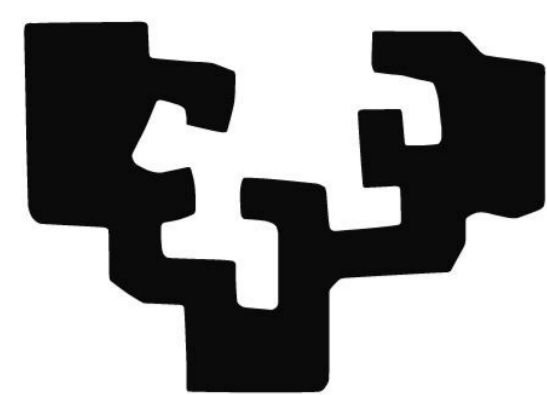


# RELATIONSHIP BETWEEN GENE EXPRESSION OF STEAROYL-COA DESATURASES (SCD1 & SCD5) AND THE FATTY ACID PROFILE IN ADIPOSE TISSUE OF CATTLE BREEDS IN THE BASQUE REGION

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## INTRODUCTION

➤ The **concern of consumers** regarding the amount and type of fat in the diet has been **increased** in relation with the negative implications of saturated FAs (SFA) while some monounsaturated FAs (MUFA) and polyunsaturated FAs have been recognized as beneficial for health.

➤ The stearoyl-CoA 9-desaturase (**SCD**) is a **lipogenic enzyme** that catalyzes the conversion of some SFA to MUFA. The SCD1 genotype has been associated with the FA composition in beef and dairy cattle but also **transcription factors** like **SREBP1** that control SCD and FA biosynthesis.

➤ Therefore, differences in the **expression level** of previously associated **SCD1**, **SREBP1** and a **novel SCD5** could affect expression and differences in FA composition of adipose tissues in beef cattle.

## MATERIAL & METHODS

**Survey**  
Three commercial groups:  
Pirenaica breed < 30 mo, n=62  
Salers breed < 30 mo, n= 12  
Friesian breed > 30 mo, n=15

➤ Correlate **SERBP1** and SCD isoforms, (**SCD1 & SCD5**).

➤ Correlate **gene expression** of **SCD1**, **novel SCD5** and **FA profile** in backfat tissue from cattle breeds in the basque Country.



## GENE EXPRESSION

**RNA extraction**

**Reverse Transcription**

- ReverTra Ace®
- cDNA

**Real-Time PCR**

- Taqman probes

**SPEARMAN**

**DATA ANALYSIS**

**ANOVA**

## FATTY ACID PROFILE

SP2560,100m  
• GC 175°C. Total FAMES  
• GC 150°C. *Trans*-18:1

SLB-IL111,100m

CLA Isomers

**GC/FID**

**Direct Methylation**

+ I.S. (23:0Me)



Bovine backfat samples were collected from animals slaughtered in a commercial abattoir located in Basque country, northern Spain over 5 weeks in June-July.

Least square means of age at slaughter and carcass traits of cattle sampled.

	Pirenaica (n=62)	Salers (n=12)	Friesian (n=15)	SEM
Age at slaughter (month)	17.1 (10.3-90.2)	12.6 (10.3-14)	63.2 (31.2-93)	3.6
Cold carcass weight (kg)	297 (187-530)	324 (286-357)	274 <sup>b</sup> (196-346)	7.3
Conformation	10.6 (8-15)	8.4 (8-10)	2.8 <sup>c</sup> (1-5)	0.33
Fat cover	5.4 (2-9)	5.7 (5-7)	3.1 (1-7)	0.21

SEM: standard error of the mean;

