Supplementary Material

# Supplementary Figures

1.1 The gene expression and expression density distribution in each sample

**Supplementary Figure 1.** (A) The histogram of gene expression. The X-axis represents an individual sample. The Y-axis represents the number of expressed genes. The color depth represents the expression level of genes; (B) The density plot of genes’ log10 (FPKM+1) distribution visualized by CummeRbund. The X-axis represents the log10 (FPKM+1) of all the genes. The Y-axis represents the genes’ distribution density. The twelve groups were shown indifferent colors.

1.2 The volcano plot for differentially expressed genes in each group

**Supplementary Figure 2.** Volcano plot for differentially expressed genes (DEGs). The X-axis represents the difference multiple after log2 conversion, the Y-axis represents the significant value after-log10 conversion. Red represents up-regulated DEGs. Green represents down-regulated DEGs. Grey represents no-DEGs. (A) DEGs of Group TNNI2; (B) DEGs of Group ACTA1; (C) DEGs of Group TNNI2-ACTA1 V1;

1.3 The KEGG analysis for DEGs

**Supplementary Figure 3.** The column diagrams for KEGG analysis of DEGs. The X-axis represents the numbers of DEGs. The Y-axis represents the functions of pathways. Each color respective the fairish biological process. (A) DEGs of Group TNNI2; (B) DEGs of Group ACTA1; (C) DEGs of Group TNNI2-ACTA1 V1.

# Supplementary Tables

2.1 Identification of chimeric RNA by RT-PCR and the primer sequences were shown in Supplementary Table 1.

Supplementary Table 1. Primer sequences for Chimeric RNAs identification

|  |  |
| --- | --- |
| Chimeric RNA | Primer Sequences (5'-3') |
| ALDOA-ACTA1 | F: CGAGAACACCGAGGAGAACCG |
| R: TTAGAAGCATTTGCGGTGGACG |
| MYH1-ACTA1 | F: CTCCTTCAGGTCCTCTTGGC |
| R: TTAGAAGCATTTGCGGTGGACG |
| TNNT3-ACTA1 | F: ATGTCGGACGAGGAAGTAGAACAC |
| R: TTAGAAGCATTTGCGGTGGACG |
| TNNI2-ACTA1 | F: ATGGGGGATGAGGAGAAGCGC |
| R: TTAGAAGCATTTGCGGTGGACG |

2.2 The primer sequences for expression plasmid constructions were shown in Supplementary Table 2.

Supplementary Table 2. Primer sequences for expression plasmid constructions

|  |  |  |
| --- | --- | --- |
| Gene | Primer Sequences (5'-3') | Production length (bp) |
| TNNI2 | F:GAATTCCGATGGGGGATGAGGAGAAGC | 549 |
| R:GGTACCCTAGGACTCCGTCTCGAACA |
| ACTA1 | F:GAATTCCGATGTGTGACGAAGACGAG | 1134 |
| R:GGTACCTTAGAAGCATTTGCGG |
| TNNI2-ACTA1-V1 | F: GAATTCCGATGGGGGATGAGGAGAAGC | 870 |
| TNNI2-ACTA1-V2 | 819 |
| TNNI2-ACTA1-V3 | 525 |
| TNNI2-ACTA1-V4 | 720 |
| TNNI2-ACTA1-V5 | R: GGTACCTTAGAAGCATTTGCGG | 423 |
| TNNI2-ACTA1-V6 | 234 |
| TNNI2-ACTA1-V7 | 369 |
| TNNI2-ACTA1-V8 | 414 |

2.3 The primer sequences for detect the changes of cell cycle related genes were shown in Supplementary Table 3.

Supplementary Table 3. Primer sequences for the cell cycle related genes

|  |  |  |
| --- | --- | --- |
| Gene | Primer Sequences (5'-3') | Production length (bp) |
| CCND1 | F: TGCATCTACACCGACAACTCCA | 222 |
| R: GTTGGAAATGAACTTCACGTCTGT |
| CCND2 | F: CTGGATGCTGGAGGTCTGTGAG | 218 |
| R: GAGGCTTGATGGAGTTGTCGGT |
| CCND3 | F: TGGATGCTGGAGGTGTGTGAGG | 220 |
| R: GGCGGGGAGAGACAGAGTGGTC |
| CCNE1 | F: TGCCTTGTATCATTTCTCTT | 302 |
| R: GCTTCTTACTGCTCGGTG |
| CCNE2 | F: ATTCCCCTCAAGAAGCCCAAAT | 156 |
| R: TAATGCAAGGACTGATCCCCCC |
| GAPDH | F: CGGCACAGTCAAGGCGGAGAAC | 212 |
| R: CATCGGCAGAAGGGGCAGAGAT |

2.4 Real-time PCR was used to validate the RNA-Seq data. The primer sequences for this assay were shown in Supplementary Table 4.

