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**INTERPRETIVE SUMMARY: A genomic analysis about the origins of extant casein variation in goats.** *By Guan et al.*, Genetic variation in the casein loci has multiple effects on milk protein composition and other dairy traits. Here, we have investigated whether the emergence of caprine casein variation predates goat domestication by comparing casein diversity of bezoars (wild goats) and domestic goats. Our results show that much of the casein diversity is shared between both groups, indicating that probably a significant part of casein polymorphisms already segregated in the wild ancestor of domestic goats.

## **RUNNING HEAD: ORIGINS OF GOAT CASEIN VARIATION**

**A genomic analysis about the origins of extant casein variation in goats**

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## ABSTRACT

The variation of the casein genes has a strong impact on the milk composition of goats. Despite the fact that many casein polymorphisms have been identified so far, we do not know yet whether they are evolutionary ancient (*i.e.* they existed before domestication) or young (*i.e.* they emerged after domestication). Herewith, we have identified casein polymorphisms in a data set of 106 caprine whole-genome sequences corresponding to bezoars (*Capra aegagrus*, the ancestor of domestic goats) and four domestic goat (*Capra hircus*) populations from Europe (EU), Africa (AF), Far East (FE) and Near East (NE). Domestic and wild goat populations shared a substantial amount of casein SNPs *i.e.* from 36.1% (*CSN2*) to 55.1% (*CSNIS2*). The comparison of casein variation amongst bezoars and the four domestic goat populations (EU, AF, FE and NE) also evidenced that more than 50% of the casein SNPs are shared by two or more populations, and 18-44% are shared by all populations. Moreover, the majority of casein alleles reported in domestic goats also segregate in the bezoar, including several alleles displaying significant associations with milk composition (*e.g.* A/B alleles of the *CSNIS1* and *CSN3* genes, A-allele of the *CSN2* gene). We conclude that much of the current diversity of the caprine casein genes comes from ancient standing variation segregating in the ancestor of modern domestic goats.

**Key words:** Domestication, standing variation, next generation sequencing, single nucleotide polymorphism

## INTRODUCTION

Caseins represent 80% of the protein content of milk and they have a strong impact on dairy traits as well as on cheese yield and texture (Remeuf *et al.*, 1991). Goat caseins  $\alpha_{S1}$ ,  $\alpha_{S2}$ ,  $\beta$  and  $\kappa$  are encoded by the *CSN1S1*, *CSN1S2*, *CSN2* and *CSN3* genes, respectively, which map to a 250 kb region on chromosome 6 in the order *CSN1S1*-*CSN2*-*CSN1S2*-*CSN3* (Rijnkels, 2002). The polymorphism of these four genes has been implicated in the variation of milk yield and composition (protein and fat contents) as well as in the determination of milk rheological properties and the yield and organoleptic attributes of cheese (revised in Martin *et al.*, 1999, Moioli *et al.*, 2007, Amills *et al.*, 2012).

The domestication of the bezoar (*Capra aegagrus*) in the Fertile Crescent 10,000 years before present (**YBP**) gave birth to domestic goats (*Capra hircus*), an important economic resource in developing countries (Zeder and Hesse 2000, Naderi *et al.*, 2008). Despite the fact that many reports describing the variability of the goat casein genes have been published so far (Martin *et al.*, 2002, Moioli *et al.*, 2007, Amills, 2014), we do not know yet if casein polymorphisms are evolutionary ancient (*i.e.* they existed before domestication) or young (*i.e.* they emerged after domestication). Herewith, we have addressed this question by identifying casein polymorphisms from 106 caprine whole-genome sequences and comparing the allelic variation of the four casein genes in (1) two populations: bezoars and domestic goats, (2) five populations: bezoars and four groups of domestic goats from Europe (**EU**), Africa (**AF**), Far East (**FE**) and Near East (**NE**). In this way, we aimed to find out whether extant genetic variation in the goat casein genes was already present before domestication (as standing variation

segregating in the bezoar) or if it emerged in the context of the evolutionary processes that took place during and well after domestication.

## MATERIALS AND METHODS

### *Retrieval of Goat Whole-Genome Sequences*

Whole genome sequences from 110 wild and domestic goats (Becker *et al.*, 2014, Benjelloun *et al.*, 2015, Reber *et al.*, 2015, Menzi *et al.*, 2016, Wang *et al.*, 2016, Li *et al.*, 2017, Alberto *et al.*, 2018) were retrieved from the NCBI Sequence Read Archive (SRA, <https://www.ncbi.nlm.nih.gov/sra>, **Supplementary Table S1**). More specifically, this data set included genome sequences from bezoars (N=22) as well as 4 domestic goat populations from Europe (Alpine, N=2; Chamois Colored, N=2; Grisons Striped, N=1; Saanen, N=6; Coppernecked, N=1; Tessin Grey, N=1), Africa (local Moroccan population, N=20), Far East (Inner Mongolia Cashmere goat, N=9, Liaoning Cashmere goat, N=10; Tibetan goat, N=16) and Near East (local Iranian breed, N=20). We retrieved all goat genome sequences that were available at the moment of initiating our experiment. All raw data in SRA format were converted into the fastq format by using the fastq-dump 2.8.2 tool available in the SRA-toolkits package (<https://www.ncbi.nlm.nih.gov/sra/docs/toolkitsoft/>).

### *Discovery and Annotation of Genomic Variants*

In order to obtain high quality single nucleotide polymorphisms (SNPs) and insertion/deletions (INDELs), fastq files were filtered with the Trimomatic software

(version 0.36, Bolger *et al.*, 2014). Only paired-end reads were used in the alignment step. Sequences were aligned to the goat reference genome (**ARS1**, Bickhart *et al.*, 2017) with the BWA MEM algorithm with default settings (Li, 2013). Files with Sequence Alignment Map (**SAM**) format were sorted and converted into binary format to remove PCR duplicates and to realign INDEL regions with the Picard tool (<https://broadinstitute.github.io/picard/>). The HaplotypeCaller function of the Genome Analysis Toolkit (**GATK**, version 3.8) was employed to generate vcf files by considering default parameters (McKenna *et al.*, 2010). Finally, a hard filtering step was performed by following the GATK Best Practices recommendations. The SNP dataset was then imputed and phased by using the Beagle 4.1 software (Browning *et al.*, 2016) in order to improve genotype calls based on genotype likelihoods.

### ***Investigation of Population Structure***

We have used the autosomal SNPs identified with GATK (McKenna *et al.*, 2010) to investigate the population structure of bezoars and domestic goats. A thinned set of autosomal SNPs was selected with the command “*--hwe 0.001 --maf 0.05 --geno 0.3 --indep-pairwise 50 5 0.2*” of the PLINK v1.9 software (Purcell *et al.*, 2007). Beforehand, individuals with pi-hat values, estimated on the basis of an identity-by-descent (**IBD**) matrix, above 0.4 were removed from the data set to avoid biases produced by relatedness. By doing so, four individuals (2 European and 2 Far Eastern goats) were excluded and the final data set was based on 106 caprine genomes. A neighbor-joining tree was constructed with the MEGA7 software (Kumar *et al.*, 2016) on the basis of an identity-by-state (**IBS**) distance matrix (Purcell *et al.*, 2007). Principal components analyses (**PCA**) based on 11,226,125 SNPs with a whole-genome distribution and 1,221

SNPs mapping to the casein genes were performed with the PLINK v1.9 software (Purcell *et al.*, 2007) by using the flag “--pca” with default parameters. In addition, the ADMIXTURE software (version 1.3.0, Alexander *et al.*, 2009) was employed to estimate population structure with a block relaxation algorithm. The K-values were set from 2 to 5, and the K-value with the lowest cross-validation error was identified with the method of Alexander and Lange (2011). Moreover, we repeated the ADMIXTURE analysis by just considering a data set of 1,221 SNPs mapping to the casein genes.

### *Annotating the Variation of Caprine Casein Genes*

The genomic coordinates of the goat casein genes (*CSN1S1*, *CSN2*, *CSN1S2* and *CSN3*) in the ARS1 reference genome (Bickhart *et al.*, 2017), were used to retrieve polymorphisms mapping to these four loci with VCFtools 1.8 (Danecek *et al.* 2011, <https://samtools.github.io/bcftools/bcftools.html>). Casein polymorphisms were classified and their effects were predicted with the SnpEff 4.3 software (Cingolani *et al.*, 2012). Moreover, the SIFT Annotator (Vaser *et al.*, 2015) was employed to predict deleteriousness of missense SNPs. When the SIFT predicted score is less than 0.05, the amino acid substitution is classified as deleterious (Vaser *et al.*, 2015). Otherwise, it is tolerated or neutral. By following the strategy outlined in **Supplementary Figure S1**, we were able to convert sequence data into casein alleles or groups of alleles. Such classification, which was based on information provided by Marletta *et al.* (2007), took into account several missense mutations that are outlined in **Supplementary Figure S1**. We were unable to discriminate between the B4 and E alleles of the *CSN1S1* gene because we could not trace the presence of the LINE insertion characteristic of the E-allele (repetitive elements are usually filtered out before the alignment step). The



SnpEff 4.3 software did not detect any mutation introducing a premature stop codon, so we did not identify null alleles in the casein genes. It is difficult to know whether this is due to a biological reality (absence of null alleles in the analysed populations) or to an annotation problem associated with SnpEff 4.3. On the other hand, the O1-allele and O2-allele of the *CSN1S1* gene are large copy number variants whose genomic coordinates have not been reported at a fine resolution. Maybe they could be detected with softwares such as Cn.MOPS or CNVnator, but the main limitation of our experiment is that we have a very heterogeneous data set composed by whole-genome sequences generated with different types of libraries, platforms and, more importantly, coverages, so to detect copy number variants based on read depth would be quite inaccurate. We have not used INDEL information to classify alleles because we consider that INDEL calling from sequence data can be quite unreliable. Indeed, O’Rawe *et al.* (2013) compared the concordance rates among INDELs detected by the GATK Unified Genotyper (v1.5), SOAPindel (v1.0) and SAMtools (v0.1.18) and concluded that there was just a 26.8% agreeing across all three softwares. Hasan *et al.* (2015) compared the performance of seven INDEL calling tools and reported that the number of common INDELs called by all seven tools was very low. By this reason, we decided to report the B2, F and D alleles as a group.

The nucleotide diversity ( $\pi$ -value, average number of pairwise differences between all individuals in the population) of the casein loci (based on 1,221 SNPs mapping to casein genes) was calculated with the VCFtools software (Danecek *et al.* 2011) by using the “--site-pi” command. The same conditions were used to estimate nucleotide diversity at the whole genome level. All results in this study were visualized under the R software environment (<https://www.r-project.org/>).

## RESULTS

### *Genome-wide Analysis of Population Structure*

By using a data set of 106 whole-genome sequences (**Supplementary Table S1**) from domestic goats and bezoars, a total of 31 billion paired-end reads were mapped to the goat reference genome ARS1 (Bickhart *et al.*, 2017). The average sequencing depth was 9.92× and the average mapping rate > 99% (**Supplementary Table S1**). Analysis of the sequence data with the GATK package (McKenna *et al.*, 2010) made possible to identify 51 million SNPs. The majority of these SNPs were biallelic, and only 509,001 sites displayed three or more alleles. Moreover, 35.17% of SNPs had MAFs > 0.05 (17.94 million), while rare (MAF between 0.01 and 0.05) and very rare (MAF < 0.01) SNPs displayed frequencies of 29.72% and 36.74%, respectively. The average ratio of transitions-to-transversions was 2.11 for the whole data set, a result consistent with previous reports (Guan *et al.*, 2016, Li *et al.*, 2017).

After filtering, 11,226,125 autosomal SNPs were used to assess the population structure of the 106 bezoars and domestic goats (four highly related individuals with  $\pi$  values above 0.4 were removed). The PCA and the neighbor-joining tree (**Figures 1a and 1b**) evidenced that individuals clustered according to their geographic origin. In the PCA, bezoars and domestic goats from the Near East occupy an intermediate position between Far Eastern goats and those from Europe and Africa. Moreover, Far Eastern domestic goats form a tight cluster, while bezoars have a more scattered distribution (**Figure 1b**). At K=2, the Admixture analysis showed the existence of two different backgrounds in domestic goats *i.e.* Africa/Europe vs Far East, while Near Eastern goats displayed an intermediate or admixed background (**Figure 2**). At the K-

value with the lowest cross-validation error ( $K = 3$ ), bezoars formed a distinctive group clearly differentiated from domestic goats (**Figure 2**). At  $K=4$ , we observed the existence of two genetically differentiated subgroups in Far Eastern goats, while at  $K=5$  European and African goats displayed different genetic backgrounds (**Figure 2**). When we repeated the PCA and Admixture analysis by using a panel of 1,221 SNPs mapping to the casein genes, we observed a substantial weakening of population structure (**Supplementary Figure S2**). This result might be due to the fact that this second analysis is based on a very reduced set of SNPs (1,221 SNPs instead of the 11,226,125 SNPs employed in the first analysis).

### ***Characterization of the Variation of the Goat Casein Genes***

We identified hundreds of SNPs in the *CSN1S1* (455 SNPs, 6 missense), *CSN2* (194 SNPs, 5 missense), *CSN1S2* (292 SNPs, 11 missense) and *CSN3* (280 SNPs, 9 missense) genes (**Table 1, Supplementary Tables S2-S4**). In the four casein genes, the broad majority of SNPs were intronic, and the second most abundant category was represented by SNPs located in upstream and downstream genic regions (**Supplementary Table S4**). The annotation of SNPs with the SnpEff software (Cingolani *et al.*, 2012) showed that the majority of casein polymorphisms are expected to have low or moderate effects. Indeed, only one SNP (g.85982647G>A) affecting a splice site in the *CSN1S1* gene (G-allele) was predicted to have a high impact (**Supplementary Tables S2-S4**). The SIFT annotator (Vaser *et al.*, 2015) captured additional missense SNPs predicted to be functionally relevant (**Supplementary Tables S2-S4**). Additionally, the majority of casein SNPs identified in our investigation had MAFs above 0.05 (47.1%), a result consistent with that obtained in the analysis of

genome-wide diversity. With regard to INDELs, we have found 81 in *CSN1S1*, 25 in *CSN2*, 59 in *CSN1S2* and 49 in *CSN3* (**Supplementary Table S2**). However, we did not use INDELs in subsequent analyses because INDEL calling is still an error-prone process and the rate of false positives might be high due to alignment artifacts and to the fact that most of the INDEL calling tools lack accurate methods for checking sequencing errors before calling INDEL (Hasan *et al.* 2015). Indeed, concordance rates of INDEL calls between algorithms and sequencing platforms are reportedly low (Fang *et al.* 2014).

Casein SNP variation of bezoars and domestic goats was analysed (**Figure 3**). Domestic and wild populations shared a substantial amount of casein SNPs *i.e.* from 36.1% (*CSN2*) to 55.1% (*CSN1S2*). The comparison of casein variation amongst the five populations (bezoars and domestic goats from Europe, Africa, Near East and Far East) also evidenced that more than 50% casein SNPs are shared by two or more populations and 18% (*CSN3*) - 44% (*CSN1S1*) SNPs are shared by all populations (**Figure 3**). Nucleotide diversity in the casein loci was quite similar in bezoar and domestic goat populations (**Figure 4a**), with the exception of Far Eastern goats that showed a reduced level of variation (t-test,  $P < 0.05$ ). Moreover, the nucleotide diversity of the casein loci happened to be higher (t-test,  $P < 0.001$ ) than that observed along the autosomal genome (**Figure 4b**).

We have used the pipeline reported in **Supplementary Figure S1** to detect casein alleles or groups of alleles based on sequence data (**Table 1**). In the *CSN1S1* gene, the A/I/N/O group of alleles was quite frequent in all populations, with an average frequency above 0.5. Moreover, we were able to detect combinations of SNPs that do not correspond to any of the *CSN1S1* alleles catalogued by Marletta *et al.* (2007) *e.g.* H<sub>8</sub>P<sub>16</sub>Q<sub>77</sub>R<sub>100</sub>A<sub>195</sub>, H<sub>8</sub>L<sub>16</sub>Q<sub>77</sub>R<sub>100</sub>A<sub>195</sub>, H<sub>8</sub>P<sub>16</sub>Q<sub>77</sub>R<sub>100</sub>T<sub>195</sub> and H<sub>8</sub>L<sub>16</sub>E<sub>77</sub>K<sub>100</sub>A<sub>195</sub>. These

novel haplotypes were especially frequent in Far Eastern goats. In the *CSN1S2*, *CSN2* and *CSN3* genes the most abundant alleles were A (average frequency = 0.54), C (average frequency = 0.67) and A/B (average frequency = 0.68), respectively. On the other hand, we have also identified certain alleles in the *CSN1S1* (B1, C and G), *CSN1S2* (E) and *CSN3* (I, K and M) genes that are rare (average frequency < 0.05) or very rare (average frequency < 0.01). Five of these rare alleles were present in Far Eastern goats at low frequencies, and two of them (the K and I alleles of the *CSN3* gene) segregated exclusively in this population. We were unable to identify the D-allele of the *CSN1S2* gene, and the null alleles plus the A1-allele of the *CSN2* gene also remained undetected in our data set.

In certain cases, frequencies of casein alleles were quite divergent amongst populations. For instance, the H-allele of the *CSN3* gene is relatively common in Far Eastern goats but rare in goats from Africa, Europe or the Near East (**Table 1**), and the D-allele of the *CSN3* gene is quite frequent in goats from the Near and Far East but it is completely absent in the remaining caprine populations (**Table 1**). In the *CSN1S1* gene, the B3 allele segregates at moderate frequencies in African goats but it does not segregate in the European population. Importantly, we have found that the majority of casein alleles are present in the population of bezoars, indicating that their existence probably predates domestication. This finding is further supported by the segregation of the majority of casein alleles in two or more of the analysed populations (**Table 1**), despite the fact that they are separated by considerable geographic distances.

## DISCUSSION

A relevant evolutionary question that we aimed to answer in the current study is whether extant casein genetic variation segregating in domestic goats comes from standing variation (already present in bezoars before their domestication) or if it did emerge after goat domestication and dispersal (novel variation). Before analyzing casein variation, we investigated the genetic relationships and population structure of the five caprine populations under analysis (bezoars and goats from Europe, Africa, Near East and Far East). Our results showed that individuals clustered according to their geographic origin (**Figure 1**). Goats were domesticated in a geographic area covering from the Central Zagros to Eastern Anatolia (Zeder and Hesse, 2000, Naderi *et al.*, 2008, reviewed in Pereira and Amorim, 2010) and subsequently they spread into Europe, Africa and Asia (Pereira and Amorim, 2010). The existence of genetic differentiation between the five populations analysed in our study (**Figure 1**) is compatible with the hypothesis that different gene pools migrated through the Mediterranean and Danubian corridors in Europe, the Central Steppe and the Indus Valley in Asia, and North Africa (Pereira and Amorim, 2010). Indeed, the analysis of goat ancient genomes has shown that goats were domesticated at multiple locations (and time periods) in the Fertile Crescent (Daly *et al.* 2018). Genetic drift combined with the existence of differences in breed management, reproductive isolation and selection goals probably contributed to the establishment of genetic differences between Asian, European and African goats.

The analysis of population structure with ADMIXTURE evidenced the existence of Western (Africa and Europe) and Eastern (Far East) genetic backgrounds, while the genetic background of Near Eastern domestic goats shared both components ( $K = 3$ , **Figure 2**). The third distinctive genetic background was represented by bezoars from

the Near East ( $K = 3$ , **Figure 2**). The analysis of mitochondrial variation of Iranian wild boars revealed the segregation of not only Middle East haplotypes but also of haplotypes that are typically found in wild boars from the West (Europe and Africa) and Far East (Khalilzadeh *et al.*, 2016). These results highlight that Iran has been an important contact zone between the East and the West, and also a key hotspot of genetic diversity (Khalilzadeh *et al.*, 2016). Moreover, we also detected the existence of two different backgrounds in Far Eastern goats, reflecting the existence of two different populations ( $K=5$ , **Figure 2**) *i.e.* Tibetan goats and two Cashmere breeds (Wang *et al.* 2016, Li *et al.*, 2017). Furthermore, Inner Mongolia Cashmere goats (**IMCG**) display a genetic background intermediate between Tibetan (**TB**) and Liaoning Cashmere goats (**LNCG**, **Figure 2**). This result points to the Mongolian Plateau as a critical hub for the dispersal of goats across East Asia (Pereira and Amorim, 2010), as reported for cattle (Ajmone-Marsan *et al.*, 2010) and sheep (Zhao *et al.*, 2017).

We have annotated casein polymorphisms according to the genomic coordinates provided in the ARS1 assembly of the goat genome (Bickhart *et al.*, 2017). Obviously, this annotation may differ from the one employed in previous publications. For instance, the missense *CSN3* Asn74Ser and Val86Ile polymorphisms identified by us (**Supplementary Table S2**) correspond to the Asn53Ser and Val65Ile substitutions reported by Marletta *et al.* (2007). These differences might be due, for instance, to the fact that amino acid residue numbering in a protein sequence may begin with the first amino acid of either the leader peptide or the mature protein sequence. Moreover, whole-genome sequencing with a modest coverage (average of  $9.92\times$  in the current work) can yield thousands of false polymorphisms that are produced by sequencing errors (Robasky *et al.*, 2014). However, these drawbacks should not have a strong impact on the main conclusions of our study because we did not intend to build a

curated catalogue of casein variation in goats, something that sooner or later will be reported in the Ensembl database (<https://www.ensembl.org>). On the contrary, we aimed to investigate the geographic distribution of caprine casein variation in order to make inferences about the origins of such variation (*i.e.* to ascertain if it comes from standing or novel variation).

The comparison of the nucleotide diversity of the casein loci in bezoars vs domestic goats showed that they have similar levels of variation (**Figure 4a**). In contrast, goats from the Far East displayed lower levels of diversity, a feature that might be due to an ancient founder effect associated with goat dispersal after domestication. Moreover, the nucleotide diversity of the casein loci was remarkably higher than that observed in the autosomal genome (**Figure 4b**). Two preferential recombination sites have been reported in the casein cluster (Bevilacqua *et al.* 2002, Hayes *et al.* 2006), a circumstance that is known to promote the generation of diversity. Moreover, the casein genes are not indispensable to sustain life, so purifying selection is probably less intense than in other genomic regions containing housekeeping genes.

In the four casein genes a substantial amount of SNPs (36-55%) were shared between the wild and domestic forms. Importantly, the number of analysed bezoars was relatively low, so we cannot rule out the possibility that the percentage of shared variation between bezoars and domestic goats may increase if sample size is also augmented. The variation shared between the wild and the domestic forms might have an ancestral origin, but such pattern could be also produced by an introgression of the bezoar population with domestic goats. However, the analysis of **Figure 1** does not provide evidence about the existence of introgressed bezoars in our data set. Moreover, the comparison of casein polymorphisms across the five populations evidenced that more than 50% of the polymorphisms are shared between two or more populations, and



that between 18-44% are shared by all populations. Casein diversity shared by all five populations probably has an ancestral origin (*i.e.* its existence probably predates the post-domestication dispersal of goats). These results indicate that a considerable proportion of casein variation might have been already present in the bezoar before the domestication process.

Our findings agree well with other studies demonstrating that genetic variants of agricultural importance such as those related with tomato fruit size, maize plant architecture (*e.g.* teosinte branched 1), seasonality controls and seed size were already present as standing variation in the wild progenitors of domestic plant species (Larson *et al.*, 2014). One exception to this general trend would be that of mutations that could be deleterious in the wild but not in a domestic context, but in principle mutations with functional consequences on the casein genes are not expected to have any effect on the biological efficacy of the individuals harbouring them. These results contrast strongly with those obtained in dogs, where a number of mutations with large phenotypic effects are present in dogs but not in wolves, implying that these mutations probably emerged during or after domestication and reached detectable allelic frequencies because they were selected for (Boyko *et al.*, 2010, Larson *et al.*, 2014). We have also observed that a relevant fraction of the casein diversity is not shared across populations (**Figure 3**). This variation might be represented by either mutations that emerged after the domestication and dispersal of goats or they may be due to insufficient sampling or to sequencing errors (because of limited genomic coverage).

The allelic frequencies of the casein genes reported in **Table 1** were consistent with previous studies, although it is important to emphasize that such frequencies can be very variable even when comparing breeds reared in the same geographic location *e.g.* the *CSN1S1* A and E alleles are the most frequent ones in Italian Saanen and Alpine

breeds (Frattini *et al.* 2014), while in Sarda goats the most abundant *CSN1S1* allele is B (Vacca *et al.* 2014). In the *CSN1S1* gene, we observed that A-I-N-O1-O2, the B2-D-F and the B4-E groups of alleles were well represented in the European and African populations (**Table 1**). The genotyping of the *CSN1S1* gene in French (Grosclaude *et al.* 1994, Pepin *et al.* 1994, Carillier-Jacquín *et al.* 2016) and Italian (Sacchi *et al.* 2005, Caroli *et al.* 2006, Gigli *et al.* 2008, Mastrangelo *et al.* 2013, Frattini *et al.* 2014) goats showed that the A and F-alleles are quite abundant, while in Spanish (Jordana *et al.* 1996, Caravaca *et al.* 2008) and African (Caroli *et al.* 2007) goats the B/E and A/B pairs of alleles are the most frequent ones, respectively. In strong contrast, the C, G, N and O1 alleles tend to have low frequencies in Italian (Sacchi *et al.* 2005, Caroli *et al.* 2006, Gigli *et al.* 2008, Mastrangelo *et al.* 2013, Frattini *et al.* 2014) and African breeds (Caroli *et al.* 2007). According to our results (**Table 1**), the A-I-N-O1-O2 group of alleles is prevalent in Near Eastern and Far Eastern domestic goats as well as in bezoars. A previous study focused on Indian and Turkish goats (Chessa *et al.* 2007) also reflected the same trend, with high frequencies of the A-allele in the majority of the analysed populations. With regard to the *CSN1S2* and *CSN2* genes, we found that the A and C alleles, respectively, were the majority ones, a finding that is concordant with what has been published in European, African, Turkish and Indian goats (Sacchi *et al.* 2005, Caroli *et al.* 2006, Caroli *et al.* 2007, Chessa *et al.* 2007, Gigli *et al.* 2008, Vacca *et al.* 2014, Tortorici *et al.* 2014, Kusza *et al.* 2016, Grobler *et al.* 2017). In the *CSN3* gene, the A and B alleles were predominant in most populations (**Table 1**), as previously published in a broad array of caprine breeds (Yahyaoui *et al.* 2003, Prinzenberg *et al.* 2005, Caroli *et al.* 2007, Chessa *et al.* 2007, Kiplagat *et al.* 2010, Di Gerlando *et al.* 2015). Interestingly, the D-allele was frequent in Far and Near Eastern goats, and the G/L group of alleles in Near Eastern goats and bezoars (**Table 1**). The

genetic analysis of the *CSN3* locus in Turkish and Indian goats has evidenced that the D-allele is relatively frequent, and that the G-allele also segregates in these two populations but at lower frequencies (Prinzenberg *et al.* 2005, Chessa *et al.* 2007). The *CSN3* D and G alleles, in contrast, are rare in African (Caroli *et al.* 2007) and the majority of European breeds (Yahyaoui *et al.* 2003, Prinzenberg *et al.* 2005), with the exception of several Italian populations (Sacchi *et al.* 2005, Di Gerlando *et al.* 2015).

In summary, our main finding is that a significant number of casein alleles (or groups of alleles) are present in the bezoar, suggesting that they existed before domestication. Noteworthy, a number of the casein alleles detected in the bezoar have been associated with dairy traits in domestic goats. For instance, the A and B alleles of the *CSN1S1* gene determine a high content of CSN1S1 in milk and they increase milk protein, casein and fats contents and they also improve cheese yield (revised in Martin *et al.*, 1999, Moioli *et al.*, 2007, Amills *et al.*, 2012, Amills, 2014). The A-allele of the *CSN2* gene and the B-allele of the *CSN3* gene have been also associated with a higher protein content (Caravaca *et al.* 2009, Vacca *et al.* 2014). We have also found that several *CSN3* polymorphisms that are very rare in European breeds display significant frequencies in goat populations from other continents, emphasizing the need to investigate their effects on dairy traits.

## CONCLUSIONS

The main conclusion that can be derived from our work is that a relevant fraction of the casein variation segregating in domestic goats probably emerged before the domestication process.

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**Table 1** Frequencies of alleles or groups of alleles identified in the bezoars (BE) and domestic goats from Europe (EU), Africa (AF), Near East (NE) and Far East (FE) in current study.

	Allele	AF (N=20)	BE (N=22)	EU (N=11)	FE (N=33)	NE (N=20)	Total (N=106)
<i>CSN1S1</i>	A-I-N-O1-O2	0.30	0.55	0.27	0.57	0.67	0.51
	B1	0	0.02	0	0.03	0	0.01
	B2-D-F	0.13	0.11	0.41	0.02	0	0.09
	B3	0.27	0.16	0	0.02	0.10	0.11
	B4-E	0.30	0.09	0.27	0.06	0.05	0.13
	C	0	0	0	0.03	0.08	0.02
	G	0	0	0.05	0	0	0.01
	Unreported	0	0.07	0	0.27	0.1	0.12
<i>CSN1S2</i>	A	0.45	0.62	0.64	0.59	0.43	0.54
	B	0	0.02	0	0.14	0	0.05
	C	0.43	0.10	0.09	0.18	0.50	0.26
	E	0	0.02	0	0.05	0	0.02
	F	0.12	0.24	0.27	0.04	0.07	0.13
<i>CSN2</i>	A	0.58	0.22	0.25	0.24	0.25	0.30
	C	0.39	0.75	0.60	0.76	0.75	0.67
	C1	0.03	0.03	0.15	0	0	0.03
<i>CSN3</i>	A	0.50	0.25	0.05	0.19	0.30	0.27
	B	0.45	0.52	0.95	0.23	0.25	0.41
	D	0	0	0	0.24	0.28	0.13
	G-L	0	0.14	0	0	0.10	0.05
	H	0	0.09	0	0.23	0	0.09
	I	0	0	0	0.08	0	0.02
	K	0	0	0	0.03	0	0.01
	M	0.05	0	0	0	0.07	0.02



## LEGENDS TO FIGURES

**Figure 1** (a) Neighbor-joining tree and (b) principal components analysis (PCA) of 106 bezoars (BE) and domestic goats from Europe (EU), Africa (AF), Near East (NE) and Far East (FE) based on a data set of 11,226,125 autosomal SNPs. The neighbor-joining tree was built according to an identity by state (IBS) distance matrix constructed with the PLINK software (Purcell *et al.* 2007) with default parameters. The PCA considered the principal components 1 (PC1) and 2 (PC2), which explained 14.20% (6.20/eigenvalues) and 13.54% (5.91/eigenvalues) of the variance, respectively.

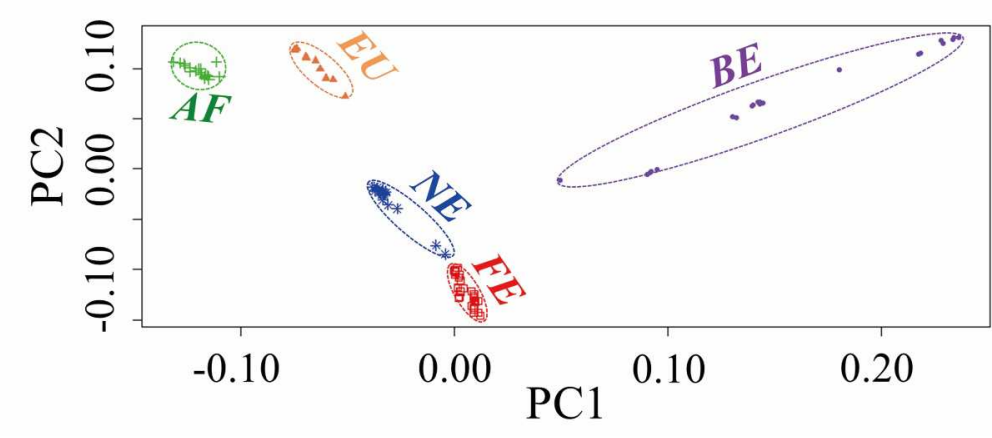
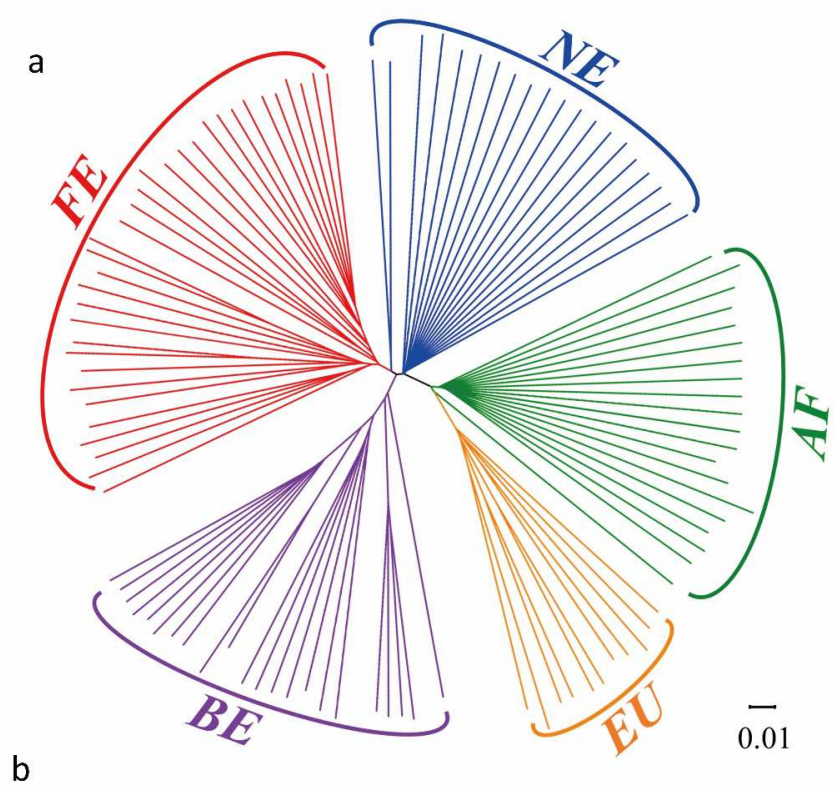
**Figure 2.** ADMIXTURE analysis of 106 bezoars (BE) and domestic goats from Europe (EU), Africa (AF), Near East (NE) and Far East (FE) based on a data set of 11,226,125 autosomal SNPs. Each bar represents one individual and the length of the colored bar represents the proportion of the goat genome inherited from each ancestral population. In the Far East group, the following subpopulations are indicated: TB, Tibetan; IMCG, Inner Mongolia Cashmere goats; LNCG, Liaoning Cashmere goats.

**Figure 3a-d.** Venn diagrams depicting the  $\alpha_{S1}$ - (CSN1S1),  $\alpha_{S2}$ - (CSN1S2),  $\beta$ - (CSN2) and  $\kappa$ - (CSN3) casein SNPs shared between bezoars (BE) and domestic goats (DG). 3e-h. Venn diagrams depicting the  $\alpha_{S1}$ - (CSN1S1),  $\alpha_{S2}$ - (CSN1S2),  $\beta$ - (CSN2) and  $\kappa$ - (CSN3) casein SNPs shared between bezoars (BE) and domestic goats from Europe (EU), Africa (AF), Near East (NE) and Far East (FE).

