Supplementary information

Table S1. Composition of feeds and intake for the low-calorie (LC), high-calorie (HC), and thiamine-treated HC (THC) sheep, expressed as dry matter.

Composition	Oat Hay	Concentrate	Ground Corn	Soybean meal	
Moisture (%)	11.0	14.9	16.3	13.6	
Crude protein (%)	10.0	18.4	9.4	53.0	
Crude Fat (%)	3	3.5	4.1	1.6	
NDF (%)	56.0	22.6	9.2	8.0	
ADF (%)	31.6	9.9	2.6	5.9	
ME, MCal/kg	2.2	3.2	3.9	2.8	
					Total Intake
LC average intake (Kg) ± SD.	0.96±0.35	-	0.28±0.08	0.27±0.08	1.52±0.48
LC average intake (ME, MCal/kg)	1.87±0.67	-	0.95±0.27	0.68±0.19	3.50±1.07
HC average intake (Kg) ± SD.	0.09±0.02	1.79±0.28	-	-	1.88±0.28
HC average intake (ME, MCal/Kg)	0.17±0.03	5.00±0.79	-	-	5.16±0.78
THC average intake (Kg) ± SD.	0.09±0.01	1.83±0.29	-		1.93±0.28
THC average intake (ME, MCal/Kg)	0.18±0.03	5.11±0.80	-	-	5.29±0.79

Table S2. Physical body and blood plasma parameters for the low calorie (LC), high calorie (HC), and thiamine treated-high calorie (THC) sheep.

	LC	HC	THC	SEM	*P*-values		
					ANOVA	Dietary effects[1]	Thiamine effects[2]
Initial BW (kg)	25.8	25.2	25.8	0.9	0.94	0.76	0.77
Final BW (kg)	47.5	71.3	70.4	2.1	<.0001	<.0001	0.70
Body length (m)	0.85	0.98	0.93	0.01	<.0001	<.0001	0.02
Wither's height (m)	0.69	0.74	0.74	0.006	<.0001	<.0001	0.7
Heart girth (cm)	89.0	103.3	102.3	1.4	<.0001	<.0001	0.61
Fasting Body weight, kg	44.5	72.5	68.5	2.3	<.0001	<.0001	0.11
Fasting Weight loss, kg	-1.08	-0.18	-0.78	0.14	0.03	0.009	0.08
Fasting Plasma TG, mg/dL	20.1	20.5	16.8	1.0	0.28	0.85	0.15

BW: body weight, BL: body length, SEM: Standard error of mean.

[1] Dietary effects were obtained from contrast *t*-test between HC and LC animals.

[2] Thiamine effects were obtained from contrast *t*-test between THC and HC animals.

