

## Supplementary figures

**Fig. S1** Characterizations of decellularized heart. (a) Immunofluorescent staining of native and decellularized heart thin sections showing the presence/absence of DAPI-positive nuclei (blue), actinin (green) or Cx43 (red). Nuclei and contractile proteins were not detected in decellularized heart. Scale bars, 50  $\mu\text{m}$ . (b) DNA quantification of native hearts and decellularized heart. Values are means  $\pm$  SD,  $n=3$ . (c) Masson's trichrome staining of the decellularized matrix showed good retention of collagen.

**Fig. S2** Characterization of NSCs specific marker. (a) Sphere NSCs was identified and immunostained to identify nestin-the NSCs specific marker. DAPI-nucleus (b) Photograph of recellularized constructs under the perfusion culture on day 14 post recellularization. (c) Immunofluorescent staining of recellularized constructs for vWF- vascularization specific marker. (d) Immunofluorescent staining of recellularized constructs for DAPI and nestin after different days (day7, day14) of culturing. The nestin+ cells were counted over days of perfusion (Right figure). Error bars represent SD ( $n=3$ ), determined using unpaired t-test. \* $P < 0.05$ ; \*\* $P < 0.01$ ; \*\*\* $P < 0.001$ .

**Fig. S3** Co-immunostaining of neuron specific marker MAP2 (red) and astrocytes specific marker GFAP (green) after 7 days or 14 days of perfusion culturing.

**Fig. S4** Characterization of cell type specific markers. (a) GFAP (green) and  $\alpha$ -actinin (red), (b) Cx43 (green) and  $\alpha$ -actinin (red) after 14 days of culturing. (c) Flow cytometry analysis characterized the percentage of  $\alpha$ -actinin positive cells.

**Fig. S5** Histological analysis of recellularized constructs after different days (day7, day14) of perfusion. The sections of the recellularized constructs were immunostained with anti-GATA4, anti-c-kit and anti-Nkx2-5 antibodies.

**Fig. S6** Characterizations of decellularized brain. (a) SEM images of native brain and decellularized brain. (b) H&E staining of sections from the native brain and decellularized brain. (c) Immunostaining of native brain and decellularized brain with anti-laminin, anti-Collagen I, anti-Collagen III, anti-Collagen IV and anti-Fibronectin antibodies. No nuclear staining (DAPI) was observed in decellularized brain.

**Fig. S7** Quantitative proteomic profiling of decellularized heart. (a) The schematic image of the TMT labeling comparatively proteomic analysis of decellularized heart matrix and decellularized brain matrix. (b) Summary of the differently expressed proteins between decellularized heart and decellularized brain.

**Fig. S8** Analysis of the differently expressed proteins between decellularized heart and decellularized brain. (a) Functional enrichment analysis. (b) KEGG Pathway enrichment analysis.

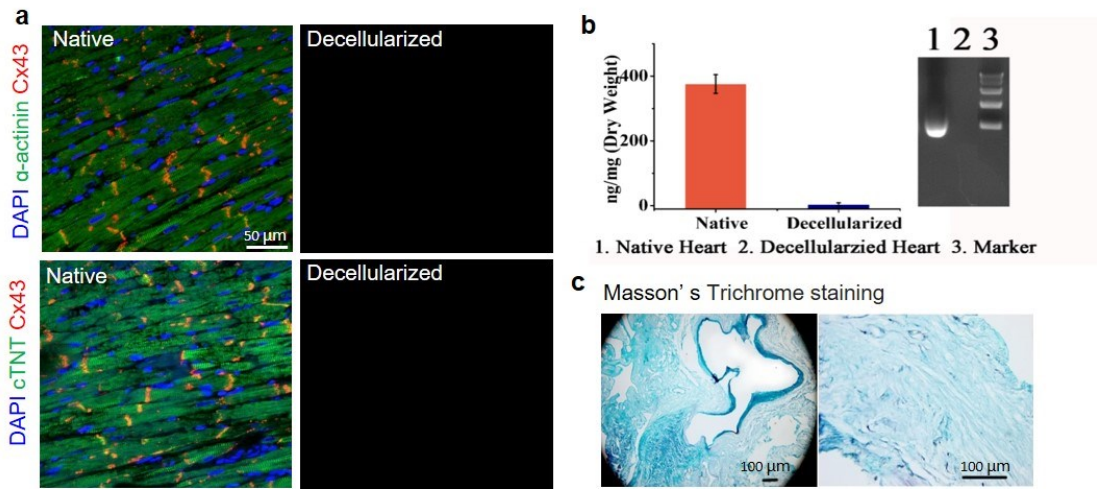
**Fig. S9** GO-based enrichment and clustering analysis of up-regulated proteins (heart-vs-brain) based on cellular component. Q1 ( $0 < \text{Ratio T/C} < 1/2$ ), Q2 ( $1/2 \leq \text{Ratio T/C} < 1/1.5$ ), Q3 ( $1.5 < \text{Ratio T/C} \leq 2$ ) and Q4 ( $\text{Ratio T/C} > 2$ ).

