

# Additional file 2 - Supplementary tables and figures of *ROH*

Table S2.1: Filter (`bcftools filter -i`) used to filter the SNP files before further processing with PLINK.

Autosome files	Filter-text
SNP VCFs	QUAL>30

Table S2.2: 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	1602	1622.8	1655.5	1666.1	1715.0	1737	92.2	55.2
0.2	8	1215	1241.5	1258.0	1273.6	1316.0	1340	74.5	46.0
0.3	7	891	891.8	906.0	920.6	945.5	985	53.8	35.0
0.4	8	630	642.8	661.0	664.1	674.2	723	31.5	30.3
0.5	8	454	458.2	474.0	478.4	486.0	526	27.8	25.2
0.6	8	310	323.5	342.0	338.1	350.5	365	27.0	19.2
0.7	7	229	235.0	248.5	247.1	254.2	272	19.2	14.6
0.8	8	170	176.2	179.0	182.9	189.0	200	12.8	11.0
0.9	7	124	128.8	133.5	136.6	144.0	157	15.2	10.9
1.0	6	95	100.0	103.5	106.1	110.0	123	10.0	9.4
1.1	8	63	76.2	78.5	81.4	84.8	101	8.5	12.7
1.2	8	40	59.8	62.5	64.5	69.8	85	10.0	13.9
1.3	8	30	47.5	52.5	53.1	60.2	71	12.8	12.8
1.4	6	24	40.5	41.0	43.2	46.5	60	6.0	11.2
1.5	6	19	32.5	33.5	35.5	37.2	53	4.8	10.3
1.6	7	17	26.5	28.5	30.0	32.2	47	5.8	8.8
1.7	7	13	23.5	25.0	26.4	28.5	44	5.0	8.7
1.8	8	12	17.5	20.5	21.5	23.0	37	5.5	7.5
1.9	7	12	14.2	17.5	19.0	20.8	35	6.5	7.5
2.0	7	7	12.5	14.5	16.8	19.8	33	7.2	8.0
2.1	8	6	8.8	13.5	14.6	18.2	30	9.5	7.7
2.2	7	5	7.8	13.0	13.9	17.2	30	9.5	8.0
2.3	7	4	7.8	12.0	13.1	17.0	28	9.2	7.6
2.4	8	4	6.8	10.0	11.9	15.2	27	8.5	7.4
2.5	7	4	6.8	8.5	11.1	13.0	27	6.2	7.5
2.6	7	4	6.5	8.0	10.6	12.0	27	5.5	7.5
2.7	7	4	5.8	7.5	10.0	11.8	25	6.0	6.9
2.8	6	4	4.0	7.5	9.4	11.5	24	7.5	6.8
2.9	6	4	4.0	7.0	8.6	9.8	22	5.8	6.1
3.0	6	3	4.0	7.0	8.1	8.5	22	4.5	6.1
3.1	8	2	3.8	6.5	7.6	8.5	21	4.8	6.0
3.2	8	1	3.8	6.0	7.2	8.2	21	4.5	6.2
3.3	8	1	3.8	5.5	7.1	8.2	21	4.5	6.2
3.4	7	1	3.8	5.0	6.6	7.5	19	3.8	5.6
3.5	7	1	3.8	5.0	6.6	7.5	19	3.8	5.6

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
3.6	7	1	3.8	5.0	6.4	7.5	17	3.8	5.0
3.7	7	1	3.8	4.5	5.8	6.5	15	2.8	4.3
3.8	7	1	3.0	4.5	5.6	6.5	15	3.5	4.3
3.9	6	1	3.0	4.0	5.5	6.5	15	3.5	4.4
4.0	6	1	3.0	4.0	5.5	6.5	15	3.5	4.4
4.1	7	1	2.8	4.0	5.4	6.5	15	3.8	4.5
4.2	6	0	2.0	4.0	5.0	6.5	14	4.5	4.4
4.3	6	0	2.0	4.0	4.9	6.5	13	4.5	4.1
4.4	6	0	2.0	4.0	4.9	6.5	13	4.5	4.1
4.5	6	0	2.0	4.0	4.9	6.5	13	4.5	4.1
4.6	6	0	2.0	4.0	4.8	6.2	13	4.2	4.0
4.7	6	0	2.0	4.0	4.8	6.2	13	4.2	4.0
4.8	6	0	2.0	4.0	4.6	5.5	13	3.5	4.0
4.9	6	0	2.0	4.0	4.6	5.5	13	3.5	4.0
5.0	7	0	2.0	3.5	4.4	5.5	12	3.5	3.7

Table S2.3: 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	699.4	725.6	744.3	756.0	784.9	838.5	59.4	44.9
0.2	8	638.7	667.6	684.9	696.4	724.9	779.9	57.2	45.3
0.3	8	552.0	580.3	597.7	609.1	635.5	700.3	55.2	47.4
0.4	8	461.3	488.3	511.0	519.7	544.4	610.5	56.1	47.4
0.5	8	385.2	403.4	422.3	436.6	457.8	538.7	54.4	49.5
0.6	8	312.5	327.2	347.6	360.0	370.8	472.8	43.5	50.9
0.7	8	252.0	271.7	289.0	301.1	310.3	409.9	38.6	49.0
0.8	8	205.7	222.7	241.1	253.2	266.3	355.9	43.5	48.3
0.9	8	167.0	183.5	199.5	214.0	228.0	320.2	44.5	49.7
1.0	8	139.8	158.0	163.1	185.1	200.6	293.7	42.6	49.6
1.1	8	106.6	133.4	140.1	159.2	172.1	275.9	38.7	53.5
1.2	8	80.1	113.0	124.4	139.8	151.7	259.9	38.7	55.0
1.3	8	67.5	101.5	112.5	125.6	135.2	242.3	33.7	53.2
1.4	8	59.3	86.7	93.0	112.3	126.7	227.4	40.0	52.2
1.5	8	52.0	76.1	82.3	101.1	112.2	217.2	36.1	51.6
1.6	8	48.9	65.7	74.6	92.6	103.2	207.9	37.5	50.7
1.7	8	42.4	63.0	67.3	86.6	94.5	203.0	31.5	50.8
1.8	8	38.7	52.2	61.1	78.1	86.7	190.7	34.5	49.3
1.9	8	31.3	48.0	55.6	73.5	81.7	186.9	33.7	49.6
2.0	8	29.4	39.7	51.7	69.1	79.7	183.1	40.0	50.3
2.1	8	23.2	36.2	47.5	64.8	74.6	177.0	38.3	49.8
2.2	8	21.1	34.0	46.4	63.2	72.4	177.0	38.4	50.4
2.3	8	21.1	33.5	44.2	61.5	70.7	172.5	37.2	49.4
2.4	8	18.7	31.2	39.8	58.5	66.6	170.2	35.4	49.4
2.5	8	18.7	27.5	38.6	56.7	61.1	170.2	33.6	49.8
2.6	8	16.2	27.5	37.3	55.4	58.6	170.2	31.1	50.1
2.7	8	16.2	25.5	36.0	53.8	57.9	165.0	32.4	48.6
2.8	8	13.4	23.4	36.0	52.0	57.2	162.2	33.8	48.3
2.9	8	13.4	23.4	34.5	49.9	52.2	156.5	28.8	46.4
3.0	8	13.4	21.2	34.5	48.4	48.6	156.5	27.4	46.4

