Supplementary Figures

Figure S1. Genomewide distribution of recombination rate using the approach of Sandor et al. (2012). These estimates were calculated from observed crossover frequencies. Fitting a gamma distribution on the observed estimates (red line) provided a prior distribution for the subsequent Bayesian inference on recombination rates (parameters given in the box). See methods for details.

Figure S2. Distribution of recombination intensities among intervals of the HD SNP array. The green curve represents the distribution under the null hypothesis that there is no hotspots ($\log10(\lambda_i) = 0$). It is estimated by fitting a mixture of Gaussian distribution to the observed distribution and extracting the relevant component. Intervals where recombination intensity was particularly high (FDR = 5%) were considered as harbouring recombination hotspots and are shown in red.

Figure S3. Validation of imputed genotypes for the GWAS. The figure shows the proportion of correct genotype calls as a function of their posterior probability calculated with BIMBAM.

Figure S4. *RNF212* gene structure in various species. *RNF212* gene is not annotated on the ovine reference genome Oar_v3.1, but can be located at the telomeric end of OAR6 (116,4Mb) by homologies (dashed lines) with the *RNF212* gene from Ovis aries musinon (Oor1_1.0). Some anotated predicted non-coding RNA sequence (nc_RNA in brown) were part of the *RNF212* sequence. The ovine *RNF212* gene is also partly present in the unplaced scaffold005259, that can be virtually located in the largest assembly gap (in blue). In Ovis orientalis musimon, the *RNF212* gene exibited 14 putative exons with alternative splicing (mRNA models in green). Homology analysis (dashed lines) with annotated *RNF212* gene in other ruminant species (bovine on BTA6 and caprine on CHI6) indicated a good gene structure conservation between ovine and bovine *RNF212*, but only a partial conservation with goat *RNF212*, where the six last predicted exons match with intronic region in ovine. When compared to human *RNF212* on HSA4 and mouse *RNF212* on MMU5 chromosomes, only four to five exons are conserved with ruminants indicated a non-conserved gene structure. Red lines located SNP associated with global recombination rate (GRR) in the present study, and those previously shown in bovine (Sandor et al. 2012; Kadri et al. 2016) , in human (Kong et al. 2008; Chowdhury et al. 2009; Fledel-Alon et al. 2011; Kong et al. 2014) and in mouse (Fujiwara et al. 2014). Gene scales are in base pair and gene structures were constructed with CLC Main Workbench software v7.7.3 using the NCBI query module (Qiagen Aarhus).

Figure S5. Patterns of recombination along Sheep autosomes. Left: recombination rate of one megabase windows along metacentric chromosomes (1,2,3). Center: recombination rate of one megabase windows along acrocentric chromosomes (4-26). Right: recombination rate of one megabase windows against distance to nearest chromosome end.

Figure S6. Recombination rates of Sheep autosomes. Left: from recombination rate estimates in windows of one megabase. Right: from recombination rate estimates in SNP

array intervals. Top: for each chromosome. Bottom: as a function of chromosome physical size. Dotted line: c = f(log(size)), dashed line: c = f(1/size)**.**

Figure S7. Distribution of recombination on the genome. The figure represents the proportion of the physical genome size affected by recombination, for increasing coverage of the genetic map. The Gini corresponding to the brown area on the figure is 0.52.

Figure S8. Relative intensity of population to meiotic recombination rates in windows of 1 Mb along the sheep genome.

Figure S9. Posterior standard deviation of recombination rates on the medium density SNP array with different datasets. Soay: dataset from Johnston et al. (2016), only male meioses were used. Lacaune: dataset from this study. Both: combination of the two datasets.

Figure S10. Effect of insemination month on the average number of crossovers per meiosis. Top: estimated mean GRR (dots) and 95% confidence intervals (vertical lines). Bottom: number of inseminations per month.

Figure S11. Individual variation in recombination rates among Lacaune Males. Additive genetic values on Genome-wide Recombination Rate genetic for all Lacaune sires of our dataset (in black) and for the 345 FID (in grey). The vertical black line is placed at the mean.

Figure S12. Local alignments of the Sheep and Human genome around the OAR7 QTL region. Dotplot of the alignements of sheep OAR7 on human HSA14. Vertical cyan bars are located at significant SNP positions. Three functional candidate genes surrounding the association signal (shaded) are indicated.

Figure S13. Linkage disequilibrium between *RNF212* polymorphisms and chromosome 6 QTL SNPs. The top figure represents the mRNA and the protein of *RNF212*. The four genotyped mutations are indicated : the two first are intronic and the two others are exonic. We replace the gene on a zoom on the chromosome 6 QTL (middle figure). The four left solid lines highlight the mutations, whereas the dashed lines represent the 3 most significant SNPs. Middle points show the intermediate SNPs between the mutations and the significant SNPs. Finally, the figure at the bottom indicates the pairwise LD between the mutations and all the SNPs presented on the middle figure. It highlights two haplotype blocks : one between the 3 most significant mutations and another between the 3 most significant SNPs.

Figure S1.

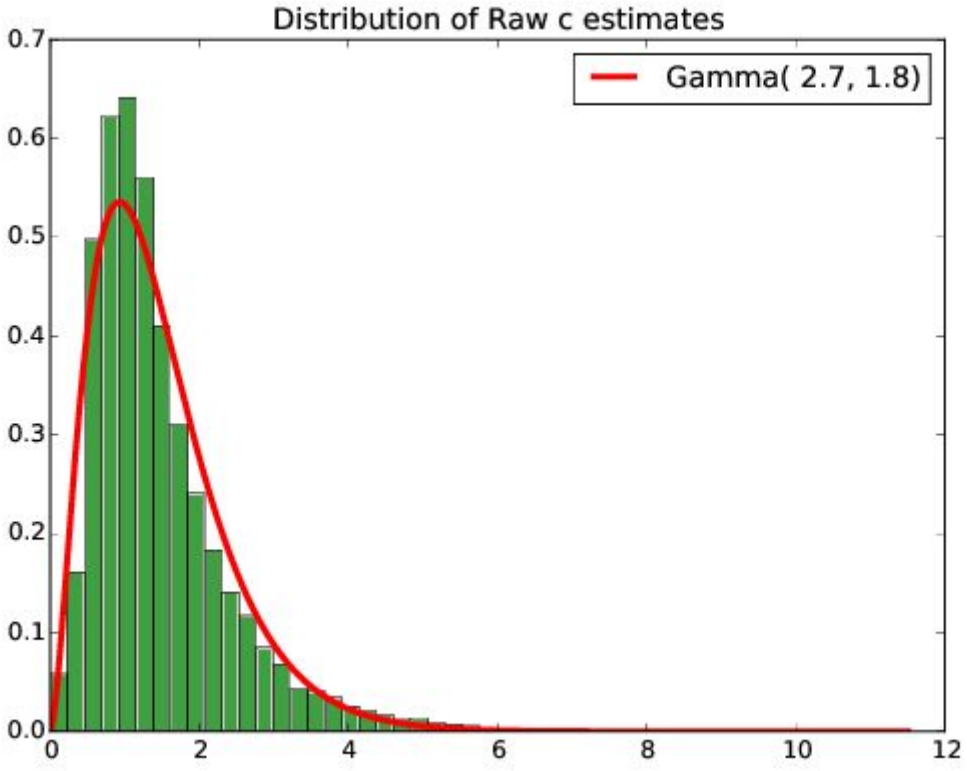
Distribution of Raw c estimates
Gamma(2.7, 1.8)
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0
2
4
6
8
10
12

Figure S2.

