SUPPLEMENT

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Table *S1*. Proteomic identification of the increase of relative content of renal proteins of hypertensive rats in comparison with that of the control animals (experiment 1).

№	Uniprot accession number	Uniprot gene number	Uniprot protein name	Function	Localization	-LOG (P-value)	Difference	Fold change
1	I7FKL4	*Mbp*	Myelin basic protein	4	M	4,067	2,768	6,813
2	A0A8I5Y2B8	*ENSRNOG00000062500*	Thioredoxin-dependent peroxiredoxin	4	C	3,064	2,287	4,880
3	P01835	*IGKC*	Ig kappa chain C region, B allele	4	C	2,066	2,080	4,227
4	G3V983	*Gstm1*	Glutathione S-transferase	4	C, Mch, ER,N, PM	2,632	2,044	4,125
5	P38718	*Mpc2*	Mitochondrial pyruvate carrier 2	2	Mch	2,061	1,996	3,988
6	Q6PDV1	*Lyz2*	Lysozyme	6	C	4,358	1,943	3,846
7	F1LQM1	*Mup4l1*	Alpha-2u-globulin (L type)	3	S	5,648	1,637	3,111
8	B5DEL8	*Ndufs5*	NADH dehydrogenase	1	Mch, M	2,893	1,476	2,781

			[ubiquinone] iron-sulfur protein 5					
9	Q9Z2M4	*Decr2*	Peroxisomal 2,4-dienoyl-CoA reductase [(3E)-enoyl-CoA-producing	7	Per	3,842	1,475	2,780
10	A0A8I5ZTR6	*Col6a3*	Collagen type VI alpha 3 chain	2	S	1,649	1,473	2,776
11	F1LM05	*Serpina3l*	Serine (or cysteine) peptidase inhibitor, clade A, member 3N	3	Extra	2,689	1,400	2,639
12	A0A8I5ZR70	*Rdx*	Radixin	2	PM,C, M	2,003	1,309	2,478
13	P27139	*Ca2*	Carbonic anhydrase 2	3	C, PM	4,114	1,301	2,463
14	G3V7Y3	*Atp5f1d*	ATP synthase F1 subunit delta	1	Mch	1,890	1,273	2,417
15	Q5RJN0	*Ndufs7*	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	1	Mch	2,139	1,245	2,371
16	P20760	*Igg-2a*	Ig gamma-2A chain C region	4	PM	3,667	1,228	2,342
17	A0A8I6B5K9	*Tpm3*	Tropomyosin 3	2	C	2,284	1,188	2,279
18	D3ZF07	*Rpl27al3*	Large ribosomal subunit protein uL15	6	C	1,340	1,152	2,222
19	Q66HG3	*Cndp1*	Beta-Ala-His dipeptidase	6	S	1,494	1,144	2,210
20	D4A3V2	*Ndufa6*	NADH dehydrogenase [ubiquinone] 1	1	Mch	2,510	1,115	2,165

			alpha subcomplex subunit 6					
21	Q6LDS4	*Sod1*	Superoxide dismutase [Cu-Zn]	4	Mch, L	4,299	1,097	2,138
22	A0A8I6 AN99	*Ubb-ps1*	Ubiquitin B, pseudogene 1	6	C, N	2,113	1,012	2,017

Here and in all the tables:

Protein functions:

1. Proteins/enzymes involved in energy generation and carbohydrate metabolism.
2. Proteins involved in cytoskeleton formation and exocytosis.
3. Proteins involved in signal transduction and regulation of enzyme activity.
4. Antioxidant and protective proteins/enzymes.
5. Protein regulators of gene expression, cell division and differentiation.
6. Enzymes involved in metabolism of proteins, amino acids, and other nitrogenous compounds.
7. Enzymes involved in metabolism of lipids.

Protein localization: C – cytoplasm, N – nucleus, M – membranes, PM – plasma membrane, Mch – mitochondria, ER – endoplasmic reticulum, G – Golgi, L – lysosomes, Mictotub – microtubules, Ve – vesicles, Per – peroxisomes, S – secreted proteins, Extra – extracellular space.

