

Additional file 6 - Supplementary tables and figures of *ROH*

Table S6.1: Filter (`bcftools filter -i`) used to filter the SNP files before further processing with PLINK.

Autosome files	Filter-text
SNP VCFs	FILTER='PASS' & QUAL>30 & FMT/DPU>10

Table S6.2: Summary of the number of runs of homozygosity *NSEG* on autosomes from the PLINK report (`--homozyg --homozyg-kb`) for variable minimum *ROH* length (Mb).

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
0.1	8	1430	1496.5	1513.5	1520.0	1549.8	1600	53.2	51.4
0.2	7	1140	1188.2	1193.5	1210.6	1247.0	1283	58.8	47.5
0.3	8	871	884.5	890.0	907.1	937.2	961	52.8	34.7
0.4	7	637	660.2	663.5	676.0	700.5	721	40.2	29.9
0.5	7	460	483.2	491.5	499.1	524.0	545	40.8	29.3
0.6	8	320	345.8	352.5	355.6	364.2	390	18.5	21.7
0.7	7	245	256.0	261.5	264.9	271.2	290	15.2	14.5
0.8	7	185	189.0	192.0	197.6	205.2	217	16.2	12.4
0.9	7	140	147.8	150.0	152.1	156.2	169	8.5	8.7
1.0	8	101	114.2	117.5	118.8	126.5	133	12.2	10.8
1.1	7	83	87.0	92.5	93.2	96.2	111	9.2	9.2
1.2	6	59	69.0	74.5	74.4	77.5	91	8.5	9.5
1.3	7	46	58.0	63.0	61.8	67.2	71	9.2	8.4
1.4	8	37	44.8	48.0	48.8	51.8	63	7.0	7.7
1.5	8	27	36.5	40.0	40.0	43.5	51	7.0	7.5
1.6	7	25	30.8	35.0	34.4	36.8	44	6.0	5.8
1.7	7	18	27.0	29.0	29.5	32.2	41	5.2	6.5
1.8	7	15	22.8	26.0	25.0	27.2	33	4.5	5.3
1.9	6	13	19.0	21.5	21.8	25.0	30	6.0	5.1
2.0	7	11	16.8	19.5	19.6	21.5	30	4.8	5.6
2.1	7	10	13.2	16.0	17.0	20.0	27	6.8	5.9
2.2	8	7	11.8	15.5	15.4	18.2	27	6.5	6.4
2.3	5	7	10.8	13.5	13.8	15.5	25	4.8	5.8
2.4	7	6	9.0	12.5	12.5	14.5	23	5.5	5.6
2.5	7	5	7.5	12.5	11.9	13.8	22	6.2	5.6
2.6	7	4	7.2	11.5	11.1	12.8	22	5.5	5.8
2.7	7	4	5.0	10.5	10.1	12.5	20	7.5	5.4
2.8	6	4	4.8	9.0	9.2	11.2	20	6.5	5.3
2.9	6	4	4.8	8.5	8.5	9.5	18	4.8	4.6
3.0	7	3	4.8	8.0	8.0	9.2	17	4.5	4.4
3.1	6	2	4.5	8.0	7.6	9.0	17	4.5	4.7
3.2	6	2	4.5	8.0	7.5	8.2	17	3.8	4.6
3.3	5	2	4.5	8.0	7.4	8.0	17	3.5	4.6
3.4	6	1	4.5	7.5	7.1	8.0	17	3.5	4.8
3.5	6	1	4.5	7.0	7.0	8.0	17	3.5	4.8

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
3.6	6	1	4.5	7.0	6.9	8.0	16	3.5	4.5
3.7	6	1	4.5	7.0	6.8	8.0	15	3.5	4.2
3.8	7	1	3.8	6.5	6.4	8.0	14	4.2	4.0
3.9	7	1	3.8	6.5	6.4	8.0	14	4.2	4.0
4.0	6	1	3.0	6.5	6.2	8.0	14	5.0	4.1
4.1	6	1	3.0	6.5	6.2	8.0	14	5.0	4.1
4.2	7	1	2.8	5.5	5.9	8.0	14	5.2	4.2
4.3	6	1	2.8	5.0	5.8	8.0	14	5.2	4.2
4.4	6	1	2.8	5.0	5.8	8.0	14	5.2	4.2
4.5	6	1	2.8	5.0	5.8	8.0	14	5.2	4.2
4.6	8	1	2.8	4.5	5.2	7.2	12	4.5	3.6
4.7	7	1	2.8	4.5	5.1	7.0	12	4.2	3.5
4.8	7	1	2.8	4.5	5.1	7.0	12	4.2	3.5
4.9	7	1	2.8	4.5	5.1	7.0	12	4.2	3.5
5.0	7	1	2.8	4.5	5.0	7.0	11	4.2	3.3

Table S6.3: Summary of the total length of runs $KB/1000$ on autosomes from the PLINK report (`--homozyg --homozyg-kb`) for variable minimum ROH length (Mb).

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
0.1	8	704.8	720.0	747.8	754.8	782.0	833.4	62.0	43.5
0.2	8	655.2	672.7	699.4	707.3	735.6	788.6	62.9	44.9
0.3	8	580.2	597.9	619.8	632.0	660.0	722.3	62.1	47.4
0.4	8	497.9	518.9	539.5	551.4	577.6	639.9	58.7	47.0
0.5	8	426.1	442.0	455.1	472.2	497.7	564.0	55.6	46.3
0.6	8	346.8	366.3	377.5	393.7	411.5	496.3	45.2	47.6
0.7	8	292.8	304.1	321.1	335.0	348.4	438.4	44.3	47.5
0.8	8	238.4	250.0	271.6	284.9	299.2	389.7	49.2	50.7
0.9	8	203.2	207.9	230.8	246.3	266.4	353.1	58.5	51.1
1.0	8	166.3	183.8	197.7	214.7	234.9	323.9	51.0	51.9
1.1	8	140.4	150.8	168.3	187.9	205.4	306.1	54.6	54.9
1.2	8	112.8	130.1	149.4	166.3	183.3	285.5	53.1	55.7
1.3	8	96.5	119.9	136.9	150.5	163.9	271.8	44.0	55.5
1.4	8	84.3	99.3	116.7	133.0	148.0	248.8	48.7	53.6
1.5	8	69.8	87.1	104.5	120.3	136.1	240.1	49.1	54.9
1.6	8	66.6	80.5	95.3	111.7	124.6	233.9	44.1	54.2
1.7	8	55.1	73.1	86.3	103.6	115.1	228.9	42.1	55.4
1.8	8	49.9	64.4	81.8	95.8	106.4	215.0	42.1	52.9
1.9	8	46.1	58.9	76.3	89.8	96.7	209.4	37.8	52.7
2.0	8	42.2	50.2	71.4	85.7	95.7	209.4	45.6	54.6
2.1	8	33.0	44.9	64.2	80.3	92.7	203.3	47.8	55.1
2.2	8	24.4	42.2	63.1	76.8	89.0	203.3	46.8	56.5
2.3	8	24.4	39.9	58.6	73.1	82.8	198.8	42.9	55.4
2.4	8	22.0	35.8	56.3	70.2	80.4	194.2	44.6	54.8
2.5	8	22.0	31.5	56.3	68.7	78.5	191.7	47.0	54.7
2.6	8	19.5	30.8	53.7	66.8	76.0	191.7	45.1	55.2
2.7	8	19.5	25.7	51.1	64.1	75.3	186.4	49.6	54.4
2.8	8	16.7	25.7	47.0	61.7	71.9	186.4	46.2	54.7
2.9	8	16.7	25.7	45.5	59.6	66.9	180.7	41.2	52.7
3.0	8	16.7	24.1	44.1	58.1	66.2	177.7	42.1	52.0

