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## Supplemental information

# Long noncoding RNA LUCAT1 enhances the survival and therapeutic effects of mesenchymal stromal cells post-myocardial infarction

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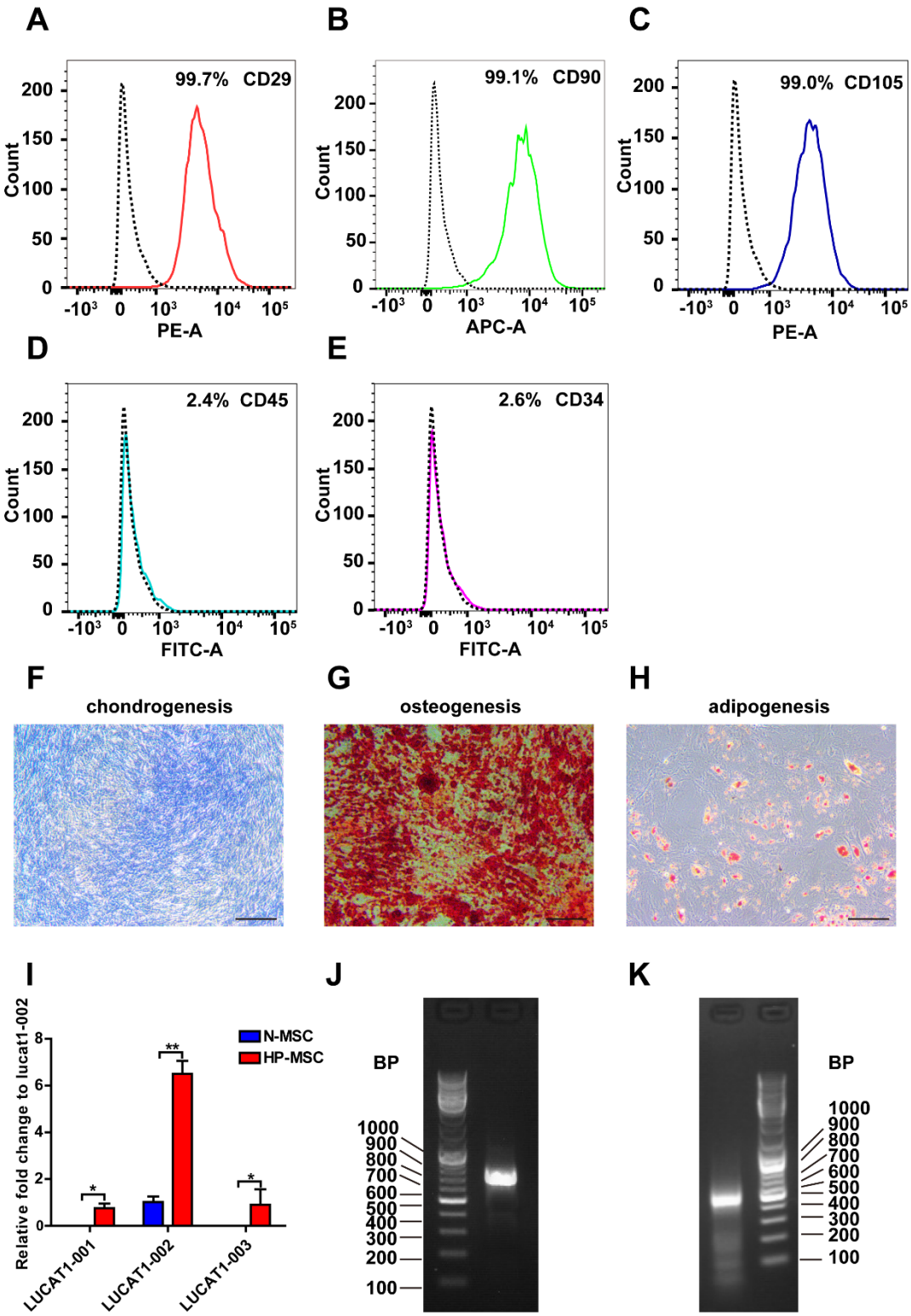
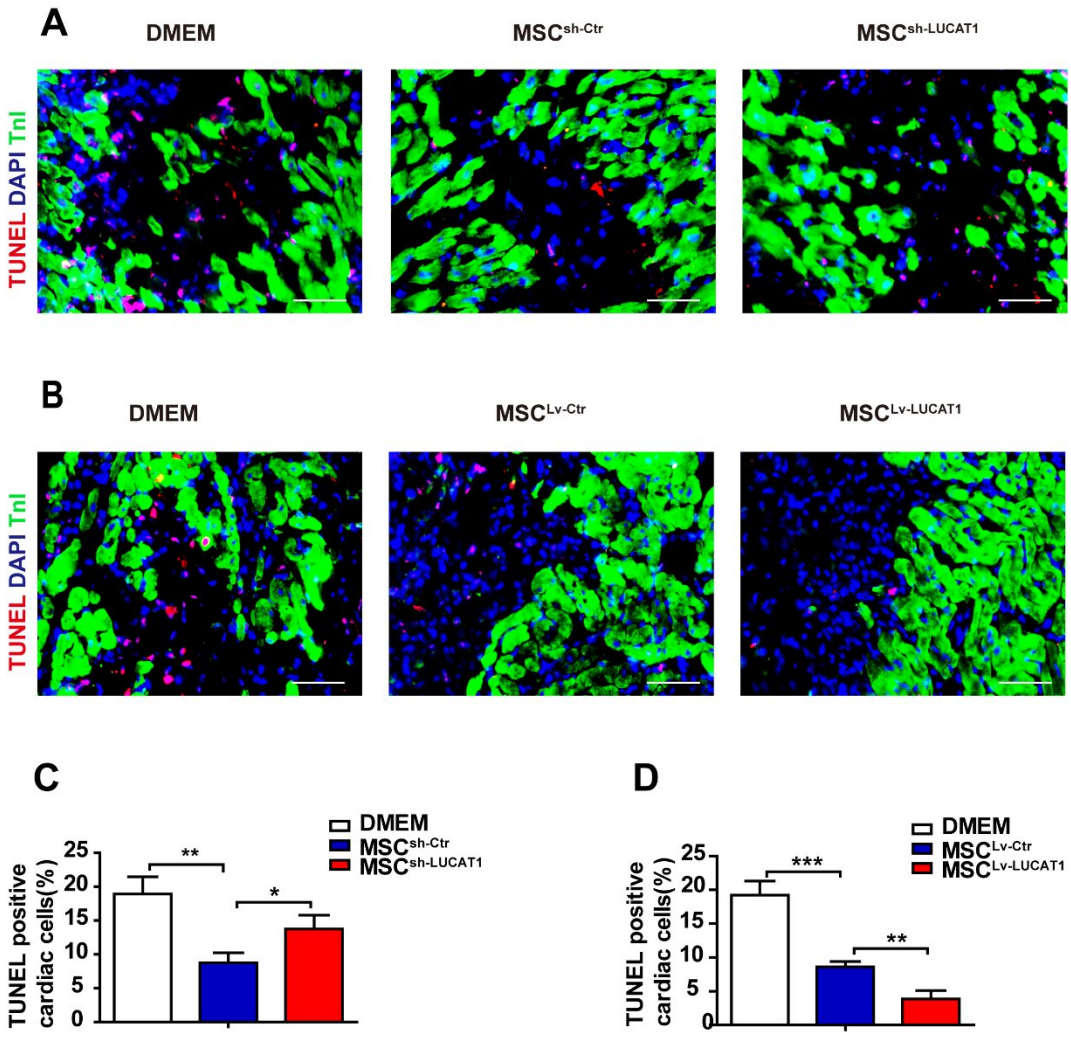
## SUPPLEMENTAL INFORMATION

