

Lipid metabolism

Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
3-ketoacyl-CoA thiolase	P42765	0.66		Beta-oxidation
3-ketoacyl-CoA thiolase peroxisomal	P09110	0.36		Beta-oxidation
Acetyl-coenzyme A synthetase 2-like	Q9NUB1	0.14		Beta-oxidation
Acyl-CoA dehydrogenase family member 9	Q9H845	0.26		Beta-oxidation
Delta(3 5)-Delta(2 4)-dienoyl-CoA isomerase	Q13011	0.14		Beta-oxidation
Enoyl-CoA delta isomerase 1	P42126	0.14		Beta-oxidation
Long-chain-fatty-acid--CoA ligase 1	P33121	0.37		Beta-oxidation
Medium-chain specific acyl-CoA dehydrogenase (ACADm)	P11310	0.09	0.16	Beta-oxidation
Peroxisomal multifunctional enzyme type 2	P51659	0.33		Beta-oxidation
Short/branched chain specific acyl-CoA dehydrogenase	P45954	0.11		Beta-oxidation
Short-chain specific acyl-CoA dehydrogenase	P16219	0.17	0.30	Beta-oxidation
Very long-chain specific acyl-CoA dehydrogenase	P49748	0.32	0.35	Beta-oxidation
Trifunctional enzyme subunit alpha	P40939	0.19		Beta-oxidation
Trifunctional enzyme subunit beta	P55084	0.28		Beta-oxidation
2 4-dienoyl-CoA reductase	Q16698	0.08		Beta-oxidation
Enoyl-CoA hydratase mitochondrial	P30084	0.22		Beta-oxidation
3-hydroxyacyl-CoA dehydrogenase type-2	Q99714	0.25		Beta-oxidation
Hydroxyacyl-coenzyme A dehydrogenase	Q16836	0.21		Beta-oxidation
Acetyl-CoA acetyltransferase	P24752	0.17		Beta-oxidation

Table S1

Lipid metabolism (cont.)

Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
Trans-2-enoyl-CoA reductase	Q9BV79	0.19		Fatty acid biosynthesis
Estradiol 17-beta-dehydrogenase 8	Q92506	0.18	0.31	Fatty acid biosynthesis
Mitochondrial carnitine/acylcarnitine carrier protein	O43772	0.17	0.24	Fatty acid oxidation
Acyl-CoA-binding protein	P07108	0.18		Fatty acid oxidation
Acyl-coenzyme A thioesterase 9	Q9Y305	0.35		Fatty acid oxidation
Carnitine O-acetyltransferase	P43155	0.25		Fatty acid oxidation
Carnitine O-palmitoyltransferase 1	Q92523	0.34		Fatty acid oxidation
Carnitine O-palmitoyltransferase 2	P23786	0.24		Fatty acid oxidation
Malonyl-CoA decarboxylase	O95822	0.15		Fatty acid oxidation
Microsomal glutathione S-transferase 3	O14880	0.33		Fatty acid oxidation
Fatty acid-binding protein	P05413	0.12	0.21	Fatty acid transport
D-beta-hydroxybutyrate dehydrogenase	Q02338	0.09	0.21	Fatty acid catabolism
Acid ceramidase	Q13510	0.21	0.28	Sphingolipid metabolism
Prostaglandin E synthase 2	Q9H7Z7	0.34		Prostaglandin biosynthesis
Prostaglandin reductase 2	Q8N8N7	0.19		Prostaglandin biosynthesis
Phosphatidate cytidyltransferase 2	O95674	0.28		Lipid biosynthesis
Phosphatidylinositol transfer protein alpha isoform	Q00169	0.30		Lipid transport
Apolipoprotein A-I Binding Protein	Q8NCW5	0.25	0.34	Lipid transport
Perilipin-3	O60664	0.49		Formation and maintenance of lipid storage droplets
Succinyl-CoA:3-ketoacid coenzyme A transferase 1	P55809	0.10		Ketone body catabolism
Prosaposin	P07602	0.33	0.38	Sphingolipid metabolism

Table S1 (cont.)

Carbohydrate metabolism				
Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
Malate dehydrogenase	P40926	0.13		Gluconeogenesis
Phosphoglycolate phosphatase	A6NDG6	0.19		Gluconeogenesis
Glycogen [starch] synthase	P13807	0.13		Gluconeogenesis
Glycogenin-1	P46976	0.37		Gluconeogenesis
Phosphoglucomutase-1	P36871	0.40		Glycogen degradation
Glycogen phosphorylase	P11216	0.38		Glycogen degradation
Adenylosuccinate synthetase isozyme 1	Q8N142	0.20		Glycolysis
Aldose reductase	P15121	0.25		Glycolysis
Alpha-enolase	P06733	0.63		Glycolysis
Aspartate aminotransferase cytoplasmic	P17174	0.13		Glycolysis
Aspartate aminotransferase mitochondrial	P00505	0.15		Glycolysis
ATP-dependent 6-phosphofructokinase	P08237	0.17		Glycolysis
Beta-enolase	P13929	0.20		Glycolysis
Fructose-bisphosphate aldolase A	P04075	0.44		Glycolysis
Fructose-bisphosphate aldolase C	P09972	0.14		Glycolysis
Glucose-6-phosphate isomerase	P06744	0.35		Glycolysis
Glyceraldehyde-3-phosphate dehydrogenase	P04406	0.54		Glycolysis
Hexokinase-1	P19367	0.29		Glycolysis
Malate dehydrogenase cytoplasmic	P40925	0.22		Glycolysis
Mitochondrial pyruvate carrier 2	O95563	0.11		Glycolysis
Phosphoglycerate mutase 1	P18669	0.58		Glycolysis
Phosphoglycerate mutase 2	P15259	0.19		Glycolysis
Syndapin III	Q9UKS6	0.35		Glycolysis
Triosephosphate isomerase	P60174	0.38		Glycolysis
Dihydrolipoyl dehydrogenase	P09622	0.20		Glycolysis
Lectin, Mannose Binding 1	P49257	0.26		Glycoprotein transport
Glucosamine-6-phosphate isomerase 1	P46926	0.37		Glycosaminoglycan metabolism
UDP-glucose 6-dehydrogenase	O60701	0.39		Glycosaminoglycan metabolism
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2	O60825	0.31		Fructose metabolism
Saccharopine dehydrogenase-like oxidoreductase	Q8NBX0	0.34		Glycolipid biosynthetic
Probable D-lactate dehydrogenase	Q86WU2	0.27		D-lactate catabolic
Aldehyde dehydrogenase mitochondrial	P05091	0.34		Acetate synthesizes

Table S1 (cont.)

