## Supplementary methods

### Table S1. Primers used in RT-qPCR

| Gene   | Primer sequence (5’-3’)                  | Product size (bp) |
|--------|------------------------------------------|-------------------|
| SOX2   | Forward TGGACAGTTACGGCGACAT              | 215               |
|        | Reverse CGAGTAGGACATGCTGTAAGGT           |                   |
| REX1   | Forward GCCCTATGTAGTGCTCATTGTA           | 96                |
|        | Reverse ACCCCCTATGACGGCATATCATTA         |                   |
| OCT4   | Forward CGAGAAGGATGTTGTCGGAGG           | 136               |
|        | Reverse CAGAGAAAAGGACACTTGTC            |                   |
| NANOG  | Forward AGATGCCTCACAAGGAGACT             | 96                |
|        | Reverse GTTTCCTTGGGACTGTTG              |                   |
| TNNT2  | Forward CATGGAGAAGGACACTGAATG            | 108               |
|        | Reverse CACGCCACGCATTTCGTC              |                   |
| MYH6   | Forward CCACCAGTTCGACAGAT                | 127               |
|        | Reverse CACAGAAAGGCCCCAGTAG              |                   |
| NKKX2-5| Forward CAACTGCGCCACAGCGGCCAA           | 105               |
|        | Reverse GGGCCACGCTCTTCTTTT              |                   |
| GATA4  | Forward TGGCCTTGATCCTCACCAG             | 126               |
|        | Reverse TAGCCCTTGGGAGACCTT               |                   |
| TBX5   | Forward CAGACTCGCCACAGCGGCCAA           | 237               |
|        | Reverse GGGCCACGCTCTTCTTTTC             |                   |
| DES    | Forward CTAGCCCAAGGGGTTCCTGAG            | 109               |
|        | Reverse ACTCTATGCTGTGCTGCTG             |                   |
| GAPDH  | Forward AGTCCCTGCACACTCAG                | 123               |
|        | Reverse TACCTTTATGATGACATGACAGG          |                   |
| SCN5A  | Forward TCATCGTAGATCCCTCTCTG             | 318               |
|        | Reverse GGCCCTTGGTTCCGACAGTT            |                   |
| CACNA1D| Forward GGGCAATGGGACCTCATATAAA          | 141               |
|        | Reverse TTACCTGGTTCCGAGTGCAATT          |                   |
| KCNJ12 | Forward GCCAGCTAGGCTCTGTTTGT            | 152               |
|        | Reverse CTCAGAACACATCCTAAGGTAC          |                   |
| KCND3  | Forward AGAGAGCTGATAAAGCAGG             | 209               |
|        | Reverse CAGGGCTGAGCGAGGTTGAT            |                   |
| HCN2   | Forward GCCGCTGATCCCGATCCAT              | 230               |
|        | Reverse AGTCAGGAGGAGTGACAGTTACCAT       |                   |
| PPARGC1A| Forward GCAATTGAAGGAGCGCGTTGGA          | 134               |
|        | Reverse CTGCTCCATCATCCCGGAGAT           |                   |
| NRF1   | Forward AGGGCTTGGGAGGAAAGAAG            | 303               |
|        | Reverse CCAACCTGGAATAAGTGAGAC           |                   |
| HIF1A  | Forward CCAACATACCAACACCTCAG            | 302               |
|        | Reverse TCCGCTGCTGACTGTCCCTT            |                   |
Extracellular Flux analysis

Extracellular Flux analysis was done using Seahorse XFp Extracellular Flux analyzer, Cell Mito Stress Test Kit and Cell Energy Phenotype Test Kit (Agilent Technologies, USA). The device simultaneously detects changes in oxygen concentration and in proton concentration (or pH) in the assay medium.

**Cell Energy Phenotype Test Kit** measures the basal oxygen consumption rate (OCR) and then OCR after the injection of the stressor mix (1 μM of Oligomycin and 1 μM of FCCP). Oligomycin inhibits ATP production by the mitochondria and causes a compensatory increase in the rate of glycolysis as the cells attempt to meet their energy demands via the glycolytic pathway. FCCP depolarizes the mitochondrial membrane and drives OCR higher as the mitochondria attempt to restore the mitochondrial membrane potential. The main parameters are as follows:

- **Oxygen consumption rate (OCR):** The rate of decrease of oxygen concentration in the assay medium. OCR is a measure of the rate of mitochondrial respiration of the cells.
- **Extracellular acidification rate (ECAR):** The rate of increase in proton concentration (or decrease in pH) in the assay medium. ECAR is a measure of the rate of glycolysis of the cells.
- **Baseline phenotype:** OCR and ECAR of cells at starting assay conditions.
- **Stressed phenotype:** OCR and ECAR of cells in the presence of stressor compounds.
- **Metabolic potential:** Percentage increase of stressed OCR over baseline OCR and stressed ECAR over baseline ECAR. Metabolic potential is the measure of cells' ability to meet the energy demand via respiration and glycolysis.