Table *S2*. Proteomic identification of the increase of relative content of renal proteins of hypertensive rats in comparison with that of the control animals (experiment 2).

№	Uniprot accession number	Uniprot gene number	Uniprot protein name	Function	Localization	-LOG (P-value)	Difference	Fold change
1	A0A8I5ZTR6	*Col6a3*	Collagen type VI alpha 3 chain	2	S	2,830	3,581	11,969
2	P12075	*Cox5b*	Cytochrome c oxidase subunit 5B, mitochondrial	1	Mch	2,808	2,982	7,900
3	P38718	*Mpc2*	Mitochondrial pyruvate carrier 2	2	Mch	2,126	2,852	7,222
4	P01835	*IGKC*	Ig kappa chain C region, B allele	4	C	1,842	2,626	6,174
5	G3V7Y3	*Atp5f1d*	ATP synthase F1 subunit delta	1	Mch	2,741	2,533	5,788
6	A0A8I5ZR70	*Rdx*	Radixin	2	PM, C, M	3,592	2,172	4,508
7	Q5RJN0	*Ndufs7*	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	1	Mch	3,415	2,136	4,395
8	F1LQM1	*Mup4l1*	Alpha-2u-globulin (L type)	3	S	4,130	2,104	4,300
9	G3V983	*Gstm1*	Glutathione S-transferase	4	C, Mch, ER, N, PM	3,688	2,064	4,181
10	Q6PDV1	*Lyz2*	Lysozyme	6	C	4,056	1,785	3,447

11	B5DEL8	*Ndufs5*	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	1 1	Mch, M	2,940	1,757	3,379
12	Q6LDS4	*Sod1*	Superoxide dismutase [Cu-Zn]	4	Mch, L	5,631	1,669	3,179
13	P25093	*Fah*	Fumarylacetoacetase	6	C	3,047	1,626	3,087
14	A0A8I6AN99	*Ubb-ps1*	Ubiquitin B, pseudogene 1	6	C, N	3,153	1,589	3,008
15	A0A8L2QWG8	*Atp5pb*	ATP synthase subunit b	1	Mch	1,923	1,465	2,762
16	A0A8I6B5K9	*Tpm3*	Tropomyosin 3	2	C	1,807	1,348	2,545
17	B0BNE5	*Esd*	S-formylglutathione hydrolase	4	C	3,601	1,302	2,465
18	Q09073AT	*Slc25a5*	ADP/ATP translocase 2	2	M	2,934	1,296	2,456
19	S5RZM8	*Mt-co2*	Cytochrome c oxidase subunit 2	1	M, Mch	3,248	1,273	2,417
20	Q6IN22	*Ctsb*	Cathepsin B	6	PM, L	3,682	1,264	2,402
21	P20760	*Igg-2a*	Ig gamma-2A chain C region	4	PM	3,192	1,262	2,399
22	A0A8L2Q0J0	*Atp1b1*	Sodium/potassium-transporting ATPase subunit beta	2	PM, M	1,732	1,224	2,336
23	A6I7B6	*Hbb*	Globin a4	2	Extra	2,501	1,223	2,334
24	A0A0G2K0X4	*Rac1*	Rac family small GTPase 1	3	C	3,156	1,143	2,208

25	P27139	*Ca2*	Carbonic anhydrase 2	3	C, PM	4,143	1,127	2,184
26	F1LM05	*Serpina3l*	Serine (or cysteine) peptidase inhibitor, clade A, member 3N	3	Extra	2,192	1,109	2,157
27	D3ZF07	*Rpl27al3*	Large ribosomal subunit protein uL15	6	C	1,697	1,076	2,109

Table *S3*. Proteomic identification of the increase of relative content of renal proteins of hypertensive rats in comparison with that of the control animals (experiment 3).

