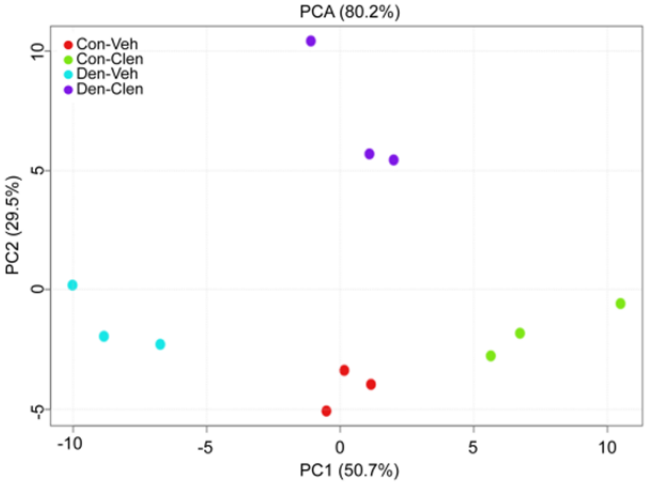


Supplemental Figure 1



**Supplemental Figure 1** Principal component analysis (PCA) of muscle tissue protein FSRs for the contralateral limb in vehicle-treated (Con-Veh, n=3) and clenbuterol-treated (Con-Clen, n=3) rats, as well as denervated limb in vehicle-treated (Den-Veh) and clenbuterol-treated (Den-Clen) rats.

Supplemental Table 1: Correlation of fractional synthesis of creatine-kinase M-type (CK-M) and carbonic anhydrase 3 (CA-3) with that of muscle proteins in rat gastrocnemius. Pearson correlation coefficients between fractional synthesis of CK-M and CA-3 in the rat gastrocnemius muscle or plasma and fractional syntheses of other proteins measured in the gastrocnemius muscle.

