

Scotland's Rural College

## **Variants in the 3'UTR of the ovine Acetyl-Coenzyme A Acyltransferase 2 gene are associated with dairy traits and exhibit differential allelic expression**

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1 **Interpretive summary**

2 **Variants in the 3'UTR of the ovine Acetyl-Coenzyme A Acyltransferase 2 gene**

3 **are associated with dairy traits and exhibit differential allelic expression.** *By*

4 *Miltiadou et al.* The present study shows that the ovine *ACAA2* gene is associated

5 with milk production, milk protein percentage and milk fat yield. Additionally, we

6 demonstrated that the mRNA expression in homozygous animals for each allele of the

7 *ACAA2* gene differs by several orders of magnitude in hepatic and mammary gland

8 tissues and the *ACAA2* variants are expressed at different levels in the udder of

9 heterozygous animals, suggesting the existence of regulatory variation within the

10 ovine *ACAA2* gene. These findings support the hypothesis that the *ACAA2* gene is a

11 functional candidate affecting dairy traits in sheep.

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28 **Variants in the 3'UTR of the ovine Acetyl-Coenzyme A Acyltransferase 2 gene**  
29 **are associated with dairy traits and exhibit differential allelic expression.**

30

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**ABSTRACT**

53 The Acetyl-CoA acyltransferase 2 (*ACAA2*) gene encodes an enzyme of the thiolase  
54 family that is involved in mitochondrial fatty acid elongation and degradation by  
55 catalyzing the last step of the respective  $\beta$ -oxidation pathway. The increased energy  
56 needs for gluconeogenesis and triglyceride synthesis during lactation are met  
57 primarily by increased fatty acid oxidation. Therefore, the *ACAA2* enzyme plays an  
58 important role in the supply of energy and carbon substrates for lactation and may  
59 thus affect milk production traits. This study investigates the association of the  
60 *ACAA2* gene with important sheep traits and the putative functional involvement of  
61 this gene in dairy traits. A single nucleotide substitution (SNP), a T to C transition  
62 located in the 3' untranslated region (UTR) of the *ACAA2* gene, was used in mixed  
63 model association analysis with milk yield, milk protein yield and percentage, milk fat  
64 yield and percentage, and litter size at birth. The SNP was significantly associated  
65 with total lactation production and milk protein percentage, with respective additive  
66 effects of  $6.81 \pm 2.95$  kg and  $-0.05 \pm 0.02$  %. Additionally, a significant dominance  
67 effect of  $0.46 \pm 0.21$  was detected for milk fat yield. Homozygous TT and  
68 heterozygous CT animals exhibited higher milk yield compared to homozygous CC  
69 animals, while the latter exhibited increased milk protein percentage. Expression  
70 analysis from age, lactation and parity matched female sheep showed that mRNA  
71 expression of the *ACAA2* gene from TT animals was 2.8 and 11.8 fold higher in liver  
72 and mammary gland, respectively. In addition, by developing an allelic expression  
73 imbalance (AEI) assay, it was estimated that the T allele was expressed at an average  
74 of 18% more compared to the C allele in the udder of randomly selected ewes. We  
75 demonstrated for the first time that the variants in the 3'UTR of the ovine *ACAA2*  
76 gene are differentially expressed in homozygous ewes of each allele and exhibit AEI

## CIS-REGULATORY DNA VARIATION IN THE OVINE ACAA2 GENE

77 within heterozygotes in a tissue specific manner, supporting the existence of cis-  
78 regulatory DNA variation in the ovine *ACAA2* gene. This is the first study reporting  
79 differential allelic imbalance expression of a candidate gene associated with milk  
80 production traits in dairy sheep.

81

82 Key words (up to 4): *ACAA2* association, 3' *UTR* Cis-acting SNP, gene expression,

83 dairy sheep

# THE OVINE ACAA2 GENE IS AFFECTED BY CIS-REGULATORY DNA VARIATION

84

## INTRODUCTION

85 Milk yield represents more than two thirds of the total income of the dairy sheep  
86 industry (Carta et al., 2009) and therefore the improvement of milk production is the  
87 most important breeding objective. In Mediterranean countries, however, most of the  
88 ovine milk produced is used for the production of cheese commercialized as products  
89 of protected designation of origin (PDO) and other quality labels (Arranz and  
90 Gutierrez-Gil, 2012). Thus, farmers' income is additionally determined by total solids  
91 that affect cheese yield (De Rancourt et al., 2006) and, therefore, increased milk fat  
92 and protein content is also highly desirable from an economic perspective (Ramon *et*  
93 *al.*, 2010). Although traditional breeding programs have achieved appreciable genetic  
94 gains mainly for milk yield, application of selection schemes assisted by molecular  
95 information could expedite improvement (Carta et al., 2009). Moreover, marker  
96 assisted selection could be of special interest for dairy sheep, due to the great regional  
97 diversity of breeds, funding limitations, organizational difficulties (Arranz and  
98 Gutierrez-Gil, 2012) and small population sizes (Garcia-Gamez et al., 2012).

99 To date, there are few reports of genome-wide association studies (GWAS) and  
100 genome scans based on linkage mapping that detect quantitative trait loci (QTL) and  
101 quantitative trait mutations (QTM) for ovine dairy traits (reviewed by Arranz and  
102 Gutierrez-Gil, 2012; Garcia-Gamez et al., 2012; 2013; Gutierrez-Gil et al., 2014). In a  
103 whole genome QTL study performed in Churra ewes, Gutierrez-Gil et al. (2009)  
104 detected suggestive QTL for milk, fat and protein yields, mapped in a region of the  
105 ovine chromosome 23 (OAR23) harbouring the Acetyl-CoA acyltransferase 2  
106 (ACAA2) gene. The ACAA2 gene encodes an enzyme of the thiolase family, also  
107 known as 3-oxoacyl-CoA thiolase or mitochondrial 3-ketoacyl-CoA thiolase. The  
108 ACAA2 enzyme catalyzes the last step in mitochondrial fatty acid  $\beta$ -oxidation, thus

109 playing a central role in the supply of energy for the animal (Bartlett and Eaton,  
110 2004). Therefore, due to the chromosomal location of the ovine *ACAA2* gene in  
111 relation to the QTL described by Gutierrez-Gil et al., (2009) and its functional role in  
112 lipid metabolism, it was regarded as a putative functional and positional candidate  
113 gene that may affect milk yield and composition.

114 Genes encoding enzymes of the thiolase family have been correlated with  
115 production traits in other livestock species. Single nucleotide polymorphisms (SNPs)  
116 detected in the porcine *ACAA2* gene are reported to be associated with daily weight  
117 gain and loin muscle area (Li HD, 2008). An important paralog of the *ACAA2* gene,  
118 the acetyl-CoA acetyltransferase 2 (*ACAT2*) gene has been associated with production  
119 and fertility traits (milk protein content, productive life and conception and pregnancy  
120 rates) in Holstein cattle (Cochran et al., 2013), while SNPs within the swine *ACAT2*  
121 gene were suggested to influence the metabolic functions of the corresponding  
122 enzyme and thus may affect growth performance (Sodhi et al., 2014).

123 Our previous study showed that the entire mRNA (coding and untranslated  
124 regions) of the ovine *ACAA2* gene is monomorphic in Chios sheep, one of the most  
125 productive and extensively used breeds in Greece and Cyprus (Chatziplis et al., 2012),  
126 with the exception of a SNP (HM537015:g.2982T>C) located in the 3' untranslated  
127 region (*UTR*) of the gene (Orford et al, 2012). The SNP was significantly associated  
128 with milk yield, at first lactation and across first to third lactations in Chios sheep.  
129 Animals from a closed nucleus research flock at the Agricultural Research Institute of  
130 Cyprus, carrying the g.2982TT or g.2982CT genotype had significantly higher milk  
131 yield than those with the g.2982CC genotype and the g.2982T>C SNP explained 10%  
132 of the additive genetic variance for milk yield when data up to third lactation from a  
133 single flock were analysed (Orford et al., 2012).

