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Genomic consequences of intensive inbreeding in an isolated wolf population

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Supplementary Table S1. Identity, sex (M, male; F, female), origin, pedigree-based inbreeding (F_P), and the generations to the most remote ancestor (i.e. the depth of the pedigree) for each of the 97 wolves included in the study. The individuals were chosen based a sampling scheme consisting of (i) all wolves sampled before 1991 (temporal class 1983-1990) plus all immigrants and (ii) randomly selected wolves within five predefined inbreeding classes and three temporal classes.

ID	Sex	Origin	F_P	Generations to most remote ancestor	Inbreeding class	Temporal class
D-05-18	M	Immigrant	0	-	-	-
D-77-01	M	Immigrant	0	-	-	-
D-79-01	F	Immigrant	0	-	-	-
D-85-01*	F	Immigrant	0	-	-	-
G23-13*	M	Immigrant	0	-	-	-
G31-13*	F	Immigrant	0	-	-	-
G82-10	F	Immigrant	0	-	-	-
M-02-15	M	Immigrant	0	-	-	-
M-05-01	M	Immigrant	0	-	-	-
M-07-02	M	Immigrant	0	-	-	-
M-09-03*	M	Immigrant	0	-	-	-
M-10-10*	M	Immigrant	0	-	-	-
D-84-03	M	Scandinavian born	0	1	0-0.1	1983-1990
D-85-02	M	Scandinavian born	0	1	0-0.1	1983-1990
D-86-01	M	Scandinavian born	0	1	0-0.1	1983-1990
D-89-01	M	Scandinavian born	0.25	2	0.2-0.3	1983-1990
D-91-01	F	Scandinavian born	0.25	2	0.2-0.3	1983-1990
D-89-03	F	Scandinavian born	0.25	2	0.2-0.3	1983-1990
D-92-05	M	Scandinavian born	0.25	2	0.2-0.3	1983-1990
D-93-02	F	Scandinavian born	0.25	2	0.2-0.3	1983-1990
D-93-03	F	Scandinavian born	0.375	3	0.3-0.4	1983-1990
M-98-02	M	Scandinavian born	0.375	3	0.3-0.4	1983-1990
D-92-06	M	Scandinavian born	0.375	3	0.3-0.4	1983-1990
D-94-01	F	Scandinavian born	0.375	3	0.3-0.4	1983-1990
D-92-01	M	Scandinavian born	0	2	0-0.1	1991-1998
D-99-02	M	Scandinavian born	0	2	0-0.1	1991-1998
D-93-01	M	Scandinavian born	0	2	0-0.1	1991-1998
D-92-02	M	Scandinavian born	0	2	0-0.1	1991-1998
D-96-01	M	Scandinavian born	0	2	0-0.1	1991-1998
M-98-03	F	Scandinavian born	0	2	0-0.1	1991-1998
M-98-08	M	Scandinavian born	0.125	4	0.1-0.2	1991-1998
M-00-09	M	Scandinavian born	0.125	4	0.1-0.2	1991-1998
D-00-15	M	Scandinavian born	0.125	4	0.1-0.2	1991-1998
D-01-18	M	Scandinavian born	0.125	4	0.1-0.2	1991-1998
D-05-23	M	Scandinavian born	0.234	5	0.2-0.3	1991-1998
M-01-10	F	Scandinavian born	0.234	5	0.2-0.3	1991-1998
M-03-07	F	Scandinavian born	0.234	5	0.2-0.3	1991-1998
M-98-01	F	Scandinavian born	0.281	5	0.2-0.3	1991-1998
M-03-06	M	Scandinavian born	0.188	6	0.1-0.2	1999-2006
M-09-17	M	Scandinavian born	0.188	6	0.1-0.2	1999-2006
G9-05	M	Scandinavian born	0.188	6	0.1-0.2	1999-2006
D-10-20	F	Scandinavian born	0.188	6	0.1-0.2	1999-2006
D-07-24	F	Scandinavian born	0.215	8	0.2-0.3	1999-2006
D-06-14	F	Scandinavian born	0.261	7	0.2-0.3	1999-2006
M-09-05	M	Scandinavian born	0.227	7	0.2-0.3	1999-2006
D-00-12	F	Scandinavian born	0.281	5	0.2-0.3	1999-2006

