

Additional File #1

Human glycolipid transfer protein (*GLTP*) genes: organization, transcriptional status and evolution

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Figure S1 –RT-PCR/Restriction Analyses of Human *GLTP* and *GLTPi* cDNA in Various Human Cells

Different *GLTP* clones, produced by 37 PCR cycles and cloned using pGEM-T, were digested by *Bsp*HI and analyzed by agarose gel electrophoresis. The top panel (A) shows the *Bsp*HI restriction map for the different *GLTP* ORFs in pGEM-T. The middle (B) right panel shows the restriction analysis of various clones in which the RNA extracts were 3xDNase treated prior to RT-PCR (42 PCR cycles). Two clones containing the intronless *GLTP* ORF are clearly evident. No-RT PCR analysis revealed genomic DNA to be the source of the two clones [middle (B) left panel]. Similar occurrences of clones from the intronless *GLTP* ORF were evident in the absence of DNase I treatment after 37 PCR cycles. The lower (C) panel shows restriction analyses of various clones in which the RNA extracts were treated with DNase I. Intronless *GLTP* ORF was not detectable among the clones when the RT-PCR cycle number was 37 or less.

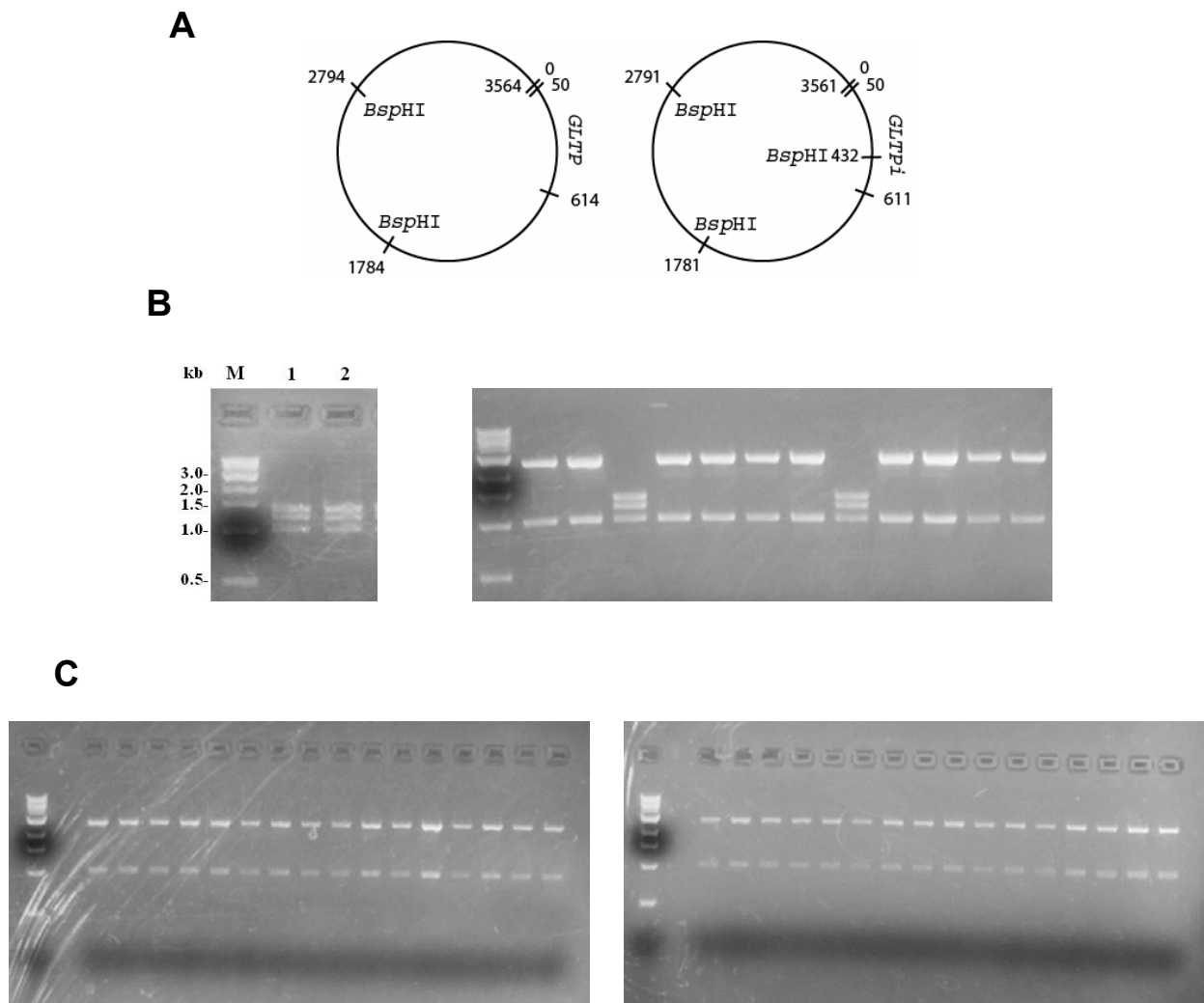


Figure S2 -CpG Islands in Human *GLTP* genes

Human *GLTPi* (intronless) --- locus 11p15.1 --- CpG Island

TCACTGTGATCATGAAACATACCAAAAAAAGGGCTGTGACTGCCCGGGCGCTGACGGCGGCGCG
GGGGGTGCGGTGTGGAACCCCGCGGTGCCCGCTGGGGCATCACCGTGGGCCTCGAACCCGAAATGG
CTCTGCTGACCGAACACCTGCTGAAGCGTTGCCCGCGGACAAGCAGATCGAGACTGGGCCCTTCC
TCGAGGCGGTGTCCCACCTGCGGCCCTTTTCGATTGCCCTTGGGTCCCCAGTGTTTA

