Supplement Table 1: Mass spectroscopic identification of INrf2 and PGAM5 proteins peptides. Control 293 cells and INrf2-293 cells were treated with tetracycline (0.5μg/ml) for 24h for induction of Flag-INrf2 protein in INrf2-293 cells. 10 mg cell lysates were immunoprecipitated with anti-Flag antibodies, the immune complexes were separated by SDS-PAGE and gels were stained with CBB (as shown in Fig. 2A). Gel slices containing bands indicated by arrows in figure 2A were reduced, alkylated, and digested with trypsin. Tryptic peptides were desalted and subjected to LC-MS/MS analysis. Some of INrf2 and PGAM5 proteins peptide identified by LC-MS/MS were presented below.

INrf2 a.a.	INrf2 Peptide Sequence	charge State	XCorr	PGAM5 a.a.	PGAM5 Peptide Sequence	Charge State	XCorr
					AGGDAEPRPAEPP		
51-61	TFSYTLEDHTK	2	2.38	33-52	AWAGGAR	2	2.95
72-84	LSQQLCDVTLQVK	2	3.93	41-52	PAEPPAWAGGAR	2	2.98
98-108	VVLASSSPVFK	2	3.64	53-64	PGPGVWDPNWDR	2	3.08
117-131	EQGMEVVSIEGIHPK	2	3.86	65-74	REPLSLINVR	2	3.41
	CVLHVMNGAVMYQ						
151-169	IDSVVR	2	3.87	66-74	EPLSLINVR	1	1.63
					RNVESGEEELASKLDH		
203-216	AREYIYMHFGEVAK	3	3.43	76-93	YK	3	4.87
205-216	EYIYMHFGEVAK	2	3.81	77-88	NVESGEEELASK	1	2.46
262-269	FYVQALLR	2	3.25	77-88	NVESGEEELASK	2	4.15
					NVESGEEELASKLDHY		
288-296	CEILQSDSR	2	3.41	77-93	K	2	4.98
	YEPERDEWHLVAPM						
443-459	LTR	3	3.75	99-104	HIFLIR	1	1.70
460-470	RIGVGVAVLNR	2	3.25	105-116	HSQYHVDGSLEK	2	4.10
461-470	IGVGVAVLNR	2	1.97	105-118	HSQYHVDGSLEKDR	2	5.73
471-483	LLYAVGGFDGTNR	2	4.35	119-125	TLTPLGR	1	1.66
484-494	LNSAECYYPER	2	3.32	126-134	EQAELTGLR	1	1.57
499-507	MITAMNTIR	2	2.82	135-141	LASLGLK	1	1.77
	SGAGVCVLHNCIYA						
	AGGYDGQDQLNSV						
508-536	ER	3	4.96	135-144	LASLGLKFNK	2	2.78
602-614	SGVGVAVTMEPCR	2	3.81	142-152	FNKIVHSSMTR	2	3.22
602-615	SGVGVAVTMEPCRK	2	3.26	153-162	AIETTDIISR	2	4.02
	YEPERDEWHLVAPM						
443-459	LTR	3	3.75	204-209	IEAAFR	1	1.76
460-470	RIGVGVAVLNR	2	3.25	241-251	ALQFPPEGWLR	2	3.28

MS/MS spectra were searched against a UniProt human protein database using Sorcerer™-SEQUEST® (Sage-N Research). Database search parameters were as follows: enzyme – trypsin; cleavage – full; precursor mass tolerance – 1.5Da; fragment ion tolerance – 0.5 Da; missed cleavages – 2; modifications – Cys carbamidomethylation (+57.02), and Met oxidation (+15.99). The quality of protein assignments was assessed using ProteinProphet. Proteins with probabilities ≥ 1.0 and ≥ 2 unique peptides were accepted as confidently identified proteins. The quality of peptide assignments was assessed using the following Xcorr vs. charge state filter: 1+: ≥ 1.5, 2+: ≥ 2.5, 3+: ≥ 3.0, and 4+: ≥ 3.5.