ID	Sex	Origin	F_P	Generations to most remote ancestor	Inbreeding class	Temporal class
D-10-29	M	Scandinavian born	0.227	7	0.2-0.3	1999-2006
D-10-30	M	Scandinavian born	0.27	6	0.2-0.3	1999-2006
M-00-10	M	Scandinavian born	0.313	5	0.3-0.4	1999-2006
M-06-03	M	Scandinavian born	0.302	7	0.3-0.4	1999-2006
D-06-16	F	Scandinavian born	0.305	5	0.3-0.4	1999-2006
M-06-04	F	Scandinavian born	0.302	7	0.3-0.4	1999-2006
D-11-17	F	Scandinavian born	0.324	7	0.3-0.4	1999-2006
M-01-06	F	Scandinavian born	0.305	5	0.3-0.4	1999-2006
M-05-07	F	Scandinavian born	0.302	7	0.3-0.4	1999-2006
D-08-20	M	Scandinavian born	0.324	7	0.3-0.4	1999-2006
D-07-09	F	Scandinavian born	0.438	8	0.4-0.5	1999-2006
D-07-17	M	Scandinavian born	0.438	8	0.4-0.5	1999-2006
D-08-08	F	Scandinavian born	0.438	8	0.4-0.5	1999-2006
M-07-06	M	Scandinavian born	0.437	8	0.4-0.5	1999-2006
D-08-10	F	Scandinavian born	0.434	6	0.4-0.5	1999-2006
D-07-28	M	Scandinavian born	0.434	6	0.4-0.5	1999-2006
G67-15	F	Scandinavian born	0	1	0-0.1	2007-2014
M-10-04	F	Scandinavian born	0	8	0-0.1	2007-2014
G47-11	F	Scandinavian born	0	9	0-0.1	2007-2014
G37-10	M	Scandinavian born	0	8	0-0.1	2007-2014
M-11-02	F	Scandinavian born	0	8	0-0.1	2007-2014
G100-14	M	Scandinavian born	0	1	0-0.1	2007-2014
D-10-53	M	Scandinavian born	0	9	0-0.1	2007-2014
G106-13	M	Scandinavian born	0.166	10	0.1-0.2	2007-2014
G111-14	M	Scandinavian born	0.158	10	0.1-0.2	2007-2014
G139-12	F	Scandinavian born	0.158	10	0.1-0.2	2007-2014
G109-11	M	Scandinavian born	0.139	9	0.1-0.2	2007-2014
G100-12	M	Scandinavian born	0.139	9	0.1-0.2	2007-2014
D-08-21	M	Scandinavian born	0.223	8	0.2-0.3	2007-2014
G87-12	F	Scandinavian born	0.274	9	0.2-0.3	2007-2014
D-11-58	F	Scandinavian born	0.257	8	0.2-0.3	2007-2014
D-08-19	F	Scandinavian born	0.267	8	0.2-0.3	2007-2014
D-10-50	M	Scandinavian born	0.275	8	0.2-0.3	2007-2014
G32-12	M	Scandinavian born	0.306	8	0.3-0.4	2007-2014
D-10-68	M	Scandinavian born	0.311	8	0.3-0.4	2007-2014
G32-15	F	Scandinavian born	0.361	11	0.3-0.4	2007-2014
G126-13	M	Scandinavian born	0.307	9	0.3-0.4	2007-2014
G97-13	M	Scandinavian born	0.306	8	0.3-0.4	2007-2014
G174-13	F	Scandinavian born	0.311	10	0.3-0.4	2007-2014
D-11-22	F	Scandinavian born	0.352	9	0.3-0.4	2007-2014
D-07-16	M	Scandinavian born	0.434	6	0.4-0.5	2007-2014
G58-15	F	Scandinavian born	0.462	9	0.4-0.5	2007-2014
G50-12	M	Scandinavian born	0.413	9	0.4-0.5	2007-2014
G175-13	M	Scandinavian born	0.413	9	0.4-0.5	2007-2014
D-10-15	F	Scandinavian born	0.486	9	0.4-0.5	2007-2014
D-10-23	F	Scandinavian born	0.486	9	0.4-0.5	2007-2014
G34-10	F	Scandinavian born	0.47	8	0.4-0.5	2007-2014
D-10-44	M	Scandinavian born	0.486	9	0.4-0.5	2007-2014
G110-11	F	Scandinavian born	0.41	8	0.4-0.5	2007-2014

