

Supplementary Table 1. The NCBI accession numbers of 18S rRNA sequences of selected yeast strains included in the phylogenetic analysis. For two *K. humilis* strains, YMX004033 and KAHU0_CLIB1323v1, the Previous name, if appropriate, is given in the Assembly column, Accession is the contig/scaffold with nucleotide coordinates, and the GI is the successive number. Additionally, the strain name for *K. humilis* strains KAHU0_CLIB1323v1 is its Assembly.

Name	Strain	Assembly	Accession	GI
<i>Candida albicans</i>	SC5314		XR_002086442.1	1111963232
<i>Candida glabrata</i>	NRRL Y-65		NG_063242.1	1543850743
<i>Kazachstania humilis</i>	YMX004033	ASM2031349v2	JAIWYV020000005.1_5923-7719	1
	YMX004033	ASM2031349v2	JAIWYV020000017.1_199854-201651	3
	KAHU0_CLIB1323v1	KAHU0_CLIB1323v1	CAKOGS010000006.1_797070-798856	1
	KAHU0_CLIB1323v1	KAHU0_CLIB1323v1	CAKOGS010000006.1_806039-807826	2
	KAHU0_CLIB1323v1	KAHU0_CLIB1323v1	CAKOGS010000006.1_815005-816802	3
	KAHU0_CLIB1323v1	KAHU0_CLIB1323v1	CAKOGS010000011.1_7842-9638	5
	KAHU0_CLIB1323v1	KAHU0_CLIB1323v1	CAKOGS010000011.1_16823-18617	6
	KAHU0_CLIB1323v1	KAHU0_CLIB1323v1	CAKOGS010000011.1_25773-27565	7
	KAHU0_CLIB1323v1	KAHU0_CLIB1323v1	CAKOGS010000011.1_34765-36562	8
	AS.1		KM516765.1	731189348
	JCM 9613	<i>Candida humilis</i>	AB054677.1	18147567
	JCM 9852	<i>Candida humilis</i>	AB054678.1	18147568
	NRRL Y-17074	<i>Candida humilis</i>	AY046243.1	31746899
<i>Kazachstania servazzii</i>	ATCC 58439	<i>Saccharomyces servazzii</i>	NG_064888.1	1632313344
	DO2	<i>Saccharomyces servazzii</i>	AY251624.1	29470195
<i>Kazachstania telluris</i>	CBS 2419 (type strain)	<i>Arxiozyma telluris</i>	Y15809.1	3954803
	CBS 2675	<i>Arxiozyma telluris</i>	Y15849.1	3962382
	CBS 2676	<i>Arxiozyma telluris</i>	Y15848.1	3962381
	CBS 2678	<i>Arxiozyma telluris</i>	Y15847.1	3962380
	CBS 2685 (type strain)	<i>Arxiozyma telluris</i>	Y15806.1	3962378
	CBS 2760 (type strain)	<i>Arxiozyma telluris</i>	Y15808.1	3954541
	CBS 2778	<i>Arxiozyma telluris</i>	Y15851.1	3962384
	CBS 2985	<i>Arxiozyma telluris</i>	Y15850.1	3962383
	NCYC 2475	<i>Arxiozyma telluris</i>	Y15807.1	3962379
	NRRL YB-4302		NG_063241.1	1543850742
<i>Magnusiomyces capitatus</i>	CBS 162.80	<i>Magnusiomyces capitatus</i>	NG_070302.1	1884649521
	Mandori	<i>Dipodascus capitatus</i>	AB083079.1	27531041
	Tuguri	<i>Dipodascus capitatus</i>	AB083080.1	27531042
<i>Naumovozyma</i>	CBS 4309 (type strain)		XR_002431959.1	1199953578

<i>castellii</i>	strain)			
<i>Saccharomyces cerevisiae</i>	S288C		NR_132213.1	831416138

Supplementary Table 2. Localization of 18S rRNA genes identified in the *Kazachstania humilis* MAW1 genome assembly.

