Table S1. The detail information of 16S rRNA gene sequences for all samples.

sample	clean_tags	singleton%	chimeras%	Effective_tags	OTUs
NP-1	129360 ± 38390	12.9 ± 3.0	0.9 ± 0.6	110071 ± 29399	350±90
NP-2	165016 ± 7095	12.4 ± 0.2	0.0 ± 0.0	144516 ± 6596	324 ± 18
NP-3	79459 ± 2292	1.1 ± 0.7	1.3 ± 1.6	77554 ± 1313	217 ± 22
YCR1	81558 ± 779	2.5 ± 0.3	0.8 ± 0.3	78885 ± 973	66 ± 11
YCR2	94343 ± 48465	10.4 ± 2.1	0.4 ± 0.3	83208 ± 40808	187 ± 158
YCG3	90605 ± 3067	3.3 ± 0.3	1.2 ± 0.3	86560 ± 3338	68 ± 5
SW-1	67819 ± 797	3.8 ± 0.4	0.6 ± 0.0	64801 ± 555	850 ± 34
SW-2	67686 ± 3452	4.3 ± 1.3	1.0 ± 0.4	64061 ± 3077	708 ± 195
SW-3	64041 ± 2515	2.5 ± 1.8	0.1 ± 0.1	62311 ± 2322	401 ± 129

Data are expressed as mean ± SD (n = 3).