Gastrocnemius Muscle Proteins	Muscle CK-M fractional synthesis vs. other gastrocnemius muscle proteins fractional synthesis: Pearson correlation coefficient r, two-tailed p-value, n	Plasma CK-M fractional synthesis vs. other gastrocnemius muscle proteins fractional synthesis: Pearson correlation coefficient r, two-tailed p-value, n	Muscle CA-3 fractional synthesis vs. other gastrocnemius muscle proteins fractional synthesis: Pearson correlation coefficient r, two-tailed p-value, n	Plasma CA-3 fractional synthesis vs. other gastrocnemius muscle proteins fractional synthesis: Pearson correlation coefficient r, two-tailed p-value, n
2-oxoglutarate dehydrogenase, mitochondrial	r = 0.958, p < 0.0001, n = 17	r = 0.9748, p < 0.0001, n = 15	r = 0.9321, p < 0.0001, n = 17	r = 0.9488, p < 0.0001, n = 17
3-mercaptopyruvate sulfurtransferase	r = 0.8819, p < 0.0001, n = 13	r = 0.9202, p < 0.0001, n = 12	r = 0.7977, p < 0.005, n = 13	r = 0.8444, p < 0.0005, n = 13
60 kDa heat shock protein, mitochondrial	r = 0.9126, p < 0.0001, n = 16	r = 0.931, p < 0.0001, n = 14	r = 0.8324, p < 0.0001, n = 16	r = 0.8094, p < 0.0001, n = 16
Aconitate hydratase, mitochondrial	r = 0.9314, p < 0.0001, n = 24	r = 0.948, p < 0.0001, n = 22	r = 0.8418, p < 0.0001, n = 24	r = 0.8761, p < 0.0001, n = 24
Actin	r = 0.8741, p < 0.0001, n = 24	r = 0.857, p < 0.0001, n = 22	r = 0.9257, p < 0.0001, n = 24	r = 0.882, p < 0.0001, n = 24
Adenylate kinase isoenzyme 1	r = 0.9957, p < 0.0001, n = 24	r = 0.9687, p < 0.0001, n = 22	r = 0.9073, p < 0.0001, n = 24	r = 0.9737, p < 0.0001, n = 24
ADP/ATP translocase 1	r = 0.9263, p < 0.0001, n = 20	r = 0.933, p < 0.0001, n = 18	r = 0.9322, p < 0.0001, n = 20	r = 0.9068, p < 0.0001, n = 20
Alpha-enolase	r = 0.982, p < 0.0001, n = 24	r = 0.972, p < 0.0001, n = 22	r = 0.8705, p < 0.0001, n = 24	r = 0.9353, p < 0.0001, n = 24
Aspartate aminotransferase, cytoplasmic	r = 0.8461, p < 0.0001, n = 24	r = 0.8571, p < 0.0001, n = 22	r = 0.6658, p < 0.0005, n = 24	r = 0.8051, p < 0.0001, n = 24
Aspartate aminotransferase, mitochondrial	r = 0.9568, p < 0.0001, n = 24	r = 0.961, p < 0.0001, n = 22	r = 0.9204, p < 0.0001, n = 24	r = 0.9179, p < 0.0001, n = 24
ATP synthase subunit alpha, mitochondrial	r = 0.9182, p < 0.0001, n = 24	r = 0.9286, p < 0.0001, n = 22	r = 0.8368, p < 0.0001, n = 24	r = 0.881, p < 0.0001, n = 24
ATP synthase subunit beta, mitochondrial	r = 0.9548, p < 0.0001, n = 24	r = 0.965, p < 0.0001, n = 22	r = 0.8629, p < 0.0001, n = 24	r = 0.9174, p < 0.0001, n = 24
Beta-enolase	r = 0.9887, p < 0.0001, n = 24	r = 0.9811, p < 0.0001, n = 22	r = 0.8657, p < 0.0001, n = 24	r = 0.9433, p < 0.0001, n = 24
Carbonic anhydrase 3	r = 0.914, p < 0.0001, n = 24	r = 0.8977, p < 0.0001, n = 22	r = 1	r = 0.9038, p < 0.0001, n = 24
Citrate synthase, mitochondrial	r = 0.9524, p < 0.0001, n = 14	r = 0.9505, p < 0.0001, n = 12	r = 0.9155, p < 0.0001, n = 14	r = 0.8727, p < 0.0001, n = 14
Creatine kinase M-type	r = 1	r = 0.9771, p < 0.0001, n = 22	r = 0.914, p < 0.0001, n = 24	r = 0.9688, p < 0.0001, n = 24
Creatine kinase S-type, mitochondrial	r = 0.8289, p < 0.0001, n = 23	r = 0.8336, p < 0.0001, n = 21	r = 0.6496, p < 0.001, n = 23	r = 0.8099, p < 0.0001, n = 23
Cytochrome c oxidase subunit 5A, mitochondrial	r = 0.9465, p < 0.0001, n = 19	r = 0.937, p < 0.0001, n = 17	r = 0.7961, p < 0.0001, n = 19	r = 0.9033, p < 0.0001, n = 19
Dihydrolipoyl dehydrogenase, mitochondrial	r = 0.7097, p < 0.005, n = 15	r = 0.6923, p < 0.01, n = 14	r = 0.6604, p < 0.01, n = 15	r = 0.6735, p < 0.01, n = 15
Electron transfer flavoprotein subunit alpha, mitochondrial	r = 0.8915, p < 0.0001, n = 23	r = 0.8266, p < 0.0001, n = 21	r = 0.7398, p < 0.0001, n = 23	r = 0.8748, p < 0.0001, n = 23
Fatty acid-binding protein, heart	r = 0.8732, p < 0.0001, n = 17	r = 0.8673, p < 0.0001, n = 15	r = 0.757, p < 0.0005, n = 17	r = 0.845, p < 0.0005, n = 17
Four and a half LIM domains protein 1	r = 0.9624, p < 0.0001, n = 20	r = 0.945, p < 0.0001, n = 18	r = 0.9423, p < 0.0001, n = 20	r = 0.9322, p < 0.0001, n = 20
Fructose-bisphosphate aldolase A	r = 0.9945, p < 0.0001, n = 24	r = 0.9799, p < 0.0001, n = 22	r = 0.8912, p < 0.0001, n = 24	r = 0.9558, p < 0.0001, n = 24
Fumarate hydratase, mitochondrial	r = 0.9218, p < 0.0001, n = 23	r = 0.9267, p < 0.0001, n = 21	r = 0.8103, p < 0.0001, n = 23	r = 0.8588, p < 0.0001, n = 23
Galectin-1	r = 0.8867, p < 0.0001, n = 22	r = 0.8502, p < 0.0001, n = 20	r = 0.9022, p < 0.0001, n = 22	r = 0.8593, p < 0.0001, n = 22
Glucose-6-phosphate isomerase	r = 0.9911, p < 0.0001, n = 24	r = 0.9705, p < 0.0001, n = 22	r = 0.8765, p < 0.0001, n = 24	r = 0.9612, p < 0.0001, n = 24
Glyceraldehyde-3-phosphate dehydrogenase	r = 0.9802, p < 0.0001, n = 24	r = 0.9735, p < 0.0001, n = 22	r = 0.8469, p < 0.0001, n = 24	r = 0.9427, p < 0.0001, n = 24
Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic	r = 0.9793, p < 0.0001, n = 24	r = 0.9673, p < 0.0001, n = 22	r = 0.8857, p < 0.0001, n = 24	r = 0.9444, p < 0.0001, n = 24
Glycogen phosphorylase, muscle form	r = 0.9887, p < 0.0001, n = 24	r = 0.9712, p < 0.0001, n = 22	r = 0.8666, p < 0.0001, n = 24	r = 0.9542, p < 0.0001, n = 24
GTP-binding protein SAR1b	r = 0.7995, p < 0.0001, n = 22	r = 0.839, p < 0.0001, n = 20	r = 0.6263, p < 0.005, n = 22	r = 0.772, p < 0.0001, n = 22
Heat shock cognate 71 kDa protein	r = 0.9681, p < 0.0001, n = 24	r = 0.9575, p < 0.0001, n = 22	r = 0.9181, p < 0.0001, n = 24	r = 0.9621, p < 0.0001, n = 24
Heat shock-related 70 kDa protein 2	r = 0.9567, p < 0.0001, n = 22	r = 0.9477, p < 0.0001, n = 20	r = 0.8899, p < 0.0001, n = 22	r = 0.9464, p < 0.0001, n = 22
Histidine triad nucleotide-binding protein 1	r = 0.9799, p < 0.0001, n = 20	r = 0.9634, p < 0.0001, n = 18	r = 0.8707, p < 0.0001, n = 20	r = 0.9651, p < 0.0001, n = 20
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	r = 0.9153, p < 0.0001, n = 16	r = 0.9273, p < 0.0001, n = 14	r = 0.7567, p < 0.001, n = 16	r = 0.8713, p < 0.0001, n = 16
Isocitrate dehydrogenase [NADP], mitochondrial	r = 0.8735, p < 0.0001, n = 23	r = 0.8783, p < 0.0001, n = 21	r = 0.7557, p < 0.0001, n = 23	r = 0.8267, p < 0.0001, n = 23
L-lactate dehydrogenase A chain	r = 0.9955, p < 0.0001, n = 24	r = 0.9738, p < 0.0001, n = 22	r = 0.9005, p < 0.0001, n = 24	r = 0.9617, p < 0.0001, n = 24
L-lactate dehydrogenase B chain	r = 0.9332, p < 0.0001, n = 12	r = 0.8535, p < 0.005, n = 10	r = 0.8208, p < 0.005, n = 12	r = 0.9412, p < 0.0001, n = 12
Malate dehydrogenase, cytoplasmic	r = 0.9082, p < 0.0001, n = 24	r = 0.905, p < 0.0001, n = 22	r = 0.7289, p < 0.0001, n = 24	r = 0.8408, p < 0.0001, n = 24
Malate dehydrogenase, mitochondrial	r = 0.9445, p < 0.0001, n = 24	r = 0.9549, p < 0.0001, n = 22	r = 0.8911, p < 0.0001, n = 24	r = 0.9116, p < 0.0001, n = 24
Myoglobin	r = 0.8057, p < 0.0001, n = 24	r = 0.8331, p < 0.0001, n = 22	r = 0.6355, p < 0.001, n = 24	r = 0.7721, p < 0.0001, n = 24
Myosin light chain 1/3, skeletal muscle isoform	r = 0.9597, p < 0.0001, n = 24	r = 0.9404, p < 0.0001, n = 22	r = 0.8997, p < 0.0001, n = 24	r = 0.9436, p < 0.0001, n = 24
Nucleoside diphosphate kinase A	r = 0.9734, p < 0.0001, n = 13	r = 0.9262, p < 0.0001, n = 11	r = 0.9456, p < 0.0001, n = 13	r = 0.9653, p < 0.0001, n = 13
Nucleoside diphosphate kinase B	r = 0.9432, p < 0.0001, n = 22	r = 0.9481, p < 0.0001, n = 20	r = 0.8873, p < 0.0001, n = 22	r = 0.9403, p < 0.0001, n = 22
Parvalbumin alpha	r = 0.9357, p < 0.0001, n = 24	r = 0.8887, p < 0.0001, n = 22	r = 0.9148, p < 0.0001, n = 24	r = 0.9169, p < 0.0001, n = 24
Peroxiredoxin-2	r = 0.9547, p < 0.0001, n = 21	r = 0.9591, p < 0.0001, n = 19	r = 0.8336, p < 0.0001, n = 21	r = 0.9252, p < 0.0001, n = 21
Phosphatidylethanolamine-binding protein 1	r = 0.9032, p < 0.0001, n = 21	r = 0.9147, p < 0.0001, n = 19	r = 0.8015, p < 0.0001, n = 21	r = 0.8852, p < 0.0001, n = 21
Phosphoglucosmutase-1	r = 0.9812, p < 0.0001, n = 24	r = 0.9759, p < 0.0001, n = 22	r = 0.8592, p < 0.0001, n = 24	r = 0.9499, p < 0.0001, n = 24
Phosphoglycerate kinase 1	r = 0.9942, p < 0.0001, n = 24	r = 0.9837, p < 0.0001, n = 22	r = 0.9042, p < 0.0001, n = 24	r = 0.9666, p < 0.0001, n = 24
Phosphoglycerate mutase 1	r = 0.9937, p < 0.0001, n = 24	r = 0.9739, p < 0.0001, n = 22	r = 0.9017, p < 0.0001, n = 24	r = 0.9677, p < 0.0001, n = 24
Phosphoglycerate mutase 2	r = 0.9935, p < 0.0001, n = 24	r = 0.9791, p < 0.0001, n = 22	r = 0.8939, p < 0.0001, n = 24	r = 0.9722, p < 0.0001, n = 24
Profilin-1	r = 0.7676, p < 0.005, n = 13	r = 0.745, p < 0.01, n = 11	r = 0.832, p < 0.0005, n = 13	r = 0.767, p < 0.005, n = 13
Protein DJ-1	r = 0.9826, p < 0.0001, n = 24	r = 0.968, p < 0.0001, n = 22	r = 0.9107, p < 0.0001, n = 24	r = 0.9586, p < 0.0001, n = 24
Protein NDRG2	r = 0.8866, p < 0.0001, n = 20	r = 0.8296, p < 0.0001, n = 18	r = 0.6632, p < 0.005, n = 20	r = 0.8339, p < 0.0001, n = 20
Pyruvate kinase isozymes M1/M2	r = 0.9897, p < 0.001, n = 24	r = 0.9768, p < 0.001, n = 22	r = 0.8682, p < 0.001, n = 24	r = 0.9562, p < 0.0001, n = 24
Rho GDP-dissociation inhibitor 1	r = 0.9314, p < 0.001, n = 8	r = 0.8882, p < 0.01, n = 7	r = 0.9176, p < 0.005, n = 8	r = 0.8088, p < 0.05, n = 8
Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	r = 0.9888, p < 0.0001, n = 24	r = 0.9813, p < 0.0001, n = 22	r = 0.8848, p < 0.0001, n = 24	r = 0.9598, p < 0.0001, n = 24
Superoxide dismutase [Cu-Zn]	r = 0.903, p < 0.0001, n = 20	r = 0.8624, p < 0.0001, n = 18	r = 0.7654, p < 0.0001, n = 20	r = 0.8689, p < 0.0001, n = 20
Triosephosphate isomerase	r = 0.9928, p < 0.0001, n = 24	r = 0.9863, p < 0.0001, n = 22	r = 0.8921, p < 0.0001, n = 24	r = 0.9591, p < 0.0001, n = 24
Tripartite motif-containing protein 72	r = 0.8728, p < 0.0001, n = 21	r = 0.8844, p < 0.0001, n = 19	r = 0.7823, p < 0.0001, n = 21	r = 0.8451, p < 0.0001, n = 21
Tropomyosin alpha-1 chain	r = 0.844, p < 0.0001, n = 15	r = 0.8033, p < 0.001, n = 14	r = 0.802, p < 0.0005, n = 15	r = 0.8885, p < 0.0001, n = 15
Tubulin alpha-1B chain	r = 0.9127, p < 0.0001, n = 12	r = 0.9038, p < 0.005, n = 10	r = 0.933, p < 0.0001, n = 12	r = 0.902, p < 0.0001, n = 12

Supplemental Table 2: Correlation of fractional synthesis of creatine kinase M-type (CK-M) and carbonic anhydrase 3 (CA-3) with that of muscle proteins in rat quadriceps. Pearson correlation coefficients between fractional synthesis of CK-M and CA-3 in the rat quadriceps muscle or plasma and fractional syntheses of other proteins measured in the quadriceps muscle.