**Figure 4.** Nucleotide diversity of the (a) casein loci in the bezoars (BE) and domestic goats from Africa (AF), Europe (EU), Near East (NE) and Far East (FE) and (b) the

757 casein loci vs the autosomal genome. Each bar represents the mean nucleotide diversity  
758 and its standard error. The standard error ( $2.08 \times 10^{-5}$ ) of the estimate of the nucleotide  
759 diversity corresponding to the autosomal genome is very small, so it is not been  
760 depicted in the graph.  
761

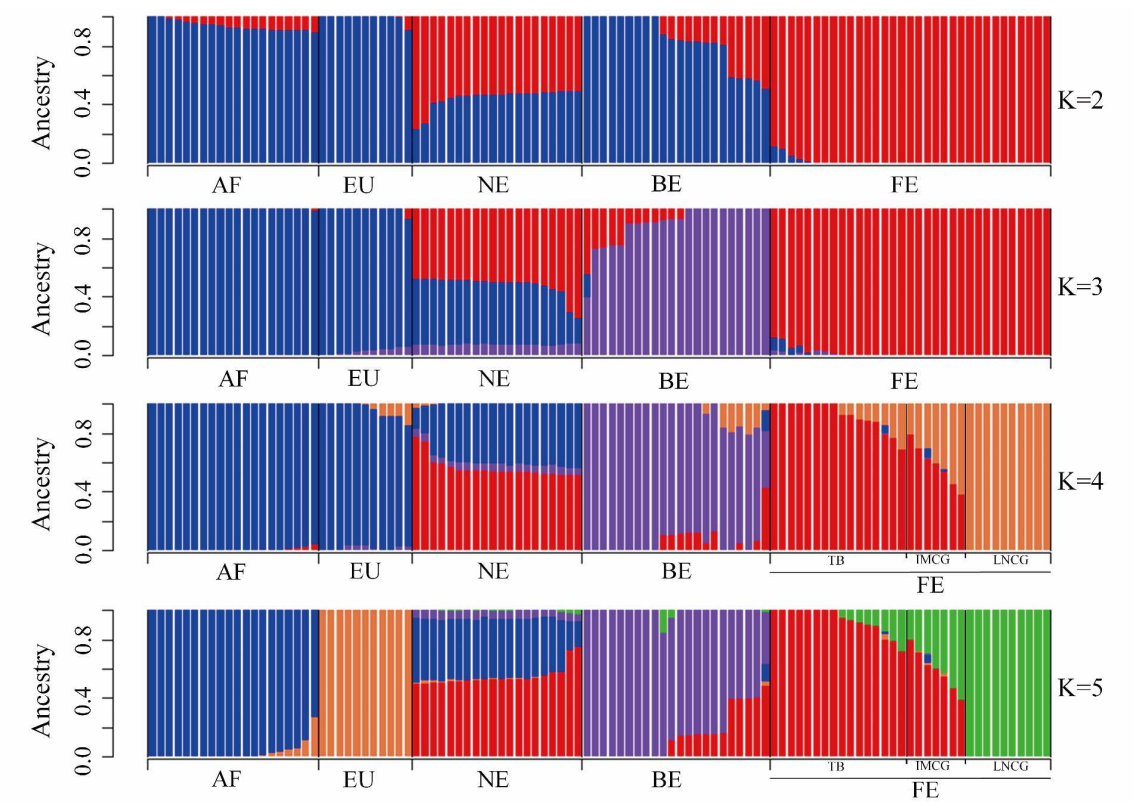
762 **Figure 1**



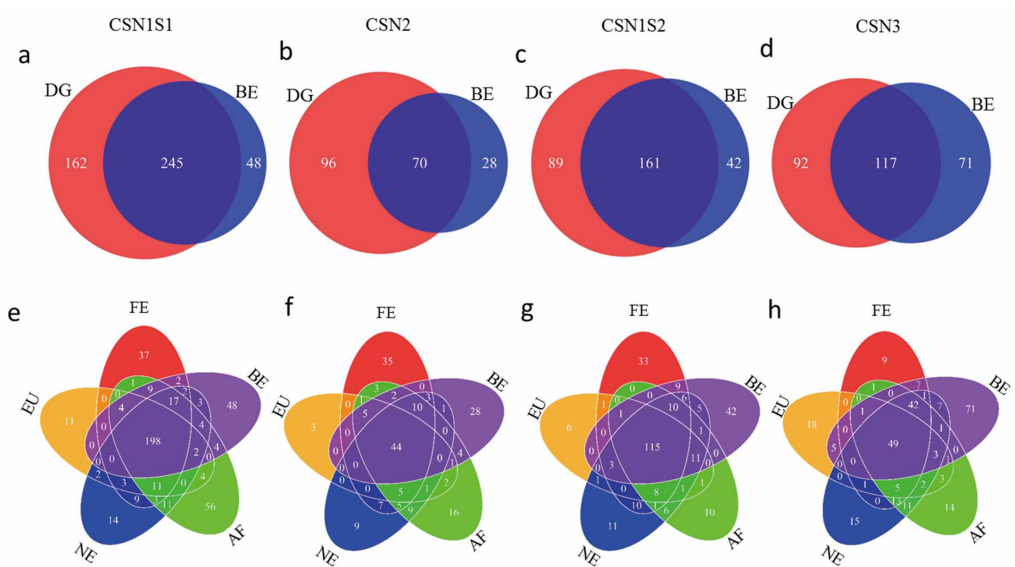
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**Figure 2**



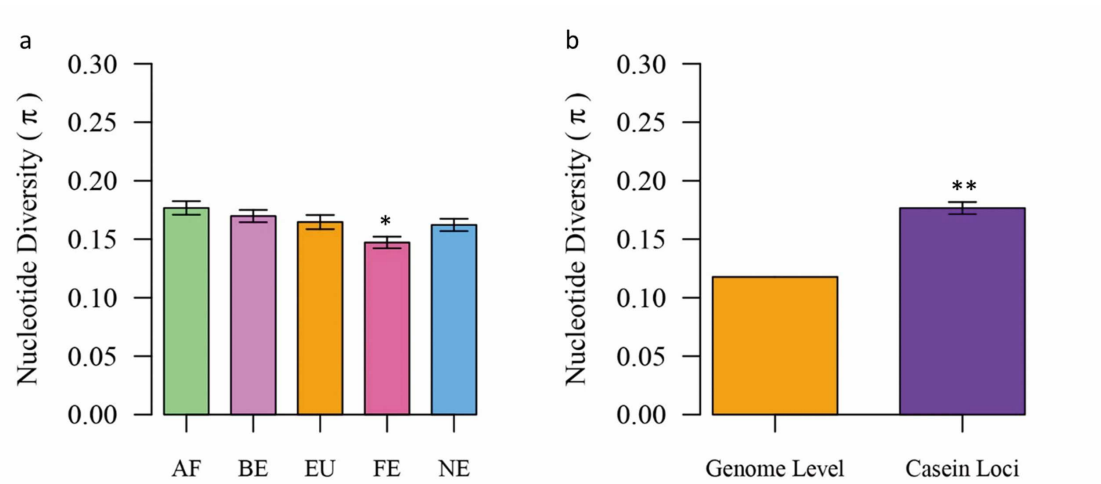
768 **Figure 3**



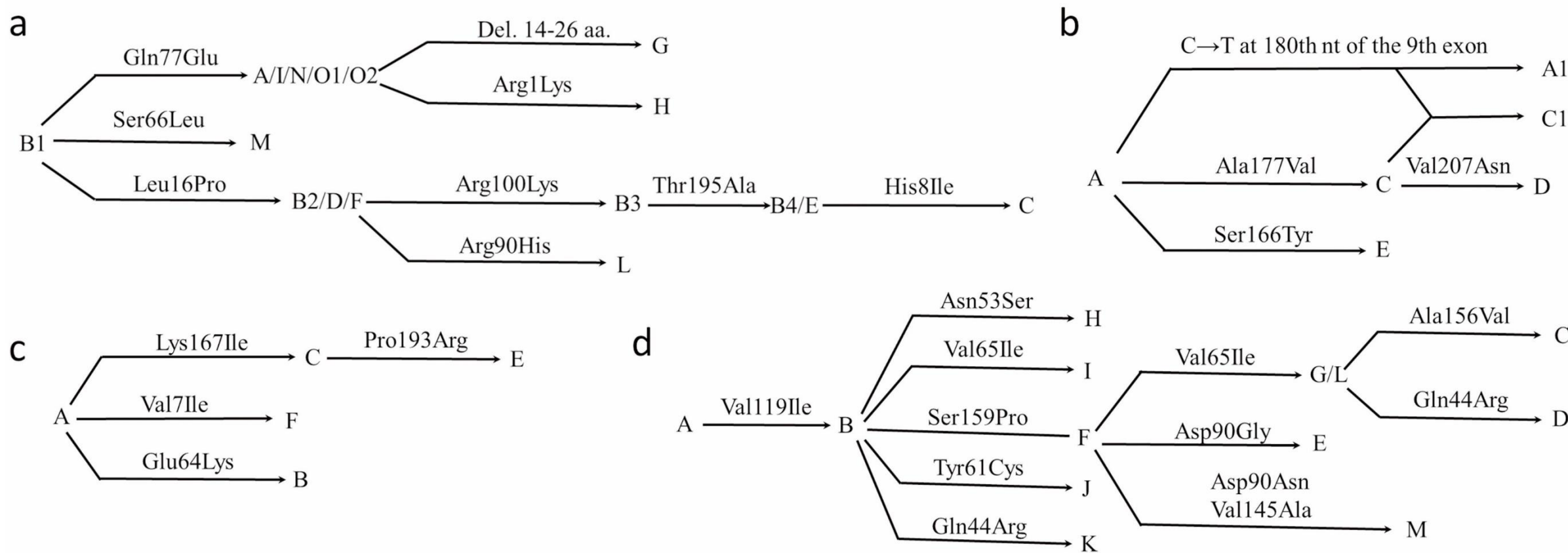
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770

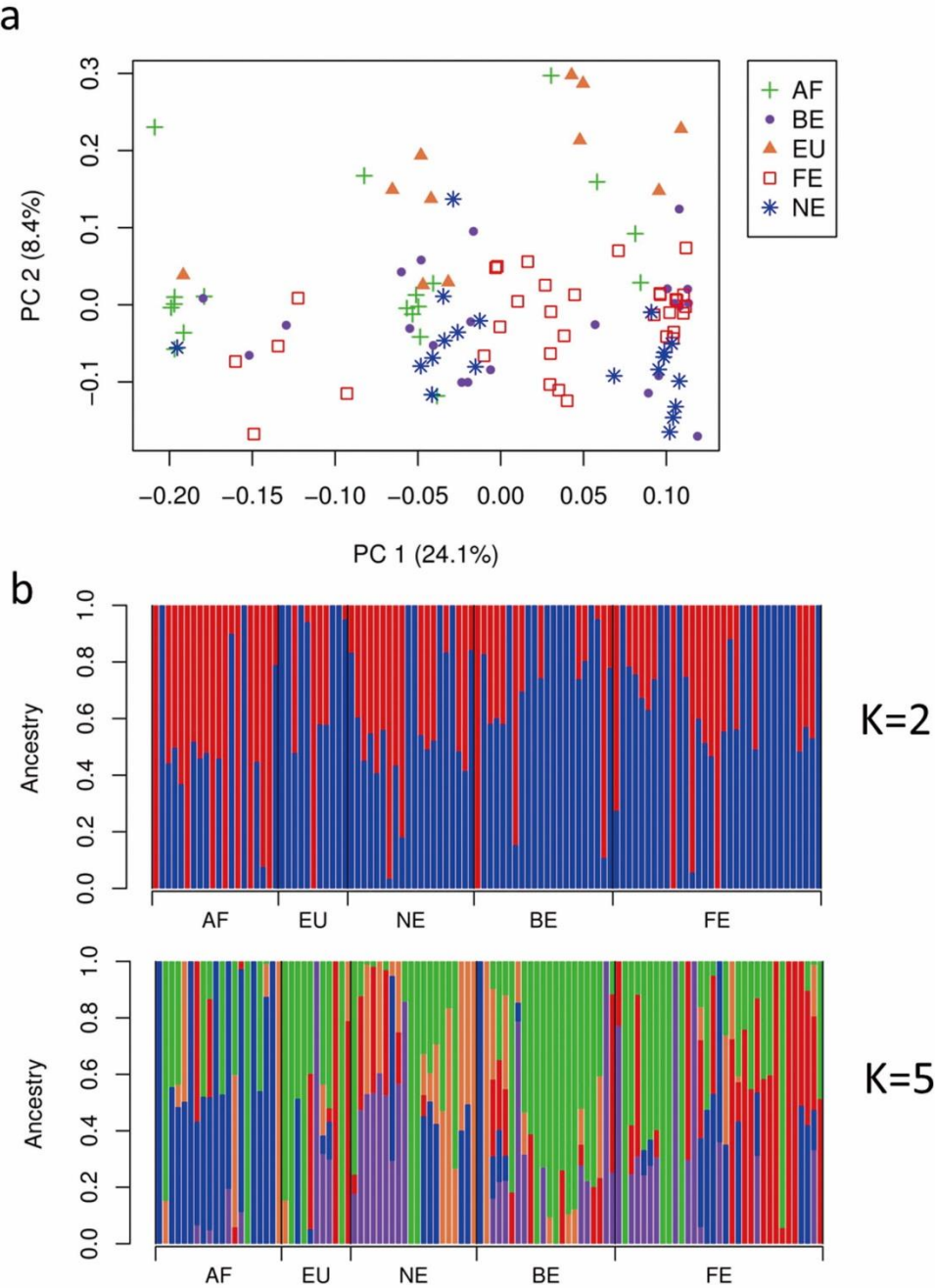
**Figure 4**



**Supplementary Figure S1.** The strategy used for inferring alleles of *CSN1S1* (a), *CSN2* (b), *CSN1S2* (c) and *CSN3* gene (d), which was based on information provided by Marletta *et al.* (2007).



**Supplementary Figure S2.** Principal components analysis (**PCA**, a) and ADMIXTURE analysis (b) based on 1,221 SNPs mapping to casein genes in bezoars (BE) and four domestic goat populations corresponding to Europe (EU), Africa (AF), Near East (NE) and Far East (FE).





Supplementary Table 1. List of the caprine whole-genome sequences used in the current study

Organism	SRA ID	Sample name	Breed	Region	Country	Latitude	Longitude	Sex	Age	Tissue	Total reads	Mapped Reads	Mapping Rate	Depth	Publication
<i>Capra aegagrus</i>	ERR219211	IRCA-C3-1002	-	Near East	Iran	38.63	45.16	male	missing	missing	407117878	406691266	99.90%	11.07	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340328	IRCA-M7-0652	-	Near East	Iran	36.65	50.27	female	missing	missing	189475827	189292834	99.90%	6.53	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340329	IRCA-I11-0002	-	Near East	Iran	34.60	48.21	male	missing	missing	166826202	166574223	99.85%	5.72	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340330	IRCA-N8-0006	-	Near East	Iran	36.44	50.59	male	108 months	missing	368676764	368229077	99.88%	12.88	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340331	IRCA-I6-5237	-	Near East	Iran	37.16	48.39	male	missing	missing	341870050	341568819	99.91%	12.10	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340333	IRCA-I11-0001	-	Near East	Iran	34.60	48.20	male	missing	missing	187650854	187441350	99.89%	6.55	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340334	IRCA-C3-1001	-	Near East	Iran	38.63	45.16	male	missing	missing	369791011	369512004	99.92%	12.90	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340335	IRCA-K12-0005	-	Near East	Iran	34.21	49.05	male	missing	missing	193643194	193368011	99.86%	6.76	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340336	IRCA-F3-0597	-	Near East	Iran	38.88	46.66	male	missing	missing	187438444	187276068	99.91%	6.59	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340338	IRCA-K7-0009	-	Near East	Iran	36.68	49.37	male	missing	missing	334178821	333916774	99.92%	11.80	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340340	IRCA-G2-5063	-	Near East	Iran	39.18	47.13	male	missing	missing	359913613	358204161	99.53%	12.60	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340341	IRCA-I11-0003	-	Near East	Iran	34.60	48.21	male	missing	missing	149716312	149436381	99.81%	5.26	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340342	IRCA-F3-0600	-	Near East	Iran	38.92	46.87	male	missing	missing	186534047	186281194	99.86%	6.53	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340343	IRCA-F2-5064	-	Near East	Iran	39.25	46.84	male	missing	missing	212276200	211009172	99.40%	7.54	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340344	IRCA-F2-5026	-	Near East	Iran	39.16	46.69	male	missing	missing	333435356	333017953	99.87%	11.66	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340345	IRCA-F2-5066	-	Near East	Iran	39.08	46.93	male	missing	missing	87018563	86992885	99.97%	9.75	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340347	IRCA-G2-0568	-	Near East	Iran	39.35	47.47	male	missing	missing	138763744	138734320	99.98%	11.27	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340348	IRCA-M12-0008	-	Near East	Iran	34.18	50.34	male	missing	missing	117206276	117177563	99.98%	9.67	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR340426	IRCA-G2-5065	-	Near East	Iran	39.16	47.13	male	missing	missing	180075946	180023075	99.97%	11.76	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR470100	IRCA-M7-5041	-	Near East	Iran	36.55	50.42	male	60 months	missing	321131238	320984037	99.95%	13.53	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR470104	IRCA-N8-5141	-	Near East	Iran	36.37	50.60	male	84 months	missing	424483520	424062497	99.90%	14.80	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra aegagrus</i>	ERR470106	IRCA-M7-5147	-	Near East	Iran	36.60	50.35	male	60 months	missing	447109081	427812381	95.68%	14.16	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR297229	IRCH-F4-5093	local breed	Near East	Iran	38.30	46.61	female	12 months	missing	379151641	378857509	99.92%	12.54	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR299449	IRCH-D6-5189	local breed	Near East	Iran	37.47	45.88	female	36 months	missing	381861059	381557832	99.92%	12.75	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR299456	IRCH-B4-5209	local breed	Near East	Iran	38.15	44.84	female	36 months	missing	372195363	371909016	99.92%	5.25	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR313197	IRCH-E7-5193	local breed	Near East	Iran	36.95	46.25	male	24 months	missing	353043634	352780840	99.93%	12.08	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR313198	IRCH-C6-5204	local breed	Near East	Iran	37.18	45.21	female	60 months	missing	341402089	341135717	99.92%	11.98	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR313199	IRCH-D7-5132	local breed	Near East	Iran	36.98	45.59	male	12 months	missing	393673889	393380804	99.93%	9.86	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR313200	IRCH-C3-5039	local breed	Near East	Iran	38.86	45.06	female	48 months	missing	390966886	390649355	99.92%	13.43	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR313202	IRCH-E5-5053	local breed	Near East	Iran	37.92	46.09	female	18 months	missing	377246573	376965429	99.93%	12.35	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR313204	IRCH-F3-5044	local breed	Near East	Iran	38.52	46.85	female	24 months	missing	377551996	377266564	99.92%	12.44	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR313206	IRCH-G5-5185	local breed	Near East	Iran	37.97	47.08	male	12 months	missing	346949355	346682466	99.92%	12.37	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR313207	IRCH-D5-5240	local breed	Near East	Iran	37.81	45.57	female	36 months	missing	383771191	383470239	99.92%	13.23	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR313209	IRCH-E6-5087	local breed	Near East	Iran	37.22	46.08	female	24 months	missing	353888406	353603653	99.92%	11.86	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR313210	IRCH-F11-5140	local breed	Near East	Iran	34.90	46.91	female	24 months	missing	377093111	376795608	99.92%	12.92	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR313211	IRCH-C5-5206	local breed	Near East	Iran	37.78	45.06	male	12 months	missing	372728543	372448647	99.92%	12.93	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR313212	IRCH-B3-5031	local breed	Near East	Iran	38.65	44.94	female	36 months	missing	370069849	369780083	99.92%	12.74	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR313213	IRCH-B5-5032	local breed	Near East	Iran	37.97	44.95	male	missing	missing	374971142	374684198	99.92%	13.09	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR313215	IRCH-F5-5133	local breed	Near East	Iran	37.91	46.62	female	36 months	missing	368403194	368120979	99.92%	12.60	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR340332	IRCH-G4-5194	local breed	Near East	Iran	38.39	47.43	female	72 months	missing	325235527	324988396	99.92%	11.25	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR340337	IRCH-G3-5210	local breed	Near East	Iran	38.53	47.16	male	12 months	missing	315414552	315186734	99.93%	11.29	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR340339	IRCH-C7-5144	local breed	Near East	Iran	36.73	45.24	male	12 months	missing	329508630	329279092	99.93%	11.49	Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR313259	MOCH-V10-1083	local populations	Africa	Morocco	missing	missing	male	missing	missing	444198628	443875264	99.93%	15.07	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR313264	MOCH-R13-1104	local populations	Africa	Morocco	missing	missing	female	missing	missing	446770484	446770484	99.92%	14.60	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR315501	MOCH-AA7-2026	local populations	Africa	Morocco	missing	missing	female	missing	missing	442877435	442548200	99.93%	14.75	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR315503	MOCH-N16-1231	local populations	Africa	Morocco	missing	missing	female	missing	missing	459159122	458811288	99.92%	15.36	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR315504	MOCH-AA6-2034	local populations	Africa	Morocco	missing	missing	female	missing	missing	444073531	443746453	99.93%	14.63	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR315506	MOCH-M16-1227	local populations	Africa	Morocco	missing	missing	female	missing	missing	474100441	473568522	99.89%	15.67	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR315511	MOCH-M18-1285	local populations	Africa	Morocco	missing	missing	female	missing	missing	438785780	438405607	99.91%	14.70	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR345977	MOCH-N10-3078	local populations	Africa	Morocco	missing	missing	female	missing	missing	357516082	357415502	99.97%	13.99	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR345980	MOCH-T4-3026	local populations	Africa	Morocco	missing	missing	female	missing	missing	431590733	431462319	99.97%	14.37	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR229484	MOCH-Q10-0090	local populations	Africa	Morocco	missing	missing	female	missing	missing	446045210	445692981	99.92%	15.05	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>

<i>Capra hircus</i>	ERR234310	MOCH-J19-1309	local populations	Africa	Morocco	missing	missing	female	missing	missing	438000396	437874904	99.97%	14.41	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR234316	MOCH-X9-2235	local populations	Africa	Morocco	missing	missing	female	missing	missing	435430167	435329501	99.98%	14.82	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR246145	MOCH-T8-2261	local populations	Africa	Morocco	missing	missing	female	missing	missing	437183185	436819138	99.92%	14.72	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR246149	MOCH-U8-2266	local populations	Africa	Morocco	missing	missing	female	missing	missing	438150896	437813623	99.92%	14.81	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR248918	MOCH-K16-1367	local populations	Africa	Morocco	missing	missing	female	missing	missing	470456851	470092257	99.92%	15.92	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR248919	MOCH-Z5-2083	local populations	Africa	Morocco	missing	missing	female	missing	missing	440653104	440328693	99.93%	14.93	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR248931	MOCH-J17-1355	local populations	Africa	Morocco	missing	missing	female	missing	missing	463796214	463416061	99.92%	15.89	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR248932	MOCH-X5-2098	local populations	Africa	Morocco	missing	missing	female	missing	missing	455014622	454677124	99.93%	15.45	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR248934	MOCH-Z7-2010	local populations	Africa	Morocco	missing	missing	female	missing	missing	101427172	101407401	99.98%	13.49	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR276219	MOCH-X7-2064	local populations	Africa	Morocco	missing	missing	female	missing	missing	461343083	460978000	99.92%	15.35	Benjelloun et al., 2015, Alberto et al., 2018, <a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	SRR3144601	BST001	Grisons Striped	Europe	Switzerland	missing	missing	female	2 years	blood	125108812	124679903	99.66%	5.30	Becker et al., 2014, Reber et al., 2015, Menzi et al., 2016
<i>Capra hircus</i>	SRR3144619	CAG038	Tessin Grey	Europe	Switzerland	missing	missing	male	2 years	blood	145153962	144914652	99.84%	6.43	Becker et al., 2014, Reber et al., 2015, Menzi et al., 2016
<i>Capra hircus</i>	SRR3144621	GFG024	Chamois Colored	Europe	Switzerland	missing	missing	female	2 years	blood	129023757	128810529	99.83%	5.50	Becker et al., 2014, Reber et al., 2015, Menzi et al., 2016
<i>Capra hircus</i>	SRR3144622	GFG034	Chamois Colored	Europe	Switzerland	missing	missing	female	2 years	blood	148032999	147777485	99.83%	6.33	Becker et al., 2014, Reber et al., 2015, Menzi et al., 2016
<i>Capra hircus</i>	SRR3144623	KHZ098	Coppernecked	Europe	Switzerland	missing	missing	female	adult	blood	173029651	172682305	99.80%	7.33	Becker et al., 2014, Reber et al., 2015, Menzi et al., 2016
<i>Capra hircus</i>	SRR3144624	SAN041	Saanen	Europe	Switzerland	missing	missing	female	2 years	blood	115862069	115529708	99.71%	4.92	Becker et al., 2014, Reber et al., 2015, Menzi et al., 2016
<i>Capra hircus</i>	SRR3144625	SAN049	Saanen	Europe	Switzerland	missing	missing	female	2 years	blood	389873370	387863717	99.48%	13.16	Becker et al., 2014, Reber et al., 2015, Menzi et al., 2016
<i>Capra hircus</i>	SRR3144630	SAN075	Saanen	Europe	Switzerland	missing	missing	female	2 years	blood	266551249	265295464	99.53%	9.01	Becker et al., 2014, Reber et al., 2015, Menzi et al., 2016
<i>Capra hircus</i>	SRR3144633	SAN081	Saanen	Europe	Switzerland	missing	missing	male	2 years	blood	157071301	156719106	99.78%	6.84	Becker et al., 2014, Reber et al., 2015, Menzi et al., 2016
<i>Capra hircus</i>	ERR470101	FRCH-SA-0001	Saanen	Europe	France	46.57	-0.28	female	missing	missing	214954141	214848480	99.95%	12.59	<a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR470102	FRCH-SA-0002	Saanen	Europe	France	47.69	-0.87	female	missing	missing	277215487	277150745	99.98%	12.11	<a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR470103	FRCH-AL-0001	Alpine	Europe	France	47.04	0.79	female	missing	missing	426904442	426583336	99.92%	14.50	<a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	ERR470105	FRCH-AL-0002	Alpine	Europe	France	46.69	-0.36	female	missing	missing	405734455	405424639	99.92%	13.66	<a href="https://nextgen.epfl.ch/">https://nextgen.epfl.ch/</a>
<i>Capra hircus</i>	SRR1999390	Tibetan goat1	Tibetan goat	Far East	China	missing	missing	missing	adult	blood	287025996	286464263	99.80%	9.53	<a href="https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710">https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710</a>
<i>Capra hircus</i>	SRR1999396	Tibetan goat3	Tibetan goat	Far East	China	missing	missing	missing	adult	blood	308865310	307958383	99.71%	9.82	<a href="https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710">https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710</a>
<i>Capra hircus</i>	SRR1999407	Tibetan goat4	Tibetan goat	Far East	China	missing	missing	missing	adult	blood	313674863	312793091	99.72%	10.35	<a href="https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710">https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710</a>
<i>Capra hircus</i>	SRR1999408	Tibetan goat5	Tibetan goat	Far East	China	missing	missing	missing	adult	blood	288189075	287928895	99.91%	8.97	<a href="https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710">https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710</a>
<i>Capra hircus</i>	SRR1999409	Tibetan goat6	Tibetan goat	Far East	China	missing	missing	missing	adult	blood	315982304	315572549	99.87%	10.33	<a href="https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710">https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710</a>
<i>Capra hircus</i>	SRR1999410	Tibetan goat7	Tibetan goat	Far East	China	missing	missing	missing	adult	blood	405301838	404754502	99.86%	8.86	<a href="https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710">https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710</a>
<i>Capra hircus</i>	SRR1999411	Tibetan goat8	Tibetan goat	Far East	China	missing	missing	missing	adult	blood	293213699	292906984	99.90%	10.16	<a href="https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710">https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710</a>
<i>Capra hircus</i>	SRR1999413	Tibetan goat10	Tibetan goat	Far East	China	missing	missing	missing	adult	blood	412382631	411734620	99.84%	7.84	<a href="https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710">https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710</a>
<i>Capra hircus</i>	SRR1999415	Tibetan goat11	Tibetan goat	Far East	China	missing	missing	missing	adult	blood	428534092	427622808	99.79%	8.45	<a href="https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710">https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710</a>
<i>Capra hircus</i>	SRR1999416	Tibetan goat12	Tibetan goat	Far East	China	missing	missing	missing	adult	blood	295628082	295252906	99.87%	9.79	<a href="https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710">https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710</a>
<i>Capra hircus</i>	SRR1999419	Tibetan goat13	Tibetan goat	Far East	China	missing	missing	missing	adult	blood	273463552	272700672	99.72%	9.10	<a href="https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710">https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710</a>
<i>Capra hircus</i>	SRR1999477	Tibetan goat14	Tibetan goat	Far East	China	missing	missing	missing	adult	blood	329230508	328728792	99.85%	10.33	<a href="https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710">https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710</a>
<i>Capra hircus</i>	SRR1999645	Tibetan goat16	Tibetan goat	Far East	China	missing	missing	missing	adult	blood	314647084	314216409	99.86%	10.14	<a href="https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710">https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710</a>
<i>Capra hircus</i>	SRR1999646	Tibetan goat15	Tibetan goat	Far East	China	missing	missing	missing	adult	blood	283134647	283134647	99.86%	9.17	<a href="https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710">https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710</a>
<i>Capra hircus</i>	SRR1999647	Tibetan goat17	Tibetan goat	Far East	China	missing	missing	missing	adult	blood	377981754	377555276	99.89%	7.52	<a href="https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710">https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP057710</a>
<i>Capra hircus</i>	SRR5149617	High-altitude goat	Tibetan goat	Far East	China	missing	missing	female	adult	blood	206817767	206321898	99.76%	9.74	Tang et al. 2017
<i>Capra hircus</i>	SRR4051866	a19-13	Inner Mongolia cashmere goat	Far East	China	missing	missing	female	adult	blood	128206465	128102831	99.92%	4.12	Wang et al., 2016, Li et al., 2017
<i>Capra hircus</i>	SRR4051928	a33-14	Inner Mongolia cashmere goat	Far East	China	missing	missing	female	adult	blood	146283012	146166904	99.92%	4.79	Wang et al., 2016, Li et al., 2017
<i>Capra hircus</i>	SRR4051964	a48-12	Inner Mongolia cashmere goat	Far East	China	missing	missing	female	adult	blood	184310811	184143736	99.91%	5.03	Wang et al., 2016, Li et al., 2017
<i>Capra hircus</i>	SRR4052103	a13-13	Inner Mongolia cashmere goat	Far East	China	missing	missing	female	adult	blood	136347816	135998335	99.74%	3.36	Wang et al., 2016, Li et al., 2017
<i>Capra hircus</i>	SRR4052272	a30-1	Inner Mongolia cashmere goat	Far East	China	missing	missing	female	adult	blood	116077351	115965880	99.90%	3.07	Wang et al., 2016, Li et al., 2017
<i>Capra hircus</i>	SRR4052346	a43-3	Inner Mongolia cashmere goat	Far East	China	missing	missing	female	adult	blood	136708343	136530426	99.87%	4.55	Wang et al., 2016, Li et al., 2017
<i>Capra hircus</i>	SRR4052349	a45-5	Inner Mongolia cashmere goat	Far East	China	missing	missing	female	adult	blood	169591085	169194844	99.77%	5.50	Wang et al., 2016, Li et al., 2017
<i>Capra hircus</i>	SRR5557418	Chir 183	Inner Mongolia cashmere goat	Far East	China	missing	missing	female	missing	blood	79642650	70717205	88.79%	1.19	Qiao et al. 2017
<i>Capra hircus</i>	SRR5557598	Chir 458	Inner Mongolia cashmere goat	Far East	China	missing	missing	female	missing	blood	75256299	65014732	86.39%	1.16	Qiao et al. 2017
<i>Capra hircus</i>	SRR4064255	a18-1	Liaoning cashmere	Far East	China	missing	missing	female	7 years	blood	91410380	91306970	99.89%	3.08	Wang et al., 2016, Li et al., 2017
<i>Capra hircus</i>	SRR4064259	a21-4	Liaoning cashmere	Far East	China	missing	missing	female	8 years	blood	88853679	88777183	99.91%	2.69	Wang et al., 2016, Li et al., 2017
<i>Capra hircus</i>	SRR4067780	a24-2	Liaoning cashmere	Far East	China	missing	missing	female	3 years	blood	123294860	122994567	99.76%	3.95	Wang et al., 2016, Li et al., 2017
<i>Capra hircus</i>	SRR4067798	a33-3	Liaoning cashmere	Far East	China	missing	missing	female	4 years	blood	124034168	123928016	99.91%	3.76	Wang et al., 2016, Li et al., 2017
<i>Capra hircus</i>	SRR4068049	a37-4	Liaoning cashmere	Far East	China	missing	missing	female	6 years	blood	102633262	102370930	99.74%	3.00	Wang et al., 2016, Li et al., 2017
<i>Capra hircus</i>	SRR4068051	a38-5	Liaoning cashmere	Far East	China	missing	missing	female	9 years	blood	80436139	80322946	99.86%	2.50	Wang et al., 2016, Li et al., 2017
<i>Capra hircus</i>	SRR4068053	a47-3	Liaoning cashmere	Far East	China	missing	missing	female	3 years	blood	122176975	121912696	99.78%	3.76	Wang et al., 2016, Li et al., 2017

<i>Capra hircus</i>	SRR4068056	a52-10	Liaoning cashmere	Far East	China	missing	missing	female	3 years	blood	117189492	117070791	99.90%	3.30	Wang et al., 2016, Li et al., 2017
<i>Capra hircus</i>	SRR4068057	a54-13	Liaoning cashmere	Far East	China	missing	missing	female	5 years	blood	103703020	103604843	99.91%	3.15	Wang et al., 2016, Li et al., 2017
<i>Capra hircus</i>	SRR4068058	a56-10	Liaoning cashmere	Far East	China	missing	missing	female	3 years	blood	115716990	115260683	99.61%	3.48	Wang et al., 2016, Li et al., 2017

