

Analysis of mesenchymal stem cell proteomes in situ in the ischemic heart

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Supplementary Information

Supplementary Figures

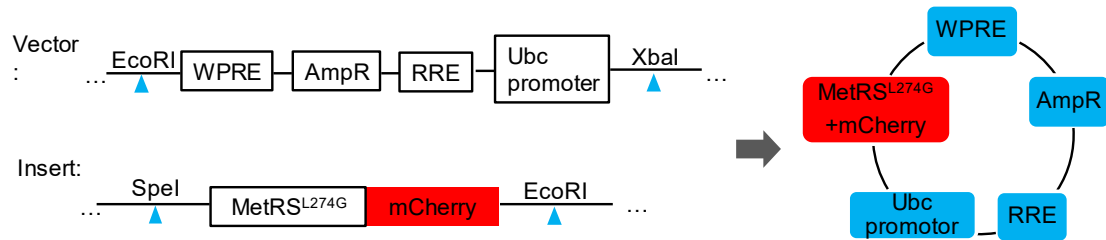


Figure S1: Cloning of lentiviral vector MetRS^{L274G}-mCherry: (Upper left panel) Backbone plasmid FUGW were digested with restriction enzyme EcoRI and XbaI to obtain a 9.1 kb fragment. (Lower left panel) MetRS^{L274G}-mCherry insert was created by amplifying a 3.6kb fragment of plasmid MaRSC via PCR with primers containing Spel and EcoRI restriction sites at the ends (primer sequences reported in Methods), then digested with restriction enzyme Spel and EcoRI (Right panel) The lentiviral plasmid MetRS^{L274G}-mCherry was obtained by ligating backbone and insert.

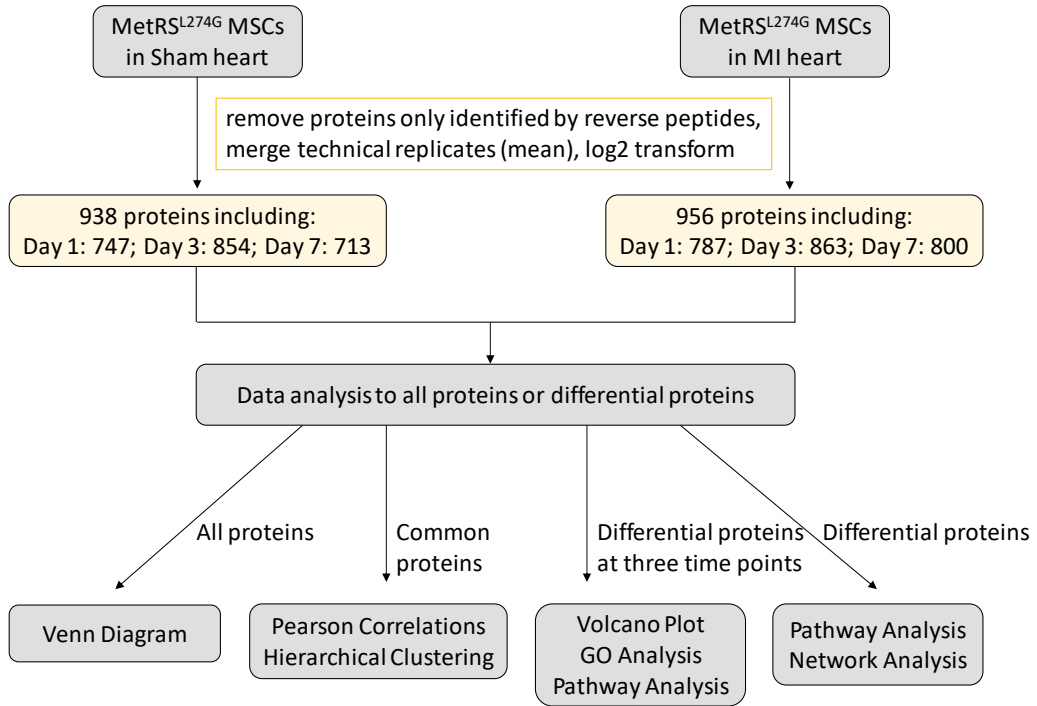


Figure S2. Workflow of mass spectrometry and data analysis.