**Cell Mito Stress Test Kit** measures mitochondrial function in the cell by detecting OCR at the baseline level and after the addition of electron transfer chain (ETC) modulators: Oligomycin inhibits ATP synthase (complex V) and the decrease in OCR following injection of Oligomycin correlates to the mitochondrial respiration associated with cellular ATP production. Carbonyl cyanide-4 (trifluoromethoxy) phenylhydrazone (FCCP) is an uncoupling agent that collapses the proton gradient and disrupts the mitochondrial membrane potential. As a result, electron flow through the ETC is uninhibited and oxygen is maximally consumed by complex IV. The third injection is a mix of Rotenone, a complex I inhibitor, and Antimycin A, a complex III inhibitor. This combination shuts down mitochondrial respiration and enables the calculation of non-mitochondrial respiration driven by processes outside the mitochondria.

The main parameters are as follows:

- **Basal respiration:** Oxygen consumption used to meet cellular ATP demand and resulting from mitochondrial proton leak. Calculated as (Last measurement before the first injection) - (Non-mitochondrial respiration rate).
- **ATP Production:** The decrease in oxygen consumption rate upon injection of Oligomycin represents the portion of basal respiration that was being used to drive ATP production. Shows ATP produced by the mitochondria that contributes to meeting the energy needs of the cell. Calculated as (Last rate measurement before Oligomycin in-
• H+ (Proton) leak: Remaining basal respiration not coupled to ATP production. Proton leak can be a sign of mitochondrial damage or can be used as a mechanism to regulate the mitochondrial ATP production. Calculated as (Minimum rate measurement after Oligomycin injection) – (Non-mitochondrial respiration).

• Maximal respiration: The maximal oxygen consumption rate attained by adding the uncoupler FCCP. FCCP mimics a physiological “energy demand” by stimulating the respiratory chain to operate at maximum capacity, which causes rapid oxidation of substrates to meet this metabolic challenge. Shows the maximum rate of respiration that the cell can achieve. Calculated as (Maximum rate measurement after FCCP injection) – (Non-mitochondrial respiration).

• Spare respiratory capacity: This measurement indicates the capability of the cell to respond to an energetic demand as well as how closely the cell is to respire to its theoretical maximum. The cell's ability to respond to demand can be an indicator of cell fitness or flexibility. Calculated as (Maximal respiration) – (Basal respiration).