**Fig. S10** GO-based enrichment and clustering analysis of up-regulated proteins (heart-vs-brain) based on molecular function. Q1 ( $0 < \text{Ratio T/C} < 1/2$ ), Q2 ( $1/2 \leq \text{Ratio T/C} < 1/1.5$ ), Q3 ( $1.5 < \text{Ratio T/C} \leq 2$ ) and Q4 ( $\text{Ratio T/C} > 2$ ).

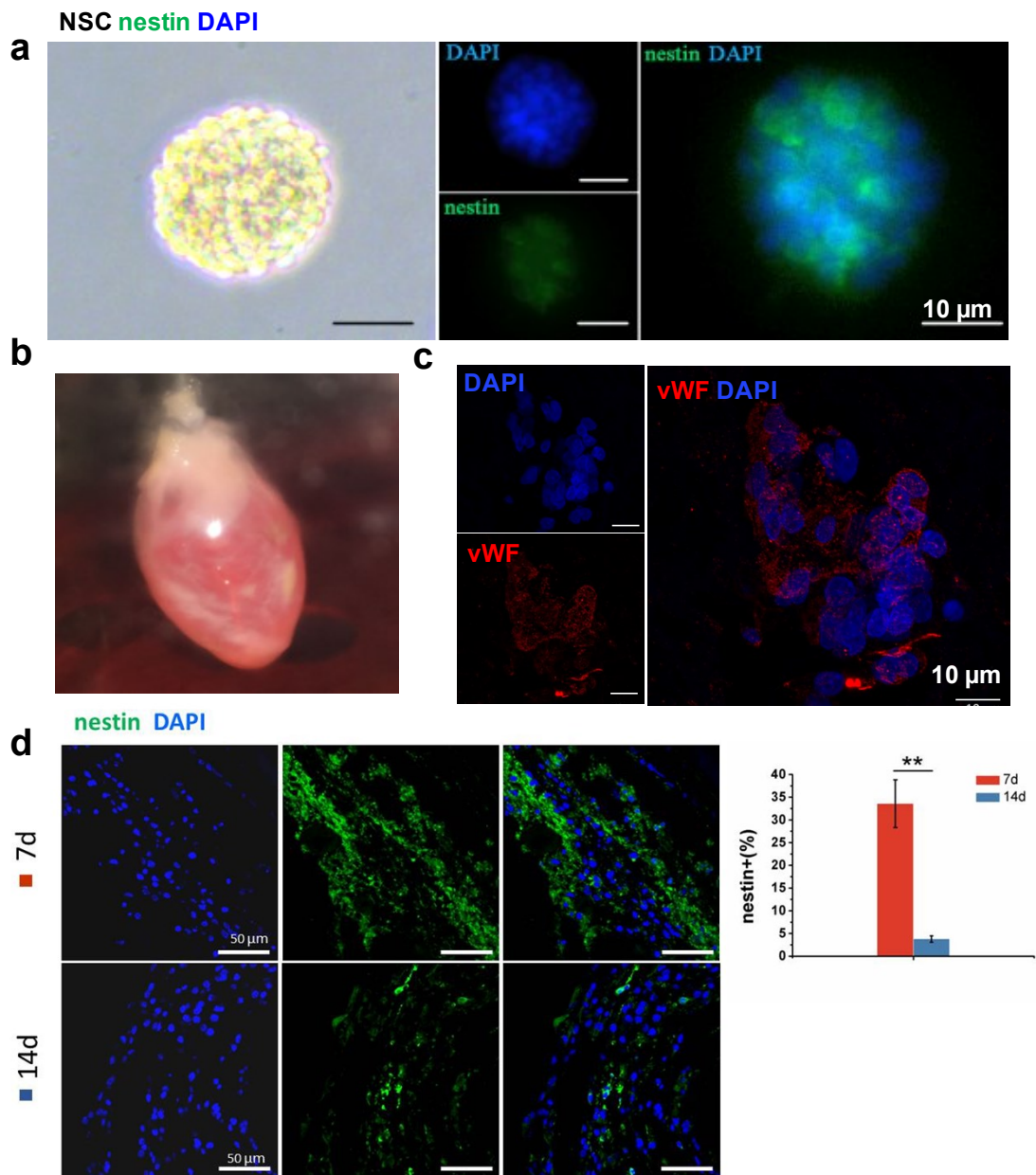
**Fig. S11** GO-based enrichment and clustering analysis of up-regulated proteins (heart-vs-brain) based on biological process. Q1 ( $0 < \text{Ratio T/C} < 1/2$ ), Q2 ( $1/2 \leq \text{Ratio T/C} < 1/1.5$ ), Q3 ( $1.5 < \text{Ratio T/C} \leq 2$ ) and Q4 ( $\text{Ratio T/C} > 2$ ).

