

Supplementary material

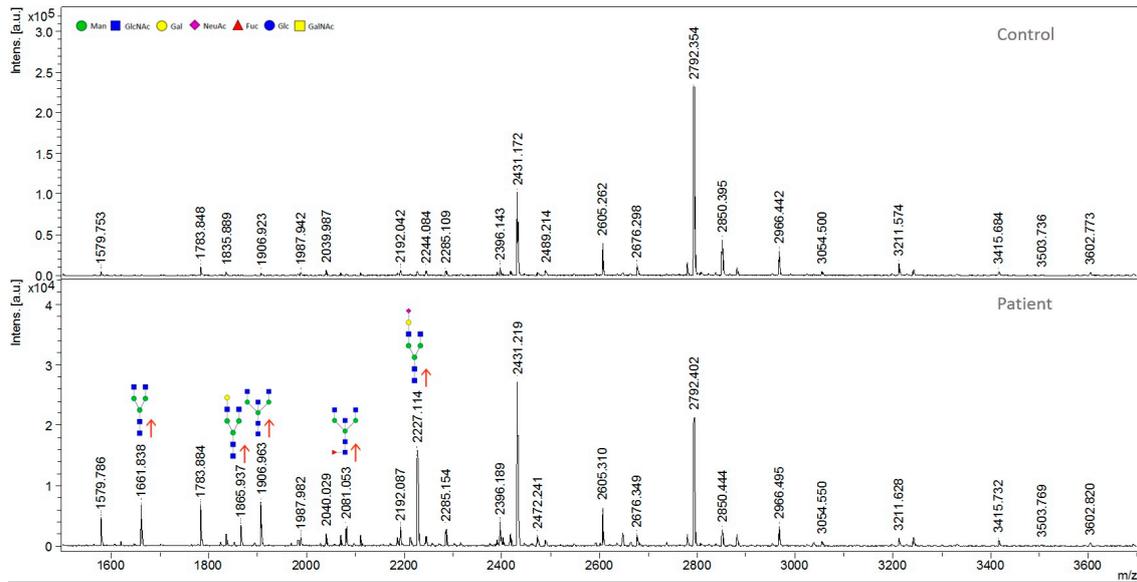


Figure S1. MALDI-TOF/TOF MS of increased hypogalactosylated derivatized N-glycans released from the patient's and control blood serum.

