

Additional file 9 - Supplementary tables and figures of *ROH* with McQuillan2008 *ROH* parameters: `-homozyg -homozyg-snp 25 -homozyg-kb hkb -homozyg-gap 100` for minimum *ROH* > 500kb.

Table S9.1: Filter (`bcftools filter -i`) used to filter the SNP files before further processing with PLINK.

Autosome files	Filter-text
SNP VCFs	QUAL>30

Table S9.2: Summary of the number of runs of homozygosity *NSEG* on autosomes from the PLINK report (`--homozyg --homozyg-snp 25 --homozyg-kb hkb --homozyg-gap 100`) for variable minimum *ROH* length (Mb).

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
0.5	8	441	447.5	464.0	475.4	509.2	523	61.8	33.4
0.6	7	287	297.0	301.0	313.6	333.5	352	36.5	24.6
0.7	8	194	201.8	204.0	214.2	228.0	251	26.2	19.8
0.8	7	132	142.8	146.0	153.0	165.8	180	23.0	16.7
0.9	8	94	99.8	104.5	113.1	125.5	145	25.8	19.0
1.0	8	67	75.2	81.0	86.0	91.8	117	16.5	17.2
1.1	8	44	53.2	59.5	63.2	67.2	97	14.0	17.4
1.2	8	31	40.8	47.0	51.0	54.5	88	13.8	18.1
1.3	7	22	34.0	40.0	42.4	46.2	76	12.2	17.2
1.4	7	18	26.0	30.0	34.1	39.0	63	13.0	14.3
1.5	7	12	21.0	23.5	27.6	30.5	58	9.5	14.1
1.6	7	11	16.0	21.0	23.9	26.2	53	10.2	13.0
1.7	8	10	12.8	18.0	20.6	21.8	49	9.0	12.4
1.8	8	7	10.5	14.0	16.8	17.5	43	7.0	11.4
1.9	8	7	8.8	11.5	14.9	14.8	41	6.0	11.1
2.0	7	6	7.0	9.5	12.8	12.8	36	5.8	9.9
2.1	5	6	6.0	8.0	11.4	11.0	33	5.0	9.1
2.2	6	5	5.8	7.0	10.5	9.8	33	4.0	9.4
2.3	6	3	5.5	7.0	9.2	8.0	29	2.5	8.3
2.4	7	2	4.5	6.0	8.2	7.2	29	2.8	8.6
2.5	8	2	3.8	5.5	7.9	7.2	28	3.5	8.4
2.6	6	1	3.5	5.0	7.0	6.0	27	2.5	8.3
2.7	7	1	2.8	4.5	6.2	6.0	23	3.2	7.0
2.8	6	1	2.0	4.0	5.6	5.2	21	3.2	6.4
2.9	5	1	2.0	4.0	5.2	4.5	19	2.5	5.8
3.0	5	1	1.8	4.0	4.9	4.2	18	2.5	5.5
3.1	7	0	1.8	3.0	4.2	4.2	16	2.5	5.0
3.2	6	0	1.8	3.0	3.9	4.0	14	2.2	4.3
3.3	5	0	0.8	2.0	2.9	3.0	12	2.2	3.9
3.4	5	0	0.8	2.0	2.6	3.0	10	2.2	3.2

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
3.5	5	0	0.8	2.0	2.6	3.0	10	2.2	3.2
3.6	5	0	0.8	1.5	2.4	3.0	9	2.2	2.9
3.7	5	0	0.8	1.0	2.0	2.2	8	1.5	2.6
3.8	5	0	0.0	1.0	1.6	2.2	6	2.2	2.1
3.9	5	0	0.0	0.5	1.5	2.2	6	2.2	2.1
4.0	5	0	0.0	0.5	1.5	2.2	6	2.2	2.1
4.1	5	0	0.0	0.5	1.5	2.2	6	2.2	2.1
4.2	5	0	0.0	0.5	1.2	2.2	4	2.2	1.6
4.3	5	0	0.0	0.5	1.2	2.2	4	2.2	1.6
4.4	5	0	0.0	0.5	1.2	2.2	4	2.2	1.6
4.5	5	0	0.0	0.5	1.2	2.2	4	2.2	1.6
4.6	5	0	0.0	0.5	1.2	2.2	4	2.2	1.6
4.7	4	0	0.0	0.5	1.1	2.2	3	2.2	1.4
4.8	4	0	0.0	0.5	1.1	2.2	3	2.2	1.4
4.9	4	0	0.0	0.5	1.1	2.2	3	2.2	1.4
5.0	4	0	0.0	0.5	1.0	2.0	3	2.0	1.2

Table S9.3: Summary of the total length of runs  $KB/1000$  on autosomes from the PLINK report (`--homozyg --homozyg-snp 25 --homozyg-kb hkb --homozyg-gap 100`) for variable minimum  $ROH$  length (Mb).