**Fig. S12** NSCs were seeded in 2D heart decellularized coating wells and cultured for 14 days. Immunofluorescent analysis of NSCs with neural lineage specific markers GFAP, MAP2 and cardiac specific markers  $\alpha$ -actinin, GATA4.

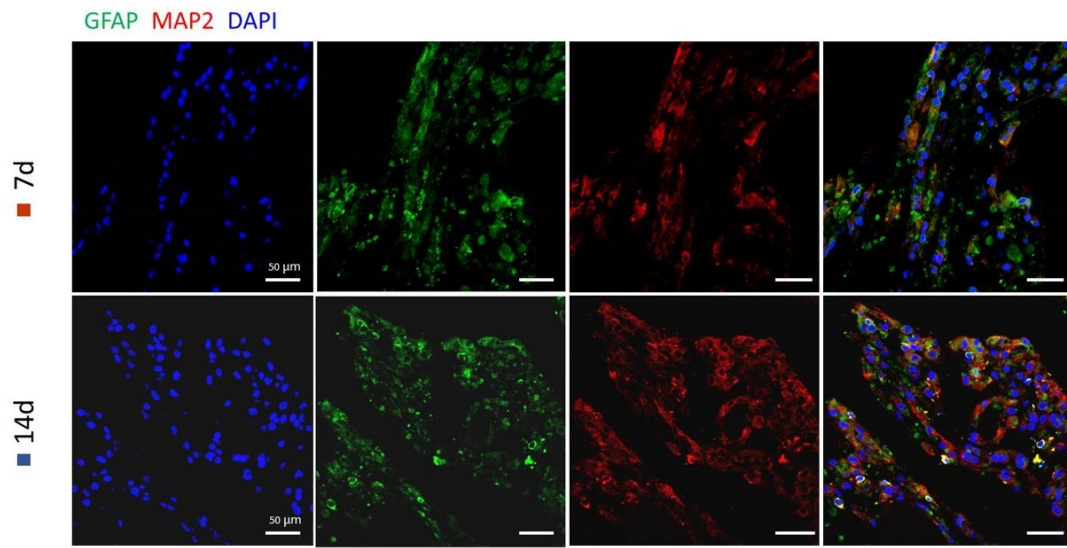
**Fig. S1**



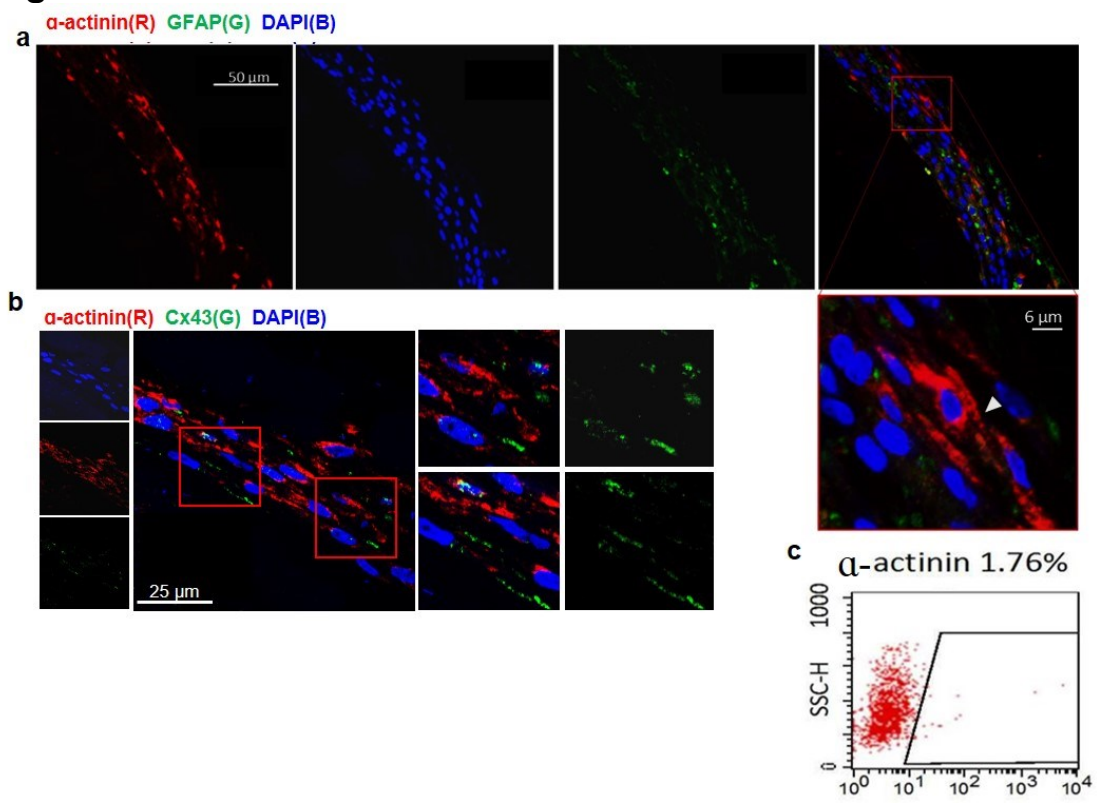
**Fig. S2**



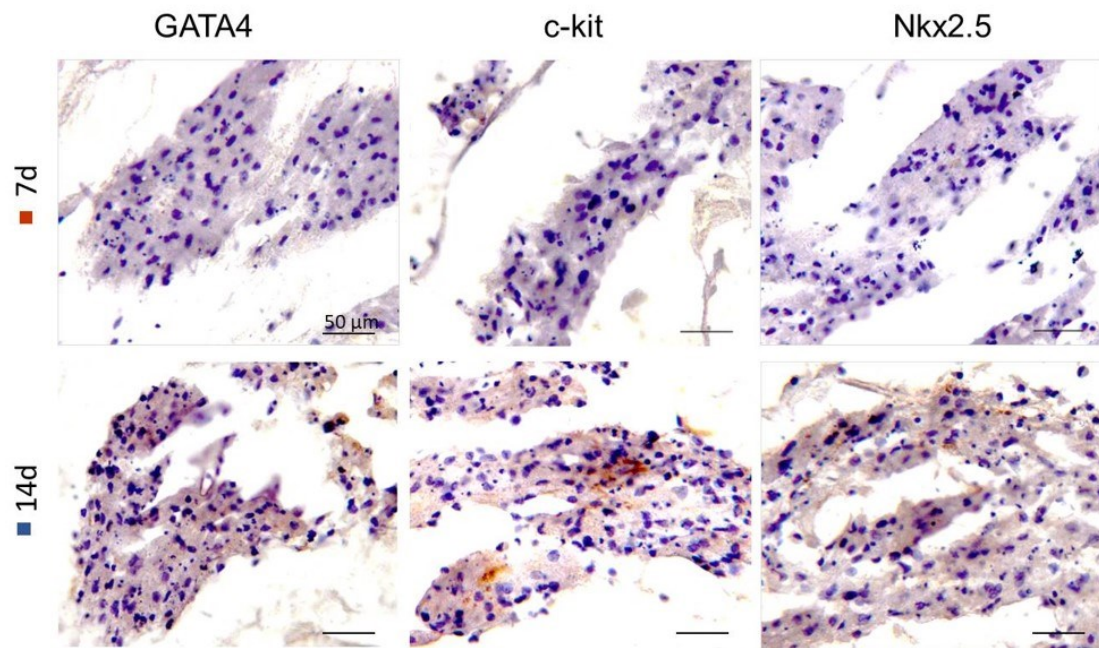