Number	Contig	Start position	End position
1	tig00000119	236954	238745
2	tig00000119	191471	193261
3	tig00000119	218764	220557
4	tig00000119	209655	211450
5	tig00000119	245974	247735
6	tig00000119	200552	202351
7	tig00000119	227874	229664
8	tig00000120	8934	10732
9	tig00000120	35	1680
10	tig00000121	4447	6201

Supplementary Table 3. Selected yeast proteins with toxic activity against microorganisms, used for Blast searches of the *Kazachstania humilis* MAW1 genome assembly, grouped by general function, with the location of the coding sequence if not chromosomal DNA. The functions are mainly retrieved from UniProtKB [1].

UniProtKB Accession	Name	Strain	Function	Reference
J7S427	Vac14_Fig4_bd domain-containing protein	<i>Kazachstania naganishii</i> CBS 8797	Phosphatidylinositol biosynthetic process; PAS complex	[2]
J7S410	cellulase domain-containing protein	<i>Kazachstania naganishii</i> CBS 8797	Hydrolase activity, hydrolyzing O-glycosyl compounds	[2]
J8Q1Q0	Exg1p	<i>Saccharomyces arboricola</i> H-6	Hydrolase activity, hydrolyzing O-glycosyl compounds; cellular glucan metabolic process; extracellular region; fungal-type cell wall	[3]
G8B7X9	cellulase domain-containing protein, XOG1	<i>Candida parapsilosis</i> CDC317	Hydrolase activity, hydrolyzing O-glycosyl compounds; carbohydrate metabolic process; cellular anatomical entity	
B9WE14	Arginase	<i>Candida dubliniensis</i> CD36	Arginase activity; metal ion binding; regulation of nitrogen compound metabolic process; regulation of primary metabolic process	
P09807	Killer toxin subunit γ , RF3	<i>Kluyveromyces lactis</i> CBS2359/152; pGKL1 / k1 plasmid	Toxin	[4]
M3HTE7	U4/U5/U6 small nuclear ribonucleoprotein prp3	<i>Candida maltose</i> Xu316	mRNA splicing, via spliceosome; U4/U6 x U5 tri-snRNP complex	

P01546	K1, M1-1 protoxin	<i>S. cerevisiae</i> ; (ScV-M1) TF325 dsDNA	Ionophoric toxin; recognizes β -1,6-D-glucan	[5-9]
E9PA29	K2, K2 killer toxin	<i>S. cerevisiae</i> ; M2-1 dsDNA	Ionophoric toxin; recognizes β -1,6-D-glucan	[5, 10, 11]
P22313	killer toxin KHR, KHR1	<i>Saccharomyces cerevisiae</i>	Toxin	[12]
P39690	killer toxin KHS, KHS1	<i>Saccharomyces cerevisiae</i>	Toxin	[13]
Q00569	K5, panomycocin	<i>Wickerhamomyces anomalous</i> NCYC434, BCA15, BCU24, BS91, DBVPG 3003, ATCC 96603	Hydrolysis of β -1,6-/ β -1,3-glucan	[14-18]
A5A0Q7	KpKt, endo-b-1,3-glucanase	<i>Tetrapisispora Phaffii</i> DBVPG6076	Hydrolysis β -1,6-/ β -1,3-glucan	[19, 20]
Q7LZU3	K28 / Killer toxin K28	<i>S. cerevisiae</i> ; M28 virus dsDNA	Inhibits DNA synthesis; recognizes α -1,3-mannoprotein	[6, 21]
P09805	zymocin, killer toxin subunits alpha/beta	<i>Kluyveromyces lactis</i> NRRL Y-1140; pGK1-1 dsDNA	Exochitinase activity; tRNA ^{Glu} cleavage; cell-cycle perturbation	[4, 22-24]
Q707V3	PaT / Fam-a protein	<i>Millerozyma acaciae</i> NRRL Y18665; pPac1-2 linear plasmids	Exochitinase activity; tRNA ^{Gln} cleavage	[25, 26]
Q7Z8R9 (γ subunit) Q7Z8R6 (α and β subunits)	PiT, Egg protein	<i>Babjeviella inositovora</i> NRRL Y-18709; pPin1-3 killer plasmid	rRNA cleavage; binds to chitin	[27, 28]
Q90121	KP4, KP4 killer toxin	<i>Ustilago maydis</i> ; virus P4 dsRNA	Inhibits voltage-gated calcium channels	[29, 30]
P16948	KP6	<i>Ustilago maydis</i> ; virus P6	K ⁺ depletion	[31]
P19972	SMKT, SMK1, salt-mediated killer protoxin 1	<i>Millerozyma farinosa</i> KK1	Membrane permeabilization	[32, 33]
Q8NJU1	Zygocin, killer toxin zygocin	<i>Zygosaccharomyces bailii</i> 412	Membrane permeabilization, Mannoprotein target	[34, 35]
P10410	HMK, HM-1, Killer toxin HM-1	<i>Cyberlindnera mrakii</i> IFO0895	Inhibits β -1,3-glucan synthesis	[36-38]
D6NTN8	Klus	<i>Saccharomyces cerevisiae</i> dsRNA	Unknown	[39]

