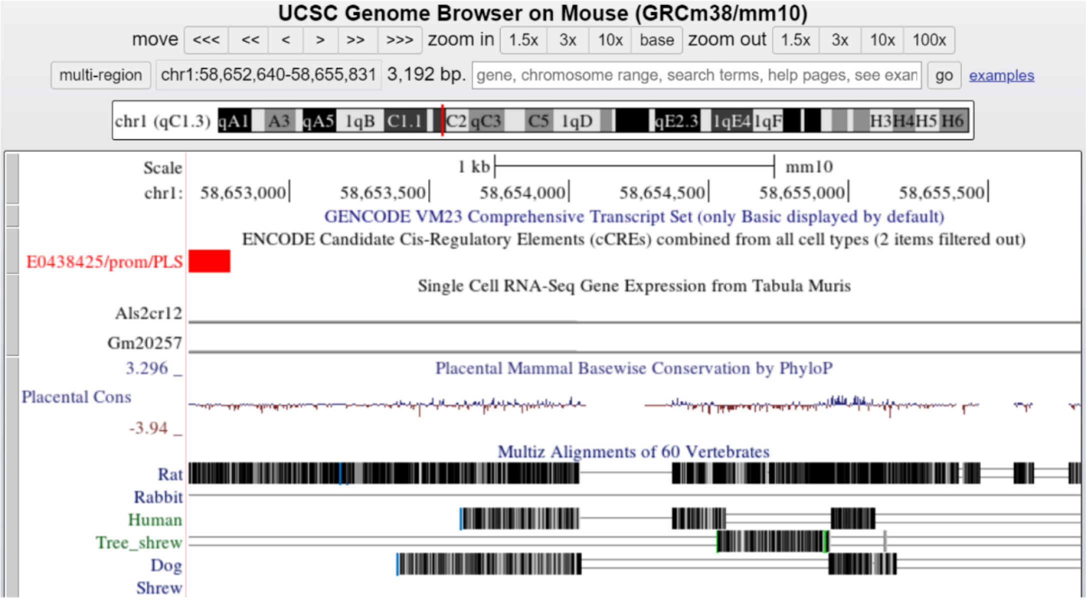
Figure S-1



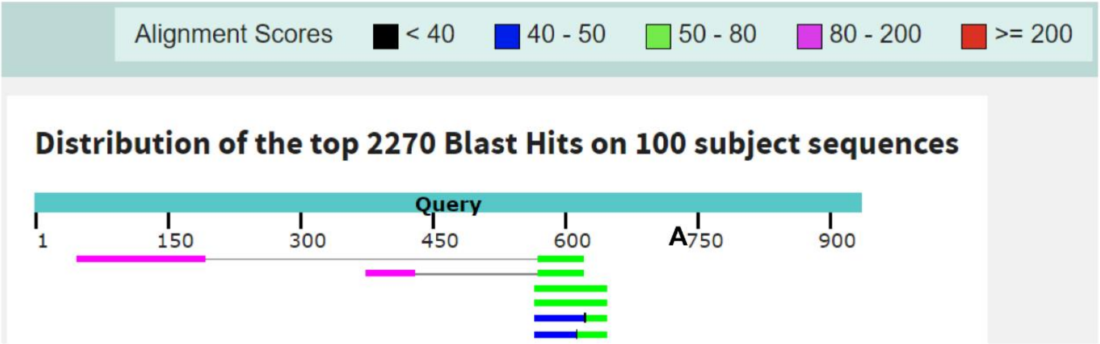
Gm20257-NR_045007(RefSeq,936) chr1: 58652640-58655831
1 gaagtctctg agacctgagc ctctcaagcg gccacttagg ggcagacaga ggagatgaca
61 ttcttagcat cctgactggc gtgaactatg acgtgagcaa taaagacgac aggaggaaca
121 agggaaagca gatgacacag cccaccttca cactacggaa gaagctcttc ttccctccct
181 aatgatgtgt gctctccaca gttcacatgg cttatctgtg cacttttgtg tggatgagtc
241 taatttattt tttaggattt cttttgtttt ttaggttaca cttacatcat ttccccttt
301 cctcccttca aatccttcta tgtaatgttc caatttcaaa tacatgacct cctttctcat
361 taactgttgt acacacacac acacacacac acacacacac acacacacac acatttctaa
421 atataaccta cccagtttgt atactgtcac ttagatgtat gttttgtttt gcttttttaa
481 attggagcaa cctttggtag gctaatcaca ctccaaggca ggtccctctc ccaagaatag
541 ctgggcaaca caaactgaat tccatgggtt cacctttaat cccagcactc tggaggcaga
601 ggcaggagga tctctgagtt caaagccaac ctgctctaca tagcaagttc tgagatagcc
661 aggactacac agagaaagct tgtcttgaaa aaaacaaact tgaagatgca tgagtaagaa
721 agcaagactg gaacataaac ctgtttaaca gaatgggtga atgacgggag cagggacctg
781 gggcaagtta acagagtggg tgaaagaaca tggacctgag acaagttaac aaagggggtg
841 aatgatggga gcggggacct ggggtgagaa aggggtgaat atcatcagca ttttgctgca
901 tgaaattctc agaggtaata aaaaatatta aacttt

