

Appendix from Su et al., “Right ventricular protein expression profile in end-stage heart failure” (Pulm. Circ., vol. 5, no. 3, p. 000)

Table S1. Ischemic LV ($n = 6$) versus ischemic RV ($n = 6$) proteomic results

Cluster, protein	Gene	MW, kDa	Unique peptides	Spectral counts	Peptide covered, %	LV/RV AV ratio	<i>P</i> , <i>t</i> test
Cluster 1						1.41	0.012
Mu-crystallin homolog	<i>CRYM</i>	34	1	1	3		
Cluster 2						1.61	0.051
Tropomyosin 1 alpha	<i>TPM1</i>	33	18	26	41		
Mu-crystallin homolog	<i>CRYM</i>	34	4	4	14		
Cluster 3						2.04	0.03
Tropomyosin 1 alpha	<i>TPM1</i>	33	19	25	42		
Cluster 4						2.61	0.021
Thioredoxin-like protein 1	<i>TXNL1</i>	32	4	5	17		
Cluster 5						2.75	0.019
Actinin-2 fragment	<i>ACTN2</i>	104	9	10	11		

Note: Unique peptides: no. of peptides unique to the parent protein in question identified by tandem mass spectrometry; spectral counts: no. of spectral counts identified by tandem mass spectrometry; peptide covered: percentage of the entire parent peptide identified by the digested peptide fragments identified by tandem mass spectrometry mapped back to the entire parent peptide. AV: average abundance; LV: left ventricle; MW: molecular weight; RV: right ventricle.

Table S2. Nonischemic LV ($n = 6$) versus nonischemic RV ($n = 6$) proteomic results

Cluster, protein	Gene	MW, kDa	Unique peptides	Spectral counts	Peptide covered, %	LV/RV AV ratio	P , t test
Cluster 1						1.36	0.028
Mitochondrial inner membrane protein ^a	<i>IMMT</i>	84	29	38	31		
Cluster 2						1.29	0.029
Mu-crystallin homolog	<i>CRYM</i>	34	1	1	3		
Cluster 3						1.49	0.046
Tropomyosin 1 alpha	<i>TPM1</i>	33	13	14	41		
Mu-crystallin homolog	<i>CRYM</i>	34	9	12	23		
Clusterin	<i>CLUS</i>	52	5	7	13		
Cluster 4						1.43	0.026
Tropomyosin 1 alpha	<i>TPM1</i>	33	19	25	42		
Cluster 5						1.35	0.013
Ubiquinone biosynthesis protein COQ9 (mitochondrial)	<i>COQ9</i>	36	8	9	22		
Cluster 6 ^b						1.28	0.047
ATP synthase subunit d	<i>ATP5H</i>	18	18	23	43		
Cluster 7						1.3	0.056
Cathepsin D	<i>CATD</i>	45	8	12	14		
Prohibitin	<i>PHB</i>	30	8	10	29		

Note: Unique peptides: no. of peptides unique to the parent protein in question identified by tandem mass spectrometry; spectral counts: no. of spectral counts identified by tandem mass spectrometry; peptide covered: percentage of the entire parent peptide identified by the digested peptide fragments identified by tandem mass spectrometry mapped back to the entire parent peptide. AV: average abundance; LV: left ventricle; MW: molecular weight; RV: right ventricle.

^a Mitofilin, p87/89, cell proliferation-inducing gene 4 protein.

^b Also some background from myosin light chain 3 (*MYL3*).

