Supplementary

**Table S1.** The bacterial relative abundance in genus level of the two Moutai-flavor Daqu samples.

|  |  |  |  |
| --- | --- | --- | --- |
| No. | Genus name | The relative abundance (%) | |
| GT01 | GT02 |
| 1 | *Brevibacterium* | 2.30 | 0 |
| 2 | *Corynebacterium* | 0.30 | 0 |
| 3 | *Brachybacterium* | 0.40 | 0 |
| 4 | *Glycomyces* | 0.30 | 0 |
| 5 | *Microbacterium* | 0.10 | 0 |
| 6 | *Arthrobacter* | 0.10 | 0 |
| 7 | *Saccharomonospora* | 0.20 | 0 |
| 8 | *Saccharopolyspora* | 1.10 | 0.20 |
| 9 | *Streptomyces*. | 1.50 | 0 |
| 10 | *Nonomuraea* | 0.10 | 0 |
| 11 | *Bacteroides* | 0.10 | 0 |
| 12 | *Dyadobacter* | 0.10 | 0 |
| 13 | *Flavobacterium* | 0.10 | 0 |
| 14 | *Chryseobacterium* | 0.20 | 0 |
| 15 | *Olivibacter* | 0.20 | 0 |
| 16 | *Pedobacter* | 0.10 | 0 |
| 17 | *Sphingobacterium* | 2.20 | 0 |
| 18 | *Bacillus* | 17.80 | 56.50 |
| 19 | *Kurthia* | 0.40 | 0 |
| 20 | *Scopulibacillus* | 0 | 0.20 |
| 21 | *Staphylococcus* | 3.80 | 0.10 |
| 22 | *Planifilum* | 0 | 0.70 |
| 23 | *Thermoactinomyces* | 5.00 | 15.40 |
| 24 | *Lactobacillus* | 2.00 | 0.30 |
| 25 | *Leuconostoc* | 0.20 | 0.40 |
| 26 | *Weissella* | 0.10 | 0.10 |
| 27 | *Lactococcus* | 0.20 | 0 |
| 28 | *Tepidimicrobium* | 0.10 | 0 |
| 29 | *Ochrobactrum* | 0.20 | 0 |
| 30 | *Methylobacterium* | 0.10 | 0 |
| 31 | *Paracoccus* | 0.10 | 0 |
| 32 | *Acetobacter* | 0.20 | 0 |
| 33 | *Sphingomonas* | 0.10 | 0 |
| 34 | *Rhodospirillum* | 0.10 | 0 |
| 35 | *Comamonas* | 0.40 | 0 |
| 36 | *Delftia* | 0.10 | 0 |
| 37 | *Hydrogenophaga* | 0 | 0.10 |
| 38 | *Myxococcus* | 0.10 | 0 |
| 39 | *Citrobacter* | 0.10 | 0.10 |
| 40 | *Enterobacter* | 0.40 | 0.60 |
| 41 | *Erwinia* | 0.20 | 0.60 |
| 42 | *Escherichia* | 0.10 | 0 |
| 43 | *Klebsiella* | 0.10 | 0 |
| 44 | *Proteus* | 27.10 | 0 |
| 45 | *Providencia* | 0.30 | 0 |
| 46 | *Acinetobacter* | 1.20 | 0.10 |
| 47 | *Enhydrobacter* | 0 | 0 |
| 48 | *Pseudomonas* | 1.40 | 0 |
| 49 | *Luteimonas* | 0.20 | 0 |
| 50 | *Pseudoxanthomonas* | 0.10 | 0 |
| 51 | *Stenotrophomonas* | 0.40 | 0 |
| 52 | Unclassified | 27.60 | 24.50 |

**Table S2.** The mold relative abundance in genus level of the two Moutai-flavor Daqu samples.

|  |  |  |  |
| --- | --- | --- | --- |
| No. | Genus name | The relative abundance (%) | |
| GT01 | GT02 |
| 1 | *Lichtheimia* | 5.40 | 9.50 |
| 2 | *Rhizomucor* | 0.60 | 0.70 |
| 3 | *Thamnostylum* | 0 | 0.10 |
| 4 | *Thermomucor* | 0 | 2.20 |
| 5 | *Mucor* | 0.50 | 0.70 |
| 6 | *Rhizopus* | 33.60 | 17.10 |
| 7 | *Bispora* | 0 | 0.80 |
| 8 | *Neocatenulostroma* | 2.30 | 3.80 |
| 9 | *Aspergillus* | 56.50 | 61.30 |
| 10 | *Elaphomyces* | 0.20 | 0.20 |
| 11 | *Pseudotulostoma* | 0.10 | 0 |
| 12 | *Paecilomyces* | 0 | 0.10 |
| 13 | *Galactomyces* | 0.30 | 0.20 |
| 14 | *Ceratolenta* | 0.10 | 0.20 |
| 15 | *Myrothecium* | 0 | 0.10 |
| 16 | *Tolypocladium* | 0 | 1.20 |
| 17 | *Graphium* | 0 | 0.30 |
| 18 | *Diatrypasimilis* | 0.30 | 0.60 |
| 19 | *Puccinia* | 0 | 0.20 |
| 20 | Unclassified | 0.10 | 0.60 |

**Table S3.** The yeast relative abundance in genus level of the two Moutai-flavor Daqu samples.

|  |  |  |  |
| --- | --- | --- | --- |
| No. | Genus name | The relative abundance (%) | |
| GT01 | GT02 |
| 1 | *Hyphopichia* | 0.50 | 1.40 |
| 2 | *Galactomyces* | 0 | 0.50 |
| 3 | *Wickerhamomyces* | 0. | 0.90 |
| 4 | *Pichia* | 0.10 | 14.30 |
| 5 | *Nakaseomyces* | 0 | 0.10 |
| 6 | *Saccharomyces* | 0 | 0.50 |
| 7 | *Saccharomycopsis* | 99.40 | 80.00 |
| 8 | *Trichomonascus* | 0 | 2.20 |
| 9 | Unclassified | 0 | 0.1 |

**Table S4.** Alpha-diversity index of the two Moutai-flavor Daqu samples.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample | **C**hao | **A**ce | **S**impson | **S**hannon |
| GT01 | 312.973 | 308.3545 | 0.724148 | 3.312139 |
| GT02 | 673.1589 | 689.5607 | 0.915248 | 5.562487 |