Table S1. Furukawa et al.

Table S1. Primers used for quantitative PCR

gene name		primer sequence (5' – 3')	amplicon size (bp)	accession number
g6pca.1	**F**	TTGTTTCAGGATTGGATGTATTG	131	NM_001003512
	R	GAAGCAGCAAAGCCACAG		
g6pca.2	**F**	CACACGGCTGCTCTCTTCT	89	NM_001163806
	R	GATAAGCAGTACGGGATGATG		
pck1	**F**	CAGTAAACACGGCTGAAGACAC	122	NM_214751
	R	CGGTTTTGATGCACTTGAGA		
pck2	**F**	TCTGGCAGAAGGAAACACA	116	NM_213192
	R	TCAATCCCTCACTCTCTCCTC		
glud1a	**F**	CACTTCTGATTTTCAAGAAAGGA	125	NM_212576
	R	CAAGGTTATACCGGTTGGCT		
glud1b	**F**	TGAGTGGCTGAAGAACCTGA	84	NM_199545
	R	ATCAGCAGGTGGTAGTTGGAG		
glsa	**F**	ATCAGCAGGTGGTAGTTGGAG	114	NM_001045044
	R	GGGCTGTAGGTGTTGTGATAG		
glsb	**F**	CTATAGGATGGAGACTGTTGGAGA	117	XM_688079
	R	TGACCCGAATGAGAACCAG		
gls2a	**F**	TTTCTGGGTTGGAGGACTTG	100	BX927144, ENSDARG00000069095
	R	TGCAAACCTGTGCTTTTGAG		
gls2b	**F**	ACAGAAACAAGTCGGTGGTG	110	NM_001083825, ENSDARG00000002917
	R	GTCATAGTCCCTCAACTCCATATTC		
gls-like	**F**	GAGCTGGTTTCAACCTTCCA	142	ENSDARG00000062781
	R	CCAGGTCCCCTCTATAAGCAG		
rpl13a	**F**	TCTGGAGGACTGTAAGAGGTATGC	150	NM_212784.1
	R	TCAGACGCACAATCTTGAGAGCAG		

F, forward; R, reverse.

Table S2. Primers used to generate templates for RNA probe synthesis

gene name		primer sequence (5' – 3')	amplicon size (bp)
g6pca.1	**F**	CCGTCCACTTACAGATCAAATAC	957
	R	GAAGCAGCAAAGCCACAG	
g6pca.2	**F**	CTCATTACAAAGATGCCCAAG	970
	R	GATAAGCAGTACGGGATGATG	
pck1	**F**	CGCTCATCATGCCTCCTC	2007
	R	CGGTTTTGATGCACTTGAGA	
pck2	**F**	CAATTTCACCTGCACCAAAG	1931
	R	TCAATCCCTCACTCTCTCCTC	
glud1a	**F**	CAGGACCCCGTGTAAAGGA	1166
	R	CAAGGTTATACCGGTTGGCT	
glud1b	**F**	ATGGTGGAGGGCTTCTTTG	1199
	R	ATCAGCAGGTGGTAGTTGGAG	
glsa	**F**	TTCGAGGGCGTTAAAGGAG	1695
	R	GGGCTGTAGGTGTTGTGATAG	
glsb	**F**	GCTTCAATTGTGCTGAAGGAG	1763
	R	TGACCCGAATGAGAACCAG	
gls2a	**F**	TGCTGGAAAATGGGAAAGAG	1327
	R	TGCAAACCTGTGCTTTTGAG	
gls2b	**F**	TCCAGTGTCTCATTTCACTGCT	1294
	R	GTCATAGTCCCTCAACTCCATATTC	
gls-like	**F**	ATCTCTCAGACGTAAATGGAGAAAG	1619
	R	CCAGGTCCCCTCTATAAGCAG	

F, forward; R, reverse.

Table S3. List of mRNA localization detected by *in situ* hybridization

gene name	localization	putative function
g6pca.1	yolk syncytial layer, liver (ER)	glucose production
g6pca.2	yolk syncytial layer, liver (ER)	glucose production
pck1	liver (cytosolic)	PEP synthesis, cataplerosis
pck2	liver, intestinal bulb (mitochondrial)	PEP synthesis, cataplerosis
glud1a	liver, intestinal bulb (mitochondrial)	glutamate catabolism
glud1b	liver, intestinal bulb (mitochondrial)	glutamate catabolism
glsa	brain (cytosolic)	glutamine catabolism
glsb	pectoral fin (cytosolic)	glutamine catabolism
gls2a	liver (mitochondrial)	glutamine catabolism
gls2b	liver, intestinal bulb (mitochondrial)	glutamine catabolism
gls-like	swim bladder (no data)	(glutamine catabolism?)

Putative intracellular localization of the protein product was written in parentheses. ER, endoplasmic reticulum; PEP, phosphoenolpyruvate.