• Nonmitochondrial respiration: Oxygen consumption that persists due to a subset of cellular enzymes continuing to consume oxygen after Rotenone and Antimycin A addition. This is important for getting an accurate measure of mitochondrial respiration. Calculated as the minimum rate measurement after Rotenone/Antimycin A injection.
| Pathway ID  | Pathway Description                                      | Observed gene count | False discovery rate | Matching proteins in your network (IDs) | Matching proteins in your network (labels) |
|------------|----------------------------------------------------------|---------------------|----------------------|----------------------------------------|------------------------------------------|
| GO.0003209 | cardiac atrium morphogenesis                            | 5                   | 1.97e-10             | ENSP00000309913,ENSP00000327758,ENSP00000334458,ENSP00000348634,ENSP00000356286 | GATA4,MYH6,NKX2-5,TBX5,TNNNT2            |
| GO.0003230 | cardiac atrium development                              | 5                   | 1.97e-10             | ENSP00000309913,ENSP00000327758,ENSP00000334458,ENSP00000348634,ENSP00000356286 | GATA4,MYH6,NKX2-5,TBX5,TNNNT2            |
| GO.0003229 | ventricular cardiac muscle tissue development            | 5                   | 1.42e-09             | ENSP00000309913,ENSP00000327758,ENSP00000334458,ENSP00000348634,ENSP00000356286 | GATA4,MYH6,NKX2-5,TBX5,TNNNT2            |
| GO.0003208 | cardiac ventricle morphogenesis                         | 5                   | 4.48e-09             | ENSP00000309913,ENSP00000327758,ENSP00000334458,ENSP00000348634,ENSP00000356286 | GATA4,MYH6,NKX2-5,TBX5,TNNNT2            |
| GO.0003231 | cardiac ventricle development                           | 5                   | 3.38e-08             | ENSP00000309913,ENSP00000327758,ENSP00000334458,ENSP00000348634,ENSP00000356286 | GATA4,MYH6,NKX2-5,TBX5,TNNNT2            |
| GO.0051891 | positive regulation of cardioblast differentiation       | 3                   | 2.15e-07             | ENSP00000309913,ENSP00000327758,ENSP00000334458 | GATA4,NKX2-5,TBX5                        |
| GO.0008016 | regulation of heart contraction                         | 5                   | 2.26e-07             | ENSP00000327758,ENSP00000334458,ENSP00000348634,ENSP00000356286,ENSP00000363071 | DES,GATA4,MYH6,NKX2-5,TNNNT2             |
| GO.0051146 | striated muscle cell differentiation                     | 5                   | 3.05e-07             | ENSP00000309913,ENSP00000327758,ENSP00000334458,ENSP00000348634,ENSP00000356286 | GATA4,MYH6,NKX2-5,TBX5,TNNNT2            |
| GO.0003007 | heart morphogenesis                                     | 5                   | 6.7e-07              | ENSP00000309913,ENSP00000327758,ENSP00000334458,ENSP00000348634,ENSP00000356286 | GATA4,MYH6,NKX2-5,TBX5,TNNNT2            |
| GO.0055007 | cardiac muscle cell differentiation                      | 4                   | 1.9e-06              | ENSP00000309913,ENSP00000327758,ENSP00000334458,ENSP00000348634 | GATA4,MYH6,NKX2-5,TBX5                  |
| GO.0060413 | atrial septum morphogenesis                             | 3                   | 2.91e-06             | ENSP00000309913,ENSP00000327758,ENSP00000334458 | GATA4,NKX2-5,TBX5                        |
| GO.0003283 | atrial septum development                               | 3                   | 5.15e-06             | ENSP00000309913,ENSP00000327758,ENSP00000334458 | GATA4,NKX2-5,TBX5                        |
| GO.0055002 | striated muscle cell development                        | 4                   | 7.11e-06             | ENSP00000327758,ENSP00000334458,ENSP00000348634,ENSP00000356286 | GATA4,MYH6,NKX2-5,TNNNT2                 |
| GO.0007507 | heart development                                       | 5                   | 1.24e-05             | ENSP00000309913,ENSP00000327758,ENSP00000334458,ENSP00000348634,ENSP00000356286 | GATA4,MYH6,NKX2-5,TNNNT2                 |
| GO.0061061 | muscle structure development                            | 5                   | 1.3e-05              | ENSP00000309913,ENSP00000327758,ENSP00000334458,ENSP00000348634,ENSP00000356286 | TBX5,TNNNT2,MYH6,NKX2-5,TNNNT2           |
| GO.0045214 | sarcomere organization                                 | 3                   | 2.71e-05             | ENSP00000327758,ENSP00000348634,ENSP00000356286 | GATA4,MYH6,NKX2-5,TNN2                  |
| GO.0048729 | tissue morphogenesis                                    | 5                   | 3.84e-05             | ENSP00000309913,ENSP00000327758,ENSP00000334458,ENSP00000348634,ENSP00000356286 | GATA4,MYH6,NKX2-5,TBX5,TNNNT2            |
| GO.0030049 | muscle filament sliding                                 | 3                   | 5.16e-05             | ENSP00000327758,ENSP00000348634,ENSP00000356286,ENSP00000363071 | MYS6,TNN2,MYH6,TNNNT2                    |
| GO.0055010 | ventricular cardiac muscle tissue morphogenesis         | 3                   | 6.34e-05             | ENSP00000327758,ENSP00000348634,ENSP00000356286 | MYH6,NKX2-5,TNN2                        |
| GO.0060420 | regulation of heart growth                              | 3                   | 6.62e-05             | ENSP00000327758,ENSP00000348634 | GATA4,MYH6,NKX2-5,TBX5                  |
| Pathway ID    | Pathway description                                      | Observed gene count | False discovery rate | Matching proteins in your network (IDs) | Matching proteins in your network (labels) |
|--------------|----------------------------------------------------------|---------------------|----------------------|-----------------------------------------|-------------------------------------------|