## SUPPLEMENTAL FIGURES AND LEGENDS



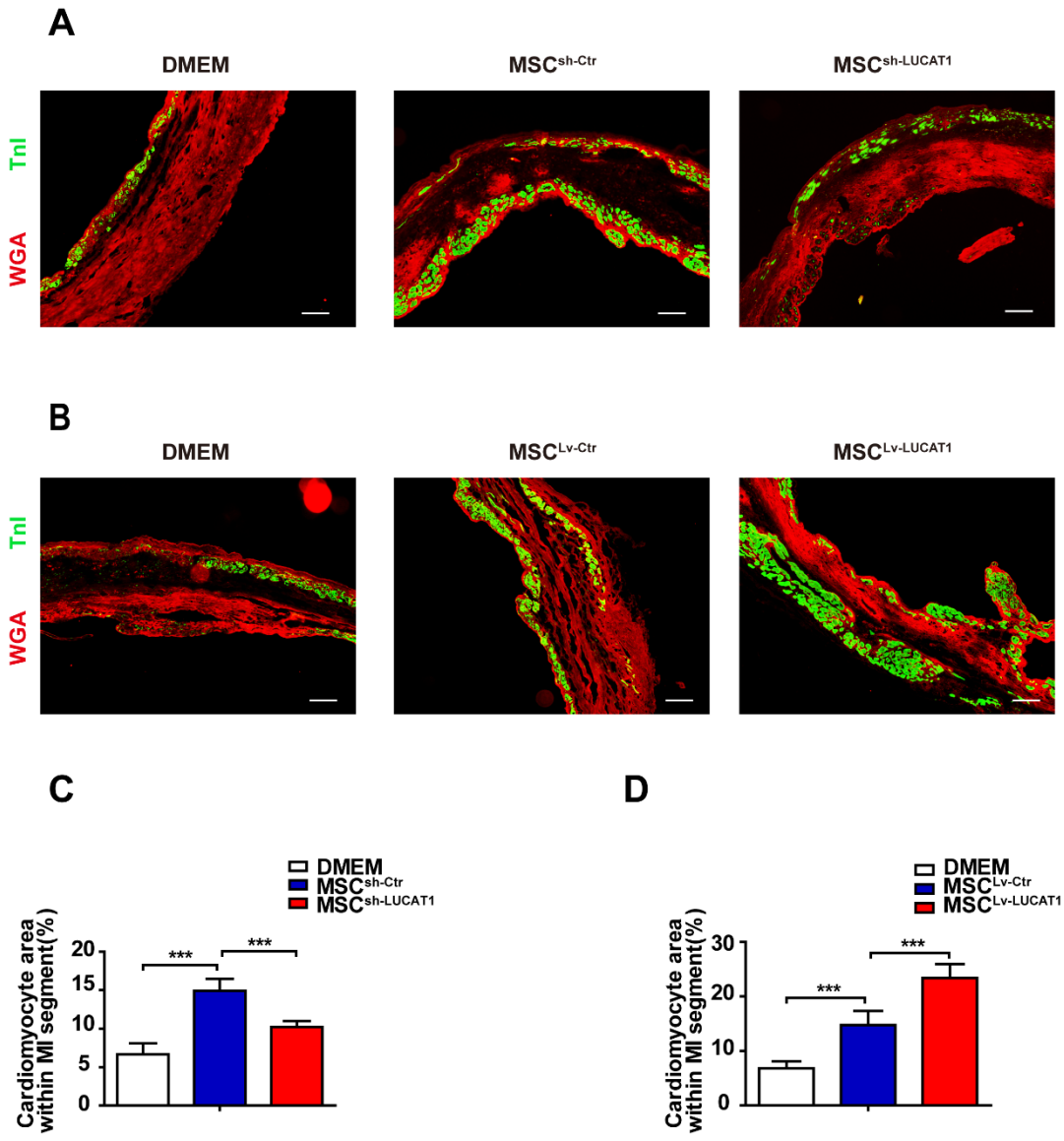
**Supplementary Figure S1. MSCs identification and characterization of LUCAT1 in MSCs**

Characterization of MSCs: positive for mesenchymal cell surface markers PE-CD29 (A), APC-CD90 (B), PE-CD105 (C), and negative for the hematopoietic surface marker FITC-CD45 (D) and endothelial cell surface marker FITC-CD34 (E). The chondrogenesis, osteogenesis and adipogenesis differentiation of MSCs were shown with toluidine eblue staining (F, dark blue), alizarin red staining (G, dark red) and oil red O-staining (H, red), respectively (bar = 100 μm). I, LUCAT1-002 was the longest transcripts and expressed higher both in N-MSCs and HP-MSCs compared with other transcripts, validated by qRT-PCR with three pairs of non-overlapping primers to each transcript (n = 3). 5′ (J) and 3′ (K) rapid amplification of cDNA ends (RACE) assays were showed by gel electrophoresis image of PCR products. Data are presented as mean ± SEM. * $p$ <0.05, ** $p$ <0.01, *** $p$ <0.001.