№	Uniprot accession number	Uniprot gene number	Uniprot protein name	Function	Localization	-LOG (P-value)	Difference	Fold change
1	P01835	*IGKC*	Ig kappa chain C region, B allele	4	C	2,576	3,339	10,118
2	P0DP31	*Calm3*	Calmodulin-3	3	C	2,299	2,894	7,432
3	Q641W3	*Nufip1*	FMR1-interacting protein NUFIP1	5	N	3,462	2,514	5,711
4	F1LQM1	*Mup4l1*	Alpha-2u-globulin (L type)	3	S	5,646	2,360	5,134
5	A0A8I5ZTF9	*Akr1b1*	Aldo-keto reductase family 1 member B1	7	C	4,428	2,268	4,815
6	Q6LDS4	*Sod1*	Superoxide dismutase [Cu-Zn]	4	Mch, L	5,367	2,210	4,626
7	P20760	*Igg-2a*	Ig gamma-2A chain C region	4	PM	6,377	2,075	4,214
8	A0A8I5ZTR6	*Col6a3*	Collagen type VI alpha 3 chain	2	S	2,222	2,047	4,132
9	G3V983	*Gstm1*	Glutathione S-transferase	4	C, Mch, ER, N, PM	2,517	1,920	3,783
10	B2RZC1	*Rbp4*	Retinol-binding protein	2	S	3,032	1,757	3,379
11	P12346	*Tf*	Serotransferrin	2	S	5,997	1,611	3,054

12	P11030	*Dbi*	Acyl-CoA-binding protein	7	ER, G	1,717	1,610	3,052
13	Q66HG3	*Cndp1*	Beta-Ala-His dipeptidase	6	S	1,972	1,598	3,028
14	P27139	*Ca2*	Carbonic anhydrase 2	3	C, PM	4,595	1,520	2,867
15	Q5M876	*Acy3*	N-acyl-aromatic-L-amino acid amidohydrolase (carboxylate-forming)	6	C, PM	3,745	1,402	2,643
16	A0A8I5ZXS2	*Dld*	Dihydrolipoyl dehydrogenase	1	Mch, Ve	5,548	1,345	2,540
17	Q6AY30	*Sccpdh*	Saccharopine dehydrogenase-like oxidoreductase	Ve	7	1,801	1,336	2,525
18	F1RLE1	*COMMD10*	COMM domain containing 10	5	N	1,739	1,329	2,512
19	Q6PDV1	*Lyz2*	Lysozyme	6	C	5,832	1,323	2,501
20	F1LM05	*Serpina3l*	Serine (or cysteine) peptidase inhibitor, clade A, member 3N	3	Extra	1,792	1,253	2,383

Table *S4.* Proteomic identification of the increase of relative content of renal proteins of hypertensive rats in comparison with that of the control animals (experiment 4).

№	Uniprot accession number	Uniprot gene number	Uniprot protein name	Function	Localization	-LOG (P-value)	Difference	Fold change
1	A0A8I5ZTR6	*Col6a3*	Collagen type VI alpha 3 chain	2	S	3,150	4,155	17,816
2	P01835	*IGKC*	Ig kappa chain C region, B allele	4	C	2,108	3,885	14,777
3	P12075	*Cox5b*	Cytochrome c oxidase subunit 5B, mitochondrial	1	Mch	2,752	3,026	8,146
4	P0DP31	*Calm3*	Calmodulin-3	3	C	3,886	2,852	7,222
5	F1LQM1	*Mup4l1*	Alpha-2u-globulin (L type)	3	S	4,546	2,827	7,095
6	Q6LDS4	*Sod1*	Superoxide dismutase [Cu-Zn]	4	Mch, Lys	6,249	2,782	6,879
7	A0A8I5ZTF9	*Akr1b1*	Aldo-keto reductase family 1 member B1	7	C	5,678	2,144	4,419
8	G3V7Y3	*Atp5f1d*	ATP synthase F1 subunit delta	1	Mch	2,393	2,124	4,358
9	P20760	*Igg-2a*	Ig gamma-2A chain C region	4	PM	4,614	2,110	4,316
10	G3V983	*Gstm1*	Glutathione S-transferase	4	C, Mch, ER, N, PM	3,535	1,939	3,835
11	A0A8I5ZR70	*Rdx*	Radixin	2	PM,C, M	3,161	1,904	3,741
12	P25093	*Fah*	Fumarylacetoacetase	6	C	1,318	1,868	3,651