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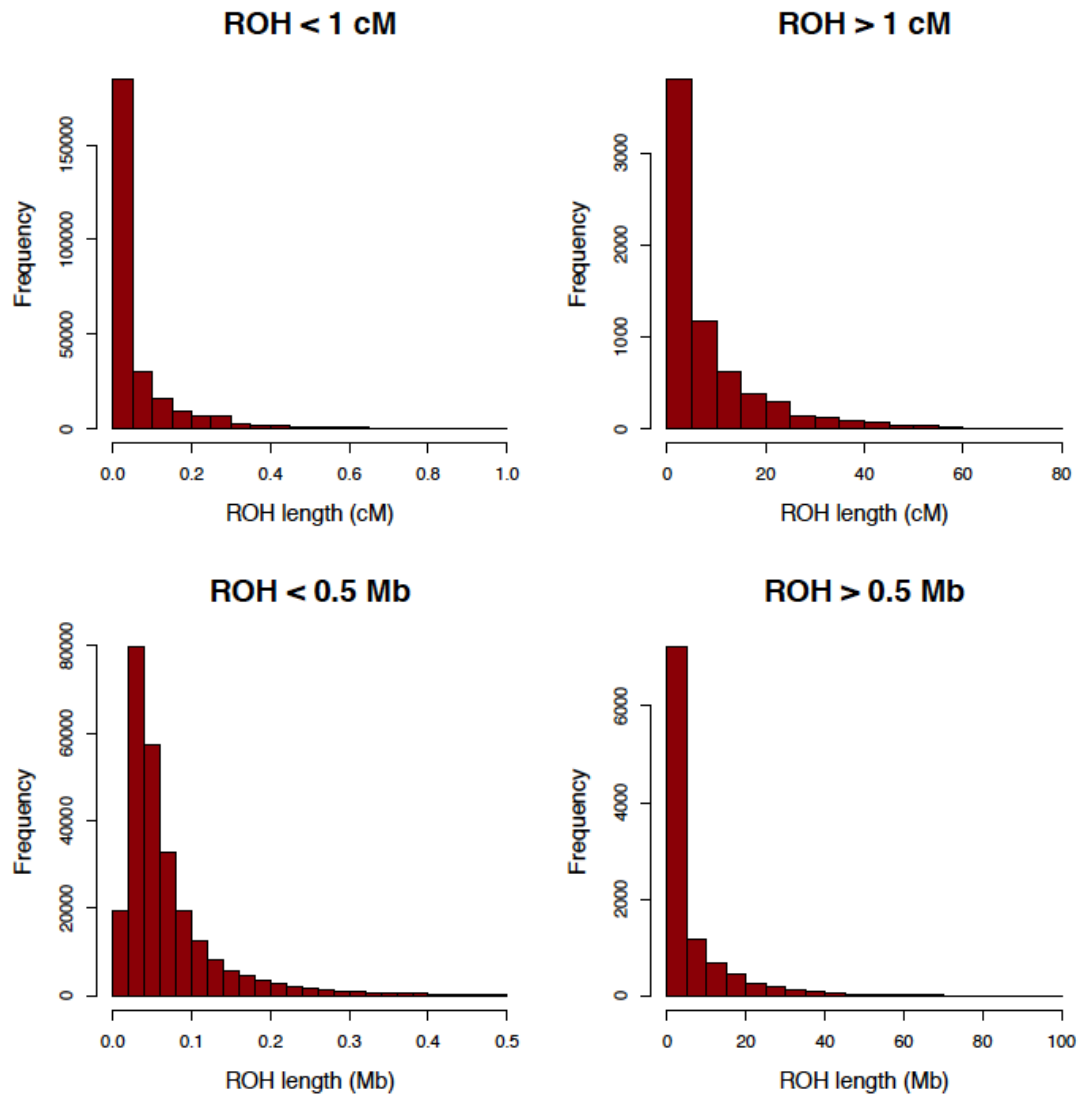
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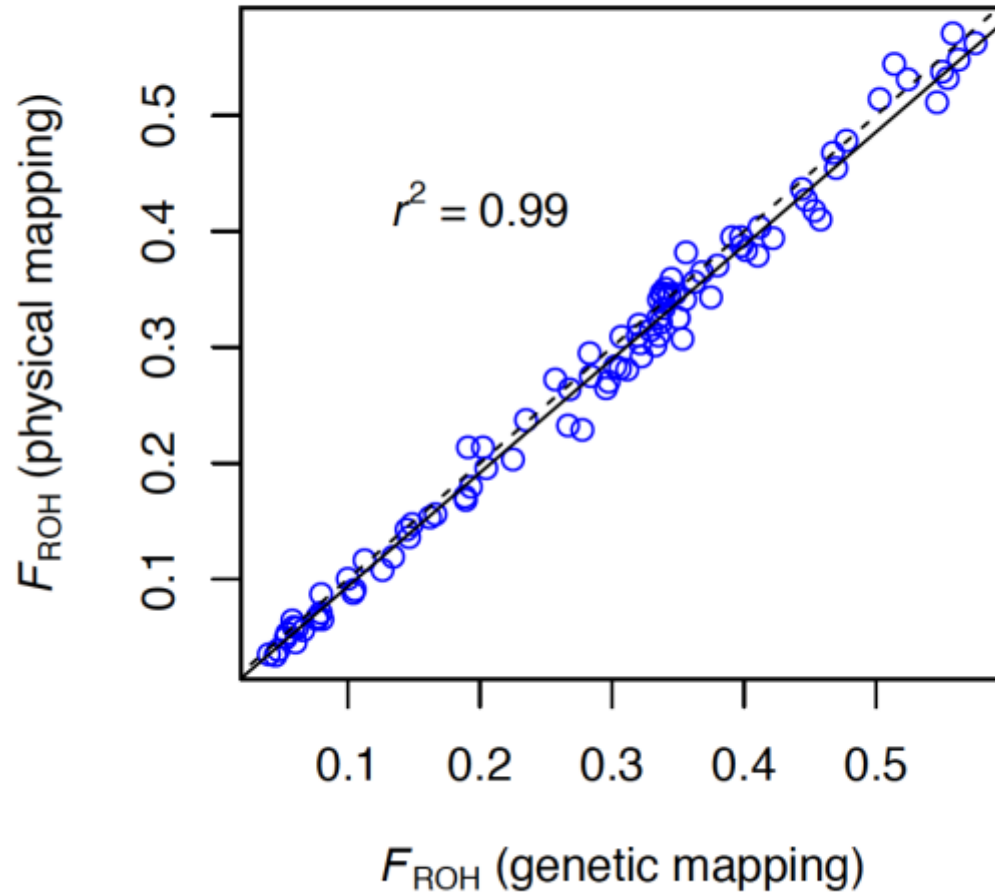
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Supplementary Table 2. ROH regions with statistically significant deficit of ROH abundance. Shown are the chromosome with start and stop position (in Mb), segment lengths (Mb), mean recombination rate (cM/Mb), nucleotide diversity (π), the number of SNPs present in the segment, and ROH density. Note that adjacent 100 kb windows with statistically significant permutation tests were joined in the table.