Supplementary Table 4. Primer sequences for the real-time PCR to validate the RNA-Seq data

|  |  |  |
| --- | --- | --- |
| Gene | Primer Sequences (5'-3') | Production length (bp) |
| KLF7 | F: ATTAACGCCCCCGTCGTCCCCT | 208 |
| R: TCCTTGTTCGCTGTCGCTCTGT |
| CLK | F: GATGAACGCACACTGAAAAACA | 148 |
| R: CACAAGGCTGAGACCAACCTAA |
| ENO3 | F: CTGCTGGAAAAGAAACTAAGTG | 174 |
| R: AATGTGACGGTAGAGTGGGACC |
| PTGES | F: GGATGCTCAGAGACACGGAGGC | 114 |
| R: CCCAGGAACAGGAAGGGGTAAA |
| EIF4A2 | F: CATCTATGCTTACGGTTTTGAG | 114 |
| R: GCTGTCTTGCCAGTACCTGACT |
| WNT16 | F: ACCACGGGAAAAGAGAGCAAAG | 100 |
| R: ACCGGCAGTCTAGTGACATCAG |
| PRRX1 | F: GAGAAAGCAGCGGAGAAACAGG | 234 |
| R: GAGTAGGATTTGAGGAGGGAAG |
| BACE2 | F: CCTCCGCAGAAGCTGCAGATAC | 190 |
| R: TGACAACGTCCTCCCCAACAAG |
| KLF12 | F: GGTACATCCGTCCCCAGTGTCC | 228 |
| R: TTCTCTCCTGTGTGCGTCCTTC |
| NCOA3 | F: GAGGGTGTGGGGACTTCTCTTT | 120 |
| R: GGGACTCTTGGAATCCTGACTG |
| DDR2 | F: GCCATCATTGTCATCATCCTCT | 284 |
| R: CCCACTATTTCATCTTCACCTG |
| PRG4 | F: GACTACTTTGCACAATGGGACA | 240 |
| R: TTGGAAATCAGTTTGGGATACC |
| CAST | F: CAAGTCAGGAGAACAGAAAGGA | 126 |
| R: GTTGAAGCAGAGGAAGGCGATA |
| MEF2A | F: AGTTCACTTGTGTCCCCGTCTT | 130 |
| R: TGCCTGTACTTGGTGGTCTCTG |
| GAPDH | F: CGGCACAGTCAAGGCGGAGAAC | 212 |
| R: CATCGGCAGAAGGGGCAGAGAT |

2.5 These 49 Chimeric RNAs were jointly predicted by Star-Fusion and Fusionmap. The specific information was shown in Supplementary Table 5.

Supplementary Table 5. The specific information of Chimeric RNAs were jointly predicted by Star-Fusion and Fusionmap

