Spot Number	Accession Number (GI)	Mascot Score	Molecular Weight	Protein Name	Change-Novel	Change-Habituated	Mitochondria	Biosynthesis Process	Energy Metabolism
1023	211235	483	42080	• Creatine kinase, brain	▲▲		+	+	
942	211235	273	44414	• Creatine kinase, brain	▲▲		+	+	
649	60592998	350	56150	• 3-Oxoacid CoA transferase 1	▲▲		+	+	
646	60592998	420	56150	• 3-Oxoacid CoA transferase 1	▲		+	+	
1112	226855	404	38624	• Aldolase C	▲▲		+	+	
1085	226855	356	38624	• Aldolase C	▲		+	+	
1300	50754481	137	37360	Pyruvate dehydrogenase (lipoamide) beta	▲		+	+	
691	8163560	775	55015	Vacuolar ATP synthase subunit B	▽▽		+		+
1487	45382251	125	26184	Ubiquitin carboxyl-terminal esterase L3	▽▽				
808	45384010	284	41738	Actin, gamma-enteric smooth muscle	▽▽				
974	45382927	534	42080	Actin, beta	▽				
1450	3851612	118	33374	Succinate dehydrogenase Ip subunit	▽▽	▽	+		+
854	118098116	81	57258	4-Aminobutyrate aminotransferase	▽	▽▽	+	+	
696	45383566	565	60263	• ATP synthase subunit alpha	▽▽	▽	+		+
690	45383566	395	42262	• ATP synthase subunit alpha	▽▽	▽▽	+		+
1574	118093103	163	28017	• similar to Prdx3 protein	▽	▽▽	+		
1571	118093103	209	28304	• similar to Prdx3 protein		▲▲	+		
1185	50753625	66	24394	similar to Neuronal calcium binding protein 2		▲▲			
654	60592998	316	56150	• 3-Oxoacid CoA transferase 1		▽▽	+	+	
331	119331078	508	77697	Dynamin 1-like		▽▽	+		
1156	57529654	206	37053	Aldo-keto reductase family 1, member A1		▽▽		+	
348	57529753	751	79526	NADH-ubiquinone oxidoreductase, 75 kDa		▽▽	+		+
922	46048768	282	47617	Alpha-enolase		▽		+	
1254	71895681	133	36714	Electron transfer flavoprotein alpha polypept		▽	+		

Table S5. Annotated protein spots from DIGE experiment, identified by MS/MS sequencing (*Supporting Information*). Triangles (black up, white down) point direction of change relative to Silence (two triangles = $p < .05$; one = $p < 0.1$). Plusses (+) indicate GO terms from annotation of orthologous chicken proteins. Bullets (•) indicate same protein detected in multiple spots.