cpa111	0.046	-1.23	-0.007	0.024
Cpa112	1	1000	-1.17	0.008
Cpa113	1	1000	-1.78	0.004
Cpa114	1	1000	-2.38	0.002
msild12	1	1000	-2.60	0.002
msild13	1	1000	-1.11	0.009
msild17	1	1000	-0.96	0.010
msild24	1	1000	-2.23	0.003
msild27	1	1000	-2.31	0.003
msild32	1	1000	-2.35	0.003

Table S5. Power of the 24 microsatellite loci in 10 samples of Atlantic herring *Clupea harengus*. The Norwegian local spring-spawning herring were excluded from the analysis. Estimations of the resolution power of the microsatellite loci were performed using POWSIM (Ryman & Palm 2006). N_e : effective population size.

Expected F_{ST}	Average F_{ST}	χ^2 -test	Fisher's test	N_e	Generation (t)	Runs
0.0000	0.0000	0.077	0.075	1,000	0	1,000
0.0000	0.0000	0.089	0.076	5,000	0	1,000
0.0010	0.0010	1.000	1.000	500	1	1,000
0.0010	0.0010	1.000	1.000	1,000	2	1,000
0.0010	0.0010	1.000	1.000	5,000	10	1,000
0.0025	0.0025	1.000	1.000	1,000	5	1,000
0.0050	0.0050	1.000	1.000	1,000	10	1,000

The resolution power was assessed by simulating different expected levels of F_{ST} according to the effective population size (N_e) and generations (t) and to the Nei (1987) formula: $F_{ST} = 1 - (1 - 1/2N_e)^t$. The significance, evaluated using Fisher's exact tests as well as χ^2 tests, reflects the power to detect any given level of differentiation (average F_{ST}) with the sampling design developed during our study. N_e values used during the test are based on estimates calculated from fisheries data. "Runs" denotes the number of simulations performed. The setting $F_{ST} = 0$ and $t = 0$ estimates α (type I error; in the absence of genetic drift).

Table S6. Genetic differentiation among samples. Pairwise F_{ST} (above diagonal) and p-values (below diagonal) among 14 samples of Atlantic herring *Clupea harengus* based on allelic frequencies at 24 microsatellite loci. See Table 1 in the main text for sample codes.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	0	-0.0010	-0.0008	-0.0003	0.0006	-0.0007	-0.0003	0.0003	0.0008	0.0007	0.0074*	0.0127*	0.0106*	0.0110*
2	0.998	0	-0.0006	-0.0004	-0.0002	0.0001	-0.0005	-0.0001	0.0012	-0.0004	0.0082*	0.0154*	0.0117*	0.0115*
3	0.907	0.850	0	-0.0002	-0.0009	-0.0008	-0.0014	0.0001	0.0007	-0.0013	0.0064*	0.0124*	0.092*	0.0010*
4	0.494	0.803	0.490	0	0.0005	-0.0001	-0.0001	0.0003	0.0011	0.0024	0.0087*	0.0150*	0.0122*	0.0116*
5	0.127	0.808	0.598	0.117	0	-0.0005	-0.0001	0.0011	0.0012	0.0015	0.0088*	0.0160*	0.0130*	0.0115*
6	0.928	0.929	0.916	0.639	0.038	0	0.0009	-0.0003	0.0001	0.0002	0.0082*	0.0115*	0.0122*	0.0122*
7	0.972	0.951	0.986	0.590	0.310	0.957	0	-0.0007	-0.0001	0.0003	0.0073*	0.0113*	0.0093*	0.0101*
8	0.138	0.811	0.720	0.024	0.038	0.912	0.972	0	-0.0001	0.0008	0.0067*	0.0120*	0.0090*	0.0092*
9	0.097	0.766	0.549	0.122	0.018	0.332	0.497	0.014	0	-0.0001	0.0074*	0.0127*	0.0121*	0.0122*
10	0.112	0.783	0.989	0.001	0.006	0.359	0.155	0.416	0.083	0	0.0075*	0.0119*	0.0115*	0.0107*
11	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0	0.0182*	0.0079*	0.0069*
12	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0	0.0160*	0.0169*
13	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0	0.0022
14	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0

Values in bold differ significantly from zero (Fisher's exact test, $p < 0.05$).