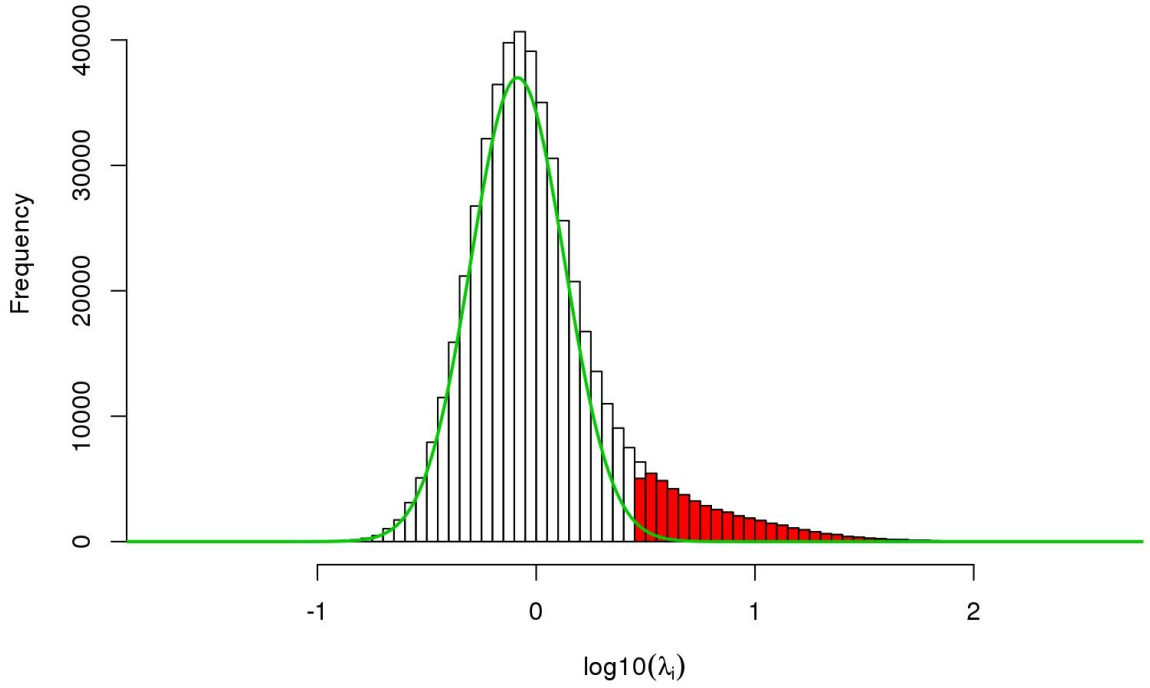

Figure S3.

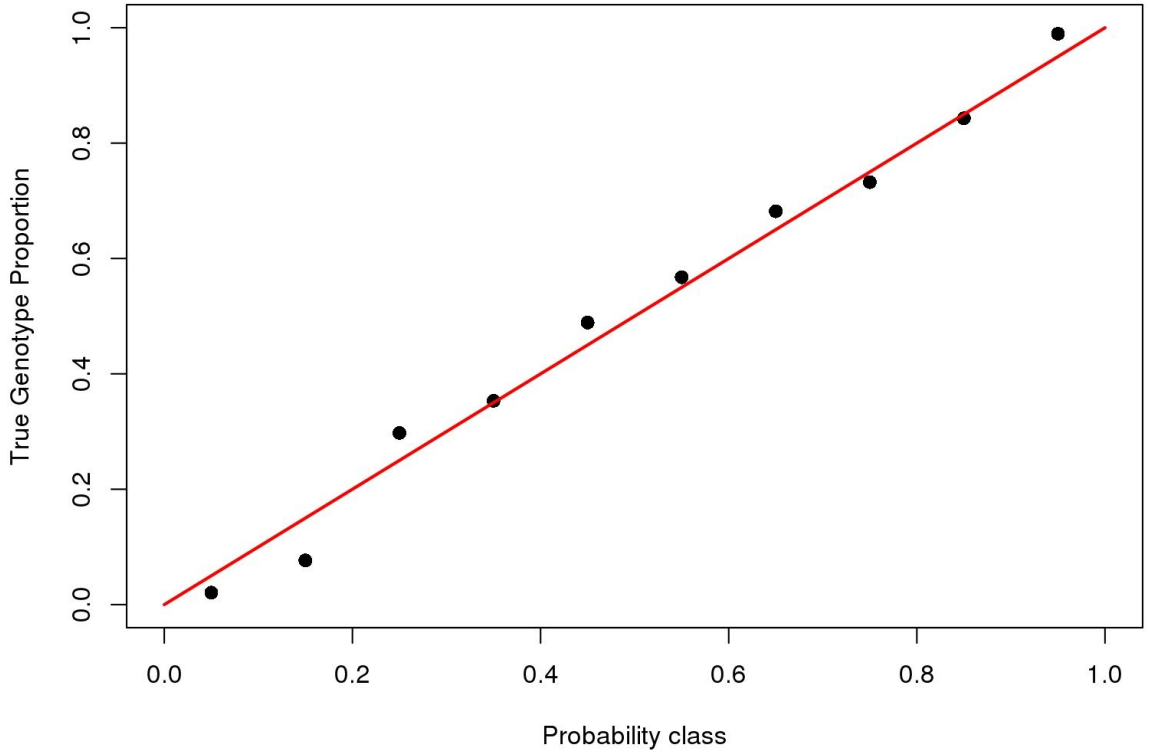
True Genotype Proportion
0.0
0.2
0.4
0.6
0.8
1.0
Probability class
0.0
0.2
0.4
0.6
0.8
1.0

Figure S4.