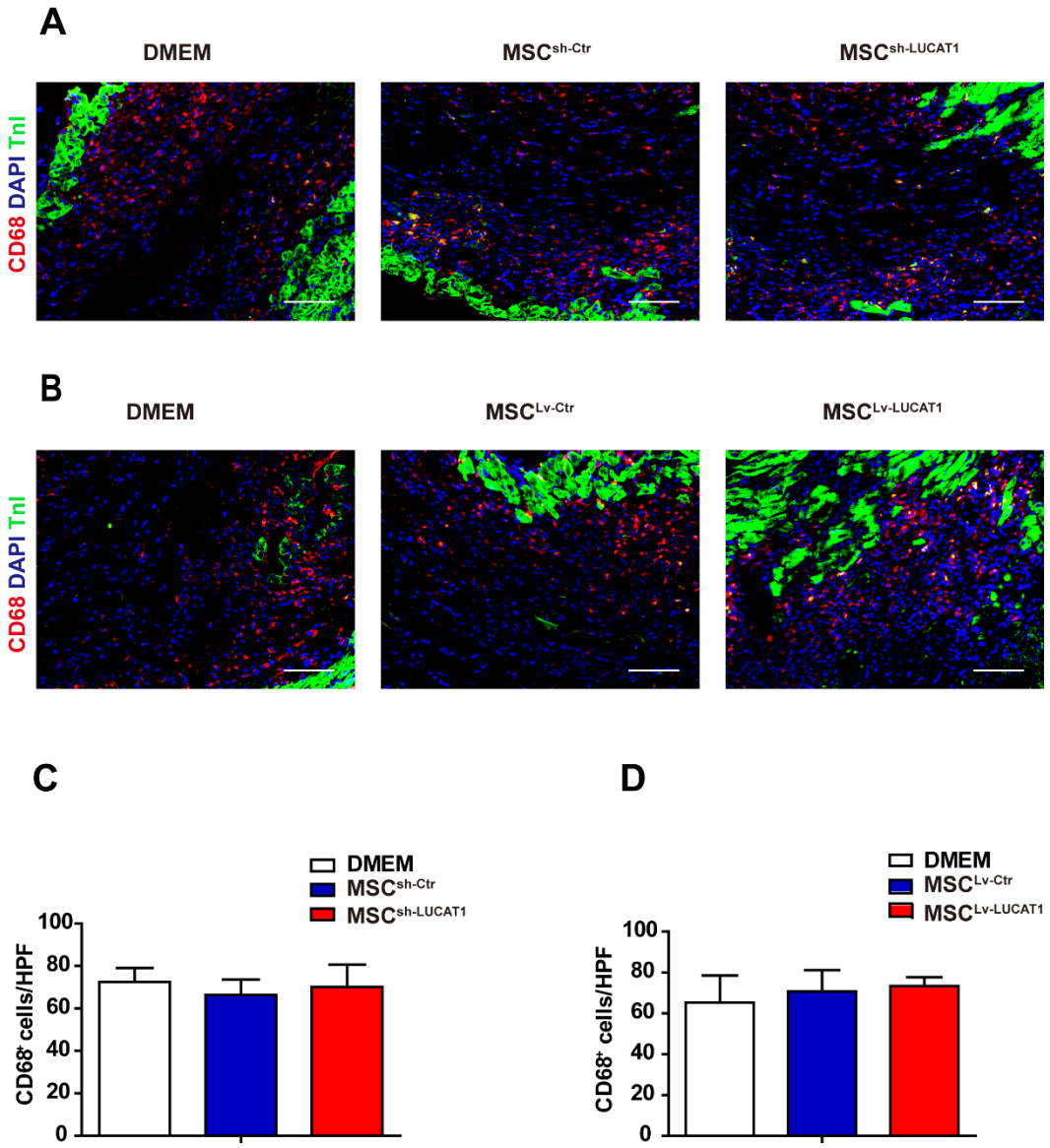

**Supplementary Figure S2. The TUNEL staining of the infarct border area at 3 days post MI**

A and B, TUNEL staining of apoptotic cells in border area. bar=50μm. C and D, Quantitative analysis of TUNEL positive cardiac cells in border zone. n=5 for each group. *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$.



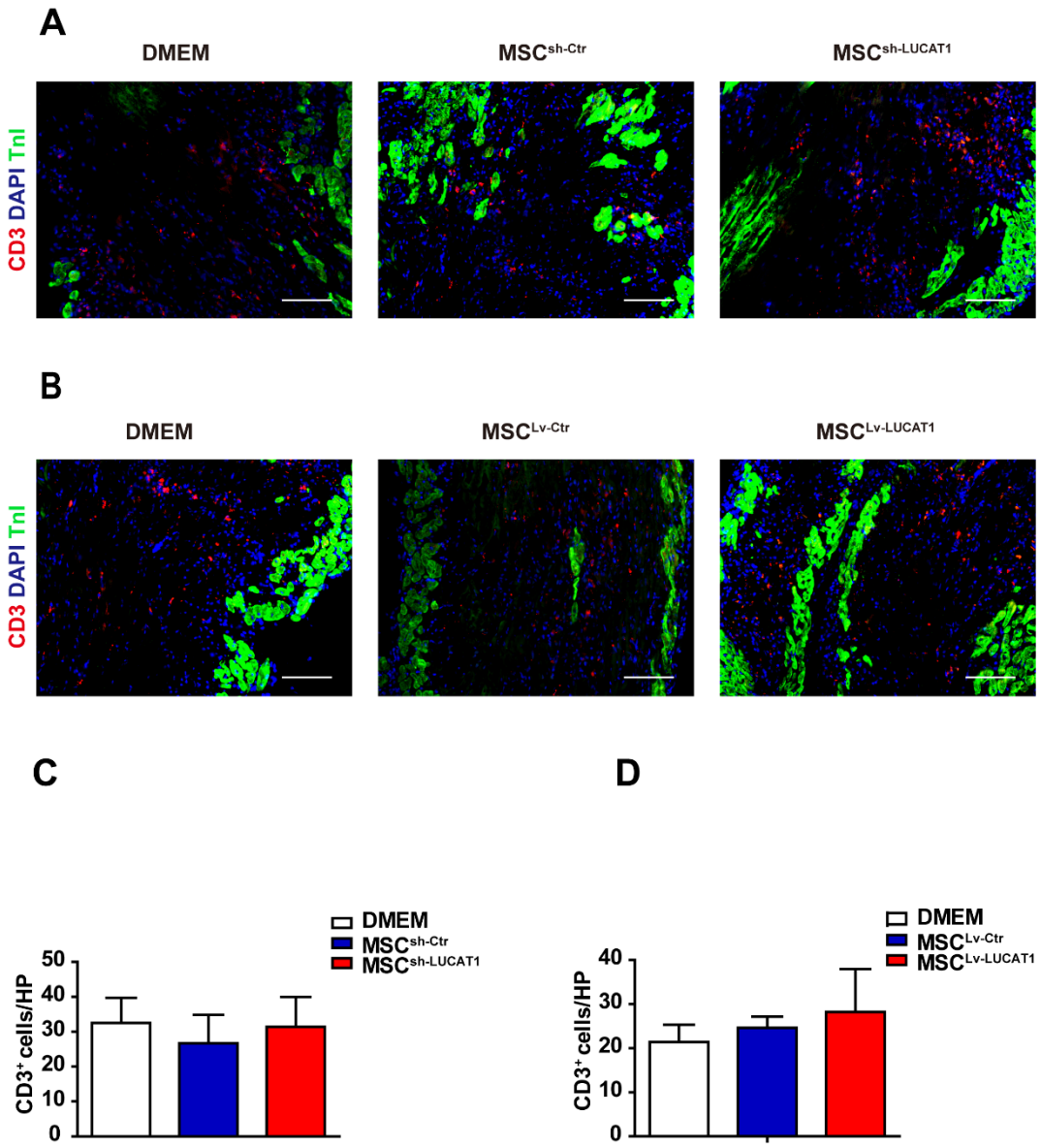

**Supplementary Figure S3. The wheat-germ agglutinin (WGA) staining of MI segments at 28 days post MI treated with LUCAT1 knockdown or overexpression MSCs**

A and B, The infarct area was stained with WGA (red), troponinI (TnI) (green). bar=100um. C and D, Quantitative analysis of TnI positive area within MI segment. n=5 for each group. ***$P < 0.001$.



