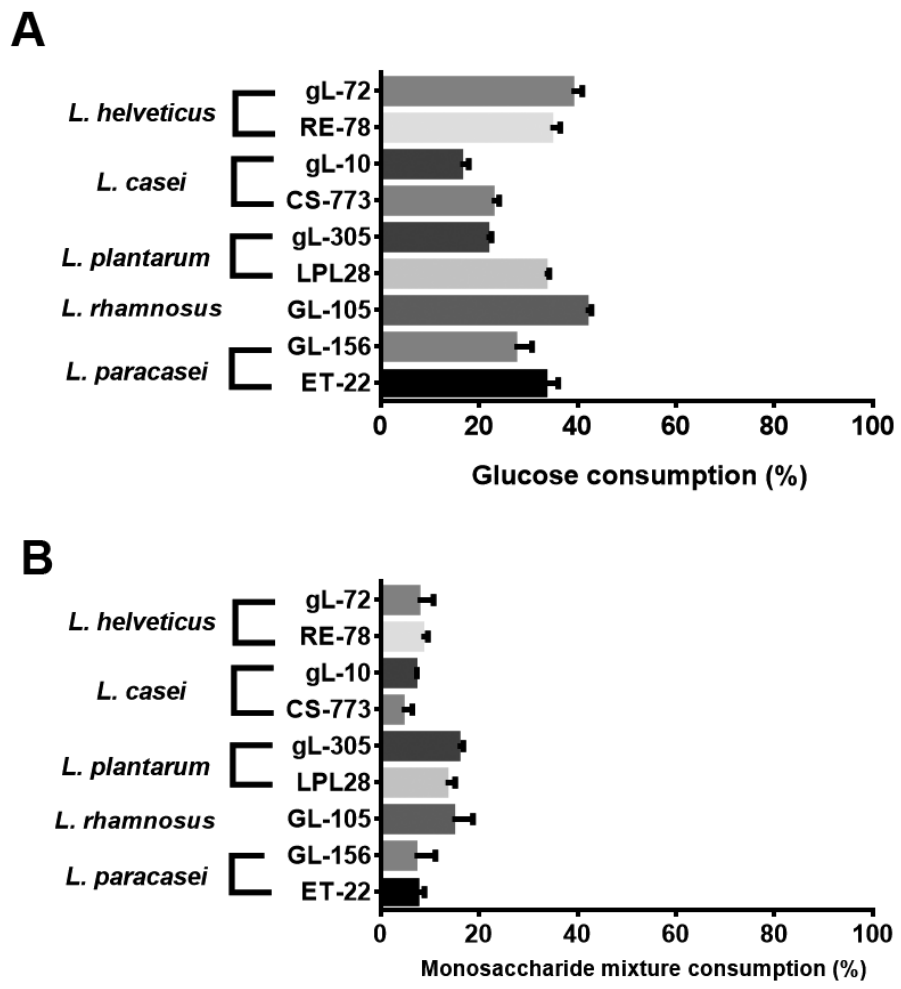
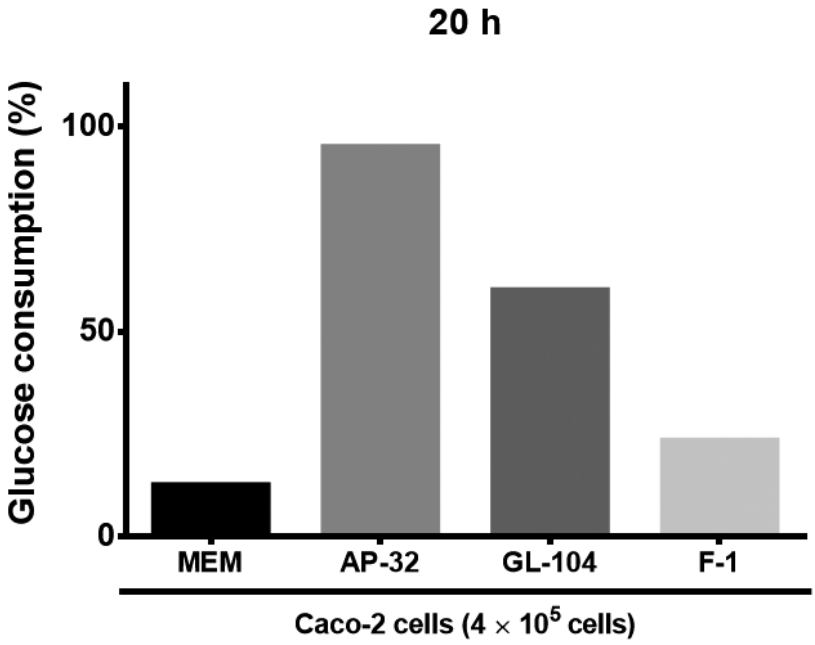
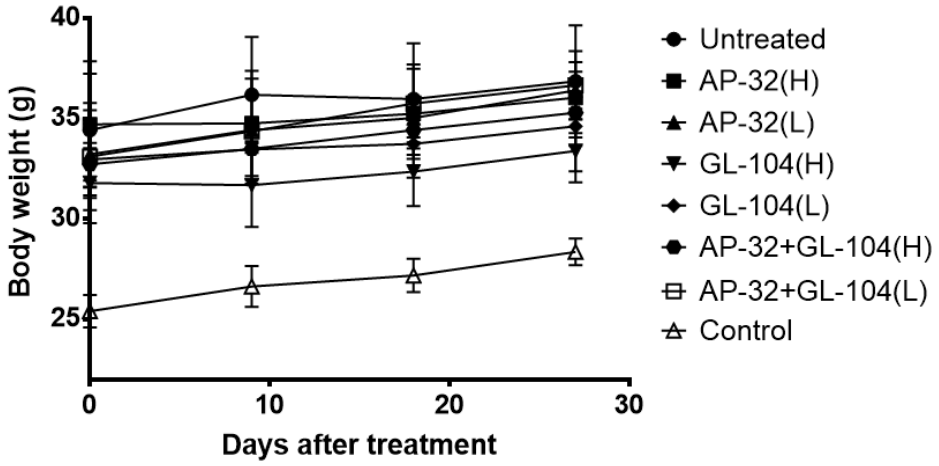
Supplemental Material