| GO.0055013   | cardiac muscle cell development                           | 3                   | 7.42e-05             | ENSP00000327758,ENSP00000334458,ENSP00000348634 | GATA4,MYH6,NKX2-5,TBX5                    |
| GO.0003281   | ventricular septum development                           | 3                   | 7.72e-05             | ENSP00000309913,ENSP00000327758,ENSP00000334458 | GATA4,NKX2-5                             |
| GO.0060048   | cardiac muscle contraction                               | 3                   | 7.8e-05              | ENSP00000327758,ENSP00000348634,ENSP00000363071 | MYH6,NKX2-5,MYH6,NKX2-5,TBX5             |
| GO.0003285   | septum secundum development                              | 2                   | 8.02e-05             | ENSP00000327758,ENSP00000334458             | GATA4,NKX2-5                             |
| GO.0030239   | myofibril assembly                                       | 3                   | 9.09e-05             | ENSP00000327758,ENSP00000334458             | MYH6,NKX2-5,MYH6,NKX2-5,TBX5             |
| GO.0003012   | muscle system process                                    | 4                   | 9.7e-05              | ENSP00000327758,ENSP00000334458,ENSP00000363071 | GATA4,NKX2-5                             |
| GO.0072358   | cardiovascular system development                        | 5                   | 0.000109             | ENSP00000327758,ENSP00000348634,ENSP00000363071 | GATA4,MYH6,NKX2-5,TBX5                  |
| GO.0072359   | circulatory system development                           | 5                   | 0.000109             | ENSP00000327758,ENSP00000334458,ENSP00000363071 | GATA4,MYH6,NKX2-5,TBX5                  |
| GO.0060047   | heart contraction                                        | 3                   | 0.000112             | ENSP00000327758,ENSP00000348634,ENSP00000363071 | GATA4,MYH6,NKX2-5,TBX5                  |
| GO.0003166   | bundle of His development                                | 2                   | 0.000129             | ENSP00000327758,ENSP00000334458,ENSP00000363071 | GATA4,MYH6,NKX2-5,TBX5                  |
| GO.0003164   | His-Purkinje system development                          | 2                   | 0.00019              | ENSP00000327758,ENSP00000334458,ENSP00000363071 | GATA4,MYH6,NKX2-5,TBX5                  |
| GO.0048644   | muscle organ morphogenesis                               | 3                   | 0.000207             | ENSP00000327758,ENSP00000334458,ENSP00000363071 | GATA4,MYH6,NKX2-5,TBX5                  |
| GO.0048646   | anatomical structure formation involved in morphogenesis  | 5                   | 0.000246             | ENSP00000327758,ENSP00000348634,ENSP00000363071 | GATA4,MYH6,NKX2-5,TBX5                  |
| GO.0003228   | atrial cardiac muscle tissue development                 | 2                   | 0.000247             | ENSP00000327758,ENSP00000348634,ENSP00000363071 | GATA4,MYH6,NKX2-5,TBX5                  |
| GO.00030509  | BMP signaling pathway                                    | 3                   | 0.000247             | ENSP00000327758,ENSP00000334458,ENSP00000348634 | GATA4,MYH6,NKX2-5,TBX5                  |
| GO.0005509   | atrial cardiac muscle tissue morphogenesis               | 2                   | 0.000247             | ENSP00000327758,ENSP00000348634,ENSP00000363071 | GATA4,MYH6,NKX2-5,TBX5                  |
| GO.0071773   | cellular response to BMP stimulus                        | 3                   | 0.000294             | ENSP00000327758,ENSP00000334458,ENSP00000348634 | GATA4,MYH6,NKX2-5,TBX5                  |
| GO.0060070   | canonical Wnt signaling pathway                          | 3                   | 0.0003                | ENSP00000327758,ENSP00000334458,ENSP00000348634 | GATA4,MYH6,NKX2-5,TBX5                  |
| GO.0060290   | transdifferentiation                                     | 3                   | 0.000432             | ENSP00000327758,ENSP00000334458,ENSP00000348634 | GATA4,TBX5                              |
| GO.0044057   | regulation of system process                             | 4                   | 0.000449             | ENSP00000327758,ENSP00000334458,ENSP00000363071 | GATA4,TBX5                              |
| GO.0003211   | cardiac ventricle formation                              | 2                   | 0.000663             | ENSP00000327758,ENSP00000334458,ENSP00000363071 | GATA4,TBX5                              |
| GO.0007512   | adult heart development                                  | 2                   | 0.0013               | ENSP00000327758,ENSP00000334458,ENSP00000363071 | GATA4,TBX5                              |
| GO.0003181   | atrioventricular valve morphogenesis                     | 2                   | 0.00148              | ENSP00000327758,ENSP00000334458             | GATA4,TBX5                              |
| GO.0006937   | regulation of muscle contraction                         | 3                   | 0.00154              | ENSP00000327758,ENSP00000348634,ENSP00000363071 | GATA4,TBX5                              |
| GO.0003215   | cardiac right ventricle morphogenesis                    | 2                   | 0.00164              | ENSP00000327758,ENSP00000334458             | GATA4,TBX5                              |
| GO.0003171   | atrioventricular valve development                       | 2                   | 0.00204              | ENSP00000327758,ENSP00000348634,ENSP00000363071 | GATA4,TBX5                              |
