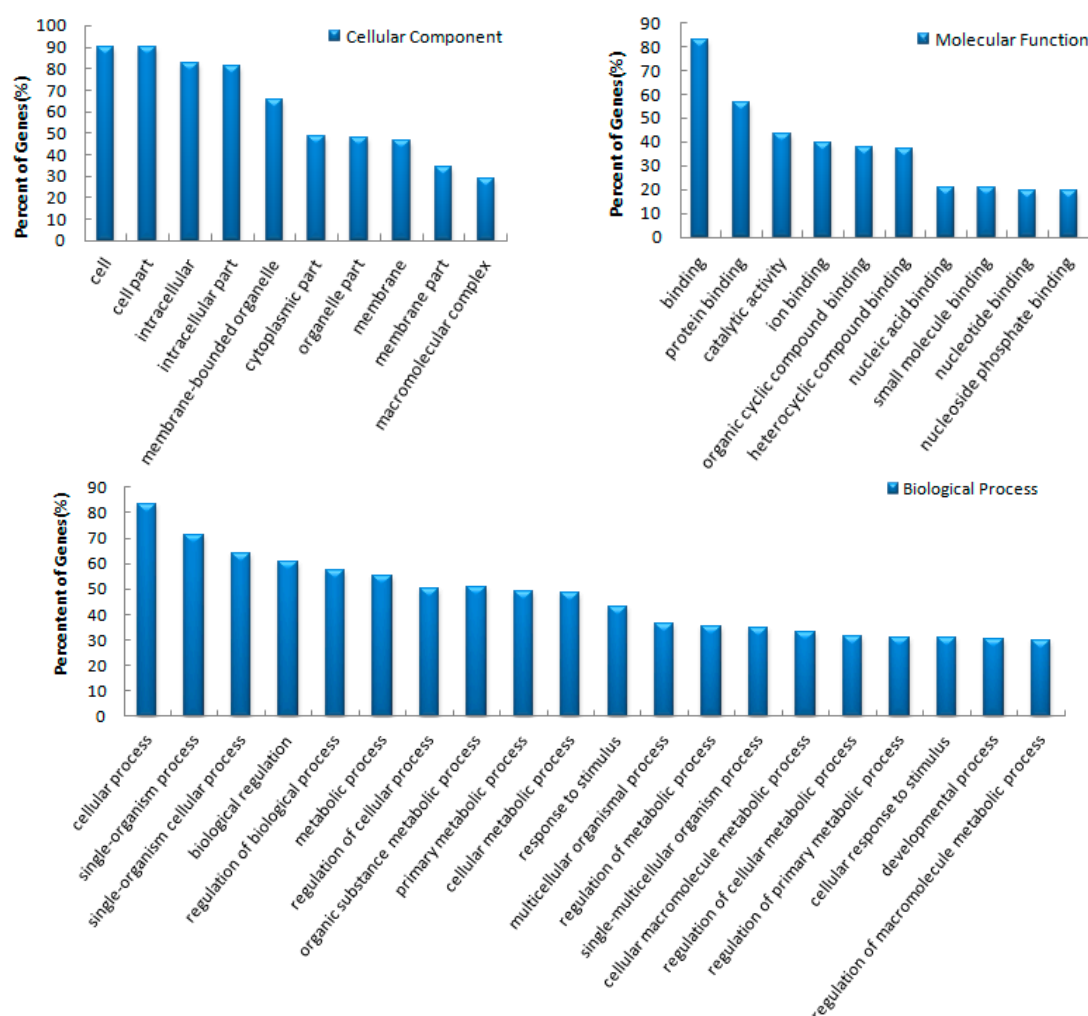


# Supplementary Materials: Deep Sequencing and Screening of Differentially Expressed microRNAs Related to Milk Fat Metabolism in Bovine Primary Mammary Epithelial Cells

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**Figure S1.** GO analyses of predicted targets of differentially expressed miRNAs. The top twenty categories enriched in biological processes and top ten categories enriched in both the cellular components and molecular functions.