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
3.1	8	7.3	21.2	34.5	46.9	46.3	153.5	25.1	46.1
3.2	8	4.2	21.2	33.0	45.7	45.5	153.5	24.3	46.5
3.3	8	4.2	21.2	33.0	45.3	43.1	153.5	21.9	46.6
3.4	8	4.2	21.2	29.6	43.7	43.0	146.8	21.8	44.7
3.5	8	4.2	21.2	29.6	43.7	43.0	146.8	21.8	44.7
3.6	8	4.2	21.2	29.6	42.8	43.0	139.7	21.8	42.3
3.7	8	4.2	21.2	26.0	40.5	42.1	132.4	20.9	40.0
3.8	8	4.2	20.3	26.0	40.0	42.1	132.4	21.9	40.3
3.9	8	4.2	20.3	24.0	39.5	42.1	132.4	21.9	40.5
4.0	8	4.2	20.3	24.0	39.5	42.1	132.4	21.9	40.5
4.1	8	4.2	17.2	24.0	39.0	42.1	132.4	24.9	40.8
4.2	8	0.0	16.2	24.0	37.5	42.1	128.2	25.9	40.3
4.3	8	0.0	16.2	24.0	36.9	42.1	124.0	25.9	39.0
4.4	8	0.0	16.2	24.0	36.9	42.1	124.0	25.9	39.0
4.5	8	0.0	16.2	24.0	36.9	42.1	124.0	25.9	39.0
4.6	8	0.0	16.2	24.0	36.4	41.0	124.0	24.8	38.7
4.7	8	0.0	16.2	24.0	36.4	41.0	124.0	24.8	38.7
4.8	8	0.0	16.2	24.0	35.8	37.4	124.0	21.2	38.7
4.9	8	0.0	16.2	24.0	35.8	37.4	124.0	21.2	38.7
5.0	8	0.0	16.2	21.5	34.5	37.4	119.0	21.2	37.3

Table S2.4: 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	0.43	0.43	0.45	0.45	0.46	0.52	0.03	0.03
0.2	8	0.51	0.52	0.54	0.55	0.56	0.64	0.03	0.04
0.3	8	0.62	0.63	0.64	0.66	0.67	0.79	0.04	0.05
0.4	8	0.73	0.75	0.75	0.78	0.79	0.96	0.04	0.08
0.5	8	0.84	0.86	0.88	0.91	0.93	1.13	0.07	0.10
0.6	8	0.96	0.99	1.01	1.06	1.10	1.33	0.11	0.12
0.7	8	1.07	1.12	1.15	1.22	1.27	1.59	0.15	0.17
0.8	8	1.21	1.26	1.30	1.38	1.41	1.91	0.15	0.23
0.9	8	1.35	1.42	1.45	1.56	1.57	2.22	0.16	0.29
1.0	8	1.43	1.56	1.63	1.73	1.74	2.53	0.18	0.35
1.1	8	1.60	1.72	1.80	1.92	1.92	2.79	0.20	0.38
1.2	8	1.72	1.93	1.99	2.12	2.12	3.06	0.20	0.43
1.3	8	1.84	2.03	2.16	2.32	2.37	3.41	0.34	0.52
1.4	8	1.91	2.27	2.34	2.53	2.58	3.79	0.31	0.58
1.5	8	2.02	2.40	2.59	2.77	2.89	4.10	0.48	0.66
1.6	8	2.12	2.66	2.82	2.96	3.02	4.42	0.36	0.70
1.7	8	2.19	2.73	3.07	3.15	3.36	4.61	0.63	0.74
1.8	8	2.42	3.05	3.21	3.43	3.58	5.15	0.53	0.86
1.9	8	2.61	3.26	3.38	3.61	3.70	5.34	0.44	0.86
2.0	8	2.67	3.47	3.57	3.89	4.45	5.55	0.98	0.90
2.1	8	2.91	3.62	4.03	4.17	4.70	5.90	1.08	0.96
2.2	8	3.01	3.71	4.21	4.33	4.95	5.90	1.24	1.01
2.3	8	3.01	3.76	4.25	4.49	5.14	6.16	1.38	1.16
2.4	8	3.12	4.03	4.52	4.67	5.26	6.30	1.23	1.12
2.5	8	3.12	4.24	4.73	4.79	5.26	6.30	1.02	1.05

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
2.6	8	3.24	4.38	4.82	4.87	5.38	6.30	0.99	1.01
2.7	8	3.24	4.44	5.01	5.01	5.51	6.60	1.07	1.06
2.8	8	3.36	4.70	5.18	5.17	5.66	6.76	0.96	1.03
2.9	8	3.36	5.00	5.22	5.32	5.82	7.11	0.83	1.09
3.0	8	3.36	5.00	5.37	5.55	6.50	7.15	1.50	1.28
3.1	8	3.67	5.00	5.54	5.66	6.51	7.31	1.51	1.24
3.2	8	4.16	5.00	5.75	5.82	6.76	7.31	1.77	1.15
3.3	8	4.16	5.00	5.97	5.87	6.76	7.31	1.77	1.16
3.4	8	4.16	5.04	6.26	6.02	6.76	7.73	1.72	1.21
3.5	8	4.16	5.04	6.26	6.02	6.76	7.73	1.72	1.21
3.6	8	4.16	5.04	6.26	6.08	6.76	8.22	1.72	1.32
3.7	8	4.16	5.30	6.26	6.27	7.04	8.83	1.74	1.44
3.8	8	4.16	5.50	6.26	6.32	7.04	8.83	1.54	1.39
3.9	8	4.16	5.69	6.26	6.37	7.04	8.83	1.35	1.36
4.0	8	4.16	5.69	6.26	6.37	7.04	8.83	1.35	1.36
4.1	8	4.16	5.69	6.26	6.56	7.43	8.83	1.74	1.58
4.2	8	0.00	6.12	6.27	6.17	7.43	9.16	1.31	2.79
4.3	8	0.00	6.12	6.27	6.22	7.43	9.54	1.31	2.85
4.4	8	0.00	6.12	6.27	6.22	7.43	9.54	1.31	2.85
4.5	8	0.00	6.12	6.27	6.22	7.43	9.54	1.31	2.85
4.6	8	0.00	6.12	6.27	6.26	7.69	9.54	1.58	2.86
4.7	8	0.00	6.12	6.27	6.26	7.69	9.54	1.58	2.86
4.8	8	0.00	6.13	6.41	6.30	7.69	9.54	1.57	2.86
4.9	8	0.00	6.13	6.41	6.30	7.69	9.54	1.57	2.86
5.0	8	0.00	6.19	6.41	6.38	7.69	9.92	1.50	2.92