**Fig. S3**



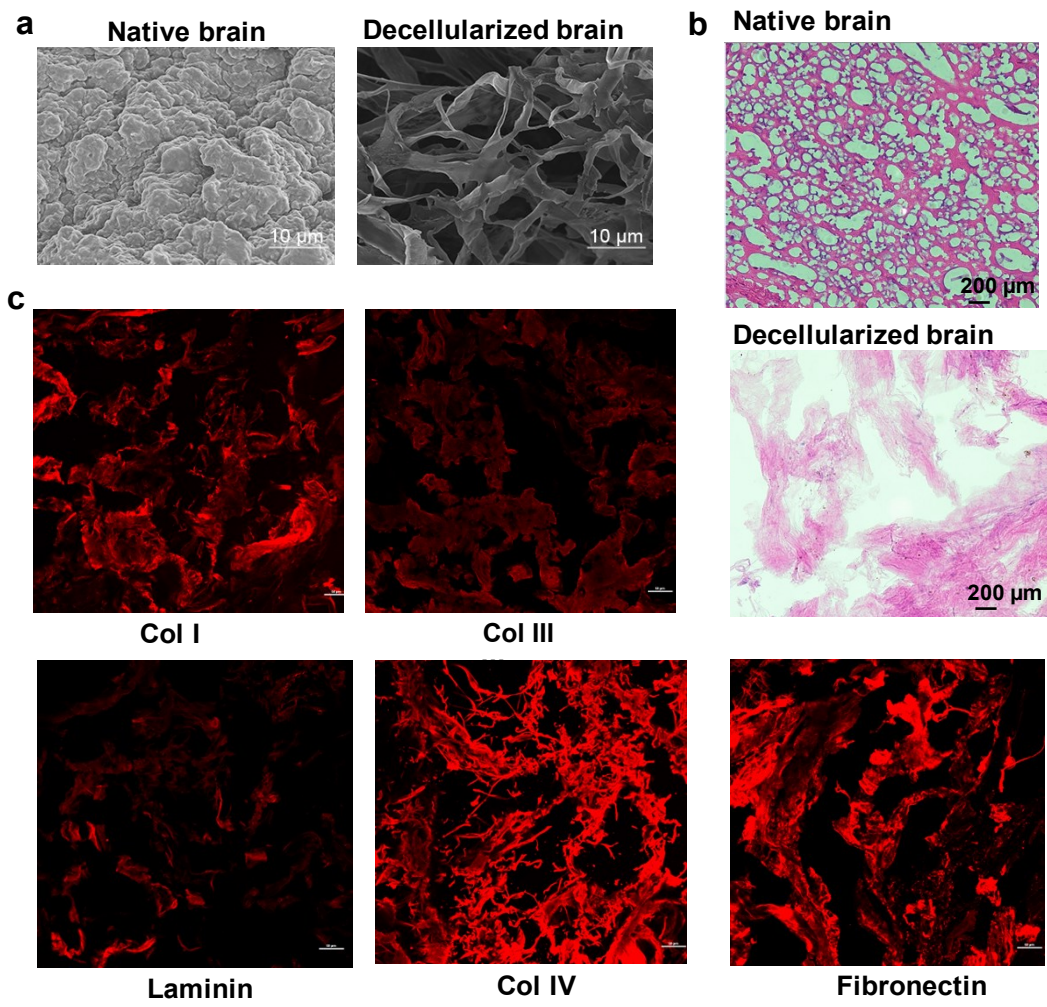
**Fig. S4**



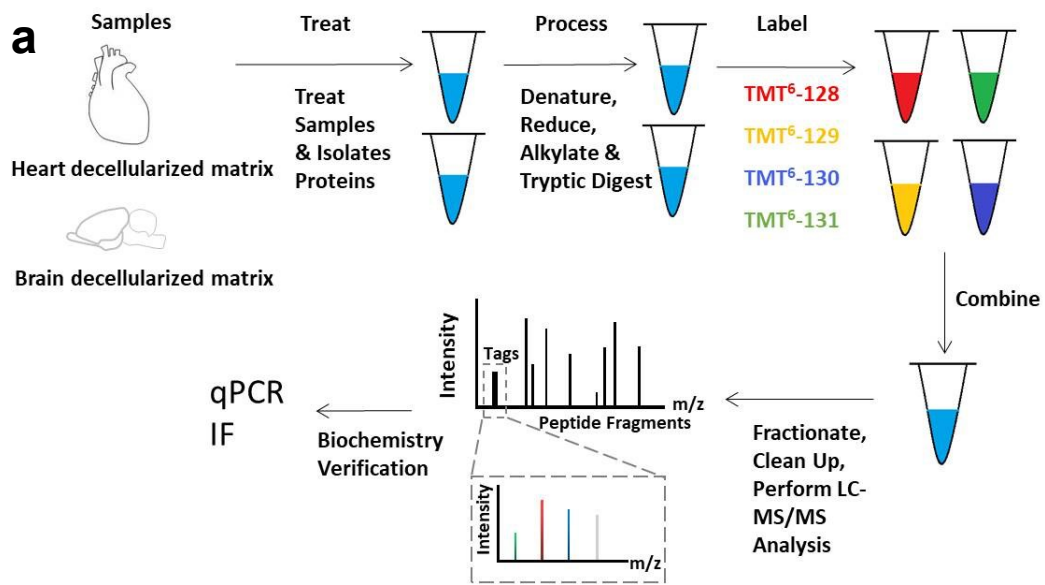
**Fig. S5**



**Fig. S6**



**Fig. S7**



**b**

Name	Identified	Quantified
