

Supplementary Table 1 : Centromeres of *Z. rouxii*, *K. thermotolerans* and *S. kluyveri*

ZYRO	size	<i>S.cerevisiae</i> homologs(left)	dist. (kb)	Centromere coord.	dist. (kb)	<i>S.cerevisiae</i> homologs (right)	CDEI	CDEII (AT%)	CDEIII
Zyro0A	167	<i>YBL001-X-X</i>	2.1	369077-369243	0.2	<i>YBR001c-YDR002w-YBR002c</i>	ATCAGGTG	134bp (82)	TGTGTTATGTTTCCGAACAGAAAAA
Zyro0B	167	<i>YJR002w-YJR001w-YLR001c</i>	0.3	788730-788896	0.4	<i>YLL001w-YLL002w-YJL001w</i>	ATCACATG	134bp (87)	TGTGGCTTACTTCCGAAACCTCTAA
Zyro0C	167	<i>YOL003c-YOL002c-YOL001w</i>	0.2	581961-581795	0.2	<i>YOR001w-YML001w-X</i>	GTCATGTG	134bp (84)	TGTATTTGTGTTCCGAAGATAAATT
Zyro0D	167	<i>YIL002c-YIL001w-YEL001c</i>	0.2	807719-807885	0.3	<i>YIR001c-YER002w-YER003c</i>	GTCACATG	134bp (86)	AGTTTGTGGTTTCCGAACCTTGATT
Zyro0E	169	<i>X-YCR003w-YCR002c</i>	0.9	335012-334844	0.1	<i>YNL001w-YCL001w-YCL002c</i>	ATCACGTG	136bp (82)	TGTACCTCGGTTCCGAAGATAAAAA
Zyro0F	167	<i>YFL001w-YPL002c-YPL001w</i>	0.1	372701-372867	0.3	<i>YFR001w-YPR001w-YPR002w</i>	GTCATGTG	134bp (82)	TGTTTTAGAGTTCCGAAGCTTAGAAA
Zyro0G	167	<i>YGL002w-YAR002w-YGL001c</i>	0.4	852551-852385	0.1	<i>YGR001c-YAL001c-YAL002w</i>	ATCACATG	134bp (89)	TGTCTACGGCTTCCGAAGATAAAAA

KLTH	size	<i>S.cerevisiae</i> homologs (left)	dist. (kb)	Centromere coord.	dist. (kb)	<i>S.cerevisiae</i> homologs (right)	CDEI	CDEII(AT%)	CDEIII
Klth0A	137	<i>YFL001w-YPL002c-YPL001w</i>	0.05	186515-186379	0.4	<i>YFR001w-YFR002w-YFR003c</i>	GTCACCTG	104bp (80)	TGTTAGTGGCTTCCGAAAATATTTA
Klth0B	126	<i>YJL001w-YLL002w-YLL001w</i>	0.1	238312-238187	0.1	<i>YLR001c-X-YJR001w</i>	CACACGTG	93bp (76)	TGTTTATCAGTTCCGAACGCAAAAA
Klth0C	128	<i>YOL003c-YOL002c-YOR001w</i>	0.1	912837-912964	1.3	<i>YOL001w-YML001w-X</i>	ATCAGCTG	95bp (86)	TGTATATGGGTTCCGAAGACACAAT
Klth0D	127	<i>YKL003c-YKL002w-YKL001c</i>	0.6	555337-555463	0.2	<i>YKR001c-YKR002w-YKR003w</i>	GTCACCTG	94bp (84)	ATTATTTGTTTTCCGAAACATTAAA
Klth0E	127	<i>YAL003w-YAL002w-YGL001c</i>	0.3	761047-760921	0.2	<i>YGR001c-YAL001c-YAR002w</i>	ATCACCTG	94bp (76)	ATTCTGCGGTTTCCGAACATTTATT
Klth0F	126	<i>YIL002c-YIL001w-YEL001c</i>	0.3	1078717-1078842	0.2	<i>YIR001c-YER002w-YER003c</i>	ACCACGTG	93bp (84)	TATGCTTGTGTTTTCCGAAAATATTTT
Klth0G	134	<i>YBR002c-YDR002w-YBR001c</i>	0.1	1432769-1432902	0.6	<i>YBL001c-YBL002w-YBL003</i>	ATCATATG	101bp (82)	TGATTATGAGCTCCGAAATATTTAA
Klth0H	127	<i>YCL004w-YCL001w-YNL001w</i>	0.2	1062917-1063043	1.0	<i>YCR002c-YCR003w-X</i>	CGCACGTG	95bp (76)	CTGCTAAGTGTTCCGAAACAAGTTT

SAKL	size	<i>S.cerevisiae</i> homologs (left)	dist. (kb)	Centromere coord.	dist. (kb)	<i>S.cerevisiae</i> homologs (right)	CDEI	CDEII (AT%)	CDEIII
Sakl0A	196	<i>YKL003c-YKL002w-YKL001c</i>	0.6	777082-777277	0.3	<i>YKR001c-YKR002w-YKR003w</i>	ATCACGTG	163bp (91)	TGTTTTTGCTTTCCGAAATTATAAA
Sakl0B	196	<i>YFL001w-YPL002c-YPL001w</i>	0.1	272171-272366	0.4	<i>YFR001w-YPR001w-YPR002w</i>	ATCACGTG	163bp (88)	TGTTTGAGAATTCCGAAAAAAGAAA
Sakl0C	197	<i>YBL003c-YBL002w-YBL001c</i>	1.1	1009526-1009330	0.5	<i>YBR001c-YDR002w-YBR002c</i>	AGCACGTG	164bp (83)	AGTTTTAGTTTTCCGAAAGTATTTA
Sakl0D	198	<i>X-YCR003w-YCR002c</i>	0.9	737092-737289	0.3	<i>YNL001w-YCL001w-YCL002c</i>	GTCACGTG	165bp (92)	AGTTTGTGCACTCCGAAACTTAAAA
Sakl0E	186	<i>YOR002w-YML001w-YOL001w</i>	1.1	108420-108235	0.5	<i>YOR001w-YOL002c-YOL003c</i>	CTCACGTG	153bp (90)	AGTTTGTGCACTCCGAAACTTAAAA
Sakl0F	197	<i>YIL002c-YIL001w-YEL001c</i>	0.5	383306-383110	0.6	<i>YIR001c-YER002w-YER003c</i>	GCCACGTG	164bp (92)	TGTTTTTGATCTCCGAACACTTTAC
Sakl0G	199	<i>YJL001w-YLL002w-YLL001w</i>	3.5	1064569-1064371	0.4	<i>YLR001c-X-YJR001w</i>	GTCACATG	166bp (90)	ATTATATGAGTTCCGAAAGCTAGAT
Sakl0H	198	<i>YAL002w-YBR015c-YGL001c</i>	0.6	1963796-1963599	0.4	<i>YGR001c-YAL001c-YGR229c</i>	CTCACGTG	165bp (94)	AGTTTTTGATTCCGAAAAATTTTT

The table describes the centromeres of *Z. rouxii*, *K. thermotolerans* and *S. kluyveri* with their size in base-pair (column 2) and their position on each chromosome (column 5, coordinates refer to the sequence deposited to EMBL at the date of this publication). Two centromeres of *Z. rouxii* were previously characterized (Pribylova et al. 2007). As in *S. cerevisiae*, centromeres of *Z. rouxii*, *K. thermotolerans* et *S. kluyveri* are short, suggesting that all hemiascomycetous yeasts have kinetochores with a single microtubule-binding site. For each centromere, the *S. cerevisiae* homologues of the centromere-proximal CDSs are indicated (left and right flanking genes, respectively, columns 3 and 7) and X indicates a CDS without similarity in the *S. cerevisiae* genome. The distances separating centromeres from the first adjacent CDS on either side are given (columns 4 and 6).

Supplementary Table 2 : Equivalence between centromeres

<i>Z. rouxii</i> 7 chromosomes	<i>K. thermotolerans</i> 8 chromosomes	<i>S. kluyveri</i> 8 chromosomes	<i>K. lactis</i> 6 chromosomes	<i>A. gossypii</i> 7 chromosomes
A (w)	G (c)	C (w)	⁽¹⁾	E (w)
B (w)	B (w)	G (w)	F (c) ⁽²⁾	⁽³⁾
C (c)	C (c)	E (c)	⁽⁴⁾	C (c)
D (w)	F (w)	F (w)	D (c)	D (w)
E (w)	H (w)	D (c)	A (c) ⁽⁵⁾	A (w)
F (w)	A (w)	B (w)	E (c) ⁽⁶⁾	G (w)
G (c)	E (w)	H (w)	C (w)	F (c)
⁽⁷⁾	D (w)	A (w)	B (c)	B (c)

Centromere equivalence is based on conserved syntenic blocks around them. Centromeres are identified by letters following chromosome nomenclature. Relative centromere orientation within blocks are indicated in brackets (w / c). Note the conserved centromeric organization within syntenic blocks across all five species for two chromosomes (bold). Other arrangements are as follows :

- (1) a conserved syntenic block of 11 orthologs exists on chromosome KLLA0E but lacks the centromeric sequence
- (2) identification of this centromere is based on a block of 7 orthologs on one side, no synteny is detectable on the other side
- (3) a conserved syntenic block of 4 orthologs exists on chromosome ERGO0C and another block of 7 orthologs exists on chromosome ERGO0A. Breakage occurred at the centromeric sequence which is no longer detectable.
- (4) a conserved syntenic block of 15 orthologs exists on chromosome KLLA0D but lacks the centromeric sequence
- (5) identification of this centromere is based on a block of 4 orthologs on one side, no synteny is detectable on the other side
- (6) identification of this centromere is based on a block of 4 orthologs on one side, no synteny is detectable on the other side
- (7) a conserved syntenic block of 9 orthologs exists on chromosome ZYRO0B showing a trace of ancient centromeric sequence

Supplementary Table 3: Segmental duplications in protoploid *Saccharomycetaceae*

Species	Total nb of segments	Size range (kb)	Significant segmental duplications after elimination of subtelomeric regions and known transposable elements
<i>Z. rouxii</i>	35	1 – 6	none
<i>K. thermotolerans</i>	35	1 - 15.5	a 3.3 kb segment triplicated on chr. B, E and H
<i>S. kluyveri</i>	70	1 – 5.7	a 3.3 kb segment tandemly duplicated on chr. E
<i>K. lactis</i>	60	1 - 6.7	a 6.7 kb segment duplicated on chr. A and C a 5.5 kb segment duplicated on chr. B and D
<i>A. gossypii</i>	1	1.8	none

All dispersed or tandemly duplicated chromosomal segments larger than 1kb and showing over 90 % sequence identity were computed for each yeast genome. The triplicated segment of *K. thermotolerans* encompasses two genes (KLTH0B05038g and KLTH0B05060g) on chromosome B, two genes (KLTH0E14938g and KLTH0E14960g) on chromosome E and two genes (KLTH0H00484g and KLTH0H00506g) on chromosome H. The duplicated segment of *S. kluyveri* encompasses two genes (SAKL0E02618g and SAKL0E02640g) on chromosome E and two genes (SAKL0E02684g and SAKL0E02706g) on the same chromosome. The first duplicated segment of *K. lactis* encompasses four genes (KLLA0A04521g, KLLA0A04543g, KLLA0A04565g and KLLA0A04587g) on chromosome A and four genes (KLLA0C05148g, KLLA0C05170g, KLLA0C05192g and KLLA0C05214g) on chromosome C. The second duplicated segment of *K. lactis* encompasses three genes on chromosome D (KLLA0D10109g, KLLA0D10131g and KLLA0D10153g) and one gene (KLLA0B05379g) and two pseudogenes (KLLA0B05305g and KLLA05342g) on chromosome B.

Supplementary Table 4: Codon usage and number of tRNA genes

AA		C	AC	ZYRO		KLTH		SAKL		KLLA		ERGO	
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F	Phe	TTT	---	2.46	-	2.05	-	2.63	-	1.98	-	1.66	-
F	Phe	TTC	(GAA)	1.87	8+	2.33	7+	1.79	8+	2.40	5	2.28	6+
L	Leu	TTA	(TAA)	2.70	4	1.01	2	1.93	3	2.41	3	0.83	2
L	Leu	TTG	(CAA)	2.86	10+	2.08	8+	3.19	11+	3.20	7+	1.94	7+
L	Leu	CTT	---	1.28	-	1.85	-	1.01	-	1.44	-	1.27	-
L	Leu	CTC	(GAG)	0.57	1	1.57	2	0.60	1	0.62	1	1.59	1
L	Leu	CTA	(TAG)	1.33	5+	1.15	3+	1.47	3+	1.39	2+	1.30	4+
L	Leu	CTG	(CAG)	0.88	-	2.11	3+	1.51	1+	0.64	1+	3.10	1+
I	Ile	ATT	(AAT)	2.90	11	2.09	10	2.58	12	2.78	7	1.71	9
I	Ile	ATC	(GAT)	1.57	1	2.01	-	2.13	-	2.04	-	2.17	-
I	Ile	ATA	(TAT)	1.15	1+	1.19	1+	1.17	1+	1.52	1+	1.16	1+
m	iMet	ATG	(CAT)	2.09	4	2.01	4	1.98	5	2.08	3	2.19	3
M	Met	ATG	(CAT)		5		4		5		3		4
V	Val	GTT	(AAC)	2.39	12	2.07	11	2.36	14	2.29	7	1.38	8
V	Val	GTC	---	1.06	-	1.62	-	1.50	-	1.22	-	1.59	-
V	Val	GTA	(TAC)	1.25	2(*)	0.79	1	0.99	1	1.21	1	0.87	2
V	Val	GTG	(CAC)	1.33	4	1.74	3	1.28	3	1.29	2	2.66	4
S	Ser	TCT	(AGA)	2.28	12	1.90	9	2.48	11+	2.45	6	1.37	7
S	Ser	TCC	---	1.16	-	1.51	-	1.57	-	1.28	-	1.46	-
S	Ser	TCA	(TGA)	1.99	3+	1.47	2	1.32	2	1.96	2	0.95	2
S	Ser	TCG	(CGA)	0.76	2+	1.36	2+	0.91	1+	0.96	1+	1.73	3+
P	Pro	CCT	(AGG)	1.48	3	1.43	2	1.26	1	1.30	1	1.00	1
P	Pro	CCC	---	0.68	-	1.05	-	0.67	-	0.45	-	1.06	-
P	Pro	CCA	(TGG)	2.10	10	1.42	8+	1.89	10+	1.99	7+	1.25	6+
P	Pro	CCG	---	0.47	-	0.75	-	0.63	-	0.56	-	1.54	-
T	Thr	ACT	(AGT)	2.10	10	1.51	9	1.97	11	2.18	6	1.12	7
T	Thr	ACC	---	1.11	-	1.44	-	1.64	-	1.23	-	1.46	-
T	Thr	ACA	(TGT)	1.53	2	1.44	2	1.51	2	1.66	2	1.21	2
T	Thr	ACG	(CGT)	0.68	2	1.03	1	0.78	1	0.77	1	1.65	2
A	Ala	GCT	(AGC)	2.21	12	2.03	10	2.07	13	2.26	7	1.49	7
A	Ala	GCC	---	1.10	-	1.82	-	1.50	-	1.04	-	2.00	-
A	Ala	GCA	(TGC)	2.00	9	1.64	3+	1.57	4	1.73	3	1.71	4
A	Ala	GCG	(CGC)	0.52	-	1.55	2	0.65	-	0.58	-	2.66	2

	AA	C	AC	ZYRO		KLTH		SAKL		KLLA		ERGO	
	-----	---	---	-----		-----		-----		-----		-----	
Y	Tyr	TAT	---	1.77	-	1.10	-	1.49	-	1.80	-	1.17	-
Y	Tyr	TAC (GTA)		1.49	7+	1.97	6+	1.88	7+	1.55	5+	2.10	4+
*	Och	TAA	---	-		-		-		-		-	
*	Amb	TAG	---	-		-		-		-		-	
H	His	CAT	---	1.50	-	0.96	-	1.17	-	1.50	-	1.00	-
H	His	CAC (GTG)		0.74	6	1.24	5	1.04	6	0.69	4	1.40	5
Q	Gln	CAA (TTG)		3.17	10	2.02	5	2.57	10	2.82	6	1.24	4
Q	Gln	CAG (CTG)		1.32	3	2.22	5	1.71	1+	1.39	1+	3.02	4+
N	Asn	AAT	---	3.42	-	1.80	-	2.40	-	3.11	-	1.60	-
N	Asn	AAC (GTT)		1.95	9	2.81	7	2.84	9	2.44	6	2.49	6
K	Lys	AAA (TTT)		3.70	7+	2.90	4+	3.67	5+	3.79	4+	1.76	3+
K	Lys	AAG (CTT)		2.98	14	3.59	14	3.33	14	3.27	9	3.90	9
D	Asp	GAT	---	4.48	-	2.43	-	3.28	-	4.21	-	2.38	-
D	Asp	GAC (GTC)		1.44	14	3.16	10	2.50	13	1.85	8	3.26	10
E	Glu	GAA (TTC)		4.93	10	3.31	6	4.31	13	4.70	8	2.42	3
E	Glu	GAG (CTC)		1.89	4	3.45	11	2.47	3(#)	2.00	2	4.14	8
C	Cys	TGT	---	0.87	-	0.54	-	0.77	-	0.84	-	0.49	-
C	Cys	TGC (GCA)		0.37	4	0.80	4	0.54	5	0.40	3	0.88	3
*	Opa	TGA	---	-		-		-		-		-	
W	Trp	TGG (CCA)		1.10	6+	1.09	5+	1.07	5+	1.09	4+	1.13	5+
R	Arg	CGT (ACG)		0.90	5	0.67	4+	0.74	5+	0.69	3+	0.73	4+
R	Arg	CGC	---	0.20	-	1.04	-	0.39	-	0.19	-	1.66	-
R	Arg	CGA	---	0.28	-	0.42	-	0.22	-	0.30	-	0.38	-
R	Arg	CGG (CCG)		0.13	1	0.52	1	0.24	1	0.20	1	1.34	2
S	Ser	AGT	---	1.73	-	1.02	-	1.31	-	1.37	-	0.80	-
S	Ser	AGC (GCT)		0.75	5+	1.75	3+	1.23	4+	0.80	2+	1.65	3+
R	Arg	AGA (TCT)		2.45	8	1.51	9	1.97	12	2.21	7	0.92	6
R	Arg	AGG (CCT)		0.92	2	0.96	1	1.04	1	0.77	1	0.83	1
G	Gly	GGT	---	3.28	-	1.56	-	2.46	-	2.54	-	1.30	-
G	Gly	GGC (GCC)		0.66	17	2.02	15	1.37	15	0.68	7	2.38	11
G	Gly	GGA (TCC)		1.19	5	1.19	3	0.87	2	1.26	2+	0.89	2
G	Gly	GGG (CCC)		0.54	2	0.92	2	0.61	2	0.63	1	1.38	2
Total number of tDNAs				272		229		257		163		190	
Nr of anticodons				43		44		43		43		44	

The first column (AA) indicates the charged amino acid (in one- and three-letter codes), the second one (C) the codon and the third one (AC) the anticodon found (between brackets). For each genome, the first value is the codon usage (in % of the 61 sense codons) and the second one the number of tRNA genes (“-” no tRNA gene). The “+” signs denote genes with intron. Data for *K. lactis* and *A. gossypii* are taken from (Marck et al. 2006) and updated for tDNA-Leu (CAG).

