

**TABLE S1** Numbers of sequences and the observed OTUs, estimated OTU richness (Ace, Chao 1), diversity index (Shannon), and estimated sample coverage for 16S rRNA gene libraries of MT-Daqu samples.

Sample ID	Raw reads	Trim reads	coverage	OTUs	Ace	Chao	Shannon
Day 0	1564	1144	96.71%	64	138	127	2.21
Day 2	2161	1729	98.71%	80	101	92	2.80
Day 4	1544	1129	95.83%	134	218	183	3.97
Day 6	1595	1151	97.39%	96	126	118	3.25
Day 8	1582	1081	98.51%	78	90	87	3.49
Day 10	1882	1073	97.39%	73	103	105	2.55
Day 12	1451	1071	98.13%	74	91	91	3.22
Day 17	1860	1314	98.16%	81	104	98	3.03
Day 27	15592	11749	98.94%	263	836	481	3.54
Day 32	2856	2057	98.44%	93	131	138	3.21

**TABLE S2** Number of sequences and the observed OTUs, estimated OTU richness (Ace, Chao 1), diversity index (Shannon), and estimated sample coverage for ITS rRNA gene libraries of MT-Daqu samples

Sample ID	Raw reads	Trim Reads	coverage	OTUs	Ace	Chao	Shannon
Day 0	88206	87707	99.99%	105	110	107	1.98
Day 2	57036	56864	99.96%	99	123	111	2.14
Day 4	96710	96495	99.99%	89	99	98	1.67
Day 6	51620	51287	99.97%	104	117	115	2.6
Day 8	49797	49578	99.96%	78	96	91	1.96
Day 10	36426	36187	99.97%	59	72	67	1.1
Day 12	46299	45618	99.97%	81	90	87	1.44
Day 17	39277	38819	99.96%	70	86	85	1.46
Day 27	33016	32778	99.93%	86	112	118	2.19
Day 32	37538	37097	99.97%	54	66	63	1.18

**TABLE S3** Bacterial OTUs differentially distributed in the MT-Daqu microbiotas formed at different temperature

OTU ID	T37 <sup>a</sup>		T50		P-value	Taxonomy
	Mean (%)	Variance	Mean (%)	Variance		
OTU010	13.09	0.04	22.73	0.02	0.01	<i>Bacillus licheniformis</i>
OTU017	1.75	0.00	5.24	0.04	0.04	<i>Thermoactinomyces vulgaris</i>
OTU022	0.24	0.00	9.16	0.01	0.00	<i>Lactobacillus fermentum</i>
OTU027	0.03	0.00	0.08	0.00	0.01	<i>Lactobacillus buchneri</i>
OTU041	0.01	0.00	0.11	0.00	0.04	<i>Staphylococcus sciuri subsp</i>
OTU042	0.05	0.00	0.18	0.00	0.02	<i>Lactobacillus paracasei</i>
OTU071	5.83	0.02	9.54	0.00	0.03	<i>Lactobacillus farciminis</i>
OTU004	4.34	0.01	0.43	0.00	0.02	<i>Staphylococcus gallinarum strain</i>
OTU016	2.26	0.00	0.68	0.00	0.03	<i>Lactobacillus brevis</i>
OTU044	4.36	0.03	0.78	0.00	0.04	<i>Pediococcus pentosaceus</i>
OTU058	26.48	0.01	21.31	0.08	0.04	<i>Weissella confusa</i>
OTU116	3.44	0.00	0.79	0.00	0.01	<i>Lactobacillus plantarum</i>
OTU122	0.11	0.00	0.00	0.00	0.00	<i>Saccharopolyspora rectivirgula</i>

<sup>a</sup> MT-Daqu bricks with the temperature of  $52.5\pm 0.8$  °C in the fermentation room after 4 d of fermentation were moved to two different rooms with controlled temperatures at 50 °C (T50 group) and 37 °C (T37 group), respectively. Red background, 7 bacterial OTUs showing higher relative abundance in MT-Daqu microbiota in the T50 group; Blue background, 6 bacterial taxa showing higher relative abundance in MT-Daqu fermented at 37 °C.

