

Supplementary Data to:

**Dicistronic tRNA-5S rRNA genes in *Yarrowia lipolytica*:
an alternative TFIIIA-independent way for expression of 5S rRNA genes**

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- 1- Alignment of the 117 5S rRNA gene copies from *Yarrowia lipolytica*.
- 2- Coordinates of the 47 tRNA-5S rRNA dicistronic genes and of a single tRNA-tRNA-5S rRNA tricistronic gene.
- 3- Coordinates of the 13 tDNA-Trp (CCA)-RUF70 dicistronic genes.
- 4- Sequences of oligonucleotides used for RT-PCR and cloning.
- 5- Sequences and alignment of TFIIIA orthologs in hemiascomycetes.

1- Alignment of the 117 5S rRNA gene copies from *Yarrowia lipolytica*.

First line in blue is 5S rRNA gene from *Saccharomyces cerevisiae*. Gene names in italic denote the 8 uncomplete copies of the 5S rRNA gene and one (*YALIOA08974r*) interrupted by a *ylt1* transposable element (the end of the sequence is not listed). There are 108 full length copies of which 48 are located 3' adjacent to a tRNA gene (hilited in yellow).

	1				50
<i>SACE_5S</i>	GGTTGCGGCC	ATATCTACCA	GAAAGCACCG	TTTCCCGTCC	GATCAACTGT
<i>YALIOE25527r</i>TCTCTGA	GTTTGACTGT
<i>YALIOE25229r</i>GCC	ATATCCTGGA	G.TGGTACAG	CTTCCTATCC	GACCAGCAAT
<i>YALIOA00786r</i>ATTCTGGT	GAAAATACGG	CTTCTCGTCC	CATCAGCCTT
<i>YALIOE28694r</i>	GAAATAATGG	CTCCCCGTTT	GATCAACCAT
<i>YALIOF01414r</i>GT	GAAAATACGG	CTT.CCGTCC	GATCAGCCGT
<i>YALIOD23754r</i>AT	GAAAATACGG	CTT.CGGTCT	GATCTGCCAT
<i>YALIOA08893r</i>CAT
<i>YALIOB14932r</i>	AGTTGCAGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOA08974r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOE30439r</i>	GGTTACGACC	ATATCTTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOA18082r</i>	GGTCCAGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOC20843r</i>	AGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOB04666r</i>	GGTTACGGCC	ATATCTTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOF09898r</i>	AGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOC10404r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOC12300r</i>	GGTTACGGCC	ATATCTTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOA06235r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTTC	GATCAGCCAT
<i>YALIOA13451r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTTC	GATCAGCCAT
<i>YALIOC11189r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTTC	GATCAGCCAT
<i>YALIOA04211r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOA04567r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOA12461r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOA12993r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOC07218r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOC09413r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOC17613r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOC22811r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOE08116r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOA12773r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOB00332r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOB13026r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOB17576r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOB18830r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOB21734r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOC01806r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOC03115r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOC04754r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOD10199r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOD10349r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOD26035r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOE00354r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOE12795r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOE19835r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOE27322r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOE29801r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOF05366r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOF18060r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOF19934r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOF25947r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOF26941r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOA07269r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOE07357r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOE30241r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOF26739r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOC09055r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOD05425r</i>	GGTTACGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTCC	GATCAGCCAT
<i>YALIOB07137r</i>	GGTTGCGGCC	ATATCCTGGT	GAAAATACGG	CTTCCCGTTC	GATCAGCCAT

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 YALIO05660r AGTTGCGGCT ATATCCTGGT GAAAATACGG CTTCCCGTCC GATCAGCCAT
 YALIOB09114r CTCAACGGCC ATATCCTGGT GAAAATACGG CTTCCCGTCC GATCAGCCAT
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SACE_5S AGTTAAGCTG G..TAAGAGC CTGACCGAGT AGTGTAGTGG GTGACCATAC

YALIOE25527r AGCTGATCGG AC.TGGAAGC CGTATT...T TCTTCAGGAT ATGGCC....

YALIOE25229r AGTCAAGCAC C..AGAGAGC CCAGTT.GTT ATTGTAGTTG GATACCATA.

YALIOA00786r AGTCAACCAC C..AGGGAGC CTAG.....

YALIOE28694r AGTAAAGCAC C..AGAGAG.

YALIOF01414r AGTCAAGCAC C..AGATAGC CCAATT.AGT ATTGTAGTGG GAGACCCTAC

YALIOD23754r AGTCAAGCAC C..AGAGAGC CCAG.....