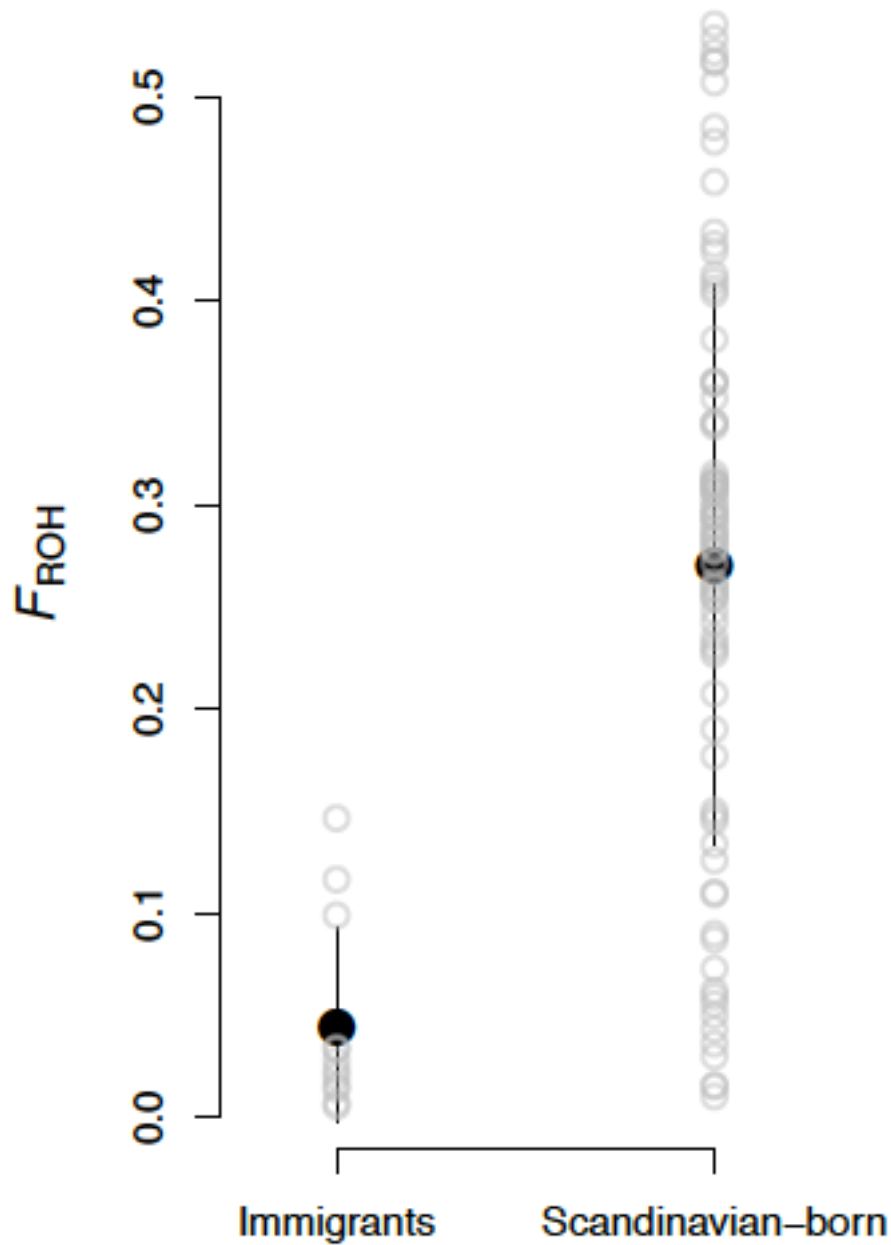
Chr.	Start (Mb)	End (Mb)	Length (Mb)	Mean Rec. Rate. (cM/Mb)	π	SNPs	ROH Density
3	91.8	91.89	0.09	0.39	0.0001	40	8.9
11	26.7	28.2	1.5	0.6	0.0008	3,486	9
11	28.3	29.3	1	0.55	0.0012	3,545	10.1
11	72.4	73.1	0.7	1.69	0.0025	5,202	10.1
14	0	0.2	0.2	0.57	0.0005	271	3.5
16	59.3	59.6	0.3	1.27	0.0001	122	7.2
20	54.7	54.9	0.2	0.55	0.0005	312	10.3
20	55.7	55.9	0.2	2	0.0012	678	10.5
21	0	0.1	0.1	11.53	0.0004	164	10.9
22	55.8	56.1	0.3	0.86	0.0017	1,474	10



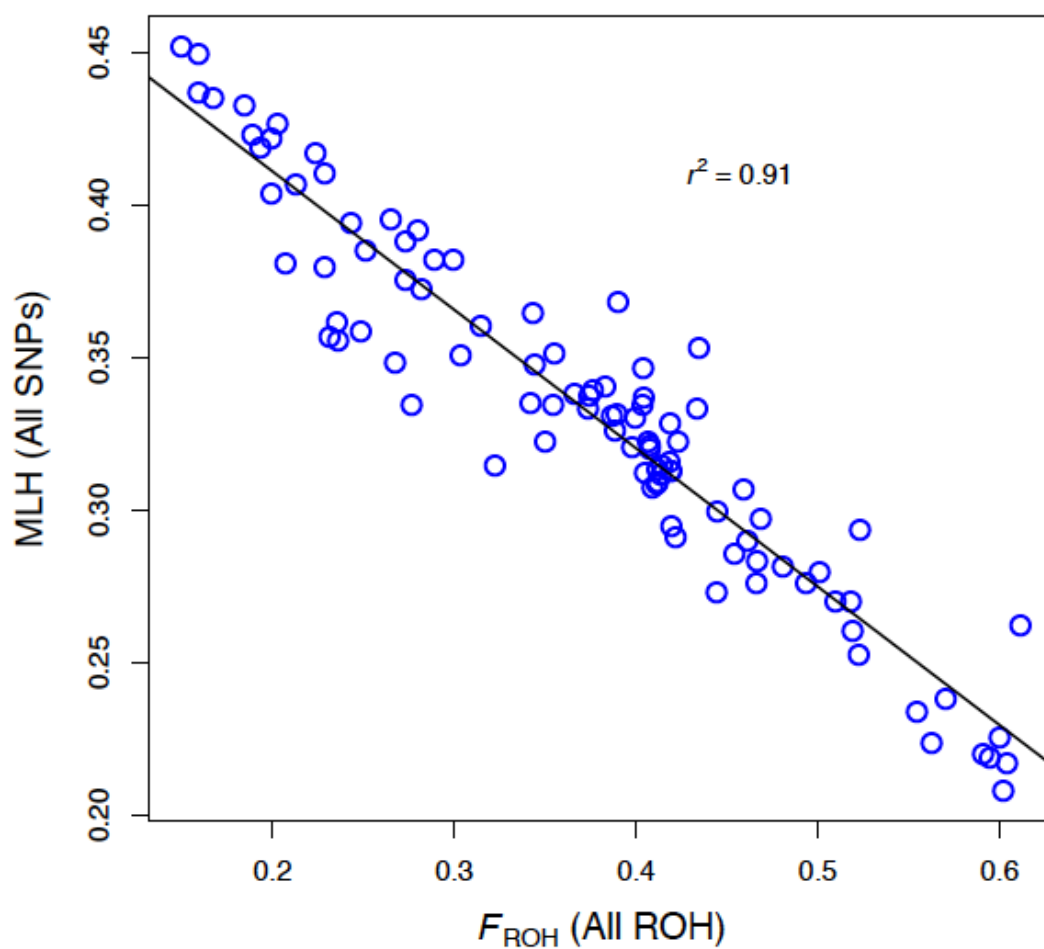
Supplementary Figure 1. Distribution of the lengths of ROH. The genetic map lengths (in cM) of ROH are shown in the two upper panels. The lower two panels show the physical lengths (in Mb) of ROH.