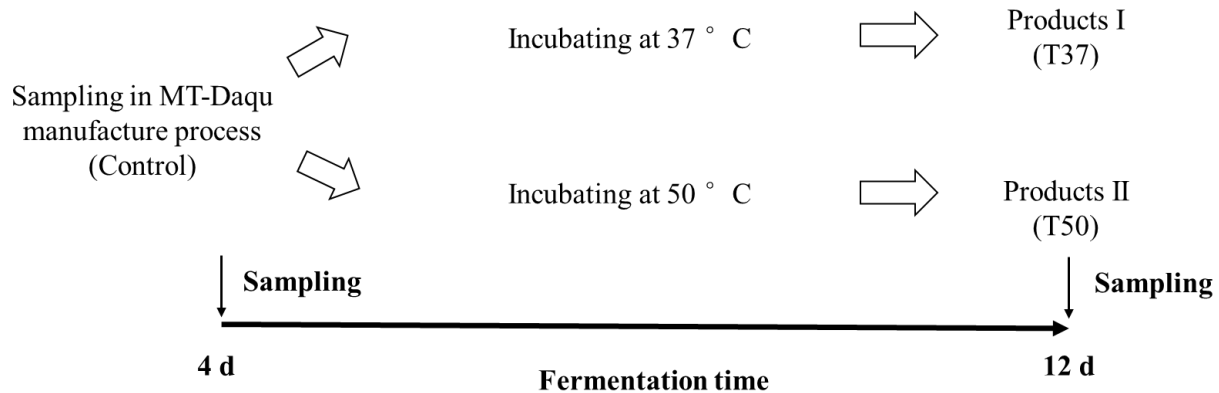
**TABLE S4** Fungal OTUs differentially distributed in the MT-Daqu microbiotas formed at different temperature

OTU ID	T37 <sup>a</sup>		T50		P-value	Taxonomy
	Mean (%)	Variance	Mean (%)	Variance		
OTU010	0.30	0.00	0.68	0.00	0.01	<i>Thermoascus sp</i>
OTU043	45.08	13.44	98.01	0.00	0.03	<i>Thermoascus sp</i>
OTU004	0.91	0.00	0.00	0.00	0.02	<i>Aspergillus penicillioides</i>
OTU016	0.64	0.00	0.04	0.00	0.02	<i>Epicoccum nigrum</i>
OTU028	0.01	0.00	0.00	0.00	0.04	<i>Cladosporium ramotenellum</i>
OTU045	0.60	0.00	0.06	0.00	0.03	<i>Gibberella zeae</i>
OTU051	46.28	9.29	0.01	0.00	0.01	<i>Aspergillus amstelodami</i>

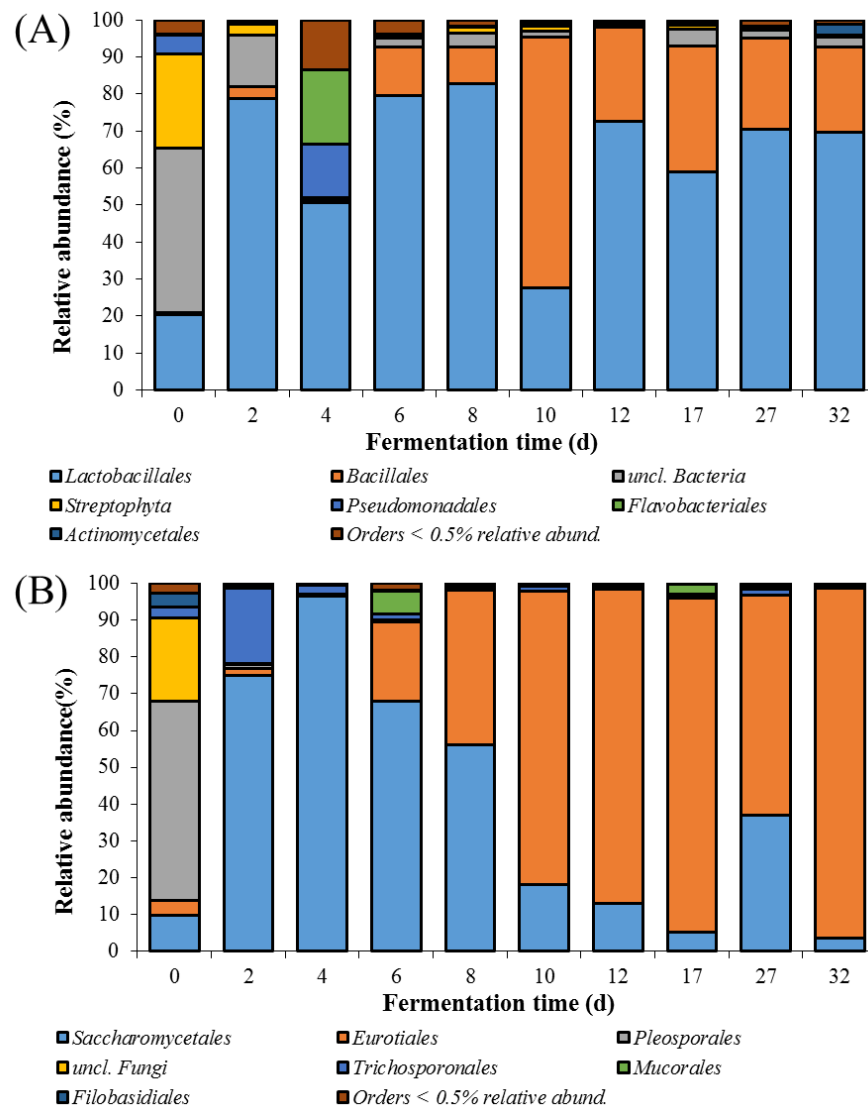
<sup>a</sup> MT-Daqu bricks with the temperature of  $52.5\pm 0.8$  °C in the fermentation room after 4 d of fermentation were moved to two different rooms with controlled temperatures at 50 °C (T50 group) and 37 °C (T37 group), respectively. Red background, 2 fungal OTUs with higher relative abundance in MT-Daqu microbiota fermented at 50 °C; Blue background, 5 fungal taxa with higher relative abundance in MT-Daqu fermented at 37 °C.



