Supplementary Tables

Table S1. Sequence-processing statistics for bacterial 16S rRNA gene amplicons.

Fermentation stage	Input reads	Filtered reads	Input passed filter (%)	Denoised reads	Merged reads	Input merged (%)	Non-chimeric reads[1]	Input non-chimeric (%)	ASVs
10 °Brix	64,672	63,696	98.49	62,400	56,138	86.80	25,237	39.02	38
5 °Brix	82,631	81,639	98.80	80,539	71,470	86.49	28,379	34.34	49
2 °Brix	70,061	69,149	98.70	68,051	59,948	85.57	23,031	32.87	40

[1]Non-chimeric reads represent the final post-DADA2 sequencing depth used for downstream processing. Percentages were calculated relative to the input reads. ASV, amplicon sequence variant.

Table S2. Sequence-processing statistics for fungal ITS1 amplicons.

Fermentation stage	Input reads	Filtered reads	Input passed filter (%)	Denoised reads	Merged reads	Input merged (%)	Non-chimeric reads[1]	Input non-chimeric (%)	ASVs
10 °Brix	212,195	205,997	97.08	205,399	200,255	94.37	118,059	55.64	51
5 °Brix	175,492	168,497	96.01	168,050	160,906	91.69	124,337	70.85	35
2 °Brix	80,171	78,344	97.72	78,205	77,708	96.93	73,717	91.95	32

[1]Non-chimeric reads represent the final post-DADA2 sequencing depth used for downstream processing. Percentages were calculated relative to the input reads. ASV, amplicon sequence variant.