Table S2.5: 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	0.243	0.252	0.258	0.262	0.272	0.291	0.021	0.016
0.2	8	0.222	0.232	0.238	0.242	0.252	0.271	0.020	0.016
0.3	8	0.192	0.201	0.207	0.211	0.221	0.243	0.019	0.016
0.4	8	0.160	0.169	0.177	0.180	0.189	0.212	0.019	0.016
0.5	8	0.134	0.140	0.147	0.152	0.159	0.187	0.019	0.017
0.6	8	0.108	0.114	0.121	0.125	0.129	0.164	0.015	0.018
0.7	8	0.087	0.094	0.100	0.105	0.108	0.142	0.013	0.017
0.8	8	0.071	0.077	0.084	0.088	0.092	0.124	0.015	0.017
0.9	8	0.058	0.064	0.069	0.074	0.079	0.111	0.015	0.017
1.0	8	0.049	0.055	0.057	0.064	0.070	0.102	0.015	0.017
1.1	8	0.037	0.046	0.049	0.055	0.060	0.096	0.013	0.019
1.2	8	0.028	0.039	0.043	0.049	0.053	0.090	0.013	0.019
1.3	8	0.023	0.035	0.039	0.044	0.047	0.084	0.012	0.018
1.4	8	0.021	0.030	0.032	0.039	0.044	0.079	0.014	0.018
1.5	8	0.018	0.026	0.029	0.035	0.039	0.075	0.013	0.018
1.6	8	0.017	0.023	0.026	0.032	0.036	0.072	0.013	0.018
1.7	8	0.015	0.022	0.023	0.030	0.033	0.070	0.011	0.018
1.8	8	0.013	0.018	0.021	0.027	0.030	0.066	0.012	0.017
1.9	8	0.011	0.017	0.019	0.026	0.028	0.065	0.012	0.017
2.0	8	0.010	0.014	0.018	0.024	0.028	0.064	0.014	0.017

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
2.1	8	0.008	0.013	0.016	0.022	0.026	0.061	0.013	0.017
2.2	8	0.007	0.012	0.016	0.022	0.025	0.061	0.013	0.017
2.3	8	0.007	0.012	0.015	0.021	0.025	0.060	0.013	0.017
2.4	8	0.006	0.011	0.014	0.020	0.023	0.059	0.012	0.017
2.5	8	0.006	0.010	0.013	0.020	0.021	0.059	0.012	0.017
2.6	8	0.006	0.010	0.013	0.019	0.020	0.059	0.011	0.017
2.7	8	0.006	0.009	0.012	0.019	0.020	0.057	0.011	0.017
2.8	8	0.005	0.008	0.012	0.018	0.020	0.056	0.012	0.017
2.9	8	0.005	0.008	0.012	0.017	0.018	0.054	0.010	0.016
3.0	8	0.005	0.007	0.012	0.017	0.017	0.054	0.009	0.016
3.1	8	0.003	0.007	0.012	0.016	0.016	0.053	0.009	0.016
3.2	8	0.001	0.007	0.011	0.016	0.016	0.053	0.008	0.016
3.3	8	0.001	0.007	0.011	0.016	0.015	0.053	0.008	0.016
3.4	8	0.001	0.007	0.010	0.015	0.015	0.051	0.008	0.015
3.5	8	0.001	0.007	0.010	0.015	0.015	0.051	0.008	0.015
3.6	8	0.001	0.007	0.010	0.015	0.015	0.049	0.008	0.015
3.7	8	0.001	0.007	0.009	0.014	0.015	0.046	0.007	0.014
3.8	8	0.001	0.007	0.009	0.014	0.015	0.046	0.008	0.014
3.9	8	0.001	0.007	0.008	0.014	0.015	0.046	0.008	0.014
4.0	8	0.001	0.007	0.008	0.014	0.015	0.046	0.008	0.014
4.1	8	0.001	0.006	0.008	0.014	0.015	0.046	0.009	0.014
4.2	8	0.000	0.006	0.008	0.013	0.015	0.045	0.009	0.014
4.3	8	0.000	0.006	0.008	0.013	0.015	0.043	0.009	0.014
4.4	8	0.000	0.006	0.008	0.013	0.015	0.043	0.009	0.014
4.5	8	0.000	0.006	0.008	0.013	0.015	0.043	0.009	0.014
4.6	8	0.000	0.006	0.008	0.013	0.014	0.043	0.009	0.013
4.7	8	0.000	0.006	0.008	0.013	0.014	0.043	0.009	0.013
4.8	8	0.000	0.006	0.008	0.012	0.013	0.043	0.007	0.013
4.9	8	0.000	0.006	0.008	0.012	0.013	0.043	0.007	0.013
5.0	8	0.000	0.006	0.007	0.012	0.013	0.041	0.007	0.013