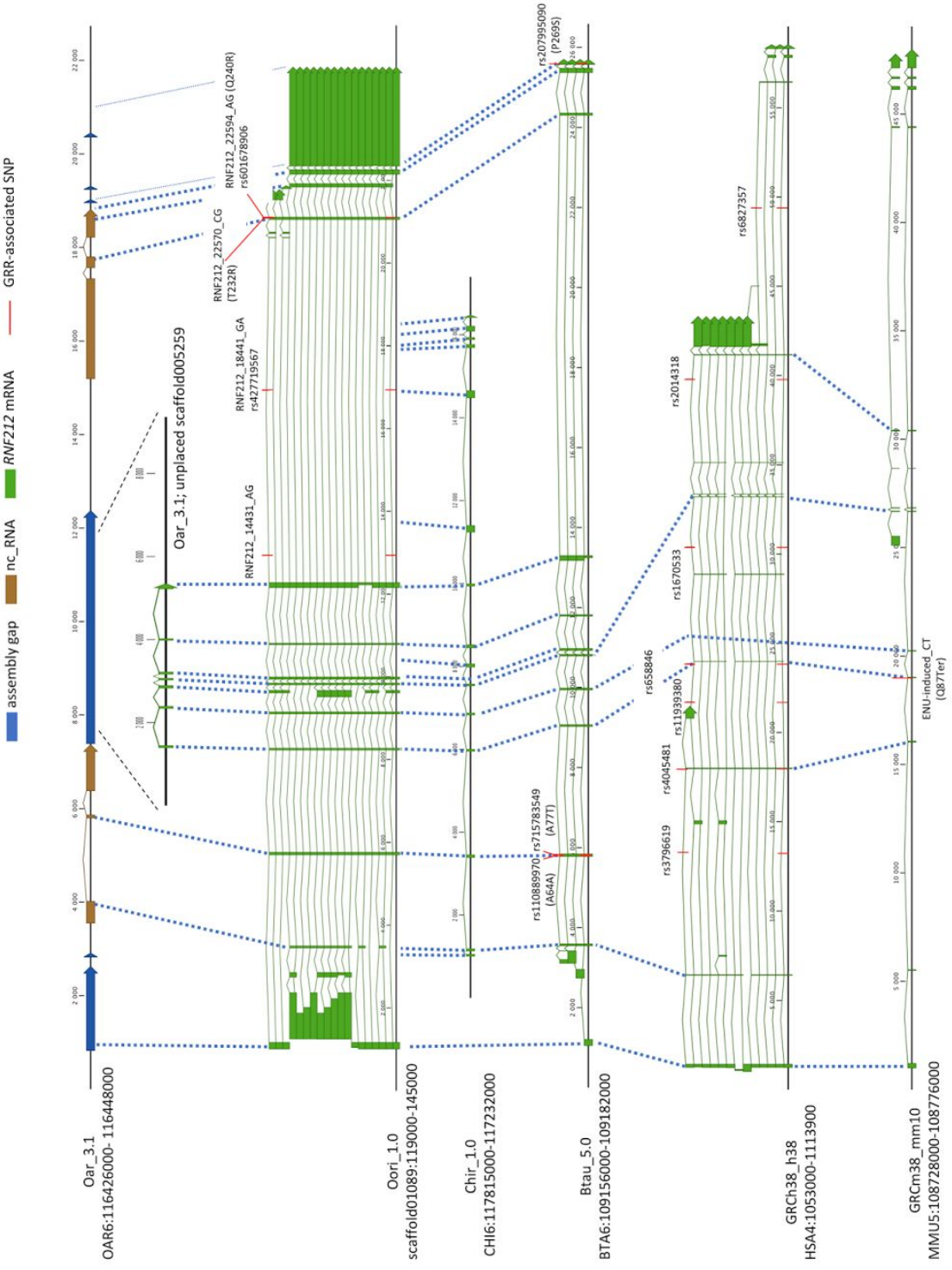
assembly gap
nc_RNA
RNF212 mRNA
GRR-associated SNP
Oar_3.1; unplaced scaffold005259
RNF212_14431_AG
RNF212_18441_GA
rs427719567
RNF212_22570_CG
(T232R)
RNF212_22594_AG (Q240R)
rs601678906
rs207995090
(P269S)
rs110889970
rs715783549
(A64A)
(A77T)
rs3796619
rs4045481
rs11939380
rs6658846
rs1670533
rs2014318
rs6827357
ENU-induced_CT
(Q87Ter)
Oar_3.1
OAR6:116426000- 116448000
Oori_1.0
scaffold01089:119000-145000
Chir_1.0
CHI6:117815000-117232000
Btau_5.0
BTA6:109156000-109182000
GRCh38_h38
HSA4:1053000-1113900
GRCm38_mm10
MMU5:108728000-108776000

Figure S5.

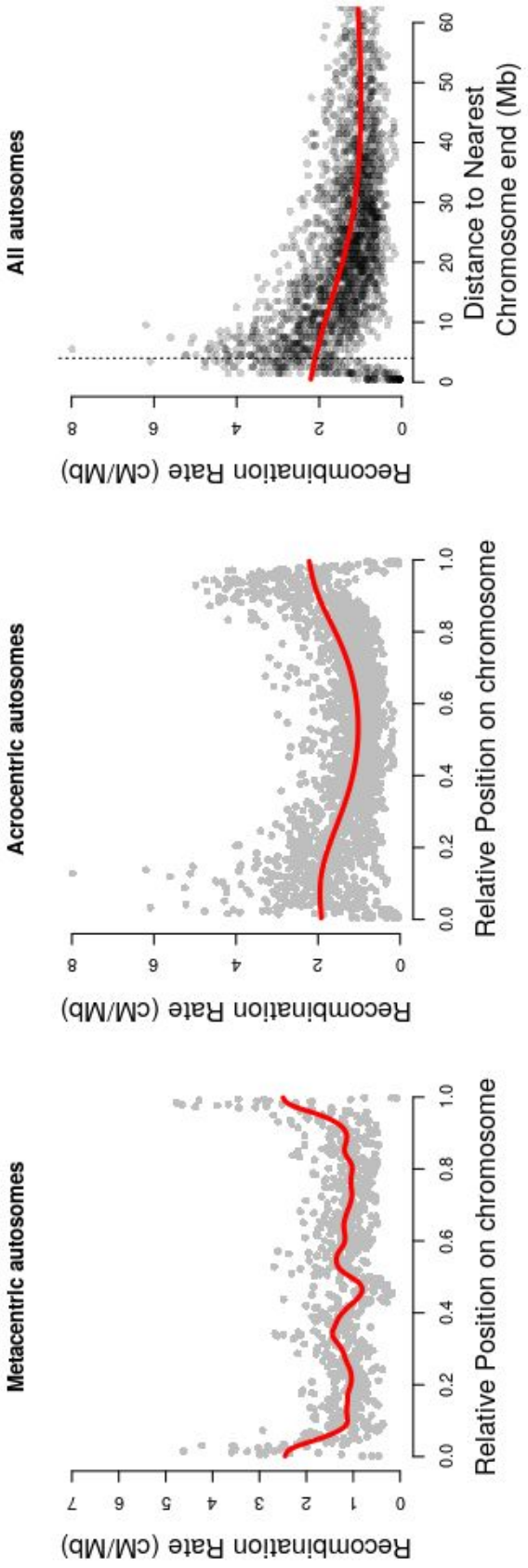
All autosomes
Recombination Rate (cM/Mb)
Distance to Nearest Chromosome end (Mb)
Acrocentric autosomes
Recombination Rate (cM/Mb)
Relative Position on chromosome
Metacentric autosomes
Recombination Rate (cM/Mb)
Relative Position on chromosome

Figure S6.