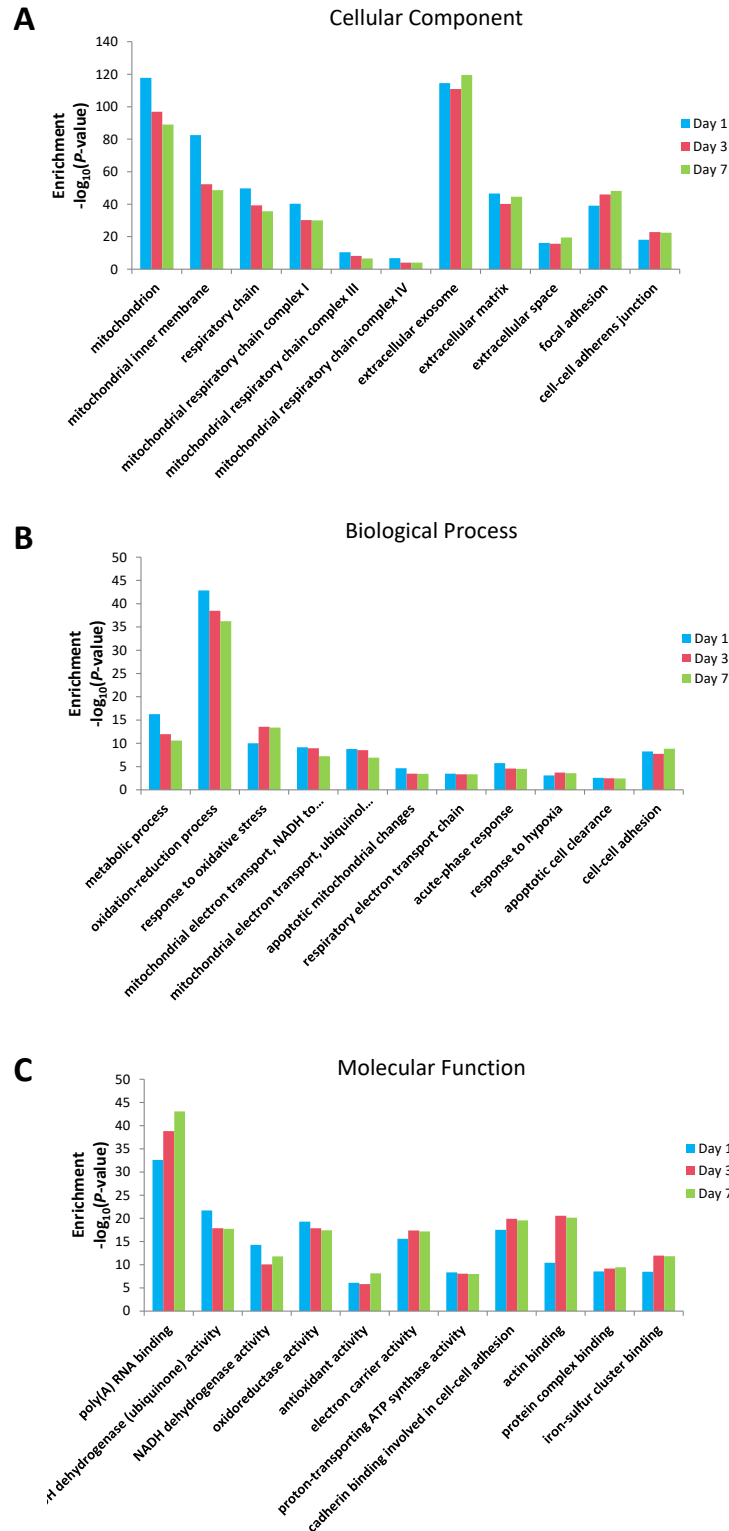


Figure S3: Gene Ontology analyses of MSC proteomes in the Sham heart: The significantly enriched GO terms for cellular components (A), biological processes (B) and molecular function (C) at day 1, 3, or day 7 in the Sham hearts. n=5 for each time point.