As previously observed for other hemiascomycetes (Marck et al. 2006), *Z. rouxii*, *K. thermotolerans*, *S. kluyveri*, *K. lactis*, and *A. gossypii*, follow the bacterial-type sparing rule to read CTY Leu and CGA Arg codons. Namely, all yeasts (except *Y. lipolytica*) read both CTT and CTC codons with tRNA-Leu (GAG), as do bacteria, instead of tRNA-Leu (AAG), as do other eukaryotes. Similarly, CGA codons are read by tRNA-Arg (ACG) instead of tRNA-Arg

(TCG). The “G₃₄ or A₃₄ sparing” rule applies to all species except *Z. rouxii*, where a tDNA-Ile (GAT) is found in addition to the 11 copies of tDNA-Ile (AAT). Hemiascomycetes also use additional sparing rules that reduce their total number of tRNA species to only 43 or 44, compared to the complete eukaryotic set of 46 (Marck et al. 2006). Following the “C₃₄ sparing” rule, the tDNA-Ala (CGC) is generally absent from the *Saccharomycetaceae*, except for *K. thermotolerans* and *A. gossypii*. The case of tDNA-Leu (CAG) is interesting. It was thought to be absent from all species of *Saccharomycetaceae*, except *K. waltii* (Marck et al. 2006), but we now found copies of this tDNA in *S. kluyveri* and *K. thermotolerans*, two members of clade 10. In addition, two previously overlooked tDNA-Leu (CAG) were recently identified in *K. lactis* and *A. gossypii* (M. Santos, personal communication). These genes were previously overlooked because their introns are exceptionally long (288-nt and 150-nt for *K. lactis* and *A. gossypii*, respectively). In *S. kluyveri*, this intron is 134-nt long, but it is only 20- and 19-nt long in *K. thermotolerans* and *K. waltii*, respectively. The tDNA-Leu (CAG) is not found in *Z. rouxii*. (*) the two copies of tDNA Val (TAC) in *Z. rouxii* differ extensively in sequence. (#) one copy of tDNA Gly (CTC) in *S. kluyveri* differs significantly in sequence from the other two. It is identical to the 13 copies of tDNA Gly (TTC) except for the anticodon.

Supplementary Table 5: Pairs of potentially co-transcribed tRNA genes

Species	tDNA pairs and intervals in bp			nb of occurrences in genome
<i>Z. rouxii</i>	Arg (TCT)	15/16	Asp (GTC)	3x
<i>K. thermotolerans</i>	none			
<i>S. kluyveri</i>	His (GTG)	9	Val (AAC)	1x
	Arg (TCT)	19	Asp (GTC)	1x
<i>K. lactis</i>	Arg (TCT)	13/21	Asp (GTC)	2x
	His (GTG)	38	Val (AAC)	1x
<i>A. gossypii</i>	Ser (AGA)	5/4	Asp (GTC)	2x
	Thr (CGT)	26	Thr (CGT)	1x
	Arg (ACG)	19	Arg (ACG)	1x
	Leu (TAA)	9	Val (TAC)	1x
	His (GTG)	3	Val (AAC)	1x

Potentially di-cistronic tDNAs are listed for each genome, indicating the upstream tRNA type, the distance between base 73 of the first tRNA gene and base 1 of the following tRNA gene, and the downstream tRNA type. Each tRNA type is identified by the charged amino acid and the anticodon (in brackets). Note the short intervals and absence of Pol III-terminator in them. For comparison, the next shortest distances between two successive tDNA loci along chromosomes are 119, 86, 143, 91 and 70 nucleotides for *Z. rouxii*, *K. thermotolerans*, *S. kluyveri*, *K. lactis* and *A. gossypii*, respectively, and their orientation is random. The number of occurrences of the same di-cistronic tDNA in each genome is indicated. Intervals vary slightly between paralogous copies (indicated by n/n). Pairs of two identical tDNAs are shown in bold. Data for *K. lactis* and *A. gossypii* were previously published (Marck et al. 2006).

Supplementary Table 6: Genes for non-coding RNAs

RNA	ncRNA class	gene type	gene product	<i>ZYRO</i>	<i>KLTH</i>	<i>SAKL</i>	<i>KLLA</i>	<i>ERGO</i> (#)
polymerase								
II	snoRNA	intronic	snR18 (U18 RNA)	110	109	113	108	122
II	snoRNA	intronic	snR24 (U24 RNA)	90	86	92	91	83
II	snoRNA	intronic	snR38	93	108	117	114	106
II	snoRNA	intronic	snR39	89	92	89	90	85
II	snoRNA	intronic	snR54	110	111	95	95	84
II	snoRNA	polycistronic cluster 1	snR72	88	82	83	88	92
II	snoRNA	polycistronic cluster 1	snR73	100	107	106	104	101
II	snoRNA	polycistronic cluster 1	snR74	89	78	83	82	74
II	snoRNA	polycistronic cluster 1	snR75	91	88	89	83	85
II	snoRNA	polycistronic cluster 1	snR76	99	101	97	107	87
II	snoRNA	polycistronic cluster 1	snR77	84	81	94	85	82
II	snoRNA	polycistronic cluster 1	snR78	78	84	86	83	78
II	snoRNA	polycistronic cluster 2	snR55	85	92	96	102	89
II	snoRNA	polycistronic cluster 2	snR57	88	84	99	96	86
II	snoRNA	polycistronic cluster 2	snR61	96	88	86	92	83
II	snoRNA	polycistronic cluster 3	snR41	136	135	123	138	135
II	snoRNA	polycistronic cluster 3	snR51	93	147	115	147	147
II	snoRNA	polycistronic cluster 3	snR70	198	205	185	205	153
II	snoRNA	polycistronic cluster 4	snR53	131	131	113	131	95
II	snoRNA	polycistronic cluster 4	snR67	122	121	100	122	122
II	snoRNA	polycistronic cluster 5	snR128 (U14 RNA)	130	166	127	165	123
II	snoRNA	polycistronic cluster 5	snR190	144	230	164	236	141
II	snoRNA	single	snR4	151	162	-	-	148
II	snoRNA	single	snR13	102	106	102	115	110
II	snoRNA	single	snR39b	94	104	98	101	99
II	snoRNA	single	snR40	100	97	101	96	93
II	snoRNA	single	snR45	201	210	202	201	184
II	snoRNA	single	snR47	101	106	106	109	97
II	snoRNA	single	snR48	123	118	114	113	121
II	snoRNA	single	snR50	99	-	107	100	73
II	snoRNA	single	snR56	99	108	120	96	92
II	snoRNA	single	snR58	109	90	84	95	89
II	snoRNA	single	snR60	144	129	134	136	113
II	snoRNA	single	snR62	-	85	102	110	96
II	snoRNA	single	snR63	189	234	241	259	228
II	snoRNA	single	snR64	113	120	121	122	105
II	snoRNA	single	snR65	96	111	108	116	108
II	snoRNA	single	snR66	113	94	95	100	89
II	snoRNA	single	snR68	108	112	105	116	87
II	snoRNA	single	snR69	109	97	105	107	123
II	snoRNA	single	snR71	104	93	106	98	103
II	snoRNA	single	snR79	90	99	108	113	85
II	snoRNA	single	U3 RNA	(*) 377	409	343	399	300
II	snRNA	single	U1 RNA	559	488	451	523	478
II	snRNA	single	U2 RNA	137	114	114	111	159
II	snRNA	single	U4 RNA	154	145	141	148	142
II	snRNA	single	U5 RNA	155	163	163	143	125
III	snoRNA	single	snR52	116	106	144	129	87
III	snRNA	single	U6 RNA	103	103	108	101	103
III	SRP_RNA	single	SRP RNA	534	431	447	485	382
III	RNase_P_RNA	single	RNase P RNA	342	332	335	540	379

The table lists the genes for non-coding RNA molecules (ncRNAs) found in each yeast species, ordered by RNA polymerase, ncRNA class according to the International Nucleotide Sequence Database Collaboration nomenclature (http://www.insdc.org/page.php?page=rna_vocab) and gene type (single: free standing genes; intronic: embedded within spliceosomal introns; or part of polycistronic clusters). The last five columns indicate the predicted nucleotide length of each RNA molecule (- : gene not found). (*) the gene encoding U3 RNA is duplicated in *Z. rouxii*. (#) see complete annotation at <http://agd.vital-it.ch/index.html>. The RNA moities of telomerases were not annotated.

Supplementary Table 7. Class I and class II transposable elements.

	Class I elements		Class II elements
	Ty1-like	Ty3-like	Rover (hAT-like)
<i>Z. rouxii</i>	-	0 (6)	-
<i>K. thermotolerans</i>	0 (<i>ca.</i> 60*)	-	2 (11)
<i>S. kluyveri</i>	3 (<i>ca.</i> 200*)	0 (1)	1 (4)
<i>K. lactis</i>	0 (<i>ca.</i> 35*)	-	0 (2)
<i>A. gossypii</i>	-	0 (3)	1**

For each yeast species, the table indicates the number of full-length and degenerated (brackets) class I and class II transposable elements (- absence of any trace of the element). The classification of LTR-retrotransposons is according to Neuvéglise et al. (2002). Most degenerated elements (*) are solo LTRs. Note the complete absence of Ty4, Ty5, Tca2 and non-LTR class I elements. The newly discovered class II transposable elements (hAT-like elements), called Rover family, is absent *Z. rouxii*. The Rover elements in *K. thermotolerans* and *S. kluyveri* can be subdivided into two subfamilies. The ORF encoded by *A. gossypii*-Rover (**) was previously annotated AFR535C (Dietrich et al. 2004). Note that the *ca.* 1 Mb long, GC-rich chromosomal segment of *S. kluyveri* shows no trace of Ty1-like elements or solo-LTRs (*ca.* 20 expected if distribution were random in entire genome, Payen *et al.*, submitted).

Supplementary Table 8: Statistical distribution of paralogous loci in genomes

Species	Synsomic coverage	Total paralogous pairs (*)	Synsomic paralogs (expected)	Synsomic paralogs (observed)	Relative variation (%)	Antisomic paralogs (observed)
<i>ZYRO</i>	0.14919	1011	150.8	147	-2.5	864
<i>KLTH</i>	0.13451	1044	140.4	128	-8.9	916
<i>SAKL</i>	0.13489	1125	151.8	166	+9.4	959
<i>KLLA</i>	0.18078	1007	192.9	194	+0.6	813
<i>ERGO</i>	0.15676	838	131.4	127	-3.3	711

Synsomic coverage is the probability for two loci to fall on the same chromosome, assuming a random distribution of loci ($\sum_{i=1-n} c_i^2$ where c is the relative size of each chromosome over the entire genome (rDNA excluded) and n the total number of chromosomes). Figures indicate the number of pairs of paralogs observed on the same chromosome (synsomic) or on two distinct chromosomes (antisomic). In order to limit the numerical influence of large families, only one pair of paralogs, taken at random, was considered for families of ≥ 3 members. (*) TGAs are not included (see Suppl. Table 9).

Supplementary Table 9: Tandem gene arrays

Yeast species	Total number of tandem gene arrays with					Total nb of arrays	Total nb of genes in TGAs	Total nb of protein families in TGAs
	1 gene and 1 pseudogene	2 gene copies	3 gene copies	4 gene copies	5 gene copies			
<i>ZYRO</i>	8	31	6	1	1	47	97	43
<i>KLTH</i>	6	25	4	1	1	37	77	35
<i>SAKL</i>	4	42	3	2	-	51	105	49
<i>KLLA</i>	2	32	2	-	-	36	72	38
<i>ERGO</i>	1	23	5	2	-	31	70	35

Tandem gene arrays were identified using an original, automated Blast comparison procedure of successive genes followed by manual curation that will be published separately (Despons et al. in prep.). Since proteins encoded by members of TGAs were separately assigned in our general protein family classification using slightly different criteria (see **Methods**), TGAs may contain gene copies whose products were attributed to distinct families in complex cases (usually large families of proteins containing repeats). Given the evolutionary conservation of some TGAs (see **Suppl. Table 10**), a total of 108 protein families have members encoded by TGAs in at least one yeast species.

The largest tandem gene arrays include:

- *Z. rouxii*: one TGA of 5 genes encoding proteins similar to the *BAR1* aspartyl protease involved in pheromone hydrolysis in *S. cerevisiae* (a shorter TGA of these genes exist in *A. gossypii*, see **Suppl. Table 10**); and one TGA of 4 genes encoding proteins similar to the *FLR1* plasma membrane multidrug transporter of *S. cerevisiae* (shorter TGAs of these genes exist in other species, see **Suppl. Table 10**).
- *K. thermotolerans*: one TGA of 5 genes encoding proteins with similarity to the *PEP1* trans-membrane sorting receptor of *S. cerevisiae*; and one TGA of 4 genes similar to the *COS9* gene of *S. cerevisiae* (shorter TGAs of these genes exist in other species, see **Suppl. Table 10**).
- *S. kluyveri*: two TGAs of 4 genes similar, respectively, to the *FRE3* ferric reductase and to the *CAN1* plasma membrane permease of *S. cerevisiae* (shorter TGAs of these genes exist in other species, see **Suppl. Table 10**).
- *A. gossypii*: two TGAs of 4 genes similar, respectively, to the *CWP1* gene and to the *YIR035C-YIR036C* genes of *S. cerevisiae*.

