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SUPPORTING INFORMATION:

Introgression drives repeated evolution of winter coat color polymorphism in hares

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SUPPLEMENTARY METHODS

Samples and whole genome sequencing

We generated whole-genome sequencing data at individual low coverage for 59 mountain hares (*Lepus timidus*) collected from the Faroe Islands (N=20 diploid individuals), Fennoscandia (N=19; Sweden, Finland, Norway) and the Alps (N=20; Austria, Italy, France, Switzerland) (Tables S1 and S2). Genomic DNA was extracted from ear or organ tissues with PureLink Genomic DNA Mini Kit (Invitrogen) and quantified with Qubit fluorometer (Invitrogen). Double-indexed libraries were prepared according to a modified version of the protocol of Meyer and Kircher (1). Briefly, genomic DNA was sheared with Bioruptor® Pico and up to 500 ng of sheared DNA was used for blunt-end repair, adapter ligation and adapter fill-in. Indexing polymerase chain reactions (PCRs) was performed in 50 µl reactions containing 1X Herculase II reaction buffer, 250 µM each dNTP, 0.2 µM P5 and P7 indexing primers, 0.5 µl Herculase II polymerase and 3.5 µl DNA template. The PCR profiles were as follows: initial denaturation 98ºC – 2 min, 10 or 16 cycles: 98ºC – 20 s, 60ºC – 20 s, 72ºC – 20 s, and final elongation 72ºC - 5 min. The indexed libraries were quantified with quantitative PCR (qPCR), pooled and sequenced at low individual coverage in five lanes of an Illumina HiSeq 1500 sequencer in three separate runs (125 bp paired-end) at CIBIO-InBIO's New-Gen sequencing platform, Portugal.

In addition, whole-genome sequencing data at higher individual coverage from specimens from six *Lepus* species was analyzed, representing mountain hares (*L. timidus*) from the Faroe Islands, the Alps and Fennoscandia, European brown hares (*L. europaeus*) from Iberia and central Europe, two Iberian hares (*L. granatensis*) from the Iberian Peninsula, one broom hare (*L. castroviejoi*) from the Iberian Peninsula, one winter-brown and two winter-white snowshoe hares (*L. americanus*), and two black-tailed jackrabbits (*L. californicus*) (from 2, 3, 4 and this work) (Table S3).

Sequence data processing

The raw Illumina reads of whole-genome low coverage sequence data for 59 mountain hares were demultiplexed and their quality was assessed with FastQC (https://www.bioinformatics.babraham.ac.uk/projects/fastqc/). We removed adapters and filtered low quality reads using Trimmomatic (5) with the following settings: TRAILING:15, SLIDINGWINDOW:4:15,

MINLEN:30. The cleaned read pairs were mapped to a hare pseudo-reference (3) using bwa-mem with default settings (6). This reference was built by replacing in the European rabbit (*Oryctolagus cuniculus*) reference genome fixed differences to the group of three hare species (*L. americanus*, *L. granatensis* and *L. timidus*) (3). The European rabbit is related to hares (~11.8 million years divergence; 7) and its reference genome has high quality chromosome-level assembly and annotation (8). PCR duplicates were removed with PICARD (http://broadinstitute.github.io/picard/) and reads were locally realigned with GATK IndelRealigner (9). Then, for each individual, we calculated mean coverage and the proportion of properly mapped reads using Samtools (10). Two specimens with depth >2X were randomly subsampled to <1.5X to avoid overrepresentation of individual samples (Table S2). Sequencing resulted in a total coverage of 16.8X for Faroese hares, 17.1X for Alpine hares, and 18.0X for Fennoscandian hares. The resulting BAM files were used as inputs for further analyses. Taking advantage of sequencing individually barcoded DNA libraries, for all analyses using low coverage data, only sites represented by at least six different individuals from each population were used, to avoid strong biases in the representation the sequenced specimens.

The raw reads of higher coverage data were processed as described above, except the Trimmomatic settings, which were as follows: TRAILING:20, SLIDINGWINDOW:4:20, MINLEN:36. Adapters were removed with cutadapt (11). SNP calling for the whole chromosome 4 was performed with Samtools (mpileup) and Bcftools (call -m) separately for each individual. Resulting vcf files were filtered (bcftools filter) for minimum depth of 6X, maximum depth of 2 times the average depth, and a minimum QUAL of 50.

Genetic diversity

We used PoPoolation (12) to calculate genome-wide nucleotide diversity (π) and theta (θ) for each population separately (Fig. S8C). For each population, mpileup files with masked SNPs in the proximity of indels (--indel-window 5) were used as input to estimate diversity indices in 200 kb non-overlapping windows, using the following parameters: --min-count 4 --min-coverage 10 --max-coverage 51 --min-qual 20 --min-covered-fraction 0.25.

Population structure and evolutionary relationship

Principal component analysis (PCA) based on low individual coverage data was performed with ANGSD (13), using a single-read sampling approach (IBS) appropriate for low-depth data (Fig. S1A). Genotype-likelihoods were calculated using the Samtools method, as implemented in ANGSD (-GL 1). For all ANGSD analyses we used the following filtering criteria: -uniqueOnly 1 -remove_bads 1 -trim 0 -C 50 -baq 2 -minMapQ 20 -minQ 20 -SNP_pval 1e-6. The PCA was based on 123,995 SNPs sampled every 20 kb with PLINK --bp-space command (14) to reduce non-independence due to linkage. The proportion of variance explained by each component was calculated with the R function *prcomp*.

A neighbor-joining tree (NJ) was constructed based on pairwise genetic distances between individuals (Fig. S1B). The distances were estimated with ngsDist (15) and ngsTools (16) from genotype posterior probabilities generated with ANGSD (-doGeno 8 -doPost 1), based on 127,413 polymorphic sites sampled at least every 20 kb. We performed 100 bootstrapped replicates by randomly sampling with replacement blocks of 100 SNPs (-n_boot_rep 100 -boot_block_size 100). Trees were generated using FastME (17).

We also constructed a population tree based on allele frequencies (Fig. 1D), as implemented in TreeMix (18). First, allele frequencies were estimated with ANGSD, using the European rabbit genome reference (OryCun2.0, Ensembl, release 80) to determine the ancestral state (-doMajorMinor 5 -doMaf 1). Then, the ANGSD output was converted into the TreeMix input (allele counts at each SNP) with custom python scripts (available at https://github.com/evochange/far), sampling sites at least every 20 kb, resulting in 136,834 SNPs. TreeMix was run 1,000 times.

For both the NJ and TreeMix analyses, the snowshoe hare (*L. americanus*) was used as outgroup. Trees were summarized with SumTrees of the DendroPy library (19) and visualized with FigTree (http://tree.bio.ed.ac.uk/software/figtree/).

Approximate Bayesian Computation

The introduction of mountain hares into the Faroe Islands was modelled using Approximate Bayesian Computation (ABC; 20). The demographic scenario was built in accordance with the historical information about the introduction, but with wide uniform prior distributions to allow parameter inference (Table S4). Briefly, it consisted of an ancestral population of size N_{FSC} (effective population size of the Fennoscandia population) that split at time *Ti* generations ago (the time of the introduction into the Faroe Islands; a generation

length of two years was considered; 21); while the Fennoscandian effective population size (N_{FSC}) was kept constant, a growth rate of g was set for the Faroese population, from the time of introduction (T_i) until the present (effective population size N_{FAR}). Simulations were performed under a mutation rate estimated from the data, with a transition rate set to 0.33.

The data was characterized by the following summary statistics: number of segregating sites (S), nucleotide diversity (θ_π), Watterson's theta ($\theta_{Watterson}$), and Tajima's D per population, and F_{ST} between populations, including their means, standard deviations and medians (27 summary statistics). The summary statistics were calculated using PoPoolation2 (22) and npstat (23), pooling the sequencing data for each population. For the empirical dataset, we removed sites overlapping coding regions and repeats, sites with a base quality <30, and reads with a mapping quality <30. Only sites represented by at least 10 individuals in each population (determined by the individual barcodes) and with coverage between 10X and 51X per population were retained. The summary statistics were calculated from independent windows (at least 100 kb apart) of 2 kb with at least 85% of the window covered, which resulted in 501 windows. Demographic inference is sensible to the inclusion of sequencing errors as rare variants (24, 25), and we thus filtered empirical and simulated datasets to include SNPs with at least three observations of the minor allele. This approach has been suggested to be preferable to the potential bias introduced by sequencing errors (26).

Simulations of the demographic model (Fig. 1E) were performed using fastsimcoal26 (27) with 100,000 replicates. We simulated 501 windows of 2 kb under a finite-site model, considering 20 diploid individuals (40 haploid) from FAR and 19 diploids (38 haploid) from FSC, as in our dataset. We generated Arlequin files in diploid formats (-g), outputting whole DNA sequences (-S). These files were converted to population bam files, that were used to produce mpileup and sync files, inputs for npstat and PoPoolation2. Summary statistics were calculated as for the empirical dataset, in 501 2 kb non-overlapping windows for each simulation.

Parameter estimation was performed using ABCtoolbox package (28). Summary statistics were transformed via Partial Least Squares (PLS), using the *PLS* R package (29), and the root mean squared error plots (RMSEP) were inspected to determine the number of PLS components. The marginal density P-value and the Tukey P-value, both based on 1,000 retained simulations (1% closest to the empirical data), were used to evaluate whether the model was able to reproduce the empirical summary statistics. While our approach did

not explicitly model the occurrence of sequencing errors, filtering the empirical and simulated datasets for minimum allele counts allowed recovering well the empirical statistics under our demographic scenario (marginal density P-value = 0.73; Tukey P-value = 0.74). We used the PLS transformed statistics to estimate demographic parameters by applying the ABC-GLM algorithm (30) and retaining 1% of the simulations closest to the observed data (Fig. S2, Table S4). Finally, the accuracy of parameter estimates was assessed by cross-validation, based on 1,000 random simulations for which the true parameter values were known (pseudo-observed datasets) (Fig. S3).

Detection of differentiation and association outliers

Scans of differentiation were performed using an array of tests based either on pooled sequence data per population/phenotype (ensuring a minimum representation of six individuals) or from genotype likelihoods, as implemented in PoPoolation2 (22) and ANGSD (13), respectively.

A genome scan of Population Branch Statistic (PBS; 31) was performed in 20 kb non-overlapping windows (Fig. 2A). Given three structured populations (Fig. S1A) and the closer relationship of Faroese and Fennoscandian populations (Fig. 1D, Fig. S1B), this statistic is suited to identify localized strong allele frequency changes in the specific branch of the Faroese hares, which deviate from the genome-wide norm, and may result from recent selective sweeps (31). PBS was calculated in 20 kb non-overlapping windows, based on allele frequencies estimated from individual genotype likelihoods, as implemented in ANGSD (13). The European rabbit reference was used to determine the ancestral state (-anc). PBS values were plotted against chromosome position using the *qqman* R package.

Association tests based on allele frequency differences between cases and controls using genotype likelihoods were performed in ANGSD (-doAsso 1), setting the Faroese individuals (winter-grey phenotype) as cases and the remaining individuals (from Alps and Fennoscandia) as controls (Fig. S4E). For this analysis, additional filters for minimum (-setMinDepth 30) and maximum (setMaxDepth 150) depth were used. The resulting likelihood ratio statistic (LRT) was converted to $-\log_{10}(P)$ values assuming a chi-square distribution with one degree of freedom. The mean $-\log_{10}(P)$ values for windows of 100 SNPs were plotted against chromosome positions with a custom R script (available at https://github.com/evochange/far). The Bonferroni correction for multiple tests was used to determine the significance threshold, which was set to $p < 6.15 \times 10^{-7}$.

In addition, the scan was performed for single pairwise comparisons, i.e. Faroese hares vs. Alpine hares and Faroese hares vs. Fennoscandian hares, adjusting coverage and significance thresholds (Fig. S4).

For PoPoolation2 analyses, concatenated bam files were used to produce mpileup files with Samtools, removing reads with mapping quality lower than 20. The mpileup files were then converted to synchronized files requiring base qualities of at least 20 and masking 5 bp on either side of inferred insertion-deletions (--indel-window 5). The synchronized file was then used as an input to calculate F_{ST} (--karlsson-fst) and Fisher Exact Tests (FET) in non-overlapping 20 kb windows, containing at least 30 SNPs (Fig. S4A and B). Analyses contrasting Faroese hares with Alpine hares and Fennoscandian hares pooled together were performed using the following parameters: --min-count 4, --min-coverage 10, --max-coverage 51,105 --window-size 20000 --step-size 20000 --min-covered-fraction 0.25 --pool-size 40:78. The maximum coverage was chosen to be 3 times the mean coverage of each concatenated bam. For FET, a Bonferroni-corrected significance threshold was used and set at $p < 3.7x10^{-7}$. Analyses contrasting Faroese hares and Alpine hares, and Faroese hares and Fennoscandian hares were done adjusting coverage and significance thresholds and pool sizes (Table S4).

Discovery of structural variants

The Faroese mountain hare genome sequenced at 6.9X was used to inspect the longest candidate region (mapped to chromosome 4) for structural variation, including deletions, insertions, inversions, duplications and translocations. Lumpy (32), which uses read-pair, split-read and read-depth information to detect structural variation, Delly (33), which relies on read-pair and split-read information, and BreakDancer, which uses read-pair information (34), were used with default settings. In addition, candidate structural variants were confirmed through visual inspection of the bam files in IGV (Integrative Genomics Viewer; 35, 36). A candidate insertion-deletion was detected and validated using a three-primer PCR assay, which resulted in distinguishable PCR products: one forward primer anchored close to the insertion-deletion (*LTM_indel_F1*), one forward primer within the insertion (*LTM_indel_F01*), and a reverse primer immediately after the insertion-deletion (*LTM_indel_R*) (Table S5). The sequences of the amplified fragments were confirmed by Sanger sequencing.

SNP and insertion-deletion genotyping

To confirm the genotype-phenotype association within the candidate regions in chromosomes 4 and 15, clarify the segregation patterns of the inferred variants and remove the confounding effect of population structure that could create spurious signals of association in our genome scans, we genotyped 59 SNPs and the inferred insertion-deletion in 97 *L. timidus* individuals from the same sampling localities included in the genome scans: FAR, N = 35; FSC, N = 34; ALP, N = 28 (Table S1, Fig. S5). DNA extraction for the additional samples was performed as previously described. In addition, 29 individuals from Sweden and Russia, deposited in the collection of the Swedish Museum of Natural History, originally sampled during winter and for which the winter color phenotype could be assessed – grey (N = 15), white (N = 14) – were also included in the genotyping assay (Tables S1, S6 and S7). DNA extraction of museum skin samples was performed in dedicated laboratory facilities suitable for manipulation of samples with low content of endogenous DNA, following Dabney et al. (37). All genotyped SNPs were chosen for having allele frequency differences between the Faroese and other populations between 0.75 and 1, according to the PoPoolation2 analysis (snp-frequency-diff.pl), and were located in windows showing extreme PBS. Thirty-six and five SNPs were agglomerated in the regions of *Agouti* and *USP38*, respectively, and the remaining 18 were located in other windows of extreme PBS scattered along the genome. SNPs were genotyped using the MassARRAY technology at the Genome Transcriptome Facility in the University of Bordeaux, France. The insertion-deletion was genotyped using the devised three-primer PCR approach described above with some modifications for the museum samples (indicated in parentheses). PCRs were performed in 6 µl reactions containing 2.1 µl Qiagen Multiplex PCR Master Mix (2.4 µl for museum samples), 0.2 µl primer F1, 0.1 µl primer F2, 0.3 µl primer R, 2.8 µl water (2.4 µl) and 0.5 µl template DNA. The PCR profile was as follows: 95ºC - 15 min, 35 cycles of 95ºC - 30 s, 62ºC - 30 s (60 s) and 72ºC - 35 s (40 s), and 72ºC - 10 min. For the museum samples showing greater level of DNA degradation, an independent validation of the genotypes was performed using another three-primer PCR approach (primers *LTM_indel*_F2, *LTM_indel_F3* and *LTM_indel_R*; Table S5). A volume of 0.3 µl of each primer was used in these additional PCR reactions. Significance of the associations of SNPs and the insertion-deletion with the winter color phenotype was tested using *SNPassoc* R package (38).