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
0.5	8	340.9	359.4	374.9	391.3	417.2	485.5	57.8	47.5
0.6	8	262.3	275.5	286.3	303.1	319.4	400.0	43.9	44.9
0.7	8	194.3	214.5	227.9	238.8	248.0	334.3	33.5	44.0
0.8	8	148.1	168.4	184.7	193.1	202.4	281.2	34.0	41.8
0.9	8	115.8	132.2	149.6	159.3	168.4	251.5	36.1	43.7
1.0	8	90.4	107.7	119.7	133.6	147.0	224.9	39.3	42.8
1.1	8	66.7	86.1	98.3	109.8	120.5	203.9	34.5	43.5
1.2	8	51.7	73.7	82.8	95.7	105.8	193.6	32.1	44.5
1.3	8	40.4	65.4	75.4	85.0	93.7	178.6	28.4	43.2
1.4	8	35.0	54.6	59.9	73.9	87.0	161.0	32.4	39.8
1.5	8	26.2	45.1	52.1	64.5	73.8	153.7	28.7	39.7
1.6	8	24.7	37.4	48.2	58.7	63.4	146.0	25.9	38.2
1.7	8	23.1	32.1	43.3	53.4	55.1	139.4	23.1	37.5
1.8	8	16.8	29.7	35.4	46.6	47.8	128.9	18.1	35.7
1.9	8	16.8	25.9	30.4	43.1	42.7	125.1	16.8	35.1
2.0	8	15.4	23.4	26.5	39.0	38.8	115.5	15.5	32.9
2.1	8	14.7	21.5	25.5	36.2	32.1	109.4	10.6	31.4
2.2	8	12.6	20.3	23.8	34.3	29.4	109.4	9.1	31.9
2.3	8	8.8	17.3	23.1	31.5	28.8	100.3	11.6	29.6
2.4	8	5.6	13.3	22.3	29.1	26.5	100.3	13.2	30.2
2.5	8	5.6	11.5	21.5	28.2	25.8	97.9	14.3	29.7
2.6	8	3.1	10.9	19.7	26.0	23.4	95.3	12.5	29.3
2.7	8	3.1	8.8	18.9	24.0	22.6	84.7	13.8	26.0
2.8	8	3.1	6.8	17.0	22.2	21.4	79.1	14.6	24.6
2.9	8	3.1	6.8	15.5	21.2	21.4	73.4	14.6	22.8
3.0	8	3.1	6.0	15.5	20.1	20.6	70.5	14.6	22.0
3.1	8	0.0	6.0	14.0	18.2	18.4	64.5	12.3	20.5
3.2	8	0.0	6.0	14.0	17.0	17.6	58.2	11.5	18.3

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
3.3	7	0.0	2.8	10.7	13.7	14.3	51.7	11.5	16.9
3.4	7	0.0	2.8	10.7	12.9	14.3	45.1	11.5	14.8
3.5	7	0.0	2.8	10.7	12.9	14.3	45.1	11.5	14.8
3.6	7	0.0	2.8	9.0	12.0	14.3	41.6	11.5	13.8
3.7	7	0.0	2.8	5.3	10.7	14.3	37.9	11.5	13.0
3.8	6	0.0	0.0	5.3	9.3	14.3	30.5	14.3	11.2
3.9	5	0.0	0.0	3.4	8.8	14.3	30.5	14.3	11.6
4.0	5	0.0	0.0	3.4	8.8	14.3	30.5	14.3	11.6
4.1	5	0.0	0.0	3.4	8.8	14.3	30.5	14.3	11.6
4.2	5	0.0	0.0	3.4	7.7	14.3	22.2	14.3	9.5
4.3	5	0.0	0.0	3.4	7.7	14.3	22.2	14.3	9.5
4.4	5	0.0	0.0	3.4	7.7	14.3	22.2	14.3	9.5
4.5	5	0.0	0.0	3.4	7.7	14.3	22.2	14.3	9.5
4.6	5	0.0	0.0	3.4	7.7	14.3	22.2	14.3	9.5
4.7	5	0.0	0.0	3.4	7.2	13.5	20.8	13.5	8.6
4.8	5	0.0	0.0	3.4	7.2	13.5	20.8	13.5	8.6
4.9	5	0.0	0.0	3.4	7.2	13.5	20.8	13.5	8.6
5.0	5	0.0	0.0	3.4	6.5	12.3	20.8	12.3	7.9

Table S9.4: Summary of the average length of runs  $KBAVG/1000$  on autosomes from the PLINK report (`--homozyg --homozyg-snp 25 --homozyg-kb hkb --homozyg-gap 100`) for variable minimum  $ROH$  length (Mb).

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
0.5	8	0.77	0.79	0.80	0.82	0.83	0.95	0.05	0.06
0.6	8	0.88	0.92	0.94	0.96	0.99	1.14	0.08	0.08
0.7	8	1.00	1.05	1.07	1.11	1.15	1.33	0.10	0.11
0.8	8	1.12	1.17	1.21	1.25	1.28	1.56	0.11	0.14
0.9	8	1.23	1.29	1.36	1.39	1.41	1.73	0.12	0.16
1.0	8	1.34	1.43	1.49	1.53	1.55	1.92	0.12	0.19
1.1	8	1.51	1.58	1.64	1.70	1.73	2.10	0.15	0.20
1.2	8	1.62	1.70	1.76	1.83	1.91	2.20	0.21	0.20
1.3	8	1.80	1.82	1.84	1.96	2.03	2.35	0.21	0.22
1.4	8	1.84	1.95	2.00	2.10	2.22	2.56	0.27	0.24
1.5	8	1.95	2.11	2.19	2.27	2.40	2.65	0.30	0.25
1.6	8	2.00	2.22	2.36	2.38	2.53	2.75	0.30	0.26
1.7	8	2.13	2.29	2.50	2.50	2.68	2.85	0.38	0.26
1.8	8	2.35	2.39	2.65	2.69	3.00	3.09	0.61	0.31
1.9	8	2.37	2.45	2.82	2.82	3.10	3.44	0.65	0.40
2.0	8	2.40	2.61	2.94	2.97	3.26	3.65	0.65	0.43
2.1	8	2.45	2.61	3.20	3.10	3.36	3.92	0.75	0.51
2.2	8	2.51	2.67	3.27	3.19	3.53	3.92	0.86	0.52
2.3	8	2.58	2.90	3.35	3.28	3.57	3.92	0.67	0.49
2.4	8	2.79	2.95	3.35	3.42	3.72	4.42	0.77	0.56
2.5	8	2.79	3.06	3.36	3.48	3.79	4.42	0.74	0.59
2.6	8	3.06	3.11	3.44	3.66	3.95	5.03	0.85	0.69
2.7	8	3.06	3.20	3.51	3.74	4.05	5.03	0.85	0.73
2.8	8	3.06	3.38	3.63	3.84	4.27	5.03	0.89	0.71
2.9	8	3.06	3.40	3.74	3.87	4.27	5.03	0.87	0.70
3.0	8	3.06	3.43	3.77	3.94	4.27	5.45	0.84	0.79

