Table S1: Annotated genes with functions in sugar fermentation

Enzyme/Protein	*S. cerevisiae*		*H. uvarum*		%aa identity
Hexose transporter	*HXT1*	*YHR094C*	*HuHXT1*	***HUVA_0D00240***	56
	HXT2	*YMR011W*	*HuHXT2*	*HUVA_0L01320*	54
	HXT3	*YDR345C*		*HUVA_0L01320*	55
	HXT4	*YHR092C*		*HUVA_0L01320*	54
	HXT5	*YHR096C*		*HUVA_0L01320*	52
	HXT6	*YDR343C*		*HUVA_0L01320*	57
	HXT7	*YDR342C*		*HUVA_0L01320*	57
	HXT8	*YJL214W*		*HUVA_0L01320*	56
	HXT9	*YJL219W*		*HUVA_0L01320*	56
	HXT10	*YFL011W*		*HUVA_0L01320*	52
	HXT11	*YOL156W*		*HUVA_0L01320*	55
	HXT12	*YIL170W*		*HUVA_0L01320*	48
	HXT13	*YEL069C*		*HUVA_0L01320*	50
	HXT14	*YNL318C*	*HuHXT14*	***HUVA_0B02500***	33
	HXT15	*YDL245C*		*HUVA_0L01320*	49
	HXT16	*YJR158W*		*HUVA_0L01320*	49
	HXT17	*YNR072W*		*HUVA_0L01320*	50
Hexokinase/Glucokinase	*HXK1*	*YFR053C*	*HuHXK2*	*HUVA_0D01460*	71
	HXK2	*YGL253W*		*HUVA_0D01460*	72
	Glk1	*YCL040W*		*HUVA_0D01460*	36
Phosphoglucose isomerase	*PGI1*	*YBR196C*	*HuPGI1*	***HUVA_0A01480***	71
Phosphofructokinase	*PFK1*	*YGR240C*	*HuPFK1*	***HUVA_0H01120***	57
	PFK2	*YMR205C*	*HuPFK2*	***HUVA_0V00740***	56
Aldolase	*FBA1*	*YKL060C*	*HuFBA1*	***HUVA_0G01470***	76
Triosephoshate isomerase	*TPI1*	*YDR050C*	*HuTPI1*	***HUVA_0D00480***	68
Triosephosphate-dehydrogenase	*TDH1*	*YJL052W*	*HuTDH3*	*HUVA_0B02070*	78
	TDH2	*YJR009C*		*HUVA_0B02070*	82
	TDH3	*YGR192C*		*HUVA_0B02070*	83
Phoshpoglycerate kinase	*PGK1*	*YCR012W*	*HuPGK1*	***HUVA_0F00810***	73
Phosphoglycerate mutase	*GPM1*	*YKL152C*	*HuGPM1*	***HUVA_0B02300***	76
Enolase	*ENO1*	*YGR254W*	*HuENO2*	*HUVA_0H00510*	82
	ENO2	*YHR174W*		*HUVA_0H00510*	81
Pyruvate kinase	*PYK1*	*YAL038W*	*HuPYK1*	***HUVA_0S00560***	77
Pyruvate decarboxylase	*PDC1*	*YLR044C*	*HuPDC1*	***HUVA_0S00750***	78
Alcohol dehydrogenase	*ADH1*	*YOL086C*	*HuADH1*	*HUVA_0N01010*	72
	ADH2	*YMR303C*		*HUVA_0N01010*	71
	ADH3	*YMR083W*	*HuADH3*	***HUVA_0N01040***	67

Amino acid identities were calculated from global sequence alignments using the needle Programm of the EMBOSS software package. The location of each homolog in *H. uvarum* is given by a trivial name and the systemic gene name of the annotation.

[1] The three annotated hexose transporters of *H. uvarum* are indicated. A BLAST search against the nucleotide sequence translated in all six frames independent of annotated open reading frames shows the presence of five more sequences with homology to hexose transporters in the *H. uvarum* genome. Whether these encode functional homologs or pseudogenes remains to be determined.

[2] The corrected sequence of *HuPFK1* was used for this comparison as explained in the main manuscript, rather than the annotated genome sequence.