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
3.1	8	10.6	24.1	44.1	57.0	65.4	177.7	41.3	52.7
3.2	8	10.6	24.1	44.1	56.6	63.6	177.7	39.5	52.6
3.3	8	10.6	24.1	44.1	56.1	62.2	177.7	38.1	52.5
3.4	8	7.3	24.1	42.4	55.3	62.2	177.7	38.1	53.1
3.5	8	7.3	24.1	40.7	54.9	62.2	177.7	38.1	53.2
3.6	8	7.3	24.1	40.7	54.4	62.2	174.2	38.1	52.0
3.7	8	7.3	24.1	40.7	54.0	62.2	170.5	38.1	50.8
3.8	8	7.3	22.6	38.8	52.6	62.2	166.8	39.6	50.1
3.9	8	7.3	22.6	38.8	52.6	62.2	166.8	39.6	50.1
4.0	8	7.3	21.6	38.8	52.1	62.2	166.8	40.6	50.5
4.1	8	7.3	21.6	38.8	52.1	62.2	166.8	40.6	50.5
4.2	8	7.3	20.6	34.6	50.5	62.2	166.8	41.6	51.3
4.3	8	7.3	20.6	32.5	50.0	62.2	166.8	41.6	51.4
4.4	8	7.3	20.6	32.5	50.0	62.2	166.8	41.6	51.4
4.5	8	7.3	20.6	32.5	50.0	62.2	166.8	41.6	51.4
4.6	8	7.3	20.6	30.2	47.7	59.4	157.7	38.9	48.5
4.7	8	7.3	20.6	30.2	47.1	57.6	157.7	37.0	48.4
4.8	8	7.3	20.6	30.2	47.1	57.6	157.7	37.0	48.4
4.9	8	7.3	20.6	30.2	47.1	57.6	157.7	37.0	48.4
5.0	8	7.3	20.6	30.2	46.5	57.6	152.7	37.0	46.8

Table S6.4: Summary of the average length of runs *KBAVG/1000* on autosomes from the PLINK report (`--homozyg --homozyg-kb`) for variable minimum *ROH* length (Mb).

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
0.1	8	0.47	0.47	0.49	0.50	0.50	0.58	0.03	0.04
0.2	8	0.55	0.56	0.57	0.59	0.59	0.69	0.04	0.05
0.3	8	0.65	0.66	0.68	0.70	0.71	0.83	0.05	0.06
0.4	8	0.76	0.77	0.79	0.82	0.83	1.00	0.06	0.08
0.5	8	0.86	0.88	0.91	0.95	0.97	1.20	0.09	0.11
0.6	8	0.99	1.01	1.05	1.11	1.16	1.44	0.15	0.15
0.7	8	1.10	1.14	1.19	1.27	1.33	1.71	0.20	0.20
0.8	8	1.25	1.29	1.36	1.44	1.48	2.04	0.19	0.26
0.9	8	1.38	1.44	1.52	1.62	1.65	2.39	0.21	0.33
1.0	8	1.45	1.61	1.69	1.81	1.83	2.77	0.22	0.41
1.1	8	1.60	1.75	1.89	2.00	2.01	3.06	0.26	0.46
1.2	8	1.73	1.91	2.06	2.21	2.21	3.48	0.30	0.55
1.3	8	1.89	2.06	2.19	2.40	2.46	3.83	0.40	0.62
1.4	8	2.00	2.25	2.46	2.68	2.65	4.61	0.40	0.82
1.5	8	2.16	2.52	2.68	2.93	2.91	5.00	0.39	0.89
1.6	8	2.27	2.60	2.89	3.14	3.27	5.32	0.67	0.96
1.7	8	2.33	2.90	3.15	3.37	3.57	5.58	0.67	1.00
1.8	8	2.47	3.11	3.31	3.68	3.91	6.51	0.80	1.25
1.9	8	2.57	3.27	3.54	3.94	4.27	6.98	1.00	1.38
2.0	8	2.70	3.49	3.77	4.10	4.42	6.98	0.93	1.31
2.1	8	3.00	3.81	4.04	4.38	4.49	7.53	0.68	1.39
2.2	8	3.41	3.93	4.28	4.60	4.88	7.53	0.95	1.31
2.3	8	3.48	4.11	4.59	4.88	5.24	7.95	1.13	1.43
2.4	8	3.67	4.21	4.92	5.13	5.42	8.44	1.21	1.52
2.5	8	3.67	4.29	4.99	5.30	5.78	8.71	1.49	1.59

