experimental conditions detailed in Table S1. Sequencing experiments revealed the existence of eight and three single nucleotide polymorphisms (SNPs) at the promoter and 3′-UTR of the goat *LALBA* gene respectively (Table S2 and Fig. S1). We also found eight additional putative polymorphic sites at exonic (all synonymous) and intronic regions. The potential functional significance of substitutions detected at the *LALBA* promoter was evaluated with the TFSEARCH software (http://www.cbrc.jp/research/db/TFSEARCH.html). This analysis showed that polymorphisms at SNPs c.-440C>T and c.-358C>T may destroy putative E2F (c.-440C>T, allele T) and p300 and CdxA (c.-358C>T, allele C) transcription factor binding sites. Analysis with UTRSCAN[3] did not reveal any coincidence between SNPs c.*130C>T, c.*203C>T and c.*214C>T and 3′-UTR functional motifs.

Performance of an association analysis between LALBA *variation and milk lactose content:* Because SNPs mapping to *LALBA* regulatory regions may affect the synthesis of this protein and, consequently, lactose levels, we decided to genotype four promoter and two 3′-UTR *LALBA* SNPs in 175 Murciano-Granadina goats with lactose records (two to three per goat, 497 in total) measured with a CombiFoss 600FC instrument.[4] Genotyping was carried out at the Veterinary Service of Molecular Genetics (http://www.svgm.es/eng/index.php) using an OpenArray Real-Time PCR platform. Analysis of the data with a mixed model for repeated measurements did not reveal any significant association between *LALBA* variation and lactose levels (Table 1). It might be argued that this negative outcome is caused by the limited sample size of the resource population. However, it should be stressed that two to three lactose registers have been obtained in each animal. This is expected to very significantly decrease the variance attributable to factors associated with the special environment. Besides, each one of the genotypic means compared in Table 1 has been inferred with data from at least 20 individuals. Finally, the *P*-values shown in Table 1 are very far from the 0.05 level of nominal significance, and even more distant from the Bonferroni correction threshold ($P = 0.01$), so we do not expect that an increase in population size would render significant associations. In conclusion, our work has remarkably enlarged the catalog of caprine *LALBA* SNPs, but we did not obtain any solid evidence of a causal effect of *LALBA* genotype on milk lactose content.

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Supporting information

Additional supporting information may be found in the online version of this article.
Figure S1 Electropherograms showing polymorphic sites at the goat *LALBA* gene.
Table S1 PCR conditions and primers used for the amplification of the goat *LALBA* gene and annealing temperatures.
Table S2 Polymorphisms identified in the goat *LALBA* gene.

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Association analysis of variant near *ZNF389* with ewe cumulative production in three sheep breeds

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Description: Genome-wide association identified a gene region including *ZNF389* as highly associated with small ruminant lentivirus (SRLV) proviral concentration among infected sheep.[1] Within this region, a deletion variant near *ZNF389* was associated with control of SRLV proviral concentration in multiple sheep flocks.[2] Because proviral concentration is a measure of viral replication also correlated with disease,[3] this deletion variant may be predictive for SRLV disease severity. However, an open question is whether this deletion variant could also be associated with production or other traits that might enhance or detract from its value in selective sheep breeding.[4]

Animals and phenotypes: We sampled 764 Idaho Rambouillet, Polypay and Columbia ewes as described.[2] SRLV testing was performed by validated assay as described[5] (Appendix S1) to establish lifetime and partial-lifetime SRLV-negative status. Phenotypes included birth weight; weaning weight; mature weights at 3 and 4 years; milk score; udder scores at 3 and 4 years; and lifetime measures of fleece weight, number of

lambs born, number born alive, number born dead, weight of lambs born and weight of lambs weaned (Appendix S1).

Genotypes and analysis: The deletion variant was g.29500068_29500069delAT relative to NC_019477.1 (rs397514112). Genotyping was performed as described[2] (Table S1). Analysis employed the mixed model or glimmix procedure in SAS v9.2 (SAS Institute) as described.[6,7] For each analysis, the production trait of interest was included as the dependent variable. Other model terms included breed, sire, year of birth, age in years, age at last lambing and genotype as described (Appendix S1). Bonferroni correction accounted for multiple testing.

Comments: The *ZNF389* deletion variant was not consistently associated with any tested production traits between lifetime and partial-lifetime SRLV-negative groups (Tables S1 and S4). Insertion homozygotes previously associated with reduced SRLV proviral concentration were associated with lower birth weight in the partial-lifetime group (Bonferroni $P = 0.033$; Table S4), but the weight difference was small (0.41 kg) and not replicated in the lifetime group (nominal $P = 0.41$; Table S2). Further, there was no association with weaning or later weights (Tables S2 and S4). These results showed no consistent association of the *ZNF389* deletion variant with ewe lifetime production. Other breeds and additional traits, such as wool diameter and infectious disease traits besides control of SRLV, should be examined to more fully assess this locus.

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Conflict of interest: The authors have no conflict of interest to declare.

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Supporting information

Additional supporting information may be found in the online version of this article.

Appendix S1 Additional Methods Description.
Table S1 *ZNF389* deletion variant genotype counts among lifetime SRLV-negative ewes.
Table S2 Association results between *ZNF389* deletion variant and production phenotypes in lifetime SRLV-negative ewes.
Table S3 *ZNF389* deletion variant genotype counts among partial-lifetime group SRLV-negative ewes.
Table S4 Association results between ZNF389 deletion variant and production phenotypes among partial-lifetime group SRLV-negative ewes.

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An updated felCat5 SNP manifest for the Illumina Feline 63k SNP genotyping array

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Background: The development of the first Illumina Infinium iSelect 63k Cat DNA genotyping array has been a milestone in feline research. Since its release in February 2011, the International Cat Genome Sequencing Consortium released a new version of the feline genome assembly (Felis_catus 6.2/felCat5; GenBank assembly ID GCA_000181335.2). As inconsistencies between genome assemblies can complicate genome-wide association studies, we compare SNP locations of the manifest provided with the Illumina Infinium iSelect 63k Cat DNA genotyping array with the most recent feline genome assembly, felCat5. We make the resultant updated SNP manifest available to the cat research community.

Methods: A FASTA file was created using the SNP identifier and the genomic sequence in top orientation from the current feline SNP manifest. For each probe, the longest of the two flanking sequences either side of the variant was selected to create the BLAST input file, and a nucleotide basic local alignment search (BLAST)[1] against the Felis_catus 6.2/felCat5 whole-genome assembly, September 2011 build, downloaded from UCSC Genome Browser (http://genome.ucsc.edu/) was performed. The single best hit for each sequence was retained. A custom perl script was used to extract the position of each array marker relative to the felCat5 assembly from the BLAST output, rejecting hits that failed to reach the base position immediately adjacent to the SNP and those where the *E* value was greater than 1e-05. Hits that were rejected as well as