

## **Supplemental tables**

**Table 1A.** Microarray results of intestinal genes differentially upregulated, under glucose perfusion only, between 20d and 10d old pups.

access number	symbol	name and function	Mean fold change 20G vs 10G	SE	Frequency
<b>Metabolism activity</b>					
M26854	Cyp2b15	cytochrome P450, 2b19	3.92	2.46	5
U39943	C5yp2J3	cytochrome P450 monooxygenase	2.73	1.00	5
M73714	Aldh3a2	aldehyde dehydrogenase family 3, subfamily A2	2.60	1.10	5
X81395	Ces1	carboxylesterase 1	2.44	0.75	4
M58364	Gch	GTP cyclohydrolase 1	2.38	1.26	4
M10149	Aldob	aldolase B	2.26	0.48	4
AF170918	Aldh9a1	aldehyde dehydrogenase family 9, subfamily A1	2.09	0.40	5
D10655	Dlat	dihydrolipoamide acetyltransferase	1.92	0.32	4
NM_017272	Aldh1a4	aldehyde dehydrogenase family 1, subfamily A4	1.85	0.44	5
AF106944	Prdx3	peroxiredoxin 3	1.85	0.34	4
NM_013052	Ywhah	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, polypeptide	1.64	0.33	5
U21662	Mgat2	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	1.61	0.21	4
<b>Transcription activity/transcription factor</b>					
NM_012864	Mmp7	matrix metalloproteinase 7	2.06	0.73	5
NM_017365	Pdlim1	PDZ and LIM domain 1	1.59	0.22	4
D83948	Rbm10	RNA binding motif protein 10	1.55	0.21	5
<b>Transporter activity</b>					
NM_017251	Gjb1	gap junction membrane channel protein beta 1	2.55	0.37	5
NM_017216	Slc3a1	neutral amino acid transporter, member 1	2.30	0.90	5
NM_012914	Atp2a3	ATPase, Ca <sup>++</sup> transporting, ubiquitous	2.10	0.76	5
U01344	Nat2	N-Acetyltransferase-2	1.86	0.27	4
NM_013034	Slc6a4	serotonin transporter	1.65	0.16	4
NM_017126	Fdx1	ferredoxin 1	1.64	0.27	4
NM_017326	Calm2	calmodulin 2	1.54	0.14	5
<b>Cell communication</b>					
NM_031971	Hspa1a	heat shock 70kD protein 1A	7.39	11.55	5
L08134	Sgp158	proline-rich glycoprotein (sgp158)	2.48	1.26	5

AF260258	Synj2bp	synaptojanin 2 binding protein	2.34	0.75	5
NM_013129	Il15	interleukin 15	2.33	0.66	5
Z11875	Muc	intestinal mucin peptide	2.27	0.59	5
AF281661	Ppp1r1b	protein phosphatase 1, regulatory (inhibitor) subunit 1B	2.22	1.53	4
NM_013222	Gfer	growth factor, erv1 -like	2.19	0.50	4
NM_019259	C1qbp	complement component 1, q subcomponent binding protein	1.94	0.27	5
U09583	Frk	src related tyrosine kinase	1.86	0.25	4
AB042887	Ramp1	receptor (calcitonin) activity modifying protein 1	1.86	0.35	4
NM_013012	Prkg2	protein kinase, cGMP- dependent, type II	1.83	0.31	5
U53922	Hsj2	DnaJ-like protein	1.77	0.39	5
AF035951		similar to KIFC1	1.75	0.21	5
AB010119	Tctex1	t-complex testis expressed 1	1.73	0.30	4
<b>Immune activity</b>					
AF068861	Defb2	beta defensin-2	6.55	3.63	5
AF115768		similar to Defensin 5 precursor (RD-5) (Enteric defensin)	5.22	3.87	5
<b>Unclassified</b>					
U36786	VN7	putative pheromone receptor VN7	1.97	0.50	4
S78734		similar to ribosomalprotein S24	1.74	0.25	4
NM_012609	Nfl	neurofibromatosis 1	1.59	0.34	4

Table 1A shows upregulated genes that changed by more than 1.5 fold in at least four of five samples and whose fold change is significant ( $P < 0.05$ ). Values are mean  $\pm$  SE for each gene;  $n = 5$  experiments. Values indicate the fold increase in the expression of a gene in 20d old G-perfused compared with 10d old G-perfused intestine