Predicted genomic sequence for fully methylated CpG sites

TTATTGTGATTATGAAAAATATATTAATAAAAAAAGGGTTGTGATTGTTTCGGGCGTTGACGGCGGCGCG
GGGGGTGCGGTGTGGAACCTTCGCGGTGTCCGTTGGGGTATTATCGTGGGTTTCGAATTCGAAATGG
TTTGTGTTGATCGAATATTTGTTGAAGTCGTTGTTCCCGGATAAGTAGATCGAGATTGGGTTTTTTT
TCGAGGCGGTGTTTTATTGTTCGTTTTTTTCGATTGTTTGGGTTTTTAGTGTTTA

CpG island (yellow highlighted sequence), identified by MethPrimer [34] consisted of -119 bases upstream of ATG translation start site along with the initial 97 ORF bases. COBRA analysis involved PCR amplification of the 255 base sequence using primers delineated by the double underlined sequences.

GLTP (5-exon/4-intron)---locus 12q24.11 --- CpG Island

-1000gaggatgttacttggtgggagaggatgaatgtgaagttacaaagtataaatggagaggatgtttct
tggagtgtgtggtctgtgtaaatggagaggatgaatgtgaagttacaaagtgtaaagggcgtgaatggaga
ggatgaagtgaagttgcaaagcgtttacattcctgtcattgctaaggtgctttttgatttaggtctagga
agtcagccttatgttccctgacctccaggccctatttttctgcctcacaacagggtacatcagactgttgag
ggcagactggaccacccagattttcgggaagcaggagttgtccagcagggcagtggctgagttagactgtgact
tcagcagtggttcaacagggtataaggtcattgaagaccagaatcaagcaatcgagcgtcctcgtcggttgt
agcgaagagaaacggtgaccacacaggagagcagtgctccacccagggtcacttgggggtactggggtacaatt
ttgggggaaacgggggtcctggggagcgttggctgggtggggctgtaacccgagcgtggtggggcggttgtg
agctgtgacctggcccgagtcggcccgcccgattggggggccaaaacggggggcgggggaggccacacctg
gggaagactcacctgggagcggctcacttgggcccctcggggacccatgaacgggcgcacctcctctgcgtc
ccgcccccgccggcccccccgccaatggggggcgcgagacactcggcgggcgcgagattggggagccggt
gagcggggggcgggggcgcgcccgcccgagtttaggcgctcggccggcgggcgcgctgagcgcctcggctac
gagggcgccggtgcggcggaagtggcgacgctggcgtccCGGAGCCTGCGCGGGCGGCTGTGACGGCCC
CGGCGCTGACGGCGCGGCGGGGGGGCGGTGTGACGCCCGCGGCGCGGCTGGGGCATCACCGCGGGCC
TCGACCCCGAAATGCGCTGCTGGCCGACACTTGCTGAAGCCGCTGCCCGCGGACAAGCAGATCGAGACC
GGGCCCCCTTCGAGGCGGTGTCCCACCTGCCGCCCTTCTTCGgtgagcgggaatggagggggggaggcggc
ccgcagccccacgcgcacccggaatcctccttcccccgagcatcccccaaccatctctgcctagacacccc

CpG island (yellow highlighted sequence), identified by MethPrimer [34] consisted of -476 bases adjacent to ATG translation start site, all of the Exon 1 ORF and a portion of Intron 1. 70 CpGs occur between -460 & 0 and 18 CpGs occur in the Exon 1 ORF + Intron region. Further upstream (-1000 & -500), only 9 CpGs occur. COBRA analysis, using primers delineated by the double underlined sequences, involved PCR amplification of the intervening 201 base sequence containing 11 CpGs.

Table S1

Number of synonymous substitutions per site (K_s), non-synonymous substitutions per site (K_a) and confidence intervals

Species ^b	No. bp ^c	K_s	P=0.05		P=0.01		$C. I.$ ^a		P=0.05		P=0.01	
			Min.	Max.	Min.	Max.	K_a		Min.	Max.	Min.	Max.
<i>GLTP</i>												
Hom/Pan	627	0.0190	0.0000	0.0434	0.0000	0.0570	0.0000		0.0000	0.0000	0.0000	0.0000
Hom/Mac	627	0.1018	0.0566	0.1559	0.0446	0.1733	0.0000		0.0000	0.0000	0.0000	0.0000
Pan/Mac	627	0.0921	0.0497	0.1434	0.0391	0.1629	0.0000		0.0000	0.0000	0.0000	0.0000
Bos/Sus	627	0.0413	0.0098	0.0862	0.0048	0.1046	0.0000		0.0000	0.0000	0.0000	0.0000
Rat/Mus	627	0.2241	0.1466	0.3166	0.1213	0.3526	0.0020		0.0000	0.0082	0.0000	0.0116
Dan(chr5)/(chr10)	627	1.9912	1.4206	2.8613	1.2447	3.3960	0.1942		0.1402	0.2492	0.1240	0.2723
<i>GLTPi</i>												
Hs-Pan	624	0.0296	0.0049	0.0639	0.0000	0.0746	0.0156		0.0047	0.0295	0.0023	0.0345
Hs-Mac	624	0.0889	0.0419	0.1341	0.0310	0.1498	0.0658		0.0411	0.0939	0.0336	0.1039
Pan-Mac	624	0.0988	0.0487	0.1556	0.0394	0.1792	0.0599		0.0385	0.0876	0.0304	0.0992