	Supplementary Table S2. Polymorphisms (SNPs in black, INDEL in red) detected in the goat casein genes (CSN1S1)																		
	Chromosome	Position	Ref allele	Alt_allele	QUAL	Variant_type	Effect	Nucleotide substitution	AA substitution	Subst. literature	Alt_freq	SIFT_score	SIFT_median	SIFT_prediction	AF	BE	EU	FE	NE
	6	85978500	G	A	828.77	5_prime_UTR_variant	MODIFIER	c.-82G>A			0.4151				0.7000	0.3864	0.6818	0.2727	0.2500
	6	85978529	A	G	1026.77	5_prime_UTR_variant	MODIFIER	c.-53A>G			0.1085				0.2750	-	0.3182	0.0606	0.0250
	6	85978639	G	A	1217.77	upstream_gene_variant	MODIFIER	c.-14842G>A			0.4340				0.7000	0.4318	0.6818	0.2879	0.2750
	6	85978648	A	G,C	1242.77	upstream_gene_variant	MODIFIER	c.-14833A>C			0.4340				0.7000	0.4318	0.6818	0.2879	0.2750
	6	85978841	A	G	39.77	upstream_gene_variant	MODIFIER	c.-14640A>G			0.0047				-	-	-	0.0152	-
	6	85978933	G	A	170.77	upstream_gene_variant	MODIFIER	c.-14548G>A			0.0094				-	0.0455	-	-	-
	6	85979000	A	T	860.77	upstream_gene_variant	MODIFIER	c.-14481A>T			0.4528				0.7000	0.4318	0.6818	0.3485	0.2750
	6	85979027	C	T	786.77	upstream_gene_variant	MODIFIER	c.-14454C>T			0.4340				0.7000	0.4318	0.6818	0.3030	0.2500
	6	85979093	G	T	60.74	upstream_gene_variant	MODIFIER	c.-14388G>T			0.0094				-	-	-	0.0303	-
	6	85979123	A	G	421.77	upstream_gene_variant	MODIFIER	c.-14358A>G			0.0613				-	0.2955	-	-	-
	6	85979294	C	T	822.77	upstream_gene_variant	MODIFIER	c.-14187C>T			0.4764				0.7000	0.4318	0.7273	0.3788	0.3250
	6	85979316	G	A	175.77	upstream_gene_variant	MODIFIER	c.-14165G>A			0.0047				0.0250	-	-	-	-
	6	85979372	C	T	218.77	upstream_gene_variant	MODIFIER	c.-14109C>T			0.0047				0.0250	-	-	-	-
	6	85979379	G	T	24.78	upstream_gene_variant	MODIFIER	c.-14102G>T			0.0047				-	-	-	0.0152	-
	6	85979447	A	G	221.77	upstream_gene_variant	MODIFIER	c.-14034A>G			0.0047				-	-	-	-	0.0250
	6	85979465	A	C	313.78	upstream_gene_variant	MODIFIER	c.-14016A>C			0.0283				-	0.1364	-	-	-
	6	85979518	T	G	242.77	upstream_gene_variant	MODIFIER	c.-13963T>G			0.0047				-	-	-	-	0.0250
	6	85979525	A	T	775.77	upstream_gene_variant	MODIFIER	c.-13956A>T			0.4670				0.7500	0.4091	0.7273	0.3333	0.3250
	6	85979526	A	T	775.77	upstream_gene_variant	MODIFIER	c.-13955A>T			0.1792				0.3250	0.0682	-	0.2273	0.1750
	6	85979559	T	C	452.77	upstream_gene_variant	MODIFIER	c.-13922T>C			0.0660				0.1500	0.0227	-	0.0606	0.0750
	6	85979624	T	C	109.77	upstream_gene_variant	MODIFIER	c.-13857T>C			0.0047				0.0250	-	-	-	-
	6	85979652	C	A	1147.77	upstream_gene_variant	MODIFIER	c.-13829C>A			0.6887				0.8000	0.9545	1.0000	0.4545	0.5000
	6	85979710	G	C	265.77	upstream_gene_variant	MODIFIER	c.-13771G>C			0.0047				0.0250	-	-	-	-
	6	85979715	G	A	1162.77	upstream_gene_variant	MODIFIER	c.-13766G>A			0.4575				0.7000	0.4318	0.6818	0.3636	0.2750
	6	85979745	C	T	451.77	upstream_gene_variant	MODIFIER	c.-13736C>T			0.0189				0.0750	0.0227	-	-	-
	6	85979787	A	G	101.03	upstream_gene_variant	MODIFIER	c.-13694A>G			0.0142				-	-	-	0.0455	-
	6	85979851	A	G	971.77	upstream_gene_variant	MODIFIER	c.-13630A>G			0.4623				0.7000	0.4091	0.6818	0.3939	0.2750
	6	85979873	T	C	79.77	upstream_gene_variant	MODIFIER	c.-13608T>C			0.0094				-	-	-	0.0303	-
	6	85979926	T	C	922.77	upstream_gene_variant	MODIFIER	c.-13555T>C			0.4481				0.7000	0.4091	0.6818	0.3485	0.2750
	6	85980048	G	C	945.77	intron_variant	MODIFIER	c.51+39G>C			0.4434				0.7000	0.4091	0.6818	0.3333	0.2750
	6	85980071	T	C	601.77	intron_variant	MODIFIER	c.51+62T>C			0.0330				-	-	-	0.0606	0.0750
	6	85980182	C	G	392.77	intron_variant	MODIFIER	c.51+173C>G			0.0425				0.1250	-	-	-	0.1000
	6	85980234	G	T	702.77	intron_variant	MODIFIER	c.51+225G>T			0.0094				-	-	-	-	0.0500
	6	85980337	G	A	970.77	intron_variant	MODIFIER	c.51+328G>A			0.0660				-	0.3182	-	-	-
	6	85980427	G	A	155.77	intron_variant	MODIFIER	c.51+418G>A			0.0094				-	-	-	0.0303	-
	6	85980442	C	T,A	511.77	intron_variant	MODIFIER	c.51+433C>A			0.0802				0.1000	0.0682	0.3636	0.0303	-
	6	85980463	A	C	360.77	intron_variant	MODIFIER	c.51+454A>C			0.0189				0.1000	-	-	-	-
	6	85980533	G	T	139.03	intron_variant	MODIFIER	c.51+524G>T			0.0189				-	0.0909	-	-	-
	6	85980570	A	G	1084.77	intron_variant	MODIFIER	c.51+561A>G			0.4717				0.7000	0.4318	0.7727	0.3333	0.3500
	6	85980624	C	T	226.77	intron_variant	MODIFIER	c.51+615C>T			0.0189				-	-	0.0455	0.0152	0.0500
	6	85980625	G	A	223.77	intron_variant	MODIFIER	c.51+616G>A			0.0094				-	-	0.0455	-	0.0250
	6	85980643	G	A	339.77	intron_variant	MODIFIER	c.51+634G>A			0.0425				0.1250	-	-	-	0.1000
	6	85980706	G	A	187.77	intron_variant	MODIFIER	c.51+697G>A			0.0047				0.0250	-	-	-	-
	6	85980721	A	G	785.77	intron_variant	MODIFIER	c.51+712A>G			0.4481				0.7000	0.4318	0.6818	0.3333	0.2750
	6	85980810	T	C	39.77	intron_variant	MODIFIER	c.51+801T>C			0.0047				-	-	0.0455	-	-
	6	85980845	A	G	316.77	intron_variant	MODIFIER	c.51+836A>G			0.0425				0.1250	-	-	-	0.1000
	6	85980874	A	G	936.77	intron_variant	MODIFIER	c.52-821A>G			0.3774				0.5750	0.4091	0.5909	0.2879	0.1750
	6	85980896	T	A	10.2	intron_variant	MODIFIER	c.52-799T>A			0.0047				-	-	-	0.0152	-
	6	85980905	A	G	553.77	intron_variant	MODIFIER	c.52-790A>G			0.0708				0.0250	0.0455	-	0.1818	-
	6	85980968	C	T	26.78	intron_variant	MODIFIER	c.52-727C>T			0.0047				-	-	-	-	0.0250
	6	85981008	G	A	153.77	intron_variant	MODIFIER	c.52-687G>A			0.0094				-	-	-	0.0303	-
	6	85981070	G	A	1051.77	intron_variant	MODIFIER	c.52-625G>A			0.4623				0.7000	0.4091	0.6818	0.3939	0.2750
	6	85981078	A	G	731.77	intron_variant	MODIFIER	c.52-617A>G			0.0189				0.1000	-	-	-	-
	6	85981115	T	C	771.77	intron_variant	MODIFIER	c.52-580T>C			0.1226				0.2750	0.0909	0.3182	0.0455	0.0250
	6	85981136	G	C	869.77	intron_variant	MODIFIER	c.52-559G>C			0.3160				0.5000	0.3636	0.6818	0.1061	0.2250
	6	85981181	G	A	814.77	intron_variant	MODIFIER	c.52-514G>A			0.4340				0.7000	0.4091	0.6818	0.3030	0.2750
	6	85981193	C	T	305.77	intron_variant	MODIFIER	c.52-502C>T			0.0189				-	0.0909	-	-	-
	6	85981280	C	T	228.84	intron_variant	MODIFIER	c.52-415C>T			0.0283				-	0.0455	-	0.0606	-
	6	85981351	A	G	136.77	intron_variant	MODIFIER	c.52-344A>G			0.0047				0.0250	-	-	-	-
	6	85981474	G	T	923.77	intron_variant	MODIFIER	c.52-221G>T			0.1085				0.1750	0.0682	-	0.1515	0.0750
	6	85981549	G	A	657.77	intron_variant	MODIFIER	c.52-146G>A			0.0094				-	-	-	-	0.0500
	6	85981622	T	C	200.84	intron_variant	MODIFIER	c.52-73T>C			0.0189				-	0.0909	-	-	-
	6	85981710	C	A	376.78	missense_variant	MODERATE	c.67C>A, c.68A>T	p.His23Ile	p.His8Ile	0.0330	0.03	2.74	DELETERIOUS	-	-	-	0.0606	0.0750
	6	85981735	T	C	363.77	splice_region_variant	LOW	c.84+8T>C			0.0283				-	0.1364	-	-	-
	6	85981739	T	A	794.77	intron_variant	MODIFIER	c.84+12T>A			0.4481				0.7000	0.4318	0.6818	0.3333	0.2750
	6	85981746	T	C	306.77	intron_variant	MODIFIER	c.84+19T>C			0.0283				-	-	0.0909	0.0303	0.0500
	6	85981799	T	A	862.77	intron_variant	MODIFIER	c.84+72T>A			0.4623				0.7000	0.4091	0.6818	0.3939	0.2750
	6	85981816	G	T	863.77	intron_variant	MODIFIER	c.84+89G>T			0.4623				0.7000	0.4091	0.6818	0.3939	0.2750
	6	85981818	C	T	208.77	intron_variant	MODIFIER	c.84+91C>T			0.0047				-	-	-	-	0.0250

6	85981851	C	T	884.77	intron_variant	MODIFIER	c.84+124C>T			0.3160				0.5000	0.2955	0.6818	0.1667	0.2000
6	85981916	A	G	236.77	intron_variant	MODIFIER	c.84+189A>G			0.0047				0.0250	-	-	-	-
6	85981928	G	A	146.77	intron_variant	MODIFIER	c.84+201G>A			0.0094				-	0.0455	-	-	-
6	85981976	A	G	243.77	intron_variant	MODIFIER	c.84+249A>G			0.0094				-	-	-	0.0303	-
6	85982020	T	A	670.77	intron_variant	MODIFIER	c.84+293T>A			0.0802				0.1000	0.0909	0.3636	0.0152	-
6	85982105	A	T	846.77	intron_variant	MODIFIER	c.84+378A>T			0.3160				0.5000	0.3409	0.6818	0.1364	0.2000
6	85982132	C	T	140.77	intron_variant	MODIFIER	c.84+405C>T			0.0142				-	-	0.0455	-	0.0500
6	85982136	G	A	951.77	intron_variant	MODIFIER	c.84+409G>A			0.4528				0.7000	0.4318	0.6818	0.3485	0.2750
6	85982149	T	C	951.77	intron_variant	MODIFIER	c.84+422T>C			0.4434				0.7000	0.4091	0.6818	0.3333	0.2750
6	85982210	C	T	542.77	intron_variant	MODIFIER	c.85-398C>T			0.0047				-	0.0227	-	-	-
6	85982261	A	G	411.77	intron_variant	MODIFIER	c.85-347A>G			0.0425				0.1250	-	-	-	0.1000
6	85982286	C	T	109.77	intron_variant	MODIFIER	c.85-322C>T			0.0094				-	-	-	0.0303	-
6	85982287	G	A	490.77	intron_variant	MODIFIER	c.85-321G>A			0.0613				0.1500	0.0227	-	0.0758	0.0250
6	85982533	G	A	306.77	intron_variant	MODIFIER	c.85-75G>A			0.0047				-	0.0227	-	-	-
6	85982583	A	G	535.77	intron_variant	MODIFIER	c.85-25A>G			0.0660				0.1750	-	0.3182	-	-
6	85982615	T	C	1616.77	missense_variant	MODERATE	c.92T>C	p.Leu31Pro	p.Leu16Pro	0.4292	0.1	2.86	TOLERATED	0.7000	0.3864	0.6818	0.3030	0.2750
6	85982631	C	G	1603.77	synonymous_variant	LOW	c.108C>G	p.Leu36Leu		0.4292				0.7000	0.3636	0.6818	0.3182	0.2750
6	85982647	G	A	111.77	splice_donor_variant	HIGH	c.123+1G>A			0.0047				-	-	0.0455	-	-
6	85982740	A	G	1246.77	intron_variant	MODIFIER	c.123+94A>G			0.4340				0.7000	0.4318	0.6818	0.2879	0.2750
6	85982793	A	G	1137.77	intron_variant	MODIFIER	c.123+147A>G			0.4387				0.7000	0.4091	0.6818	0.3182	0.2750
6	85982829	G	A	258.77	intron_variant	MODIFIER	c.123+183G>A			0.0094				-	0.0455	-	-	-
6	85982853	A	G	1124.77	intron_variant	MODIFIER	c.123+207A>G			0.4245				0.7000	0.4318	0.6818	0.2576	0.2750
6	85982911	T	C	1147.77	intron_variant	MODIFIER	c.124-182T>C			0.4340				0.7000	0.4318	0.6818	0.2879	0.2750
6	85982914	G	A	264.77	intron_variant	MODIFIER	c.124-179G>A			0.0047				0.0250	-	-	-	-
6	85982925	C	T	836.77	intron_variant	MODIFIER	c.124-168C>T			0.0094				-	-	-	-	0.0500
6	85982965	T	C	165.77	intron_variant	MODIFIER	c.124-128T>C			0.0094				-	-	-	0.0303	-
6	85983009	T	C	273.8	intron_variant	MODIFIER	c.124-84T>C			0.0142				-	0.0682	-	-	-
6	85983179	T	C	1125.77	intron_variant	MODIFIER	c.147+63T>C			0.3066				0.5000	0.2955	0.6818	0.1364	0.2000
6	85983185	C	T	1113.77	intron_variant	MODIFIER	c.147+69C>T			0.4292				0.7000	0.4091	0.6818	0.2879	0.2750
6	85983257	C	A	1047.77	intron_variant	MODIFIER	c.147+141C>A			0.4340				0.7000	0.3864	0.6818	0.3182	0.2750
6	85983281	A	G	146.77	intron_variant	MODIFIER	c.147+165A>G			0.0047				0.0250	-	-	-	-
6	85983289	T	A	1065.77	intron_variant	MODIFIER	c.147+173T>A			0.4292				0.7000	0.3864	0.6818	0.3030	0.2750
6	85983335	A	C	1047.77	intron_variant	MODIFIER	c.148-205A>C			0.4057				0.7000	0.3864	0.6818	0.2273	0.2750
6	85983337	A	G	540.77	intron_variant	MODIFIER	c.148-203A>G			0.1038				0.2000	0.0682	-	0.1212	0.0750
6	85983410	G	T	758.77	intron_variant	MODIFIER	c.148-130G>T			0.0802				0.1000	0.0909	0.3636	0.0152	-
6	85983448	A	G	891.77	intron_variant	MODIFIER	c.148-92A>G			0.0566				-	0.1364	-	0.0606	0.0500
6	85983450	T	G	344.77	intron_variant	MODIFIER	c.148-90T>G			0.0236				0.0750	-	-	0.0152	0.0250
6	85983563	G	A	370.98	synonymous_variant	LOW	c.171G>A	p.Lys57Lys		0.0094				-	-	-	0.0303	-
6	85983577	A	G	1003.77	intron_variant	MODIFIER	c.171+14A>G			0.4292				0.7000	0.4091	0.6818	0.2879	0.2750
6	85983631	T	A	380.77	intron_variant	MODIFIER	c.171+68T>A			0.0047				0.0250	-	-	-	-
6	85983681	T	C	1034.77	intron_variant	MODIFIER	c.171+118T>C			0.9151				1.0000	0.9091	1.0000	0.7879	1.0000
6	85983700	G	A	1069.77	intron_variant	MODIFIER	c.171+137G>A			0.4528				0.7000	0.3864	0.6818	0.3788	0.2750
6	85983717	G	T	546.77	intron_variant	MODIFIER	c.171+154G>T			0.0802				0.1750	0.0227	-	0.0909	0.0750
6	85983745	C	T	882.77	intron_variant	MODIFIER	c.171+182C>T			0.4528				0.7000	0.4318	0.6818	0.3485	0.2750
6	85983897	G	T	479.77	intron_variant	MODIFIER	c.172-254G>T			0.0566				0.1500	0.0227	-	0.0606	0.0250
6	85983939	G	A	805.77	intron_variant	MODIFIER	c.172-212G>A			0.4387				0.7000	0.4318	0.6818	0.3030	0.2750
6	85984009	C	T	976.77	intron_variant	MODIFIER	c.172-142C>T			0.1226				0.2000	0.1136	-	0.1515	0.0750
6	85984028	C	T	960.77	intron_variant	MODIFIER	c.172-123C>T			0.4434				0.7000	0.3864	0.6818	0.3333	0.3000
6	85984094	A	G	467.77	intron_variant	MODIFIER	c.172-57A>G			0.0330				-	-	-	0.0606	0.0750
6	85984305	C	T	334.77	intron_variant	MODIFIER	c.195+131C>T			0.0613				0.1250	-	-	0.0606	0.1000
6	85984331	A	T	721.77	intron_variant	MODIFIER	c.195+157A>T			0.4575				0.7000	0.4318	0.7273	0.3333	0.3000
6	85984357	T	C	906.77	intron_variant	MODIFIER	c.195+183T>C			0.1085				0.2000	0.0682	-	0.1364	0.0750
6	85984395	A	T	860.77	intron_variant	MODIFIER	c.195+221A>T			0.3679				0.5250	0.4318	0.3636	0.2879	0.2750
6	85984423	C	T	1039.77	intron_variant	MODIFIER	c.195+249C>T			0.3774				0.5250	0.4318	0.3636	0.3182	0.2750
6	85984512	C	T	645.77	intron_variant	MODIFIER	c.195+338C>T			0.1179				0.2000	0.1136	-	0.1364	0.0750
6	85984519	C	T	241.77	intron_variant	MODIFIER	c.195+345C>T			0.0142				-	-	0.0455	0.0152	0.0250
6	85984530	G	A	229.77	intron_variant	MODIFIER	c.196-337G>A			0.0094				-	0.0455	-	-	-
6	85984603	A	G	199.77	intron_variant	MODIFIER	c.196-264A>G			0.0189				-	-	-	0.0455	0.0250
6	85984648	A	T	127.77	intron_variant	MODIFIER	c.196-219A>T			0.0236				-	-	-	0.0758	-
6	85984650	A	G	307.77	intron_variant	MODIFIER	c.196-217A>G			0.0566				0.0250	0.0455	-	0.1364	-
6	85984702	A	G	649.77	intron_variant	MODIFIER	c.196-165A>G			0.1274				0.2000	0.1136	-	0.1667	0.0750
6	85984781	T	A	997.77	intron_variant	MODIFIER	c.196-86T>A			0.4623				0.6750	0.4545	0.7273	0.3485	0.3000
6	85984785	C	T	238.77	intron_variant	MODIFIER	c.196-82C>T			0.0047				-	-	-	-	0.0250
6	85984930	A	C	901.77	intron_variant	MODIFIER	c.219+40A>C			0.4292				0.6750	0.3864	0.7273	0.3182	0.2500
6	85984938	G	T	688.77	intron_variant	MODIFIER	c.219+48G>T			0.1226				0.1750	0.1136	-	0.1970	0.0250
6	85984964	A	T	895.77	intron_variant	MODIFIER	c.219+74A>T			0.4387				0.6750	0.4091	0.7273	0.3182	0.2750
6	85985065	A	C	640.77	intron_variant	MODIFIER	c.219+175A>C			0.0991				0.1750	0.1136	-	0.1212	0.0250
6	85985092	T	C	1006.77	intron_variant	MODIFIER	c.219+202T>C			0.2123				0.3000	0.1364	0.3182	0.1667	0.2250
6	85985094	T	G	1006.77	intron_variant	MODIFIER	c.219+204T>G			0.2123				0.3000	0.1364	0.3182	0.1667	0.2250
6	85985148	C	G,A	675.77	intron_variant	MODIFIER	c.219+258C>A			0.0283				0.1000	-	-	-	0.0500
6	85985149	G	A	338.77	intron_variant	MODIFIER	c.219+259G>A			0.0047				0.0250	-	-	-	-
6	85985183	C	A	374.77	intron_variant	MODIFIER	c.219+293C>A			0.0047				0.0250	-	-	-	-

6	85985242	T	G	861.77	intron_variant	MODIFIER	c.219+352T>G			0.0802				0.1000	0.0909	0.3636	0.0152	-
6	85985289	T	C	876.77	intron_variant	MODIFIER	c.219+399T>C			0.4717				0.8000	0.4091	0.5909	0.3333	0.3750
6	85985322	G	A	903.77	intron_variant	MODIFIER	c.219+432G>A			0.4292				0.6750	0.4091	0.6818	0.3030	0.2750
6	85985357	C	T	739.77	intron_variant	MODIFIER	c.219+467C>T			0.4198				0.6750	0.4318	0.6818	0.2576	0.2750
6	85985359	G	C	667.77	intron_variant	MODIFIER	c.219+469G>C			0.1226				0.2000	0.1818	0.4091	-	0.0250
6	85985443	C	T	230.77	intron_variant	MODIFIER	c.219+553C>T			0.0425				0.0250	-	-	0.1212	-
6	85985458	G	A	860.77	intron_variant	MODIFIER	c.219+568G>A			0.4528				0.6750	0.4091	0.6818	0.3788	0.2750
6	85985503	T	C	187.77	intron_variant	MODIFIER	c.219+613T>C			0.0047				0.0250	-	-	-	-
6	85985526	G	A	272.77	intron_variant	MODIFIER	c.219+636G>A			0.0189				-	0.0909	-	-	-
6	85985599	C	T	217.77	intron_variant	MODIFIER	c.219+709C>T			0.0047				0.0250	-	-	-	-
6	85985622	T	A	921.77	intron_variant	MODIFIER	c.219+732T>A			0.3208				0.4750	0.2500	0.3182	0.3182	0.2500
6	85985630	T	C	581.77	intron_variant	MODIFIER	c.219+740T>C			0.0849				0.1750	-	0.3182	0.0455	0.0250
6	85985689	G	A	142.77	intron_variant	MODIFIER	c.220-715G>A			0.0047				-	-	-	-	0.0250
6	85985736	C	A	385.77	intron_variant	MODIFIER	c.220-668C>A			0.0613				0.1500	0.0227	-	0.0758	0.0250
6	85985762	T	C	563.77	intron_variant	MODIFIER	c.220-642T>C			0.0660				-	0.3182	-	-	-
6	85985763	A	C	273.77	intron_variant	MODIFIER	c.220-641A>C			0.0047				-	0.0227	-	-	-
6	85985765	G	T	898.77	intron_variant	MODIFIER	c.220-639G>T			0.4292				0.7000	0.4318	0.6818	0.2879	0.2500
6	85985806	A	G	310.9	intron_variant	MODIFIER	c.220-598A>G			0.0189				-	0.0909	-	-	-
6	85985820	T	C	846.77	intron_variant	MODIFIER	c.220-584T>C			0.4434				0.7000	0.4091	0.6818	0.3485	0.2500
6	85985829	T	C	367.77	intron_variant	MODIFIER	c.220-575T>C			0.0330				-	0.1591	-	-	-
6	85985836	G	A	214.77	intron_variant	MODIFIER	c.220-568G>A			0.0047				0.0250	-	-	-	-
6	85985858	T	C	106.77	intron_variant	MODIFIER	c.220-546T>C			0.0047				0.0250	-	-	-	-
6	85985890	C	G	178.77	intron_variant	MODIFIER	c.220-514C>G			0.0047				0.0250	-	-	-	-
6	85985922	C	T	71.77	intron_variant	MODIFIER	c.220-482C>T			0.0047				-	0.0227	-	-	-
6	85985952	G	A	385.77	intron_variant	MODIFIER	c.220-452G>A			0.0330				-	0.1591	-	-	-
6	85985954	T	C	424.77	intron_variant	MODIFIER	c.220-450T>C			0.0566				0.1000	-	0.0455	0.0152	0.1500
6	85985968	T	C	471.77	intron_variant	MODIFIER	c.220-436T>C			0.0047				0.0250	-	-	-	-
6	85986087	G	C	353.77	intron_variant	MODIFIER	c.220-317G>C			0.0047				0.0250	-	-	-	-
6	85986106	C	T	361.77	intron_variant	MODIFIER	c.220-298C>T			0.0047				0.0250	-	-	-	-
6	85986239	C	T	155.77	intron_variant	MODIFIER	c.220-165C>T			0.0047				-	-	-	0.0152	-
6	85986246	C	T	971.77	intron_variant	MODIFIER	c.220-158C>T			0.4151				0.7000	0.4318	0.6818	0.2424	0.2500
6	85986322	A	T,G	591.77	intron_variant	MODIFIER	c.220-82A>G			0.0377				-	0.0227	-	0.0606	0.0750
6	85986334	G	A	341.77	intron_variant	MODIFIER	c.220-70G>A			0.0047				0.0250	-	-	-	-
6	85986339	T	G	1152.77	intron_variant	MODIFIER	c.220-65T>G			0.7075				0.8750	1.0000	1.0000	0.4394	0.5000
6	85986363	A	G	187.9	intron_variant	MODIFIER	c.220-41A>G			0.0094				-	0.0455	-	-	-
6	85986379	G	A	199.77	intron_variant	MODIFIER	c.220-25G>A			0.0047				0.0250	-	-	-	-
6	85986427	G	T,C,A	415.77	synonymous_variant	LOW	c.243G>A	p.Ser81Ser		0.0660				0.1500	0.0682	-	-	0.1250
6	85986459	A	C	108.77	intron_variant	MODIFIER	c.252+23A>C			0.0047				0.0250	-	-	-	-
6	85986466	C	T	1002.77	intron_variant	MODIFIER	c.252+30C>T			0.4198				0.6750	0.4091	0.6818	0.2879	0.2500
6	85986479	G	T	195.77	intron_variant	MODIFIER	c.252+43G>T			0.0094				-	-	-	0.0303	-
6	85986502	T	C	107.77	intron_variant	MODIFIER	c.252+66T>C			0.0047				-	-	-	0.0455	-
6	85986573	C	A	183.77	intron_variant	MODIFIER	c.252+137C>A			0.0047				0.0250	-	-	-	-
6	85986644	A	T	148.77	intron_variant	MODIFIER	c.252+208A>T			0.0094				-	-	-	0.0303	-
6	85986739	A	G	246.77	intron_variant	MODIFIER	c.252+303A>G			0.0142				-	0.0682	-	-	-
6	85986773	T	C	152.77	intron_variant	MODIFIER	c.252+337T>C			0.0047				0.0250	-	-	-	-
6	85986837	T	C	137.77	intron_variant	MODIFIER	c.253-339T>C			0.0094				-	0.0455	-	-	-
6	85986847	A	G	481.77	intron_variant	MODIFIER	c.253-329A>G			0.0377				-	-	-	0.0758	0.0750
6	85986864	A	G	294.77	intron_variant	MODIFIER	c.253-312A>G			0.0047				0.0250	-	-	-	-
6	85986893	G	A	781.77	intron_variant	MODIFIER	c.253-283G>A			0.0660				0.1750	-	0.3182	-	-
6	85986905	G	A	295.77	intron_variant	MODIFIER	c.253-271G>A			0.0047				0.0250	-	-	-	-
6	85986939	T	C	227.77	intron_variant	MODIFIER	c.253-237T>C			0.0047				0.0250	-	-	-	-
6	85986951	T	A	268.77	intron_variant	MODIFIER	c.253-225T>A			0.0047				0.0250	-	-	-	-
6	85986962	C	T	906.77	intron_variant	MODIFIER	c.253-214C>T			0.4481				0.6750	0.4318	0.6818	0.3485	0.2750
6	85987033	C	T	312.77	intron_variant	MODIFIER	c.253-143C>T			0.0330				-	0.1591	-	-	-
6	85987078	A	G	562.77	intron_variant	MODIFIER	c.253-98A>G			0.0519				0.1500	0.0455	-	0.0303	0.0250
6	85987083	T	C	1036.77	intron_variant	MODIFIER	c.253-93T>C			0.4104				0.6750	0.4545	0.6818	0.2121	0.2750
6	85987138	T	C	1037.77	intron_variant	MODIFIER	c.253-38T>C			0.4198				0.7000	0.4545	0.6818	0.2273	0.2750
6	85987155	A	G	409.77	intron_variant	MODIFIER	c.253-21A>G			0.0566				0.1750	-	-	-	0.1250
6	85987162	T	G	157.77	intron_variant	MODIFIER	c.253-14T>G			0.0047				-	-	0.0455	-	-
6	85987189	A	G	529.77	missense_variant	MODERATE	c.266A>G	p.Asn89Ser		0.0047	0.35	2.74	TOLERATED	0.0250	-	-	-	-
6	85987197	C	G	866.77	missense_variant	MODERATE	c.274C>G	p.Gln92Glu	p.Gln77Glu	0.4245	0.29	2.74	TOLERATED	0.7000	0.4773	0.6818	0.2273	0.2750
6	85987210	T	C	378.77	intron_variant	MODIFIER	c.276+11T>C			0.0330				0.0250	0.1136	-	-	0.0250
6	85987242	A	T	237.84	intron_variant	MODIFIER	c.276+43A>T			0.0189				-	0.0909	-	-	-
6	85987273	T	C	36.77	intron_variant	MODIFIER	c.277-17T>C			0.0047				-	-	-	0.0152	-
6	85987307	G	A	213.77	synonymous_variant	LOW	c.294G>A	p.Lys98Lys		0.0094				-	0.0455	-	-	-
6	85987376	A	G	150.77	intron_variant	MODIFIER	c.330+33A>G			0.0047				0.0250	-	-	-	-
6	85987400	G	T	385.77	intron_variant	MODIFIER	c.330+57G>T			0.0047				-	0.0227	-	-	-
6	85987401	T	A	385.77	intron_variant	MODIFIER	c.330+58T>A			0.0047				-	0.0227	-	-	-
6	85987405	G	A	173.77	intron_variant	MODIFIER	c.330+62G>A			0.0047				0.0250	-	-	-	-
6	85987423	C	A	122.77	intron_variant	MODIFIER	c.330+80C>A			0.0047				0.0250	-	-	-	-
6	85987436	G	A	124.77	intron_variant	MODIFIER	c.330+93G>A			0.0047				0.0250	-	-	-	-
6	85987500	T	C	1174.77	intron_variant	MODIFIER	c.330+157T>C			0.3491				0.6000	0.3182	0.3182	0.2727	0.2750