## RESULTS

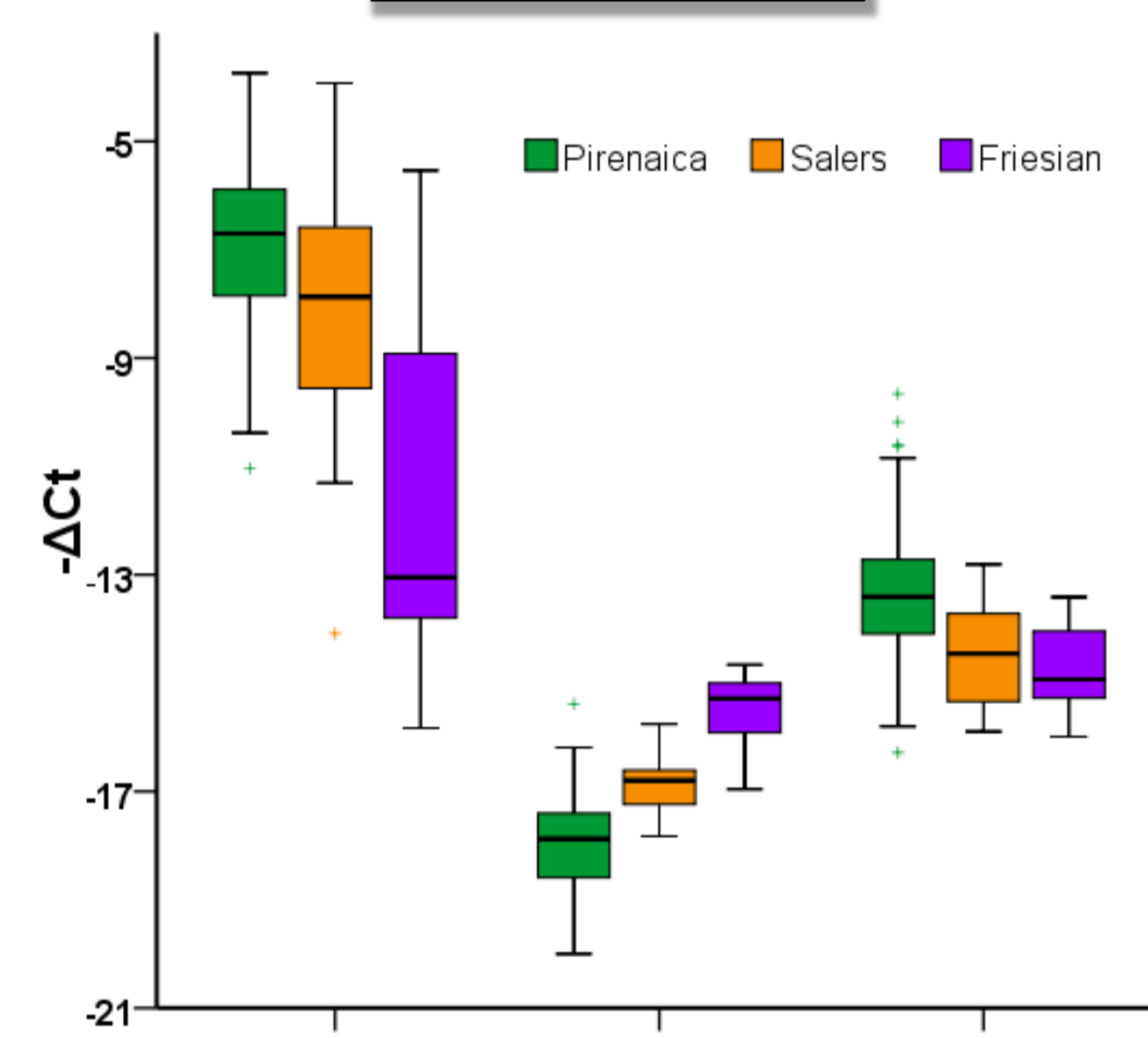


Figure 1. Relative expression levels of *SCD1*, *SCD5* and *SREBP1* mRNA of Pirenaica, Salers and Friesian cattle.

➤ When expression of **SCD1**, **SCD5** and **SREBP1** were given in relative amount ( $-\Delta Ct$ ), **significant differences** ( $P \leq 0.01$ ) were observed among genes (Fig. 1). This expression pattern was previously observed by Lengi and Corl (2007) in several tissues.