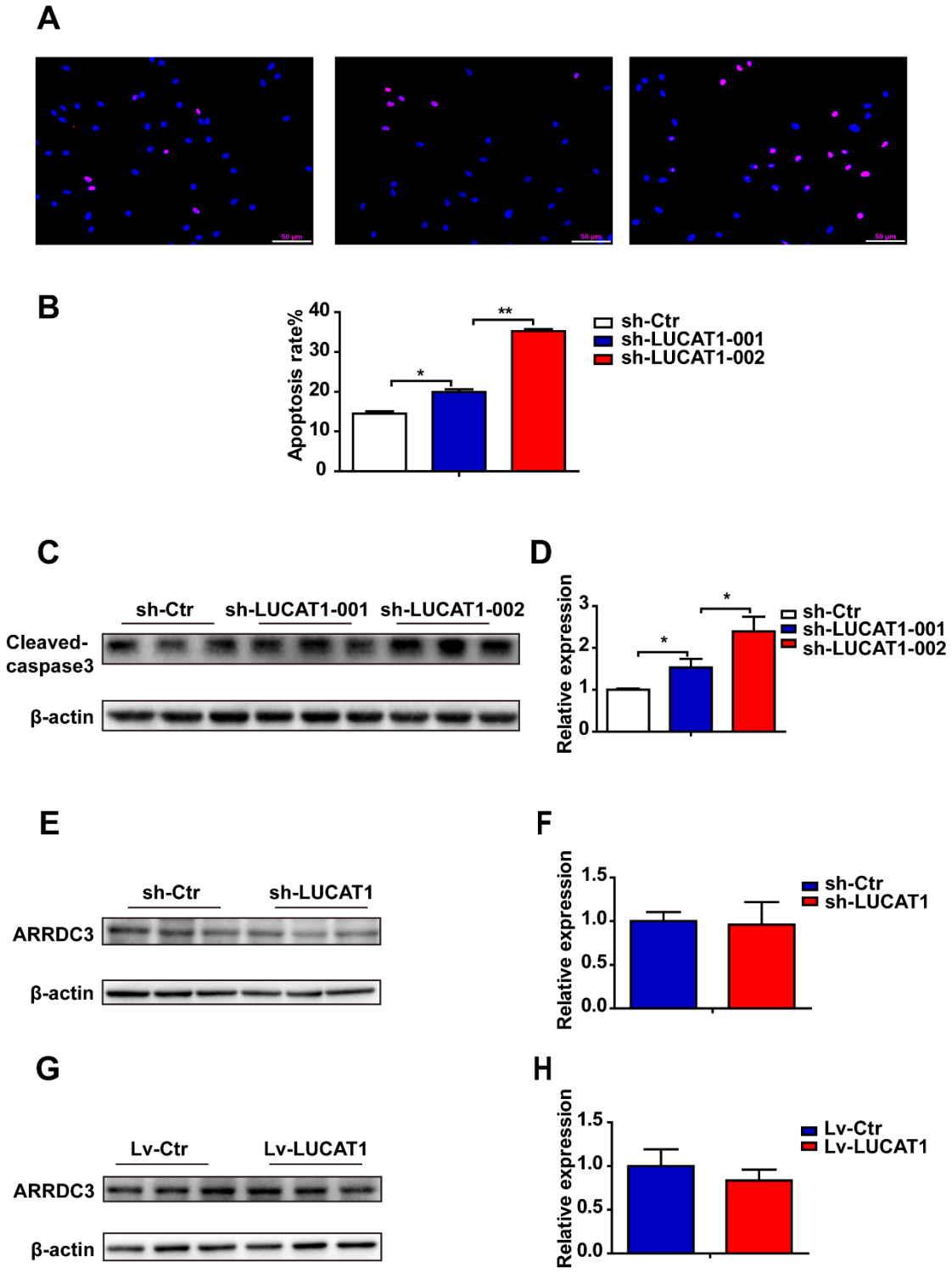

**Supplementary Figure S4. Evaluation of CD68+ inflammation cell in the border area**

A-B, Immunofluorescent staining of CD68 positive macrophages and troponin positive cardiomyocytes in the border area at 3 days post MI. bar = 100μm. C-D, Quantitative analysis of CD68 positive cells/HPF. n=5 for each group.




**Supplementary Figure S5. Evaluation of CD3+ inflammation cell in the border area**

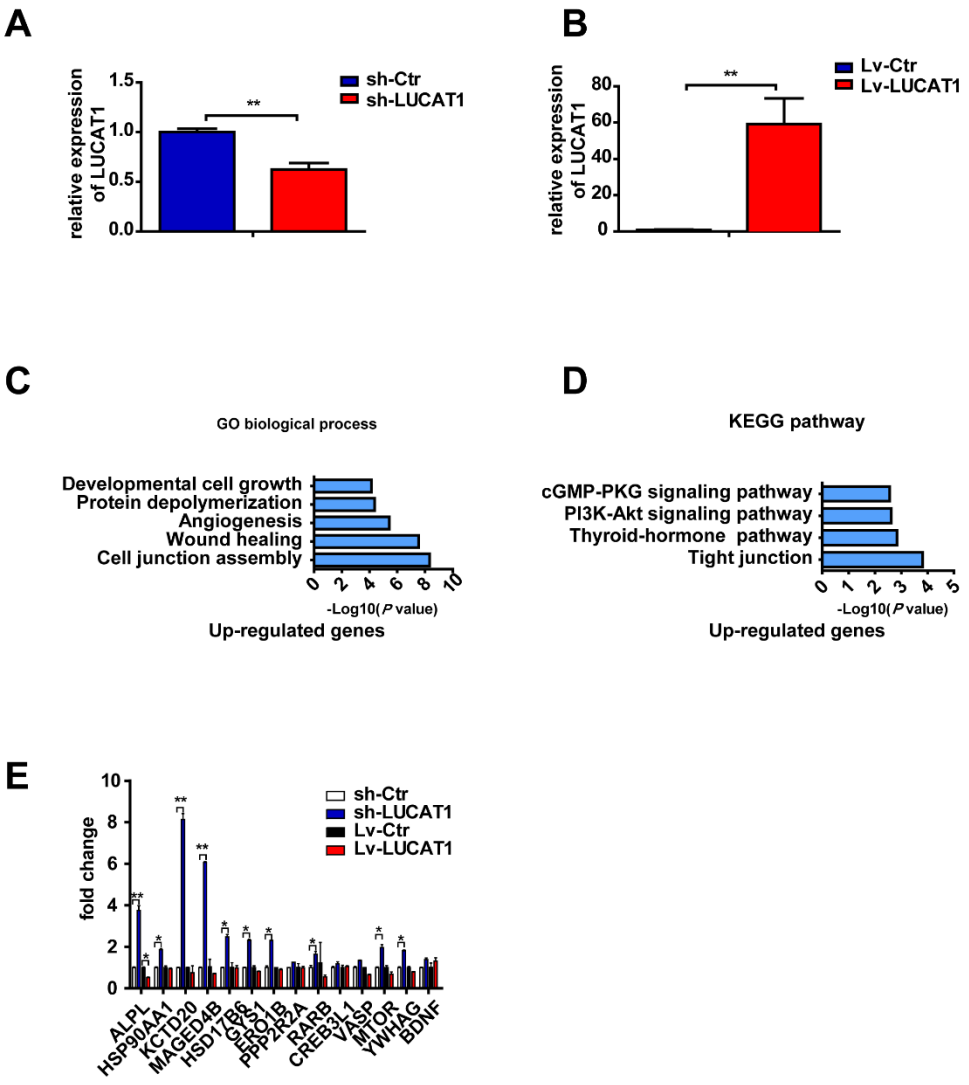
A-B, Immunofluorescent staining of CD3 positive T-lymphocytes and troponin positive cardiomyocytes in the border area at 3 days post MI. bar = 100μm. C-D, Quantitative analysis of CD3 positive cells/HPF. n=5 for each group.




