Supplementary Table S1. DNA sequnece of 26S rDNA D/D2 of *kuratsuki* sake yeasts and wild yeasts in this study.

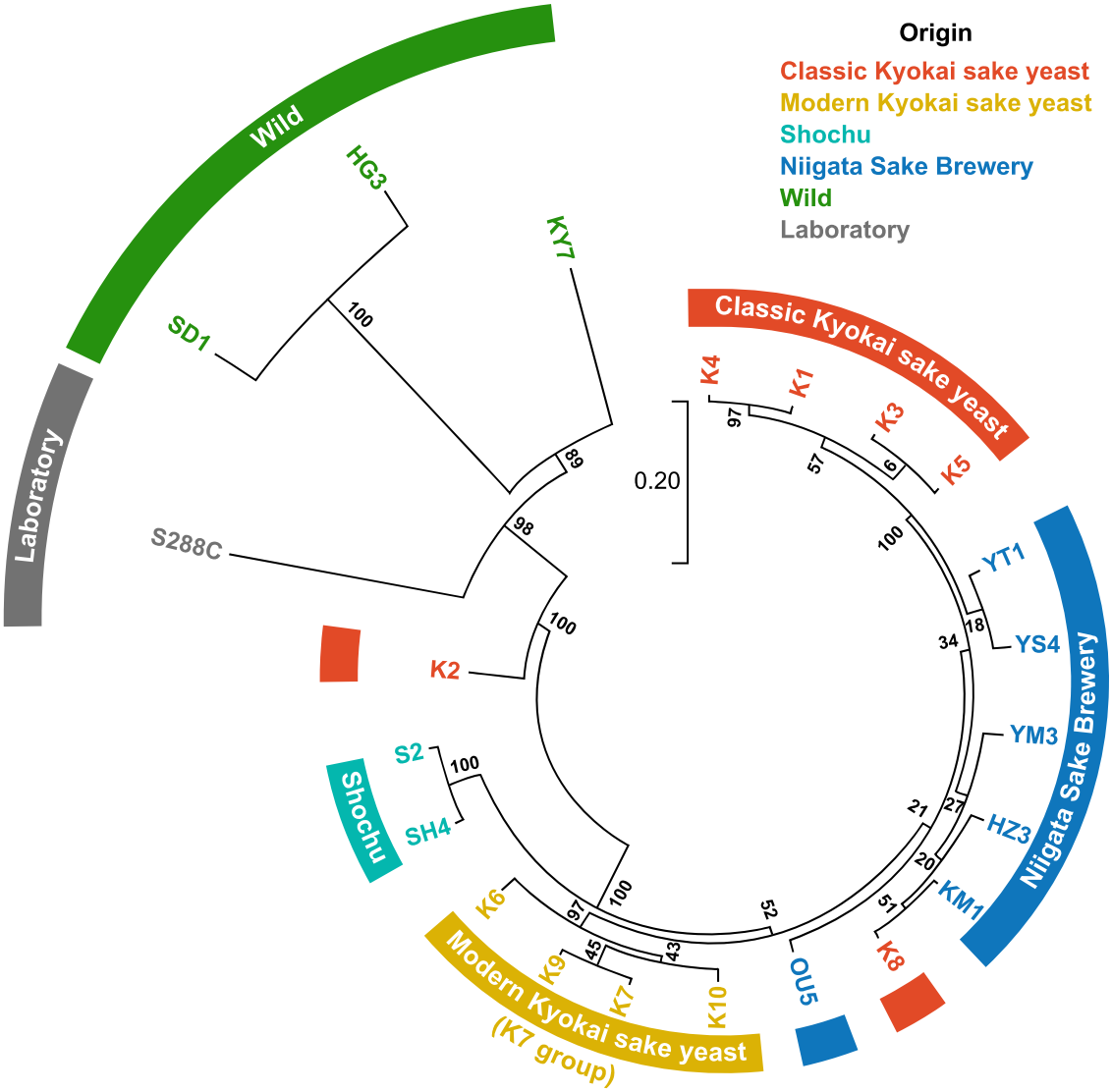
Yeast strain	DNA sequnece of 26s rDNA D1/D2
YT1	AAACCAACCGGGATTGCCTTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAA ATCTGGTACCTTCGGTGCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCC TTGTCTATGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGG AGTGCGGTTCTTTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTA AGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAG TACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATT GTTGAAAGGGAAGGGCATTTGATCAGACATGGTGTTTTGTGCCCTCTGCTCCTTGTGG GTAGGGGAATCTCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCA TAGGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGGA CTGAGGACTGCGACGTAAGTCAAGGATGCTGGCATAATGGTTATATGCCGC
OU5	AAACCAACCGGGATTGCCTTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAA ATCTGGTACCTTCGGTGCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCC TTGTCTATGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGG AGTGCGGTTCTTTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTA AGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAG TACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATT GTTGAAAGGGAAGGGCATTTGATCAGACATGGTGTTTTGTGCCCTCTGCTCCTTGTGG GTAGGGGAATCTCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCA TAGGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGGA CTGAGGACTGCGACGTAAGTCAAGGATGCTGGCATAATGGTTATATGCCGC
KM1	AAACCAACCGGGATTGCCTTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAA ATCTGGTACCTTCGGTGCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCC TTGTCTATGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGG AGTGCGGTTCTTTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTA AGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAG TACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATT GTTGAAAGGGAAGGGCATTTGATCAGACATGGTGTTTTGTGCCCTCTGCTCCTTGTGG GTAGGGGAATCTCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCA TAGGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGGA CTGAGGACTGCGACGTAAGTCAAGGATGCTGGCATAATGGTTATATGCCGC
HZ3	AAACCAACCGGGATTGCCTTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAA ATCTGGTACCTTCGGTGCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCC TTGTCTATGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGG AGTGCGGTTCTTTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTA AGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAG TACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATT GTTGAAAGGGAAGGGCATTTGATCAGACATGGTGTTTTGTGCCCTCTGCTCCTTGTGG GTAGGGGAATCTCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCA TAGGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGGA CTGAGGACTGCGACGTAAGTCAAGGATGCTGGCATAATGGTTATATGCCGC
YM3	AAACCAACCGGGATTGCCTTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAA ATCTGGTACCTTCGGTGCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCC TTGTCTATGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGG AGTGCGGTTCTTTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTA AGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAG TACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATT GTTGAAAGGGAAGGGCATTTGATCAGACATGGTGTTTTGTGCCCTCTGCTCCTTGTGG GTAGGGGAATCTCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCA TAGGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGGA CTGAGGACTGCGACGTAAGTCAAGGATGCTGGCATAATGGTTATATGCCGC

KY7	AAACCAACCGGGATTGCCTTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAA ATCTGGTACCTTCGGTGCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCC TTGTCTATGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGG AGTGCGGTTCTTTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTA AGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAG TACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATT GTTGAAAGGGAAGGGCATTTGATCAGACATGGTGTTTTGTGCCCTCTGCTCCTTGTGG GTAGGGGAATCTCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCA TAGGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGGA CTGAGGACTGCGACGTAAGTCAAGGATGCTGGCATAATGGTTATATGCCGC
SD1	AAACCAACCGGGATTGCCTTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAA ATCTGGTACCTTCGGTGCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCC TTGTCTATGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGG AGTGCGGTTCTTTGTAAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTA AGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAG TACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATT GTTGAAAGGGAAGGGCATTTGATCAGACATGGTGTTTTGTGCCCTCTGCTCCTTGTGG GTAGGGGAATCTCGCATTTCACTGGGCCAGCATCAGTTTTGGTGGCAGGATAAATCCA TAGGAATGTAGCTTGCCTCGGTAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGGA CTGAGGACTGCGACGTAAGTCAAGGATGCTGGCATAATGGTTATATGCCGC

Supplementary Table S2. Sake fermentation parameters in small-scale brewing tests (100 g of total rice).

Yeast strain	CO_2 evolution (g)	General properties				Flavor components (mg/L)					Glucose (%)	Urea (mg/L)	4-Vinyl guaiacol (μg/L)
		Sake meter	Alcohol (%)	Acidity (mL)	Amino acidity (mL)	Ethyl acetate	Isobutyl alcohol	Isoamyl acetate	Isoamyl alcohol	Ethyl caproate			
K1	27.3±0.3	-35.4±2.0	16.6±0.0	2.6±0.6	2.5±0.2	64.0±3.7	36.1±2.1	3.2±0.3	123.1±3.7	0.3±0.1	5.7±0.3	16.7±0.4	5.6±1.4
K2	24.8±0.1	-54.7±1.2	14.7±0.2	3.5±0.0	3.0±0.1	41.3±1.4	78.1±5.5	0.8±0.0	139.4±6.9	0.3±0.0	7.3±0.2	8.6±0.6	5.2±0.8
K3	30.7±0.9	-24.9±1.5	18.2±0.2	3.1±0.1	2.6±0.1	53.2±4.2	78.0±13.8	1.4±0.3	144.6±21.5	0.4±0.1	4.2±0.2	7.1±0.8	5.7±0.0
K4	30.4±0.3	-29.1±2.2	18.1±0.0	3.8±0.1	2.3±0.1	58.1±4.3	58.4±12.5	1.5±0.1	137.6±6.6	0.6±0.0	4.5±0.2	11.0±0.1	7.0±3.2