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
3.1	8	0.00	3.43	3.82	3.69	4.68	5.45	1.24	1.68
3.2	8	0.00	3.43	3.89	3.77	4.68	6.01	1.24	1.78
3.3	7	0.00	2.80	4.04	3.75	5.38	6.93	2.59	2.56
3.4	7	0.00	2.80	4.14	3.77	5.38	6.93	2.59	2.57
3.5	7	0.00	2.80	4.14	3.77	5.38	6.93	2.59	2.57
3.6	7	0.00	2.80	4.19	3.99	6.25	6.93	3.45	2.75
3.7	7	0.00	2.83	4.30	4.02	6.25	6.93	3.42	2.76
3.8	6	0.00	0.00	4.47	3.59	6.25	6.93	6.25	3.12
3.9	5	0.00	0.00	2.54	3.11	6.25	6.93	6.25	3.37
4.0	5	0.00	0.00	2.54	3.11	6.25	6.93	6.25	3.37
4.1	5	0.00	0.00	2.54	3.11	6.25	6.93	6.25	3.37
4.2	5	0.00	0.00	2.77	3.16	6.25	6.93	6.25	3.41
4.3	5	0.00	0.00	2.77	3.16	6.25	6.93	6.25	3.41
4.4	5	0.00	0.00	2.77	3.16	6.25	6.93	6.25	3.41
4.5	5	0.00	0.00	2.77	3.16	6.25	6.93	6.25	3.41
4.6	5	0.00	0.00	2.77	3.16	6.25	6.93	6.25	3.41
4.7	5	0.00	0.00	2.92	3.20	6.25	6.93	6.25	3.44
4.8	5	0.00	0.00	2.92	3.20	6.25	6.93	6.25	3.44
4.9	5	0.00	0.00	2.92	3.20	6.25	6.93	6.25	3.44
5.0	5	0.00	0.00	3.04	3.26	6.39	6.93	6.39	3.49

Table S9.5: Summary of the inferred inbreeding  $F_{ROH}$  on autosomes from the PLINK report (`--homozyg --homozyg-snp 25 --homozyg-kb hkb --homozyg-gap 100`) for variable minimum  $ROH$  length (Mb).

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
0.5	8	0.118	0.125	0.130	0.136	0.145	0.169	0.020	0.017
0.6	8	0.091	0.096	0.099	0.105	0.111	0.139	0.015	0.016
0.7	8	0.067	0.074	0.079	0.083	0.086	0.116	0.012	0.015
0.8	8	0.051	0.058	0.064	0.067	0.070	0.098	0.012	0.015
0.9	8	0.040	0.046	0.052	0.055	0.058	0.087	0.013	0.015
1.0	8	0.031	0.037	0.042	0.046	0.051	0.078	0.014	0.015
1.1	8	0.023	0.030	0.034	0.038	0.042	0.071	0.012	0.015
1.2	8	0.018	0.026	0.029	0.033	0.037	0.067	0.011	0.015
1.3	8	0.014	0.023	0.026	0.030	0.033	0.062	0.010	0.015
1.4	8	0.012	0.019	0.021	0.026	0.030	0.056	0.011	0.014
1.5	8	0.009	0.016	0.018	0.022	0.026	0.053	0.010	0.014
1.6	8	0.009	0.013	0.017	0.020	0.022	0.051	0.009	0.013
1.7	8	0.008	0.011	0.015	0.019	0.019	0.048	0.008	0.013
1.8	8	0.006	0.010	0.012	0.016	0.017	0.045	0.006	0.012
1.9	8	0.006	0.009	0.011	0.015	0.015	0.043	0.006	0.012
2.0	8	0.005	0.008	0.009	0.014	0.013	0.040	0.005	0.011
2.1	8	0.005	0.007	0.009	0.013	0.011	0.038	0.004	0.011
2.2	8	0.004	0.007	0.008	0.012	0.010	0.038	0.003	0.011
2.3	8	0.003	0.006	0.008	0.011	0.010	0.035	0.004	0.010
2.4	8	0.002	0.005	0.008	0.010	0.009	0.035	0.005	0.010
2.5	8	0.002	0.004	0.007	0.010	0.009	0.034	0.005	0.010
2.6	8	0.001	0.004	0.007	0.009	0.008	0.033	0.004	0.010
2.7	8	0.001	0.003	0.007	0.008	0.008	0.029	0.005	0.009
2.8	8	0.001	0.002	0.006	0.008	0.007	0.027	0.005	0.009

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
2.9	8	0.001	0.002	0.005	0.007	0.007	0.025	0.005	0.008
3.0	8	0.001	0.002	0.005	0.007	0.007	0.024	0.005	0.008
3.1	8	0.000	0.002	0.005	0.006	0.006	0.022	0.004	0.007
3.2	8	0.000	0.002	0.005	0.006	0.006	0.020	0.004	0.006
3.3	7	0.000	0.001	0.004	0.005	0.005	0.018	0.004	0.006
3.4	7	0.000	0.001	0.004	0.004	0.005	0.016	0.004	0.005
3.5	7	0.000	0.001	0.004	0.004	0.005	0.016	0.004	0.005
3.6	7	0.000	0.001	0.003	0.004	0.005	0.014	0.004	0.005
3.7	7	0.000	0.001	0.002	0.004	0.005	0.013	0.004	0.005
3.8	6	0.000	0.000	0.002	0.003	0.005	0.011	0.005	0.004
3.9	5	0.000	0.000	0.001	0.003	0.005	0.011	0.005	0.004
4.0	5	0.000	0.000	0.001	0.003	0.005	0.011	0.005	0.004
4.1	5	0.000	0.000	0.001	0.003	0.005	0.011	0.005	0.004
4.2	5	0.000	0.000	0.001	0.003	0.005	0.008	0.005	0.003
4.3	5	0.000	0.000	0.001	0.003	0.005	0.008	0.005	0.003
4.4	5	0.000	0.000	0.001	0.003	0.005	0.008	0.005	0.003
4.5	5	0.000	0.000	0.001	0.003	0.005	0.008	0.005	0.003
4.6	5	0.000	0.000	0.001	0.003	0.005	0.008	0.005	0.003
4.7	5	0.000	0.000	0.001	0.002	0.005	0.007	0.005	0.003
4.8	5	0.000	0.000	0.001	0.002	0.005	0.007	0.005	0.003
4.9	5	0.000	0.000	0.001	0.002	0.005	0.007	0.005	0.003
5.0	5	0.000	0.000	0.001	0.002	0.004	0.007	0.004	0.003

Table S9.6: Summary of the inferred relatedness  $R_{ROH} = 2xF_{ROH}$  on autosomes from the PLINK report (`--homozyg --homozyg-snp 25 --homozyg-kb hkb --homozyg-gap 100`) for variable minimum  $ROH$  length (Mb).