13	P11030	*Dbi*	Acyl-CoA-binding protein	7	ER, G	1,579	1,856	3,620
14	Q5RJN0	*Ndufs7*	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	1	Mch	3,004	1,825	3,543
15	P12346	*Tf*	Serotransferrin	2	S	6,425	1,757	3,380
16	B2RZC1	*Rbp4*	Retinol-binding protein	2	S	3,541	1,603	3,037
17	A0A8I5ZXS2	*Dld*	Dihydrolipoyl dehydrogenase	1	Mch, Ve	3,551	1,590	3,010
18	Q7TQ94	*Nit1*	Deaminated glutathione amidase	4	Mch, C	1,654	1,531	2,890
19	F7DLY1	*Eps8l2*	EPS8-like 2	3	C, PM, M	1,388	1,513	2,855
20	A0A8I6AN99	*Ubb-ps1*	Ubiquitin B, pseudogene 1	6	C, N	4,066	1,460	2,751
21	A0A0G2K8G2	*Acsm1*	Medium-chain acyl-CoA ligase	7	Mch	2,533	1,452	2,736
22	A0A8I5ZSP9	*Kyat1*	Kynurenine aminotransferase 1	6	C	1,850	1,389	2,618
23	P48500	*Tpi1*	Triosephosphate isomerase	1	C	4,480	1,367	2,579
24	P27139	*Ca2*	Carbonic anhydrase 2	3	C, PM	4,759	1,346	2,542
25	B5DEL8	*Ndufs5*	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	1	Mch, M	2,749	1,333	2,520
26	Q5I0D7	*Pepd*	Xaa-Pro dipeptidase	6	C	2,183	1,270	2,412

27	A0A8I6B5K9	*Tpm3*	Tropomyosin 3	2	C	1,938	1,239	2,360
28	Q07523	*Hao2*	2-Hydroxyacid oxidase 2	7	Per	3,116	1,216	2,322
29	Q6PDV1	*Lyz2*	Lysozyme	6	C	4,559	1,165	2,242
30	Q66HG3	*Cndp1*	Beta-Ala-His dipeptidase	6	S	2,876	1,160	2,235
31	Q5M876	*Acy3*	N-acyl-aromatic-L-amino acid amidohydrolase (carboxylate-forming)	6	M,C	3,314	1,109	2,157
32	A0A8I5Y808	*Mep1a*	Meprin A subunit	3	M	3,126	1,044	2,063
33	R9PXU4	*Txnrd1*	Thioredoxin reductase 1, cytoplasmic	4	N	2,103	1,038	2,053

Table *S5*. Proteomic identification of the decrease of relative content of renal proteins of hypertensive rats in comparison with that of the control animals (experiment 1).

№	Uniprot accession number	Uniprot gene number	Uniprot protein name	Function	Localization	- LOG (P-value)	Difference
1	A0A8L2Q282	*Cltrn*	Collectrin, amino acid transport regulator	2	M	1,854	0,493
2	Q9WVK3	*Pecr*	Peroxisomal trans-2-enoyl-CoA reductase	7	Per	4,572	0,489
3	A0A8L2UH84	*Pebp1*	Phosphatidylethanolamine binding protein 1	3	C	4,114	0,483
4	P68136	*ACTA1*	Actin, alpha skeletal muscle	2	C	3,597	0,475
5	P07171	*Calb1*	Calbindin	3	C, N, Synapse	4,353	0,442
6	A0A8I6A9U0	*Fgb*	Fibrinogen beta chain	3	S	3,064	0,438
7	A0A8I6AI74	*Ywhah*	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta	3	C	3,447	0,394
8	D4A1D8|	*Surf4*	Surfeit locus protein 4	2	ER, G, M	1,543	0,362
9	Q91ZW6	*Tmlhe*	Trimethyllysine dioxygenase, mitochondrial	6	Mch	4,172	0,304
10	Q6SKG1	*Acsm3*	Acyl-coenzyme A synthetase ACSM3, mitochondrial	7	Mch	2,814	0,009

Table *S6.* Proteomic identification of the decrease of relative content of renal proteins of hypertensive rats in comparison with that of the control animals (experiment 2).