^a1000 replicates for confidence intervals ($C.I.$) ^b Hom, Pan, Mac, Bos, Sus, Mus, Rat and Dan indicate *Homo sapiens*, *Pan troglodytes*, *Macaca mulatta*, *Bos taurus*, *Sus scrofa*, *Mus musculus*, *Rattus norvegicus* and *Danio rerio*, respectively. *GLTP* = functional 5-exon/4-intron *GLTP* genes and *GLTPi* = intronless *GLTP* genes. ^cNumber of base pairs compared.

FIGURE S3 -- *GLTP* and *GLTPi* Nucleotide Sequence Conservation in Primates. The nucleotide sequences are derived from the ORFs of the 5-exon/4-intron and intronless *GLTP* genes.

Hs <i>GLTP</i>	ATGGCGCTGCTGGCCGAACACTTGCTGAAGCCGCTGCCCGCGGACAAGCAGATCGAGACCGGGCCCTTCCTCGAGGCGGTGTCCACCTGCCGCCCTTCTTCGAT	105
Hs <i>GLTPi</i>	T.....A.....C.....T.....	105
Pan <i>GLTP</i>	G.....G.....T.....C.....	105
Pan <i>GLTPi</i>	T.....C.....T.....T.....	105
Mac <i>GLTP</i>	G.....A.....C.....C.....A.....	105
Mac <i>GLTPi</i>	T.....G.....T.....TA...A.....C.....	105
Hs <i>GLTP</i>	TGCCTTGGGTCCCCAGTGTTTACTCCCATCAAGGCAGACATAAGCGGCAACATCAGGAAAATCAAAGCTGTGTACGACACCAACCCAGCCAAGTTCCGGACCTG	210
Hs <i>GLTPi</i>	A.....A.....	210
Pan <i>GLTP</i>	G.....G.....	210
Pan <i>GLTPi</i>	A.....A.....	210
Mac <i>GLTP</i>	G.....G.....C.....T.....	210
Mac <i>GLTPi</i>	.A.....A.....C.....T.....	210
Hs <i>GLTP</i>	CAGAACATCCTGGAGGTGGAGAAAGAAATGTATGGAGCAGAGTGGCCCAAAGTAGGGGCCACACTGGCGCTGATGTGGCTGAAAAGAGGCCTCCGCTTCATCCAG	315
Hs <i>GLTPi</i>	C...T.....G.....	315
Pan <i>GLTP</i>	T...C.....A.....G.....	315
Pan <i>GLTPi</i>	C.....G.....A.....	315
Mac <i>GLTP</i>	T.....A.....	315
Mac <i>GLTPi</i>	A.....AA.....A.....	315
Hs <i>GLTP</i>	GTCTTCCTCCAGAGCATCTGCGACGGGGAGCGGGACGAGAACCACCCCAACCTCATCCGTGTCAACGCCACCAAGGCCTACGAGATGGCCCTCAAGAAGTACCAT	420
Hs <i>GLTPi</i>	A...A...C.....T.....C.....A.....T.....C.....	420
Pan <i>GLTP</i>	G...G...G.....C.....T.....G.....A.....	420
Pan <i>GLTPi</i>	A...A.....T...C.....A.....T.....	420
Mac <i>GLTP</i>	G...G.....C.....G.....A.....	420
Mac <i>GLTPi</i>	C...T.....	420
Hs <i>GLTP</i>	GGCTGGATCGTGCAGAAGATCTTCAGGCAGCACTGTACGCAGCACCTATAAGTCTGACTTCCTGAAAGCGCTCTCCAAGGGGCAGAATGTTACGGAGGAGGAG	525
Hs <i>GLTPi</i>	ΔΔΔ.....CT...G...C.....G.....	522
Pan <i>GLTP</i>	AGA.....AC...A...T.....	525
Pan <i>GLTPi</i>	ΔΔΔ.....C.....CT...G...C...G.....	522
Mac <i>GLTP</i>	AGA.....T.....C...A...A.....C.....A.....A.....	525
Mac <i>GLTPi</i>	A.....ΔΔΔ.....G.....A.....G.....	522
Hs <i>GLTP</i>	TGCCTGGAGAAGATCCGCCTCTTCCTAGTCAACTACACGGCGACCATCGATGTCATCTACGAGATGTACACCCAGATGAACGCTGAGCTTAAGTACAAGGTGTAG	630
Hs <i>GLTPi</i>	A.....T.....C...T.....A.....	627
Pan <i>GLTP</i>	G.....C.....T...C.....G.....A.....A.....	630
Pan <i>GLTPi</i>	T.....G.....	627
Mac <i>GLTP</i>	C...C.....T...T.....T...C.....T.....G.....	630
Mac <i>GLTPi</i>	TG.....	627

FIGURE S4 -*GLTP* ORF Conservation in Vertebrates. The nucleotide sequences are derived from the ORFs of the 5-exon/4-intron *GLTP* genes.