SNP	6	85987501	G	T	474.77	intron_variant	MODIFIER	c.330+158G>T			0.0047				0.0250	-	-	-	-
	6	85987517	C	A	281.77	intron_variant	MODIFIER	c.330+174C>A			0.0283				0.1250	-	-	-	0.0250
	6	85987563	A	G	328.77	intron_variant	MODIFIER	c.330+220A>G			0.0047				0.0250	-	-	-	-
	6	85987573	G	A	845.77	intron_variant	MODIFIER	c.330+230G>A			0.3396				0.6000	0.3636	0.3182	0.2121	0.2750
	6	85987603	C	T	40.77	intron_variant	MODIFIER	c.330+260C>T			0.0047				-	-	-	0.0152	-
	6	85987615	G	T	437.77	intron_variant	MODIFIER	c.330+272G>T			0.0142				-	0.0682	-	-	-
	6	85987646	C	A	1051.77	intron_variant	MODIFIER	c.330+303C>A			0.3443				0.6000	0.3182	0.3182	0.2576	0.2750
	6	85987650	C	T	1051.77	intron_variant	MODIFIER	c.330+307C>T			0.3396				0.6000	0.3182	0.3182	0.2576	0.2500
	6	85987658	A	T	1199.77	intron_variant	MODIFIER	c.330+315A>T			0.3302				0.6000	0.3182	0.2273	0.2576	0.2500
	6	85987785	C	T	947.77	intron_variant	MODIFIER	c.330+442C>T			0.3538				0.6000	0.3182	0.3182	0.2879	0.2750
	6	85987796	G	A	851.77	intron_variant	MODIFIER	c.330+453G>A			0.3585				0.6000	0.3182	0.3182	0.3030	0.2750
	6	85987829	C	T	947.77	intron_variant	MODIFIER	c.330+486C>T			0.3302				0.6000	0.3409	0.2727	0.2121	0.2750
	6	85987841	T	A	581.77	intron_variant	MODIFIER	c.330+498T>A			0.0330				-	-	-	0.0606	0.0750
	6	85987882	G	T	1014.77	intron_variant	MODIFIER	c.330+539G>T			0.3255				0.5750	0.3182	0.2273	0.2576	0.2500
	6	85987919	G	A	977.77	intron_variant	MODIFIER	c.330+576G>A			0.2689				0.5250	0.0909	0.3182	0.2121	0.2750
	6	85987939	G	C	916.77	intron_variant	MODIFIER	c.330+596G>C			0.3208				0.5750	0.2955	0.3182	0.2121	0.2750
	6	85987946	A	G	736.77	intron_variant	MODIFIER	c.330+603A>G			0.0519				0.2250	-	-	-	0.0500
	6	85987956	G	T	701.77	intron_variant	MODIFIER	c.330+613G>T			0.3302				0.5750	0.3182	0.3636	0.2121	0.2750
	6	85988005	A	C	245.77	intron_variant	MODIFIER	c.330+662A>C			0.0425				0.0250	0.0455	-	0.0909	-
	6	85988049	C	T	798.77	intron_variant	MODIFIER	c.331-643C>T			0.3679				0.6000	0.3409	0.3182	0.3182	0.2750
	6	85988101	A	G	1027.77	intron_variant	MODIFIER	c.331-591A>G			0.3679				0.6000	0.3409	0.2727	0.3333	0.2750
	6	85988127	T	C	897.77	intron_variant	MODIFIER	c.331-565T>C			0.3443				0.5750	0.2955	0.3182	0.3030	0.2500
	6	85988128	G	A	897.77	intron_variant	MODIFIER	c.331-564G>A			0.3443				0.5750	0.2955	0.3182	0.3030	0.2500
	6	85988138	T	C	395.77	intron_variant	MODIFIER	c.331-554T>C			0.0047				0.0250	-	-	-	-
	6	85988170	C	T	570.77	intron_variant	MODIFIER	c.331-522C>T			0.0377				0.0500	0.1136	-	0.0152	-
	6	85988209	C	T	777.77	intron_variant	MODIFIER	c.331-483C>T			0.0094				-	0.0455	-	-	-
	6	85988222	G	A	878.77	intron_variant	MODIFIER	c.331-470G>A			0.3302				0.6000	0.3409	0.2727	0.2273	0.2500
	6	85988253	A	C	881.77	intron_variant	MODIFIER	c.331-439A>C			0.3349				0.6000	0.3409	0.2727	0.2273	0.2750
	6	85988301	C	T	1048.77	intron_variant	MODIFIER	c.331-391C>T			0.3443				0.6000	0.3636	0.2727	0.2424	0.2750
	6	85988308	C	G,A	1138.77	intron_variant	MODIFIER	c.331-384C>A			0.3443				0.6000	0.3636	0.3182	0.2273	0.2750
	6	85988365	G	A	955.77	intron_variant	MODIFIER	c.331-327G>A			0.3585				0.6000	0.3409	0.3182	0.2879	0.2750
	6	85988390	G	A	1065.77	intron_variant	MODIFIER	c.331-302G>A			0.3585				0.6000	0.3636	0.2727	0.2879	0.2750
	6	85988405	C	A	401.77	intron_variant	MODIFIER	c.331-287C>A			0.0236				0.0250	0.0455	-	0.0303	-
	6	85988477	T	C	927.77	intron_variant	MODIFIER	c.331-215T>C			0.4198				0.7000	0.3409	0.4091	0.3182	0.4000
	6	85988516	A	G	981.77	intron_variant	MODIFIER	c.331-176A>G			0.3349				0.6000	0.3409	0.3182	0.2121	0.2750
	6	85988536	T	G	1051.77	intron_variant	MODIFIER	c.331-156T>G			0.3255				0.5750	0.2727	0.3182	0.2424	0.2750
	6	85988540	C	T	1006.77	intron_variant	MODIFIER	c.331-152C>T			0.3208				0.6000	0.2727	0.3182	0.2121	0.2750
	6	85988608	G	C	121.77	intron_variant	MODIFIER	c.331-84G>C			0.0047				0.0250	-	-	-	-
	6	85988643	T	A	730.77	intron_variant	MODIFIER	c.331-49T>A			0.1840				0.3250	0.1136	0.2727	0.1364	0.1500
	6	85988650	T	C	781.77	intron_variant	MODIFIER	c.331-42T>C			0.3113				0.6000	0.3409	0.2727	0.1515	0.2750
	6	85988659	T	C	953.77	intron_variant	MODIFIER	c.331-33T>C			0.4104				0.7000	0.4545	0.3636	0.1970	0.4500
	6	85988664	T	C	871.77	intron_variant	MODIFIER	c.331-28T>C			0.3019				0.5750	0.3409	0.2727	0.1364	0.2750
	6	85988682	C	T	1006.77	intron_variant	MODIFIER	c.331-10C>T			0.2925				0.5750	0.3182	0.2727	0.1212	0.2750
	6	85988705	G	A	871.77	missense_variant	MODERATE	c.344G>A	p.Arg115Lys	p.Arg100Lys	0.2830	0.07	2.68	TOLERATED	0.5750	0.2955	0.2727	0.1061	0.2750
	6	85988712	A	G	781.77	synonymous_variant	LOW	c.351A>G	p.Lys117Lys		0.2830				0.5750	0.2955	0.2727	0.1061	0.2750
	6	85988739	G	A	728.77	splice_region_variant	LOW	c.372+6G>A			0.3396				0.6000	0.3636	0.3182	0.2121	0.2750
	6	85988745	T	G	731.77	intron_variant	MODIFIER	c.372+12T>G			0.3349				0.5750	0.3636	0.3182	0.2121	0.2750
	6	85988758	A	G	49.77	intron_variant	MODIFIER	c.372+25A>G			0.0047				-	-	-	0.0152	-
	6	85988788	G	A	250.77	intron_variant	MODIFIER	c.372+55G>A			0.0236				0.0500	-	0.0455	0.0152	0.0250
	6	85988831	G	A	191.77	intron_variant	MODIFIER	c.372+98G>A			0.0047				0.0250	-	-	-	-
	6	85988840	A	G	613.77	intron_variant	MODIFIER	c.372+107A>G			0.0519				-	-	-	0.1212	0.0750
	6	85988857	G	A	608.77	intron_variant	MODIFIER	c.372+124G>A			0.0094				0.0250	-	-	-	0.0250
	6	85988911	C	T	904.77	intron_variant	MODIFIER	c.372+178C>T			0.3443				0.6000	0.3636	0.3182	0.2273	0.2750
	6	85988914	A	G	190.9	intron_variant	MODIFIER	c.372+181A>G			0.0189				0.0250	0.0682	-	-	-
	6	85988971	T	C	1082.77	intron_variant	MODIFIER	c.372+238T>C			0.3491				0.6000	0.3636	0.3182	0.2576	0.2500
	6	85989021	A	G	992.77	intron_variant	MODIFIER	c.372+288A>G			0.3396				0.6000	0.2955	0.3182	0.2727	0.2500
	6	85989107	A	T	907.77	intron_variant	MODIFIER	c.373-270A>T			0.3538				0.6000	0.3182	0.3182	0.2879	0.2750
	6	85989108	T	C	907.77	intron_variant	MODIFIER	c.373-269T>C			0.3538				0.6000	0.3182	0.3182	0.2879	0.2750
	6	85989166	T	C	277.77	intron_variant	MODIFIER	c.373-211T>C			0.0189				0.0250	0.0682	-	-	-
	6	85989187	C	T	352.77	intron_variant	MODIFIER	c.373-190C>T			0.0377				0.0500	-	0.0455	0.0303	0.0750
	6	85989190	A	C	971.77	intron_variant	MODIFIER	c.373-187A>C			0.3679				0.5750	0.3182	0.3182	0.3485	0.2750
	6	85989234	C	T	873.77	intron_variant	MODIFIER	c.373-143C>T			0.3491				0.5750	0.3182	0.3182	0.2879	0.2750
	6	85989257	T	C	949.77	intron_variant	MODIFIER	c.373-120T>C			0.2028				0.3000	0.1136	0.3182	0.1970	0.1500
	6	85989260	T	C	949.77	intron_variant	MODIFIER	c.373-117T>C			0.2028				0.3000	0.1136	0.3182	0.1970	0.1500
	6	85989481	G	T	736.77	intron_variant	MODIFIER	c.396+81G>T			0.0802				0.1000	-	0.3182	0.0758	0.0250
	6	85989491	C	T	1017.77	intron_variant	MODIFIER	c.396+91C>T			0.3726				0.6000	0.3636	0.3182	0.3333	0.2500
	6	85989585	A	T	395.77	intron_variant	MODIFIER	c.396+185A>T			0.0566				0.1000	-	0.0455	0.0303	0.1250
	6	85989632	T	C	357.89	intron_variant	MODIFIER	c.396+232T>C			0.0236				-	0.0909	-	-	0.0250
	6	85989645	A	T	871.77	intron_variant	MODIFIER	c.396+245A>T			0.4575				0.7000	0.4545	0.4091	0.3485	0.4250
	6	85989662	T	A	1307.77	intron_variant	MODIFIER	c.396+262T>A			0.9245				1.0000	0.9545	1.0000	0.7879	1.0000
	6	85989686	T	C	32.77	intron_variant	MODIFIER	c.396+286T>C			0.0047				-	-	-	0.0152	-
	6	85989691	A	C	699.77	intron_variant	MODIFIER	c.396+291A>C			0.3679				0.6000	0.3636	0.3182	0.3030	0.2750



6	85989744	C	G	355.77	intron_variant	MODIFIER	c.396+344C>G			0.0236				-	0.1136	-	-	-
6	85989768	T	C	710.77	intron_variant	MODIFIER	c.396+368T>C			0.3396				0.5750	0.2955	0.2727	0.2879	0.2750
6	85989770	G	A	710.77	intron_variant	MODIFIER	c.396+370G>A			0.3349				0.5500	0.2955	0.2727	0.2879	0.2750
6	85989813	C	T	322.77	intron_variant	MODIFIER	c.396+413C>T			0.0047				-	0.0227	-	-	-
6	85989815	C	T	622.77	intron_variant	MODIFIER	c.396+415C>T			0.3443				0.6000	0.2955	0.2727	0.2879	0.2750
6	85989826	A	T	691.77	intron_variant	MODIFIER	c.396+426A>T			0.4151				0.7000	0.3409	0.3182	0.3333	0.4000
6	85989834	T	C	729.77	intron_variant	MODIFIER	c.396+434T>C			0.3632				0.6000	0.3409	0.2727	0.3182	0.2750
6	85989894	C	T	781.77	intron_variant	MODIFIER	c.396+494C>T			0.3632				0.6000	0.3636	0.3182	0.2879	0.2750
6	85989895	A	G	781.77	intron_variant	MODIFIER	c.396+495A>G			0.3632				0.6000	0.3636	0.3182	0.2879	0.2750
6	85989926	C	G	679.77	intron_variant	MODIFIER	c.396+526C>G			0.0519				-	-	-	0.1212	0.0750
6	85989940	C	G	43.77	intron_variant	MODIFIER	c.396+540C>G			0.0047				-	-	-	0.0152	-
6	85989948	C	A	946.77	intron_variant	MODIFIER	c.396+548C>A			0.3538				0.6000	0.3864	0.3182	0.2424	0.2750
6	85989950	A	G	43.77	intron_variant	MODIFIER	c.396+550A>G			0.0047				-	-	-	0.0152	-
6	85989951	A	G	946.77	intron_variant	MODIFIER	c.396+551A>G			0.3491				0.6000	0.3636	0.3182	0.2424	0.2750
6	85989992	G	A	37.77	intron_variant	MODIFIER	c.396+592G>A			0.0047				-	-	-	-	0.0250
6	85989994	G	A	225.77	intron_variant	MODIFIER	c.396+594G>A			0.0047				0.0250	-	-	-	-
6	85990036	C	G	168.77	intron_variant	MODIFIER	c.397-559C>G			0.0047				-	-	0.0455	-	-
6	85990040	C	A,T	965.77	intron_variant	MODIFIER	c.397-555C>A			0.4198				0.4500	0.1136	0.3182	0.5000	0.6500
6	85990049	A	G	809.77	intron_variant	MODIFIER	c.397-546A>G			0.3491				0.6000	0.2955	0.3182	0.3030	0.2500
6	85990082	A	G	940.77	intron_variant	MODIFIER	c.397-513A>G			0.3208				0.6000	0.3409	0.3182	0.1970	0.2250
6	85990092	A	T	946.77	intron_variant	MODIFIER	c.397-503A>T			0.3396				0.6000	0.3409	0.3182	0.2576	0.2250
6	85990118	G	T	507.77	intron_variant	MODIFIER	c.397-477G>T			0.0377				0.0500	0.1136	-	0.0152	-
6	85990138	T	A	169.77	intron_variant	MODIFIER	c.397-457T>A			0.0047				-	-	0.0455	-	-
6	85990142	T	A	169.77	intron_variant	MODIFIER	c.397-453T>A			0.0047				-	-	0.0455	-	-
6	85990152	T	C	904.77	intron_variant	MODIFIER	c.397-443T>C			0.3302				0.6000	0.2955	0.3182	0.2273	0.2750
6	85990162	C	T	852.77	intron_variant	MODIFIER	c.397-433C>T			0.3349				0.6000	0.3182	0.3182	0.2273	0.2750
6	85990182	A	T	910.77	intron_variant	MODIFIER	c.397-413A>T			0.3208				0.6000	0.3182	0.3182	0.1818	0.2750
6	85990237	T	G	329.77	intron_variant	MODIFIER	c.397-358T>G			0.0330				0.0500	-	-	0.0152	0.1000
6	85990269	C	A	1290.77	intron_variant	MODIFIER	c.397-326C>A			0.3066				0.6000	0.2955	0.3182	0.1515	0.2750
6	85990290	G	A	385.77	intron_variant	MODIFIER	c.397-305G>A			0.0425				0.0500	0.0909	-	0.0455	-
6	85990299	G	T	977.77	intron_variant	MODIFIER	c.397-296G>T			0.3208				0.6000	0.2955	0.3182	0.2121	0.2500
6	85990349	C	T	973.77	intron_variant	MODIFIER	c.397-246C>T			0.3585				0.6000	0.3636	0.3182	0.2727	0.2750
6	85990386	C	T	241.79	intron_variant	MODIFIER	c.397-209C>T			0.0094				-	-	-	0.0303	-
6	85990408	G	A	822.77	intron_variant	MODIFIER	c.397-187G>A			0.3396				0.6000	0.3636	0.3182	0.2121	0.2750
6	85990416	A	G	871.77	intron_variant	MODIFIER	c.397-179A>G			0.3255				0.6000	0.3182	0.2727	0.2121	0.2750
6	85990432	A	G	1006.77	intron_variant	MODIFIER	c.397-163A>G			0.3302				0.6000	0.2727	0.3182	0.2424	0.2750
6	85990454	A	G,T	1064.77	intron_variant	MODIFIER	c.397-141A>G			0.3396				0.6000	0.2955	0.3182	0.2576	0.2750
6	85990531	A	G	890.77	intron_variant	MODIFIER	c.397-64A>G			0.4104				0.7000	0.3409	0.4091	0.3030	0.3750
6	85990548	T	C	992.77	intron_variant	MODIFIER	c.397-47T>C			0.3632				0.6000	0.3409	0.3182	0.3182	0.2500
6	85990699	T	C	768.77	intron_variant	MODIFIER	c.438+63T>C			0.1226				0.3250	-	0.3182	0.0606	0.0500
6	85990773	A	C	928.77	intron_variant	MODIFIER	c.438+137A>C			0.3726				0.6000	0.3182	0.3182	0.3485	0.2750
6	85990791	C	A	203.77	intron_variant	MODIFIER	c.438+155C>A			0.0094				-	0.0455	-	-	-
6	85990847	T	C	891.77	intron_variant	MODIFIER	c.438+211T>C			0.3632				0.6000	0.2955	0.3182	0.3333	0.2750
6	85990898	C	T	45.77	intron_variant	MODIFIER	c.438+262C>T			0.0047				-	-	0.0455	-	-
6	85991024	C	T	15.65	intron_variant	MODIFIER	c.438+388C>T			0.0094				-	0.0455	-	-	-
6	85991177	A	G	117.77	intron_variant	MODIFIER	c.439-359A>G			0.0047				-	0.0227	-	-	-
6	85991241	A	T	1029.77	intron_variant	MODIFIER	c.439-295A>T			0.3679				0.6000	0.3182	0.3182	0.3333	0.2750
6	85991284	G	A	731.77	intron_variant	MODIFIER	c.439-252G>A			0.1981				0.3250	0.1364	0.3636	0.1515	0.1250
6	85991345	T	C	1209.77	intron_variant	MODIFIER	c.439-191T>C			0.4151				0.7000	0.3182	0.3636	0.3333	0.4000
6	85991355	G	A	1082.77	intron_variant	MODIFIER	c.439-181G>A			0.3538				0.6000	0.3182	0.2727	0.3030	0.2750
6	85991440	G	T	989.77	intron_variant	MODIFIER	c.439-96G>T			0.3491				0.5750	0.3409	0.3182	0.2727	0.2750
6	85991446	G	T	1160.77	intron_variant	MODIFIER	c.439-90G>T			0.5660				0.8000	0.5682	0.7727	0.4394	0.4250
6	85991481	C	T	954.77	intron_variant	MODIFIER	c.439-55C>T			0.3538				0.6000	0.3182	0.3182	0.2879	0.2750
6	85991482	A	G	954.77	intron_variant	MODIFIER	c.439-54A>G			0.3538				0.6000	0.3182	0.3182	0.2879	0.2750
6	85991487	C	T	980.77	intron_variant	MODIFIER	c.439-49C>T			0.3491				0.6000	0.2955	0.3182	0.2879	0.2750
6	85991509	G	T	154.77	intron_variant	MODIFIER	c.439-27G>T			0.0094				-	-	-	0.0303	-
6	85991559	C	T	974.77	synonymous_variant	LOW	c.462C>T	p.Asn154Asn		0.3302				0.6000	0.2500	0.3182	0.2576	0.2750
6	85991580	T	C	1104.77	intron_variant	MODIFIER	c.465+18T>C			0.3396				0.6000	0.2955	0.3182	0.2576	0.2750
6	85991587	G	A	1061.77	intron_variant	MODIFIER	c.465+25G>A			0.3443				0.6000	0.2955	0.3182	0.2727	0.2750
6	85991602	C	T	576.77	intron_variant	MODIFIER	c.465+40C>T			0.1274				0.2500	0.1591	-	0.0758	0.1250
6	85991607	T	G	893.77	intron_variant	MODIFIER	c.465+45T>G			0.3491				0.6000	0.2955	0.3182	0.2879	0.2750
6	85991635	G	A	864.77	intron_variant	MODIFIER	c.465+73G>A			0.3538				0.6000	0.3182	0.3182	0.2879	0.2750
6	85991651	C	T	821.77	intron_variant	MODIFIER	c.465+89C>T			0.3491				0.6000	0.3182	0.3182	0.2727	0.2750
6	85991661	T	G	241.77	intron_variant	MODIFIER	c.465+99T>G			0.0142				-	0.0682	-	-	-
6	85991685	T	C	945.77	intron_variant	MODIFIER	c.465+123T>C			0.3538				0.6000	0.3182	0.2727	0.3030	0.2750
6	85991713	A	G	1085.77	intron_variant	MODIFIER	c.465+151A>G			0.3396				0.6000	0.2955	0.2727	0.2727	0.2750
6	85991733	G	A	118.77	intron_variant	MODIFIER	c.465+171G>A			0.0047				-	-	0.0455	-	-
6	85991803	A	T,G	863.77	intron_variant	MODIFIER	c.465+241A>G			0.3538				0.6000	0.3409	0.3182	0.2727	0.2750
6	85991807	G	A	213.77	intron_variant	MODIFIER	c.465+245G>A			0.0142				-	0.0682	-	-	-
6	85991808	G	A	163.77	intron_variant	MODIFIER	c.465+246G>A			0.0094				-	-	-	0.0303	-
6	85991817	C	T	904.77	intron_variant	MODIFIER	c.465+255C>T			0.3443				0.5750	0.3409	0.3182	0.2576	0.2750
6	85991831	A	C	946.77	intron_variant	MODIFIER	c.465+269A>C			0.3491				0.5750	0.3182	0.3182	0.2879	0.2750



6	85991850	C	T	180.77	intron_variant	MODIFIER	c.465+288C>T			0.0094				0.0250	-	0.0455	-	-
6	85991890	G	T	257.77	intron_variant	MODIFIER	c.465+328G>T			0.0047				0.0250	-	-	-	-
6	85991957	G	C	1003.77	intron_variant	MODIFIER	c.465+395G>C			0.0708				0.2000	0.0455	-	-	0.1250
6	85991994	T	A	1041.77	intron_variant	MODIFIER	c.465+432T>A			0.3160				0.5750	0.2500	0.3182	0.2424	0.2500
6	85991995	T	A	1041.77	intron_variant	MODIFIER	c.465+433T>A			0.3160				0.5750	0.2500	0.3182	0.2424	0.2500
6	85992002	T	A	328.77	intron_variant	MODIFIER	c.465+440T>A			0.0047				0.0250	-	-	-	-
6	85992080	G	A	954.77	intron_variant	MODIFIER	c.466-428G>A			0.3538				0.5750	0.3409	0.3182	0.2879	0.2750
6	85992114	T	G	378.77	intron_variant	MODIFIER	c.466-394T>G			0.0236				-	0.0909	-	-	0.0250
6	85992211	A	G	939.77	intron_variant	MODIFIER	c.466-297A>G			0.3302				0.5750	0.2727	0.2727	0.2727	0.2750
6	85992238	A	T	11.12	intron_variant	MODIFIER	c.466-270A>T			0.0047				-	-	-	0.0152	-
6	85992268	T	G	242.85	intron_variant	MODIFIER	c.466-240T>G			0.0047				0.0250	-	-	-	-
6	85992331	T	C	903.77	intron_variant	MODIFIER	c.466-177T>C			0.3679				0.6000	0.3182	0.2727	0.3485	0.2750
6	85992334	C	T	402.77	intron_variant	MODIFIER	c.466-174C>T			0.0330				-	0.1364	-	-	0.0250
6	85992335	G	A	284.77	intron_variant	MODIFIER	c.466-173G>A			0.0047				-	-	-	-	0.0250
6	85992343	T	C	403.77	intron_variant	MODIFIER	c.466-165T>C			0.0377				0.0250	0.0682	0.0909	-	0.0500
6	85992347	A	G	907.77	intron_variant	MODIFIER	c.466-161A>G			0.4292				0.6750	0.3182	0.4091	0.3788	0.4000
6	85992386	T	G	153.77	intron_variant	MODIFIER	c.466-122T>G			0.0094				-	-	-	0.0303	-
6	85992418	C	T	1070.77	intron_variant	MODIFIER	c.466-90C>T			0.5849				0.7250	0.3636	0.3636	0.6061	0.7750
6	85992483	A	T	40.77	intron_variant	MODIFIER	c.466-25A>T			0.0047				-	-	-	0.0152	-
6	85992591	C	T	160.77	intron_variant	MODIFIER	c.489+60C>T			0.0094				-	0.0455	-	-	-
6	85992672	A	C	368.77	intron_variant	MODIFIER	c.489+141A>C			0.0236				0.0500	-	0.0455	0.0152	0.0250
6	85992703	C	T	984.77	intron_variant	MODIFIER	c.489+172C>T			0.3585				0.6000	0.3864	0.3182	0.2576	0.2750
6	85992805	C	T	1096.77	intron_variant	MODIFIER	c.489+274C>T			0.3632				0.6000	0.2955	0.3182	0.3333	0.2750
6	85992812	G	C	253.77	intron_variant	MODIFIER	c.489+281G>C			0.0094				0.0250	0.0227	-	-	-
6	85992858	T	C	249.77	intron_variant	MODIFIER	c.489+327T>C			0.0047				-	-	-	-	0.0250
6	85992900	T	C	86.77	intron_variant	MODIFIER	c.489+369T>C			0.0047				-	0.0227	-	-	-
6	85992912	A	G	244.77	intron_variant	MODIFIER	c.489+381A>G			0.0047				0.0250	-	-	-	-
6	85992960	C	T	157.77	intron_variant	MODIFIER	c.490-367C>T			0.0330				-	0.0455	-	0.0758	-
6	85992975	T	C	602.77	intron_variant	MODIFIER	c.490-352T>C			0.2170				0.3250	0.1591	0.3182	0.1970	0.1500
6	85992976	G	A	466.77	intron_variant	MODIFIER	c.490-351G>A			0.0094				-	0.0455	-	-	-
6	85992980	A	G	373.77	intron_variant	MODIFIER	c.490-347A>G			0.0566				0.1000	-	0.0455	0.0303	0.1250
6	85993013	C	T	168.77	intron_variant	MODIFIER	c.490-314C>T			0.0047				-	-	0.0455	-	-
6	85993106	A	G	732.77	intron_variant	MODIFIER	c.490-221A>G			0.2217				0.3250	0.1818	0.2727	0.2121	0.1500
6	85993120	C	A	708.77	intron_variant	MODIFIER	c.490-207C>A			0.1934				0.3250	0.1364	0.2727	0.1515	0.1500
6	85993303	T	C	240.84	intron_variant	MODIFIER	c.490-24T>C			0.0377				-	-	-	0.1212	-
6	85993314	T	C	272.77	intron_variant	MODIFIER	c.490-13T>C			0.0377				0.0250	0.0682	-	0.0606	-
6	85993335	A	G	125.77	synonymous_variant	LOW	c.498A>G	p.Arg166Arg		0.0094				-	-	-	0.0303	-
6	85993353	C	T	642.77	synonymous_variant	LOW	c.516C>T	p.Asp172Asp		0.0189				0.0250	-	0.1364	-	-
6	85993377	C	T	718.77	synonymous_variant	LOW	c.540C>T	p.Tyr180Tyr		0.3491				0.6000	0.3636	0.2727	0.2576	0.2750
6	85993465	A	G	692.77	missense_variant	MODERATE	c.628A>G	p.Thr210Ala	p.Thr195Ala	0.2358	0.45	2.79	TOLERATED	0.3000	0.1591	0.2727	0.3030	0.1250
6	85993489	C	A	701.77	splice_region_variant	LOW	c.644+8C>A			0.1887				0.3250	0.1136	0.2727	0.1667	0.1250
6	85993501	C	T	813.77	downstream_gene_variant	MODIFIER	c.*13542C>T			0.3491				0.6000	0.3636	0.2727	0.2576	0.2750
6	85993527	A	G	918.77	downstream_gene_variant	MODIFIER	c.*13568A>G			0.3538				0.6000	0.3409	0.2727	0.2879	0.2750
6	85993557	T	A	1055.77	downstream_gene_variant	MODIFIER	c.*13598T>A			0.3538				0.6000	0.3409	0.2727	0.2879	0.2750
6	85993575	A	T	259.77	downstream_gene_variant	MODIFIER	c.*13616A>T			0.0047				0.0250	-	-	-	-
6	85993594	C	T	933.77	downstream_gene_variant	MODIFIER	c.*13635C>T			0.3443				0.6000	0.3409	0.2727	0.2576	0.2750
6	85993618	A	T	817.77	downstream_gene_variant	MODIFIER	c.*13659A>T			0.3443				0.6000	0.3409	0.2727	0.2727	0.2500
6	85993643	C	T	286.77	downstream_gene_variant	MODIFIER	c.*13684C>T			0.0472				0.0500	0.1136	-	0.0455	-
6	85993651	C	T	781.77	downstream_gene_variant	MODIFIER	c.*13692C>T			0.3491				0.5750	0.3409	0.3182	0.2879	0.2500
6	85993653	C	T	781.77	downstream_gene_variant	MODIFIER	c.*13694C>T			0.3538				0.6000	0.3409	0.3182	0.2879	0.2500
6	85993699	G	A	845.77	downstream_gene_variant	MODIFIER	c.*13740G>A			0.3396				0.6000	0.3409	0.2727	0.2576	0.2500
6	85993712	A	T	888.77	downstream_gene_variant	MODIFIER	c.*13753A>T			0.3396				0.5750	0.3636	0.2727	0.2576	0.2500
6	85993727	T	C	375.77	downstream_gene_variant	MODIFIER	c.*13768T>C			0.0472				0.1000	-	0.0455	0.0152	0.1000
6	85993747	C	T	219.77	downstream_gene_variant	MODIFIER	c.*13788C>T			0.0047				0.0250	-	-	-	-
6	85993765	C	T	58.74	downstream_gene_variant	MODIFIER	c.*13806C>T			0.0094				-	-	-	0.0303	-
6	85993774	A	C	1001.77	downstream_gene_variant	MODIFIER	c.*13815A>C			0.3302				0.6000	0.2955	0.3182	0.2273	0.2750
6	85993778	T	C	239.77	downstream_gene_variant	MODIFIER	c.*13819T>C			0.0047				0.0250	-	-	-	-
6	85993794	A	G	145.77	downstream_gene_variant	MODIFIER	c.*13835A>G			0.0047				-	-	0.0455	-	-
6	85993802	C	T	159.77	downstream_gene_variant	MODIFIER	c.*13843C>T			0.0047				0.0250	-	-	-	-
6	85993820	G	A	415.77	downstream_gene_variant	MODIFIER	c.*13861G>A			0.0189				-	0.0909	-	-	-
6	85993838	T	G	126.79	downstream_gene_variant	MODIFIER	c.*13879T>G			0.0189				-	-	-	0.0606	-
6	85993851	G	A	252.77	downstream_gene_variant	MODIFIER	c.*13892G>A			0.0047				-	-	-	-	0.0250
6	85993904	T	C	641.77	downstream_gene_variant	MODIFIER	c.*13945T>C			0.3019				0.5750	0.2955	0.2727	0.1667	0.2750
6	85993905	G	A	102.77	downstream_gene_variant	MODIFIER	c.*13946G>A			0.0047				-	0.0227	-	-	-
6	85993909	T	C	677.77	downstream_gene_variant	MODIFIER	c.*13950T>C			0.3019				0.5750	0.2955	0.2727	0.1667	0.2750
6	85993917	T	A	43.77	downstream_gene_variant	MODIFIER	c.*13958T>A			0.0047				-	-	-	0.0152	-
6	85993920	A	C	43.77	downstream_gene_variant	MODIFIER	c.*13961A>C			0.0047				-	-	-	0.0152	-
6	85993926	G	C	40.77	downstream_gene_variant	MODIFIER	c.*13967G>C			0.0047				-	-	-	0.0152	-
6	85993967	G	A	913.77	downstream_gene_variant	MODIFIER	c.*14008G>A			0.2170				0.3250	0.1364	0.2727	0.2273	0.1500
6	85993972	T	C	1010.77	downstream_gene_variant	MODIFIER	c.*14013T>C			0.3585				0.5750	0.3636	0.2727	0.3030	0.2750
6	85993990	T	G	404.77	downstream_gene_variant	MODIFIER	c.*14031T>G			0.0142				-	0.0682	-	-	-
6	85994045	A	T	893.77	splice_region_variant	LOW	c.645-5A>T			0.3302				0.5750	0.3409	0.2727	0.2424	0.2500

	6	85994070	G	A	1099.77	3 prime UTR variant	MODIFIER	c.*20G>A			0.3491				0.5750	0.3636	0.2727	0.2879	0.2500
	6	85994072	A	G	1099.77	3 prime UTR variant	MODIFIER	c.*22A>G			0.3491				0.5750	0.3636	0.2727	0.2879	0.2500
	6	85994113	T	C	1096.77	downstream gene variant	MODIFIER	c.*14154T>C			0.3255				0.5750	0.3409	0.2727	0.2273	0.2500
	6	85994117	G	A	1136.77	downstream gene variant	MODIFIER	c.*14158G>A			0.3349				0.5750	0.3409	0.2727	0.2576	0.2500
	6	85994176	T	C	948.77	downstream gene variant	MODIFIER	c.*14217T>C			0.0566				0.2000	-	-	-	0.1000
	6	85994216	A	G	929.77	downstream gene variant	MODIFIER	c.*14257A>G			0.2972				0.5750	0.3182	0.2727	0.1515	0.2500
	6	85994218	T	C	121.77	downstream gene variant	MODIFIER	c.*14259T>C			0.0047				0.0250	-	-	-	-
	6	85994228	T	C	354.77	downstream gene variant	MODIFIER	c.*14269T>C			0.0047				-	0.0227	-	-	-
	6	85994271	A	G	237.84	downstream gene variant	MODIFIER	c.*14312A>G			0.0094				-	0.0455	-	-	-
	6	85994538	T	C	196.9	downstream gene variant	MODIFIER	c.*14579T>C			0.0142				-	-	-	0.0455	-
	6	85994582	T	C	775.77	downstream gene variant	MODIFIER	c.*14623T>C			0.3726				0.6000	0.3409	0.3182	0.3485	0.2500
	6	85994603	A	G	384.77	downstream gene variant	MODIFIER	c.*14644A>G			0.0047				0.0250	-	-	-	-
	6	85994777	C	T	576.77	downstream gene variant	MODIFIER	c.*14818C>T			0.0708				0.2250	0.0455	-	-	0.1000
	6	85994889	G	A	744.77	3 prime UTR variant	MODIFIER	c.*48G>A			0.3396				0.5750	0.3182	0.3182	0.2727	0.2500
	6	85994922	T	C	228.84	3 prime UTR variant	MODIFIER	c.*81T>C			0.0142				-	0.0682	-	-	-
	6	85994963	G	A	755.77	3 prime UTR variant	MODIFIER	c.*122G>A			0.0566				0.2500	-	-	-	0.0500
	6	85994992	G	T	100.77	3 prime UTR variant	MODIFIER	c.*151G>T			0.0047				0.0250	-	-	-	-
	6	85995000	T	C	317.77	3 prime UTR variant	MODIFIER	c.*159T>C			0.0047				0.0250	-	-	-	-
	6	85995016	C	T	827.77	3 prime UTR variant	MODIFIER	c.*175C>T			0.4198				0.7000	0.4318	0.0909	0.3636	0.4000
	6	85995040	T	C	341.78	3 prime UTR variant	MODIFIER	c.*199T>C			0.0094				-	-	-	0.0303	-
	6	85995065	C	T	159.77	3 prime UTR variant	MODIFIER	c.*224C>T			0.0047				0.0250	-	-	-	-
	6	85995097	G	T	565.77	3 prime UTR variant	MODIFIER	c.*256G>T			0.1179				0.2500	0.1364	-	0.0606	0.1250
	6	85995112	A	G	136.77	3 prime UTR variant	MODIFIER	c.*271A>G			0.0047				0.0250	-	-	-	-
	6	85995124	T	C	103.77	3 prime UTR variant	MODIFIER	c.*283T>C			0.0047				-	-	-	-	0.0250
	6	85995157	G	A	128.77	3 prime UTR variant	MODIFIER	c.*316G>A			0.0094				-	0.0455	-	-	-
INDEL	6	85979524	TA	T	18.79	upstream gene variant	MODIFIER	c.-13956delA			0.0047				-	-	-	0.0152	-
	6	85979859	CA	C	637.73	upstream gene variant	MODIFIER	c.-13621delA			0.0425				-	-	-	0.0909	0.0750
	6	85979892	TA	T	310.73	upstream gene variant	MODIFIER	c.-13588delA			0.0142				-	-	-	0.0303	0.0250
	6	85980078	C	CAA	1087.73	intron variant	MODIFIER	c.51+69_51+70insAA			0.4198				0.7000	0.3864	0.6818	0.2727	0.2750
	6	85980207	CTT	C	271.73	intron variant	MODIFIER	c.51+199_51+200delTT			0.0047				0.0250	-	-	-	-
	6	85980785	TG	T	468.73	intron variant	MODIFIER	c.51+777delG			0.0425				0.1250	-	-	-	0.1000
	6	85980931	T	TC	931.73	intron variant	MODIFIER	c.52-764_52-763insC			0.4292				0.7000	0.4091	0.6818	0.3030	0.2500
	6	85981527	A	AT	117.87	intron variant	MODIFIER	c.52-168_52-167insT			0.0094				-	0.0455	-	-	-
	6	85981679	AT	ATT,A,ATT	59.73	intron variant	MODIFIER	c.52-15delT			0.0377				0.0250	0.1591	-	-	-
	6	85982000	A	AT	803.73	intron variant	MODIFIER	c.84+273_84+274insT			0.4717				0.7000	0.3636	0.7727	0.3939	0.3250
	6	85982011	TA	T	165.73	intron variant	MODIFIER	c.84+285delA			0.0047				0.0250	-	-	-	-
	6	85982013	TTC	T	165.73	intron variant	MODIFIER	c.84+287_84+288delTC			0.0047				0.0250	-	-	-	-
	6	85982039	C	CA	782.73	intron variant	MODIFIER	c.84+312_84+313insA			0.7075				0.8000	0.9545	0.8636	0.5758	0.4750
	6	85982445	ATT	A	409.73	intron variant	MODIFIER	c.85-162_85-161delTT			0.0047				-	0.0227	-	-	-
	6	85983623	AC	A	260.73	intron variant	MODIFIER	c.171+61delC			0.0283				-	0.1364	-	-	-
	6	85983759	G	GA	485.73	intron variant	MODIFIER	c.171+196_171+197insA			0.4481				0.7000	0.3864	0.6818	0.3636	0.2750
	6	85984180	ATTCT	A	82.73	splice region variant	LOW	c.195+7_195+10delTTCT			0.0047				-	-	-	0.0152	-
	6	85984273	T	TG	1013.73	intron variant	MODIFIER	c.195+99_195+100insG			0.4387				0.7000	0.3864	0.7273	0.3182	0.2750
	6	85985882	GA	G	211.75	intron variant	MODIFIER	c.220-521delA			0.0189				-	0.0909	-	-	-
	6	85986289	TTCTTCTA	A	311.73	intron variant	MODIFIER	c.220-114_220-76delTTAAGTGTGGGTTGTTTCCTTCTAATGAAACAATGGAAT			0.0047				0.0250	-	-	-	-
	6	85986425	TC	T	1048.73	frameshift variant	HIGH	c.242delC			0.0660				0.1500	-	0.3636	-	-
	6	85986505	A	AGTTTAC	1222.73	intron variant	MODIFIER	c.252+69_252+70insGTTTCCGTAAT			0.4292				0.7000	0.4318	0.6818	0.2727	0.2750
	6	85986675	AT	A	109.73	intron variant	MODIFIER	c.252+240delT			0.0047				0.0250	-	-	-	-
	6	85986833	T	TA	248.73	intron variant	MODIFIER	c.253-343_253-342insA			0.0047				0.0250	-	-	-	-
	6	85987157	GTT	GTTT,G,GT	249.73	intron variant	MODIFIER	c.253-18_253-17delTT			0.1651				0.1000	0.2273	0.1364	0.0303	0.4000
	6	85987159	T	TTG	372.73	intron variant	MODIFIER	c.253-17_253-16insTG			0.0094				-	0.0455	-	-	-
	6	85987160	T	TG,TA	287.73	intron variant	MODIFIER	c.253-16_253-15insA			0.0236				0.0500	-	-	0.0455	-
	6	85987166	T	AA,TA,TTA	940.73	intron variant	MODIFIER	c.253-10_253-9insTAA			0.4057				0.7000	0.4318	0.6818	0.1970	0.2750
	6	85987354	AT	A	66.73	intron variant	MODIFIER	c.330+12delT			0.0047				0.0250	-	-	-	-
	6	85987396	G	GATA	418.73	intron variant	MODIFIER	c.330+53_330+54insATA			0.0047				-	0.0227	-	-	-
	6	85987410	TA	T	319.74	intron variant	MODIFIER	c.330+68delA			0.0094				-	0.0455	-	-	-
	6	85987444	T	TAAAAC,T/	1267.73	intron variant	MODIFIER	c.330+101_330+102insA			0.3349				0.5500	0.2955	0.2727	0.2879	0.2750
	6	85987448	C	CAAAG	320.73	intron variant	MODIFIER	c.330+105_330+106insAAAG			0.0047				0.0250	-	-	-	-
	6	85987824	TC	T	84.25	intron variant	MODIFIER	c.330+482delC			0.0094				-	-	-	0.0303	-
	6	85988124	ATG	A	355.73	intron variant	MODIFIER	c.331-567_331-566delTG			0.0047				0.0250	-	-	-	-
	6	85988131	C	CAT	355.73	intron variant	MODIFIER	c.331-561_331-560insAT			0.0047				0.0250	-	-	-	-
	6	85988198	CTGTGCCA	A	238.73	intron variant	MODIFIER	c.331-493_331-466delCCAGGACTCCCTGTCCATGACCAGCATG			0.0094				-	-	-	0.0152	0.0250
	6	85988319	TCTC	T	1032.73	intron variant	MODIFIER	c.331-372_331-370delCTC			0.3302				0.6000	0.3409	0.3182	0.1970	0.2750
	6	85988504	TA	T	484.73	intron variant	MODIFIER	c.331-187delA			0.0236				0.0250	-	0.0909	-	0.0500
	6	85988539	TC	T	309.73	intron variant	MODIFIER	c.331-152delC			0.0047				-	0.0227	-	-	-
	6	85988545	T	TAAAG	952.73	intron variant	MODIFIER	c.331-147_331-146insAAAG			0.3302				0.6000	0.3182	0.3182	0.2121	0.2750
	6	85988600	GATT	G	112.73	intron variant	MODIFIER	c.331-91_331-89delATT			0.0047				0.0250	-	-	-	-
	6	85988963	A	AG	1110.73	intron variant	MODIFIER	c.372+230_372+231insG			0.3491				0.6000	0.3636	0.3182	0.2576	0.2500
	6	85989187	CA	C	962.73	intron variant	MODIFIER	c.373-189delA			0.3491				0.5250	0.3182	0.3182	0.3485	0.2250
	6	85989267	GT	G	652.73	intron variant	MODIFIER	c.373-109delT			0.3585				0.5750	0.3409	0.3182	0.3030	0.2750
	6	85989314	AT	A	644.73	intron variant	MODIFIER	c.373-62delT			0.3632				0.5750	0.3636	0.3182	0.3030	0.2750
	6	85989360	G	GT	213.73	intron variant	MODIFIER	c.373-17_373-16insT			0.0047				0.0250	-	-	-	-