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
0.5	8	0.237	0.250	0.260	0.272	0.290	0.337	0.040	0.033
0.6	8	0.182	0.191	0.199	0.210	0.222	0.278	0.030	0.031
0.7	8	0.135	0.149	0.158	0.166	0.172	0.232	0.023	0.031
0.8	8	0.103	0.117	0.128	0.134	0.141	0.195	0.024	0.029
0.9	8	0.080	0.092	0.104	0.111	0.117	0.175	0.025	0.030
1.0	8	0.063	0.075	0.083	0.093	0.102	0.156	0.027	0.030
1.1	8	0.046	0.060	0.068	0.076	0.084	0.142	0.024	0.030
1.2	8	0.036	0.051	0.057	0.066	0.073	0.134	0.022	0.031
1.3	8	0.028	0.045	0.052	0.059	0.065	0.124	0.020	0.030
1.4	8	0.024	0.038	0.042	0.051	0.060	0.112	0.022	0.028
1.5	8	0.018	0.031	0.036	0.045	0.051	0.107	0.020	0.028
1.6	8	0.017	0.026	0.033	0.041	0.044	0.101	0.018	0.027
1.7	8	0.016	0.022	0.030	0.037	0.038	0.097	0.016	0.026
1.8	8	0.012	0.021	0.025	0.032	0.033	0.089	0.013	0.025
1.9	8	0.012	0.018	0.021	0.030	0.030	0.087	0.012	0.024
2.0	8	0.011	0.016	0.018	0.027	0.027	0.080	0.011	0.023
2.1	8	0.010	0.015	0.018	0.025	0.022	0.076	0.007	0.022
2.2	8	0.009	0.014	0.017	0.024	0.020	0.076	0.006	0.022
2.3	8	0.006	0.012	0.016	0.022	0.020	0.070	0.008	0.021
2.4	8	0.004	0.009	0.015	0.020	0.018	0.070	0.009	0.021
2.5	8	0.004	0.008	0.015	0.020	0.018	0.068	0.010	0.021
2.6	8	0.002	0.008	0.014	0.018	0.016	0.066	0.009	0.020

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
2.7	8	0.002	0.006	0.013	0.017	0.016	0.059	0.010	0.018
2.8	8	0.002	0.005	0.012	0.015	0.015	0.055	0.010	0.017
2.9	8	0.002	0.005	0.011	0.015	0.015	0.051	0.010	0.016
3.0	8	0.002	0.004	0.011	0.014	0.014	0.049	0.010	0.015
3.1	8	0.000	0.004	0.010	0.013	0.013	0.045	0.009	0.014
3.2	8	0.000	0.004	0.010	0.012	0.012	0.040	0.008	0.013
3.3	7	0.000	0.002	0.007	0.010	0.010	0.036	0.008	0.012
3.4	7	0.000	0.002	0.007	0.009	0.010	0.031	0.008	0.010
3.5	7	0.000	0.002	0.007	0.009	0.010	0.031	0.008	0.010
3.6	7	0.000	0.002	0.006	0.008	0.010	0.029	0.008	0.010
3.7	7	0.000	0.002	0.004	0.007	0.010	0.026	0.008	0.009
3.8	6	0.000	0.000	0.004	0.006	0.010	0.021	0.010	0.008
3.9	5	0.000	0.000	0.002	0.006	0.010	0.021	0.010	0.008
4.0	5	0.000	0.000	0.002	0.006	0.010	0.021	0.010	0.008
4.1	5	0.000	0.000	0.002	0.006	0.010	0.021	0.010	0.008
4.2	5	0.000	0.000	0.002	0.005	0.010	0.015	0.010	0.007
4.3	5	0.000	0.000	0.002	0.005	0.010	0.015	0.010	0.007
4.4	5	0.000	0.000	0.002	0.005	0.010	0.015	0.010	0.007
4.5	5	0.000	0.000	0.002	0.005	0.010	0.015	0.010	0.007
4.6	5	0.000	0.000	0.002	0.005	0.010	0.015	0.010	0.007
4.7	5	0.000	0.000	0.002	0.005	0.009	0.014	0.009	0.006
4.8	5	0.000	0.000	0.002	0.005	0.009	0.014	0.009	0.006
4.9	5	0.000	0.000	0.002	0.005	0.009	0.014	0.009	0.006
5.0	5	0.000	0.000	0.002	0.005	0.009	0.014	0.009	0.006