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Chimeric RNA | Left Gene | Right Gene | Type | Annotation |
| CKM--ACTA1 | CKM | ACTA1 | Inter | NC\_010448.4--NC\_010456.5 |
| TPM2--ACTA1 | TPM2 | ACTA1 | Inter | NC\_010443.5--NC\_010456.5 |
| MYH1--ACTA1 | MYH1 | ACTA1 | Inter | NC\_010454.4--NC\_010456.5 |
| CKM--TNNC2 | CKM | TNNC2 | Inter | NC\_010448.4--NC\_010459.5 |
| PYGM--ACTA1 | PYGM | ACTA1 | Inter | NC\_010444.4--NC\_010456.5 |
| ACTA1--TTN | ACTA1 | TTN | Inter | NC\_010456.5--NC\_010457.5 |
| CKM--MYH2 | CKM | MYH2 | Inter | NC\_010448.4--NC\_010454.4 |
| MYLPF--ACTA1 | MYLPF | ACTA1 | Inter | NC\_010445.4--NC\_010456.5 |
| TNNI2--MYH1 | TNNI2 | MYH1 | Inter | NC\_010444.4--NC\_010454.4 |
| ACTN3--CKM | ACTN3 | CKM | Inter | NC\_010444.4--NC\_010448.4 |
| GAPDH--ACTA1 | GAPDH | ACTA1 | Inter | NC\_010447.5--NC\_010456.5 |
| CKM--MYH1 | CKM | MYH1 | Inter | NC\_010448.4--NC\_010454.4 |
| ACTN3--ACTA1 | ACTN3 | ACTA1 | Inter | NC\_010444.4--NC\_010456.5 |
| TPM1--MYH1 | TPM1 | MYH1 | Inter | NC\_010443.5--NC\_010454.4 |
| TNNT3--ENO3 | TNNT3 | ENO3 | Inter | NC\_010444.4--NC\_010454.4 |
| ALDOA--ENO3 | ALDOA | ENO3 | Inter | NC\_010445.4--NC\_010454.4 |
| ACTN3--MYH4 | ACTN3 | MYH4 | Inter | NC\_010444.4--NC\_010454.4 |
| MYLPF--ATP2A1 | MYLPF | ATP2A1 | Intra | NC\_010445.4 |
| TPM1--TNNI2 | TPM1 | TNNI2 | Inter | NC\_010443.5--NC\_010444.4 |
| GAPDH--MYH4 | GAPDH | MYH4 | Inter | NC\_010447.5--NC\_010454.4 |
| TNNT3--ACTA1 | TNNT3 | ACTA1 | Inter | NC\_010444.4--NC\_010456.5 |
| ALDOA--ACTA1 | ALDOA | ACTA1 | Inter | NC\_010445.4--NC\_010456.5 |
| TNNT3--CKM | TNNT3 | CKM | Inter | NC\_010444.4--NC\_010448.4 |
| TNNT3--TNNC2 | TNNT3 | TNNC2 | Inter | NC\_010444.4--NC\_010459.5 |
| TNNI2--ALDOA | TNNI2 | ALDOA | Inter | NC\_010444.4--NC\_010445.4 |
| ATP2A1--ACTA1 | ATP2A1 | ACTA1 | Inter | NC\_010445.4--NC\_010456.5 |
| TNNI2--ACTA1 | TNNI2 | ACTA1 | Inter | NC\_010444.4--NC\_010456.5 |
| GAPDH--CKM | GAPDH | CKM | Inter | NC\_010447.5--NC\_010448.4 |
| ALDOA--ATP2A1 | ALDOA | ATP2A1 | Intra | NC\_010445.4 |
| GAPDH--MYH1 | GAPDH | MYH1 | Inter | NC\_010447.5--NC\_010454.4 |
| ENO3--MYH4 | ENO3 | MYH4 | Intra | NC\_010454.4 |
| PYGM--GAPDH | PYGM | GAPDH | Inter | NC\_010444.4--NC\_010447.5 |
| CKM--TPT1 | CKM | TPT1 | Inter | NC\_010448.4--NC\_010453.5 |
| TNNI2--PYGM | TNNI2 | PYGM | Intra | NC\_010444.4 |
| MYH4--ACTA1 | MYH4 | ACTA1 | Inter | NC\_010454.4--NC\_010456.5 |
| MYH1--TTN | MYH1 | TTN | Inter | NC\_010454.4--NC\_010457.5 |
| CKM--ENO3 | CKM | ENO3 | Inter | NC\_010448.4--NC\_010454.4 |
| YBX3--ACTA1 | YBX3 | ACTA1 | Inter | NC\_010447.5--NC\_010456.5 |
| TPM2--TNNT3 | TPM2 | TNNT3 | Inter | NC\_010443.5--NC\_010444.4 |
| TNNI2--MYH7 | TNNI2 | MYH7 | Inter | NC\_010444.4--NC\_010449.5 |
| TNNT3--PYGM | TNNT3 | PYGM | Intra | NC\_010444.4 |
| TNNI2--CKM | TNNI2 | CKM | Inter | NC\_010444.4--NC\_010448.4 |
| TPM1--TNNT3 | TPM1 | TNNT3 | Inter | NC\_010443.5--NC\_010444.4 |
| RYR1--ACTA1 | RYR1 | ACTA1 | Inter | NC\_010448.4--NC\_010456.5 |
| MYLPF--ALDOA | MYLPF | ALDOA | Intra | NC\_010445.4 |
| MYBPC2--TNNC2 | MYBPC2 | TNNC2 | Inter | NC\_010448.4--NC\_010459.5 |
| ALDOA--EEF1A2 | ALDOA | EEF1A2 | Inter | NC\_010445.4--NC\_010459.5 |
| TPM1--MYBPC2 | TPM1 | MYBPC2 | Inter | NC\_010443.5--NC\_010448.4 |
| ALDOA--LOC110257453 | ALDOA | LOC110257453 | Inter | NC\_010445.4--NC\_010459.5 |

\* Inter: Inter-chromosomal; Intra: Intra-chromosomal.