Gene expression analysis

The expression of *Agouti* hair-cycle isoform (*Agouti-HC*) and reference genes *ACTB* and *SDHA* (Figs. 3 and S7) was quantified in skin biopsies sampled during the autumn molt from winter-grey (FAR; N=3) and winter-white hares (ALP; N=5). Skin was opportunistically sampled from the dorsum of mountain hares killed during regular hunting campaigns, representing three stages of the progressing molt: brown, intermediate and white/grey (nine skin samples from the three Faroese hares, and 15 skin samples from the 5 Alpine hares) (39). Total RNA was extracted from 30 mg of each skin sample with the RNeasy Mini Kit (Qiagen). Tissue was homogenized in a rotor-stator homogenizer (Mixer Mill MM400, Retsch) at 30 Hz for 10 min. The RNA integrity was checked with the Agilent Technologies TapeStation for a minimum RIN > 7 (Table S9). First-strand cDNA synthesis was performed using oligo (dT) primers and the GRS cDNA synthesis kit (GRISP) using 400 ng of RNA from skin sample (except for two samples that had insufficient amount of RNA, resulting in no qPCR product). Relative expression was quantified using quantitative PCR (qPCR) of the gene of interest, normalized across individuals to the reference genes. Primers amplifying the *Agouti* hair cycle isoform (*Agouti-HC*) were designed to anchor in the *Agouti-HC* non-coding exon and the first *Agouti* coding exon. All primers, both for *Agouti* and reference genes, were anchored in regions showing no polymorphisms between winter color morphs. The amplification efficiencies were calculated based on the slope of a regression line fitted to C_t values of five samples from 2-fold serial dilutions ($E = 10^{(-1/slope)} - 1$), using two replicates per sample (Table S9). Then, three replicate qPCR reactions were performed per skin sample, using 1X iTaq™ universal SYBR® green supermix (Bio-Rad), 0.4 µM each primer and 1µl cDNA (2-fold dilution of stock cDNA, except for four samples marked with asterisks in Table S9), in a total volume of 10 µl. The qPCR thermal conditions were as follows: 95°C – 30 s polymerase activation and cDNA denaturation, 40 cycles of 95°C – 5 s, 62°C – 30 s, and melting curve analysis from 65°C to 95°C, with 0.5°C increments. The raw qPCR results, presented as the threshold cycle (C_t), were used to calculate expression of the *Agouti-HC* isoform, normalized by the expression of the *ACTB* and *SDHA* genes using the formula $2^{-\Delta Ct}$, where $\Delta C_t = C_t^{\ Agouti} - C_t^{\ ref\ gene}$. We performed calculations by subtracting the mean C_t of the reference gene from each technical replicate C_t of the *Agouti* gene (Table S9), to present the relative expression as normalized individual data points. Additionally, we performed a Bayesian analysis where raw qPCR data were represented as molecule counts, and described using generalized linear mixed models under a Poisson-lognormal error distribution (40). This method is suitable also for low-abundant targets, as it uses information about no amplification status. Although

reference genes may sharpen estimates of model parameters, they are not strictly required, because normalization is performed within the model. We used the naïve model implemented in *MCMC.qpcr* R package to infer expression levels of all three genes, *Agouti, ACTB, SDHA* (Fig. S7B).

Selection analyses

Tajima's D (41) for chromosome 4 (Fig. S8D) was calculated with PoPoolation1 after subsampling the mpileup file to ensure uniform coverage (--target-coverage 10), as recommended in the software's manual. Tajima's D was estimated in 200 kb non-overlapping windows with the following parameters: --min-count 1 --min-coverage 4 --max-coverage 10 --min-qual 20 --min-covered-fraction 0.25 --dissable-corrections.

To identify signals of selective sweeps along chromosome 4, we used Pool-hmm (42), which implements a hidden Markov model to detect signatures of selective sweeps in Pool-Seq data (Figs. 2D, S8 and S9). Based on the pattern of allele frequencies, this method predicts the most likely hidden state at each site from three possible states (neutral, intermediate, selection). The hidden Markov model, takes into account also the correlation of allele frequencies between sites in addition to the site frequency spectrum (SFS), thus being more robust to bottleneck scenarios than composite likelihood ratio approaches (43). We ran Pool-hmm for pooled sequence data per population with the following parameters: -n 40 -c 10 -C 51 -q 30 -e sanger --pred -k 1e-30 --theta 0.0034 (theta estimated with PoPoolation1). To take into account the confounding effect of the strong non-equilibrium situation imposed by the demographic history, the transition probability between hidden states (k) was determined based on neutral data simulated according to the inferred demographic model using ABC (Table S4). Simulations were in addition performed retaining the extremes of the 95% high posterior density intervals that maximize the strength of the bottleneck and population growth (lower 95% HPD value for N_F and g and larger 95% HPD for N_{FAR}; Table S4). We simulated 1,000 replicates of 1 Mb regions using fastsimcoal26 (27), assuming recombination rate 1 cM/Mb ($1x10^{-8}$ per bp per generation) (44). The conservative k=1e-30 was retained, which resulted in a False Discovery Rate = 0 under the demographic scenario and 0.008 under the extreme bottleneck and growth scenario.

We also looked for signals of selective sweeps along chromosome 4 using the composite likelihood ratio test derived from genotype likelihoods, implemented in SweeD (45) (Figs. S8 and S9). This method detects signals of recent positive selection based on local deviations in the SFS relative to the background SFS.

The input for SweeD was prepared by converting the ANGSD allele frequencies output (mafs file) into the SweepFinder format, using a custom R script (available at https://github.com/evochange/far). The European rabbit allele (ancestral state) was used to determine the major allele (-doMajorMinor 5). We ran SweeD in ~20 kb windows (-grid 4570) using polymorphic sites and fixed derived sites. The significance P-value threshold for CLR was defined based on the CLR distribution from data simulated according to the demographic model inferred using ABC, using the parameters described above. We simulated 1,000 windows of 10 Mb, assuming recombination rate 1 cM/Mb (44), using *msms* (46) and used P<0.01 as the CLR significance threshold.

Finally, we estimated the probability of fixation of a rare allele ($1/2N_e$) after ~65 years of evolution under drift alone with three sets of parameters using the forward simulations implemented in SLiM3 (47). The probability of fixation at 33 and 65 generations (considering putative generation times of two and one year, respectively) was determined using 10,000 replicates of the drift process under non-equilibrium scenarios (Table S10). The three tested scenarios used 1) the modes of ABC parameter estimates for size of initial population and growth rate; 2) the low 95% HPD interval of ABC parameter estimates for size of initial population and growth rate (implying the strongest bottleneck and population growth); and 3) the historical record of four founder individuals and the growth rate needed to achieve the low 95% HPD interval value of the ABC inference for current effective population size of the Faroese hare (20,000 diploid individuals) (Table S10). Negative growth backward-in-time inferred from the ABC analysis was converted into positive growth for the forward-in-time simulations. The probability of fixation was determined by the proportion of simulations where fixation was achieved at each time point.

Topology weighting

To understand the evolutionary origin of the variants associated with winter coloration in mountain hares, we first performed a topology weighting analysis along chromosome 4, as implemented in Twisst (48), using whole-genome sequencing data from *Lepus* species obtained at higher coverage (6.1 - 29.3X; Table S3). We used genomics_general scripts available at https://github.com/simonhmartin/genomics_general to convert the vcf file to "geno" format (script: parseVCF.py), and then to calculate neighbor-joining trees in windows of 50 SNPs (script: phyml_sliding_windows.py). Topology weighting was performed considering three different sets of species/populations: 1) one winter-grey Faroese mountain hare (*L. timidus*; FAR), two winter-white

mountain hares, from the Alps and Fennoscandia (MTH), two Iberian hares (IBH), and two European brown hares - one from the Iberian Peninsula (EBH_IB) and one from central Europe (EBH_CE) (Fig. S10A); 2) one winter-grey Faroese mountain hare (FAR), two winter-white mountain hares, one from the Alps and one from Fennoscandia (MTH), two Iberian hares (IBH), one winter-white snowshoe hare (SSH_WW), and one black-tailed jackrabbit (BTJ) (Fig. S10B); 3) one winter-grey Faroese mountain hare (FAR), two winter-white mountain hares, one from the Alps and one from Fennoscandia (MTH), two Iberian hares (IBH) and one black-tailed jackrabbit (BTJ) (Fig. 4A).

f_d statistic and d_{XY}

To explore the close relationship between Faroese mountain hare and the Iberian hares at the *Agouti* region, the fraction of introgression (f_d statistic) (49) was estimated in 20 kb overlapping windows (step size 2 kb) along chromosome 4, with at least 100 genotyped SNPs per window (Fig. 4B). We used genomics_general scripts available at https://github.com/simonhmartin/genomics_general, and the following phylogenetic conformation: *P1 = FSC, P2 = FAR, P3 = IBH, O = RAB*. Genomics_general scripts were also used to calculate the absolute genetic distance (d_{XY}) between Faroese *L. timidus* and *L. granatensis*, in 20 kb overlapping windows (step size 2 kb) along chromosome 4, with at least 25% sites covered per window. From d_{XY}, the Relative Node Depth (RND; 50) was calculated by dividing d_{XY} by the distance to the European rabbit (RAB). This statistic corrects the estimated d_{XY} using the distance to an outgroup to control for local variation in mutation rate. The f_d statistic was also calculated using the European brown hare (*L. europaeus*) instead of the Iberian hare (*L. granatensis*) as *P3* (Fig. S11).

RAxML local phylogeny

An alignment of six *Lepus* species (Table S3) was generated for the genomic region showing a sharp increase in *fd* values (4:5,400,000-5,760,000) (Fig. 4B) and used to construct a local maximum-likelihood phylogeny using RAxML (51) (Fig. 4F). A phylogeny for the whole chromosome 4 was also built using the same specimens (Fig. 4E). RAxML was run with the following settings: -m GTRGAMMA -f a -x 2408 -N 100 -p 2330 and the sequence from the European rabbit reference genome was used as the outgroup.

Simulations of d_{XY}

To further test whether the low d_{XY} between the winter-grey mountain hares and the Iberian hares resulted from introgression or was instead compatible with an incomplete lineage sorting scenario, we performed coalescent simulations of species divergence. Species divergence history parameters, including effective population sizes of current and ancestral populations, time of divergence and migration rates, were estimated with G-PhoCS (52), based on high coverage data from two mountain hare individuals (Alpine and Fennoscandian; Table S3) (from 3) and two Iberian hare individuals (Table S3) (from 3). Fragments of 1 kb distancing at least 50 kb were selected from intergenic regions (at least 1 kb from the nearest gene). Repeats, identified in the rabbit reference genome with RepeatMasker and downloaded as a bed file from UCSC Genome Browser (https://genome-euro.ucsc.edu), were masked in the selected 1 kb fragments. Finally, fragments with > 40% missing data were excluded. This resulted in a dataset of 11,480 independent 1 kb loci. Model parameters were inferred assuming possible bidirectional migration. The model was run three times and the convergence of the combined run was checked with Tracer v1.7 (53) by examining the effective sample size (ESS) of each parameter. For all runs, 100,000 generations were discarded as burn-in, and 1,000,000 MCMC iterations were run, sampling every 10 iterations. To convert scaled parameter estimates, we used a mutation rate (μ) of 2.8×10^{-9} substitutions/site/generation (3), considering a divergence of 11.8 million years divergence between rabbits and hares (7) and a presumable generation length of two years (21).

The parameter values from the inferred model (Table S11) were then used in *msms* (46) to simulate 1,000 fragments of 20 kb, and test if the variance of the coalescent and lineage sorting process could retain closely related variants in the species, as seen in the empirical data. Given that the estimated local mutation rate of the *Agouti* region (using $\mu = d_{XY} / (2T_D + 4N_e)$ (54), where d_{XY} is the sequence distance between *L. timidus* and the rabbit averaged along the region, T_D is the time of divergence between hares and rabbits of 11.8 million years (7), and N_e is the ancestral effective population size (N_e = 1,000,000 assumed)) is larger than the genome-wide estimate (3.2×10^{-9} vs 2.8×10^{-9} substitutions/site/generation) we opted to perform the simulations using the latter, to increase the conservative nature of the test.

Simulations were done under four demographic models: i) the full demographic model, to assess the reliability of the demographic inference to replicate genome-wide empirical data; ii) inferred demographic model but without inter-species migration, to assess d_{XY} expectations under a strict lineage sorting model; iii)

model with strong selection in the ancestral population, leading to fixation of one variant before the split and reducing d_{XY} to a minimum, and no migration, and iv) model with selection prior to the split and with bidirectional migration. The *msms* commands were as follows:

i) full demographic model:

msms 4 1000 -t 70.8 -I 2 2 2 0 -m 1 2 0.190 -m 2 1 0.010 -n 1 0.57 -n 2 0.96 -en 0.74 2 1 -ej 0.74 1 2,

where t = 4 x 316277 x 2.8 x 10^{-9} x 20000;

ii) demographic model without migration:

msms 4 1000 -t 70.8 -I 2 2 2 -n 1 0.57 -n 2 0.96 -en 0.74 2 1 -ej 0.74 1 2;

iii) selection in ancestral population, model without migration:

msms 4 1000 -t 70.8 -I 2 2 2 0 -n 1 0.57 -n 2 0.96 -en 0.74 2 1 -ej 0.74 1 2 -N 316277 -SFC -SI 0.755 2 0 0.0000016 -Sc 0.74 2 63255 0 0 -Sp 0.5;

where selection coefficient s = 0.1, selection starts 25,000 generations ago before population split, and an initial frequency of the beneficial allele of $1/2N_e$. By using -SFC flag we kept only simulations where the beneficial allele was not lost, therefore leading to its fixation.

iv) selection in ancestral population, model with migration:

msms 4 1000 -t 70.8 -I 2 2 2 0 -m 1 2 0.190 -m 2 1 0.010 -n 1 0.57 -n 2 0.96 -en 0.74 2 1 -ej 0.74 1 2 -N 316277 -SFC -SI 0.755 2 0 0.0000016 -Sc 0.74 2 63255 0 0 -Sp 0.5;

The empirical distribution of d_{XY} along the *Agouti* association region was generated by sampling with replacement 20,000 sites from the region 1,000 times, and calculating d_{XY} for each replicate (Fig. 4D and S12A). This analysis was replicated for the divergence between the mountain hare (using the same whole-genome sequence data; Table S3) and the European brown hare (using one genome from the Iberian Peninsula and another from central Europe; Table S3). In this case, the parameters of the demographic model of divergence were inferred from 5,705 independent 1 kb loci. d_{XY} simulations were conducted as described above (Fig. S12B and C).