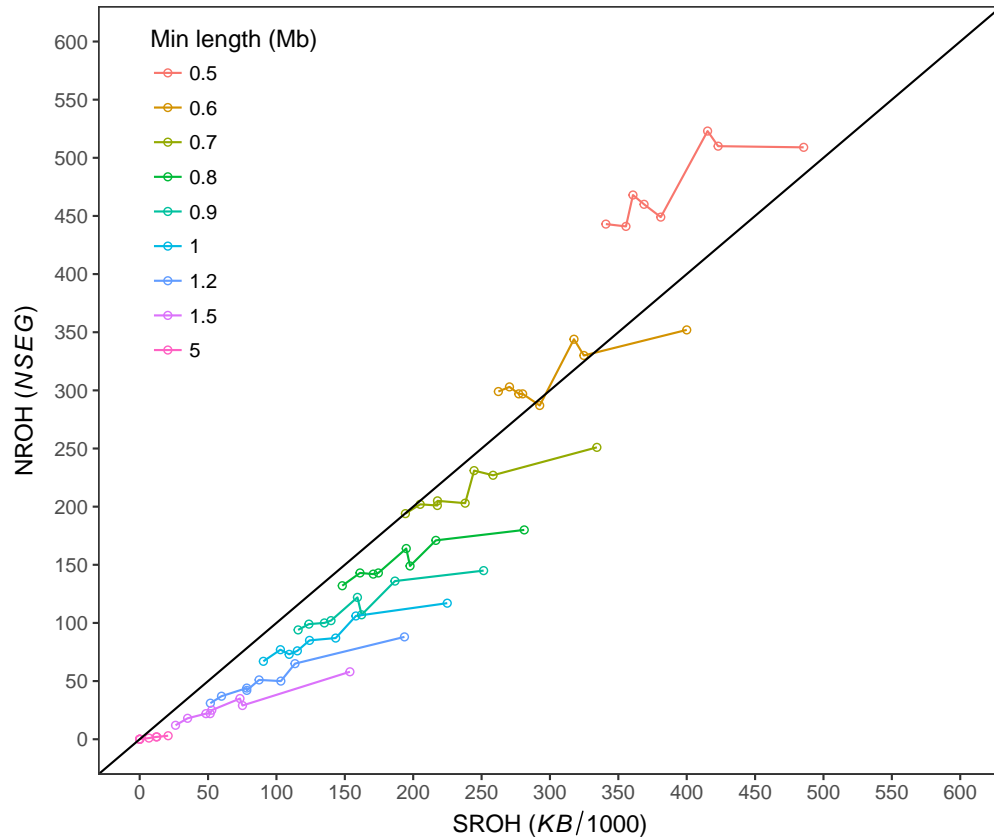


Figure S9.1: Plot of the number of runs of homozygosity  $NROH$  ( $NSEQ$ ) against the total length of runs  $SROH$  ( $KB/1000$ ) in the PLINK report for a subset 0.5 – 5Mb of the variable minimum  $ROH$  lengths. At 0.6Mb minimum length the population seems bottlenecked with most points close to or at the diagonal. Above 0.6Mb the population seems bottlenecked and consanguineous with the points below and right shifted from the diagonal. At 1.5Mb the points left shift towards the diagonal, and at 5Mb the leftmost point is back near the diagonal.

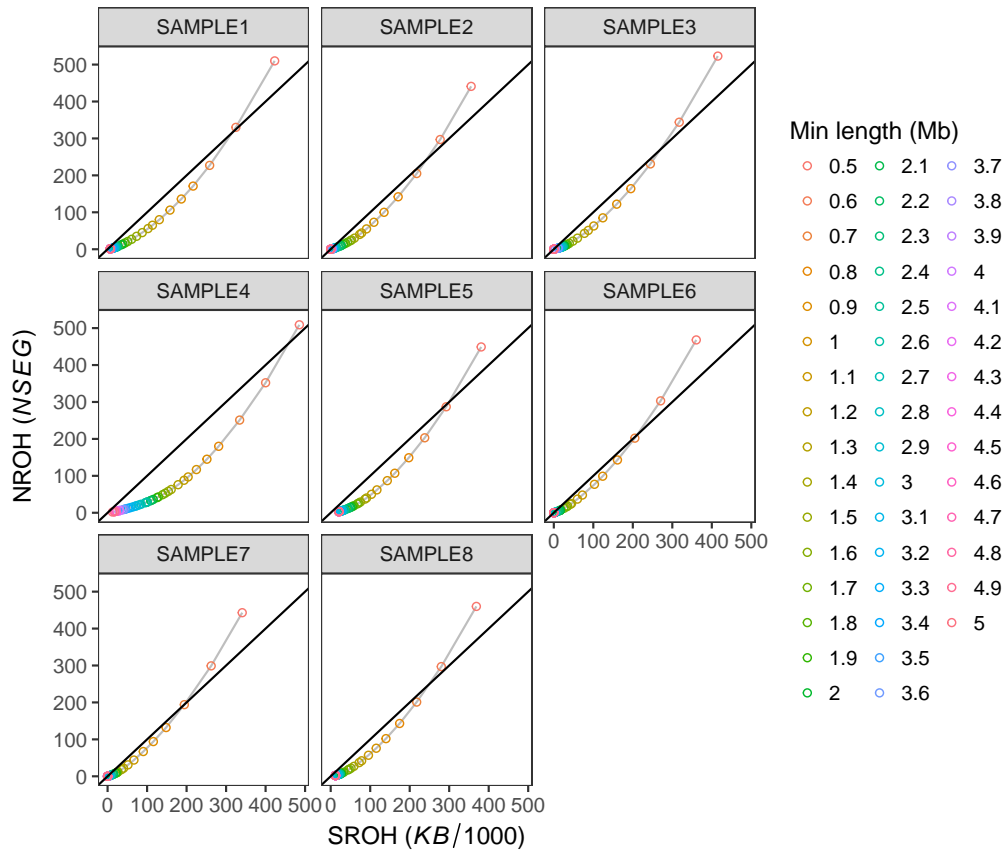


Figure S9.2: Plots of the number of runs of homozyosity NROH (*NSEQ*) against the total length of runs SROH (*KB/1000*) in the PLINK report for the minimum lengths of *ROH* > 0.5Mb. At about 1.0Mb the points are maximum shifted to the right from the diagonal.