<i>Homo</i>	:	ATGGCGCTGCTGGCCGAACACCTGCTGAAGCCGCTGCCCGCGGACAAGCAGATCGAGACCGGGCCCTTCTCGAGGCGGTGTCCCACCTGCCGCCCTTCTTCGAT	:	105
<i>Pan</i>	:	ATGGCGCTGCTGGCCGAACACCTGCTGAAGCCGCTGCCCGCGGACAAGCAGATCGAGACCGGGCCCTTCTCGAGGCGGTGTCCCACCTGCCGCCCTTCTTCGAT	:	105
<i>Mac</i>	:	ATGGCGCTGCTGGCCGAACACCTGCTGAAGCCGCTGCCCGCGGACAAGCAGATCGAGACCGGGCCCTTCTCGAGGCGGTGTCCCACCTGCCGCCCTTCTTCGAT	:	105
<i>Mus</i>	:	ATGGCGCTGCTGGCCGAACACCTGCTGAAGCCGCTGCCCGCGGACAAGCAGATCGAGACCGGGCCCTTCTCGAGGCGGTGTCCCACCTGCCGCCCTTCTTCGAT	:	105
<i>Rat</i>	:	ATGGCGCTGCTGGCCGAACACCTGCTGAAGCCGCTGCCCGCGGACAAGCAGATCGAGACCGGGCCCTTCTCGAGGCGGTGTCCCACCTGCCGCCCTTCTTCGAT	:	105
<i>Opossum</i>	:	ATGGCGCTACTGGCCGAACACCTGCTGAAGCCGCTGCCCGCGGACAAGCAGATCGAGACCGGGCCCTTCTGGAACCGGTGTCCCACCTGCCGCCCTTCTTCGAT	:	105
<i>Canis</i>	:	ATGGCGCTGCTGGCCGAACACCTGCTGAAGCCGCTGCCCGCGGACAAGCAGATCGAGACCGGGCCCTTCTCGAGGCGGTGTCCCACCTGCCGCCCTTCTTCGAT	:	105
<i>Bos</i>	:	ATGGCGCTGCTGGCCGAACACCTGCTGAAGCCGCTGCCCGCGGACAAGCAGATCGAGACCGGGCCCTTCTCGAGGCGGTGTCCCACCTGCCGCCCTTCTTCGAT	:	105
<i>Sus</i>	:	ATGGCGCTGCTGGCCGAACACCTGCTGAAGCCGCTGCCCGCGGACAAGCAGATCGAGACCGGGCCCTTCTCGAGGCGGTGTCCCACCTGCCGCCCTTCTTCGAT	:	105
<i>Xenopus</i>	:	ATGCTCTGCTTCTTTCAGCACAGATCAAGCCGCTTCTGCTGATAAACAATCGACACCTCTGCTTCTGGAATTCGTTTCCCATCTGCCCGCTTCTTCGAT	:	105
<i>Danio</i> (Chr5)	:	ATGGCTCTTCTAATGGAGCAGCAGTTCGGGCAACTTCAGCCGACAACAAGTGAACCCCGCCGCTTCTCGAGGCGGTGTCTACCTTCTCTTCTTCGAT	:	105
<i>Danio</i> (Chr10)	:	ATGGCTCTTCTTCTGAGCAGCAGTTCGCGCCGCTGTCTGACACCAAGAAATCGCCACAAGACATTTCTAGAGTCACTTCTACCTGCCGCCCTTCTTCGAT	:	105
<i>Homo</i>	:	TGCCTTGGGTCCCCAGTGTCTTACTCCCATCAAGGCAGACATAAGCGGCAACATCAAGAAAATCAAAGCTGTGTACGACACCAACCCAGCCAAGTTCGGGACCCCTG	:	210
<i>Pan</i>	:	TGCCTTGGGTCCCCAGTGTCTTACTCCCATCAAGGCAGACATAAGCGGCAACATCAAGAAAATCAAAGCTGTGTACGACACCAACCCAGCCAAGTTCGGGACCCCTG	:	210
<i>Mac</i>	:	TGCCTTGGGTCCCCAGTGTCTTACTCCCATCAAGGCAGACATAAGCGGCAACATCAAGAAAATCAAAGCTGTGTATGACACCAACCCAGCCAAGTTCGGGACCCCTG	:	210
<i>Mus</i>	:	TGCCTTGGGTCCCCAGTGTCTTACTCCCATCAAGGCAGACATAAGCGGCAACATCAAGAAAATCAAAGCTGTATGACACCAACCCAGCCAAGTTCGGGACCCCTG	:	210
<i>Rat</i>	:	TGCCTTGGGTCCCCAGTGTCTTACTCCCATCAAGGCAGACATAAGCGGCAACATCAAGAAAATCAAAGCTGTATGACACCAACCCAGCCAAGTTCGGGACCCCTG	:	210
<i>Opossum</i>	:	TGCCTTGGGTCCCCAGTGTCTTACTCCCATCAAGGCAGACATAAGCGGCAACATCAAGAAAATCAAAGCTGTATGACACCAACCCAGCCAAGTTCGGGACCCCTG	:	210
