

**Genome sequence of *Saccharomyces carlsbergensis*, the world's first pure culture lager yeast**

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**Table S1 Primers used in this study to bridge gaps between scaffolds**

Chr	Primer 1	sequence	Primer 2	sequence 2	scaffold
2/4	6479	GGCGACAGCACGACCAGTACCCC	6485	GGAAGCAGGAGTGACTGAGGC	1
4	6591	GTTGCGTGTGCACAGTAGAGGG	6611	cagtgtactccggaggagcattcac	3+42
4	6964	GTGTAATAGACGACCCATG	6965	GAAGGCTTATGCTGGAGC	42+1p
4/2	6480	GGTATGTAAGTAAAACCAG	6486	CATAAGGAAAAGTAAGCAATG	4
7	6482	CTCTTAATAAAGAAAGGTGCAAAGAA	6488	TAGTCCACCTGTACTTGGGCCG	6
7	6593	CTGATTCATAGCCTCGTAtAG	6613	GCTCAGAGTTTACCAAGAGAG	6+32
7	6481	CTTAATAAAGAAAGATGTAATAAGT	6487	GTTGTTCCAGGCATACTCGCA	2
7	6594	CCAGTAGGTCCTCTGTAAGAC	6614	CCAATGTCGACCCAGACGAG	32+77
7	6595	CAACCACCAGATTTGATGTTT	6615	GAGATTCGCCAAGCAGACGTC	77+59
8	6596	CATAAATTTGATCTTAGCATC	6616	GGACAACGTGGATAGCAAGGAC	50+22
8/15	6520	GTTATTTTCGTTCCGGTCTCAAGG	6528	CTGTAAGGATTATTTGGTCAAACCTC	27+15
8/15	6551	CTGTGATCCAAAGGCTGACTTG	6552	GTATACTACCTTATTATATGTATTAC	27+15
10	6598	GGAGAATATTGACAGTTACAC	6618	GTGAAAGTTCTTTGCAAGATG	24+23
10	6599	GGATTGCAGACCATTTCATC	6619	GAATTTTCGTTATTCCTACCTTC	25+37
10	6600	CAGATTTCCAAATTAATG	6620	GAAGAAGCTGCCATTTCCG	37+28
11	6601	CTCGAAGACAGTTCATCGTATG	6621	CTGTGTGTTCCGTAGTTCACC	53+10
12	6602	GATGACCGTAAATGCTGCTTG	6622	CGAACGACTTGTGACGACGC	5+40
13	6517	GGTGATACGGATGGTAATGGGCATCG	6526	CATTGCTACCTCTACTAAGGTT	39+51
13	6604	CTGGTGGGGCTGTGTGGATGC	6624	CTACCCGTAATCAAGTTGCC	11+41
13	6515	GCAAGTAATTCGAATTAATGG	6523	CTATTGGGTGTACCGAGTATCCTG	41+47
13	6517	GGTGATACGGATGGTAATGGGCATCG	6525	CATTGCCACCTCCACCAACGTC	39+30
13	6548	CCGTTCTACCTGAACTACGAG	6549	TCACGACTTATAGCTGCAATTAATCAC	39+30
13	6605	CCATTGTTGACCTGATTCTG	6625	GATGAAGGCCTTCGACCGTC	30+16
13	6515	GCAAGTAATTCGAATTAATGG	6524	CTTTATACGTCGCTCCCTCAG	16+47
14	6606	CAGCGAAGTGGAAGATGACC	6626	GAACATCAAGGCTTTGGACC	46+14
14	6607	GACATTGTCTTGTGGAGCC	6627	GCAATGATAAGGTGTTCTTC	14+36
15	6608	GACGAAGACAGTTAGCTTTAC	6628	GAGCGGACCATTGCAAGTGG	44+17
15	6519	gtcgtgtcgaagtcaagaacgc	6527	GTTGGGGACGAGTCGCCTTGAG	17+15
15	6550	CAGAATCCAAGGTCCAAACTACG	6528	CTGTAAGGATTATTTGGTCAAACCTC	17+15
15/8	6609	GCCATCTCATTTAGCACCAGC	6629	GTCACCATCTCTCATTCCAAG	9+43
16	6521	GCACCAGCAGAAGAGTTAGTC	6529	TGAGTCAGAATCATCAGCGGCAGAAG	18+20
16	6521	GCACCAGCAGAAGAGTTAGTC	6530	GGAGTCGAGTCGTTAGCAGCAGGCA	18+26
16	6522	GAAAGTGTGTGGGCAGGATTG	6531	CTCTTTCTCGTTATTCAGATTG	20+52