Pyruvate decarboxylation and Tricarboxylic Acid Cycle				
Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
L-lactate dehydrogenase B chain	P07195	0.27		Pyruvate decarboxylation
Pyruvate Dehydrogenase Complex Component E2	P10515	0.10		Pyruvate decarboxylation
Pyruvate dehydrogenase E1 component subunit alpha	P08559	0.16	0.24	Pyruvate decarboxylation
Pyruvate dehydrogenase E1 component subunit beta	P11177	0.10		Pyruvate decarboxylation
Pyruvate dehydrogenase protein X component mitochondrial	O00330	0.12	0.17	Pyruvate decarboxylation
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1	Q15118	0.29		Pyruvate decarboxylation
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2	Q15119	0.10		Pyruvate decarboxylation
[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1	Q9P0J1	0.35		Pyruvate decarboxylation
Pyruvate dehydrogenase phosphatase regulatory subunit	Q8NCN5	0.45		Pyruvate decarboxylation
Aconitate hydratase	Q99798	0.13		TCA cycle
Citrate synthase	O75390	0.17		TCA cycle
2-oxoglutarate dehydrogenase	Q02218	0.16		TCA cycle
2-oxoisovalerate dehydrogenase subunit alpha	P12694	0.32		TCA cycle
2-oxoisovalerate dehydrogenase subunit beta	P21953	0.15		TCA cycle
Branched Chain 2-Oxo-Acid Dehydrogenase Complex Component E2	P11182	0.12		TCA cycle
Delta-1-pyrroline-5-carboxylate dehydrogenase	P30038	0.23		TCA cycle
Glutamate dehydrogenase 1	P00367	0.50		TCA cycle
Isocitrate dehydrogenase [NAD] subunit alpha	P50213	0.32	0.47	TCA cycle
Isocitrate dehydrogenase [NAD] subunit gamma	P51553	0.12		TCA cycle
Isocitrate dehydrogenase [NADP]	P48735	0.11		TCA cycle
L-2-hydroxyglutarate dehydrogenase	Q9H9P8	0.30		TCA cycle
Methylmalonyl-CoA mutase	P22033	0.20		TCA cycle
Succinyl-CoA ligase [ADP-forming] subunit beta	Q9P2R7	0.20		TCA cycle
Succinyl-CoA ligase [GDP-forming] subunit beta	Q96I99	0.14		TCA cycle
Isocitrate dehydrogenase [NAD] subunit beta	O43837	0.12		TCA cycle
Malate Dehydrogenase (Oxaloacetate-Decarboxylating)	P23368	0.17		TCA cycle
Dihydrolipoamide S-Succinyltransferase	P36957	0.36		TCA cycle
Alpha-ketoglutarate dehydrogenase component 4	P82909	0.30		TCA cycle
Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha	P53597	0.45		TCA cycle
Glyoxylate reductase/hydroxypyruvate reductase	Q9UBQ7	0.38		Dicarboxylic acid and carboxylic acid metabolism

Table S1 (cont.)

Amino acid metabolism

Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
Cysteine desulfurase mitochondrial	Q9Y697	0.25		Alanine synthesis
S-methyl-5'-thioadenosine phosphorylase	Q13126	0.36		L-methionine biosynthesis
Calcium-binding mitochondrial carrier protein Aralar1	O75746	0.07		Amino acid transport
Branched-chain-amino-acid aminotransferase	O15382	0.13		Amino acid catabolism
3-hydroxyisobutyrate dehydrogenase	P31937	0.15		Amino-acid degradation
3-hydroxyisobutyryl-CoA hydrolase	Q6NVY1	0.27		Amino-acid degradation
Succinate-semialdehyde dehydrogenase	P51649	0.49		Amino-acid degradation
Alanine aminotransferase 1	P24298	0.39		L-alanine degradation
Methylglutaconyl-CoA hydratase	Q13825	0.47		Leucine degradation
Isovaleryl-CoA dehydrogenase	P26440	0.24	0.33	Leucine degradation
Methylcrotonoyl-CoA carboxylase beta chain	Q9HCC0	0.14		Leucine and isovaleric acid catabolism.
Methylcrotonoyl-CoA carboxylase subunit alpha	Q96RQ3	0.12		Leucine and isovaleric acid catabolism.
Methylmalonate-semialdehyde dehydrogenase	Q02252	0.24	0.38	Valine and pyrimidine metabolism
Aspartate--tRNA ligase	Q6PI48	0.33		tRNA aminoacylation
Aspartate--tRNA ligase	P14868	0.50		tRNA aminoacylation
Isoleucine--tRNA ligase	Q9NSE4	0.22		tRNA aminoacylation
Lysine--tRNA ligase	Q15046	0.34		tRNA aminoacylation
Methionine--tRNA ligase	P56192	0.56	0.50	tRNA aminoacylation
Threonine--tRNA ligase	P26639	0.40		tRNA aminoacylation
Alanine--tRNA ligase	P49588	0.08		tRNA aminoacylation
Bifunctional glutamate/proline--tRNA ligase	P07814	0.36		tRNA aminoacylation
Phenylalanine--tRNA ligase alpha subunit	Q9Y285	0.27		tRNA aminoacylation
Phenylalanine--tRNA ligase beta subunit	Q9NSD9	0.33		tRNA aminoacylation
Arginine--tRNA ligase	P54136	0.31		tRNA aminoacylation
Tryptophan--tRNA ligase	P23381	0.45		tRNA aminoacylation
Tripeptidyl-peptidase 2	P29144	1.89		Intracellular amino acid homeostasis
Amine oxidase [flavin-containing] A	P21397	0.42		Oxidative deamination
Amine oxidase [flavin-containing] B	P27338	0.27		Oxidative deamination
4-aminobutyrate aminotransferase	P80404	0.29		Gamma-aminobutyric acid catabolism
Sepiapterin reductase	P35270	0.34		Tetra-hydrobiopterin biosynthesis
Dihydropteridine reductase	P09417	0.39		Tetra-hydrobiopterin biosynthesis

Table S1 (cont.)