| GO.0060485   | mesenchyme development                                   | 3                   | 0.00204              | ENSP00000327758,ENSP00000348634,ENSP00000363071 | GATA4,TBX5                              |
| Pathway ID | Pathway description | Observed gene count | False discovery rate | Matching proteins in your network (IDs) | Matching proteins in your network (labels) |
|------------|---------------------|---------------------|---------------------|------------------------------------------|------------------------------------------|
| GO:0060045 | positive regulation of cardiac muscle cell proliferation | 2                   | 0.00225             | ENSP00000309913,ENSP00000334458          | GATA4,TBX5                                |
| GO:0053017 | cardiac muscle tissue growth | 2                   | 0.00292             | ENSP00000327758,ENSP00000334458          | GATA4,NKX2-5,DES,MYH6,NKX2-5             |
| GO:0006936 | muscle contraction     | 3                   | 0.00315             | ENSP00000327758,ENSP000003348634,ENSP00000363071 | GATA4,NKX2-5,DES,MYH6,NKX2-5,TNT2       |
| GO:0060419 | heart growth           | 2                   | 0.00315             | ENSP00000327758,ENSP00000334458          | GATA4,NKX2-5,DES,MYH6,NKX2-5,TNT2       |
| GO:0003197 | endocardial cushion development | 2                   | 0.00423             | ENSP00000327758,ENSP00000334458          | GATA4,BX5                                |
| GO:0060043 | regulation of cardiac muscle cell proliferation | 2                   | 0.00449             | ENSP00000327758,ENSP00000334458          | GATA4,NKX2-5                             |
| GO:0007517 | muscle organ development | 3                   | 0.00634             | ENSP00000327758,ENSP00000348634,ENSP00000363071 | MYH6,NKX2-5,DES,MYH6,TNT2               |
| GO:0008015 | blood circulation      | 3                   | 0.00641             | ENSP00000327758,ENSP00000348634,ENSP00000363071 | MYH6,NKX2-5,MYH6,X2-5                   |
| GO:0009790 | embryo development     | 4                   | 0.00679             | ENSP00000309913,ENSP00000327758,ENSP00000334458 | GATA4,MYH6,NKX2-5,DES,GATA4,MYH6,X2-5,TNT2 |
| GO:0051239 | regulation of multicellular organisinal process | 5                   | 0.00935             | ENSP00000309913,ENSP00000327758,ENSP00000334458 | GATA4,MYH6,NKX2-5,DES,GATA4,MYH6,X2-5,TNT2 |
| GO:1903115 | regulation of actin filament-based movement | 2                   | 0.0102              | ENSP00000334458,ENSP00000356286          | GATA4,TNNT2                              |
| GO:0043462 | regulation of ATPase activity | 2                   | 0.0115              | ENSP00000309913,ENSP00000348634,ENSP00000356286 | MYH6,DES,GATA4,MYH6,X2-5,TNT2         |
| GO:0001547 | heart looping          | 2                   | 0.0128              | ENSP00000327758,ENSP00000334458          | GATA4,NKX2-5                             |
| GO:0061371 | determination of heart left/right asymmetry | 2                   | 0.014               | ENSP00000327758,ENSP00000334458          | GATA4,NKX2-5                             |
| GO:0030029 | actin filament-based process | 3                   | 0.0169              | ENSP00000327758,ENSP00000348634,ENSP00000356286 | GATA4,NKX2-5                             |
| GO:0003489 | pattern specification process | 3                   | 0.0171              | ENSP00000309913,ENSP00000327758,ENSP00000334458 | GATA4,NKX2-5,DES,GATA4,MYH6,X2-5,TNT2 |
| GO:0001570 | vasculogenesis         | 2                   | 0.0178              | ENSP00000309913,ENSP00000327758,ENSP00000334458 | GATA4,NKX2-5,DES,GATA4,MYH6,X2-5,TNT2 |
| GO:0002009 | morphogenesis of an epithelium | 3                   | 0.0193              | ENSP00000309913,ENSP00000327758,ENSP00000334458 | GATA4,NKX2-5,DES,GATA4,MYH6,X2-5,TNT2 |
| GO:0006928 | movement of cell or subcellular component | 4                   | 0.0197              | ENSP00000309913,ENSP00000327758,ENSP00000334458 | GATA4,NKX2-5,DES,GATA4,MYH6,X2-5,TNT2 |
| GO:0044707 | single-multicellular organism process | 6                   | 0.0208              | ENSP00000309913,ENSP00000327758,ENSP00000334458 | GATA4,NKX2-5,DES,GATA4,MYH6,X2-5,TNT2 |
| GO:0035050 | embryonic heart tube development | 2                   | 0.021               | ENSP00000327758,ENSP00000334458          | GATA4,NKX2-5                             |
| GO:0055117 | regulation of cardiac muscle contraction | 2                   | 0.025               | ENSP00000327758,ENSP00000334458          | GATA4,NKX2-5                             |
| GO:200026  | regulation of multicellular organisinal development | 4                   | 0.028               | ENSP00000309913,ENSP00000327758,ENSP00000334458 | GATA4,MYH6,NKX2-5,DES,GATA4,MYH6,X2-5,TNT2 |
| GO:0009888 | tissue development      | 4                   | 0.031               | ENSP00000327758,ENSP00000334458          | GATA4,MYH6,NKX2-5,DES,GATA4,MYH6,X2-5,TNT2 |
| GO:0048598 | embryonic morphogenesis | 3                   | 0.035               | ENSP00000309913,ENSP00000327758,ENSP00000334458 | GATA4,MYH6,NKX2-5,DES,GATA4,MYH6,X2-5,TNT2 |
| GO:0035295 | tube development        | 3                   | 0.037               | ENSP00000309913,ENSP00000327758,ENSP00000334458 | GATA4,MYH6,NKX2-5,DES,GATA4,MYH6,X2-5,TNT2 |
| GO:0006357 | regulation of transcription from RNA polymerase II promoter | 4                   | 0.041               | ENSP00000309913,ENSP00000327758,ENSP00000334458 | GATA4,MYH6,NKX2-5,DES,GATA4,MYH6,X2-5,TNT2 |
| GO:0043009 | chordate embryonic development | 3                   | 0.044               | ENSP00000327758,ENSP00000334458,ENSP00000348634 | GATA4,MYH6,NKX2-5,DES,GATA4,MYH6,X2-5,TNT2 |