2.6 The clean reads quality metrics were shown in Supplementary Table 6.

Supplementary Table 6. Statistics of the mapping of sequencing reads to the reference genome Sus scrofa 11.1

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Group | Individual | Clean Reads(M) | % Uniquely Mapping | Q20 (%) |
| TNNI2 | TNNI2\_1 | 23.91 | 91.42 | 98.17 |
| TNNI2\_2 | 23.91 | 91.42 | 98.19 |
| TNNI2\_3 | 23.91 | 91.19 | 98.25 |
| ACTA1 | ACTA1\_1 | 23.91 | 91.37 | 98.16 |
| ACTA1\_2 | 23.91 | 91.29 | 98.16 |
| ACTA1\_3 | 23.9 | 91.31 | 98.18 |
| TNNI2-ACTA1 | TNNI2-ACTA1\_1 | 23.91 | 91.36 | 98.42 |
| TNNI2-ACTA1\_2 | 23.91 | 90.96 | 98.23 |
| TNNI2-ACTA1\_3 | 23.91 | 90.94 | 98.2 |
| NC | NC\_1 | 23.91 | 90.76 | 98.1 |
| NC\_2 | 23.91 | 90.92 | 98.28 |
| NC\_3 | 23.91 | 90.59 | 98.08 |

2.7 The top 30 pathways were enriched for group TNNI2 were shown in Supplementary Table 7.

Supplementary Table 7. Pathways enriched in Group TNNI2

|  |  |  |
| --- | --- | --- |
| Pathway | p-Value | q-Value |
| Focal adhesion | 2.40×10-17 | 7.92×10-15 |
| Ribosome biogenesis in eukaryotes | 7.51×10-16 | 1.24×10-13 |
| ECM-receptor interaction | 6.29×10-13 | 6.92×10-11 |
| Human papillomavirus infection | 5.09×10-12 | 4.20×10-10 |
| PI3K-Akt signaling pathway | 9.38×10-9 | 6.19×10-7 |
| Proteoglycans in cancer | 1.59×10-8 | 8.74×10-7 |
| Protein processing in endoplasmic reticulum | 2.85×10-8 | 1.34×10-6 |
| Pathways in cancer | 3.36×10-8 | 1.38×10-6 |
| Epstein-Barr virus infection | 4.64×10-8 | 1.61×10-6 |
| AGE-RAGE signaling pathway in diabetic complications | 4.87×10-8 | 1.61×10-6 |
| MAPK signaling pathway | 9.12×10-8 | 2.74×10-6 |
| Dilated cardiomyopathy (DCM) | 3.19×10-7 | 8.78×10-6 |
| Arrhythmogenic right ventricular cardiomyopathy (ARVC) | 4.65×10-7 | 1.18×10-5 |
| MicroRNAs in cancer | 5.04×10-7 | 1.19×10-5 |
| Cellular senescence | 7.01×10-7 | 1.54×10-5 |
| Hypertrophic cardiomyopathy (HCM) | 8.25×10-7 | 1.70×10-5 |
| Transcriptional misregulation in cancer | 4.49×10-6 | 8.72×10-5 |
| Human cytomegalovirus infection | 7.32×10-6 | 1.34×10-4 |
| Rap1 signaling pathway | 8.50×10-6 | 1.48×10-4 |
| Shigellosis | 1.33×10-5 | 2.19×10-4 |
| Adherens junction | 1.49×10-5 | 2.34×10-4 |
| Regulation of actin cytoskeleton | 1.80×10-5 | 2.70×10-4 |
| Axon guidance | 2.04×10-5 | 2.93×10-4 |
| Human T-cell leukemia virus 1 infection | 3.17×10-5 | 4.36×10-4 |
| Melanoma | 3.63×10-5 | 4.80×10-4 |
| EGFR tyrosine kinase inhibitor resistance | 4.06×10-5 | 5.15×10-4 |
| Prostate cancer | 4.33×10-5 | 5.30×10-4 |
| Bladder cancer | 5.23×10-5 | 6.16×10-4 |
| Amoebiasis | 6.67×10-5 | 7.59×10-4 |
| Toxoplasmosis | 7.26×10-5 | 7.98×10-4 |