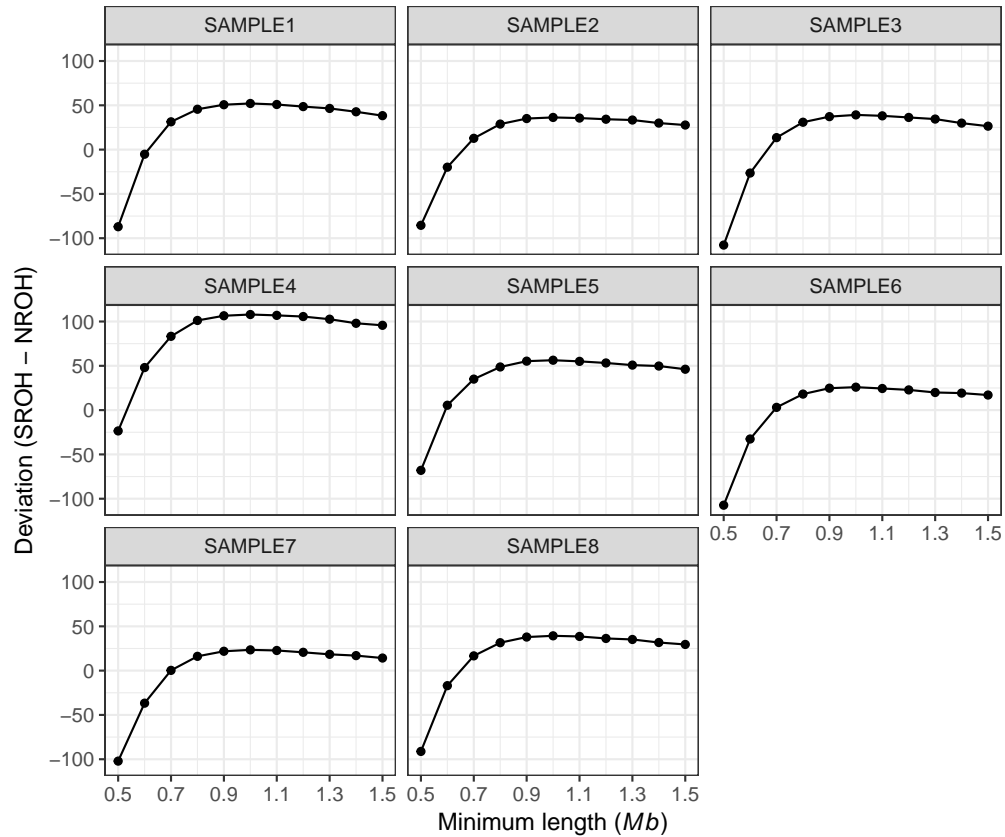


Figure S9.3: Plots of deviation  $SROH (KB/1000) - NROH (NSEQ)$  from the linear diagonal in the  $NROH$  versus  $SROH$  plots shown for minimum  $ROH$  lengths between 0.5 and 1.5Mb. For all the samples the  $SROH$  is below the diagonal (deviation  $> 0$ ) for minimum  $ROH$  lengths above 0.7 – 0.8Mb and the maximum deviation is found at 1.0Mb.

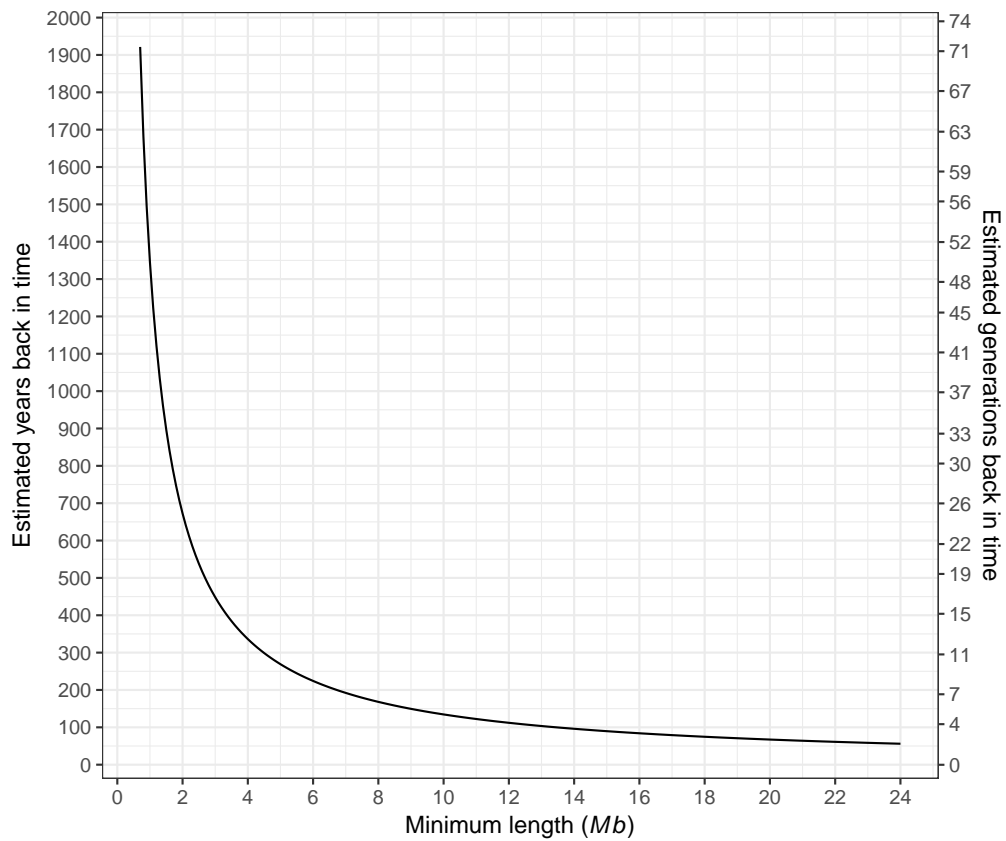


Figure S9.4: Plot of the estimated years back in time (left y-axis) and generations back in time (right y-axis) inferred from the minimum lengths of  $ROH > 0.6\text{Mb}$ . At 1Mb the estimate is 1345 years back and 50 generations back in time.