Figure S-1 The genomic location, conversion, and sequence of lncRNA Gm20257.

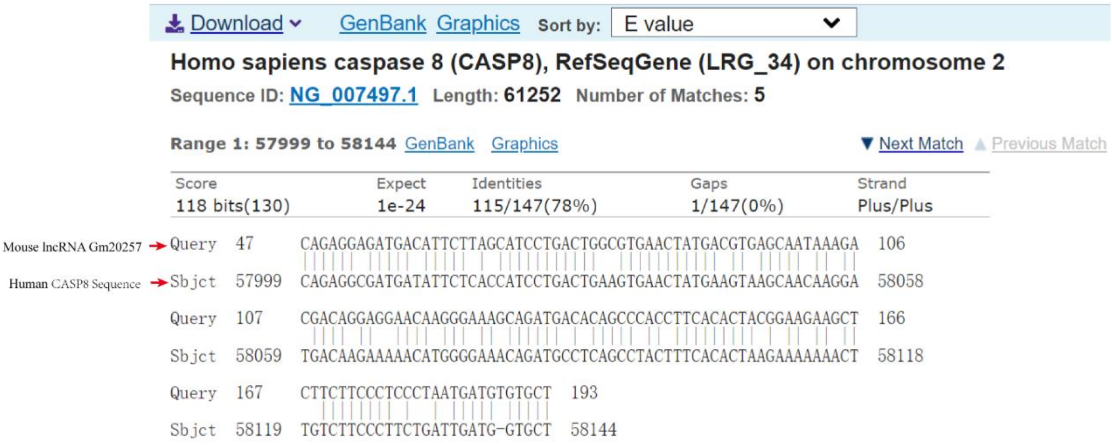
LncRNA Gm20257 locates on chromosome 1: 158652641-58655831, the genome’s full length is 3193 bp in which the exon that could transcribe to Gm20257 is 936 bp. Both exons and introns contain sequences similar to human genes.

Figure S-2

A **The Graphic Summary of the conservative sequence of lncRNA Gm20257 between mouse and human**



B **Complementarity between mouse and human**



Homo sapiens caspase 8 (CASP8), RefSeqGene (LRG_34) on chromosome 2

Sequence ID: NG_007497.1 Length: 61252 Number of Matches: 5

Range 1: 57999 to 58144

Score	Expect	Identities	Gaps	Strand
118 bits(130)	1e-24	115/147(78%)	1/147(0%)	Plus/Plus

```
Mouse lncRNA Gm20257 →Query  47     CAGAGGAGATGACATTCTTAGCATCCTGACTGGCGTGAACTATGACGTGAGCAATAAAGA  106
                                    |||||| ||||| ||||| | |||||||||||  ||||||||||| || ||||| || ||
Human CASP8 Sequence →Sbjct  57999  CAGAGGCGATGATATTCTCACCATCCTGACTGAAGTGAACTATGAAGTAAGCAACAAGGA  58058

                      Query  107    CGACAGGAGGAACAAGGGAAAGCAGATGACACAGCCCACCTTCACACTACGGAAGAAGCT  166
                                     |||| ||  |||| ||| || |||||| | ||||| || ||||||||| | || || ||
                      Sbjct  58059  TGACAAGAAAAACATGGGGAAACAGATGCCTCAGCCTACTTTCACACTAAGAAAAAAACT  58118

                      Query  167    CTTCTTCCCTCCCTAATGATGTGTGCT  193
                                      |||||||| |  | ||||| |||||
                      Sbjct  58119  TGTCTTCCCTTCTGATTGATG-GTGCT  58144
```

C **Conservative sequence**

caga ggagatgaca ttcttagcat cctgactggc gtgaactatg acgtgagcaa taaagacgac aggaggaaca
agggaaagca gatgacacag cccaccttca cactacggaa gaagctcttc ttccctccct aatgatgtgt gct

Figure S-2 The protein level of mitochondrial ETC complexes.