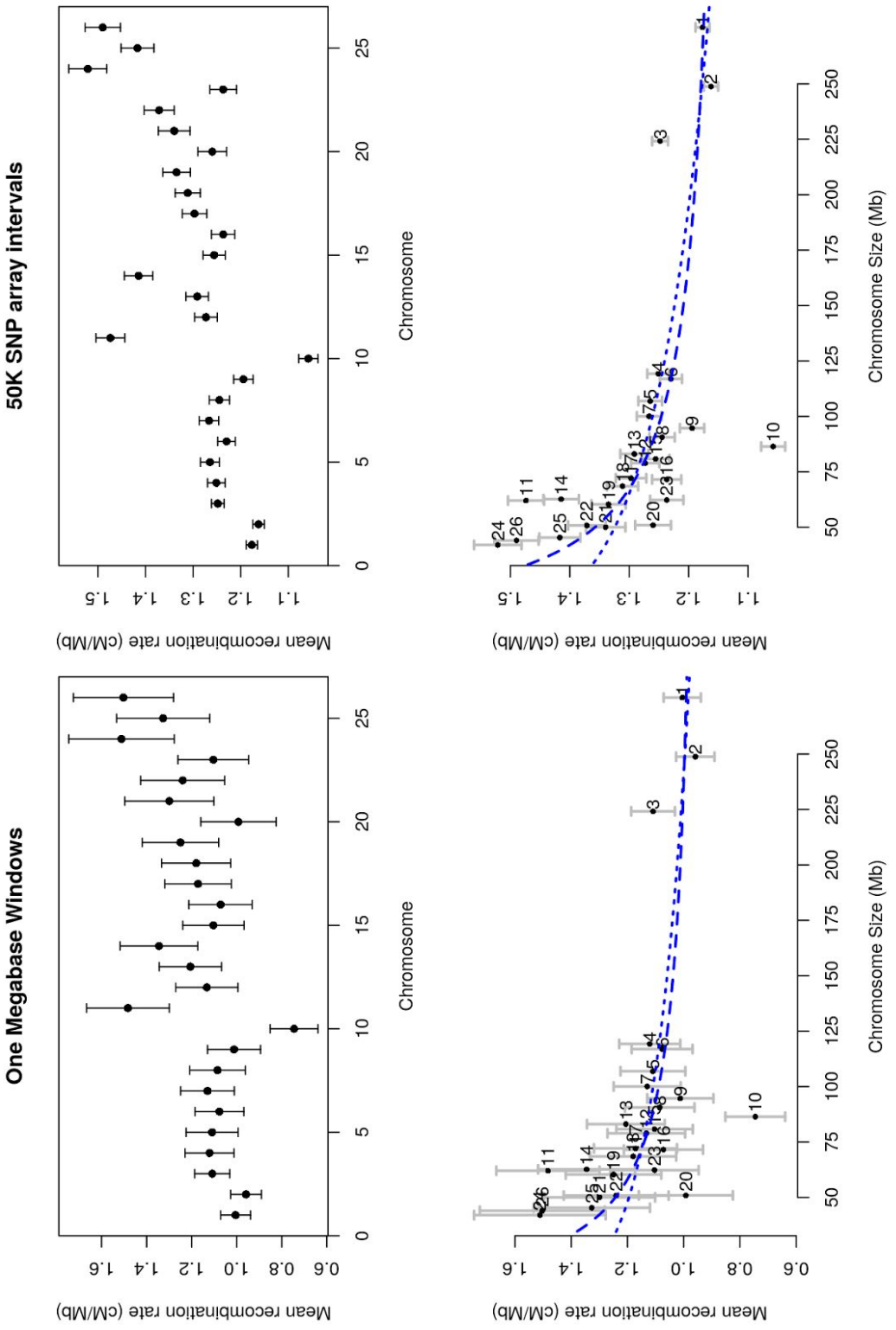
50K SNP array intervals
One Megabase Windows
Mean recombination rate (cM/Mb)
Chromosome
Chromosome Size (Mb)

Figure S7.

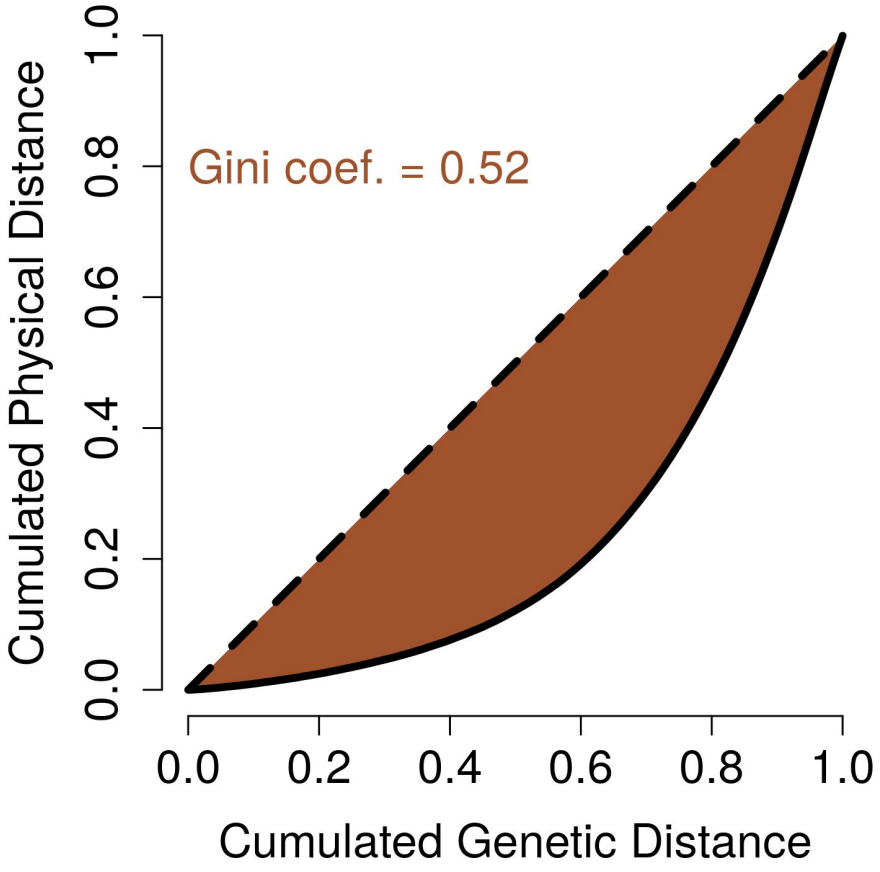
Gini coef. = 0.52
Cumulated Physical Distance
0.0
0.2
0.4
0.6
0.8
1.0
Cumulated Genetic Distance
0.0
0.2
0.4
0.6
0.8
1.0

Figure S8.