Table S3. Primer sequences used for real-time quantitative PCR

Gene	GenBank Accession	Primer	Length (bp)
Leukocytes			
GAPDH	NM_001190390.1	Forward: AAGTTCCACGGCACAGTCAA Reverse: ATGTTGGCAGGATCTCGCTC	92
YWHAZ	XM_027972757.1	Forward: AGACGGAAGGTGCTGAGAAA Reverse: CGTTGGGGATCAAGAACTTT	123
TNF	NM_001024860.1	Forward: CACGTTGTAGCCAACATCAGC Reverse: GAGGTAAAGCCCGTCAGTGG	129
CCL2	XM_004012471.2	Forward: TCGCTCAGCCAGATGCAATTA Reverse: GACACTTGCTGGTGGTGACT	112
CXCL8 (IL8)	NM_001009401.2	Forward: AAGCTGGCTGTTGCTCTCTTG Reverse: GTGGAAAGGTGTGGAATGTGT	127
IFNG	X52640	Forward: GGAGGACTTCAAAAGGCTGA Reverse: GGTTAGATTTTGGCGACAGG	110
IL1B	NM_001009465.2	Forward: GTGCTGGATAGCCCATGTGT Reverse: CAGAACACCACTTCTCGGCT	74
Liver			
AGPAT1	NM_001009746.1	Forward: TTGCGTCTGATGCTACTCCA Reverse: CTCCATCATCCCAAGCAGGTC	141
AGPAT2	XM_015094112.2	Forward: CGGTGGAGAACATGAGCATC Reverse: CGGTGGAGAACATGAGCATC	138
SREBF1	XM_027974781.1	Forward: GAGCTTCGTGGTTTCCAGA Reverse: TGTAGGAATACCCTCCGCAT	86
PPARG	NM_001100921.1	Forward: GACGACAGACAAATCACCGT Reverse: GGGGCTGATGTGCTTGAACT	88
FOXO1	XM_027973596.1	Forward: ATCGCAGTTTTCCAAGTGGC Reverse: ACTAGCGTTCGAGCTGGTTC	100
FASN	AF479289.1	Forward: CCCAGCTCAACGAAACCA Reverse: GACGAGGTCAACACCCTTCC	110
SIRT1	XM_015104377.2	Forward: TTGGGTACCGAGATGACCTT Reverse: GCATGCGAGGCTCTATCATC	94
PPARA	XM_012145989.2	Forward: GTCCCATAACGCGATTCGT Reverse: GATCTGCGGTTTCGGAATCT	110
PRKAA2	NM_001112816.1	Forward: GTCATCTCAGGCAGGCTGTA Reverse: AGGGTGCCACAAAGAAGAGC	87
PPARGC1A	XM_004009738.4	Forward: AGTGACATCGAGTGTGCTGC Reverse: CTGTCTGTATCCAAGTCGTTC	109
Perilipin 2	NM_001104932.1	Forward: ACAGCTGAGTGTGGTGACAA Reverse: CTGATGTAAGCCGAGGACAC	82
Catalase	XM_004016396.4	Forward: GCAACTACCCCTCCTGGACT Reverse: CACTGTGAGGCCAAACCTTAG	105
SOD2	NM_001280703.1	Forward: CAATAAGGAGCAGGGACGCT Reverse: TAAGCATGCTCCCACACGTC	111
GPX1	XM_004018462.4	Forward: CACCCAGATGAATGACCTGC Reverse: CGTTCTTGGCGTTTTCCTGA	102
Glycogen synthase 2	XM_004006794.4	Forward: CAACTCAGCGGCAGTCTTTG Reverse: TGACTCTGTCTGTGCGGCTA	120

PYGL	NM_001024861.1	Forward: CAGCCAGCTGTACATGAATCC Reverse: CCCGGGCGTACTCCTTAATC	107
GSK3B	XM_012178649.3	Forward: CGAGACACACCTGCACTCTT Reverse: GCATTAGCATCTGAGGCTGC	146
NFKB1	XM_004009667.3	Forward: GCAGATGGCCCATACCTTCAA Reverse: GTTGCAGATTTTGACCTGAGGG	150
TNF	NM_001024860.1	Forward: CACGTTGTAGCCAACATCAGC Reverse: GAGGTAAAGCCCGTCAGTGG	129
IL1B	NM_001009465.2	Forward: GTGCTGGATAGCCCATGTGT Reverse: CAGAACACCACTTCTCGGCT	74
CCL2	XM_004012471.2	Forward: TCGCTCAGCCAGATGCAATTA Reverse: GACACTTGCTGGTGGTGACT	112
CXCL8 (IL8)	NM_001009401.2	Forward: AAGCTGGCTGTTGCTCTCTTG Reverse: GTGGAAAGGTGTGGAATGTGT	127
PTX3	AM492193.1	Forward: CCTGCATTTGGGTCAAAGCC Reverse: CTCCACCCACCACAAGCATT	129
MTTP	XM_027970731.1	Forward: GAGCTGAAAACCACGGAAGC Reverse: TCTGAGAGAGAAGGGCATCCT	133
APOB	XM_027966544.1	Forward: TGTATGGCCTCGATCCTGAG Reverse: GGTCATACTTGGACATGGCA	88
CD36	XM_027968558.1	Forward: ATGGTACAGATGCAGCCTCA Reverse: ATGGTACAGATGCAGCCTCA	105
SLC27A5	XM_027978950.1	Forward: TTCGTATCCAGGACGCCTT Reverse: GAACAGAGGATCAGCGACGA	104
SLC27A6	XM_004008652.4	Forward: TTGGAGACACTTTCAGGTGG Reverse: CTGGCACAACCACACCATAG	114
Insulin Receptor	XM_004008549.4	Forward: ACGCCACTAATCCTTCCGTC Reverse: AGGGAGGCTTCCACTTCAGA	84
IGF1R	XM_027957015.1	Forward: GACGTGGCAATAACATCGCT Reverse: GAGTGGCGGATCTTCACGTA	112
GAPDH	NM_001190390.1	Forward: TCGGAGTGAACGGATTTGGC Reverse: ACGATGTCCACTTTGCCAGT	76
PPIA	NM_001308578.1	Forward: TTATGTGCCAGGGTGGTGAC Reverse: GCCAGGACCTGTATGCTTCA	110
YWHAZ	XM_027972757.1	Forward: ACTGGGTCTGGCCCTTAAC Reverse: CGATGTCCACAATGTCAAGT	190
RPL19	AY158223.1	Forward: AGCCTGTGACTGTCCATTCC Reverse: ACCTATACCCATATGCCTGCC	80