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YALIO0D09565r AGTCAAGCAC C..AGAGAGC CCAGTT.AGT ATTGTAGTGG GAGACCATAC
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YALIO0A08201r AGTCAAGCAC C..AGAGAGC CCAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0F01182r AGTCAAGCAC C..AGAGAGC CTAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0A17966r AGTCAAGCAC C..AGAGAGC CTAGTT.AGT ATTGTAGTGG GAGACCATAC
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YALIO0C06671r AGTCAAGCAC C..AGAGAGC CTAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0C08998r AGTCAAGCAC C..AGAGAGC CTAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0C10643r AGTCAAGCAC C..AGAGAGC CTAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0D08806r AGTCAAGCAC C..AGAGAGC CTAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0E19167r AGTCAAGCAC C..AGAGAGC CTAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0E23480r AGTCAAGCAC C..AGAGAGC CTAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0E24111r AGTCAAGCAC C..AGAGAGC CTAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0E26399r AGTCAAGCAC C..AGAGAGC CTAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0F06518r AGTCAAGCAC C..AGAGAGC CTAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0F07200r AGTCAAGCAC C..AGAGAGC CTAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0F15791r AGTCAAGCAC C..AGAGAGC CTAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0A16600r AGTCAAGCAC C..AGAGAGC CCAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0B08349r AGTCAAGCAC C..AGAGAGC CCAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0C10218r AGTCAAGCAC C..AGAGAGC CCAGTT.AGT ATTGTAGTGG GAGACCATAT
YALIO0D21203r AGTCAAGCAC C..AGAGAGC CCAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0C05312r AGTCAAGCAC C..AGAGAGC CCAGTT.AGT ATTGTAGTGG GAGACCATAC
YALIO0D16281r AGTCAAGCAC C..AGAGAGC CCAGTT.AGT ATTGTAGTGG GAGACCATAC

	101	127	
<i>SACE_5S</i>	<i>GCGAAACTCA</i>	<i>GGTGCTGCAA</i>	<i>TCTTTAT</i>
<i>YALIOE25527r</i>
<i>YALIOE25229r</i>
<i>YALIOA00786r</i>
<i>YALIOE28694r</i>
<i>YALIOF01414r</i>	CAGCATCCTG	GGTGCTGCCA	TTC....
<i>YALIOD23754r</i>
<i>YALIOA08893r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOB14932r</i>	GAGAATCC..
<i>YALIOA08974r</i>
<i>YALIOE30439r</i>	GAGAATCCTG	GGTGTGTAA	TT.....
<i>YALIOA18082r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOC20843r</i>	GAGAATCCTG	GGTGCTGTAA	TT.....
<i>YALIOB04666r</i>	GAGAATCCTG	GGTGCTGTAA	CC.....
<i>YALIOF09898r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOC10404r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOC12300r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOA06235r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOA13451r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOC11189r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOA04211r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOA04567r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOA12461r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOA12993r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOC07218r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOC09413r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOC17613r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOC22811r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOE08116r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOA12773r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOB00332r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOB13026r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOB17576r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOB18830r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOB21734r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOC01806r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOC03115r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOC04754r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOD10199r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOD10349r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOD26035r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOE00354r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOE12795r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOE19835r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOE27322r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOE29801r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOF05366r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOF18060r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOF19934r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOF25947r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOF26941r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOA07269r</i>	GAGAATCCTG	GGTGCTGTAA	TC.....
<i>YALIOE07357r</i>	GAGAATCCTG	GGTGCTGTAA	TT.....
<i>YALIOE30241r</i>	GAGAATCCTG	GGTGCTGTAA	TT.....
<i>YALIOF26739r</i>	GAGAATCCTG	GGTGCTGTAA	TT.....
<i>YALIOC09055r</i>	GAGAATCCTA	GGTGCTGTAA	TC.....
<i>YALIOD05425r</i>	GAGAATCCTA	GGTGCTGTAA	TC.....
<i>YALIOB07137r</i>	GAGAATCCTA	GGTGCTGCAA	TC.....