№	Uniprot accession number	Uniprot gene number	Uniprot protein name	Function	Localization	- LOG (P-value)	Difference
1	A0A8I5ZLR0	*Gstt3*	Glutathione transferase	4	C, Mch, ER, N, PM	5,168	0,495
2	G3V6P2	*Dlst*	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	1	Mch	4,309	0,495
3	P41498	*Acp1*	Low molecular weight phosphotyrosine protein phosphatase	6	C	3,124	0,494
4	P62890	*Rpl30*	Large ribosomal subunit protein eL30	6	C	2,209	0,494
5	A0A8L2UH84	*Pebp1*	Phosphatidylethanolamine binding protein 1	3	C	2,824	0,483
6	A0A8I6G6M3	*Cap1*	Adenylyl cyclase-associated protein	3	PM	2,159	0,469
7	Q4QRB8	*Asl*	Argininosuccinate lyase	6	C	1,994	0,469
8	A0A8I6AI74	*Ywhah*	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	3	C	2,710	0,432

			activation protein, eta				
9	Q9WVK3	*Pecr*	Peroxisomal trans-2-enoyl-CoA reductase	7	Per	3,745	0,415
10	P07171	*Calb1*	Calbindin	3	C, N, S	4,868	0,414
11	A0A8I6A9U0	*Fgb*	Fibrinogen beta chain	3	S	2,934	0,408
12	A9UMW2	*Ndufa3*	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3	1	M	2,467	0,398
13	Q6LCA5	*Prkar1a*	cAMP-dependent protein kinase type I-alpha regulatory subunit	3	M, PM	1,816	0,342
14	D4A1D8	*Surf4*	Surfeit locus protein 4	2	ER, G, M	2,363	0,296
15	Q91ZW6	*Tmlhe*	Trimethyllysine dioxygenase, mitochondrial	6	Mch	3,879	0,294
16	Q6SKG1	*Acsm3*	Acyl-coenzyme A synthetase ACSM3, mitochondrial	7	Mch	2,896	0,007

Table *S7*. Proteomic identification of the decrease of relative content of renal proteins of hypertensive rats in comparison with that of the control animals (experiment 3).

№	Uniprot accession number	Uniprot gene number	Uniprot protein name	Function	Localization	- LOG (P-value)	Difference
1	A0A8I6AH82	*Xylb*	Xylulose kinase	7	Mch	2,459	0,497
2	Q562C3	*Gcat*	Glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	6	Mch, N	1,465	0,495
3	P85971	*Pgls*	6-phosphogluconolactonase	1	C	1,516	0,488
4	A0A0G2JUM0	*Sult1c2*	Sulfotransferase	4	C, L	2,983	0,471
5	A0A8I5ZLR0	*Gstt3*	Glutathione transferase	4	C, Mch, ER, N, PM	4,146	0,463
6	D4AE56	*Ptges2*	Prostaglandin E synthase 2	7	M	1,639	0,463
7	D4A4D5	*Rplp2l2*	Large ribosomal subunit protein P2	5	C	2,217	0,461
8	A0A8I6ACM0	*Lamp2*	Lysosomal-associated membrane protein 2		M, PM	1,676	0,454
9	A0A8L2R5Y9	*Arl8b*	Small monomeric GTPase	3	C, M	3,355	0,448
10	A0A8I5ZV58	*Aass*	Aminoadipate-semialdehyde synthase	6	Mch	2,828	0,432

