

# *Lactobacillus casei* reduces susceptibility to type 2 diabetes via microbiota-mediated body chloride ion influx

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## Supplemental Tables

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Table S1 Primers for amplifying target intestinal bacteria

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Bacterial Target	Primer	Sequence (5'-3')	Reference
<i>C. scindens</i>	scindF	GCAACCTGCCTGCACT	1
	scindR	ACCGAATGCCCTGCCA	
<i>C. sordellii</i>	sordF	TCGAGCGACCTTCGG	2
	sordR	CACCACCTGTAC	
<i>C. coccoides-E.</i>	CEF	CGGTACCTGACTAAGAACG	2
<i>rectale</i> group	CER	AGTTTCATTCTTGCAGAACG	
<i>E. rectale</i>	RectaleF	CGGTACCTGACTAAGAACG	3
	RectaleR	CCTAGTATTATCGTTACGGCGTG	
<i>Lactobacillus</i>	Lac-F	AGCAGTAGGAAATCTCCA	3
	Lac-R	CACCGCTACACATGGAG	
<i>Bifidobacterium</i>	Bifid-F	CTCCTGGAAACGGGTGG	4
	Bifid-R	GGTGTTCCTCCGATATCTACA	
<i>Clostridium</i>	C4F	TACCHRAGGAGGAAGCCAC	
cluster IV	C4R	GTTCTTCCTAATCTTACGCAT	

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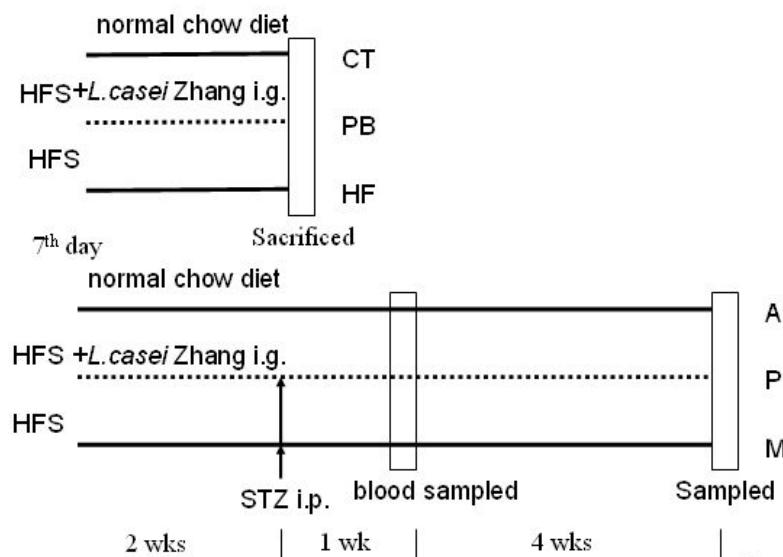
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Table S2 Primer sequences for real-time PCR