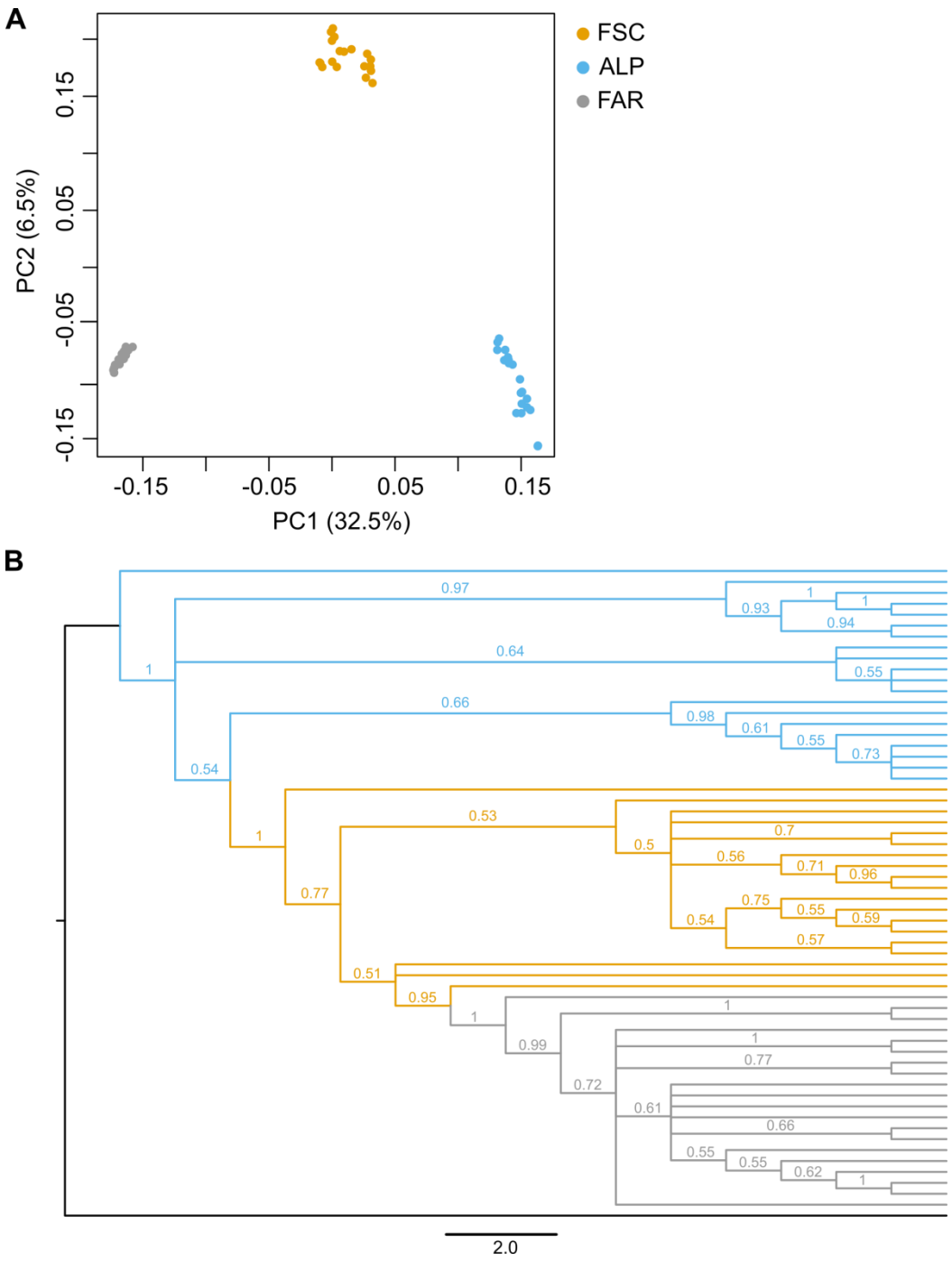

Fig. S1. Population structure and evolutionary relationships among mountain hare populations: grey - the Faroe Islands (FAR), blue - the Alps (ALP), orange - Fennoscandia (FSC). **(A)** Principal component analysis based on 123,995 polymorphic sites sampled every 20 kb to reduce non-independence. The proportion of variance of the first two principal components is shown. **(B)** A neighbor-joining tree based on individual pairwise distances, constructed with 127,413 polymorphic sites and node support derived from 100 bootstrap replicates; the black line depicts the outgroup, the snowshoe hare (*Lepus americanus*).

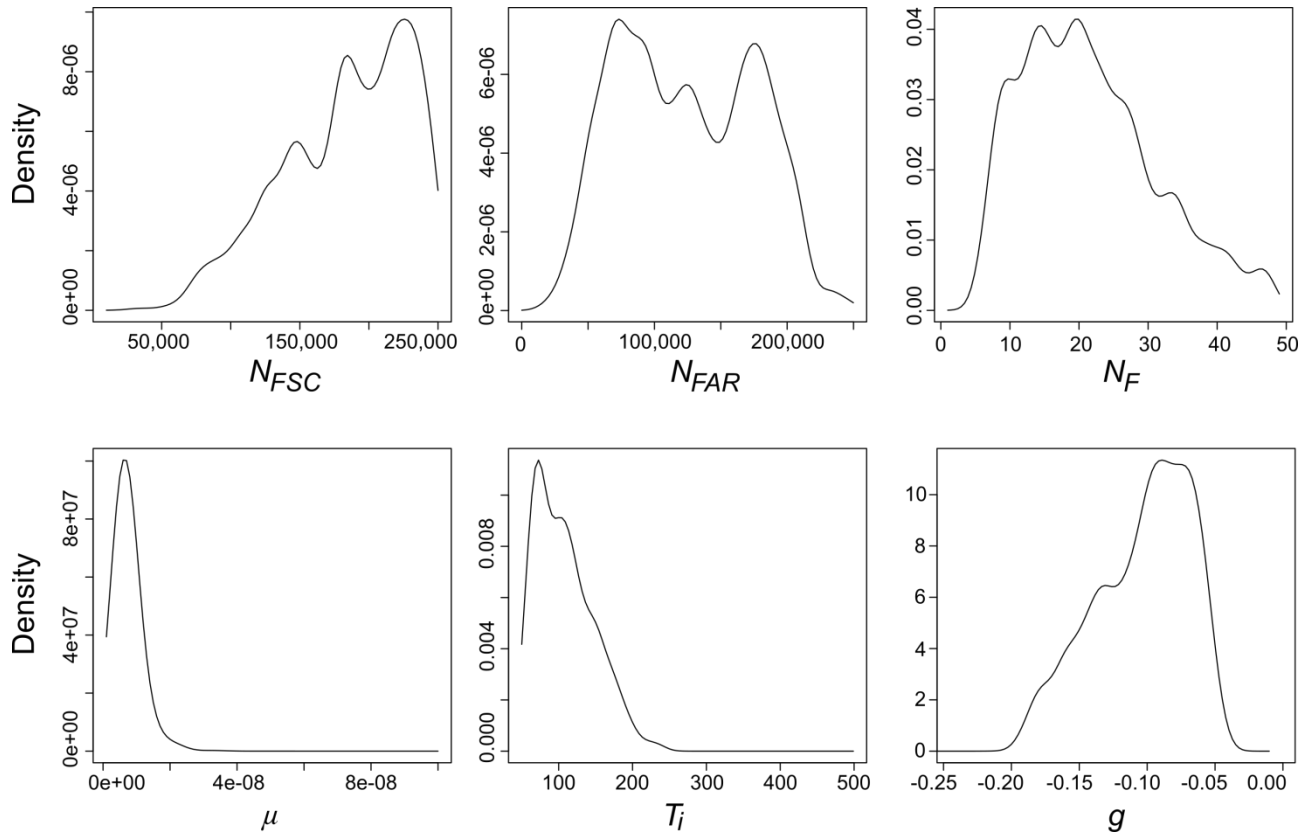

Fig. S2. Distribution of posterior probabilities of the demographic parameters inferred with ABC. N_{FSC} – effective population size (haploid numbers) of Fennoscandian population, N_{FAR} – effective population size (haploid numbers) of Faroese population, N_F – effective population size (haploid numbers) of the Faroese hare founder population, T_i – time of the introduction in generations, g – growth rate (negative value backward in time implies expansion forward in time; calculated according to the equation $N_F = N_{FAR}\, e^{gT_i}$), μ – mutation rate in units of mutations per site per generation.

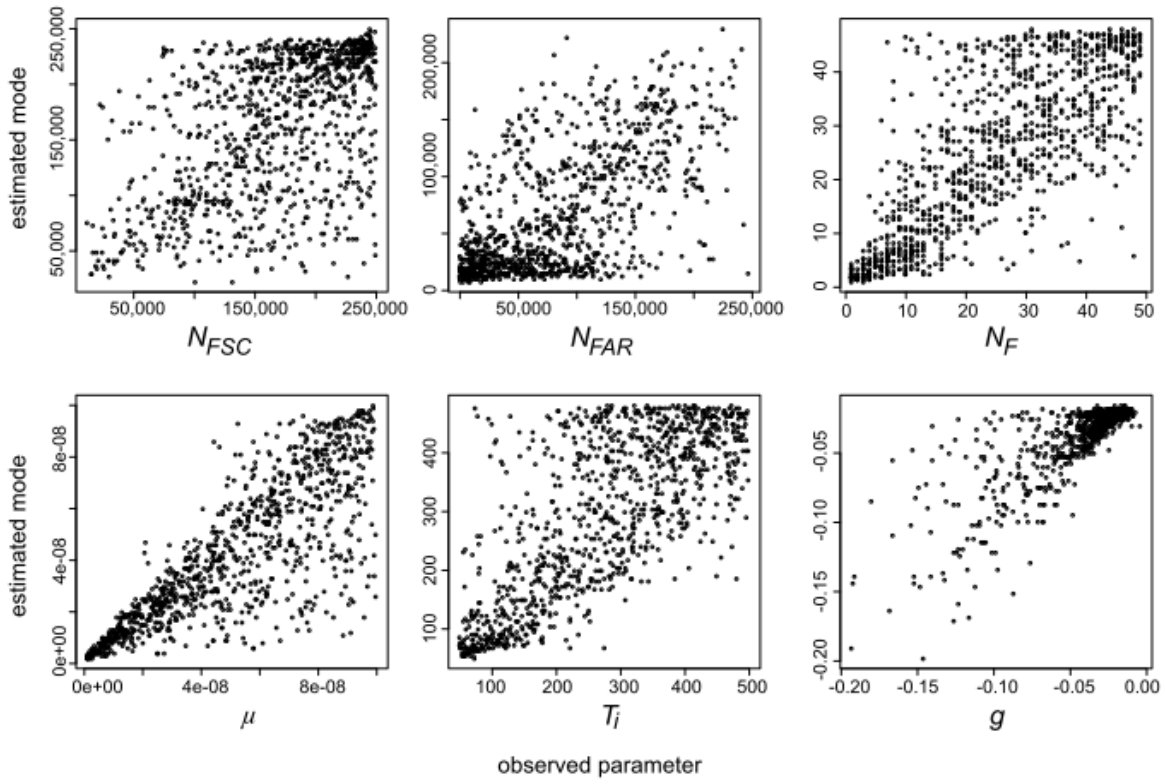

Fig. S3. Validation of parameter estimates with ABC for the model investigated, based on 1,000 parameter values picked from the prior distribution (randomValidation in ABCtoolbox). N_{FSC} – effective population size (haploid numbers) of Fennoscandian population, N_{FAR} – effective population size (haploid numbers) of Faroese population, N_F – effective population size (haploid numbers) of the Faroese hare founder population, T_i – time of the introduction in generations, g – growth rate (negative value backward in time implies expansion forward in time; calculated according to the equation $N_F = N_{FAR}\, e^{gT_i}$), μ – mutation rate in units of mutations per site per generation.

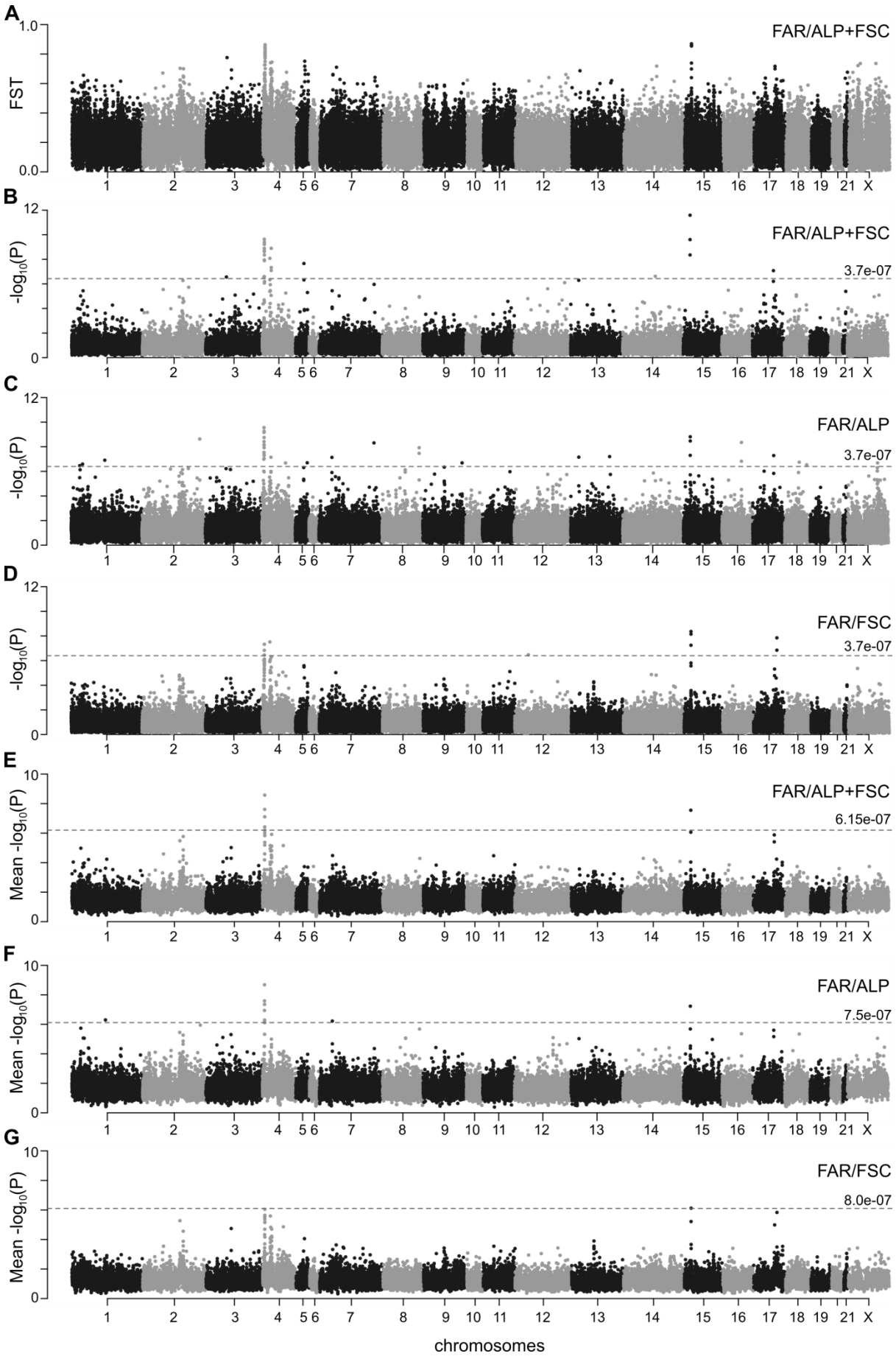
A
FST
1.0
0.0
FAR/ALP+FSC
B
-log10(P)
12
0
FAR/ALP+FSC
3.7e-07
C
-log10(P)
FAR/ALP
3.7e-07
D
-log10(P)
FAR/FSC
3.7e-07
E
Mean -log10(P)
10
0
FAR/ALP+FSC
6.15e-07
F
Mean -log10(P)
FAR/ALP
7.5e-07
G
Mean -log10(P)
FAR/FSC
8.0e-07
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 21 X
chromosomes

Fig. S4. Manhattan plots of differentiation scans and case-control association tests. **(A)** F_{ST} of Faroese hares (FAR) vs. pooled Alpine and Fennoscandian populations (ALP + FSC) estimated with PoPoolation2, based on 14,102,734 SNPs. F_{ST} values are plotted against the position of 20 kb non-overlapping windows on each chromosome. **(B)** Fisher exact test of allele frequency differences between Faroese hares (FAR) and pooled Alpine and Fennoscandian populations (ALP + FSC) estimated with PoPoolation2, based on 14,102,734 SNPs. The $-\log_{10}(P)$ values are plotted against the position of 20 kb non-overlapping windows on each chromosome. **(C)** Fisher exact test of allele frequency differences between Faroese hares (FAR) and Alpine hares (ALP). **(D)** Fisher exact test of allele frequency differences between Faroese hares (FAR) and Fennoscandian hares (FSC). **(E)** Manhattan plot of case-control association tests statistics for Faroese hares (FAR; cases) vs. Alpine and Fannoscandian hares (ALP + FSC; controls), inferred from genotype likelihoods, plotted as mean $-\log_{10}(P)$ values per windows of 100 SNPs. **(F)** Manhattan plot of case-control association tests statistics for Faroese hares (FAR; cases) vs. Alpine hares (ALP; controls). **(G)** Manhattan plot of case-control association tests statistics for Faroese hares (FAR; cases) vs. Fennoscandian hares (FSC; controls). The dashed lines represent the significance thresholds corrected for multiple tests, calculated from the data.