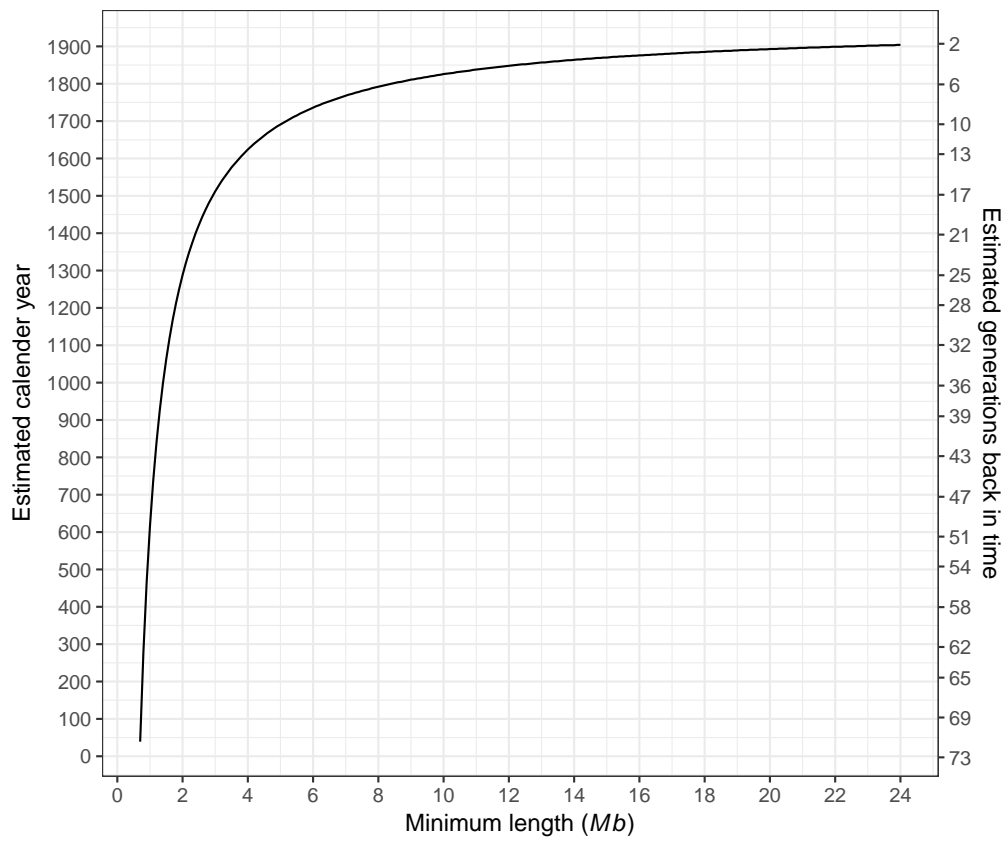


Figure S9.5: Plot of the estimated calendar year (left y-axis) and generations back in time (right y-axis) since 1960 inferred from the minimum lengths of  $ROH > 0.6\text{Mb}$ . At 1Mb the estimated calendar year is 615.

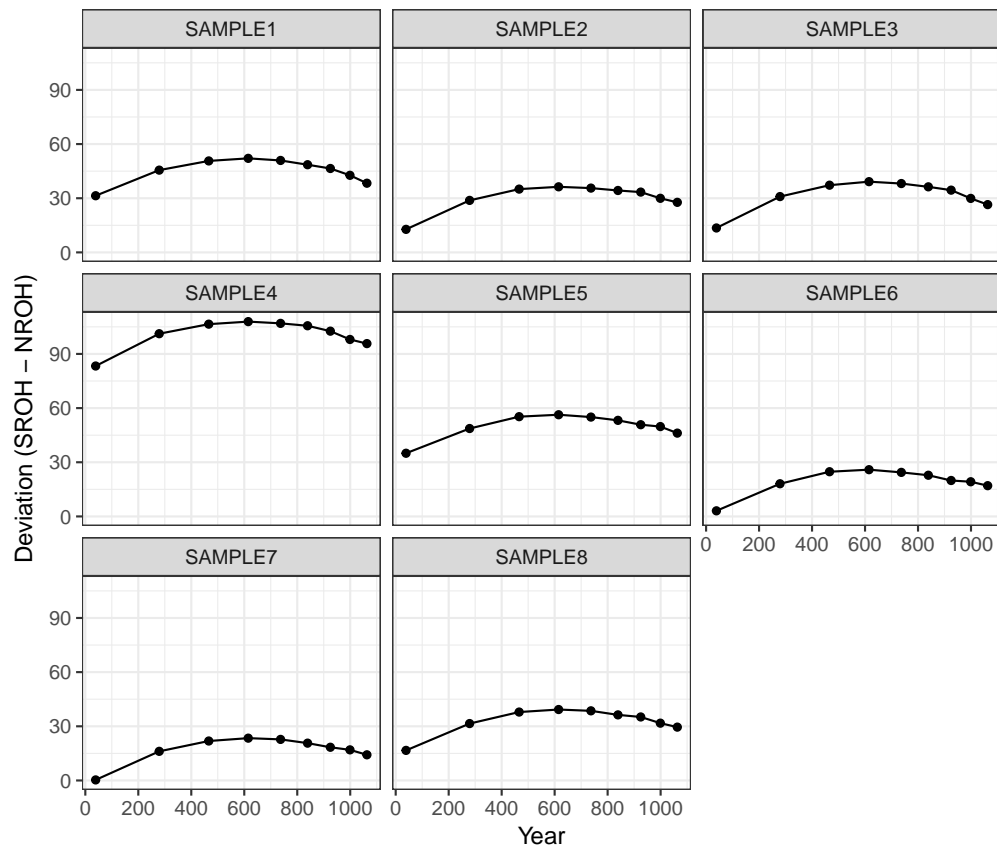


Figure S9.6: Plots of deviation  $SROH$  ( $KB/1000$ ) –  $NROH$  ( $NSEQ$ ) from the linear diagonal in the  $NROH$  versus  $SROH$  plots shown for minimum  $ROH$  lengths between 0.7 and 1.5Mb, transformed to the corresponding estimated time in years. The maximum deviation for all samples is found at 1.0Mb corresponding to year 615.

