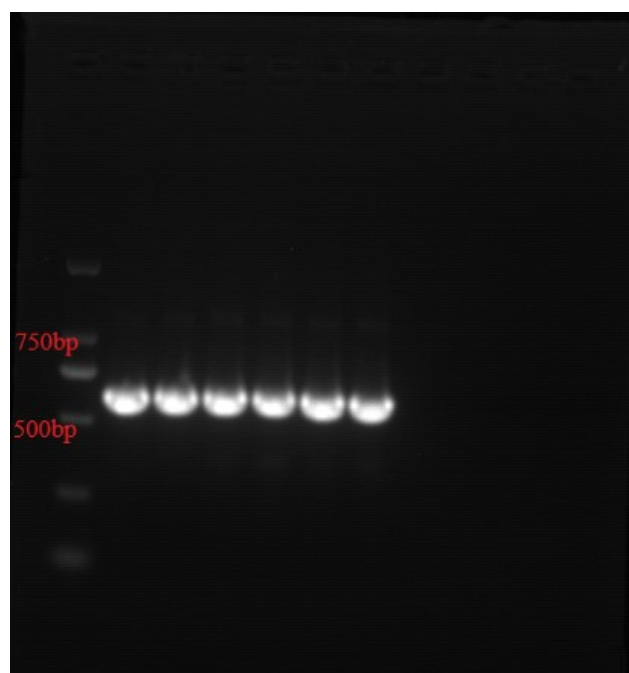


## Supplementary materials

**Figure S1.** The amplification results of *W. anomalus* 13611 by PCR.



**Table S1.** The biochemical characteristics of *W. amalus* 13611.

Items	Results	Items	Results
Cellobiose	+	Inulin	-
Maltose	+	Lactose	+
Mannitol	+	Melezitose	-
Salicin	+	Arabinose	+
Sorbitol	+	Inositol	-
Sucrose	+	Galactose	+
Raffinose	-	Xyitol	-

Note: “+” represents positive, which means it can ferment this carbohydrate; “-” represents negative, which means it cannot ferment this carbohydrate.

**Table S2.** Microbial composition of different treatments at the phylum level.

Taxon	CON	WA
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<i>Firmicutes</i>	0.681602263	0.680913589
<i>Bacteroidetes</i>	0.295815241	0.29477719
<i>Proteobacteria</i>	0.008385105	0.010656682
<i>Actinobacteria</i>	0.005389873	0.008026808
<i>Tenericutes</i>	0.003834886	0.002432855
<i>Cyanobacteria</i>	0.002461267	0.002081042
<i>Spirochaetes</i>	0.001813294	0.000791441
<i>TM7</i>	0.000262542	6.37E-05
<i>Euryarchaeota</i>	0.000184648	8.55E-05
<i>Verrucomicrobia</i>	7.59E-05	7.65E-05
<i>Chlamydiae</i>	3.85E-05	7.79E-05
<i>WPS_2</i>	7.50E-05	0
<i>Fibrobacteres</i>	6.15E-05	0
<i>Fusobacteria</i>	0	1.68E-05

**Table S3.** Microbial composition of different treatments at the family level.

<b>Taxon</b>	<b>CON</b>	<b>WA</b>
<i>Prevotellaceae</i>	0.211853208	0.217049849
<i>Streptococcaceae</i>	0.192475754	0.110284313
<i>Lactobacillaceae</i>	0.101051677	0.19637814
<i>Veillonellaceae</i>	0.129728377	0.114866823
<i>Ruminococcaceae</i>	0.109212469	0.120283486
<i>Lachnospiraceae</i>	0.066988533	0.084717074
<i>S24_7</i>	0.038723694	0.040210559
<i>[Paraprevotellaceae]</i>	0.027033673	0.023324457
<i>Unspecified_Clostridiales</i>	0.024003612	0.0166985
<i>Clostridiaceae</i>	0.023817305	0.006533932
<i>Unspecified_Bacteroidales</i>	0.016119854	0.009992676
<i>Erysipelotrichaceae</i>	0.009661119	0.011173684
<i>Christensenellaceae</i>	0.009451117	0.006942229
<i>Coriobacteriaceae</i>	0.005259145	0.007925039

**Table S4.** Microbial composition of different treatments at the genus level.

Taxon	CON	WA
<i>Prevotella</i>	0.211671438	0.217049849
<i>Streptococcus</i>	0.192475754	0.110260791
<i>Lactobacillus</i>	0.100959962	0.196327919
<i>Megasphaera</i>	0.06985205	0.059971257
<i>Unspecified_Ruminococcaceae</i>	0.046918966	0.055698637
<i>Unspecified_S24_7</i>	0.038723694	0.040210559
<i>Phascolarctobacterium</i>	0.025259203	0.030801879
<i>Gemmiger</i>	0.02225814	0.02896128
<i>[Prevotella]</i>	0.021904637	0.01980111
<i>Unspecified_Lachnospiraceae</i>	0.021950624	0.019727791
<i>Unspecified_Clostridiales</i>	0.024003612	0.0166985
<i>Blautia</i>	0.012017829	0.028191992
<i>Oscillospira</i>	0.019174787	0.016995046
<i>Mitsuokella</i>	0.016885587	0.013098312
<i>Unspecified_Bacteroidales</i>	0.016119854	0.009992676
<i>Unspecified_Clostridiaceae</i>	0.018438116	0.005136359
<i>Roseburia</i>	0.010286999	0.010273546
<i>Ruminococcus</i>	0.011335336	0.008730094
<i>Faecalibacterium</i>	0.008728718	0.008323345
<i>Unspecified_Christensenellaceae</i>	0.009451117	0.006942229
<i>Other</i>	0.101583576	0.096806828

**Table S5.** The analysis results of the bacterial taxa differentially by LEfSe.

	Mean relative abundance within the group (Logarithmic conversion value)	Location	LDA score	P value
<i>k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Lactobacillaceae</i>	5.336	WA	4.876	0.016
<i>k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Lactobacillaceae.g_Lactobacillus</i>	5.336	WA	4.876	0.016
<i>k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Lactobacillaceae.g_Lactobacillus.s_helveticus</i>	5.089	WA	4.792	0.012
<i>k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Lactobacillaceae.g_Lactobacillus.s_delbrueckii</i>	3.450	WA	3.787	0.027
<i>k_Bacteria.p_Proteobacteria.c_Betaproteobacteria</i>	3.139	CON	3.978	0.043
<i>k_Bacteria.p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales</i>	3.139	CON	4.868	0.010
<i>k_Bacteria.p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Oxalobacteraceae</i>	3.139	CON	3.778	0.043
<i>k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Streptococcaceae</i>	4.814	CON	4.370	0.021
<i>k_Bacteria.p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Oxalobacteraceae.g_Oxalobacter</i>	3.139	CON	4.044	0.043
<i>k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Streptococcaceae.g_Streptococcus</i>	4.814	CON	4.370	0.021
<i>k_Bacteria.p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Oxalobacteraceae.g_Oxalobacter.s_formigenes</i>	3.139	CON	4.106	0.043
<i>k_Bacteria.p_Firmicutes.c_Erysipelotrichi.o_Erysipelotrichales.f_Erysipelotrichaceae.g_Eubacterium.s_cylindroides</i>	2.964	CON	4.188	0.008
<i>k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Streptococcaceae.g_Streptococcus.s_alactolyticus</i>	4.814	CON	4.370	0.021