Supplementary Table 10: Conservation and specificity of tandem gene arrays (TGAs)

protein_family	ZYRO	KLTH	SAKL	KLLA	ERGO	short description
Conserved, syntenic TGAs						
GL3C0004 (TGA #1)	2	2	4	2	2	similar to <i>SACE</i> YEL063C CAN1 Plasma membrane arginine permease and <i>SACE</i> YNL268W LYP1 Lysine permease
GL3C0004 (TGA #2)	2	2	3	2	3	similar to <i>SACE</i> YKR039W GAP1 General amino acid permease and YDR508C GNP1 High-affinity glutamine permease
GL3C0007 (TGA #1)	4	2	2	1+p		similar to <i>SACE</i> YNL065W AQR1 Plasma membrane transporter of the major facilitator superfamily ; YIL121W QDR2 Multidrug transporter ; YBR008C FLR1 Plasma membrane multidrug transporter member of the major facilitator superfamily
GL3C0007 (TGA #2)			2		2	highly similar to <i>SACE</i> YNR055C
GL3C0014	2	2	2	2		similar to <i>SACE</i> YMR170C ALD2 Cytosolic aldehyde dehydrogenase; YMR170c ALD5 ; YMR169c ALD4
GL3C0019		2	2		2	highly similar to <i>SACE</i> YDL192W ARF1 and YDL137W ARF2, ADP-ribosylation factor GTPases of the Ras superfamily
GL3C0047 (1)	2	2	2	2	2	similar to <i>SACE</i> YOR130C ORT1 Ornithine transporter of the mitochondrial inner membrane; weakly similar to <i>SACE</i> YEL006W Hypothetical ORF
GL3C0073	2				2	similar to <i>SACE</i> YOL119C MCH4 Protein with similarity to mammalian monocarboxylate permeases
GL3C0142	3	3	2	3	2	similar to <i>SACE</i> YKL164C PIR1 Protein containing tandem internal repeats
GL3C0156		2	2	2		weakly similar to <i>SACE</i> YJR061W; YKL201C MNN4 Putative positive regulator of mannosylphosphate transferase
GL3C0177		2	2	2		similar to <i>SACE</i> YLR414C; weakly similar to YKL187C and YLR413W
GL3C0235 (2)	3	3	3			some similarities with <i>SACE</i> YOL048c and YAL018c
GL3C0480	2	2	2	2	2	similar to <i>SACE</i> YPL129W TAF14 Subunit of TFIID, TFIIF and SWI/SNF complexes of transcription
GL3C0507			2	2		some similarities with <i>SACE</i> YDR003W
GL3C2661 (3)	2	2	2	2	2	similar to <i>SACE</i> YAR018C KIN3 Nonessential protein kinase; YAR019C CDC15 Protein kinase of the Mitotic Exit Network
GL3R0042		2	2	2	2	similar to <i>SACE</i> YMR307W GAS1 Beta-1.3-glucanosyltransferase

GL3R0210	2			2		similar to <i>SACE</i> YMR222C FSH2 Serine hydrolase
GL3R0439	2	2	2	2	2	similar to <i>SACE</i> YOR285W; YOR286W FMP31
Conserved TGAs without clearcut syntenic conservation						
GL3C0002	2	2	2		3	similar to <i>SACE</i> High-affinity and low-affinity glucose transporters of the major facilitator superfamily
GL3C0003	2	2	2		2	similar to <i>SACE</i> YPR165W RHO1 GTP-binding protein
GL3C0005	2	2	2	2		similar to <i>SACE</i> YAL060W BDH1 NAD-dependent (2R 3R)-2 3-butanediol dehydrogenase; YAL061W putative polyol dehydrogenase; YMR152W; YNL134C; YMR083W ADH3
GL3C0009		2	2			similar to <i>SACE</i> YPR198W SGE1 Member of drug-resistance protein family
GL3C0012	5				2	similar to <i>SACE</i> YIL015W BAR1 Aspartyl protease; YLR121C YPS3 Aspartic protease; YLR120C YPS1 Aspartic protease; YDR144C MKC7 GPI- anchored aspartyl protease (yapsin) ; YIR039C YPS6 Putative GPI-anchored aspartic protease; YPL154C (PEP4)
GL3C0018 (TGA #1)			2	3	3	Similar to <i>SACE</i> YAL051W (OAF1) and YOR363C (PIP2)
GL3C0018 (TGA #2)			2			Similar to <i>SACE</i> YAL051W (OAF1) and YOR363C (PIP2)
GL3C0018 (TGA #3)			2			Similar to <i>SACE</i> YAL051W (OAF1) and YOR363C (PIP2)
GL3C0025 (TGA #1)	3		2	2	2	similar to <i>SACE</i> YDR011W SNQ2 ABC transporter; YOR153W PDR5 Short-lived membrane ABC transporter; YDR406W PDR15 ABC transporter
GL3C0025 (TGA #2)	2					highly similar to <i>SACE</i> YPL058C PDR12 ABC transporter
GL3C0028	2	2	2	2	2	similar to <i>SACE</i> YPR119W CLB2 B-type cyclin and YGR108W CLB1; YPR120C CLB5 B-type cyclin and YGR109C CLB6
GL3C0031 (6)		1+p	2			weakly similar to <i>SACE</i> YHL048W COS8
GL3C0031 (6)	2	1+p	2			weakly similar to <i>SACE</i> YGR295C COS6; some similarities with <i>SACE</i> YFL062W COS4
GL3C0031 (6)		4				some similarities with <i>SACE</i> YKL219W COS9
GL3C0031 (6)		1+p				weakly similar to <i>SACE</i> YFL062W COS4
GL3C0031 (6)		1+p				weakly similar to <i>SACE</i> YML132W COS3
GL3C0031 (6)		1+p	1+p			weakly similar to <i>SACE</i> YNL336W COS1 and YJR161C COS5
GL3C0031 (6)		1+p	2			some similarities with <i>SACE</i> YNL336W COS1 and YJR161C COS5
GL3C0039	1+p		4			weakly similar to <i>SACE</i> YOR381W FRE3 Ferric reductase; YOR384W FRE5 Putative ferric reductase
GL3C0080	2	2				highly similar to <i>SACE</i> YHR179W OYE2 NADPH oxidoreductase
GL3C0170		2	2	2	2	some similarities with <i>SACE</i> YJL079C PRY1 and YKR013W PRY2, proteins of unknown function
GL3C0377	2		1+p			similar to <i>SACE</i> YKL222C and YOR172W

GL3C0443 (4)	3	2	2	4	some similarities with <i>SACE</i> YKL096W CWP1 Cell wall mannoprotein
GL3C0536		2	2		some similarities with <i>SACE</i> YIL119C RPI1 Putative transcriptional regulator
GL3M4590 (5) (6)		1+p		2	some similarities with <i>SACE</i> YAR050W FLO1 Lectin-like protein; YAL063C; YHR211W FLO5
GL3M4590 (5) (6)		1+p			some similarities with <i>SACE</i> YAR050W FLO1 Lectin-like protein involved in flocculation
GL3R0054	2		2	1+p	similar to <i>SACE</i> YJL212C OPT1 Plasma membrane transporter; YPR194C OPT2 Oligopeptide transporter
GL3R0082	2		2		similar to <i>SACE</i> YDR384C ATO3 Plasma membrane protein; YCR010C ADY2 and YNR002C FUN34, members of the TC 9.B.33 YaaH family of putative transporters
GL3R0103	1+p		2		similar to <i>SACE</i> YMR008C PLB1 Phospholipase B (lysophospholipase)
Species-specific TGAs					
GL3C0684	1				conserved hypothetical protein
GL3R0233	2				no similarity
GL3R0426	2				similar <i>SACE</i> YER175C TMT1 Trans-aconitate methyltransferase
GL3C3802	2				some similarities with <i>SACE</i> YML111W BUL2 Component of the Rsp5p E3- ubiquitin ligase complex
GL3R0461	2				similar to <i>SACE</i> YPR159W KRE6 Protein required for beta-1 6 glucan biosynthesis
GL3C0670	2				similar to <i>SACE</i> YBR229C ROT2 Glucosidase II catalytic subunit
GL3R3311	2				similar to <i>SACE</i> YBR058C-A TSC3 involved in sphingolipid biosynthesis
GL3C0695	2				some similarities with <i>SACE</i> YMR043W MCM1 Transcription factor
GL3C0470	2				weakly similar to <i>SACE</i> YOR385W
GL3C3673	2				some similarities with <i>SACE</i> YIR019C MUC1 GPI-anchored cell surface glycoprotein
GL3C0501	2				similar to <i>SACE</i> YOR180C DCI1 Peroxisomal delta(3 5)-delta(2 4)-dienoyl-CoA isomerase
GL3C0141	2				similar to <i>SACE</i> YPL140C MKK2 Mitogen-activated kinase kinase
---	2				no similarity
GL3R0233	3				no similarity
GL3R3887		1			conserved hypothetical protein
---		1			no similarity
GL3C0196		2			similar to <i>SACE</i> YER062C HOR2 and YIL053W RHR2, two redundant DL-glycerol-3-phosphatases
GL3C3719		2			conserved hypothetical protein
GL3R0092		2			weakly similar to <i>SACE</i> YDL078C MDH3 Cytoplasmic malate dehydrogenase
GL3C0059		2			no similarity
GL3R4018		3			no similarity

GL3R3887	3	conserved hypothetical protein
GL3C0078	5	some similarities with SACE YBL017C PEP1 Type I transmembrane sorting receptor ; YJL222W
GL3R2229	1	similar to SACE YCR046C IMG1 Mitochondrial ribosomal protein
GL3R3075	1	conserved hypothetical protein
GL3R2318	2	similar to SACE YGL067W NPY1 NADH diphosphatase
GL3C0179	2	similar to SACE YMR234W RNH1 Ribonuclease H1
GL3C0482	2	similar to SACE YJL171C
GL3C3800	2	similar to SACE YJL151C SNA3 Integral membrane protein
GL3C4417	2	no similarity
GL3C0410	2	weakly similar to Candida glabrata CAGL0B02926g
GL3C0193	2	some similarities with SACE YER057C HMF1 Member of the p14.5 protein family
GL3C0110	2	similar to SACE YBL042C FUI1 High affinity uridine permease
GL3M4603 (7)	2	weakly similar to SACE YPR015C
GL3C0220	2	highly similar to SACE YBR299W MAL32 Maltase (alpha-D-glucosidase)
GL3C3541	2	conserved hypothetical protein
GL3C0110	2	highly similar to Kluyveromyces lactis KLLA0C19415g; similar to SACE YOR192C
GL3C0368	2	highly similar to Kluyveromyces lactis KLLA0A03553g; similar to SACE YAL046C
GL3C4478	3	some similarities with SACE YJL047C RTT101 Cullin family member subunit of a complex containing ubiquitin ligase activity
GL3R0920	1	conserved hypothetical protein
GL3R1456	2	some similarities SACE YGR268C HUA1
GL3C3203	2	some similarities with SACE YGL262W
GL3C3205	2	some similarities with SACE YBR250W
GL3C0667	2	some similarities with SACE YDR514C
GL3R0524	2	highly similar to SACE YDR533C
GL3R0152	2	similar to SACE YNL142W MEP2 Ammonium permease
GL3C0055	2	similar to SACE YGL039W; YGL157W; YOL151W; YDR541C NADPH- dependent Oxidoreductases
GL3C1579	2	some similarities with SACE YMR265C
GL3C4098	2	some similarities with ACE YKL096W CWP1 Cell wall mannoprotein
GL3C0369	2	similar to SACE YJL092W HPR5 DNA helicase
GL3C0011	2	highly similar to SACE YGL008C PMA1 Plasma membrane H -ATPase

GL3C0001	2		similar to SACE YDR243C PRP28 RNA helicase in the DEAD-box family; YGL078C DBP3 Putative ATP-dependent RNA helicase of the DEAD-box family
GL3C3549	2		some similarities with SACE YOR383C
GL3R0782		2	Similar to SACE YDL237W
GL3C4074		2	No homolog in SACE
GL3R0860		2	Similar to SACE YLR215C CDC123
GL3C0306		2	Similar to SACE YGL246C RAI1
GL3C0190		2	Similar to SACE YJL172W CPS1
GL3C1032		2	Similar to SACE YCL057W PRD1
GL3C4268		2	No homolog in SACE
GL3R0174		3	Similar to SACE YMR238W DFG5
GL3R0084		3	Similar to SACE YJR107W
GL3C0008		4	Similar to SACE YIR035C; YIR036C

The table indicates, for each yeast species (columns 2-6), the number of genes present in each TGA (p: pseudogene). TGAs were classified according to protein families and conserved synteny. Additional family relationships are: (1) members in GL3C0486 family; (2) members in GL3C4053 family; (3) members in GL3C2716 family; (4) members in GL3C4401, GL3U4586, GL3M4608 and GL3M4617 families; (5) members in GL3C3528 and GL3M4610 families; (6) complex subtelomeric locations; (7) members in GL3C3788 family.

Supplementary Table 11: Conservation of dispersed paralogs

#	CDS1_name	id %	CDS2_name	Protein family	Short description CDS1	Short description CDS2
1	ZYRO0A04796g	100.0	ZYRO0A02200g	GL3C019	highly similar to SACE YBR009C HHF1 and YNL030W HHF2, two identical histone H4 proteins	highly similar to SACE YBR009C HHF1 and YNL030W HHF2, two identical histone H4 proteins
1	KLTH0G16236g	100.0	KLTH0G10692g			
1	SAKL0C10714g	100.0	SAKL0E07304g			
1	KLLA0E17601g	100.0	KLLA0E08647g			
1	ERGO0E08624g	98.1	ERGO0D04664g			
2	ZYRO0A04444g	97.7	ZYRO0A09702g	GL3R0414	similar to SACE YBL002W HTB2 and YDR224C HTB1, two nearly identical histone H2B proteins	similar to SACE YDR224C HTB1 and YBL002W HTB2, two nearly identical histone H2B proteins
2	KLTH0G16500g	97.7	KLTH0E10186g			
2	SAKL0C11242g	93.2	SAKL0H12694g			
2	KLLA0E17337g	96.2	KLLA0F13310g			
2	ERGO0E08316g	90.9	ERGO0G12452g			
3	ZYRO0F04224g	71.7	ZYRO0C17754g	GL3R0345	highly similar to SACE YPL004C LSP1 Long chain base-responsive inhibitor of protein kinases Phk1p and Phk2p	highly similar SACE YGR086C PIL1 Long chain base-responsive inhibitor of protein kinases Phk1p and Phk2p
3	KLTH0A02288g	74.4	KLTH0D02992g			
3	SAKL0B02750g	75.8	SAKL0B09328g			
3	KLLA0E14411g	72.9	KLLA0F08162g			
3	ERGO0G08228g	75.5	ERGO0E00462g			
4	ZYRO0E05016g	70.8	ZYRO0B12496g	GL3C0278	highly similar to SACE YLR174W IDP2 Cytosolic NADP-specific isocitrate dehydrogenase	highly similar SACE YDL066W IDP1 Mitochondrial NADP-specific isocitrate dehydrogenase
4	KLTH0H12012g	72.4	KLTH0D14476g			
4	SAKL0D08426g	74.0	SAKL0H02860g			
4	KLLA0F12342g	73.9	KLLA0B03355g			
4	ERGO0A03872g	71.0	ERGO0E09768g			
5	ZYRO0G12936g	61.1	ZYRO0G11550g	GL3C0373	highly similar to SACE YBR084W MIS1 Mitochondrial C1-tetrahydrofolate synthase	similar to SACE YGR204W ADE3 Cytoplasmic trifunctional enzyme C1-tetrahydrofolate synthase
5	KLTH0E14366g	65.3	KLTH0B01496g			
5	SAKL0B06600g	65.1	SAKL0G14542g			
5	KLLA0E12475g	62.0	KLLA0E16545g			
5	ERGO0E12408g	62.3	ERGO0C02046g			
6	ZYRO0A12518g	54.4	ZYRO0D06974g	GL3R0183	highly similar to SACE YLR342W FKS1 Catalytic subunit of 1,3-beta-D-glucan synthase and SACE YGR032W GSC2	similar to SACE YMR306W FKS3 Protein of unknown function, has similarity to 1,3-beta-D-glucan synthase catalytic subunits Fks1p and Gsc2p
6	KLTH0G17754g	55.2	KLTH0B09856g			
6	SAKL0B04158g	58.2	SAKL0H00506g			
6	KLLA0B05841g	57.3	KLLA0C14069g			
6	ERGO0C00682g	56.5	ERGO0G00484g			
7	ZYRO0E01012g	64.9	ZYRO0F08448g	GL3C0249	similar to SACE YKL081W TEF4 Translation elongation factor EF-1gamma	similar to SACE YPL048W CAM1 Translational cofactor elongation factor-1 gamma
7	KLTH0C01342g	68.1	KLTH0E11572g			
7	SAKL0G18964g	70.7	SAKL0H11154g			
7	KLLA0F26092g	36.9	KLLA0D11594g			
7	ERGO0D12760g	36.2	ERGO0G02596g			
8	ZYRO0D16170g	52.9	ZYRO0B16038g	GL3C0396	highly similar to SACE YIL035C CKA1 alpha subunit of protein kinase CK2	highly similar to SACE YOR061W CKA2 may have a role in regulation and/or execution of the eukaryotic cell cycle alpha' subunit of casein kinase II
8	KLTH0A03542g	53.9	KLTH0F17490g			
8	SAKL0F07854g	55.4	SAKL0G00990g			
8	KLLA0E04247g	54.4	KLLA0F16467g			
8	ERGO0D06908g	52.8	ERGO0D14036g			