Abbreviations:

GAPDH, glyceraldehyde-3-phosphate dehydrogenase; YWHAZ, tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta; TNF, tumor necrosis factor; CCL2, C-C motif chemokine ligand 2; CXCL8, C-X-C motif chemokine ligand 8; IFNG, interferon gamma; IL1B, interleukin 1 beta; AGPAT1, 1-acylglycerol-3-phosphate O-acyltransferase 1; AGPAT2, 1-acylglycerol-3-phosphate O-acyltransferase 2; SREBF1, sterol regulatory element binding transcription factor 1; PPARG, peroxisome proliferator activated receptor gamma; FOXO1, forkhead box O1; FASN: Fatty acid synthase; SIRT1, sirtuin 1; SIRT3, sirtuin 3; PPARA, peroxisome proliferator activated receptor alpha; PRKAA2, protein kinase AMP-activated catalytic subunit alpha 2; PPARGC1A, PPARG coactivator 1 alpha; SOD2, superoxide dismutase 2; GPX1, glutathione peroxidase 1; PYGL, glycogen phosphorylase L; GSK3B, glycogen synthase kinase 3 beta; NFKB1, nuclear factor kappa B subunit 1; PTX3, pentraxin 3; MTTP, microsomal triglyceride transfer protein; APOB, apolipoprotein B; CD36, CD36 molecule;

SLC27A5, solute carrier family 27 member 5; SLC27A6, solute carrier family 27 member 6; PPIA, peptidylprolyl isomerase A; YWHAZ, tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta; RPL19, ribosomal protein L19.

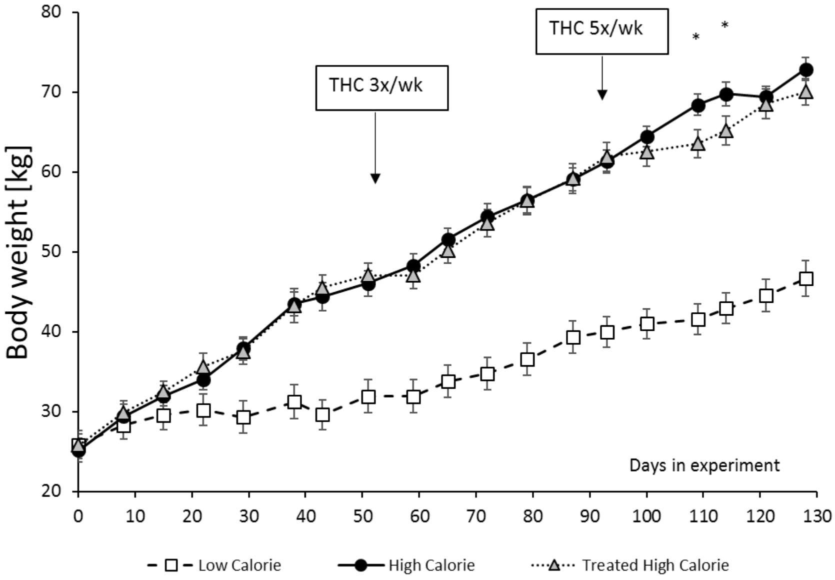

Figure S1. Body weight in the low calorie (LC), high calorie (HC) and thiamine-treated HC (THC) growing lambs. Repeated measures ANOVA analysis for HC vs. LC revealed an effect of the dietary treatment (*P* < .0001), time (*P* < .0001) and treatment x time interaction (*P* < .0001). Comparing HC with THC revealed an effect of time (*P* < .0001) and a treatment x time interaction (*P* < .0001) and a trend for thiamine treatment (*P* = 0.09). * Denotes *P* < .05 between HC and THC after Bonferroni-Holm correction.