<i>Canis</i>	:	TGCCTTGGGTCCCCAGTGTCTTACTCCCATCAAGGCAGACATAAGCGGCAACATCAAGAAAATCAAAGCTGTATGACACCAACCCAGCCAAGTTCGGGACCCCTG	:	210
<i>Bos</i>	:	TGCCTTGGGTCCCCAGTGTCTTACTCCCATCAAGGCAGACATAAGCGGCAACATCAAGAAAATCAAAGCTGTATGACACCAACCCAGCCAAGTTCGGGACCCCTG	:	210
<i>Sus</i>	:	TGCCTTGGGTCCCCAGTGTCTTACTCCCATCAAGGCAGACATAAGCGGCAACATCAAGAAAATCAAAGCTGTATGACACCAACCCAGCCAAGTTCGGGACCCCTG	:	210
<i>Xenopus</i>	:	TGCCTTGGGTCCCCAGTGTCTTACTCCCATCAAGGCAGACATAAGCGGCAACATCAAGAAAATCAAAGCTGTATGACACCAACCCAGCCAAGTTCGGGACCCCTG	:	210
<i>Danio</i> (Chr5)	:	TGCCTTGGGTCCCCAGTGTCTTACTCCCATCAAGGCAGACATAAGCGGCAACATCAAGAAAATCAAAGCTGTATGACACCAACCCAGCCAAGTTCGGGACCCCTG	:	210
<i>Danio</i> (Chr10)	:	TGCCTTGGGTCCCCAGTGTCTTACTCCCATCAAGGCAGACATAAGCGGCAACATCAAGAAAATCAAAGCTGTATGACACCAACCCAGCCAAGTTCGGGACCCCTG	:	210
<i>Homo</i>	:	CAGAACATCCTGGAGTGGAGAAAGAAATGTATGGAGCAGAGTGGCCCAAAGTAGGGGCCACACTGGCGCTGATGTGGCTGAAAAGAGGCGCTCGCTTCATCCAG	:	315
<i>Pan</i>	:	CAGAACATCCTGGAGTGGAGAAAGAAATGTATGGAGCAGAGTGGCCCAAAGTAGGGGCCACACTGGCGCTGATGTGGCTGAAGAGAGGCGCTCGCTTCATCCAG	:	315
<i>Mac</i>	:	CAGAACATCCTGGAGTGGAGAAAGAAATGTATGGAGCAGAGTGGCCCAAAGTAGGGGCCACACTGGCGCTGATGTGGCTGAAAAGAGGCGCTCGCTTCATCCAG	:	315
<i>Mus</i>	:	CAGAACATCCTGGAGTGGAGAAAGAAATGTATGGAGCAGAGTGGCCCAAAGTAGGGGCCACACTGGCGCTGATGTGGCTGAAAAGAGGCGCTCGCTTCATCCAG	:	315
<i>Rat</i>	:	CAGAACATCCTGGAGTGGAGAAAGAAATGTATGGAGCAGAGTGGCCCAAAGTAGGGGCCACACTGGCGCTGATGTGGCTGAAAAGAGGCGCTCGCTTCATCCAG	:	315
<i>Opossum</i>	:	CAGAACATCCTGGAGTGGAGAAAGAAATGTATGGAGCAGAGTGGCCCAAAGTAGGGGCCACACTGGCGCTGATGTGGCTGAAAAGAGGCGCTCGCTTCATCCAG	:	315
<i>Canis</i>	:	CAGAACATCCTGGAGTGGAGAAAGAAATGTATGGAGCAGAGTGGCCCAAAGTAGGGGCCACACTGGCGCTGATGTGGCTGAAAAGAGGCGCTCGCTTCATCCAG	:	315
<i>Bos</i>	:	CAGAACATCCTGGAGTGGAGAAAGAAATGTATGGAGCAGAGTGGCCCAAAGTAGGGGCCACACTGGCGCTGATGTGGCTGAAAAGAGGCGCTCGCTTCATCCAG	:	315
<i>Sus</i>	:	CAGAACATCCTGGAGTGGAGAAAGAAATGTATGGAGCAGAGTGGCCCAAAGTAGGGGCCACACTGGCGCTGATGTGGCTGAAAAGAGGCGCTCGCTTCATCCAG	:	315
<i>Xenopus</i>	:	CAAAATGATTCGGAAGGAGAGAAGAAATGTATGGAGCAGAGTGGCCCAAAGTAGGGGCCACACTGGCGCTGATGTGGCTGAAAAGAGGCGCTCGCTTCATCCAG	:	315
<i>Danio</i> (Chr5)	:	CAGCAATTTTGGAGGAGAGAAGAGATGCATGGAGCCGAGTGGCCCAAAGTAGGGGCCACACTGGCGCTCATGTGTTTAAAGAGGCGCTCGCTTCATCCAG	:	315
<i>Danio</i> (Chr10)	:	CAGCAATTTTGGAGGAGAGAAGAGATGCATGGAGCCGAGTGGCCCAAAGTAGGGGCCACACTGGCGCTCATGTGTTTAAAGAGGCGCTCGCTTCATCCAG	:	315