9	ZYRO0C17842g	48.5	ZYRO0B07458g	GL3C0204	similar to SACE YCR034W FEN1 Fatty acid elongase	similar to SACE YLR372W SUR4 Elongase III synthesizes 20-26-carbon fatty acids from C18-CoA primers
9	KLTH0F03740g	51.2	KLTH0D13596g			
9	SAKL0C04312g	54.3	SAKL0H03938g			
9	KLLA0C03542g	54.0	KLLA0B07777g			
9	ERGO0F20438g	53.9	ERGO0F19514g			
10	ZYRO0C03454g	54.4	ZYRO0A11088g	GL3C0320	similar to SACE YNL328C MDJ2 Protein of the mitochondrial inner membrane	similar to SACE YLR008C PAM18 Constituent of the mitochondrial import motor
10	KLTH0F19624g	51.6	KLTH0B02640g			
10	SAKL0C13662g	57.4	SAKL0G12056g			
10	KLLA0E02025g	48.6	KLLA0E09461g			
10	ERGO0G17116g	50.0	ERGO0D17248g			
11	ZYRO0D16346g	51.5	ZYRO0D03938g	GL3C0488	similar to SACE YER047C SAP1 Putative ATPase of the AAA family	similar to SACE YPL074W YTA6 Putative ATPase of the CDC48/PAS1/SEC18 (AAA) family
11	KLTH0A03696g	58.6	KLTH0E12562g			
11	SAKL0F08008g	46.0	SAKL0H10032g			
11	KLLA0E04379g	50.2	KLLA0E23409g			
11	ERGO0D06776g	46.8	ERGO0E02618g			
12	ZYRO0A04862g	49.5	ZYRO0G13662g	GL3R0356	highly similar to SACE YBR011C IPP1 Cytoplasmic inorganic pyrophosphatase	similar to SACE YMR267W PPA2 Mitochondrial inorganic pyrophosphatase
12	KLTH0G16302g	51.3	KLTH0C04312g			
12	SAKL0C10560g	49.1	SAKL0D02002g			
12	KLLA0E17667g	49.1	KLLA0E11089g			
12	ERGO0E08690g	47.5	ERGO0E14784g			
13	ZYRO0C09086g	46.6	ZYRO0B13596g	GL3C0405	highly similar to SACE YIL078W THS1 Threonyl- tRNA synthetase cytoplasmic	similar to SACE YKL194C MST1 Mitochondrial threonyl- tRNA synthetase
13	KLTH0A05192g	45.4	KLTH0D15620g			
13	SAKL0F09614g	44.8	SAKL0G16698g			
13	KLLA0F05918g	47.1	KLLA0D02772g			
13	ERGO0C03938g	46.8	ERGO0E10780g			
14	ZYRO0D17204g	46.1	ZYRO0F01650g	GL3C0187	similar to SACE YCR083W TRX3 mitochondrial thioredoxin	highly similar to gnl GLV CAGL0K00803g Candida glabrata CAGL0K00803g and similar to YLR043C uniprot P22217 SACE YLR043C TRX1 thioredoxin
14	KLTH0A07194g	44.9	KLTH0B01276g			
14	SAKL0A00814g	57.1	SAKL0G14784g			
14	KLLA0F10351g	47.5	KLLA0E16347g			
14	ERGO0G03212g	33.0	ERGO0C01826g			
15	ZYRO0A12958g	41.0	ZYRO0B03256g	GL3C0490	similar to SACE YBL064C PRX1 Mitochondrial peroxiredoxin (1-Cys Prx) with thioredoxin peroxidase activity	similar to SACE YBL064C PRX1 Mitochondrial peroxiredoxin (1-Cys Prx) with thioredoxin peroxidase activity
15	KLTH0G17314g	45.6	KLTH0C06798g			
15	SAKL0B04686g	47.7	SAKL0F12320g			
15	KLLA0A02651g	44.6	KLLA0E20285g			
15	ERGO0C00308g	42.2	ERGO0G16544g			
16	ZYRO0B09812g	31.3	ZYRO0D16654g	GL3C0506	similar to SACE YNL111C CYB5 Cytochrome b5	some similarities with SACE YNL111C CYB5 Cytochrome b5
16	KLTH0D09284g	38.2	KLTH0A04026g			
16	SAKL0E10626g	48.3	SAKL0F08316g			
16	KLLA0F23672g	46.0	KLLA0F27577g			
16	ERGO0F00374g	46.6	ERGO0D07304g			
17	ZYRO0G18898g	39.5	ZYRO0B07392g	GL3R0412	similar to SACE YJL174W KRE9 Glycoprotein involved in cell wall beta- glucan assembly	similar to SACE YJL174W KRE9 Glycoprotein involved in cell wall beta- glucan assembly
17	KLTH0F04378g	38.0	KLTH0D13684g			
17	SAKL0C04906g	47.2	SAKL0H03850g			
17	KLLA0A06468g	49.1	KLLA0E01299g			
17	ERGO0E05148g	35.4	ERGO0F19602g			
18	ZYRO0G08140g	43.1	ZYRO0G14256g	GL3C0447	similar to SACE YPL184C	similar to SACE YML117W

18	KLTH0H04906g	41.6	KLTH0C03784g			NAB6 Putative RNA-binding protein
18	SAKLOA05280g	43.4	SAKL0D01364g			
18	KLLA0E19031g	39.5	KLLA0D01485g			
18	ERGO0F04048g	41.2	ERGO0B02068g			
19	ZYRO0F01012g	36.7	ZYRO0G19140g	GL3C0216	similar to SACE YKL062W MSN4 and YMR037C MSN2 Transcriptional activators	weakly similar to SACE YER130C
19	KLTH0D08734g	37.6	KLTH0E06688g			
19	SAKL0B11330g	52.0	SAKL0H24816g			
19	KLLA0F26961g	40.4	KLLA0C17072g			
19	ERGO0B07194g	41.2	ERGO0C03498g			
20	ZYRO0C11330g	41.3	ZYRO0G09966g	GL3R0303	similar to SACE YKL062W MSN4 and YMR037C MSN2 Transcriptional activators	highly similar to SACE YGL019W CKB1 beta (38kDa) subunit of protein kinase CK2
20	KLTH0F16852g	42.2	KLTH0E07590g			
20	SAKL0G01672g	39.0	SAKL0H21692g			
20	KLLA0E21869g	43.4	KLLA0A04818g			
20	ERGO0C06776g	37.2	ERGO0G12012g			
21	ZYRO0D02002g	45.8	ZYRO0E00836g	GL3C0338	similar to SACE YER020W GPA2 Nucleotide binding alpha subunit of the heterotrimeric G protein	similar to SACE YHR005C GPA1 GTP-binding alpha subunit of the heterotrimeric G protein
21	KLTH0E01408g	35.6	KLTH0C01122g			
21	SAKL0F14608g	45.1	SAKL0G19184g			
21	KLLA0D10956g	29.6	KLLA0F25916g			
21	ERGO0B08932g	44.1	ERGO0D12936g			
22	ZYRO0F17402g	32.9	ZYRO0G03366g	GL3C0403	similar to SACE YDR507C	similar SACE YKL101W HSL1 Nim1p-related protein kinase
22	KLTH0F01672g	39.9	KLTH0D05566g			
22	SAKL0C01716g	42.2	SAKL0E02860g			
22	KLLA0C01650g	36.0	KLLA0F13552g			
22	ERGO0F22088g	45.1	ERGO0B04136g			
23	ZYRO0C15774g	36.5	ZYRO0E00792g	GL3C0385	similar to SACE YBR091C MRS5 Essential protein of the inner mitochondrial membrane	similar to SACE YHR005C-A MRS11 Essential protein of the mitochondrial intermembrane space
23	KLTH0E14872g	40.3	KLTH0C01078g			
23	SAKL0B07194g	41.4	SAKL0G19228g			
23	KLLA0B12034g	36.7	KLLA0F25872g			
23	ERGO0D02178g	38.0	ERGO0D12980g			
24	ZYRO0E01870g	37.8	ZYRO0A02838g	GL3R0339	similar to SACE YGL125W MET13 Isozyme of methylenetetrahydrofolate reductase	similar to SACE YPL023C MET12 Isozyme of methylenetetrahydrofolate reductase
24	KLTH0H06446g	39.1	KLTH0E11022g			
24	SAKL0A06952g	36.2	SAKL0H11836g			
24	KLLA0F09647g	38.7	KLLA0D12188g			
24	ERGO0A08602g	38.7	ERGO0F16544g			
25	ZYRO0E07436g	34.8	ZYRO0C00704g	GL3R0182	similar to SACE YPL221W BOP1	similar to SACE YAL053W
25	KLTH0H03564g	38.0	KLTH0D00858g			
25	SAKL0A03828g	38.5	SAKL0D14586g			
25	KLLA0B01914g	41.4	KLLA0A03355g			
25	ERGO0F02706g	37.5	ERGO0D18612g			
26	ZYRO0F00924g	39.5	ZYRO0C02838g	GL3C0223	similar to SACE YKL064W	similar to SACE YOL130W ALR1 Plasma membrane Mg(2+) transporter and YFL050C ALR2 Probable Mg(2+) transporter
26	KLTH0D08800g	37.7	KLTH0F19008g			
26	SAKL0B11418g	36.6	SAKL0C12936g			
26	KLLA0F26895g	38.5	KLLA0E07261g			
26	ERGO0B07260g	36.8	ERGO0D05324g			
27	ZYRO0B06776g	39.7	ZYRO0A09372g	GL3C0451	similar to SACE YNL281W HCH1 Heat shock protein regulator	similar to SACE YDR214W AHA1 Activator of Heat Shock Protein 90 ATPase
27	KLTH0C09284g	37.3	KLTH0F07832g			
27	SAKL0C09460g	35.1	SAKL0H13002g			

27	KLLA0C12221g	36.4	KLLA0A04147g			
27	ERGO0F13794g	38.5	ERGO0G06380g			
28	ZYRO0G08624g	36.5	ZYRO0E04686g	GL3R0352	highly similar to SACE YGL076C RPL7A and YPL198W RPL7B Proteins component of the large (60S) ribosomal subunit	similar to SACE YNL002C
28	KLTH0H04400g	34.9	KLTH0H12166g			
28	SAKL0A04686g	33.0	SAKL0D08712g			
28	KLLA0D03410g	45.2	KLLA0D04884g			
28	ERGO0F03520g	36.0	ERGO0A04136g			
29	ZYRO0C11946g	36.3	ZYRO0B04598g	GL3C0266	similar to SACE YNR036C	similar to SACE YGR118W RPS23A and YPR132W RPS23B Ribosomal proteins 28 (rp28) of the small (40S) ribosomal subunit
29	KLTH0A07018g	37.5	KLTH0F14190g			
29	SAKL0A00990g	37.5	SAKL0F03586g			
29	KLLA0F07007g	38.8	KLLA0B11231g			
29	ERGO0G03366g	35.2	ERGO0A07040g			
30	ZYRO0A04598g	35.7	ZYRO0G02662g	GL3R0316	similar to SACE YBR002C RER2 Cis-prenyltransferase	similar to SACE YMR101C SRT1 Cis-prenyltransferase
30	KLTH0G16390g	36.5	KLTH0D04906g			
30	SAKL0C11132g	37.5	SAKL0E03476g			
30	KLLA0E17205g	38.9	KLLA0B12848g			
30	ERGO0E08404g	35.5	ERGO0B04422g			
31	ZYRO0C05016g	34.0	ZYRO0G16742g	GL3R0503	similar to SACE YGL055W OLE1 Fatty acid desaturase	weakly similar to SACE YGL055W OLE1 Fatty acid desaturase
31	KLTH0H06798g	36.0	KLTH0G06358g			
31	SAKL0A07326g	39.5	SAKL0G10274g			
31	KLLA0C05566g	37.4	KLLA0C10692g			
31	ERGO0A08228g	34.5	ERGO0A02574g			
32	ZYRO0D08096g	35.7	ZYRO0C11484g	GL3R0209	similar to SACE YNR034W (SOL1) and YCR073W-A (SOL2)	similar to SACE YHR163W SOL3 Glucose-6-phosphate dehydrogenase and YGR248W (SOL4)
32	KLTH0A06864g	37.5	KLTH0H00836g			
32	SAKL0A01166g	38.0	SAKL0H02376g			
32	KLLA0C08415g	38.3	KLLA0A05390g			
32	ERGO0E14432g	31.1	ERGO0E03256g			
33	ZYRO0B14894g	29.3	ZYRO0A09416g	GL3C0251	similar to SACE YML081W	similar to SACE YDR216W ADR1 Positive transcriptional regulator controls the expression of ADH2 peroxisomal protein genes and genes required for ethanol glycerol and fatty acid utilization
33	KLTH0D18062g	22.1	KLTH0E09922g			
33	SAKL0G18062g	28.5	SAKL0H12958g			
33	KLLA0B04477g	30.1	KLLA0F13046g			
33	ERGO0E11946g	69.6	ERGO0G12210g			
34	ZYRO0B06512g	32.3	ZYRO0C06776g	GL3C0289	similar to SACE YOL100W PKH2 Serine/threonine protein kinase	similar to SACE YDR466W PKH3 Protein kinase
34	KLTH0C09548g	32.6	KLTH0G05214g			
34	SAKL0C09174g	35.9	SAKL0G06402g			
34	KLLA0C12485g	45.0	KLLA0E03587g			
34	ERGO0F13530g	33.5	ERGO0F14520g			
35	ZYRO0B09306g	33.7	ZYRO0B12650g	GL3C0260	highly similar to SACE YJL050W MTR4 Dead-box family ATP dependent helicase	similar to SACE YLR398C SKI2 blocks translation of non-poly(A) mRNAs antiviral protein putative helicase
35	KLTH0H10406g	35.3	KLTH0D14630g			
35	SAKL0D06622g	35.4	SAKL0H02706g			
35	KLLA0F01364g	39.4	KLLA0B03179g			
35	ERGO0E04070g	34.5	ERGO0E09900g			
36	ZYRO0B16478g	37.1	ZYRO0F07326g	GL3R0360	similar to SACE YIL153W RRD1 Resistant to Rapamycin Deletion	similar to SACE YPL152W RRD2 Resistant to Rapamycin Deletion
36	KLTH0E00880g	36.0	KLTH0D11176g			
36	SAKL0E15070g	31.9	SAKL0H06622g			

36	KLLA0A00462g	36.7	KLLA0F11187g			
36	ERGO0F12518g	34.6	ERGO0C07964g			
37	ZYRO0G11616g	33.6	ZYRO0G11088g	GL3C0314	similar to SACE YGR202C PCT1 Cholinephosphate cytidyltransferase	similar to SACE YGR007W MUQ1 Choline phosphate cytidyltransferase
37	KLTH0B01584g	39.1	KLTH0E08712g			
37	SAKL0G14476g	36.0	SAKL0H23012g			
37	KLLA0E16611g	34.8	KLLA0C18139g			
37	ERGO0C02112g	32.9	ERGO0F17622g			
38	ZYRO0B05764g	35.1	ZYRO0D07172g	GL3C0301	similar to SACE YOL080C REX4 Putative RNA exonuclease	similar to SACE YGR276C RNH70 3' exoribonuclease
38	KLTH0G15906g	33.7	KLTH0B09416g			
38	SAKL0C10362g	35.4	SAKL0H01034g			
38	KLLA0E17865g	34.4	KLLA0A10065g			
38	ERGO0E08932g	37.6	ERGO0G00946g			
39	ZYRO0D00990g	22.2	ZYRO0G01804g	GL3C0440	similar to SACE YPR182W SMX3 Sm or Sm-like snRNP protein	similar to SACE YDR378C LSM6 Component of small nuclear ribonucleoprotein complexes involved in RNA processing splicing and decay
39	KLTH0A00770g	36.7	KLTH0F15620g			
39	SAKL0F16082g	34.3	SAKL0G02904g			
39	KLLA0E04929g	32.9	KLLA0E02575g			
39	ERGO0E01892g	50.0	ERGO0C09438g			
40	ZYRO0B14542g	36.0	ZYRO0D11000g	GL3C0335	some similarities with SACE YPL170W DAP1 Heme-binding protein involved in regulation of cytochrome P450 protein	highly similar to SACE YPL170W DAP1 Heme-binding protein involved in regulation of cytochrome P450 protein
40	KLTH0D16566g	34.7	KLTH0D11836g			
40	SAKL0G17732g	36.5	SAKL0H05918g			
40	KLLA0B04796g	30.2	KLLA0C09757g			
40	ERGO0E11638g	34.9	ERGO0A01936g			
41	ZYRO0C07018g	34.6	ZYRO0E09570g	GL3C0393	highly similar to SACE YOR168W GLN4 Glutamine tRNA synthetase	highly similar to SACE YGL245W GUS1 Glutamyl-tRNA synthetase
41	KLTH0C10340g	34.5	KLTH0G00682g			
41	SAKL0E02134g	30.8	SAKL0F00748g			
41	KLLA0F20449g	37.0	KLLA0A00682g			
41	ERGO0G14124g	34.4	ERGO0F11880g			
42	ZYRO0G15356g	31.0	ZYRO0E09086g	GL3R0259	similar to SACE YKR028W (SAP190) and YJL098W (SAP185)	similar to SACE YFR040W (SAP155) and YGL229C (SAP4)
42	KLTH0D03388g	33.7	KLTH0G01144g			
42	SAKL0D05456g	37.8	SAKL0F01320g			
42	KLLA0F14124g	34.6	KLLA0A01155g			
42	ERGO0F07590g	33.8	ERGO0F11462g			
43	ZYRO0G20746g	32.7	ZYRO0B12254g	GL3R0429	similar to SACE YBR267W REI1	similar to SACE YLR387C REH1
43	KLTH0H10758g	34.5	KLTH0D14212g			
43	SAKL0D06996g	35.4	SAKL0H03190g			
43	KLLA0F01727g	34.4	KLLA0E05171g			
43	ERGO0E04422g	33.8	ERGO0E09504g			
44	ZYRO0F04532g	35.0	ZYRO0C09856g	GL3C0226	highly similar to SACE YFR004W RPN11 Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid	similar to SACE YDL216C RRI1 subunit of COP9 signalosome
44	KLTH0A02068g	35.2	KLTH0B07194g			
44	SAKL0B03014g	31.4	SAKL0E13046g			
44	KLLA0E14147g	33.0	KLLA0D08503g			
44	ERGO0G08470g	34.1	ERGO0B01540g			
45	ZYRO0B09702g	32.2	ZYRO0D09394g	GL3C0257	similar to YOR109w SACE INP53 Phosphatidylinositol 4,5-bisphosphate 5-phosphatase	similar to SACE YIL002C INP51 Phosphatidylinositol 4 5-bisphosphate 5-phosphatase
45	KLTH0D09174g	34.3	KLTH0F13002g			
45	SAKL0E10494g	35.3	SAKL0F04862g			
45	KLLA0F23551g	30.7	KLLA0D13860g			
45	ERGO0F00264g	34.0	ERGO0D09284g			