**Supplementary Figure S6. Effects of LUCAT1 on apoptosis and ARRDC3**

A, TUNEL staining with nuclei as identified via DAPI staining (bar = 50 μm) of control, sh-LUCAT1-001 and sh-LUCAT1-002 MSCs under 500 μM $H_2O_2$ for 1 h. B, Quantification of TUNEL-positive nuclei (n = 3). C, Cleaved caspase 3 level was

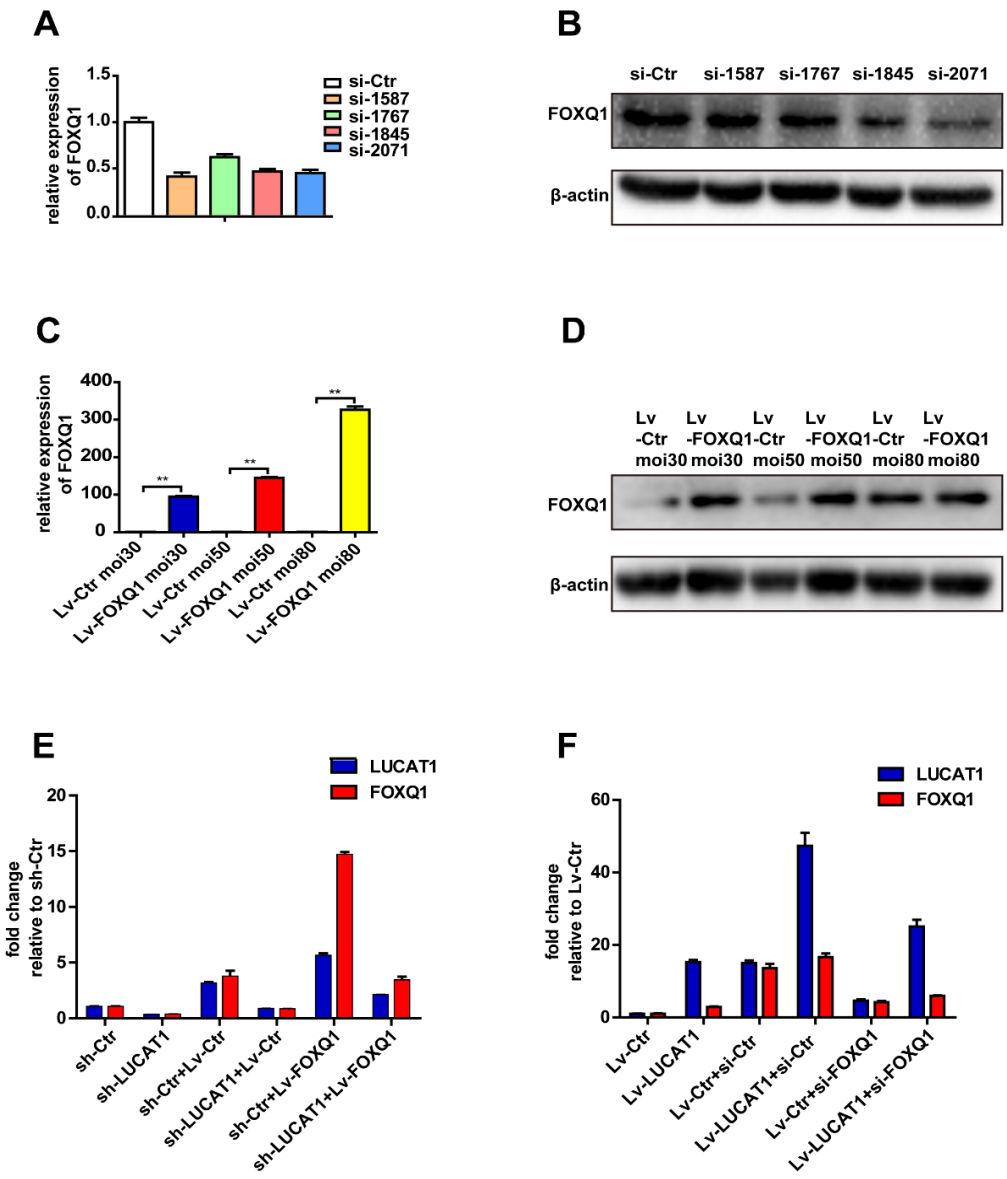
measured by western blot of control, sh-LUCAT1-001 and sh-LUCAT1-002 MSCs under conditions above. D, The quantitative analysis of Cleaved caspase 3 expression (n = 3). E, ARRDC3 level was measured by western blot of control and sh-LUCAT1 MSCs. F, The quantitative analysis of ARRDC3 expression (n = 3). G, ARRDC3 level was measured by western blot of control and Lv-LUCAT1 MSCs. H, The quantitative analysis of ARRDC3 expression (n = 3). The data are presented as mean ± SEM. * $p$ <0.05, **$p$ <0.01.




**Supplementary Figure S7. RNA sequencing analysis of the PCG expression in the**

**MSCs with LUCAT1 knockdown**

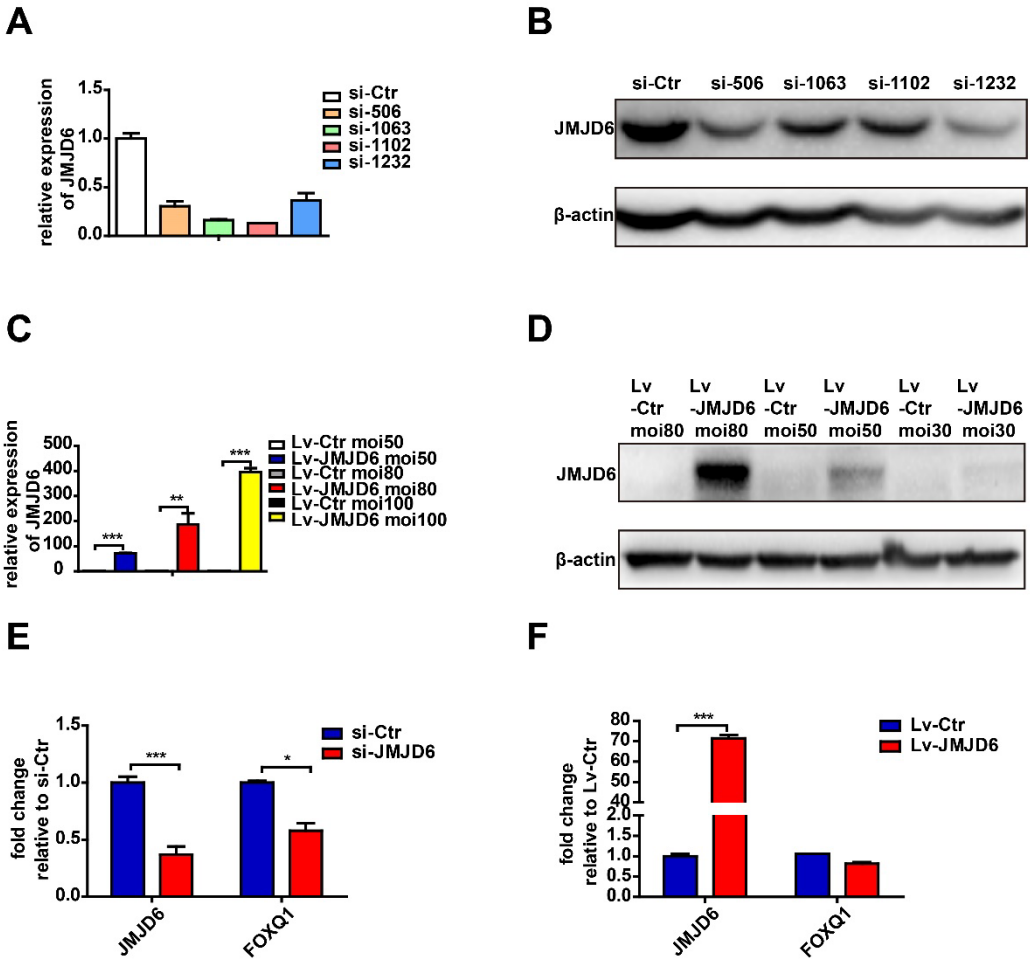
A and B, qRT-PCR showed the knockdown or overexpression efficiency of different lentivirus on LUCAT1 (n = 3). C, The GO analysis of the PCGs with downregulated expression. D, The KEGG analysis of the PCGs with downregulated expression. E, The expression of up-regulated apoptosis-related genes was analyzed through qRT-PCR when LUCAT1 was knockdown or overexpressed. Data are presented as mean ± SEM. * $p$ <0.05, ** $p$ <0.01, *** $p$ <0.001.