6	85989785	T	TAGA	700.73	intron variant	MODIFIER	c.396+385_396+386insAGA			0.3160				0.5750	0.2955	0.2273	0.2273	0.2750
6	85989835	CTAAGAA	T	34.73	intron variant	MODIFIER	c.396+436_396+449delAATCTAAGAAATTA			0.0047				-	-	-	0.0152	-
6	85989853	GAA	G	28.74	intron variant	MODIFIER	c.396+454_396+455delAA			0.0047				-	-	-	0.0152	-
6	85989859	TA	T	31.73	intron variant	MODIFIER	c.396+460delA			0.0047				-	-	-	0.0152	-
6	85989861	TA	T	31.73	intron variant	MODIFIER	c.396+462delA			0.0047				-	-	-	0.0152	-
6	85989867	CTTAATTA	A	22.75	intron variant	MODIFIER	c.396+468_396+485delGCACCTTAATTATGATAT			0.0047				-	-	-	0.0152	-
6	85989891	GGCCA	G	25.74	intron variant	MODIFIER	c.396+492_396+495delGCCA			0.0047				-	-	-	0.0152	-
6	85989898	CTCCACA	A	22.75	intron variant	MODIFIER	c.396+499_396+508delCCTCCACAAG			0.0047				-	-	-	0.0152	-
6	85989910	TTAGAAC	G	31.73	intron variant	MODIFIER	c.396+511_396+518delTTAGAACT			0.0047				-	-	-	0.0152	-
6	85989921	GTCTCTGC	A	22.75	intron variant	MODIFIER	c.396+522_396+533delTGGTCCTGCTAT			0.0047				-	-	-	0.0152	-
6	85989931	T	AGTGTTCA	846.73	intron variant	MODIFIER	c.396+531_396+532insC			0.3585				0.6000	0.3864	0.3182	0.2576	0.2750
6	85989936	TG	T	31.73	intron variant	MODIFIER	c.396+537delG			0.0047				-	-	-	0.0152	-
6	85989942	TCATTCC	T	34.73	intron variant	MODIFIER	c.396+543_396+548delCATTCC			0.0047				-	-	-	0.0152	-
6	85990259	A	AAT	1262.73	intron variant	MODIFIER	c.397-336_397-335insAT			0.3066				0.6000	0.2955	0.3182	0.1515	0.2750
6	85990894	AATTTCCA	G	693.73	intron variant	MODIFIER	c.438+259_438+276delTGTC AATTTCCATGGTTA			0.3396				0.6000	0.2727	0.2727	0.2879	0.2750
6	85991028	ATTATGC	A	811.73	intron variant	MODIFIER	c.438+393_438+398delTTATGC			0.3113				0.5750	0.2955	0.2273	0.2121	0.2750
6	85991172	T	TCTA,TTTA	1144.73	intron variant	MODIFIER	c.439-364_439-363insTTATATA			0.3538				0.7000	0.2955	0.2727	0.1818	0.4000
6	85991523	AGAAACAC	T	196.73	frameshift variant	HIGH	c.439-12_454delTTTTCTTTCCAGAAACAGCCTATGATAG			0.0047				-	-	-	-	0.0250
6	85992039	GT	G	657.73	intron variant	MODIFIER	c.466-468delT			0.3349				0.5750	0.3409	0.2727	0.2727	0.2250
6	85992178	GGGATTAA	G	190.73	intron variant	MODIFIER	c.466-329_466-301delAATCTGATAAGGGATTAAACAAGATTCAA			0.0094				0.0250	0.0227	-	-	-
6	85992237	TA	T	711.73	intron variant	MODIFIER	c.466-270delA			0.1792				0.3250	0.1136	0.2727	0.1212	0.1500
6	85992387	T	TA	63.73	intron variant	MODIFIER	c.466-121_466-120insA			0.0047				-	-	-	0.0152	-
6	85992469	AATCACAA	T	31.73	intron variant	MODIFIER	c.466-38_466-28delGAATCACAAAA			0.0047				-	-	-	0.0152	-
6	85993507	T	CCTTATCA	1312.73	downstream gene variant	MODIFIER	c.*13548_*13549insTGCTGCCTTATCAAAGG			0.9151				1.0000	0.9545	1.0000	0.7576	1.0000
6	85993870	A	ATTT,ATT	691.73	downstream gene variant	MODIFIER	c.*13911_*13912insT			0.2547				0.5500	0.1591	0.2727	0.1364	0.2500
6	85993882	TCG	T	53.7	downstream gene variant	MODIFIER	c.*13924_*13925delCG			0.0094				-	-	-	0.0303	-
6	85993897	TAATGATG	A	28.74	downstream gene variant	MODIFIER	c.*13939_*13954delATATAATGATGTTTGT			0.0047				-	-	-	0.0152	-
6	85993943	A	ATAATATA	405.73	downstream gene variant	MODIFIER	c.*13984_*13985insTAATATAT			0.0142				-	0.0455	-	-	0.0250
6	85994041	T	TTGGCAAT	142.73	splice region variant	LOW	c.645-9_645-8insAAATTTGGCAATAACAA			0.0047				-	-	-	-	0.0250
6	85994127	TC	T	1028.73	downstream gene variant	MODIFIER	c.*14169delC			0.0613				0.2000	0.0227	-	-	0.1000
6	85994531	TTG	TGTG,TTG	587.73	downstream gene variant	MODIFIER	c.*14573_*14574delTG			0.4481				0.7500	0.4773	0.4091	0.3182	0.3500
6	85994551	GTA	G	51.73	downstream gene variant	MODIFIER	c.*14593_*14594delTA			0.0047				-	-	-	0.0152	-
6	85995007	TGAG	T	53.7	3 prime UTR variant	MODIFIER	c.*167_*169delGAG			0.0094				-	-	-	0.0909	-
6	85995012	TCCACTGT	T	43.73	3 prime UTR variant	MODIFIER	c.*172_*181delCTCCACTGTA			0.0047				-	-	0.0455	-	-

	Supplementary Table S2. Polymorphisms (SNPs in black, INDEL in red) detected in the goat casein genes (CSN2)																		
	Chromosome	Position	Ref allele	Alt_allele	QUAL	Variant_type	Effect	Nucleotide substitution	AA substitution	subst. literature	Alt_freq	SIFT_score	SIFT_median	SIFT_prediction	AF	BE	EU	FE	NE
	6	86006349	T	A	230.77	3_prime_UTR_variant	MODIFIER	c.*219A>T			0.0142				-	0.0682	-	-	-
	6	86006351	T	C	427.77	3_prime_UTR_variant	MODIFIER	c.*217A>G			0.0047				-	-	-	-	0.0250
	6	86006385	T	C	96.28	3_prime_UTR_variant	MODIFIER	c.*183A>G			0.0142				-	-	-	0.0455	-
	6	86006394	G	A	813.77	3_prime_UTR_variant	MODIFIER	c.*174C>T			0.0802				0.1000	0.1136	0.3636	-	-
	6	86006395	T	C	487.77	3_prime_UTR_variant	MODIFIER	c.*173A>G			0.0142				0.0250	0.0455	-	-	-
	6	86006437	C	T	148.77	3_prime_UTR_variant	MODIFIER	c.*131G>A			0.0094				-	0.0455	-	-	-
	6	86006505	A	G	124.81	3_prime_UTR_variant	MODIFIER	c.*63T>C			0.0094				-	-	-	0.0303	-
	6	86006583	A	T	25.78	intron_variant	MODIFIER	c.769-10T>A			0.0047				-	-	-	0.0152	-
	6	86006585	A	T	25.78	intron_variant	MODIFIER	c.769-12T>A			0.0047				-	-	-	0.0152	-
	6	86006621	T	C	68.77	intron_variant	MODIFIER	c.769-48A>G			0.0047				-	-	-	-	0.0250
	6	86006689	G	T	274.77	intron_variant	MODIFIER	c.769-116C>A			0.0283				-	0.1364	-	-	-
	6	86006776	C	T	797.77	intron_variant	MODIFIER	c.769-203G>A			0.0896				0.1000	0.1364	0.3636	0.0152	-
	6	86006785	A	T	132.77	intron_variant	MODIFIER	c.769-212T>A			0.0047				0.0250	-	-	-	-
	6	86006797	T	A	1093.77	intron_variant	MODIFIER	c.769-224A>T			0.3208				0.5750	0.3182	0.3182	0.2121	0.2500
	6	86006815	A	T	236.77	intron_variant	MODIFIER	c.769-242T>A			0.0236				0.0250	0.0909	-	-	-
	6	86006864	A	G	196.77	intron_variant	MODIFIER	c.769-291T>C			0.0047				0.0250	-	-	-	-
	6	86006920	G	A	926.77	intron_variant	MODIFIER	c.769-347C>T			0.0519				0.1750	-	-	-	0.1000
	6	86007057	T	C	308.78	intron_variant	MODIFIER	c.769-484A>G			0.0142				-	0.0682	-	-	-
	6	86007097	A	G	456.77	intron_variant	MODIFIER	c.769-524T>C			0.0047				0.0250	-	-	-	-
	6	86007190	C	T	1112.77	intron_variant	MODIFIER	c.769-617G>A			0.3066				0.5750	0.2955	0.3182	0.1818	0.2500
	6	86007476	G	T	982.77	intron_variant	MODIFIER	c.768+452C>A			0.3208				0.5750	0.2955	0.3182	0.2273	0.2500
	6	86007506	T	A	603.28	intron_variant	MODIFIER	c.768+422A>T			0.1509				0.2000	0.1591	-	0.1515	0.1750
	6	86007568	C	T	346.77	intron_variant	MODIFIER	c.768+360G>A			0.0189				-	0.0909	-	-	-
	6	86007572	G	A	825.77	intron_variant	MODIFIER	c.768+356C>T			0.3208				0.5750	0.3182	0.2727	0.2273	0.2500
	6	86007588	C	A	563.77	intron_variant	MODIFIER	c.768+340G>T			0.0613				0.1250	-	0.3182	0.0152	-
	6	86007660	A	G	278.77	intron_variant	MODIFIER	c.768+268T>C			0.0377				-	0.1818	-	-	-
	6	86007724	T	G	219.77	intron_variant	MODIFIER	c.768+204A>C			0.0283				-	0.1364	-	-	-
	6	86007760	G	A	52.77	intron_variant	MODIFIER	c.768+168C>T			0.0047				-	-	0.0455	-	-
	6	86007851	T	G	169.78	intron_variant	MODIFIER	c.768+77A>C			0.0094				-	-	-	0.0303	-
	6	86007882	A	G	519.77	intron_variant	MODIFIER	c.768+46T>C			0.1745				0.2250	0.2500	-	0.1515	0.1750
	6	86008016	A	G	866.77	missense_variant	MODERATE	c.680T>C	p.Val227Ala	p.Val177Ala	0.3160	0.12	3.08	TOLERATED	0.5750	0.2727	0.2727	0.2424	0.2500
	6	86008103	G	A	105.77	missense_variant	MODERATE	c.593C>T	p.Pro198Leu		0.0094	0.12	3.08	TOLERATED	-	-	-	0.0303	-
	6	86008279	C	T	78.77	synonymous_variant	LOW	c.417G>A	p.Gln139Gln		0.0094				-	-	-	0.0303	-
	6	86008407	C	A	125.77	missense_variant	MODERATE	c.289G>T	p.Asp97Tyr		0.0047	0	3	DELETERIOUS	0.0250	-	-	-	-
	6	86008441	C	A	536.77	intron_variant	MODIFIER	c.277-22G>T			0.0472				0.0250	-	-	0.1364	-
	6	86008491	C	T	102.77	intron_variant	MODIFIER	c.277-72G>A			0.0047				-	-	0.0455	-	-
	6	86008578	C	T	779.77	intron_variant	MODIFIER	c.277-159G>A			0.1226				0.3250	-	0.3182	0.0455	0.0750
	6	86008583	G	C	309.78	intron_variant	MODIFIER	c.277-164C>G			0.0094				0.0500	-	-	-	-
	6	86008812	G	A	832.77	intron_variant	MODIFIER	c.277-393C>T			0.3396				0.5750	0.3182	0.3182	0.2727	0.2500
	6	86008813	T	C	166.77	intron_variant	MODIFIER	c.277-394A>G			0.0283				-	0.1364	-	-	-
	6	86008828	A	G	657.77	intron_variant	MODIFIER	c.277-409T>C			0.1604				0.1750	0.1818	-	0.1818	0.1750
	6	86008971	T	C	439.77	intron_variant	MODIFIER	c.277-552A>G			0.0189				0.0250	-	-	0.0152	0.0500
	6	86008987	C	A	171.77	intron_variant	MODIFIER	c.277-568G>T			0.0094				-	0.0455	-	-	-
	6	86008988	A	G	763.77	intron_variant	MODIFIER	c.277-569T>C			0.1321				0.3500	-	0.3182	0.0606	0.0750
	6	86009018	T	G	971.77	intron_variant	MODIFIER	c.277-599A>C			0.0330				0.0500	0.0227	-	0.0152	0.0750
	6	86009029	A	T	150.77	intron_variant	MODIFIER	c.277-610T>A			0.0047				-	-	-	0.0152	-
	6	86009039	A	C	381.77	intron_variant	MODIFIER	c.277-620T>G			0.0189				0.0500	-	-	0.0152	0.0250
	6	86009064	T	C	201.77	intron_variant	MODIFIER	c.277-645A>G			0.0094				-	-	-	0.0303	-
	6	86009084	C	A	18.83	intron_variant	MODIFIER	c.276+665G>T			0.0047				-	-	-	0.0152	-
	6	86009107	G	A	153.77	intron_variant	MODIFIER	c.276+642C>T			0.0094				-	-	-	0.0303	-
	6	86009297	G	A	294.78	intron_variant	MODIFIER	c.276+452C>T			0.0142				0.0250	0.0455	-	-	-
	6	86009349	C	T	346.78	intron_variant	MODIFIER	c.276+400G>A			0.0142				-	0.0682	-	-	-
	6	86009350	A	G	710.77	intron_variant	MODIFIER	c.276+399T>C			0.3349				0.5750	0.3182	0.3182	0.2576	0.2500
	6	86009395	G	A	714.77	intron_variant	MODIFIER	c.276+354C>T			0.0142				-	0.0682	-	-	-
	6	86009425	C	T	456.77	intron_variant	MODIFIER	c.276+324G>A			0.0849				0.1000	0.0909	0.3636	0.0303	-
	6	86009478	C	T	166.77	intron_variant	MODIFIER	c.276+271G>A			0.0094				-	-	-	0.0303	-
	6	86009501	A	G	1009.77	intron_variant	MODIFIER	c.276+248T>C			0.3113				0.5750	0.2727	0.2727	0.2273	0.2500
	6	86009623	C	A	264.8	intron_variant	MODIFIER	c.276+126G>T			0.0330				-	-	-	0.1061	-
	6	86009649	T	C	1093.77	intron_variant	MODIFIER	c.276+100A>G			0.3396				0.5750	0.3182	0.3182	0.2727	0.2500
	6	86009752	T	C	248.77	synonymous_variant	LOW	c.273A>G	p.Thr91Thr		0.0283				-	0.1364	-	-	-
	6	86009770	A	G	52.77	synonymous_variant	LOW	c.255T>C	p.Ser85Ser		0.0047				-	0.0227	-	-	-
	6	86009827	C	T	658.77	intron_variant	MODIFIER	c.235-37G>A			0.1509				0.2000	0.1818	-	0.1364	0.1750
	6	86009847	C	T	1096.77	intron_variant	MODIFIER	c.234+41G>A			0.2925				0.5750	0.2727	0.3182	0.1515	0.2500
	6	86009848	A	G	1096.77	intron_variant	MODIFIER	c.234+40T>C			0.2925				0.5750	0.2727	0.3182	0.1515	0.2500
	6	86009856	T	A	121.77	intron_variant	MODIFIER	c.234+32A>T			0.0047				-	-	-	-	0.0250
	6	86009867	A	G	951.77	intron_variant	MODIFIER	c.234+21T>C			0.3019				0.5750	0.2727	0.3182	0.1818	0.2500
	6	86009990	C	T	301.77	intron_variant	MODIFIER	c.211-79G>A			0.0094				-	-	-	0.0303	-
	6	86010024	G	A	199.77	intron_variant	MODIFIER	c.211-113C>T			0.0047				-	-	-	0.0152	-
	6	86010087	A	T	247.77	intron_variant	MODIFIER	c.211-176T>A			0.0047				0.0250	-	-	-	-
	6	86010104	C	T	80.77	intron_variant	MODIFIER	c.211-193G>A			0.0047				0.0250	-	-	-	-
	6	86010119	G	T	875.77	intron_variant	MODIFIER	c.211-208C>A			0.3113				0.5750	0.2045	0.2727	0.2727	0.2500
	6	86010127	A	G	301.84	intron_variant	MODIFIER	c.211-216T>C			0.0236				-	-	-	0.0606	0.0250
	6	86010178	G	A	971.77	intron_variant	MODIFIER	c.211-267C>T			0.1462				0.3750	0.1136	0.1818	0.0606	0.0750
	6	86010193	C	T	525.77	intron_variant	MODIFIER	c.211-282G>A			0.0142				-	0.0682	-	-	-
	6	86010264	C	T	227.77	intron_variant	MODIFIER	c.211-353G>A			0.0047				0.0250	-	-	-	-
	6	86010306	G	A	66.77	intron_variant	MODIFIER	c.211-395C>T			0.0047				-	-	-	0.0152	-

SNP	6	86010313	A	T	325.77	intron_variant	MODIFIER	c.211-402T>A					0.0189				-	0.0909	-	-	-
	6	86010365	C	T	778.77	intron_variant	MODIFIER	c.211-454G>A					0.0142				-	0.0682	-	-	-
	6	86010493	C	T	1082.77	intron_variant	MODIFIER	c.211-582G>A					0.3208				0.5750	0.3182	0.2727	0.2424	0.2250
	6	86010521	T	C	1231.77	intron_variant	MODIFIER	c.211-610A>G					0.3113				0.5750	0.3182	0.2727	0.1970	0.2500
	6	86010529	A	G	221.77	intron_variant	MODIFIER	c.211-618T>C					0.0047				0.0250	-	-	-	-
	6	86010553	A	G	72.77	intron_variant	MODIFIER	c.211-642T>C					0.0094				-	-	-	0.0303	-
	6	86010583	C	G	334.78	intron_variant	MODIFIER	c.211-672G>C					0.0377				-	-	-	0.0758	0.0750
	6	86010628	C	G	302.77	intron_variant	MODIFIER	c.211-717G>C					0.0047				0.0250	-	-	-	-
	6	86010629	G	A	410.77	intron_variant	MODIFIER	c.211-718C>T					0.0377				0.1500	-	-	-	0.0500
	6	86010665	C	T	382.77	intron_variant	MODIFIER	c.211-754G>A					0.0189				0.0250	-	0.1364	-	-
	6	86010669	C	T	126.77	intron_variant	MODIFIER	c.211-758G>A					0.0094				-	0.0455	-	-	-
	6	86010683	A	C	220.84	intron_variant	MODIFIER	c.211-772T>G					0.0472				0.1500	-	0.0455	-	0.0750
	6	86010699	G	A	25.78	intron_variant	MODIFIER	c.211-788C>T					0.0047				-	0.0227	-	-	-
	6	86010705	G	C	690.77	intron_variant	MODIFIER	c.211-794C>G					0.0283				-	0.0682	-	0.0303	0.0250
	6	86010731	T	C	280.77	intron_variant	MODIFIER	c.211-820A>G					0.0991				0.1500	0.1136	-	0.0758	0.1250
	6	86010735	G	A	270.77	intron_variant	MODIFIER	c.211-824C>T					0.0094				-	-	-	0.0303	-
	6	86010811	A	T	337.77	intron_variant	MODIFIER	c.211-900T>A					0.0094				-	-	-	-	0.0500
	6	86010832	T	G	69.77	intron_variant	MODIFIER	c.211-921A>C					0.0047				0.0250	-	-	-	-
	6	86010838	C	G	116.77	intron_variant	MODIFIER	c.211-927G>C					0.0094				-	-	-	0.0303	-
	6	86010846	C	T	96.77	intron_variant	MODIFIER	c.211-935G>A					0.0189				0.0250	0.0682	-	-	-
	6	86010893	C	T	324.78	intron_variant	MODIFIER	c.211-982G>A					0.0425				0.1500	-	-	-	0.0750
	6	86010894	G	A	123.78	intron_variant	MODIFIER	c.211-983C>T					0.0142				-	0.0682	-	-	-
	6	86010904	T	C	286.8	intron_variant	MODIFIER	c.211-993A>G					0.0896				0.1500	0.0682	-	0.0606	0.1500
	6	86010920	C	A	113.77	intron_variant	MODIFIER	c.211-1009G>T					0.0094				-	-	-	0.0303	-
	6	86010978	T	C	276.8	intron_variant	MODIFIER	c.211-1067A>G					0.0330				0.1750	-	-	-	-
	6	86010979	C	T	321.78	intron_variant	MODIFIER	c.211-1068G>A					0.0943				0.2750	0.0909	0.1364	0.0303	-
	6	86010981	T	G	286.8	intron_variant	MODIFIER	c.211-1070A>C					0.0943				0.2750	0.0909	0.1364	0.0303	-
	6	86010983	A	G	241.84	intron_variant	MODIFIER	c.211-1072T>C					0.0943				0.2750	0.0909	0.1364	0.0303	-
	6	86011097	T	A	736.77	intron_variant	MODIFIER	c.210+1162A>T					0.1226				0.3500	-	0.3182	0.0303	0.0750
	6	86011103	C	G	845.77	intron_variant	MODIFIER	c.210+1156G>C					0.2925				0.5750	0.2727	0.3182	0.1667	0.2250
	6	86011216	G	A	630.77	intron_variant	MODIFIER	c.210+1043C>T					0.0755				-	0.1591	-	0.0909	0.0750
	6	86011247	C	T	685.77	intron_variant	MODIFIER	c.210+1012G>A					0.1321				0.1750	0.2500	-	0.0606	0.1500
	6	86011291	G	A	796.77	intron_variant	MODIFIER	c.210+968C>T					0.8113				0.9500	0.8409	0.8182	0.5909	1.0000
	6	86011335	T	G	412.77	intron_variant	MODIFIER	c.210+924A>C					0.1934				0.4500	0.1591	0.2273	0.0909	0.1250
	6	86011358	A	G	419.77	intron_variant	MODIFIER	c.210+901T>C					0.2217				0.5250	0.1818	0.2273	0.0606	0.2250
	6	86011385	G	A	556.77	intron_variant	MODIFIER	c.210+874C>T					0.2642				0.5250	0.3182	0.1818	0.1061	0.2500
	6	86011390	T	C	598.77	intron_variant	MODIFIER	c.210+869A>G					0.2594				0.5250	0.3182	0.1818	0.0909	0.2500
	6	86011405	T	C	677.77	intron_variant	MODIFIER	c.210+854A>G					0.2642				0.5500	0.3182	0.1818	0.0909	0.2500
	6	86011501	A	G	46.77	intron_variant	MODIFIER	c.210+758T>C					0.0047				-	0.0227	-	-	-
	6	86011518	A	G,T	1159.77	intron_variant	MODIFIER	c.210+741T>C					0.3066				0.5750	0.2727	0.3182	0.2121	0.2250
	6	86011549	A	C	840.77	intron_variant	MODIFIER	c.210+710T>G					0.3302				0.5750	0.2955	0.3182	0.2576	0.2500
	6	86011552	A	G	826.77	intron_variant	MODIFIER	c.210+707T>C					0.3302				0.5750	0.2955	0.3182	0.2576	0.2500
	6	86011575	C	T	234.77	intron_variant	MODIFIER	c.210+684G>A					0.0094				-	0.0455	-	-	-
	6	86011642	T	G	52.77	intron_variant	MODIFIER	c.210+617A>C					0.0047				-	-	-	0.0152	-
	6	86011654	T	C	1026.77	intron_variant	MODIFIER	c.210+605A>G					0.0377				0.0500	0.0455	-	0.0152	0.0750
	6	86011668	T	C	11.12	intron_variant	MODIFIER	c.210+591A>G					0.0047				-	-	-	0.0152	-
	6	86011744	A	G	285.77	intron_variant	MODIFIER	c.210+515T>C					0.0047				-	-	-	-	0.0250
	6	86011787	A	G	655.77	intron_variant	MODIFIER	c.210+472T>C					0.0142				-	0.0682	-	-	-
	6	86011815	T	C	925.77	intron_variant	MODIFIER	c.210+444A>G					0.3160				0.5750				

	6	86013325	A	T	75.77	intron_variant	MODIFIER	c.94-105T>A			0.0094				-	0.0455	-	-	-
	6	86013334	A	G	442.77	intron_variant	MODIFIER	c.94-114T>C			0.0519				0.1750	-	-	-	0.1000
	6	86013355	G	A	295.77	intron_variant	MODIFIER	c.94-135C>T			0.0425				-	0.2045	-	-	-
	6	86013356	T	C	605.77	intron_variant	MODIFIER	c.94-136A>G			0.1226				0.1500	0.0909	0.3182	0.0758	0.1000
	6	86013357	G	A	169.77	intron_variant	MODIFIER	c.94-137C>T			0.0094				-	-	-	0.0303	-
	6	86013427	C	T	515.77	intron_variant	MODIFIER	c.94-207G>A			0.1226				0.1500	0.1136	0.3636	0.0455	0.1000
	6	86013443	G	A	591.77	intron_variant	MODIFIER	c.94-223C>T			0.1132				0.1500	0.1136	0.3636	0.0152	0.1000
	6	86013515	A	G	593.77	intron_variant	MODIFIER	c.94-295T>C			0.0519				0.1750	-	-	-	0.1000
	6	86013561	T	C	673.77	intron_variant	MODIFIER	c.94-341A>G			0.1226				0.1500	0.1136	0.4091	0.0303	0.1000
	6	86013570	T	G	135.77	intron_variant	MODIFIER	c.94-350A>C			0.0047				-	0.0227	-	-	-
	6	86013702	G	A	240.77	intron_variant	MODIFIER	c.94-482C>T			0.0047				0.0250	-	-	-	-
	6	86013703	C	T	414.77	intron_variant	MODIFIER	c.94-483G>A			0.0283				0.0250	-	-	0.0758	-
	6	86013727	G	A	633.77	intron_variant	MODIFIER	c.94-507C>T			0.1038				0.1500	0.0909	0.3182	0.0152	0.1000
	6	86013784	G	A	399.77	intron_variant	MODIFIER	c.94-564C>T			0.0472				-	-	-	0.1061	0.0750
	6	86013800	T	C	175.77	intron_variant	MODIFIER	c.94-580A>G			0.0047				-	-	-	0.0152	-
	6	86013811	A	T	18.59	intron_variant	MODIFIER	c.94-591T>A			0.0094				-	-	-	0.0303	-
	6	86013835	A	G	1129.77	intron_variant	MODIFIER	c.94-615T>C			0.8632				0.9250	0.9545	0.9545	0.6667	0.9750
	6	86014076	A	T,C	728.77	intron_variant	MODIFIER	c.94-856T>G			0.0613				0.0250	0.0909	0.0455	0.0758	0.0500
	6	86014126	C	T	129.77	intron_variant	MODIFIER	c.94-906G>A			0.0094				-	-	-	0.0303	-
	6	86014202	T	C	400.77	intron_variant	MODIFIER	c.94-982A>G			0.0755				0.0500	0.2500	-	0.0455	-
	6	86014228	A	C	119.77	intron_variant	MODIFIER	c.93+988T>G			0.0094				-	-	-	0.0303	-
	6	86014300	T	G	330.77	intron_variant	MODIFIER	c.93+916A>C			0.0566				-	0.2727	-	-	-
	6	86014301	T	G	994.77	intron_variant	MODIFIER	c.93+915A>C			0.5708				0.5500	0.4545	0.5455	0.5455	0.7750
	6	86014358	C	T	150.03	intron_variant	MODIFIER	c.93+858G>A			0.0142				-	-	-	0.0455	-
	6	86014420	T	G	375.77	intron_variant	MODIFIER	c.93+796A>C			0.0047				0.0250	-	-	-	-
	6	86014441	A	T	726.77	intron_variant	MODIFIER	c.93+775T>A			0.1179				0.1500	0.0909	0.4091	0.0303	0.1000
	6	86014611	C	G	247.77	intron_variant	MODIFIER	c.93+605G>C			0.0047				-	-	0.0455	-	-
	6	86014682	T	C	167.77	intron_variant	MODIFIER	c.93+534A>G			0.0094				-	-	-	0.0303	-
	6	86014735	A	G	530.77	intron_variant	MODIFIER	c.93+481T>C			0.0519				0.1750	-	-	-	0.1000
	6	86014797	A	C	87.77	intron_variant	MODIFIER	c.93+419T>G			0.0094				-	-	-	0.0303	-
	6	86014810	C	A	146.77	intron_variant	MODIFIER	c.93+406G>T			0.0047				-	-	-	-	0.0250
	6	86014864	A	C	346.77	intron_variant	MODIFIER	c.93+352T>G			0.0189				0.0250	-	-	0.0152	0.0500
	6	86014866	G	T	637.77	intron_variant	MODIFIER	c.93+350C>A			0.1604				0.2500	0.2727	-	0.1212	0.1000
	6	86014979	A	G	349.77	intron_variant	MODIFIER	c.93+237T>C			0.0047				0.0250	-	-	-	-
	6	86015172	A	T	416.77	intron_variant	MODIFIER	c.93+44T>A			0.0472				-	-	-	0.1061	0.0750
	6	86015175	A	G	244.77	intron_variant	MODIFIER	c.93+41T>C			0.0142				-	-	-	0.0303	0.0250
	6	86015185	G	A	441.77	intron_variant	MODIFIER	c.93+31C>T			0.0425				-	0.2045	-	-	-
	6	86015270	C	T	334.77	synonymous_variant	LOW	c.39G>A	p.Gln13Gln		0.0094				-	-	-	0.0303	-
	6	86015278	G	C	335.77	missense_variant	MODERATE	c.31C>G	p.Leu11Val		0.0094	0	4.32	DELETERIOUS	-	-	-	0.0303	-
INDEL	6	86007152	C	CAG	286.73	intron_variant	MODIFIER	c.769-580_769-579insCT			0.0047				-	-	-	-	0.0250
	6	86007352	T	TA	633.73	intron_variant	MODIFIER	c.768+575_768+576insT			0.2830				0.5500	0.2955	0.3182	0.1364	0.2250
	6	86007847	A	AT	895.73	intron_variant	MODIFIER	c.768+80_768+81insA			0.2736				0.5750	0.2727	0.2727	0.1212	0.2250
	6	86007903	GCA	G	244.73	intron_variant	MODIFIER	c.768+23_768+24delTG			0.0047				-	-	-	0.0152	-
	6	86009237	A	AG	931.73	intron_variant	MODIFIER	c.276+511_276+512insC			0.3396				0.6250	0.2727	0.3636	0.2273	0.3000
	6	86009273	TGTGTGCCA	T	73.73	intron_variant	MODIFIER	c.276+468_276+475delTGGCACAC			0.0047				-	-	-	0.0152	-
	6	86009795	TAAAA	TA,TAAA,TAAAAA,TAA,TAAAA	735.73	splice_region_variant	LOW	c.235-9_235-6delITTTT			0.3962				0.6250	0.3409	0.6364	0.2273	0.3750
	6	86009980	G	GA	567.73	intron_variant	MODIFIER	c.211-70_211-69insT			0.3255				0.5750	0.2955	0.2727	0.2727	0.2250
	6	86010083	TA	T,TAA	442.73	intron_variant	MODIFIER	c.211-173delT			0.3066				0.5750	0.2273	0.3182	0.2576	0.2000
	6	86011232	G	GGC	885.73	intron_variant	MODIFIER	c.210+1026_210+1027insGC			0.1368				0.1500	0.2727	-	0.0909	0.1250
	6	86011410	TAGC	T	352.74	intron_variant	MODIFIER	c.210+846_210+848delGCT			0.0472				-	0.2273	-	-	-
	6	86011593	TAATAAAATATGTCCAT	A	34.73	intron_variant	MODIFIER	c.210+623_210+665delGGGCAGACATGCAATGGACATATTTTATTATTATACCAGCAA			0.0047				-	-	-	0.0152	-
	6	86011639	ACT	A	40.73	intron_variant	MODIFIER	c.210+618_210+619delAG			0.0047				-	-	-	0.0152	-
	6	86011645	CAA	C	43.73	intron_variant	MODIFIER	c.210+612_210+613delTT			0.0047				-	-	-	0.0152	-
	6	86011650	TGCATC	T	43.73	intron_variant	MODIFIER	c.210+604_210+608delGATGC			0.0047				-	-	-	0.0152	-
	6	86011664	CAGTTTGTA	C	851.73	intron_variant	MODIFIER	c.210+585_210+594delAGTACAAACT			0.3160				0.5750	0.3182	0.3182	0.1970	0.2500
	6	86011741	CAG	C	929.73	intron_variant	MODIFIER	c.210+516_210+517delCT			0.3255				0.5750	0.2955	0.2727	0.2576	0.2500
	6	86012436	GA	G,GAAA,GAA	1201.73	intron_variant	MODIFIER	c.157-13delT			0.1557				0.3250	0.0909	0.3182	0.0606	0.1250
	6	86012437	A	AG	288.73	intron_variant	MODIFIER	c.157-14_157-13insC			0.0047				0.0250	-	-	-	-
	6	86012625	ATGGCTAACAGAAAAGC	T	397.73	intron_variant	MODIFIER	c.157-222_157-202delCTCCTTTTCTGTGTAGCCATAA			0.0377				-	0.1818	-	-	-
	6	86013668	AT	A	1035.73	intron_variant	MODIFIER	c.94-449delA			0.8019				0.9500	0.9091	0.8636	0.5152	0.9750
	6	86013800	TGAA	T	682.73	intron_variant	MODIFIER	c.94-583_94-581delTTC			0.0472				0.1500	-	-	-	0.1000
	6	86013811	A	AT	344.74	intron_variant	MODIFIER	c.94-592_94-591insA			0.0189				0.0250	-	-	0.0455	-
	6	86014176	CA	C	407.73	intron_variant	MODIFIER	c.94-957delT			0.0472				0.1750	-	-	-	0.0750
	6	86015234	GAGA	G	354.73	disruptive_inframe_deletion	MODERATE	c.72_74delTCT			0.0047				0.0250	-	-	-	-