A. The Graphic Summary of the sequence of Gm20257 with human genome by using Blast (https://blast.ncbi.nlm.nih.gov/Blast.cgi). **B.** The Alignment analysis of Gm20257 with human genome. **C.** The conservative sequence of Gm20257 with human.

Figure S-3

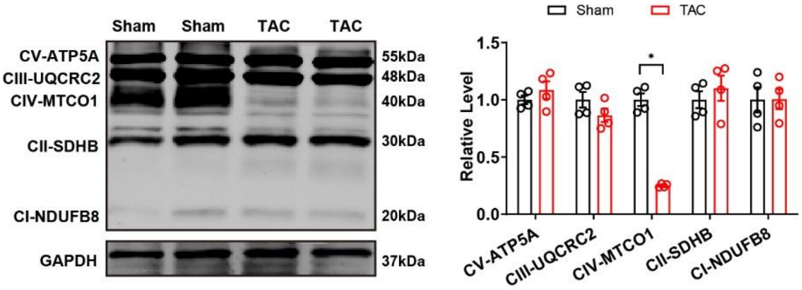
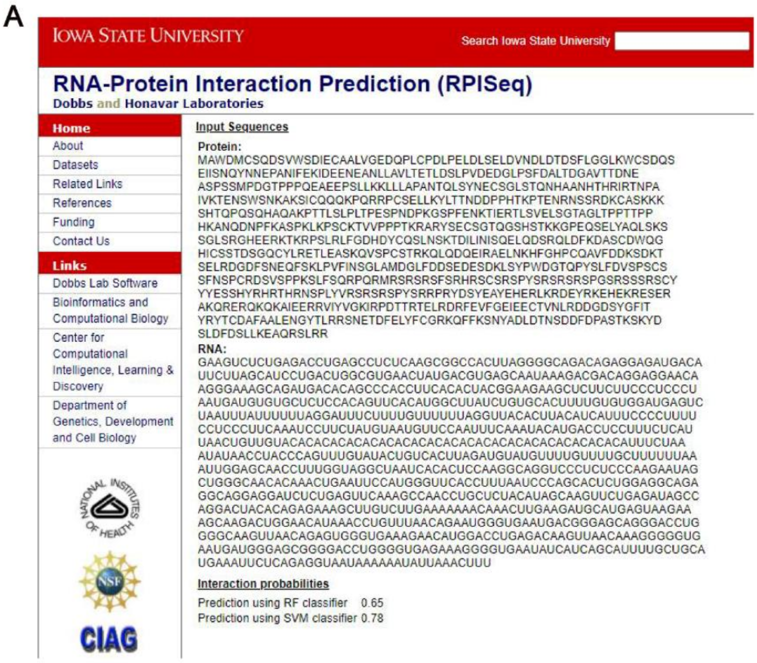


Figure S-3 The protein level of mitochondrial ETC complexes.

The protein level of the mitochondrial ETC after TAC surgery. *$P < 0.05$, $n=4$.

Figure S-4



IOWA STATE UNIVERSITY

RNA-Protein Interaction Prediction (RPISeq)

Dobbs and Honavar Laboratories

Input Sequences

Protein:

```
MAWDMCSQDSVWSDIECAALVGEDQPLCPDLPELDLSELDVNDLDTDSFLGGLKWCSDQS
EIISNQYNNEPANIFEKIDEENEANLLAVLTETLDSLPVDEDGLPSFDALTDGAVTTDNE
ASPSSMPDGTPPPQEAEEPSLLKKLLLAPANTQLSYNECSGLSTQNHAANHTHRIRTNPA
IVKTENSWSNKAKSICQQQKPQRRPCSELLKYLTTNDDPPHTKPTENRNSSRDKCASKKK
SHTQPQSQHAQAKPTTLSLPLTPESPNDPKGSPFENKTIERTLSVELSGTAGLTPPTTPP
HKANQDNPFKASPKLKPSCKTVVPPPTKRARYSECSGTQGSHSTKKGPEQSELYAQLSKS
SGLSRGHEERKTKRPSLRLFGDHDYCQSLNSKTDILINISQELQDSRQLDFKDASCDWQG
HICSSTDSGQCYLRETLEASKQVSPCSTRKQLQDQEIRAELNKHFGHPCQAVFDDKSDKT
SELRDGDFSNEQFSKLPVFINSGLAMDGLFDDSEDESDKLSYPWDGTQPYSLFDVSPSCS
SFNSPCRDSVSPPKSLFSQRPQRMRSRSRSFSRHRSCSRSPYSRSRSRSPGSRSSSRSCY
YYESSHYRHRTHRNSPLYVRSRSRSPYSRRPRYDSYEAYEHERLKRDEYRKEHEKRESER
AKQRERQKQKAIEERRVIYVGKIRPDTTRTELRDRFEVFGEIEECTVNLRDDGDSYGFIT
YRYTCDAFAALENGYTLRRSNETDFELYFCGRKQFFKSNYADLDTNSDDFDPASTKSKYD
SLDFDSLLKEAQRSLRR
```