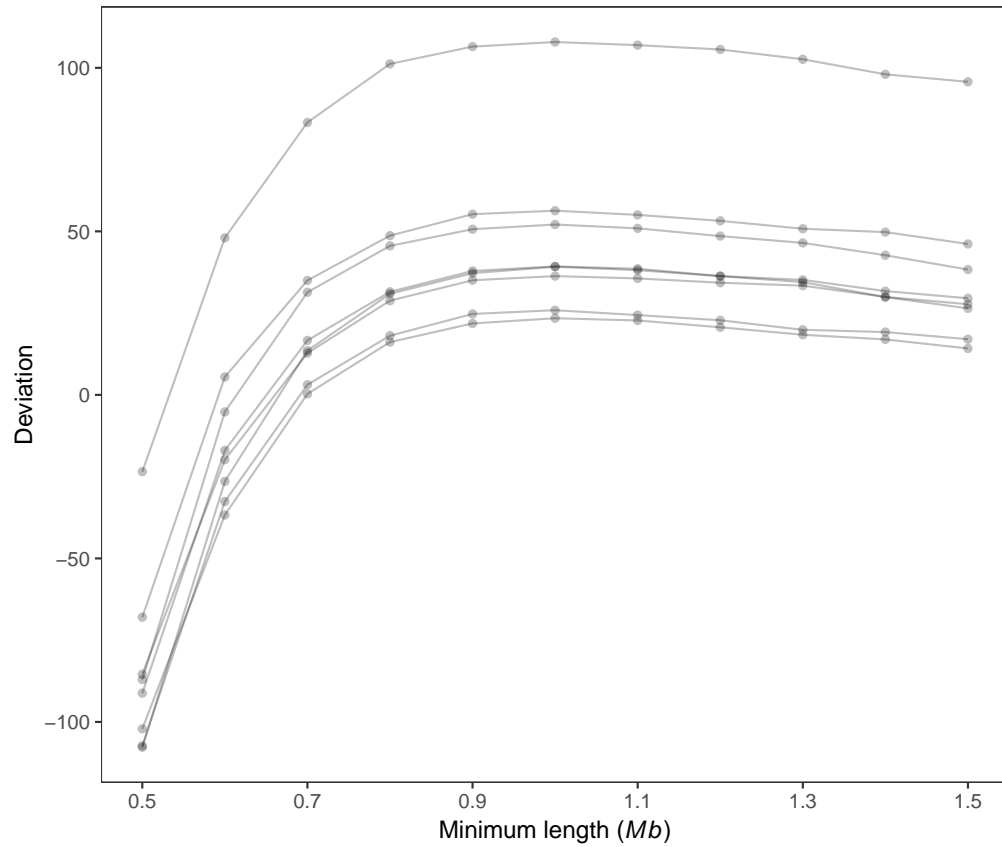


Figure S9.7: Plot of deviation  $SROH (KB/1000) - NROH (NSEQ)$  from the linear diagonal in the  $NROH$  versus  $SROH$  plots shown for minimum  $ROH$  lengths between 0.5 and 1.5Mb. For all the samples the  $SROH$  is clearly below the diagonal (deviation  $> 0$ ) for minimum  $ROH$  lengths above 0.7 – 0.8Mb and the maximum deviation is found at 1.0Mb.

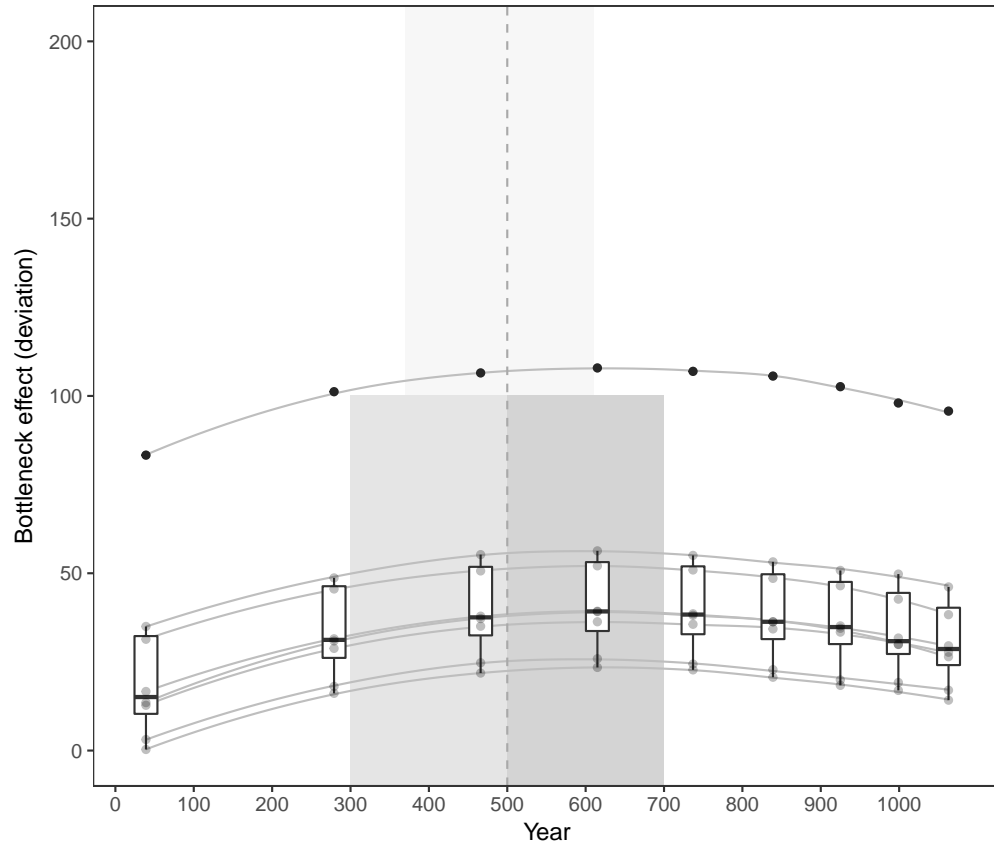


Figure S9.8: Plot of deviation from the linear diagonal in the NROH versus SROH plots shown for minimum *ROH* lengths between 0.7 and 1.5Mb, transformed to the corresponding estimated time in years. The maximum deviation for all samples is found at 1.0Mb corresponding to year 615. The three shaded rectangles illustrate the dating of the oldest archaeological findings from the Faroe Islands from two pre-Viking colonization events at year 300 – 500 (left) and 500 – 700 (right), and the first appearance of sheep DNA at year 500 (top, CI: 370 – 610).