

Supplementary Table S7. Proteome changes on aorta and heart tissue of high-fat diet *versus* standard chow diet.

Tissue	UniProt ID	Gene	Protein name	FC	p-value*
AORTA	P02680	<i>Fgg</i>	Fibrinogen gamma chain	2.228	< 0.001
	Q7TQ70	<i>Fga</i>	Ac1873	1.989	0.0010
	M0RBF1	<i>C3</i>	Complement C3	1.489	0.0019
	A0A0G2K162	<i>Epb41l2</i>	Erythrocyte membrane protein band 4.1-like 2	1.197	0.0022
	P49242	<i>Rps3a</i>	40S ribosomal protein S3a	1.302	0.0027
	Q9Z1Z9	<i>Pdlim7</i>	PDZ and LIM domain protein 7	1.239	0.0043
	A1L1M0	<i>Prkaca</i>	Protein kinase, cAMP-dependent, catalytic, alpha	1.240	0.0064
	D4A5E5	<i>Sgcb</i>	Sarcoglycan, beta	1.331	0.0085
	Q6P502	<i>Cct3</i>	T-complex protein 1 subunit gamma	1.622	0.0087
	G3V7N9	<i>C1qb</i>	Complement C1q subcomponent subunit B	2.001	0.0111
	P10860	<i>Glud1</i>	Glutamate dehydrogenase 1, mitochondrial	1.297	0.0118
	Q5RJR9	<i>Serpinh1</i>	Serine (Or cysteine) proteinase inhibitor, clade H, member 1, isoform CRA_b	1.093	0.0126
	D3ZFH5	<i>Itih2</i>	Inter-alpha-trypsin inhibitor heavy chain 2	1.698	0.0154
	P14046	<i>Ali3</i>	Alpha-1-inhibitor 3	1.494	0.0166
	B5DEZ8	<i>Plxdc2</i>	Plexin domain containing 2 (Predicted)	-1.122	0.0043
	Q5U2Q3	<i>N/A</i>	Ester hydrolase C11orf54 homolog	-1.426	0.0049
	M0RAM5	<i>Gpx1</i>	Glutathione peroxidase	-1.144	0.0071
	B5DEN5	<i>Eef1b2</i>	Eukaryotic translation elongation factor 1 beta 2	-1.260	0.0111
	D4A0T0	<i>Ndufb10</i>	NADH:ubiquinone oxidoreductase subunit B10	-1.397	0.0116
	P80254	<i>Ddt</i>	D-dopachrome decarboxylase	-1.466	0.0120
	P62775	<i>Mtpn</i>	Myotrophin	-1.416	0.0122
	Q6P686	<i>Ostf1</i>	Osteoclast-stimulating factor 1	-1.225	0.0152
	Q9WUC4	<i>Atox1</i>	Copper transport protein ATOX1	-1.819	0.0165
	A0A0G2K6J5	<i>Myl6</i>	Myosin light polypeptide 6	-1.631	0.0167
	O08557	<i>Ddah1</i>	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	-1.365	0.0190
HEART	P09605	<i>Ckmt2</i>	Creatine kinase S-type, mitochondrial	1.532	0.0015

P08010	<i>Gstm2</i>	Glutathione S-transferase Mu 2	1.386	0.0034
P16290	<i>Pgam2</i>	Phosphoglycerate mutase 2	1.260	0.0053
B4F789	<i>ApoBec2</i>	Apolipoprotein B editing complex 2 (Predicted), isoform CRA_a	1.403	0.0055
Q62651	<i>Ech1</i>	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	1.175	0.0083
B0BNE6	<i>Ndufs8</i>	NADH dehydrogenase (Ubiquinone) Fe-S protein 8 (Predicted), isoform CRA_a	1.427	0.0096
P00173	<i>Cyb5a</i>	Cytochrome b5	1.303	0.0100
Q9QZ76	<i>Mb</i>	Myoglobin	1.609	0.0100
D3ZPF0	<i>Fhl3</i>	Four and a half LIM domains 3	1.150	0.0139
E9PU42	<i>Vps26c</i>	Down syndrome critical region gene 3 (Predicted), isoform CRA_c	1.679	0.0152
A0A0G2JY31	<i>Serpina1</i>	Alpha-1-antiproteinase	1.234	0.0177
P35053	<i>Gpc1</i>	Glypican-1	1.291	0.0182
Q4V8F6	<i>Pcbp2</i>	Pcbp2 protein	-1.273	0.0022
P70623	<i>Fabp4</i>	Fatty acid-binding protein, adipocyte	-1.346	0.0157
F1LN42	<i>Tns1</i>	Tensin 1	-1.280	0.0176
P13086	<i>Suclg1</i>	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	-1.288	0.0196
M0R7S5	<i>Plin4</i>	Perilipin 4	-1.497	0.0197

FC, fold change.

T-test or Wilcoxon test of pairwise comparisons was performed depending on each protein's distribution.

* $p < 0.02$ was considered statistically significant