

## Electronic Supplementary Material (ESI) for Food & Function

### Supplementary Tables

Table S1 Content (umol/g) of cecal SCFAs after *L. rhamnosus* CCFM1060 and combined with different doses of XOS intervention

Group	Control	Model	Rosiglitazone	<i>L. rhamnosus</i>	L-LXOS	L-HXOS
Acetate	7.0 ± 1.2 <sup>a</sup>	6.7 ± 1.0 <sup>a</sup>	13.0 ± 3.4 <sup>bc</sup>	13.9 ± 1.8 <sup>c</sup>	10.8 ± 2.0 <sup>bc</sup>	10.3 ± 2.0 <sup>b</sup>
Propionate	2.9 ± 0.9 <sup>a</sup>	2.7 ± 1.0 <sup>a</sup>	4.6 ± 1.3 <sup>b</sup>	4.7 ± 0.9 <sup>b</sup>	3.7 ± 1.0 <sup>ab</sup>	2.7 ± 0.9 <sup>a</sup>
Butyrate	3.1 ± 0.9 <sup>ab</sup>	2.4 ± 0.4 <sup>a</sup>	5.2 ± 0.6 <sup>cd</sup>	6.0 ± 1.1 <sup>d</sup>	4.6 ± 0.7 <sup>c</sup>	3.8 ± 1.0 <sup>b</sup>
Total SCFAs	13.0 ± 1.7 <sup>a</sup>	11.8 ± 1.3 <sup>a</sup>	22.8 ± 3.6 <sup>c</sup>	24.5 ± 3.2 <sup>c</sup>	19.1 ± 2.4 <sup>b</sup>	16.8 ± 2.5 <sup>b</sup>

The data are presented as the mean ± standard deviation. Different letters in table indicate a significant difference between groups ( $P < 0.05$ ).

Table S2 Significantly increased KEGG pathways compared with the model group using two-sided Welch's t test at  $P < 0.05$ 

KEGG pathways	<i>L. rhamnosus</i>	L-LXOS	L-HXOS
Membrane transport	Phosphotransferase system (PTS)	PTS	PTS
Carbohydrate Metabolism	Amino sugar and nucleotide sugar metabolism	Amino sugar and nucleotide sugar metabolism	Amino sugar and nucleotide sugar metabolism
	Glycolysis/Gluconeogenesis	NS	NS
	Starch and sucrose metabolism	NS	NS
	NS	Pentose phosphate pathway	Pentose phosphate pathway
Energy metabolism	NS	Homologous recombination	Homologous recombination
Lipid Metabolism	Primary bile acid biosynthesis	Primary bile acid biosynthesis	Primary bile acid biosynthesis
	Secondary bile acid biosynthesis	Secondary bile acid biosynthesis	Secondary bile acid biosynthesis
	Glycerolipid metabolism	NS	NS
Metabolism of Other Amino Acids	Phosphonate and phosphinate metabolism	NS	NS
Nucleotic Metabolism	Purine metabolism	Purine metabolism	Purine metabolism
Glycan biosynthesis and metabolism	NS	Peptidoglycan biosynthesis	Peptidoglycan biosynthesis
Replication and repair	Mismatch repair	Mismatch repair	NS
	DNA replication	DNA replication	DNA replication
	Nucleotide excision repair	Nucleotide excision repair	Nucleotide excision repair
Metabolism of Terpenoids and Polyketides	Terpenoid backbone biosynthesis	Terpenoid backbone biosynthesis	Terpenoid backbone biosynthesis
	NS	NS	Zeatin biosynthesis
Metabolism of cofactors and vitamins	NS	One carbon pool by folate	One carbon pool by folate
Translation	NS	NS	Ribosome
	NS	NS	Aminoacyl-tRNA biosynthesis
Amino acid metabolism	NS	NS	Lysine biosynthesis
	NS	NS	Glycine, serine and threonine metabolism
Xenobiotics biodegradation and metabolism	NS	NS	Chlorocyclohexane and chlorobenzene degradation

NS, no important significance compared with the model group.

