Supplemental table 1. Overview of proteins that were significantly increased or decreased in the hyperinsulinemic (INS) or prediabetic (IGT) groups of mice, as compared with the normal glucose tolerant control mice. Upon 2-DIGE analysis, proteins were identified by mass spectrometry as described in Materials and Methods. Membrane-associated proteins are highlighted.

spot	Protein Name	FOLD CHANGE		
		NGT	**INS**	**IGT**
s2201	**polymerase I and transcript release factor**	1.00	0.59	2.12
s2632	EH domain-containing protein 2	1.00	0.77	2.01
s2640	EH domain-containing protein 2	1.00	0.72	1.98
s2448	Astrotactin 1	1.00	0.87	1.95
s2197	**polymerase I and transcript release factor**	1.00	0.59	1.75
s2244	delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase	1.00	1.10	1.73
s2189	**polymerase I and transcript release factor**	1.00	0.73	1.71
s2254	estradiol 17-beta-dehydrogenase 8	1.00	1.22	1.60
s2613	E3 ubiquitin-protein ligase TTC3	1.00	0.99	1.55
s1906	Short-chain acyl-CoA dehydrogenase, mitochondrial	1.00	1.22	1.54
s1709	adenosine kinase	1.00	0.99	1.52
s1166	Heat shock protein 8	1.00	0.91	1.52
s1513	ATP synthase subunit beta,	1.00	0.89	1.50
s2479	annexin A1	1.00	1.23	1.49
s1177	albumin precursor	1.00	1.11	1.49
s1112	Heat shock protein 8	1.00	0.99	1.47
s1521	aldehyde dehydrogenase, mitochondrial precursor	1.00	1.17	1.47
s2191	**polymerase I and transcript release factor**	1.00	0.58	1.47
s1649	cytochrome b-c1 complex subunit 1, mitochondrial	1.00	0.96	1.46
s1309	Serpin1a	1.00	0.96	1.46
s1353	vitamin D-binding protein	1.00	1.10	1.45
s1759	gamma-actin	1.00	0.99	1.42
s1527	aldehyde dehydrogenase, mitochondrial precursor	1.00	1.09	1.42
s1377	protein disulfide-isomerase A3 precursor	1.00	1.08	1.40
s1173	albumin precursor	1.00	0.97	1.40
s1171	albumin precursor	1.00	1.03	1.40
s2051	alpha-2-macroglobulin precursor	1.00	1.20	1.39
s2050	albumin precursor	1.00	1.08	1.39
s1298	Protein phosphatase 2 (formerly 2A), regulatory subunit	1.00	1.20	1.39
s1085	propionyl CoA-carboxylase alpha-subunit	1.00	1.16	1.38
s717	albumin precursor	1.00	1.12	1.38
s1480	selenium-binding protein	1.00	1.13	1.37
s1168	albumin precursor	1.00	1.12	1.36
s1503	dihydrolipoyllysine-residue succinyltransferase	1.00	1.11	1.33
s1745	vimentin	1.00	0.91	1.33
s2031	pyridoxal kinase	1.00	1.04	1.29
s2307	serum amyloid P-component precursor	1.00	1.82	1.29
s2357	guanidinoacetate N-methyltransferase	1.00	0.92	1.28
s2056	guanine nucleotide binding protein, beta 1	1.00	1.06	1.25
s1482	selenium-binding protein 1	1.00	0.93	1.24
s2445	apolipoprotein A-I	1.00	2.37	1.24
s1951	trans-1,2-dihydrobenzene-1,2-diol dehydrogenase	1.00	1.13	1.23
s1174	Heat shock protein 8	1.00	0.94	1.22
s1472	selenium-binding protein 1	1.00	1.06	1.20
s2139	**polymerase I and transcript release factor**	1.00	0.66	1.20
s2131	**polymerase I and transcript release factor**	1.00	0.67	1.19