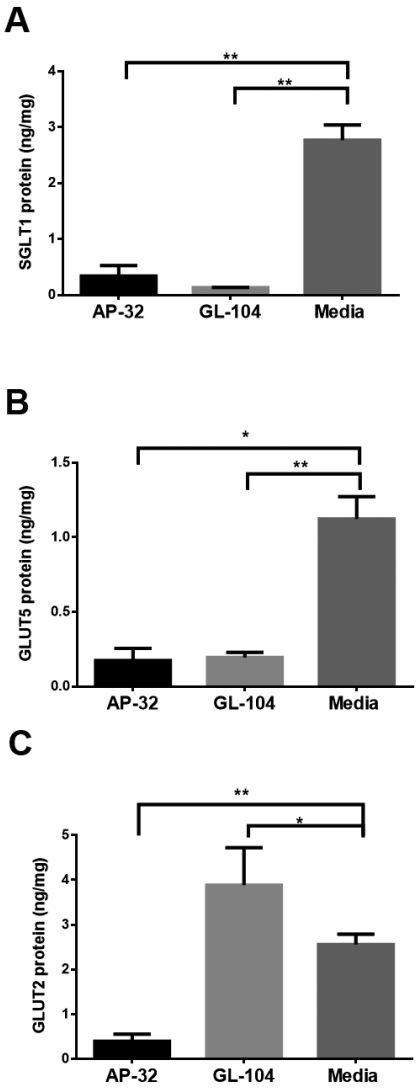
Supplemental Figure 1. *Lactobacillus* strains with low monosaccharide consumption. *Lactobacillus* species and strains (10^8 CFU) were incubated with MRS medium containing **(A)** 2% glucose or **(B)** 6% monosaccharide. Monosaccharide concentrations in MRS medium were evaluated as described in Figure 1. Bar graphs represent means ± SDs of the consumption rates from three individual experiments.



Supplemental Figure 2. *L. salivarius* AP-32 and *L. reuteri* GL-104 consumed glucose effectively in the presence of epithelial intestinal cells. Caco-2 cells were co-incubated with selected *Lactobacillus* strains as described in Figure 2. The bar graph shows the mean glucose consumption rates from two separate experiments. Minimum Essential Media (MEM) was used as the medium control.