<i>Homo</i>	:	GTCTTCTCCAGAGCATCTGCGACGGGGAGCGGGACGAGAACCACCCCAACCTCATCCGTGTCAACGCCACCAAGGCTACGAGATGGCCCTCAAGAAGTACCAT	:	420
<i>Pan</i>	:	GTCTTCTCCAGAGCATCTGCGACGGGGAGCGGGACGAGAACCACCCCAACCTCATCCGTGTCAACGCCACCAAGGCTACGAGATGGCCCTCAAGAAGTACCAT	:	420
<i>Mac</i>	:	GTCTTCTCCAGAGCATCTGCGACGGGGAGCGGGACGAGAACCACCCCAACCTCATCCGTGTCAACGCCACCAAGGCTACGAGATGGCCCTCAAGAAGTACCAT	:	420
<i>Mus</i>	:	GTCTTCTCCAGAGCATCTGCGATGGGGAACCGGACGAGAACCACCCCAACCTCATCCGTGTCAACGCCACCAAGGCTATGAGATGGCCCTCAAGAAGTACCAT	:	420
<i>Rat</i>	:	GTCTTCTCCAGAGCATCTGCGATGGGGAACCGGACGAGAACCACCCCAACCTCATCCGTGTCAACGCCACCAAGGCTATGAGATGGCCCTCAAGAAGTACCAT	:	420
<i>Opossum</i>	:	GTCTTCTCCAGAGCATCTGCGATGGGGAACCGGACGAGAACCACCCCAACCTCATCCGTGTCAACGCCACCAAGGCTATGAGATGGCCCTCAAGAAGTACCAT	:	420
<i>Canis</i>	:	GTCTTCTCCAGAGCATCTGCGATGGGGAACCGGACGAGAACCACCCCAACCTCATCCGTGTCAATGCCACCAAGGCTACGAGATGGCCCTCAAGAAGTACCAT	:	420
<i>Bos</i>	:	GTCTTCTCCAGAGCATCTGCGACGGGAGCGGGATGAGAACCACCCCAACCTCATCCGTGTCAATGCCACCAAGGCTACGAGATGGCCCTCAAGAAGTACCAT	:	420
<i>Sus</i>	:	GTCTTCTCCAGAGCATCTGCGACGGGAGCGGGATGAGAACCACCCCAACCTCATCCGTGTCAATGCCACCAAGGCTACGAGATGGCCCTCAAGAAGTACCAT	:	420
<i>Xenopus</i>	:	GTTTANGCTACAGAGTATGTGATGGAGAAAGAGATGATCAAAACCCCAATCTCATCAAGGTGAACATAACCAAGGCTATGAGATAGGGCTCAAAAATACCAT	:	420
<i>Danio</i> (Chr5)	:	GTTTCTTCTCAAGATCAAGTAGATGGTGATAAAGATGATAACAACCCCAACCTCATCAAGGTGAACGTCACTAAAGGTTATGAGATGGGTTTAAAGAGTATCAT	:	420
<i>Danio</i> (Chr10)	:	ATTTTACTCCAGAGTCTTGGCGATGGAGAGAGATGAGGACATCCCAATCTCATTCGGCTCAACATCACCAGGTTATGATCAAGCACTGAAGAGTACCAC	:	420
<i>Homo</i>	:	GGCTGGATGCTGCAGAAGATCTTCCAGGCAGCACTGTACGCAGCACCCATTAAGTCTGACTTCTGAAAGCGCTCTCCAAGGGGAGAGATGTACGGAGGAGGAG	:	525
<i>Pan</i>	:	GGCTGGATGCTGCAGAAGATCTTCCAGGCAGCACTGTACGCAGCACCCATTAAGTCTGACTTCTGAAAGCGCTCTCCAAGGGGAGAGATGTACGGAGGAGGAG	:	525
<i>Mac</i>	:	GGCTGGATGCTGCAGAAGATCTTCCAGGCAGCACTGTACGCAGCACCCATTAAGTCTGACTTCTGAAAGCGCTCTCCAAGGGGAGAGATGTACGGAGGAGGAG	:	525
<i>Mus</i>	:	GGCTGGATGCTGCAGAAGATCTTCCAGGCAGCACTGTACGCAGCACCCATTAAGTCTGACTTCTGAAAGCGCTCTCCAAGGGGAGAGATGTACGGAGGAGGAG	:	525
<i>Rat</i>	:	GGCTGGATGCTGCAGAAGATCTTCCAGGCAGCACTGTACGCAGCACCCATTAAGTCTGACTTCTGAAAGCGCTCTCCAAGGGGAGAGATGTACGGAGGAGGAG	:	525
<i>Opossum</i>	:	GGCTGGATGCTGCAGAAGATCTTCCAGGCAGCACTGTACGCAGCACCCATTAAGTCTGACTTCTGAAAGCGCTCTCCAAGGGGAGAGATGTACGGAGGAGGAG	:	525