Organism name	Uniprot ID	Sequence	Group
<i>H. sapiens</i>	P78381	KILTTA[F]FSVLMNRS[L]	Mammals
<i>P. abelii</i>	A0A2J8R8J3	KILTTA[F]FSVLMNRS[L]	
<i>C. syrichta</i>	A0A1U7UF56	KILTTA[F]FSVLMNRS[L]	
<i>P. macrocephalus</i>	A0A2Y9FGB5	KILTTA[F]FSVLMNRS[L]	
<i>B. taurus</i>	Q6YC49	KILTTA[F]FSVSMLSK[KL]	
<i>E. caballus</i>	F7C7T4	KILTTA[F]FSVFMNRS[L]	
<i>C. lupus familiaris</i>	O77592	KILTTA[F]FSVSMLSK[KL]	
<i>V. vulpes</i>	A0A3Q7SA97	KILTTA[F]FSVLMNRS[L]	
<i>P. pardus</i>	A0A6P4T3G7	KILTTA[F]FSVLMNRS[L]	
<i>O. rosmarus divergens</i>	A0A2U3VNZ3	KILTTA[F]FSVLMNRS[L]	
<i>P. vampyrus</i>	A0A6P3RXC5	KILTTA[F]FSVLMNRS[L]	
<i>P. discolor</i>	A0A6J2MGD1	KILTTA[F]FSVLMNRS[L]	
<i>M. musculus</i>	Q9ROM8	KILTTA[F]FSVLMNRS[L]	
<i>C. griseus</i>	Q99PG7	KILTTA[F]FSVLMNRS[L]	
<i>M. auratus</i>	A0A1U8CKB9	KILTTA[F]FSVLMNRS[L]	
<i>D. ordii</i>	A0A1S3GII7	KILTTA[F]FSVLMNRS[L]	
<i>H. glaber</i>	A0A0P6J5Z9	KILTTA[F]FSVLMNRS[L]	
<i>E. europaeus</i>	A0A1S3A515	KILTTA[F]FSVLMNRS[L]	
<i>L. striata domestica</i>	A0A218U883	KILTTA[F]FSVLLGTAL	Birds
<i>O. spaldingii</i>	A0A7K8G0Q9	KILTTA[F]FSVLLGTAL	
<i>B. capensis</i>	A0A7K9I2Y8	KILTTA[F]FSVLLGTSL	
<i>X. laevis</i>	A5PKQ2	KILTTA[F]FSVLLLRKSL	Amphibians
<i>P. guttatus</i>	A0A6P9D2P8	KILTTA[F]FSVLMRKS[L]	Reptiles
<i>S. salar</i>	A0A1S3LGH5	KILTTA[F]FSVLMRKS[L]	Ray-finned fishes
<i>C. gobio</i>	A0A6J2PPF1	KILTTA[F]FSVMRKS[L]	
<i>C. chanos</i>	A0A6J2W8A0	KILTTA[F]FSVMRKS[L]	
<i>P. rangq</i>	A0A6P7IV90	KILTTA[F]FSVLMRKS[L]	
<i>C. magur</i>	A0A8J4THQ4	KILTTA[F]FSVLMRKS[L]	
<i>I. punctatus</i>	W5UFK5	KILTTA[F]FSVLMRKS[L]	
<i>A. spatula</i>	A0A8J7P5A1	KILTTA[F]FSVLMRKS[L]	

Figure S2. Multiple sequence alignment (MSA) results - aligned human protein (P78381) with orthologues. Residues highlighted (Leucine with green, Valine with magenta) at position 154 in the human protein P78381.

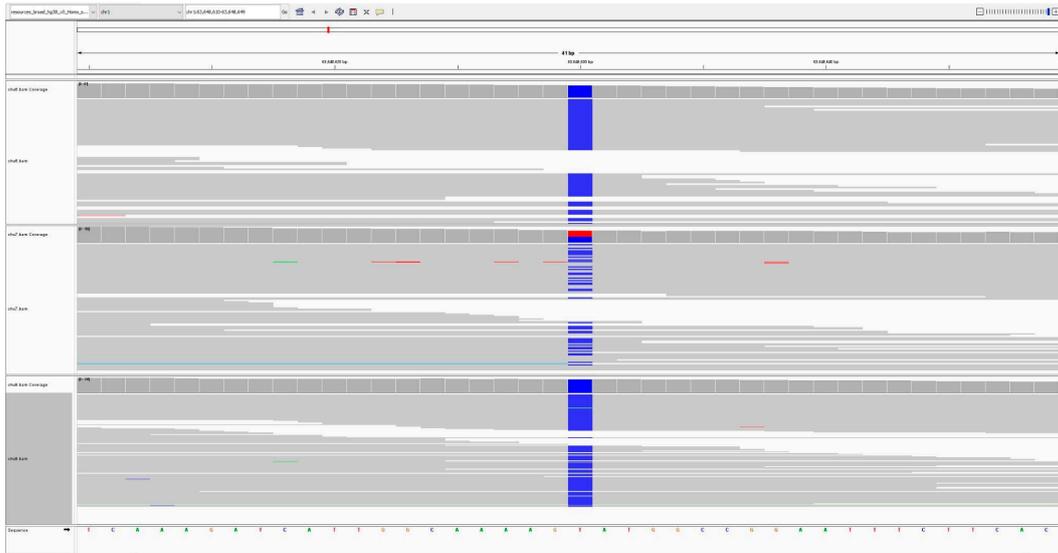


Figure S3. Screenshot from Integrative genomics viewer [37] of the mutation at position chr1: 63648630 in gene *PGM1*. The patient is labeled as chu6, parents are samples chu7 and chu8.