Gene	Primer	Sequence (5'-3')	Reference
18S	18SF	TAAGTCCCTGCCCTTGTACACA	5
	18SR	ATCCGAGGGCCTCACTAAAC	
CIC1	CIC1F	TGTGGAACGCTCAGAACTGCAGTC	6
	CIC1R	TCTAGTGCCAAGACACCTCTGAGC	
CIC-2	CIC-2F	GCAGTGATTGTCTCGAGCTCACCGG	7
	CIC-2R	CCAGCTCAGGCAGGTAGGGCAGCT	
CIC-3	CIC-3F	TTGCCTACTATCACCAACGAC	8
	CIC-3R	GCATCTCCAACCCATTACT	
CIC4	CIC4F	GAGACTCGGAGCGTCTCATCGG	9
	CIC4R	CTGTTGGCAGGCAGCTCAGGAG	
CIC5	CIC5F	TGCTGACTGTCCCTACTCAG	
	CIC5R	CAGGATGTTCCGAAGCTTCA	
CIC7	CIC7F	ATGAGCACGCCGTGACCTGCCTG	10
	CIC7R	CGAGGAAGAGATGCCTCTGTGGC	
GlyR $\alpha$ 1	GlyR1F	GCACCAAGCACTACAAACAC	11
	GlyR1R	AGGACAGGATGACGATAAGC	
GABA $\alpha$ 1	GABA1F	CTCCTACAGCAACCAGCTATAACCC	
	GABA1R	GCGGTTTGTCTCAGGCTTGAC	12
GABA $\alpha$ 2	GABA2F	AAGAGAAAGGCTCCGTATG	
	GABA2R	GCTTCTTGTGTTGGTCTGGAGTAG	
F4/80	F4/80F	ATGACCACACTTGCCATCCT	13
	F4/80R	GGCGAGTCGCTTCTAAGACA	
CD68	CD68F	TGGACTCAGCAGCTCTACCA	
	CD68R	CCTGTGGGTGGTCGTAGG	
CFTR	CFTRF	AATATCCTTAGCCCCTCGGA	14
	CFTRR	TGGTGGAAACAATGGCACTA	
FoxA2	FoxA2F	GTATGCTGGGAGCCGTGAAG	15
	FoxA2R	AGCCTCGCGCTCATGTTGC	
SLC26A3	SLC26A3F	TTCTACCCCTGTCTCGTC	16
	SLC26A3R	ACACCGTAGGAAATAGCG	
SLC26A6	SLC26A6F	CGGGAGGCAACACGCAGAT	
	SLC26A6R	GGTGGCTGAGGAACGGAAGAC	
CYP7A1	CYP7A1F	GAGCTCATGCATGCCAATGAGAAGAG	17
	CYP7A1R	AATTCCACATACCTCAGAGC	
Bestrophin-3	BEST3F	CTCATCTCCAGCAGTGTCCA	18
	BEST3R	CAGATGAGGCGACTTGAGG	
TGR5	TGR5F	TTGCTCCTGTCAGTCTGGCCTAT	19
	TGR5R	TTGGGTCTCCTCGAACGACTTGT	
T-BET	T-BETF	TCCTGTCTCCAGCCGTTCT	
	T-BETR	CGCTCACTGCTCGGAACCTCT	20
GATA-3	GATA-3 F	GGCGCGAGATGGTACTG	
	GATA-3 R	TCTGCCATTCAATTATGGTAGA	

