

Supplementary Matrials

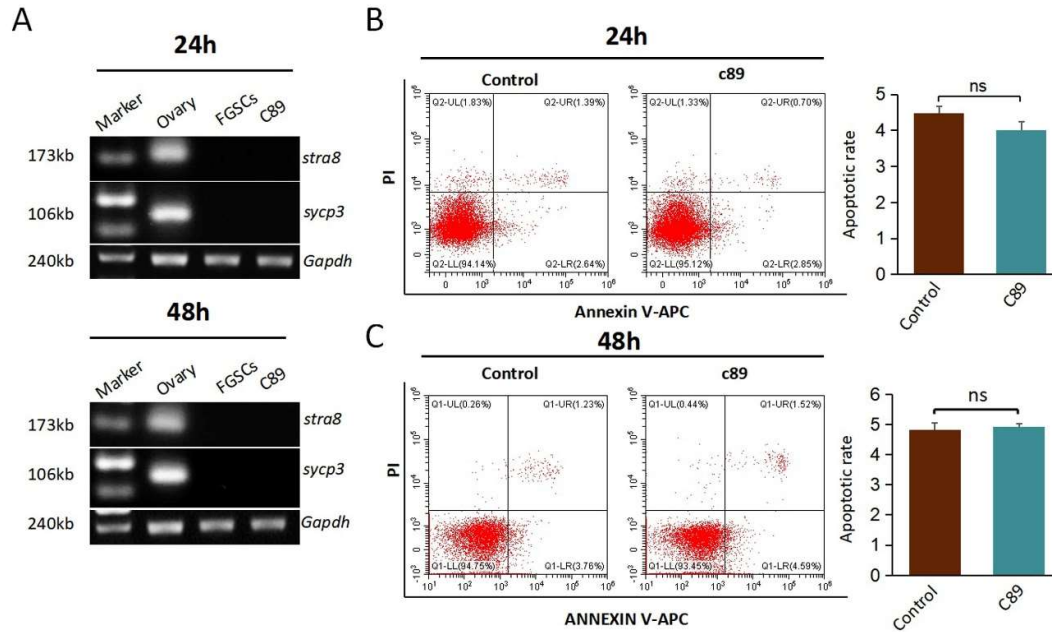


Figure 1. C89 had no effect on differentiation and apoptosis of FGSCs at 24 h or 48 h in vitro. (A) The expression of differentiation markers of FGSCs was detected by RT-PCR at 24 h and 48 h. No expressions of *Sycp3* and *Stra8* were detected in FGSCs and C89-treated FGSCs. Ovary served as the positive control. (B–) FGSC apoptosis was detected by flow cytometry. The apoptotic rate showed no significant difference between C89-treated groups and control groups at 24 h (B) or 48 h (C). ns: not significant.