46	ZYRO0D02354g	43.1	ZYRO0E08976g	GL3C0413	highly similar to SACE YNL052W (COX5A) and YIL111W (COX5B) Subunits Va and Vb of cytochrome c oxidase	similar to SACE YGL226W
46	KLTH0G09746g	31.9	KLTH0G01254g			
46	SAKL0E08360g	31.7	SAKL0F01430g			
46	KLLA0F03641g	28.5	KLLA0A01298g			
46	ERGO0D03674g	31.3	ERGO0F11352g			
47	ZYRO0G20988g	33.9	ZYRO0E09262g	GL3C0295	similar to SACE YBR281C	highly similar to SACE YFR044C
47	KLTH0H11000g	32.6	KLTH0G00990g			
47	SAKL0D07238g	32.7	SAKL0F01100g			
47	KLLA0F01991g	32.5	KLLA0A01001g			
47	ERGO0E04664g	33.4	ERGO0F11616g			
48	ZYRO0E02156g	35.0	ZYRO0F14388g	GL3C0445	similar to SACE YOR092W ECM3	similar to SACE YLR152C
48	KLTH0G08118g	35.0	KLTH0G11220g			
48	SAKL0E10010g	33.4	SAKL0H14564g			
48	KLLA0C13607g	31.6	KLLA0D17314g			
48	ERGO0C02992g	29.9	ERGO0G04972g			
49	ZYRO0F16676g	30.6	ZYRO0B16654g	GL3C0361	some similarities with SACE YNL271C BNI1 Formin nucleates the formation of linear actin filaments	some similarities with SACE YIL159W BNR1 Formin nucleates the formation of linear actin filaments
49	KLTH0F02376g	33.2	KLTH0E00704g			
49	SAKL0C02618g	35.1	SAKL0E15224g			
49	KLLA0C02321g	30.3	KLLA0F10912g			
49	ERGO0F21494g	35.1	ERGO0F12694g			
50	ZYRO0D13772g	30.3	ZYRO0B12166g	GL3C0450	similar to SACE YML032C RAD52 Protein that stimulates strand exchange	similar to SACE YDL059C RAD59 Protein involved in the repair of double-strand breaks
50	KLTH0G04862g	29.9	KLTH0D14124g			
50	SAKL0G06072g	35.4	SAKL0H03278g			
50	KLLA0B01782g	32.8	KLLA0E05259g			
50	ERGO0E15290g	34.1	ERGO0E09416g			
51	ZYRO0A04906g	32.7	ZYRO0C03058g	GL3C0325	similar to SACE YDL008W APC11 Catalytic core subunit of the Anaphase-Promoting Complex/Cyclosome (APC/C)	similar to SACE YOL133W HRT1 RING finger containing subunit of Skp1-Cullin-F-box ubiquitin protein ligases
51	KLTH0G16082g	32.3	KLTH0F19228g			
51	SAKL0C10516g	35.8	SAKL0C13178g			
51	KLLA0E17711g	29.9	KLLA0E07151g			
51	ERGO0E08734g	30.9	ERGO0D05104g			
52	ZYRO0D08514g	32.7	ZYRO0C09174g	GL3C0436	similar to SACE YCR059C YIH1 piecemeal microautophagy of the nucleus (PMN)	similar to SACE YDL177C
52	KLTH0A06424g	31.7	KLTH0A05258g			
52	SAKL0A01694g	31.9	SAKL0F09724g			
52	KLLA0C08932g	34.0	KLLA0F05797g			
52	ERGO0A05786g	30.1	ERGO0C04312g			
53	ZYRO0B03762g	27.5	ZYRO0F14212g	GL3C0283	weakly similar to SACE YER112W LSM4 component of small nuclear ribonucleoprotein complexes involved in RNA processing, splicing, and decay	similar to SACE YLR147C SMD3 involved in snRNP biogenesis and pre-mRNA splicing encodes a core snRNP protein
53	KLTH0C06248g	33.8	KLTH0G11396g			
53	SAKL0F12892g	33.8	SAKL0H14740g			
53	KLLA0E20813g	31.0	KLLA0D17160g			
53	ERGO0G01738g	33.8	ERGO0G04796g			
54	ZYRO0B01804g	32.3	ZYRO0E09284g	GL3C0400	highly similar to SACE YBR291C CTP1 Mitochondrial inner membrane citrate transporter	weakly similar to SACE YFR045W
54	KLTH0D06622g	29.9	KLTH0G00968g			
54	SAKL0A09284g	32.4	SAKL0F01078g			
54	KLLA0E18723g	31.1	KLLA0A00979g			
54	ERGO0G06952g	32.3	ERGO0F11638g			
55	ZYRO0D11726g	27.8	ZYRO0A10582g	GL3C0334	highly similar to SACE YDR404C RPB7 RNA	highly similar to SACE YKL144C RPC25 RNA

55	KLTH0G02926g	30.7	KLTH0G07546g		polymerase II subunit B16	polymerase III subunit C25
55	SAKLOG04048g	31.9	SAKLOG11506g			
55	KLLA0C06787g	30.9	KLLA0E13751g			
55	ERGO0F15114g	36.2	ERGO0C05896g			
56	ZYRO0F02508g	31.3	ZYRO0D10406g	GL3C0202	similar to SACE YFL042C	similar to SACE YDR326C and YHR080C
56	KLTH0G19030g	30.6	KLTH0E03806g			
56	SAKL0B00770g	32.3	SAKL0G08404g			
56	KLLA0D05555g	32.5	KLLA0E16919g			
56	ERGO0B10582g	29.3	ERGO0D16082g			
57	ZYRO0D15664g	29.2	ZYRO0D12298g	GL3C0230	highly similar to SACE YIL018W RPL2B and YFR031C-A RPL2A, Proteins of the large (60S) ribosomal subunit	similar to YEL050C SACE RML2 Mitochondrial ribosomal protein of the large subunit
57	KLTH0E04752g	32.1	KLTH0G03476g			
57	SAKL0F07304g	29.1	SAKL0G04554g			
57	KLLA0D16027g	31.4	KLLA0A02035g			
57	ERGO0D06358g	30.9	ERGO0A07590g			
58	ZYRO0F02904g	27.1	ZYRO0D02508g	GL3R0348	similar to SACE YFL034C-B MOB2 Component of the RAM signaling network	similar to SACE YIL106W MOB1 Mps One Binder (putative) transcriptional regulator involved in mitosis
58	KLTH0G18722g	29.6	KLTH0G09900g			
58	SAKL0B01100g	30.7	SAKL0E08206g			
58	KLLA0D05225g	31.1	KLLA0F03795g			
58	ERGO0C09856g	33.1	ERGO0D03828g			
59	ZYRO0G18568g	30.3	ZYRO0B03960g	GL3C0265	highly similar to SACE YKL170W MRPL38 Mitochondrial ribosomal protein of the large subunit	highly similar to SACE YER117W RPL23B and YBL087C RPL23A, components of the large (60S) ribosomal subunit
59	KLTH0F04708g	27.9	KLTH0C06072g			
59	SAKL0C05258g	30.3	SAKL0F13068g			
59	KLLA0A06798g	31.6	KLLA0E06997g			
59	ERGO0E05478g	31.5	ERGO0G01914g			
60	ZYRO0F05566g	32.3	ZYRO0B15994g	GL3C0473	weakly similar to SACE YOR059C	similar to SACE YOR059C
60	KLTH0C03102g	26.2	KLTH0F17446g			
60	SAKL0D12100g	36.6	SAKL0G01034g			
60	KLLA0F16709g	31.2	KLLA0F16423g			
60	ERGO0F14740g	24.1	ERGO0D13992g			
61	ZYRO0C12584g	30.0	ZYRO0D01914g	GL3R0411	similar to SACE YPR114W	similar to SACE YJR116W
61	KLTH0E05566g	31.6	KLTH0E01320g			
61	SAKL0F06292g	27.7	SAKL0F15180g			
61	KLLA0D15059g	29.5	KLLA0D10868g			
61	ERGO0A06468g	28.3	ERGO0B09020g			
62	ZYRO0G20064g	29.6	ZYRO0F07216g	GL3R0272	similar to SACE YMR113W FOL3 Dihydrofolate synthetase involved in folic acid biosynthesis	similar to SACE YOR241W MET7 Folylpolyglutamate synthetase
62	KLTH0D04664g	27.0	KLTH0D11066g			
62	SAKL0E03872g	27.8	SAKL0H06732g			
62	KLLA0B12463g	27.4	KLLA0F11297g			
62	ERGO0E00990g	33.7	ERGO0C07854g			
63	ZYRO0E07678g	29.0	ZYRO0D00968g	GL3C0332	similar to SACE YPL227C ALG5 UDP-glucose:dolichyl-phosphate glucosyltransferase	highly similar to SACE YPR183W DPM1 Dolichol phosphate mannose (Dol-P-Man) synthase of the ER membrane
63	KLTH0H03256g	29.0	KLTH0A00748g			
63	SAKL0A03542g	24.9	SAKL0F16104g			
63	KLLA0C16071g	29.7	KLLA0B03377g			
63	ERGO0F02420g	31.3	ERGO0E01870g			
64	ZYRO0G06512g	22.7	ZYRO0A05676g	GL3C0206	similar to SACE YNL121C TOM70 Translocase of Outer Mitochondrial membrane	highly similar to SACE YOR027W STI1 Heat shock protein also induced by canavanine and entry into stationary phase
64	KLTH0B05170g	27.6	KLTH0E02178g			
64	SAKL0E10956g	29.9	SAKL0G07084g			
64	KLLA0F24046g	40.0	KLLA0A07062g			

64	ERGO0B08316g	22.6	ERGO0E03058g			
65	ZYRO0D11462g	26.9	ZYRO0B08448g	GL3R0438	similar to SACE YOR147W MDM32 Mitochondrial Distribution and Morphology	highly similar to SACE YHR194W MDM31 Mitochondrial Distribution and Morphology
65	KLTH0G02596g	28.7	KLTH0D17798g			
65	SAKLOG03762g	29.7	SAKLOG18304g			
65	KLLA0C06468g	31.0	KLLA0B04246g			
65	ERGO0F14872g	24.7	ERGO0B03366g			
66	ZYRO0B01540g	27.8	ZYRO0F06952g	GL3C0212	highly similar to SACE YHR001W OSH7 Member of an oxysterol-binding protein family	similar to SACE YPL145C KES1 Member of the oxysterol binding protein family
66	KLTH0D06402g	28.6	KLTH0D10824g			
66	SAKLOA08932g	27.5	SAKLOH06974g			
66	KLLA0A02827g	28.4	KLLA0D07480g			
66	ERGO0E01540g	27.5	ERGO0C07656g			
67	ZYRO0F01078g	30.8	ZYRO0A08052g	GL3C0337	highly similar to SACE YMR035W IMP2 mitochondrial peptidase	similar to SACE YMR150c IMP1 protease, mitochondrial
67	KLTH0D08668g	25.7	KLTH0H15884g			
67	SAKLOB11264g	27.5	SAKLOE05478g			
67	KLLA0F27027g	29.0	KLLA0F07293g			
67	ERGO0B07128g	25.3	ERGO0D15488g			
68	ZYRO0F16610g	27.8	ZYRO0C04356g	GL3C0144	similar to SACE YNL267W PIK1 Phosphatidylinositol 4-kinase	similar to SACE YLR240W VPS34 Phosphatidylinositol 3-kinase
68	KLTH0F02442g	25.1	KLTH0F08404g			
68	SAKLOC02750g	27.1	SAKLOH13596g			
68	KLLA0C02387g	28.5	KLLA0D18645g			
68	ERGO0F21428g	27.2	ERGO0G05896g			
69	ZYRO0F17072g	27.4	ZYRO0G12276g	GL3C0351	similar to SACE YLR187W SKG3 and YNL278W CAF120 Part of the evolutionarily-conserved CCR4- NOT transcriptional regulatory complex involved in controlling mRNA initiation, elongation, and degradation	weakly similar to SACE YJL016W
69	KLTH0F02002g	26.3	KLTH0B02222g			
69	SAKLOC02222g	30.8	SAKLOG13838g			
69	KLLA0C01969g	28.3	KLLA0F22561g			
69	ERGO0F21824g	22.8	ERGO0G15334g			
70	ZYRO0G21736g	26.8	ZYRO0F11484g	GL3C0293	highly similar to SACE YGL100W SEH1 Nuclear pore protein homologous to Sec13p	highly similar to SACE YLR208W SEC13 Component of both the Nup84 nuclear pore sub-complex and of the COPII complex
70	KLTH0H05610g	27.8	KLTH0H01518g			
70	SAKLOA05962g	26.1	SAKLOF11022g			
70	KLLA0F06754g	26.7	KLLA0C16643g			
70	ERGO0F04598g	27.3	ERGO0C09328g			
71	ZYRO0C09812g	27.3	ZYRO0A05962g	GL3C0409	some similarities with SACE YNL186W UBP10 Ubiquitin-specific protease	similar to SACE YMR223W UBP8 Ubiquitin-specific protease
71	KLTH0B07150g	25.0	KLTH0D12760g			
71	SAKLOE13002g	28.6	SAKLOH04994g			
71	KLLA0D08459g	28.5	KLLA0C06974g			
71	ERGO0B01562g	24.2	ERGO0F18678g			
72	ZYRO0C10868g	27.8	ZYRO0F06710g	GL3R0271	similar to SACE YJL042W MHP1 Microtubule-associated protein	similar to SACE YPL137C and YOR227W
72	KLTH0G07348g	24.9	KLTH0D10582g			
72	SAKLOG11308g	27.2	SAKLOH07216g			
72	KLLA0E11815g	28.2	KLLA0D07216g			
72	ERGO0C06116g	24.4	ERGO0C07370g			
73	ZYRO0B13266g	27.8	ZYRO0F07018g	GL3R0319	similar to SACE YKL188C PXA2 subunit of a peroxisomal ABC family long-chain fatty acid transporter	similar to SACE YPL147W PXA1 subunit of a peroxisomal ABC family long-chain fatty acid transporter
73	KLTH0D15246g	27.7	KLTH0D10890g			
73	SAKLOG16280g	24.9	SAKLOH06908g			
73	KLLA0B02563g	26.2	KLLA0F11484g			
73	ERGO0E10450g	25.7	ERGO0C07722g			

74	ZYRO0A10472g	26.3	ZYRO0G10978g	GL3R0252	similar to SACE YBR168W PEX32 Peroxisomal integral membrane protein	similar to SACE YLR324W PEX30 Peroxisomal integral membrane protein
74	KLTH0E13706g	27.1	KLTH0E08602g			
74	SAKL0H08756g	26.9	SAKL0H22902g			
74	KLLA0E24641g	23.9	KLLA0C18238g			
74	ERGO0G13156g	26.5	ERGO0F17534g			
75	ZYRO0F17204g	25.7	ZYRO0B03740g	GL3C0149	similar to SACE YLR182W SWI6 Transcription cofactor that regulate transcription at the G1/S transition	similar to SACE YER111C SWI4 Involved in cell cycle dependent gene expression transcription factor
75	KLTH0F01826g	27.0	KLTH0C06270g			
75	SAKL0C01914g	29.0	SAKL0F12870g			
75	KLLA0C01826g	22.8	KLLA0E20791g			
75	ERGO0F21956g	26.2	ERGO0G01716g			
76	ZYRO0B03652g	25.7	ZYRO0A05632g	GL3C0386	highly similar to SACE YER107C GLE2 Component of the nuclear pore complex required for polyadenylated RNA export	similar to SACE YOR026W BUB3 Kinetochore checkpoint WD40 repeat protein
76	KLTH0C06358g	27.4	KLTH0E02134g			
76	SAKL0F12782g	24.7	SAKL0G07040g			
76	KLLA0E20703g	25.7	KLLA0A07106g			
76	ERGO0G01628g	26.8	ERGO0E03014g			
77	ZYRO0B16544g	27.8	ZYRO0G06798g	GL3C0217	similar to SACE YIL156W UBP7 Ubiquitin-specific protease that cleaves ubiquitin-protein fusions	some similarities with SACE YDR069C DOA4 Ubiquitin hydrolase and YER144C UBP5 Putative ubiquitin- specific protease that does not associate with the proteasome
77	KLTH0E00814g	27.9	KLTH0H07678g			
77	SAKL0E15136g	24.8	SAKL0H18986g			
77	KLLA0A00396g	22.9	KLLA0E10275g			
77	ERGO0F12584g	26.1	ERGO0F05698g			
78	ZYRO0C07502g	25.6	ZYRO0B09878g	GL3C0326	highly similar to SACE YOL005C RPB11	similar to SACE YNL113W RPC19 RNA polymerase subunit common to RNA polymerases I and III
78	KLTH0C10934g	23.3	KLTH0D09350g			
78	SAKL0E01562g	28.4	SAKL0E10692g			
78	KLLA0C06160g	26.1	KLLA0F23760g			
78	ERGO0C04686g	25.6	ERGO0F00440g			
79	ZYRO0D14124g	22.8	ZYRO0B13684g	GL3C0384	highly similar to SACE YLR268W SEC22 R-SNARE protein	highly similar to SACE YKL196C YKT6 v-SNARE (synaptobrevin) essential for endoplasmic reticulum-Golgi transport
79	KLTH0G15510g	26.7	KLTH0D15708g			
79	SAKL0A08492g	27.1	SAKL0G16786g			
79	KLLA0F20251g	25.0	KLLA0D02684g			
79	ERGO0G14300g	27.0	ERGO0E10868g			
80	ZYRO0F05324g	26.8	ZYRO0D09570g	GL3C0207	similar to SACE YEL042W GDA1 Guanosine diphosphatase located in the Golgi	similar to SACE YER005W YND1 Yeast Nucleoside Diphosphatase
80	KLTH0C03300g	25.7	KLTH0F13178g			
80	SAKL0D11924g	26.8	SAKL0F04664g			
80	KLLA0F16863g	25.4	KLLA0D13662g			
80	ERGO0F14190g	23.6	ERGO0D09438g			
81	ZYRO0F00880g	24.5	ZYRO0B12694g	GL3C0404	similar to SACE YKL065C YET1 Endoplasmic reticulum transmembrane protein	similar to SACE YDL072C YET3 Endoplasmic reticulum transmembrane protein
81	KLTH0D08866g	24.2	KLTH0D14674g			
81	SAKL0B11484g	28.3	SAKL0G15708g			
81	KLLA0F26829g	25.0	KLLA0B03091g			
81	ERGO0B07326g	25.2	ERGO0E09944g			
82	ZYRO0C17886g	24.1	ZYRO0D01936g	GL3C0317	similar to SACE YCR036W RBK1 Putative ribokinase	similar to SACE YJR105W ADO1 adenosine kinase
82	KLTH0F03696g	25.5	KLTH0E01342g			
82	SAKL0C04268g	26.6	SAKL0F15158g			
82	KLLA0C03498g	25.2	KLLA0D10890g			
82	ERGO0F20482g	24.2	ERGO0B08998g			