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
2.6	8	3.90	4.42	5.17	5.53	6.23	8.71	1.82	1.60
2.7	8	3.90	4.84	5.37	5.78	6.23	9.32	1.39	1.66
2.8	8	4.18	4.93	5.88	6.01	6.47	9.32	1.54	1.58
2.9	8	4.18	4.93	6.18	6.28	6.74	10.04	1.81	1.83
3.0	8	4.18	5.12	6.38	6.56	7.37	10.45	2.24	2.00
3.1	8	4.88	5.29	6.53	6.75	7.46	10.45	2.17	1.86
3.2	8	4.88	5.29	6.53	6.82	7.78	10.45	2.49	1.89
3.3	8	4.88	5.29	6.78	6.88	7.78	10.45	2.49	1.91
3.4	8	4.88	5.93	7.53	7.17	7.78	10.45	1.85	1.78
3.5	8	4.88	5.99	7.53	7.20	7.78	10.45	1.79	1.74
3.6	8	4.88	5.99	7.53	7.26	7.78	10.89	1.79	1.86
3.7	8	4.88	5.99	7.53	7.32	7.78	11.37	1.79	1.99
3.8	8	5.16	6.06	7.53	7.46	7.78	11.91	1.72	2.07
3.9	8	5.16	6.06	7.53	7.46	7.78	11.91	1.72	2.07
4.0	8	5.55	6.06	7.53	7.51	7.78	11.91	1.72	2.02
4.1	8	5.55	6.06	7.53	7.51	7.78	11.91	1.72	2.02
4.2	8	6.05	6.44	7.53	7.68	7.78	11.91	1.34	1.86
4.3	8	6.05	6.78	7.53	7.73	7.78	11.91	0.99	1.82
4.4	8	6.05	6.78	7.53	7.73	7.78	11.91	0.99	1.82
4.5	8	6.05	6.78	7.53	7.73	7.78	11.91	0.99	1.82
4.6	8	6.05	7.06	7.65	8.02	7.90	13.14	0.84	2.21
4.7	8	6.05	7.06	7.65	8.08	8.22	13.14	1.17	2.21
4.8	8	6.05	7.06	7.65	8.08	8.22	13.14	1.17	2.21
4.9	8	6.05	7.06	7.65	8.08	8.22	13.14	1.17	2.21
5.0	8	6.05	7.06	7.65	8.17	8.22	13.89	1.17	2.45

Table S6.5: Summary of the inferred inbreeding F_{ROH} on autosomes from the PLINK report (--homozyg --homozyg-kb) for variable minimum ROH length (Mb).

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
0.1	8	0.245	0.250	0.260	0.262	0.271	0.289	0.022	0.015
0.2	8	0.227	0.233	0.243	0.246	0.255	0.274	0.022	0.016
0.3	8	0.201	0.208	0.215	0.219	0.229	0.251	0.022	0.016
0.4	8	0.173	0.180	0.187	0.191	0.200	0.222	0.020	0.016
0.5	8	0.148	0.153	0.158	0.164	0.173	0.196	0.019	0.016
0.6	8	0.120	0.127	0.131	0.137	0.143	0.172	0.016	0.017
0.7	8	0.102	0.106	0.111	0.116	0.121	0.152	0.015	0.016
0.8	8	0.083	0.087	0.094	0.099	0.104	0.135	0.017	0.018
0.9	8	0.071	0.072	0.080	0.085	0.092	0.123	0.020	0.018
1.0	8	0.058	0.064	0.069	0.075	0.082	0.112	0.018	0.018
1.1	8	0.049	0.052	0.058	0.065	0.071	0.106	0.019	0.019
1.2	8	0.039	0.045	0.052	0.058	0.064	0.099	0.018	0.019
1.3	8	0.033	0.042	0.048	0.052	0.057	0.094	0.015	0.019
1.4	8	0.029	0.034	0.041	0.046	0.051	0.086	0.017	0.019
1.5	8	0.024	0.030	0.036	0.042	0.047	0.083	0.017	0.019
1.6	8	0.023	0.028	0.033	0.039	0.043	0.081	0.015	0.019
1.7	8	0.019	0.025	0.030	0.036	0.040	0.079	0.015	0.019
1.8	8	0.017	0.022	0.028	0.033	0.037	0.075	0.015	0.018
1.9	8	0.016	0.020	0.026	0.031	0.034	0.073	0.013	0.018
2.0	8	0.015	0.017	0.025	0.030	0.033	0.073	0.016	0.019

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
2.1	8	0.011	0.016	0.022	0.028	0.032	0.071	0.017	0.019
2.2	8	0.008	0.015	0.022	0.027	0.031	0.071	0.016	0.020
2.3	8	0.008	0.014	0.020	0.025	0.029	0.069	0.015	0.019
2.4	8	0.008	0.012	0.020	0.024	0.028	0.067	0.015	0.019
2.5	8	0.008	0.011	0.020	0.024	0.027	0.067	0.016	0.019
2.6	8	0.007	0.011	0.019	0.023	0.026	0.067	0.016	0.019
2.7	8	0.007	0.009	0.018	0.022	0.026	0.065	0.017	0.019
2.8	8	0.006	0.009	0.016	0.021	0.025	0.065	0.016	0.019
2.9	8	0.006	0.009	0.016	0.021	0.023	0.063	0.014	0.018
3.0	8	0.006	0.008	0.015	0.020	0.023	0.062	0.015	0.018
3.1	8	0.004	0.008	0.015	0.020	0.023	0.062	0.014	0.018
3.2	8	0.004	0.008	0.015	0.020	0.022	0.062	0.014	0.018
3.3	8	0.004	0.008	0.015	0.019	0.022	0.062	0.013	0.018
3.4	8	0.003	0.008	0.015	0.019	0.022	0.062	0.013	0.018
3.5	8	0.003	0.008	0.014	0.019	0.022	0.062	0.013	0.018
3.6	8	0.003	0.008	0.014	0.019	0.022	0.060	0.013	0.018
3.7	8	0.003	0.008	0.014	0.019	0.022	0.059	0.013	0.018
3.8	8	0.003	0.008	0.013	0.018	0.022	0.058	0.014	0.017
3.9	8	0.003	0.008	0.013	0.018	0.022	0.058	0.014	0.017
4.0	8	0.003	0.007	0.013	0.018	0.022	0.058	0.014	0.018
4.1	8	0.003	0.007	0.013	0.018	0.022	0.058	0.014	0.018
4.2	8	0.003	0.007	0.012	0.018	0.022	0.058	0.014	0.018
4.3	8	0.003	0.007	0.011	0.017	0.022	0.058	0.014	0.018
4.4	8	0.003	0.007	0.011	0.017	0.022	0.058	0.014	0.018
4.5	8	0.003	0.007	0.011	0.017	0.022	0.058	0.014	0.018
4.6	8	0.003	0.007	0.010	0.017	0.021	0.055	0.013	0.017
4.7	8	0.003	0.007	0.010	0.016	0.020	0.055	0.013	0.017
4.8	8	0.003	0.007	0.010	0.016	0.020	0.055	0.013	0.017
4.9	8	0.003	0.007	0.010	0.016	0.020	0.055	0.013	0.017
5.0	8	0.003	0.007	0.010	0.016	0.020	0.053	0.013	0.016

Table S6.6: Summary of the inferred relatedness $R_{ROH} = 2xF_{ROH}$ on autosomes from the PLINK report (`--homozyg --homozyg-kb`) for variable minimum ROH length (Mb).