Table S2: Annotated genes with functions in production of aromatic compounds

Functional group	*S. cerevisiae*		*H. uvarum*		%aa identity
Higher alcohols					
Amino acid permeases	*GAP1*	*YKR039W*	*HuGAP1*	***HUVA_0Q00300***	66
Transaminases	*BAT1*	*YHR208W*	*HuBAT1*	*HUVA_0G00720*	67
	BAT2	*YJR148W*		*HUVA_0G00720*	64
	ARO8	*YGL202W*	*HuARO8*	***HUVA_0J01320***	46
	ARO9	*YHR137W*	*HuARO9*	***HUVA_0O00700***	30
Decarboxylases	*PDC1*	*YLR044C*	*HuPDC1*	***HUVA_0S00750***	78
	THI3	*YOL086C*	*HuTHI3*	*HUVA_0N01010*	72
Dehydrogenases	*ADH1*	*YOL086C*	*HuADH1*	*HUVA_0N01010*	72
	ADH3	*YMR083W*	*HuADH3*	***HUVA_0N01040***	67
	SFA1	*YDL168W*	*HuSFA1*	***HUVA_0BV00120***	57
	ALD5	*YER073W*	*HuALD5*	***HUVA_0AA00210***	47
	ALD6	*YPL061W*	*HuALD6*	***HUVA_0AH00100***	54
	OYE2	*YHR179W*	*HuOYE2*	***HUVA_0AE00210***	47
	HOM2	*YDR158W*	*HuHOM2*	***HUVA_0A00230***	70
Ester compounds					
Acetyl-/Acyltransferases	*EEB1*	*YPL095C*	*HuEEB1*	***HUVA_0A01690***	41
	IAH1	*YOR126C*	*HuIAH1*	***HUVA_0A04760***	46
Glycerol production					
Dehydrogenase	*GPD1*	*YDL022W*	*HuGPD1*	***HUVA_0AC00420***	46
Phosphatase	*GPP2*	*YER062C*	*HuGPP2*	***HUVA_0Q00600***	67
Processing of aroma compounds from grape ingredients					
Glucanases and Glucosidases	*BGL2*	*YGR282C*	*HuBGL2*	***HUVA_0H01180***	44
	GRE2	*YOL151W*	*HuGRE2*	***HUVA_0A03230***	50
	YPR1	*YDR368W*	*HuYPR1*	***HUVA_0A00510***	49
	ROT2	*YBR229C*	*HuROT2*	***HUVA_0V00220***	35
	SGA1	*YIL099W*	*HuSGA1*	***HUVA_0V00520***	31
	SIM1	*YIL123W*	*HuSIM1*	***HUVA_0AI00100***	57
Xylosidases	*GRE3*	*YHR104W*	*HuGRE3*	***HUVA_0M00160***	52
				HUVA_0A04250	27
				HUVA_0B00860	29
				HUVA_0AF00390	32
				HUVA_0M00390	25
		ANI_1_1358014[1]		***HUVA_0DZ00100***	25

The table includes annotations not included in the semi automatically annotated data set submitted to Genbank.

[1] Reference: Pel HJ, de Winde JH, Archer DB, Dyer PS, Hofmann G, Schaap PJ, et al. 2007. Genome sequencing and analysis of the versatile cell factory *Aspergillus niger* CBS 513.88. Nat Biotechnol 25:221-231.