Supplementary Figure 2. Scatterplot of F_{ROH} measured using physical mapping of ROH versus F_{ROH} measured using genetic mapping of ROH. The ROH shown are those with values of $g \leq 50$. The r^2 value and the fitted solid line are from a linear regression model. The dashed line has an intercept of zero and a slope of one.



Supplementary Figure 3. The distribution of F_{ROH} for immigrants and Scandinavian-born wolves calculated using only ROH with $g \leq 10$ generations. The filled point and error bars represent the mean $\pm$ one standard deviation.



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82 **Supplementary Figure 4.** The relationship between MLH and F_{ROH} measured
 83 with the whole genome in Scandinavian wolves.

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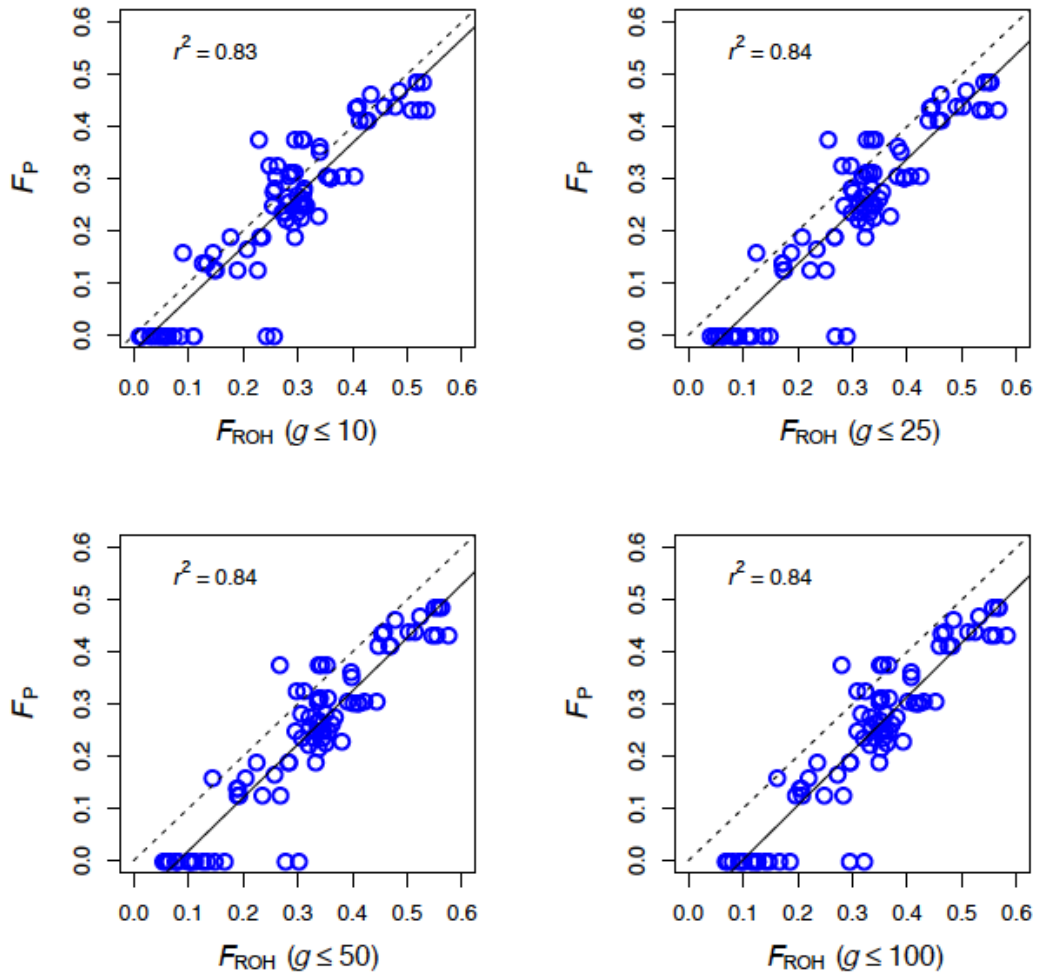
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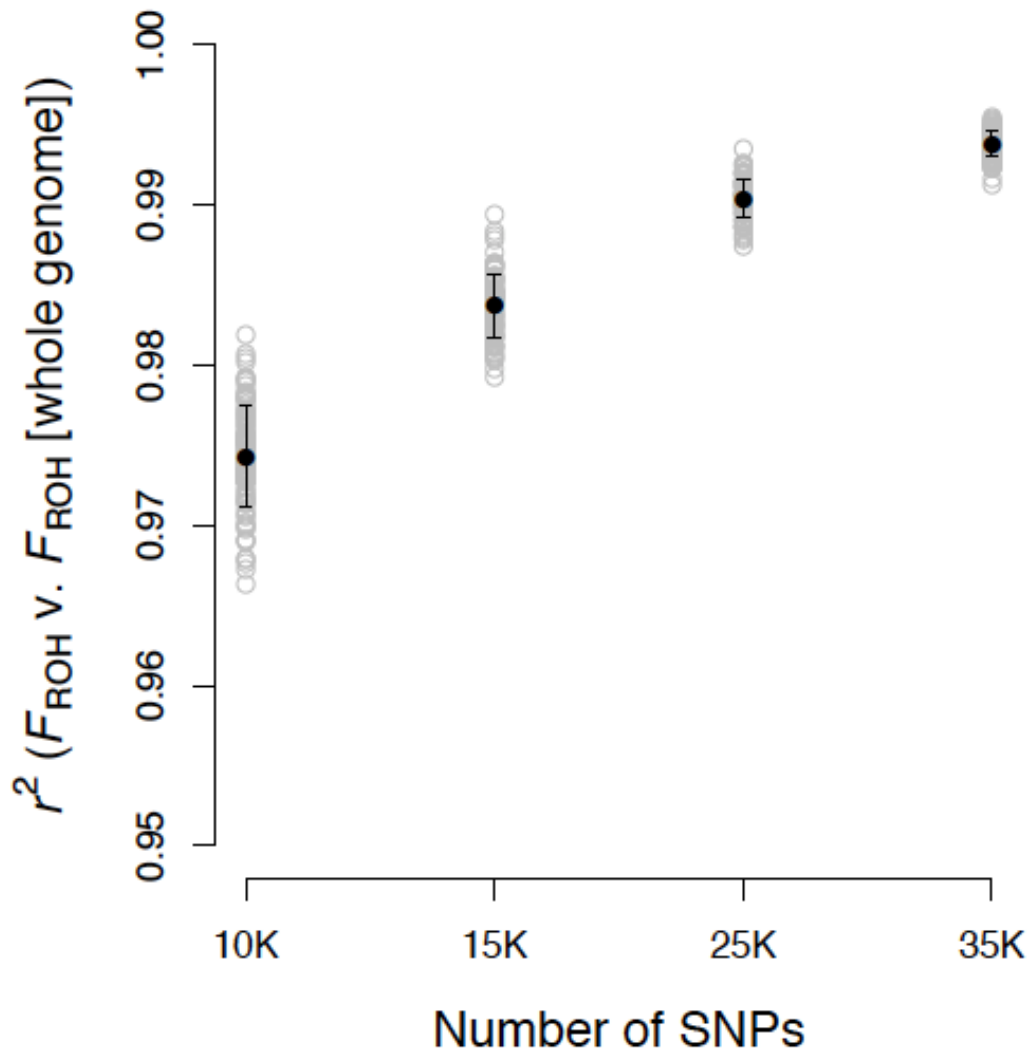
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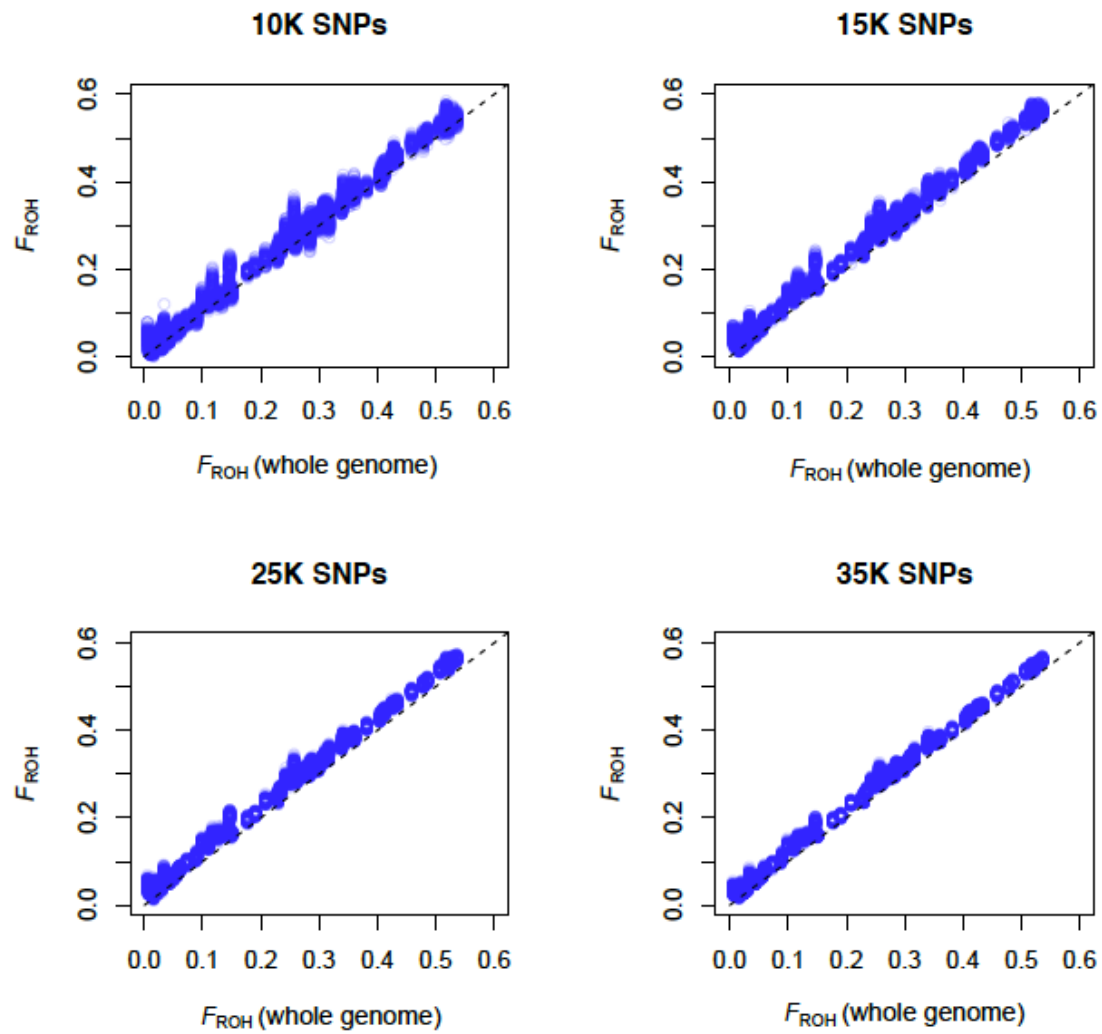
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Supplementary Figure 5. The relationship between F_P and F_{ROH} measured with the whole genome in Scandinavian wolves, after excluding immigrants from the data. F_P is shown on the y-axis, and F_{ROH} measured using ROH arising from relatively recent ancestors ($g \leq 10$ -100 generations). The dashed line has an intercept of zero and a slope of one. Points below the line thus represent cases where F_P underestimated F_{ROH} . The solid line is the fitted line from a regression of F_P versus F_{ROH} .