**Table S2 Volatile compound analysis**

<b>compound</b>		<b>WS34/70</b>			<b>CBS1513</b>			<b>CBS1503</b>		
Ethanol	% v/v	5,86	±	0,01	6,04	±	0,01	5,13	±	0,00
acetaldehyde	ppm	3,5	±	0,7	5,2	±	0,2	4,5	±	0,2
ethylacetate	mg/l	35,1	±	1,3	18,1	±	1,3	17,5	±	4,4
isobutanol	mg/l	116,8	±	11,0	194,9	±	1,4	76,6	±	27,2
isobutylacetate	mg/l	0,3	±	0,1	0,2	±	0,1	0,1	±	0,1
propanol	mg/l	31,0	±	1,1	25,4	±	0,3	24,8	±	1,2
isoamyl alcohol	mg/l	244,1	±	17,2	224,3	±	1,2	174,0	±	32,1
isoamylacetate	mg/l	7,5	±	0,8	4,9	±	0,4	2,5	±	1,1
2-phenylethanol	mg/l	57,8	±	6,4	76,9	±	7,2	60,1	±	17,9
2-phenylethyl acetate	mg/l	1,3	±	0,1	1,3	±	0,1	0,7	±	0,3
ethyl hexanoate	mg/l	0,2	±	0,1	0,2	±	0,0	0,2	±	0,1
ethyl octanoate	mg/l	0,2	±	0,0	0,2	±	0,0	0,1	±	0,0
hexanoic acid	mg/l	0,8	±	0,0	0,7	±	0,1	0,7	±	0,2
octanoic acid	mg/l	5,4	±	0,2	6,5	±	0,3	5,6	±	1,6
vinyl gäiacol	mg/l	0,7	±	0,1	0,7	±	0,1	0,8	±	0,0
Decanoic acid	mg/l	0,2	±	0,0	1,3	±	0,1	1,3	±	0,3
Total acids	mg/l	6,4	±	0,2	8,5	±	0,3	7,6	±	1,6
Sub-total alcohols	mg/l	205,6	±	17,8	297,3	±	8,8	161,4	±	44,7
Total esters	mg/l	43,3	±	2,2	23,7	±	1,8	20,3	±	5,5

**Table S3 Scaffold assembly for *S. carlsbergensis***

<i>Saccharomyces carlsbergensis</i>			
Sc Chr	Scaffolds	Se Chr	Scaffolds
I	33	I	34
II	7	II-IV	1
III	38 (TY) 35	III	31+78+35part
IV	3+42+1part	IV-II	4
V	12	V	13
VI	-	VI	29
VII	6+32+77+59	VII	2
VIII	50+22**48	VIII-XV	27+15
IX	19	IX	21
X	24 (TY) 23	X	25*37+28
XI	-	XI	53*10, 52
XII	-	XII	5+40
XIII	39+51 (TY) 11+41+47	XIII	39+30 (TY) 16+47
XIV	46 (TY) 14 (TY) 36	XIV	8
XV	44+17+15	XV-XIII	9+43
XVI	56+18*20+52	XVI	56+18+26+45+52

A “+” indicates that scaffolds were combined by PCR and sequencing. Grey boxes mark scaffolds that represent either chromosomes consisting of only one scaffold or chromosomes which were generated by merging scaffolds. Red boxes mark scaffolds with gaps containing TY-elements. A “\*\*” indicates a gap < 0.5 kb verified by PCR and “\*\*\*” indicates the region between YHR165C and YHR174W that is apparently missing in *S. carlsbergensis*.