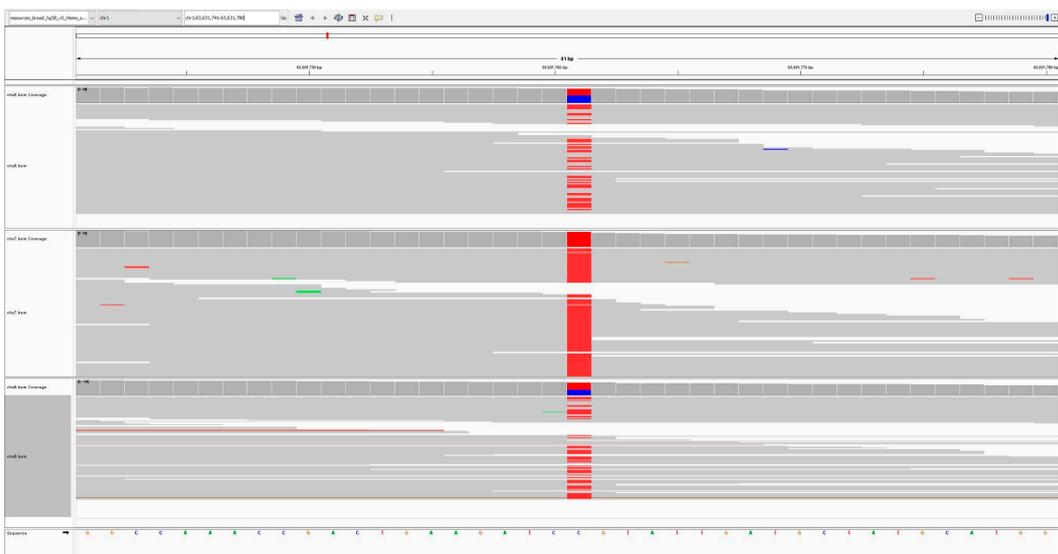


Figure S4. Screenshot from Integrative genomics viewer [37] of the mutation at position chr1: 63631761 in gene *PGM1*. The patient is labeled as chu6, parents are samples chu7 and chu8.

Subtype	SLC35A2-CDG presented patient	Galactosemia [32]	B4GALT1-CDG [33]	TMEM165-CDG [35, 36]	PGM1-CDG [36]	COGs-CDG [33, 36]
Deficient enzyme	UDP-galactose transporter	galactose-1-phosphate uridylyltransferase, galactokinase 1, UDP-galactose-4-epimerase	beta-1,4-galactosyltransferase 1	transmembrane protein 165	phosphoglucomutase 1	conserved oligomeric Golgi complex
Increased serum N-glycan biomarker						
Hex3HexNAc4 <i>m/z</i> 1661.9	+	+/-	+	+	+	-
Hex3HexNAc4Fuc1 <i>m/z</i> 1835.9	-	+/-	+	+	-	+
Hex3HexNAc5 <i>m/z</i> 1906.9	+	-	+	-	-	-
Hex3HexNAc5Fuc1 <i>m/z</i> 2081.1	+	-	+	-	-	-
Hex4HexNAc4 <i>m/z</i> 1865.1	+	+/-	-	+/-	-	+/-
Hex4HexNAc4NeuAc1 <i>m/z</i> 2227.2	+	-	+	+	+	+
Hex5HexNAc4NeuAc1 <i>m/z</i> 2431.2	-	-	-	+/-	+/-	+
Hex5HexNAc4NeuAc1 Fuc1 <i>m/z</i> 2605.3	-	-	-	+	-	+

Table S1. List of other diseases that could affect galactose metabolism and lead to similar serum glycoprofile as in SLC35A2-CDG, with respective increased levels (+) or normal levels (-) of N-glycan biomarkers. Fuc - fucose, Hex- hexose, HexNAc - N-acetylhexosamine, NeuAc - sialic acid.





Figure S7. Analysis of DNA sequence of the selected region of SLC35A2 gene - father.