134 It is well established that *UTRs* contain motifs involved in posttranscriptional  
135 regulation of gene expression (Xie et al., 2005) that may lead to differential  
136 expression of alleles associated with phenotypic diversity of production traits (Clop et  
137 al., 2006; Khatib et al., 2007; Sugimoto et al., 2015). Studies in humans (Yan et al.,  
138 2002, Bray et al., 2003), mice (Cowles et al., 2002), cattle (Khatib et al., 2007,  
139 Olbromski et al., 2013) and pig (Muráni et al., 2009) have shown that alleles of non-  
140 imprinted genes are not expressed equally at the mRNA level in heterozygous  
141 animals, a phenomenon called allelic expression imbalance (AEI). AEI is the outcome  
142 of the presence of at least one cis regulatory element in the regulatory sequences of a  
143 gene (Campbell et al., 2008) and is therefore one of the possible mechanisms  
144 underlying the effect of causative genetic variations that are not located on the  
145 translated region of a gene.

146 The objective of the current study was to provide novel insights into the  
147 association of the ovine *ACAA2* gene with important sheep traits. Firstly, we  
148 performed an association analysis of the previously identified g.2982T>C SNP with  
149 milk yield, fat and protein contents, fat and protein yields and litter size, in a  
150 population of Chios sheep from all available farms keeping production records in  
151 Cyprus. Upon confirmation of the association of the SNP with total milk production  
152 and additional detection of association with milk protein percentage, we tested the  
153 hypothesis that the *ACAA2* is a putative functional gene affecting dairy traits, by  
154 comparing the expression of the gene in different genotypes and by developing an  
155 assay to test the presence of AEI.

156

157

## MATERIALS AND METHODS

158 *Animals and phenotypic data*



159 Data were collected from 742 purebred Chios ewes from five farms. Those were  
160 one governmental farm (Orites, Cyprus) and the only 4 commercial farms in Cyprus  
161 keeping phenotypic records of purebred Chios sheep according to the regulations of  
162 the International Committee for Animal Recording (ICAR).

163 For all animals, individual records included month of lambing, year of lambing,  
164 lactation number and age of lambing. Phenotypic data were obtained for lambing  
165 years between 2009 and 2016 and included 1,514 individual records of 742 milking  
166 ewes; this data included total lactation milk yield, 1,242 observations for litter size at  
167 birth, 1,203 measurements of milk fat content and yield and 615 measurements of  
168 milk protein content and yield, respectively. Total lactation yield was calculated for  
169 each animal with the Fleischmann method with monthly tests on actual yields (sum of  
170 *am* and *pm* records, ICAR 2014). Milk samples were obtained for fat and protein  
171 analysis by combined thermo-optical procedures (LactoStar 3510, Funke Gerber,  
172 Berlin, Germany), previously calibrated for protein with the Lowry protein assay and  
173 for fat with the method 989.05 (AOAC International, 2005).

174

#### 175 ***DNA extraction and SNP genotyping***

176 Whole blood samples were obtained from all 742 ewes for DNA extraction and  
177 genotyping of the g.2982T>C SNP of the ACAA2 gene. Genomic DNA was isolated  
178 from all samples using the Genomic DNA Blood kit (Macherey-Nagel), according to  
179 the manufacturer's instructions, and DNA quality and quantity were estimated by UV  
180 absorption at 260 and 280nm. Genotyping of the Chios ewes was performed by a cost  
181 effective direct DNA sequencing protocol (Miltiadou et al., 2017), with primers  
182 amplifying the 10<sup>th</sup> exon of the gene, using conditions previously described (Orford et  
183 al., 2012).

184

185 ***Mixed model association analysis***

186 Each trait was analyzed separately with the following mixed linear model:

187 
$$Y_{jklmn} = \mu + F_i + YS_j + L_k + b_1age + b_2dur + G_l + A_m + e_{ijklmn} \quad (1)$$

188 where:

189 Y = lactation milk yield, fat yield/percentage, protein yield/percentage or litter size

190 record  $n$  of animal  $m$

191  $\mu$  = overall population mean for the trait

192 F = fixed effect of flock  $i$  (1-5)

193 YS = fixed effect of year (2009-2016) by season (1-2) of lambing interaction  $j$

194 L = fixed effect of number of lactation  $k$  (1-4)

195  $b_1$  = linear regression on age at lambing (age)

196  $b_2$  = linear regression on lactation duration (dur); yield traits only

197 G = fixed effect of genotype  $l$  in the g.2982T>C locus (1-3; CC, CT, TT)

198 A = random effect of animal  $m$

199 e = random residual effect

200

201 All lactation records were analyzed for all traits. In a separate analysis, only first

202 lactation records were considered for milk yield. In the latter case, the fixed effect of

203 number of lactation and the random animal effect were removed from the model.

204 In all cases, predicted trait values for each SNP genotype and respective standard

205 errors were derived; these values were reflective of the marginal genotypic effect on

206 each trait adjusted for all other effects fitted in the model. The predicted trait values

207 were used to estimate additive and dominance SNP effects on traits, and the

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208 proportion of phenotypic variance for each trait accounted for by the SNP locus. The  
209 equations used were:

210 Additive effect,  $a = (TT - CC) / 2$ ;

211 Dominance effect,  $d = CT - [(TT + CC) / 2]$ ,

212 Percentage of phenotypic variance ( $V_P$ ) due to SNP =  $100 * [2pq(a + d(q-p))^2] / V_P$ ,

213 where TT, CC, CT are the predicted trait values for each genotype class and p, q

214 are the allele frequencies at the SNP locus. Variance components were estimated with

215 model (1) after excluding the genotype effect. All statistical analyses were conducted

216 with the ASReml3 software (Gilmour et al., 2009).

217 Since multiple traits were analyzed, we assessed the number of independent tests in

218 order to adjust for multiple testing. For this reason, we conducted multivariate

219 analyses based on model (1) after excluding the genotype effect to assess the

220 correlation among traits. Very high correlations were found among the three

221 production traits (milk, fat, protein yield; 0.89-0.99), and between the two milk

222 concentration traits (fat and protein percentage; 0.75). Correlations between the two

223 groups of traits were near zero. Correlations of these two groups with litter size

224 ranged from 0.05 to 0.19. Consequently, we regarded three separate trait groups

225 (production, concentration and litter size) that corresponded to three distinct,

226 independent hypothesis tests. This was confirmed with a Principal Component

227 Analysis of the studied traits (Supplementary Figure 1). Subsequently, a Bonferroni

228 adjustment for multiple tests was implemented based on the Holm-Bonferroni method

229 (Holm 1979). This method works sequentially testing first the lowest nominal P-value

230 against the threshold value of  $0.05/n$ , where n is the number of independent

231 hypotheses tests (three in the present study). If this hypothesis is rejected, the next

232 lowest nominal P-value is compared to  $0.05/(n-1)$  and so on, until a hypothesis is not

233 rejected (Holm, 1979). Supplementary Table 1 includes the corresponding P-value  
234 thresholds in the case of three independent tests.

235

### 236 *Animals and tissue sampling for expression analysis*

237 Blood samples were collected from 161 first parity ewes from the biggest  
238 commercial farm in Cyprus, allowing the selection of age, parity and lactation stage  
239 matched animals. Based on the methodology described in our previous work (Orford  
240 et al., 2012), we identified animals with the genotypes g.2982TT, g.2982CT and  
241 g.2982CC, and chose 3 ewes from each genotype for subsequent biopsies and RNA  
242 extraction. All 9 selected ewes were first parity, 15-month old and had given birth to  
243 two lambs each.

244 Mammary and liver biopsies were obtained under anaesthesia, by a professional  
245 veterinarian,  $42 \pm 2$  days after lambing, a week after weaning. Liver parenchyma was  
246 sampled via puncture biopsy using ultrasonography for the selection of the  
247 appropriate biopsy site and for avoiding large vessels and other organs. Udder  
248 biopsies were taken from either the left or the right rear gland. The biopsy site was  
249 carefully selected to avoid large subcutaneous blood vessels. Preparation of the site  
250 involved shaving and washing with dilute betadine solution followed by sanitizing  
251 with ethanol (70%). Ewes were given intravenous xylazine before anesthetizing the  
252 biopsy site by subcutaneous injection of lidocaine hydrochloride. An incision was  
253 made (~0.5-1.0 cm) on the outside of the quarter using a scalpel blade (size 22). A  
254 Bard<sup>®</sup> Magnum<sup>®</sup> core biopsy instrument (Bard Peripheral Vascular, Inc., Tempe, AZ)  
255 with a Bard<sup>®</sup> Magnum<sup>®</sup> core tissue biopsy needle (MN1210, 12G × 10 cm) was used.