20      Supplemental Figures



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Fig. S1 Experimental design

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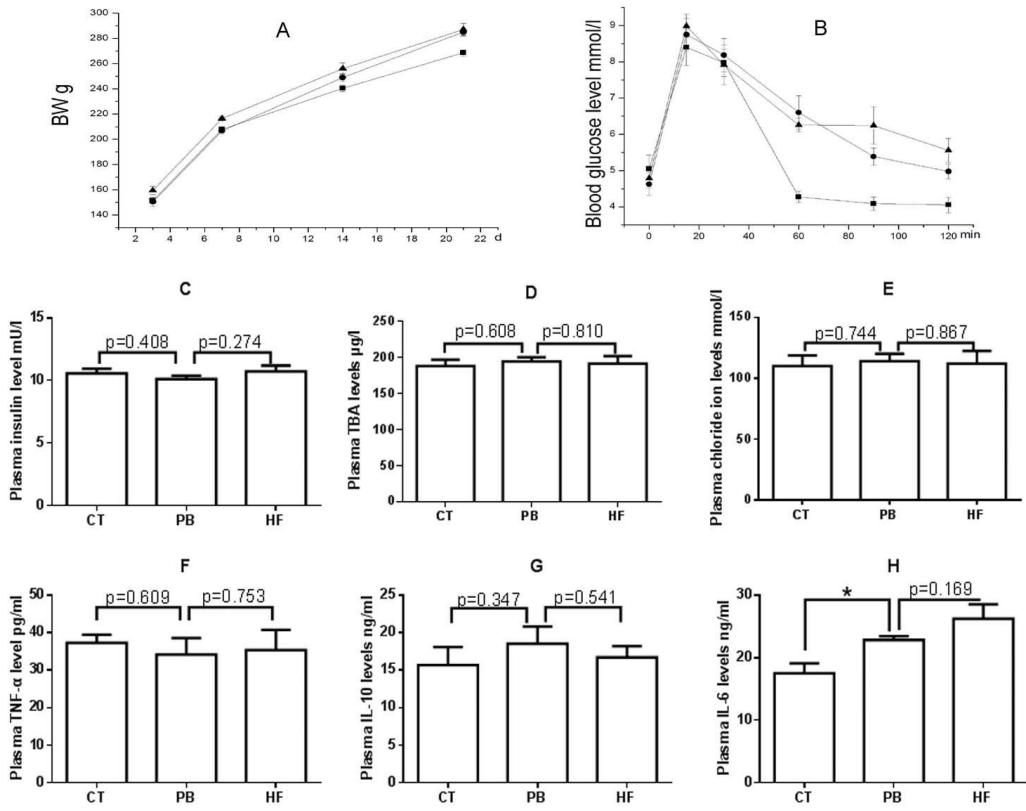
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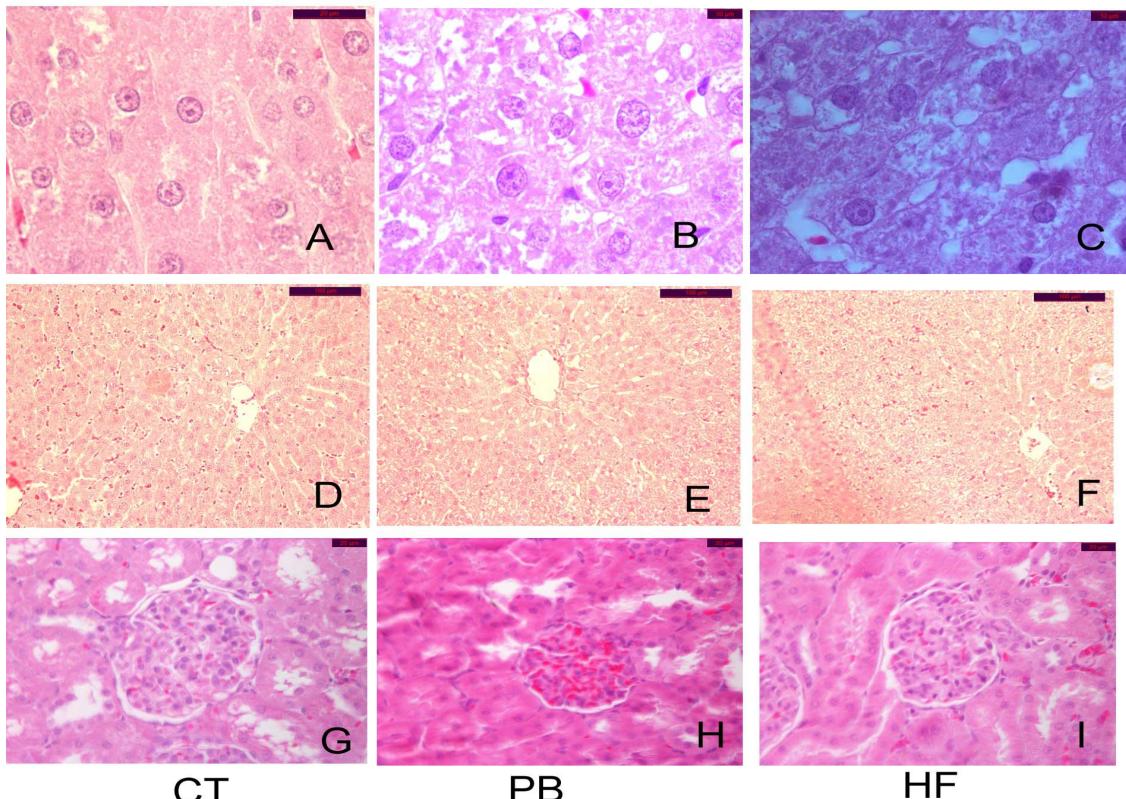
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35 Fig. S2 Comparison of body weight (A), OGTT (B), plasma insulin levels (C), plasma TBA  
 36 levels (D), plasma chloride ion levels (E), plasma TNF- $\alpha$  levels (F), plasma IL-10 levels (G), and  
 37 plasma IL-6 levels (H) between different groups. Black triangles = HF group; black circles = PB  
 38 group; black squares = CT group.\* represents  $p<0.05$ .