* Values remaining significant after Bonferroni correction ($\alpha = 0.05/91 = 0.0005$).

Table S7. Genetic differentiation among samples. Pairwise F_{ST} (above diagonal) and p-values (below diagonal) among 14 samples of Atlantic herring *Clupea harengus* based on allelic frequencies at Cpa111. See Table 1 in the main text for sample codes.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	0	-0.0066	0.0013	-0.0020	-0.0021	-0.0038	-0.0004	0.0011	-0.0048	0.0023	0.0300	0.0054	0.1196	0.0965
2	0.791	0	-0.0087	-0.0070	-0.0067	-0.0077	0.0018	0.0018	-0.0102	-0.0067	0.0282	0.0060	0.1234	0.1000
3	0.636	0.891	0	-0.0048	-0.0024	0.0004	0.0137	0.0155	-0.0052	-0.0050	0.0266	0.0162	0.1367	0.1053
4	0.616	0.313	0.445	0	-0.0049	-0.0022	0.0091	0.0109	-0.0042	-0.0002	0.0308	0.0135	0.1389	0.1078
5	0.744	0.871	0.586	0.652	0	-0.0020	0.0091	0.0137	-0.0024	0.0035	0.0288	0.0177	0.1325	0.1041
6	0.691	0.587	0.162	0.111	0.405	0	0.0044	0.0021	-0.0050	-0.0006	0.0427	0.0086	0.1435	0.1176
7	0.756	0.566	0.408	0.136	0.164	0.083	0	-0.0035	0.0010	0.0134	0.0263	-0.0003	0.0836	0.0715
8	0.424	0.483	0.217	0.124	0.110	0.261	0.517	0	-0.0014	0.0084	0.0468	-0.0038	0.1112	0.1002
9	0.750	0.893	0.923	0.492	0.646	0.342	0.465	0.698	0	-0.0048	0.0301	0.0031	0.1233	0.0998
10	0.097	0.480	0.770	0.066	0.051	0.118	0.018	0.270	0.884	0	0.0440	0.0122	0.1620	0.1277
11	0.000*	0.000*	0.007	0.000*	0.000*	0.000*	0.000*	0.000*	0.000*	0.000*	0	0.0371	0.0580	0.0334
12	0.001	0.015	0.052	0.004	0.000*	0.000*	0.002	0.027	0.019	0.001	0.000*	0	0.1042	0.0890
13	0.000*	0.000*	0.000*	0.000*	0.000*	0.000*	0.000*	0.000*	0.000*	0.000*	0.001	0.000*	0	-0.0004
14	0.000*	0.000*	0.000*	0.000*	0.000*	0.000*	0.000*	0.000*	0.000*	0.000*	0.000*	0.000*	0.320	0

Values in bold differ significantly from zero (Fisher's exact test. $p < 0.05$).

* Values remaining significant after Bonferroni correction ($\alpha = 0.05/91 = 0.0005$).

Table S8. Results from the hierarchical Bayesian cluster analysis (STRUCTURE) based on all 24 microsatellite loci and all samples. STRUCTURE was run using 350,000 burn-in and 500,000 iterations for 10 independent runs for $K = 1$ to 10 for the North Atlantic samples and from $K = 1$ to 4 for the local Norwegian fjords (samples 11, 12, 13 and 14). An admixture model with correlated allele frequencies without prior information on sample location was implemented. Bold values indicate the most likely number of clusters.

	K	Mean LnP(K)	StDev LnP(K)
North Atlantic	1	-87102	0.2898
	2	-87261	12.7600
	3	-87740	91.5819
	4	-88410	95.0116
	5	-89562	271.3621
	6	-91281	799.5722
	7	-93083	1390.0332
	8	-95410	1819.3528
	9	-95538	2152.4678
	10	-95920	1641.7548
Local fjords (all)	1	-49481	2.0991
	2	-48829	5.9326
	3	-49195	180.2179
	4	-49718	1186.7621
Local fjords (samples 11, 13 and 14)	1	-33530	1.0390
	2	-33627	23.2868
	3	-34463	254.8380

Table S9. Results from the hierarchical Bayesian cluster analysis (STRUCTURE) based only on neutral microsatellite loci and all samples. STRUCTURE was run using 350,000 burn-in and 500,000 iterations for 10 independent runs for $K = 1$ to 10 for the North Atlantic samples and from $K = 1$ to 3 for the local Norwegian fjords (samples 11, 13 and 14). An admixture model with correlated allele frequencies without prior information on sample location was implemented. Bold values indicate the most likely number of clusters.

