

Table S1. Primer pairs for RT-qPCR analysis.

Gene	Primers ¹	Sequence (5' to 3')	NCBI accession number	bp ²
<i>SCD</i>	F.501	TGCTGATCCCCACAATTCCC	NM_001285619.1	216
	R.716	CCCCATAGATACCACGGCAC		
<i>LDLR</i>	F.2403	ACAATGTCCCAACAAGCCCT	XM_005682375.3	189
	R.2591	GTACACGGGGTTGTCTGAAGT		
<i>FASN</i>	F.6850	GGGCTCCACCACCGTGTTC	NM_001285629.1	226
	R.7075	GCTCTGCTGGGCCTGCAGCTG		
<i>FADS1</i>	F.186	CGCTATTTACCTGGGACGA	XM_018043053.1	187
	R.372	CCTTGTTGATGTGGAACGCC		
<i>INSIG1</i>	F.323	TGCAGGTCCAGAGGAATGTC	NM_001286088.1	169
	R.491	CACTCCCGCTTGAACCTGTG		
<i>FADS2</i>	F.237	CCGCTGGGAGGAGATTC	XM_018043056.1	129
	R.365	GCGTAGTGCCCGATGAC		
<i>HMGCR</i>	F.2075	CGCAACCTTTACATCCG	XM_018053703.1	190
	R.2264	TCCCTCGTCCCTCTATC		
<i>SQLE</i>	F.1005	GCTGGTGTTCCTGTGCGC	XM_005688851.3	126
	R.1130	ATGAAAGGCAAGGCTGA		
<i>HMGCS1</i>	F.725	GAGGACTTCGTGGGACT	XM_005694740.3	151
	R.875	TGGATCTTCTTGCGGTA		
<i>ALDH3B1</i>	F.1303	GCTTCTGTGGGAACGACG	XM_018042919.1	179
	R.1481	CGGGTAGCGGATGGTGTA		
<i>RPS9</i>	F.243	CCTCGACCAAGAGCTGAAG	XM_018063498.1	64
	R.306	CCTCCAGACCTCACGTTTGTTTC		
<i>UXT</i>	F.391	CAGCTGGCCAAATACCTTCAA	XM_005700842.2	125
	R.515	GTGTCTGGGACCACTGTGTCAA		

¹Primer direction (F-forward, R-reverse) and hybridization position on the sequence.

²Amplicon size in base pair (bp)

SCD, stearoyl-CoA desaturase; *LDLR*, low density lipoprotein receptor; *FASN*, fatty acid synthase; *FADS1*, fatty acid desaturase 1; *FADS2*, fatty acid desaturase 2; *INSIG1*, insulin induced gene 1; *HMGCR*, 3-hydroxy-3-methylglutaryl-CoA reductase; *SQLE*, squalene epoxidase; *HMGCS1*, 3-hydroxy-3-methylglutaryl-CoA synthase 1; *ALDH3B1*, aldehyde dehydrogenase 3 family member B1; *RPS9*, ribosomal protein S9; *UXT*, ubiquitously expressed prefoldin like chaperone.