256 In addition, liver and udder *ex vivo* tissue samples were obtained from 16 randomly  
257 selected Chios ewes from an abattoir straight after slaughtering, under sterile

258 conditions. Although tissue samples obtained from the abattoir were at different and  
259 unknown parities and stages of lactation, they were taken to increase the number of  
260 heterozygous samples for allelic expression imbalance analysis, without increasing  
261 the veterinary costs required for biopsies.

262 All samples were snap frozen in liquid N<sub>2</sub> immediately after the tissue was  
263 obtained under sterile conditions and stored at -80°C until RNA extraction.

264 Animal sampling and handling and all procedures in this study were carried out in  
265 strict accordance with the national legislation for animal welfare 46I/94 and no  
266 animals were sacrificed for the purposes of this study.

267

268 ***DNA, total RNA extraction and reverse transcription***

269 Frozen tissue biopsies and ex vivo samples were homogenized using a mortar and  
270 pestle constantly covered under liquid N<sub>2</sub> and aliquoted in tubes containing ~20 mg  
271 each. DNA was extracted using the Genomic DNA Nucleospin Tissue kit (Macherey-  
272 Nagel, Germany), while ~20 mg of frozen homogenized tissue was subjected to RNA  
273 extraction using the RNA isolation Nucleospin RNA kit (Macherey-Nagel, Germany),  
274 according to manufacturer's instructions. Before reverse transcription, extracted RNA  
275 was incubated with 2U/μl rDNAase (Macherey-Nagel, Germany) for 10 min at 37°C  
276 to eliminate putative contaminating genomic DNA and then purified using the RNA  
277 clean up Nucleospin RNA Clean up XS kit (Macherey-Nagel, Germany). The  
278 concentration and quality of DNA and RNA for all samples was measured using a  
279 Nanodrop 1000 UV/VIS spectrophotometer (Thermoscientific Nanodrop  
280 Technologies LLC, USA). The RNA integrity was assessed by electrophoretic  
281 analysis of the 28S and 18S rRNA subunits.

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282 Complementary DNA (cDNA) was synthesized from 0.5 µg RNA, using the High  
283 Capacity cDNA Reverse Transcription Kit (Applied Biosystems, USA), using random  
284 hexamer primers following the manufacturer's recommendations in a final volume of  
285 20 µl. The lack of genomic DNA contamination was verified by a PCR amplification  
286 using primers amplifying intron 2 of the prolactin gene (*PRL*), as described by Orford  
287 et al. (2010) and by including a control without reverse transcriptase during cDNA  
288 synthesis of each sample. These controls were used for conventional PCR  
289 amplification of the *ACAA2* exon 10, as we have previously described (Orford et al.,  
290 2012) and for subsequent real time PCR (RT-PCR) and verified lack of genomic  
291 contamination.

292

### 293 *ACAA2 mRNA expression*

294 *ACAA2* relative expression in liver and udder was assessed by quantitative Reverse  
295 Transcriptase PCR (qRT-PCR). *ACAA2* qRT-PCR was performed with the primers  
296 used for genotyping as described above and expression levels were normalized by the  
297 expression of reference genes, ovine β-actin (*ACTB*) for liver samples and ovine β2  
298 microglobulin (*ovB2M*) for udder samples, utilizing primers: ovACTB Forward  
299 (GCAAAGACCTCTACGCCAAC) and ovACTB Reverse  
300 (TGATCTTGATCTTCATCGTGCT) (Sari et al., 2009) and for ovB2M Forward  
301 (CTGTGCTGTCTGGACTGG) and ovB2M Reverse  
302 TTTCCATCTTCTGGCGGGTG (designed using the NCBI/Primer-BLAST tool). For  
303 each gene and cDNA sample qRT-PCR reactions were performed in triplicates.  
304 Reactions of no template negative control and 5 point 1:5 serial dilutions of reference  
305 cDNA, to obtain the reaction standard curves and calculate amplification efficiencies,  
306 were also performed in triplicates. Reactions for *ACAA2* expression were performed

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307 in a final volume of 20 $\mu$ l containing 1 $\times$  KAPA SYBR fast qPCR Master Mix (Kapa  
308 Biosystems), 100 nM of each of *ACAA2\_SNP* Forward and Reverse primers, 1 $\times$ ROX  
309 low and cDNA. Reactions for *ACTB* and *B2M* were performed in a final volume of  
310 10 $\mu$ l containing 1 $\times$  KAPA SYBR fast qPCR Master Mix (Kapa Biosystems), 200nM  
311 of each of the ovACTB or ovB2M Forward and Reverse primers, 1 $\times$ ROX low and  
312 cDNA. Cycling conditions included a 3 min initial denaturation step at 95 $^{\circ}$ C followed  
313 by 40 cycles of: (i) denaturation for 3 sec at 95 $^{\circ}$ C and primer annealing and template  
314 extension for 30 sec at 60 $^{\circ}$ C, for *ACAA2* (ii) denaturation for 3 sec at 95 $^{\circ}$ C, primer  
315 annealing at 62 $^{\circ}$ C for 20 sec and template extension at 72 $^{\circ}$ C for 30 sec, for *ACTB* and  
316 (iii) denaturation for 3 sec at 95 $^{\circ}$ C, primer annealing at 64 $^{\circ}$ C for 15 sec and template  
317 extension at 72 $^{\circ}$ C for 30 sec, for *B2M*. For all three genes, a melting curve analysis  
318 was performed following the amplification cycles consisting of 15 s at 95 $^{\circ}$ C, 30 s at  
319 the respective annealing temperature for each gene and continuous heating and data  
320 collection up to 95 $^{\circ}$ C at a rate of 1% temperature increase per 30 seconds, to evaluate  
321 specificity of the amplification. Reactions were optimized for amplification efficiency  
322 to be between 85-95% and linear standard curve fit ( $r^2$ ) to be greater than 0.990 for all  
323 genes. Raw data were analyzed with the 7500 software v2.3 (Applied Biosystems,  
324 USA), and mean Ct values and PCR reaction efficiencies were exported. The  
325 normalized expression (nQ) of *ACAA2* was calculated according to the delta-Ct  
326 method (Livak and Schmittgen, 2001), i.e.  $nQ = E_{ACAA2}^{(\min_{ACAA2\_Ct} -$   
327  $\text{sample}_{ACAA2\_Ct})} / E_{ref}^{(\min_{ref\_Ct} - \text{sample}_{ref\_Ct})}$ , where E is the PCR efficiency for a given  
328 gene (values are greater than 1 and 2 corresponds to ideal doubling of templates per  
329 cycle, 100% = 2) estimated based on standard cDNA dilution series reactions,  
330  $\min_{gene\_Ct}$  is the minimum Ct value among all samples for a given gene and  
331  $\text{sample}_{gene\_Ct}$  is the Ct value for a given gene and sample. To express *ACAA2* nQ as

332 fold change relative to nQ in CC genotype (nrQ) nQ for each sample was divided by  
 333 mean nQ in CC samples. Data were then analyzed using the mixed models procedure  
 334 of SAS software (SAS, 2005) with genotype as the fixed effect. Mean comparisons  
 335 were performed with Tukey's adjustment with significance level set at 0.05.

336

337 ***Allelic Expression Imbalance (AEI) analysis***

338 Sequencing of the *ACAA2* gene from genomic DNA and cDNA of each sample  
 339 was initially used as a semi-quantitative approach to detect differential expression of  
 340 the *ACAA2* alleles. RT-PCR products amplified from heterozygous individuals were  
 341 sequenced and data were analyzed using Applied Biosystems' Sequencing Analysis  
 342 (Applied Biosystems, USA). The SNP was identified by visually inspecting each base  
 343 in sequencing traces. Allelic variation was estimated by comparing the proportions of  
 344 the peak heights of the two alternative alleles of the SNP.