YALI0D19299r GAGAATCTCC GGTGCTGCAA TC.....
YALI0D05660r GAGAATCCTG GATGCTGCAA TT.....
YALI0B09114r GAGAATCCTG GGTGCTGCAA TC.....
YALI0A03916r GAGAATCCTA GGTGCTGCAA TT.....
YALI0A06760r GAGAATCCTA GGTGCTGCAA TT.....
YALI0B19987r GAGAATCCTA GGTGCTGCAA TTC.....
YALI0C13717r GAGAATCCTA GGTGCTGCAA TT.....
YALI0C20922r GAGAATCCTA GGTGCTGCAA TT.....
YALI0D04840r GAGAATCCTA GGTGCTGCAA TT.....
YALI0D10627r GAGAATCCTA GGTGCTGCAA TT.....
YALI0E07756r GAGAATCCTA GGTGCTGCAA TT.....
YALI0E14252r GAGAATCCTA GGTGCTGCAA TT.....
YALI0F08157r GAGAATCCTA GGTGCTGCAA TT.....
YALI0F10581r GAGAATCCTA GGTGCTGCAA TT.....
YALI0F16880r GAGAATCCTA GGTGCTGCAA TT.....
YALI0A06644r GAGAATCCTG GGTGCTGCAA TT.....
YALI0C21571r GAGAATCCTG GGTGCTGCAA TT.....
YALI0F12523r GAGAATCCTG GGTGCTGCAA TT.....
YALI0F16725r GAGAATCCTG GGTGCTGCAA TT.....
YALI0A14888r GAGAATCCTG GGTGCTGCAA TT.....
YALI0D00104r GAGAATCCTG GGTGCTGCAA TT.....
YALI0A10884r GAGAATCCTG GGTGCTGCAA TT.....
YALI0A15326r GAGAATCCTG GGTGCTGCAA TT.....
YALI0A16145r GAGAATCCTG GGTGCTGCAA TT.....
YALI0B09988r GAGAATCCTG GGTGCTGCAA TT.....
YALI0B23485r GAGAATCCTG GGTGCTGCAA TT.....
YALI0C00099r GAGAATCCTG GGTGCTGCAA TT.....
YALI0C19525r GAGAATCCTG GGTGCTGCAA TT.....
YALI0C24453r GAGAATCCTG GGTGCTGCAA TT.....
YALI0D09565r GAGAATCCTG GGTGCTGCAA TT.....
YALI0E11511r GAGAATCCTG GGTGCTGCAA TT.....
YALI0F00099r GAGAATCCTG GGTGCTGCAA TT.....
YALI0F13964r GAGAATCCTG GGTGCTGCAA TT.....
YALI0F15687r GAGAATCCTG GGTGCTGCAA TT.....
YALI0F16461r GAGAATCCTG GGTGCTGCAA TT.....
YALI0F23886r GAGAATCCTG GGTGCTGCAA TT.....
YALI0A10493r GAGAATCCTT GGTGTTGCAA TT.....
YALI0C18833r GAGAATCCTT GGTGCTGCAA TT.....
YALI0A08201r GAGAATCCTA GGTGCTGCAA TC.....
YALI0F01182r GAGAATCCTG GGTGCTGCAA TC.....
YALI0A17966r GAGAATCCTG GGTGCTGCAA TC.....
YALI0B20515r GAGAATCCTG GGTGCTGCAA TC.....
YALI0C05542r GAGAATCCTG GGTGCTGCAA TC.....
YALI0C06671r GAGAATCCTG GGTGCTGCAA TC.....
YALI0C08998r GAGAATCCTG GGTGCTGCAA TC.....
YALI0C10643r GAGAATCCTG GGTGCTGCAA TC.....
YALI0D08806r GAGAATCCTG GGTGCTGCAA TC.....
YALI0E19167r GAGAATCCTG GGTGCTGCAA TC.....
YALI0E23480r GAGAATCCTG GGTGCTGCAA TC.....
YALI0E24111r GAGAATCCTG GGTGCTGCAA TC.....
YALI0E26399r GAGAATCCTG GGTGCTGCAA TC.....
YALI0F06518r GAGAATCCTG GGTGCTGCAA TC.....
YALI0F07200r GAGAATCCTG GGTGCTGCAA TC.....
YALI0F15791r GAGAATCCTG GGTGCTGCAA TC.....
YALI0A16600r GAGAATCCTA GGTGCTGCAA TC.....
YALI0B08349r GAGAATCCTG GGTGCCGCAA TC.....
YALI0C10218r GAGAATCCTG GGTGCTGCAA TC.....
YALI0D21203r GAGAATCCTG GGTGCTGCAA TC.....
YALI0C05312r GAGAATCCTG GGTGCTGCAA TC.....
YALI0D16281r GAGAATCCTG GGTGCTGCAA TC.....

2- Coordinates of the 47 tRNA-5S rRNA dicistronic genes and of a single tRNA-tRNA-5S rRNA tricistronic gene.

