# Interference with DGAT Gene-Inhibited TAG Accumulation and Lipid Droplet Synthesis in Bovine Preadipocytes

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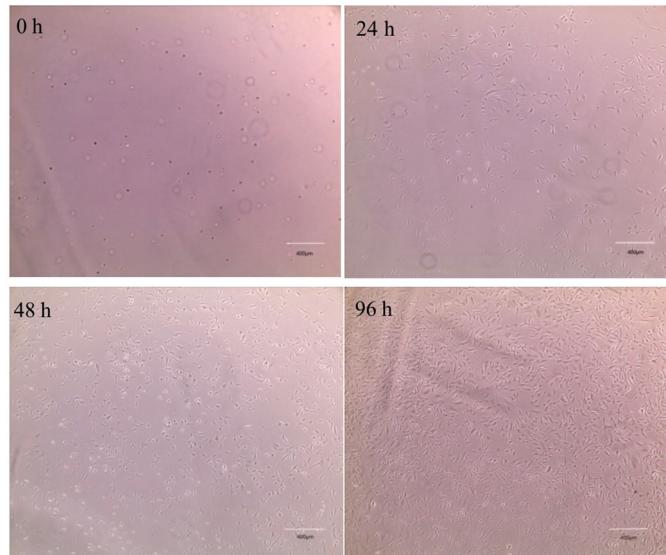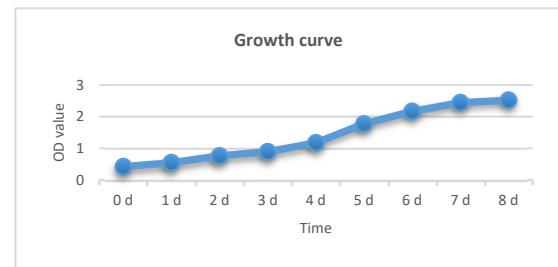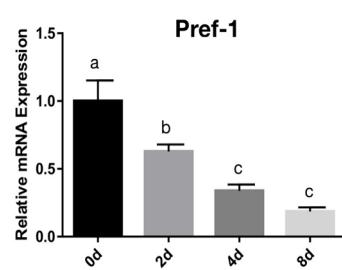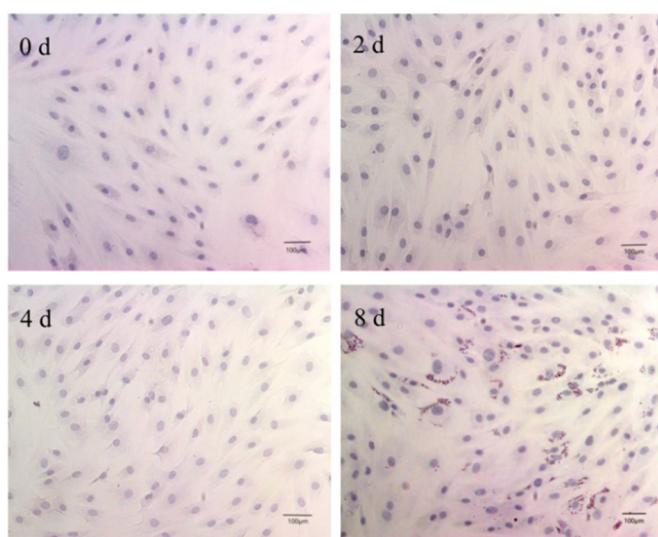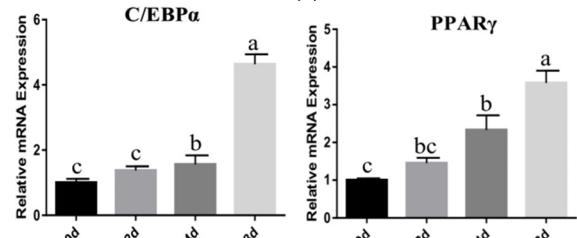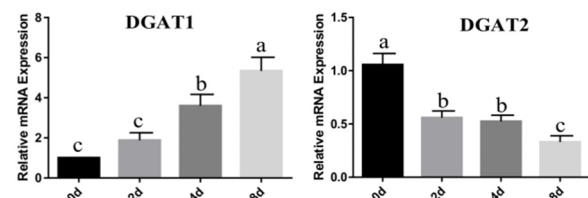
**Figure S1**. Isolation, culture, identification, and timing expression of DGAT gene in bovine adipocytes. **(a)** Morphology of cells (Scale bars: 400 μm). The newly inoculated cells were reduced into small spherical shapes (0 h). After 24 h, part of the cells with irregular triangles had attached to the wall (24 h), and then the attached cells gradually began to spread and