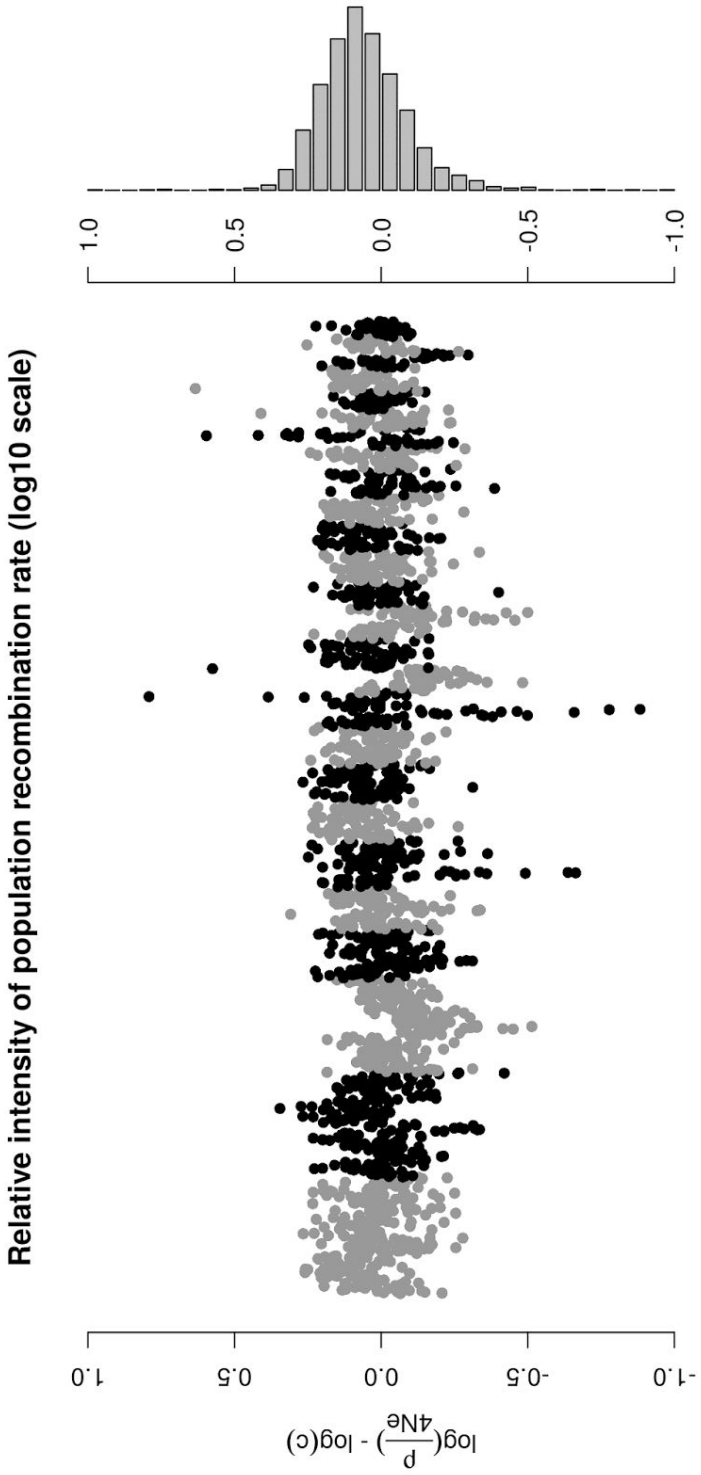
Relative intensity of population recombination rate (log10 scale)
1.0
0.5
0.0
-0.5
-1.0
log(ρ/4Ne) - log(c)

Figure S9.

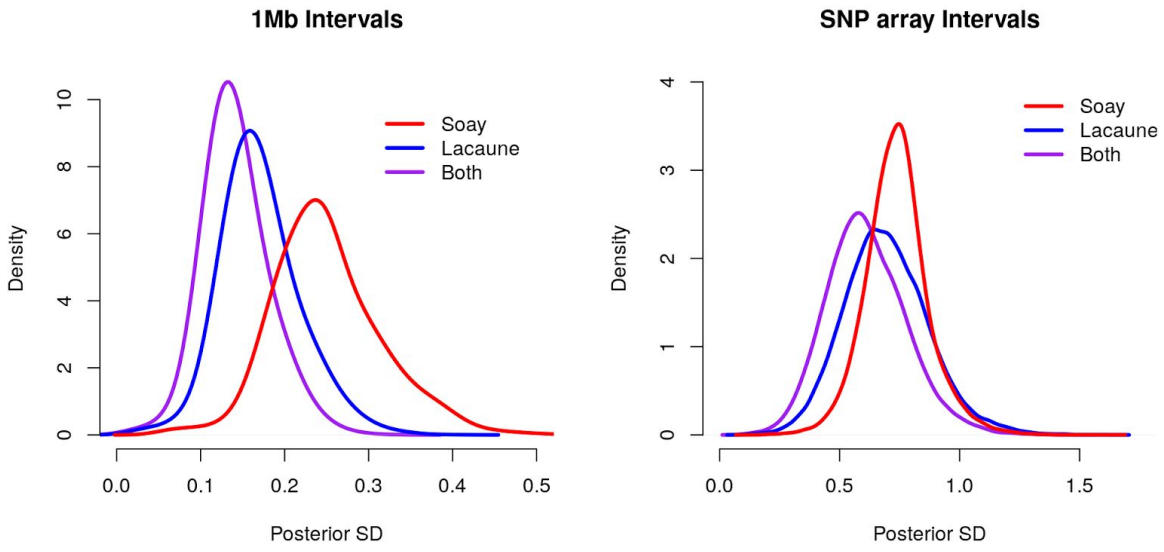
1Mb Intervals
Density
Posterior SD
Soay
Lacaune
Both
0
2
4
6
8
10
0.0
0.1
0.2
0.3
0.4
0.5
SNP array Intervals
Density
Posterior SD
Soay
Lacaune
Both
0
1
2
3
4
0.0
0.5
1.0
1.5

Figure S10.

