

Table S1. qPCR performance of the genes analyzed in *Longissimus* muscle.

Gene ¹	Median Ct ²	Median Δ Ct ³	Slope ⁴	(R ²) ⁵	Efficiency ⁶	Relative mRNA abundance ⁷
<i>MYOG</i>	23.845	6.5435	-3.48	0.987	1.937	0.0132
<i>MYOD1</i>	23.943	6.6706	-3.43	0.988	1.958	0.0113
<i>PAX7</i>	29.550	12.2835	-3.25	0.993	2.032	0.0002
<i>MYF5</i>	26.935	9.6754	-3.22	0.995	2.045	0.0010
<i>MYH1</i>	15.355	-2.9116	-3.28	0.992	2.019	7.7358
<i>MYH2</i>	16.995	-1.2911	-3.25	0.999	2.031	2.4961
<i>MYH7</i>	16.173	-1.0751	-3.41	0.997	1.965	2.0676
<i>MEF2C</i>	25.195	7.0340	-3.49	0.994	1.935	0.0096
<i>AGPAT1</i>	26.992	9.7029	-3.19	0.990	2.059	0.0009
<i>PPARGC1A</i>	25.538	8.2646	-3.41	0.990	1.965	0.0038
<i>PPARG</i>	27.927	10.6139	-3.43	0.989	1.958	0.0008
<i>ZFP423</i>	24.021	6.8094	-3.55	0.987	1.913	0.0121
<i>CEBPA</i>	26.395	7.6611	-3.19	0.992	2.056	0.0040
<i>CEBPB</i>	27.030	8.2960	-3.35	0.995	1.989	0.0033
<i>FABP4</i>	21.913	3.4202	-3.19	0.991	2.057	0.0848

¹*MYOG* Myogenin, *MYOD1* Myogenic differentiation 1, *PAX7* Paired box protein 7, *MYF5* Myogenic factor 5, *MYH1* Myosin heavy chain 1, *MYH2* Myosin heavy chain 2, *MYH7* Myosin heavy chain 7, *MEF2C* Myocyte enhancer factor 2C, *AGPAT1* Acyl-glycerol phosphate acyltransferase 1, *PPARGC1A* PPARG coactivator 1 alpha, *PPARG* Peroxisome proliferator activated receptor gamma, *ZFP423* Zinc finger protein 423, *C/EBPA* CCAAT enhancer binding protein alpha, *C/EBPB* CCAAT enhancer binding protein beta, *FABP4* Fatty acid binding protein 4. ²The median is calculated considering all steers. ³The median of Δ Ct is calculated as [Ct gene – geometrical mean of Ct internal controls] for each steer. ⁴Slope of the standard curve. ⁵R² stands for the coefficient of determination of the standard curve. ⁶Efficiency is calculated as $[10(-1 / \text{Slope})]$. ⁷Relative mRNA abundance = $1 / \text{Efficiency Median } \Delta\text{Ct}$

Table S2. qPCR performance of the genes analyzed in subcutaneous adipose tissue

Gene ¹	Median Ct ²	Median Δ Ct ³	Slope ⁴	(R ²) ⁵	Efficiency ⁶	Relative mRNA Abundance ⁷
<i>FASN</i>	16.948	-3.2600	-3.37	0.999	1.981	9.2823
<i>SREBP1</i>	22.131	1.9597	-3.22	0.983	2.045	0.2461
<i>PPARG</i>	23.709	3.6456	-3.39	0.998	1.974	0.0839
<i>ADFP</i>	21.908	1.5577	-3.45	0.990	1.948	0.3539
<i>SCD</i>	15.892	-4.5701	-3.55	0.992	1.913	19.3803
<i>FABP4</i>	16.304	-3.8287	-3.40	0.992	1.969	13.3892
<i>PPARGC1A</i>	28.331	-4.5180	-3.30	0.981	2.011	23.4826
<i>ZFP423</i>	23.849	3.2014	-3.55	0.983	1.914	0.1251
<i>ACACA</i>	20.851	0.5347	-3.53	0.995	1.921	0.7053
<i>CEBPA</i>	23.241	3.2014	-3.20	0.996	2.056	0.0995
<i>CEBPB</i>	26.974	6.7941	-3.44	0.990	1.952	0.0106

¹*FASN* Fatty acid synthase, *SREBP1* Sterol regulatory element binding transcription factor 1, *ADFP* Adipose differentiation-related protein, *SCD* Stearoyl-CoA desaturase, *ACACA* Acetyl-CoA carboxylase alpha. ²The median is calculated considering all steers. ³The median of Δ Ct is calculated as [Ct gene – geometrical mean of Ct internal controls] for each steer. ⁴Slope of the standard curve. ⁵R² stands for the coefficient of determination of the standard curve. ⁶Efficiency is calculated as $[10(-1 / \text{Slope})]$. ⁷Relative mRNA abundance = $1 / \text{Efficiency Median } \Delta\text{Ct}$