**FIG S1** A flow diagram of MT-Daqu production



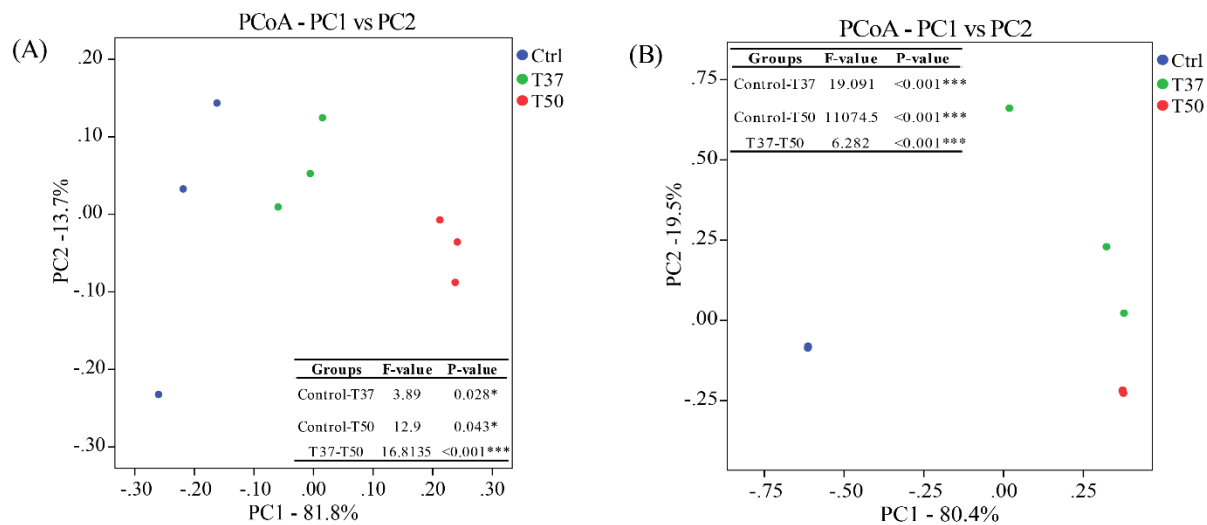
**FIG S2** A flow diagram of exploring microbes differentially distributed in the MT-Daqu microbiotas formed at different temperature



**FIG S3** Temporal patterns of microbial community during the fermentation process of MT-Daqui.

(A) Temporal profile for the relative abundance of bacterial taxa represented at the order level; (B)

Temporal profile for the relative abundance of fungal taxa represented at the order level.



**FIG S4** Comparison the structures of bacterial community (A) and fungal community (B) based on Bray-Curtis distance matrices. MT-Daqu bricks in the fermentation room after 4 d of fermentation (Ctrl group) were moved to two different rooms with controlled temperatures at 50 °C (T50 group) and 37 °C (T37 group), respectively. *P*-values<0.05 showed that significant difference of community structure existed between two treatment groups.