Table S2.6: 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	0.486	0.504	0.517	0.525	0.545	0.582	0.041	0.031
0.2	8	0.443	0.463	0.475	0.483	0.503	0.541	0.040	0.031
0.3	8	0.383	0.403	0.415	0.423	0.441	0.486	0.038	0.033
0.4	8	0.320	0.339	0.355	0.361	0.378	0.424	0.039	0.033
0.5	8	0.267	0.280	0.293	0.303	0.318	0.374	0.038	0.034
0.6	8	0.217	0.227	0.241	0.250	0.257	0.328	0.030	0.035
0.7	8	0.175	0.189	0.201	0.209	0.215	0.285	0.027	0.034
0.8	8	0.143	0.155	0.167	0.176	0.185	0.247	0.030	0.034
0.9	8	0.116	0.127	0.139	0.149	0.158	0.222	0.031	0.035
1.0	8	0.097	0.110	0.113	0.128	0.139	0.204	0.030	0.034
1.1	8	0.074	0.093	0.097	0.111	0.119	0.192	0.027	0.037
1.2	8	0.056	0.078	0.086	0.097	0.105	0.180	0.027	0.038
1.3	8	0.047	0.070	0.078	0.087	0.094	0.168	0.023	0.037
1.4	8	0.041	0.060	0.065	0.078	0.088	0.158	0.028	0.036
1.5	8	0.036	0.053	0.057	0.070	0.078	0.151	0.025	0.036

Mb	distinct	min	q1	med	mean	q3	max	iqr	sd
1.6	8	0.034	0.046	0.052	0.064	0.072	0.144	0.026	0.035
1.7	8	0.029	0.044	0.047	0.060	0.066	0.141	0.022	0.035
1.8	8	0.027	0.036	0.042	0.054	0.060	0.132	0.024	0.034
1.9	8	0.022	0.033	0.039	0.051	0.057	0.130	0.023	0.034
2.0	8	0.020	0.028	0.036	0.048	0.055	0.127	0.028	0.035
2.1	8	0.016	0.025	0.033	0.045	0.052	0.123	0.027	0.035
2.2	8	0.015	0.024	0.032	0.044	0.050	0.123	0.027	0.035
2.3	8	0.015	0.023	0.031	0.043	0.049	0.120	0.026	0.034
2.4	8	0.013	0.022	0.028	0.041	0.046	0.118	0.025	0.034
2.5	8	0.013	0.019	0.027	0.039	0.042	0.118	0.023	0.035
2.6	8	0.011	0.019	0.026	0.038	0.041	0.118	0.022	0.035
2.7	8	0.011	0.018	0.025	0.037	0.040	0.115	0.023	0.034
2.8	8	0.009	0.016	0.025	0.036	0.040	0.113	0.023	0.034
2.9	8	0.009	0.016	0.024	0.035	0.036	0.109	0.020	0.032
3.0	8	0.009	0.015	0.024	0.034	0.034	0.109	0.019	0.032
3.1	8	0.005	0.015	0.024	0.033	0.032	0.107	0.017	0.032
3.2	8	0.003	0.015	0.023	0.032	0.032	0.107	0.017	0.032
3.3	8	0.003	0.015	0.023	0.031	0.030	0.107	0.015	0.032
3.4	8	0.003	0.015	0.021	0.030	0.030	0.102	0.015	0.031
3.5	8	0.003	0.015	0.021	0.030	0.030	0.102	0.015	0.031
3.6	8	0.003	0.015	0.021	0.030	0.030	0.097	0.015	0.029
3.7	8	0.003	0.015	0.018	0.028	0.029	0.092	0.015	0.028
3.8	8	0.003	0.014	0.018	0.028	0.029	0.092	0.015	0.028
3.9	8	0.003	0.014	0.017	0.027	0.029	0.092	0.015	0.028
4.0	8	0.003	0.014	0.017	0.027	0.029	0.092	0.015	0.028
4.1	8	0.003	0.012	0.017	0.027	0.029	0.092	0.017	0.028
4.2	8	0.000	0.011	0.017	0.026	0.029	0.089	0.018	0.028
4.3	8	0.000	0.011	0.017	0.026	0.029	0.086	0.018	0.027
4.4	8	0.000	0.011	0.017	0.026	0.029	0.086	0.018	0.027
4.5	8	0.000	0.011	0.017	0.026	0.029	0.086	0.018	0.027
4.6	8	0.000	0.011	0.017	0.025	0.028	0.086	0.017	0.027
4.7	8	0.000	0.011	0.017	0.025	0.028	0.086	0.017	0.027
4.8	8	0.000	0.011	0.017	0.025	0.026	0.086	0.015	0.027
4.9	8	0.000	0.011	0.017	0.025	0.026	0.086	0.015	0.027
5.0	8	0.000	0.011	0.015	0.024	0.026	0.083	0.015	0.026

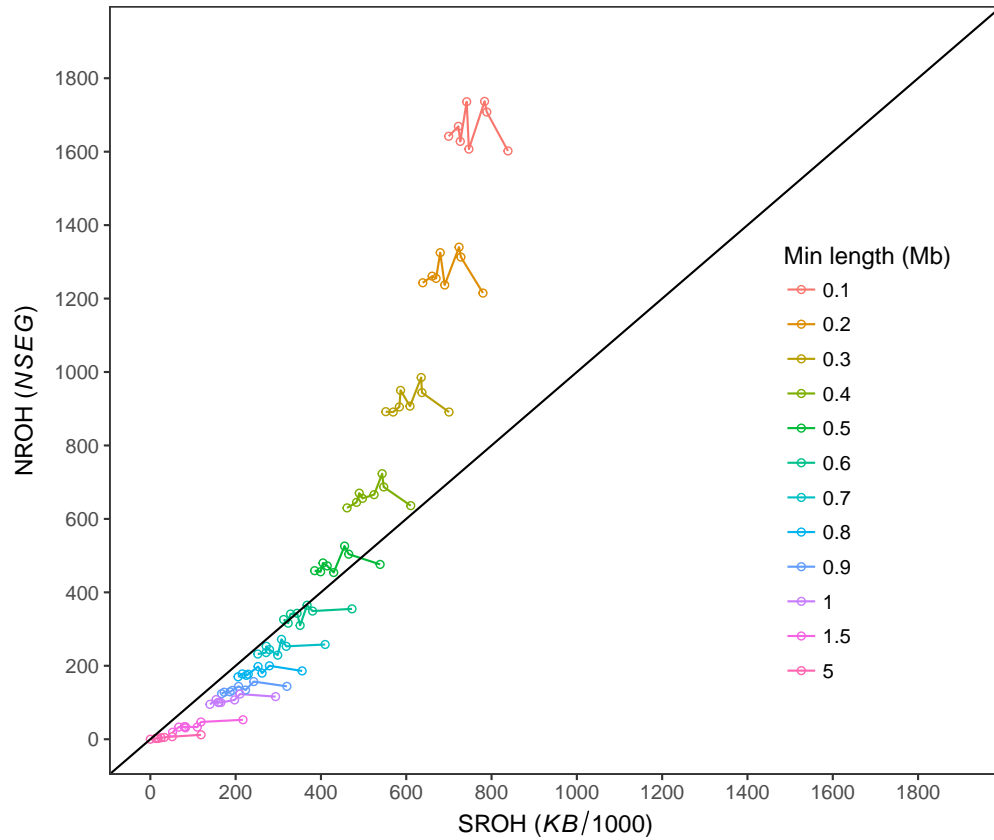


Figure S2.1: Plot of the number of runs of homozygosity NROH ( $NSEQ$ ) against the total length of runs SROH ( $KB/1000$ ) in the PLINK report for a subset of the variable minimum  $ROH$  lengths 0.1 – 5Mb. NROH dominates over SROH with all points above the diagonal, until the minimum length increases 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.