	K	Mean LnP(K)	StDev LnP(K)
North Atlantic	1	-85817	0.1871
	2	-85981	25.6621
	3	-86425	74.1802
	4	-87096	124.9924
	5	-88564	489.7930
	6	-90622	1073.9283
	7	-92667	2955.3703
	8	-94162	2935.9272
	9	-96560	3065.5698
	10	-97251	3204.5460
Local fjords	1	-32919	0.6579
	2	-32999	21.2130
	3	-33709	251.2843

Fig. S1. Results of the Bayesian cluster analysis performed in STRUCTURE for all microsatellite loci and all samples. Two clusters were detected both at the $LnP(K)$ (left figure) and ΔK levels (right figure). STRUCTURE was run using 350,000 burn-in and 500,000 iterations for 10 independent runs for $K = 1$ to 10 using an admixture model with correlated allele frequencies. No prior information on sample location was implemented.

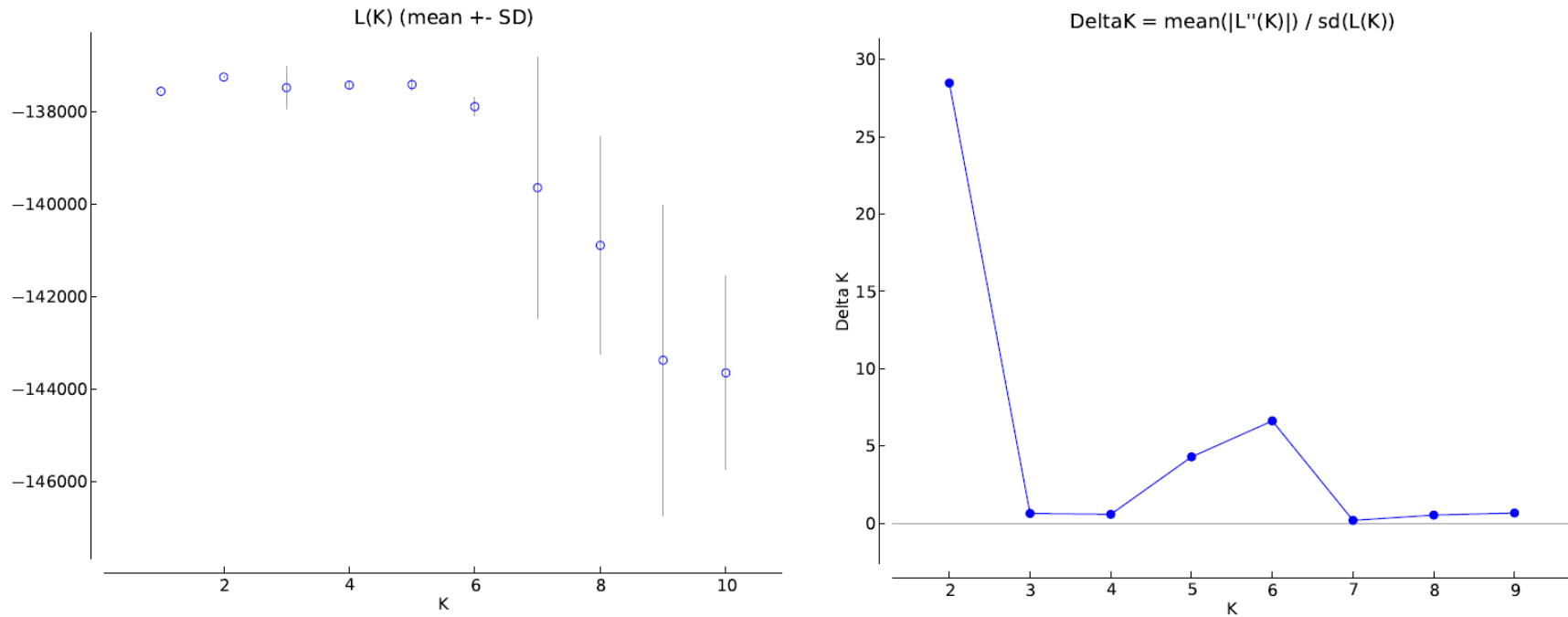