<i>Canis</i>	:	GGCTGGATGCTGCAGAAGATCTTCCAGGCAGCACTGTACGCAGCACCCATTAAGTCTGACTTCTGAAAGCGCTCTCCAAGGGGAGAGATGTACGGAGGAGGAG	:	525
<i>Bos</i>	:	GGCTGGATGCTGCAGAAGATCTTCCAGGCAGCACTGTACGCAGCACCCATTAAGTCTGACTTCTGAAAGCGCTCTCCAAGGGGAGAGATGTACGGAGGAGGAG	:	525
<i>Sus</i>	:	GGCTGGATGCTGCAGAAGATCTTCCAGGCAGCACTGTACGCAGCACCCATTAAGTCTGACTTCTGAAAGCGCTCTCCAAGGGGAGAGATGTACGGAGGAGGAG	:	525
<i>Xenopus</i>	:	GGCTGGATGCTGCAGAAGATCTTCCAGGCAGCACTGTACGCAGCACCCATTAAGTCTGACTTCTGAAAGCGCTCTCCAAGGGGAGAGATGTACGGAGGAGGAG	:	525
<i>Danio</i> (Chr5)	:	GGCTGGATGCTGCAGAAGATCTTCCAGGCAGCACTGTACGCAGCACCCATTAAGTCTGACTTCTGAAAGCGCTCTCCAAGGGGAGAGATGTACGGAGGAGGAG	:	525
<i>Danio</i> (Chr10)	:	GGCTGGATGCTGCAGAAGATCTTCCAGGCAGCACTGTACGCAGCACCCATTAAGTCTGACTTCTGAAAGCGCTCTCCAAGGGGAGAGATGTACGGAGGAGGAG	:	525
<i>Homo</i>	:	TGCCTGGAGAAGATCCGCCCTCTTCTTACTCAACTACACGGGCACCATCGATGTCATCTACGAGATGTACACCCAGATGAACGGCTGAGCTTAACTACAAGGTGTAG	:	630
<i>Pan</i>	:	TGCCTGGAGAAGATCCGCCCTCTTCTTACTCAACTACACGGGCACCATCGATGTCATCTACGAGATGTACACCCAGATGAACGGCTGAGCTTAACTACAAGGTGTAG	:	630
<i>Mac</i>	:	TGCCTGGAGAAGATCCGCCCTCTTCTTACTCAACTACACGGGCACCATCGATGTCATCTACGAGATGTACACCCAGATGAATGCCGAGCTTAACTACAAGGTGTAG	:	630
<i>Mus</i>	:	TGCCTGGAGAAGATCCGCCCTCTTCTTACTCAACTACACGGGCACCATCGATGTCATCTACGAGATGTACACCAAGATGAATGCCGAGCTTAACTACAAGGTGTAG	:	630
<i>Rat</i>	:	TGCCTGGAGAAGATCCGCCCTCTTCTTACTCAACTACACGGGCACCATCGATGTCATCTACGAGATGTACACCAAGATGAATGCCGAGCTTAACTACAAGGTGTAG	:	630
<i>Opossum</i>	:	TGCCTGGAGAAGATCCGCCCTCTTCTTACTCAACTACACGGGCACCATCGATGTCATCTACGAGATGTACACCAAGATGAACGGCTGAGCTTAACTACAAGGTGTAG	:	630
<i>Canis</i>	:	TGCCTGGAGAAGATCCGCCCTCTTCTTACTCAACTACACGGGCACCATCGATGTCATCTACGAGATGTACACCAAGATGAACGGCTGAGCTTAACTACAAGGTGTAG	:	630
<i>Bos</i>	:	TGCCTGGAGAAGATCCGCCCTCTTCTTACTCAACTACACGGGCACCATCGATGTCATCTACGAGATGTACACCAAGATGAACGGCTGAGCTTAACTACAAGGTGTAG	:	630
<i>Sus</i>	:	TGCCTGGAGAAGATCCGCCCTCTTCTTACTCAACTACACGGGCACCATCGATGTCATCTACGAGATGTACACCAAGATGAACGGCTGAGCTTAACTACAAGGTGTAG	:	630
<i>Xenopus</i>	:	TGCCTGGAGAAGATCCGCCCTCTTCTTACTCAACTACACGGGCACCATCGATGTCATCTACGAGATGTACACCAAGATGAATGCCGAGCTTAACTACAAGGTGTAG	:	630
<i>Danio</i> (Chr5)	:	TGTTTGGACAAGATCCGCCGAGTCTCTTAAATTTTACAGCTACTAATGACGCCATCTATGAAATGTACACCAAGATGAATGCCGAGCTTAACTACAAGGTGTAG	:	630
<i>Danio</i> (Chr10)	:	TGTTTGGACAAGATCCGCCGAGTCTCTTAAATTTTACAGCTACTAATGACGCCATCTATGAAATGTACACCAAGATGAATGCCGAGCTTAACTACAAGGTGTAG	:	630