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
0.1	8	0.489	0.500	0.519	0.524	0.543	0.579	0.043	0.030
0.2	8	0.455	0.467	0.485	0.491	0.511	0.547	0.044	0.031
0.3	8	0.403	0.415	0.430	0.439	0.458	0.501	0.043	0.033
0.4	8	0.346	0.360	0.375	0.383	0.401	0.444	0.041	0.033
0.5	8	0.296	0.307	0.316	0.328	0.345	0.391	0.039	0.032
0.6	8	0.241	0.254	0.262	0.273	0.286	0.344	0.031	0.033
0.7	8	0.203	0.211	0.223	0.233	0.242	0.304	0.031	0.033
0.8	8	0.165	0.174	0.189	0.198	0.208	0.271	0.034	0.035
0.9	8	0.141	0.144	0.160	0.171	0.185	0.245	0.041	0.036
1.0	8	0.115	0.128	0.137	0.149	0.163	0.225	0.035	0.036
1.1	8	0.097	0.105	0.117	0.130	0.143	0.213	0.038	0.038
1.2	8	0.078	0.090	0.104	0.115	0.127	0.198	0.037	0.039
1.3	8	0.067	0.083	0.095	0.104	0.114	0.189	0.031	0.039
1.4	8	0.059	0.069	0.081	0.092	0.103	0.173	0.034	0.037
1.5	8	0.048	0.060	0.073	0.084	0.094	0.167	0.034	0.038

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
1.6	8	0.046	0.056	0.066	0.078	0.086	0.162	0.031	0.038
1.7	8	0.038	0.051	0.060	0.072	0.080	0.159	0.029	0.038
1.8	8	0.035	0.045	0.057	0.067	0.074	0.149	0.029	0.037
1.9	8	0.032	0.041	0.053	0.062	0.067	0.145	0.026	0.037
2.0	8	0.029	0.035	0.050	0.059	0.066	0.145	0.032	0.038
2.1	8	0.023	0.031	0.045	0.056	0.064	0.141	0.033	0.038
2.2	8	0.017	0.029	0.044	0.053	0.062	0.141	0.032	0.039
2.3	8	0.017	0.028	0.041	0.051	0.057	0.138	0.030	0.038
2.4	8	0.015	0.025	0.039	0.049	0.056	0.135	0.031	0.038
2.5	8	0.015	0.022	0.039	0.048	0.055	0.133	0.033	0.038
2.6	8	0.014	0.021	0.037	0.046	0.053	0.133	0.031	0.038
2.7	8	0.014	0.018	0.035	0.044	0.052	0.129	0.034	0.038
2.8	8	0.012	0.018	0.033	0.043	0.050	0.129	0.032	0.038
2.9	8	0.012	0.018	0.032	0.041	0.046	0.125	0.029	0.037
3.0	8	0.012	0.017	0.031	0.040	0.046	0.123	0.029	0.036
3.1	8	0.007	0.017	0.031	0.040	0.045	0.123	0.029	0.037
3.2	8	0.007	0.017	0.031	0.039	0.044	0.123	0.027	0.037
3.3	8	0.007	0.017	0.031	0.039	0.043	0.123	0.026	0.036
3.4	8	0.005	0.017	0.029	0.038	0.043	0.123	0.026	0.037
3.5	8	0.005	0.017	0.028	0.038	0.043	0.123	0.026	0.037
3.6	8	0.005	0.017	0.028	0.038	0.043	0.121	0.026	0.036
3.7	8	0.005	0.017	0.028	0.037	0.043	0.118	0.026	0.035
3.8	8	0.005	0.016	0.027	0.036	0.043	0.116	0.028	0.035
3.9	8	0.005	0.016	0.027	0.036	0.043	0.116	0.028	0.035
4.0	8	0.005	0.015	0.027	0.036	0.043	0.116	0.028	0.035
4.1	8	0.005	0.015	0.027	0.036	0.043	0.116	0.028	0.035
4.2	8	0.005	0.014	0.024	0.035	0.043	0.116	0.029	0.036
4.3	8	0.005	0.014	0.023	0.035	0.043	0.116	0.029	0.036
4.4	8	0.005	0.014	0.023	0.035	0.043	0.116	0.029	0.036
4.5	8	0.005	0.014	0.023	0.035	0.043	0.116	0.029	0.036
4.6	8	0.005	0.014	0.021	0.033	0.041	0.109	0.027	0.034
4.7	8	0.005	0.014	0.021	0.033	0.040	0.109	0.026	0.034
4.8	8	0.005	0.014	0.021	0.033	0.040	0.109	0.026	0.034
4.9	8	0.005	0.014	0.021	0.033	0.040	0.109	0.026	0.034
5.0	8	0.005	0.014	0.021	0.032	0.040	0.106	0.026	0.032