Table S3: Annotated genes related to stress response pathways

Functional group	*S. cerevisiae*		*H. uvarum*		%aa identity
High osmolarity glycerol (HOG)	*SHO1*	*YER118C*	*HuSHO1*	***HUVA_0AF00310***	38
	MSB2	*YGR014W*	*HuMSB2*	***HUVA_0A03570***	25
	STE20	*YHL007C*	*HuSTE20*	***HUVA_0X00390***	23
	STE50	*YCL032W*	*HuSTE50*	***HUVA_0J00440***	30
	CDC42	*YLR229C*	*HuCDC42*	***HUVA_0A01310***	93
	OPY2	*YPR075C*	*HuOPY2*	***HUVA_0A02790***	24
	YPD1	*YDL235C*	*HuYPD1*	***HUVA_0W00350***	33
	SSK2	*YNR031C*	*HuSSK2*	***HUVA_0D01160***	31
	HOG1	*YLR113W*	*HuHOG1*	***HUVA_0A00590***	58
Cell wall integrity (CWI)	*MID2*	*YLR332W*	*HuMID2*	***HUVA_0C02040***	29
	ROM2	*YLR371W*	*HuROM2*	*HUVA_0G01240*	33
	ROM1	*YGR070W*		*HUVA_0G01240*	31
	RHO1	*YPR165W*	*	***HUVA_0AE00480***	71
	PKC1	*YBL105C*	*HuPKC1*	***HUVA_0AQ00100***	54
	BCK1	*YJL095W*	*HuBCK1*	***HUVA_0AA00400***	33
	MKK1	*YOR231W*	*HuMKK1*	*HUVA_0AH00240*	38
	MKK2	*YPL140C*		*HUVA_0AH00240*	37
	SLT2	*YHR030C*	*HuSLT2*	*HUVA_0B02480*	69
	KDX1	*YKL161C*		*HUVA_0B02480*	50
General stress response (GSR)	*CDC25*	*YLR310C*	*HuCDC25*	***HUVA_0Q00190***	23
	RAS2	*YNL098C*	*	*HUVA_0AL00310*	33
	CYR1	*YJL005W*	*HuCYR1*	***HUVA_0B02920***	41
	BCY1	*YIL033C*	*HuBCY1*	***HUVA_0A03310***	36
	TPK1	*YJL164C*	*HuTPK2*	*HUVA_0M00380*	59
	TPK3	*YKL166C*		*HUVA_0M00380*	59
	TPK2	*YPL203W*		*HUVA_0M00380*	70
Oxidative stress response (OSR)	*YBP1*	*YBR216C*	*HuYBP1*	***HUVA_0P00160***	22
	HYR1	*YIR037W*	*HuHYR1*	***HUVA_0M01240***	62
	YAP1	*YML007W*	*HuYAP1*	***HUVA_0BI00110***	24
	SOD1	*YJR104C*	*HuSOD1*	***HUVA_0D00160***	66
	SOD2	*YHR008C*	*HuSOD2*	***HUVA_0D00380***	48
	CTT1	*YGR088W*	*HuCTT1*	***HUVA_0A02280***	43
	GSH1	*YJL101C*	*HuGSH1*	***HUVA_0F00240***	43
	GSH2	*YOL049W*	*HuGSH2*	***HUVA_0I01200***	46
	TRX1	*YLR043C*	*HuTRX1*	***HUVA_0D01370***	43
	TRX2	*YGR209C*	*HuTRX2*	***HUVA_0R00460***	26

* Non-syntenic homologs. Most likely false positives due to high sequence conservation in the protein family.