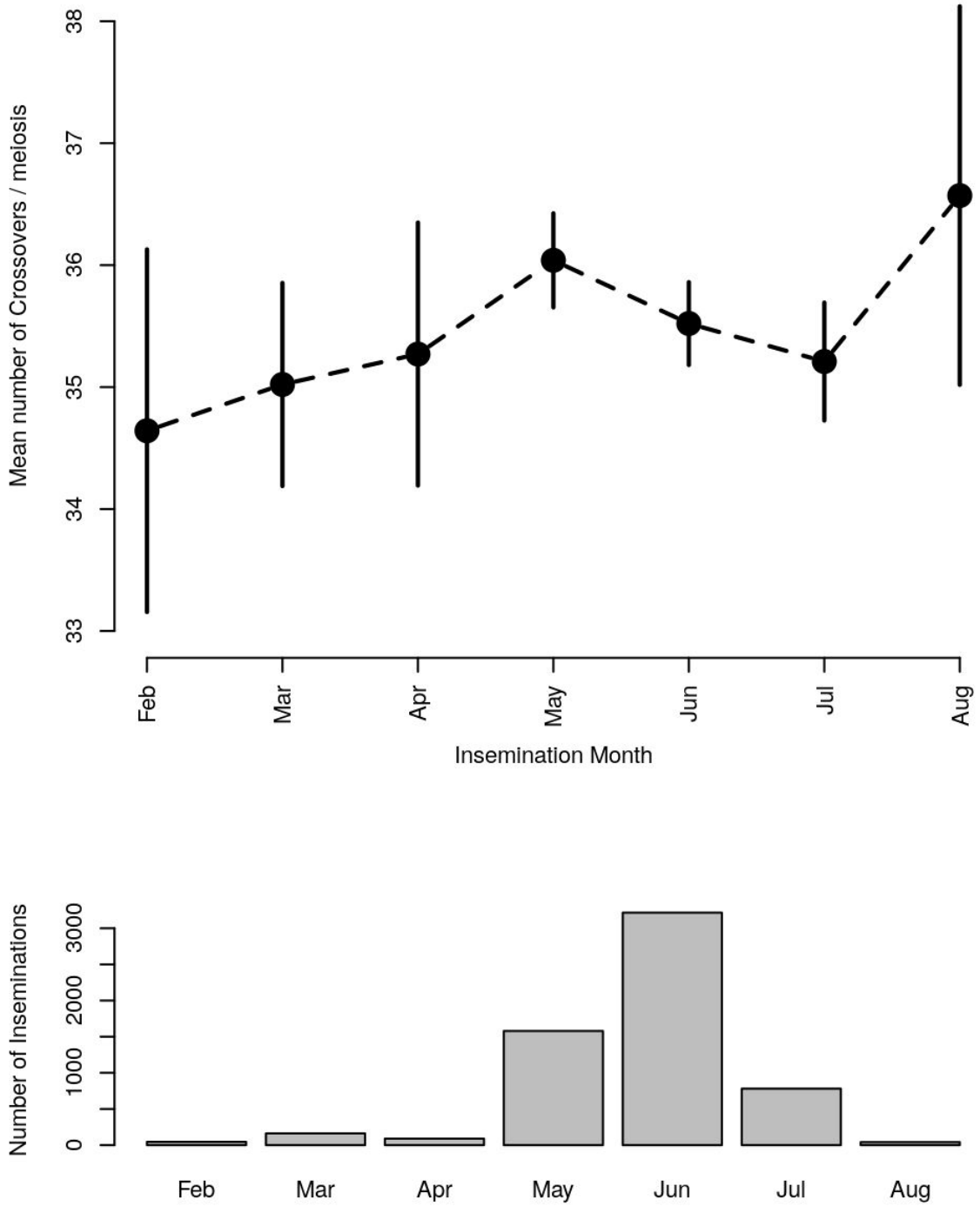
Mean number of Crossovers / meiosis
33
34
35
36
37
38
Feb
Mar
Apr
May
Jun
Jul
Aug
Insemination Month
Number of Inseminations
0
1000
2000
3000
Feb
Mar
Apr
May
Jun
Jul
Aug

Figure S11.

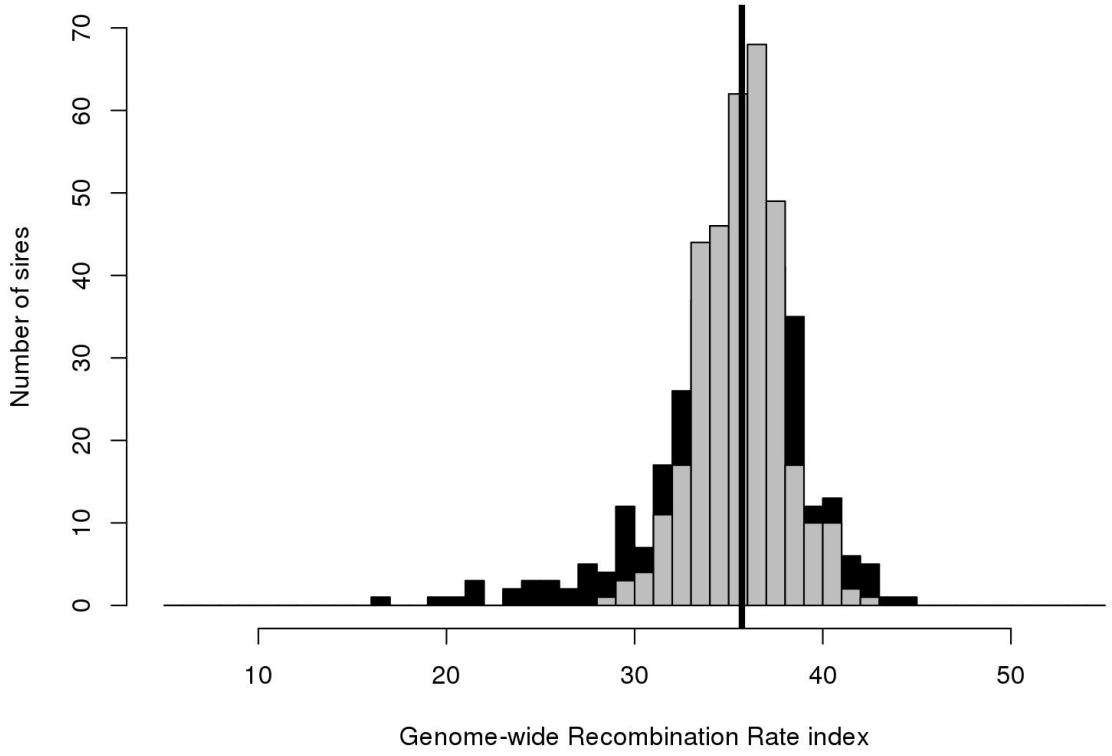
Number of sires
0
10
20
30
40
50
60
70
10
20
30
40
50
Genome-wide Recombination Rate index

Figure S12.