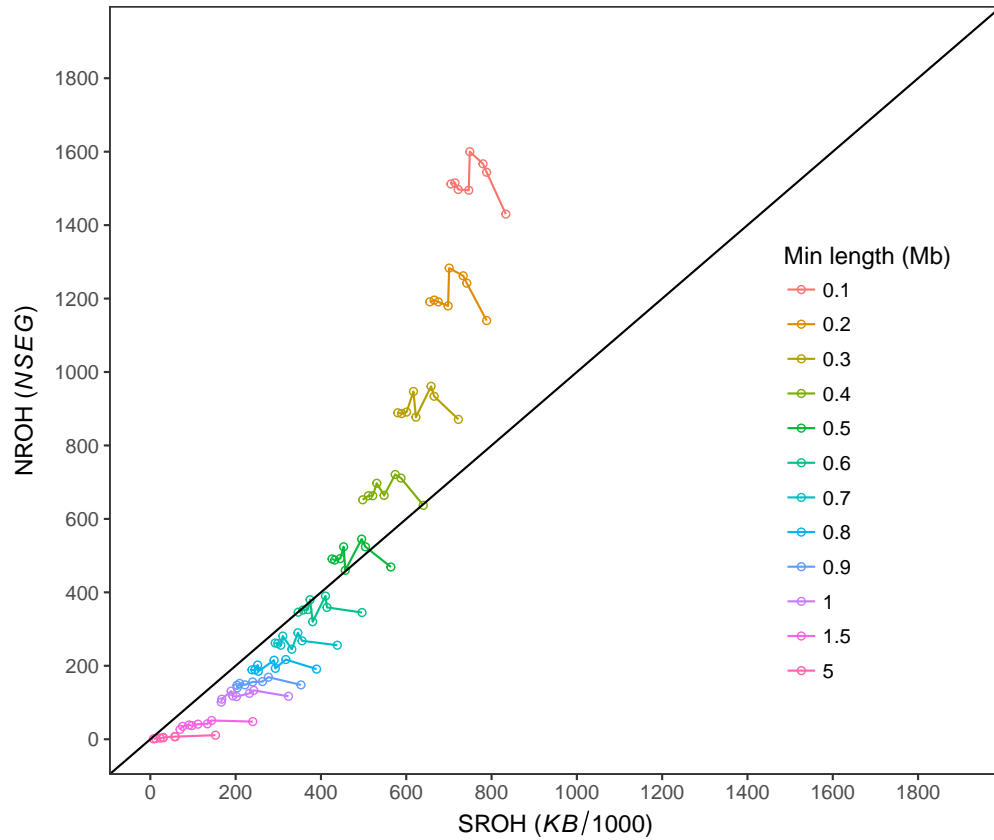


Figure S6.1: Plot of the number of runs of homozygosity NROH (*NSEQ*) against the total length of runs SROH (*KB/1000*) in the PLINK report for a subset of the variable minimum *ROH* lengths 0.1 – 5Mb. NROH dominates over SROH with all points above the diagonal, until the minimum length increases to 0.5 – 0.6Mb, where the population seems bottlenecked with most points close to or at the diagonal. For minimum lengths above 0.6Mb, the population seems bottlenecked and consanguineous with most points below and right shifted from the diagonal.

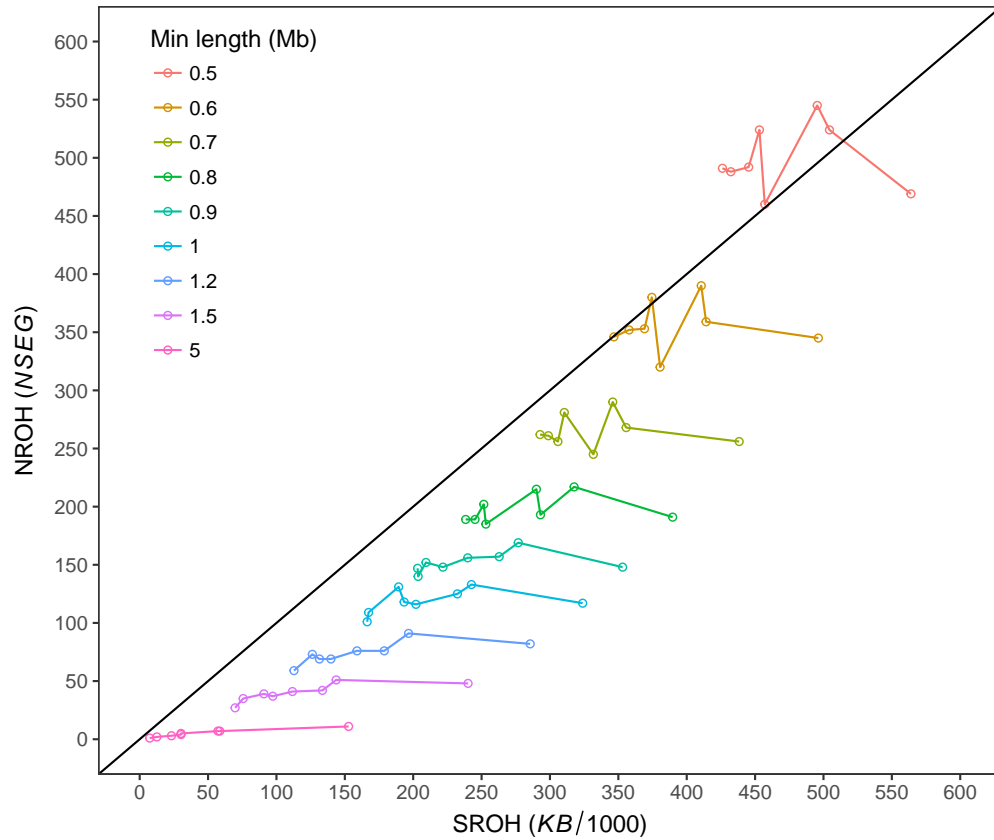


Figure S6.2: Plot of the number of runs of homozygosity $NROH$ ($NSEQ$) against the total length of runs $SROH$ ($KB/1000$) in the PLINK report for a subset 0.5 – 5Mb of the variable minimum ROH lengths. At 0.6Mb minimum length the population seems bottlenecked with most points close to or at the diagonal. 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.