Mitochondrial Respiration				
Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
ADP/ATP translocase 1	P12235	0.12		ADP/ATP transport
ADP/ATP translocase 2	P05141	0.25		ADP/ATP transport
Adenine phosphoribosyltransferase	P07741	0.37	0.47	AMP formation
Adenylate kinase 2	P54819	0.11		AMP/ATP metabolism
Adenylate kinase isoenzyme 1	P00568	0.33		AMP/ATP metabolism
Mitochondrial chaperone BCS1	Q9Y276	0.41		Assembly of complex III
Mitochondrial 2-oxoglutarate/malate carrier protein	Q02978	0.09	0.17	Dicarboxylic acids transport
Electron transfer flavoprotein subunit alpha	P13804	0.13		Electron transfer
Electron transfer flavoprotein-ubiquinone oxidoreductase	Q16134	0.08	0.14	Electron transfer
Creatine kinase B-type	P12277	0.33		Energy transduction(ATP-->Creatine)
Creatine kinase M-type	P06732	0.15		Energy transduction(ATP-->Creatine)
Creatine kinase S-type	P17540	0.04		Energy transduction(ATP-->Creatine)
Lactoylglutathione lyase	Q04760	0.39		Methylglyoxal degradation
Phosphate carrier protein	Q00325	0.14		Phosphate groups transport
Thioredoxin reductase 2	Q9NNW7	0.38		Regulation of mitochondrial redox homeostasis
Protein phosphatase 1K	Q8N3J5	0.29		Regulation of the mitochondrial permeability transition pore
NAD(P) transhydrogenase	Q13423	0.09		Transhydrogenation between NADH and NADP
Atypical kinase ADCK3	Q8NI60	0.16	0.27	Ubiquinone biosynthetic
Ubiquinone biosynthesis O-methyltransferase	Q9NZJ6	0.18		Ubiquinone biosynthetic
Ubiquinone biosynthesis protein COQ9	O75208	0.07		Ubiquinone biosynthetic
Coenzyme Q5, Methyltransferase	Q5HYK3	0.28	0.37	Ubiquinone biosynthesis
Coenzyme Q6, Monooxygenase	Q9Y2Z9	0.28		Ubiquinone biosynthesis

Table S1 (cont.)

Mitochondrial respiration_Complex I				
Protein	UniProtKB	HTN-T2DM vs. Ctrl (fold change)	HTN-T2DM vs. HTN (fold change)	
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 5	Q5TEU4	0.33	0.32	
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10	O95299	0.20		
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	Q86Y39	0.15		
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	Q9UI09	0.14		
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	Q9P0J0	0.13		
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	O43678	0.26	0.15	
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	Q16718	0.07		
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	P56556	0.13		
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	P51970	0.08		
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9	Q16795	0.06		0.15
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1	O75438	0.08	0.22	
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	O96000	0.08		
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11	Q9NX14	0.11		
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	O43676	0.07		0.14
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	O95168	0.10		0.19
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5	O43674	0.09	0.20	
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6	O95139	0.51		
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	P17568	0.12		
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8	O95169	0.39		
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	Q9Y6M9	0.15		

Table S1 (cont.)

Mitochondrial respiration_Complex I (Cont.)			
Protein	UniProtKB	HTN-T2DM vs. Ctrl (fold change)	HTN-T2DM vs. HTN (fold change)
NADH dehydrogenase [ubiquinone] 1 subunit C2	O95298	0.08	
NADH dehydrogenase [ubiquinone] flavoprotein 1	P49821	0.08	0.17
NADH dehydrogenase [ubiquinone] flavoprotein 2	P19404	0.18	0.30
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2	O75306	0.06	
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3	O75489	0.15	
NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	O43920	0.13	
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7	O75251	0.26	0.39
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8	O00217	0.08	
NADH-ubiquinone oxidoreductase chain 1	P03886	0.14	
NADH-ubiquinone oxidoreductase chain 4	P03905	0.14	
NADH-ubiquinone oxidoreductase chain 5	P03915	0.33	
NADH-ubiquinone oxidoreductase 75 kDa subunit	P28331	0.08	
NADH-cytochrome b5 reductase 1	Q9UHQ9	0.29	
Acyl carrier protein mitochondrial	O14561	0.17	
Iron-sulfur protein NUBPL	Q8TB37	0.31	

Table S1 (cont.)

Mitochondrial respiration_Complex II			
Protein	UniProtKB	HTN-T2DM vs. Ctrl (fold change)	HTN-T2DM vs. HTN (fold change)
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit (SDHB)	P21912	0.10	
Succinate dehydrogenase cytochrome b560 subunit	Q99643	0.16	
Succinate dehydrogenase [ubiquinone] flavoprotein subunit	P31040	0.16	0.26

Mitochondrial respiration_Complex III			
Protein	UniProtKB	HTN-T2DM vs. Ctrl (fold change)	HTN-T2DM vs. HTN (fold change)
Cytochrome b-c1 complex subunit 1	P31930	0.07	0.14
Cytochrome c	P99999	0.07	
Cytochrome b-c1 complex subunit Rieske	P47985	0.09	0.20
Cytochrome b-c1 complex subunit 7	P14927	0.09	
Cytochrome b-c1 complex subunit 9	Q9UDW1	0.11	
Cytochrome b-c1 complex subunit 6	P07919	0.11	
Cytochrome c1 heme protein	P08574	0.11	
Cytochrome b-c1 complex subunit 8	O14949	0.12	
Cytochrome b-c1 complex subunit 2	P22695	0.13	
Cytochrome b	P00156	0.14	
Cytochrome b5	P00167	0.45	
Cytochrome b5 type B	O43169	0.38	

Table S1 (cont.)

Mitochondrial respiration_Complex IV

protein	UniProtKB	HTN-T2DM vs. Ctrl (fold change)	HTN-T2DM vs. HTN (fold change)
Cytochrome c oxidase subunit 5A	P20674	0.08	
Cytochrome c oxidase subunit 5B	P10606	0.10	0.15
Cytochrome c oxidase subunit 4 isoform 1	P13073	0.11	
Cytochrome c oxidase subunit 2	P00403	0.11	
Cytochrome c oxidase subunit 6C	P09669	0.14	
Cytochrome c oxidase subunit 3	P00414	0.18	
Cytochrome c oxidase assembly factor 3 homolog	Q9Y2R0	0.32	
Cytochrome c oxidase subunit 1	P00395	0.48	
Cytochrome c oxidase subunit 6B1	P14854	0.56	
Cytochrome c oxidase subunit NDUFA4	O00483	0.20	