345 Subsequently, the detection of AEI was based on quantitative analysis of mRNA  
 346 transcripts using a TaqMan probe qRT-PCR assay (Livak, 1999, Chen et al., 2008) in  
 347 order to detect deviations from the null hypothesis expecting equimolar ratio between  
 348 the two alleles in heterozygous samples. TaqMan qPCR reactions were performed in  
 349 10  $\mu$ l reaction volumes containing 1 $\times$  Type-it® Fast SNP Probe PCR Master Mix  
 350 (Qiagen, USA), 400 nM of each PCR primer and 200 nM of each TaqMan probes  
 351 (primer and probe sequences as described in the *DNA extraction and SNP genotyping*  
 352 section), and liver or udder cDNA or gDNA from *ACAA2* heterozygous ewes. A 7500  
 353 Real Time PCR system (Applied Biosystems, USA) was used with a cycling profile  
 354 that included a 5 min denaturation step at 95°C and 40 cycles of 15 sec at 95°C and  
 355 30 sec at 62°C.



## CIS-REGULATORY DNA VARIATION IN THE OVINE ACAA2 GENE

356 Pooled genomic (g) DNA from three *ACAA2* heterozygous animals (genotype  
357 confirmed by several replications of genotyping reactions) was used as standard  
358 gDNA and 5 points of 1:4 serial dilutions were used to construct the standard curve  
359 for relative *ACAA2* T and C allele quantification (Fig. 1A-C). The T:C allele copy  
360 ratio is expected to equal 1 in all dilutions.

361 The quantitation relative to standard curve method was employed, using the  
362 homonymous option of the ABI 7500v2.3 software to extract the value for  
363 “normalized quantity” of T allele at each qPCR reaction, having set the C allele as the  
364 “endogenous control”. The “normalized quantity” of the T allele was computed as the  
365 quantity of T allele divided by the quantity of C allele and thus corresponds to the  
366 ratio of T:C *ACAA2* allele quantity. T and C allele quantities in each qPCR reaction  
367 were computed from the respective Ct values and the linear prediction function for  
368 each of the *ACAA2* alleles, computed by the software based on standard gDNA  
369 dilution series. The quantity of T and C alleles in the standard gDNA was set at the  
370 same arbitrary value and thus T:C ratio equalled 1 at all points of the dilution series of  
371 the standard gDNA. The T:C ratio for each sample, i.e. the mean normalized quantity  
372 of the three replicates performed with each cDNA or gDNA, was divided by the  
373 average normalized quantity of the T allele in all the gDNA samples to obtain the  
374 corrected T:C ratio for each cDNA sample. Average corrected T:C ratio in the gDNA  
375 samples equalled 1 and ranged between 0.90-1.09. Standard gDNA dilution series  
376 reactions were performed in each qPCR run. In all runs, efficiency values for both T  
377 and C allele amplification were very similar (102.01% for T and 101.23% for C in run  
378 1 and 102.66% for T and 102.74% for C in run 2). Linear standard curve  $r^2$  values  
379 were 0.997 for T, 0.996 for C in run 1 and 0.998 for T and 0.998 for C in run 2.

380 Statistical analysis of the T:C ratios in cDNA or gDNA was performed using the  
381 mixed models procedure of SAS software (SAS, 2005) with tissue (liver or udder) as  
382 the fixed effect. Means are presented as ordinary means and se. Least square mean  
383 pairwise comparisons were performed with Tukey's adjustment with significance  
384 level set at 0.05.

385

386

## RESULTS

### 387 *Association of the ACAA2 gene with sheep traits*

388 Allelic frequencies in the g.2982C/T SNP locus were 0.54 for the T allele and 0.46  
389 for the C allele; genotypic frequencies were 0.27, 0.54 and 0.19 for TT, CT and CC,  
390 respectively. Genotypic frequencies were found to deviate from the Hardy-Weinberg  
391 equilibrium ( $p = 0.019$ ).

392 Marginal predicted means for the three genotype classes for all production traits  
393 are presented in Table 1. After applying Holm-Bonferroni correction, the SNP was  
394 significantly associated with milk yield at first lactation ( $P < 0.01$ ) and all lactations  
395 ( $P < 0.025$ ), with respective additive effects of  $10.61 \pm 3.56$  kg and  $6.81 \pm 2.95$  and  
396 respective positive dominance effects of  $13.02 \pm 4.26$  kg and  $8.67 \pm 3.53$  (Table 2).  
397 Significant differences were found between the CC and CT genotype pairs ( $P < 0.01$ )  
398 and between the CC and TT classes ( $P < 0.025$ ) at the g.2982T>C SNP locus for milk  
399 yield (Table 1). These results overall suggest a complete dominance effect at the  
400 locus, since heterozygous CT animals exhibit similar predicted mean values compared  
401 to homozygous TT animals. Based on the estimated allelic effects and the allele  
402 frequencies observed in the sample, it was estimated that the g.2982T>C SNP  
403 explained 2.25% and 0.62% of the total phenotypic variance for 1<sup>st</sup> lactation and for  
404 all lactations, respectively (Table 2). Overall, these results suggest a stronger

405 association in first lactation milk yield, whereas the effect was reduced in subsequent  
406 lactations.

407 After applying Holm-Bonferroni correction, the SNP was also associated with  
408 protein percentage ( $P < 0.01$ ), with a significant additive effect of  $-0.05 \pm 0.02$  (Table  
409 1). Pairwise contrasts between the predicted protein percentage values showed  
410 significant differences between the genotype classes CC and CT ( $P < 0.001$ ) and  
411 between CC and TT ( $P < 0.025$ ), with CC animals exhibiting higher protein  
412 percentage, whereas differences between CT and TT were not significant (Table 1). It  
413 was estimated that the SNP explained 1.68% of the phenotypic variance for protein  
414 percentage (Table 1). Additionally, there was a dominance effect of  $0.46 \pm 0.21$  ( $p =$   
415  $0.027$ ) and  $0.41 \pm 0.21$  ( $p = 0.048$ ) of the SNP on fat and protein yields, respectively.  
416 Homozygous TT and heterozygous CT animals exhibited significantly higher milk fat  
417 yield compared to homozygous CC ewes ( $P < 0.025$  and  $P < 0.001$ , respectively). No  
418 significant associations of the SNP genotype with fat percentage, protein yield or litter  
419 size at birth were found.

420

#### 421 *mRNA expression analysis*

422 The expression of *ACAA2* was found to be significantly increased in TT compared  
423 to CC udder and liver biopsies from age matched, at the same lactation stage and  
424 parity ewes that gave birth to two lambs each. In particular, homozygous TT animals  
425 showed a 2.8 fold increase in mRNA expression levels compared to homozygous CC  
426 animals in liver ( $P < 0.05$ ), while TT ewes exhibited an 11.8 fold increase in mRNA  
427 of the *ACAA2* gene in the udder compared to CC ewes ( $P < 0.05$ ) (Fig. 2A). *ACAA2*  
428 mRNA expression of heterozygous animals showed a tendency for reduction  
429 compared to homozygous TT animals only in liver ( $p = 0.07$ ), while it did not

430 significantly differ from homozygous CC animals. Heterozygous mRNA expression  
431 in the udder exhibited a very high standard deviation (Fig. 2A) and did not differ  
432 significantly from homozygote expression.

433 The expression of *ACAA2* was also assessed in liver and udder *ex vivo* samples  
434 from 1 CC, 10 CT and 5 TT ewes (Fig. 2B). These ewes were selected at random and  
435 were not age matched nor at the same milking season or lactation stage. Expression of  
436 *ACAA2* was found to be significantly increased in the liver compared to the udder ( $P$   
437  $< 0.0001$ ), but no significant differences were observed between CT and TT ewes in  
438 either the liver or the udder ( $P > 0.05$ ). Since only one ewe from the slaughterhouse  
439 was genotyped as CC, it was not possible to make comparisons between  
440 homozygotes.

441

#### 442 *Allelic expression imbalance analysis (AEI)*

443 To test whether the differences observed between homozygous TT and CC  
444 animals, was due to AEI between the T and C alleles, the transcription of T and C  
445 alleles was quantified in liver and udder of heterozygous individuals. Sequencing of  
446 genomic DNA and cDNA from 12 heterozygous samples (3 from biopsies and 9 from  
447 slaughterhouse) was initially performed to evaluate semi-quantitatively whether there  
448 was allelic expression imbalance. The allele specific expression levels were evaluated  
449 by comparing the peak heights of C and T in cDNA samples from heterozygous  
450 individuals compared to the peak heights of the respective genomic DNA. Although  
451 in all genomic DNA samples from heterozygotes, peak heights of both nucleotides at  
452 the SNP position were tangential, suggesting no preferential amplification, peak  
453 heights from heterozygous cDNA samples were different, with the T allele exhibiting  
454 a higher peak compared to the C allele (Fig. 3).