Gene #	Begin	End	Strand	Gene type	intergenic distance
-----	-----	-----	-	-----	--
YALIOA04211r	456779	456897	c	5SRNA	4
YALIOA04213r	456902	456972	c	tRNA Gly (GCC) cove=64.77	
YALIOA04565r	484054	484124		tRNA Gly (GCC) cove=64.77	4
YALIOA04567r	484129	484247		5SRNA	
YALIOA06235r	614877	614995	c	5SRNA	4
YALIOA06237r	615000	615070	c	tRNA Gly (GCC) cove=64.77	
YALIOA07269r	712090	712208	c	5SRNA	4
YALIOA07271r	712213	712283	c	tRNA Gly (GCC) cove=64.77	
YALIOA12461r	1297180	1297298	c	5SRNA	4
YALIOA12463r	1297303	1297383	c	tRNA Glu (CTC) cove=60.91	
YALIOA12771r	1318253	1318323		tRNA Gly (GCC) cove=64.77	4
YALIOA12773r	1318328	1318446		5SRNA	
YALIOA12991r	1334940	1335010		tRNA Gly (GCC) cove=64.77	4
YALIOA12993r	1335015	1335133		5SRNA	
YALIOA13451r	1385398	1385516	c	5SRNA	4
YALIOA13453r	1385521	1385608	c	tRNA Asp (GTC) cove=57.55	
YALIOA18082r	1883168	1883286	c	5SRNA	4
YALIOA18084r	1883291	1883371	c	tRNA Glu (CTC) cove=60.91	
YALIOB00330r	25708	25788		tRNA Glu (CTC) cove=58.38	4
YALIOB00332r	25793	25911		5SRNA	
YALIOB04664r	636203	636273		tRNA Gly (GCC) cove=64.77	5
YALIOB04666r	636279	636397		5SRNA	
YALIOB07137r	946403	946521	c	5SRNA	7
YALIOB07139r	946529	946600	c	tRNA Thr (AGT) cove=74.31	
YALIOB13024r	1745449	1745519		tRNA Gly (GCC) cove=64.77	4
YALIOB13026r	1745524	1745642		5SRNA	
YALIOB17576r	2299263	2299381	c	5SRNA	4
YALIOB17578r	2299386	2299473	c	tRNA Asp (GTC) cove=56.78	
YALIOB18830r	2475555	2475673	c	5SRNA	4
YALIOB18832r	2475678	2475748	c	tRNA Gly (GCC) cove=64.77	
YALIOB21734r	2859341	2859459	c	5SRNA	4
YALIOB21736r	2859464	2859544	c	tRNA Glu (CTC) cove=60.91	
YALIOC01804r	251371	251441		tRNA Gly (GCC) cove=64.77	4
YALIOC01806r	251446	251564		5SRNA	
YALIOC03113r	417851	417921		tRNA Gly (GCC) cove=64.77	4
YALIOC03115r	417926	418044		5SRNA	
YALIOC04752r	624935	625005		tRNA Gly (GCC) cove=64.77	4
YALIOC04754r	625010	625128		5SRNA	
YALIOC07216r	963247	963317		tRNA Gly (GCC) cove=64.77	4
YALIOC07218r	963322	963440		5SRNA	
YALIOC09053r	1238222	1238292		tRNA Gly (GCC) cove=64.77	5
YALIOC09055r	1238298	1238416		5SRNA	
YALIOC09413r	1286546	1286664	c	5SRNA	5
YALIOC09416r	1286670	1286740	c	tRNA Gly (GCC) cove=64.77	
YALIOC10404r	1447991	1448109	c	5SRNA	5
YALIOC10406r	1448115	1448185	c	tRNA Gly (GCC) cove=64.77	
YALIOC10643r	1473976	1474094		5SRNA	

YALIO1C11187r	1543852	1543922		tRNA Gly (GCC) cove=64.77	5
YALIO1C12298r	1705002	1705072		tRNA Gly (GCC) cove=64.77	4
YALIO1C12300r	1705077	1705195		5SRNA	
YALIO1C17611r	2463226	2463296		tRNA Gly (GCC) cove=64.77	4
YALIO1C17613r	2463301	2463419		5SRNA	
YALIO1C20843r	2795011	2795129	c	5SRNA	4
YALIO1C20845r	2795134	2795214	c	tRNA Glu (CTC) cove=60.14	
YALIO1C22811r	3062616	3062734	c	5SRNA	4
YALIO1C22814r	3062739	3062809	c	tRNA Gly (GCC) cove=64.77	
YALIO1D05423r	705811	705891		tRNA Glu (CTC) cove=60.91	4
YALIO1D05425r	705896	706014		5SRNA	
YALIO1D10197r	1289703	1289788		tRNA Asp (GTC) cove=57.93	4
YALIO1D10199r	1289793	1289911		5SRNA	
YALIO1D10349r	1303013	1303131	c	5SRNA	4
YALIO1D10351r	1303136	1303221	c	tRNA Asp (GTC) cove=57.16	
YALIO1D26035r	3463039	3463157	c	5SRNA	4
YALIO1D26037r	3463162	3463242	c	tRNA Glu (CTC) cove=60.77	
YALIO1E00352r	36748	36828		tRNA Glu (CTC) cove=60.77	4
YALIO1E00354r	36833	36951		5SRNA	
YALIO1E07357r	843297	843415	c	5SRNA	5
YALIO1E07359r	843421	843491	c	tRNA Gly (GCC) cove=64.77	
YALIO1E08116r	956044	956162	c	5SRNA	4
YALIO1E08118r	956167	956257	c	tRNA Asp (GTC) cove=58.99	
YALIO1E12749r	1552681	1552761		tRNA Lys (CTT) cove=65.44	17
YALIO1E12793r	1552779	1552870		tRNA Glu (CTC) cove=60.47	4
YALIO1E12795r	1552875	1552993		5SRNA	
YALIO1E19833r	2367494	2367564		tRNA Gly (GCC) cove=64.77	4
YALIO1E19835r	2367569	2367687		5SRNA	
YALIO1E27322r	3238316	3238434	c	5SRNA	4
YALIO1E27324r	3238439	3238509	c	tRNA Gly (GCC) cove=64.77	
YALIO1E29799r	3531926	3532007		tRNA Glu (CTC) cove=60.26	4
YALIO1E29801r	3532012	3532130		5SRNA	
YALIO1E30239r	3569382	3569452		tRNA Gly (GCC) cove=64.77	4
YALIO1E30241r	3569457	3569575		5SRNA	
YALIO1E30437r	3585610	3585695		tRNA Asp (GTC) cove=57.93	4
YALIO1E30439r	3585700	3585818		5SRNA	
YALIO1F05366r	802929	803047	c	5SRNA	4
YALIO1F05368r	803052	803122	c	tRNA Gly (GCC) cove=64.77	
YALIO1F09898r	1346340	1346458	c	5SRNA	4
YALIO1F09900r	1346463	1346547	c	tRNA Gln (CTG) cove=57.33	
YALIO1F18060r	2405305	2405423	c	5SRNA	4
YALIO1F18062r	2405428	2405498	c	tRNA Gly (GCC) cove=64.77	
YALIO1F19932r	2665039	2665126		tRNA Asp (GTC) cove=57.69	4
YALIO1F19934r	2665131	2665249		5SRNA	
YALIO1F25947r	3337927	3338045	c	5SRNA	5
YALIO1F25949r	3338051	3338138	c	tRNA Asp (GTC) cove=56.91	
YALIO1F26739r	3413815	3413933	c	5SRNA	4
YALIO1F26741r	3413938	3414008	c	tRNA Gly (GCC) cove=64.77	
YALIO1F26939r	3429923	3429993		tRNA Gly (GCC) cove=64.77	4
YALIO1F26941r	3429998	3430116		5SRNA	

