

Supplementary data Table 1. Protein spots identified by MALDI-TOF / MS.

Spot ID	Accession Number	Protein Name	Score	Matched Peptide	Sequence Coverage	Theoretical MW/PI	Ratio
Cell growth and proliferation							
65	gi 55562869	translationally-controlled tumor protein	58	8	30%	19450/4.76	∞
26	gi 300797951	mago-nashi homolog B	65	9	48%	23381/8.35	11.64
22	gi 543829	adenine phosphoribosyl-transferase (APRT)	101	9	42%	19533/6.17	5.78
21	gi 46485421	bis(5'-nucleosyl)-tetraphosphatase	61	8	71%	16919/5.35	3.09
49	gi 150383503	UMP-CMP kinase	107	12	47%	22155/5.66	0.47
51	gi 13929006	RAB2A, member RAS oncogene family	63	8	48%	23521/6.08	0.42
56	gi 209364558	centrosomal protein 290	62	29	13%	289504/5.91	0
Energy metabolism							
59	gi 1083805	sterol esterase (EC 3.1.1.13) precursor	144	16	30%	67027/5.31	∞
68	gi 51858584	solute carrier family 27 (fatty acid transporter), member 2	63	15	33%	70650/8.82	∞
70	gi 293357526	PREDICTED: amylase 2a5, pancreatic	70	6	59%	11933/9.64	∞
73	gi 61556993	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	60	8	22%	47840/8.33	∞
18	gi 6978515	apolipoprotein A-I	130	16	50%	30043/5.52	3.59
44	gi 11560131	dimethylarginine dimethylaminohydrolase 1	144	21	44%	31805/5.75	0.49
36	gi 25990263	mitochondrial aldehyde dehydrogenase	161	19	40%	53809/5.70	0.47
43	gi 6981112	isovaleryl Coenzyme A dehydrogenase	142	22	33%	46862/8.03	0.46
45	gi 15100179	malate dehydrogenase 1, NAD (soluble)	73	12	35%	36631/6.16	0.46
34	gi 149063967	phosphoenolpyruvate carboxykinase 2	153	30	45%	67708/7.89	0.45
33	gi 57528264	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	227	34	41%	79564/6.66	0.34
50	gi 157786894	pyrroline-5-carboxylate reductase 1	134	23	46%	32206/6.36	0.34
31	gi 62654757	similar to methylmalonyl-CoA mutase, mitochondrial precursor	126	24	32%	91977/7.59	0.32
32	gi 129684	propionyl-CoA carboxylase alpha chain, mitochondrial precursor	200	28	34%	78289/6.33	0.3
40	gi 13591949	glycine amidinotransferase	99	19	35%	48724/7.17	0.26
41	gi 13591949	glycine amidinotransferase	153	27	42%	48724/7.17	0.26
35	gi 148747576	asparagine synthetase	222	29	44%	64776/6.01	0.18
Gene expression and protein modification							
71	gi 109458729	PREDICTED: liprin-alpha-3	61	20	16%	149841/5.95	∞
72	gi 149018901	zic family member 4, isoform CRA_a	70	9	85%	7787/10.69	∞
75	gi 55391508	albumin	89	14	22%	68714/6.09	∞
23	gi 149048541	carboxypeptidase B1, isoform CRA_b	61	12	39%	43653/5.50	15.35
24	gi 149068328	importin 7 (predicted), isoform CRA_e	50	10	32%	42425/6.80	9.56
46	gi 16758848	endoplasmic reticulum protein 29	114	12	48%	28614/6.23	0.47

37	gi 8393693	laminin receptor 1	96	15	42%	32917/4.80	0.41
52	gi 51172600	ubiquitin-fold modifier conjugating enzyme 1	105	11	55%	19651/6.90	0.41
42	gi 72255515	serine (or cysteine) proteinase inhibitor, clade B, member 1a	182	26	49%	42700/5.92	0.21
53	gi 8393322	protein disulfide isomerase associated 3	247	27	49%	57010/5.88	0
54	gi 9506571	eukaryotic translation initiation factor 2, subunit 1 alpha	234	28	53%	36371/5.02	0
55	gi 8394221	ribosomal protein S3a	143	22	51%	30154/9.75	0
58	gi 9507019	sec1 family domain containing 1	216	33	48%	72559/6.09	0