83	ZYRO0D08118g	22.9	ZYRO0B02970g	GL3C0365	similar to SACE YNR033W ABZ1	similar to SACE YER090W TRP2 anthranilate synthase Component I
83	KLTH0A06842g	25.0	KLTH0C07084g			
83	SAKL0A01188g	26.7	SAKL0F12034g			
83	KLLA0C08448g	27.6	KLLA0E19999g			
83	ERGO0E14410g	22.8	ERGO0B10098g			
84	ZYRO0A12452g	23.7	ZYRO0B01210g	GL3C0344	highly similar to SACE YLR340W RPP0 Conserved ribosomal protein P0	highly similar to SACE YKL009W MRT4 Protein involved in mRNA turnover and ribosome assembly, localizes to the nucleolus
84	KLTH0G17820g	25.7	KLTH0D06050g			
84	SAKL0B04092g	26.3	SAKL0E02288g			
84	KLLA0B05918g	25.7	KLLA0B13563g			
84	ERGO0C00748g	22.5	ERGO0B05148g			
85	ZYRO0B07678g	32.4	ZYRO0B11132g	GL3C0367	similar to SACE YGR062C COX18	similar to SACE YER154W OXA1 Translocase of the mitochondrial inner membrane
85	KLTH0D13376g	30.8	KLTH0H07304g			
85	SAKL0H04180g	20.0	SAKL0H18568g			
85	KLLA0B08019g	18.6	KLLA0E00925g			
85	ERGO0F19250g	21.7	ERGO0G11572g			
86	ZYRO0G14190g	23.1	ZYRO0G02508g	GL3C0231	similar to SACE YMR278W	highly similar to SACE YMR105C PGM2 Phosphoglucosyltransferase
86	KLTH0C03872g	24.2	KLTH0D04796g			
86	SAKL0D01474g	26.7	SAKL0E03630g			
86	KLLA0D01573g	24.7	KLLA0B12694g			
86	ERGO0B01980g	23.6	ERGO0B04268g			
87	ZYRO0B03784g	25.0	ZYRO0C01848g	GL3R0309	similar to SACE YER113C	similar to SACE YLR083C EMP70 Protein whose 24kDa cleavage product is found in endosome-enriched membrane fractions
87	KLTH0C06226g	23.7	KLTH0G13882g			
87	SAKL0F12914g	24.0	SAKL0H17248g			
87	KLLA0E20835g	25.5	KLLA0F18931g			
87	ERGO0G01760g	22.1	ERGO0G10538g			
88	ZYRO0E03652g	25.7	ZYRO0C09944g	GL3C0372	highly similar to SACE YEL013W VAC8 Phosphorylated vacuolar membrane protein	highly similar to SACE YNL189W SRP1 karyopherin alpha homolog of 60 kDa
88	KLTH0H13926g	23.2	KLTH0B07282g			
88	SAKL0D10736g	23.5	SAKL0E13134g			
88	KLLA0A11286g	23.1	KLLA0D08580g			
88	ERGO0E07172g	24.6	ERGO0B01452g			
89	ZYRO0F04136g	23.0	ZYRO0B11836g	GL3C0379	similar to SACE YPL008W CHL1	highly similar to SACE YER171W RAD3 5' to 3' DNA helicase subunit of Nucleotide Excision Repair Factor 3 and subunit of RNA polymerase II transcription initiation factor TFIIH
89	KLTH0A02376g	23.6	KLTH0G14300g			
89	SAKL0B02662g	25.2	SAKL0H17776g			
89	KLLA0F27181g	24.3	KLLA0C17776g			
89	ERGO0G08140g	23.5	ERGO0G10934g			
90	ZYRO0D04554g	25.3	ZYRO0G01078g	GL3C0390	similar to SACE YAL035W FUN12 GTPase required for general translation initiation	similar to SACE YOL023W IFM1 Mitochondrial translation initiation factor 2
90	KLTH0D01606g	22.7	KLTH0H13530g			
90	SAKL0B10758g	24.0	SAKL0D10274g			
90	KLLA0F23265g	23.3	KLLA0A10923g			
90	ERGO0D17886g	24.2	ERGO0E07546g			
91	ZYRO0D01056g	24.3	ZYRO0G16962g	GL3C0280	highly similar to SACE YPR181C SEC23 cytoplasmic GTPase-activating protein	weakly similar to SACE YHR035W
91	KLTH0A00814g	24.4	KLTH0G06138g			
91	SAKL0F16038g	24.5	SAKL0G10010g			
91	KLLA0E04885g	23.1	KLLA0C10461g			
91	ERGO0E01936g	23.0	ERGO0A02794g			

92	ZYRO0C09438g	24.4	ZYRO0G10934g	GL3R0224	highly similar to SACE YDL132W CDC53 Cullin structural protein of SCF complexes	similar to SACE YGR003W CUL3
92	KLTH0H02464g	20.8	KLTH0E08558g			
92	SAKL0F10054g	23.6	SAKL0H22858g			
92	KLLA0F05467g	24.2	KLLA0C18282g			
92	ERGO0D11770g	26.2	ERGO0F17490g			
93	ZYRO0B15400g	21.3	ZYRO0A13200g	GL3C0228	highly similar to SACE YHR148W IMP3 Component of the SSU processome	highly similar to SACE YPL081W RPS9A and YBR189W RPS9B, components of the small (40S) ribosomal subunit
93	KLTH0C01958g	24.8	KLTH0E12826g			
93	SAKL0G15268g	24.8	SAKL0H09768g			
93	KLLA0E15995g	24.8	KLLA0E23673g			
93	ERGO0D06270g	22.5	ERGO0E02376g			
94	ZYRO0C05544g	27.5	ZYRO0B01298g	GL3C0366	similar to SACE YNR006W VPS27 hydrophilic protein has cysteine rich putative zinc finger	similar to SACE YHL002W HSE1 Subunit of the endosomal Vps27p-Hse1p complex
94	KLTH0A05676g	19.5	KLTH0D06138g			
94	SAKL0A02464g	28.4	SAKL0E02200g			
94	KLLA0F06446g	18.8	KLLA0B13475g			
94	ERGO0F01430g	23.8	ERGO0B05060g			
95	ZYRO0C03256g	24.4	ZYRO0C09306g	GL3C0299	similar to SACE YNL321W Protein of unknown function potential Cdc28p substrate	similar to SACE YDL128W VCX1
95	KLTH0F19404g	24.4	KLTH0A05368g			
95	SAKL0C13398g	22.4	SAKL0F09878g			
95	KLLA0E21033g	22.5	KLLA0F05632g			
95	ERGO0D04928g	24.2	ERGO0F09350g			
96	ZYRO0A04378g	23.4	ZYRO0C03718g	GL3C0222	similar to SACE YDL002C NHP10 likely component of the INO80, ATP-dependent chromatin-remodeling complex	similar to SACE YDR174W HMO1 Chromatin associated high mobility group (HMG)
96	KLTH0G16566g	24.1	KLTH0F09020g			
96	SAKL0C11308g	21.9	SAKL0H14234g			
96	KLLA0E17403g	22.0	KLLA0D18029g			
96	ERGO0E08250g	26.3	ERGO0G05280g			
97	ZYRO0G01166g	23.7	ZYRO0G16852g	GL3C0354	highly similar to SACE YOL021C DIS3 Nucleolar exosome component involved in rRNA processing and RNA degradation	similar to SACE YDR293C SSD1 Protein that interacts with components of the TOR pathway
97	KLTH0H13420g	24.8	KLTH0G06248g			
97	SAKL0D10186g	22.9	SAKL0G10142g			
97	KLLA0A10835g	23.0	KLLA0C10571g			
97	ERGO0E07634g	22.9	ERGO0A02706g			
98	ZYRO0A02068g	22.0	ZYRO0F13046g	GL3C0388	highly similar to SACE YNL025C SSN8 Component of RNA polymerase II holoenzyme involved in RNA pol II carboxy-terminal domain phosphorylation	similar to SACE YPR025C CCL1 Cyclin associated with protein kinase Kin28p which is the TFIIH-associated carboxy-terminal domain (CTD) kinase
98	KLTH0G10560g	24.4	KLTH0C05720g			
98	SAKL0E07480g	25.3	SAKL0F13398g			
98	KLLA0E08163g	24.4	KLLA0E06689g			
98	ERGO0D04532g	20.6	ERGO0G02244g			
99	ZYRO0F07964g	23.1	ZYRO0D12694g	GL3C0442	similar to SACE YDL113C ATG20 Protein required for transport of aminopeptidase I (Lap4p) through the cytoplasm-to-vacuole targeting pathway	similar to SACE YDR425W SNX41 Sorting nexin that mediates retrieval from endosomes
99	KLTH0F09328g	24.1	KLTH0G03894g			
99	SAKL0E06710g	22.3	SAKL0G05060g			
99	KLLA0E09175g	23.6	KLLA0B00803g			
99	ERGO0D02574g	23.3	ERGO0D13772g			
100	ZYRO0D04972g	22.8	ZYRO0B14344g	GL3C0381	similar to SACE YAL042W ERV46 Protein localized to COPII-coated vesicles forms a complex with Erv41p	similar to SACE YML067C ERV41 Protein in COPII-coated vesicles
100	KLTH0D01144g	29.7	KLTH0D16324g			
100	SAKL0D14234g	19.0	SAKL0G17512g			
100	KLLA0C12947g	22.3	KLLA0B04950g			

100	ERGO0D18238g	22.3	ERGO0E11462g			
101	ZYRO0C14674g	25.1	ZYRO0G13112g	GL3C0248	similar to SACE YBR233W PBP2	similar to SACE YBL032W HEK2
101	KLTH0H06050g	26.2	KLTH0E14520g			
101	SAKL0A06424g	19.1	SAKL0B06798g			
101	KLLA0F10703g	20.4	KLLA0E12321g			
101	ERGO0F05038g	22.3	ERGO0E12584g			
102	ZYRO0D16368g	26.4	ZYRO0C03960g	GL3C0263	similar to SACE YIL039W	similar to SACE YDR182W CDC1 Putative membrane protein of unknown function involved in Mn2 homeostasis
102	KLTH0A03718g	22.1	KLTH0F08800g			
102	SAKL0F08030g	21.9	SAKL0H13992g			
102	KLLA0E04401g	22.2	KLLA0D18238g			
102	ERGO0D06754g	20.0	ERGO0G05500g			
103	ZYRO0F09482g	23.0	ZYRO0A13354g	GL3C0380	similar to SACE YOR275C RIM20 Protein involved in proteolytic activation of Rim101p in response to alkaline pH, member of the PalA/AIP1/Alix family	similar to SACE YPL084W BRO1 Cytoplasmic class E vacuolar protein sorting (VPS) factor that coordinates deubiquitination in the multivesicular body pathway by recruiting Doa4p to endosomes
103	KLTH0D12408g	25.2	KLTH0E13002g			
103	SAKL0H05346g	20.9	SAKL0H09614g			
103	KLLA0C07348g	19.6	KLLA0E23871g			
103	ERGO0E16104g	23.6	ERGO0G12914g			
104	ZYRO0A05940g	20.5	ZYRO0C04004g	GL3C0422	similar to SACE YOR281C PLP2	similar to SACE YDR183W PLP1
104	KLTH0D12782g	21.9	KLTH0F08756g			
104	SAKL0H04972g	22.0	SAKL0H13948g			
104	KLLA0C06952g	23.7	KLLA0D18282g			
104	ERGO0F18700g	23.0	ERGO0G05544g			
105	ZYRO0B13750g	20.5	ZYRO0B07480g	GL3C0290	similar to SACE YLR425W TUS1 Guanine nucleotide exchange factor (GEF)	similar to SACE YLR371W ROM2 GDP/GTP exchange protein
105	KLTH0D15752g	23.2	KLTH0D13574g			
105	SAKL0G16874g	23.0	SAKL0H03960g			
105	KLLA0D02618g	22.0	KLLA0B07799g			
105	ERGO0E10890g	22.1	ERGO0F19492g			
106	ZYRO0D11110g	17.2	ZYRO0B14454g	GL3C0448	similar to SACE YDR388W RVS167 BAR adaptor protein subunit of a complex (Rvs161p- Rvs167p) that regulates actin endocytosis	some similarities with SACE YDR388W RVS167 BAR adaptor protein, subunit of a complex (Rvs161p-Rvs167p) that regulates actin endocytosis
106	KLTH0F15114g	18.1	KLTH0D16434g			
106	SAKL0G03454g	27.3	SAKL0G17600g			
106	KLLA0E03059g	25.0	KLLA0B04862g			
106	ERGO0F08888g	21.7	ERGO0E11550g			
107	ZYRO0D11616g	26.5	ZYRO0B08514g	GL3C0420	similar to SACE YDR398W UTP5 Nucleolar protein component of the small subunit (SSU) processome	similar to SACE YHR196W UTP9 Nucleolar protein component of the small subunit (SSU) processome
107	KLTH0G02772g	22.4	KLTH0D17732g			
107	SAKL0G03916g	20.8	SAKL0G18370g			
107	KLLA0C06633g	18.4	KLLA0B04180g			
107	ERGO0F15026g	20.9	ERGO0B03300g			
108	ZYRO0A02420g	20.2	ZYRO0D03982g	GL3C0358	similar to SACE YDL122W UBP1 Ubiquitin-specific protease	weakly similar to SACE YPL072W UBP16 Putative ubiquitin-specific protease
108	KLTH0G10934g	20.7	KLTH0E12540g			
108	SAKL0E07106g	22.8	SAKL0H10076g			
108	KLLA0E08801g	22.4	KLLA0E23387g			
108	ERGO0G17028g	22.0	ERGO0E02662g			
109	ZYRO0F16500g	19.3	ZYRO0C10516g	GL3C0318	similar to SACE YGL140C	similar to SACE YDL231C BRE4 Zinc finger protein containing five transmembrane domains
109	KLTH0F02552g	21.6	KLTH0B07810g			
109	SAKL0C02860g	20.5	SAKL0E13684g			
109	KLLA0C02497g	23.8	KLLA0D19118g			

109	ERGO0F21318g	19.5	ERGO0B00990g			
110	ZYRO0G01584g	20.8	ZYRO0B12122g	GL3C0247	similar to SACE YOL034W SMC5 Structural maintenance of chromosomes protein	similar to SACE YLR383W RHC18 Protein involved in structural maintenance of chromosomes required for interchromosomal and sister chromatid recombination
110	KLTH0D02816g	20.2	KLTH0D14080g			
110	SAKL0B09526g	20.6	SAKL0H03322g			
110	KLLA0F07997g	22.8	KLLA0E05303g			
110	ERGO0E00286g	19.5	ERGO0E09372g			
111	ZYRO0D01100g	18.6	ZYRO0G16940g	GL3C0425	similar to SACE YPR179C HDA3 Subunit of a possibly tetrameric trichostatin A-sensitive class II histone deacetylase complex	similar to SACE YDR295C HDA2 Subunit of a possibly tetrameric trichostatin A-sensitive class II histone deacetylase complex
111	KLTH0A00858g	21.0	KLTH0G06160g			
111	SAKL0F15994g	19.2	SAKL0G10032g			
111	KLLA0E04841g	17.1	KLLA0C10483g			
111	ERGO0E01980g	26.7	ERGO0A02772g			
112	ZYRO0B03278g	19.5	ZYRO0D01650g	GL3C0256	similar to SACE YBL066C SEF1 putative transcription factor	similar to SACE YLR451W LEU3 Zinc-finger transcription factor that regulates genes involved in branched chain amino acid biosynthesis and ammonia assimilation
112	KLTH0C06776g	19.2	KLTH0F18392g			
112	SAKL0F12342g	20.3	SAKL0F15444g			
112	KLLA0E20307g	20.2	KLLA0D10593g			
112	ERGO0G16566g	22.6	ERGO0B09284g			
113	ZYRO0D02662g	20.4	ZYRO0B13442g	GL3C0347	highly similar to SACE YIL103W DPH1 Protein required along with Dph2p Kti11p Jjj3p and Dph5p for synthesis of diphthamide	similar to SACE YKL191W DPH2 Protein required along with Dph1p Kti11p Jjj3p and Dph5p for synthesis of diphthamide
113	KLTH0G10054g	20.2	KLTH0D15422g			
113	SAKL0E08030g	20.7	SAKL0G16500g			
113	KLLA0F03971g	19.5	KLLA0D02948g			
113	ERGO0D03982g	20.6	ERGO0E10604g			
114	ZYRO0C10340g	22.4	ZYRO0F09988g	GL3C0362	similar to SACE YNL207W RIO2 Protein required for cell viability	similar to SACE YOR119C RIO1 Essential protein that plays a role in cell cycle progression
114	KLTH0B07722g	20.7	KLTH0F16104g			
114	SAKL0E13552g	18.9	SAKL0G02486g			
114	KLLA0D19008g	19.3	KLLA0E21121g			
114	ERGO0B01100g	19.9	ERGO0E14168g			

The table indicates the series of pairs of paralogs in which both members are conserved among the five protoploid yeast species. For all series (number in column 1, classified by decreasing values of sequence conservation) are indicated the two genes concerned (columns 2 and 4), the % of amino-acid identity of their products (column 3) and the corresponding protein family (column 5). For each series, the five genes listed vertically are orthologs confirmed by synteny, and their short description is given by columns 6 and 7.