Table S3 Differential KEGG pathways compared with the *L.rhamnosus* group using two-sided Welch's t test at  $P < 0.05$ 

OKGG	L-LXOS	L-HXOS
Carbohydrate Metabolism	Pyruvate metabolism↓	NS
	Butanoate metabolism↓	NS
	Starch and sucrose metabolism↓	Starch and sucrose metabolism↓
	C5-Branched dibasic acid metabolism↑	C5-Branched dibasic acid metabolism↑
Energy metabolism	Nitrogen metabolism↓	NS
	NS	Methane metabolism↓
Lipid Metabolism	Fatty acid metabolism↓	NS
	Glycerolipid metabolism↓	Glycerolipid metabolism↓
	Glycerophospholipid metabolism↓	Glycerophospholipid metabolism↓
Metabolism of Other Amino Acids	Glutathione metabolism↓	NS
	Phosphonate and phosphinate metabolism↓	Phosphonate and phosphinate metabolism↓
Glycan biosynthesis and metabolism	NS	Lipopolysaccharide biosynthesis↑
	N-Glycan biosynthesis↑	N-Glycan biosynthesis↑
	Other glycan degradation↑	Other glycan degradation↑
Metabolism of Terpenoids and Polyketides	NS	Zeatin biosynthesis↑
Metabolism of cofactors and vitamins	Thiamine metabolism↓	Thiamine metabolism↓
	NS	Riboflavin metabolism↓
	NS	Pantothenate and CoA biosynthesis↑
	NS	Vitamin B6 metabolism↑
	NS	One carbon pool by folate↑
	NS	Porphyrin and chlorophyll metabolism↓
	NS	Folate biosynthesis↓
	NS	Ribosome↑
Translation	NS	Ribosome↑
	Tyrosine metabolism↓	Tyrosine metabolism↓
	NS	D-Arginine and D-ornithine metabolism↓
	NS	Valine, leucine and isoleucine biosynthesis↑
Xenobiotics biodegradation and metabolism	NS	D-Glutamine and D-glutamate metabolism↑
	Nitrotoluene degradation↓	Nitrotoluene degradation↓
	Aminobenzoate degradation↓	NS
Folding, sorting and degradation	Sulfur relay system↓	Sulfur relay system↓

↑, significantly increased compared with the *L.rhamnosus* group; ↓, significantly decreased compared with the *L.rhamnosus* group; NS, no important significance compared with the *L.rhamnosus* group.

## Supplementary Figures

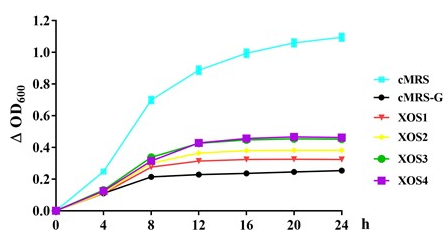


Fig. S1 Growth of *L. rhamnosus* CCFM1060 on different doses of XOS substrates *in vitro*. cMRS-G, cMRS medium without glucose; XOS1-4, cMRS medium without glucose but containing 25, 37.5, 50, 62.5 mg/ml XOS, respectively.

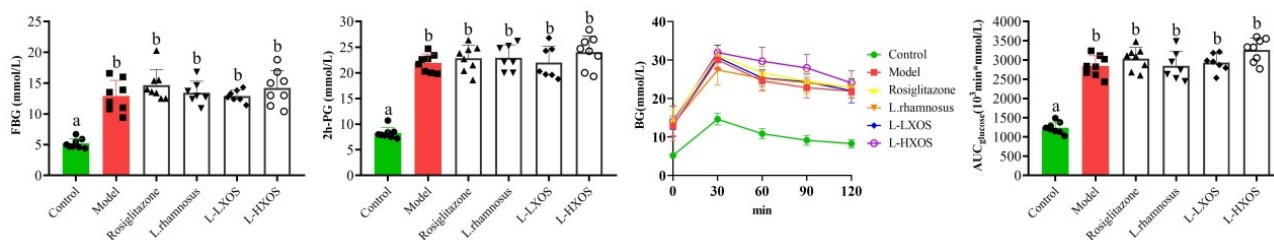


Fig. S2 FBG and OGTT 1 weeks after STZ injection. Graphs show mean  $\pm$  standard deviation;  $n = 8$ . Different superscript letters in a column indicate statistical differences between groups ( $P < 0.05$ ).

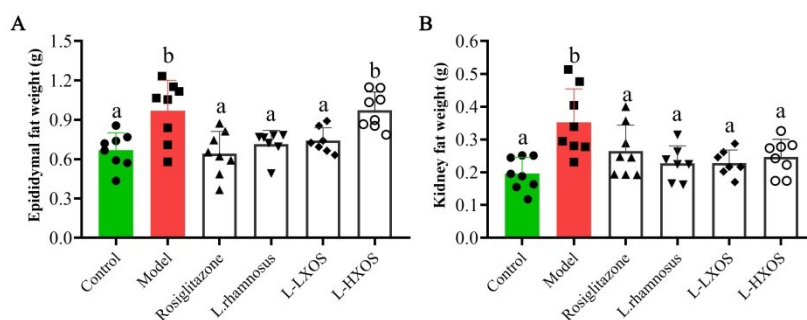


Fig. S3 Effects of *L. rhamnosus* CCFM1060 and combined with different doses of XOS on the adipose tissue of diabetic mice. (A) Epididymal fat weight. (B) Kidney fat weight. Graphs show mean  $\pm$  standard deviation;  $n = 8$ . Different superscript letters in a column indicate statistical differences between groups ( $P < 0.05$ ).