Mitochondrial respiration_Complex V

protein	UniProtKB	HTN-T2DM vs. Ctrl (fold change)	HTN-T2DM vs. HTN (fold change)
ATP synthase subunit gamma mitochondrial	P36542	0.11	
ATP synthase subunit f mitochondrial	P56134	0.11	
ATP synthase subunit e mitochondrial	P56385	0.12	
ATP synthase-coupling factor 6 mitochondrial	P18859	0.12	
ATP synthase subunit d mitochondrial	O75947	0.12	
ATP synthase subunit O mitochondrial	P48047	0.13	
ATP synthase F(0) complex subunit B1 mitochondrial	P24539	0.15	
ATP synthase membrane subunit K	Q96IX5	0.17	0.29
ATP synthase subunit beta mitochondrial	P06576	0.18	
ATP synthase mitochondrial F1 complex assembly factor 2	Q8N5M1	0.20	0.29
ATP synthase subunit alpha mitochondrial	P25705	0.21	
ATP synthase subunit delta mitochondrial	P30049	0.27	
ATP synthase protein 8	P03928	0.40	
ATP synthase subunit g mitochondrial	O75964	0.45	

Mitochondrial homeostasis				
Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
M-AAA Protease-Interacting Protein 1	Q8WWC4	0.44		Exchange of metabolites and ions
Sodium/potassium-transporting ATPase subunit alpha-1	P05023	0.42		Exchange of metabolites and ions
Sodium/potassium-transporting ATPase subunit alpha-3	P13637	0.11	0.18	Exchange of metabolites and ions
Voltage-dependent anion-selective channel protein 1	P21796	0.17		Exchange of metabolites and ions
Voltage-dependent anion-selective channel protein 2	P45880	0.23	0.35	Exchange of metabolites and ions
Voltage-dependent anion-selective channel protein 3	Q9Y277	0.23		Exchange of metabolites and ions
Heat shock protein 75 kDa	Q12931	0.38		Maintaince of mitochondrial function and polarization
MICOS complex subunit MIC26	Q9BUR5	0.14		Maintenance of crista junctions
MICOS complex subunit MIC27	Q6UXV4	0.19		Maintenance of crista junctions
MICOS complex subunit MIC60	Q16891	0.14	0.25	Maintenance of crista junctions
Lon Peptidase 1	P36776	0.09		Maintenance of miochondrial inner homeostasis
LETM1 and EF-hand domain-containing protein 1	O95202	0.19		Maintenance of miochondrial morphology
Prohibitin	P35232	0.35		Maintenance of miochondrial morphology
Prohibitin-2	Q99623	0.26		Maintenance of miochondrial morphology
Protein deglycase DJ-1	Q99497	0.37		Maintenance of miochondrial morphology
Stress-70 protein	P38646	0.16		Maintenance of miochondrial morphology
ATPase family AAA domain-containing protein 1	Q8NBU5	0.21		Maintaince of mitochondrial morphology
Sorting and assembly machinery component 50 homolog	Q9Y512	0.15		Maintenance of mitochondrial cristae
DnaJ homolog subfamily A member 3	Q96EY1	0.23		Maintenance of mitochondrial morphology
DnaJ homolog subfamily C member 11	Q9NVH1	0.27		Maintenance of mitochondrial morphology
Dynamin-1-like protein	O00429	0.26		Mitochondrial and peroxisomal division
Mitofusin-2	O95140	0.28		Mitochondrial clustering and fusion
Transcription factor A	Q00059	0.20		Mitochondrial DNA transcription
Mitochondrial fission 1 protein	Q9Y3D6	0.18		Mitochondrial fission
Dynamin-like 120 kDa protein	O60313	0.21		Mitochondrial fusion and fission
Mitochondrial carrier homolog 2	Q9Y6C9	0.29		Mitochondrial fussion
Mitochondrial Matrix Protein P1	P10809	0.31		Mitochondrial organiazation
Mitochondrial import inner membrane translocase subunit TIM50	Q3ZCQ8	0.23		Mitochondrial protein import
Mitochondrial import receptor subunit TOM22 homolog	Q9NS69	0.19		Mitochondrial protein import
Mitochondrial import receptor subunit TOM40 homolog	O96008	0.41		Mitochondrial protein import
Mitochondrial import receptor subunit TOM70	O94826	0.21		Mitochondrial protein import
28S ribosomal protein S27	Q92552	0.23		Mitochondrial protein synthesis
sirtuin-5	Q9NXA8	0.29		NAD-dependent lysine metabolism

Table S1 (cont.)

Oxidative stress and Inflammation

Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
Ig gamma-3 chain C region	P01860	3.72		Anti-inflammation
Ig gamma-4 chain C region	P01861	2.76	2.94	Anti-inflammation
Ig heavy chain V-III region GAL	A0A0C4DH32	3.85		Anti-inflammation
NLR family member X1	Q86UT6	0.32		Anti-inflammation
Proteasome activator complex subunit 1	Q06323	0.45		Anti-inflammation
Proteasome activator complex subunit 2	Q9UL46	0.21		Anti-inflammation
UBX domain-containing protein 1	Q04323	0.40		Anti-inflammation
Alpha-aminoadipic semialdehyde dehydrogenase	P49419	0.13		Anti-oxidation
Extracellular superoxide dismutase [Cu-Zn]	P08294	3.83		Anti-oxidation
Peroxiredoxin-5 mitochondrial	P30044	0.26		Anti-oxidation
Superoxide dismutase [Cu-Zn]	P00441	0.41		Anti-oxidation
Superoxide dismutase [Mn] mitochondrial	P04179	0.16		Anti-oxidation
Thioredoxin-dependent peroxide reductase	P30048	0.17		Anti-oxidation
5-oxoprolinase	O14841	0.41		Glutathione metabolic
Glutathione S-transferase kappa 1	Q9Y2Q3	0.27		Glutathione metabolic
PRA1 family protein 3	O75915	0.56		Glutathione metabolic
Cytosol aminopeptidase	P28838	0.19		Glutathione metabolic
Glutamate--cysteine ligase catalytic subunit	P48506	0.43	0.55	Glutathione synthesizes
Complement C1q Binding Protein	Q07021	0.27	0.42	Inflammation
Complement C1r subcomponent	P00736	2.02		Inflammation
Complement component C7	P10643	4.32		Inflammation
Complement component C8 alpha chain	P07357	0.60		Inflammation
Complement component C6	P13671	0.49		Inflammation
Membrane primary amine oxidase	Q16853	6.17	3.72	Inflammation
Nicotinate phosphoribosyltransferase	Q6XQN6	0.34		NAD biosynthesis
NAD(P)H dehydrogenase [quinone] 1	P15559	0.42	0.61	Quinone detoxification
Elongation factor 1-beta	P24534	0.31		Translation elongation
Quinone oxidoreductase	Q08257	0.34		Detoxification of xenobiotics

Table S1 (cont.)