Quadriceps Muscle Proteins	Muscle CK-M fractional synthesis vs. other quadriceps muscle proteins fractional synthesis: Pearson correlation coefficient r, two-tailed p-value, n	Plasma CK-M fractional synthesis vs. other quadriceps muscle proteins fractional synthesis: Pearson correlation coefficient r, two-tailed p-value, n	Muscle CA-3 fractional synthesis vs. other quadriceps muscle proteins fractional synthesis: Pearson correlation coefficient r, two-tailed p-value, n	Plasma CA-3 fractional synthesis vs. other quadriceps muscle proteins fractional synthesis: Pearson correlation coefficient r, two-tailed p-value, n
Aconitate hydratase, mitochondrial	r = 0.9508, p < 0.0001, n = 20	r = 0.949, p < 0.0001, n = 18	r = 0.8317, p < 0.0001, n = 20	r = 0.9128, p < 0.0001, n = 20
Actin	r = 0.9778, p < 0.0001, n = 23	r = 0.9541, p < 0.0001, n = 22	r = 0.9063, p < 0.0001, n = 23	r = 0.9479, p < 0.0001, n = 23
Adenylate kinase isoenzyme 1	r = 0.9784, p < 0.0001, n = 24	r = 0.9735, p < 0.0001, n = 22	r = 0.8392, p < 0.0001, n = 24	r = 0.9454, p < 0.001, n = 24
Aspartate aminotransferase, cytoplasmic	r = 0.8018, p < 0.0001, n = 20	r = 0.7825, p < 0.0001, n = 18	r = 0.469, p < 0.05, n = 20	r = 0.7299, p < 0.005, n = 20
Beta-enolase	r = 0.9919, p < 0.0001, n = 24	r = 0.9788, p < 0.0001, n = 22	r = 0.8088, p < 0.0001, n = 24	r = 0.9357, p < 0.0001, n = 24
Carbonic anhydrase 3	r = 0.8647, p < 0.0001, n = 20	r = 0.86, p < 0.0001, n = 18	r = 1	r = 0.8819, p < 0.0001, n = 24
Creatine Kinase M-type	r = 1	r = 0.9844, p < 0.0001, n = 22	r = 0.8647, p < 0.0001, n = 24	r = 0.9512, p < 0.0001, n = 24
Fructose-bisphosphate aldolase A	r = 0.9966, p < 0.0001, n = 24	r = 0.9838, p < 0.0001, n = 22	r = 0.8478, p < 0.0001, n = 24	r = 0.9474, p < 0.0001, n = 24
Glucose-6-phosphate isomerase	r = 0.9895, p < 0.0001, n = 24	r = 0.9895, p < 0.0001, n = 22	r = 0.8466, p < 0.0001, n = 24	r = 0.9517, p < 0.0001, n = 24
Glyceraldehyde-3-phosphate dehydrogenase	r = 0.9873, p < 0.0001, n = 24	r = 0.9762, p < 0.0001, n = 22	r = 0.804, p < 0.0001, n = 24	r = 0.9316, p < 0.0001, n = 24
Glycogen phosphorylase, muscle form	r = 0.9915, p < 0.0001, n = 24	r = 0.9831, p < 0.0001, n = 22	r = 0.82, p < 0.0001, n = 24	r = 0.9489, p < 0.0001, n = 24
L-lactate dehydrogenase A chain	r = 0.9916, p < 0.0001, n = 24	r = 0.9821, p < 0.0001, n = 22	r = 0.8445, p < 0.0001, n = 24	r = 0.9489, p < 0.0001, n = 24
Malate dehydrogenase, mitochondrial	r = 0.9432, p < 0.0001, n = 21	r = 0.9418, p < 0.0001, n = 19	r = 0.7594, p < 0.0005, n = 21	r = 0.9106, p < 0.0001, n = 21
Myoglobin	r = 0.7591, p < 0.0001, n = 24	r = 0.7649, p < 0.0001, n = 22	r = 0.4823, p < 0.05, n = 24	r = 0.715, p < 0.0001, n = 24
Myosin Light Chain-1/3	r = 0.9834, p < 0.0001, n = 24	r = 0.9749, p < 0.0001, n = 22	r = 0.865, p < 0.0001, n = 24	r = 0.9511, p < 0.0001, n = 24
Parvalbumin alpha	r = 0.9588, p < 0.0001, n = 24	r = 0.9347, p < 0.0001, n = 22	r = 0.8939, p < 0.0001, n = 24	r = 0.9327, p < 0.0001, n = 24
Phosphoglucomutase-1	r = 0.9631, p < 0.0001, n = 24	r = 0.9518, p < 0.0001, n = 22	r = 0.7644, p < 0.0001, n = 24	r = 0.9197, p < 0.0001, n = 24
Phosphoglycerate kinase 1	r = 0.9654, p < 0.0001, n = 24	r = 0.9601, p < 0.0001, n = 22	r = 0.7792, p < 0.0001, n = 24	r = 0.8947, p < 0.0001, n = 24
Phosphoglycerate mutase 2	r = 0.995, p < 0.0001, n = 24	r = 0.9857, p < 0.0001, n = 22	r = 0.8514, p < 0.0001, n = 24	r = 0.9446, p < 0.0001, n = 24
Pyruvate Kinase M1/M2	r = 0.9886, p < 0.0001, n = 24	r = 0.9783, p < 0.0001, n = 22	r = 0.8098, p < 0.0001, n = 24	r = 0.933, p < 0.0001, n = 24
Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	r = 0.9427, p < 0.0001, n = 17	r = 0.9428, p < 0.0001, n = 16	r = 0.8179, p < 0.0005, n = 17	r = 0.9168, p < 0.0001, n = 17
Triosephosphate isomerase	r = 0.9928, p < 0.0001, n = 24	r = 0.9843, p < 0.0001, n = 22	r = 0.8382, p < 0.0001, n = 24	r = 0.9527, p < 0.0001, n = 24
Tropomyosin	r = 0.9673, p < 0.0001, n = 24	r = 0.9563, p < 0.0001, n = 24	r = 0.8386, p < 0.0001, n = 24	r = 0.9372, p < 0.0001, n = 24

Supplemental Table 3A: Human Muscle FSR. Values represent mean, SD for FSR of 273 proteins measured in the vastus lateralis muscle of 2-5 subjects who were sedentary and 2-6 subjects who underwent sprint interval training

Protein	Sedentary	Sprint	Sedentary	Sprint	Sedentary	Sprint
	FSR/week Mean	FSR/week Mean	FSR/week SD	FSR/week SD	FSR/week N	FSR/week N
Aspartate aminotransferase, cytoplasmic	7.2%	12.0%	0.8%	3.1%	5	6
Heat shock 70 kDa protein 1A/1B	13.2%	18.6%	2.7%	2.9%	5	6
Fructose-1,6-bisphosphatase isozyme 2	12.9%	20.2%	1.9%	5.2%	5	5
Phosphoglycerate mutase 2	5.7%	8.5%	1.0%	1.8%	5	6
Pyruvate kinase isozymes M1/M2	9.5%	15.3%	1.6%	4.4%	5	6
Malate dehydrogenase, cytoplasmic	7.2%	11.5%	1.4%	3.3%	5	6
Creatine kinase S-type, mitochondrial	9.0%	13.8%	2.2%	3.3%	5	6
ATP synthase subunit beta, mitochondrial	8.5%	12.4%	1.8%	2.8%	5	6
Fatty acid-binding protein, heart	6.2%	9.3%	1.4%	2.3%	5	5
Fructose-bisphosphate aldolase A	10.5%	15.9%	1.7%	4.7%	5	6
Triosephosphate isomerase	5.4%	8.3%	0.9%	2.5%	5	6
ATP synthase subunit alpha, mitochondrial	9.3%	13.4%	1.8%	3.5%	5	6
2-oxoglutarate dehydrogenase, mitochondrial	15.5%	25.4%	2.6%	10.5%	5	6
Phosphoglycerate kinase 1	5.7%	8.6%	1.0%	2.6%	5	6
L-lactate dehydrogenase A chain	7.6%	13.1%	1.6%	5.4%	5	6
Ferritin heavy chain	17.9%	33.6%	3.1%	10.8%	3	3
Filamin-A	17.7%	25.7%	2.6%	7.9%	5	5
Glyceraldehyde-3-phosphate dehydrogenase	7.0%	11.5%	0.4%	4.6%	5	6
Myosin light chain 1/3, skeletal muscle isoform	10.0%	12.9%	2.7%	1.6%	5	6
Filamin-C	16.1%	25.3%	1.7%	10.3%	5	6
Fumarate hydratase, mitochondrial	9.7%	15.7%	1.7%	6.1%	5	6
Glucose-6-phosphate isomerase	6.3%	9.0%	0.7%	2.9%	5	6
Phosphoglycerate mutase 1	6.3%	9.0%	0.7%	2.8%	5	6
Aldose reductase	5.2%	7.4%	0.6%	2.2%	5	5
14-3-3 protein gamma	17.6%	32.3%	4.6%	16.5%	5	6
Beta-enolase	6.3%	8.8%	0.8%	2.6%	5	6
60 kDa heat shock protein, mitochondrial	9.3%	13.6%	1.5%	4.3%	5	5
Tropomyosin alpha-1 chain	7.6%	10.3%	0.8%	2.9%	5	6
Filamin-B	17.4%	25.3%	2.2%	9.5%	5	5
Apolipoprotein A-I	72.6%	74.9%	4.6%	0.0%	4	4
Histidine triad nucleotide-binding protein 1	7.5%	6.1%	0.3%	0.5%	2	2
Ubiquitin-like modifier-activating enzyme 1	16.5%	21.3%	1.2%	5.8%	5	6
Superoxide dismutase [Cu-Zn]	5.5%	12.4%	1.0%	8.5%	5	4
LIM domain-binding protein 3	19.7%	12.7%	4.3%	0.9%	3	2
Aspartate aminotransferase, mitochondrial	7.4%	10.2%	2.2%	2.6%	5	6
ADP/ATP translocase 1	10.4%	14.3%	2.4%	4.0%	5	6
Electron transfer flavoprotein subunit beta	8.8%	13.6%	3.2%	2.9%	4	3
Flavin reductase (NADPH)	8.7%	10.8%	1.1%	2.4%	5	6
Tubulin beta-4A chain	8.8%	10.8%	1.6%	0.5%	4	3
Nucleoside diphosphate kinase A	6.5%	9.5%	2.4%	2.5%	5	4
ATP synthase subunit O, mitochondrial	5.9%	9.6%	2.1%	0.5%	3	2
Myosin-7	10.8%	22.1%	1.6%	18.4%	5	6
Adenylate kinase isoenzyme 1	4.7%	5.8%	0.5%	1.3%	5	5
Myosin-6	11.2%	22.4%	1.7%	18.3%	5	6
Gamma-enolase	5.0%	6.8%	0.8%	2.3%	5	6
Nucleoside diphosphate kinase B	7.1%	9.6%	2.1%	2.5%	5	5
Cofilin-1	10.6%	13.5%	1.7%	3.4%	5	5
1,4-alpha-glucan-branching enzyme	20.8%	27.1%	0.8%	5.8%	3	3
Myosin-2	11.2%	18.3%	1.0%	10.1%	5	5
Alpha-enolase	5.2%	6.9%	0.8%	2.2%	5	6
Alpha-actinin-3	6.7%	4.6%	1.3%	0.9%	3	2
NADP-dependent malic enzyme	17.3%	7.0%	7.0%	1.4%	2	2
Phosphatidylethanolamine-binding protein 1	6.5%	7.7%	1.5%	1.1%	5	6
UTP--glucose-1-phosphate uridylyltransferase	15.8%	19.0%	2.1%	3.9%	5	5
Phosphoglucomutase-1	7.7%	10.5%	0.4%	4.1%	5	6
Heat shock protein beta-6	21.7%	30.3%	4.9%	12.2%	5	6
ES1 protein homolog, mitochondrial	8.2%	11.4%	2.3%	3.2%	5	3
Heat shock cognate 71 kDa protein	14.1%	17.4%	1.0%	4.8%	5	5
Creatine kinase B-type	7.9%	14.6%	4.8%	3.9%	3	3
Troponin I, fast skeletal muscle	11.1%	15.9%	1.6%	6.9%	5	6
Peroxisredoxin-6	9.1%	10.7%	1.5%	1.8%	5	6
Protein disulfide-isomerase	20.6%	14.8%	2.2%	2.9%	2	2
Heat shock-related 70 kDa protein 2	15.5%	19.6%	1.6%	6.1%	5	5
Enoyl-CoA delta isomerase 1, mitochondrial	14.8%	9.2%	5.0%	3.3%	3	3
Alpha-1-antitrypsin	60.4%	41.4%	21.0%	34.9%	5	5
Myomesin-2	5.3%	6.9%	0.3%	2.3%	5	6
Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	12.3%	15.7%	1.2%	4.9%	5	6
Four and a half LIM domains protein 1	9.4%	13.1%	0.8%	5.5%	5	6
Cofilin-2	10.6%	13.2%	1.4%	3.7%	5	5
Elongation factor 1-alpha 2	14.7%	18.5%	1.2%	5.8%	5	5
Isopentenyl-diphosphate Delta-isomerase 2	25.5%	13.4%	9.8%	0.6%	2	2
Glutathione S-transferase P	7.5%	9.1%	1.3%	2.2%	5	5
Myosin-4	11.6%	18.1%	1.7%	9.7%	5	5
Peroxisredoxin-1	11.8%	14.2%	2.0%	3.3%	5	5
Ubiquinone biosynthesis protein COQ9, mitochondrial	7.3%	9.1%	1.6%	2.4%	5	5
Tripartite motif-containing protein 72	10.4%	12.3%	2.4%	1.8%	5	5
Lumican	18.7%	11.7%	9.0%	3.1%	3	4
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase	3.8%	5.6%	1.0%	2.2%	4	3
L-lactate dehydrogenase B chain	8.9%	11.9%	0.4%	4.9%	5	6
Glycogen debranching enzyme	9.9%	13.2%	1.8%	5.3%	5	6