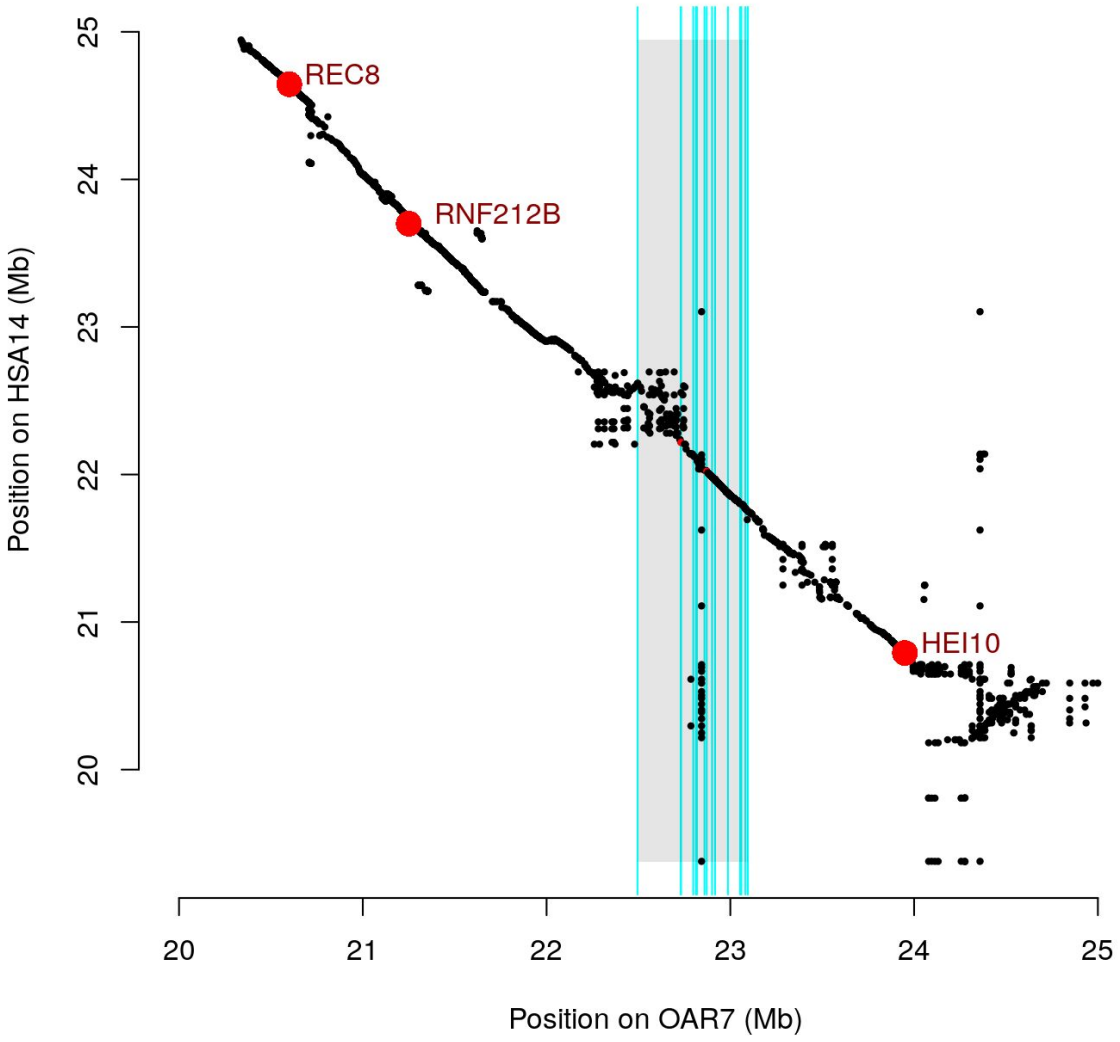
REC8
RNF212B
HEI10
Position on HSA14 (Mb)
Position on OAR7 (Mb)
20
21
22
23
24
25

Figure S13.