Cytoskeleton regulation and Muscle contraction

Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
Spectrin alpha chain non-erythrocytic 1	Q13813	0.44		Actin binding
Synaptopodin 2-like protein	Q9H987	0.15	0.21	Actin binding
Tropomyosin alpha-1 chain	P09493	0.25	0.35	Actin binding
Tropomyosin alpha-4 chain	P67936	0.24		Actin binding
Troponin C slow skeletal and cardiac muscles	P63316	0.18		Actin binding
Transgelin	Q01995	2.81		Actin cross-linking/gelling protein
Alpha-actinin-2	P35609	0.12		Actin cytoskeleton organization
Alpha-actinin-4	O43707	0.38		Actin cytoskeleton organization
Dihydropyrimidinase-related protein 3	Q14195	2.15	2.32	Actin filament organization
Unconventional myosin-Ic	O00159	1.65		Actin-based molecular motors
Filamin-C	Q14315	0.35		Actin-cross-linking protein
Myopalladin	Q86TC9	0.37		Tether to alpha-actinin
Gelsolin	P06396	1.54		Assemble and disassemble of actin
Nebulette	O76041	0.17	0.28	Assemble of Z-disk
Obscurin	Q5VST9	0.52		Assembly of myosin
Troponin T cardiac muscle	P45379	0.07	0.13	Bindg to tropomyosin and troponin-C
Troponin I cardiac muscle	P19429	0.04		Blocking actin-myosin in relaxation
T-complex protein 1 subunit epsilon	P48643	0.17		Fold of actin and tubulin
Ras-related protein R-Ras	P10301	1.79		Organization of the actin cytoskeleton
Nesh-Binding Protein	Q7Z7G0	3.10		Regulation of actin cytoskeleton reorganization
Xin actin-binding repeat-containing protein 1	Q702N8	0.21		Protects actin filaments from depolymerization
Xin actin-binding repeat-containing protein 2	A4UGR9	2.94		Protects actin filaments from depolymerization

Suppl. Table 1 (cont.)

Cytoskeleton regulation and Muscle contraction (Cont.)

Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
Calcium/calmodulin-dependent protein kinase type II subunit beta	Q13554	0.22		Ca ²⁺ homeostasis
Protein S100-A1	P23297	0.09		Ca ²⁺ homeostasis
Sodium/calcium exchanger 1	P32418	0.08		Ca ²⁺ homeostasis
Calcium/calmodulin-dependent protein kinase type II subunit delta	Q13557	0.31		Ca ²⁺ homeostasis
Vesicle-associated membrane protein-associated protein B/C	O95292	0.33		Ca ²⁺ homeostasis
Aspartyl/asparaginyl beta-hydroxylase	Q12797	1.37		Ca ²⁺ homeostasis
Sarcalumenin	Q86TD4	0.06		Calcium transport.
Sarcoplasmic reticulum histidine-rich calcium-binding protein	P23327	0.12		Calcium transport.
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	P16615	0.24		Translocation of calcium
Calsequestrin-2	O14958	0.12		Stores calcium for muscle function
Myoglobin	P02144	0.07		Storage and facilitated transfer of oxygen
Catenin alpha-1	P35221	0.41		Cell adhesion
Catenin alpha-3	Q9UI47	0.24		Cell adhesion
Catenin beta-1	P35222	0.12		Cell adhesion
Cell surface glycoprotein MUC18	P43121	2.38		Cell adhesion
Talin-2	Q9Y4G6	0.35		Cell adhesion
Cadherin-2	P19022	0.11	0.18	Calcium-dependent cell adhesion
Nidogen-2	Q14112	0.49		Cell-extracellular matrix interaction
Dermatopontin	Q07507	2.30		Cell-matrix interactions and matrix assembly.
Gap junction alpha-1 protein	P17302	0.14		Gap junction communication

Cytoskeleton regulation and Muscle contraction (Cont.)

Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
Calpain-1 catalytic subunit	P07384	0.60		Cytoskeletal remodeling
Calpain-2 catalytic subunit	P17655	0.39		Cytoskeletal remodeling
Dystroglycan 1	Q14118	0.48		Cytoskeleton and extracellular interaction
Plakophilin-2	Q99959	0.06		Cytoskeleton and extracellular interaction
Dystrophin	P11532	0.27		Cytoskeleton and the extracellular interaction
Alpha-sarcoglycan	Q16586	0.13		Cytoskeleton and the extracellular interaction
Beta-sarcoglycan	Q16585	0.30	0.39	Cytoskeleton and the extracellular interaction
Delta-sarcoglycan	Q92629	0.33		Cytoskeleton and the extracellular interaction
Gamma-sarcoglycan	Q13326	0.12		Cytoskeleton and the extracellular interaction
Sarcospan	Q14714	0.22		Cytoskeleton and the extracellular interaction
LIM domain-binding protein 3	O75112	0.13		Cytoskeleton assemble
Myosin-9	P35579	0.73		Cytoskeleton reorganization
Junction plakoglobin	P14923	0.58		Influence the arrangement and function of cytoskeleton

Cytoskeleton regulation and Muscle contraction (Cont.)

Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
Cathepsin Z	Q9UBR2	0.27		Carboxy-monopeptidase
Proline synthase co-transcribed bacterial homolog protein	O94903	0.27		Intracellular homeostatic regulation
Myocardial zonula adherens protein	P0CAP1	0.27		Intracellular signal transduction
Desmin	P17661	0.28		Intracytoplasmic filamentous network
Microfibrillar-associated protein 5	Q13361	0.23		Maintaining large vessel integrity
Vimentin	P08670	2.46		Maintenance of cellular morphology
Transmembrane protein 65	Q6PI78	0.24		Cardiac development and function
Histone-lysine N-methyltransferase SMYD1	Q8NB12	0.11		Cardiomyocyte differentiation
Basic Leucine Zipper And W2 Domains 2	Q9Y6E2	0.28		Cell differentiation
Nucleophosmin	P06748	0.41		Cell proliferation
Prostaglandin reductase 3	Q8N4Q0	0.36		Negative regulation of fat cell differentiation
Cysteine and glycine-rich protein 3	P50461	0.08		Organization of cytosolic structures
Desmoplakin	P15924	0.32		Organization of the desmosomal Cadherin-plakoglobin complexes
Muscular LMNA-interacting protein	Q5VWP3	0.17		Protection against cardiac hypertrophy
Latent-transforming growth factor beta-binding protein 4	Q8N2S1	0.35		Regulation of integrin-dependent Activation of TGF-beta.
PDZ and LIM domain protein 5	Q96HC4	0.20		Scaffolding PKC to the Z-disk region
Laminin subunit beta-2	P55268	1.64		Constituent of basement membranes

Table S1 (cont.)