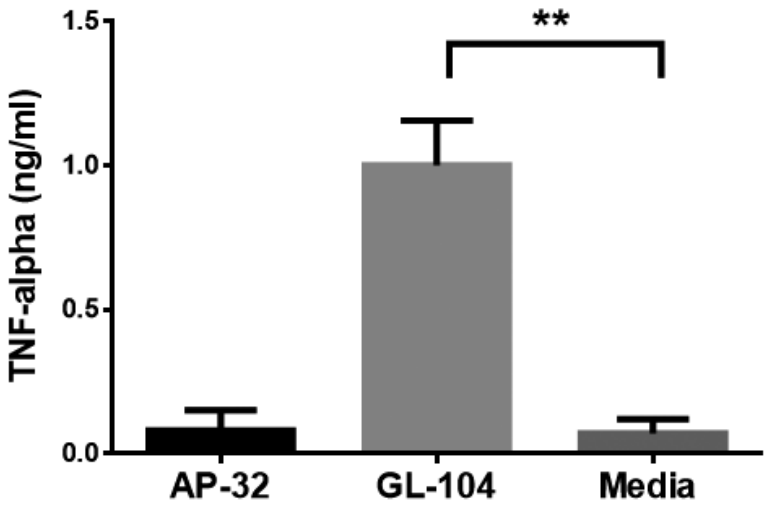


Supplemental Figure 3. Changes in body weights of probiotic-treated db/db mice. Data represent means + SDs from three independent experiments. Nondiabetic db/m mice served as a blank control, and untreated db/db mice served as the experimental control.



Supplemental Figure 4. Expression of hexose transporter protein in the presence of probiotics. Caco-2 cells were treated with AP-32 and GL-104 as previously described in Fig 2. Cells were lysed and proteins were extracted. Expression of SGLT1, GLUT5, and GLUT2 proteins was analyzed using ELISA kits. Data were normalized with the amount of total proteins and shown as means + SDs from two independent experiments. Cells treated with MEM containing 0.45% glucose alone

served as a control **p < 0.01; *p < 0.05.



Supplemental Figure 5. TNF-α production in Caco-2 cells after probiotic treatment. Caco-2 cells were treated with AP-32 and GL-104 as previously described in Fig 2. TNF-α in the cultural media was evaluated by ELISA. Data represent means + SDs from two independent experiments. Cells treated with MEM containing 0.45% glucose serve as a control. **p < 0.01.

Supplemental Table 1. PCR primers

GLUT2	Forward	CGT CTC CTT TGA CAT TTC CTT C
	Reverse	GGT GGA GAA AAC AGC CTA GAG AT
GLUT5	Forward	GCA ACA GGA TCA GAG CAT GA
	Reverse	TCG CAG GCA CGA TAG AAA AT
SGLT1	Forward	CTC TTC ACC ATG GAC ATC TAC
	Reverse	TCG TTG ACA GGG TGC TAA TAG
GAPDH	Forward	CCA TGG AGA AGG CTG GGG
	Reverse	CAA AGT TGT CAT GGA TGA CC

Supplemental Table 2. Serum biochemistry analysis

Treatments [a]	AST [b]	ALT [b]	BUN[c]	CREA[c]
AP-32 (H)	151.8 ± 57.9	89.5 ± 40.4**	27.4 ± 3.3***	0.2 ± 0.04
AP-32 (L)	142.9 ± 75.3	107.4 ± 48.4*	30.7 ± 5.1*	0.26 ± 0.06
GL-104 (H)	166.3 ± 80.6	105.6 ± 34.0*	29.5 ± 5.7**	0.23 ± 0.03
GL-104 (L)	135.7 ± 42.8	99.5 ± 62.2*	28.2 ± 4.6**	0.26 ± 0.04
AP-32+GL-104 (H)	144.9 ± 57.4	99.2 ± 17.4**	27.9 ± 1.9***	0.24 ± 0.04
AP-32+GL-104 (L)	137.6 ± 92.7	109.1 ±26.2**	27.7 ± 5.7**	0.26 ± 0.06
Untreated	172.7 ± 66.1	169.1 ± 44.6	37.7 ± 3.8	0.27 ± 0.12
db/m	78.1 ±14.9**	38.3 ± 18.8***	41.7 ± 12.4	0.31 ± 0.13

[a] Mice were treated with a (H) high (1.025×10^9 cfu/kg/day) or (L) low dose (5.125×10^9 CFU/kg/day) of probiotics.

[b] Activities of aspartate aminotransferase (AST) and alanine aminotransferase(ALT). Data are represented as means ± SD (U/L).

[c] Renal function assays: blood urea nitrogen (BUN) and creatinine (CREA) were evaluated. Data are represented mean ± SD (mg/dL).

*p <0.05,**p <0.01,***p <0.005.