Table S3. Paired LV ($n = 8$) versus RV dysfunction ($n = 8$) proteomic results

Cluster, protein	Gene	MW, kDa	Unique peptides	Spectral counts	Peptide covered, %	Unpaired		Paired	
						LV/RV AV ratio	P, <i>t</i> test	LV/RV AV ratio	P, <i>t</i> test
Cluster 1						1.3	0.01	1.34	0.026
Mu-crystallin homolog	<i>CRYM</i>	34	1	1	3				
Cluster 2						NS	NS	1.37	0.04
Tropomyosin 1 alpha	<i>TPM1</i>	33	19	25	42				
Cluster 3						1.31	0.035	1.35	0.012
Ubiquinone biosynthesis protein COQ9 (mitochondrial)	<i>COQ9</i>	36	8	9	22				
Cluster 4 ^a						NS	NS	1.23	0.017
Troponin I	<i>TNNI3</i>	24	8	13	32				
Serum amyloid P-component	<i>SAMP</i>	25	7	13	28				
ER protein 29	<i>ERP29</i>	29	6	11	27				
Cluster 5						1.81	0.022	1.88	0.023
Actinin-2 fragment	<i>ACTN2</i>	104	9	10	11				

Note: Unique peptides: no. of peptides unique to the parent protein in question identified by tandem mass spectrometry; spectral counts: no. of spectral counts identified by tandem mass spectrometry; peptide covered: percentage of the entire parent peptide identified by the digested peptide fragments identified by tandem mass spectrometry mapped back to the entire parent peptide. AV: average abundance; LV: left ventricle; MW: molecular weight; NS: not significant; RV: right ventricle.

^a Also weaker evidence for heat-shock protein 27 (*HSP27*) and NADH dehydrogenase (ubiquinone) iron-sulfur protein 3, mitochondrial (*NDUFS3*).

Table S4. Paired LV ($n = 4$) versus RV no dysfunction ($n = 4$) proteomic results

Cluster, protein	Gene	MW, kDa	Unique peptides	Spectral counts	Peptide covered, %	Unpaired		Paired	
						LV/RV AV ratio	<i>P</i> , <i>t</i> test	LV/RV AV ratio	<i>P</i> , <i>t</i> test
Cluster 1						NS	NS	1.37	0.011
Transferrin	<i>TRFE</i>	77	17	27	21				
Cluster 2 ^a						1.47	0.047	1.49	0.046
Myosin 7	<i>MYH7</i>	223	15	19	7				
RuvB-like 2	<i>RUVB2</i>	51	14	19	28				
Fibrin(ogen) gamma	<i>FIBG</i>	52	10	13	18				
Cluster 3						1.47	0.036	NS	NS
Mu-crystallin homolog	<i>CRYM</i>	34	1	1	3				
Cluster 4						1.55	0.042	NS	NS
Tropomyosin 1 alpha	<i>TPM1</i>	33	18	26	41				
Mu-crystallin homolog	<i>CRYM</i>	34	4	4	14				
Cluster 5 ^b						1.36	0.048	NS	NS
WDR44	<i>B7Z964</i>	37	23	34	49				
Desmin	<i>DES</i>	54	8	9	19				
Cluster 6						2.68	0.014	2.61	0.024
Tropomyosin 1 alpha	<i>TPM1</i>	33	19	25	42				
Cluster 7						1.42	0.018	1.41	0.0012
Ubiquinone biosynthesis protein COQ9 (mitochondrial)	<i>COQ9</i>	36	8	9	22				
Cluster 8 ^c						NS	NS	1.77	0.0067
Troponin I	<i>TNNI3</i>	24	7	10	28				
Serum amyloid P-component	<i>SAMP</i>	25	6	10	26				

Note: Unique peptides: no. of peptides unique to the parent protein in question identified by tandem mass spectrometry; spectral counts: no. of spectral counts identified by tandem mass spectrometry; peptide covered: percentage of the entire parent peptide identified by the digested peptide fragments identified by tandem mass spectrometry mapped back to the entire parent peptide. AV: average abundance; LV: left ventricle; MW: molecular weight; NS: not significant; RV: right ventricle.

^a Also weaker evidence for desmin (*DES*).

^b Also weaker evidence for heme oxygenase 2 (*HMOX2*), lactate dehydrogenase B (*LDHB*), and pyruvate dehydrogenase β (*PDHB*).

^c Also heat-shock protein 27 (*HSP27*).