deform into uniform and complete single-compartment adipocytes and presented a long and narrow spindle fibroblast-like cell shape (48 h). The proliferation rate of the cells in continued culture was relatively slow, and the cell proliferation reached more than 80%, ready to enter the differentiation stage (96 h). **(b)** The cells had stable growth characteristics. From 2 to 7 days, the cell vitality was significantly enhanced and entered the exponential growth phase. After 7 to 8 days, entering the plateau phase, the cell proliferation rate slowed down significantly, and then gradually withdrew from the cell proliferation cycle. **(c)** Oil red O staining (Scale bars: 100 μm) and **(d-e)** time sequence expression of precursor adipocytes, lipid marker genes, and *DGAT* genes. The results were presented as the mean ± SEM (n = 3). The different letters (a−e) represent significant differences ($p < 0.05$) in gene expression.



(**a**)

(**b**)

(c)



(d)
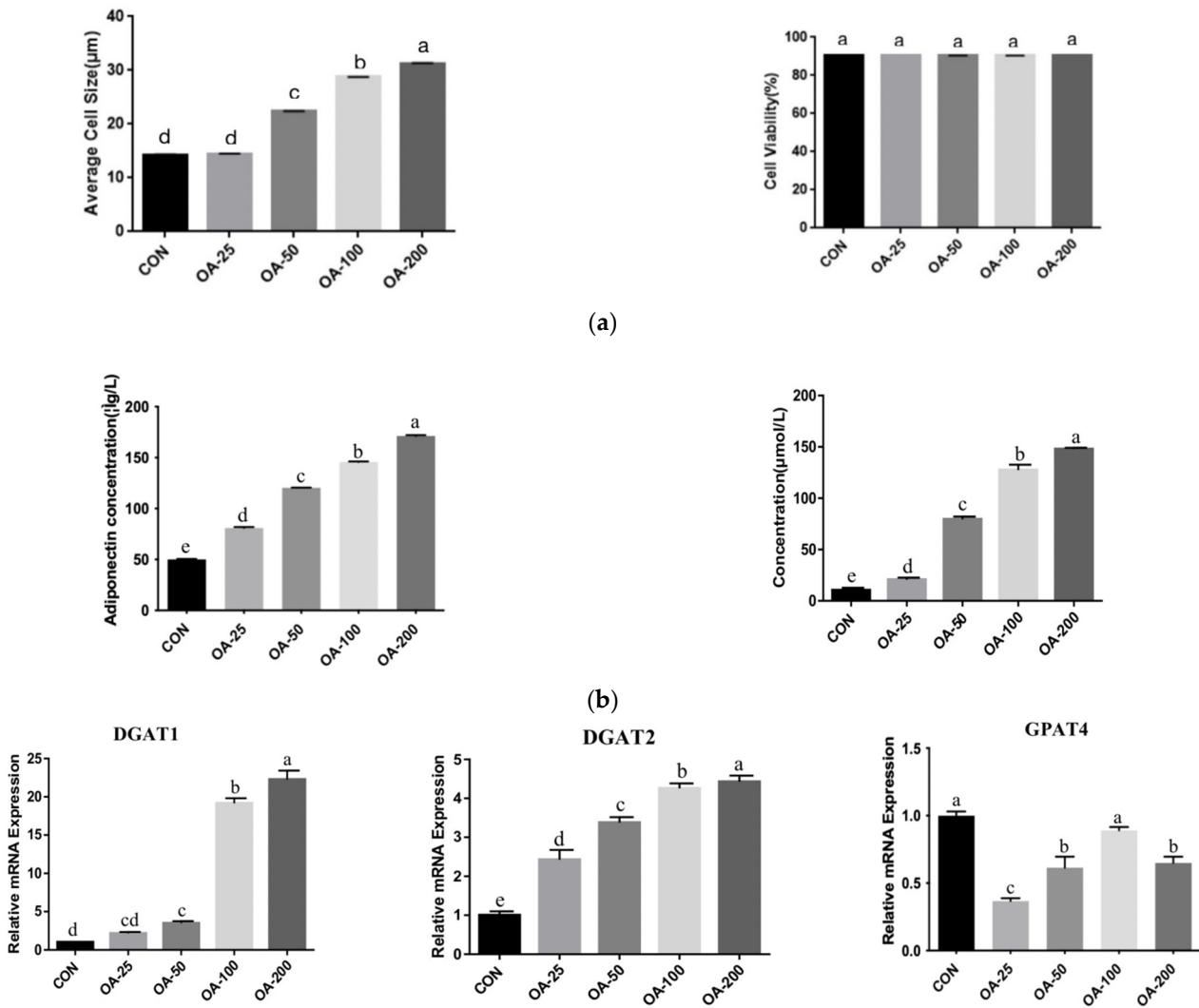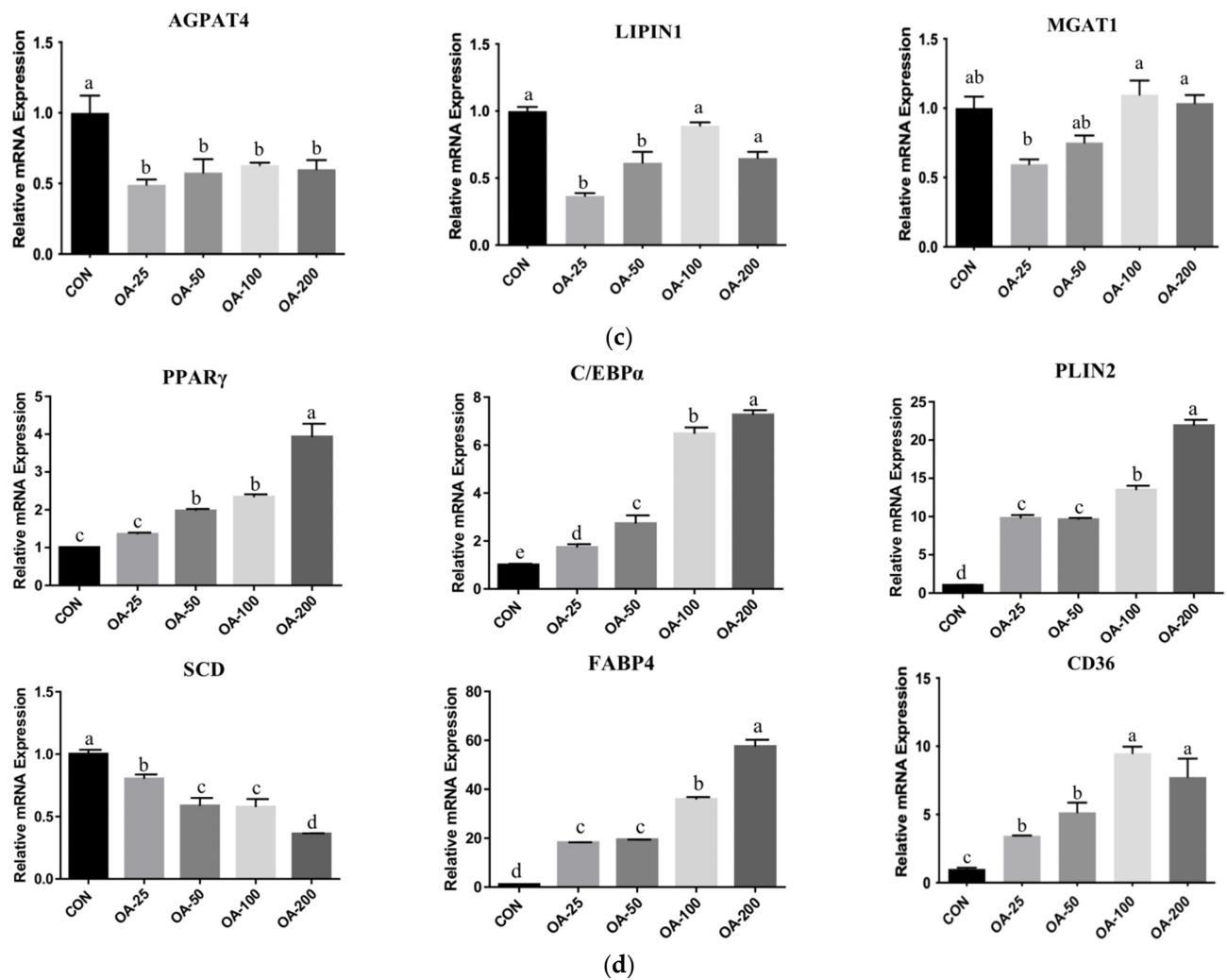
**Figure S2.** Differentiation of bovine preadipocytes induced by different concentrations of oleic acid. (a) Cell size and cell viability. (b) Concentration of triglycerides and adiponectin. (c) Expression of genes related to triglyceride synthesis pathway. (d) Expression of genes related to lipid metabolism. The results were presented as the mean ± SEM (n = 3). The different letters (a–e) represent significant differences ($p < 0.05$) in gene expression.