Supplementary Table 4. Selected proteins performing accompanying roles in the toxic activity of yeasts against other microorganisms, used for Blast searches of the *Kazachstania humilis* MAW1 genome assembly, with the location of the coding sequence if not chromosomal DNA. The functions are mainly retrieved from UniProtKB [1].

UniProtKB Accession	Name	Strain	Function	Reference
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P09806 P05469	RF4	<i>Kluyveromyces lactis</i> CBS2359/152 pGKL1 and pGKL2 plasmids	Immunity determinant	[4, 24, 40-42]
P17260	KRE1, killer toxin-resistance protein 1	<i>Saccharomyces cerevisiae</i>	Acts as the plasma membrane receptor for the yeast K1 viral toxin	[43-47]
P27809	KRE2, glycolipid 2-alpha-mannosyltransferase	<i>Saccharomyces cerevisiae</i>		[48-50]
P22023	KRE5, killer toxin-resistance protein 5	<i>Saccharomyces cerevisiae</i>	Required for β -1-6-D-glucan synthesis and normal cell growth	[51]
W0TH48	KRE1	<i>Kluyveromyces marxianus</i> DMKU3-1042		[52]
W0TAU5	KRE5, killer toxin-resistance protein 5	<i>Kluyveromyces marxianus</i> DMKU3-1042		[52]
A0A5P2U3X4	KRE1	<i>Kluyveromyces lactis</i> CBS 2105		[53]
A0A5P2U364	KRE1	<i>Kluyveromyces lactis</i> CBS 2105		[53]
A0A5P2U6V5	KRE1	<i>Kluyveromyces lactis</i> CBS 2105		[53]
A0A5P2U8G6	KRE1	<i>Kluyveromyces lactis</i> CBS 2105		[53]
A0A5P2U9Q3	Kre2/Ktr6	<i>Kluyveromyces lactis</i> CBS 2105		[53]
A0A5P2TZB3	Kre5	<i>Kluyveromyces lactis</i> CBS 2105		[53]
P43497	Cwp2p	<i>Saccharomyces cerevisiae</i>	Plasma membrane receptor for <i>Pichia membranifaciens</i> killer toxin	[54, 55]
P34253	KTI12	<i>Saccharomyces cerevisiae</i>	Regulates elongator complex γ -toxin target (TOT) activity, resulting in G1 block by <i>K. lactis</i> toxin zymocin (pGKL1 killer toxin)	[56-67]
P09620	KEX1, pheromone-processing carboxypeptidase KEX1	<i>Saccharomyces cerevisiae</i>	Protease with a carboxypeptidase B-like function involved in the C-terminal processing of the lysine and arginine residues from the precursors of K1, K2 and K28 killer toxins and α -factor (mating pheromone)	[68-75]
P13134	KEX2, Kexin	<i>Saccharomyces cerevisiae</i>	Processing of precursors of α -factors and killer toxin	[76-78]
P09231	KEX1, Protease KEX1	<i>Kluyveromyces lactis</i> NRRL Y-1140	Probably involved in the processing of the precursor of m1-toxin and alpha-factor	[79]
Q6CKK4	KEX1, pheromone-processing carboxypeptidase KEX1	<i>Kluyveromyces lactis</i> NRRL Y-1140	Protease with a carboxypeptidase B-like function involved in the C-terminal processing of the lysine and arginine residues from protein precursors	
Q4P8U8	KEX1, Pheromone-processing carboxypeptidase	<i>Ustilago maydis</i> 521	Protease with a carboxypeptidase B-like function involved in the C-terminal processing of the lysine	