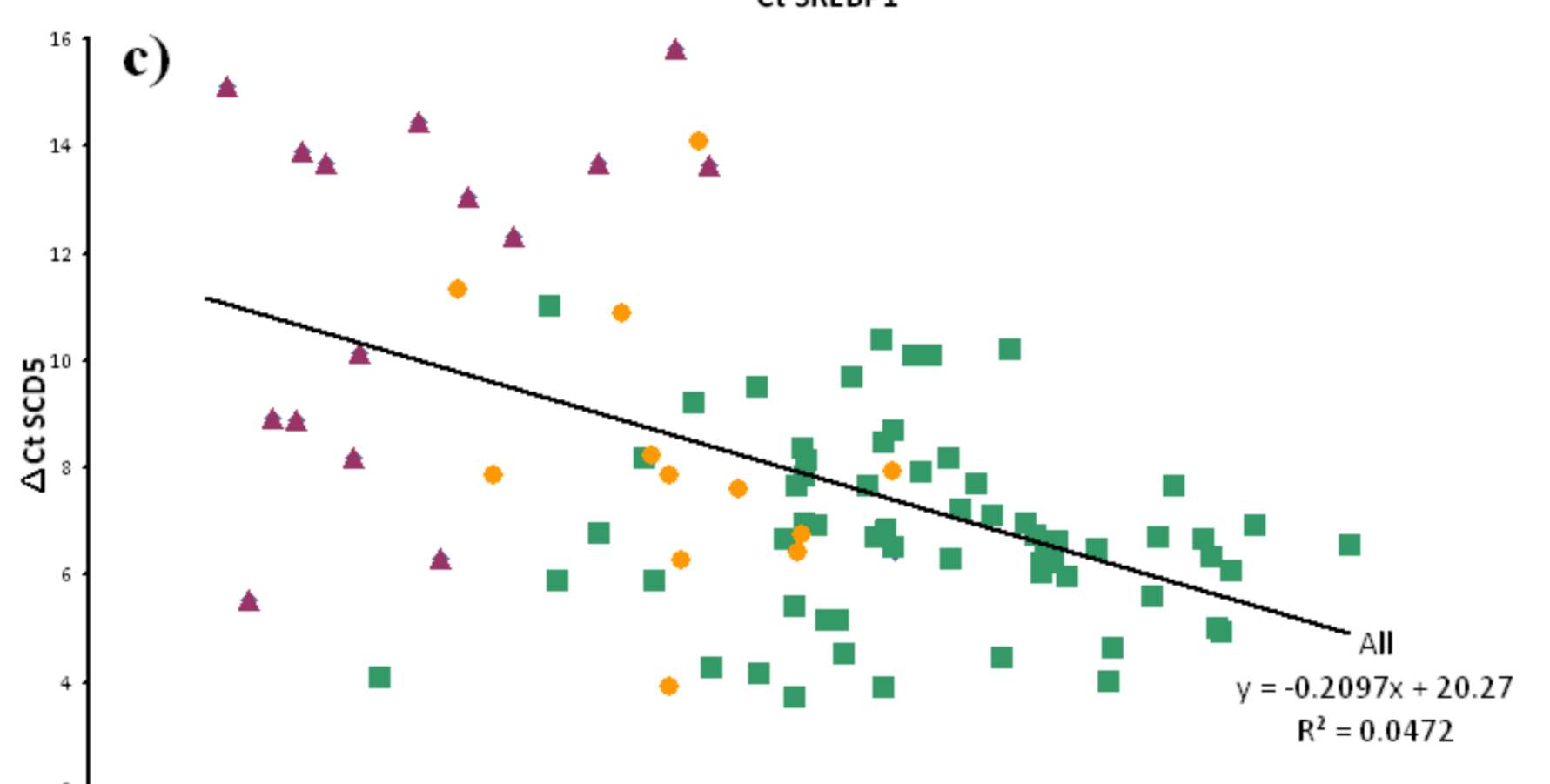