11	D4AD05	*Crocc*	Ciliary rootlet coiled-coil, rootletin	2	N	0,723	0,410
12	A0A8L2QY15	*H2aj*	Histone H2A	5	N	3,270	0,407
13	A0A8I6A9B3	*Hspa12a*	Heat shock protein family A (Hsp70) member 12A	4	C, M, Mch	1,870	0,386
14	B2RYS0	*Cox7a2*	Cytochrome c oxidase subunit 7A2, mitochondrial	1	Mch	2,851	0,359
15	Q9WVK3	*Pecr*	Peroxisomal trans-2-enoyl-CoA reductase	7	Per	5,436	0,341
16	Q91ZW6	*Tmlhe*	Trimethyllysine dioxygenase, mitochondrial	6	Mch	4,722	0,319
17	D3ZNJ5	*Inmt*	Indolethylamine N-methyltransferase	4	C	3,379	0,162
18	Q6SKG1	*Acsm3*	Acyl-coenzyme A synthetase ACSM3, mitochondrial	7	Mch	3,801	0,038

Table *S8*. Proteomic identification of the decrease of relative content of renal proteins of hypertensive rats in comparison with that of the control animals (experiment 4).

№	Uniprot accession number	Uniprot gene number	Uniprot protein name	Function	Localization	-LOG (P-value)	Difference
1	P07171	*Calb1*	Calbindin	3	C, N, S	3,404	0,496
2	A0A8I6A9B3	*Hspa12a*	Heat shock protein family A (Hsp70) member 12A	4	C, M, Mch	1,335	0,495
3	M0RD75	*Rps6*	40S ribosomal protein S6	5	C	2,587	0,494
4	G3V8C3	*Vim*	Vimentin	2	Pm, N	4,733	0,494
5	A0A0G2JUM0	*Sult1c2*	Sulfotransferase	4	C, L	2,143	0,487
6	Q562C3	*Gcat*	Glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	6	Mch, N	2,240	0,483
7	A0A8I6AH82	*Xylb*	Xylulose kinase	7	Mch	2,691	0,481
8	A0A8I6AFW7	*Acot9*	Acyl-CoA thioesterase 9	7	Mch	2,068	0,479
9	P11951	*Cox6c2*	Cytochrome c oxidase subunit 6C-2	1	Mch	1,953	0,452
10	A0A8L2UK87	*Actr1a*	Alpha-centractin	2	C	1,359	0,448
11	Q5I0J9	*Aspdh*	Aspartate dehydrogenase domain-containing protein	6	C	2,562	0,433
12	A0A8L2R5Y9	*Arl8b*	Small monomeric GTPase	3	C, M	2,096	0,430

13	A0A8I5ZLR0	*Gstt3*	Glutathione transferase	4	C, Mch, ER, N, PM	4,597	0,420
14	A0A8I5ZV58	*Aass*	Aminoadipate-semialdehyde synthase	6	Mch	2,941	0,410
15	Q9QX79	*Fetub*	Fetuin-B	3	Secreted	1,876	0,407
16	D4AE56	*Ptges2*	Prostaglandin E synthase 2	7	M	1,782	0,403
17	P85971	*Pgls*	6-phosphogluconolactonase	1	C	2,326	0,399
18	D4AD05	*Crocc*	Ciliary rootlet coiled-coil, rootletin	2	N	2,025	0,360
19	D4A4D5	*Rplp2l2*	Large ribosomal subunit protein P2	5	C	2,480	0,325
20	Q91ZW6	*Tmlhe*	Trimethyllysine dioxygenase, mitochondrial	6	Mch	4,173	0,309
21	Q9WVK3	*Pecr*	Peroxisomal trans-2-enoyl-CoA reductase	7	Per	4,372	0,289
22	B2RYS0	*Cox7a2*	Cytochrome c oxidase subunit 7A2, mitochondrial	1	Mch	3,207	0,228
23	D3ZNJ5	*Inmt*	Indolethylamine N-methyltransferase	4	C	4,305	0,173
24	Q6SKG1	*Acsm3*	Acyl-coenzyme A synthetase ACSM3, mitochondrial	7	Mch	3,988	0,031