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| Pathway ID | Pathway description                      | Observed gene count | False discovery rate | Matching proteins in your network (IDs)          | Matching proteins in your network (labels) |
|-----------|-----------------------------------------|---------------------|----------------------|------------------------------------------------|-------------------------------------------|
| 5410      | Hypertrophic cardiomyopathy (HCM)       | 3                   | 0.000219             | ENSP00000348634,ENSP00000356286,ENSP000363071 | DES, MYH6, TN                            |
| 5414      | Dilated cardiomyopathy                 | 3                   | 0.000219             | ENSP00000348634,ENSP00000356286,ENSP000363071 | DES, MYH6, TN                            |
| 4260      | Cardiac muscle contraction             | 2                   | 0.0189               | ENSP00000348634,ENSP00000356286                  | MYH6, TNNT2                              |
| 4919      | Thyroid hormone signaling pathway      | 2                   | 0.0332               | ENSP00000334458,ENSP00000348634                  | GATA4, MYH6                              |
| 4261      | Adrenergic signaling in cardiomyocytes | 2                   | 0.0399               | ENSP00000348634,ENSP00000356286                  | MYH6, TNNT2                              |
| #Pathway ID | Pathway description | Observed gene count | False discovery rate | Matching proteins in your network (IDs) | Matching proteins in your network (labels) |
|------------|---------------------|---------------------|----------------------|----------------------------------------|------------------------------------------|
| GO.0030016 | myofibril           | 3                   | 0.0166               | ENSP0000034834,ENSP00000356286,ENSP00000363071 | DES,MYH6,TNNT2                           |