Cytoskeleton regulation and Muscle contraction (Cont.)

Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
Chloride intracellular channel protein 1	O00299	2.23		Chloride transport
Sodium/potassium-transporting ATPase	P05026	0.20		Exchange of Na ⁺ and K ⁺ ions
Cytoplasmic aconitate hydratase	P21399	0.37		Iron sensor.
Glycerol-3-phosphate dehydrogenase 1-like protein	Q8N335	0.33		Regulating cardiac sodium current
cAMP-dependent protein kinase type I-alpha regulatory subunit	P10644	0.37		Regulation of cAMP signaling
cAMP-dependent protein kinase type II-alpha regulatory subunit	P13861	0.34		Regulatory subunit of the cAMP-dependent protein kinases
14-3-3 protein beta/alpha	P31946	0.44		Signal transduction
14-3-3 protein epsilon	P62258	0.48		Signal transduction
14-3-3 protein zeta/delta	P63104	1.64		Signal transduction
LIM domain only protein 7	Q8WWI1	0.30		Signal transduction
Phosphodiesterase 1C	Q14123	0.47		Signal transduction
Protein NipSnap homolog 2	O75323	0.32		Vesicular transport
Protein NipSnap homolog 3B	Q9BS92	0.14		Vesicular transport
Transmembrane emp24 domain-containing protein 10	P49755	0.56		Vesicular transport
Vesicle-fusing ATPase	P46459	2.15	2.30	Vesicular transport
EH domain-containing protein 4	Q9H223	0.57		Membrane reorganization/tubulation
Ras-related protein Rab-18	Q9NP72	0.47		Membrane trafficking in organelles and vesicles transport
Ras-related protein Rab-7a	P51149	0.49		Membrane trafficking in organelles and vesicles transport
Dystrobrevin alpha	Q9Y4J8	0.38		Stability of synapses
Alpha-1-syntrophin	Q13424	0.31		Synapse formation
Elongation factor 1-delta	P29692	0.50		Translation elongation
Elongation factor 2	P13639	0.49		Translation elongation

Table S1 (cont.)

Cytoskeleton regulation and Muscle contraction (Cont.)				
Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
Ryanodine receptor 2	Q92736	1.36		Contraction of cardiac muscle
Junctophilin-2	Q9BR39	0.44		Excitation-contraction coupling
Voltage-dependent calcium channel subunit alpha-2/delta-1	P54289	0.45		Excitation-contraction coupling
Myomesin-1	P52179	0.07		Major component of the vertebrate myofibrillar M band
Myomesin-2	P54296	0.09		Major component of the vertebrate myofibrillar M band
Myomesin-3	Q5VTT5	0.10		Link the intermediate filament cytoskeleton to the M-disk
Tubulin alpha-8 chain	Q9NY65	0.15		Major constituent of microtubules
Actin alpha skeletal muscle	P68133	0.11		Major contractile protein
Myosin-binding protein C cardiac-type	Q14896	0.06	0.13	Modulation of muscle contraction
Myosin regulatory light chain 2 ventricular/cardiac muscle isoform	P10916	0.09		Muscle contraction
Myosin-11	P35749	5.93	3.81	Muscle contraction
Myosin-6	P13533	1.37		Muscle contraction
Myosin-7	P12883	0.10		Muscle contraction
Myosin light chain 3	P08590	0.08		Regulatory light chain of myosin.
Myosin light chain 4	P12829	0.11		Regulatory light chain of myosin.
Myosin light polypeptide 6	P60660	4.09		Regulatory light chain of myosin.
Zinc finger homeobox protein 4	Q86UP3	0.10		Muscle differentiation
Calponin-1	P51911	3.57		Regulation and modulation of muscle contraction
Heat shock protein beta-2	Q16082	0.29		Maintenance of muscle structure and function
Heat shock protein beta-7	Q9UBY9	0.22		Regulation of heart contraction
Caldesmon	Q05682	4.45	2.63	Regulation of actomyosin interactions
Myosin regulatory light polypeptide 9	P24844	6.44	3.58	Regulation of cell contractile activity
Myosin light chain kinase 3	Q32MK0	0.42	0.44	Promotes sarcomere formation
Telethonin	O15273	0.26		Sarcomere assemble
Alpha-parvin	Q9NVD7	2.06		Sarcomere organization
Protein unc-45 homolog B	Q8IWX7	0.18		Proper folding of the myosin motor domain
Protein phosphatase 1 regulatory subunit 12C	Q9BZL4	0.30		Regulates myosin phosphatase activity.
Synemin	O15061	0.30		Structural support in muscle
LIM and calponin homology domains-containing protein 1	Q9UPQ0	0.09		Activation of non-muscle myosin IIa

Table S1 (cont.)

Fibrosis

Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
Serpin H1	P50454	1.39	0.19	Collagen biosynthetic
Collagen alpha-1(XVIII) chain	P39060	3.47		Extracellular matrix organization
Collagen alpha-1(XXVIII) chain	Q2UY09	0.42		Extracellular matrix organization
Hyaluronan and proteoglycan link protein 1	P10915	0.12		Structre of extracellular matrix
Fibronectin	P02751	3.07		Fibril formation
Fibulin-1	P23142	1.58		Fibril formation
Collagen alpha-2(I) chain	P08123	2.76		Fibrillar forming collagen
Decorin	P07585	3.81		Fibrils formation
Myozenin-2	Q9NPC6	0.05		Myofibrillogenesis
Keratin type I cytoskeletal 19	P08727	2.47		Organization of myofibers
EMILIN-1	Q9Y6C2	3.08		Formation of the elastic fiber
Lumican	P51884	2.88		Interstitial collagenous matrices
Collagen alpha-1(VI) chain	P12109	1.78		Major structural component of microfibrils
Collagen alpha-2(VI) chain	P12110	2.00		Major structural component of microfibrils
Collagen alpha-3(VI) chain	P12111	2.00		Major structural component of microfibrils

Table S1 (cont.)