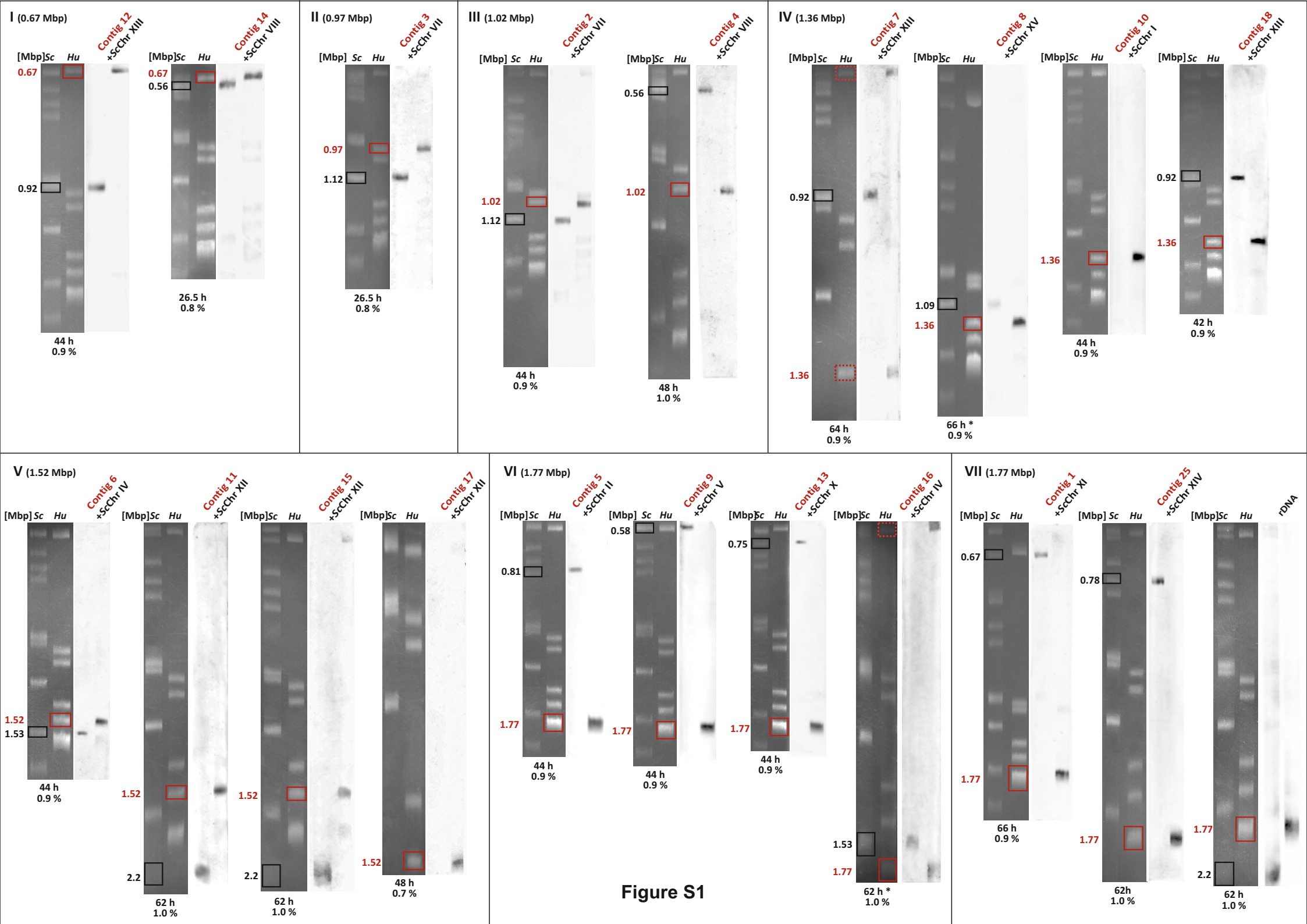

I (0.67 Mbp)
Contig 12 +ScChr XIII
Contig 14 +ScChr VIII
[Mbp] Sc Hu
0.67
0.92
0.67
0.56
44 h 0.9 %
26.5 h 0.8 %
II (0.97 Mbp)
Contig 3 +ScChr VII
0.97
1.12
26.5 h 0.8 %
III (1.02 Mbp)
Contig 2 +ScChr VII
Contig 4 +ScChr VIII
1.02
1.12
0.56
1.02
44 h 0.9 %
48 h 1.0 %
IV (1.36 Mbp)
Contig 7 +ScChr XIII
Contig 8 +ScChr XV
Contig 10 +ScChr I
Contig 18 +ScChr XIII
0.92
1.36
1.09
1.36
1.36
0.92
1.36
64 h 0.9 %
66 h * 0.9 %
44 h 0.9 %
42 h 0.9 %
V (1.52 Mbp)
Contig 6 +ScChr IV
Contig 11 +ScChr XII
Contig 15 +ScChr XII
Contig 17 +ScChr XII
1.52
1.53
1.52
2.2
1.52
2.2
1.52
44 h 0.9 %
62 h 1.0 %
62 h 1.0 %
48 h 0.7 %
VI (1.77 Mbp)
Contig 5 +ScChr II
Contig 9 +ScChr V
Contig 13 +ScChr X
Contig 16 +ScChr IV
0.81
1.77
0.58
1.77
0.75
1.77
1.53
1.77
44 h 0.9 %
44 h 0.9 %
44 h 0.9 %
62 h * 1.0 %
VII (1.77 Mbp)
Contig 1 +ScChr XI
Contig 25 +ScChr XIV
rDNA
0.67
1.77
0.78
1.77
2.2
1.77
66 h 0.9 %
62h 1.0 %
62 h 1.0 %

Figure S1

Figure S1: FIGE separation and Southern hybridizations of chromosomes from *H. uvarum*. Chromosomes from *S. cerevisiae* (standard, left lanes) and the adapted type strain of *H. uvarum* described in the main manuscript (right lanes) were separated by FIGE under the conditions indicated below the gels (e.g. upper left corner a separation for 44 h in a gel with 0.9% agarose). DNA was stained with ethidium bromide (left, white bands on gray background). Gels were blotted and hybridized with a mixture of DIG-labeled probes with one probe for the indicated chromosomes of *S. cerevisiae* (e.g. + ScChrXIII in the upper left image) and three different labeled PCR products from the indicated contigs (e.g. Contig 12 shown in red in the upper left image). The latter mixture was used to ensure that each contig is indeed represented by a continuous correctly assembled sequence and gives only one signal. Signals in the hybridization corresponding to the chromosomes in the ethidium bromide stained gels are boxed, with *H. uvarum* chromosomes boxed in red. Estimated chromosome sizes are given at the left of the gels in megabase pairs (Mbp). Hybridizations are ordered by chromosome numbers (I-VII). Note that in FIGE chromosomes migrate inversely correlated to their size. See text and legend to Fig. 3 for more details.