K5	27.5±0.6	-39.7±2.5	16.6±0.3	3.3±0.1	2.5±0.2	43.0±8.3	58.3±11.4	1.6±0.4	143.3±25.2	0.3±0.1	5.9±0.3	7.6±0.5	3.4±0.3
K6	28.6±0.2	-38.1±1.3	16.8±0.2	3.5±0.1	2.7±0.3	70.4±6.3	77.7±1.0	3.7±0.3	147.3±5.4	0.6±0.0	5.5±0.2	8.0±0.5	4.9±0.4
K7	27.2±1.5	-39.1±7.8	16.3±0.7	3.6±0.2	2.5±0.1	79.7±11.0	84.8±3.3	4.6±1.2	164.2±7.9	0.9±0.1	6.0±1.2	8.8±0.3	6.4±1.3
K8	26.3±0.6	-47.5±0.5	15.6±0.1	3.3±0.3	2.6±0.1	62.8±3.3	70.5±0.2	0.9±0.0	127.2±3.3	0.5±0.0	6.6±0.1	8.6±0.3	5.2±1.1
K9	28.1±0.2	-36.8±3.0	16.9±0.1	3.7±0.1	2.5±0.1	69.0±2.0	63.7±1.1	2.8±0.1	138.0±2.8	0.6±0.0	5.3±0.4	8.4±0.2	4.1±0.9
K10	30.5±0.3	-24.5±2.4	18.3±0.1	2.8±0.0	2.5±0.1	111.5±2.0	51.6±4.8	7.1±0.4	161.2±5.9	0.8±0.0	4.2±0.4	12.1±0.4	3.9±0.2
S2	26.9±0.3	-46.6±0.7	16.0±0.1	3.9±0.1	2.3±0.1	30.8±3.4	52.3±2.5	0.8±0.1	138.4±6.2	0.4±0.0	6.5±0.1	6.5±0.2	3.7±0.2
SH4	27.0±0.2	-45.0±0.8	16.2±0.2	3.8±0.1	2.2±0.2	32.8±1.8	55.6±2.8	0.9±0.0	142.9±2.6	0.4±0.0	6.4±0.1	6.6±0.3	3.3±0.2
YS4	29.8±0.6	-30.9±2.6	17.9±0.3	3.1±0.1	2.5±0.1	78.9±6.1	128.4±9.0	5.0±0.7	215.9±16.2	0.5±0.1	5.0±0.3	8.3±0.5	4.4±1.2
YT1	24.9±0.5	-51.3±0.9	14.9±0.1	3.8±0.0	2.4±0.1	60.0±3.0	49.9±1.6	1.1±0.1	131.5±5.1	0.4±0.0	7.1±0.1	6.6±0.7	3.4±0.7
OU5	30.6±0.3	-28.5±2.0	18.4±0.2	3.2±0.0	2.1±0.1	98.3±8.3	67.4±5.3	5.0±0.7	151.1±5.0	0.9±0.1	4.9±0.2	13.4±0.4	3.9±0.6
KM1	27.1±0.4	-38.1±2.4	16.5±0.1	3.5±0.1	2.1±0.1	65.6±4.4	57.7±3.3	1.2±0.1	137.9±1.7	0.6±0.1	5.7±0.3	6.1±0.5	2.2±0.4
HZ3	24.0±0.3	-52.6±0.7	14.5±0.1	3.3±0.1	2.5±0.0	63.2±1.2	41.9±3.5	0.8±0.1	107.1±3.4	0.3±0.0	7.4±0.1	8.4±0.6	1.9±1.0
YM3	21.6±0.2	-66.4±0.5	12.9±0.1	4.0±0.1	2.4±0.1	57.1±2.3	38.2±1.6	0.7±0.0	109.2±2.1	0.4±0.0	8.3±0.1	7.0±0.6	2.2±0.5
HG3	21.4±0.3	-66.9±2.6	13.0±0.0	4.0±0.2	2.2±0.1	48.8±3.0	48.9±2.7	0.7±0.1	128.2±5.0	0.5±0.0	8.6±0.1	7.1±0.7	98.2±12.9
KY7	20.4±0.6	-73.4±0.8	12.1±0.0	4.2±0.2	2.3±0.1	41.5±1.0	53.3±2.6	0.6±0.0	134.6±2.7	0.5±0.0	9.6±0.2	6.5±0.1	60.7±5.0
SD1	20.1±0.1	-71.7±0.9	12.1±0.2	4.0±0.1	2.4±0.2	44.2±0.8	55.0±3.3	0.5±0.0	122.1±3.0	0.4±0.1	9.6±0.3	6.3±0.2	61.9±4.1
S288C	22.7±0.2	-60.1±0.9	13.9±0.0	3.0±0.1	2.7±0.0	32.6±0.4	49.4±1.1	0.5±0.0	101.5±1.1	0.5±0.0	8.6±0.0	6.0±0.1	91.6±4.4

Values are averages from three independent brewing experiments.



Supplementary Fig. S1 kuribayashi *et al.*