Supplementary Table S2. Polymorphisms (SNPs in black, INDEL in red) detected in the goat casein genes (CSN1S2)																			
	Chromosome	Position	Ref allele	Alt allele	QUAL	Variant_type	Effect	Nucleotide substitution	AA substitution	subst. literature	Alt_freq	SIFT_score	SIFT_median	SIFT_prediction	AF	BE	EU	FE	NE
	6	86076861	T	G	777.77	5_prime_UTR_variant	MODIFIER	c.-76T>G			0.2972				0.2000	0.4773	0.2727	0.1515	0.4500
	6	86076886	C	T	718.77	5_prime_UTR_variant	MODIFIER	c.-51C>T			0.2972				0.2000	0.4545	0.3182	0.1515	0.4500
	6	86076980	C	T	495.77	upstream_gene_variant	MODIFIER	c.-2108C>T			0.1792				0.0250	0.0909	0.0455	0.3788	0.1750
	6	86077054	T	C	178.77	upstream_gene_variant	MODIFIER	c.-2034T>C			0.0047				-	-	0.0455	-	-
	6	86077055	T	C	188.77	upstream_gene_variant	MODIFIER	c.-2033T>C			0.0047				-	-	0.0455	-	-
	6	86077057	G	T	25.78	upstream_gene_variant	MODIFIER	c.-2031G>T			0.0047				-	-	-	0.0152	-
	6	86077186	G	A	268.77	upstream_gene_variant	MODIFIER	c.-1902G>A			0.0283				-	0.0455	-	0.0455	0.0250
	6	86077193	G	C	84.77	upstream_gene_variant	MODIFIER	c.-1895G>C			0.0047				-	0.0227	-	-	-
	6	86077343	G	A	242.77	upstream_gene_variant	MODIFIER	c.-1745G>A			0.0047				-	0.0227	-	-	-
	6	86077378	C	T	620.77	upstream_gene_variant	MODIFIER	c.-1710C>T			0.3113				0.2250	0.4318	0.3182	0.1818	0.4750
	6	86077496	C	T	10.2	intron_variant	MODIFIER	c.-13+572C>T			0.0047				-	-	-	0.0152	-
	6	86077505	C	G	545.77	intron_variant	MODIFIER	c.-13+581C>G			0.0943				0.2500	-	0.2727	0.0455	0.0250
	6	86077654	A	G	157.77	intron_variant	MODIFIER	c.-13+730A>G			0.0236				-	0.0455	-	0.0303	0.0250
	6	86077666	A	C	280.77	intron_variant	MODIFIER	c.-13+742A>C			0.0047				-	0.0227	-	-	-
	6	86077672	A	G	894.77	intron_variant	MODIFIER	c.-13+748A>G			0.2972				0.2250	0.4318	0.3182	0.1364	0.4750
	6	86077862	G	A	188.77	intron_variant	MODIFIER	c.-13+938G>A			0.0189				-	-	-	0.0303	0.0500
	6	86077879	A	T	869.77	intron_variant	MODIFIER	c.-13+955A>T			0.2925				0.2000	0.4318	0.3182	0.1364	0.4750
	6	86077932	C	T	97.77	intron_variant	MODIFIER	c.-13+1008C>T			0.0047				-	-	0.0455	-	-
	6	86077956	C	T	350.77	intron_variant	MODIFIER	c.-13+1032C>T			0.0047				-	0.0227	-	-	-
	6	86078007	A	G	549.77	intron_variant	MODIFIER	c.-12-1069A>G			0.3774				0.3250	0.3864	0.4091	0.4545	0.2750
	6	86078043	C	A	29.77	intron_variant	MODIFIER	c.-12-1033C>A			0.0047				-	-	0.0455	-	-
	6	86078062	C	T	261.77	intron_variant	MODIFIER	c.-12-1014C>T			0.0094				-	0.0227	-	-	0.0250
	6	86078137	A	G	108.77	intron_variant	MODIFIER	c.-12-939A>G			0.0047				-	-	-	0.0152	-
	6	86078216	A	T	397.77	intron_variant	MODIFIER	c.-12-860A>T			0.0047				0.0250	-	-	-	-
	6	86078217	C	T	732.77	intron_variant	MODIFIER	c.-12-859C>T			0.3113				0.2250	0.4773	0.3182	0.1515	0.4750
	6	86078276	T	C	760.77	intron_variant	MODIFIER	c.-12-800T>C			0.0236				-	0.0682	-	-	0.0500
	6	86078336	C	T	398.77	intron_variant	MODIFIER	c.-12-740C>T			0.0047				-	0.0227	-	-	-
	6	86078369	G	C	401.77	intron_variant	MODIFIER	c.-12-707G>C			0.0094				-	0.0455	-	-	-
	6	86078370	G	A	724.77	intron_variant	MODIFIER	c.-12-706G>A			0.3066				0.2250	0.4318	0.3182	0.1667	0.4750
	6	86078373	G	T	18.59	intron_variant	MODIFIER	c.-12-703G>T			0.0094				-	-	-	0.0303	-
	6	86078400	T	C	421.77	intron_variant	MODIFIER	c.-12-676T>C			0.1745				0.1500	0.1136	0.1364	0.0758	0.4500
	6	86078677	T	A	159.77	intron_variant	MODIFIER	c.-12-399T>A			0.0094				-	-	-	0.0303	-
	6	86078872	G	A	58.74	intron_variant	MODIFIER	c.-12-204G>A			0.0094				-	-	-	0.0303	-
	6	86078947	T	C	620.77	intron_variant	MODIFIER	c.-12-129T>C			0.2217				0.0500	0.2955	0.0455	0.3636	0.1750
	6	86078967	T	C	865.77	intron_variant	MODIFIER	c.-12-109T>C			0.3160				0.2250	0.4773	0.3182	0.1667	0.4750
	6	86078991	A	G	486.77	intron_variant	MODIFIER	c.-12-85A>G			0.1132				0.2750	-	0.4091	0.0303	0.0500
	6	86079078	C	A	254.77	splice_region_variant	LOW	c.-10C>A			0.0094				0.0250	-	-	-	0.0250
	6	86079086	G	A	1141.77	5_prime_UTR_variant	MODIFIER	c.-2G>A			0.7500				0.5500	0.9773	0.7727	0.6818	0.8000
	6	86079087	T	C	1141.77	5_prime_UTR_variant	MODIFIER	c.-1T>C			0.7500				0.5500	0.9773	0.7727	0.6818	0.8000
	6	86079098	T	C	395.77	missense_variant	MODERATE	c.11T>C	p.Phe4Ser		0.2358	0	2.59	DELETERIOUS	0.0500	0.3182	0.0455	0.3939	0.1750
	6	86079121	G	A	405.77	missense_variant	MODERATE	c.34G>A	p.Val12Ile		0.0094	0.07	2.55	TOLERATED	-	-	-	-	0.0500
	6	86079145	A	C	533.77	splice_region_variant	LOW	c.51+7A>C			0.1132				0.2750	-	0.3636	0.0455	0.0500
	6	86079206	A	G	348.77	intron_variant	MODIFIER	c.51+68A>G			0.2264				0.0500	0.3182	-	0.3788	0.1750
	6	86079307	A	G	254.77	intron_variant	MODIFIER	c.51+169A>G			0.0047				-	-	-	-	0.0250
	6	86079355	G	A	85.77	intron_variant	MODIFIER	c.51+217G>A			0.0283				-	-	-	0.0606	0.0500
	6	86079432	G	T,A	222.77	intron_variant	MODIFIER	c.51+294G>A			0.0094				-	0.0455	-	-	-
	6	86079506	A	G	710.77	intron_variant	MODIFIER	c.51+368A>G			0.5708				0.2750	0.7955	0.3182	0.6364	0.6500
	6	86079521	C	T	388.77	intron_variant	MODIFIER	c.51+383C>T			0.0047				0.0250	-	-	-	-
	6	86079607	A	G	217.77	intron_variant	MODIFIER	c.51+469A>G			0.0189				0.0250	-	0.0455	0.0152	0.0250
	6	86079749	A	G	119.77	intron_variant	MODIFIER	c.51+611A>G			0.0094				-	-	0.0455	-	0.0250
6	86079850	A	T	836.77	intron_variant	MODIFIER	c.51+712A>T			0.9858				1.0000	0.9773	1.0000	0.9848	0.9750	
6	86079970	T	C	566.77	intron_variant	MODIFIER	c.51+832T>C			0.0802				0.1250	0.0455	0.2273	0.0455	0.0500	
6	86080015	G	A	861.77	intron_variant	MODIFIER	c.51+877G>A			0.2925				0.1500	0.4545	0.3182	0.1667	0.4500	
6	86080077	C	T	814.77	intron_variant	MODIFIER	c.52-880C>T			0.1415				0.3000	0.0455	-	0.1364	0.1750	
6	86080096	T	G	943.77	intron_variant	MODIFIER	c.52-861T>G			0.9340				1.0000	0.9091	0.9091	0.8788	1.0000	
6	86080198	C	T	265.77	intron_variant	MODIFIER	c.52-759C>T			0.0094				-	0.0227	-	-	0.0250	
6	86080224	C	T	651.77	intron_variant	MODIFIER	c.52-733C>T			0.0802				-	0.0682	-	0.1818	0.0500	
6	86080225	G	A	453.77	intron_variant	MODIFIER	c.52-732G>A			0.1226				0.0500	0.2955	-	0.0909	0.1250	
6	86080248	C	T	316.77	intron_variant	MODIFIER	c.52-709C>T			0.0519				0.0250	0.0455	-	0.0606	0.1000	
6	86080262	C	T	578.77	intron_variant	MODIFIER	c.52-695C>T			0.0236				-	-	-	0.0758	-	
6	86080294	C	T	227.77	intron_variant	MODIFIER	c.52-663C>T			0.0142				0.0250	-	-	-	0.0500	
6	86080380	A	T	86.77	intron_variant	MODIFIER	c.52-577A>T			0.0283				-	0.0227	-	0.0758	-	

6	86080424	G	A	218.77	intron_variant	MODIFIER	c.52-533G>A			0.0047				0.0250	-	-	-	-
6	86080481	T	G	618.77	intron_variant	MODIFIER	c.52-476T>G			0.2453				0.0500	0.3636	0.2273	0.3485	0.1500
6	86080520	T	C	227.8	intron_variant	MODIFIER	c.52-437T>C			0.0047				-	-	-	0.0152	-
6	86080539	C	G	78.77	intron_variant	MODIFIER	c.52-418C>G			0.0047				-	-	-	0.0152	-
6	86080574	C	A	1053.77	intron_variant	MODIFIER	c.52-383C>A			0.6415				0.8250	0.2273	0.5000	0.7273	0.8500
6	86080578	G	A	1117.77	intron_variant	MODIFIER	c.52-379G>A			0.7217				0.6250	0.8182	1.0000	0.5909	0.7750
6	86080602	A	G	440.77	intron_variant	MODIFIER	c.52-355A>G			0.0142				-	0.0682	-	-	-
6	86080610	A	C	295.77	intron_variant	MODIFIER	c.52-347A>C			0.0094				-	0.0455	-	-	-
6	86080612	T	A	954.77	intron_variant	MODIFIER	c.52-345T>A			0.5708				0.3250	0.8409	0.5909	0.4394	0.7250
6	86080651	A	C	998.77	intron_variant	MODIFIER	c.52-306A>C			0.7453				0.8250	0.6591	0.9091	0.8182	0.5500
6	86080664	C	T	318.77	intron_variant	MODIFIER	c.52-293C>T			0.0047				-	0.0227	-	-	-
6	86080714	A	G	347.77	intron_variant	MODIFIER	c.52-243A>G			0.0330				-	0.0227	-	0.0758	0.0250
6	86080760	G	C	948.77	intron_variant	MODIFIER	c.52-197G>C			0.1415				0.3500	0.0682	-	0.0909	0.1750
6	86080782	T	A	198.77	intron_variant	MODIFIER	c.52-175T>A			0.0142				-	0.0682	-	-	-
6	86080855	C	A	221.84	intron_variant	MODIFIER	c.52-102C>A			0.0377				-	-	-	0.0758	0.0750
6	86080886	C	T	430.77	intron_variant	MODIFIER	c.52-71C>T			0.2075				0.1500	0.3409	0.2727	0.1515	0.1750
6	86080905	G	A	447.77	intron_variant	MODIFIER	c.52-52G>A			0.0519				-	0.2500	-	-	-
6	86080919	G	A	835.77	intron_variant	MODIFIER	c.52-38G>A			0.4717				0.5000	0.4773	0.6364	0.4848	0.3250
6	86080927	A	G	351.77	intron_variant	MODIFIER	c.52-30A>G			0.0047				-	-	-	-	0.0250
6	86080943	G	A	172.78	intron_variant	MODIFIER	c.52-14G>A			0.0094				-	-	-	0.0303	-
6	86080969	G	A	665.77	missense_variant	MODERATE	c.64G>A	p.Val22Ile	p.Val7Ile	0.1321	0.4	2.65	TOLERATED	0.1250	0.2273	0.2727	0.0455	0.1000
6	86080994	C	T	289.77	intron_variant	MODIFIER	c.78+11C>T			0.0330				-	-	-	0.0606	0.0750
6	86080999	G	T	1089.77	intron_variant	MODIFIER	c.78+16G>T			0.9009				1.0000	0.8409	0.9545	0.8030	1.0000
6	86081022	T	G	467.77	intron_variant	MODIFIER	c.78+39T>G			0.0283				0.0250	-	0.1818	-	0.0250
6	86081049	A	G	79.77	intron_variant	MODIFIER	c.78+66A>G			0.0047				-	0.0227	-	-	-
6	86081080	C	T	1205.77	intron_variant	MODIFIER	c.78+97C>T			0.7123				0.8750	0.5682	0.8182	0.7121	0.6500
6	86081134	A	G	202.77	intron_variant	MODIFIER	c.78+151A>G			0.0047				-	-	-	0.0152	-
6	86081135	T	G	819.77	intron_variant	MODIFIER	c.78+152T>G			0.5000				0.4750	0.5227	0.6818	0.5606	0.3000
6	86081164	C	T	31.77	intron_variant	MODIFIER	c.78+181C>T			0.0047				-	-	-	0.0152	-
6	86081202	C	A	147.77	intron_variant	MODIFIER	c.78+219C>A			0.0142				-	-	-	0.0455	-
6	86081216	A	G	250.77	intron_variant	MODIFIER	c.78+233A>G			0.0094				0.0250	-	-	-	0.0250
6	86081280	T	C	289.77	intron_variant	MODIFIER	c.78+297T>C			0.0094				0.0250	-	-	-	0.0250
6	86081283	G	A	1029.77	intron_variant	MODIFIER	c.78+300G>A			0.5236				0.7500	0.3409	0.5909	0.5455	0.4250
6	86081383	A	G	721.77	intron_variant	MODIFIER	c.79-391A>G			0.2972				0.2500	0.3409	0.3182	0.1970	0.4500
6	86081390	T	C	579.77	intron_variant	MODIFIER	c.79-384T>C			0.2406				0.1500	0.2955	0.0909	0.1818	0.4500
6	86081416	G	A	19.81	intron_variant	MODIFIER	c.79-358G>A			0.0047				-	-	-	0.0152	-
6	86081439	A	G	661.77	intron_variant	MODIFIER	c.79-335A>G			0.0802				0.2500	-	0.1818	0.0303	0.0250
6	86081441	A	G	308.77	intron_variant	MODIFIER	c.79-333A>G			0.0849				0.0250	0.1136	-	0.1061	0.1250
6	86081450	A	G	317.78	intron_variant	MODIFIER	c.79-324A>G			0.1132				-	0.2045	-	0.1818	0.0750
6	86081493	A	G	304.77	intron_variant	MODIFIER	c.79-281A>G			0.0283				0.0250	0.0682	-	-	0.0500
6	86081581	T	A	620.77	intron_variant	MODIFIER	c.79-193T>A			0.0708				-	-	-	0.1515	0.1250
6	86081651	T	C	326.78	intron_variant	MODIFIER	c.79-123T>C			0.0377				-	0.1818	-	-	-
6	86081728	G	A	227.77	intron_variant	MODIFIER	c.79-46G>A			0.0047				-	-	-	-	0.0250
6	86081865	A	T	176.77	intron_variant	MODIFIER	c.103-21A>T			0.0047				-	0.0227	-	-	-
6	86081932	A	G	419.77	splice_region_variant	LOW	c.144+5A>G			0.0094				-	-	-	-	0.0500
6	86081940	T	G	79.77	intron_variant	MODIFIER	c.144+13T>G			0.0047				-	-	-	-	0.0250
6	86081947	G	A	804.77	intron_variant	MODIFIER	c.144+20G>A			0.2877				0.4000	0.3182	0.5909	0.1667	0.1750
6	86082011	C	A	46.77	intron_variant	MODIFIER	c.144+84C>A			0.0047				-	-	-	0.0152	-
6	86082099	G	A	826.77	intron_variant	MODIFIER	c.144+172G>A			0.1557				0.3250	0.0227	-	0.1818	0.1750
6	86082170	G	T	222.77	intron_variant	MODIFIER	c.145-142G>T			0.0047				-	0.0227	-	-	-
6	86082213	A	G	1146.77	intron_variant	MODIFIER	c.145-99A>G			0.9811				1.0000	1.0000	1.0000	0.9394	1.0000
6	86082469	A	G	23.79	intron_variant	MODIFIER	c.171+131A>G			0.0047				-	-	-	0.0152	-
6	86082493	C	T	975.77	intron_variant	MODIFIER	c.171+155C>T			0.4057				0.4000	0.4091	0.0455	0.5758	0.3250
6	86082578	G	A	292.77	intron_variant	MODIFIER	c.171+240G>A			0.0047				0.0250	-	-	-	-
6	86082708	C	T	85.77	intron_variant	MODIFIER	c.171+370C>T			0.0283				-	-	-	0.0909	-
6	86082752	T	A	863.77	intron_variant	MODIFIER	c.172-384T>A			0.5708				0.5500	0.5455	0.5000	0.7121	0.4250
6	86082774	A	G	542.77	intron_variant	MODIFIER	c.172-362A>G			0.1415				0.3250	0.0682	0.4091	0.0455	0.0500
6	86083035	A	G	252.77	intron_variant	MODIFIER	c.172-101A>G			0.0094				-	0.0455	-	-	-
6	86083274	C	T	636.77	intron_variant	MODIFIER	c.198+112C>T			0.2358				0.3250	0.0909	0.4545	0.2879	0.1000
6	86083302	T	C	768.77	intron_variant	MODIFIER	c.198+140T>C			0.1698				0.1250	0.3182	0.0909	-	0.3750
6	86083375	A	T	190.77	intron_variant	MODIFIER	c.198+213A>T			0.0047				-	0.0227	-	-	-
6	86083446	C	G	390.77	intron_variant	MODIFIER	c.199-166C>G			0.0142				-	0.0455	-	-	0.0250
6	86083468	T	C	1023.77	intron_variant	MODIFIER	c.199-144T>C			0.4245				0.5250	0.5000	0.4545	0.3636	0.3250
6	86083573	G	C	201.77	intron_variant	MODIFIER	c.199-39G>C			0.0047				-	-	-	-	0.0250
6	86083659	A	T	506.77	intron_variant	MODIFIER	c.225+21A>T			0.0142				-	0.0455	-	0.0152	-
6	86083669	G	A	471.77	intron_variant	MODIFIER	c.225+31G>A			0.0377				-	0.1818	-	-	-



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6	86083904	C	T	500.77	intron_variant	MODIFIER	c.225+266C>T			0.1226				0.1250	0.1136	0.0909	-	0.3500
6	86083934	C	A	901.77	intron_variant	MODIFIER	c.225+296C>A			0.4434				0.5250	0.4318	0.4545	0.4242	0.4000
6	86084055	G	A	899.77	intron_variant	MODIFIER	c.225+417G>A			0.4811				0.5250	0.4773	0.4545	0.5000	0.4250
6	86084117	C	G	953.77	intron_variant	MODIFIER	c.225+479C>G			0.1038				0.1000	0.0682	0.0909	-	0.3250
6	86084134	G	A	950.77	intron_variant	MODIFIER	c.225+496G>A			0.9906				1.0000	1.0000	1.0000	0.9697	1.0000
6	86084271	T	C	530.77	intron_variant	MODIFIER	c.226-478T>C			0.1179				0.1250	0.1136	0.0909	-	0.3250
6	86084300	T	C	582.77	intron_variant	MODIFIER	c.226-449T>C			0.1132				0.1000	0.1136	0.0909	-	0.3250
6	86084309	C	T	446.77	intron_variant	MODIFIER	c.226-440C>T			0.2311				0.3500	0.1136	0.3182	0.3030	0.0750
6	86084333	T	G	451.77	intron_variant	MODIFIER	c.226-416T>G			0.1132				0.1250	0.0909	0.0909	-	0.3250
6	86084339	G	A	731.77	intron_variant	MODIFIER	c.226-410G>A			0.0283				-	0.1136	-	-	0.0250
6	86084492	A	C	447.77	intron_variant	MODIFIER	c.226-257A>C			0.0283				-	0.0227	-	0.0606	0.0250
6	86084621	C	T	519.77	splice_region_variant	LOW	c.199-8C>T			0.0094				-	-	-	-	0.0500
6	86084638	G	A	410.77	missense_variant	MODERATE	c.208G>A	p.Glu79Lys	p.Glu64Lys	0.0566	0.13	2.56	TOLERATED	-	0.0227	-	0.1667	-
6	86084692	C	T	136.77	intron_variant	MODIFIER	c.226-57C>T			0.0142				-	0.0682	-	-	-
6	86084847	T	C	297.77	intron_variant	MODIFIER	c.270+54T>C			0.0094				-	0.0455	-	-	-
6	86084942	A	G	184.77	intron_variant	MODIFIER	c.271-113A>G			0.0047				0.0250	-	-	-	-
6	86084950	T	A	355.77	intron_variant	MODIFIER	c.271-105T>A			0.0094				-	-	-	0.0303	-
6	86084966	T	G	737.77	intron_variant	MODIFIER	c.271-89T>G			0.1179				0.1250	0.1136	0.0909	-	0.3250
6	86084994	T	G	829.77	intron_variant	MODIFIER	c.271-61T>G			0.1179				0.1250	0.1136	0.0909	-	0.3250
6	86085104	C	T	115.77	missense_variant	MODERATE	c.320C>T	p.Pro115Leu		0.0142	0.8	2.64	TOLERATED	-	-	0.0455	0.0303	-
6	86085160	G	C	1016.77	missense_variant	MODERATE	c.376G>C	p.Ala134Pro		0.9623	1	2.7	TOLERATED	1.0000	1.0000	1.0000	0.8788	1.0000
6	86085212	T	G	150.41	intron_variant	MODIFIER	c.393+35T>G			0.0094				-	-	-	0.0303	-
6	86085213	A	T	482.77	intron_variant	MODIFIER	c.393+36A>T			0.0519				0.0500	0.0455	0.0455	0.0758	0.0250
6	86085224	C	T	175.77	intron_variant	MODIFIER	c.393+47C>T			0.0566				0.1500	0.0227	0.1364	0.0303	-
6	86085320	G	A	60.74	intron_variant	MODIFIER	c.393+143G>A			0.0094				-	-	-	0.0303	-
6	86085388	A	G	505.77	intron_variant	MODIFIER	c.393+211A>G			0.0425				-	0.2045	-	-	-
6	86085509	C	T	1021.77	intron_variant	MODIFIER	c.394-199C>T			0.4670				0.5250	0.4318	0.5000	0.4545	0.4500
6	86085537	A	G	1173.77	intron_variant	MODIFIER	c.394-171A>G			0.9292				1.0000	0.9545	1.0000	0.8788	0.8750
6	86085554	A	G	951.77	intron_variant	MODIFIER	c.394-154A>G			0.3726				0.4500	0.2500	0.5455	0.3485	0.3750
6	86085602	C	T	990.77	intron_variant	MODIFIER	c.394-106C>T			0.2311				0.1250	0.2500	0.1364	0.2273	0.3750
6	86085705	T	C	103.28	splice_region_variant	LOW	c.394-3T>C			0.0142				-	-	-	0.0455	-
6	86085714	G	A	140.77	missense_variant	MODERATE	c.400G>A	p.Glu142Lys		0.0094	0.14	2.67	TOLERATED	-	-	-	-	0.0500
6	86085800	C	T	786.77	intron_variant	MODIFIER	c.420+66C>T			0.1038				0.0750	0.0909	0.0909	-	0.3250
6	86085937	C	T	398.77	intron_variant	MODIFIER	c.420+203C>T			0.0425				-	0.2045	-	-	-
6	86085957	T	C	514.77	intron_variant	MODIFIER	c.420+223T>C			0.1934				0.3500	0.2273	0.3182	0.0758	0.1250
6	86086078	G	A	328.77	intron_variant	MODIFIER	c.420+344G>A			0.0377				-	-	-	0.0606	0.1000
6	86086173	A	G	1078.77	intron_variant	MODIFIER	c.420+439A>G			0.1698				0.1750	0.1136	0.5000	0.1212	0.1250
6	86086263	T	C	655.77	intron_variant	MODIFIER	c.421-444T>C			0.1226				0.1500	0.0227	0.5000	0.0606	0.1000
6	86086327	C	T	195.77	intron_variant	MODIFIER	c.421-380C>T			0.0047				-	-	-	-	0.0250
6	86086472	A	G	147.03	intron_variant	MODIFIER	c.421-235A>G			0.0142				-	0.0227	-	0.0303	-
6	86086494	A	T	1050.77	intron_variant	MODIFIER	c.421-213A>T			0.2736				0.4250	0.1136	0.0909	0.2273	0.4750
6	86086535	C	T	216.77	intron_variant	MODIFIER	c.421-172C>T			0.0047				-	0.0227	-	-	-
6	86086636	T	C	557.77	intron_variant	MODIFIER	c.421-71T>C			0.3538				0.1000	0.6591	0.0455	0.4242	0.3250
6	86086777	C	T	897.77	intron_variant	MODIFIER	c.447+44C>T			0.0755				0.1250	-	0.5000	-	-
6	86086880	T	C	767.77	intron_variant	MODIFIER	c.447+147T>C			0.1226				0.1500	0.0682	0.5455	0.0152	0.1000
6	86087089	G	T	118.77	intron_variant	MODIFIER	c.447+356G>T			0.0047				-	0.0227	-	-	-
6	86087198	T	A	334.78	intron_variant	MODIFIER	c.447+465T>A			0.0377				-	0.1818	-	-	-
6	86087279	C	T	753.77	intron_variant	MODIFIER	c.447+546C>T			0.1462				0.1500	0.0682	0.5000	0.1061	0.1000
6	86087295	A	G	620.77	intron_variant	MODIFIER	c.447+562A>G			0.1368				0.1500	0.0682	0.5000	0.0758	0.1000
6	86087421	A	C	1051.77	intron_variant	MODIFIER	c.447+688A>C			0.9528				1.0000	0.9545	1.0000	0.9091	0.9500
6	86087422	A	T	1051.77	intron_variant	MODIFIER	c.447+689A>T			0.9528				1.0000	0.9545	1.0000	0.9091	0.9500
6	86087434	G	T	1007.77	intron_variant	MODIFIER	c.447+701G>T			0.9623				1.0000	0.9545	1.0000	0.9394	0.9500
6	86087527	C	T	767.77	intron_variant	MODIFIER	c.447+794C>T			0.1415				0.1500	0.0227	0.5455	0.1061	0.1000
6	86087647	A	G	156.77	intron_variant	MODIFIER	c.448-786A>G			0.0047				-	0.0227	-	-	-
6	86087692	C	T	347.78	intron_variant	MODIFIER	c.448-741C>T			0.0094				-	0.0455	-	-	-
6	86087723	C	T	598.77	intron_variant	MODIFIER	c.448-710C>T			0.1321				0.1500	0.0682	0.4545	0.0758	0.1000
6	86087749	T	C	826.77	intron_variant	MODIFIER	c.448-684T>C			0.1415				0.1500	0.0682	0.4545	0.1061	0.1000
6	86087772	C	A	856.77	intron_variant	MODIFIER	c.448-661C>A			0.1415				0.1500	0.0682	0.5000	0.0909	0.1000
6	86087822	C	T	882.77	intron_variant	MODIFIER	c.448-611C>T			0.3160				0.0750	0.4318	0.0455	0.4848	0.3000
6	86087879	G	A	871.77	intron_variant	MODIFIER	c.448-554G>A			0.2547				0.4250	0.1136	0.0455	0.1667	0.5000
6	86087888	C	T	679.77	intron_variant	MODIFIER	c.448-545C>T			0.1179				0.3250	0.0455	0.3182	0.0303	0.0250
6	86088001	A	G	728.77	intron_variant	MODIFIER	c.448-432A>G			0.1321				0.1500	0.0682	0.4091	0.0909	0.1000
6	86088079	G	A	131.77	intron_variant	MODIFIER	c.448-354G>A			0.0047				-	0.0227	-	-	-
6	86088144	A	C	581.77	intron_variant	MODIFIER	c.448-289A>C			0.1415				0.1500	0.0682	0.4545	0.1061	0.1000
6	86088167	A	C	592.77	intron_variant	MODIFIER	c.448-266A>C			0.1085				0.3250	-	0.3182	0.0303	0.0250
6	86088181	T	C	612.77	intron_variant	MODIFIER	c.448-252T>C			0.0849				-	0.0455	0.0455	0.1970	0.0500