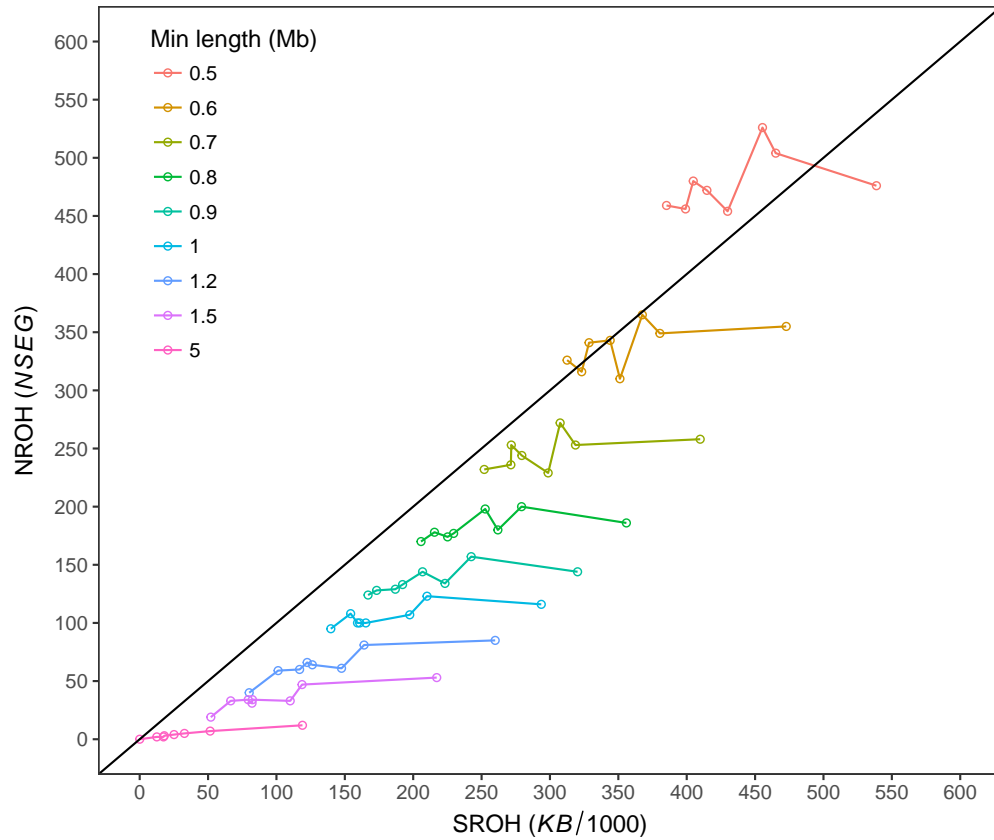


Figure S2.2: Plot of the number of runs of homozygosity NROH ( $NSEQ$ ) against the total length of runs SROH ( $KB/1000$ ) in the PLINK report for a subset 0.5 – 5Mb of the variable minimum  $ROH$  lengths. At 0.6Mb minimum length the population seems bottlenecked with most points close to or at the 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.



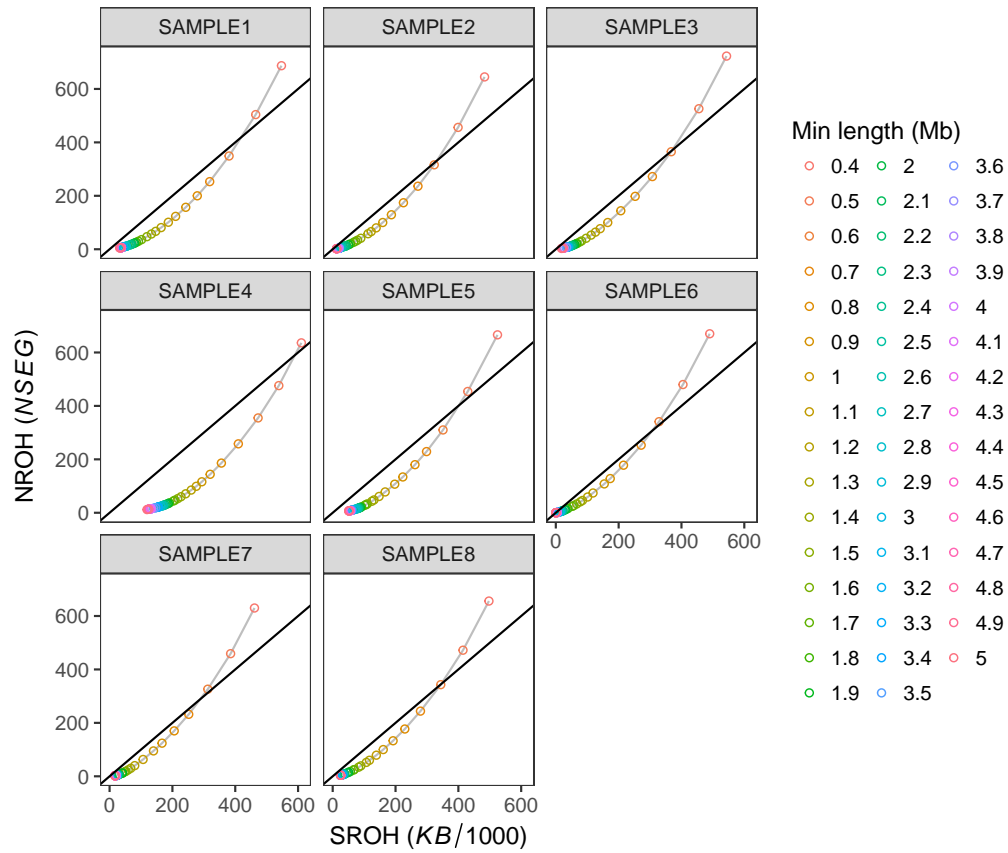


Figure S2.3: Plots of the number of runs of homozygosity NROH (*NSEQ*) against the total length of runs SROH (*KB/1000*) in the PLINK report for the minimum lengths of *ROH* > 0.3Mb. At about 1.0Mb the points are maximum shifted to the right from the diagonal.