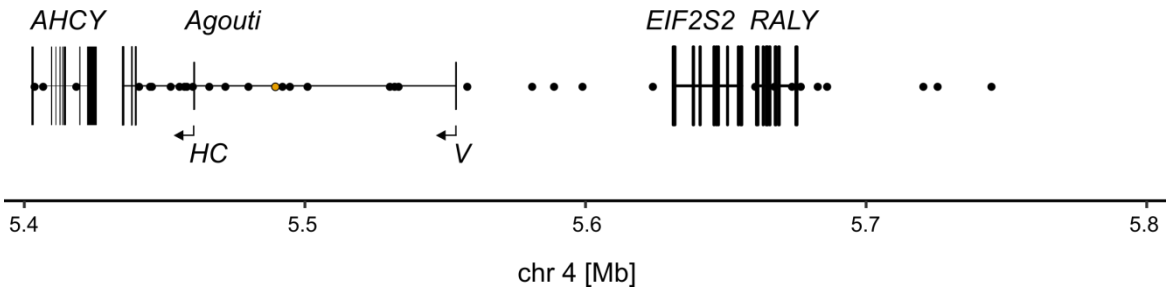

Fig. S5. Distribution of 36 genotyped SNPs (black dots) and one insertion-deletion (orange dot) along the association region in chromosome 4, including the structure of four genes: *AHCY*, *Agouti* (*HC* – non-coding exon of the hair-cycle isoform, *V* – non-coding exon of the ventral isoform), *EIF2S2* and *RALY*.

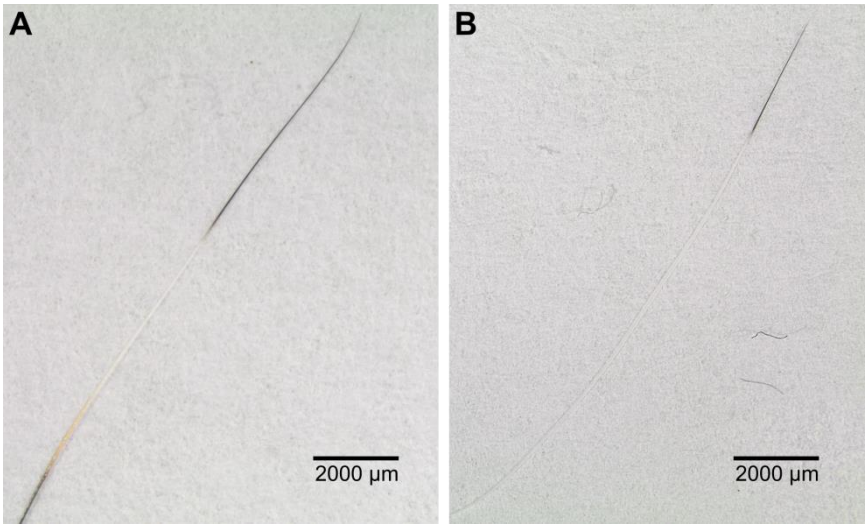

Fig. S6. Two common types of hairs present in Faroese mountain hares. **(A)** Black hair with white band. **(B)** White hair with black tip.

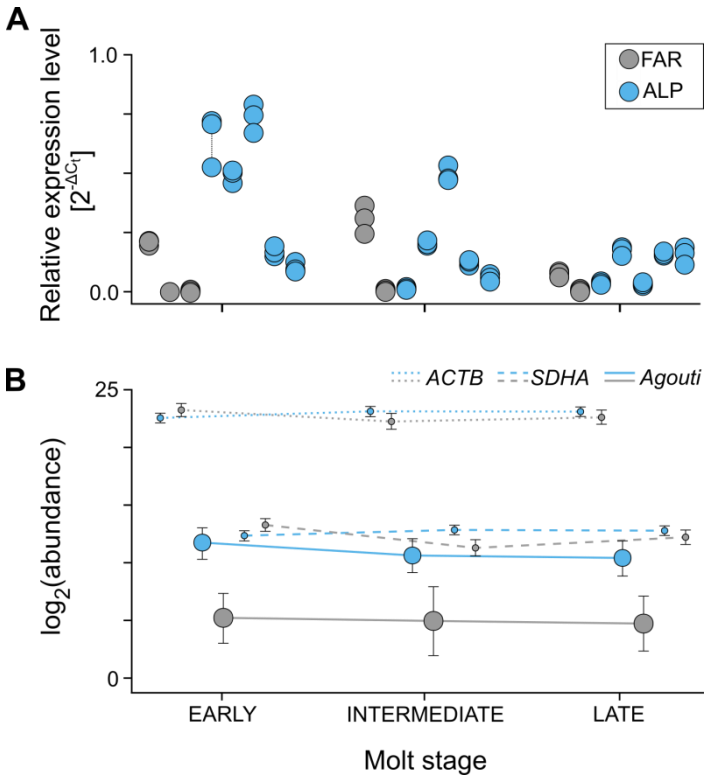

Fig. S7. Expression of the *Agouti* hair-cycle isoform in mountain hares during the autumn molt. Skin tissue samples were collected from the dorsum, representing the brown, intermediate, and white/grey stages of the molt. **(A)** The expression level ($2^{-\Delta Ct}$) is shown as relative to the reference gene *SDHA* (see Fig. 3 for the analysis using *ACTB* as reference gene). Each point represents one relative measure and dashed lines connect technical replicates. **(B)** The expression level ($\log_2$(abundance)) estimated using the naïve model of *MCMC.qpcr* R package. The points are posterior means and the whiskers denote 95% credible intervals. See Table S10 for sequences of primers and raw C_t values.

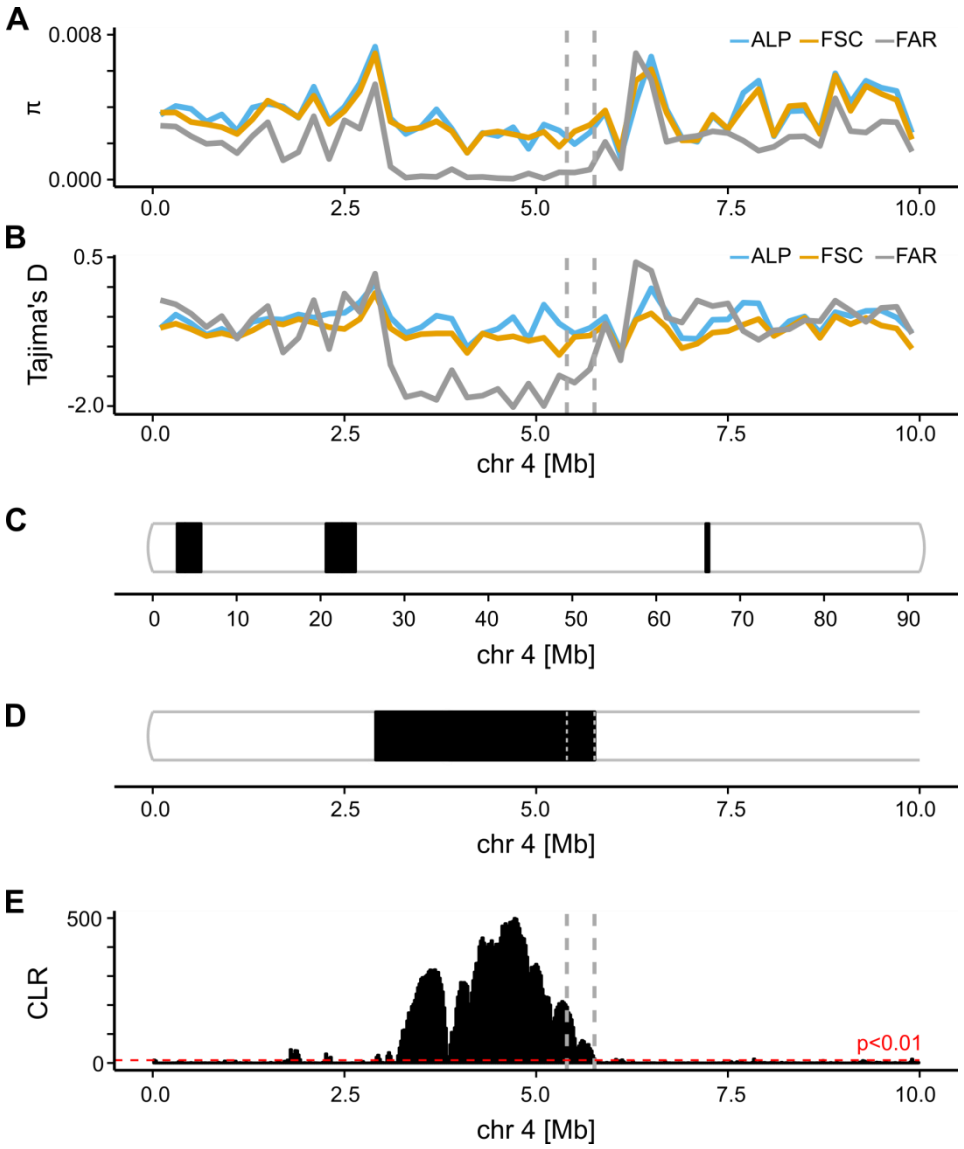

Fig. S8. Signatures of selective sweeps in Faroese mountain hares. **(A)** Nucleotide diversity (π) along the first 10 Mb of chromosome 4. **(B)** Tajima's D along the first 10 Mb of chromosome 4. **(C)** Selective sweeps detected by Pool-hmm along the whole chromosome 4. **(D)** Selective sweep detected by Pool-hmm along the first 10 Mb of chromosome 4 **(E)** SweeD Composite Likelihood Ratio (CLR) along the first 10 Mb of chromosome 4. The red line represents the CLR threshold based on demographic simulations ($p < 0.01$). Vertical dashed grey lines delimit the association region: 4:5,400,000-5,760,000 bp in A, B, E.

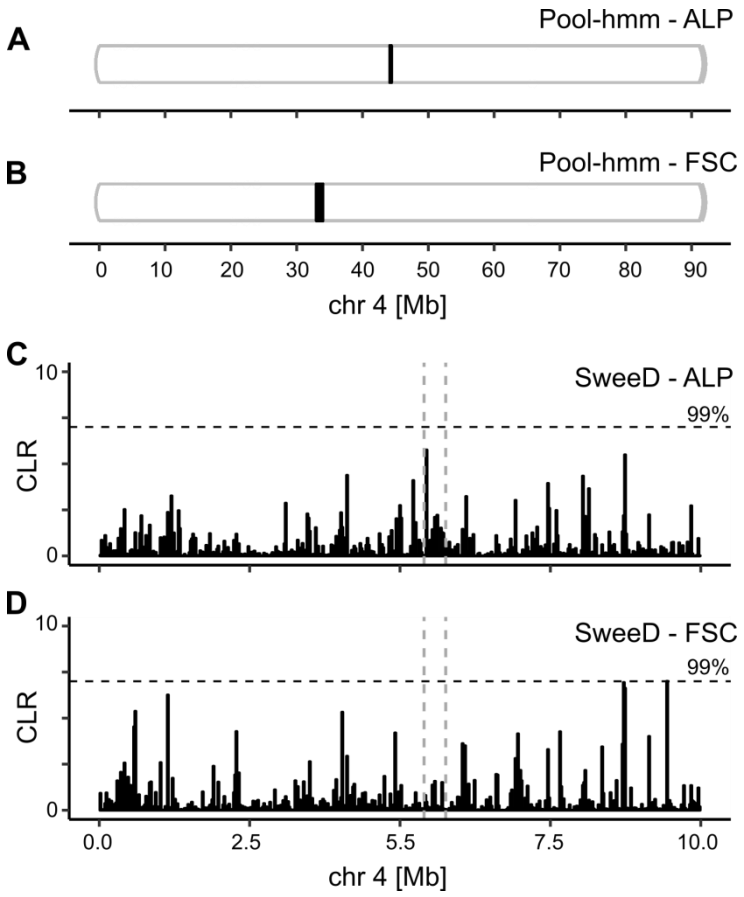

Fig. S9. Selection scans at the *Agouti* association region in Alpine and Fennoscandian populations of the mountain hare. **(A)** Selective sweeps detected in chromosome 4 of Alpine hares using Pool-hmm. **(B)** Selective sweep detected in chromosome 4 of Fennoscandian hares using Pool-hmm. **(C)** SweeD Composite Likelihood Ratio (CLR) in the first 10 Mb of chromosome 4 in the Alpine hares. **D)** SweeD CLR in the first 10 Mb of chromosome 4 in the Fennoscandian hares. Grey vertical dashed lines represent the *Agouti* association region. The horizontal dashed line represents the 99% CLR cutoff (chromosome 4 empirical distribution).

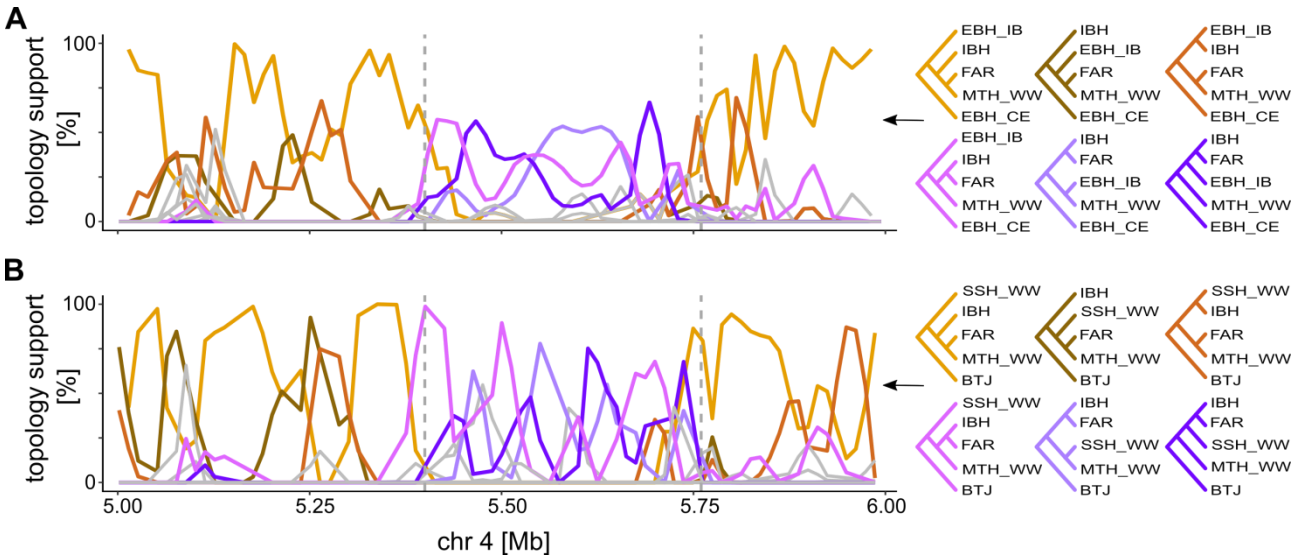

Fig. S10. Twisst topology weightings along the *Agouti* association region in chromosome 4 (delimited by dashed lines). All topologies include winter-grey (FAR) and winter-white (MTH_WW) mountain hares (*Lepus timidus*) and the Iberian hares (IBH; *L. granatensis*). Topology support is plotted with loess smoothing (span = 0.075). Only the most common topologies are shown in detail (the remaining ones are represented in grey). **(A)** Analyses include two European brown hares (*L. europaeus*), from the Iberian Peninsula (EBH_IB) and central Europe (EBH_CE). **(B)** Analyses include the black-tailed jackrabbit (BTJ; *L. californicus*) and a winter-white snowshoe hare (SSH_WW; *L. americanus*).