6	86088315	G	A	887.77	intron_variant	MODIFIER	c.448-118G>A			0.1321				0.1250	0.0682	0.4091	0.1061	0.1000
6	86088407	T	G	507.77	intron_variant	MODIFIER	c.448-26T>G			0.1745				0.0750	0.3182	-	0.1515	0.2500
6	86088555	C	T	564.77	synonymous_variant	LOW	c.481C>T	p.Leu169Leu		0.0896				-	0.0455	0.0455	0.2121	0.0500
6	86088596	T	C	492.77	splice_region_variant	LOW	c.516+6T>C			0.1179				0.3250	0.0682	0.3182	0.0152	0.0250
6	86088658	C	T	935.77	intron_variant	MODIFIER	c.516+68C>T			0.9387				1.0000	1.0000	0.9091	0.8636	0.9500
6	86088676	A	T	11.12	intron_variant	MODIFIER	c.516+86A>T			0.0047				-	-	-	0.0152	-
6	86088680	A	C	63.41	intron_variant	MODIFIER	c.516+90A>C			0.0094				-	-	-	0.0303	-
6	86088687	G	C	858.77	intron_variant	MODIFIER	c.516+97G>C			0.7925				0.6750	0.8636	0.5909	0.8030	0.9250
6	86088716	G	A	808.77	intron_variant	MODIFIER	c.516+126G>A			0.1321				0.1500	0.0227	0.4091	0.1212	0.1000
6	86088736	A	G	414.77	intron_variant	MODIFIER	c.516+146A>G			0.0094				-	0.0455	-	-	-
6	86088752	C	A	887.77	upstream_gene_variant	MODIFIER	c.-16620C>A			0.8349				0.6750	0.8864	0.5909	0.9242	0.9250
6	86088766	T	C	145.03	upstream_gene_variant	MODIFIER	c.-16606T>C			0.0094				-	-	-	0.0303	-
6	86088978	C	T	735.77	upstream_gene_variant	MODIFIER	c.-16394C>T			0.1462				0.1500	0.0682	0.5000	0.1061	0.1000
6	86089078	A	G	924.77	upstream_gene_variant	MODIFIER	c.-16294A>G			0.1321				0.1500	0.0682	0.4545	0.0758	0.1000
6	86089096	C	T	496.77	upstream_gene_variant	MODIFIER	c.-16276C>T			0.1132				0.1250	0.0909	0.0909	-	0.3250
6	86089185	C	A	112.77	upstream_gene_variant	MODIFIER	c.-16187C>A			0.0047				-	-	-	0.0152	-
6	86089260	A	G	449.77	upstream_gene_variant	MODIFIER	c.-16112A>G			0.1085				0.0750	0.2500	-	0.0606	0.1250
6	86089401	A	T	1065.77	missense_variant	MODERATE	c.521A>T	p.Lys182Ile	p.Lys167Ile	0.2783	0.07	2.77	TOLERATED	0.4250	0.1136	0.0909	0.2273	0.5000
6	86089408	C	G	244.77	missense_variant	MODERATE	c.528C>G	p.Ser184Arg		0.0047	0.12	2.77	TOLERATED	-	-	-	-	0.0250
6	86089479	C	G	379.77	missense_variant	MODERATE	c.599C>G	p.Pro208Arg	p.Pro193Arg	0.0236	0	2.64	DELETERIOUS	-	0.0455	-	0.0455	-
6	86089508	C	G	63.77	missense_variant	MODERATE	c.628C>G	p.Pro218Ala		0.0094	0.03	2.72	DELETERIOUS	-	-	-	0.0303	-
6	86089935	G	T	565.77	upstream_gene_variant	MODIFIER	c.-15437G>T			0.3821				0.2250	0.6364	0.0909	0.3333	0.5000
6	86089942	T	G	538.77	upstream_gene_variant	MODIFIER	c.-15430T>G			0.1321				0.3250	0.0682	0.4545	0.0152	0.0250
6	86089950	G	T	174.77	upstream_gene_variant	MODIFIER	c.-15422G>T			0.0142				-	-	-	0.0303	0.0250
6	86090047	A	G	1117.77	upstream_gene_variant	MODIFIER	c.-15325A>G			0.9292				1.0000	0.9545	1.0000	0.8333	0.9500
6	86090061	G	A	1003.77	upstream_gene_variant	MODIFIER	c.-15311C>A			0.1085				0.3000	-	-	0.0758	0.1500
6	86090095	T	A	535.77	upstream_gene_variant	MODIFIER	c.-15277T>A			0.0377				-	0.1818	-	-	-
6	86090113	T	A	142.77	upstream_gene_variant	MODIFIER	c.-15259T>A			0.0047				-	0.0227	-	-	-
6	86090117	G	A	757.77	upstream_gene_variant	MODIFIER	c.-15255G>A			0.1321				0.1500	0.0682	0.5000	0.0606	0.1000
6	86090195	G	A	484.77	upstream_gene_variant	MODIFIER	c.-15177G>A			0.0519				-	0.2500	-	-	-
6	86090253	G	T	213.77	upstream_gene_variant	MODIFIER	c.-15119G>T			0.0094				0.0250	-	-	-	0.0250
6	86090351	C	G	172.78	upstream_gene_variant	MODIFIER	c.-15021C>G			0.0094				-	-	-	0.0303	-
6	86090378	T	C	308.77	upstream_gene_variant	MODIFIER	c.-14994T>C			0.0094				-	0.0455	-	-	-
6	86090502	T	G	290.77	upstream_gene_variant	MODIFIER	c.-14870T>G			0.0047				0.0250	-	-	-	-
6	86090539	C	T	684.77	upstream_gene_variant	MODIFIER	c.-14833C>T			0.1132				0.3250	-	0.3636	0.0303	0.0250
6	86090567	G	A	43.77	upstream_gene_variant	MODIFIER	c.-14805G>A			0.0094				-	0.0455	-	-	-
6	86090578	T	A	408.77	upstream_gene_variant	MODIFIER	c.-14794T>A			0.0943				-	0.0455	0.0909	0.2121	0.0500
6	86090594	A	C	647.77	upstream_gene_variant	MODIFIER	c.-14778A>C			0.1179				0.3000	0.0455	0.3636	0.0303	0.0250
6	86090598	A	G	620.77	upstream_gene_variant	MODIFIER	c.-14774A>G			0.1321				0.1500	0.0682	0.4545	0.0758	0.1000
6	86090619	A	C	69.77	upstream_gene_variant	MODIFIER	c.-14753A>C			0.0047				-	-	-	0.0152	-
6	86090620	C	T	660.77	upstream_gene_variant	MODIFIER	c.-14752C>T			0.1321				0.1500	0.0455	0.4545	0.0909	0.1000
6	86090729	C	G	1045.77	upstream_gene_variant	MODIFIER	c.-14643C>G			0.8160				0.6750	0.8864	0.5909	0.8636	0.9250
6	86090733	G	A,T	1045.77	upstream_gene_variant	MODIFIER	c.-14639G>A			0.3160				0.4500	0.1591	0.0909	0.2879	0.5250
6	86090785	A	G	18.59	upstream_gene_variant	MODIFIER	c.-14587A>G			0.0094				-	0.0455	-	-	-
6	86090896	T	G	37.77	upstream_gene_variant	MODIFIER	c.-14476T>G			0.0047				0.0250	-	-	-	-
6	86090899	A	G	28.77	upstream_gene_variant	MODIFIER	c.-14473A>G			0.0047				0.0250	-	-	-	-
6	86090996	T	C	19.81	upstream_gene_variant	MODIFIER	c.-14376T>C			0.0047				-	-	0.0455	-	-
6	86091022	T	C	152.03	upstream_gene_variant	MODIFIER	c.-14350T>C			0.0283				-	0.0227	-	0.0758	-
6	86091038	A	T	294.77	upstream_gene_variant	MODIFIER	c.-14334A>T			0.0189				-	-	-	0.0303	0.0500
6	86091040	A	T	62.74	upstream_gene_variant	MODIFIER	c.-14332A>T			0.0189				-	-	-	0.0606	-
6	86091046	T	A	231.84	upstream_gene_variant	MODIFIER	c.-14326T>A			0.0283				-	0.0455	-	0.0606	-
6	86091057	A	T	1277.77	upstream_gene_variant	MODIFIER	c.-14315A>T			0.2264				0.4000	0.1136	0.0909	0.0758	0.5000
6	86091066	A	C	1006.77	upstream_gene_variant	MODIFIER	c.-14306A>C			0.1226				0.1250	0.0227	0.5000	0.0758	0.1000
6	86091082	A	G	303.77	upstream_gene_variant	MODIFIER	c.-14290A>G			0.0802				0.2500	-	0.1818	0.0303	0.0250
6	86091085	C	T	61.74	upstream_gene_variant	MODIFIER	c.-14287C>T			0.0094				-	-	-	0.0303	-
6	86091086	G	C	1006.77	upstream_gene_variant	MODIFIER	c.-14286G>C			0.1274				0.1500	0.0227	0.5000	0.0606	0.1250
6	86091126	A	G	27.77	upstream_gene_variant	MODIFIER	c.-14246A>G			0.0047				-	-	-	0.0152	-
6	86091181	G	A	906.77	upstream_gene_variant	MODIFIER	c.-14191G>A			0.9811				1.0000	1.0000	1.0000	0.9394	1.0000
6	86091318	G	T	785.77	upstream_gene_variant	MODIFIER	c.-14054G>T			0.1462				0.1500	0.0682	0.4545	0.1212	0.1000
6	86091366	A	G	166.77	upstream_gene_variant	MODIFIER	c.-14006A>G			0.0094				-	0.0455	-	-	-
6	86091409	A	G	1253.77	upstream_gene_variant	MODIFIER	c.-13963A>G			0.2689				0.4250	0.1136	0.0909	0.1970	0.5000
6	86091437	A	G	214.77	upstream_gene_variant	MODIFIER	c.-13935A>G			0.0094				-	0.0455	-	-	-
6	86091489	C	G	46.77	upstream_gene_variant	MODIFIER	c.-13883C>G			0.0047				-	-	-	0.0152	-
6	86091746	A	G	357.77	upstream_gene_variant	MODIFIER	c.-13626A>G			0.0094				0.0250	-	-	-	0.0250
6	86091875	G	T	756.77	upstream_gene_variant	MODIFIER	c.-13497G>T			0.1368				0.1500	0.0682	0.5000	0.0758	0.1000
6	86091883	A	G	72.77	upstream_gene_variant	MODIFIER	c.-13489A>G			0.0047				-	0.0227	-	-	-

	6	86091990	A	G	1025.77	upstream_gene_variant	MODIFIER	c.-13382A>G			0.8443				0.6750	0.9318	0.6364	0.9091	0.9250
	6	86091991	C	T	691.77	upstream_gene_variant	MODIFIER	c.-13381C>T			0.1462				0.1500	0.0682	0.5000	0.1061	0.1000
	6	86092101	T	C	272.77	upstream_gene_variant	MODIFIER	c.-13271T>C			0.0377				-	0.0455	-	0.0909	-
	6	86092122	T	C	663.77	upstream_gene_variant	MODIFIER	c.-13250T>C			0.3821				0.1000	0.7045	0.0455	0.4848	0.3250
	6	86092123	G	A	535.77	upstream_gene_variant	MODIFIER	c.-13249G>A			0.0377				-	-	-	0.0758	0.0750
	6	86092199	A	G	705.77	upstream_gene_variant	MODIFIER	c.-13173A>G			0.2877				0.4250	0.1364	0.0909	0.2273	0.5250
	6	86092271	A	G	460.77	upstream_gene_variant	MODIFIER	c.-13101A>G			0.1132				0.1000	0.1136	0.0909	-	0.3250
	6	86092314	A	G	571.77	upstream_gene_variant	MODIFIER	c.-13058A>G			0.3349				0.1000	0.6818	0.0455	0.3485	0.3250
	6	86092351	T	A	358.77	upstream_gene_variant	MODIFIER	c.-13021T>A			0.1132				0.1500	0.0227	0.4091	0.0606	0.1000
	6	86092432	G	A	556.77	upstream_gene_variant	MODIFIER	c.-12940G>A			0.1179				0.1500	0.0227	0.3636	0.0909	0.1000
	6	86092435	C	T	556.77	upstream_gene_variant	MODIFIER	c.-12937C>T			0.1179				0.1500	0.0227	0.3636	0.0909	0.1000
	6	86092456	C	T	226.84	upstream_gene_variant	MODIFIER	c.-12916C>T			0.0425				-	0.2045	-	-	-
	6	86092457	C	T	507.77	upstream_gene_variant	MODIFIER	c.-12915C>T			0.2736				0.4250	0.1591	0.0909	0.1818	0.5000
	6	86092490	A	C	565.77	upstream_gene_variant	MODIFIER	c.-12882A>C			0.2547				0.4250	0.1364	0.0909	0.1364	0.5000
	6	86092506	A	G	848.77	upstream_gene_variant	MODIFIER	c.-12866A>G			0.9245				1.0000	0.9545	1.0000	0.7879	1.0000
	6	86092551	C	T	389.77	upstream_gene_variant	MODIFIER	c.-12821C>T			0.0519				0.0750	0.0682	-	0.0152	0.1000
	6	86092557	A	T	127.03	upstream_gene_variant	MODIFIER	c.-12815A>T			0.0189				-	-	-	0.0606	-
	6	86092634	A	G	727.77	upstream_gene_variant	MODIFIER	c.-12738A>G			0.2311				0.4250	0.0909	0.0909	0.1061	0.4750
	6	86092671	C	T	337.77	upstream_gene_variant	MODIFIER	c.-12701C>T			0.0330				-	0.0455	-	0.0758	-
	6	86092746	C	G	294.77	upstream_gene_variant	MODIFIER	c.-12626C>G			0.0236				-	-	-	0.0303	0.0750
	6	86092851	A	G	30.77	upstream_gene_variant	MODIFIER	c.-12521A>G			0.0047				-	-	0.0455	-	-
	6	86092858	G	A	724.77	upstream_gene_variant	MODIFIER	c.-12514G>A			0.1604				0.1500	0.0909	0.5000	0.1364	0.1000
	6	86092887	T	C	111.77	upstream_gene_variant	MODIFIER	c.-12485T>C			0.0094				-	0.0455	-	-	-
	6	86092891	A	G	204.77	upstream_gene_variant	MODIFIER	c.-12481A>G			0.0047				0.0250	-	-	-	-
	6	86092917	T	A	267.77	upstream_gene_variant	MODIFIER	c.-12455T>A			0.0047				0.0250	-	-	-	-
	6	86093184	A	G	1196.77	upstream_gene_variant	MODIFIER	c.-12188A>G			0.8443				0.6750	0.9091	0.6364	0.9242	0.9250
	6	86093225	C	A	1178.77	upstream_gene_variant	MODIFIER	c.-12147C>A			0.2925				0.4250	0.1591	0.0909	0.2424	0.5000
	6	86093330	G	C	1032.77	3_prime_UTR_variant	MODIFIER	c.*91G>C			0.9811				1.0000	0.9545	1.0000	0.9697	1.0000
	6	86093348	T	C	482.77	3_prime_UTR_variant	MODIFIER	c.*109T>C			0.1274				0.1500	0.0227	0.5000	0.0758	0.1000
	6	86093378	G	C	521.77	3_prime_UTR_variant	MODIFIER	c.*139G>C			0.1462				0.1500	0.0682	0.5000	0.1061	0.1000
	6	86093399	C	T	711.77	3_prime_UTR_variant	MODIFIER	c.*160C>T			0.2783				0.4750	0.1364	0.8636	0.1515	0.1250
	6	86093465	T	C	85.77	3_prime_UTR_variant	MODIFIER	c.*226T>C			0.0047				-	0.0227	-	-	-
INDEL	6	86078000	T	TC	730.75	intron_variant	MODIFIER	c.-13+1076_-12-1075insC			0.3208				0.2250	0.5000	0.3182	0.1667	0.4750
	6	86078390	ATCT	A	673.73	intron_variant	MODIFIER	c.-12-685_-12-683delTCT			0.1274				0.2750	0.0682	0.4091	0.0303	0.0500
	6	86078422	A	ATT	720.73	intron_variant	MODIFIER	c.-12-654_-12-653insTT			0.0236				-	0.0682	-	-	0.0500
	6	86078654	T	TA	605.73	intron_variant	MODIFIER	c.-12-422_-12-421insA			0.8821				0.9750	0.8409	0.9545	0.8485	0.8500
	6	86078661	A	AT	341.73	intron_variant	MODIFIER	c.-12-415_-12-414insT			0.0142				0.0250	-	-	-	0.0500
	6	86078883	ATGTTG	A	851.73	intron_variant	MODIFIER	c.-12-192_-12-188delTGTTG			0.3066				0.2250	0.4318	0.3182	0.1667	0.4750
	6	86078914	CGTT	C	627.73	intron_variant	MODIFIER	c.-12-161_-12-159delGTT			0.0236				-	0.0682	-	-	0.0500
	6	86078941	AATCTAC	A	112.73	intron_variant	MODIFIER	c.-12-134_-12-121delATGAATCTACTTTT			0.0047				-	0.0227	-	-	-
	6	86080908	AT	A	13.91	intron_variant	MODIFIER	c.52-48delT			0.0047				-	-	-	0.0152	-
	6	86080975	CCAGTG/	T	28.74	frameshift_variant	HIGH	c.71_77delCCAGTGA			0.0047				-	-	-	0.0152	-
	6	86080985	CTCTTAGC	T	25.74	splice_region_variant	LOW	c.78+3_78+23delAAGATACTCTTAGGATCAACA			0.0047				-	-	-	0.0152	-
	6	86080993	TC	T	310.75	intron_variant	MODIFIER	c.78+11delC			0.0566				-	0.2727	-	-	-
	6	86081053	TC	T	31.73	intron_variant	MODIFIER	c.78+71delC			0.0047				-	-	-	0.0152	-
	6	86081060	A	AG	28.74	intron_variant	MODIFIER	c.78+77_78+78insG			0.0047				-	-	-	0.0152	-
	6	86081065	TTTTCAC	T	28.74	intron_variant	MODIFIER	c.78+83_78+90delTTTTCACC			0.0047				-	-	-	0.0152	-
	6	86081076	TAGAACT	T	31.73	intron_variant	MODIFIER	c.78+94_78+111delGAGCCTAGAACTATAGAA			0.0047				-	-	-	0.0152	-
	6	86081098	AGAAAAT	G	37.73	intron_variant	MODIFIER	c.78+116_78+123delAGAAAATT			0.0047				-	-	-	0.0152	-
	6	86081473	G	GA,GAA	334.73	intron_variant	MODIFIER	c.79-301_79-300insA			0.1509				0.0500	0.3182	0.1818	0.1061	0.1250
	6	86081842	CTTTA	C	367.74	intron_variant	MODIFIER	c.103-43_103-40delTTTA			0.0566				0.0250	0.2273	-	-	0.0250
	6	86085171	C	CA	153.73	frameshift_variant	HIGH	c.388dupA			0.0047				-	-	-	-	0.0250
	6	86085209	G	TTT,GTT,C	258.73	intron_variant	MODIFIER	c.393+32_393+33insT			0.0236				0.0250	0.0455	0.0455	0.0152	-
	6	86085210	T	TTG	113.73	intron_variant	MODIFIER	c.393+33_393+34insTG			0.0047				-	-	-	0.0152	-
	6	86085212	TA	T	46.73	intron_variant	MODIFIER	c.393+36delA			0.0047				-	0.0227	-	-	-
	6	86085213	AT	A	706.73	intron_variant	MODIFIER	c.393+37delT			0.4292				0.3250	0.5000	0.4545	0.4242	0.4500
	6	86085223	TC	T	37.73	intron_variant	MODIFIER	c.393+47delC			0.0047				-	0.0227	-	-	-
	6	86085227	TCTG	T	163.73	intron_variant	MODIFIER	c.393+51_393+53delCTG			0.0236				0.0750	-	0.0909	-	-
	6	86085531	C	CA	35.73	intron_variant	MODIFIER	c.394-177_394-176insA			0.0047				-	-	-	-	0.0250
	6	86085679	TTTTTTT,CTTTTTT		70.73	intron_variant	MODIFIER	c.394-28_394-21delTTTTTTTTT			0.0142				0.0250	-	-	-	0.0500
	6	86086829	AAT	A	720.73	intron_variant	MODIFIER	c.447+97_447+98delAT			0.3443				0.1000	0.6136	0.0455	0.4242	0.3250
	6	86086982	CT	C	450.73	intron_variant	MODIFIER	c.447+250delT			0.3208				0.1000	0.6818	0.0455	0.3485	0.2500
	6	86087843	AAC	A	264.73	intron_variant	MODIFIER	c.448-589_448-588delAC			0.0094				-	-	-	0.0303	-
	6	86088414	CTT	C,CT,CTT	498.73	intron_variant	MODIFIER	c.448-18_448-17delTT			0.3632				0.2000	0.3864	0.5455	0.3485	0.4250
	6	86088598	T	TA	28.74	intron_variant	MODIFIER	c.516+8_516+9insA			0.0047				-	-	-	0.0152	-
	6	86089298	CTGTT	C	112.73	upstream_gene_variant	MODIFIER	c.-16073_-16070delTGTT			0.0094				-	-	-	-	0.0500

6	86089579	AG	A	182.73	upstream_gene_variant	MODIFIER	c.-15792delG			0.0094				-	-	-	-	0.0500
6	86089875	T	TA	675.73	upstream_gene_variant	MODIFIER	c.-15497_-15496insA			0.2689				0.4250	0.1136	0.0909	0.2121	0.4750
6	86089925	ATGTT	A	682.73	upstream_gene_variant	MODIFIER	c.-15446_-15443delTGTT			0.1132				0.1500	0.0227	0.4091	0.0606	0.1000
6	86089933	TG	T	787.73	upstream_gene_variant	MODIFIER	c.-15438delG			0.2217				0.4500	0.0909	0.4545	0.1061	0.2000
6	86089934	GGTTTT	TGTTTT,G	682.73	upstream_gene_variant	MODIFIER	c.-15438_-15437insT			0.1698				0.1750	0.2500	0.4091	0.0758	0.1000
6	86089935	GTTTTT	G	140.73	upstream_gene_variant	MODIFIER	c.-15436_-15432delTTTTT			0.0047				-	-	-	-	0.0250
6	86089939	T	TTG	342.73	upstream_gene_variant	MODIFIER	c.-15433_-15432insTG			0.1226				0.0750	0.2727	-	0.0909	0.1250
6	86089949	GAAATG	AAATGT	72.73	upstream_gene_variant	MODIFIER	c.-15422_-15414delGGAAATGTA			0.0142				-	-	-	0.0303	0.0250
6	86090203	A	AT	584.73	upstream_gene_variant	MODIFIER	c.-15169_-15168insT			0.1179				0.1500	0.0227	0.5000	0.0455	0.1000
6	86090586	AC	A	326.74	upstream_gene_variant	MODIFIER	c.-14785delC			0.0189				0.0250	0.0455	-	-	0.0250
6	86090836	T	TAA	197.73	upstream_gene_variant	MODIFIER	c.-14536_-14535insAA			0.0047				-	0.0227	-	-	-
6	86090894	G	GGGAGA	28.74	upstream_gene_variant	MODIFIER	c.-14478_-14477insGGAGA			0.0047				0.0250	-	-	-	-
6	86090895	G	AGAGGGT	34.73	upstream_gene_variant	MODIFIER	c.-14477_-14476insGAGAGGGAGAGGGTGGGATGATT			0.0047				0.0250	-	-	-	-
6	86091013	TTGACA	T	149.73	upstream_gene_variant	MODIFIER	c.-14358_-14354delTGACA			0.0330				-	0.0455	-	0.0758	-
6	86091017	TTTTATT	TTTTATT	270.73	upstream_gene_variant	MODIFIER	c.-14354delA			0.0283				-	-	0.0455	-	0.1250
6	86091019	TTATTTT	T	270.73	upstream_gene_variant	MODIFIER	c.-14352_-14344delTTTATTTTA			0.0142				0.0250	-	-	-	0.0500
6	86091020	TTATTTT	T	98.25	upstream_gene_variant	MODIFIER	c.-14351_-14344delTTATTTTA			0.0094				-	-	-	0.0303	-
6	86091022	TATTTTA	T	1185.73	upstream_gene_variant	MODIFIER	c.-14349_-14344delATTTTA			0.4858				0.5000	0.8182	0.0909	0.2727	0.6750
6	86091023	ATTTTTT	A	867.73	upstream_gene_variant	MODIFIER	c.-14348_-14309delTTTTATTTTTTTTTTAAATTTTTTATTTTTTTTTTAAATTTT			0.1226				0.1250	0.0227	0.5000	0.0758	0.1000
6	86091027	TA	T	187.87	upstream_gene_variant	MODIFIER	c.-14344delA			0.0377				-	0.0455	-	0.0909	-
6	86091034	TTTTA	T	704.73	upstream_gene_variant	MODIFIER	c.-14337_-14334delTTTA			0.3113				0.2000	0.7273	0.0909	0.1061	0.4250
6	86091035	TTTA	T	1130.73	upstream_gene_variant	MODIFIER	c.-14336_-14334delTTA			0.1745				0.3000	0.1136	-	0.1818	0.2000
6	86091068	TAATTCT	T	997.73	upstream_gene_variant	MODIFIER	c.-14303_-14290delCTTTAATTCTTACA			0.1179				0.1250	0.0227	0.5000	0.0606	0.1000
6	86091088	TCCCA	T	1000.73	upstream_gene_variant	MODIFIER	c.-14283_-14280delCCCA			0.1179				0.1250	0.0227	0.5000	0.0606	0.1000
6	86091655	GA	G	563.73	upstream_gene_variant	MODIFIER	c.-13716delA			0.5330				0.2500	0.8409	0.5455	0.5909	0.3750

Supplementary Table S2. Polymorphisms (SNPs in black, INDEL in red) detected in the goat casein genes (CSN3)																		
Chromosome	Position	Ref allele	Alt allele	QUAL	Variant_type	Effect	Nucleotide substitution	AA substitution	subst. literature	Alt_freq	SIFT_score	SIFT_median	SIFT_prediction	AF	BE	EU	FE	NE
6	86197357	G	C	274.77	intron_variant	MODIFIER	c.-6+47G>C			0.0047				0.0250	-	-	-	-
6	86197402	C	A	208.78	intron_variant	MODIFIER	c.-6+92C>A			0.0047				-	0.0227	-	-	-
6	86197531	T	G	660.28	intron_variant	MODIFIER	c.-6+221T>G			0.5519				0.5500	0.5909	0.3636	0.5455	0.6250
6	86197697	C	T	313.77	intron_variant	MODIFIER	c.-6+387C>T			0.0094				-	0.0455	-	-	-
6	86197703	T	C	944.77	intron_variant	MODIFIER	c.-6+393T>C			0.1604				0.4500	-	-	0.0758	0.2750
6	86197766	A	G	624.77	intron_variant	MODIFIER	c.-6+456A>G			0.0330				-	0.0227	0.2727	-	-
6	86197775	T	C	851.77	intron_variant	MODIFIER	c.-6+465T>C			0.0094				0.0500	-	-	-	-
6	86197776	C	T	750.77	intron_variant	MODIFIER	c.-6+466C>T			0.1840				0.0750	0.2727	0.3182	0.1061	0.2500
6	86197903	G	T	590.77	intron_variant	MODIFIER	c.-6+593G>T			0.0236				-	-	0.2273	-	-
6	86197933	G	A	678.77	intron_variant	MODIFIER	c.-6+623G>A			0.0330				-	0.0227	0.2727	-	-
6	86198001	T	C	657.77	intron_variant	MODIFIER	c.-6+691T>C			0.2170				0.0750	0.2955	0.3182	0.1818	0.2750
6	86198097	A	G	1193.77	intron_variant	MODIFIER	c.-6+787A>G			0.0943				0.4000	-	-	0.0303	0.0500
6	86198114	A	G	1039.77	intron_variant	MODIFIER	c.-6+804A>G			0.0377				-	0.0455	0.2727	-	-
6	86198175	T	C	260.77	intron_variant	MODIFIER	c.-6+865T>C			0.0283				-	0.1364	-	-	-
6	86198178	A	G	709.77	intron_variant	MODIFIER	c.-6+868A>G			0.1226				0.0500	0.2273	-	0.0758	0.2250
6	86198192	T	C	125.77	intron_variant	MODIFIER	c.-6+882T>C			0.0047				-	0.0227	-	-	-
6	86198214	A	G	152.77	intron_variant	MODIFIER	c.-6+904A>G			0.0283				-	0.1364	-	-	-
6	86198239	A	G	266.77	intron_variant	MODIFIER	c.-6+929A>G			0.0047				-	-	-	-	0.0250
6	86198253	C	T	88.77	intron_variant	MODIFIER	c.-6+943C>T			0.0047				-	0.0227	-	-	-
6	86198254	A	G	88.77	intron_variant	MODIFIER	c.-6+944A>G			0.0047				-	0.0227	-	-	-
6	86198298	A	G	989.77	intron_variant	MODIFIER	c.-6+988A>G			0.7972				0.6000	0.8409	0.6818	0.8636	0.9000
6	86198325	A	G	745.03	intron_variant	MODIFIER	c.-6+1015A>G			0.1509				0.0250	-	-	0.3030	0.2750
6	86198344	G	A	313.77	intron_variant	MODIFIER	c.-6+1034G>A			0.0094				-	0.0455	-	-	-
6	86198436	G	A	159.77	intron_variant	MODIFIER	c.-6+1126G>A			0.0283				-	0.1364	-	-	-
6	86198500	C	T	586.77	intron_variant	MODIFIER	c.-6+1190C>T			0.2028				0.0750	0.2727	0.3182	0.1515	0.2750
6	86198520	C	A	241.77	intron_variant	MODIFIER	c.-6+1210C>A			0.0047				-	-	-	-	0.0250
6	86198530	C	T	574.77	intron_variant	MODIFIER	c.-5-1214C>T			0.2453				0.0750	0.2955	0.5909	0.1818	0.2750
6	86198606	A	G	629.77	intron_variant	MODIFIER	c.-5-1138A>G			0.2217				0.0750	0.2955	0.5909	0.1061	0.2750
6	86198725	C	T	61.77	intron_variant	MODIFIER	c.-5-1019C>T			0.0047				-	0.0227	-	-	-
6	86198726	G	C	949.77	intron_variant	MODIFIER	c.-5-1018G>C			0.7547				0.6250	0.8864	0.6818	0.6818	0.9000
6	86198899	G	A	635.77	intron_variant	MODIFIER	c.-5-845G>A			0.2358				0.0750	0.2955	0.5909	0.1515	0.2750
6	86198906	T	C	221.77	intron_variant	MODIFIER	c.-5-838T>C			0.0047				-	0.0227	-	-	-
6	86198964	C	A	568.77	intron_variant	MODIFIER	c.-5-780C>A			0.0236				-	-	-	-	0.1250
6	86199016	T	C	387.77	intron_variant	MODIFIER	c.-5-728T>C			0.0755				-	0.0682	-	0.1970	-
6	86199111	G	A	238.77	intron_variant	MODIFIER	c.-5-633G>A			0.0142				-	0.0682	-	-	-
6	86199195	T	C	1052.77	intron_variant	MODIFIER	c.-5-549T>C			0.2358				0.0750	0.3182	0.5909	0.1364	0.2750
6	86199227	G	A	573.77	intron_variant	MODIFIER	c.-5-517G>A			0.0613				0.0250	0.0455	0.3182	0.0152	0.0500
6	86199247	G	A	293.77	intron_variant	MODIFIER	c.-5-497G>A			0.0047				-	-	-	-	0.0250
6	86199257	A	G	35.77	intron_variant	MODIFIER	c.-5-487A>G			0.0047				-	-	-	0.0152	-
6	86199315	T	C	160.77	intron_variant	MODIFIER	c.-5-429T>C			0.0047				-	0.0227	-	-	-
6	86199401	G	A	846.77	intron_variant	MODIFIER	c.-5-343G>A			0.0943				0.4000	-	-	0.0303	0.0500
6	86199471	G	A	527.77	intron_variant	MODIFIER	c.-5-273G>A			0.0283				-	0.0227	0.2273	-	-
6	86199526	T	C	883.77	intron_variant	MODIFIER	c.-5-218T>C			0.1179				0.3750	-	0.3182	0.0152	0.0500
6	86199543	A	G	199.77	intron_variant	MODIFIER	c.-5-201A>G			0.0047				-	0.0227	-	-	-
6	86199548	A	G	199.77	intron_variant	MODIFIER	c.-5-196A>G			0.0047				-	0.0227	-	-	-
6	86199577	C	T	1017.77	intron_variant	MODIFIER	c.-5-167C>T			0.0377				-	0.1818	-	-	-
6	86199578	G	A	345.78	intron_variant	MODIFIER	c.-5-166G>A			0.0330				-	0.1591	-	-	-
6	86199773	G	A	58.77	missense_variant	MODERATE	c.25G>A	p.Val9Met		0.0047	0.07	2.7	TOLERATED	-	0.0227	-	-	-
6	86199914	A	G	757.77	intron_variant	MODIFIER	c.57+109A>G			0.1745				0.0750	0.2955	0.3182	0.0455	0.2750
6	86200043	T	G	460.77	intron_variant	MODIFIER	c.57+238T>G			0.0283				-	-	0.2727	-	-
6	86200086	A	T	357.77	intron_variant	MODIFIER	c.57+281A>T			0.0566				0.0250	0.0682	0.2273	0.0152	0.0500
6	86200140	C	T	298.77	intron_variant	MODIFIER	c.57+335C>T			0.0377				-	-	0.0455	0.0455	0.1000
6	86200141	G	A	322.78	intron_variant	MODIFIER	c.57+336G>A			0.0330				-	0.1591	-	-	-
6	86200156	T	C	562.77	intron_variant	MODIFIER	c.57+351T>C			0.0472				-	0.1818	-	0.0303	-
6	86200169	C	A	573.77	intron_variant	MODIFIER	c.57+364C>A			0.1698				0.0750	0.2955	0.3182	0.0303	0.2750
6	86200190	T	C	601.77	intron_variant	MODIFIER	c.57+385T>C			0.0377				-	0.1818	-	-	-
6	86200192	A	G	646.77	intron_variant	MODIFIER	c.57+387A>G			0.0377				-	0.1818	-	-	-
6	86200199	G	T	30.77	intron_variant	MODIFIER	c.57+394G>T			0.0047				-	-	0.0455	-	-
6	86200202	C	A	767.77	intron_variant	MODIFIER	c.57+397C>A			0.0896				0.0500	0.1818	-	0.0152	0.2000
6	86200203	T	C	767.77	intron_variant	MODIFIER	c.57+398T>C			0.0896				0.0500	0.1818	-	0.0152	0.2000
6	86200217	A	G	612.77	intron_variant	MODIFIER	c.57+412A>G			0.0283				-	-	0.2727	-	-
6	86200239	T	C	196.77	intron_variant	MODIFIER	c.57+434T>C			0.0142				-	-	-	-	0.0750
6	86200242	T	A	789.77	intron_variant	MODIFIER	c.57+437T>A			0.2028				0.0750	0.3182	0.5909	0.0303	0.2750
6	86200313	C	T	699.77	intron_variant	MODIFIER	c.57+508C>T			0.2500				0.1000	0.4318	0.3182	0.1515	0.3250
6	86200373	C	G	306.77	intron_variant	MODIFIER	c.57+568C>G			0.0660				-	0.0682	-	0.1667	-
6	86200420	T	A	258.8	intron_variant	MODIFIER	c.57+615T>A			0.0094				-	0.0455	-	-	-
6	86200441	T	C	902.77	intron_variant	MODIFIER	c.57+636T>C			0.3255				0.1000	0.4318	0.3182	0.3788	0.3500
6	86200590	G	A	538.77	intron_variant	MODIFIER	c.57+785G>A			0.0283				-	-	0.2727	-	-
6	86200700	C	T	281.77	intron_variant	MODIFIER	c.57+895C>T			0.0047				-	-	-	-	0.0250
6	86200725	T	C	422.77	intron_variant	MODIFIER	c.57+920T>C			0.1415				0.0750	0.0909	0.2727	0.0909	0.2750
6	86200781	A	T	255.77	intron_variant	MODIFIER	c.57+976A>T			0.0236				0.0500	-	-	-	0.0750
6	86200839	C	T	1009.77	intron_variant	MODIFIER	c.57+1034C>T			0.0377				-	0.1818	-	-	-