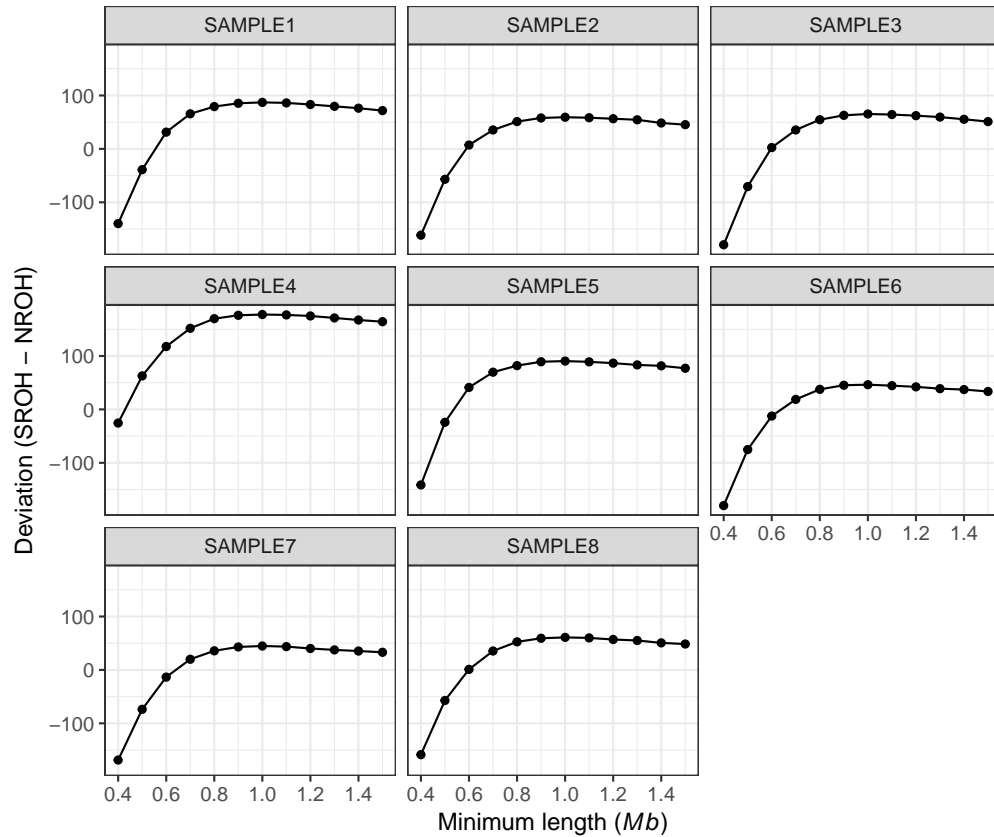


Figure S2.4: Plots of deviation  $SROH (KB/1000) - NROH (NSEQ)$  from the linear diagonal in the  $NROH$  versus  $SROH$  plots shown for minimum  $ROH$  lengths between 0.4 and 1.5Mb. For all the samples the  $SROH$  is clearly below the diagonal (deviation  $> 0$ ) for minimum  $ROH$  lengths above 0.7 – 0.8Mb and the maximum deviation is found at 1.0Mb.

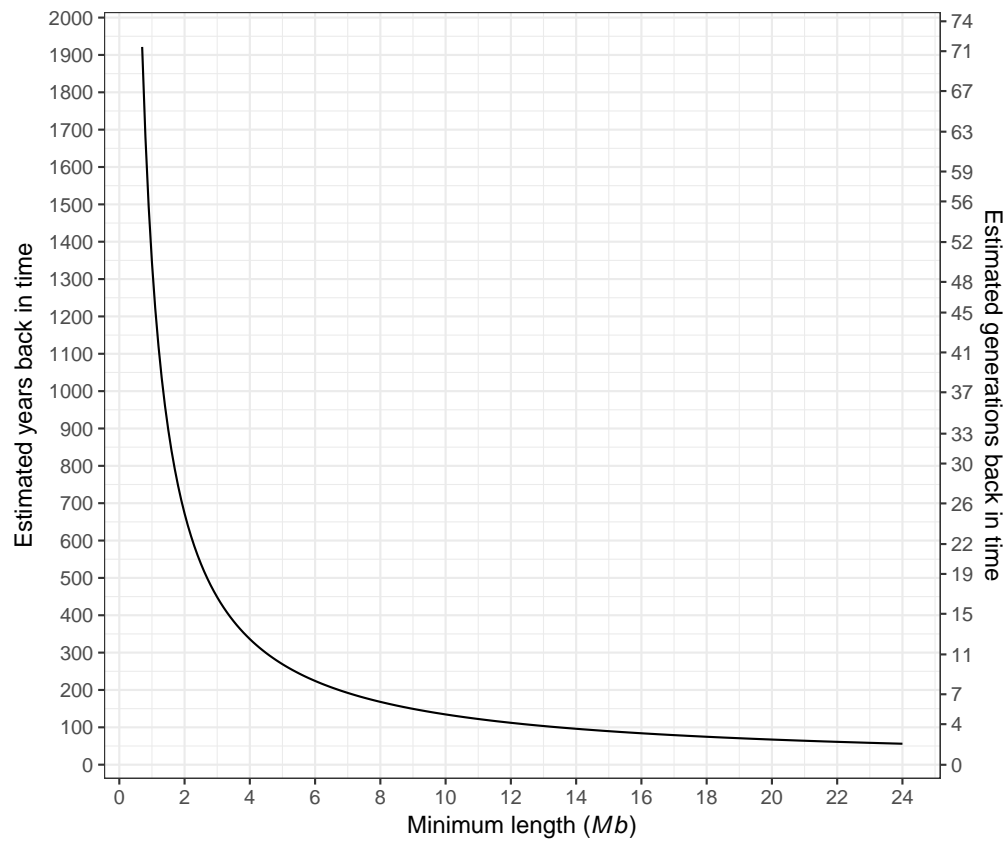


Figure S2.5: Plot of the estimated years back in time (left y-axis) and generations back in time (right y-axis) inferred from the minimum lengths of  $ROH > 0.6\text{Mb}$ . At 1Mb the estimate is 1345 years back and 50 generations back in time.