FIGURE S5 - Conservation of GLTP Amino Acid Sequence in Vertebrates.

The amino acid sequences are derived from the ORFs of the 5-exon/4-intron *GLTP* genes. CLUSTAL FORMAT for T-COFFEE Version_1.41, CPU=11.20 sec, SCORE=69, Nseq=9, Len=209

<i>Homo</i>	MALLAEHLLKPLPADKQIETGPFLEAVSHLPPFFDCLGSPVFTPIKADISGNITKIKAVY	60
<i>Pan</i>	MALLAEHLLKPLPADKQIETGPFLEAVSHLPPFFDCLGSPVFTPIKADISGNITKIKAVY	60
<i>Macaca</i>	MALLAEHLLKPLPADKQIETGPFLEAVSHLPPFFDCLGSPVFTPIKADISGNITKIKAVY	60
<i>Canis</i>	MALLAEHLLKPLPADKQIETGPFLEAVSHLPPFFDCLGSPVFTPIKADISGNITKIKAVY	60
<i>Bos</i>	MALLAEHLLRPLPADKQIETGPFLEAVSHLPPFFDCLGSPVFTPIKADISGNITKIKAVY	60
<i>Mus</i>	MALLAEHLLKPLPADRQIETGPFLEAVAHLPFFDCLGSPVFTPIKADISGNITKIKAVY	60
<i>Monodelphis</i>	MALLAEHLLKPLPADKQIETRPFLDAVAHLPPFFDCLGSPIFTPIKADISGNIKTIRAVY	60
<i>Xenopus</i>	MSVLLQHQFKPLPADKQIDTCCFLDSVSHLPAFFDCLGSAIFSPIKADITGNISKIRSVY	60
<i>Danio</i> (chr.5)	MALLMEHQFRQLPADKQVETRPFLEAVSHLPPFFDCLGSAVFSPIKADIAGNITKIKAVY	60
<i>Danio</i> (chr.10)	MALLLDQQFAPLSDTKEIATKTFLSEVSHLPPFFDCLGSKVFAPIKSDINGNITKIKAVY	60
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<i>Homo</i>	DTNPAKFRTLQNILEVEKEMYGAEWPKVGATLALMWLKRGLRFIQVFLQSIDGERDENH	120
<i>Pan</i>	DTNPAKFRTLQNILEVEKEMYGAEWPKVGATLALMWLKRGLRFIQVFLQSIDGERDENH	120
<i>Macaca</i>	DTNPAKFRTLQNILEVEKEMYGAEWPKVGATLALMWLKRGLRFIQVFLQSIDGERDENH	120
<i>Canis</i>	DTNPAKFRTLQNILEVEKEMYGAEWPKVGATLALMWLKRGLRFIQVFLQSIDGERDENH	120
<i>Bos</i>	DTNP TKFRTLQNILEVEKEMYGAEWPKVGATLALMWLKRGLRFIQVFLQSIDGERDENH	120
<i>Mus</i>	DTDPAKFKTLQNILEVEKMGYGAEWPKVGATLALLWLKRGLRFIQVFLQSIDGERDENH	120
<i>Monodelphis</i>	DTDP TKFRTLQNILEAEKEMYGAEWPKVGATLALMWLKRGLRFIQVLLQSIDGERDENR	120
<i>Xenopus</i>	ESNP SKFKTLQMILEGEKE LHGPQWPKVGATLALMWLKRGLKF IQV MLQSIADGERDDQN	120
<i>Danio</i> (chr.5)	DSNP TRFKTLQQILEAEKEMHGAEWPKVGATLALMWLKRGLRFIQVLLQSLVDGDKDDNN	120
<i>Danio</i> (chr.10)	DSDPVKYETLQQILIEKSSYGEWPKVGATLALMWLKRGLRFIQILLQSLADGERDEDN	120
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<i>Homo</i>	PNLIRVNATKAYEMALKKYHGWIVQKIFQAALYAAPYKSDFLKALSKGQNVTEEECLEKI	180
<i>Pan</i>	PNLIRVNATKAYEMALKKYHGWIVQKIFQAALYAAPYKSDFLKALSKGQNVTEEECLEKI	180
<i>Macaca</i>	PNLIRVNATKAYEMALKKYHGWIVQKIFQAALYAAPYKSDFLKALSKGQNVTEEECLEKI	180
<i>Canis</i>	PNLIRVNATKAYEMALKKYHGWIVQKIFQAALYAAPYKSDFLKALSKGQNVTEEECLEKV	180
<i>Bos</i>	PNLIRVNATKAYEMALKKYHGWIVQKIFQAALYAAPYKSDFLKALSKGQNVTEEECLEKI	180
<i>Mus</i>	PNLIRVNANKAYEMALKKYHGWLVQKIFKAALYAAPYKSDFLKALSKGQNVTEEECLEKI	180
<i>Monodelphis</i>	PNLIRVNVTKAYEMALKKYHGWLVQKIFQGALYAAPYKSDFLKALSKGQDIP EEEECLEKI	180
<i>Xenopus</i>	PNLIRVNI TKAYEIALKKYHGWVQKIFQTALIAAPYKDDFLKALSKGQTVKEEECEIEKI	180
<i>Danio</i> (chr.5)	PNLIRVNVTKAYEMALKKYHGWIVQKLFQAALYAAPYRSDFLRALSKGREVKDEECLDKV	180
<i>Danio</i> (chr.10)	PNLIRVNI TKAYDQALKRYHGWIVQKVFKAALFAAPCRSDFLKALSKDQEVAEEDCLAKV	180
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<i>Homo</i>	RLFLVNYTATIDVIYEMYTQMNAELNYKV	209
<i>Pan</i>	RLFLVNYTATIDVIYEMYTQMNAELNYKV	209
<i>Macaca</i>	RLFLVNYTATIDVIYEMYTQMNAELNYKV	209
<i>Canis</i>	RLFLVNYTATIDVIYEMYTRMNAELNYKV	209
<i>Bos</i>	RLFLVNYTATIDVIYEMYTRMNAELNYKV	209
<i>Mus</i>	RLFLVNYTATIDAIYDMYTKMNAELDYTV	209
<i>Monodelphis</i>	RLFLVNF TATIDVIYEMYTKMNAELNYKV	209
<i>Xenopus</i>	RQFLVNYTTTIEAIYIMYNKMNAELDYKA	209
<i>Danio</i> (chr.5)	RQFLVNF TATNDAIYEMYTKMNADLDYKV	209
<i>Danio</i> (chr.10)	RQFLINF TATVDAIYEMYSTMNAELDYL	209
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