3- Coordinates of the 13 tDNA-Trp (CCA)-RUF70 dicistronic genes.

The 13 tDNA-Trp (CCA)-RUF70 dicistronic genes are numbered according to their location in the genome from chromosomes A to F. Start coordinate of tDNA is that of mature nt #1, end coordinate is that of nt #73, start coordinate of RUF70 genes are that of the nucleotide following nt #73 of tDNA, end coordinate is that of the first nucleotide following the terminal T-track (see Fig. 2).

	tDNA-Trp (CCA)		RUF70 gene	
	start	end	start	end
1 A <	861901	861816	861815	861774
2 A >	1404668	1404753	1404754	1404832
3 A <	1424537	1424452	1424451	1424374
4 A <	1568219	1568134	1568133	1568048
5 B >	2652246	2652332	2652333	2652406
6 C <	286336	286251	286250	286173
7 C >	664941	665028	665029	665104
8 C <	2551313	2551228	2551227	2551156
9 D <	210924	210839	210838	210762
10 E <	1739685	1739600	1739599	1739511
11 E <	2547332	2547246	2547245	2547173
12 F <	1021277	1021192	1021191	1021113
13 F <	3423047	3422964	3422963	3422887

4- Sequences of oligonucleotides used for RT-PCR and cloning.

Oligos for RT-PCR	forward	reverse
tDNA-Gly (GCC)-5S RNA	GCGCCGATGGTTTAGTGGTAA	ATTACAGCACCCAGGATTCTCG
tDNA-Asp (GTC)-5S RNA	TCCGCAATAGTTTAGTGGCTAG	ATTACAGCACCCAGGATTCTCG
tDNA-Glu (CTC)-5S RNA	TCCGATATAGTGTAGGGGCTAT	ATTACAGCACCCAGGATTCTCG
tDNA-Gln (CTG)-5S RNA	GGTTGTATAGTGTAGCGGTTAT	ATTACAGCACCCAGGATTCTCG
tDNA-Thr (AGT)-5S RNA	GCCTTCGTGGCCAAGTGGTAAG	ATTGCAGCACCTAGGATTCTCG
tDNA-Lys (CTT)-		
tDNA-Glu (CTC)-5S RNA	GCCTGGCTAGCTCAATCGGTAG	ATTACAGCACCCAGGATTCTCG
tDNA-Trp (CCA)-RUF70	GATGTGGTGGCTCAATGGTAGAG	TACACCGATCAGCTGAAGCTATG

Oligos used for cloning

tDNA-Gly (GCC)-5S RNA	TTGTCGTGGTCTCGTGGTAGTG	ATAACGGCAGAAGAACACAGCC	(#1)
tDNA-Asp (GTC)-5S RNA	TTTCATCACATTTGCTCTCTTCG	TATACATCGATGGGCAGATTAC	(#3)
tDNA-Glu (CTC)-5S RNA	CTGAATCTTTGCGATGTGCGCT	ACGTGACTAGAGTGGTTGTTCC	(#2)
tDNA-Gln (CTG)-5S RNA	TTGTCGTCTGTAACGCTCCTAC	GATTGTGCGACTCAAGCACAAG	(#1)
tDNA-Thr (AGT)-5S RNA	AGGCCAAAACAGCGAAGATACG	CACATGGCAAAACACATGGGC	(#1)
tDNA-Lys (CTT)-			
tDNA-Glu (CTC)-5S RNA	TCTCGAGGTAGTGAATCATGGC	CCAATTGCATATGCAAGTCGGG	(#0)
tDNA-Trp (CCA)-RUF70	AGCTGTTTTGCGCATAATCCTG	TACACCGATCAGCTGAAGCTATG	

5- Sequences and alignment of TFIIIA orthologs in hemiascomycetes and *S. pombe*.