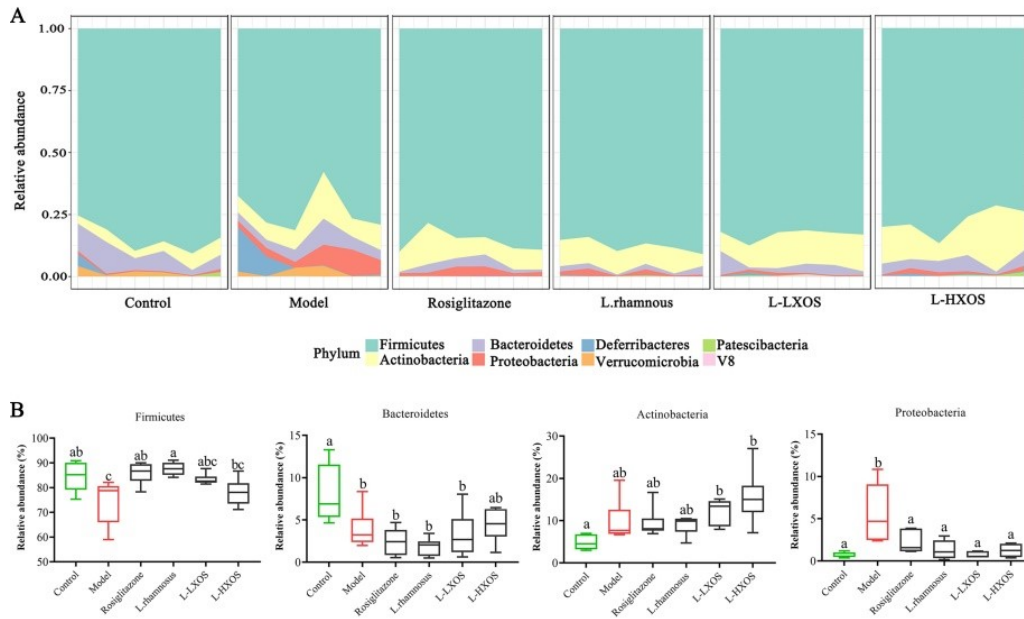


Fig. S4 Effects of *L. rhamnosus* CCFM1060 and combined with different doses of XOS on the structure at the phylum level of the gut flora (A) Microbial distribution at the phylum level. (B) Relative abundance of *Actinobacteria*, *Bacteroidetes*, *Firmicutes* and *Proteobacteria*. Graphs show mean  $\pm$  SD; n = 6; Different superscript letters in a column indicate statistical differences between groups ( $P < 0.05$ ).

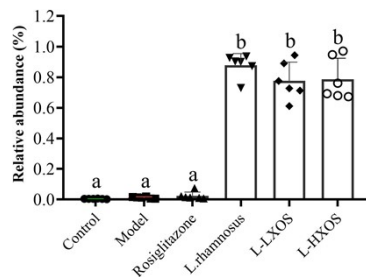


Fig. S5 Effects of *L. rhamnosus* CCFM1060 and combined with different doses of XOS on relative abundance of the *L. rhamnosus* in the intestine of mice. Different superscript letters in a column indicate statistical differences between groups ( $P < 0.05$ )

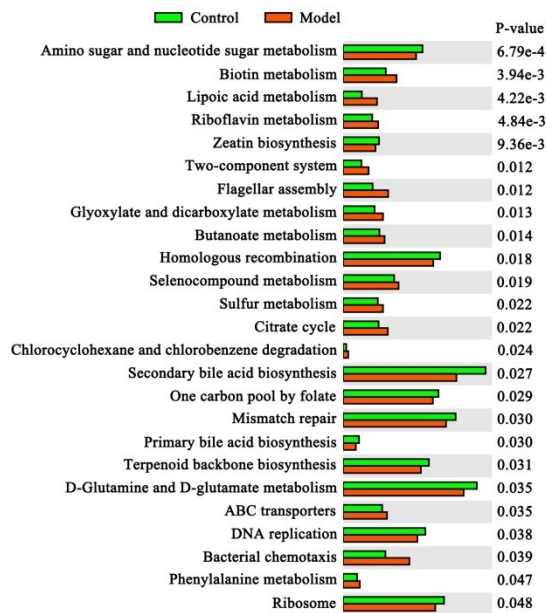


Fig. S6 Differential KEGG pathways between the model and control groups using two-sided Welch's t test at  $P < 0.05$