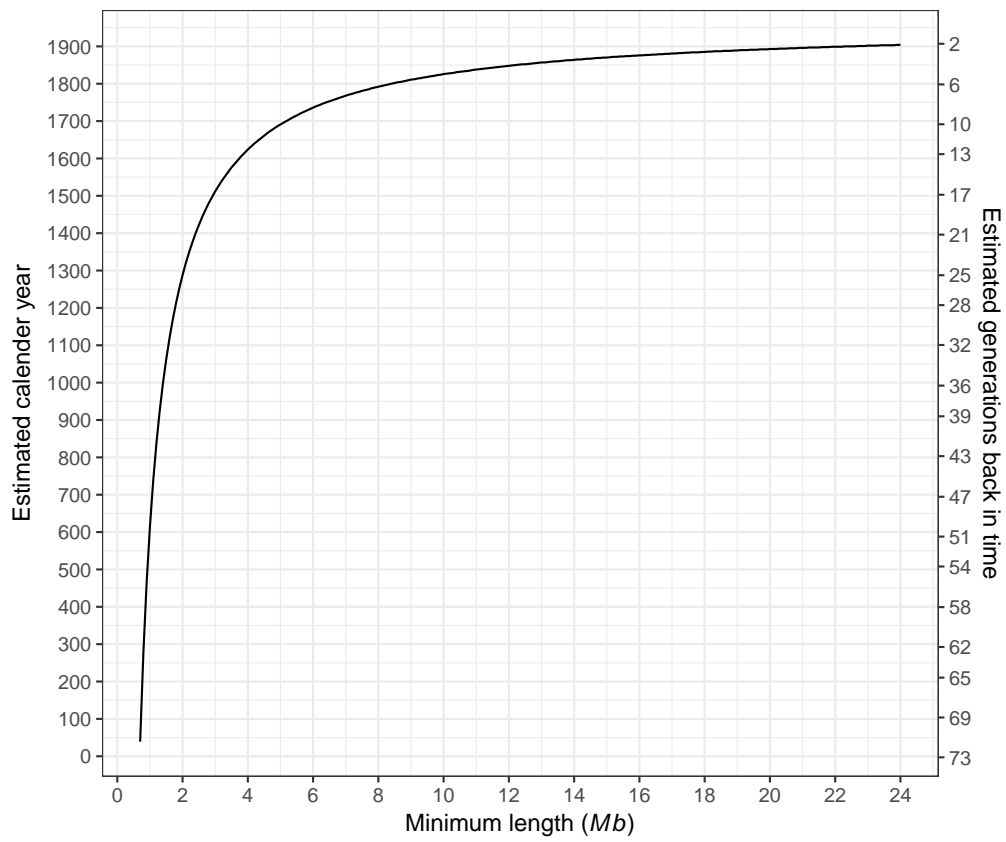


Figure S2.6: Plot of the estimated calendar year (left y-axis) and generations back in time (right y-axis) since 1960 inferred from the minimum lengths of  $ROH > 0.6\text{Mb}$ . At 1Mb the estimated calendar year is 615.

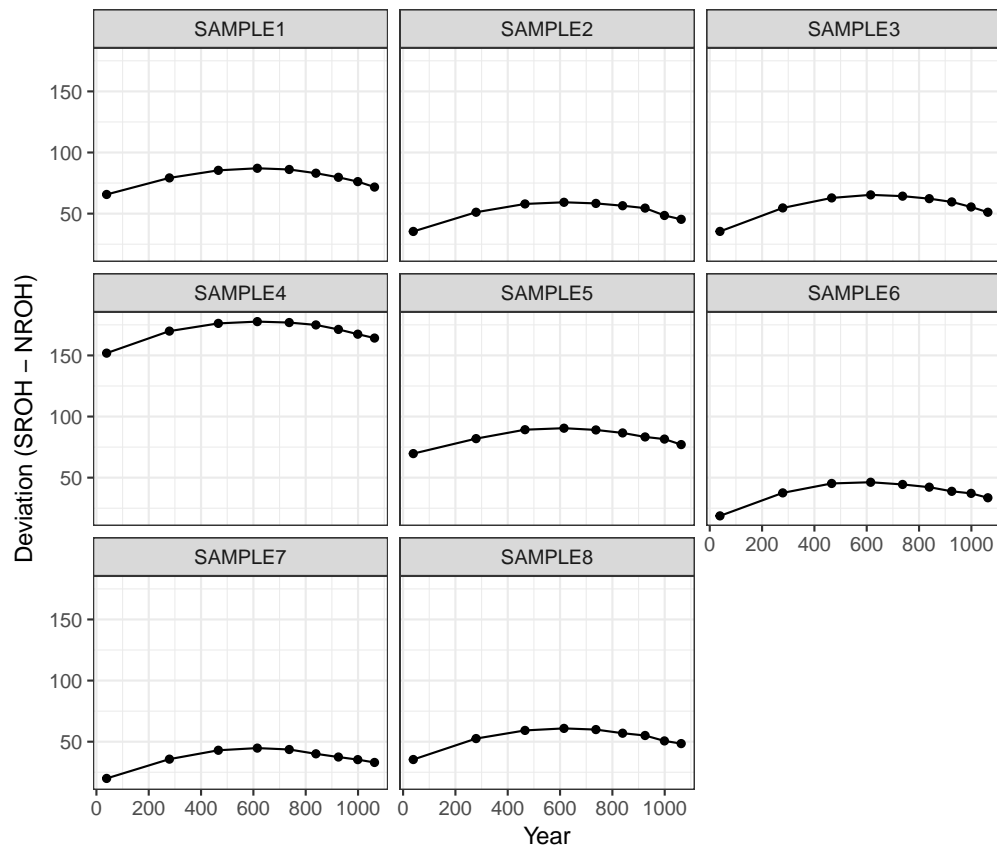


Figure S2.7: Plots of deviation  $SROH$  ( $KB/1000$ ) –  $NROH$  ( $NSEQ$ ) from the linear diagonal in the  $NROH$  versus  $SROH$  plots shown for minimum  $ROH$  lengths between 0.7 and 1.5Mb, transformed to the corresponding estimated time in years. The maximum deviation for all samples is found at 1.0Mb corresponding to year 615.