2.8 The top 30 pathways were enriched for group ACTA1 were shown in Supplementary Table 8.

Supplementary Table 8. Pathways enriched in Group ACTA1

|  |  |  |
| --- | --- | --- |
| Pathway | p-Value | q-Value |
| Ribosome | 9.11×10-14 | 3.03×10-11 |
| Focal adhesion | 1.12×10-9 | 1.86×10-7 |
| Protein processing in endoplasmic reticulum | 1.75×10-8 | 1.94×10-6 |
| Kaposi sarcoma-associated herpesvirus infection | 4.92×10-8 | 4.09×10-6 |
| Epstein-Barr virus infection | 9.60×10-8 | 6.39×10-6 |
| Proteoglycans in cancer | 1.96×10-7 | 1.09×10-5 |
| Viral carcinogenesis | 1.03×10-6 | 4.88×10-5 |
| Parkinson disease | 1.83×10-6 | 7.60×10-5 |
| Mitophagy - animal | 2.64×10-6 | 9.77×10-5 |
| Cellular senescence | 4.19×10-6 | 1.36×10-4 |
| Hypertrophic cardiomyopathy (HCM) | 4.67×10-6 | 1.36×10-4 |
| Dilated cardiomyopathy (DCM) | 4.91×10-6 | 1.36×10-4 |
| Shigellosis | 8.23×10-6 | 2.11×10-4 |
| Human papillomavirus infection | 9.50×10-6 | 2.26×10-4 |
| Fluid shear stress and atherosclerosis | 1.07×10-5 | 2.38×10-4 |
| HIF-1 signaling pathway | 1.22×10-5 | 2.54×10-4 |
| Alzheimer disease | 1.61×10-5 | 3.15×10-4 |
| MicroRNAs in cancer | 1.72×10-5 | 3.18×10-4 |
| TNF signaling pathway | 2.77×10-5 | 4.85×10-4 |
| Viral myocarditis | 3.54×10-5 | 5.80×10-4 |
| Oxidative phosphorylation | 3.78×10-5 | 5.80×10-4 |
| p53 signaling pathway | 3.83×10-5 | 5.80×10-4 |
| Human T-cell leukemia virus 1 infection | 4.63×10-5 | 6.71×10-4 |
| AGE-RAGE signaling pathway in diabetic complications | 5.21×10-5 | 7.23×10-4 |
| Bacterial invasion of epithelial cells | 7.91×10-5 | 1.05×10-3 |
| Non-alcoholic fatty liver disease (NAFLD) | 9.35×10-5 | 1.20×10-3 |
| EGFR tyrosine kinase inhibitor resistance | 1.01×10-4 | 1.25×10-3 |
| Endocytosis | 1.72×10-4 | 2.0×10-3 |
| Small cell lung cancer | 1.80×10-4 | 2.0×10-3 |
| ECM-receptor interaction | 1.86×10-4 | 2.0×10-3 |

2.9 All the pathways were enriched for group TNNI2-ACTA1 V1 were shown in Supplementary Table 9.

Supplementary Table 9. Pathways enriched in Group TNNI2-ACTA1 V1

|  |  |  |
| --- | --- | --- |
| Pathway | p-Value | q-Value |
| TNF signaling pathway | 1.59×10-4 | 1.28×10-2 |
| Legionellosis | 3.87×10-4 | 1.57×10-2 |
| Viral protein interaction with cytokine and cytokine receptor | 1.34×10-3 | 3.10×10-2 |
| IL-17 signaling pathway | 1.53×10-3 | 3.10×10-2 |
| Cytokine-cytokine receptor interaction | 4.31×10-3 | 7.0×10-2 |
| Influenza A | 7.30×10-3 | 9.86×10-2 |
| Chemokine signaling pathway | 1.07×10-2 | 1.20×10-1 |
| Viral carcinogenesis | 1.19×10-2 | 1.20×10-1 |
| Human T-cell leukemia virus 1 infection | 1.95×10-2 | 1.60×10-1 |
| Shigellosis | 2.0×10-2 | 1.60×10-1 |
| Rheumatoid arthritis | 2.38×10-2 | 1.60×10-1 |
| AGE-RAGE signaling pathway in diabetic complications | 2.84×10-2 | 1.60×10-1 |
| NF-kappa B signaling pathway | 2.89×10-2 | 1.60×10-1 |
| C-type lectin receptor signaling pathwaycardiomyopathy (ARVC) | 3.0×10-2 | 1.60×10-1 |
| Parathyroid hormone synthesis, secretion and action | 3.05×10-2 | 1.60×10-1 |
| Chagas disease (American trypanosomiasis) | 3.16×10-2 | 1.60×10-1 |
| Osteoclast differentiation | 4.21×10-2 | 1.81×10-1 |
| Yersinia infection | 4.21×10-2 | 1.81×10-1 |
| Fluid shear stress and atherosclerosis | 4.78×10-2 | 1.81×10-1 |
| Apoptosis | 4.85×10-2 | 1.81×10-1 |
| Apelin signaling pathway | 4.85×10-2 | 1.81×10-1 |
| Signaling pathways regulating pluripotency of stem cells | 4.91×10-2 | 1.81×10-1 |