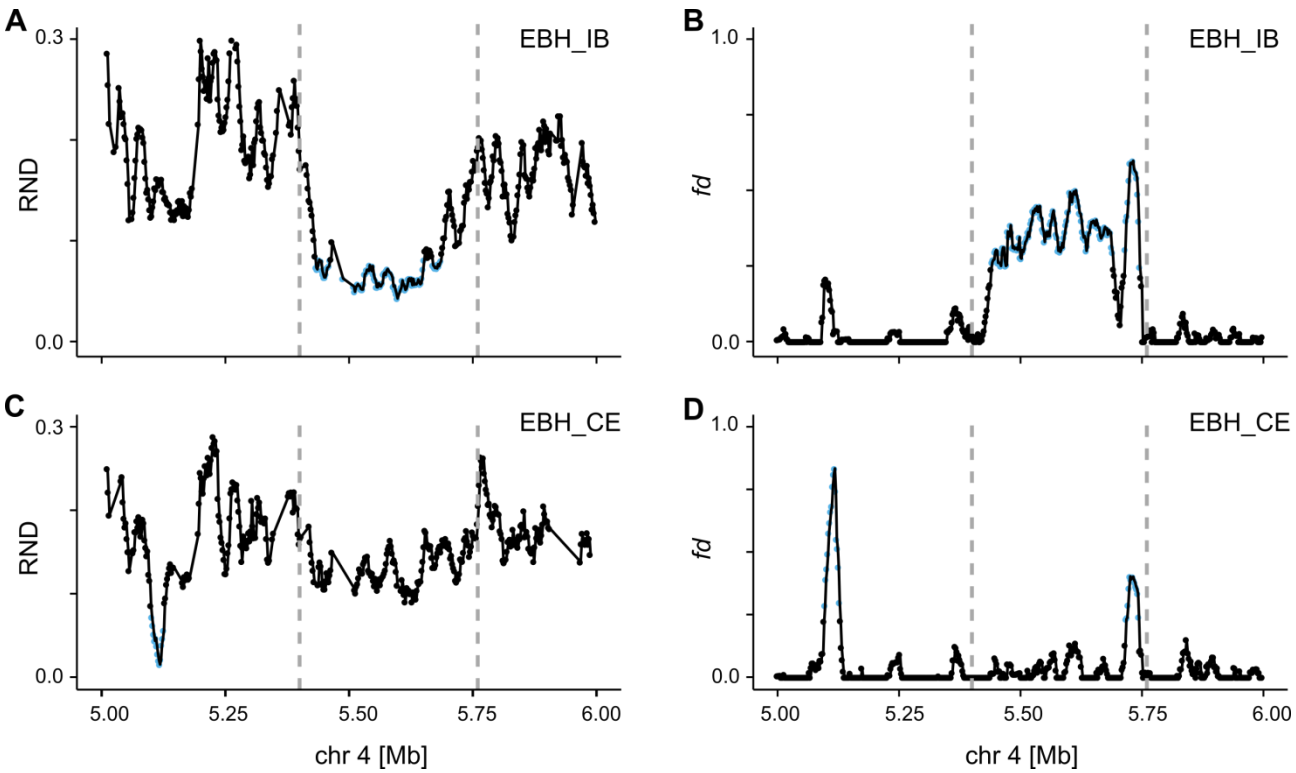

Fig. S11. Signatures of variant sharing between Faroese mountain hare (*Lepus timidus*) and the European brown hare (*L. europaeus*) from the Iberian Peninsula (EBH_IB) and central Europe (EBH_CE). **(A)** Relative node depth (RND) between the Faroese mountain hare and the European brown hare from the Iberian Peninsula (EBH_IB). **(B)** Fraction of introgression (*f_d* statistic) estimated with the following phylogenetic conformation: *P1 = FSC, P2 = FAR , P3 = EBH_IB, O = RAB*. **(C)** RND between the Faroese mountain hare and the brown hare from central Europe (EBH_CE). **(D)** *f_d* statistic estimated with the following phylogenetic conformation: *P1 = FSC, P2 = FAR , P3 = EBH_CE, O = RAB*. In all plots, blue dots represent 1% lowest (RND) or highest (*f_d*) values along the chromosome 4 empirical distribution. FSC - Fennoscandian mountain hare; RAB – European rabbit.

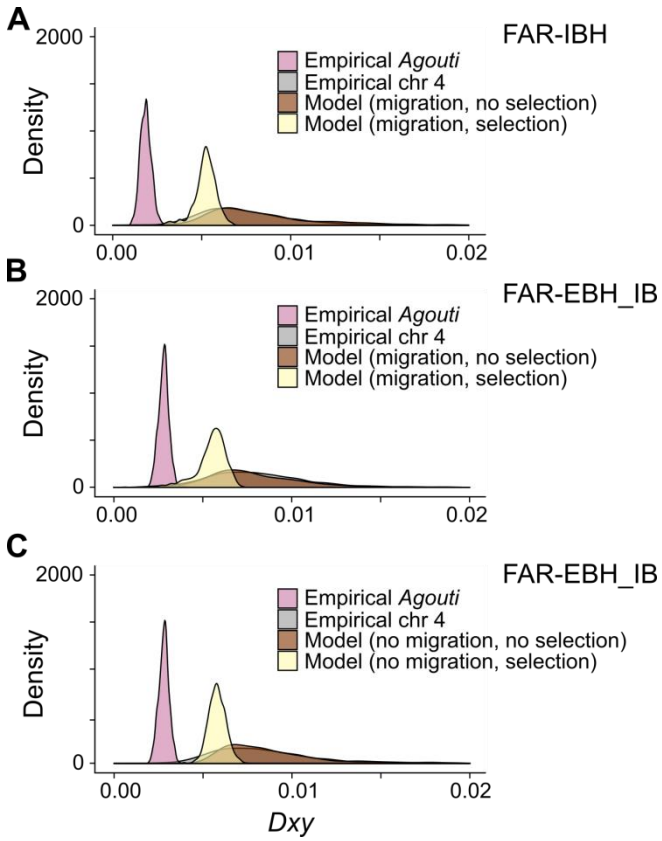

Fig. S12. Distributions of d_{XY}. **(A)** d_{XY} between the Faroese mountain hare (*Lepus timidus*) and the Iberian hare (*L. granatensis*; IBH); simulated data derived from a model assuming bidirectional migration. **(B)** d_{XY} between the Faroese mountain hare (*L. timidus*) and the European brown hare (*L. europaeus)* from the Iberian Peninsula (EBH_IB); simulated data derived from a model assuming bidirectional migration. with simulations including migration. **(C)** d_{XY} between the Faroese mountain hare (*L. timidus*) and the European brown hare (*L. europaeus*) from the Iberian Peninsula (EBH_IB); simulated data derived from a model assuming no migration.

Table S1. Mountain hare specimens used in this study: samples' code, populations of origin (FAR - the Faroe Islands, FSC - Fennoscandia, RUS - Russia, ALP - the Alps), localities, and data collected (WGS – low individual coverage whole-genome sequencing; SNP Genotyping; qPCR – quantitative PCR). Specimens from the Swedish Museum of Natural History are indicated as MG – museum winter-grey and MW – museum winter-white in the "Population" column. NCBI Sequence read archive (SRA) BioSample accession numbers for the sequence data are indicated.

Sample code	Population	Locality	WGS (SRA BioSample)	SNP Genotyping	qPCR
LTM.3655	FAR	Kollafjørður - Sjóvarhagi, Niðaripartur	SAMN12710257	X	-
LTM.3656	FAR	Kollafjørður - Sjóvarhagi, Niðaripartur	SAMN12710258	X	-
LTM.3658	FAR	Kollafjørður - Sjóvarhagi, Niðaripartur	-	X	-
LTM.3659	FAR	Kaldbak - Áarhagi, Heimafyri	-	X	-
LTM.3661	FAR	Kaldbak - Áarhagi, Heimafyri	SAMN12710259	X	-
LTM.3663	FAR	Kaldbak - Áarhagi, Heimafyri	-	X	-
LTM.3664	FAR	Kaldbak - Býggjarhagi, Yngstugimbrar	SAMN12710260	X	-
LTM.3667	FAR	Kaldbak - Býggjarhagi, Yngstugimbrar	SAMN12710261	X	-
LTM.3668	FAR	Kaldbak - Býggjarhagi, Yngstugimbrar	-	X	-
LTM.3670	FAR	Velbastað - Lambahagi	SAMN12710262	X	-
LTM.3672	FAR	Velbastað - Lambahagi	-	X	-
LTM.3673	FAR	Velbastað - Lambahagi	SAMN12710263	X	-
LTM.3674	FAR	Velbastað - Lambahagi	-	X	-
LTM.3675	FAR	Nólsoy - Borðan	SAMN12710264	X	-
LTM.3677	FAR	Nólsoy - Borðan	SAMN12710265	X	-
LTM.3678	FAR	Nólsoy - Borðan	-	X	-
LTM.3680	FAR	Nólsoy - Heimarahelvt	-	X	-
LTM.3682	FAR	Nólsoy - Heimarahelvt	SAMN12710266	X	-
LTM.3683	FAR	Nólsoy - Heimarahelvt	SAMN12710267	X	-
LTM.3688	FAR	Hestur - Øll oyggin	SAMN12710268	X	-
LTM.3691	FAR	Hestur - Øll oyggin	-	X	-
LTM.3692	FAR	Hestur – Øll oyggin	SAMN12710269	X	-
LTM.3695	FAR	Vestmanna - Dalar, Eystanfyri	SAMN12710270	X	-
LTM.3696	FAR	Vestmanna - Dalar, Eystanfyri	SAMN12710271	X	-
LTM.3697	FAR	Vestmanna - Dalar, Eystanfyri	-	X	-
LTM.3698	FAR	Vestmanna - Dalar, Eystanfyri	-	X	-
LTM.3699	FAR	Saksun - Svartá, Fyri Uttan	-	X	-
LTM.3702	FAR	Saksun - Svartá, Fyri Uttan	SAMN12710272	X	-
LTM.3703	FAR	Saksun - Svartá, Fyri Uttan	-	X	-
LTM.3707	FAR	Saksun - Svartá, Fyri Uttan	SAMN12710273	X	-
LTM.3978	FAR	Kollafjørður - Signabøshagi	SAMN12710256	X	X
LTM.3979	FAR	Kvívík - Fjallið	-	X	X
LTM.3980	FAR	Kvívík - Fjallið	SAMN12710274	X	-
LTM.3981	FAR	Kvívík - Fjallið	-	X	X
LTM.3982	FAR	Kvívík - Fjallið	SAMN12710275	X	-
NRM588802	FSC/MG	Skåne, Sweden	-	X	-
NRM588803	FSC/MG	Skabersjo, Sweden	-	X	-
NRM588806	FSC/MG	Barseback, Sweden	-	X	-
NRM588810	FSC/MG	Gotland, Sweden	-	X	-

NRM588812	FSC/MG	Grundfors, Sweden	-	X	-
NRM588831	FSC/MG	Barseback, Sweden	-	X	-
NRM588832	FSC/MG	Uppsala, Sweden	-	X	-
NRM588833	FSC/MG	Uppsala, Sweden	-	X	-
NRM588834	FSC/MG	Uppsala, Sweden	-	X	-
NRM588861	FSC/MG	Hällefors, Sweden	-	X	-
NRM588870	FSC/MG	Hällefors, Sweden	-	X	-
NRM588871	FSC/MG	Hällefors, Sweden	-	X	-
NRM595175	RUS/MG	Kamchatka - Petropavlovsk, Russia	-	X	-
NRM588865	FSC/MG	Hällefors, Sweden	-	X	-
NRM588815	FSC/MW	Hällefors, Sweden	-	X	-
NRM588809	FSC/MW	Småland, Sweden	-	X	-
NRM588845	FSC/MW	Kinnekulle, Sweden	-	X	-
NRM588850	FSC/MW	Hällefors, Sweden	-	X	-
NRM588852	FSC/MW	Hällefors, Sweden	-	X	-
NRM588857	FSC/MW	Hällefors, Sweden	-	X	-
NRM588866	FSC/MW	Hällefors, Sweden	-	X	-
NRM588862	FSC/MW	Hällefors, Sweden	-	X	-
NRM592555	RUS/MW	Kamchatka - Petropavlovsk, Russia	-	X	-
NRM592556	RUS/MW	Kamchatka - Petropavlovsk, Russia	-	X	-
NRM598844	FSC/MW	Kinnekulle, Sweden	-	X	-
NRM588859	FSC/MW	Hällefors, Sweden	-	X	-
NRM588860	FSC/MW	Hällefors, Sweden	-	X	-
NRM588838	FSC/MW	Stockholmstrakten, Sweden	-	X	-
NRM588851	FSC/MW	Hällefors, Sweden	-	X	-
LTM.2012	FSC	Finland	SAMN12710276	X	-
LTM.1726	FSC	Finland	SAMN12710277	X	-
LTM.1727	FSC	Finland	-	X	-
LTM.1728	FSC	Finland	-	X	-
LTM.1729	FSC	Finland	SAMN12710278	X	-
LTM.1730	FSC	Finland	SAMN12710279	X	-
LTM.1731	FSC	Finland	SAMN12710280	X	-
LTM.1732	FSC	Finland	-	X	-
LTM.1733	FSC	Finland	SAMN12710286	X	-
LTM.1734	FSC	Finland	-	X	-
LTM.2191	FSC	Finland	SAMN12710281	X	-
LTM.2192	FSC	Finland	SAMN12710282	X	-
LTM.1749	FSC	Norway	SAMN12710283	X	-
LTM.1750	FSC	Norway	SAMN12710284	X	-
LTM.1751	FSC	Norway	SAMN12710285	X	-
LTM.1752	FSC	Sweden	-	X	-
LTM.1754	FSC	Sweden	SAMN12710287	X	-
LTM.1755	FSC	Sweden	SAMN12710288	X	-
LTM.1756	FSC	Sweden	SAMN12710289	X	-
LTM.1757	FSC	Sweden	SAMN12710290	X	-
LTM.1758	FSC	Sweden	-	X	-
LTM.1759	FSC	Sweden	-	X	-
LTM.1760	FSC	Sweden	-	X	-
LTM.1761	FSC	Sweden	-	X	-

LTM.1762	FSC	Sweden	SAMN12710291	X	-
LTM.1763	FSC	Sweden	SAMN12710292	X	-
LTM.1764	FSC	Sweden	-	X	-
LTM.1765	FSC	Sweden	-	X	-
LTM.1766	FSC	Sweden	SAMN12710293	X	-
LTM.1768	FSC	Sweden	-	X	-
LTM.1769	FSC	Sweden	-	X	-
LTM.1770	FSC	Sweden	-	X	-
LTM.1771	FSC	Sweden	-	X	-
LTM.1772	FSC	Sweden	SAMN12710294	X	-
LTM.1798	ALP	Italy	SAMN12710295	-	-
LTM.1800	ALP	Italy	SAMN12710296	-	-
LTM.1806	ALP	Italy	-	X	-
LTM.1814	ALP	Italy	-	X	-
LTM.1816	ALP	Italy	-	X	-
LTM.1817	ALP	Italy	SAMN12710297	X	-
LTM.1818	ALP	Italy	-	X	-
LTM.1820	ALP	Italy	-	X	-
LTM.1823	ALP	Italy	-	X	-
LTM.1825	ALP	Austria	SAMN12710298	X	-
LTM.1827	ALP	Austria	SAMN12710299	X	-
LTM.1828	ALP	Austria	SAMN12710300	X	-
LTM.2772	ALP	France	SAMN12710301	X	X
LTM.2773	ALP	France	SAMN12710302	X	-
LTM.2774	ALP	France	-	X	-
LTM.2775	ALP	France	SAMN12710303	X	-
LTM.2776	ALP	France	SAMN12710304	X	-
LTM.3106	ALP	France	-	X	-
LTM.3107	ALP	France	-	X	-
LTM.3108	ALP	France	SAMN12710305	X	-
LTM.3109	ALP	France	SAMN12710306	X	-
LTM.3110	ALP	France	SAMN12710307	X	-
LTM.3112	ALP	Switzerland	-	X	X
LTM.3113	ALP	Switzerland	-	-	X
LTM.3114	ALP	Switzerland	-	-	X
LTM.3116	ALP	Switzerland	SAMN12710308	X	X
LTM.3122	ALP	Switzerland	SAMN12710309	X	-
LTM.3199	ALP	Switzerland	SAMN12710310	X	-
LTM.3207	ALP	Switzerland	SAMN12710311	X	-
LTM.3228	ALP	Switzerland	SAMN12710312	X	-
LTM.3253	ALP	Switzerland	SAMN12710313	X	-
LTM.3262	ALP	Switzerland	SAMN12710314	X	-

Table S2. Sequencing statistics for low individual coverage data: samples' codes, populations (FAR – the Faroe Islands, FSC – Fennoscandia, ALP – the Alps), number of raw paired reads, percentage of mapped reads and final mean coverage per site. Values in parentheses represent final mean coverage after subsampling.