Apoptosis

Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
Annexin A2	P07355	1.39	1.46	Apoptosis
Annexin A4	P09525	3.98	3.02	Apoptosis
Annexin A5	P08758	2.27	1.80	Apoptosis
Apoptosis-inducing factor 1	O95831	0.12		Apoptosis
Bcl-2-like protein 13	Q9BXK5	0.25		Apoptosis
Protein FAM162A	Q96A26	0.11		Apoptosis
28S ribosomal protein S29	P62273	0.21		Apoptosis
Casein kinase II subunit alpha	P68400	0.33		Apoptosis
Peptidyl-prolyl cis-trans isomerase F	P30405	0.21		Apoptosis
Alpha-crystallin B chain	P02511	0.23		Anti-apoptosis
BAG family molecular chaperone regulator 3	O95817	0.28		Anti-apoptosis

Table S1 (cont.)

Cellular physiology				
Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
Regulator of microtubule dynamics protein 1	Q96DB5	0.24		Mitotic regulation
Heterogeneous nuclear ribonucleoprotein A1-like 2	Q32P51	0.56		mRNA processing
Heterogeneous nuclear ribonucleoprotein K	P61978	0.65		mRNA processing
Heterogeneous nuclear ribonucleoprotein L	P14866	0.39		mRNA processing
Heterogeneous nuclear ribonucleoprotein M	P52272	0.53		mRNA processing
Heterogeneous nuclear ribonucleoproteins C1/C2	P07910	0.66		mRNA processing
Single-stranded DNA-binding protein	Q04837	0.27		mtDNA replication
Spliceosome RNA helicase DDX39B	Q13838	0.40		Nuclear export of spliced and unspliced mRNA.
Importin subunit beta-1	Q14974	0.28		Nuclear protein import
Importin-5	O00410	0.58		Nuclear protein import
Transportin-1	Q92973	0.67		Nuclear protein import
Lamin A/C	P02545	1.58		Nuclear stability,Cardiac homeostasis
Ankyrin repeat domain-containing protein 1	Q15327	0.27		Nuclear transcription factor
Core histone macro-H2A.1	O75367	0.34		Nucleosome assembly
Histone H1.0	P07305	0.31		Nucleosome assembly
Histone H2A.V	Q71UI9	0.33	0.42	Nucleosome assembly
Histone H2A.Z	P0C0S5	0.33	0.42	Nucleosome assembly
Histone H2B type 1-B	P33778	0.71		Nucleosome assembly
Histone H2B type 1-J	P06899	0.71		Nucleosome assembly
Histone H2B type 1-O	P23527	0.71		Nucleosome assembly
Histone H2B type 2-E	Q16778	0.71		Nucleosome assembly
Nucleosome assembly protein 1-like 4	Q99733	0.46		Nucleosome assembly.
Adenylate kinase 4 mitochondrial	P27144	0.15		Maintaining cellular nucleotides homeostasis
GTP:AMP phosphotransferase AK3 mitochondrial	Q9UIJ7	0.35		Maintaining cellular nucleotides homeostasis
ATP-dependent RNA helicase A	Q08211	0.32	0.46	DNA replication
Lamin-B2	Q03252	0.49		Nuclear stability
X-ray repair cross-complementing protein 6	P12956	0.35		Chromosome translocation.
Coiled-coil domain-containing protein 141	Q6ZP82	0.31		Radial migration and centrosomal function.
Adenylyl cyclase-associated protein 1	Q01518	2.30		Regulation of filament dynamics
RNA-binding protein Musashi homolog 2	Q96DH6	0.54		Development and cell cycle regulation

Table S1 (cont.)

Cellular physiology (cont.)

Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
Tripeptidyl-peptidase 1	O14773	0.22		Peptide catabolic
Small nuclear ribonucleoprotein Sm D3	P62318	0.42		pre-mRNA splicing
Heat shock protein HSP 90-alpha	P07900	0.62		Proper folding of specific target proteins
Heat shock protein HSP 90-beta	P08238	0.61	0.64	Proper folding of specific target proteins
Elongation factor 1-alpha 2	Q05639	0.10		Protein biosynthesis.
78 kDa glucose-regulated protein	P11021	0.46		Protein folding
DnaJ homolog subfamily B member 4	Q9UDY4	0.41		Protein folding
Heat shock cognate 71 kDa protein	P11142	0.46		Protein quality control
DnaJ homolog subfamily A member 4	Q8WW22	0.47		Protein refolding
60S acidic ribosomal protein P0	P05388	0.50		Protein synthesis
60S ribosomal protein L12	P30050	0.53		Protein synthesis
60S ribosomal protein L13a	P40429	0.39		Protein synthesis
60S ribosomal protein L14	P50914	0.40		Protein synthesis
60S ribosomal protein L15	P61313	0.33	0.52	Protein synthesis
60S ribosomal protein L17	P18621	0.28		Protein synthesis
60S ribosomal protein L23	P62829	0.39		Protein synthesis
60S ribosomal protein L30	P62888	0.35		Protein synthesis
60S ribosomal protein L4	P36578	0.42		Protein synthesis
60S ribosomal protein L5	P46777	0.32		Protein synthesis
60S ribosomal protein L6	Q02878	0.41	0.62	Protein synthesis
60S ribosomal protein L7	P18124	0.48		Protein synthesis
60S ribosomal protein L9	P32969	0.47		Protein synthesis
Eukaryotic translation initiation factor 2 subunit 1	P05198	0.54		Protein synthesis
Eukaryotic translation initiation factor 2 subunit 3	P41091	0.23		Protein synthesis
Eukaryotic translation initiation factor 5	P55010	0.36		Protein synthesis
60S acidic ribosomal protein P2	P05387	0.43		Protein synthesis.
Elongation factor Tu	P49411	0.43		Protein synthesis.
Syntaxin-7	O15400	0.57		Protein trafficking

Table S1 (cont.)

Cellular physiology (Cont.)

Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
DNA damage-binding protein 1	Q16531	0.36		Protein ubiquitination
Cathepsin B	P07858	0.18		Protein degradation
Protein S100-A13	Q99584	0.27	0.36	Proteins export
Proteasome subunit alpha type-3	P25788	0.27		Proteolytic degradation
Proteasome subunit alpha type-4	P25789	0.61		Proteolytic degradation
Proteasome subunit alpha type-5	P28066	0.29		Proteolytic degradation
Proteasome subunit alpha type-6	P60900	0.41		Proteolytic degradation
Protein phosphatase 1 regulatory subunit 7	Q15435	0.44		Regulatory subunit of protein phosphatase 1
26S proteasome non-ATPase regulatory subunit 12	O00232	0.39		Maintenance of protein homeostasis
Ubiquitin carboxyl-terminal hydrolase 5	P45974	1.49		Ubiquitin-dependent protein catabolic
Lupus La Protein	P05455	0.31		RNA metabolism
40S ribosomal protein S2	P15880	0.35	0.55	rRNA maturation.
40S ribosomal protein S24	P62847	0.33	0.52	rRNA maturation.
40S ribosomal protein S6	P62753	0.39		rRNA maturation.
40S ribosomal protein S7	P62081	0.22		rRNA maturation.
40S ribosomal protein S8	P62241	0.44		rRNA maturation.
Dual specificity protein phosphatase 3	P51452	0.36		Negative regulate cellular proliferation and differentiation
Ribophorin I	P04843	0.37	0.43	Protein N-glycosylation
Presequence protease	Q5JRX3	0.28		Peptide cleavage and degradation

Table S1 (cont.)