Proteins	3477	2275

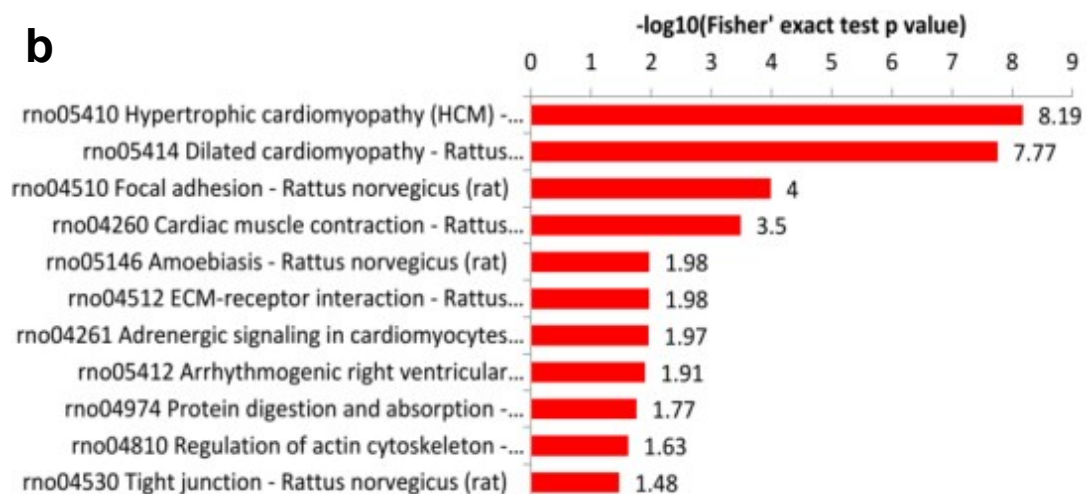
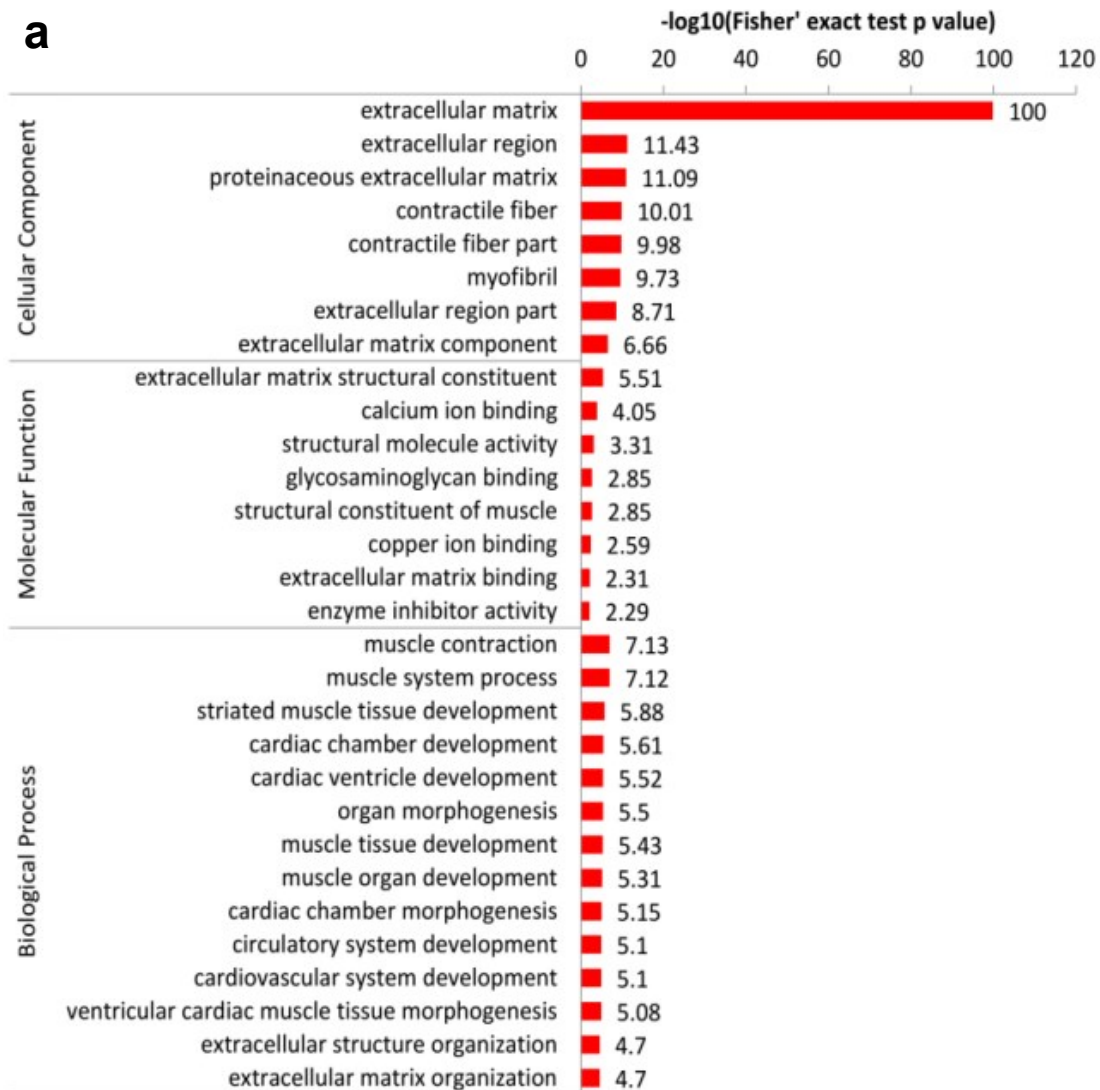
**Table 1** Summary of identified and quantified proteins