Amino acid sequence of TFI_{II}A orthologues were aligned with MAFFT (Kato et al., 2002) and visualized with Genedoc (<http://www.psc.edu/biomed/genedoc>). SACE, *Saccharomyces cerevisiae* YPR186c; CAGL, *Candida glabrata* CAGL0G10021g; VAPO, *Vanderwaltozyma polyspora* A7TF03_VANPO; KLLA, *Kluyveromyces lactis* KLLA0B03454g; ERGO, *Eremothecium gossypii* AEL278Wp (Q758N3_ASHGO); DEHA, *Debaryomyces hansenii* DEHA0C07623g; CAAL, *Candida albicans* CA1157|PZF1; YALI, *Yarrowia lipolytica* YALI0F05104g, SCPO, *Schizosaccharomyces pombe* SPAC144.09c (NP_594670).

Cys and His residues of the 9 zinc fingers common to all TFI_{II}A's in Hemiascomycetes are indicated in bold under the alignment; those from the 10th zinc finger specific to TFI_{II}A of *Y. lipolytica* are indicated in italics.

Kato K, Misawa K, Kuma K & Miyata T (2002) MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. *Nucleic Acids Res* 30(14): 3059-3066.

Saccharomyces cerevisiae (SACE)

```
>YPR186c Tfc2 (Pzf1) 429 aa
MGGEVLNNEGMP LAELKQETIPISRSESSESLNSLTSTRSSSSNRPKTYF
CDYDGCDAFTRPSILTEHQLSVHQGLRAFQCDKCAKSFVKKSHLERHLY
THSDTKPFQCSYCGKGVTTROQLKRHEVTHTKSFICPEEGCNLRFYKHPQ
LRAHILSVHLKLTCPHCNKSFORPYRLRNHISKHHDPEVENPYQCTFAG
CCKEFRIWSQLQSHIKNDHPKPKCPCSKPCVGENGLQMHMIHDDSLVT
KNWKCHICPDMFSRKHDLTHYGSIHTEEDIPELKYKISDIQQLVQDH
GVQLGNSKHSNEQDEEKISNRLRKRRLTENNNVEFLQNEVDLEKRLESG
ENGLNLLLNTVGRKYRCFYNNCSRFTFKTKKEYEKHIDKHKVHELKLIKILQ
EKEENKTLVDQNHKEPFI IQKETQSAGDK
```