	KEX1		and arginine residues from protein precursors; promotes cell fusion and is involved in the programmed cell death (by similarity)	
P38179	Alg3, Dol-P-Man:Man(5)GlcNAc(2)-PP-Dol α -1,3-mannosyltransferase	<i>Saccharomyces cerevisiae</i>	Adds the first Dol-P-Man derived mannose in an α -1,3 linkage to Man5GlcNAc2-PP-Dol; sensitive to <i>H. mrakii</i> HM-1 killer toxin	[80, 81]
P23900	Fps1, glycerol uptake/efflux facilitator protein	<i>Saccharomyces cerevisiae</i>	Channel protein for glycerol; has a role in both glycerol influx and efflux; plays a role in osmoregulation: under osmotic stress the channel is apparently closed to allow accumulation of glycerol in the cell under hyperosmotic conditions	[82]
P18414	Erd2	<i>Saccharomyces cerevisiae</i>	Required for the retention of luminal endoplasmic reticulum proteins; determines the specificity of the luminal ER protein retention system; also required for normal vesicular traffic through the Golgi; this receptor strongly recognizes H-D-E-L and weakly recognizes D-D-E-L and K-D-E-L	[83-86]

Supplementary Table 5. Statistics for Illumina PE reads used for the assembly of the *K. humilis* MAW1 genome, before and after filtration (F – forward, R – reverse).

Statistics	F raw reads	F clean reads	R raw reads	R clean reads
Mean read length	288.7	226.6	291.5	178.5
Mean read quality	22.3	29.6	17.6	27.7
Number of reads	1105532	935589	1105532	935589
Total bases	319153383	212010680	322259796	167040671

Supplementary Table 6. Statistics for Nanopore reads used for the assembly of the *K. humilis* MAW1 genome, before and after filtering.

Statistics	Raw reads	Clean reads
Mean read length	7823.1	8188.1
Mean read quality	10.8	11.6
Number of reads	392690	291705
Total bases	3072061280	2388514783
N50	9276	9480
Number, percentage, and bases of reads above quality cutoffs		
Q5	390991 (99.6) 3071.0	291705 (100.0) 2388.5
Q7	377652 (96.2) 3004.0	291705 (100.0) 2388.5
Q10	292260 (74.4) 2388.8	291705 (100.0) 2388.5
Q12	106760 (27.2) 887.6	106621 (36.6) 887.6
Q15	0 (0.0) 0.0	0 (0.0%) 0.0Mb
The top three longest reads and their mean base quality		
1:	172574 (6.4)	94368 (11.7)
2:	102396 (6.3)	86916 (12.1)
3:	94368 (11.7)	86408 (11.6)

Supplementary Table 7. Similarity matrix of 18S rDNA sequences identified in the genome assembly of *K. humilis* MAW1.

[illegible]

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