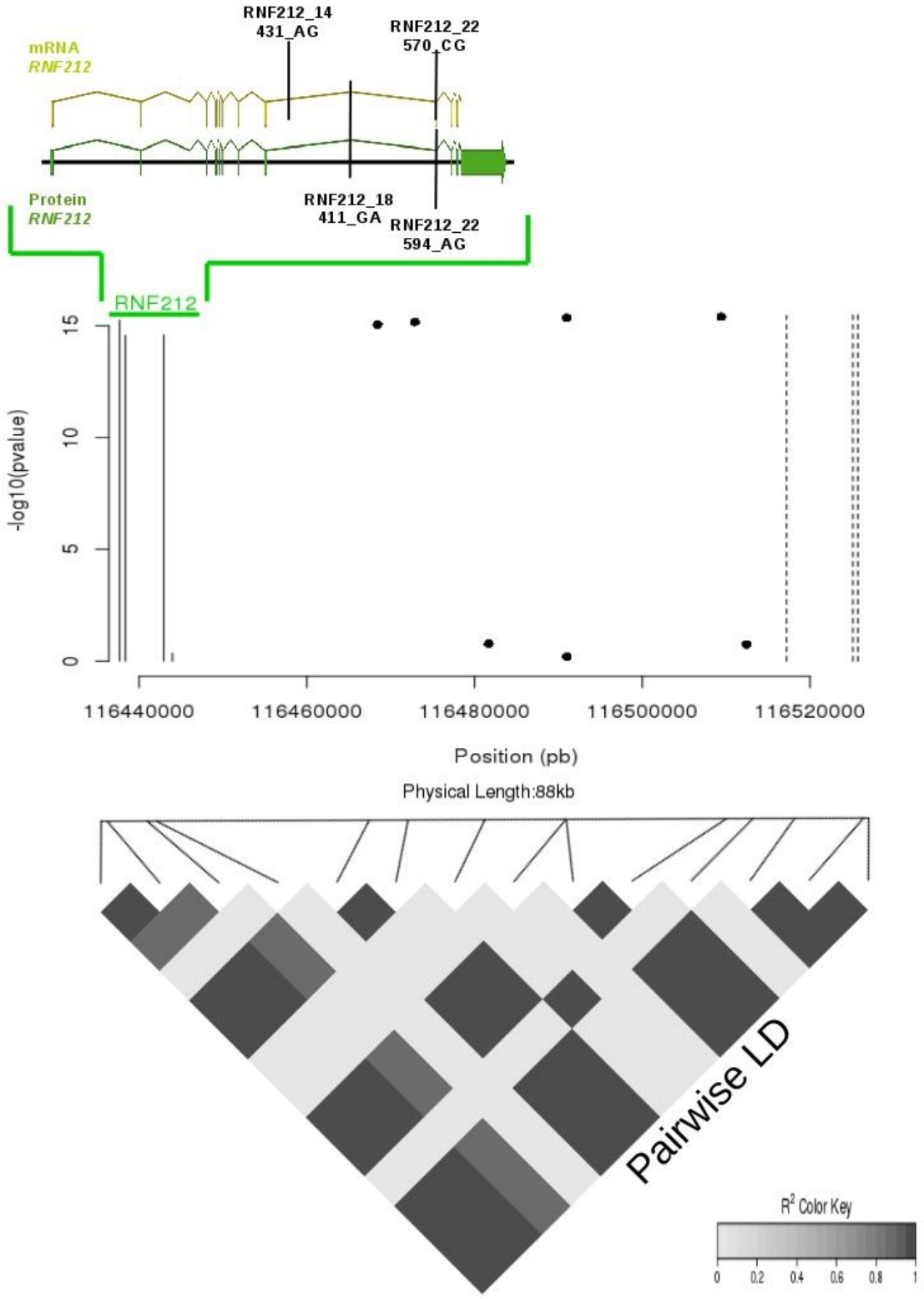
RNF212_14
431_AG
RNF212_22
570_CG
mRNA
RNF212
Protein
RNF212
RNF212_18
411_GA
RNF212_22
594_AG
RNF212
-log10(pvalue)
0
5
10
15
116440000
116460000
116480000
116500000
116520000
Position (pb)
Physical Length:88kb
Pairwise LD
R2 Color Key
0
0.2
0.4
0.6
0.8
1

Table S1: Primers used for resequencing exons of RNF212 and genotyping mutations.

Primer Name	Sequence 5' to 3'	Amplified fragment	Application
OAR6_RNF212_116426312	GTCCCTTCCTGCCTTGGTAC	781bp	sequencing exon1
OAR6_RNF212_116427093	CTCACTCCCCCGTCTCCTC		
OAR6_RNF212_116425796	CAGTGACACCCCACCCTAAT	2354bp	sequencing exon 1-1'
OAR6_RNF212_116428149	ACATGAGCCCTGCTTCTGTC		
OAR6_RNF212_116428877	TGGGAGATAATCTGGGCTGA	434bp	sequencing exon 2
OAR6_RNF212_116429310	TCTCCTAGCACACCAAGCAA		
OAR6_RNF212_116430870	CCCTCGAGTGTTTCCTGACT	271bp	sequencing exon 3
OAR6_RNF212_116431140	CAGTGTCTCTCGCCTTCAGA		
OAR6_RNF212_116432814	ACTAGATCCCGCATGCTGTC	872bp	sequencing exon 4
OAR6_RNF212_116433675	ATGGCTGACCTCAGAGAGGA		
OAR6_RNF212_116434284	GAAGTGGGATTGGTGCAGAT	1127bp	sequencing exon 5-5'-6-7
OAR6_RNF212_116435410	CACCCCTCTGCTTGGAGAC		
OAR6_RNF212_116435488	CTAGAGCCCCTGGTGAAGTG	775bp	sequencing exon 8
OAR6_RNF212_116436262	CCATCAGGCCTCTCCTTG		
OAR6_RNF212_116437201	CCTTCATCCACTCACCACCT	422bp	sequencing exon 9
OAR6_RNF212_116437622	CGCTTCCACAACGACACC		
OAR6_RNF212_116437703	CTTGGCTTCCTGTCCTCTTG	1805bp	sequencing part intron9
OAR6_RNF212_116439507	AGGGCGGCATATCTAAGGTT		

OAR6_RNF212_1 16437913	GGTCTCAGGCTGG CAGTTG	555bp	sequencing part intron9
OAR6_RNF212_1 16437358	ACTGCTTCCATTCC TCCAGA		genotyping RFLP BsrBI, SNP_14431_AG
OAR6_RNF212_1 16441598	AAGATGTTCCTTGG CTGGTG	541bp	sequencing part intron9
OAR6_RNF212_1 16442037	TTTGATCAACCTCC CATTCC		genotyping RFLP RsaI, SNP_18441_GA
OAR6_RNF212_1 16443189	GCTGTGAGTGGGT CTGGACT	865bp	sequencing part intron9
OAR6_RNF212_1 16444053	ACACAGGGACATG AGCACAG		
OAR6_RNF212_1 16441598	AAGATGTTCCTTGG CTGGTG	437bp	sequencing part intron9
OAR6_RNF212_1 16442037	TTTGATCAACCTCC CATTCC		
OAR6_RNF212_1 16445907	GCCCTCCTCAGAG CCAGA	662bp	sequencing exon 10
OAR6_RNF212_1 16446568	CTCCAGGGTGTTC GTGATG		genotyping RFLP Bsu36I, SNP_22570_CG and SNP_22594_AG
OAR6_RNF212_1 16445601	GTTGGTCACGGAA GGGGTAC	1522bp	sequencing exon 10-10'
OAR6_RNF212_1 16445343	CCACAGGTCCAGC GGGAG		
OAR6_RNF212_1 16447360	GTGCCCTTCGAAA CTGAGAC	706bp	sequencing exon 11, part exon 12
OAR6_RNF212_1 16448065	CACAGCTGGAGAC ACACGAG		

Description of Supplemental Files:

File S1: Recombination maps in the Lacaune male populations on 1 megabase intervals

File S2: Recombination maps in the Lacaune male populations on SNP array intervals

File S3: Graphical representation of Lacaune recombination maps

File S4: Recombination maps of the High-Density SNP array

File S5: Recombination rates in Lacaune, Soay, and Soay+Lacaune in SNP array intervals

File S6: Genome-wide Single SNP association results in the Lacaune population

File S7: Genome-wide Bayesian Sparse Linear Mixed Model results in the Lacaune population

File S8: Single SNP association results in the Lacaune population in the distal end of OAR6, including mutations in RNF212

File S9: Bayesian Sparse Linear Mixed Model results in the Lacaune population in the distal end of OAR6, including mutations in RNF212

File S10: Supplemental methods. Documentation of computer scripts for data analysis.