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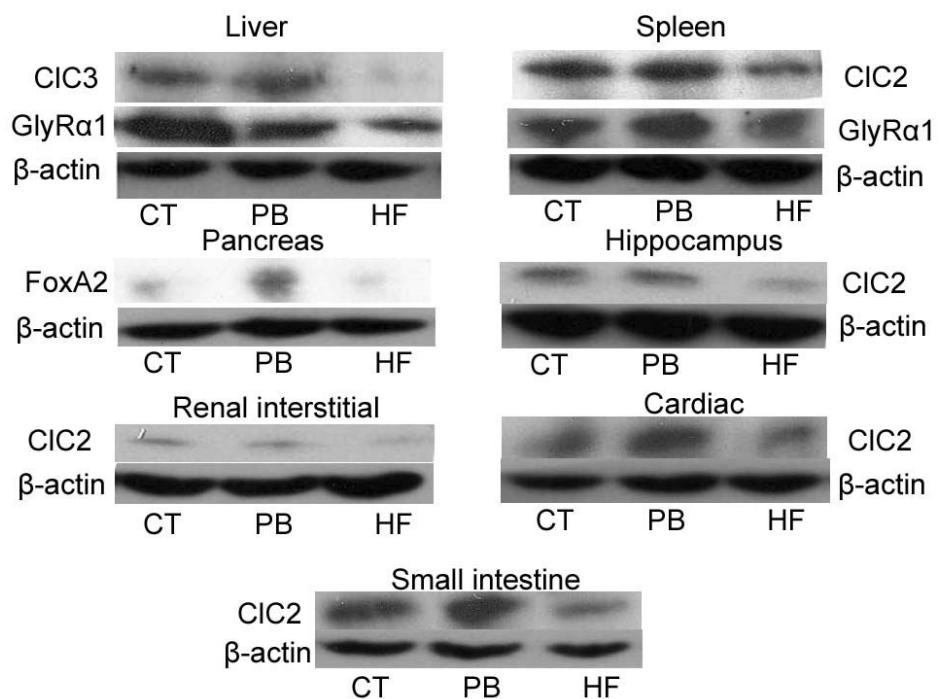
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42 Fig. S3 Hepatic (A-F) and renal (G-I) tissue sections of three groups of rat

43 CT: A( $\times 1000$ ), D( $\times 200$ ), G( $\times 1000$ ); PB: B( $\times 1000$ ), E( $\times 200$ ), H( $\times 1000$ ); HF: C ( $\times 1000$ ), F ( $\times 200$ ), I ( $\times 1000$ ).

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45 The CT rats exhibited an intact structure of hepatic lobule (A and D), whereas HF  
 46 rats showed preliminary fatty liver morphology with compressed liver sinusoids,  
 47 disarranged hepatic cords and large areas of fatty vacuolization but no inflammatory  
 48 infiltration (C and F). Compared to HF rats, hepatic structure was clear and areas of  
 49 fatty vacuolization were reduced in PB (B and E). No significant lesion was observed  
 50 in renal glomerulus of all three groups (G, H and I). However, both the kidneys of PB  
 51 and HF rats exhibited fewer renal tubular cavities (white areas) compared with the CT  
 52 rats (G, H and I).



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54 Fig. S4 The levels of target proteins in the three groups of rats

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66     **Supplemental references**

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