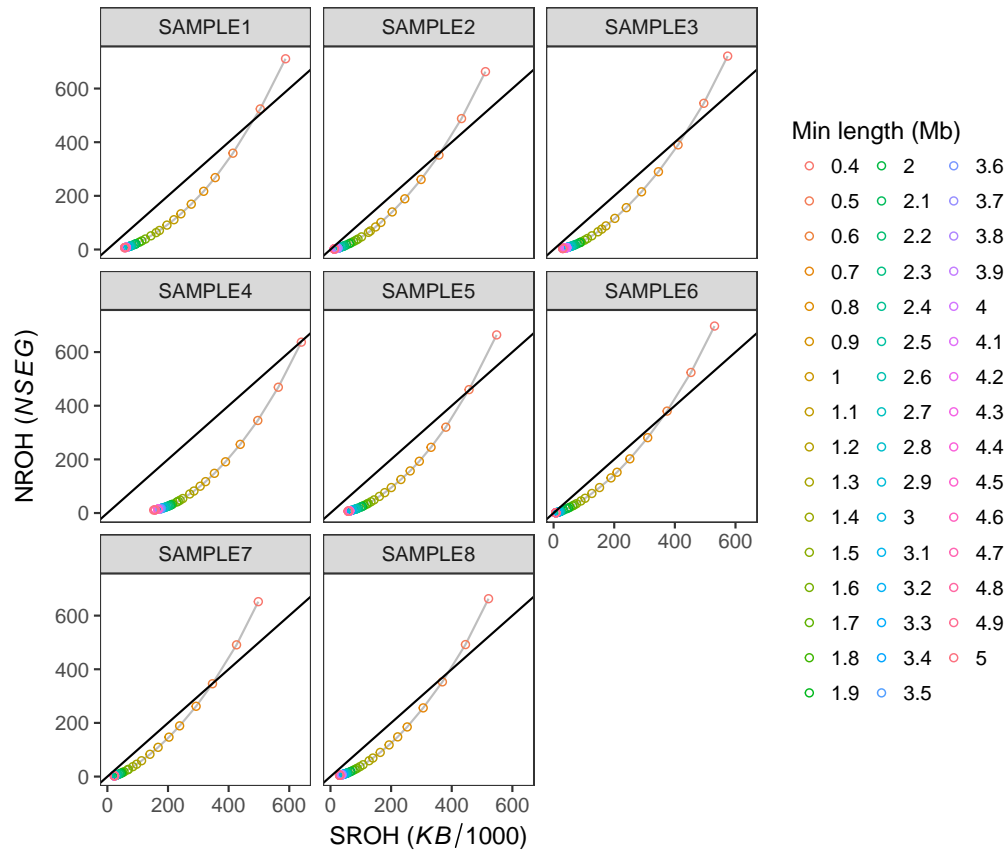


Figure S6.3: Plots of the number of runs of homozygosity NROH (*NSEQ*) against the total length of runs SROH (*KB/1000*) in the PLINK report for the minimum lengths of *ROH* > 0.3Mb. At about 1.0Mb the points are maximum shifted to the right from the diagonal.

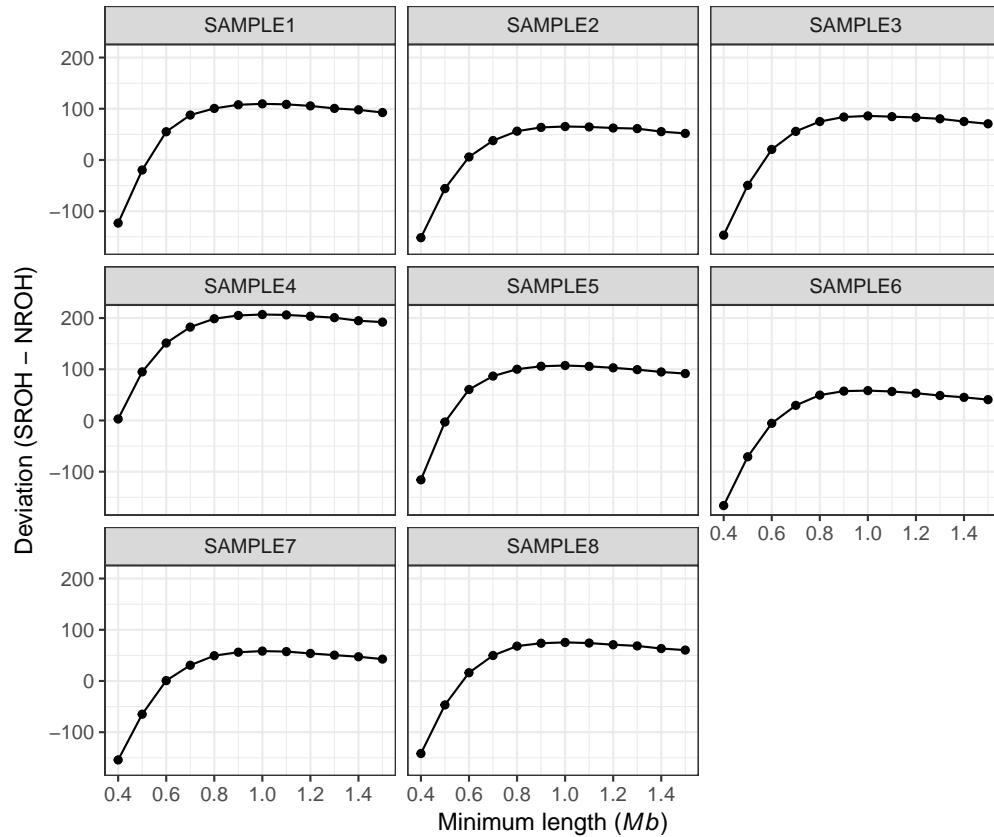


Figure S6.4: Plots of deviation $SROH (KB/1000) - NROH (NSEQ)$ from the linear diagonal in the $NROH$ versus $SROH$ plots shown for minimum ROH lengths between 0.4 and 1.5Mb. For all the samples the $SROH$ is clearly below the diagonal (deviation > 0) for minimum ROH lengths above 0.7 – 0.8Mb and the maximum deviation is found at 1.0Mb.

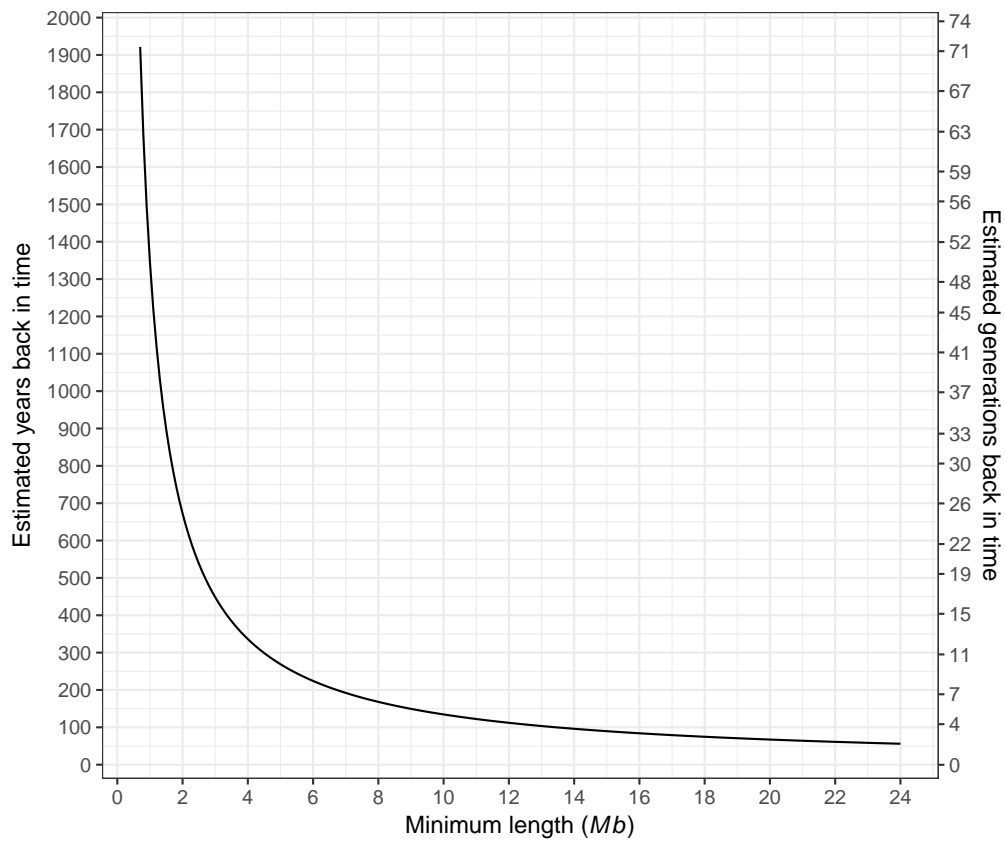


Figure S6.5: Plot of the estimated years back in time (left y-axis) and generations back in time (right y-axis) inferred from the minimum lengths of $ROH > 0.6\text{Mb}$. At 1Mb the estimate is 1345 years back and 50 generations back in time.