Sample code	Population	Nr. raw paired reads	Mapped reads [%]	Final coverage [X]
LTM.3661	FAR	12,829,381	96.9	0.90
LTM.3670	FAR	10,096,944	96.4	0.78
LTM.3664	FAR	9,567,273	96.8	0.72
LTM.3675	FAR	16,454,576	96.9	1.28
LTM.3682	FAR	20,538,870	96.9	1.52
LTM.3692	FAR	7,959,334	96.9	0.61
LTM.3702	FAR	11,256,419	97.2	0.82
LTM.3695	FAR	6,476,635	96.7	0.50
LTM.3696	FAR	14,221,459	97.0	1.06
LTM.3655	FAR	16,520,101	96.8	1.28
LTM.3656	FAR	8,655,408	96.8	0.68
LTM.3673	FAR	12,022,197	96.7	0.94
LTM.3667	FAR	9,083,660	96.7	0.71
LTM.3677	FAR	8,137,461	96.8	0.64
LTM.3683	FAR	7,759,607	96.9	0.61
LTM.3688	FAR	9,575,665	97.0	0.75
LTM.3707	FAR	10,459,376	97.2	0.82
LTM.3978	FAR	9,293,011	96.9	0.73
LTM.3980	FAR	8,439,113	96.9	0.67
LTM.3982	FAR	10,041,109	96.8	0.79
LTM.1749	FSC	10,208,547	96.7	0.76
LTM.1750	FSC	12,886,291	96.6	0.96
LTM.1751	FSC	11,483,086	96.7	0.88
LTM.1756	FSC	8,474,247	97.3	0.62
LTM.1757	FSC	7,057,106	96.6	0.50
LTM.1755	FSC	50,218,055	97.0	3.90 (1.36)
LTM.1762	FSC	10,110,536	96.3	0.76
LTM.1766	FSC	16,209,093	96.7	1.23
LTM.1772	FSC	20,187,925	97.0	1.54
LTM.1754	FSC	9,787,414	97.0	0.76
LTM.1763	FSC	9,234,634	96.3	0.71
LTM.1726	FSC	14,219,520	96.7	1.00
LTM.2012	FSC	33,688,533	96.7	2.34 (1.17)
LTM.1730	FSC	10,693,297	96.7	0.73
LTM.1731	FSC	16,246,618	96.4	1.08
LTM.2191	FSC	18,605,267	96.5	1.19
LTM.2192	FSC	10,434,252	96.7	0.60
LTM.1729	FSC	14,318,970	97.2	1.11
LTM.1733	FSC	14,029,706	97.2	1.05
LTM.2772	ALP	10,288,174	96.8	0.77
LTM.2773	ALP	10,609,990	96.9	0.80
LTM.2775	ALP	15,163,631	96.9	1.14

LTM.3109	ALP	11,707,114	96.9	0.88
LTM.3108	ALP	9,937,167	96.9	0.78
LTM.3110	ALP	8,673,602	97.2	0.68
LTM.2776	ALP	8,934,439	96.8	0.69
LTM.1825	ALP	12,022,278	96.7	0.86
LTM.1827	ALP	21,154,620	97.0	1.39
LTM.1828	ALP	8,937,741	97.0	0.70
LTM.1800	ALP	8,386,434	96.8	0.64
LTM.1798	ALP	14,207,625	96.4	1.06
LTM.1817	ALP	12,615,520	96.7	0.94
LTM.3116	ALP	15,012,254	97.0	1.06
LTM.3122	ALP	8,589,038	96.8	0.60
LTM.3253	ALP	15,715,612	97.1	1.08
LTM.3199	ALP	11,477,056	97.0	0.80
LTM.3228	ALP	12,101,462	97.1	0.76
LTM.3207	ALP	8,995,964	96.9	0.70
LTM.3262	ALP	9,693,029	97.0	0.74

Table S3. Information on higher depth individual whole-genome resequencing data used in this study: species, samples' codes, localities of origin (FAR – Faroe Islands; FSC – Fennoscandia; ALP – Alps), coverage, NCBI Sequence Read Archive (SRA) BioSample accession number and reference.

Species	Sample code	Origin	Coverage [X]	SRA BioSample	Reference
L. timidus	LTM.3978	FAR/Signabøur	6.9	SAMN12710256	this study
	LTM.2012	FSC/Finland	17.9	SAMN07526960	(3)
	LTM.3109	ALP/France	22.0	SAMN07526962	(3)
L. europaeus	LER.1515	Spain/Navarra	15.7	SAMN12618118	(2)
	LER.1639	Austria/Vienna	10.8	SAMN12618122	(2)
L. granatensis	LGR.2553	Spain/Ciudad Real	20.8	SAMN07526967	(3)
	LGR.2544	Spain/Navarra	21.8	SAMN07526972	(3)
L. americanus	Allab3	USA/Pennsylvania	6.8	SAMN08146528	(4)
	DOlsen1	USA/Utah	6.8	SAMN08146529	(4)
	A0961	USA/Montana	29.3	SAMN08146494	(4)
L. californicus	MacKay2	USA/Nevada	6.1	SAMN08146530	(4)
	MacKay3	USA/Nevada	7.1	SAMN08146531	(4)
L. castroviejoi	LCS.1991	Spain/León	10.0	SAMN12640762	this study

Table S4. Approximate Bayesian Computation demographic modelling. Prior and posterior distributions of parameters' estimate (marginal density P-value: 0.73, Tukey depth P-value: 0.74), based on PLS transformed data. N_{FSC} – effective population size of the Fennoscandian population; N_{FAR} – effective population size of the Faroese population; N_F – effective population size of the Faroese hare founder population; T_i – time of the introduction in generations; μ – mutation rate in units of mutations per site per generation; g – growth rate (negative value backward in time implies expansion forward in time; calculated according to the equation $N_F = N_{FAR}\, e^{gT_i}$). Effective population sizes are reported as haploid numbers.

Parameter	Prior		Posterior characteristics				
	Min	Max	Mode	Mean	Median	HDI95-lower	HDI95-upper
N_{FSC}	10,000	250,000	225,758	182,100	188,760	96,793	249999
N_{FAR}	10	250,000	73,216	123,794	120,565	39,143	212,645
N_F	2	50	20	21	20	6	42
T_i	50	500	73	109	104	50	184
μ	1e-9	1e-7	6.0e-09	7.7e-09	7.3e-09	1e-09	1.6e-08
g	-	-	-0.080	-0.094	-0.088	-0.166	-0.036

Table S5. Sequences of PCR primers used to confirm and genotype the insertion-deletion detected in the *Agouti* association region. The coordinates on the European rabbit reference genome are shown (*OryCun2.0*). The reverse primer (*LTM_indel_R*) is common to all three PCRs.

Primer	**Sequence (5'-3')**	**Coordinates**	**PCR product [bp]**
LTM_indel_F1	GACAATACCATGGGCCATAAA	4:5,489,246-	266 (deletion)
LTM_indel_F01	AAGAGCAGCTGGGAAACAAA	4:5,490,280-	406 (no deletion)
LTM_indel_F2	GAGATCTCTGAAATACCCAAATA	4:5,489,350-	165 (deletion)
LTM_indel_F3	TTCTGGGTCTCCTACATCAGGT	4:5,490,513-	173 (no deletion)
LTM_indel_R	TGCTGCTGTGGCGTAAGTAG	4:5,490,666-	

Table S6. Genotypes at selected SNPs and insertion-deletion along the *Agouti* region (chromosome 4). Rows depict individuals and columns represent site coordinates according to the rabbit genome (*OryCun2.0*). Colors are concordant with Fig. 2C, i.e. black: homozygous Faroese variant, light grey: homozygous alternative variant, dark grey: heterozygous, and white: missing data.

Origin	Specimen Code	*Agouti region (chromosome 4)*																																		
		5387616	5404147	5407210	5419007	5441387	5445294	5445964	5452657	5455802	5457584	5458411	5460551	5466404	5472145	5480355	INDEL	5492509	5495138	5501424	5530769	5532471	5533873	5558350	5581471	5589277	5599413	5624495	5660971	5667845	5674077	5677222	5683247	5686590	5720878	5725962	5739201	5745165
FSC/MG	NRM588802	TT	GG	TT	CC	GG	AA	AA	AA	TT	0	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FSC/MG	NRM588803	GT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TC	GT	CA	CT	CT	CT	AG	CT	CA	CA
FSC/MG	NRM588806	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FSC/MG	NRM588810	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FSC/MG	NRM588812	GT	GA	TC	TC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FSC/MG	NRM588831	GT	GA	TC	TC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FSC/MG	NRM588832	GT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	GA	TC	TC	GT	CA	CT	CT	CT	AG	CT	CA	CA
FSC/MG	NRM588833	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FSC/MG	NRM588834	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	0	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC/MG	NRM588861	GT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FSC/MG	NRM588870	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	0	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FSC/MG	NRM588871	GT	GA	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
RUS/MG	NRM595175	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FSC/MG	NRM588865	GT	AA	CC	TT	AG	GA	GA	CA	TC	CC	CA	TT	CT	AA	CT	HET	CT	TC	CT	AA	CT	CA	GA	GT	GA	GA	TC	TC	GT	CA	CT	CT	CT	AG	CT	CA	CA
FSC/MW	NRM588815	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	AG	TT	INS	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC/MW	NRM588809	GG	AA	CC	TC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	INS	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC/MW	NRM588845	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	INS	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC/MW	NRM588850	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CA	CC	TT	GG	TT	INS	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC/MW	NRM588852	GT	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	INS	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC/MW	NRM588857	GT	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	AG	TT	INS	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC/MW	NRM588866	GG	GA	TT	CC	AA	GG	GG	CC	CC	TT	CC	CC	TT	AG	TT	INS	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC/MW	NRM588862	TT	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	AG	TT	INS	TT	TT	TT	0	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
RUS/MW	NRM592555	GT	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	AA	TT	INS	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
RUS/MW	NRM592556	GT	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	AA	TT	INS	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC/MW	NRM598844	GT	GA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	AG	TT	INS	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC/MW	NRM588859	GT	GA	TC	TC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	INS	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC/MW	NRM588860	GT	GA	TC	TC	AA	GG	GG	CC	CC	TT	CA	CC	TT	GG	TT	INS	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC/MW	NRM588838	GG	AA	CC	TT	AG	GA	GA	CA	TC	CT	CA	TC	CT	AG	CT	HET	CT	TC	CT	0	CT	CA	GA	GT	GA	GA	TC	TC	GT	CA	CT	CT	CT	AG	CT	CA	CA
FSC/MW	NRM588851	GT	GA	TC	TC	AG	GA	GA	CA	TC	CT	CA	TC	CT	AG	CT	HET	CT	TC	CT	0	CT	CA	GA	GT	GA	GA	TC	TC	GT	CA	CT	CT	CT	AG	CT	CA	CA
FAR	LTM.3655	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3656	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	0	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3658	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3659	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3661	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	0	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3663	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3664	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3667	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3668	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	0	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3670	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	0	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3672	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	0	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3673	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3674	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	0	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3675	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3677	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3678	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	0	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3680	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	0	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3682	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3683	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3688	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3691	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3692	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3695	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3696	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3697	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3698	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	0	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3699	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	0	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3702	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3703	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3707	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	0	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3978	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	DEL	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC

FAR	LTM.3979	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	0	**DEL**	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3980	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	**DEL**	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3981	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	0	**DEL**	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FAR	LTM.3982	TT	GG	TT	CC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	**DEL**	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FSC	LTM.2012	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	AG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1726	GT	GA	TC	TC	AG	GA	GA	CA	TC	CT	CA	TT	CT	AA	CT	**HET**	CT	TC	CT	GG	CT	CA	GA	GT	GA	GA	TC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1727	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	AG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1728	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1729	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	AG	TT	**INS**	TT	TT	TT	GG	CC	AA	GA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1730	GG	GA	TC	TC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1731	GT	GA	TC	TC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	0	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1732	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1733	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1734	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.2191	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.2192	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1749	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1750	GT	GA	TC	TC	AG	GA	GA	CA	TC	CT	CA	TC	CT	AG	CT	**HET**	CT	TC	CT	0	CT	CA	GA	GT	GA	GA	TC	TC	GT	CA	CT	CT	CT	AG	CT	CA	CA
FSC	LTM.1751	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1752	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	AG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1754	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	AG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1755	TT	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	AG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1756	GG	AA	CC	TT	AG	GA	GA	CA	TC	CT	CA	TC	CT	AG	CT	**HET**	CT	TC	CT	0	CT	CA	GA	GT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1757	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1758	GT	GA	TC	TC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1759	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	AG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1760	GT	GA	TC	TC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1761	0	GA	TC	TC	AG	GA	GA	CA	TC	CT	CA	TC	CT	AG	CT	**HET**	CT	TC	CT	0	CT	CA	GA	GT	GA	GA	TC	TC	GT	CA	CT	CT	CT	AG	CT	CA	CA
FSC	LTM.1762	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	AA	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1763	GT	GA	TC	TC	AG	GA	GA	CA	TC	CT	0	TC	CT	AG	CT	**HET**	CT	TC	CT	AA	CT	CA	GA	GT	GA	GA	TC	TC	GT	CA	CT	CT	CT	AG	CT	CA	CA
FSC	LTM.1764	GT	GA	TC	TC	AG	GA	GA	CA	TC	CT	CA	TC	CT	AG	CT	**HET**	CT	TC	CT	0	CT	CA	GA	GT	GA	GA	TC	TC	GT	CA	CT	CT	CT	AG	CT	CA	CA
FSC	LTM.1765	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1766	GT	GA	TC	TC	GG	AA	AA	AA	TT	CC	AA	TT	CC	AA	CC	**DEL**	CC	CC	CC	AA	TT	CC	GG	GG	GG	AA	TT	TT	GG	CC	CC	TT	CC	AA	TT	AA	CC
FSC	LTM.1768	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1769	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	AG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1770	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1771	GT	AA	CC	TT	AA	GG	GG	CC	CC	0	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
FSC	LTM.1772	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.1806	GG	AA	CC	CC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.1814	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.1816	GG	AA	CC	TC	AA	GG	GG	CC	CC	0	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.1817	GT	AA	CC	TC	AG	GG	GA	CC	CC	TT	CA	CC	CT	AG	TT	**INS**	CT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.1818	GG	AA	CC	CC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.1820	GT	AA	CC	TC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.1823	GG	AA	CC	TC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.1825	GG	AA	CC	TC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.1827	GG	AA	CC	TC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.1828	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.2772	GG	AA	CC	CC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.2773	GG	AA	CC	TC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.2774	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.2775	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.2776	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.3106	GG	AA	CC	TC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.3107	TT	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	AA	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.3108	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.3109	GG	AA	CC	TC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.3110	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.3112	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.3116	GG	AA	CC	TC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.3122	GT	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.3199	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.3207	GG	AA	CC	TC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.3228	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.3253	GG	AA	CC	TT	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA
ALP	LTM.3262	GG	AA	CC	TC	AA	GG	GG	CC	CC	TT	CC	CC	TT	GG	TT	**INS**	TT	TT	TT	GG	CC	AA	AA	TT	AA	GG	CC	CC	TT	AA	TT	CC	TT	GG	CC	CC	AA

Table S7. Genotypes at selected SNPs in the *USP38* gene region (chromosome 15) and genome-wide. Rows depict individuals and columns represent site coordinates according to the rabbit genome (*OryCun2.0*; chromosome: site). Colors are concordant with Fig. 2C, i.e. black: homozygous Faroese variant, light grey: homozygous alternative variant, dark grey: heterozygous, and white: missing data.