**Table S8.** Six screened miRNAs whose target gene candidates were annotated to the pathway related to fatty acid metabolism.

Gene Symbol	Gene Description
bta-miR-33a	
Unsaturated fatty acid biosynthetic process	
<i>ELOVL5</i>	ELOVL family member 5
<i>ALOX15</i>	arachidonate 15-lipoxygenase
<i>ELOVL 6</i>	hypothetical LOC533333
<i>SC4MOL</i>	sterol-C4-methyl oxidase-like
bta-miR-21*	
Unsaturated fatty acid biosynthetic process	
<i>CD74</i>	CD74 molecule
<i>PTGIS</i>	prostaglandin I2 (prostacyclin) synthase
<i>PTGS1</i>	prostaglandin-endoperoxide synthase 1
<i>SYK</i>	spleen tyrosine kinase
Fatty acid biosynthetic process	
<i>PTGIS</i>	prostaglandin I2 (prostacyclin) synthase
<i>PTGS1</i>	prostaglandin-endoperoxide synthase 1
<i>SYK</i>	spleen tyrosine kinase
Fatty acid metabolic process	
<i>ADIPOQ</i>	adiponectin, C1Q and collagen domain containing
<i>CPT1</i>	carnitine palmitoyltransferase 1B (muscle)
bta-miR-152	
Fatty acid biosynthetic process	
<i>PTGS2</i>	prostaglandin-endoperoxide synthase 2
<i>PRKAG3</i>	protein kinase, AMP-activated, gamma 3 non-catalytic subunit
<i>QKI</i>	quaking homolog, KH domain RNA binding
<i>SC5DL</i>	sterol-C5-desaturase-like
Fatty acid metabolic process	
<i>PRKAA1</i>	protein kinase, AMP-activated, alpha 1 catalytic subunit
<i>UCP3</i>	uncoupling protein 3 (mitochondrial, proton carrier)
bta-miR-224	
Unsaturated fatty acid biosynthetic process	
<i>ALOX15</i>	arachidonate 5-lipoxygenase-activating protein
<i>GST</i>	microsomal glutathione S-transferase 2
<i>PTGS1</i>	prostaglandin-endoperoxide synthase 1
Fatty acid biosynthetic process	
<i>ELOVL 5</i>	ELOVL family member 5, elongation of long chain fatty acids
<i>ALOX15</i>	arachidonate5-lipoxygenase-activating protein
<i>LPL</i>	lipoprotein lipase
<i>GST</i>	microsomal glutathione S-transferase 2
<i>PTGS1</i>	prostaglandin-endoperoxide synthase 1
bta-miR-877	
Unsaturated fatty acid biosynthesis process	
<i>EDN1</i>	endothelin 1
<i>HPGD</i>	hydroxyprostaglandin dehydrogenase 15-(NAD)
<i>PDPN</i>	podoplanin
<i>PTGIS</i>	prostaglandin I2 (prostacyclin) synthase

Table S8. Cont.

Gene Symbol	Gene Description
Fatty acid metabolic process	
<i>EDN1</i>	endothelin 1
<i>HADHB</i>	hydroxyacyl-Coenzyme A dehydrogenase beta subunit
<i>PDPN</i>	podoplanin
<i>PTGIS</i>	prostaglandin I2 (prostacyclin) synthase
<i>PRKAG1</i>	protein kinase, AMP-activated, gamma 1 non-catalytic subunit
bta-miR-29b	
Fatty acid biosynthetic process	
<i>LPL</i>	lipoprotein lipase
<i>PLP</i>	proteolipid protein RG Bos taurus

bta-miR-21\*, sequence is from the opposite arm of bta-miR-21.

Table S10. Primer sequences of candidate target genes for qRT-qPCR.