Other factors				
Protein	UniprotKB	HTN-T2DM vs. Ctrl (Fold-change)	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
5'-AMP-activated protein kinase catalytic subunit alpha-2	P54646	0.47		Cellular energy metabolism
Sulfite oxidase	P51687	0.25		Sulfur metabolism
Propionyl-CoA carboxylase alpha chain	P05165	0.28		Metabolites catabolism
26S proteasome non-ATPase regulatory subunit 13	Q9UNM6	0.47		ATP-dependent degradation of ubiquitinated proteins.
26S proteasome non-ATPase regulatory subunit 2	Q13200	0.53		ATP-dependent degradation of ubiquitinated proteins.
26S proteasome non-ATPase regulatory subunit 4	P55036	0.22		ATP-dependent degradation of ubiquitinated proteins.
AFG3-like protein 2	Q9Y4W6	0.15		Axonal and neuron development
Prolyl endopeptidase	P48147	0.26		Maturation of hormones and neuropeptides
D-dopachrome decarboxylase	P30046	0.32		Melanin biosynthesis
Pyridoxal kinase	O00764	0.45		Cofactor metabolism.
Olfactomedin-like protein 3	Q9NRN5	2.11		Dorsoventral patterning
Retinol dehydrogenase 13	Q8NBN7	0.25		Retinol metabolism
Retinol dehydrogenase 14	Q9HBH5	0.49		Retinol metabolism

Table S1 (cont.)

Protein	UniprotKB	HTN vs. Ctrl (Fold-change)	Cellular function (Heart)
[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1	Q9P0J1	0.47	Pyruvate decarboxylation
Glucosamine-6-phosphate isomerase 1	P46926	0.54	Carbohydrate metabolism
UDP-glucose 6-dehydrogenase	O60701	0.62	Carbohydrate metabolism
Cytochrome b5 type B	O43169	0.60	Mitochondrial respiration(complex III)
Cytochrome c oxidase subunit 6B1	P14854	0.66	Mitochondrial respiration(complex IV)
Succinate-semialdehyde dehydrogenase	P51649	0.64	Amino-acid degradation
Sepiapterin reductase	P35270	0.44	Tetra-hydrobiopterin biosynthesis
Tripeptidyl-peptidase 2	P29144	1.77	Intracellular amino acid homeostasis
LETM1 and EF-hand domain-containing protein 1	O95202	0.59	Maintenance of mitochondrial morphology
Mitofusin-2	O95140	0.44	Mitochondrial clustering and fusion
Mitochondrial import inner membrane translocase subunit TIM50	Q3ZCQ8	0.33	Mitochondrial protein import
NAD(P)H dehydrogenase [quinone] 1	P15559	0.69	Quinone detoxification
NLR family member X1	Q86UT6	0.36	Anti-inflammation
UBX domain-containing protein 1	Q04323	0.54	Anti-inflammation
Complement C1q Binding Protein	Q07021	0.63	Inflammation
Annexin A2	P07355	1.39	Apoptosis
Talin-2	Q9Y4G6	0.52	Cell adhesion
Junction plakoglobin	P14923	0.75	Cytoskeleton and extracellular interaction
Myosin-6	P13533	1.88	Muscle contraction

Table S2

Protein	UniprotKB	HTN vs. Ctrl (Fold-change)	Cellular function (Heart)
Heterogeneous nuclear ribonucleoprotein A1-like 2	Q32P51	0.74	mRNA processing
Spliceosome RNA helicase DDX39B	Q13838	0.66	Nuclear export of spliced and unspliced mRNA
Core histone macro-H2A.1	O75367	0.47	Nucleosome assembly
Histone H2B type 1-B	P33778	0.72	Nucleosome assembly
Histone H2B type 1-J	P06899	0.72	Nucleosome assembly
Histone H2B type 1-O	P23527	0.72	Nucleosome assembly
Histone H2B type 2-E	Q16778	0.72	Nucleosome assembly
Lupus La Protein	P05455	0.54	RNA metabolism
40S ribosomal protein S2	P15880	0.63	rRNA maturation.
40S ribosomal protein S24	P62847	0.63	rRNA maturation.
40S ribosomal protein S7	P62081	0.47	rRNA maturation.
Asparagine--tRNA ligase cytoplasmic	O43776	0.69	tRNA aminoacylation
Lysine--tRNA ligase	Q15046	0.37	tRNA aminoacylation
DnaJ homolog subfamily B member 4	Q9UDY4	0.48	Protein folding
60S ribosomal protein L13a	P40429	0.48	Protein synthesis
60S ribosomal protein L15	P61313	0.62	Protein synthesis
60S ribosomal protein L17	P18621	0.62	Protein synthesis
60S ribosomal protein L23	P62829	0.63	Protein synthesis
60S ribosomal protein L5	P46777	0.46	Protein synthesis
60S ribosomal protein L6	Q02878	0.66	Protein synthesis
26S protease regulatory subunit 6B	P43686	0.47	Maintenance of protein homeostasis
Protein S100-A13	Q99584	0.76	Proteins export

Table S2 (cont.)

Protein	UniprotKB	HTN-T2DM vs. HTN (Fold-change)	Cellular function (Heart)
Ras-related protein Rap-1b	P61224	2.28	Membrane trafficking in organelles and vesicles transport
ATP-citrate synthase	P53396	2.13	TCA cycle
Alpha-adducin	P35611	2.09	Cytoskeleton assemble
Guanine nucleotide-binding protein subunit alpha-11	P29992	1.66	Transmembrane transduction
10 kDa heat shock protein mitochondrial	P61604	1.37	Mitochondrial protein import
DNA-(apurinic or apyrimidinic site) lyase	P27695	0.63	Oxidation

Table S3