Name	Up-regulated	Down-regulated
Proteins	364	573

**Table 2** Summary of differentially quantified proteins



**Fig. S8**



**Fig. S9**

**Cellular Component**

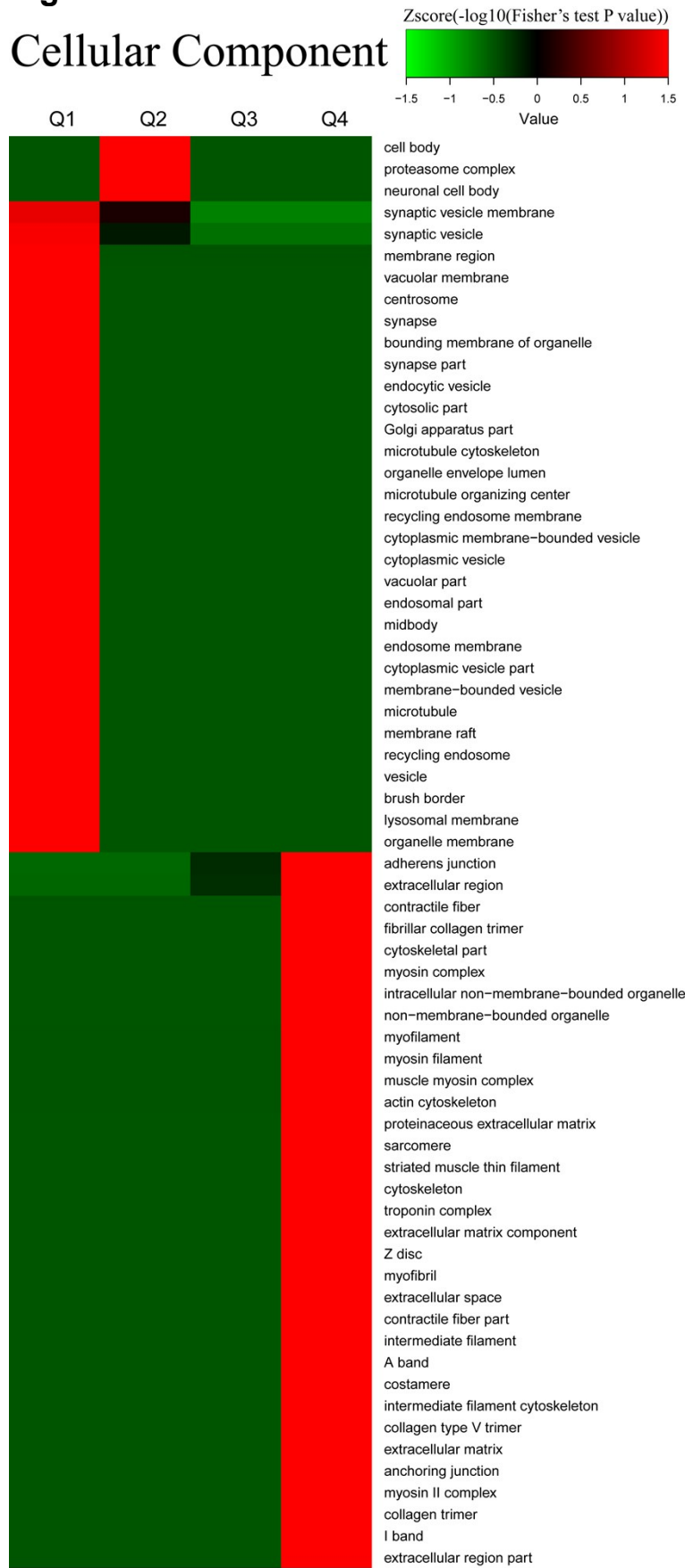


Fig. S10

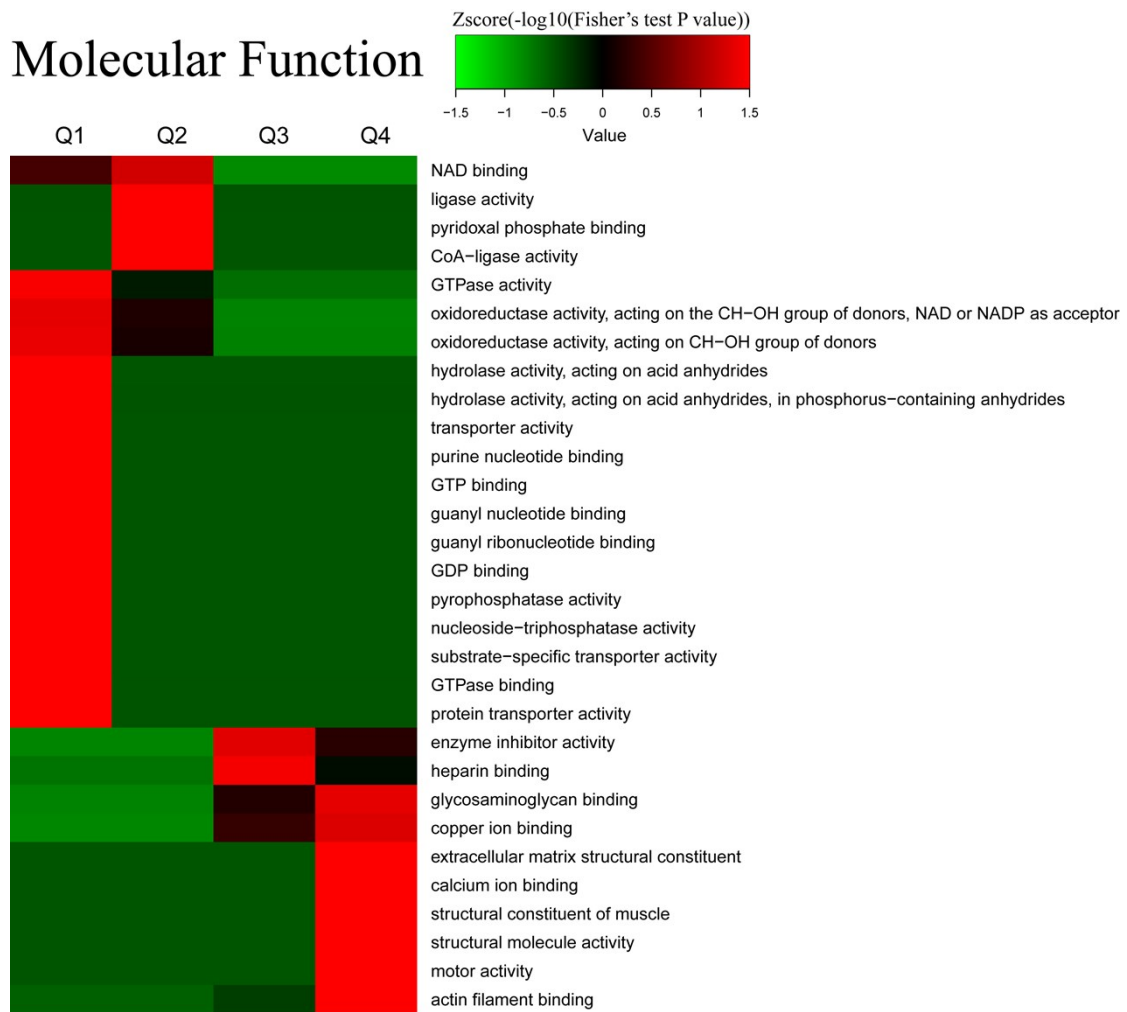
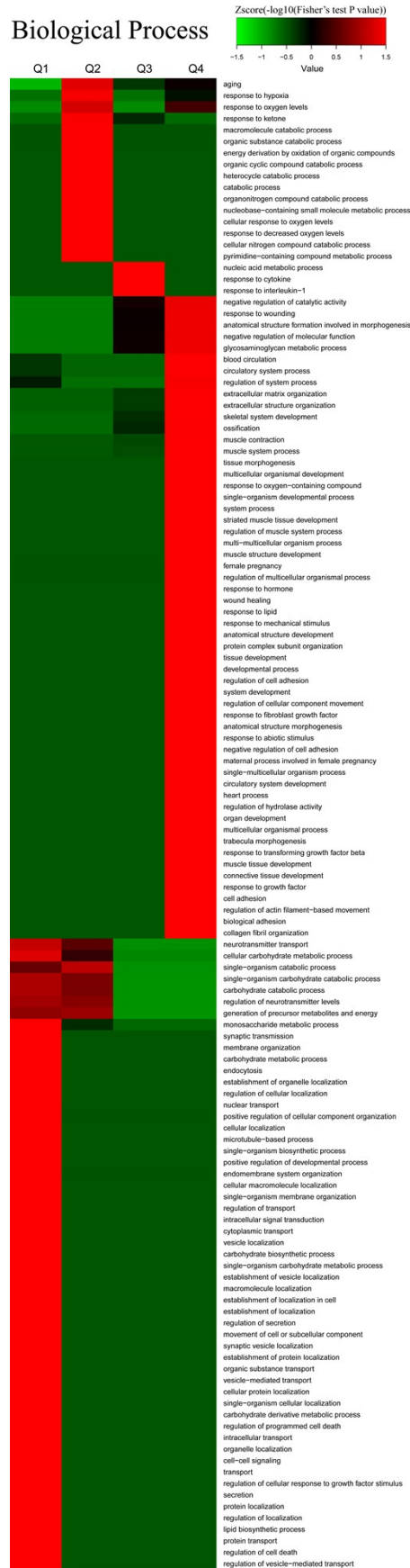


Fig. S11



**Fig. S12**