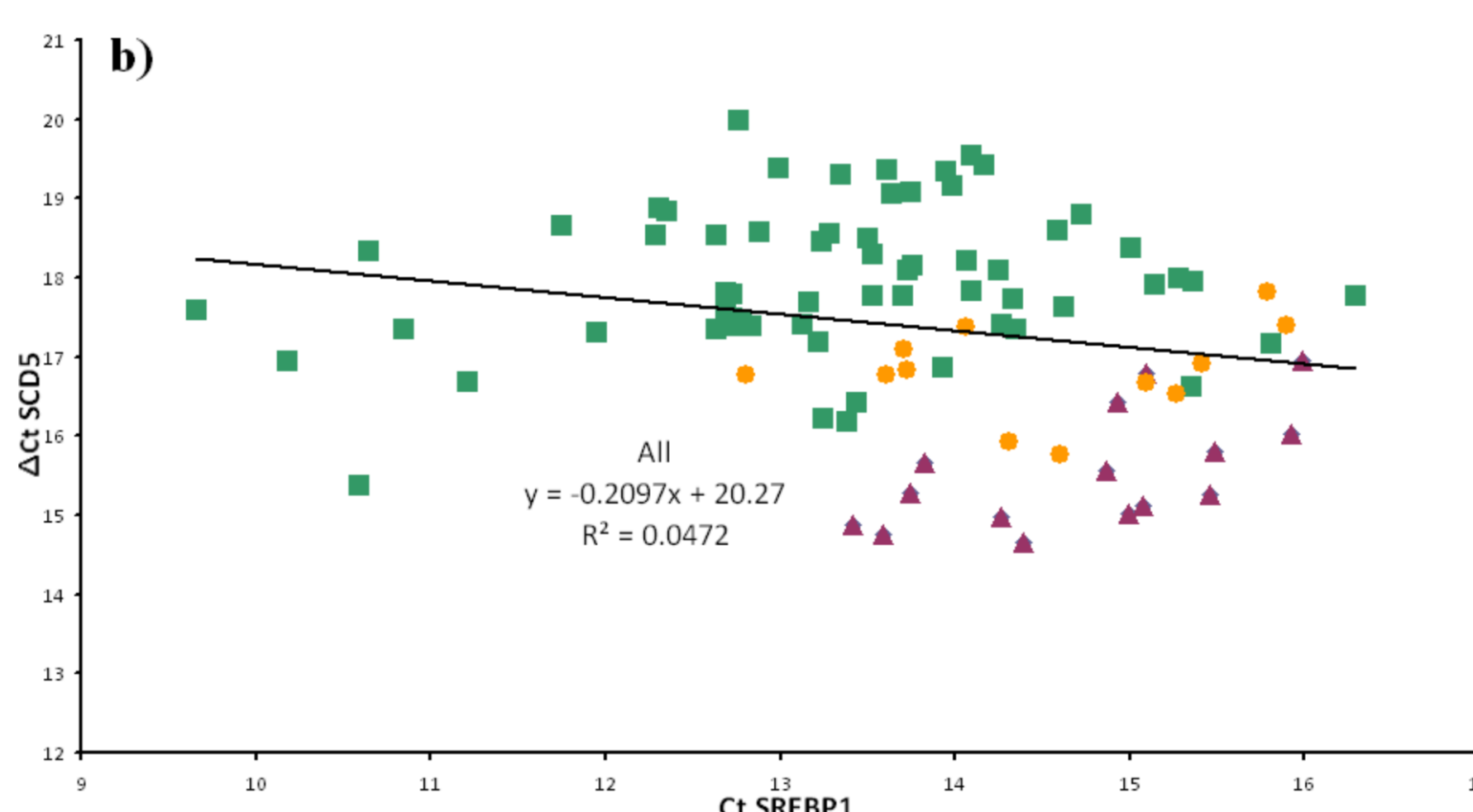