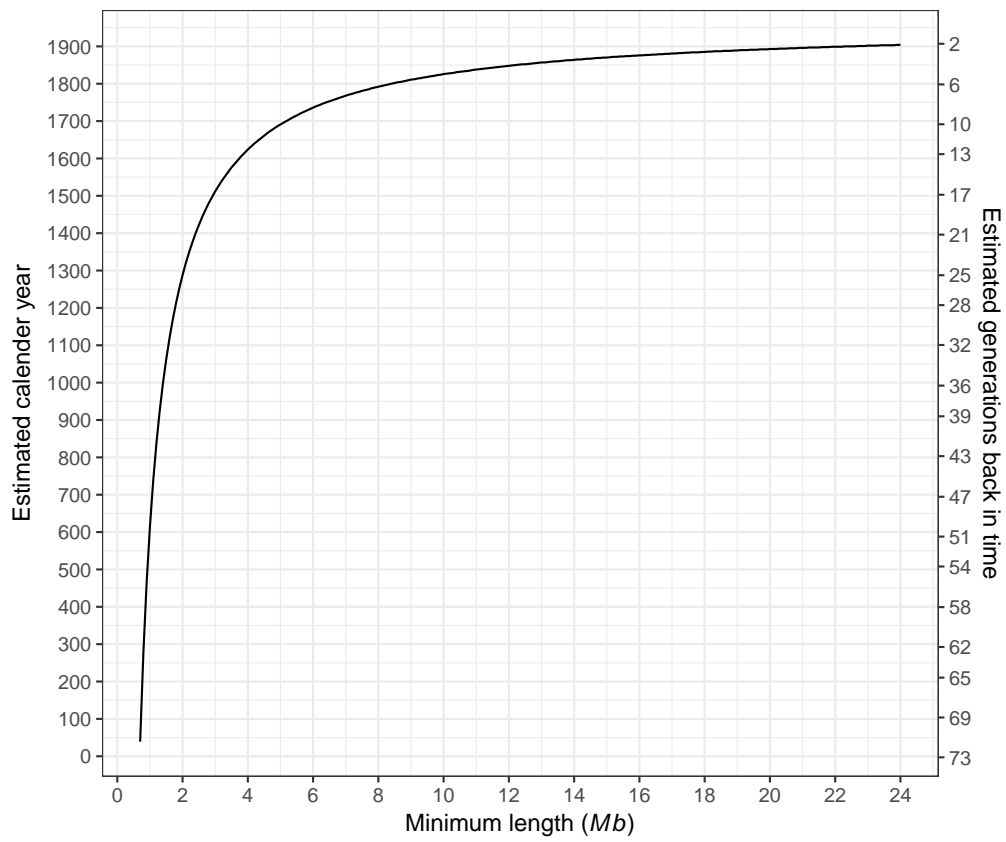


Figure S6.6: Plot of the estimated calendar year (left y-axis) and generations back in time (right y-axis) since 1960 inferred from the minimum lengths of $ROH > 0.6\text{Mb}$. At 1Mb the estimated calendar year is 615.

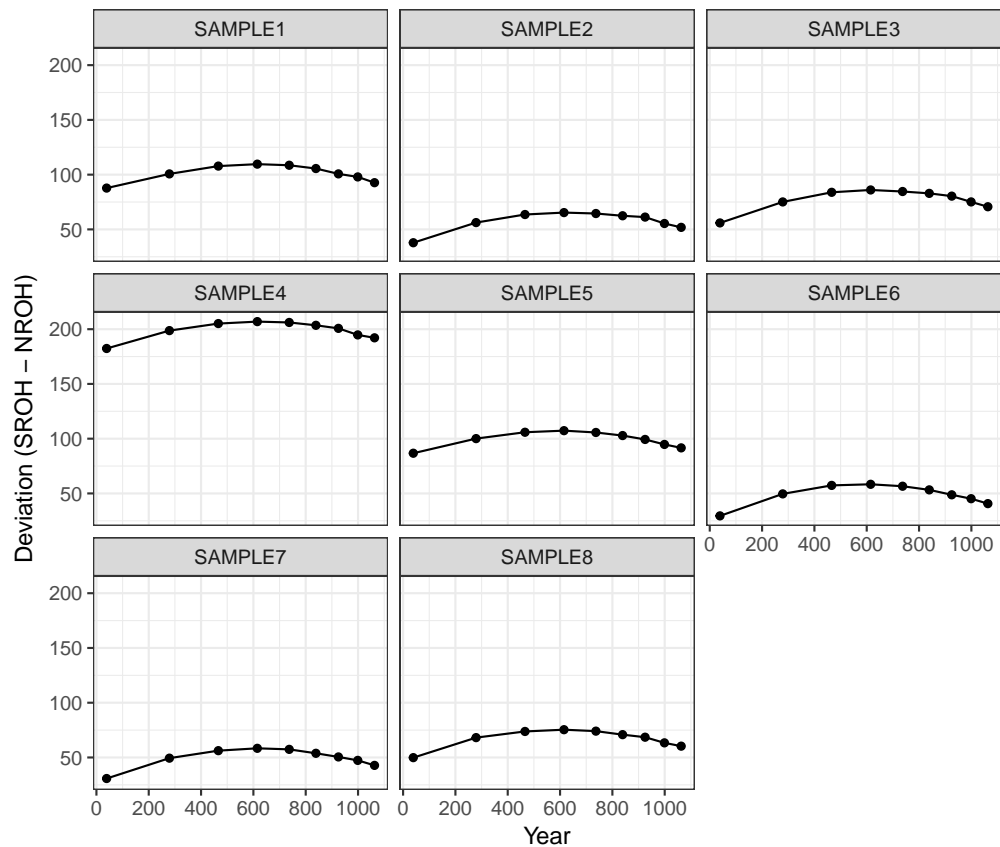


Figure S6.7: Plots of deviation $SROH$ ($KB/1000$) – $NROH$ ($NSEQ$) from the linear diagonal in the $NROH$ versus $SROH$ plots shown for minimum ROH lengths between 0.7 and 1.5Mb, transformed to the corresponding estimated time in years. The maximum deviation for all samples is found at 1.0Mb corresponding to year 615.