Fig. S2. Results of the Bayesian cluster analysis performed in STRUCTURE for all microsatellite loci and the fjord samples. Two clusters were detected both at the $\text{LnP}(K)$ (left figure) and ΔK levels (right figure). STRUCTURE was run using 350,000 burn-in and 500,000 iterations for 10 independent runs for $K = 1$ to 5 using an admixture model with correlated allele frequencies. No prior information on sample location was implemented.

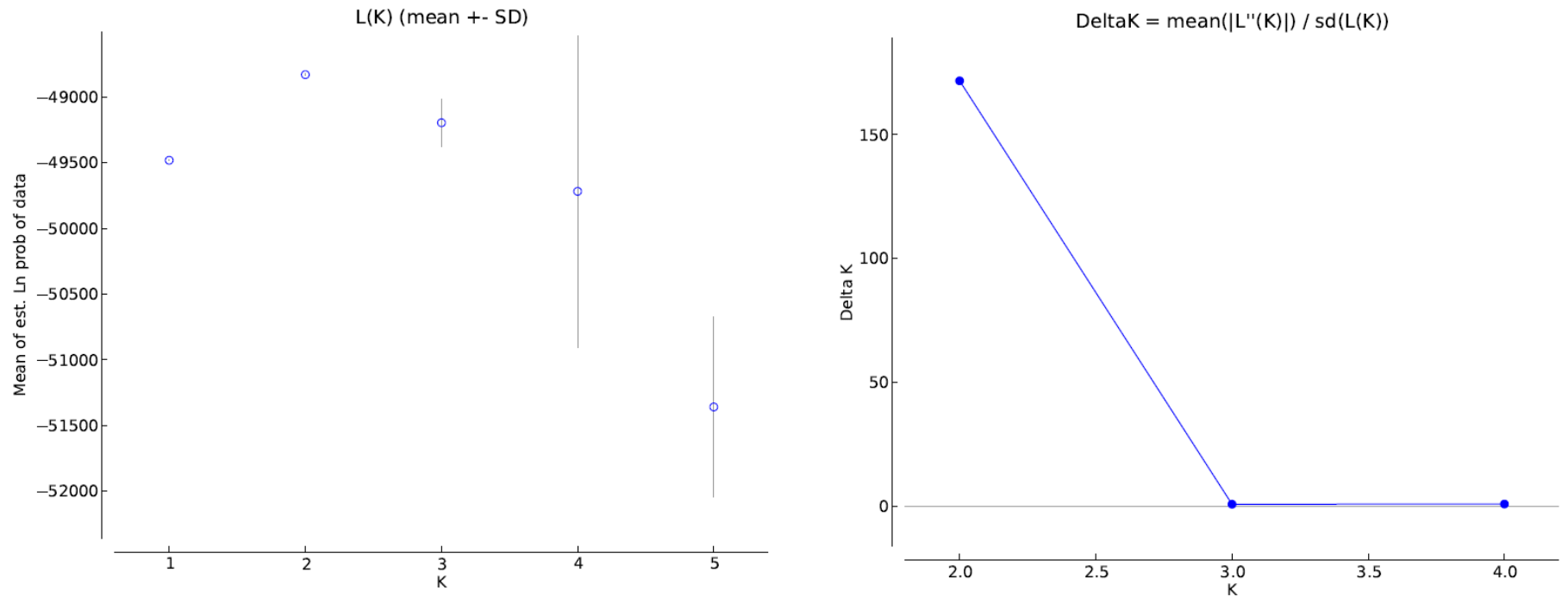


Fig. S3. Results of the Bayesian cluster analysis performed in STRUCTURE for neutral microsatellite loci only and all samples. Three clusters were detected both at the $LnP(K)$ (left figure) and ΔK levels (right figure). STRUCTURE was run using 350,000 burn-in and 500,000 iterations for 10 independent runs for $K = 1$ to 10 using an admixture model with correlated allele frequencies. No prior information on sample location was implemented. No additional clusters were detected.