Creatine kinase M-type	6.2%	8.0%	0.8%	2.9%	5	6
Troponin T, slow skeletal muscle	13.9%	18.9%	1.8%	6.0%	3	3
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	21.2%	25.1%	5.3%	4.2%	5	4
Fatty acid-binding protein, adipocyte	19.7%	35.7%	7.9%	16.1%	3	2
Vinculin	16.7%	21.2%	4.2%	6.3%	5	5
Carbonic anhydrase 3	4.3%	6.1%	0.8%	2.8%	5	6
Long-chain-fatty-acid--CoA ligase 1	12.2%	16.7%	6.2%	3.7%	5	4
Kelch repeat and BTB domain-containing protein 10	24.5%	20.1%	0.6%	3.3%	2	2
Troponin C, slow skeletal and cardiac muscles	18.9%	29.3%	3.0%	16.8%	5	4
Myosin-binding protein C, fast-type	20.8%	26.7%	2.2%	7.0%	3	2
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	7.4%	9.9%	3.0%	3.4%	5	6
Aldehyde dehydrogenase X, mitochondrial	15.9%	22.2%	2.9%	4.8%	2	2
Malate dehydrogenase, mitochondrial	7.6%	9.6%	1.6%	3.4%	5	6
Cytosolic 10-formyltetrahydrofolate dehydrogenase	18.5%	23.5%	3.8%	7.5%	5	3
Protein DJ-1	6.9%	8.1%	1.2%	1.8%	5	6
Band 3 anion transport protein	6.4%	4.2%	2.8%	0.2%	4	3
Beta-actin-like protein 2	5.1%	6.4%	0.7%	2.2%	5	6
Tubulin beta chain	9.2%	11.5%	2.1%	3.2%	5	3
Carbonic anhydrase 1	7.2%	8.8%	2.4%	2.2%	5	6
Reticulon-2	11.6%	10.6%	1.0%	0.3%	3	2
Tropomyosin alpha-3 chain	8.7%	10.1%	0.6%	2.5%	5	6
Ig gamma-2 chain C region	12.0%	7.3%	5.8%	5.2%	5	3
Actin, alpha cardiac muscle 1	4.5%	5.4%	0.3%	1.7%	5	6
Cysteine and glycine-rich protein 3	19.6%	7.8%	0.4%	9.7%	2	2
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	10.3%	8.9%	1.0%	1.3%	3	2
Glutathione S-transferase Mu 1	5.6%	8.4%	0.8%	2.9%	2	4
Alpha-actinin-4	9.1%	41.9%	2.8%	46.6%	3	2
Enoyl-CoA hydratase, mitochondrial	9.2%	11.3%	1.9%	3.5%	5	5
Transforming protein RhoA	27.9%	53.7%	11.4%	24.4%	2	2
Tubulin beta-4B chain	9.5%	11.8%	2.5%	2.9%	5	3
Peroxiredoxin-2	8.0%	9.4%	2.9%	1.6%	5	6
Tubulin alpha-4A chain	17.7%	20.1%	3.6%	1.6%	5	3
Retinal dehydrogenase 1	13.6%	11.4%	1.8%	3.5%	4	3
Superoxide dismutase [Mn], mitochondrial	7.7%	9.9%	1.5%	4.2%	5	6
Ig alpha-1 chain C region	57.8%	46.1%	18.2%	16.2%	3	4
Myoglobin	3.6%	4.3%	0.5%	1.3%	5	6
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	11.5%	8.2%	3.8%	0.5%	3	2
Cytoplasmic aconitate hydratase	14.5%	17.5%	4.4%	4.7%	5	4
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	7.7%	9.5%	2.1%	3.4%	5	6
Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	8.1%	9.5%	1.4%	2.5%	5	6
Serum albumin	22.9%	28.3%	8.4%	11.0%	5	6
Ig kappa chain C region	16.8%	26.0%	5.5%	16.4%	4	6
Protein-arginine deiminase type-2	14.4%	8.3%	8.0%	0.9%	3	2
NAD(P) transhydrogenase, mitochondrial	8.9%	21.9%	1.9%	25.4%	3	5
Ig gamma-1 chain C region	15.9%	19.5%	3.7%	7.2%	5	5
Actin, alpha skeletal muscle	4.4%	5.2%	0.3%	1.7%	5	6
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	25.1%	32.4%	5.8%	9.2%	3	2
Alpha-crystallin B chain	18.6%	22.3%	4.6%	7.0%	5	6
Citrate synthase, mitochondrial	8.9%	11.0%	3.5%	3.4%	5	5
Dysferlin	9.8%	10.8%	0.0%	1.8%	3	2
Alpha-actinin-1	7.7%	10.1%	1.9%	3.6%	3	3
ATP synthase subunit b, mitochondrial	6.8%	8.6%	1.7%	3.1%	5	3
Myosin regulatory light chain 2, skeletal muscle isoform	6.9%	8.5%	2.1%	3.1%	5	6
Glutathione S-transferase Mu 4	6.0%	8.3%	0.3%	3.0%	2	4
WD repeat-containing protein 1	5.8%	7.3%	0.3%	1.8%	2	2
POTE ankyrin domain family member E	4.5%	5.4%	0.5%	2.0%	5	6
Annexin A6	16.3%	12.5%	0.3%	8.5%	3	4
Polyubiquitin-C	52.5%	67.6%	16.5%	12.6%	5	3
Myosin-1	11.4%	13.7%	1.3%	4.8%	5	4
Synaptophysin-like protein 2	2.2%	3.1%	0.9%	1.4%	4	2
Isoleucine--tRNA ligase, mitochondrial	15.0%	12.5%	3.4%	0.9%	3	2
Calsequestrin-1	10.0%	5.3%	11.2%	1.3%	4	5
Tubulin alpha-8 chain	17.4%	20.0%	4.8%	2.2%	4	3
Neutral alpha-glucosidase AB	23.2%	16.2%	3.1%	9.2%	2	2
Trifunctional enzyme subunit alpha, mitochondrial	7.0%	6.1%	1.9%	0.5%	5	4
Cytochrome b-c1 complex subunit 1, mitochondrial	9.6%	12.4%	1.6%	5.0%	3	2
ATP synthase subunit d, mitochondrial	7.0%	9.2%	1.7%	3.7%	3	3
Electron transfer flavoprotein subunit alpha, mitochondrial	9.9%	11.8%	2.5%	4.5%	5	6
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	16.3%	22.1%	5.0%	8.8%	3	2
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	16.6%	19.4%	4.3%	4.9%	5	3
Inter-alpha-trypsin inhibitor heavy chain H2	68.2%	74.9%	9.5%	0.0%	2	2
Protein NDRG2	36.1%	32.1%	6.5%	19.4%	5	3
Troponin T, fast skeletal muscle	11.8%	10.3%	1.4%	3.0%	3	3
Thioredoxin-dependent peroxide reductase, mitochondrial	11.8%	14.6%	4.2%	6.1%	5	5
Glutathione S-transferase Mu 3	9.4%	8.7%	0.7%	1.3%	3	2
Acylphosphatase-2	15.4%	12.3%	5.3%	2.5%	4	2
Glycogen [starch] synthase, muscle	15.8%	17.3%	4.3%	1.9%	5	4
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	8.1%	9.1%	1.6%	0.4%	3	2
Cytochrome b-c1 complex subunit 2, mitochondrial	8.4%	9.4%	1.0%	1.8%	3	2
Galectin-1	8.5%	10.4%	1.9%	3.5%	3	2
ATP synthase subunit g, mitochondrial	5.6%	6.8%	1.2%	2.5%	3	2
Ig gamma-4 chain C region	11.2%	16.4%	0.6%	11.0%	3	2
Vitamin D-binding protein	74.9%	74.9%	0.0%	0.0%	2	2
PWWP domain-containing protein MUM1	5.8%	8.6%	0.6%	4.6%	2	4
Cytochrome b-c1 complex subunit 7	11.7%	14.8%	0.4%	5.3%	2	2
Heat shock protein beta-1	15.3%	19.1%	3.9%	9.8%	5	5
Importin subunit beta-1	26.7%	18.3%	0.1%	17.6%	2	2
Cullin-associated NEDD8-dissociated protein 2	33.7%	40.7%	13.4%	16.1%	4	3
Annexin A5	15.0%	16.5%	1.8%	3.4%	4	3

