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Supplement of

Nutritional modification of *SCD*, *ACACA* and *LPL* gene expressions in different ovine tissues

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Table S1. The composition and nutritional value of complete mixture for lambs control group (diet I).

Compltere mixture – control group (diet I)	
Individual components %	
Barley	15.0
Wheat bran	15.0
Oat	15.0
Wheat	13.0
Soybean post-extraction meal	21.0
Dried grass	16.0
Mel stern	2.5
NaCl	1.0
Mineral-vitamin supplement	1.5
The composition of integrities in the ration, kg:	
	10.3
Metabolisable energy, MJ	190.0
Total protein, g	159.0
Useful protein nBO, g	28.2
Protein UDP,%	26.2
Crude fat, g	251.0
Starch, g	501.0
Nitrogen free extraction NFE, g	80.8
Ash content, g	87.5
Crude fiber, g	140.0
Acid detergent fiber ADF, g	247.0
Neutral detergent fiber NDF, g	11.7
Calcium, g	5.1
Phosphorus, g	2.1
Sodium, g	3.9
Magnesium, g	
Fatty acid concentration (presented as % of total fatty acid content)	
Linoleic acid (C18:2)	9.8
Poliunsaturated fatty acid n3 + n6	11.3

Table S2. The composition and nutritional value of the mixture for experimental groups (diets II and III).

Compltere mixture –experimental groups (diets II and III)	
Individual components %	
Barley	17.0
Wheat bran	8.9
Oat	13.0
Wheat	14.0
Soybean post-extraction meal	20.0
Dried grass	1.2
Mel stern	2.5
NaCl	0.1
Mineral-vitamin suplement	1.9
Corn	8.9
Flour from wheat grain	8.9
Post-extracted rapeseed meal	1.5
Dried molasses beet pulp	0.5
Beer yeast	1.5
The composition of integrities in the ration, kg:	
	10.6
Metabolisable energy, MJ	185.0
Total protein, g	159.0
Useful protein nBO, g	27.4
Protein UDP,%	26.2
Crude fat, g	334.0
Starch, g	531.0
Nitrogen free extraction NFE, g	77.3
Ash content, g	55.2
Crude fiber, g	115.0
Acid detergent fiber ADF, g	195.0
Neutral detergent fiber NDF, g	13.7
Calcium, g	6.0
Phosphorus, g	2.5
Sodium, g	2.5
Magnesium, g	
Fatty acid concentration (presented as % of total fatty acid content)	
Linoleic acid (C18:2)	11.4
Poliunsaturated fatty acid n3 + n6	12.4

Table S3. Sequences of primers, probes, and PCR efficiencies of the investigated genes and endogenous controls.

Gene symbol	Gene name	GenBank Accession No.	Primer sequence	Probe sequence (MGB)	Label	Amplicon length (bp)	PCR efficiency
<i>SCD1</i>	Stearoyl-Coenzyme Adesaturaze 1	FJ513370.1	FTTCCAGATCTCTAGCTCCTACACAAC R CAATTTGCCCCCTCCATTCT	CACCATCACAGCACCT	FAM	86	1.92
<i>ACACA</i>	acetyl-CoA carboxylase alpha	NM_001009256.1	F AGCCTGCCCTAGCTTTCCA R CCCGAGATACAAGTGCATCTTG	AGAAATTTTGACCTTACTGCCAT	FAM	76	2.02
<i>LPL</i>	Lipoprotein Lipase	NM_001009394	F CCTAACGGAGGCACTTTCCA R TGCAATCACACGGAGAGCTT	CCAGGATGTAACATTG	FAM	59	2.01
<i>ATP5G2</i>	H(+)-transporting ATP synthase	NM_001009468	Custom real-time PCR assays with VIC equivalent labeled double dye probe (Taqman style) – PrimerDesign Ltd.		VIC	141	2.00
<i>RPS2</i>	Ribosomal protein S2 mRNA	DQ520732	Custom real-time PCR assays with VIC equivalent labeled double dye probe (Taqman style) – PrimerDesign Ltd.		VIC	87	1.97