**Supplementary Figure S8. mRNA levels of LUCAT1 and FOXQ1 in rescue experiment**

A and B, qRT-PCR and western blotting showed the knockdown efficiency of different FOXQ1 siRNA in MSCs (n = 3). C and D, qRT-PCR and western blotting revealed the efficiency of FOXQ1 overexpression lentivirus at different multiplicities of infection (MOI) (n = 3). E and F, qRT-PCR detected the expression levels of LUCAT1 and FOXQ1 under different treatments (n = 3). Data are presented as mean

± SEM. * $p$ <0.05, ** $p$ <0.01, *** $p$ <0.001.




**Supplementary Figure S9. mRNA level of FOXQ1 following JMJD6 knockdown or overexpressed treatment**

A and B, qRT-PCR and western blotting showed the knockdown efficiency of JMJD6 siRNA in MSCs (n = 3). C and D, qRT-PCR and western blotting revealed the efficiency of JMJD6 overexpression lentivirus at different MOI levels (n = 3). E and F, qRT-PCR results demonstrated that the mRNA level of FOXQ1 with JMJD6 knockdown or overexpressed treatment (n = 3). Data are presented as mean ± SEM. * $p$ <0.05, ** $p$ <0.01, *** $p$ <0.001.

**Table S1: SiRNA sequence**

| siRNA | sense sequence（5'-3'） | anti-sense sequence（5'-3'） |
|---|---|---|
| FOXQ1-homo-1587 | CUCCAUCAAACGUGCCUUATT | UAAGGCACGUUUGAUGGAGTT |
| FOXQ1-homo-1767 | CAGGCUUCGUCUUAUUUCUTT | AGAAAUAAGACGAAGCCUGTT |
| FOXQ1-homo-1845 | GGGAACCUUUCCACACUAUTT | AUAGUGUGGAAAGGUUCCCTT |
| FOXQ1-homo-2071 | CAACGGGCUACAGCUUUAUTT | AUAAAGCUGUAGCCCGUUGTT |
| JMJD6-homo-1232 | GGGAGACCAAAGUUAUCAATT | UUGAUAACUUUGGUCUCCCTT |
| JMJD6-homo-1063 | CUGGCCACCUGAAUUCAAATT | UUUGAAUUCAGGUGGCCAGTT |
| JMJD6-homo-1137 | GGCAUGUUGUCCUCAAUCUTT | AGAUUGAGGACAACAUGCCTT |
| JMJD6-homo-506 | CGGUAUGAAAGACCUUACATT | UGUAAGGUCUUUCAUACCGTT |

**Table S2： The list of primers**

| **lncRNA qPCR primers** | **Forward Primers** | **Reverse Primers** |
|---|---|---|
| LUCAT1 | CTGGCTCCTTTCCTCACAAG | AGCTTGCAGTGAACCGAGAT |
| RP11-841O20.2 | GATGGATTGAGGAGTCTGGCT | ACATTTTGCTCACTCCTGAACC |
| NEAT1 | CTCTCCATTTCCCCATCTGA | GCTGCTGCCAAACATCTACA |
| RP11-274H2.3 | TGCCAACTCATCGGAACAGA | TTCTCAACAGCAGTGGTCCC |
| MIR210HG | CTATGCATTCCAGGCTCCAT | TCGGCTTGGTTATTTCTTGC |

| **mRNA qPCR primers** | **Forward Primers** | **Reverse Primers** |
|---|---|---|
| ACTB | CGAAAGTTGCCTTTTATGGCTC | GCGGCGATATCATCATCCA |
| GAPDH | TCTCTGCTCCTCCTGTTCGAC | ACCAGAGTTAAAAGCAGCCCT |
| JMJD6 | AAGACCTTACAAGCCCGTGG | GGGTGTTCACCATAGCTGCT |
| FOXQ1 | TCGGAAGACCAGGGTAGAGC | AGGGACGAACACCTCCAACT |
| DRP2 | ACGGAATCAGAAGGTTAGAGCTG | AGGGAGCTGAAGCTTTCCAC |
| MAPK10 | CCTTTTGTCAGGGATTCGATAAAC | ACAAACTATGCCCTGAGCCC |
| RARB | A TGGAGTTGGGTGGACTTTTCT | TCAATTGATTGAGCAGTGTGCC |
| OLR1 | GCAAATTGTTCAGGACTTCATCCA | GGTATGTCTGGGAGACAGCG |
| CDH18 | CACCACAGCTCCATCAAGGT | TGGAGTGCAGCTTTCCAACA |
| ART3 | CCTGTCTCAGCTCTCACTGTC | ACACTTCAGCCTTCACCTGG |
| NR4A3 | TCTAAAGACGGAACCGCCAC | AAAAGGTGATGAGGGCCTGG |
| EPHA1 | TTCGAGACCTTGTGTCTGGC | CCTGACACTGGGAACACCTC |
| GADD45G | CAGCCAAAGTCTTGAACGTGG | TCCTCGTTGGGGTTCGAAAT |
| POLQ | TGACCAAACAGGATTGTCACGA | AGCTGGCGCCTATTTTCACT |
| ABCC2 | TGCATCTAGGCAAGGTTAACGA | GTCCAGGAATGAGGAATTCCAAAAA |
| PCLAF | AGAAAAGTGGTGGCTGCTCG | TCCTTTTTGCCACTTGGGAGT |
| CCL7 | CCCTCACCCTCCAACATGAAA | TAGCTCTCCAGCCTCTGCTTA |
| E2F2 | CAACATCCAGTGGGTAGGCA | GGCAATCACTGTCTGCTCCT |
| COL10A1 | CAGCACGCAGAATCCATCTGA | AACTGTGTCTTGGTGTTGGGT |
| GRM1 | CAGTCCACACGGAAGGGAAT | AAGCCTCTCTCGGAGTTTGC |
| NR0B1 | GAAGATCCTCACCACCAGGC | GGCACGTCCGGGTTAAAGA |
| SKA3 | CGGCGCCGAGATTCAAACTA | TCAAAGTCGCTTTCCTCTCCG |
| HMMR | TTTCCAATTGGCTAACGCCG | GGAGATGGTGCACAACCAGA |
| CENPM | CAGGGCGGTTTGAAAGATCG | GGACTTTGCCAAGTGGACCT |
| MAGED4B | GGATGAGGGTAGCGACGAAG | TTTCCGGATCCAGCTGCAAT |
| SERF1B | GCCCGTGGAAATCAACGAGA | AGACTTCTTCTCATTAGCTGCCT |
| ALPL | AACATCAGGGACATTGACGTG | GTATCTCGGTTTGAAGCTCTTCC |
| KCTD20 | TGACAGTGACAGGTTATTGCG | AGGCATAGTCAAGTGAGAGGTC |
| HSD17B6 | GGACTGGTGAACAATGCAGG | ACACAGTAGCCTCCTACAAAGA |
| ERO1B | CCGAGGCGAAGATGATGGAG | ACAGGGTCAAAGCGGTGTTT |
| GJD3 | GCTGTTCGTCGTCTACTCCAT | ACCGCGAAATAGAAGAGCACG |
| KLHDC3 | CCGCATTCGAGTCTTTGACAC | GTCATGGAAGTGCCGGTTC |
| BMF | AACCCCAGCGACTCTTTTATG | GGCAATCTGTACCTCTGCTTG |
| LIPA | TTACAACCAGAGTTATCCTCCCA | CCAAATGAAGTCAAGATGCTCCC |