Cytochrome c oxidase subunit 5B, mitochondrial	9.8%	8.0%	3.2%	0.9%	3	2
Angiotensinogen	35.3%	51.0%	34.4%	33.8%	3	2
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	16.6%	19.2%	3.3%	6.7%	5	2
Protein-L-isoaspartate(D-aspartate) O-methyltransferase	10.3%	7.1%	6.1%	1.1%	3	2
Myosin light chain 3	4.1%	4.6%	1.1%	1.4%	5	6
Mitochondrial 2-oxoglutarate/malate carrier protein	8.7%	9.9%	1.5%	2.5%	3	2
Hemoglobin subunit alpha	7.4%	6.7%	2.3%	1.6%	5	6
Ubiquitin carboxyl-terminal hydrolase 5	16.7%	14.9%	3.2%	1.2%	2	2
Carbonic anhydrase 2	5.9%	6.5%	1.4%	1.6%	5	5
Apolipoprotein B-100	48.2%	64.9%	37.8%	17.3%	2	3
Prohibitin-2	4.6%	6.4%	1.5%	4.4%	3	2
Actin, cytoplasmic 2	4.6%	5.2%	0.5%	2.1%	5	6
Protein S100-A1	18.1%	20.6%	6.0%	5.6%	4	3
Catalase	9.2%	11.0%	2.9%	5.0%	4	5
Microsomal glutathione S-transferase 3	12.7%	15.3%	3.1%	5.9%	3	2
Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic	12.8%	14.3%	1.9%	5.0%	5	5
SH3 domain-binding glutamic acid-rich protein	18.8%	22.0%	2.5%	8.4%	4	4
Mitochondrial inner membrane protein	8.8%	6.9%	1.7%	7.1%	3	2
Glycogen phosphorylase, brain form	9.3%	8.4%	2.3%	3.7%	5	6
Spectrin alpha chain, erythrocyte	10.8%	8.4%	4.9%	1.5%	2	2
Acyl-CoA-binding protein	5.0%	6.0%	0.3%	2.2%	2	2
Rab GDP dissociation inhibitor beta	10.7%	11.4%	1.5%	0.8%	3	2
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	20.2%	24.4%	6.2%	9.7%	3	2
Acetyl-CoA acetyltransferase, mitochondrial	8.2%	9.9%	2.1%	6.1%	5	6
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	12.8%	14.1%	1.9%	4.3%	5	6
UPF0366 protein C11orf67	9.7%	10.7%	3.6%	0.4%	2	3
Ryanodine receptor 1	16.3%	11.9%	11.7%	9.1%	5	4
Alpha-2-macroglobulin	39.1%	45.8%	20.9%	16.0%	5	5
Heat shock protein HSP 90-beta	57.2%	56.4%	21.5%	26.1%	5	2
Glycogen phosphorylase, muscle form	10.0%	11.3%	2.2%	5.0%	5	6
Protein-cysteine N-palmitoyltransferase HHAT-like protein	3.7%	4.5%	0.9%	2.7%	3	2
GTP-binding protein SAR1b	48.8%	41.8%	13.3%	16.3%	2	2
S-formylglutathione hydrolase	5.4%	6.4%	2.9%	0.1%	4	2
Leucine-rich PPR motif-containing protein, mitochondrial	38.7%	43.2%	17.5%	8.0%	3	2
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	15.4%	18.0%	5.6%	6.0%	3	2
DNA damage-binding protein 1	33.3%	30.1%	10.0%	10.6%	5	5
Cytochrome b-c1 complex subunit Rieske, mitochondrial	10.5%	12.0%	2.3%	4.3%	3	2
Dihydropyridol dehydrogenase, mitochondrial	10.6%	13.1%	2.5%	8.9%	5	5
Ig lambda-2 chain C regions	21.4%	23.2%	9.9%	0.6%	4	2
Hemopexin	46.7%	56.5%	19.0%	26.0%	2	2
Transitional endoplasmic reticulum ATPase	36.5%	30.7%	13.7%	6.5%	3	2
Phosphorylase b kinase regulatory subunit beta	14.1%	15.4%	4.2%	1.8%	3	2
CDGSH iron-sulfur domain-containing protein 1	9.9%	12.1%	2.9%	5.3%	2	2
Hexokinase-1	20.9%	16.8%	10.5%	2.2%	3	2
Troponin C, skeletal muscle	21.1%	20.2%	3.2%	6.1%	4	5
PDZ and LIM domain protein 3	25.7%	29.9%	5.1%	12.2%	3	3
Alpha-actinin-2	7.0%	8.3%	2.3%	5.1%	4	3
Aldehyde dehydrogenase, mitochondrial	31.7%	28.2%	9.8%	3.9%	3	3
Aconitate hydratase, mitochondrial	11.3%	13.3%	2.0%	7.0%	5	6
Peptidyl-prolyl cis-trans isomerase A	13.0%	14.6%	1.0%	4.7%	2	3
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	9.7%	10.6%	3.2%	1.5%	3	2
Myosin-binding protein C, slow-type	18.2%	19.7%	4.4%	6.1%	5	5
Glutathione S-transferase omega-1	7.3%	7.7%	0.7%	1.1%	2	2
Heat shock protein HSP 90-alpha	53.0%	41.8%	16.0%	28.7%	4	3
Glutathione S-transferase Mu 2	7.5%	7.2%	1.3%	2.3%	5	5
Myc box-dependent-interacting protein 1	17.0%	18.9%	2.2%	6.1%	2	2
Serotransferrin	51.2%	52.0%	17.9%	20.8%	5	5
Myosin-8	11.9%	12.7%	2.0%	4.3%	5	4
Titin	17.4%	17.0%	2.2%	6.4%	4	5
Ig gamma-3 chain C region	17.4%	18.5%	6.6%	5.7%	4	3
14-3-3 protein epsilon	13.6%	14.3%	2.6%	3.8%	5	5
Plectin	15.1%	16.5%	2.8%	7.3%	5	3
Leucine-rich repeat-containing protein 20	16.9%	15.8%	4.5%	0.8%	5	2
Hemoglobin subunit beta	7.4%	7.0%	2.6%	1.7%	5	6
L-xylulose reductase	8.2%	8.8%	0.2%	2.7%	2	2
Translationally-controlled tumor protein	62.4%	63.3%	21.7%	20.1%	3	3
Prolyl endopeptidase	12.4%	13.6%	3.2%	6.4%	3	2
Programmed cell death 6-interacting protein	28.1%	38.4%	3.7%	27.2%	2	2
Clathrin heavy chain 1	39.6%	40.0%	14.1%	9.4%	4	2
Voltage-dependent anion-selective channel protein 1	11.8%	12.7%	4.9%	4.3%	3	2
Ankyrin repeat domain-containing protein 2	18.6%	32.1%	4.7%	37.2%	5	3
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	19.8%	16.9%	11.2%	4.8%	3	2
Carboxymethylenebutenolidase homolog	7.5%	7.2%	2.5%	4.7%	4	5
Atrial natriuretic peptide receptor 1	4.4%	5.1%	2.6%	4.6%	4	5
ATP synthase subunit f, mitochondrial	9.4%	8.6%	4.5%	2.4%	2	2
Troponin I, slow skeletal muscle	21.0%	21.2%	6.6%	4.6%	5	6
Isocitrate dehydrogenase [NADP], mitochondrial	8.4%	8.5%	2.3%	2.1%	5	5
Importin-5	48.9%	43.1%	21.9%	9.5%	2	2
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform	12.3%	12.9%	1.0%	4.6%	5	5
Sarcalumenin	12.4%	12.0%	6.8%	6.7%	5	6
Complement component 1 Q subcomponent-binding protein, mitochondrial	16.6%	16.1%	4.8%	6.9%	2	2
Cytochrome c oxidase subunit 2	8.9%	9.3%	2.0%	3.5%	3	2
Fructose-bisphosphate aldolase C	8.4%	8.8%	2.9%	4.4%	5	5
Hemoglobin subunit delta	7.1%	6.9%	2.8%	1.9%	5	6
Isochorismatase domain-containing protein 2, mitochondrial	9.1%	9.7%	1.8%	6.2%	4	2
Reticulon-4	12.7%	12.8%	2.5%	1.3%	3	2
Trifunctional enzyme subunit beta, mitochondrial	16.7%	17.2%	2.4%	5.5%	3	2
14 kDa phosphohistidine phosphatase	6.3%	6.4%	0.5%	1.3%	2	2
Complement C3	70.3%	62.6%	9.2%	24.6%	4	4

Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	15.7%	15.8%	1.9%	0.9%	3	2
Rab GDP dissociation inhibitor alpha	11.9%	11.7%	2.5%	1.2%	2	2
Heat shock 70 kDa protein 4	30.4%	28.3%	14.6%	5.3%	2	3
Acyl-protein thioesterase 1	14.2%	14.1%	4.7%	6.6%	2	2
Tropomyosin beta chain	9.2%	9.4%	2.2%	3.4%	5	6
Phosphate carrier protein, mitochondrial	8.9%	9.4%	2.8%	5.7%	3	3
Myomesin-1	10.3%	10.9%	1.3%	6.8%	5	4
Succinate-semialdehyde dehydrogenase, mitochondrial	6.1%	6.0%	2.5%	1.7%	3	2
Stress-70 protein, mitochondrial	48.4%	36.4%	37.5%	5.4%	2	2
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	7.3%	7.5%	0.5%	4.8%	3	2
ATP synthase subunit gamma, mitochondrial	7.8%	7.8%	2.8%	3.8%	3	2
Cytochrome c	6.8%	7.4%	0.7%	6.9%	2	3
Cullin-associated NEDD8-dissociated protein 1	16.3%	15.8%	8.6%	4.5%	2	2
6-phosphofructokinase, muscle type	16.7%	21.8%	2.5%	19.5%	5	6
Profilin-1	15.2%	15.2%	2.8%	2.6%	2	2

Supplemental Table 3B: Human Muscle FSR. Values represent mean, SD for FSR of proteins in the different gene ontological clusters, measured in the vastus lateralis muscle of 3-5 subjects who were sedentary and 4-6 subjects who underwent sprint interval training

Proteins in Gene Ontology Term (Level 5)	Sedentary FSR/week Mean	Sprint FSR/week Mean	Sedentary FSR/week SD	Sprint FSR/week SD	Sedentary FSR/week N	Sprint FSR/week N
<b>Glucose Metabolic Process GO:0006006</b>						
2-oxoglutarate dehydrogenase, mitochondrial	15.5%	25.4%	2.6%	10.5%	5	6
6-phosphofructokinase, muscle type	16.7%	21.8%	2.5%	19.5%	5	6
Alpha-crystallin B chain	18.6%	22.3%	4.6%	7.0%	5	6
Alpha-enolase	5.2%	6.9%	0.8%	2.2%	5	6
Beta-enolase	6.3%	8.8%	0.8%	2.6%	5	6
Fructose-1,6-bisphosphatase isozyme 2	12.9%	20.2%	1.9%	5.2%	5	5
Fructose-bisphosphate aldolase A	10.5%	15.9%	1.7%	4.7%	5	6
Fructose-bisphosphate aldolase C	8.4%	8.8%	2.9%	4.4%	5	5
Gamma-enolase	5.0%	6.8%	0.8%	2.3%	5	6
Glucose-6-phosphate isomerase	6.3%	9.0%	0.7%	2.9%	5	6
Glyceraldehyde-3-phosphate dehydrogenase	7.0%	11.5%	0.4%	4.6%	5	6
Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic	12.8%	14.3%	1.9%	5.0%	5	5
Glycogen [starch] synthase, muscle	15.8%	17.3%	4.3%	1.9%	5	4
Glycogen debranching enzyme	9.9%	13.2%	1.8%	5.3%	5	6
Glycogen phosphorylase, brain form	9.3%	8.4%	2.3%	3.7%	5	6
Glycogen phosphorylase, muscle form	10.0%	11.3%	2.2%	5.0%	5	6
L-lactate dehydrogenase A chain	7.6%	13.1%	1.6%	5.4%	5	6
L-lactate dehydrogenase B chain	8.9%	11.9%	0.4%	4.9%	5	6
Malate dehydrogenase, cytoplasmic	7.2%	11.5%	1.4%	3.3%	5	6
Malate dehydrogenase, mitochondrial	7.6%	9.6%	1.6%	3.4%	5	6
Phosphoglucosmutase-1	7.7%	10.5%	0.4%	4.1%	5	6
Phosphoglycerate kinase 1	5.7%	8.6%	1.0%	2.6%	5	6
Phosphoglycerate mutase 1	6.3%	9.0%	0.7%	2.8%	5	6
Phosphoglycerate mutase 2	5.7%	8.5%	1.0%	1.8%	5	6
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform	12.3%	12.9%	1.0%	4.6%	5	5
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	7.4%	9.9%	3.0%	3.4%	5	6
Pyruvate kinase isozymes M1/M2	9.5%	15.3%	1.6%	4.4%	5	6
Triosephosphate isomerase	5.4%	8.3%	0.9%	2.5%	5	6
UTP--glucose-1-phosphate uridylyltransferase	15.8%	19.0%	2.1%	3.9%	5	5
<b>Striated Muscle Contraction GO:0006941</b>						
Phosphoglycerate mutase 2	5.7%	8.5%	1.0%	1.8%	5	6
Fructose-bisphosphate aldolase A	10.5%	15.9%	1.7%	4.7%	5	6
Myosin light chain 1/3, skeletal muscle isoform	10.0%	12.9%	2.7%	1.6%	5	6
Tropomyosin alpha-1 chain	7.6%	10.3%	0.8%	2.9%	5	6
Myosin-2	11.2%	18.3%	1.0%	10.1%	5	5
Troponin I, fast skeletal muscle	11.1%	15.9%	1.6%	6.9%	5	6
Myosin-6	11.2%	22.4%	1.7%	18.3%	5	6
Myosin-7	10.8%	22.1%	1.6%	18.4%	5	6
Troponin C, slow skeletal and cardiac muscles	18.9%	29.3%	3.0%	16.8%	5	4
Actin, alpha cardiac muscle 1	4.5%	5.4%	0.3%	1.7%	5	6
Myoglobin	3.6%	4.3%	0.5%	1.3%	5	6
Myosin-1	11.4%	13.7%	1.3%	4.8%	5	4
Myosin light chain 3	4.1%	4.6%	1.1%	1.4%	5	6
Troponin C, skeletal muscle	21.1%	20.2%	3.2%	6.1%	4	5
Myomesin-1	10.3%	10.9%	1.3%	6.8%	5	4
Titin	17.4%	17.0%	2.2%	6.4%	4	5
<b>Regulation of Apoptosis GO:0042981</b>						
Heat shock 70 kDa protein 1A/1B	13.2%	18.6%	2.7%	2.9%	5	6
60 kDa heat shock protein, mitochondrial	9.3%	13.6%	1.5%	4.3%	5	5
Superoxide dismutase [Cu-Zn]	5.5%	12.4%	1.0%	8.5%	5	4
Nucleoside diphosphate kinase A	6.5%	9.5%	2.4%	2.5%	5	4
Nucleoside diphosphate kinase B	7.1%	9.6%	2.1%	2.5%	5	5
Cofilin-1	10.6%	13.5%	1.7%	3.4%	5	5
Glutathione S-transferase P	7.5%	9.1%	1.3%	2.2%	5	5
Elongation factor 1-alpha 2	14.7%	18.5%	1.2%	5.8%	5	5
Peroxisredoxin-1	11.8%	14.2%	2.0%	3.3%	5	5
Superoxide dismutase [Mn], mitochondrial	7.7%	9.9%	1.5%	4.2%	5	6
Peroxisredoxin-2	8.0%	9.4%	2.9%	1.6%	5	6
Alpha-crystallin B chain	18.6%	22.3%	4.6%	7.0%	5	6
Thioredoxin-dependent peroxide reductase, mitochondrial	11.8%	14.6%	4.2%	6.1%	5	5
Heat shock protein beta-1	15.3%	19.1%	3.9%	9.8%	5	5
Catalase	9.2%	11.0%	2.9%	5.0%	4	5
14-3-3 protein epsilon	13.6%	14.3%	2.6%	3.8%	5	5
<b>Cellular Respiration GO:0045333</b>						
Malate dehydrogenase, cytoplasmic	7.2%	11.5%	1.4%	3.3%	5	6
Fumarate hydratase, mitochondrial	9.7%	15.7%	1.7%	6.1%	5	6
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	7.4%	9.9%	3.0%	3.4%	5	6
Malate dehydrogenase, mitochondrial	7.6%	9.6%	1.6%	3.4%	5	6
Superoxide dismutase [Mn], mitochondrial	7.7%	9.9%	1.5%	4.2%	5	6
Cytoplasmic aconitate hydratase	14.5%	17.5%	4.4%	4.7%	5	4
Citrate synthase, mitochondrial	8.9%	11.0%	3.5%	3.4%	5	5
NAD(P) transhydrogenase, mitochondrial	8.9%	21.9%	1.9%	25.4%	3	5
Catalase	9.2%	11.0%	2.9%	5.0%	4	5
Aconitate hydratase, mitochondrial	11.3%	13.3%	2.0%	7.0%	5	6
Dihydropyridol dehydrogenase, mitochondrial	10.6%	13.1%	2.5%	8.9%	5	5
Isocitrate dehydrogenase [NADP], mitochondrial	8.4%	8.5%	2.3%	2.1%	5	5