RNA:

```
GAAGUCUCUGAGACCUGAGCCUCUCAAGCGGCCACUUAGGGGCAGACAGAGGAGAUGACA
UUCUUAGCAUCCUGACUGGCGUGAACUAUGACGUGAGCAAUAAAGACGACAGGAGGAACA
AGGGAAAGCAGAUGACACAGCCCACCUUCACACUACGGAAGAAGCUCUUCUUCCCUCCCU
AAUGAUGUGUGCUCUCCACAGUUCACAUGGCUUAUCUGUGCACUUUUGUGUGGAUGAGUC
UAAUUUAUUUUUUAGGAUUUCUUUUGUUUUUUAGGUUACACUUACAUCAUUUCCCCUUUU
CCUCCCUUCAAAUCCUUCUAUGUAAUGUUCCAAUUUCAAAUACAUGACCUCCUUUCUCAU
UAACUGUUGUACACACACACACACACACACACACACACACACACACACACACAUUUCUAA
AUAUAACCUACCCAGUUUGUAUACUGUCACUUAGAUGUAUGUUUUGUUUUGCUUUUUUAA
AUUGGAGCAACCUUUGGUAGGCUAAUCACACUCCAAGGCAGGUCCCUCUCCCAAGAAUAG
CUGGGCAACACAAACUGAAUUCCAUGGGUUCACCUUUAAUCCCAGCACUCUGGAGGCAGA
GGCAGGAGGAUCUCUGAGUUCAAAGCCAACCUGCUCUACAUAGCAAGUUCUGAGAUAGCC
AGGACUACACAGAGAAAGCUUGUCUUGAAAAAAACAAACUUGAAGAUGCAUGAGUAAGAA
AGCAAGACUGGAACAUAAACCUGUUUAACAGAAUGGGUGAAUGACGGGAGCAGGGACCUG
GGGCAAGUUAACAGAGUGGGUGAAAGAACAUGGACCUGAGACAAGUUAACAAAGGGGGUG
AAUGAUGGGAGCGGGGACCUGGGGUGAGAAAGGGGUGAAUAUCAUCAGCAUUUUGCUGCA
UGAAAUUCUCAGAGGUAAUAAAAAAUAUUAAACUUU
```

Interaction probabilities

```
Prediction using RF classifier    0.65
Prediction using SVM classifier 0.78
```

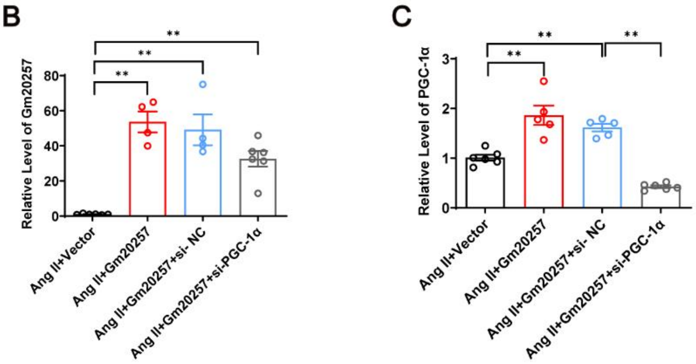


Figure S-4 The predicted interaction of PGC-1α and Gm20257 and the mRNA

level of Gm20257 and PGC-1α.

A. The prediction for interaction between PGC-1α and lncRNA Gm20257. Interaction probabilities generated by RPISeq range from 0 to 1. Predictions with probabilities > 0.5 were considered “positive”. **B, C.** Cardiomyocytes were transfected with Gm20257 overexpression plasmid or transfected with Gm20257 overexpression plasmid simultaneous with small interfering RNA of PGC-1α or NC, Ang II + vector group was used as the control. The mRNA expression of lncRNA Gm20257 and PGC-1α (***P* <0.01, *n*=4 - 6 in A; *n*=5 - 6 in B).