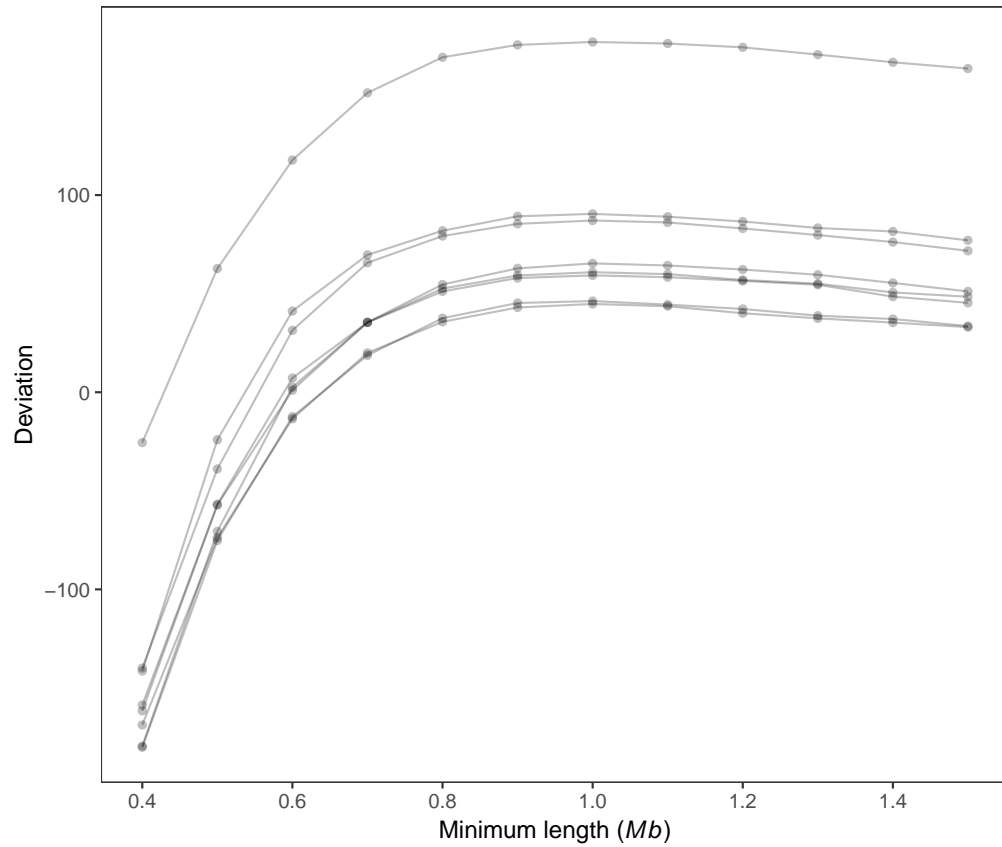


Figure S2.8: Plot of deviation  $SROH (KB/1000) - NROH (NSEQ)$  from the linear diagonal in the NROH versus SROH plots shown for minimum  $ROH$  lengths between 0.4 and 1.5Mb. For all the samples the SROH is clearly below the diagonal (deviation  $> 0$ ) for minimum  $ROH$  lengths above 0.7 – 0.8Mb and the maximum deviation is found at 1.0Mb.

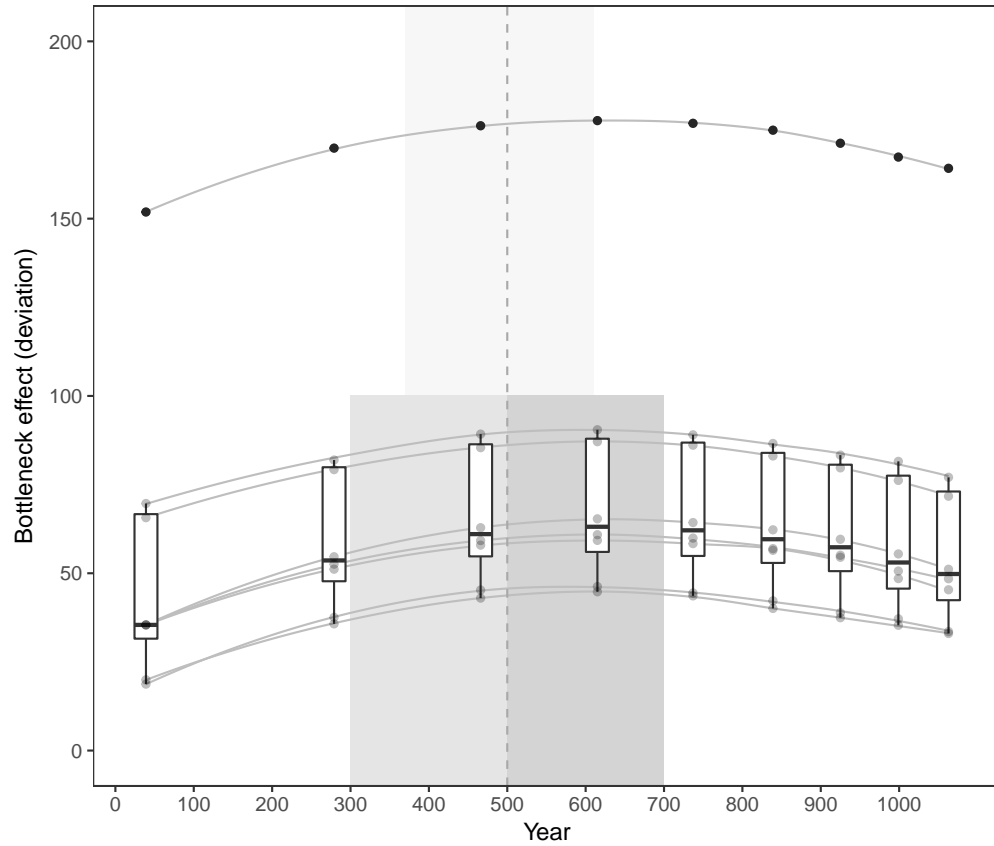


Figure S2.9: Plot of deviation from the linear diagonal in the NROH versus SROH plots shown for minimum *ROH* lengths between 0.7 and 1.5Mb, transformed to the corresponding estimated time in years. The maximum deviation for all samples is found at 1.0Mb corresponding to year 615. The three shaded rectangles 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).