

SUPPLEMENTARY ONLINE DATA

FGT-1 is the major glucose transporter in *C. elegans* and is central to aging pathways

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Table S1 Primers used for cloning the putative glucose transporter genes from a *C. elegans* cDNA library

Gene Name	Gene size (bp)	Primer name	Primer sequence (5'→3')
<i>fgt-1a</i>	1479	H17aFOR H17aREV	AAATGGGTGTCACGACC GCATTACTTCTCTCTCG
<i>fgt-1b</i>	1533	H17bFOR H17bREV H17int	ATGTCGGAAAATCAAGAAGTG TACTTCTCTCTCGAATTCCG GGCCACTGATCTTTGCC
R09B5.11	1551	R09FOR R09REV R09intFOR R09intREV	ATGAACGCC GTTGTGCC CCGACTATGAACATATCCG GGTGCCAA TGTTCTTACC CGTAAGAAACATTGGCACC
C35A11.4	1548	C35FOR C35REV C35intFOR C35intREV	ATGGTGAAGCACCCAGTTTCCG CTAGAGTCGATAAGATAAGG CTGTGAGATTGATGAAGCC GGCTTCATCAATCTCACAG
F14E5.1	1419	F14FOR F14REV F14intFOR F14intREV	ATGTCAAATAGATTGTGGCC TCATTTTTTTAAGTTCATT GGAGATGGTACAGATGC GCATCTGTACCATCTCC
Y39E4B.5	1518	Y39FOR Y39REV Y39intFOR Y39intREV	ATGCGGTGGCAAACGATTCG TTAGTAAATCGAAGATGTC CATGAGCGAATATCAAGCC GGCTTGATTCGCTCATG
F48E3.2	1467	F48FOR F48REV F48intFOR F48intREV	CCAGTGACAACATGCAAAAACCTAATTGG GGCTGTATTATAATTATTCAITCC CGTCGTGGGTTTTTTGTTGGG CCCAACAAAACCCACGACG
K09C4.5	1575	K4.5FOR K4.5REV K4.5intFOR K4.5intREV	CCATTAGCAATCATGTATTCAATGCGCC GGCAATGAAGCAAGCAACATCGCAGG GGAGAAGAATTTGACACAGG CCTGTGTCAAATCTTCTCC
T08B1.1	1776	T08FOR T08REV T08intFOR T08intREV	ATGTCAGAATTGAAGAAG CAGTCTTCTTCCACATTGG CGTCCTGACCTACGCTATGG CCATAGCGTAGGTCAGGACC

Table S2 Insertion sites for the exofacial HA tag in putative *C. elegans* transporters

The influenza HA epitope (peptide sequence, IDYPYDVPDYAE) was introduced using the sense oligonucleotide: 5'-TGAGATCGATTATCCTTATGATGTTCTGATTATGC-3' and the antisense oligonucleotide: 5'-TCAGCATAATCAGGAACATCATAAGGATAATCGATC-3'. A specific restriction enzyme site (Bsu36I) was created by site-directed mutagenesis (at the position indicated in the Table) so that the sticky ends could be produced after the digestion. Subsequently the HA tag was ligated into the sequence with correct orientation. The consequent mutated amino acids for each protein are listed.

Gene name	Position of the HA insertion	Mutated amino acid
H17B01.1a	Thr ⁵⁷ -Glu ⁵⁸	–
H17B01.1b	Pro ⁷⁰ -Gly ⁷¹	–
R09B5.11	Pro ⁷¹ -Gly ⁷²	–
C35A11.4	Met ⁴² -Asn ⁴³	Met ⁴² →Pro, Asn ⁴³ →Asp
F14E5.1	Thr ⁵⁵ -Glu ⁵⁶	–
Y39E4B.5	Leu ⁴⁵ -Arg ⁴⁶	Arg ⁴⁶ →Ala, Gln ⁴⁷ →Glu, Pro ⁴⁸ →Ala
F48E3.2	Asn ⁴² -Glu ⁴³	–
K09C4.5	Pro ⁵¹ -Thr ⁵²	Thr ⁵² →Ala
K09C4.1	Thr ⁵⁴ -Glu ⁵⁵	Thr ⁵⁴ →Glu
T08B1.1	Asp ⁷⁶ -Trp ⁷⁷	Asp ⁷⁶ →Glu, Trp ⁷⁷ →Gly

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The gene and protein names for *fgt-1a* and *fgt-1b* and FGT-1A and -1B have been deposited in WormBase (<http://www.wormbase.org>) under accession numbers NM_061580.4 and NM_061581.1 respectively.

Table S3 Positions of charged residues in putative TM segments

Charged residues in putative TM segments were identified following sequence alignment (Figure S1). The Table includes charged residues within the central eight residues in the proposed TM regions, but excludes charged residues in the first or last three residues of the proposed helices. The membrane topology of each putative transporter was set up to maximize alignment with the hGLUT1 TM regions and at the same time taking account of the membrane topology predicted by the SOSUI program.