Candida glabrata (CAGL)

```
>CAGL0G10021g 394 aa
MEANDVFDSQVPLSRSSSVGSMSSVASGSSVRSKTYLCEYDNCDAFTRP
SLLTEHQNTVHLGRKPWKNQCESSFTKKIHLEHLYTHTDERPFYCSFC
GGLITRQQLKRHEVTHTKSFNCEYEGCNESFYKHPQLRAHILAVHLQSL
KCHECNKSFORPYRLKNHIAKHHNPVFNAYQCTFSVCSKSFKTWSALRL
HVKNDDHPKPKCPCSKPCVGEDGLNMHMKIH DENLVSRNWKCHICNDQSF
AKKLELLDHYSNSHSEEIPAYLLEQKVVPYVETNVTGKTECEKSPTKKYV
KATDMLAIRTEITLNRFFDGGKDAMTLLLNTVGRKFRCPYSKCYRSFKTE
EKYNIHIEKHRIHEQKLELETSGLQADIEPDRQSTALEKEE
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Vanderwaltozyma polyspora (VAPO)

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> A7TF03 | A7TF03_VANPO
MEELSLWKSECTPPLQRTNTGGGGGSSGSVTSSTASRSKRFFCDYDGCDA
KAFSRPVLLTDHQQSVHLRIKPFKCDQCSAFSKKSHLERHLFSHSSEKP
FTCAVCNKGLTTRQQLKRHEITHTKSFVCPHDGCSESFYKHPQLRSHILA
VHLQKLRQCQKDFORPYRLRLHIAKHHNPVFNAYQCTFGGCSLSFKT
WTALQTHTKNDHPKPKCAICDKPCVGEAGLQMHMEVHNEFLVAKNWKCSK
CDPPI SFVKKNELITHYLEIHKEELPPGLVESASEPTSKVAESPANEILT
RAKRRKLNNASAVLNEEKLEEYLESGNSGLSLLLNTVGRRLKCKYLGCSR
TFKTEERYDKHIIHRKIHLEKLIKIAITKEDTDKE
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Kluyveromyces lactis (KLLA)

>KLLA0B03454g 472 aa

MKFIKQAMRCDWVRRFTPIHGIPNRVMDYLGNVVVATDESVMVAPTYN
KENEVRQNVVGENDDDDQCCVPTPPLTRSEMSVMSMASVTSTVSVSSS
QRSKVYFCDYQGCNKSFTRPSSLTEHQLTVHHGIKPFKCDTCGKEFAKKS
HLNRHMFSTDDKPFCTCSICGKGVTTROQLKRHEITHTKSFHCSYEGCNE
SFYKHPQLRSHILSVHEKLTCPHCNKTFQRPYRLKNHIDKHHNPESTGM
YQCDFLSTDFVSTWSSLOQHIKQCHPKLPICGKPCVAESGLRNHMMI
HDESLVTKNWKCSSCPDTSFAKKTQLVQHYESHKDVPPELLLLPTDADE
DTNIKVNTDIKISETEDSFSSGKKTLLDFPSFSKRRKVDLGSVEAEIKI
KKYIESGKTTKSLLLNTVQKRCPCYTNCNRTFKSKEKFDTHIEKHKIHE
LKMKILEDENQKSSKNDHARKI

Eremothecium gossypii (ERGO)

>AEL278W (NP_984582) 476 aa

MCSCQAIWSWIDQSDQSGCVLFASVAQPLGRHRNLGAPSLEQVKIGGKSS
PDRAHLTIIGCAARSRGKMEAHKLVHGLEELPVDEVTDYALSRTTSAGS
TVSLSSVESTASSTRKTHYCDYEGCYKAFTRPSLLTEHQOTAHQIRAY
QCEQCGRGFTKKSHLERHLFSHSETKPFCTVCGKGVTTROQLRRHEITH
TKSFKCPHEGCGEAFYKHPQLRSHVLAVHEQKLTCTHCDKRFQRPYRLKT
HIAKHHGPASQFRYQCTNAGCVQCFETWSALQOHLHTDHPKLPBGVCGKL
CVGETGLQMHMTVHDESRVIKNWKCVCSDTTYAKMADLLAHYMKTHGDS
IPKELIEHVNAESPVVHVDEQQREDPEIVRPQKRRKNSDNTIMGSLQTE
EKIRKLIESGRGLSLLNNTAGRKKRCPYLGCSRVPFKTEDKYDLHISKHK
INDLKVKLLEDKLTAAAAGKDPACG

Debaryomyces hansenii (DEHA)

>DEHA0C07623g 452 aa

MESSETASVSSRASSSSARPKNYICDEPDCGKAYSKPSLLEQHKRSHTNE
RPFKSETGCDKSFRLKSHLQAHLLEDQESKPFQCATCGKGVNTLQHL
KRHEITHTKSFICTFEGCNESFYKHQSLRHHTLSVHEKLLCNKCNKSN
RPYRLAQHNIKYHSDSPAYQCDHQGCFGNFMTWSALQLHIKTEHPKIKCP
ICGKGCVGKGLRSHMNIHDEEKIVKLWNCNYCNIGKFKADLIDHYNT
YHDRNLPDDLKPIEREQLDKLLSEKDNIDFNLTLEGLQSKGFVEVPSD
EEKEENDYMSNGLQASHKSLNSLNLTLSEKASIVDLILNNYLKRKVPKP
KKNCDRMFSRDYDLERHLKWHESHLLKIEAFLKSLELEKVPDSNMHDKR
LFPENDEPVMATKRHHAMESDDDFELDDLIDEELKSIQAGQTASNNTTN
VK

Candida albicans (CAAL)

>PZF1 (EAK91019) 412 aa

MSEDETKSISLSSSSSRPKKYICTYEGCDKAYNRPSLLEQHLRTHS
NDRPYKCTVEDCDKAFFRKSHLETHIVSHSEKPFHCSVCGKGVNSRQHL
KRHEITHTKSFKCTFENCQEAIFYKHQSLRHHILSVHEKTLTCKQCCKVFT
RPSKLAQHKLKHGGSPAYQCDHPGCFKNFQTWSVLQFHQSHPKLKCP
KCGKGCVGKGLSSHMLSHDDSTMIKIWTCDYCDVGKFAKKNELVEHYNI
FHDGNI PDDLKETEVEVKLENLLDQGSKLNNLHELETEKLVKVEEDEEDEE
DSLDEKRSVRSDSMSAQRSIKSFTASLEGSKSVSKLISNSGKKINCPKN
NCDRMFSREYDLRRHLKWHDDNLQRIESFLNSIEKEETPEGEPLVKKARM
DLLPNETSVISR

Yarrowia lipolytica (YALI)

>YALIOF05104g 655 aa
