Table S2: Number of genes/proteins enriched in GO categories and pathways.

TERMS	Proteomics (-log P value)	Genomics (-log P value)	No of proteins	No of cDNA
Components				
Mitochondrion	7.7	3.7	16	14
Mitochondrion Inner Membrane	5.9	1.4	9	4
Cytoplasm	5.7	0.5	30	30
Contractile Fiber	5.2	2.1	5	3
Mitochondrial Envelope	5.1	1.1	9	4
Mitochondrion Matrix	3.9	3.9	8	6
Mitochondrion Lumen	3.9	3.9	8	6
Membrane enclosed Lumen	0.7	2.8	4	14
Extracellular Space	0.1	3.3	4	24
GO Biological Processes				
cardiac muscle contraction	7.8	0.9	5	1
heart contraction	6.0	1.0	5	1
striated muscle contraction	5.8	0.6	5	1
glucose metabolic process	4.1	0.8	5	1
fatty acid beta-oxidation	2.4	3.4	2	3
fatty acid metabolic process	2.4	4.2	4	7
fatty acid catabolic process	2.1	3	2	3
carboxylic acid catabolic process	2.0	2.9	6	8
involuntary skeletal muscle contraction	2.0	1.9	1	1
positive regulation of muscle development	1.7	1.5	1	1
blood vessel morphogenesis	0.7	3.7	3	5
blood vessel development	0.6	3.4	3	5
vasculature development	0.6	3.4	3	5
GO Metabolic Functions				
phosphopyruvate Hydratase activity	7.3	0	3	0
peroxiredoxin activity	6.4	0	3	0
hydro-lyase activity	4.9	0.8	4	1
carbon-oxygen lyase activity	4.7	0.6	4	1
catalytic activity	3.3	2.5	21	35
acyl-CoA dehydrogenase activity	1.4	2.8	1	2
endopeptidase activity	0.5	8.0	1	13
serine-type endopeptidase activity	0.5	12.9	1	13
serine hydrolase activity	0.4	12.2	1	13
Canonical Pathways				
Glycolysis and gluconeogenesis p.3	6.0	0	4	0
Cytoskeleton remodeling Alpha-1A adrenergic receptor-dependent inhibition of PI3	4.5	0	3	0
Oxidative phosphorylation	3.3	0.5	4	1
Cytoskeleton remodeling Regulation of actin cytoskeleton by Rho GTPases	2.7	1.3	2	1
Prostaglandin 2 biosynthesis and metabolism	2.5	0	3	
Development Beta-adrenergic receptors signaling via cAMP	1.9	0.8	2	1
Butanoate metabolism	1.7	1.8	2	2
Mitochondrial long chain fatty acid beta-oxidation	0.6	4.6	1	4
Propionate metabolism p.1	0	3.5	0	4
Cell adhesion ECM remodeling	0	3.4	0	3