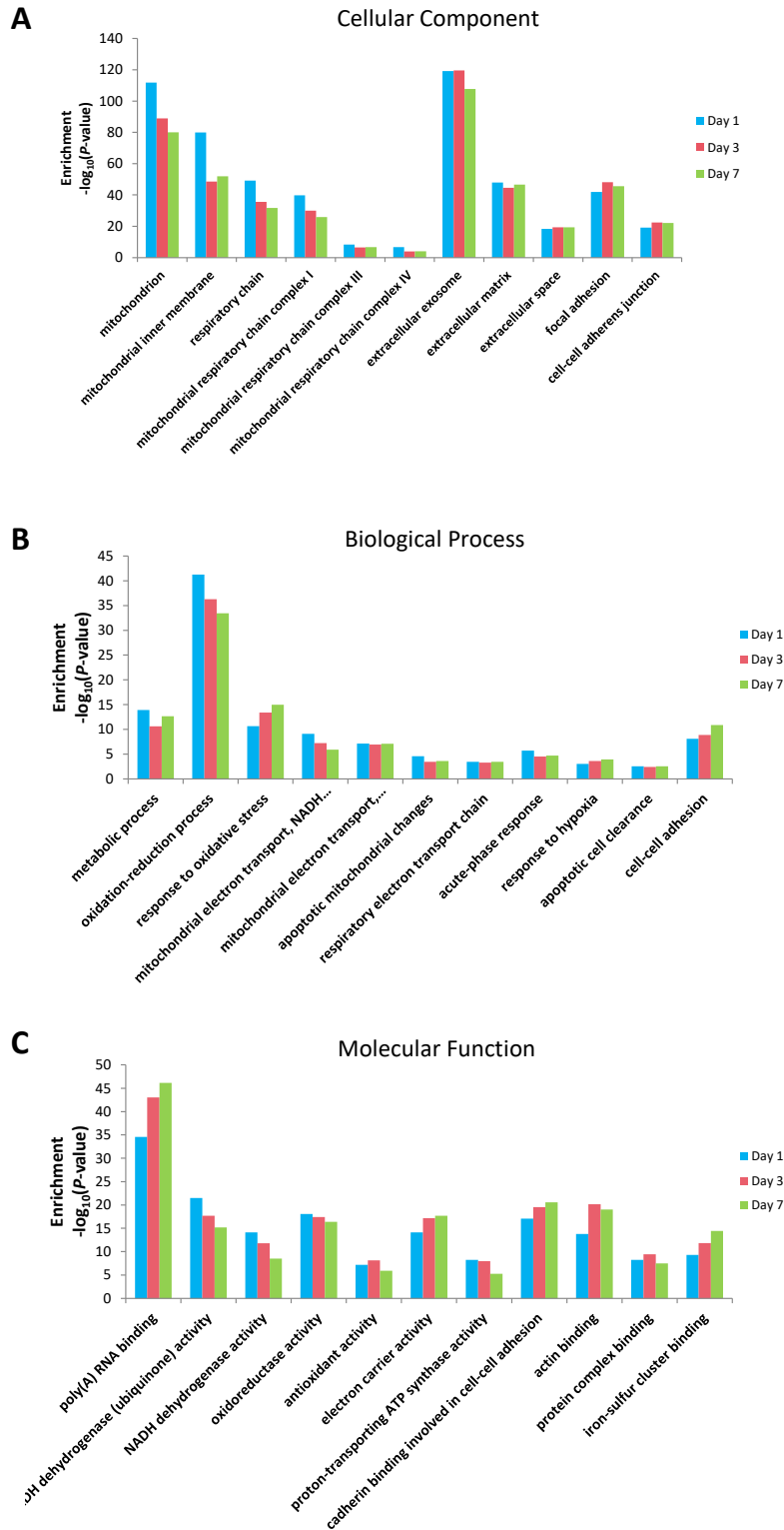


Figure S4: Gene Ontology analysis of MSC proteomes in the MI heart: The significantly enriched GO terms for cellular components (**A**), biological processes (**B**) and molecular function (**C**) at day 1, 3 or 7 in the MI hearts. n=5 for each time point.