**Table S3： Information of antibodies**

| | company | | Western blot | ChIP | RIP | IHC |
|---|---|---|---|---|---|---|
| Histone H3 [Asym-dimethyl Arg2] Antibody | Novus biologicals | NB21-1002 | 1:1000 | 1:50 | | |
| Histone H4R3me2s (symmetric) antibody (pAb) | Active motif | 61187 | 1:1000 | 1:50 | | |
| Anti-JMJD6 | Abcam | ab65770 | 1:1000 | 1:50 | 1:50 | |
| Anti-FOXQ1 | Abcam | ab51340 | 1:1000 | | | |
| Bcl2 | Cell Signaling Technology | 15071 | 1:1000 | | | |
| Bax | Cell Signaling Technology | 2774 | 1:1000 | | | |
| Cleaved Caspase3 antibody | Cell Signaling Technology | 9661 | 1:1000 | | | |
| β-Actin | Cell Signaling Technology | 4970 | 1:3000 | | | |
| Anti-GFP | Abcam | ab290 | | | | 1:200 |
| Anti-TroplinI | Abcam | ab8295 | | | | 1:200 |
| Anti-CD3 | Abcam | ab16669 | | | | 1:200 |
| Anti-CD68 | Abcam | ab125212 | | | | 1:200 |
| Wheat germ agglutinin (WGA) | Thermofisher Scientific | W32464 | | | | 100ug/ml |
| Donkey Anti-Mouse IgG H&L (DyLight® 488) | Abcam | ab96875 | | | | 1:3000 |
| Donkey Anti-Rabbit IgG H&L (DyLight® 550) | Abcam | ab96892 | | | | 1:3000 |
| Donkey Anti-Goat IgG H&L (DyLight® 488) | Abcam | ab96931 | | | | 1:3000 |
| Donkey polyclonal Secondary Antibody to Rabbit IgG - H | Abcam | ab150073 | | | | 1:3000 |

ChIP:Chromatin immunoprecipitation; RIP:RNA-binding protein immunoprecipitation; IHC:immunohistochemistry

**Table S4： The list of proteins predicted to be only pulled down by sense sequence (see the attached Excel table S4 for details).**

**Table S5： The list of RACE and ChIP primers**

**RACE primers**

**adaptor primers:**

| | |
|---|---|
| 5’adaptor | GCTGTCAACGATACGCTACGTAACGGCATGACAGTGCCCCCCCCCCCCCCC |
| 3’adaptor | GCTGTCAACGATACGCTACGTAACGGCATGACAGTGTTTTTTTTTTTTTTT |
| 5.3’outer | TT GCTGTCAACGATACGCTACGTAAC |
| 5.3’inner | GCTACGTAACGGCATGACAGTG |
| **5’ RACE:** | |
| RC351-R4 | TGTCTAGGACAGCTCCTAGCTCATATTTAGTGTT |
| RC351-R3 | GAAAAATGGGATGCTAACATAAGGCCAAC |
| RC351-RT4 | TCAGAGCTCAGGCTATACAT |
| RC351-RT3 | CTTCCATACCAATTTGTTCA |
| **3’ RACE:** | |
| RC351-F3 | CTTTGAATGCAGCCAAACACAAATTTGTAA |
| RC351-F4 | CATGTATTTTATGTGTGGCCCAAGACAATT |

**ChIP Primers**

| **Promoter area(-)** | **Forward Primer(5'-3')** | **Reverse Primer(5'-3')** |
|---|---|---|
| -147~-488 | CCCAAAAAGCAGCCATTCCC | ACGCCGAGTTTCCTCCTTTT |
| -399~-766 | TCCGTCGCTTTTTGTGCAAC | CACTTGTGTCCCTGCGGAAG |
| -757~-1156 | GACACAAGTGCAGGCACAG | GCGGCGTATGTGCTTCTGTA |
| -1056~-1281 | GCGCATACAATTTCAAGCCCA | GCAGTGACCTCTTTCGGGAG |
| -1261~-1643 | TAAACTGCGTCCCCGAACTC | CCGGCCCAATATAACCCTGC |
| -1619~-2019 | CCGCCGCAGGGTTATATTGG | GCTTTTTCTCTGGAGGGGCT |