**Table S1.** Information of clean data.

| Sample | Trimmed_Read_Number | Trimmed_Bases | Useful_read% | Useful_bases% |
|---|---|---|---|---|
| sh-1-1 | 36366626 | 5454993900 | 91.06 | 91.06 |
| sh-1-2 | 40975778 | 6146366700 | 91.31 | 91.31 |
| sh-1-3 | 42154940 | 6323241000 | 92.56 | 92.56 |
| sh-NC-1 | 38316996 | 5747549400 | 93.13 | 93.13 |
| sh-NC-2 | 35927164 | 5389074600 | 92.61 | 92.61 |
| sh-NC-3 | 36048608 | 5407291200 | 92.93 | 92.93 |
| sh-2-1 | 44365810 | 6654871500 | 91.75 | 91.75 |
| sh-2-2 | 38107086 | 5716062900 | 92.88 | 92.88 |
| sh-2-3 | 43070816 | 6460622400 | 92.32 | 92.32 |
| sh-1+2-1 | 40170616 | 6025592400 | 92.99 | 92.99 |
| sh-1+2-2 | 43323888 | 6498583200 | 92.47 | 92.47 |
| sh-1+2-3 | 40149380 | 6022407000 | 91.74 | 91.74 |

**Table S2.** Summary of sequencing data and reference genome comparison.

| Sample | Clean Reads | TotalMapped | Multiple Mapped | Uniquely Mapped | Map Events | Mapped to Gene | Mapped to Inter Gene | Mapped to Exon |
|---|---|---|---|---|---|---|---|---|
| sh-NC-1 | 44026548 | 42389681 (96.28%) | 1002846 (2.37%) | 41386835 (97.63%) | 41386835 | 36471282 (88.12%) | 4915553 (11.88%) | 33540110 (91.96%) |
| sh-NC-2 | 42622942 | 40922553 (96.01%) | 1120749 (2.74%) | 39801804 (97.26%) | 39801804 | 34979444 (87.88%) | 4822360 (12.12%) | 32691531 (93.46%) |
| sh-NC-3 | 43119516 | 41501907 (96.25%) | 1093019 (2.63%) | 40408888 (97.37%) | 40408888 | 35378530 (87.55%) | 5030358 (12.45%) | 32742709 (92.55%) |
| sh-1-1 | 36366626 | 35017719 (96.29%) | 926080 (2.64%) | 34091639 (97.36%) | 34091639 | 30616505 (89.81%) | 3475134 (10.19%) | 28646689 (93.57%) |
| sh-1-2 | 40975778 | 39468963 (96.32%) | 1049040 (2.66%) | 38419923 (97.34%) | 38419923 | 34574231 (89.99%) | 3845692 (10.01%) | 32528805 (94.08%) |
| sh-1-3 | 42154940 | 40498526 (96.07%) | 1138229 (2.81%) | 39360297 (97.19%) | 39360297 | 34520961 (87.71%) | 4839336 (12.29%) | 31736725 (91.93%) |
| sh-2-1 | 44365810 | 42604283 (96.03%) | 1106723 (2.60%) | 41497560 (97.40%) | 41497560 | 37195112 (89.63%) | 4302448 (10.37%) | 34794332 (93.55%) |