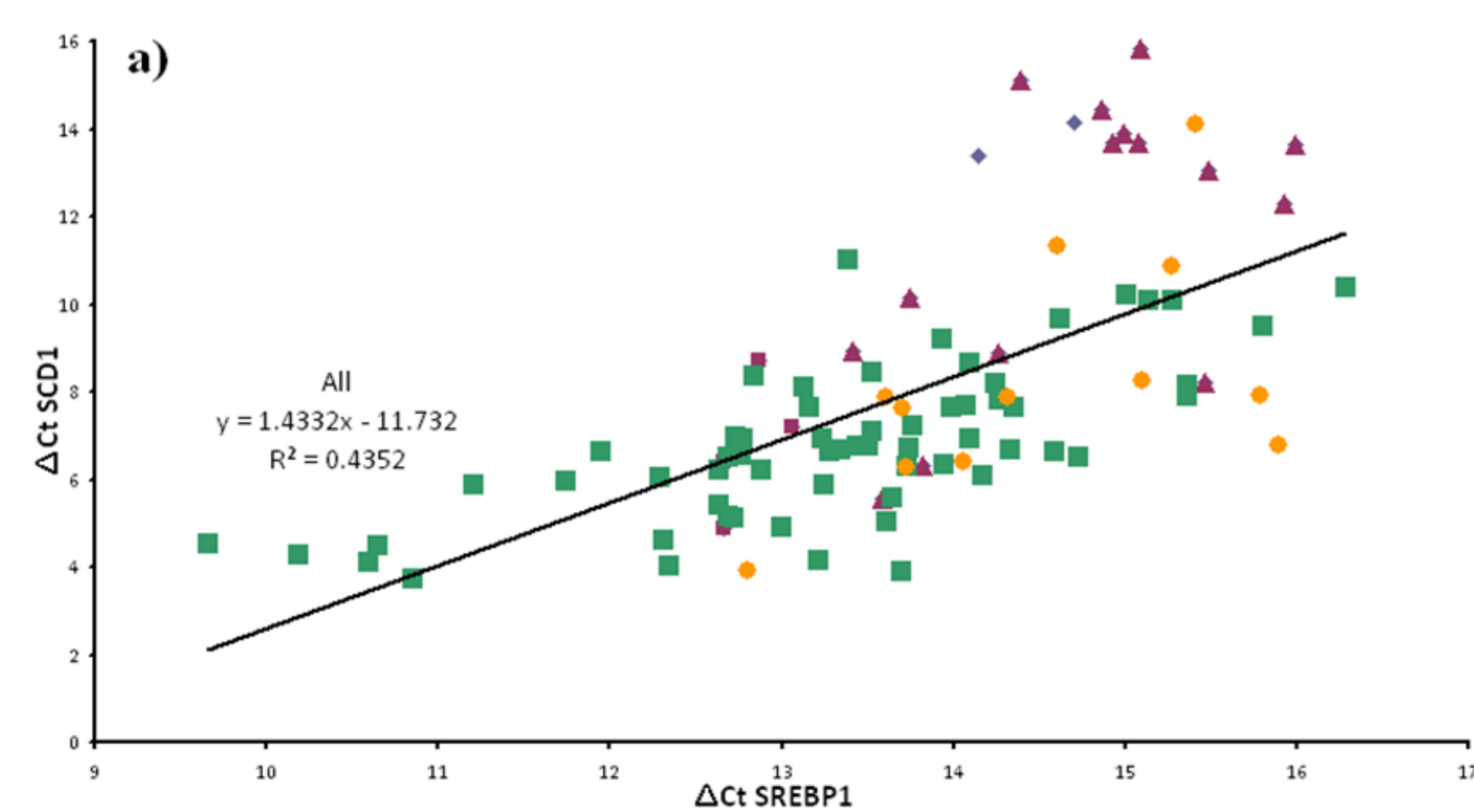


