Table S8. Catabolic genes predicted in HMO utilization by *B. longum* subsp. *infantis* ATCC15697

Pathway[1]	Gene name	Gene symbol	Locus tag
Leloir pathway genes			
	galactokinase	*galK*	Blon_2062
	UDP-glucose 4-epimerase	*galE*	Blon_2171
	galactose-1-phosphate uridylyltransferase	*galT*	Blon_2172
	phosphoglucomutase	*pgm*	Blon_2184
Central fermentative pathway genes			
1	glucokinase	*glkA*	Blon_0565
1	glucose-6-phosphate isomerase	*gpi*	Blon_0417
2	fructose-6-phosphate phosphoketolase	*xfp*	Blon_1722
3	transaldolase	*tal*	Blon_1095
4	transketolase	*tkt*	Blon_1096
5	ribose 5-phosphate isomerase	*rpiA*	Blon_2191
6	ribulose 5-phosphate epimerase	*rpe*	Blon_1368
7	xylulose-5-phosphate phosphoketolase	*xfp*	Blon_1722
8	acetate kinase	*ackA*	Blon_1731
9	glyceraldehyde-3-phosphate dehydrogenase	*gap*	Blon_0900
10	phosphoglycerate kinase	*pgk*	Blon_1087
11	phosphoglycerate mutase	*pmg*	Blon_2152
12	enolase	*eno*	Blon_1836
13	pyruvate kinase	*pyk*	Blon_1745
14	lactate dehydrogenase	*ldh*	Blon_0840
Sialic acid genes			
15	N-acetylneuraminate lyase	*nanA*	Blon_2349
16	N-acetylmannosamine kinase	*nanK*	Blon_0644
17	N-acetylmannosamine-6-phosphate 2-epimerase	*nanE*	Blon_0645
N-acetylglucosamine genes			
18	N-acetylhexosamine 1-kinase	*nahK*	Blon_2173
19	phosphoglucosamine mutase	*glmM*	Blon_2031
20	N-acetylglucosamine-6-phosphate deacetylase	*nagA*	Blon_0882
21	glucosamine-6-phosphate isomerase	*nagB*	Blon_0881
Fucose genes			
?	fucose isomerase	*fucI*	NOT FOUND
?	fuculose kinase	*fucK*	NOT FOUND
?	L-fuculose phosphate aldolase	*fucA*	NOT FOUND
22	lactaldehyde reductase	*fucO*	Blon_0540
23	triose-phosphate isomerase	*tpiA*	Blon_1088

[1] Number refers to representation in figure 2.