Stress and inflammation

60	gi 529586	fibrinogen B-beta-chain	79	11	33%	33926/8.06	∞
61	gi 16757980	orosomucoid 1	87	7	25%	23560/5.64	∞
62	gi 33086640	Ba1-647	67	10	26%	42447/6.11	∞
63	gi 71830	fibrinogen gamma-B chain precursor	79	11	30%	50468/5.56	∞
15	gi 33086640	Ba1-647	72	10	20%	42447/6.11	12.31
17	gi 71830	fibrinogen gamma-B chain precursor	79	13	37%	50468/5.56	6.34
19	gi 33086640	Ba1-647	73	12	24%	42447/6.11	3.88
16	gi 29028310	platelet-activating factor acetylhydrolase II	62	8	25%	43464/6.23	3.1
14	gi 51259324	fibrinogen gamma chain	93	16	33%	49620/5.85	2.88
28	gi 70794740	interleukin-1 receptor-associated kinase 2	56	15	25%	69193/5.97	2.49
48	gi 11968132	peroxiredoxin 3	75	9	40%	28589/7.14	0.43
47	gi 16758274	peroxiredoxin 4	123	11	39%	30988/6.18	0.42
39	gi 149069193	similar to Glutathione S-transferase A1	69	5	87%	7280/6.08	0.41

Etc

64	gi 293357925	PREDICTED: ATP/GTP binding protein-like 2	56	20	27%	102305/8.77	∞
66	gi 149029060	rCG41048, isoform CRA_a	75	45	13%	440273/5.00	∞
67	gi 33086658	Cc1-6	59	8	25%	43052/8.46	∞
69	gi 149025754	rCG28529, isoform CRA_b	86	10	26%	57093/7.92	∞
74	gi 149066873	nucleoporin 107, isoform CRA_a	62	17	17%	1006809/5.31	∞
30	gi 157817027	coiled-coil-helix-coiled-coil-helix domain containing 3	46	15	31%	42141/9.42	8.6
27	gi 293354252	PREDICTED: FSHD region gene 1	44	7	32%	20183/6.24	7.22
29	gi 149041991	rCG58343	62	13	34%	55697/9.88	5.26
13	gi 38181879	Clu protein	64	8	26%	51431/5.53	3.42
20	gi 1487990	Ott	59	7	29%	26968/11.98	3.4
11	gi 58865656	lymphocyte cytosolic protein 1	90	14	34%	70078/5.15	3.03
12	gi 33086660	Cc1-8	105	20	22%	107343/8.35	2.59
25	gi 149044856	spectrin beta 2, isoform CRA_a	55	28	15%	273893/5.41	2.32
38	gi 84781638	ectoderm-neural cortex protein 2	64	13	21%	65798/6.32	0.26
57	gi 149052721	rCG33997	56	6	88%	4682/9.35	0

∞ : protein spots newly introduced in the PPX 2-DE gel.

Supplementary data Table 2. Genes reproducibly up-regulated or down-regulated by partial pancreatectomy.

A. Up-regulated genes

Gene / Protein	Target of Assay	ACCESS NO.	REFERENCE
actin related protein homolog	protein / mRNA	gi 34879484, NM_016860	[1], [2]
ADP-ribosylation factor	Protein / mRNA	P41276, BG142914	[2], [3]
albumin	Protein	gi 19705431, gi 55391508	[1], [*]
amyloid beta precursor like protein	mRNA	NM_009691, XM_001055798	[2], [4]
apolipoprotein A-I	Protein	gi 55747, gi 6978515	[1], [*]
cytokeratin 8	protein / mRNA	gi 203734	[1], [4]
fibrinogen gamma chain precursor	Protein	gi 1346007, gi 71830	[1], [*]
lymphocyte cytosolic protein 1	Protein	gi 34875362, gi 58865656	[1], [*]
MAPK1	Protein	gi 1942172, 204052	[1], [3]
<i>Reg3</i>	mRNA	NM_0011036, NM_0011260, NM_013893, NM_172077	[2], [4]
serine proteinase inhibitor	protein / mRNA	gi 55824765, gi 34935459, gi 34875374, NM_025429	[1], [2]
sterol esterase	Protein	311386, gi 1083805	[3], [*]
translationally-controlled tumor protein	protein / mRNA	NM_009429, gi 55562869	[2], [*]
x-box binding protein 1	mRNA	NM_013842, NM_001004210	[2], [4]