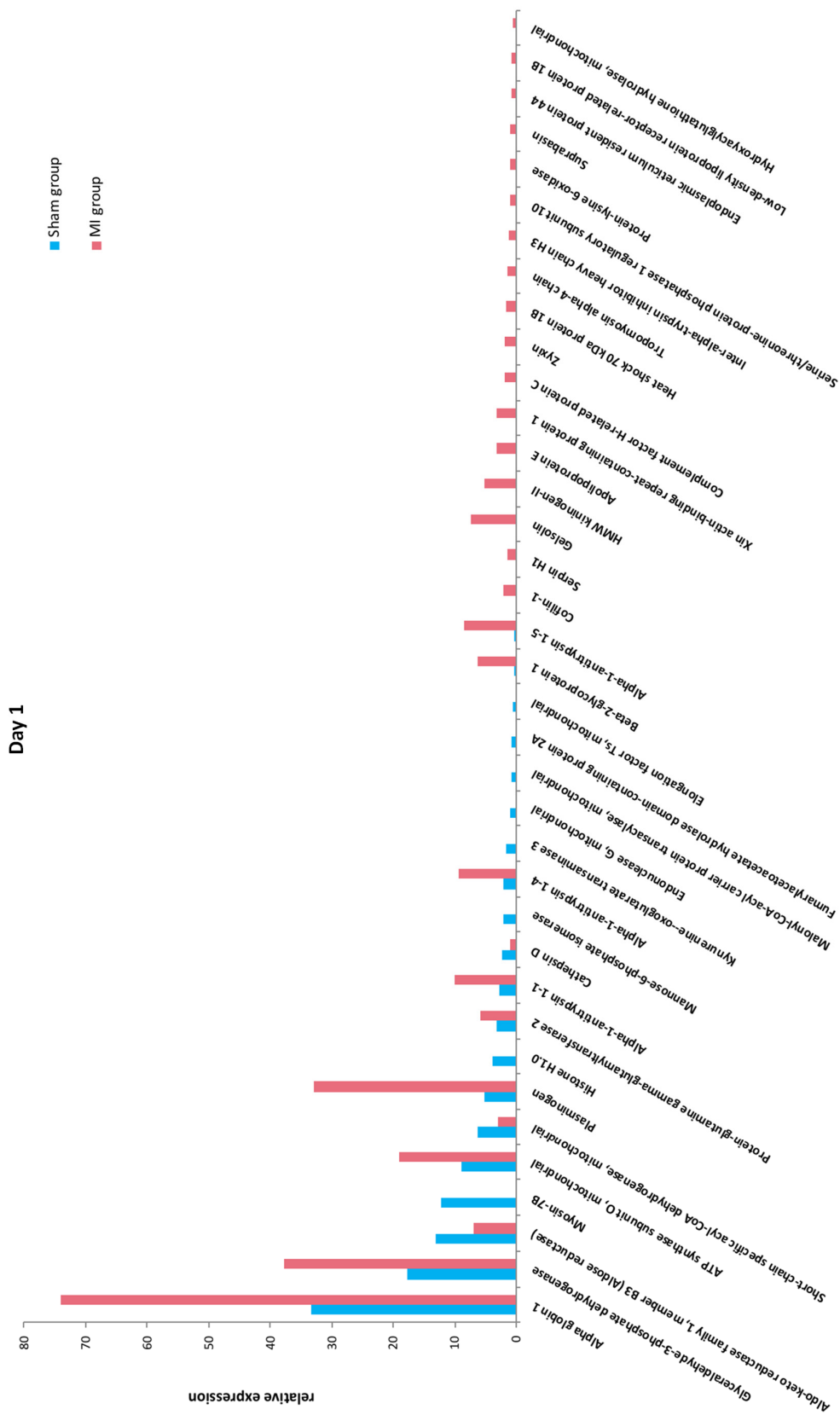


Figure S5: The relative expression levels of the differentially expressed proteins (fold change ≥ 1.5) in the MSCs transplanted for 1 day in the MI vs. Sham heart.