| sh-2-2 | 38107086 | 36636777 (96.14%) | 936978 (2.56%) | 35699799 (97.44%) | 35699799 | 32098875 (89.91%) | 3600924 (10.09%) | 30060957 (93.65%) |
| sh-2-3 | 43070816 | 41277842 (95.84%) | 1181981 (2.86%) | 40095861 (97.14%) | 40095861 | 34812914 (86.82%) | 5282947 (13.18%) | 32063210 (92.10%) |
| sh-1+2-1 | 40170616 | 38605876 (96.10%) | 1007014 (2.61%) | 37598862 (97.39%) | 37598862 | 33730066 (89.71%) | 3868796 (10.29%) | 31599534 (93.68%) |
| sh-1+2-2 | 43323888 | 41295601 (95.32%) | 1140781 (2.76%) | 40154820 (97.24%) | 40154820 | 35535525 (88.50%) | 4619295 (11.50%) | 33119936 (93.20%) |
| sh-1+2-3 | 40149380 | 38497340 (95.89%) | 1120920 (2.91%) | 37376420 (97.09%) | 37376420 | 32347092 (86.54%) | 5029328 (13.46%) | 30001243 (92.75%) |

**Table S3.** Sequence information of PCR primers

| Gene | Sense Strand (5'→3' ) | Length (bp) | Gene ID |
|---|---|---|---|
| *GAPDH* | F-ACTCTGGCAAAGTGGATGTTGTC R-GCATCACCCCACTTGATGTTG | 143 | NM_001034034 |

| | | | |
|---|---|---|---|
| FABP3 | F-GAGACCACAGCAGATGACAGGAAAG<br>R-CGTCAACCATCTCCCGCACAAG | 118 | NM_174313.2 |
| OLR1 | F-CTTGTCTTTGGATGCCCAGT<br>R-ATTGACAACCCCATCCAGAA | 108 | NM_174132.2 |
| ACSL1 | F-TCCACAAGGGCTTCAAGGCA<br>R-TGGCTTCAGTTCCGAGGGTG | 144 | NM_001076085.1 |
| ACOX2 | F-GGAAAGCCAGCCAGCGATTC<br>R-AGCCGTCATGGAGGAAGTCG | 101 | NM_001102015.2 |
| PIK3CD | F-TCCTGGACAAGATCCTGGAG<br>R-AGGTCCTTCTCGTGCTCGTA | 130 | NM_001205548.2 |
| STRADB | F-CCTCATTTCTGGTGATGGCCTAGTG<br>R-CCTATGCCTCTGTCCGTGCTTAAC | 82 | NM_001192081.2 |
| FBP1 | F-AGAAGGCAGGAGGAATGGCTACC<br>R-GATGATGGGCGACTTCTGATGGATG | 86 | NM_001034447.2 |
| CFTR | F-GAGGCAGTCCGTTCTGAACCTTATG<br>R-TTCGTGTGGATGTCGCTGTCTTTC | 86 | NM_174018.2 |
| SFRP2 | F-TCCTGGAGACCAAGAGCAAGACC<br>R-GAGCCACAGCACCGACTTCTTC | 80 | NM_001034393.1 |
| MAPK10 | F-GACCACGAGCGAATGTCTTACCTG<br>R-CCCTGTGAATAATCCCAGCAGAGTG | 82 | NM_001083728.3 |
| SFRP4 | F-AACGACAGTGGTGGATGTGAAAGAG<br>R-CTTGATGAGGCAGGATGTGTGGAC | 116 | NM_001075764.1 |
| WNT2 | F-CTGTCTCGTTGGAATCTGGCTCTG<br>R-TGTCACACATCACCCTGGAGGAG | 119 | NM_001013001.1 |