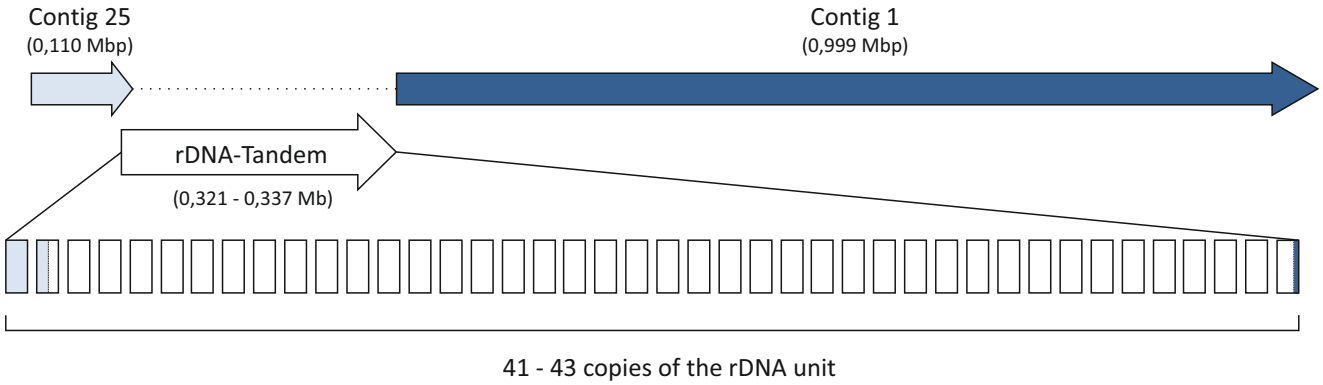
Figure S2

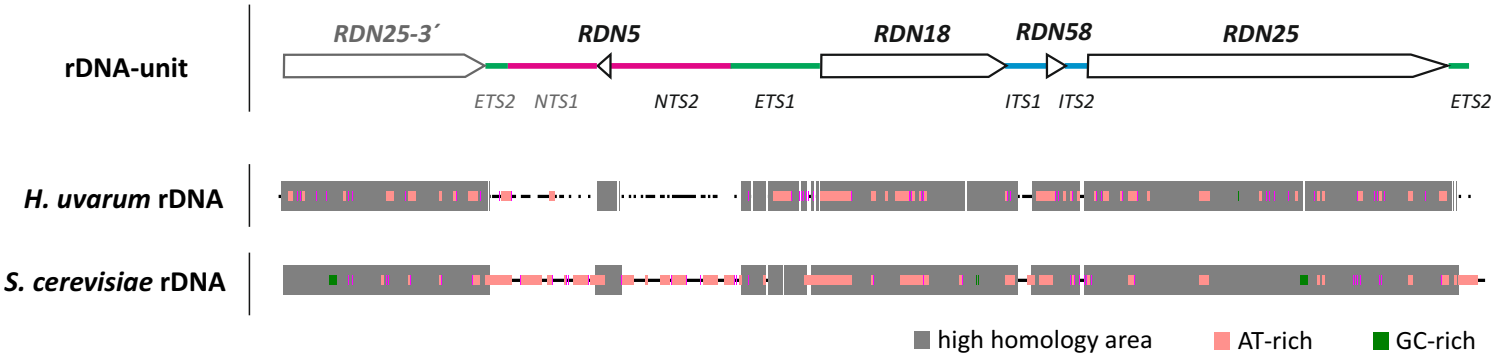
Contig16::CGAGTTGGAGTTGCTACCGTAAGAATCGGAGTTATCGTTAC**CGTAT**
GAGCTCTTTTTACCGTAAGAATCGGAGTTATCATTACCATATGAGTTAGAGTTGTC
ATTACCGTAGGAATTGGAGTTGCTACCGTAAGAATCGGAGTTATCGTTACCGTATG
AGCTCTTTTTACCGTAAGAATCGGAGTTATCATTACCATATGAGTTAGAGTTGTCA
TTACCGTAGGAATTGGAGTTGCTACCGTAAGAATCGGAATTATCGTTACCGTATGA
GCTCTTTTTACCGTAAGAATTGGAGTTATCATCATCATAAGAATTTTTCTTACCGT
AAGAATTGGAGTTATCGTTACCGTAGGAATTGGAGTTGCTACCGTAAGAATCAGAG
TTATCGTTACCGTAGGAATTGGAGTTGCTACCATATGAGTTAGAGTTATCATTACC
ATATGAGTTGGAGTTGCTACCGTATGAGTTAGAGTTATCATTACCATATGAGTTGG
AGTTGCTACCGTATGAGTTAGAGTTATCATTACCATATGAGTTGTCGTTACCGTAG
GAATTGCTGTTATCATTACCGTAGGAATTGGAGTTATCGTTACCGTATGAGTTGTC
GTTACCATTAGAGCCAGAATTGTTGTTACCATTGTTACCGAACTTCTTTTGGGCAA
AGTCAAAACCTTGGTCTACATATTTGGATGCATTAGAACCAAATTGCTCGTTAGCT
TTTTTTTCAACAAATTGTTTAGCGTTATCAAATAAACCCATTTTTAGTTATCTTTT
AAAGTTATTACTACTTGAAAATCTTTTGAAATTATTGTAAAAATATTTTCTATGGT
TAATTTTCATGTATTTTATTCTAATAATATTAAAATGTTATTTATTTAATAGATTA
TCTTAACACTTTTTACACACACCCTTGTTTATATAGTCGTAAATATTTAGACATAT
AGATAAATTTTTCAGTATATG**::Contig13**