Supplementary Table 12: Species-specific formation of dispersed paralogs

Fam. Size	Protein family	CDS	Short description
<i>Z. rouxii</i>			
2	GL3C0630	ZYRO0D09702g ZYRO0G20372g	weakly similar to SACE YPR154W PIN3 Protein that induces appearance of prion when overproduced weakly similar to SACE YPR154W PIN3 Protein that induces appearance of prion when overproduced
2	GL3C0706	ZYRO0A03256g ZYRO0G05060g	weakly similar to SACE YDR028C REG1 Regulatory subunit of type 1 protein phosphatase Glc7p similar to SACE YNL166C BNI5 Protein involved in organization of septins at the mother-bud neck
2	GL3C0903	ZYRO0D14102g ZYRO0F13816g	Zygosaccharomyces rouxii sod2 Na ⁺ /H ⁺ antiporter similar to SACE YLR138W NHA1 Na ⁺ /H ⁺ antiporter
2	GL3C0982	ZYRO0C13662g ZYRO0F02640g	weakly similar to SACE YJL020C BBC1 Protein possibly involved in assembly of actin patches weakly similar to SACE YJL020C BBC1 Protein possibly involved in assembly of actin patches
2	GL3R0496	ZYRO0F13552g ZYRO0G11528g	similar to SACE YJR019C TES1 Thioesterase peroxisomal acyl-CoA thioesterase similar to SACE YJR019C TES1 Thioesterase peroxisomal acyl-CoA thioesterase
2	GL3R0659	ZYRO0F04246g ZYRO0G13816g	highly similar to SACE YML106W URA5 Orotate phosphoribosyltransferase 1 highly similar to SACE YML106W URA5 Orotate phosphoribosyltransferase 1
2	GL3R0660	ZYRO0C10406g ZYRO0F06072g	weakly similar to SACE YPL123C RNY1 RNase member of the T(2) family of endoribonucleases similar to SACE YPL123C RNY1 RNase member of the T(2) family of endoribonucleases
2	GL3R0775	ZYRO0B15356g ZYRO0G11638g	highly similar to SACE YJR016C ILV3 Dihydroxyacid dehydratase highly similar to SACE YJR016C ILV3 Dihydroxyacid dehydratase
2	GL3R0872	ZYRO0B00528g ZYRO0C17116g	highly similar to SACE YPR086W SUA7 Transcription factor TFIIIB required for initiation and start site selection by RNA polymerase II highly similar to SACE YPR086W SUA7 Transcription factor TFIIIB required for initiation and start site selection by RNA polymerase II
2	GL3R3015	ZYRO0A06050g ZYRO0F13574g	weakly similar to SACE YOR279C RFM1 DNA-binding protein that directs the Hst1p histone deacetylase to some of the promoters regulated by Sum1p weakly similar to SACE YOR279C RFM1 DNA-binding protein that directs the Hst1p histone deacetylase to some of the promoters regulated by Sum1p
<i>K. thermotolerans</i>			
2	GL3C0549	KLTH0D17930g KLTH0G00418g	similar to SACE YJR130C STR2 Cystathionine gamma-synthase converts cysteine into cystathionine similar to SACE YLL058W
2	GL3C0569	KLTH0A05214g KLTH0G17424g	similar to SACE YIL079C AIR1 and YDL175C AIR2 similar to SACE YIL079C
2	GL3C0590	KLTH0B00440g KLTH0E05676g	similar to SACE YFL054C similar to SACE YLL043W FPS1 Plasma membrane glycerol channel member of the major intrinsic protein family
2	GL3C0711	KLTH0C10516g KLTH0H02684g	similar to SACE YOR380W RDR1 Transcriptional repressor involved in the control of multidrug resistance weakly similar to SACE YPL248C GAL4 DNA-binding transcription factor
2	GL3C0754	KLTH0C00814g KLTH0E03256g	similar to SACE YKL015W PUT3 Positive regulator of proline utilization genes weakly similar to SACE YJL206C
2	GL3C0942	KLTH0C09570g KLTH0G04092g	similar to SACE YOL098C similar to SACE YDR430C CYM1 Cytosolic metalloprotease

2	GL3C0956	KLTH0B00176g KLTH0G19624g	similar to SACE YER152C similar to SACE YER152C
2	GL3R0474	KLTH0B00418g KLTH0D16412g	highly similar to SACE YFL053W DAK2 Dihydroxyacetone kinase highly similar to SACE YML070W DAK1 Dihydroxyacetone kinase
2	GL3R0904	KLTH0D12958g KLTH0F06204g	similar to SACE YOR289W similar to SACE YOR289W
3	GL3R0661	KLTH0B08470g KLTH0F19866g KLTH0H00286g	some similarities with SACE YNL234W Similar to globins and has a functional heme-binding domain involved in glucose signaling or metabolism regulated by Rgt1p some similarities with SACE YNL234W Similar to globins and has a functional heme-binding domain involved in glucose signaling or metabolism regulated by Rgt1p some similarities with SACE YNL234W similar to globins and has a functional heme-binding domain involved in glucose signaling or metabolism regulated by Rgt1p
<i>S. kluyveri</i>			
2	GL3C0553	SAKL0B08008g SAKL0E09658g	similar to SACE YBR114W RAD16 Protein subunit of Nucleotide Excision Repair Factor 4 (NEF4) member of the SWI/SNF family weakly similar to SACE YBR114W RAD16 Protein subunit of Nucleotide Excision Repair Factor 4 (NEF4) member of the SWI/SNF family
2	GL3C0557	SAKL0B12496g SAKL0G09064g	highly similar to SACE YHR208W BAT1 Mitochondrial branched-chain amino acid aminotransferase some similarities SACE YHR208W BAT1 Mitochondrial branched-chain amino acid aminotransferase
2	GL3C0694	SAKL0B02178g SAKL0E13596g	weakly similar SACE YFL010C WWM1 WW domain containing protein interacting with Metacaspase (MCA1) no similarity
2	GL3C0710	SAKL0F13354g SAKL0H21890g	similar to SACE YBL097W BRN1 Essential protein required for chromosome condensation weakly similar to SACE YBL097W BRN1 Essential protein required for chromosome condensation
2	GL3C0713	SAKL0D05302g SAKL0F06622g	highly similar to SACE YKR026C GCN3 Alpha subunit of the translation initiation factor eIF2B highly similar SACE YPR118W Methylthioribose-1-phosphate isomerase
2	GL3C0794	SAKL0B00594g SAKL0H25894g	similar to SACE YLR078C BOS1 v-SNARE (vesicle specific SNAP receptor) localized to the endoplasmic reticulum membrane and necessary for vesicular transport from the ER to the Golgi similar to SACE YHL031C GOS1 v-SNARE protein involved in Golgi transport homolog of the mammalian protein GOS-28/GS28
2	GL3C0976	SAKL0F07370g SAKL0H25982g	similar to SACE YFR033C QCR6 ubiquinol-cytochrome c oxidoreductase subunit 6 (17 kDa) weakly similar to SACE YFR033C QCR6 ubiquinol-cytochrome c oxidoreductase subunit 6 (17 kDa)
2	GL3C1461	SAKL0D13816g SAKL0E08096g	conserved hypothetical protein similar to SACE YNL044W YIP3 Interacts with YPT proteins
2	GL3C3180	SAKL0H15686g SAKL0H17116g	some similarities with SACE YDR143C SAN1 Ubiquitin-protein ligase weakly similar to SACE YDR143C SAN1 Ubiquitin-protein ligase
2	GL3R0843	SAKL0E05742g SAKL0H03762g	similar to SACE YDL052C SLC1 fatty acyltransferase similar to SACE YDL052C SLC1 fatty acyltransferase
2	GL3R2315	SAKL0C05632g SAKL0H10648g	similar to SACE YBR163W similar to SACE YBR163W
2	GL3R2424	SAKL0F01738g SAKL0H20526g	conserved hypothetical protein conserved hypothetical protein
3	GL3R0604	SAKL0C01760g SAKL0C03586g SAKL0D08272g	weakly similar to SACE YLR247C weakly similar to SACE YLR247C similar to SACE YLR247C
3	GL3R0923	SAKL0B00220g	similar to SACE YIL162W SUC2

	SAKL0D11946g	similar to SACE YIL162W SUC2
	SAKL0F01122g	similar to SACE YIL162W SUC2
5	GL3R0543	SAKL0B12826g weakly similar to SACE YBR158W AMN1 Involved in daughter cell separation and Chromosome STability
		SAKL0G00110g weakly similar to SACE YBR158W AMN1 Involved in daughter cell separation and Chromosome Stability
		SAKL0G00132g weakly similar to SACE YBR158W AMN1 Involved in daughter cell separation and Chromosome Stability
		SAKL0G19866g weakly similar to SACE YBR158W AMN1 Involved in daughter cell separation and Chromosome Stability
		SAKL0H10824g similar to SACE YBR158W AMN1 Involved in daughter cell separation and Chromosome Stability

K. lactis

2	GL3C0665	KLLA0E00243g similar to SACE YPR200C ARR2 Arsenate reductase required for arsenate resistance
		KLLA0E16589g similar to SACE YGR203W Probable protein tyrosine phosphatase of the CDC25-like phosphatase family
2	GL3C0688	KLLA0A02233g highly similar to SACE YOR157C PUP1 Endopeptidase with trypsin- like activity that cleaves after basic residues
		KLLA0D11506g highly similar to SACE YFR050C PRE4 20S proteasome beta-type subunit
2	GL3C0736	KLLA0B07227g similar to SACE YJL163C
		KLLA0E24883g weakly similar to SACE YJL163C
2	GL3C0876	KLLA0A12089g similar to Bacillus clausii ABC3243 paiA Septation and degradation transcriptional repressor of sporulation
		KLLA0C09845g similar to SACE YOR253W NAT5 Subunit of the N-terminal acetyltransferase NatA
2	GL3C0944	KLLA0D15356g some similarities with SACE YIR023W DAL81 Positive regulator of genes in multiple nitrogen degradation pathways
		KLLA0E18195g similar to SACE YIR023W DAL81 Positive regulator of genes in multiple nitrogen degradation pathways
2	GL3C1005	KLLA0A04587g highly similar to SACE YOR187W TUF1 Mitochondrial translation elongation factor Tu
		KLLA0C05214g highly similar to SACE YOR187W TUF1 Mitochondrial translation elongation factor Tu
2	GL3R0562	KLLA0C14949g weakly similar to SACE YOL137W
		KLLA0E07063g similar to SACE YOL137W BSC6 Protein of unknown function containing 8 putative transmembrane segments
2	GL3R0834	KLLA0A04543g similar to SACE YLR295C ATP14 Subunit h of the F0 sector of mitochondrial F1F0 ATP synthase
		KLLA0C05170g similar to SACE YLR295C ATP14 Subunit h of the F0 sector of mitochondrial F1F0 ATP synthase
2	GL3R2918	KLLA0A04565g weakly similar to SACE YLR298C YHC1 U1 snRNP protein required for pre- mRNA splicing
		KLLA0C05192g weakly similar to SACE YLR298C YHC1 U1 snRNP protein required for pre- mRNA splicing

A. gossypii

2	GL3C0709	ERGO0D10186g Syntenic homolog of SACE YPR112C (MRD1)
		ERGO0G11110g Syntenic homolog of SACE YER165W (PAB1)
2	GL3M4606	ERGO0B09350g Syntenic homolog of SACE YPR161C (SGV1)
		ERGO0F10538g Syntenic homolog of SACE YKL139W (CTK1)
2	GL3M4611	ERGO0C11308g Syntenic homolog of SACE YOL051W (GAL11)
		ERGO0F01034g Syntenic homolog of SACE YMR164C (MSS11)
2	GL3R0346	ERGO0F11088g Non-syntenic homolog of SACE YKR093W (PTR2)
		ERGO0G00220g No homolog in SACE
2	GL3R0841	ERGO0B02178g Syntenic homolog of SACE YMR284W (YKU70)

		ERGO0F16126g	Syntenic homolog of SACE YMR284W (YKU70)
3	GL3R0662	ERGO0D00264g	Syntenic homolog of SACE YNL244C (SUI1)
		ERGO0E18766g	Syntenic homolog of SACE YNL244C (SUI1)
		ERGO0F20856g	Syntenic homolog of SACE YNL244C (SUI1)
3	GL3R0858	ERGO0D00242g	Syntenic homolog of SACE YNL246W
		ERGO0E18788g	Syntenic homolog of SACE YNL246W (VPS75)
		ERGO0F20834g	Syntenic homolog of SACE YNL246W (VPS75)

The table indicates the series of dispersed paralogs specific to one of the protoploid yeasts corresponding to a unique gene in all other species.

Supplementary Table 13: Paralogous series of species-specific genes

Fam. size	Protein family	CDS	Short description
<i>Z. rouxii</i>			
2	GL3C3673	ZYRO0C10120g ZYRO0F02728g	no similarity some similarities with SACE YIR019C MUC1 GPI-anchored cell surface glycoprotein
2	GL3C3937	ZYRO0E10428g ZYRO0G00198g	similar to SACE YDR539W some similarities with SACE YDR539W
2	GL3C4506	ZYRO0D16918g ZYRO0F11132g	no similarity no similarity
2	GL3R4028 (1)	ZYRO0E10340g ZYRO0F18634g	highly similar to Aspergillus oryzae AO090012000349 Choline dehydrogenase and related flavoproteins highly similar to Aspergillus oryzae AO090012000349 Choline dehydrogenase and related flavoproteins
2	GL3R4324 (1)	ZYRO0A13552g ZYRO0G22572g	similar to Aspergillus oryzae AO090005000547 Predicted protein similar to Aspergillus oryzae AO090005000547 Predicted protein
3	GL3C3802	ZYRO0C01100g ZYRO0C05874g ZYRO0C05896g	some similarities with SACE YML111W BUL2 Component of the Rsp5p E3-ubiquitin ligase complex some similarities with SACE YML111W BUL2 Component of the Rsp5p E3-ubiquitin ligase complex some similarities with SACE YML111W BUL2 Component of the Rsp5p E3-ubiquitin ligase complex
3	GL3C4103	ZYRO0C18326g ZYRO0F15796g ZYRO0F18546g	some similarities with SACE YPR065W no similarity no similarity
5	GL3C3825	ZYRO0A10868g ZYRO0D09658g ZYRO0E04774g ZYRO0G10230g ZYRO0G10692g	no similarity no similarity no similarity no similarity no similarity
10	GL3R0925	ZYRO0A00154g ZYRO0A00264g ZYRO0A11374g ZYRO0A13838g ZYRO0A13904g ZYRO0B00132g ZYRO0C00220g ZYRO0E00308g ZYRO0F05434g ZYRO0G00154g	no similarity no similarity no similarity no similarity no similarity no similarity no similarity no similarity no similarity no similarity
20	GL3R0233	ZYRO0A00132g ZYRO0A00198g ZYRO0A00242g ZYRO0A11198g ZYRO0A11242g ZYRO0A11286g ZYRO0A11308g ZYRO0A11352g ZYRO0A13860g ZYRO0A13926g	some similarities with SACE YKL219W COS9 some similarities with SACE YJR161C COS5 some similarities with SACE YHL044W Putative integral membrane protein, member of DUP240 gene family no similarity no similarity no similarity no similarity no similarity no similarity no similarity

