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Table S1: MinION sequencing metrics for *Brettanomyces* sequencing

	Median read length (bp)	Median read quality (QV)	Number of reads	Read length N50 (bp)	Total bases (Gb)
<i>B. anomalus</i>	4 685	8.7	296 479	7 859	1.65
<i>B. custersianus</i>	6 695	7.9	180 237	10 588	1.35
<i>B. naardenensis</i>	4 249	8.9	83 581	9 336	0.497
<i>B. nanus</i>	14 912	10.8	28 586	30 870	0.508

Table S2: Predicted genes, gene density, and orthogroup duplicity for the *Brettanomyces* genomes

	Number of genes	Total genic sequence (bp)	Total genic sequence (% of genome)	Orthogroups with multiple genes (% of orthogroups)
<i>B. anomalus</i>	5 735	8 571 724	62.2	10.4*
<i>B. bruxellensis</i>	5 293	8 469 775	64.2	6.0
<i>B. custersianus</i>	5 255	8 094 938	75.4	5.4
<i>B. naardenensis</i>	5 334	8 393 268	75.2	5.6
<i>B. nanus</i>	5 083	7 960 011	78.1	5.2
<i>S. cerevisiae</i> (S288C)	6 445	9 008 924	74.1	9.7

* Averaged between H1 and H2

Table S3: Constrained tree topology tests for *Brettanomyces* invertases (depicted in Figure S4)

Tree	logL	deltaL	Bp-RELL	p-KH	p-SH	c-ELW	p-AU
a	-112583.8414	0	1	1	1	1	1
b	-112793.0893	209.25	0	0	0	6.92e-51	3.59e-06
c	-112833.7503	249.91	0	0	0	2.55e-69	4.67e-08
d	-112818.1804	234.34	0	0	0	1.86e-62	4.28e-34

Columns are as follows: Tree, the tree depicted in Figure S4; logL, the log likelihood; deltaL, the difference from the maximal logL in the set; bp-RELL, bootstrap proportion using REll method (Kishino et al., 1990); p-KH, p-value of one sided Kishino-Hasegawa test (Kishino and Hasegawa, 1989); p-SH, p-value of Shimodaria-Hasegawa test (Ota et al., 2000); c-ELW, Expected likelihood weight (Strimmer and Rambaut, 2002); p-AU, p-value of approximately unbiased (AU) test (Shimodaira, 2002).

Table S4: Saccharomycetaceae species used with *Brettanomyces* species in OrthoFinder

Species	Genome accession
<i>Agaricus bisporus</i>	GCF_000300575.1
<i>Babjeviella inositovora</i>	GCF_001661335.1
<i>Candida albicans</i>	GCF_000182965.3
<i>Candida boidinii</i>	GCA_001599335.1
<i>Candida glabrata</i>	GCF_000002545.3
<i>Candida tenuis</i>	GCF_000002545.3
<i>Citeromyces matritensis</i>	GCA_003243085.1
<i>Debaryomyces hansenii</i>	GCF_000006445.2
<i>Eremothecium gossypii</i>	GCF_000091025.4
<i>Hansenispora osmophila</i>	GCA_001747045.1
<i>Kazachstania africana</i>	GCF_000304475.1
<i>Kluyveromyces lactis</i>	GCF_000002515.2
<i>Komagataella phaffii</i>	GCF_000027005.1
<i>Lachancea thermotolerans</i>	GCF_000142805.1
<i>Lodderomyces elongisporus</i>	GCF_000149685.1
<i>Nadsonia fulvescens</i>	GCA_001661315.1
<i>Nakaseomyces bscillisporus</i>	GCA_001046975.1
<i>Naumovozya dairenensis</i>	GCF_000227115.2
<i>Ogataea methanolica</i>	GCA_001600755.1
<i>Ogataea parapolyomorpha</i>	GCF_000187245.1
<i>Ogataea polymorpha</i>	GCF_001664045.1
<i>Pachysolen tannophilus</i>	GCA_001661245.1
<i>Pichia membranifaciens</i>	GCF_001661235.1
<i>Saccharomyces bayanus</i>	GCA_000167035.1
<i>Saccharomyces boulardii</i>	GCA_001413975.1
<i>Saccharomyces cerevisiae</i>	GCF_000146045.2
<i>Saccharomyces eubayanus</i>	GCF_001298625.1
<i>Saccharomyces mikatae</i>	GCA_000166975.1
<i>Saccharomyces paradoxus</i>	GCA_002079145.1
<i>Saccharomyces uvarum</i>	GCA_002242645.1
<i>Spathaspora xylofermentans</i>	GCA_002105455.1
<i>Torulaspora delbrueckii</i>	GCF_000243375.1
<i>Wickerhamiella sorbophila</i>	GCF_002251995.1
<i>Wickerhamomyces anomalus</i>	GCF_001661255.1
<i>Wickerhamomyces ciferrii</i>	GCF_000313485.1
<i>Zygosaccharomyces parabolii</i>	GCA_001984395.2

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