Figure S2: Putative sequence of the gap between contigs 13 and 16 of the annotated genome sequence from *H. uvarum*. Sequences in blue and underlined represent the ends of contigs 13 and 16, as indicated. Sequence in black and bold letters was obtained by cloning and Sanger sequencing of four independent PCR products. Since the sequence at the end of contig 16 is highly repetitive, the exact size of the gap cannot be determined.

Figure S3

A





Segment	*ETS2*	*NTS1*	*RDN5*	*NTS2*	*ETS1*	*RDN18*	*ITS1*	*RDN58*	*ITS2*	*RDN25*
***H. uvarum* [bps]**	157	472	120	637	625	1786	290	158	212	3383
***S. cerevisiae* [bps]**	211	915		1243	700	1800	362		233	3396
Identity [%]	45	33	95	31	61	94	51	89	52	91

B

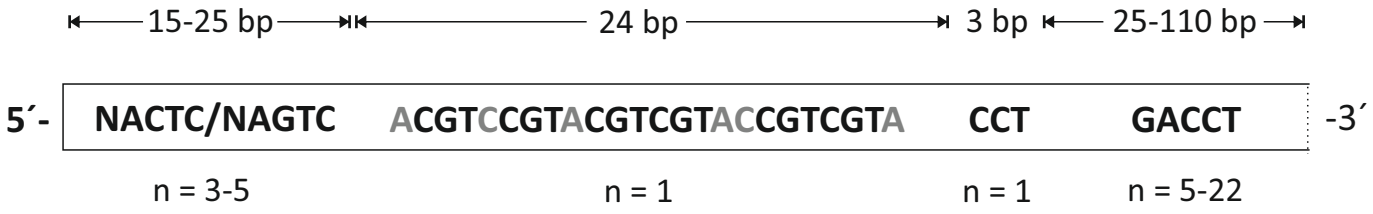


Figure S3: Arrangement of rDNA units in *H. uvarum* as compared to *S. cerevisiae*. (A) Schematic representation of the localization of rDNA units between contigs 25 and 1. Contig arrows indicate the orientation from 5' to 3' of the annotated sequence, with light and dark blue regions indicating the overlaps of the flanking rDNA units. Genes annotated according to the S. cerevisiae rDNA repeats are given below (*RDN#*), as are the schematic results of sequence alignments with regions of high homology. The table shows lengths and identities of the different sequence parts between *H. uvarum* and *S. cerevisiae* units. ETS1/2 = external transcribed spacers, NTS1/2 = non-transcribed spacers, ITS1/2 = internal transcribed spacers.

(B) Organization and consensus sequence of putative telomeres in *H. uvarum*. Lengths (above) and numbers (below) of conserved sequence elements are indicated. Black letters indicate three bp repeats within the conserved 24 bp motive.