6	86200921	T	C	618.77	intron variant	MODIFIER	c.57+1116T>C				0.1415				0.0500	-	-	0.2727	0.2500
6	86200971	A	G	647.77	intron variant	MODIFIER	c.57+1166A>G				0.1698				0.4500	0.0227	-	0.0909	0.2750
6	86201166	A	G	191.77	intron variant	MODIFIER	c.57+1361A>G				0.0330				-	0.1591	-	-	-
6	86201245	C	T	839.77	intron variant	MODIFIER	c.57+1440C>T				0.1604				0.4500	-	-	0.0758	0.2750
6	86201279	A	G	429.77	intron variant	MODIFIER	c.57+1474A>G				0.0236				0.0500	-	-	-	0.0750
6	86201298	G	A	1004.77	intron variant	MODIFIER	c.57+1493G>A				0.0094				0.0500	-	-	-	-
6	86201317	A	G	201.77	intron variant	MODIFIER	c.57+1512A>G				0.0283				-	-	0.2727	-	-
6	86201340	A	G	853.77	intron variant	MODIFIER	c.57+1535A>G				0.8019				0.6250	0.8864	0.6818	0.8333	0.9000
6	86201393	A	C	234.77	intron variant	MODIFIER	c.57+1588A>C				0.0047				-	0.0227	-	-	-
6	86201434	G	A	583.77	intron variant	MODIFIER	c.57+1629G>A				0.0330				-	0.1591	-	-	-
6	86201469	C	A	511.77	intron variant	MODIFIER	c.57+1664C>A				0.0283				-	-	0.2727	-	-
6	86201470	G	A	881.77	intron variant	MODIFIER	c.57+1665G>A				0.4528				0.5000	0.6364	0.3182	0.4091	0.3500
6	86201532	G	T	835.77	intron variant	MODIFIER	c.57+1727G>T				0.3019				0.1250	0.2727	0.3182	0.2727	0.5500
6	86201554	A	C	880.77	intron variant	MODIFIER	c.57+1749A>C				0.7877				0.6000	0.9318	0.6364	0.7879	0.9000
6	86201589	T	G	378.77	intron variant	MODIFIER	c.57+1784T>G				0.0047				0.0250	-	-	-	-
6	86201710	C	T	475.77	intron variant	MODIFIER	c.57+1905C>T				0.0047				-	-	-	-	0.0250
6	86201775	T	C	361.77	intron variant	MODIFIER	c.57+1970T>C				0.0896				0.0250	0.1136	-	0.1515	0.0750
6	86201829	G	A	430.77	intron variant	MODIFIER	c.57+2024G>A				0.0330				-	0.0227	0.2727	-	-
6	86201843	T	C,A	948.77	intron variant	MODIFIER	c.57+2038T>A				0.8113				0.6250	0.8182	0.6818	0.9091	0.9000
6	86201870	C	T	564.77	intron variant	MODIFIER	c.57+2065C>T				0.0047				-	0.0227	-	-	-
6	86202017	C	T	360.77	intron variant	MODIFIER	c.57+2212C>T				0.0236				0.0250	0.0227	0.1364	-	-
6	86202049	G	C	475.77	intron variant	MODIFIER	c.57+2244G>C				0.0330				-	0.1591	-	-	-
6	86202103	G	T	539.77	intron variant	MODIFIER	c.57+2298G>T				0.2406				0.0500	0.2273	0.6364	0.3030	0.1250
6	86202104	G	T	539.77	intron variant	MODIFIER	c.57+2299G>T				0.2406				0.0500	0.2273	0.6364	0.3030	0.1250
6	86202115	C	T	740.77	intron variant	MODIFIER	c.57+2310C>T				0.2453				0.1000	0.1818	-	0.3030	0.5000
6	86202210	C	T	172.77	intron variant	MODIFIER	c.57+2405C>T				0.0047				-	0.0227	-	-	-
6	86202369	T	A	265.77	intron variant	MODIFIER	c.57+2564T>A				0.0047				-	0.0227	-	-	-
6	86202401	C	A	493.77	intron variant	MODIFIER	c.57+2596C>A				0.0283				-	-	0.2727	-	-
6	86202439	C	A	67.77	intron variant	MODIFIER	c.57+2634C>A				0.0047				-	0.0227	-	-	-
6	86202473	C	G	626.77	intron variant	MODIFIER	c.57+2668C>G				0.2170				0.1000	0.2045	-	0.2121	0.4750
6	86202519	C	T	158.77	intron variant	MODIFIER	c.57+2714C>T				0.0047				-	0.0227	-	-	-
6	86202532	C	A	670.77	intron variant	MODIFIER	c.57+2727C>A				0.2264				0.1000	0.1818	-	0.2424	0.5000
6	86202547	A	G	861.77	intron variant	MODIFIER	c.57+2742A>G				0.8066				0.6250	0.9318	0.6818	0.8333	0.8750
6	86202557	T	A	316.77	intron variant	MODIFIER	c.57+2752T>A				0.0142				0.0250	-	0.0909	-	-
6	86202654	C	T	892.77	intron variant	MODIFIER	c.57+2849C>T				0.2123				0.0500	0.2045	-	0.2576	0.4250
6	86202749	G	A	1027.77	intron variant	MODIFIER	c.57+2944G>A				0.3632				0.4750	0.2045	0.3636	0.2879	0.5500
6	86202766	A	G	325.77	intron variant	MODIFIER	c.57+2961A>G				0.0236				0.0500	-	-	-	0.0750
6	86202774	T	A,C	668.77	intron variant	MODIFIER	c.57+2969T>A				0.3538				0.1250	0.3182	-	0.5000	0.5750
6	86202785	A	C	151.03	intron variant	MODIFIER	c.57+2980A>C				0.0189				-	-	-	0.0606	-
6	86202816	T	A	431.77	intron variant	MODIFIER	c.57+3011T>A				0.0142				0.0250	-	0.0909	-	-
6	86202819	C	T	826.77	intron variant	MODIFIER	c.57+3014C>T				0.4953				0.1500	0.4318	0.5909	0.6515	0.6000
6	86202834	T	G	859.77	intron variant	MODIFIER	c.57+3029T>G				0.2547				0.0750	0.2045	-	0.3333	0.5000
6	86202839	A	G	323.77	intron variant	MODIFIER	c.57+3034A>G				0.1038				0.0250	0.0682	-	0.2424	0.0500
6	86202890	A	C	941.77	intron variant	MODIFIER	c.57+3085A>C				0.3113				0.4750	0.5000	0.0909	0.1818	0.2750
6	86202910	T	G	249.77	intron variant	MODIFIER	c.57+3105T>G				0.0047				-	-	-	-	0.0250
6	86202932	A	C	430.77	intron variant	MODIFIER	c.57+3127A>C				0.0283				-	-	0.2727	-	-
6	86202947	G	A	315.77	intron variant	MODIFIER	c.57+3142G>A				0.0094				-	0.0227	-	-	0.0250
6	86202971	C	T	912.77	intron variant	MODIFIER	c.57+3166C>T				0.1179				0.3750	-	0.3182	0.0152	0.0500
6	86203026	T	C	849.77	intron variant	MODIFIER	c.57+3221T>C				0.2358				0.0750	0.1818	-	0.3182	0.4500
6	86203045	C	T	699.77	intron variant	MODIFIER	c.57+3240C>T				0.2406				0.0750	0.2045	-	0.3182	0.4500
6	86203194	T	A	124.77	intron variant	MODIFIER	c.57+3389T>A				0.0047				-	0.0227	-	-	-
6	86203231	T	A	418.77	intron variant	MODIFIER	c.57+3426T>A				0.0377				-	0.1818	-	-	-
6	86203242	A	G	781.77	intron variant	MODIFIER	c.57+3437A>G				0.4623				0.1000	0.4318	0.5455	0.6212	0.5500
6	86203257	G	A	36.77	intron variant	MODIFIER	c.57+3452G>A				0.0047				-	-	0.0455	-	-
6	86203336	A	G	691.77	intron variant	MODIFIER	c.58-3423A>G				0.0283				-	-	0.2727	-	-
6	86203518	G	A	278.77	intron variant	MODIFIER	c.58-3241G>A				0.0047				-	0.0227	-	-	-
6	86203557	T	C	166.77	intron variant	MODIFIER	c.58-3202T>C				0.0142				-	0.0682	-	-	-
6	86203558	G	T	166.77	intron variant	MODIFIER	c.58-3201G>T				0.0142				-	0.0682	-	-	-
6	86203575	A	C	184.84	intron variant	MODIFIER	c.58-3184A>C				0.0142				-	0.0682	-	-	-
6	86203584	A	G	181.77	intron variant	MODIFIER	c.58-3175A>G				0.0189				-	-	-	0.0606	-
6	86203623	A	C	749.77	intron variant	MODIFIER	c.58-3136A>C				0.2311				0.0750	0.2045	-	0.2576	0.5000
6	86203734	T	C	449.77	intron variant	MODIFIER	c.58-3025T>C				0.0236				0.0250	-	0.1818	-	-
6	86203810	A	T	701.77	intron variant	MODIFIER	c.58-2949A>T				0.0236				-	-	0.2273	-	-
6	86203868	A	C	279.77	intron variant	MODIFIER	c.58-2891A>C				0.0047				0.0250	-	-	-	-
6	86203931	C	G	41.77	intron variant	MODIFIER	c.58-2828C>G				0.0047				-	-	-	0.0152	-
6	86203933	T	C	682.77	intron variant	MODIFIER	c.58-2826T>C				0.1745				0.0500	0.1818	0.2727	0.2424	0.1250
6	86203934	C	T	781.77	intron variant	MODIFIER	c.58-2825C>T				0.2594				0.1000	0.1818	-	0.3485	0.5000
6	86203953	A	T	691.77	intron variant	MODIFIER	c.58-2806A>T				0.0283				-	-	0.2727	-	-
6	86203961	C	T	691.77	intron variant	MODIFIER	c.58-2798C>T				0.2217				0.0500	0.2045	0.5455	0.2879	0.1250
6	86204053	C	T	693.77	intron variant	MODIFIER	c.58-2706C>T				0.2358				0.1000	0.2045	-	0.2576	0.5000
6	86204125	T	A	442.77	intron variant	MODIFIER	c.58-2634T>A				0.0330				-	-	0.3182	-	-
6	86204129	A	T	107.28	intron variant	MODIFIER	c.58-2630A>T				0.0330				0.0250	0.0455	-	0.0303	0.0500
6	86204131	T	C	107.28	intron variant	MODIFIER	c.58-2628T>C				0.0189				-	0.0455	-	0.0303	-
6	86204137	C	G	62.74	intron variant	MODIFIER	c.58-2622C>G				0.0283				0.0250	0.0455	-	0.0303	0.0250
6	86204138	T	G	62.74	intron variant	MODIFIER	c.58-2621T>G				0.0283				0.0250	0.0455	-	0.0303	0.0250

6	86204142	T	A	266.77	intron variant	MODIFIER	c.58-2617T>A			0.0047				-	0.0227	-	-	-
6	86204257	T	C	247.77	intron variant	MODIFIER	c.58-2502T>C			0.0142				-	0.0682	-	-	-
6	86204339	C	T	183.1	intron variant	MODIFIER	c.58-2420C>T			0.1321				0.0500	0.2045	0.4545	-	0.1750
6	86204380	G	A	197.84	intron variant	MODIFIER	c.58-2379G>A			0.1840				0.3500	0.1818	-	0.0303	0.3750
6	86204408	G	A	263.78	intron variant	MODIFIER	c.58-2351G>A			0.3538				0.4500	0.6136	0.2727	0.0909	0.4500
6	86204433	C	T	84.77	intron variant	MODIFIER	c.58-2326C>T			0.0047				0.0250	-	-	-	-
6	86204739	C	T	319.78	intron variant	MODIFIER	c.58-2020C>T			0.0425				-	0.2045	-	-	-
6	86204909	G	T	218.84	intron variant	MODIFIER	c.58-1850G>T			0.3208				0.8250	0.2273	0.1818	0.1515	0.2750
6	86205444	T	G	57.74	intron variant	MODIFIER	c.58-1315T>G			0.0094				-	0.0455	-	-	-
6	86205468	C	T	12.05	intron variant	MODIFIER	c.58-1291C>T			0.0047				0.0250	-	-	-	-
6	86205537	G	C	13.95	intron variant	MODIFIER	c.58-1222G>C			0.0047				0.0250	-	-	-	-
6	86205592	C	T	49.77	intron variant	MODIFIER	c.58-1167C>T			0.0047				-	-	-	0.0152	-
6	86205593	G	A	145.9	intron variant	MODIFIER	c.58-1166G>A			0.0425				0.0500	0.0682	0.0909	-	0.0500
6	86205602	T	C	52.74	intron variant	MODIFIER	c.58-1157T>C			0.0142				-	0.0682	-	-	-
6	86205621	A	C	53.9	intron variant	MODIFIER	c.58-1138A>C			0.0047				-	-	-	0.0152	-
6	86205628	T	C	196.9	intron variant	MODIFIER	c.58-1131T>C			0.0236				-	-	0.2273	-	-
6	86205629	G	A	196.9	intron variant	MODIFIER	c.58-1130G>A			0.0236				-	-	0.2273	-	-
6	86205641	C	T	47.88	intron variant	MODIFIER	c.58-1118C>T			0.0047				-	0.0227	-	-	-
6	86205657	A	G	134.77	intron variant	MODIFIER	c.58-1102A>G			0.0094				-	0.0227	-	0.0152	-
6	86205745	A	T	44.77	intron variant	MODIFIER	c.58-1014A>T			0.0047				-	0.0227	-	-	-
6	86205753	T	C	390.77	intron variant	MODIFIER	c.58-1006T>C			0.0519				0.0250	0.0455	0.2727	-	0.0500
6	86205782	C	T	248.8	intron variant	MODIFIER	c.58-977C>T			0.0283				-	-	0.2727	-	-
6	86206019	C	T,G	200.8	intron variant	MODIFIER	c.58-740C>G			0.1698				0.3500	0.2500	-	0.0303	0.2250
6	86206112	A	G	27.78	intron variant	MODIFIER	c.58-647A>G			0.0047				-	0.0227	-	-	-
6	86206133	T	G	91.03	intron variant	MODIFIER	c.58-626T>G			0.0189				-	0.0455	-	-	0.0500
6	86206183	T	C	49.74	intron variant	MODIFIER	c.58-576T>C			0.0094				-	-	-	-	0.0500
6	86206218	C	T	50.74	intron variant	MODIFIER	c.58-541C>T			0.0094				-	-	-	-	0.0500
6	86206269	G	A	321.78	intron variant	MODIFIER	c.58-490G>A			0.3774				0.9000	0.3182	0.4545	0.1212	0.3000
6	86206299	G	A	115.9	intron variant	MODIFIER	c.58-460G>A			0.0708				0.0500	0.1364	0.2273	0.0303	-
6	86206413	A	G	442.77	intron variant	MODIFIER	c.58-346A>G			0.1745				0.4250	-	-	0.0909	0.3500
6	86206557	G	A	275.77	intron variant	MODIFIER	c.58-202G>A			0.0047				-	0.0227	-	-	-
6	86206570	C	T	333.03	intron variant	MODIFIER	c.58-189C>T			0.0236				0.0500	-	-	-	0.0750
6	86206606	G	C	142.77	intron variant	MODIFIER	c.58-153G>C			0.0047				-	0.0227	-	-	-
6	86206632	A	G	849.77	intron variant	MODIFIER	c.58-127A>G			0.1557				0.0500	0.2045	0.3182	0.1667	0.1000
6	86206637	A	T	310.77	intron variant	MODIFIER	c.58-122A>T			0.0094				-	0.0227	-	-	0.0250
6	86206785	A	G	1020.77	synonymous variant	LOW	c.84A>G	p.Gln28Gln		0.3066				0.4750	0.4545	0.0909	0.1970	0.2750
6	86206804	C	T	1007.77	intron variant	MODIFIER	c.90+13C>T			0.2500				0.4750	0.2727	0.0455	0.1515	0.2750
6	86206829	T	C	425.77	intron variant	MODIFIER	c.90+38T>C			0.0047				-	0.0227	-	-	-
6	86206836	C	T	811.77	intron variant	MODIFIER	c.90+45C>T			0.1226				0.3750	-	0.3182	0.0303	0.0500
6	86206854	G	T	894.77	intron variant	MODIFIER	c.90+63G>T			0.4575				0.1500	0.4091	0.5909	0.5303	0.6250
6	86206912	T	A	167.77	intron variant	MODIFIER	c.90+121T>A			0.0047				0.0250	-	-	-	-
6	86206915	T	C	391.77	intron variant	MODIFIER	c.90+124T>C			0.0236				0.0500	-	-	-	0.0750
6	86206948	G	A	767.9	intron variant	MODIFIER	c.90+157G>A			0.2500				0.1000	0.1818	-	0.3182	0.5000
6	86206984	G	A	746.77	intron variant	MODIFIER	c.90+193G>A			0.2500				0.1000	0.2045	-	0.3030	0.5000
6	86207029	G	A	764.77	intron variant	MODIFIER	c.90+238G>A			0.2358				0.0500	0.2045	-	0.3333	0.4250
6	86207133	C	T	123.77	intron variant	MODIFIER	c.90+342C>T			0.0047				0.0250	-	-	-	-
6	86207177	A	G	53.74	intron variant	MODIFIER	c.90+386A>G			0.0094				-	0.0455	-	-	-
6	86207335	G	T	556.77	intron variant	MODIFIER	c.90+544G>T			0.0849				0.0500	-	-	0.0303	0.3500
6	86207344	G	A	601.77	intron variant	MODIFIER	c.90+553G>A			0.3396				0.1500	0.5909	0.5909	0.0909	0.5250
6	86207355	T	C	11.12	intron variant	MODIFIER	c.90+564T>C			0.0047				-	0.0227	-	-	-
6	86207376	T	A	769.77	intron variant	MODIFIER	c.90+585T>A			0.5708				0.6250	0.8864	0.6818	0.1212	0.8500
6	86207426	T	C	232.77	intron variant	MODIFIER	c.90+635T>C			0.0236				0.0500	-	-	-	0.0750
6	86207440	A	C	742.77	intron variant	MODIFIER	c.90+649A>C			0.5189				0.6000	0.8864	0.3636	0.0606	0.8750
6	86207488	A	G	112.77	intron variant	MODIFIER	c.90+697A>G			0.0047				0.0250	-	-	-	-
6	86207502	A	G	401.28	intron variant	MODIFIER	c.90+711A>G			0.1226				0.0750	0.1136	-	0.0152	0.4250
6	86207524	A	C	378.77	intron variant	MODIFIER	c.90+733A>C			0.0283				0.0500	-	-	-	0.1000
6	86207577	G	A	452.77	intron variant	MODIFIER	c.90+786G>A			0.1462				0.1000	0.1818	-	-	0.4750
6	86207588	T	C	165.77	intron variant	MODIFIER	c.90+797T>C			0.0047				-	0.0227	-	-	-
6	86207619	C	T	68.77	intron variant	MODIFIER	c.90+828C>T			0.0047				0.0250	-	-	-	-
6	86207639	A	G	543.77	intron variant	MODIFIER	c.90+848A>G			0.2547				0.1500	0.3864	0.2727	0.0455	0.5500
6	86207698	A	T	164.77	intron variant	MODIFIER	c.90+907A>T			0.0094				-	0.0227	-	-	0.0250
6	86207759	G	A	50.77	intron variant	MODIFIER	c.90+968G>A			0.0047				-	0.0227	-	-	-
6	86207828	C	T	28.77	intron variant	MODIFIER	c.91-1029C>T			0.0047				-	0.0227	-	-	-
6	86207832	A	G	180.77	intron variant	MODIFIER	c.91-1025A>G			0.0047				-	0.0227	-	-	-
6	86207856	C	T	80.77	intron variant	MODIFIER	c.91-1001C>T			0.0047				-	0.0227	-	-	-
6	86207858	G	A	101.77	intron variant	MODIFIER	c.91-999G>A			0.0047				-	0.0227	-	-	-
6	86207875	G	T	339.77	intron variant	MODIFIER	c.91-982G>T			0.0047				-	0.0227	-	-	-
6	86207913	A	C	51.74	intron variant	MODIFIER	c.91-944A>C			0.0094				-	-	-	0.0303	-
6	86207931	G	A	541.77	intron variant	MODIFIER	c.91-926G>A			0.0991				0.3750	-	0.1818	-	0.0500
6	86208015	T	G	826.77	intron variant	MODIFIER	c.91-842T>G			0.1415				0.4500	-	-	0.0152	0.2750
6	86208019	G	A	1112.77	intron variant	MODIFIER	c.91-838G>A			0.7217				1.0000	0.8864	0.8182	0.2727	0.9500
6	86208022	A	G	206.77	intron variant	MODIFIER	c.91-835A>G			0.0047				-	0.0227	-	-	-
6	86208101	A	T	892.77	intron variant	MODIFIER	c.91-756A>T			0.6321				0.6000	0.8864	0.5909	0.3788	0.8250
6	86208220	T	C	41.77	intron variant	MODIFIER	c.91-637T>C			0.0047				-	0.0227	-	-	-
6	86208320	T	G	178.77	intron variant	MODIFIER	c.91-537T>G			0.0236				-	0.0682	-	-	0.0500



6	86208350	G	A	219.77	intron variant	MODIFIER	c.91-507G>A			0.0094				-	0.0227	-	-	0.0250
6	86208373	T	C	1067.77	intron variant	MODIFIER	c.91-484T>C			0.1651				0.4250	0.0682	0.3182	0.0606	0.1000
6	86208414	T	C	504.77	intron variant	MODIFIER	c.91-443T>C			0.0236				0.0500	-	-	-	0.0750
6	86208422	T	C	36.77	intron variant	MODIFIER	c.91-435T>C			0.0047				-	-	-	0.0152	-
6	86208434	C	T	763.77	intron variant	MODIFIER	c.91-423C>T			0.0189				-	-	-	-	0.1000
6	86208501	A	T	267.77	intron variant	MODIFIER	c.91-356A>T			0.0330				-	0.1591	-	-	-
6	86208636	G	T	712.77	intron variant	MODIFIER	c.91-221G>T			0.1226				0.4000	-	0.3182	-	0.0750
6	86208637	A	T	351.77	intron variant	MODIFIER	c.91-220A>T			0.0047				-	-	-	-	0.0250
6	86208685	T	C	275.77	intron variant	MODIFIER	c.91-172T>C			0.0047				-	-	-	-	0.0250
6	86208747	T	G	1103.77	intron variant	MODIFIER	c.91-110T>G			0.4198				0.5500	0.2045	-	0.4242	0.7500
6	86208815	G	A	740.77	intron variant	MODIFIER	c.91-42G>A			0.2358				0.1000	0.2045	-	0.2879	0.4500
6	86208826	C	G	820.77	intron variant	MODIFIER	c.91-31C>G			0.2075				0.0500	0.2045	-	0.2727	0.3750
6	86208883	C	T	360.77	synonymous variant	LOW	c.117C>T	p.Phe39Phe	p.Phe18Phe	0.0189				0.0750	-	-	0.0152	-
6	86208958	T	C	895.77	synonymous variant	LOW	c.192T>C	p.Tyr64Tyr	p.Tyr43Tyr	0.2594				0.1000	0.2045	-	0.3636	0.4500
6	86208960	A	G	646.77	missense variant	MODERATE	c.194A>G	p.Gln65Arg	p.Gln44Arg	0.1745	0.14	2.76	TOLERATED	0.0500	-	-	0.3636	0.2750
6	86208977	C	A	175.77	missense variant	MODERATE	c.211C>A	p.Leu71Ile		0.0047	0.11	2.76	TOLERATED	0.0250	-	-	-	-
6	86208987	A	G	530.77	missense variant	MODERATE	c.221A>G	p.Asn74Ser	p.Asn53Ser	0.0802	0.21	2.82	TOLERATED	-	0.0682	-	0.2121	-
6	86208997	G	A	203.77	synonymous variant	LOW	c.231G>A	p.Leu77Leu	p.Leu56Leu	0.0094				-	0.0227	-	-	0.0250
6	86209022	G	A	697.77	missense variant	MODERATE	c.256G>A	p.Val86Ile	p.Val65Ile	0.2123	0.17	2.77	TOLERATED	0.0500	0.2045	-	0.2879	0.3750
6	86209097	G	A	213.77	missense variant	MODERATE	c.331G>A	p.Asp111Asn	p.Asp90Asn	0.0236	0.36	3.09	TOLERATED	0.0500	-	-	-	0.0750
6	86209184	A	G	807.77	missense variant	MODERATE	c.418A>G	p.Ile140Val	p.Ile119Val	0.2642	0.17	2.75	TOLERATED	0.4750	0.2500	0.0455	0.1970	0.3000
6	86209263	T	C	206.77	missense variant	MODERATE	c.497T>C	p.Val166Ala	p.Val145Ala	0.0236	0.21	2.78	TOLERATED	0.0500	-	-	-	0.0750
6	86209304	T	C	410.77	missense variant	MODERATE	c.538T>C	p.Ser180Pro	p.Ser159Pro	0.2028	1	2.78	TOLERATED	0.0750	0.1364	-	0.2424	0.4500
6	86209404	C	A	62.74	intron variant	MODIFIER	c.*34+25C>A			0.0094				-	-	-	0.0303	-
6	86209492	G	T	517.77	intron variant	MODIFIER	c.*34+113G>T			0.1981				0.0500	0.1818	-	0.2727	0.3500
6	86209519	C	T	759.77	intron variant	MODIFIER	c.*34+140C>T			0.1745				0.0500	0.1136	0.2727	0.3333	0.0500
6	86209526	A	T	40.77	intron variant	MODIFIER	c.*34+147A>T			0.0047				-	-	-	-	0.0250
6	86209547	C	T	561.77	intron variant	MODIFIER	c.*34+168C>T			0.2123				0.0500	0.1818	-	0.3030	0.3750
6	86209594	T	C	194.77	intron variant	MODIFIER	c.*34+215T>C			0.0047				-	0.0227	-	-	-
6	86209600	G	A	554.77	intron variant	MODIFIER	c.*34+221G>A			0.2406				0.0750	0.2045	-	0.3182	0.4500
6	86209676	C	A	673.77	intron variant	MODIFIER	c.*34+297C>A			0.2311				0.1000	0.1818	-	0.2879	0.4500
6	86209704	C	G	289.77	intron variant	MODIFIER	c.*34+325C>G			0.0047				-	-	-	-	0.0250
6	86209768	A	G	697.77	intron variant	MODIFIER	c.*34+389A>G			0.1274				0.3750	-	0.3182	0.0152	0.1000
6	86209797	A	C	76.77	intron variant	MODIFIER	c.*34+418A>C			0.0047				-	0.0227	-	-	-
6	86209968	T	C	202.77	intron variant	MODIFIER	c.*34+589T>C			0.0047				0.0250	-	-	-	-
6	86209997	T	C	1109.77	intron variant	MODIFIER	c.*34+618T>C			0.1274				0.3750	-	0.3182	0.0152	0.1000
6	86210032	G	A	980.77	intron variant	MODIFIER	c.*34+653G>A			0.4198				0.1500	0.3409	0.5909	0.5303	0.5000
6	86210141	G	A	355.77	intron variant	MODIFIER	c.*34+762G>A			0.0708				-	0.1591	-	0.1212	-
6	86210163	A	C	828.77	intron variant	MODIFIER	c.*34+784A>C			0.2453				0.1000	0.2045	-	0.3182	0.4500
6	86210290	G	C	100.77	intron variant	MODIFIER	c.*34+911G>C			0.0047				-	0.0227	-	-	-
6	86210384	T	C	283.77	intron variant	MODIFIER	c.*35-833T>C			0.0613				-	0.2273	-	0.0152	0.0500
6	86210410	A	G	284.77	intron variant	MODIFIER	c.*35-807A>G			0.0094				-	-	0.0909	-	-
6	86210563	T	C	790.77	intron variant	MODIFIER	c.*35-654T>C			0.2264				0.0750	0.1818	-	0.2879	0.4500
6	86210710	C	T	878.77	intron variant	MODIFIER	c.*35-507C>T			0.2170				0.0500	0.2045	-	0.3030	0.3750
6	86210763	A	G	813.77	intron variant	MODIFIER	c.*35-454A>G			0.2311				0.1000	0.1818	-	0.2879	0.4500
6	86210814	A	G	123.78	intron variant	MODIFIER	c.*35-403A>G			0.0047				-	0.0227	-	-	-
6	86210899	G	C	150.77	intron variant	MODIFIER	c.*35-318G>C			0.0236				-	0.1136	-	-	-
6	86210947	C	T	428.77	intron variant	MODIFIER	c.*35-270C>T			0.0236				0.0500	-	-	-	0.0750
6	86210964	C	G	638.41	intron variant	MODIFIER	c.*35-253C>G			0.2264				0.1000	0.2045	-	0.2576	0.4500
6	86211014	G	T	356.77	intron variant	MODIFIER	c.*35-203G>T			0.0377				-	0.1818	-	-	-
6	86211031	G	C	556.77	intron variant	MODIFIER	c.*35-186G>C			0.1698				0.0500	-	-	0.3030	0.3500
6	86211050	T	C	923.77	intron variant	MODIFIER	c.*35-167T>C			0.1321				0.4500	-	-	0.0303	0.2000
6	86211074	A	G	202.77	intron variant	MODIFIER	c.*35-143A>G			0.0047				-	0.0227	-	-	-
6	86211075	T	C	243.77	intron variant	MODIFIER	c.*35-142T>C			0.0330				-	0.1591	-	-	-
6	86211096	A	T	792.77	intron variant	MODIFIER	c.*35-121A>T			0.1887				0.4500	-	-	0.1364	0.3250
6	86211128	T	G	672.77	intron variant	MODIFIER	c.*35-89T>G			0.2075				0.0500	0.1818	-	0.2879	0.3750
6	86211321	C	T	334.78	3 prime UTR variant	MODIFIER	c.*139C>T			0.0377				-	0.1818	-	-	-
6	86211337	T	C	237.77	3 prime UTR variant	MODIFIER	c.*155T>C			0.0330				-	0.1591	-	-	-
6	86197576	TAAAA	TAAA,TAA,TA,T	477.82	intron variant	MODIFIER	c.-6+267 -6+270delAAAA			0.3538				0.575	0.45455	0.63636	0.04546	0.375
6	86198350	ACAAT	A	637.73	intron variant	MODIFIER	c.-6+1041 -6+1044delCAAT			0.2170				0.075	0.29546	0.31818	0.18182	0.275
6	86198648	TA	T	298.73	intron variant	MODIFIER	c.-5-1095delA			0.0330				-	0.02273	0.27273	-	-
6	86198978	CAAG	C	547.73	intron variant	MODIFIER	c.-5-765 -5-763delAAG			0.0330				-	0.02273	0.27273	-	-
6	86199535	A	ATTC	772.73	intron variant	MODIFIER	c.-5-209 -5-208insTTC			0.1179				0.05	0.22727	-	0.06061	0.225
6	86200085	TA	T	265.73	intron variant	MODIFIER	c.57+281delA			0.0142				0.075	-	-	-	-
6	86200532	TCAGATGTTTATTTTC	T	115.73	intron variant	MODIFIER	c.57+728 57+742delCAGATGTTTATTTTC			0.0047				-	-	-	-	0.025
6	86201431	GC	G	337.74	intron variant	MODIFIER	c.57+1627delC			0.0236				0.025	-	0.18182	-	-
6	86203237	TA	T	831.73	intron variant	MODIFIER	c.57+3433delA			0.9387				1	0.95455	1	0.84849	0.975
6	86203503	CTT	C	372.73	intron variant	MODIFIER	c.58-3255 58-3254delTT			0.0377				0.075	-	0.09091	-	0.075
6	86203515	AG	A	109.74	intron variant	MODIFIER	c.58-3243delG			0.0094				-	0.02273	-	0.01515	-
6	86203670	CTATT	C	289.73	intron variant	MODIFIER	c.58-3088 58-3085delTATT			0.0047				-	0.02273	-	-	-
6	86203859	CA	C	762.73	intron variant	MODIFIER	c.58-2899delA			0.2123				0.05	0.20455	-	0.27273	0.4
6	86203928	TCTC	T	136.73	intron variant	MODIFIER	c.58-2830 58-2828delCTC			0.0047				-	-	-	-	0.025
6	86204116	ATT	AT,A	533.73	intron variant	MODIFIER	c.58-2642 58-2641delTT			0.5472				0.525	0.77273	0.63636	0.39394	0.525
6	86204120	T	TAGTTAGCATGTATCTGTCA,TAG,TAGTTAGCATGTATCTG	145.73	intron variant	MODIFIER	c.58-2639 58-2638insAG			0.0849				0.05	0.06818	-	0.06061	0.225
6	86204122	T	TAGCA	145.73	intron variant	MODIFIER	c.58-2637 58-2636insAGCA			0.0519				0.025	0.04546	-	0.0303	0.15



INDEL	6	86204126	A	ATCTGTC	98.25	intron_variant	MODIFIER	c.58-2633_58-2632insTCTGTC			0.0377				0.025	0.04546	-	0.0303	0.075
	6	86204245	CTT	CT,CTTT,C,CTTTT	574.73	intron_variant	MODIFIER	c.58-2513_58-2512delTT			0.2217				0.325	0.20455	0.27273	0.07576	0.35
	6	86204257	T	TC	127.87	intron_variant	MODIFIER	c.58-2502_58-2501insC			0.0330				-	0.15909	-	-	-
	6	86204283	T	TA	461.73	intron_variant	MODIFIER	c.58-2476_58-2475insA			0.1415				0.05	0.18182	0.5	0.0303	0.175
	6	86205991	A	ACT	86.25	intron_variant	MODIFIER	c.58-768_58-767insCT			0.0094				-	0.04546	-	-	-
	6	86206433	T	TTC	412.74	intron_variant	MODIFIER	c.58-326_58-325insTC			0.1651				0.05	0.18182	0.54546	0.12121	0.125
	6	86206436	AAG	A	445.73	intron_variant	MODIFIER	c.58-322_58-321delAG			0.1651				0.05	0.18182	0.54546	0.12121	0.125
	6	86206659	C	CT	618.73	intron_variant	MODIFIER	c.58-100_58-99insT			0.1887				0.05	0.22727	0.59091	0.16667	0.1
	6	86207321	A	ATAT	664.73	intron_variant	MODIFIER	c.90+530_90+531insTAT			0.5660				0.6	0.79546	0.63636	0.21212	0.825
	6	86207322	TA	T	38.7	intron_variant	MODIFIER	c.90+532delA			0.0189				-	-	-	0.06061	-
	6	86207364	A	AATATT	682.73	intron_variant	MODIFIER	c.90+573_90+574insATATT			0.2736				0.15	0.40909	0.59091	-	0.525
	6	86207410	AAT	A	220.73	intron_variant	MODIFIER	c.90+620_90+621delAT			0.0236				0.05	-	-	-	0.075
	6	86207495	GATATATATC	G	592.73	intron_variant	MODIFIER	c.90+705_90+713delATATATATC			0.1981				0.45	0.36364	-	-	0.2
	6	86207560	TA	T	49.73	intron_variant	MODIFIER	c.90+770delA			0.0047				-	-	-	-	0.025
	6	86207657	T	TTATATAATTA	288.73	intron_variant	MODIFIER	c.90+866_90+867insTATATAATTA			0.0047				-	0.02273	-	-	-
	6	86207982	ATATAT	A	435.73	intron_variant	MODIFIER	c.91-874_91-870delTATAT			0.0047				0.025	-	-	-	-
	6	86207983	TATA	T	316.73	intron_variant	MODIFIER	c.91-873_91-871delATA			0.0236				0.05	-	-	-	0.075
	6	86208138	C	CATATA	682.73	intron_variant	MODIFIER	c.91-719_91-718insATATA			0.2642				0.475	0.40909	0.09091	0.10606	0.25
	6	86208142	T	TAATAC	736.73	intron_variant	MODIFIER	c.91-715_91-714insAATAC			0.1792				0.1	0.22727	-	0.09091	0.45
	6	86208262	G	GA	137.73	intron_variant	MODIFIER	c.91-595_91-594insA			0.0094				-	0.04546	-	-	-
	6	86208410	CAT	CATAT,CCTAT,CCTATAT,C	530.19	intron_variant	MODIFIER	c.91-447_91-446insCT			0.1934				0.075	0.13636	0.09091	0.25758	0.325
	6	86208422	T	TATATAC,TATATATATAC,TATAC	692.73	intron_variant	MODIFIER	c.91-435_91-434insATAC			0.1462				0.025	0.20455	-	0.12121	0.325
	6	86208428	T	TAC	199.73	intron_variant	MODIFIER	c.91-429_91-428insAC			0.0047				-	-	-	-	0.025
	6	86208432	TAC	TACAC,T	646.73	intron_variant	MODIFIER	c.91-424_91-423delAC			0.1887				0.375	0.11364	0.13636	0.15152	0.175
	6	86208470	T	TAC	849.73	intron_variant	MODIFIER	c.91-387_91-386insAC			0.1981				0.075	0.18182	-	0.19697	0.45
	6	86208472	GT	G	101.73	intron_variant	MODIFIER	c.91-384delT			0.0047				-	0.02273	-	-	-
	6	86208627	AT	A	359.73	intron_variant	MODIFIER	c.91-229delT			0.1792				0.05	0.15909	0.54546	0.22727	0.05
	6	86208635	TG	T	342.73	intron_variant	MODIFIER	c.91-221delG			0.0047				-	-	-	-	0.025
	6	86208674	TGGAA	T	193.73	intron_variant	MODIFIER	c.91-182_91-179delGGAA			0.0047				-	0.02273	-	-	-
	6	86209704	CATG	C	817.73	intron_variant	MODIFIER	c.*34+326_*34+328delATG			0.1934				0.05	0.15909	0.54546	0.27273	0.05
	6	86210002	AAT	A	637.73	intron_variant	MODIFIER	c.*34+624_*34+625delAT			0.2075				0.05	0.18182	-	0.28788	0.375
	6	86210754	A	AATAGGACATCTGGTAAG	902.73	intron_variant	MODIFIER	c.*35-463_*35-462insATAGGACATCTGGTAAG			0.2311				0.1	0.18182	-	0.28788	0.45