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455 To further confirm the initial results from the semi-quantitative method consistent  
456 with AEI in *ACAA2* gene, we developed an AEI assay using TaqMan probes to  
457 estimate the T:C transcription ratio in cDNA samples corrected by the mean T:C ratio  
458 in gDNA samples and ultimately test for deviations from the expected ratio of 1 in the  
459 absence of AEI. Results of the assay for the control gDNA reactions showed that  
460 observed T:C ratios were, as expected, very close to 1 (average non-corrected ratio  
461 was 1.052). *ACAA2* AEI was observed in individual ewes in both the liver and the  
462 udder (Fig. 4). The average corrected T:C ratio in the liver cDNA was 1.026, not  
463 significantly different from the average corrected gDNA ratio (mean = 1,  $p = 0.67$ ).  
464 On the contrary, corrected T:C ratio of transcription in the udder of heterozygous  
465 animals was 1.18, significantly increased compared to both gDNA and liver cDNA  
466 mean corrected T:C ratios ( $p = 0.0054$  and  $0.0134$  respectively). Therefore, we  
467 observed a moderate and tissue specific imbalance in the allelic expression of the two  
468 *ACAA2* alleles in favour of allele T in the udder, but not in the liver of heterozygous  
469 animals.

470

471

### DISCUSSION

472 The study confirmed the previously observed association of the  
473 HM537015:g.2982T>C *ACAA2* SNP with milk yield in an extended population of  
474 Chios sheep from multiple flocks and showed that the g.2982T>C SNP of the *ACAA2*  
475 gene is also associated with milk protein percentage and milk fat yield. Investigation  
476 of the expression of the *ACAA2* gene from the three different genotypes and allelic  
477 expression imbalance analysis (AEI) of heterozygous samples supported the  
478 hypothesis that *ACAA2* is a functional gene affecting dairy traits. To the best of our

479 knowledge, this is the first study showing differential allelic imbalance expression of  
480 a candidate gene associated with milk production traits in dairy sheep.

481 Consistent with our previous study (Orford et al., 2012), the g.2982T>C SNP, was  
482 significantly associated with milk yield, with the T allele exhibiting positive additive  
483 and dominance effects, mainly attributed to first lactation production data.  
484 Confirmation of a previously detected association using a bigger and different data set  
485 strengthens the evidence for the observed association (Sasaki et al., 2013). The overall  
486 effects estimated in the present study, however, were lower compared to Orford et al.,  
487 (2012), possibly due to the increased variation introduced from the use of multiple  
488 flocks managed in different ways, as a substantial fraction of the environmental  
489 variance for production traits is attributed to farm (Carta et al., 2009; Sasaki et al.,  
490 2013). In the current analysis, we adjusted for the systematic effect of the flock and,  
491 therefore, the estimates are more representative and indicative of the true effect of the  
492 gene in the population. The reasons why the effects are more important in the first  
493 lactation than in the rest of lactations are not clear at this stage and therefore further  
494 research is needed.

495 In the present study, additional evidence about the correlation of the *ACAA2* gene  
496 with important sheep traits is provided, as the g.2982T>C SNP was found to be  
497 significantly associated with milk protein percentage. Homozygous CC animals  
498 exhibited superior values for protein percentage compared to both homozygous TT  
499 and heterozygous CT animals, in contrast to their inferior values estimated for total  
500 milk yield (Table 1). This is consistent with the negative genetic correlation between  
501 those two traits (Bencini and Pulina, 1997; Fuertes et al., 1998). Since, protein yield  
502 was not significantly associated with this SNP, the decrease on protein content could  
503 be attributed to a dilution effect, due to the increase of milk yield (Emery, 1988).

504 Similarly, milk yield is known to be negatively correlated to fat content (Fuertes et  
505 al., 1998). However, although the marginal predicted mean for the fat content from  
506 CC ewes was higher compared to that of the other genotypes in the present study, the  
507 differences were not significant and the investigated SNP was not significantly  
508 associated with milk fat percentage (Tables 1 and 2), in consistence with the results of  
509 Orford et al. (2012). In agreement with other studies where fat is the most variable  
510 component of ovine milk (Othmane et al., 2002; Pulina et al., 2005), in the current  
511 study, standard errors for fat content were double compared to those for protein  
512 content. Therefore, low precision of data for fat content may be a reason for not  
513 detecting the association of the studied SNP with fat percentage. However, there is a  
514 significant association of the SNP with fat yield (Table 2). In addition, homozygous  
515 CC animals exhibit significantly lower fat yields, compared to heterozygous CT and  
516 homozygous TT animals (Table 1), that could be attributed to decreased milk yield  
517 with similar fat content.

518 Since fat and protein content are crucial for cheese-making, the potential use of the  
519 studied SNP in a selection scheme requires applied research to identify whether each  
520 additional unit of milk production compensates for the lower cheese yield due to  
521 lower protein percentage, based on farmer prices and cheese yield for a certain type of  
522 cheese. Using current prices in Cyprus for sheep milk and the values of each genotype  
523 in Table 1, the producer is going to get 1.012 euros extra per additional liter, whereas  
524 the price of the milk is reduced only by 0.012 (from 1.024 to 1.012) per liter due to  
525 the lower protein and fat content. Therefore, selecting for the T allele is expected to  
526 be beneficial. However, prior to incorporation of the SNP in any breeding program,  
527 negative effects of selection on other important traits, for instance fertility, need to be  
528 excluded. To facilitate further research, the SNP has been incorporated into the sheep

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529 HD SNP chip developed by the International Sheep Genomics Consortium (ISGC) for  
530 functional studies (James Kijas, Csiro, Australia, personal communication).

531 Allele frequencies of the g.2982T>C polymorphism genotyped were similar to the  
532 previously observed (T:0.56; C:0.44; Orford et al., 2012). However, genotypic  
533 frequencies were found to deviate from the Hardy-Weinberg (H-W) equilibrium in the  
534 studied population, in contrast to the previously observed frequencies from a single  
535 experimental flock (Orford et al., 2012), due to higher frequencies of TT and CT ewes  
536 carrying the favourable for milk yield T allele. This could be possibly explained by  
537 the fact that farmers select animals mainly based on milk yield, due to low meat prices  
538 during the last decade, whereas the selection indices used at the experimental flock  
539 (Orford et al., 2012) combine the individual capacity of young stock for growth and  
540 milk production (Mavrogenis and Constantinou, 1991).

541 The candidate gene approach followed in the current study is an alternative to QTL  
542 and GWA studies that can be very powerful in the identification of loci even with  
543 small effects on the trait, if the candidate gene represents a true causative gene  
544 (Andersson, 2001). Otherwise, an association detected could occur due to linkage  
545 disequilibrium to linked or non-linked causative genes (Andersson, 2001). Therefore,  
546 the polymorphism in the 3' UTR mRNA of the ACAA2 gene that was found  
547 significantly associated with dairy traits, can be either the functional polymorphism to  
548 which the genetic variance can be attributed or can be in linkage disequilibrium with  
549 the functional polymorphism or both. Since the ACAA2 g.2982T>C SNP is in the  
550 untranslated region of the gene and thus does not affect the protein produced, it may be  
551 a functional polymorphism playing a regulatory role, by causing alterations in the  
552 expression levels of the gene. Identification of regulatory variants requires studying  
553 two alleles of a gene under identical circumstances and comparing the expression



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554 associated with each allele (Cowles et al., 2002). For that reason, the expression of the  
555 *ACAA2* variants was investigated in first parity, age, lactation stage and litter size  
556 matched ewes that were managed, fed and sampled uniformly to eliminate  
557 confounding sampling and environmental effects. The practical difficulties of  
558 obtaining those uniform conditions resulted in the selection of 3 animals per  
559 genotype. Three biological replicates are accepted as a minimum number of animals  
560 for mRNA expression analysis, as shown by recent published studies (Shi H. et. al,  
561 2015; Yao D. W. et al., 2016 a, b; Weller et al., 2016). The expression of the gene in  
562 both the udder and the liver was significantly influenced by the animals' genotype,  
563 with ewes homozygous for the T allele showing significantly increased expression, by  
564 several orders of magnitude, compared to ewes homozygous for the C allele. The  
565 reasons why heterozygous mRNA expression in the udder exhibited a very high  
566 standard deviation needs to be elucidated by further research.

