Class description	Ingredients	Grams	Caloric information (Kcal)
Protein	Casein, Latic, 30 Mesh	200.00g	— 20% Kcal
	Cystine, L	3.00g	
Carbohydrate	Lodex 10	125.00g	— 20% Kcal
	Sucrose, Fine Granulated	72.80g	
Fiber	Solka Floc, FCC200	50.00g	
Fat	Lard	245.00g	— 60% Kcal
	Soybean Oil, USP	25.00g	
Mineral	S10026B	50.00g	
Vitamin	Choline Bitartrate	2.00g	
	V10001C	1.00g	
Dye	Dye, Blue FD&C#1, Alum. Lake 35-42%	0.05g	
Total		773.85g	
Energy density			5.21 Kcal/g

Table S1. Ingredients of HFD (D12492, Research diet)

Figure S1.

(A)

100% Verrucomicrobia 90% 40 Relative abundance (%) 80% **** 30 70% Fibrobacteres Fusobacteria 20-Euryarchaeota Cyanobacteria Unknown Phylum **10** Tenericutes Actinobacteria Deferribacteres 0 1x10⁹ 4x10⁹ Met300 NFD Con N/A Verrucomicrobia HAC01 Proteobacteria 10% Bacteroid etes HFD+STZ Firmicutes 0% NFD Con 1x10⁹ 4x109 Met300

Figure S1. Changes in fecal bacterial community in *L. plantarum* HAC01 treated group and the metformin treated group with diabetes induced mouse. (A) Average relative abundance of the phylum level in each group. (B) Relative abundance of the phylum Verrucomicrobia in each group NFD: Normal fat diet; HFD+STZ_Con: High-fat diet + streptozotocin (STZ); HFD+STZ_1x10⁹-4x10⁹ HAC01: HFD+STZ + 1x10⁹- 4x10⁹ CFU/day *L. plantarum* HAC01; Met300: Metformin 300 mg/kg. The ends of the whiskers represent the minimum and maximum, the bottom and top of the box are the 1st and 3rd quartiles, and the line within the box is the median. Statistical significance was as follows: p<0.05 and ****p<0.0001 vs Con (n=10 per group).

(B)

Figure S2.

(A) (B) 4X10^9 Con Propionibacteriacea **4**X10^9 pionibacteriales Con p Proteobacteria nerellacea c Deltaproteobacteria istensenellaceae stridiaceae] f Desulfovibrionaceae Desulfovibrionacea Desulfovibrionales ulfovibrionales f Rikenellaceae obacteriaceae probacteriales f_Pseudomonadaceae udomonadaceae c Gammaproteobacteria inculturedrumenbacter o: Enterobacteriales Akkermansiaceae o Verrucomicrobiales f Enterobacteriaceae f Tannerellaceae Christensenellaceae Propionibacteriales Propionibacteriaceae Clostridiaceae1 unculturedrumehbacterium Actinóbacteria Verrucomicrobiales Verrucomicrobia Akkermansiaceae Verrucomicrobiae E009306091 Proteobacteria -6.0 -4.8 -3.6 -2.4 -1.2 0.0 1.2 2.4 3.6 6.0 4.8 LDA SCORE (log 10)

Figure S2. LEfSe analysis of fecal microbiota in *L. plantarum* $4 \ge 10^9$ HAC01-treated group and control group. (A) Cladogram generated by LEfSe indicating differences at phylum, class, and family levels between the two groups. Regions in green indicate taxa enriched in high fat diet and streptozotocin affected while regions in green indicate taxa enriched in $4 \ge 10^9$ HAC01-treated group . Differing taxa are listed on the right side of the cladogram. (B) Bar graph showing LDA scores. Significance determined using default parameters (Kruskal Wallis test p <0.05 and LDA score >2).

Figure S3.

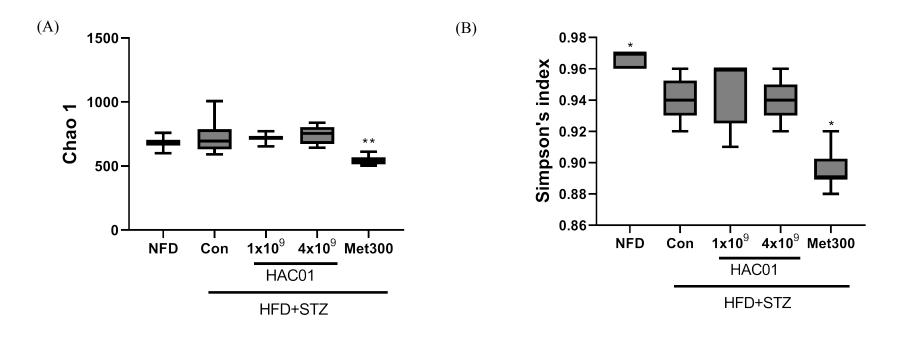


Figure S3. The richness and diversity of *L. plantarum* HAC01 treated group and the metformin treated group with diabetes induced mouse. (A) Chao 1. (B) Simpson's index. NFD: Normal fat diet; HFD+STZ_Con: High-fat diet + streptozotocin (STZ); HFD+STZ_1x10⁹-4x10⁹ HAC01: HFD+STZ + 1x10⁹- 4x10⁹ CFU/day *L. plantarum* HAC01; Met300: Metformin 300 mg/kg. The ends of the whiskers represent the minimum and maximum, the bottom and top of the box are the 1st and 3rd quartiles, and the line within the box is the median. Statistical significance was as follows: *p<0.05 and **p<0.01 vs Con (n=10 per group).

Figure S4.

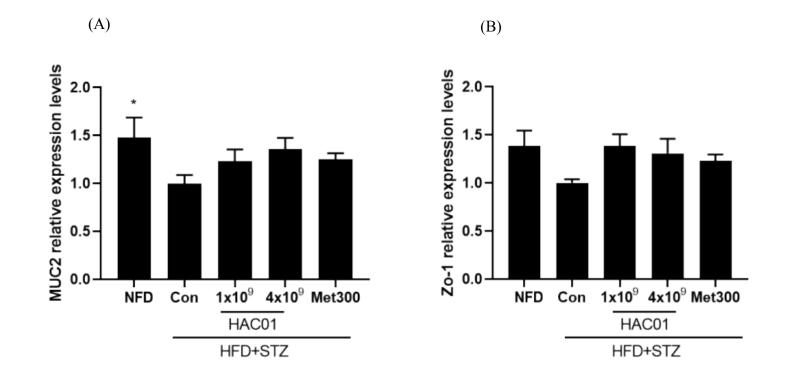


Figure S4. Effect of *L. plantarum* HAC01 on gut permeability in HFD+STZ-induced diabetic mice. (A) MUC2 mRNA expression levels and (B) Zo-1 mRNA expression levels. NFD: Normal fat diet; HFD+STZ_Con: High-fat diet + streptozotocin (STZ); HFD + STZ_1x10⁹-4x10⁹ HAC01: HFD + STZ +1x10⁹-4x10⁹ CFU/day *L. plantarum* HAC01; Met300: Metformin 300 mg/kg. Data are expressed as mean \pm SEM (n=10). **p*<0.05 vs the HFD + STZ_Con group.