Figure S4

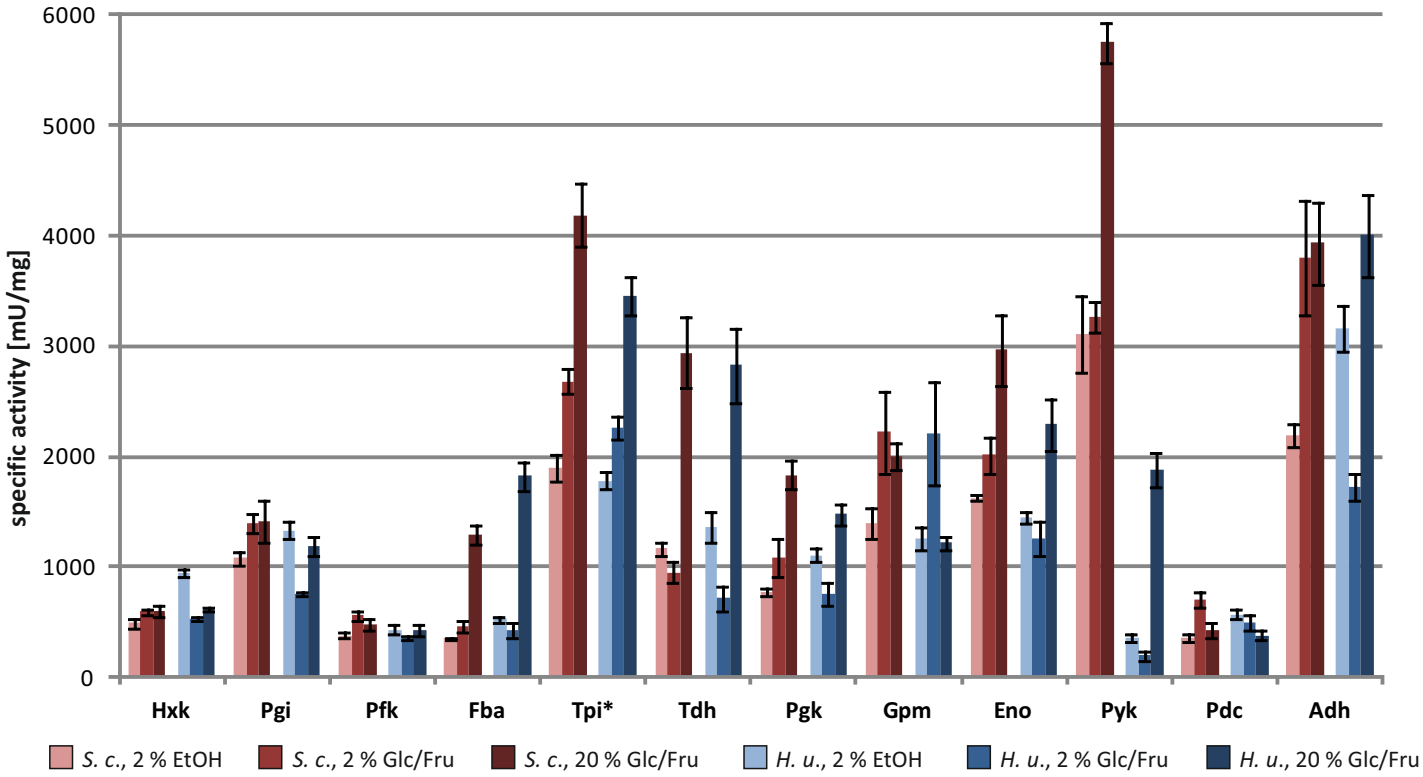


Figure S4: Comparative analysis of specific enzyme activities in the fermentative pathway from *H. uvarum* and *S. cerevisiae* on different carbon sources. Cells from the two yeast species were grown on rich medium with the carbon sources as indicated below. Glucose and fructose were applied in equal amounts to reach the indicated total sugar concentrations. Red colours designate activities in crude extracts from *S. cerevisiae*, blue colours in those from *H. uvarum*. Compare Table 2 in the main text for enzyme abbreviations. Tpi*: in order to show the activities for triosephosphate isomerase in the same graph, they were all diminished by a factor of 10, i.e. the specific activity for *S. cerevisiae* grown on 2 % Glc/Fru is approximately 26.000 mU/mg protein.