s1481	selenium-binding protein 1	1.00	0.91	1.19
s2495	peroxiredoxin-2	1.00	0.88	1.18
s561	vinculin	1.00	0.81	1.17
s2143	**polymerase I and transcript release factor**	1.00	0.64	1.17
s1895	vimentin	1.00	0.65	1.17
s1558	aldehyde dehydrogenase	1.00	3.01	1.16
s1103	78 kDa glucose-regulated protein precursor	1.00	0.81	1.13
s2321	**polymerase I and transcript release factor**	1.00	0.98	1.13
s2145	**polymerase I and transcript release factor**	1.00	0.67	1.13
s2212	Electron transferring flavoprotein, alpha polypeptide	1.00	0.92	1.13
s2339	proteasome activator complex subunit 1	1.00	1.75	1.13
s1332	epoxide hydrolase 2	1.00	0.86	1.13
s1962	Cavin-3	1.00	0.80	1.12
s2352	proteasome subunit alpha type-5	1.00	1.42	1.11
s2070	**polymerase I and transcript release factor**	1.00	0.60	1.10
s1896	aldehyde dehydrogenase 2	1.00	1.29	1.10
s2207	Gamma-actin	1.00	1.79	1.07
s1835	septin-2 b	1.00	0.70	1.04
s2063	Serpina1a	1.00	1.69	1.01
s1711	beta-centractin	1.00	0.87	1.01
s2373	immunoglobulin light chain variable region	1.00	0.55	1.00
s1108	78 kDa glucose-regulated protein precursor	1.00	0.74	0.96
s2161	annexin A6 isoform a	1.00	1.73	0.94
s2369	immunoglobulin kappa light chain variable region	1.00	1.59	0.93
s1421	Aldehyde dehydrogenase 3 family, member B1	1.00	1.64	0.93
s2002	Cavin-3	1.00	0.80	0.92
s2519	**polymerase I and transcript release factor**	1.00	2.55	0.87
s963	albumin precursor	1.00	1.31	0.86
s1458	Serpina1a	1.00	1.36	0.84
s2168	annexin A5	1.00	1.34	0.84
s1575	ribonuclease inhibitor isoform a	1.00	1.21	0.84
s1495	Serpina1a	1.00	1.41	0.79
s960	albumin precursor	1.00	1.17	0.79
s2773	Ferritin light chain 1	1.00	1.14	0.79
s2378	HIRA-interacting protein (HIRIP5)	1.00	1.56	0.79
s1765	BiP	1.00	2.46	0.77
s1486	Serpina1a	1.00	1.53	0.77
s1511	Serpina1c	1.00	1.42	0.75
s2393	peroxiredoxin-6	1.00	0.67	0.75
s1528	Serpina1a	1.00	1.44	0.74
s2768	ferritin heavy chain	1.00	1.22	0.73
s2126	annexin A6	1.00	1.05	0.72
s1388	protein disulfide-isomerase A3 precursor	1.00	1.33	0.70
s2180	annexin A5	1.00	1.87	0.69
s1903	haptoglobin precursor	1.00	0.57	0.60

Supplemental table 2. Mean log standardized abundance values (LSA) ± SEM for the PTRF isoforms found in the 2D-DIGE analysis. The zero value for LSA corresponds to the internal standard as described in material and methods.

spot	**Protein Name**	**NGT** (LSA)	INS (LSA)	**IGT** (LSA)
s2321	polymerase I and transcript release factor	-0.003 ± 0.026	-0.013 ± 0.025	0.052 ± 0.02
s2145	polymerase I and transcript release factor	0.009 ± 0.072	-0.164 ± 0.057	0.062 ± 0.05
s2143	polymerase I and transcript release factor	-0.006 ± 0.054	-0.197 ± 0.052	0.064 ± 0.064
s2070	polymerase I and transcript release factor	0.025 ± 0.063	-0.2 ± 0.083	0.066 ± 0.046
s2139	polymerase I and transcript release factor	0.003 ± 0.045	-0.178 ± 0.052	0.082 ± 0.058
s2131	polymerase I and transcript release factor	0.024 ± 0.034	-0.152 ± 0.064	0.1 ± 0.073
s2197	polymerase I and transcript release factor	-0.128 ± 0.085	-0.36 ± 0.104	0.114 ± 0.081
s2191	polymerase I and transcript release factor	-0.025 ± 0.054	-0.264 ± 0.081	0.141 ± 0.093
s2189	polymerase I and transcript release factor	-0.084 ± 0.076	-0.219 ± 0.068	0.149 ± 0.084
s2201	polymerase I and transcript release factor	-0.13 ± 0.112	-0.363 ± 0.115	0.197 ± 0.106
s2519	polymerase I and transcript release factor	-0.166 ± 0.033	0.241 ± 0.115	-0.227 ± 0.015

Supplemental Figure 1. Two day confluent 3T3-L1 cells stably overexpressing PTRF (PTRF cells) or the empty vector (CONTROL) were differentiated into adipocytes, harvested at different time points, and then analyzed with propidium iodide staining to assess cell cycle distribution by FACS analysis. Results are expressed as mean ± SEM of two independent experiments.