Strain	Putative charged residue positions in TM segments											
	TM1	TM2	TM3	TM4	TM5	TM6	TM7	TM8	TM9	TM10	TM11	TM12
FGT-1A		Asp ⁷⁸		Arg ¹⁴²				Asp ³⁴⁶				
FGT-1B		Asp ⁹⁶		Arg ¹⁶⁰				Asp ³⁶⁴				
R09B5.11	Asp ⁶¹	Asp ⁹⁷		Arg ¹⁶¹	Lys ¹⁹⁰			Lys ³⁵⁴ , Asp ³⁶⁶				
C35A11.2				Arg ¹²⁴		Glu ¹⁹¹	Asp ²⁹⁷	Asp ³¹⁰ , Asp ³²⁸ , Arg ³²⁹			Arg ⁴¹⁶	
F14E5.1		Asp ⁶⁰		Arg ¹²⁴	Glu ¹⁵⁹ , Asp ¹⁷⁵			Lys ³⁰⁹	Lys ³⁵⁷ , Arg ³⁵⁹			
Y39E4B.5				Arg ¹²² , Asp ¹³³	Glu ¹⁵⁷ , Lys ¹⁷⁵	Arg ¹⁸²		Asp ³²⁴ , Arg ³²⁵			Asp ⁴¹⁸	
F48E3.2		Glu ⁵⁷		Arg ¹²¹	Glu ¹⁵⁶		Arg ²⁶⁶ , Asp ²⁹⁰	Lys ³⁰⁴				
K09C4.5	Asp ²⁰		Arg ⁹⁷	Arg ¹³⁴	Asp ¹⁶²		Asp ²⁷³	Asp ³¹⁹ , Arg ³¹¹	Lys ³³⁸	Glu ³⁶⁵ , Glu ³⁶⁹		
K09C4.1	Asp ²⁰	Glu ⁷⁰	Arg ⁹⁷		Lys ¹⁶⁶	Glu ¹⁹¹	Asp ²⁸¹ , Asp ²⁹²	Asp ³²⁷ , Lys ³¹⁹	Lys ³⁴² , Lys ³⁴⁵ , Glu ³⁵⁴	Glu ³⁷³ , Arg ³⁸⁸		

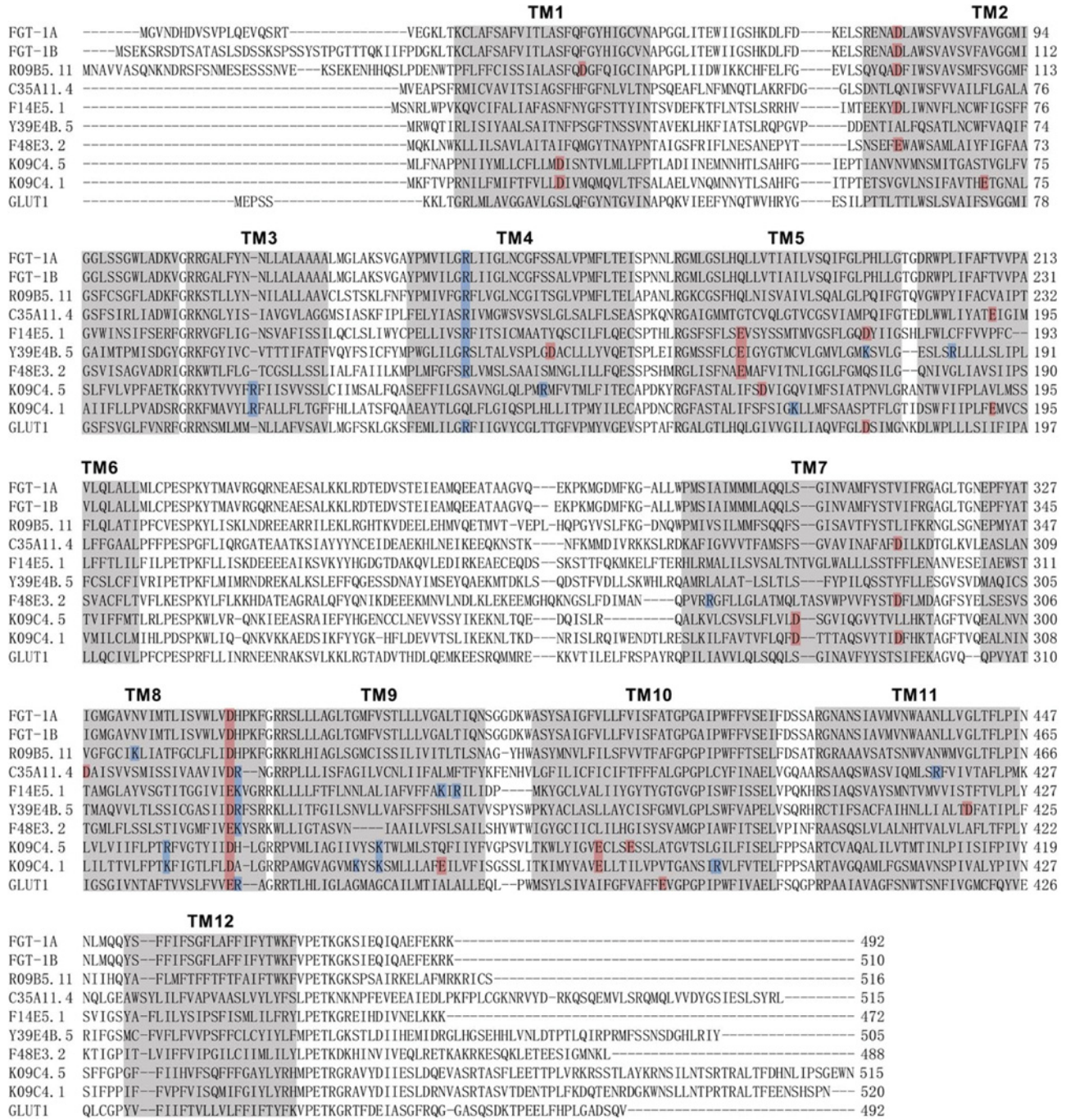


Figure S1 Alignments of GLUT1 with putative transporters cloned from *C. elegans*

Many of the putative *C. elegans* transporters have charged residues (blue and red shading) in regions that correspond to the mammalian GLUT protein TM regions. We propose that this property may be associated with poor ability to facilitate glucose transport and that the property is likely to be more associated with alternative transported substrates.

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