567 To assess whether the observed genotype effects in the expression of the *ACAA2*  
568 gene could be attributed to allelic expression imbalance (AEI), an AEI assay using  
569 TaqMan probes was designed. The advantage of measuring AEI compared to total  
570 transcript levels is the reduction of the confounding effect of trans-acting factors,  
571 because the alleles are compared within and not across individuals (Bray et al., 2003;  
572 Cowles et al., 2002; Forton et al., 2007). The results obtained are in support of  
573 differential expression of the two alleles of the *ACAA2* gene due to a cis-acting  
574 mechanism. Differential allelic expression has been found in a large proportion of  
575 human (Bray et al., 2003; Yan et al., 2002), mouse (Campbell et al., 2008) and cattle  
576 (Karim et al., 2011, Olbromski et al., 2013, Sasaki et al., 2013) genes and there is  
577 growing evidence that polymorphisms in regulatory DNA and the resulting variability  
578 in gene expression, can explain a significant proportion of disease susceptibility and

579 quantitative trait phenotypic variance (Bray et al., 2003, Khatib, 2007, Karim et al.,  
580 2011, Sasaki et al., 2013).

581 Consistent with other studies (Yan et al., 2002; Bray et al., 2003), the differential  
582 allelic expression of the *ACAA2* gene varied among individuals in post-mortem  
583 random samples, with an overall observed increase of T relative to C allele expression  
584 in the udder of heterozygous ewes close to 20%. Previous studies in cattle indicate  
585 that even small gene expression imbalances may result in large phenotypic variance of  
586 complex traits (Karim et al., 2011, Sasaki et al., 2013). Interestingly, mean AEI of the  
587 *ACAA2* gene was only significant in the udder but not in the liver. Such tissue specific  
588 AEI has also been reported for cattle genes (Olbromski et al., 2013, Chamberlain et  
589 al., 2015). This finding, together with the observed difference between mammary  
590 gland and liver in the average mRNA gene expression in TT relative to CC ewes (11.8  
591 and 2.8 fold increase, respectively), suggest an organ specific differential expression.  
592 Preferential, or higher expression in organs related to a quantitative trait is an  
593 important criterion for the selection of functional candidate genes (Ron and Weller,  
594 2007; Stickens et al., 2010).

595 Since no other polymorphisms have been detected in the mRNA sequence of the  
596 *ACAA2* gene, the differential mRNA expression of homozygotes and the observed  
597 AEI in the mammary gland could be attributed to the g.2982T>C SNP acting in cis to  
598 modulate gene transcription or mRNA survival (Pesole et al., 2001). Analysis of the  
599 region harbouring the SNP, using the MicroInspector program found differences in  
600 potential miRNA binding sites between the two alleles (Orford et al., 2012). However,  
601 since this in-silico analysis requires functional experimental support, the possibility of  
602 another cis acting regulatory polymorphism in linkage disequilibrium with the  
603 g.2982C>T SNP, e.g. in the promoter region of the gene, cannot be excluded.

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604 Moreover, it is also likely that other trans-acting factors or mutations in other genes in  
605 linkage disequilibrium with *ACAA2*, found here to be associated with milk yield and  
606 protein content, may explain part of the QTL for milk, fat and protein yields observed  
607 in the region harbouring the *ACAA2* gene (Gutierrez- Gil et al., 2009).

608 *ACAA2* is involved in mitochondrial fatty acid elongation and degradation (KEGG  
609 database: <http://www.kegg.jp/>), by catalyzing the last step of the respective  $\beta$ -  
610 oxidation pathway. In agreement with our data, although *ACAA2* is predominantly  
611 expressed in liver, it has also been reported to be expressed in the mammary gland  
612 (<http://www.genecards.org/cgi-bin/carddisp.pl?gene=ACAA2>; Paten et al., 2015). In  
613 mammals, excess energy is stored primarily as triglycerides, which are mobilized  
614 when energy demands arise. During periods of underfeeding or in early lactation,  
615 ruminants cover their increased energy demands by mobilizing fat from the adipose  
616 tissue (Drackley, 1999). Fatty acids coming from triglycerides are taken up by the  
617 liver where they are either used as energy source or converted to ketone bodies that  
618 may be released into the blood and used as energy or substrates for de novo fatty acid  
619 synthesis in the mammary gland. In addition, it is estimated that gluconeogenesis is  
620 usually increased two- to three-fold during early lactation to meet the demands of the  
621 mammary gland for lactose and triglyceride synthesis (Drackley, 2000; Vernon,  
622 2005). The increased energy needs for gluconeogenesis and triglyceride synthesis are  
623 met primarily by increased fatty acid oxidation. Additionally, a recent transcriptomics  
624 analysis of the ovine mammary gland has shown increased expression of genes of the  
625  $\beta$ -oxidation pathway during late pregnancy (Paten et al., 2015). This contributes to the  
626 development of the udder that is crucial for subsequent lactation, as the number of  
627 active secretory cells primarily determines milk yield (Pollott GE, 2004). Therefore,  
628 although the mechanism by which the *ACAA2* gene could be linked to increased milk

629 yield and decreased protein percentage needs to be elucidated, increased *ACAA2*  
630 expression at the mRNA level is likely to result in higher levels of the enzyme and  
631 thus elevated amount of energy and carbon substrates for mammary development and  
632 lactation.

633

634

### CONCLUSION

635 In the current study, we demonstrated that the variants in the 3'UTR of the *ACAA2*  
636 gene, which are associated with milk yield, protein percentage and fat yield, are  
637 differentially expressed in homozygous ewes of each allele and exhibit AEI within  
638 heterozygotes in a tissue specific manner, suggesting the existence of a cis-acting  
639 regulatory DNA mechanism. These findings support the hypothesis that the *ACAA2*  
640 gene is a functional candidate affecting dairy traits.

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642

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653

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654 **Table 1.** Predicted genotype means and standard errors of the genotypic classes CC,  
 655 CT and TT at the g.2982T>C ACAA2 locus and significance of genotype contrasts for  
 656 each trait.

<i>Trait</i>	all lactations milk yield <sup>1</sup>	1 <sup>st</sup> lactation milk yield <sup>1</sup>	milk protein percentage	milk fat percentage	milk protein yield <sup>1</sup>	milk fat yield <sup>1</sup>
Genotyped means ± SE <sup>2</sup>						
CC	245.23 ± 4.44 <sup>a</sup>	170.21 ± 5.28 <sup>a</sup>	5.29 ± 0.02 <sup>a</sup>	5.19 ± 0.05	8.78 ± 0.25	12.87 ± 0.26 <sup>a</sup>
CT	260.71 ± 2.76 <sup>c</sup>	193.85 ± 3.33 <sup>d</sup>	5.23 ± 0.01 <sup>c</sup>	5.20 ± 0.03	9.42 ± 0.16	13.62 ± 0.17 <sup>d</sup>
TT	258.85 ± 3.88 <sup>b</sup>	191.44 ± 4.77 <sup>c</sup>	5.20 ± 0.02 <sup>c</sup>	5.14 ± 0.04	9.23 ± 0.25	13.44 ± 0.23 <sup>b</sup>

657 <sup>1</sup>Yields are in kg.

658 <sup>2</sup>Marginal genotype means ( ± standard error) predicted from the mixed model analyses

659 <sup>a-e</sup>Means within a column with two different superscripts differ as: <sup>a,b</sup>*P* < 0.025; <sup>a,c</sup>*P* < 0.010; <sup>a,d</sup>*P* <  
 660 0.001 after Holm-Bonferroni adjustment.

661

662 **Table 2.** SNP allelic effects and percentage of phenotypic variance explained by the  
 663 g.2982T>C SNP of the ACAA2 gene.