Supplemental Table 4: Correlation of muscle and plasma creatine kinase M-type (CK-M) and carbonic anhydrase 3 (CA-3) with other muscle proteins in humans. Pearson correlation coefficients of muscle and plasma CK-M and CA-3 FSR with FSR of muscle proteins measured in human quadriceps of the same subject.

Protein Name	Number of Subjects	Muscle CK-M FSR vs. Muscle Protein FSR		Plasma CK-M FSR vs. Muscle Protein FSR		Muscle CA-3 FSR vs. Muscle Protein FSR		Plasma CA-3 FSR vs. Muscle Protein FSR	
		Pearson Correlation Coefficient	P (two-tailed)	Pearson Correlation Coefficient	P (two-tailed)	Pearson Correlation Coefficient	P (two-tailed)	Pearson Correlation Coefficient	P (two-tailed)
<b>Myofibril</b>									
Actin, alpha cardiac muscle 1	17	0.8738	< 0.0001	0.7256	0.001	0.8156	< 0.0001	0.7139	0.0013
Actin, alpha skeletal muscle	17	0.8985	< 0.0001	0.7401	0.0007	0.8427	< 0.0001	0.6932	0.002
Filamin-B	16	0.9192	< 0.0001	0.8618	< 0.0001	0.8512	< 0.0001	0.6753	0.0041
Filamin-C	17	0.9413	< 0.0001	0.9238	< 0.0001	0.9048	< 0.0001	0.7616	0.0004
Myomesin-2	17	0.9678	< 0.0001	0.8385	< 0.0001	0.9392	< 0.0001	0.7827	0.0002
Myosin light chain 1/3, skeletal muscle isoform	16	0.705	0.0023	0.6892	0.0031	0.5345	0.0271	0.668	0.0034
Myosin regulatory light chain 2, skeletal muscle isoform	16	0.871	< 0.0001	0.7218	0.0016	0.7901	0.0002	0.4922	0.0447
Myosin-2	16	0.8848	< 0.0001	0.7789	0.0004	0.8813	< 0.0001	0.5737	0.0202
Myosin-4	15	0.9106	< 0.0001	0.7274	0.0021	0.8577	< 0.0001	0.5064	0.0453
Myosin-6	17	0.7624	0.0004	0.6003	0.0108	0.7533	0.0005	0.5575	0.0201
Myosin-7	16	0.7724	0.0005	0.622	0.011	0.7456	0.0006	0.5518	0.0216
PDZ and LIM domain protein 3	13	0.8716	0.0001	0.9448	< 0.0001	0.776	0.0018	0.8643	0.0003
Titin	16	0.8155	0.0001	0.7043	0.0023	0.878	< 0.0001	0.7569	0.0017
Tropomyosin alpha-1 chain	17	0.9369	< 0.0001	0.8489	< 0.0001	0.8997	< 0.0001	0.7926	0.0001
Tropomyosin alpha-3 chain	17	0.7989	0.0001	0.7543	0.0005	0.7562	0.0004	0.7243	0.001
Tropomyosin beta chain	17	0.7314	0.0008	0.6454	0.0051	0.8047	< 0.0001	0.7328	0.0008
Troponin C, skeletal muscle	15	0.7177	0.0026	0.6303	0.0118	0.7102	0.003	0.6228	0.0131
Troponin C, slow skeletal and cardiac muscles	14	0.8882	< 0.0001	0.7912	0.0007	0.8359	0.0002	0.7701	0.0013
Troponin I, fast skeletal muscle	17	0.9444	< 0.0001	0.9115	< 0.0001	0.8961	< 0.0001	0.8021	0.0001
Troponin T, slow skeletal muscle	11	0.8102	0.0025	0.8445	0.0011	0.8731	0.0004	0.6549	0.0208
<b>Cytoplasm</b>									
14 kDa phosphohistidine phosphatase	10	0.8182	0.0038	0.7401	0.0144	0.6549	0.0399	0.6552	0.0207
14-3-3 protein gamma	17	0.9078	< 0.0001	0.8461	< 0.0001	0.8481	< 0.0001	0.7639	0.0004
6-phosphofructokinase, muscle type	17	0.8022	0.0001	0.748	0.0006	0.8156	< 0.0001	0.7204	0.0011
Actin, cytoplasmic 2	17	0.7765	0.0002	0.6318	0.0065	0.7614	0.0004	0.6122	0.009
Adenylate kinase isoenzyme 1	16	0.8409	< 0.0001	0.768	0.0005	0.7846	0.0003	0.6368	0.008
ADP/ATP translocase 1	17	0.7225	0.0011	0.5866	0.0133	0.7275	0.0009	0.6014	0.0107
Aldose reductase	16	0.8958	< 0.0001	0.7989	0.0002	0.8171	0.0001	0.5983	0.0144
Alpha-actinin-2	13	0.8373	0.0004	0.6666	0.0128	0.8449	0.0003	0.7283	0.0048
Alpha-crystallin B chain	17	0.8704	< 0.0001	0.9478	< 0.0001	0.7917	0.0002	0.8251	< 0.0001
Alpha-enolase	17	0.9197	< 0.0001	0.7515	0.0005	0.8234	< 0.0001	0.7185	0.0012
Aspartate aminotransferase, cytoplasmic	17	0.8818	< 0.0001	0.8152	< 0.0001	0.8484	< 0.0001	0.6684	0.0034
Beta-actin-like protein 2	17	0.7949	0.0001	0.6862	0.0024	0.7814	0.0002	0.5948	0.0118
Beta-enolase	17	0.9496	< 0.0001	0.82	< 0.0001	0.871	< 0.0001	0.7687	0.0003
Carbonic anhydrase 2	16	0.7644	0.0006	0.9032	< 0.0001	0.6097	0.0122	0.8421	< 0.0001
Carbonic anhydrase 3	17	0.9308	< 0.0001	0.8136	< 0.0001	1			
Carboxymethylenebutenolidase homolog	15	0.7652	0.0009	0.8604	< 0.0001	0.6768	0.0056	0.7245	0.0015
Cofilin-1	16	0.8399	< 0.0001	0.8987	< 0.0001	0.7673	0.0005	0.7058	0.0022
Cofilin-2	16	0.8585	< 0.0001	0.8834	< 0.0001	0.7928	0.0002	0.7215	0.0016
Creatine kinase M-type	17	1				0.9308	< 0.0001	0.8216	< 0.0001
Cytosolic 10-formyltetrahydrofolate dehydrogenase	12	0.7433	0.0056	0.8121	0.0013	0.6651	0.0183	0.6462	0.0317
Elongation factor 1-alpha 2	16	0.9184	< 0.0001	0.8917	< 0.0001	0.8234	< 0.0001	0.746	0.0009
Fatty acid-binding protein, heart	16	0.6148	0.0113	0.5415	0.0303	0.5056	0.0457	0.5183	0.0397
Filamin-A	16	0.8812	< 0.0001	0.8763	< 0.0001	0.8094	0.0001	0.6617	0.0052
Flavin reductase (NADPH)	17	0.7424	0.0006	0.7087	0.0015	0.7464	0.0006	0.6114	0.0091
Four and a half LIM domains protein 1	17	0.9675	< 0.0001	0.907	< 0.0001	0.9437	< 0.0001	0.8181	< 0.0001
Fructose-1,6-bisphosphatase isozyme 2	16	0.8863	< 0.0001	0.758	0.0007	0.7971	0.0002	0.6561	0.0058
Fructose-bisphosphate aldolase A	17	0.9616	< 0.0001	0.8894	< 0.0001	0.8722	< 0.0001	0.8169	< 0.0001
Gamma-enolase	17	0.8979	< 0.0001	0.7216	0.0011	0.7882	0.0002	0.6899	0.0022
Glucose-6-phosphate isomerase	17	0.9104	< 0.0001	0.8136	< 0.0001	0.8282	< 0.0001	0.7383	0.0007
Glutathione S-transferase Mu 1	13	0.6634	0.0134	0.7674	0.0022	0.57	0.042	0.6868	0.0095
Glutathione S-transferase Mu 2	16	0.6945	0.0028	0.7758	0.0004	0.5709	0.0209	0.6458	0.0069
Glutathione S-transferase Mu 4	13	0.6613	0.0138	0.6795	0.0106	0.673	0.0117	0.6502	0.0161
Glycerolaldehyde-3-phosphate dehydrogenase	17	0.9552	< 0.0001	0.8622	< 0.0001	0.9271	< 0.0001	0.7353	0.0008
Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic	16	0.9128	< 0.0001	0.8634	< 0.0001	0.8005	0.0002	0.6696	0.0045
Glycogen debranching enzyme	17	0.8655	< 0.0001	0.8963	< 0.0001	0.8172	< 0.0001	0.8144	< 0.0001
Glycogen phosphorylase, muscle form	17	0.8895	< 0.0001	0.8861	< 0.0001	0.84	< 0.0001	0.8648	< 0.0001
Heat shock 70 kDa protein 1A/1B	17	0.743	0.0006	0.7668	0.0003	0.558	0.0199	0.6693	0.0033
Heat shock cognate 71 kDa protein	16	0.9148	< 0.0001	0.8834	< 0.0001	0.8711	< 0.0001	0.712	0.002
Heat shock protein beta-1	16	0.9142	< 0.0001	0.9016	< 0.0001	0.8188	0.0001	0.7783	0.0004
Heat shock protein beta-6	17	0.8065	< 0.0001	0.7956	0.0001	0.7178	0.0012	0.7431	0.0006
Heat shock-related 70 kDa protein 2	16	0.8964	< 0.0001	0.8293	< 0.0001	0.8875	< 0.0001	0.6148	0.0113
Kelch repeat and BTB domain-containing protein 10	11	0.8272	0.0017	0.8917	0.0002	0.654	0.0291	0.7848	0.0042
L-lactate dehydrogenase A chain	17	0.8993	< 0.0001	0.8345	< 0.0001	0.8855	< 0.0001	0.7475	0.0006
L-lactate dehydrogenase B chain	17	0.9087	< 0.0001	0.9049	< 0.0001	0.9093	< 0.0001	0.7527	0.0005
Malate dehydrogenase, cytoplasmic	17	0.8725	< 0.0001	0.8736	< 0.0001	0.8126	< 0.0001	0.7587	0.0004
Myoglobin	17	0.9591	< 0.0001	0.8478	< 0.0001	0.8598	< 0.0001	0.8432	< 0.0001
Nucleoside diphosphate kinase B	16	0.6087	0.0123	0.5412	0.0304	0.5321	0.0339	0.6266	0.0094
Peroxiredoxin-1	16	0.7574	0.0007	0.8188	0.0001	0.606	0.0128	0.6381	0.0078
Peroxiredoxin-6	17	0.7769	0.0002	0.8336	< 0.0001	0.6398	0.0057	0.7938	0.0001
Phosphatidylethanolamine-binding protein 1	17	0.6793	0.0027	0.8389	< 0.0001	0.5093	0.0368	0.772	0.0003
Phosphoglucomutase-1	17	0.9305	< 0.0001	0.8994	< 0.0001	0.9064	< 0.0001	0.766	0.0003
Phosphoglycerate kinase 1	17	0.8862	< 0.0001	0.7583	0.0004	0.8911	< 0.0001	0.692	0.0021
Phosphoglycerate mutase 1	17	0.9382	< 0.0001	0.793	0.0001	0.8928	< 0.0001	0.7542	0.0005
Phosphoglycerate mutase 2	17	0.8786	< 0.0001	0.8199	< 0.0001	0.7981	0.0001	0.7389	0.0007
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform	16	0.7209	0.0016	0.7123	0.002	0.747	0.0009	0.6795	0.0038
Plectin	14	0.8408	0.0002	0.8485	0.0001	0.7679	0.0013	0.8783	< 0.0001
POTE ankyrin domain family member E	17	0.817	< 0.0001	0.6836	0.0025	0.8034	0.0001	0.5525	0.0214