B. Down-regulated genes

Gene / Protein	Target of Assay	ACCESS NO.	REFERENCE
L-arginine: glycine amidinotransferase	Protein	gi 13591949	[1], [*]
isovaleryl coenzyme A dehydrogenase	Protein	gi 6981112	[1], [*]
phosphoenolpyruvate carboxykinase 2	Protein	gi 34874156, gi 149063967	[1], [*]

[1] Yang et al; [2] De Leon et al; [3] Shin et al; [4] Choi et al; [*] Present study

Supplementary data Table 3. Summary of the five omic studies on partial pancreatectomy.

Study	Animal	Mode of Partial Pancreatectomy	Sampling Time	Analytical Method	Protein/Gene Identification
Yang et al. (Ref. 17)	Wistar rats; 150~160g	90%	72 hrs	2-DE/MS and mass fingerprinting analyses.	91 spots with at least 1.5-fold change in the expression (41 up-regulated spots and 50 down-regulated spots) were selected and 53 proteins were identified and listed.
De Leon et al. (Ref. 18)	BALB/c mice; 8~9 week old male	~50% and exendin-4 treatment	12, 24 and 48 hrs	cDNA Microarray (PancChip4.0)	The expressions of about 10,000 pancreas-enriched mRNA were identified. Listed 100 genes differentially expressed at 24 hrs after operation and 38 genes at 48 hrs after operation.
Shin et al. (Ref. 19)	Wistar-Kyoto rats; 5 weeks old	60%	48 hrs	2-DE and MALDI-TOF/MS analyses	137 spots with significant ($p < 0.05$) change in the expression (76 up-regulated spots and 61 down-regulated spots) were selected and 121 proteins were identified. Listed 64 identified proteins.
Choi et al. (Ref. 20)	Sprague-Dawley rats; 8 week old male;	60%	48 hrs	cDNA subtractive hybridization	418 cDNA clones were checked with restriction enzyme and 95 clones were selected for DNA sequencing. Identified 12 genes up-regulated after operation.
Present study	Sprague-Dawley rats; 8 week old male;	60%	48 hrs	2-DE and MALDI-TOF analyses	65 spots with at least 2-fold change in the expression (37 up-regulated spots and 28 down-regulated spots) were selected and 61 proteins were identified and listed.

Supplementary data Table 4. Novel genes or proteins identified from five different omics studies on partial pancreatectomy.

Study	Novel Genes or Protein identified
De Leon et al (Ref. 18)	Gene transcript : Barstead stromal cell line MPLRB8 (CV677934), Ko mouse embryo 11 5dpc (AA387288), Melton Mouse E16 5 Pancreas Library 2 M16B2 (BG141869), Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 (BI677082, BI677037, BI963673, BI901383, BI440178, BI963629, BI962378), Mitochondrial fission factor (NM_029409), Mus musculus adult male tongue (AK009749, AK049931), NIH_MGC_140 Mus musculus cDNA clone (CF586721, CF586560), RNA binding motif protein 26 (NM_134077), Soares mouse NML Mus musculus (AA237895), Soares_thymus_2NbMT (AA204455), Stratagene mouse heart (#937316) Mus musculus cDNA clone (CV700478), Sugano mouse kidney mkia (AI182303, AI315959), von Willebrand factor A domain containing 5A (NM_172767)
Shin et al (Ref. 19)	Protein : 30S ribosomal protein S19 (gi 133850), GPN-loop GTPase 2 (gi 19527098), Suppressor of IKBKE 1 (gi 13385140), Unnamed protein product (gi 12835985, gi 12853241)
Choi et al (Ref. 20)	Gene transcript : Exostoses 1 (XM_216920), LOC502894 (NM_001025064)
Present study	Protein : Coiled-coil-helix-coiled-coil-helix domain containing 3 (gi 157817027), FSHD region gene 1 (gi 293354252), rCG28529 (gi 149025754), rCG33997 (gi 149052721), rCG41048 (gi 149029060), rCG58343 (gi 149041991)

Note : Novel proteins were not identified from Yang et al. (Ref. 17) other than the reproducibly regulated proteins that are listed in Supplementary data Table 2.