Glycoproteomic profiling provides candidate MI predictors of later progression to heart failure

Kristine Y Deleon-Pennell PhD[1,2*], Osasere K Ero MBBS[1], Yonggang Ma PhD[1],

Rugmani Padmanabhan Iyer PhD[1], Elizabeth R Flynn BS[1], Ingrid Espinoza PhD[3],

Solomon K. Musani PhD[4], Ramachandran S Vasan MD[5], Michael E Hall MD, MS[1,4,6],

Ervin R Fox MD, MPH[4,6], and Merry L Lindsey PhD[1,2*]

[1]Mississippi Center for Heart Research, Department of Physiology and Biophysics, UMMC, Jackson, MS; [2]Research Service, G.V. (Sonny) Montgomery Veterans Affairs Medical Center, Jackson, MS; [3]Department of Preventive Medicine and Cancer Institute, UMMC, Jackson, MS; [4]Jackson Heart Study, UMMC, Jackson, MS; [5]Preventive Medicine and Epidemiology and Cardiology, Department of Medicine, Boston University School of Medicine; and [6]Division of Cardiology, UMMC, Jackson, MS

*Corresponding author information:

Kristine Y. DeLeon-Pennell, Ph.D.   or   Merry L. Lindsey, Ph.D.

(phone) 843-789-6839   (phone) 601-815-1329

(fax) 843-876-5068   (fax) 601-984-1817

Email: deleonky@musc.edu   Email: mllindsey@umc.edu

Department of Physiology and Biophysics

University of Mississippi Medical Center

2500 North State St., Jackson, MS 39216-4505, USA.

Short title: Glycoproteomic profiling provides indicators of heart failure

Supporting Information

Table S1. Regression analysis of mass spectroscopy peak intensity values versus densitometry of protein measured by immunoblotting. Protein quantification correlated with peak intensity of proteins identified by mass spectroscopy and showed a positive relationship between the two methods.

Accession #	Protein Name	Densitometry		Correlation	
		MI	MI+HF	r	p value
31377806	Polymeric immunoglobulin receptor	0.62±0.01	1.11±0.40	0.663	<0.0001
4502511	Complement C9	8.81±0.92	13.38±1.58	0.499	<0.0001
4502165	Apolipoprotein F	0.46±0.02	0.57±0.05	0.288	0.032
42761474	CD59 glycoprotein	0.22±0.01	0.20±0.01	0.281	0.033
4502161	Apolipoprotein C-IV	0.59±0.05	0.57±0.04	0.194	0.140
4507725	Transthyretin	0.24±0.03	0.26±0.06	0.035	0.788

Table S2. Glycoproteomic results; values for individual samples are intensity units of the peptides. Definition of terms: Xcorr- peptide score, m/z [Da]- mass/charge, and RT (min)- retention time.
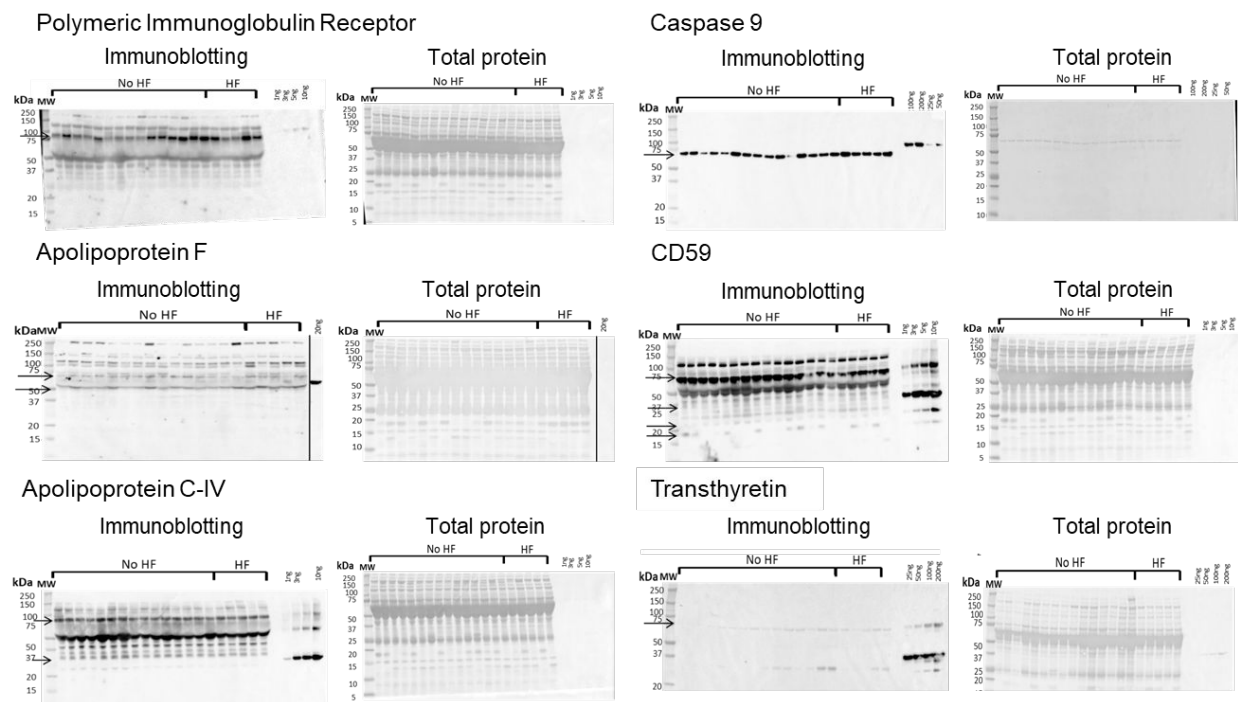
Figure S1

Polymeric Immunoglobulin Receptor

Caspase 9

Apolipoprotein F

CD59

Apolipoprotein C-IV

Transthyretin

Figure S1. Immunoblotting of top 6 proteins identified by glycoproteomics show strong correlation between two proteomic techniques. n=15 no HF and 5 HF.