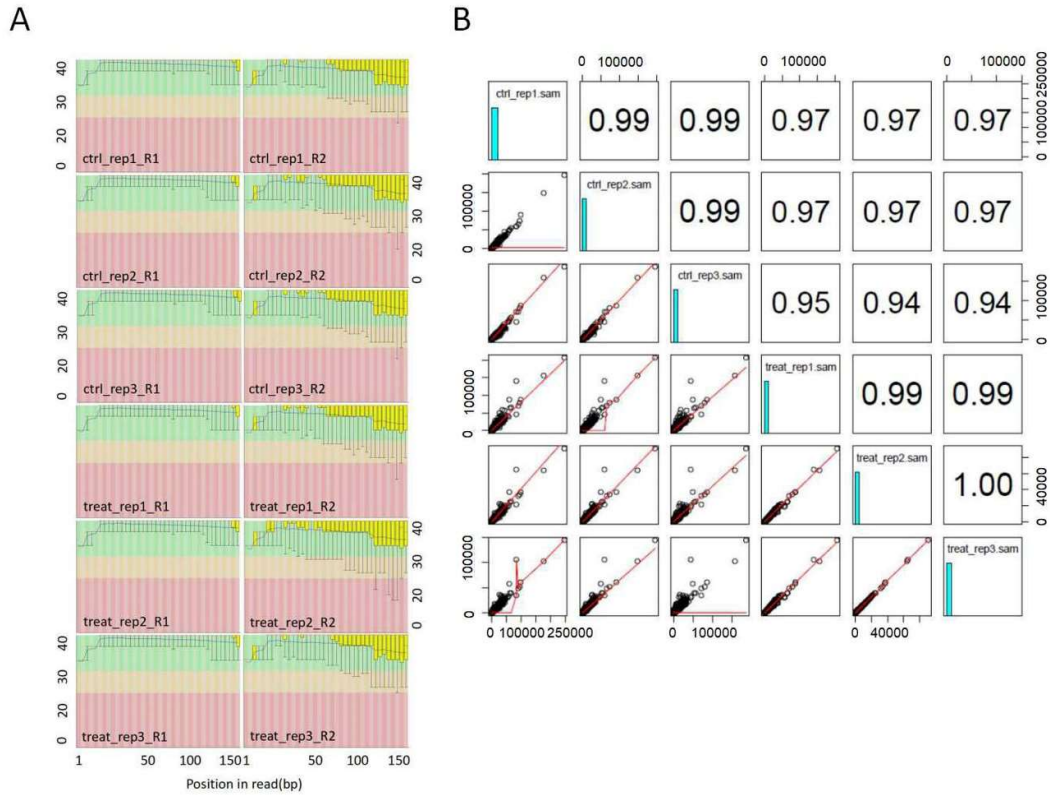


Figure 2. RNA-Seq quality control. **(A)** The Fast-QC data showing the position-specific sequencing quality in each replicated group. Data filtering criteria: Q-score higher than 10 (error rate < 10%). **(B)** The correlation plots of each replicated sample. The correlation coefficient of each replicated sample showed very good consistency. Ctrl: DMSO-treated group, treat: C89-treated group.

| Differentiation related genes | | | | Apoptosis related genes | | | |
|-------------------------------|-------------|----------------|-------------|-------------------------|-------------|----------------|-------------|
| Symbol | BaseMean | Log2FoldChange | P-value | Symbol | BaseMean | Log2FoldChange | P-value |
| <i>Stra8</i> | 0 | NA | NA | <i>Fasl</i> | 0.398275911 | -0.046778161 | NA |
| <i>Sycp3</i> | 0.821181976 | -0.138526804 | NA | <i>Casp1</i> | 0 | NA | NA |
| <i>Sycp2</i> | 0 | NA | NA | <i>Cox6b2</i> | 2.327389915 | 0.251237924 | NA |
| <i>Sycp1</i> | 44.15313238 | 0.209594478 | 0.626644766 | <i>Apaf1</i> | 716.1501603 | -0.153586386 | 0.304142427 |
| <i>Syce1</i> | 0 | NA | NA | <i>Atm</i> | 1217.959625 | -0.121556373 | 0.601505372 |
| <i>Dmc1</i> | 0.856228319 | 0.06892028 | NA | <i>Casp8</i> | 1215.923173 | 0.103682703 | 0.539648625 |

Figure 3. RNA-Seq results of some differentiation- and apoptosis-related genes. **(A)** The fragments per kilobase million (FRPK) of some differentiation-related genes. **(B)** The FRPK of some apoptosis related genes. NA, not available.

Table S1: the sequence of primes used for PCR

| PCR | Forward (5'-3') | Reverse (5'-3') |
|----------------|---------------------------|--------------------------------|
| <i>Gapdh</i> | GTCGTGGAGTCTACTGGTGTC | GAGCCCTTCCACAATGCCAAA |
| <i>Stra8</i> | ACAACCTAAGGAAGGCAGTTTAC | GACCTCCTCTAAGCTGTTGGG |
| <i>Sycp3</i> | AGCCAGTAACCAGAAAATTGAGC | CCACTGCTGCAACACATTCATA |
| <i>Bcl2</i> | CATGCCGTCCGAGAAGACCT | GATGAGCCGGACATCTTCCACT |
| <i>Trp53</i> | GGAATCTCACCCCATCCA | CAGTAAGCCAAGATCACGCC |
| <i>ATG7</i> | GCCTATATGTA CTGCTTCATCCA | CATTCAGGGGTGTGCCTCA |
| <i>Rubicon</i> | AACCTCACCCACCATCTTCTTAGCG | CACAGAGTTAAGTGCATAATTGGCATAAAG |