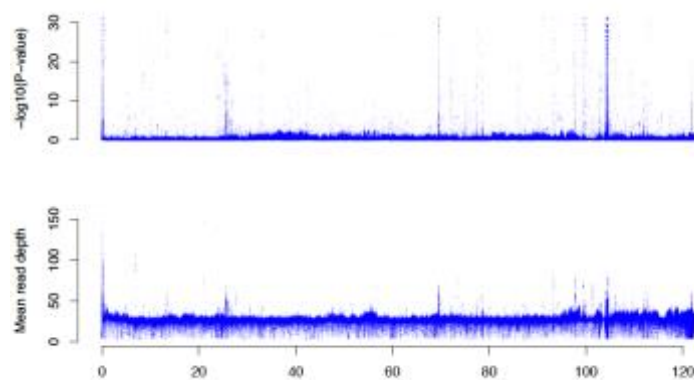


Supplementary Figure 6. The precision of F_{ROH} as a function of the number of SNPs ($\times 10^3$) analyzed. The r^2 from regressions of F_{ROH} (estimated with subsamples of SNPs) versus F_{ROH} calculated from the whole genome (using ROH with $g \leq 10$) is shown on the y-axis. The number of subsampled SNPs is shown on the x-axis. The gray points represent the r^2 values from each of the 100 analyses for each number of SNPs. The black points and error bars represent the mean r^2 $\pm$ one standard deviation of r^2 for each number of SNPs analyzed.



Supplementary Figure 7. F_{ROH} measured with 10,000-35,000 subsampled SNPs plotted against F_{ROH} measured with the whole genome in Scandinavian wolves.

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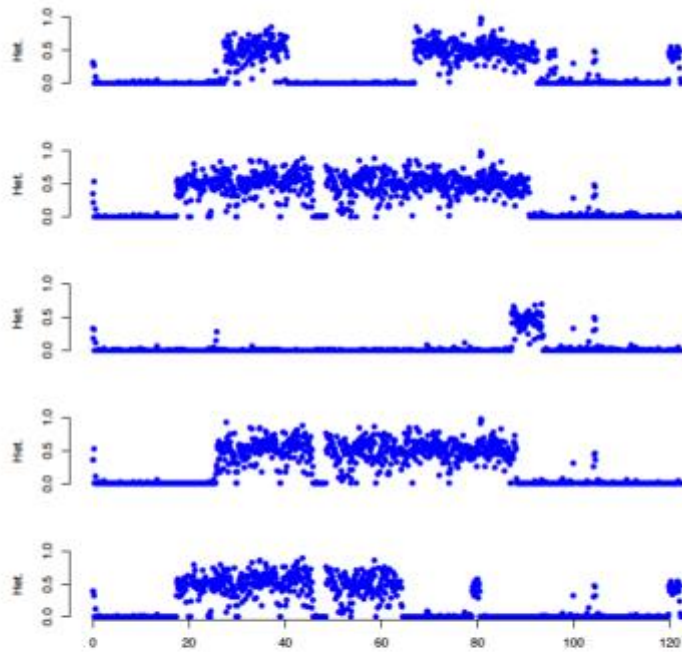
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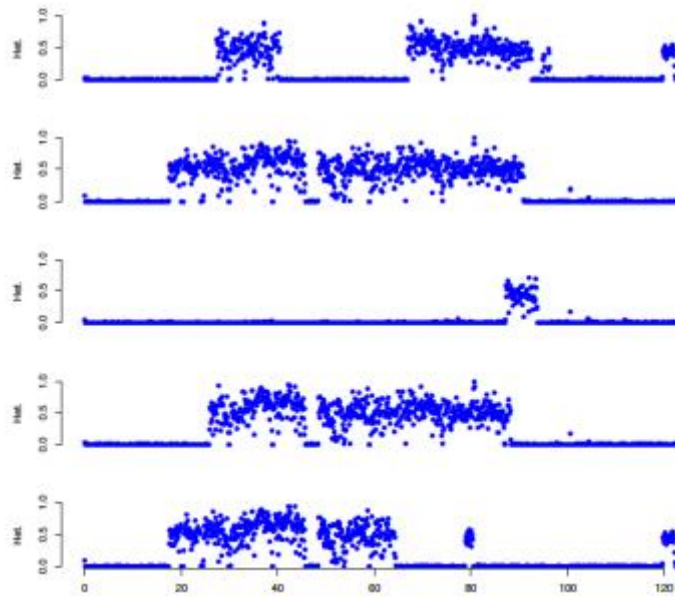
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127 **Supplementary Figure 8.** *P*-values from tests for excess of heterozygotes
128 relative to Hardy-Weinberg proportions (top panel), and mean sequence read
129 depth (lower panel), across all SNPs on chromosome 1.

