

Table 3A. Microarray results of intestinal genes differentially upregulated, under glucose and fructose perfusion, between 20d and 10d old pups

Access number	symbol	name and function	20F vs 10F			20G vs 10G		
			Mean fold change	SE	F	Mean fold change	SE	F
Metabolism								
NM_012771	Lyz	lysozyme	4.60	4.60	5	3.60	2.04	4
NM_019370	LOC54410	alkaline phosphodiesterase	4.36	0.70	5	4.90	0.73	5
X59737	Ckmt1	creatine kinase, mitochondrial 1, ubiquitous	4.12	1.73	5	4.49	1.90	5
NM_012554	Eno1	enolase 1, alpha	2.81	1.21	5	2.60	1.44	5
M29853	Cyp4b1	cytochrome P450, subfamily 4B, polypeptide 1	2.58	1.92	4	4.57	2.21	5
X15800	Pkm2	pyruvate kinase, muscle	2.49	1.00	4	2.90	1.27	4
NM_012839	Cyca	cytochrome c, somatic	2.37	0.59	4	2.25	0.54	5
D38381	Cyp3a18	cytochrome P450, 3a18	2.35	0.61	4	2.29	0.42	5
M63662	rPAM-4 type	Peptidylglycine alpha-amidating monooxygenase	2.24	0.40	5	3.99	1.82	5
NM_017025	Ldha	lactate dehydrogenase A	2.12	0.25	5	2.33	0.40	5
NM_012570	Glud1	glutamate dehydrogenase 1	1.96	0.43	5	2.28	0.51	5
M31788	Pgk1	phosphoglycerate kinase 1	1.94	0.51	4	2.60	0.78	5
NM_017201	Ahcy	S-adenosylhomocysteine hydrolase	1.87	0.48	4	1.81	0.29	4
AB049189	St14	membrane bound arginine specific serine protease	1.74	0.19	4	2.39	0.72	4
NM_017005	Fh1	fumarate hydratase 1	1.69	0.26	4	1.94	0.55	5
S74321		cytochrome bc-1 complex core P	1.66	0.10	4	1.75	0.50	4
Nucleotide/DNA metabolism								
U90888	Ampd3	adenosine monophosphate deaminase 3	4.33	1.97	5	6.15	3.43	5
AJ000347	Bpnt1	3(2),5-bisphosphate nucleotidase	2.36	0.30	4	2.54	0.39	5
D85035	Dpyd	dihydropyrimidine dehydrogenase	1.94	0.37	4	1.75	0.34	4
Drug metabolism								
NM_012792	Fmo1	flavin containing monooxygenase 1	3.03	0.51	5	3.30	1.29	5
L19998	Sult1a1	sulfotransferase family 1A, phenol-preferring, member 1	2.81	2.22	5	2.98	1.49	5
NM_017272	Aldh1a4	aldehyde dehydrogenase family 1, subfamily A4	2.11	0.34	5	1.85	0.44	4
NM_013215	Afar	aflatoxin B1 aldehyde reductase	2.05	0.54	5	1.74	0.56	4
Signal transduction activity								
NM_031654	Rabggt1	Rab geranylgeranyl transferase, a subunit	2.11	0.63	5	1.73	0.37	4
NM_013106	Gnai3	guanine nucleotide binding protein, alpha inhibiting 3	1.97	0.34	4	2.34	0.53	5
Development/proliferation/differentiation								
AF161715	Nphs1	nephrin	3.31	1.79	5	2.94	1.35	4
U66461	Pin	dynein, cytoplasmic, light chain 1	3.06	1.050	5	4.04	1.18	5

L11995	Ccnb1	cyclin B1	2.84	0.93	5	3.07	0.62	5
M63665	Krt21	cytokeratin 21	2.72	0.98	4	2.34	0.79	4
AF007890	LOC246267	resection-induced TPI (rs11)	2.15	0.43	5	2.13	1.03	4
M64388	Olf41	olfactory receptor 41	2.14	0.24	4	2.09	0.40	5
U24174	Cdkn1a	cyclin-dependent kinase inhibitor 1A	1.99	0.32	4	2.00	0.59	4
AF031483	Hfb2	Hfb2 protein	1.65	0.12	4	1.67	0.53	4
Transport								
NM_013033	Slc5a1	sodium/glucose cotransporter (SGLT1)	2.61	0.48	5	2.68	0.31	4
NM_012653	Slc9a2	solute carrier family 9, member 2	2.39	0.38	5	2.93	0.60	5
U36992	Cyp7b1	cytochrome P450, subfamily 7B, polypeptide 1	2.15	0.57	5	2.27	0.19	5
D12771	Slc25a5	solute carrier family 25 member 5	2.03	0.4	4	1.69	0.50	5
AJ223355	Slc25a10	dicarboxylate transporter	1.99	0.50	5	2.08	0.34	5
J02627	Cyp2e1	cytochrome P450, subfamily 2E, polypeptide 1	1.87	0.12	5	2.16	0.47	5
AJ238278	Xpo1	exportin 1 (CRM1, yeast, homolog)	1.72	0.32	4	2.01	0.30	4
Translation								
AJ005161		Rattus rattus mRNA for mitochondrial translational elongation factor	1.82	0.41	4	2.18	0.66	5
J01877		ribosomal RNA	1.69	0.37	4	2.24	0.25	5
Hormone metabolism								
NM_017081	Hsd11b2	hydroxysteroid 11-beta dehydrogenase 2	3.69	2.24	5	3.84	1.35	5
S68284		progesterin receptor form B	2.28	0.97	5	3.62	2.44	5
NM_017363	Csh1	chorionic somatomammotropin hormone 1	1.92	0.42	4	2.25	0.91	4
U10188	Plk	polo-like kinase homolog (Drosophila)	1.88	0.37	4	2.19	0.76	4
Immunity/inflammation								
U32681	Dmbt1	ebnerin	3.42	1.57	5	3.90	1.45	5
AF120100		thiopurine S-methyltransferase	2.17	0.53	5	2.77	1.21	4
Unknown								
AF010434		Rattus norvegicus MARRLC9B mRNA, partial cds	3.86	3.57	5	4.55	3.70	5
U25148	Myh1	myosin, heavy polypeptide-like	3.24	0.75	5	4.05	0.87	5
AF156554	Myh1	myosin, heavy polypeptide-like	2.70	1.08	5	4.03	1.37	5
AF010437		Rattus norvegicus MARRLC2A mRNA, partial cds	2.24	1.06	4	2.22	0.91	4
NM_017187	Hmgb2	high mobility group box 2	2.09	0.30	4	2.29	1.41	5
K02598	Csn10	casein kappa	1.81	0.33	4	2.17	0.63	5
U12526		Ultraviolet B radiation-activated UV96 mRNA, partial sequence	1.72	0.28	4	2.01	0.59	5

Table 3A shows genes upregulated that changed by more than 1.5 fold and less than 5 fold in at least four of five samples under glucose or fructose perfusion mean \pm SE for each gene; $n = 5$ experiments. F = frequency. Values of the “20F vs 10F” column indicate the fold increase in the expression of a gene in 20 d old F-perfused compared with 10 d old F-perfused intestine. Values of the “20G vs 10G” column indicate the fold increase in the expression of a gene in 20 d old G-perfused compared with 10 d old G-perfused intestine.