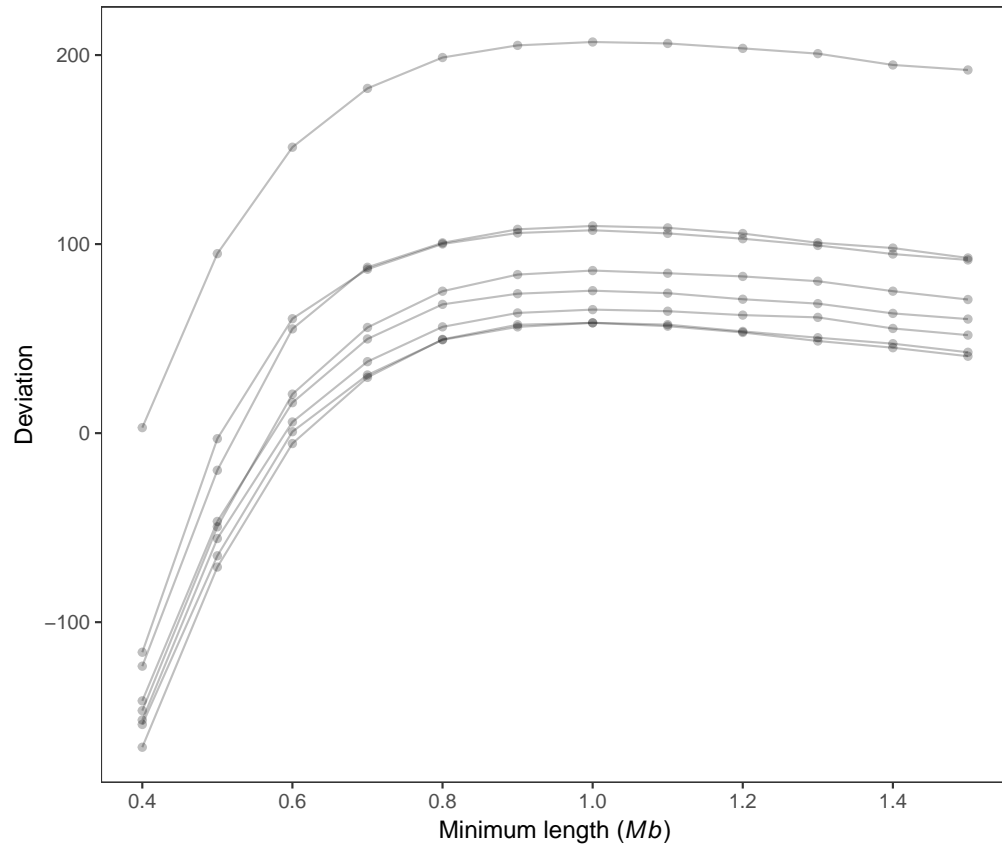


Figure S6.8: Plot of deviation $SROH (KB/1000) - NROH (NSEQ)$ from the linear diagonal in the $NROH$ versus $SROH$ plots shown for minimum ROH lengths between 0.4 and 1.5Mb. For all the samples the $SROH$ is clearly below the diagonal (deviation > 0) for minimum ROH lengths above 0.7 – 0.8Mb and the maximum deviation is found at 1.0Mb.

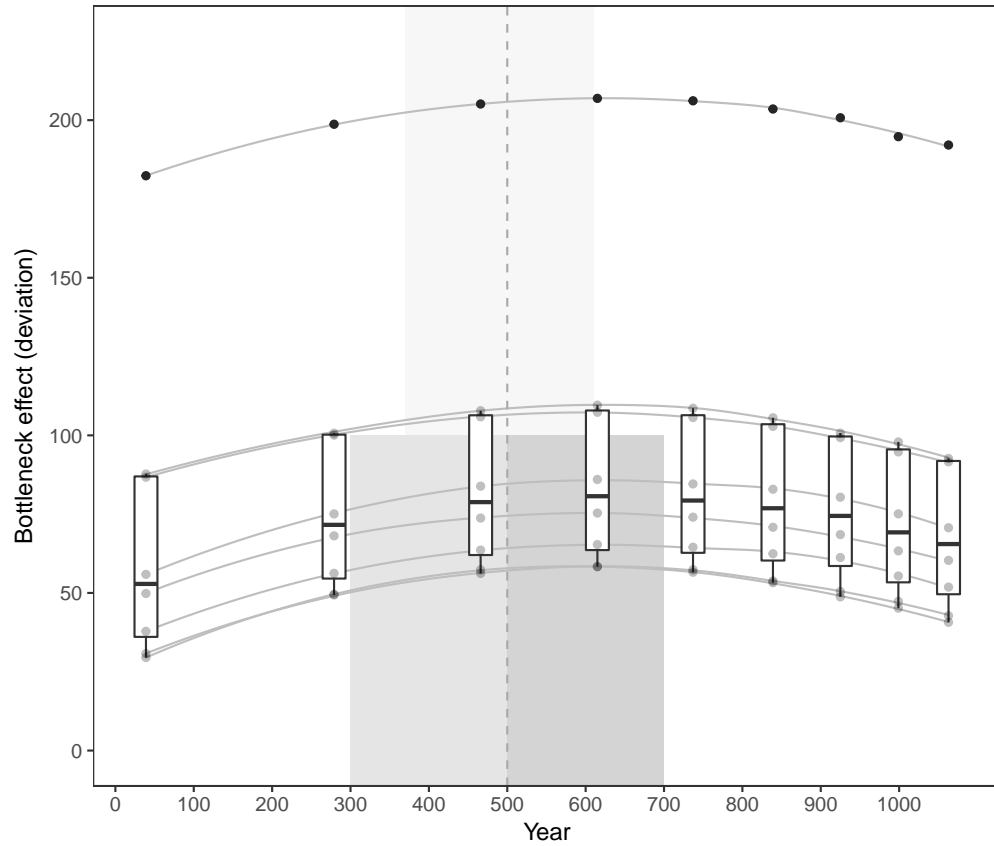


Figure S6.9: Plot of deviation from the linear diagonal in the NROH versus SROH plots shown for minimum *ROH* lengths between 0.7 and 1.5Mb, transformed to the corresponding estimated time in years. The maximum deviation for all samples is found at 1.0Mb corresponding to year 615. The three shaded rectangles 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).