ZYRO0B00110g	no similarity
ZYRO0B17006g	weakly similar to SACE YGL051W MST27 and YAR033W MST28 Putative integral membrane proteins, involved in vesicle formation; member of DUP240 gene family
ZYRO0C00198g	some similarities with SACE YKL219W COS9
ZYRO0D00176g	no similarity
ZYRO0D00220g	no similarity
ZYRO0D00264g	no similarity
ZYRO0E00286g	no similarity
ZYRO0F05368g	no similarity
ZYRO0F05412g	some similarities with SACE YHL048W COS8
ZYRO0G00132g	some similarities with SACE YKL219W COS9

K. thermotolerans

2	GL3C4023	KLTH0F00110g	conserved hypothetical protein
		KLTH0F19954g	conserved hypothetical protein
2	GL3C4283	KLTH0B05060g	conserved hypothetical protein
		KLTH0E14938g	conserved hypothetical protein
2	GL3R3968	KLTH0B10164g	conserved hypothetical protein
		KLTH0E00286g	conserved hypothetical protein
2	GL3R3973	KLTH0A00462g	some similarities with SACE YDR400W URH1 uridine nucleosidase (uridine ribohydrolase)
		KLTH0E00154g	conserved hypothetical protein
2	GL3R4294	KLTH0F00132g	conserved hypothetical protein
		KLTH0F19932g	conserved hypothetical protein
4	GL3R3887	KLTH0C07700g	conserved hypothetical protein
		KLTH0C07722g	conserved hypothetical protein
		KLTH0F12276g	conserved hypothetical protein
		KLTH0H12914g	conserved hypothetical protein
5	GL3C0059	KLTH0B10318g	no similarity
		KLTH0B10428g	no similarity
		KLTH0D00132g	no similarity
		KLTH0G00132g	no similarity
		KLTH0G00396g	conserved hypothetical protein
5	GL3R3664	KLTH0A07810g	highly similar to SACE YJL213W
		KLTH0B00264g	highly similar to SACE YJL213W
		KLTH0C11968g	highly similar to SACE YJL213W
		KLTH0E16874g	highly similar to SACE YJL213W
		KLTH0H00132g	highly similar to SACE YJL213W

S. kluyveri

2	GL3C3704	SAKL0E01848g	no similarity
		SAKL0H17578g	no similarity
2	GL3R4319	SAKL0F09944g	no similarity
		SAKL0H01408g	no similarity
3	GL3C0410	SAKL0E05324g	weakly similar to Candida glabrata CAGL0B02926g
		SAKL0E05346g	weakly similar to Candida glabrata CAGL0B02926g
		SAKL0H24090g	weakly similar to Candida glabrata CAGL0D00286g
3	GL3C4061	SAKL0A10582g	conserved hypothetical protein
		SAKL0A10648g	some similarities with SACE YPR015C
		SAKL0D15136g	some similarities with SACE YPR015C
3	GL3R4027 (1)	SAKL0B00110g	no similarity

		SAKL0C14080g	no similarity
		SAKL0E00110g	some similarities with <i>Xylella fastidiosa</i> XF_0626
4	GL3C3889	SAKL0C03872g	no similarity
		SAKL0C03916g	no similarity
		SAKL0C10648g	weakly similar to SACE YPR065W Heme-dependent repressor of hypoxic genes
		SAKL0D09922g	conserved hypothetical protein
6	GL3R3665 (1)	SAKL0B01782g	similar to Yellowstone A-Prime CYA_2439 ISSoc2 resolvase
		SAKL0B05940g	similar to <i>Caldicellulosiruptor saccharolyticus</i> DSM 8903 CsacDRAFT_1700 Regulatory protein MerR
		SAKL0G04686g	similar to <i>Caldicellulosiruptor saccharolyticus</i> DSM 8903 CsacDRAFT_1700 Regulatory protein MerR
		SAKL0H03674g	weakly similar to Yellowstone A- Prime CYA_2425 ISSoc2 resolvase
		SAKL0H06314g	similar to Yellowstone A-Prime CYA_2425 ISSoc2 resolvase
		SAKL0H06600g	similar to <i>Synechococcus</i> sp. (strain JA-3-3Ab) (<i>Cyanobacteria</i> bacterium Yellowstone A-Prime) ISSoc2 resolvase
<i>K. lactis</i>			
2	GL3C4579	KLLA0A11957g	conserved hypothetical protein
		KLLA0C19063g	conserved hypothetical protein
2	GL3R4112	KLLA0D06193g	conserved hypothetical protein
		KLLA0E04599g	no similarity
3	GL3C3955	KLLA0B14531g	conserved hypothetical protein
		KLLA0C00330g	conserved hypothetical protein
		KLLA0C03113g	<i>Kluyveromyces lactis</i> KLLA0C03113g Sla2 protein
3	GL3R4104	KLLA0A12001g	no similarity
		KLLA0B00220g	conserved hypothetical protein
		KLLA0D00209g	conserved hypothetical protein
7	GL3C3543	KLLA0A00143g	conserved hypothetical protein
		KLLA0B00166g	conserved hypothetical protein
		KLLA0C00154g	conserved hypothetical protein
		KLLA0D00157g	conserved hypothetical protein
		KLLA0D19987g	conserved hypothetical protein
		KLLA0E00155g	no similarity
		KLLA0F00176g	no similarity
7	GL3R3212	KLLA0A00154g	conserved hypothetical protein
		KLLA0B00187g	conserved hypothetical protein
		KLLA0C00176g	no similarity
		KLLA0D00187g	no similarity
		KLLA0D19965g	conserved hypothetical protein
		KLLA0E00177g	no similarity
		KLLA0F00220g	no similarity
<i>A. gossypii</i>			
2	GL3C4268	ERGO0D00110g	no similarity
		ERGO0G00132g	no similarity
3	GL3R3997	ERGO0D00308g	no similarity
		ERGO0E18722g	no similarity
		ERGO0F20900g	no similarity

The table indicates the series of dispersed paralogs specific to one of the protoplloid yeasts with no clearcut homolog in the other species. (1) putative cases of lateral gene transfers that will be published elsewhere (Rolland et al. submitted).

Supplementary Table 14: Species-specific family expansions

Protein family	ZYRO	KLTH	SAKL	KLLA	ERGO	CDS	Brief description
<i>Z. rouxii</i>							
GL3C0055	10	4	3	2	0	ZYRO0A13574g ZYRO0B00330g ZYRO0B16742g ZYRO0C18546g ZYRO0E10362g ZYRO0F05214g ZYRO0F18656g ZYRO0G00242g ZYRO0G15400g ZYRO0G22506g	similar to SACE YGL039W and YGL157W similar to SACE YGL039W and YGL157W similar to SACE YGL039W and YGL157W similar to SACE YGL039W and YGL157W similar to SACE YGL039W and YGL157W similar to SACE YOL151W GRE2 NADPH-dependent methylglyoxal reductase (D- lactaldehyde dehydrogenase) similar to SACE YOL151W GRE2 NADPH-dependent methylglyoxal reductase (D- lactaldehyde dehydrogenase) similar to SACE YGL039W and YGL157W similar to SACE YOL151W GRE2 NADPH-dependent methylglyoxal reductase (D- lactaldehyde dehydrogenase) similar to SACE YGL039W and YGL157W
GL3C0080	6	3	2	1	1	ZYRO0C11902g ZYRO0C11924g ZYRO0F12144g ZYRO0F13618g ZYRO0F16852g ZYRO0G15444g	similar to SACE YHR179W OYE2 Widely conserved NADPH oxidoreductase containing flavin mononucleotide (FMN) similar to SACE YHR179W OYE2 Widely conserved NADPH oxidoreductase containing flavin mononucleotide (FMN) similar to SACE YHR179W OYE2 Widely conserved NADPH oxidoreductase containing flavin mononucleotide (FMN) similar to SACE YHR179W OYE2 Widely conserved NADPH oxidoreductase containing flavin mononucleotide (FMN) similar to SACE YHR179W OYE2 Widely conserved NADPH oxidoreductase containing flavin mononucleotide (FMN) similar to SACE YHR179W OYE2 Widely conserved NADPH oxidoreductase containing flavin mononucleotide (FMN)
GL3C0186	6	1	0	0	0	ZYRO0A01122g ZYRO0A08206g ZYRO0D10780g ZYRO0F16874g ZYRO0G18876g ZYRO0G19866g	similar to SACE YOR388C FDH1 NAD()-dependent formate dehydrogenase similar to SACE YOR388C FDH1 NAD()-dependent formate dehydrogenase similar to SACE YOR388C FDH1 NAD()-dependent formate dehydrogenase similar to SACE YNL274C Putative hydroxyisocaproate dehydrogenase similar to SACE YOR388C FDH1 NAD()-dependent formate dehydrogenase similar to SACE YOR388C FDH1 NAD()-dependent formate dehydrogenase
GL3R0232	5	2	2	2	1	ZYRO0B16764g ZYRO0C17820g	similar to SACE YDR256C CTA1 Catalase A breaks down hydrogen peroxide in the peroxisomal matrix similar to SACE YGR088W CTT1 Cytosolic catalase T has a role in protection from oxidative damage by hydrogen peroxide

							ZYRO0E10318g	similar to SACE YDR256C CTA1 Catalase A breaks down hydrogen peroxide in the peroxisomal matrix
							ZYRO0F08426g	similar to SACE YDR256C CTA1 Catalase A breaks down hydrogen peroxide in the peroxisomal matrix
							ZYRO0G22462g	similar to SACE YGR088W CTT1 Cytosolic catalase T has a role in protection from oxidative damage by hydrogen peroxide
GL3C0522	4	1	2	1	0		ZYRO0A00286g	similar to SACE YPL088W Putative aryl alcohol dehydrogenase
							ZYRO0D02816g	similar to SACE YPL088W Putative aryl alcohol dehydrogenase
							ZYRO0F04840g	similar to SACE YPL088W Putative aryl alcohol dehydrogenase
							ZYRO0G20504g	similar to SACE YPL088W Putative aryl alcohol dehydrogenase
K. thermotolerans								
GL3R0092	3	6	3	3	3		KLTH0C01188g	highly similar to SACE YKL085W MDH1 Mitochondrial malate dehydrogenase
							KLTH0D00440g	conserved hypothetical protein
							KLTH0E09614g	similar to SACE YDL078C MDH3 Cytoplasmic malate dehydrogenase
							KLTH0F18854g	similar to SACE YOL126C MDH2 Cytoplasmic malate dehydrogenase
							KLTH0G19536g	similar to SACE YDL078C MDH3 Cytoplasmic malate dehydrogenase
							KLTH0G19558g	similar to SACE YDL078C MDH3 Cytoplasmic malate dehydrogenase
S. kluyveri								
GL3M4590	4	6	12	5	3		SAKL0A00572g	some similarities with SACE YCR089W FIG2 Cell wall adhesin expressed specifically during mating
							SAKL0A02200g	some similarities with SACE YHR211W FLO5 and YAR050W FLO1 Lectin-like proteins involved in flocculation
							SAKL0C09130g	some similarities with SACE YHR211W FLO5 and YAR050W FLO1 Lectin-like proteins involved in flocculation
							SAKL0D09944g	some similarities with SACE YIR019C MUC1 GPI-anchored cell surface glycoprotein
							SAKL0E00528g	some similarities with SACE YHR211W FLO5 and YAR050W FLO1 Lectin-like proteins involved in flocculation
							SAKL0E15378g	some similarities with SACE YHR211W FLO5 and YAR050W FLO1 Lectin-like proteins involved in flocculation
							SAKL0G19910g	some similarities with SACE YAL063C
							SAKL0H00176g	conserved hypothetical protein
							SAKL0H00286g	conserved hypothetical protein
							SAKL0H21340g	no similarity
							SAKL0H21362g	some similarities with SACE YIR019C MUC1 GPI-anchored cell surface glycoprotein
							SAKL0H23188g	some similarities with SACE YIR019C MUC1 GPI-anchored cell surface glycoprotein
GL3C0107	2	3	6	3	1		SAKL0D02486g	similar to SACE YDR242W AMD2 Putative amidase
							SAKL0E04994g	conserved hypothetical protein
							SAKL0E15312g	similar to SACE YDR242W AMD2 Putative amidase
							SAKL0H01254g	similar to SACE YMR293C

						SAKL0H11990g	similar to SACE YDR242W AMD2 Putative amidase
						SAKL0H23804g	similar to SACE YDR242W AMD2 Putative amidase
GL3R0543	1	1	5	1	1	SAKL0B12826g	similar to SACE YBR158W AMN1 Involved in daughter cell separation and Chromosome Stability
						SAKL0G00110g	similar to SACE YBR158W AMN1 Involved in daughter cell separation and Chromosome Stability
						SAKL0G00132g	similar to SACE YBR158W AMN1 Involved in daughter cell separation and Chromosome Stability
						SAKL0G19866g	similar to SACE YBR158W AMN1 Involved in daughter cell separation and Chromosome Stability
						SAKL0H10824g	similar to SACE YBR158W AMN1 Involved in daughter cell separation and Chromosome Stability
GL3C0086	1	1	4	2	1	SAKL0C03102g	conserved hypothetical protein
						SAKL0C03124g	conserved hypothetical protein
						SAKL0G04004g	similar to SACE YDR402C DIT2 Sporulation-specific enzyme required for spore wall maturation involved in the production of a soluble LL-dityrosine-containing precursor of the spore wall
						SAKL0H11176g	conserved hypothetical protein
<i>K. lactis</i>							
GL3C0074	1	4	4	12	0	KLLA0A00132g	similar to SACE YKL221W MCH2 Protein with similarity to mammalian monocarboxylate permeases
						KLLA0B00143g	similar to SACE YKL221W MCH2 Protein with similarity to mammalian monocarboxylate permeases
						KLLA0C00132g	similar to SACE YKL221W MCH2 Protein with similarity to mammalian monocarboxylate permeases
						KLLA0C06677g	similar to SACE YKL221W MCH2 Protein with similarity to mammalian monocarboxylate permeases
						KLLA0C17336g	similar to SACE YKL221W MCH2 Protein with similarity to mammalian monocarboxylate permeases
						KLLA0D00143g	similar to SACE YKL221W MCH2 Protein with similarity to mammalian monocarboxylate permeases
						KLLA0D10131g	similar to SACE YKL221W MCH2 Protein with similarity to mammalian monocarboxylate permeases
						KLLA0D20009g	similar to SACE YKL221W MCH2 Protein with similarity to mammalian monocarboxylate permeases
						KLLA0E00133g	similar to SACE YKL221W MCH2 Protein with similarity to mammalian monocarboxylate permeases
						KLLA0F00154g	similar to SACE YKL221W MCH2 Protein with similarity to mammalian monocarboxylate permeases
						KLLA0F11077g	weakly similar to SACE YNL125C ESBP6 Protein with similarity to monocarboxylate permeases
						KLLA0F24200g	weakly similar to SACE YNL125C ESBP6 Protein with similarity to monocarboxylate permeases
GL3C0221	2	2	2	7	0	KLLA0A00110g	conserved hypothetical protein
						KLLA0C00110g	conserved hypothetical protein
						KLLA0C06699g	conserved hypothetical protein
						KLLA0D13002g	conserved hypothetical protein

						KLLA0D20031g	conserved hypothetical protein
						KLLA0E00111g	conserved hypothetical protein
						KLLA0F00132g	conserved hypothetical protein
GL3C3528	0	2	0	5	0	KLLA0B00308g	some similarities with SACE YAR050W
						KLLA0B14916g	some similarities with SACE YHR211W FLO5
						KLLA0C19316g	Lectin-like protein involved in flocculation
						KLLA0D00275g	some similarities with SACE YAL063C
						KLLA0E25147g	some similarities with SACE YAL063C
GL3R0383	0	2	2	5	0	KLLA0A00176g	similar to SACE YBR092C PHO3 Constitutively expressed acid phosphatase
						KLLA0B00286g	similar to SACE YBR092C PHO3 Constitutively expressed acid phosphatase
						KLLA0C19338g	similar to SACE YBR092C PHO3 Constitutively expressed acid phosphatase
						KLLA0D00258g	similar to SACE YBR092C PHO3 Constitutively expressed acid phosphatase
						KLLA0E24949g	similar to SACE YBR092C PHO3 Constitutively expressed acid phosphatase
<i>A. gossypii</i>							
GL3M4603	0	0	1	2	6	ERGO0D08272g	Syntenic homolog of SACE YPR015C
						ERGO0D08316g	Syntenic homolog of SACE YPR013C
						ERGO0D16368g	no similarity
						ERGO0E06490g	no similarity
						ERGO0G03696g	no similarity
						ERGO0G12518g	no similarity
GL3R0084	1	1	2	1	5	ERGO0B08954g	Syntenic homolog of SACE YJR107W
						ERGO0C02222g	Non-syntenic homolog of SACE YJR107W
						ERGO0E18656g	Non-syntenic homolog of SACE YJR107W; Tandem gene triplication in this genome'
						ERGO0E18678g	Non-syntenic homolog of SACE YJR107W; Tandem gene triplication in this genome'
						ERGO0E18700g	Non-syntenic homolog of SACE YJR107W; Tandem gene triplication in this genome'

The table indicates, for each yeast species, all series of dispersed paralogs of four members of more, that are at least twice more numerous than paralogs of the same family in other species. Number of genes per species are indicated in columns 2 to 6. Expansions are shadowed, and the corresponding genes are listed in column 7 with their brief description in column 8.