Figure 2. Correlation between gene expression in cattle breeds. a) Correlation between *SREBP1* and *SCD1* gene expression. b) Correlation between *SREBP1* and *SCD5* gene expression. c) Correlation between *SCD1* and *SCD5* gene expression.

➤ The correlation between **SREBP1** and **SCD5** was not clear due to differences between breeds (Fig. 2.b).

➤ The general correlation between **SCD1** and **SCD5** are negatively correlated ( $P \leq 0.001$ ) (Fig. 2.c).

➤ In general, when SCD1 expression was positively correlated with an individual FA, SCD5 expression was negatively correlated and vice versa (Fig. 3).

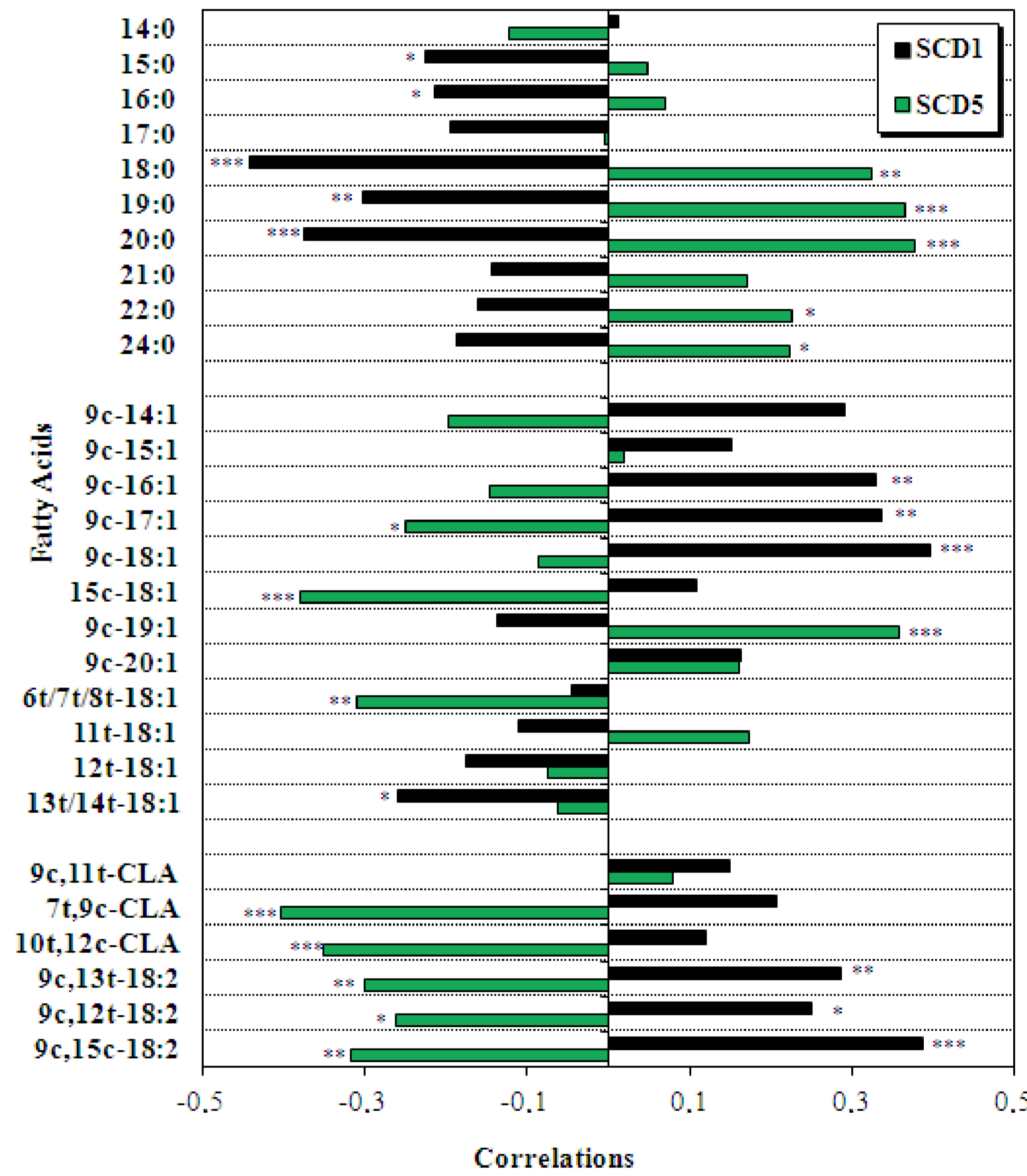


Figure 3. Correlations between expression level of *SCD1* and *SCD5* with 28 potentially related FAs fatty acids for overall population.

➤ Salers provided the most similar correlation pattern to the overall population while Friesians did not show any significant correlation. This could be due to a higher age compared to the other breeds.

➤ *SCD1* expression was significantly higher in Pirenaica but similar *cis*-MUFA contents were found in Pirenaica and Salers ( $p > 0.05$ ) that could be associated to uncontrolled factors like feeding or potential higher expression of *SCD5* in Salers breed as it was observed in Fig. 1.

## CONCLUSIONS

The gene expression of **SREBP1** and **SCD1** in Pirenaica were the highest ( $p < 0.05$ ) and also the correlation between **SREBP1** and **SCD1** expression. Moreover, *cis*-MUFA content in Pirenaica was significantly higher than in Friesian breed. Interestingly, the effect of **SCD5** on FA profile of backfat tissue was in contrast to that of **SCD1**.

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