<i>Trait</i>	all lactations milk yield	1 <sup>st</sup> lactation milk yield	milk protein percentage	milk fat percentage	milk protein yield	milk fat yield
a <sup>1</sup> ± SE	6.81 ± 2.95	10.61 ± 3.56	-0.05 ± 0.02	-0.03 ± 0.03	0.23 ± 0.18	0.28 ± 0.17
p <sup>2</sup>	0.021*	0.003*	0.003*	0.370	0.200	0.100
d <sup>3</sup> ± SE	8.67 ± 3.53	13.02 ± 4.26	0.02 ± 0.02	0.04 ± 0.04	0.41 ± 0.21	0.46 ± 0.21
p <sup>4</sup>	0.014*	0.002*	0.41	0.322	0.048*	0.027*
% V <sub>p</sub> due to SNP <sup>5</sup>	0.62%	2.25%	1.68%	0.33%	0.44%	0.41%

664 <sup>1</sup>a = additive effect; positive additive genetic effect (a > 0) indicates T allele increased the trait.

665 <sup>2</sup>*P* value for assessing the additive effect on the trait; \*significant post Holm-Bonferroni adjustment for  
 666 three independent tests.

667 <sup>3</sup>d = dominance effect.

668 <sup>4</sup>*P* value for assessing the dominance effect on the trait \*significant post Holm-Bonferroni adjustment  
 669 for three independent tests.

670 <sup>5</sup>Estimated using allele frequencies observed in sample (p = 0.46 for allele C and q = 0.54 for T).

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854

**FIGURE CAPTIONS**

855 **Figure 1. Allelic expression imbalance TaqMan Assay for the quantification of**  
 856 **the ACAA2 allele T:C transcription ratio. A.** Amplification plots of TaqMan probe  
 857 PCR from ACAA2 TT (top), TC (middle) and CC (bottom) individuals. **B.**  
 858 Amplification plot of serial dilution of standard gDNA pooled from three ACAA2 TC  
 859 ewes. **C.** Log<sub>10</sub>Quantity and threshold cycle (Ct) relationship graph for T and C  
 860 alleles. Red dots represent standard gDNA dilution series reactions. Linear standard  
 861 curves for T and C alleles (targets), standard curve slope, Y-intersection,  $r^2$  and  
 862 efficiency values are shown.

863 **Figure 2. Expression of the ACAA2 gene in liver and udder. A.** ACAA2 expression  
 864 in liver and udder samples (taken  $42 \pm 2$  days after lambing) of CC, CT and TT first  
 865 parity, 15 month old ewes that gave birth to two lambs each relative to the mean  
 866 normalized expression in CC ewes. Expression was normalized by  $\beta$ -actin and  $\beta$ -  
 867 microglobulin (B2M) expression in liver and udder, respectively. n=3 for all means  
 868 except udder CT (n=2). **B.** Mean normalized expression of the ACAA2 gene in *ex vivo*  
 869 liver and udder samples from CC, CT and TT ewes, normalized by corresponding *b*-  
 870 actin transcription and relative to mean normalized transcription in the liver of TT  
 871 individuals. CC: n=1, CT: n=10 (udder) n=9 (liver), TT: n=4 (udder) n=5 (liver). Bars  
 872 represent mean relative normalized transcription and standard error of the mean is  
 873 shown. Means with different letters are significantly different ( $P < 0.05$ ).

874 **Figure 3.** Sequencing of heterozygous samples from gDNA and cDNA from liver (A)  
 875 and udder (B). The T/C SNP is shown in light blue shade. The peak heights of the T  
 876 and C alleles are the same in gDNA, whereas the peak height of the T allele is higher  
 877 compared to the C allele in cDNA of the same samples.

878 **Figure 4.** Allelic expression imbalance of the *ACAA2* gene. Graph shows TaqMan  
879 assay corrected T:C ratios in the liver and udder of heterozygous ewes. Horizontal  
880 lines represent mean corrected T:C allele in the cDNA from liver (mean=1.03, n=12)  
881 and udder (mean=1.18, n=11) and in gDNA (mean=1, n=11) of *ACAA2* heterozygous  
882 ewes. Open circles represent corrected T:C ratios for individual ewes. \*  $P < 0.05$ , \*\* $P$   
883  $< 0.01$ .

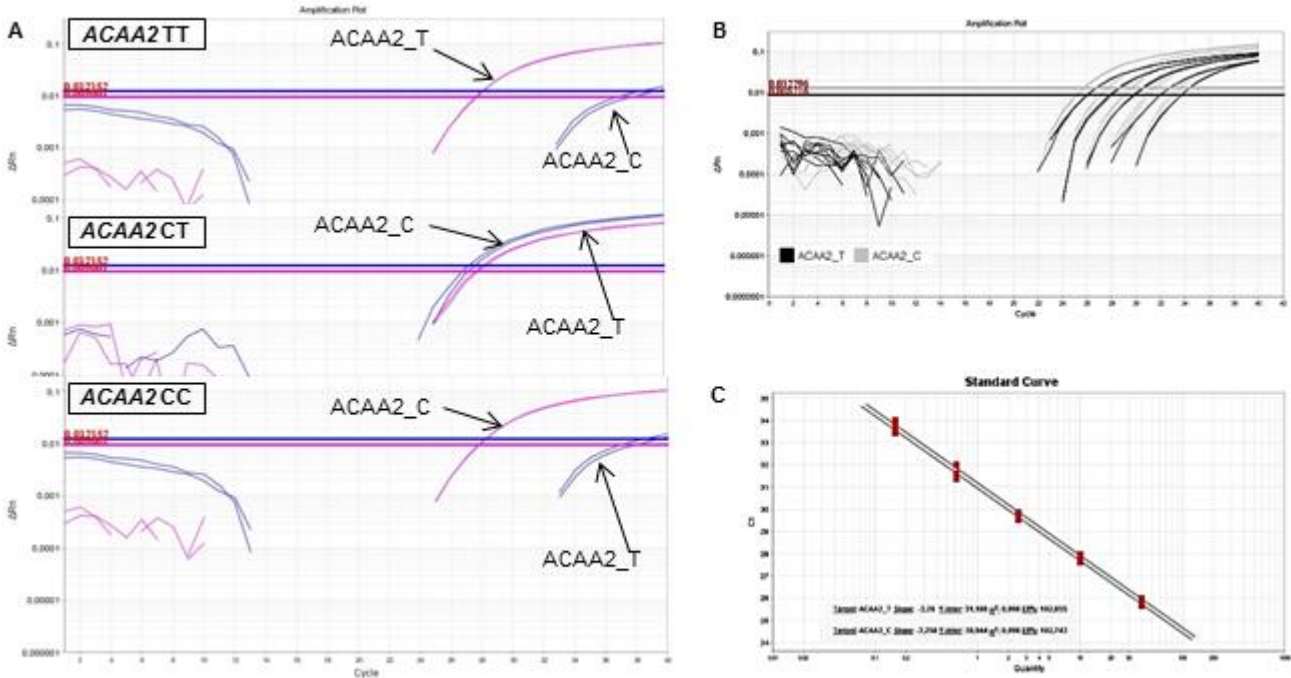
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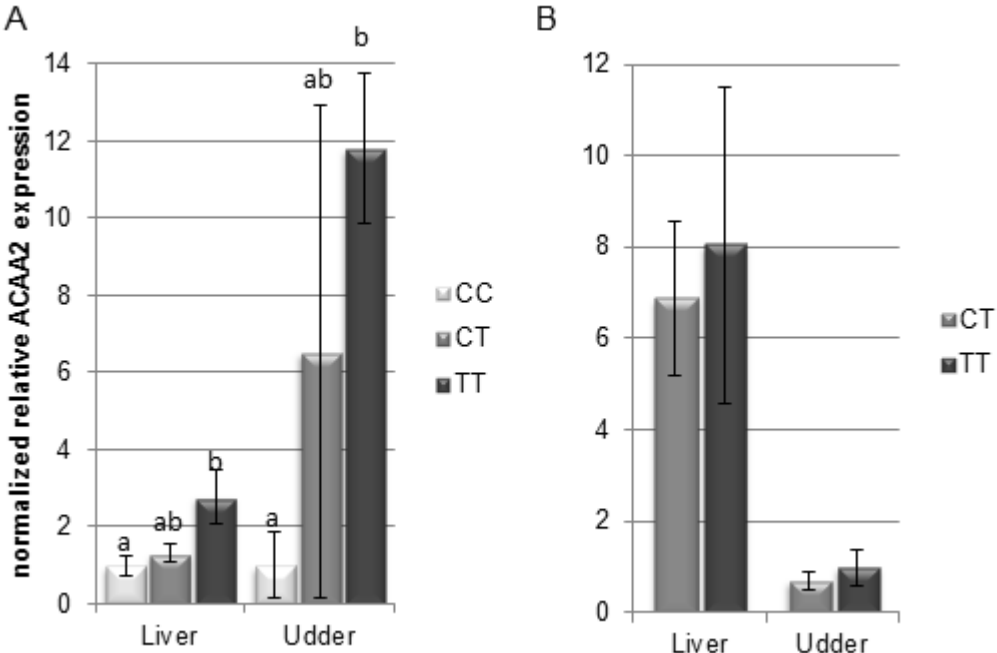
Miltiadou et al. **Figure 1**