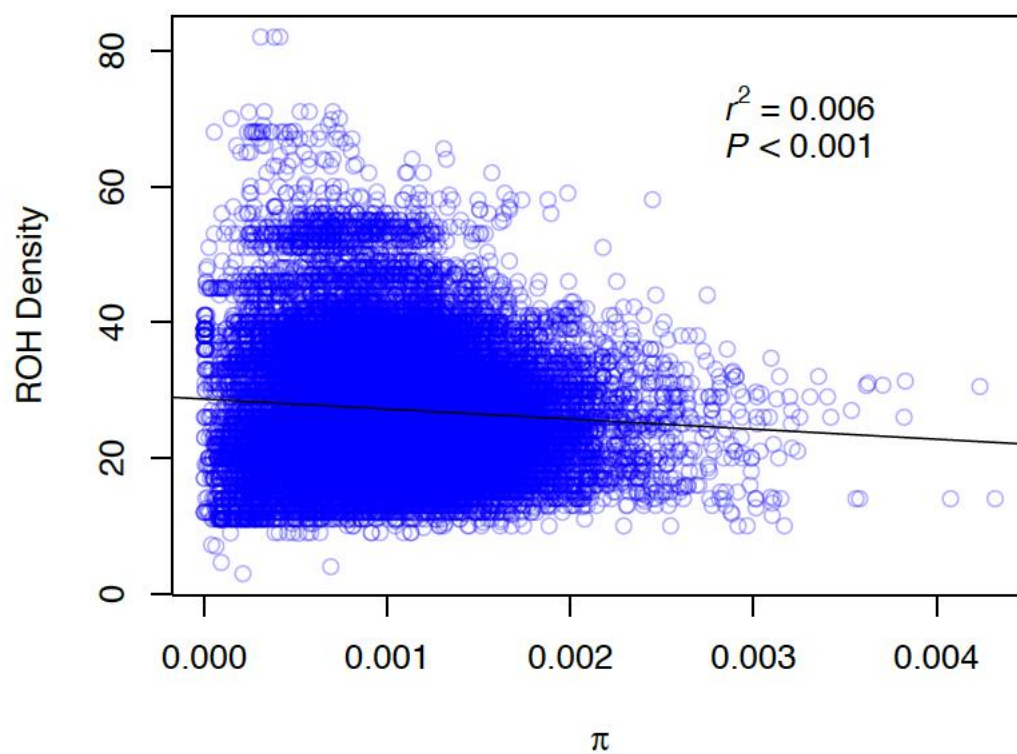
A



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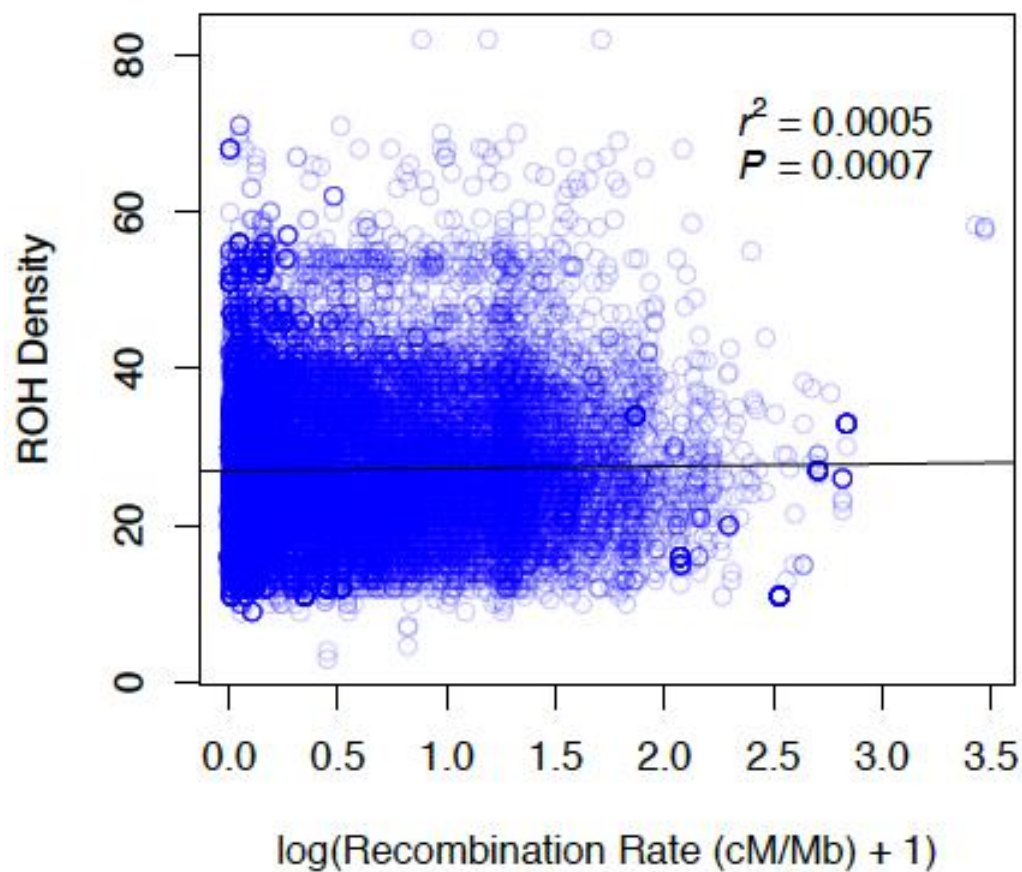


Supplementary Figure 9. Heterozygosity across chromosome 1 in 100 kb windows for five wolves. The results shown are from analysis of data not filtered based on sequence read depth and deviation from Hardy-Weinberg proportions (A), and after filtering SNPs based on sequence read depth and deviation from Hardy-Weinberg proportions as described in the main text (B).



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140 **Supplementary Figure 10.** ROH density versus π measured in 100 kb windows
141 of the 97 wolf genomes. The P -value, r^2 , and solid black fitted line are from a
142 linear regression model.

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Supplementary Figure 11. Scatterplot of ROH density versus the log-transformed recombination rate (cM/Mb) in 100 kb windows of the 97 wolf genomes. The P -value, r^2 , and solid black fitted line are from a linear regression model.