RACE:The 5' and 3' rapid amplification of cDNA ends

**Table S6: Full length of LUCAT1 different transcripts**

**Full length of LUCAT1-002**

TTTAAACAGAAGGCTCCAGGAGACATACAATCAACACTCCACTCAGACAA

TGCCCAGACCTCCAGAAACCATGTGTCAAGCTCGGATTGCCTTAGACAGG

TGCAATTTAAGAACAGCTTTCATCCTCTTTTCTCTCATATTGTCACACTATG

TGTTCTGACTTCTGGCTCCTTTCCTCACAAGAAGCTCACCCAGCTGGAACT

CTTATGGGACCTTGGCACCAGAGACCACAAATTCCTCTTTGAAGTTTTCTA

ACAGCAACAATGGTATTTCTGACTTGGCTTTCTTGTATTTCTCTCACGTTAA

CAAAATTGGTTCAGCATCTACCATGGGCTACATGCTGAGCTACAGAGTTT

CGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCGCGCGATCTCGGTTCACTG

CAAGCTCCACCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCCTCCTGAGT

AGCTGGGACTACAGGCGCCCGCCACCACACCCAGGAATCCAACTTGCTGT

TTGCTATCACATGTGCTATACATGCTGTTGATGAAACTGCTAAAGGGGCTG

AATGTGACTGACGTCTTTGGAAGGATGAGACTTAGCGTGCCTGTACAGTT

GTGTCCAAATGCTGTCCTCATCTCCCAATGAAAAGGTATTGTAAATAAAG

AGAAAGATCAGAGGCTTATTTTAAACACTAAATATGAGCTAGGAGCTGTC

CTAGACACTATGTAAAAGTTTTATTTAGTTCTCACTGTAATGTTGGCCTTA

TGTTAGCATCCCATTTTTCAGACTGAGGAAATTATGGCTCAGAGAGGTTAA

GAGACTTATTGAAGGTCACACAGCTCCACAAACTTTGGTGTAGATTGAAC

GTGTACATGGGTCTATGTGACTTTGAATCTTGCATTCTTTACATTATTGGA

ATATTTCACAGAAGGAAAATGACATATTAACATGGCAATAAGATTTCTGG

TTCCAGTCTGGTTACTGGTCTTCCAAGAGTGTTATAGGATGTATAGCCTGA

GCTCTGAAGCTTTGTTCTGAAGCATGCTATCAATATGAACAAATTGGTATG

GAAGGAAGCCACAAATTATATACTAAAATCTAGTTCATCAGAGGAAAATA

TAGTTAAATACATTTACATTCCCAGAACTGTTAATATTGAAGAATAAAAC

ACACAGTGGGAAAGAGACGAAGAGAAAATACGCCTGTTTTTATGACTTGT

TGATATCTACAGGGTTTTTCCTTAAGCCTCACAACAATTTACAGCATTGCC

AGCAGCATTCAGTACATTCAGAACAGGATAATTTCACCCGCAGCTGAACT

AGGGCCATGCCTGGGACAGACAGAGAATGGCCTTCCAGCAGACATGCCA

AGAAGCAAGCCAGGGTCAGTGAGTGAAGAGGAGGGCAGGCCCATTTGAA

GCAACACAGTTTATGTAAGTGTGATCTAACTGCTTTCACTGGAAATGGGTC

AGACTCCAGTTGAGAGAACCAGGGGCCTGAATGACCCCAGCAAAATCACT

GTGGCAATTCTTTCAATCACCTCTGAGAATATGGCCCTGTGACGACATAAT

GACGTTTGGATTAATTCCAGTCGGCTGTGTTTTCCCCTCCTTTCTTGCCTCC

CCGTAGTTGATTTGCCAAATTTTTTTTGTTTGCTTAAATACGCGGAACTAA

ACAGGATACATTATATGACAGTCTGTGATAAATTTACCACTGGGAATAGG

GAAAAAGTATGGGATAAAGAAATAGGTATTTTTCGCCTCTCACAGCTGTG

ATTCAGTTCTGACTCAAAAGGAAGTGTGCCACCTACTGAATCACAGAAAC

CACTTCCTGTGGCTGTTTGGTTTATTCTGGAGGAGCATCAGGCCAAGTGCT

GCCCTGCCCTGACCCTGACTGGCTCTTCAGAGCCAAGGCATTCACAGCTTG

AGGTGGTTTGGCCTCAGACTCTTGAGAACATTGCATATTAAATTACAAGTG

TTTCGTTTCCTAGCAAGGAGTCTTTAGCAACATGAAAACGAACGTGTGTTA

TTTGCAAACCAAGTATATCATTACTGAACCTGAATATCCTTACTTTTTCAT

AAGGTACGTATTCCGGATGACCACTCTTAAGATCTGAATGTACACTGGTTC

TGTTTTTCCTGAGGGGAACTTGGGCAGTCTGCAGGGTGGCATTTACCAGCT

GAGGGACTTCAAGAGCACCCTTTAATCAGTGTGGCAGCACTCAACTTGTA

TTCACTCACTCAGAGTATTTTTGAGCATGTACTTATTGCCATGTGCTGTGCT

AGGTAGGGGTAGAGGGTACAGTGGTGAACAAGACCCCACAGCTCCTGAC

CTCATGGCTCATGTGTTCTACACCATAAGGGAATCAAGCTGTGTCTCCCGG

GGCAGGGGCCTTCCTCTGTTCACCATGCAGCCCCAGCATCTAGCACCTGG

CGTTGCATAAAGGAGGCTCTAAATCAAGCTTGTCCAACCCAAGGCCCACG

GGCCACATGTGGCCCAGGATGGCTTTGAATGCAGCCAAACACAAATTTGT

AAACTTTCTTAAAACATTATAAGATTTGTGTGTATGTGTTTTAGTCCATCA

GCTATTGTTAGTGTTCATGTATTTTATGTGTGGCCCAAGACAATTCTTCTAT

GTGGCCCAAGGAAACCAAAGATTGAACACTCCTGCTCTAAATACTTGTTT

GTTGAATAGATACATGAAAAGAAAGAAGGAGAGAAGGAAGAAAGGAGG

GCGGAAGGAAAGGAAGAAGGGAGAGAAGAAGAGAAGAAAGAAGCAGAG

AAAGGAAGAGAAAAGAAATTACGGCCAGTGCGGTGGCTCACGCCTGTAA

TCCTAGCACTTTGGGAGGCCTAAGCGGGCTGATCACCTGAGGTCAGGAGT

TCGTAAGCCAGCCTGGCCAACATGGTGAAACCCTATCTCTACTAAAAATA

CAAAAATCAGCAGGGCATGGTGGTGCGTGCCTGTAATCCCAGCTACCTGG

GAGGCTGAGGTAGGAGAATCGCTGGAACCCGAGAGGCGGAGGCTGCAGT

GAGTTGAGATCATGTCACTGCACTCCAGGCTGGGCAACAGAGTGAGACTC

TGTCTCAGAAAAAAAAAAAAAAA

**Full length of LUCAT1-001**

GAATCAACACTCCACTCAGACAATGCCCAGACCTCCAGAAACCATGTGTC

AAGCTCGGATTGCCTTAGACAGGTGCAATTTAAGAACAGCTTTCATCCTCT

TTTCTCTCATATTGTCACACTATGTGTTCTGACTTCTGGCTCCTTTCCTCAC

AAGAAGCTCACCCAGCTGGAACTCTTATGGGACCTTGGCACCAGAGACCA

CAAATTCCTCTTTGAAGTTTTCTAACAGCAACAATGGTATTTCTGACTTGG

CTTTCTTGTATTTCTCTCACGTTAACAAAATTGGTTCAGCATCTACCATGG

GCTACATGCTGAGCTACAGAGTTTCGCTCTGTCGCCCAGGCTGGAGTGCA

GTGGCGCGCGATCTCGGTTCACTGCAAGCTCCACCTCCCGGGTTCACGCC

ATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGACTACAGGCGCCCGCCACC

ACACCCAGGAATCCAACTTGCTGTTTGCTATCACATGTGCTATACATGCTG

TTGATGAAACTGCTAAAGGGGCTGAATGTGACTGACGTCTTTGGAAGGAT

GAGACTTAGCGTGCCTGTACAGTTGTGTCCAAATGCTGTCCTCATCTCCCA

ATGAAAAGGAACAAAACCCATCAGAAGATGTCAGAAGATAAGGATTTTT

GTCCTGATGCTACACTTACCAGCTGTCCCTCAGTGTTCTACTTCTTAAAAA

AAGAGAGATGGATAAACAGAGGCAACCCGAGGATAAAGGCCTTGCTCAG

TGTCACACATTTCAGTCACTAAATAAGACACAATGGATGCCAGTATTCTC

ATCCCCTCACAAATAAAGAGCCTTCAAGCTCTTGCAGTCAACAAGAACTT

TTGGAATGATTTCACTGCCTGAAAAGGCAGATACATAGGTGACACCCACA

AATAGGAAGAAAATCAACCTGAACCTGAGTGTGTGGGCTCACTGACTCTA

AGCAGTAGAGACAGAAGAAAAATAAAGTTTTAGCAAAGAAGGGTTCTGA

AAGAAAATAAATATAGCTCGTTATCAAGTGCTGTTTTTACACAGTAAAAC

ATGGGCAAAATTACTCTTCTTTAAGTAGTAATTCTTATCTCTTGATTAAGT

CACCTACTCATTCATTTAATAAATACATACTGATTGTTTTCTAAAAAAAAA

AAAAAAAAA