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Miltiadou et al. **Figure 2**

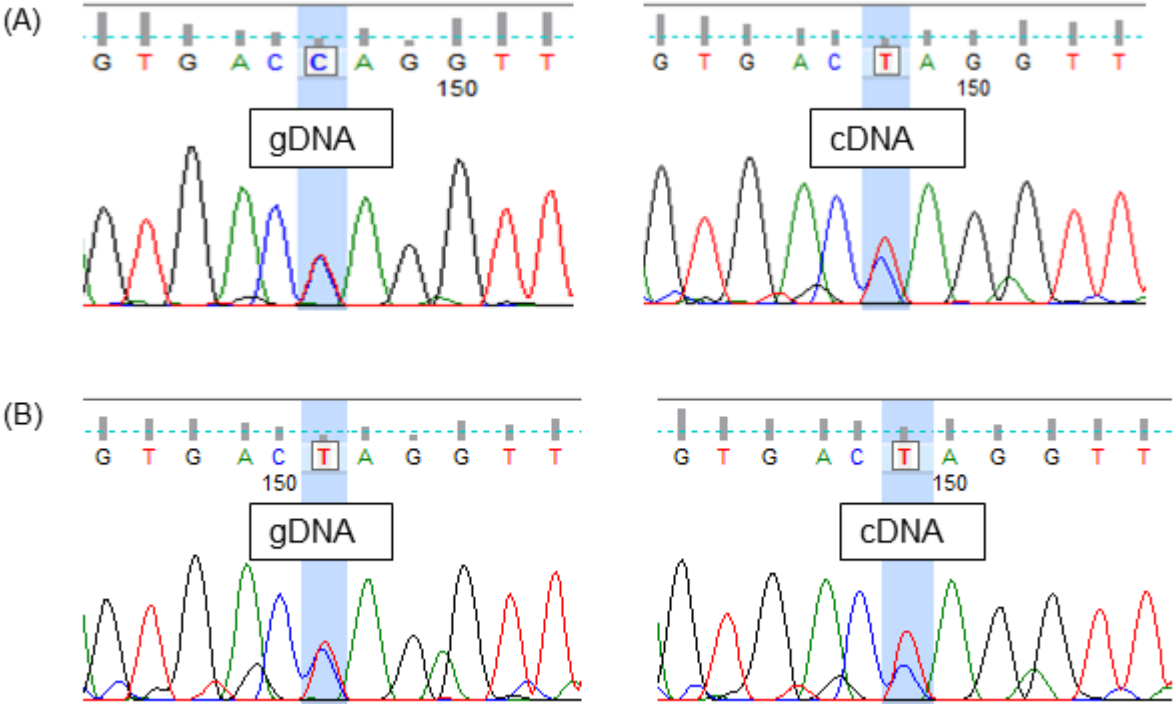


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Miltiadou et al. **Figure 3**

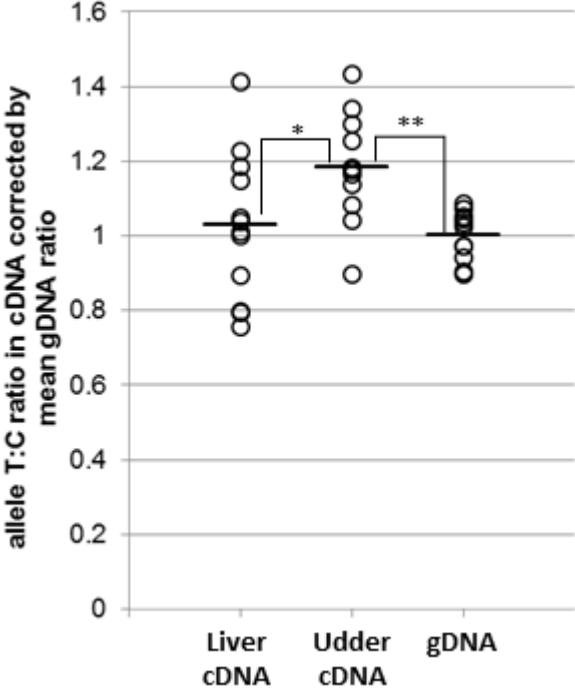


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Miltiadou et al. **Figure 4**



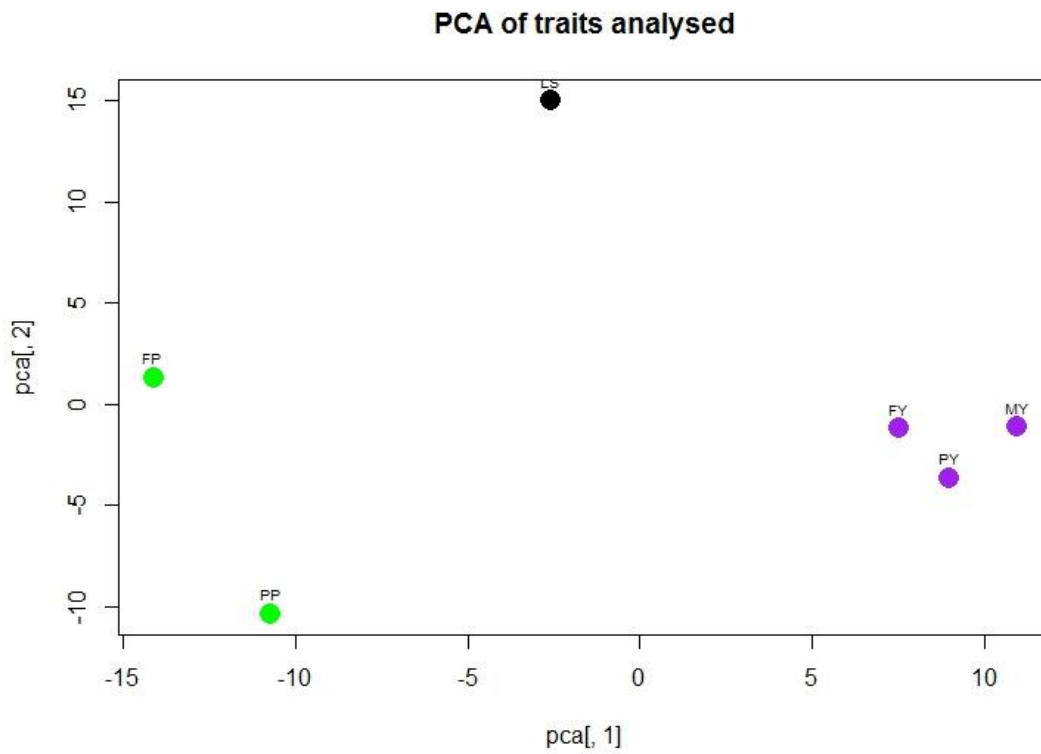
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898 **Appendix**

899 **Supplementary Figure 1:** Principal Component Analysis of studied traits: milk yield  
 900 (MY), protein yield (PY), fat yield (FY), protein percentage (PP), fat percentage (FP)  
 901 and litter size (LS).



902

903 Supplementary Table 1

<i>P</i> values after Holm-Bonferroni adjustment		
Lowest <i>P</i> value	Second lowest <i>P</i> value	Third and later lowest <i>P</i> value
<i>P</i> = 0.0167	<i>P</i> = 0.025	<i>P</i> = 0.05

904