Gene Name	Primer Sequence (5'-3')	Size (bp)	Annealing Temperature (°C)
<i>ELOVL5</i>	F: GTGGAGGAGAAGCGGACA R: TTGCGGAGGATGAAGAAGA	100	60
<i>ALOX15</i>	F: TGGACTGGCCCTACGAATAC R: GATGGAAGTTGGGAAGAGGA	124	60
<i>ELOVL6</i>	F: CCTCCATCTCAAAGGACTGC R: GGCCTTCTCTCTACCTCTGG	101	60
<i>SC4MOL</i>	F: CTGGGTGACTGTTTCGTTTGA R: ATGTGGTGGAAATCGTGATG	120	60
<i>PTGS2</i>	F: GGGCGATGAGCAGTTGTT R: GCAGCAATACGGTTCTGGTA	168	60
<i>PRKAG3</i>	F: CTCCGCTTCTGGATTACCTG R: GTGACAAAGTCGGGAGGAAC	101	60
<i>QKI</i>	F: GAACTCCTCACCCCTACTGCTG R: TAGCCACCGCACCTAATACA	150	60
<i>SC5DL</i>	F: TGAAGATCCCAACTCCATT R: AAGCCCAGGATGCTTGTGT	118	60
<i>PRKAA1</i>	F: CGCCATACCCTTGATGAATTA R: ATCATTGGCCGACTTGAC	102	60
<i>UCP3</i>	F: CACCTGCTCACCGACAAC R: CATATACCGCGTCTTCACCA	175	60
<i>ALOX5AP</i>	F: ACGAAAGCAAGACCCACAAT R: TACATCAGCCCAGCAAAGG	165	60
<i>GST</i>	F: GGACAGATGACAGGGTGGA R: TCGTGTGGTAGATTCGTGCT	142	60
<i>PTGS1</i>	F: GTGCCATCCGAACTCCAT R: AAGGTTGAAGCCACATCAC	100	60
<i>LPL</i>	F: AACTTGCCACCTCATTCCT R: TACATTCCTGTCACCGTCCA	124	60
<i>EDN1</i>	F: CTGGACATCATCTGGGTCAA R: GGCATCTCTTCTGTGGACT	101	60

Table S10. Cont.

Gene Name	Primer Sequence (5'-3')	Size (bp)	Annealing Temperature (°C)
<i>HADHB</i>	F: TCAACACTCCAGAGCACGTT R: CACACTGGCATCTCTTCCTG	127	60
<i>HPGD</i>	F: AACCTACCTGGGCTTGGATT R: GCGTTCAGTCTCACACCACT	117	60
<i>PDPN</i>	F: TCAGAAAGGTGGCTTGTCAG R: AGGGCGAGTATCTTCCCATT	198	60
<i>PTGIS</i>	F: CAAAGATGGGAAGCGACTG R: GTCAGCACAAGGAACACGAA	122	60
<i>PRKAG1</i>	F: ATCCAGCCTTTGCCTCTGT R: GGACTCAGCCTCCTCCATAC	117	60
<i>CD74</i>	F: ATGAAGAACGCCACCAAGTA R: TTCCAGTCCAAGCCATCC	114	60
<i>SYK</i>	F: CTGGACCCTTTGAGGACTTG R: CTGAGGTTTCTGGCTGATGA	155	60
<i>ADIPOQ</i>	F: AGGGAGAACCTGGAGAAAAGTG R: TTGGTAAAGCGAATGGGAAC	110	60
<i>CPT1</i>	F: ACCTGAACGAAGACCTCCAA R: CCACCATGCAAGTTCAGG	100	60
<i>PLP</i>	F: TTCCTGAACGAAGATTCACAA R: AGCTTCGGAAGCAATCGGA	112	60
<i>GAPDH</i>	F: CGTGTCTGTTGTAGGATCTGACCTGC R: CAACCTGGTCCTCTAGTGTAGCCTT	176	58