Origin	Specimen Code	*Usp38 region (chromosome:site)*					*Genome wide (chromosome:site)*															
		15:21226763	15:21236641	15:21351940	15:21352956	15:21373227	1:34929 82	1:23257458	2:1113582 24	3:688624 73	3:1445514 71	4:72246 15	4:207793 95	4:219990 72	4:232361 52	4:238188 53	5:329094 37	6:131284 52	7:451944 36	12:917999 89	13:768437 55	14:430055 58	17:744891 91	18:481934 91
FSC/MG	NRM588802	0	0	AA	GG	GG	TT	0	TT	0	CC	CC	0	0	TC	TT	0	0	AA	0	0	0	GG	TT
FSC/MG	NRM588803	GG	CC	AA	GG	GG	GT	GG	0	0	CT	TC	GG	GG	CC	TT	CC	GG	AA	AA	GA	TC	GG	CC
FSC/MG	NRM588806	GG	CC	AA	GG	GG	TT	0	TT	CG	CC	CC	GG	GG	TC	TT	AA	GG	AA	GG	GG	TT	GG	TT
FSC/MG	NRM588810	GG	CC	AA	GG	GG	GT	GG	TT	CC	CC	TC	GG	GG	TC	CT	CC	GG	AA	AG	GG	TT	GG	CT
FSC/MG	NRM588812	GG	CC	AG	GA	GT	TT	GG	TT	CG	TT	CC	GG	GG	TC	TT	CA	GG	AA	GG	GG	TT	AG	CT
FSC/MG	NRM588831	GG	CC	AA	GG	GG	TT	GG	TT	0	TT	TC	GG	GA	TT	TT	CA	GG	AG	AG	GG	TC	GG	TT
FSC/MG	NRM588832	AA	TT	GG	AA	TT	TT	GA	TA	CG	CC	TC	GG	GG	TC	TT	CC	CG	AG	GG	0	TT	GG	TT
FSC/MG	NRM588833	GG	CC	AA	GG	GG	TT	GG	TT	0	CC	TC	0	GG	CC	TT	CA	CC	AA	GG	GG	TC	AA	CT
FSC/MG	NRM588834	GG	CC	AA	GG	GG	TT	GA	TT	CG	CC	TC	GG	GG	TT	TT	AA	CG	AG	GG	GA	TC	AG	TT
FSC/MG	NRM588861	GG	CC	AA	GG	GG	GT	AA	TT	CC	CC	CC	GG	GG	TT	CT	CA	CG	AA	GG	GA	TC	GG	TT
FSC/MG	NRM588870	AG	TC	AA	GG	GT	GT	GG	TA	0	CC	CC	0	GG	TT	TT	CC	CG	AA	GG	GG	CC	GG	TT
FSC/MG	NRM588871	GG	CC	AA	GG	GG	GT	AA	AA	CC	CC	CC	GG	GG	TT	CT	CC	CG	AA	AA	GA	TC	GG	CT
RUS/MG	NRM595175	GG	CC	AA	GG	GG	GT	GG	TT	CG	CC	CC	GG	GG	TC	TT	CA	CG	AG	AG	GA	0	GG	TT
FSC/MG	NRM588865	GG	CC	AA	GG	GG	TT	GG	TT	CG	CT	CC	GG	GG	TC	CT	CA	GG	AG	AG	GA	TT	AG	CT
FSC/MW	NRM588815	GG	CC	AA	GG	GG	TT	GA	TT	CC	CT	CC	GG	GG	TC	TT	CC	CG	AG	AG	0	TC	GG	TT
FSC/MW	NRM588809	AG	TC	AA	GG	GG	TT	GG	TT	CG	CT	CC	GG	GG	TT	TT	CC	CG	AA	AG	GG	TC	AA	CT
FSC/MW	NRM588845	AG	TC	AG	GA	GT	TT	0	TT	0	CC	CC	0	AA	TT	TT	CC	CC	AA	AG	GG	TT	GG	TT
FSC/MW	NRM588850	GG	CC	AA	GG	GG	TT	AA	TT	CC	CT	TT	GG	GG	TT	TT	CA	CG	AA	AA	GA	TC	GG	CT
FSC/MW	NRM588852	AG	TC	AA	GG	GG	TT	GA	0	CC	CC	CC	GG	GG	TC	TT	AA	CG	AA	GG	GG	TC	GG	CT
FSC/MW	NRM588857	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GG	GG	TT	TT	CC	CG	AA	GG	GA	TC	GG	TT
FSC/MW	NRM588866	GG	CC	AA	GG	GG	TT	GG	TT	CG	CT	CC	GG	AA	TT	CT	0	CG	AG	GG	GA	0	GG	TT
FSC/MW	NRM588862	AG	TC	AG	GA	GG	TT	GA	0	CC	CC	CC	GG	GA	TC	CT	CA	CG	AA	AG	AA	CC	GG	TT
RUS/MW	NRM592555	GG	CC	AA	GG	GG	TT	AA	TT	CC	CC	CC	GG	GG	TT	TT	CC	CG	AA	GG	AA	TT	GG	TT
RUS/MW	NRM592556	GG	CC	AA	GG	GG	TT	GA	TT	CC	CC	CC	GG	GG	TT	TT	CC	CG	AG	GG	GA	TT	GG	TT
FSC/MW	NRM598844	GG	CC	AA	GG	GG	TT	AA	TT	CC	CC	CC	GG	GA	TT	TT	CC	CG	AG	AG	GG	TT	GG	TT
FSC/MW	NRM588859	AG	TC	AA	GG	GG	GT	GA	TA	CC	CT	TC	GG	GA	TC	TT	0	CG	AG	GG	0	0	GG	TT
FSC/MW	NRM588860	GG	CC	AG	GA	GT	TT	0	TT	CG	CC	CC	GG	GG	TT	CC	CA	CC	GG	AG	GA	CC	GG	CT
FSC/MW	NRM588838	GG	CC	AA	GG	GG	GT	GG	TT	CC	CC	CC	GA	GA	TT	TT	CC	GG	AG	GG	GG	TT	GG	TT
FSC/MW	NRM588851	AG	TC	AG	GA	GT	TT	GA	TT	CC	CC	TC	GG	GG	TT	CT	CA	GG	AG	GG	AA	TT	AG	CT
FAR	LTM.3655	AA	0	GG	AA	TT	GG	AA	AA	GG	TT	TT	AA	AA	CC	CC	AA	CC	GG	AA	AA	0	AA	CC
FAR	LTM.3656	AA	TT	GG	AA	TT	GG	AA	AA	GG	TT	TT	AA	AA	CC	CC	CA	CC	GG	AA	AA	CC	AG	CC
FAR	LTM.3658	AA	0	GG	AA	TT	GT	AA	AA	GG	TT	TT	GA	GA	TC	CC	AA	CC	GG	AG	AA	0	AG	CC
FAR	LTM.3659	AA	TT	GG	AA	TT	GG	AA	AA	GG	TT	TT	AA	AA	CC	CC	AA	CC	AG	AA	AA	CC	AA	CC
FAR	LTM.3661	AA	TT	GG	AA	TT	GT	AA	AA	GG	TT	TT	GA	GA	TC	CT	AA	CC	GG	AA	AA	CC	AA	CC
FAR	LTM.3663	AA	TT	GG	AA	TT	GG	AA	AA	GG	TT	TT	GG	GG	TT	CC	CA	CC	GG	AA	AA	CC	AA	CC
FAR	LTM.3664	AG	TC	AG	GA	TT	GG	AA	AA	GG	TT	TT	GA	GA	TC	CT	AA	CC	GG	AG	AA	CC	AA	CC
FAR	LTM.3667	AG	0	AG	GA	TT	GT	AA	AA	GG	TT	TT	AA	AA	CC	CC	AA	CC	GG	AA	AA	CC	AA	0
FAR	LTM.3668	AA	0	GG	AA	TT	GG	0	AA	0	TT	TC	AA	AA	CC	CC	AA	0	GG	AA	0	0	AA	CC
FAR	LTM.3670	AA	TT	GG	AA	TT	GG	AA	AA	GG	TT	TT	GA	GA	TC	CC	AA	CC	GG	GG	AA	CC	AA	CC
FAR	LTM.3672	AG	TC	AG	GA	TT	GG	AA	AA	GG	TT	TT	AA	AA	CC	CC	AA	CC	GG	AA	AA	CC	AA	CC
FAR	LTM.3673	AA	0	GG	AA	TT	GG	AA	AA	GG	TT	TC	AA	AA	CC	CC	AA	CC	GG	AA	AA	CC	AA	CC
FAR	LTM.3674	AA	TT	GG	AA	TT	GT	AA	AA	GG	TT	TT	AA	AA	CC	CC	AA	CC	GG	AA	AA	CC	AA	CC
FAR	LTM.3675	AA	TT	GG	AA	TT	GG	AA	AA	GG	TT	TC	AA	AA	CC	CC	AA	CC	GG	AA	AA	CC	AA	CC
FAR	LTM.3677	AA	TT	GG	AA	TT	GG	AA	AA	GG	TT	TT	AA	AA	CC	CC	AA	CC	GG	AA	AA	CC	AA	CC
FAR	LTM.3678	AG	TC	AG	GA	TT	GG	AA	AA	GG	TT	TT	AA	AA	CC	CC	AA	CC	GG	AG	AA	CC	AA	CC
FAR	LTM.3680	AG	TC	AG	GA	TT	GG	AA	AA	GG	TT	TT	GA	GA	TC	CT	CA	CC	GG	AG	AA	CC	AA	CC
FAR	LTM.3682	AA	TT	GG	AA	TT	GG	AA	AA	GG	TT	TT	AA	AA	CC	CC	AA	CC	GG	AA	AA	0	AA	CC
FAR	LTM.3683	AA	TT	GG	AA	TT	GG	AA	AA	GG	TT	TT	AA	AA	CC	CC	AA	CC	GG	AA	AA	CC	AG	CC
FAR	LTM.3688	AA	0	GG	AA	TT	GG	AA	TA	GG	TT	TT	AA	AA	TC	CT	AA	CC	GG	AA	AA	0	AA	CC
FAR	LTM.3691	AA	TT	GG	AA	TT	GG	AA	A	GG	TT	TT	AA	AA	CC	CC	AA	CC	GG	AA	AA	CC	AA	CC
FAR	LTM.3692	AA	TT	GG	AA	TT	GG	AA	TA	GG	CT	TT	AA	AA	CC	CC	AA	CC	GG	AG	AA	CC	AA	CC
FAR	LTM.3695	AA	TT	GG	AA	TT	GG	AA	TA	GG	TT	TT	GG	GA	TT	CT	AA	CC	GG	AA	AA	CC	AA	CC
FAR	LTM.3696	AA	TT	GG	AA	TT	GG	AA	TA	GG	TT	TT	AA	AA	CC	CC	AA	CC	GG	AA	AA	CC	AA	CC
FAR	LTM.3697	AG	0	AG	GA	TT	GG	AA	AA	CG	CT	TT	GA	GA	TT	CT	AA	CC	GG	AA	AA	CC	AA	CC
FAR	LTM.3698	AA	TT	AG	GA	TT	TT	AA	AA	GG	TT	TT	AA	AA	CC	CC	AA	CC	GG	AA	AA	CC	AA	CC
FAR	LTM.3699	AG	TC	AG	GA	TT	GT	AA	AA	CG	CT	TT	AA	GA	TT	CC	AA	CC	GG	AG	AA	CC	AA	CC
FAR	LTM.3702	AG	0	AG	GA	GT	GG	AA	AA	0	CT	TC	AA	AA	CC	CC	AA	CC	GG	AA	AA	0	AA	CC
FAR	LTM.3703	AA	TT	GG	AA	TT	GG	AA	AA	GG	TT	TT	GA	GA	TC	CC	AA	CC	GG	AA	AA	CC	AG	CC
FAR	LTM.3707	AA	TT	GG	AA	TT	GT	AA	AA	GG	TT	TT	AA	AA	CC	CC	AA	CC	GG	AG	AA	CC	AA	CC
FAR	LTM.3978	AA	TT	GG	AA	TT	GG	AA	AA	CC	TT	TT	AA	AA	TC	CC	AA	CC	GG	AA	AA	CC	AA	CC