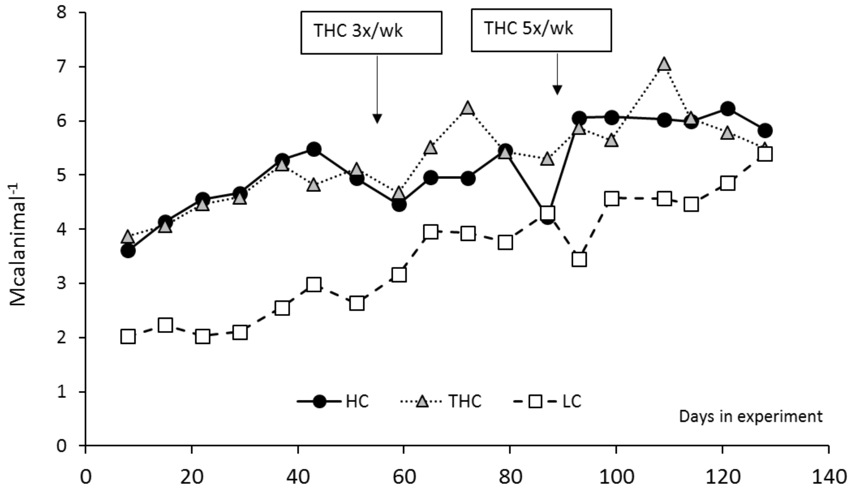

Figure S2. Daily group-average caloric intake in the low calorie (LC), high calorie (HC), and thiamine treated HC (THC) animals.

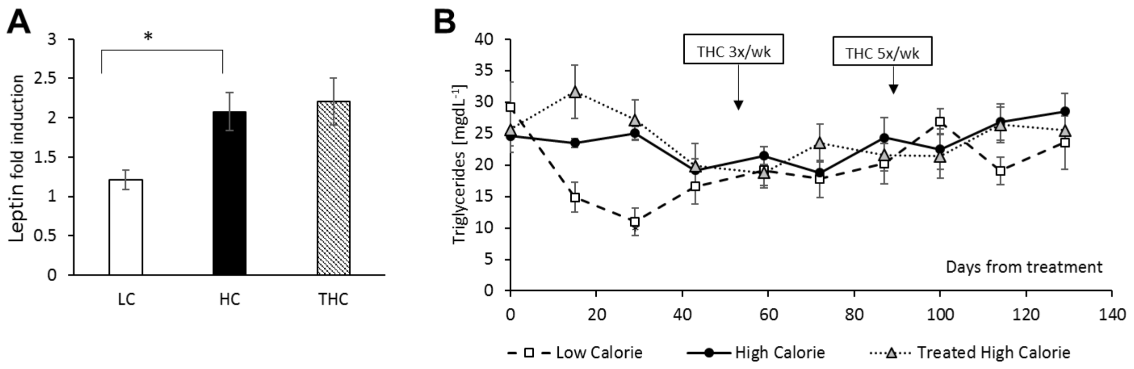

Figure S3. Plasma triglyceride and fasting leptin levels in the low calorie (LC), high calorie (HC) and thiamine-treated HC (THC) sheep. (**A**) Fasting plasma leptin concentration. One-way ANOVA detected an effect of the dietary treatment (*P* = 0.02). (**B**) Plasma triglycerides levels. Repeated-measures ANOVA analysis revealed an effect of the dietary treatment (HC vs. LC) (*P* = 0.02), time (*P* = 0.001), and treatment by time interaction (*P* = 0.01). * Denotes *P* < 0.05 by contrast t-tests.

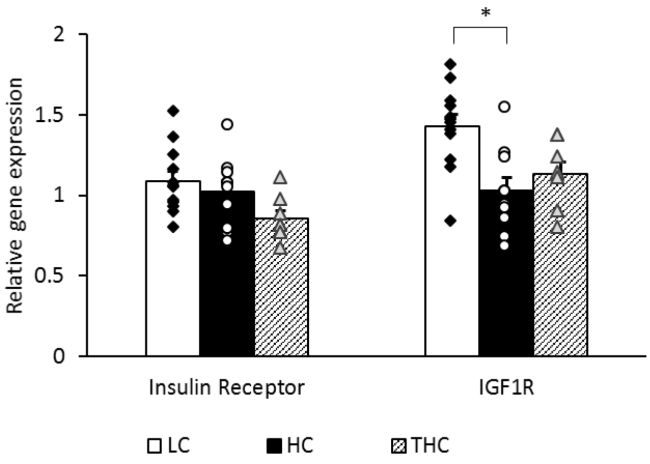

Figure S4. Comparative hepatic expression of genes involved in insulin sensitivity in the low-calorie (LC), high-calorie (HC), and thiamine-treated HC (THC) sheep. One way ANOVA detected an effect of treatment for Insulin receptor (*P*< 0.04) and *IGF1R* (*P*< 0.002). * Denotes *P* < 0.05 by contrast t-tests.

Abbreviations*:*

IGF1R, Insulin-like growth factor 1 receptor