Protein DJ-1	17	0.7644	0.0004	0.8162	< 0.0001	0.6547	0.0043	0.7458	0.0006
Purine nucleoside phosphorylase	10	0.8797	0.0008	0.8968	0.0004	0.8421	0.0022	0.8102	0.0045
Pyruvate kinase isozymes M1/M2	17	0.9188	< 0.0001	0.8613	< 0.0001	0.8557	< 0.0001	0.7671	0.0003
SH3 domain-binding glutamic acid-rich protein	15	0.8178	0.0002	0.835	0.0001	0.7784	0.0006	0.7178	0.0057
Superoxide dismutase [Cu-Zn]	15	0.9208	< 0.0001	0.7539	0.0012	0.946	< 0.0001	0.6532	0.0083
Thioredoxin	8	0.9148	0.0014	0.9314	0.0008	0.7154	0.046	0.8252	0.0062
Triosephosphate isomerase	17	0.9635	< 0.0001	0.8843	< 0.0001	0.911	< 0.0001	0.7943	0.0001
Tubulin alpha-4A chain	14	0.7285	0.0031	0.7604	0.0016	0.6237	0.0171	0.5571	0.0385
Ubiquitin-like modifier-activating enzyme 1	17	0.8794	< 0.0001	0.7779	0.0002	0.8234	< 0.0001	0.7306	0.0009
UTP--glucose-1-phosphate uridylyltransferase	16	0.7929	0.0002	0.8207	< 0.0001	0.6938	0.0029	0.7882	0.0003
Vinculin	16	0.8305	< 0.0001	0.9087	< 0.0001	0.6938	0.0029	0.7508	0.0008
<b>Mitochondrion</b>									
2-oxoglutarate dehydrogenase, mitochondrial	17	0.8593	< 0.0001	0.8676	< 0.0001	0.8579	< 0.0001	0.7298	0.0009
60 kDa heat shock protein, mitochondrial	16	0.8311	< 0.0001	0.7926	0.0003	0.6971	0.0027	0.6656	0.0049
Acetyl-CoA acetyltransferase, mitochondrial	17	0.6441	0.0053	0.7329	0.0008	0.6341	0.0063	0.6834	0.0025
Aconitate hydratase, mitochondrial	17	0.8108	< 0.0001	0.7116	0.0014	0.7616	0.0004	0.6818	0.0026
Aspartate aminotransferase, mitochondrial	17	0.8987	< 0.0001	0.8613	< 0.0001	0.794	0.0001	0.8102	< 0.0001
ATP synthase subunit alpha, mitochondrial	17	0.8629	< 0.0001	0.8161	< 0.0001	0.8001	0.0001	0.7608	0.0004
ATP synthase subunit b, mitochondrial	14	0.6518	0.0115	0.82	0.0003	0.5744	0.0317	0.7538	0.0018
ATP synthase subunit beta, mitochondrial	17	0.8801	< 0.0001	0.8316	< 0.0001	0.7746	0.0003	0.7929	0.0001
Citrate synthase, mitochondrial	16	0.6703	0.0045	0.5543	0.0259	0.6781	0.0039	0.5347	0.0329
Creatine kinase S-type, mitochondrial	17	0.841	< 0.0001	0.7516	0.0005	0.7919	0.0002	0.7073	0.0015
Cytochrome c	8	0.8521	0.0072	0.7709	0.0251	0.8298	0.0108	0.6644	0.0361
Dihydropyridol dehydrogenase, mitochondrial	16	0.9037	< 0.0001	0.775	0.0004	0.9481	< 0.0001	0.7273	0.0014
Enoyl-CoA hydratase, mitochondrial	16	0.8553	< 0.0001	0.7808	0.0004	0.8303	< 0.0001	0.6966	0.0027
ES1 protein homolog, mitochondrial	14	0.7316	0.0029	0.6684	0.009	0.573	0.0322	0.6557	0.0109
Fumarate hydratase, mitochondrial	17	0.861	< 0.0001	0.8126	< 0.0001	0.8545	< 0.0001	0.6702	0.0032
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	17	0.4947	0.0435	0.6665	0.0035	0.4833	0.0494	0.5623	0.0188
Isocitrate dehydrogenase [NADP], mitochondrial	16	0.7448	0.0009	0.837	< 0.0001	0.5366	0.0321	0.7845	0.0003
Malate dehydrogenase, mitochondrial	17	0.86	< 0.0001	0.7719	0.0003	0.8115	< 0.0001	0.7559	0.0004
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	17	0.8366	< 0.0001	0.7021	0.0017	0.8061	< 0.0001	0.6954	0.0019
Superoxide dismutase [Mn], mitochondrial	17	0.8146	< 0.0001	0.8644	< 0.0001	0.771	0.0003	0.7528	0.0005
Thioredoxin-dependent peroxide reductase, mitochondrial	16	0.7835	0.0003	0.6068	0.0127	0.7745	0.0004	0.5935	0.0154
Ubiquinone biosynthesis protein COQ9, mitochondrial	16	0.7608	0.0006	0.7537	0.0007	0.647	0.0067	0.6905	0.0031
<b>Endoplasmic Reticulum</b>									
Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	17	0.9513	< 0.0001	0.9053	< 0.0001	0.9071	< 0.0001	0.7687	0.0003
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	17	0.9015	< 0.0001	0.9358	< 0.0001	0.8461	< 0.0001	0.851	< 0.0001
<b>Nucleus</b>									
PWWP domain-containing protein MUM1	6	0.9101	0.0118	0.9284	0.0075	0.8876	0.0182	0.8983	0.0383