FAR	LTM.3979	AA	TT	GG	AA	TT	GG	AA	AA	GG	CT	TT	GA	GA	TC	CC	AA	CC	GG	AA	AA	CC	AA	CC
FAR	LTM.3980	AA	TT	GG	AA	TT	GT	AA	TA	GG	TT	TT	AA	AA	CC	CC	AA	CC	GG	AA	AA	CC	AA	CC
FAR	LTM.3981	AA	TT	GG	AA	TT	GG	AA	TA	CG	CT	TT	AA	AA	CC	CC	AA	CC	GG	AA	AA	CC	AA	CC
FAR	LTM.3982	AA	TT	GG	AA	TT	GG	AA	AA	GG	TT	TT	AA	AA	CC	CC	CA	CC	GG	AA	AA	CC	AG	CC
FSC	LTM.2012	AG	TC	AA	GG	GG	TT	0	TA	CC	CC	TC	GG	GG	TC	TT	AA	GG	AA	AG	GG	TT	GG	CT
FSC	LTM.1726	AG	TC	AA	GG	GG	TT	0	TT	CC	CC	CC	GG	GG	TT	TT	CA	GG	AA	AG	GG	TT	AG	TT
FSC	LTM.1727	GG	CC	AA	GG	GG	GT	AA	TT		CC	CC	GG	GG	TT	TT	CC	GG	AA	AG	GG	TT	GG	CC
FSC	LTM.1728	GG	CC	AA	GG	GG	TT	0	TT	CC	CC	TC	GG	GA	TC	TT	CC	CG	GG	GG	GG	TT	AG	CT
FSC	LTM.1729	GG	CC	AA	GG	GG	TT	AA	TT	CC	CC	CC	GG	GG	TT	TT	CC	GG	AA	AA	GG	TT	GG	CT
FSC	LTM.1730	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	TC	GG	GG	TT	TT	CC	CG	AA	AG	GG	TT	GG	TT
FSC	LTM.1731	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GG	GA	TT	TT	CC	CG	AA	GG	GG	TT	GG	TT
FSC	LTM.1732	GG	TC	AA	GG	GG	TT	0	TT	CC	CC	TT	GG	GA	TT	TT	CC	CG	AG	GG	GA	TT	GG	TT
FSC	LTM.1733	AG	TC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GG	GA	TT	TT	CA	CG	AA	AG	GG	CC	AG	TT
FSC	LTM.1734	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	TC	GG	GG	TT	TT	CC	CG	AG	GG	GG	TT	GG	TT
FSC	LTM.2191	GG	TC	AA	GG	GG	TT	0	TT	CC	CC	CC	GG	GG	TT	TT	CC	GG	AG	AG	GG	TT	GG	CT
FSC	LTM.2192	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	TC	GG	GA	TC	TT	CC	GG	AA	AG	GG	TT	GG	TT
FSC	LTM.1749	AG	TC	AA	GG	GG	GT	AA	TT	CC	CC	TC	GG	GG	TT	CT	CC	GG	AA	GG	GG	TC	GG	TT
FSC	LTM.1750	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	TC	GG	GG	TT	CC	CC	GG	AG	GG	GA	CC	GG	TT
FSC	LTM.1751	GG	CC	AA	GG	GG	TT	GG	0	0	CT	CC	GG	GG	TT	TT	CA	CC	AG	GG	AA	TC	AG	TT
FSC	LTM.1752	GG	CC	AA	GG	GG	GT	GA	0	0	CC	CC	0	AA	TC	TT	0	GG	GG	AG	GG	TT	AG	TT
FSC	LTM.1754	GG	CC	AA	GG	GG	TT	AA	TT	CC	CC	CC	GG	GG	TT	TT	CA	GG	AG	GG	GG	TT	GG	TT
FSC	LTM.1755	GG	CC	AA	GG	GG	TT	GG	TA	CC	CC	TC	GA	GG	TT	TT	CC	CG	AA	GG	GG	TT	GG	CT
FSC	LTM.1756	GG	CC	AA	GG	GG	GT	GG	TT	CC	CT	CC	GG	GG	TC	TT	CA	GG	AG	GG	GA	CC	GG	CT
FSC	LTM.1757	GG	CC	AA	GG	GG	TT	GG	0	CC	CT	CC	GG	GG	TT	TT	CA	CG	AA	AG	GG	TC	GG	CT
FSC	LTM.1758	AG	TC	AG	GA	GT	TT	GG	TT	CC	CC	TC	GG	GA	TT	TT	CA	GG	AG	GG	GG	TC	GG	TT
FSC	LTM.1759	GG	CC	AA	GG	GG	TT	0	TT	0	CC	CC	GG	GA	TT	CT	AA	GG	AA	AG	GG	0	GG	TT
FSC	LTM.1760	GG	CC	AA	GG	GG	TT	AA	TT	CG	CT	TC	GG	GG	TT	CT	CC	CC	AA	GG	GG	TC	AG	TT
FSC	LTM.1761	GG	CC	AG	GA	GT	TT	0	TT	0	CC	TC	GG	GG	TT	TT	CA	GG	AG	AG	GG	0	GG	CT
FSC	LTM.1762	GG	CC	AA	GG	GG	GG	GG	TT	CC	CC	CC	GG	GA	TT	TT	CA	CG	AA	GG	GG	TT	GG	TT
FSC	LTM.1763	GG	CC	AA	GG	GG	GT	GA	TA	0	CC	TC	GG	GG	TT	TT	CC	CG	AG	AA	GG	TC	GG	TT
FSC	LTM.1764	GG	CC	AA	GG	GG	TT	GG	TA	0	CC	CC	GG	GG	TT	TT	CC	0	AG	GG	GG	0	GG	TT
FSC	LTM.1765	GG	CC	AA	GG	GG	TT	AA	TT	CC	CC	CC	GG	GG	TT	TT	CC	CG	AG	GG	GA	0	GG	TT
FSC	LTM.1766	AG	0	AA	GG	GG	TT	AA	TT	CC	CC	CC	GG	GA	TC	CT	CC	GG	AG	GG	0	0	GG	CT
FSC	LTM.1768	AG	0	AA	GG	GG	TT	GG	TT	CC	CC	TC	GG	GG	TC	TT	0	GG	AG	GG	GG	0	GG	TT
FSC	LTM.1769	GG	0	AA	GG	GG	TT	0	TA	CC	CC	CC	GG	GG	TT	TT	0	GG	AG	AG	GG	0	AG	CT
FSC	LTM.1770	GG	CC	AA	GG	GG	GT	GG	TA	0	CC	CC	GG	GG	TT	TT	CA	CG	GG	GG	GA	0	AG	CC
FSC	LTM.1771	GG	CC	AA	GG	GG	GT	0	TA	0	CC	TC	0	GA	TT	TT	CC	0	AA	GG	AA	0	AG	TT
FSC	LTM.1772	GG	CC	AA	GG	GG	TT	AA	TT	CC	CC	CC	GG	GG	TT	TT	CC	CG	AG	GG	GA	TC	GG	TT
ALP	LTM.1806	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GG	GG	TT	TT	CC	GG	AA	GG	GG	TC	GG	TT
ALP	LTM.1814	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GG	GG	TT	TT	CC	GG	AA	GG	GG	TT	GG	TT
ALP	LTM.1816	GG	CC	AA	GG	GG	TT	GG	TT	0	CC	TC	GG	GG	TT	CT	CC	GG	AA	GG	GG	TT	GG	TT
ALP	LTM.1817	GG	CC	AA	GG	GG	TT	GG	TT	CC	CT	CC	GG	GG	TT	TT	CC	GG	AA	GG	GG	TT	GG	TT
ALP	LTM.1818	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	AA	GA	TT	TT	CC	GG	AA	GG	GG	CC	GG	TT
ALP	LTM.1820	GG	CC	AA	GG	GG	TT	GG	TT	CC	CT	CC	GG	GG	TT	TT	CC	GG	AA	GG	GG	TT	GG	TT
ALP	LTM.1823	GG	CC	AA	GG	GG	TT	GG	TT	0	CC	CC	GA	GG	TT	TT	CC	CG	AA	GG	GG	0	GG	TT
ALP	LTM.1825	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GG	AA	TT	TT	CC	GG	AA	GG	GG	TT	GG	TT
ALP	LTM.1827	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GG	AA	TT	TT	CC	GG	AA	GG	GG	TT	GG	TT
ALP	LTM.1828	GG	CC	AA	GG	GG	TT	GG	TT	0	CC	CC	GG	GG	TT	TT	0	GG	AA	GG	0	0	GG	CT
ALP	LTM.2772	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GG	GG	TT	TT	CC	CG	AA	GG	GG	TT	GG	TT
ALP	LTM.2773	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	TC	GG	GG	TC	TT	CC	GG	AA	GG	GG	TT	GG	TT
ALP	LTM.2774	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	TC	GA	GA	CC	TT	CA	CG	AA	GG	GG	TT	GG	TT
ALP	LTM.2775	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GA	AA	TC	TT	CC	CC	AA	GG	GG	TT	GG	TT
ALP	LTM.2776	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GA	GA	TT	CT	CC	CG	AA	GG	GG	TT	GG	TT
ALP	LTM.3106	GG	CC	AA	GG	GG	TT	GG	TT	0	CC	CC	GG	GG	TT	TT	CC	GG	AA	GG	GG	0	GG	TT
ALP	LTM.3107	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GG	GG	TT	TT	CC	GG	AA	GG	GG	TT	GG	TT
ALP	LTM.3108	GG	0	AA	GG	GG	TT	0	TT	0	CC	CC	GG	GG	TC	TT	0	0	AA	GG	0	0	GG	TT
ALP	LTM.3109	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GG	GG	TC	TT	CC	CC	AA	GG	GG	TT	GG	TT
ALP	LTM.3110	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GG	GG	TT	TT	0	GG	AA	GG	GG	TT	GG	TT
ALP	LTM.3112	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GG	GG	TT	CT	CC	GG	AG	GG	GG	TT	GG	TT
ALP	LTM.3116	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GG	GG	TT	TT	CC	GG	AA	AG	GG	TT	GG	TT
ALP	LTM.3122	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	TC	GG	GG	TT	TT	CA	CC	AA	GG	GG	TT	GG	TT
ALP	LTM.3199	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GG	GG	TC	CT	CC	GG	AG	GG	GG	TT	GG	TT
ALP	LTM.3207	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	CC	GG	AA	TT	TT	CC	GG	AA	AG	GG	TT	GG	TT
ALP	LTM.3228	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	TC	GG	GG	TT	CT	CC	GG	AA	AG	GG	TT	GG	TT
ALP	LTM.3253	GG	CC	AA	GG	GG	TT	GG	TT	0	CC	CC	GG	GG	TC	TT	CC	GG	AA	GG	GG	TT	GG	TT
ALP	LTM.3262	GG	CC	AA	GG	GG	TT	GG	TT	CC	CC	TC	GG	GG	TT	CT	CC	GG	AA	GG	GG	TT	GG	TT

Table S8. Variants at two genotyped SNPs (4:5,457,584 and 4:5,460,551) showing perfect association with winter coat color in the mountain hare, in other *Lepus* species and several other mammals (from Ensembl).

Species	**4:5,457,584**	**4:5,460,551**
mountain hare (*L. timidus*); winter-white	T	C
mountain hare (*L. timidus*); winter-grey	C	T
Iberian hare (*L. granatensis*)	C	T
European brown hare (*L. europaeus*); Iberia	T/C	T/C
European brown hare (*L. europaeus*); central Europe	T	C
snowshoe hare (*L. americanus*)	T	C
black-tailed jackrabbit (*L. californicus*)	T	C
broom hare (L. castroviejoi)	T	C
rabbit (Oryctolagus cuniculus)	T	C
mouse		C
pika		C
horse		C
sheep		C
goat		C
pig		C
human		C

Table S9. Gene expression analyses. **(A)** Sequences of primers used in quantitative PCR (qPCR) and amplification efficiencies. **(B)** Raw threshold cycle (C_t) values for the *Agouti-HC* isoform and the reference genes, *ACTB* and *SDHA*, in skin sampled at three stages of the autumn molt (early, intermediate, late). qPCR reactions of samples marked with the asterisks were run using undiluted cDNA (2-fold dilution was used for remaining ones).

A)

Primer	**Sequence (5'-3')**	**Efficiency [%]**	**PCR product [bp]**
LTM_agouti_hc_F	GGTCATCAGTGGGTTTCTCC	100% (R^2 = 0.932)	164
LTM_agouti_hc_R	CTCTGCTCTGGCTTCCCTTA		
LTM_actb_F	GAAGATCTGGCACCACACCTTC	118% (R^2 = 0.924)	162
LTM_actb_R	CCTGGATGGCCACGTACATG		
LTM_sdha_F	CCCTTGTAGTTGGTAGGAATGC	88% (R^2 = 0.971)	181
LTM_sdha_R	CCCGACAAGGATCACGTCTA		

B)

Molt stage	**Sample**	**RIN**	**C_t *Agouti***	**C_t *ACTB***	**C_t *SDHA***
EARLY	FAR3978	9.7	24.60, 24.46, 24.49	16.05, 16.18, 16.11	22.29, 22.18, 22.28
	FAR3979*	8.4	35.41 - -	15.06, 15.01, 15.02	21.64, 21.22, 21.46
	FAR3981*	9.8	35.73, 35.09, 34.84	15.61, 15.50, 16.26	21.09, 21.19, 21.28
	AFR2772	7.8	24.56, 24.59, 25.02	16.81, 16.87, 17.05	23.99, 24.03, 24.24
	SUI3112	8.1	23.96, 23.83, 23.80	17.16, 17.11, 17.08	22.84, 22.88, 22.80
	SUI3113	8.8	24.19, 23.66, 23.96	16.12, 16.12, 16.14	22.70, 22.85, 23.12
	SUI3114	9.5	27.24, 27.10, 26.89	17.95, 18.06, 17.86	24.55, 24.52, 24.47
	SUI3116	8.0	26.62, 26.42, 26.83	16.86, 16.62, 16.56	23.41, 23.41, 23.49
INTER-MEDIATE	FAR3978	7.7	27.39, 26.82, 27.05	17.76, 17.28, 17.78	25.43, 25.10, 25.55
	FAR3979*	7.1	34.16, 34.79, 32.66	14.70, 14.77, 14.89	22.04, 21.91, 22.12
	FAR3981	9.7	- - -	- - -	- - -
	AFR2772	8.8	29.65, 29.89, 30.18	16.76, 16.88, 16.71	23.56, 23.75, 24.10
	SUI3112	8.1	24.91, 24.86, 24.75	16.39, 16.35, 16.36	22.45, 22.92, 22.28
	SUI3113	8.9	24.41, 24.26, 24.41	16.63, 16.58, 16.53	23.27, 23.29, 23.48
	SUI3114	9.2	26.81, 26.61, 26.58	17.15, 17.06, 16.93	23.60, 23.70, 23.64
	SUI3116	9.8	25.48, 25.80, 26.26	15.73, 15.40, 15.39	21.76, 21.69, 21.79
LATE	FAR3978	7.8	28.46, 28.69, 28.33	17.48, 17.36, 17.61	24.66, 24.61, 24.74
	FAR3979*	9.0	34.83, 32.37, 33.87	14.88, 14.66, 14.61	21.31, 21.08, 21.20
	FAR3981	9.8	- - -	- - -	- - -
	AFR2772	7.5	27.87, 28.07, 28.10	16.37, 16.52, 16.49	23.15, 23.26, 23.60
	SUI3112	8.4	24.74, 24.99, 24.75	16.16, 16.05, 15.96	22.41, 22.11, 22.30
	SUI3113	8.7	27.91, 27.76, 28.07	16.19, 16.20, 16.34	23.10, 23.17, 23.22
	SUI3114	9.0	26.41, 26.37, 26.27	17.23, 17.28, 17.13	23.75, 23.74, 23.67
	SUI3116	8.9	25.36, 25.56, 26.07	16.35, 16.20, 16.63	22.74, 22.95, 23.16

Table S10. Probability of fixation of a rare allele due to genetic drift alone after 65 years of evolution (33-65 generations, generation time of two or one year, respectively) under three demographic scenarios, based on 10,000 SLiM simulations. All scenarios consider an initial allele frequency of $1/2N_F$, where N_F is the effective population size of the founder (diploid individuals; $2N_F$ report haploid numbers): 1 – mode of the HPD of the ABC inference; 2 – lower 95% HPD of the ABC inference, 3 – historical record. Three growth rate parameters were used: 1 – mode of the HPD of ABC inference; 2 – lower 95% HPD interval of the ABC inference; 3 – parameter value implying growth from N_F to the lowest 95% HPD interval of the current effective population size in Faroese hares, inferred with ABC. ABC inference is shown in Table S4. The P-value indicates the proportion of simulations where fixation was achieved after *n* generations.

Scenario	**Founder size ($2N_F$)**	**Initial allele freq**	**Growth rate**	**P-value (33 gen)**	**P-value (65 gen)**
1	20	1/20	0.08	0.001	0.001
2	6	1/6	0.16	0.032	0.032
3	8	1/8	0.10	0.037	0.039

Table S11. Demographic parameters inferred with G-PhoCS for the history of divergence between **(A)** the mountain hare (MTH) and the Iberian hare (IBH), and **(B)** the mountain hare (MTH) and the European brown hare (EBH). For conversion of raw estimates, mutation rate $\mu = 2.8 \times 10^{-9}$ substitutions/site/generation and generation time of two years were used. Mean values of estimated parameters are presented with 95% HPD intervals in parentheses.

A)

G-PhoCS parameter	Demographic parameter (95% HPD interval)
theta MTH	302,893 (297,910 - 307,805) diploid individuals
theta IBH	181,768 (178,425 - 185,125) diploid individuals
theta ANC	316,277 (307,424 - 325,346) diploid individuals
Tau	929,964 (910,339 - 948,925) generations
m IBH → MTH	0.010 (0.004 – 0.016) migrants/generation
m MTH → IBH	0.190 (0.176 – 0.205) migrants/generation

B)

G-PhoCS parameter	Demographic parameter (95% HPD interval)
theta MTH	258,446 (252,298 - 264,617) diploid individuals
theta EBH	290,491 (283,049 - 298,025) diploid individuals
theta ANC	286,732 (274,707 - 298,795) diploid individuals
tau	1,017,571 (990,225 – 1,045,596) generations
m EBH → MTH	0.079 (0.065 – 0.095) migrants/generation
m MTH → EBH	0.283 (0.251 – 0.315) migrants/generation

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