

Supplemental Table 1. List of the differentially expressed genes in GK rat liver after treatment with 0.05% pyroglutamic acid compared to control diet.

Probe Set ID	Functional Category ¹	Gene Title	Gene Symbol	Fold change ²
10912908	Genetic Information Processing; Folding, Sorting and Degradation/Environmental Information Processing; Signal Transduction; Jak-STAT	cytokine inducible SH2-containing protein	Cish	7.91
10860900	Metabolism; Enzyme Families; Protein kinases	pyruvate dehydrogenase kinase, isozyme 4	Pdk4	3.90
10785326		solute carrier family 25, member 30	Slc25a30	3.34
10894812		ankyrin repeat and sterile alpha motif domain containing	Anks1b	2.76
10779309		Spetex-2E protein	Spetex-2E	2.57
10927472	Metabolism; Glycan Biosynthesis and Metabolism; Glycosyltransferases (other)	mannosyl (alpha-1,3)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	Mgat4a	2.09
10742940	Environmental Information Processing; Signaling Molecules and	olfactory receptor 1425	Olr1425	2.08
10878787	Metabolism; Lipid Metabolism; Fatty acid metabolism (other)	cytochrome P450, family 4, subfamily a, polypeptide 3	Cyp4a3	2.02
10878780	Metabolism; Lipid Metabolism; Fatty acid metabolism (other)	cytochrome P450, family 4, subfamily a, polypeptide 2	Cyp4a2	2.01
10745782	Metabolism; Glycan Biosynthesis and Metabolism; Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	phosphatidylinositol glycan anchor biosynthesis, class W	Pigw	0.50
10904189	Metabolism; Glycan Biosynthesis and Metabolism; Glycosyltransferases (other)	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	St3gal1	0.50
10932917	Metabolism; Carbohydrate Metabolism; Fructose and mannose metabolism	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	Pfkfb1	0.50
10901166	Organismal Systems; Endocrine System; PPAR signaling pathway	angiopoietin-like 4	Angptl4	0.50
10762426		harakiri, BCL2 interacting protein (contains only BH3 domain)	Hrk	0.49
10832197		SNF1-like kinase	Snf1lk	0.49
10931475		feminization 1 homolog a (C. elegans)	Fem1a	0.49
10832772	Genetic Information Processing; Folding, Sorting and Degradation; Ubiquitin system /Environmental Information Processing; Genetic Information Processing; Transcription; Transcription factors/ Environmental Information Processing; Signaling Molecules and Interaction; Receptors and channels	Rho-related BTB domain containing 1	Rhobtb1	0.49
10765517		nuclear receptor subfamily 1, group I, member 3	Nr1i3	0.48
10822080		similar to 60S ribosomal protein L7a	RGD1566229	0.48
10738399	Metabolism; Carbohydrate Metabolism; Glycolysis / Gluconeogenesis (other)	glucose-6-phosphatase, catalytic subunit	G6pc	0.47
10907542	Metabolism; Metabolism of Other Amino Acids; Taurine and hypotaurine metabolism	cysteine sulfenic acid decarboxylase	Csad	0.47
10908543		dedicator of cytokinesis 6	Dock6	0.47
10771492		similar to GPI-gamma 4; GPIgamma4	RGD1562220	0.46
10812881		similar to 60S ribosomal protein L17 (L23) (Amino acid starvation-induced protein) (ASI)	LOC499522	0.45
10769361	Metabolism; Xenobiotics Biodegradation and Metabolism; Drug metabolism - cytochrome P450	flavin containing monooxygenase 1	Fmo1	0.45
10720555		similar to DNA-directed RNA polymerase II largest subunit (RPB1)	LOC688574	0.43

10917116	Genetic Information Processing; Folding, Sorting and Degradation;	zinc finger and BTB domain containing 16	Zbtb16	0.43
10815317	Organismal Systems; Endocrine System; Insulin signaling pathway / Genetic Information Processing; Transcription; Transcription factors	forkhead box O1	Foxo1	0.42
10751931	Environmental Information Processing; Signaling Molecules and Interaction; Glycan binding proteins	B-cell CLL/lymphoma 6	Bcl6	0.40
10857626	Environmental Information Processing; Signaling Molecules and	ER degradation enhancer, mannosidase alpha-like 1	Edem1	0.40
10729847	Organismal Systems; Endocrine System; Insulin signaling pathway	protein phosphatase 1, regulatory (inhibitor) subunit 3C	Ppp1r3c	0.39
10778254	Metabolism; Carbohydrate Metabolism; Glycolysis / Gluconeogenesis (other)	glucokinase	Gck	0.39
10723822	Metabolism; Glycan Biosynthesis and Metabolism;	tsukushin	Tsku	0.37
10889269	lipin 1		Lpin1	0.36
10877935	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3		Mllt3	0.34
10733310	Genetic Information Processing; Transcription; Transcription factors	zinc finger protein 354A	Zfp354a	0.30
10875324	Metabolism; Lipid Metabolism; Primary bile acid biosynthesis (other)	cytochrome P450, family 7, subfamily a, polypeptide 1	Cyp7a1	0.24
10815281		CCR4 carbon catabolite repression 4-like (S. cerevisiae) Ccrn4l		0.18

Values are means, n=3 independent experiments. ¹ The classification of category was performed using Kyoto Encyclopedia of Genes and Genomes (KEGG) database. ² Relative value to control group.