(A)

A	L. zymae
B	L. plantarum
C	L. futsaii
D	L. brevis
E	L. paraplantarum
F	L. unclassified
G	L. spicheri
H	L. acidifarinae
I	L. alimentarius
J	L. pentosus
K	L. paralimentarius
L	L. namurensis
M	L. versmoldensis
N	P. inopinatus
O	P. parvulus
P	P. cellicola
Q	P. damnosus
R	P. ethanolidurans
S	A. sp_L
T	A. anaerophilus

● FIRMICUTES
● PROTEOBACTERIA

(B)

A	S. stipitis
B	D. fabryi
C	D. hansenii
D	Pic. kudriavzevii
E	K. africana
F	C. phage CR5
G	L. phage LP65
H	L. plantarum
I	L. crustorum
J	L. mindensis
K	L. futsaii
L	L. kimchiensis
M	L. alimentarius
N	L. paralimentarius
O	L. farciminis
P	M. minutulum
Q	Pec. carotovorum
R	V. furnissii
S	V. fluvialis
T	V. litoralis

● ASCOMYCOTA
● FIRMICUTES
● PROTEOBACTERIA
● VIRUSES UNCLASSIFIED

Supplementary Figure S1 Taxonomy of the microbial community in matured industrial ZP (A) and QP (B) using metagenomic sequencing. Only the species with abundance in top 100 was presented and the top 20 were labeled by stars. The size of star and the color thickness of the outside ring represent the abundance of species. L.: *Lactobacillus*, P.: *Pediococcus*, A.: *Arcobacter*, S.: *Scheffersomyces*, D.: *Debaryomyces*, Pic.: *Pichia*, K.: *Kazachstania*, C.: *Cronobacter*, M.: *Marinospirillum*, Pec.: *Pectobacterium*, V.: *Vibrio*.