MFHEAELSDTPDGIHYDLPSRPTSAAASSASSPVSSSEWIEVKDAHGNPKR
VPERKGLFFPTRGETYGDWNGNVPKEKTTVKRTLAVHCPEEGCDKAYSR
PSLLKQHLSHYNERCFVCTYEGCGKGFRRSHLKAHTNSHTVAKRYHCS
FCAKGFNTRQHLLRHEVTHKSIKHCPHQDCSKQCRTEVQLLEHCVADHAT
WKHQCTYPECGRAIGSERQMZYHWERDHNQTPQYKCPHDECEEVASQWIK
LQKHVSKAHRNWLCHHCEGIFDDVQSMYEHEKSVHGLSVLYRGGHRTPGY
VRQLWTCPEESCGHQSFDKDLYAKHYVSHNKAPVRDMFESVAEYDITPEI
IPYFEKPEKLTRKGRSERTSLEGKSGEEYQLPSERPAKRQRREVSKPTN
TAASIVDKITGAGYSDSRTIPCVVETCMHRFNRYDLDRHVAANHATNCA
VCPFGSHILTEVRDHMSDEHRTEWPAECYQASPDAAHIKIHLAYLRGETPE
VEPVNTTSQNMKNLHYPTPGLRRNAPRGQSNSSYNSPLHSPIIQVPQRA
HSESPMHMYGNSYQPIQHTSPISVTSYPTQTPTPGSIGSPAPLQQLNEAV
EYAPFDLPLSAMSSAYVSPALSHSILAGGHMEYSSNEEVNFTKDSIDP
ELFRQ

Schizosaccharomyces pombe (SCPO)

>SPAC144.09c (NP_594670) 374 aa
MCHFNELSIEIESKNLRSAKKIFHCPYEECGKKYSRPSLLEQHLRTHSNE
RPFVCDYTGCSKAFYRKSHLKIHKRCHTNVVKPFCHYDGCDAQFYTQOHL
ERHIEVHRKPKPYACTWEGCDECFSKHQQLRSHISACHTHLLPYPTYQD
CELRFATKQKLQNHVNRAHEKIIISYSCPHESC VGHEGF EKWSQLQNHIRE
AHVPSCSICGRQFKTAAHLRHHVVLHQTTLEERKTYHCPMEGCKKSFTRS
SALKKHISVIHEGNMAFHCDSCGTFKGYKHM LQRHLERGTCKKAHKPYIN
ECGIKHDGIEGVAIHDQKEKELSSNLVSDVAKKIINEVTGHGYKEAREYS
CSFPECNYRFKRLYDMHRHLNSHH

SACE : -----MGGEVLNN-EGMPLA-----ELKQETIP----- : 22
CAGL : -----MEANDVFD-SQV-----P----- : 12
VAPO : -----M-EELSLW-----KSEC---TPP----- : 14
KLLA : -----MKFIEKTO-AMRCDWVRRFTPIHGIPNRVMDYLGNVVATDESVMVAPTYNKENEVQRNVVGENDDDDQCCVPTPP----- : 75
ERGO : MCSQAIWSWIDQSDQSGCVLFAVSAQPLGRHRNLGAPSLQVQKIGGKSSPDRHLTIIGCAARSRGKGMHAHKLHVHGLEELPVDEVTDY : 90
DEHA : ----- : -
CAAL : ----- : -
YALI : -----MFHEAELSDTPDGI THYDLP SRPTS AASSASSPV SSEWIEVKD-----AHGNPKRVP ERKGLF : 58
SCPO : -----MCHFNE----- : 6

100 * 120 * 140 * 160 * 180
SACE : -I R S E S E S L N S L T S T R S S --- S S N P K T Y F C D Y D G C D K A F I R P S I L T E H O L S V H Q G L R A F Q C --- D K C A K S F V K K S H L E R H L Y T H S D T : 105
CAGL : -L S R S S S V G G M S S V A S --- G S S V S R S T Y L C E D N C D K A F I R P S I L T E H O N T V H L G R K F W K C --- N Q C E S S F T K K I H L E R H L Y T H D E : 92
VAPO : -L Q R T N T G G G G G S S G S V T S --- S T A S S R K R F C D Y D G C D K A F I R P V I L L T D H Q C S V H L R I K E F F K C --- D Q C D S A F S K K S H L E R H L P S H S S E : 98
KLLA : -L T R S E S M D S V M S M A S V T S T V S V S S O S V V F C D Y Q C C N K S F I R P S I L T E H O L T V H H G I K E F F K C --- D T C G R E F A K K S H L N R H M P S H D D : 162
ERGO : A L S R T S A G S T V S L S S V E S T --- A S S T R K T H Y C D E G C Y K A F I R P S I L T E H O Q T A H O G I R A Y Q C --- E Q C G R G F T K K S H L E R H L P S H S E T : 175
DEHA : -M E S S E T A S V S S R A S --- S S A R P K N Y I C D E P D C G K A Y S K P S L L E O H K R S -H T N E R E F F K C S E T G C D N S F I R K S H L Q A H L L S H E D Q : 80
CAAL : -M S E S D E T K S I S S L I S S --- S S S S P K K I I C T Y E G C D K A Y N R P S L L E O H L R T -H S N D R E F Y K C T V E D C D K A F I R K S H L E T H I V S H S E K : 82
YALI : F P I R G E T Y G D A W N G N V P K E K --- T V K T L L A H V P E E G C D K A Y S R P S L L K O H L R S -H Y N E R C F V C T Y E G C G R G F P R R S H L K A H T N S H V A : 144
SCPO : -L S T E I E S K N L R S A --- K K I T H C P E E C G K Y S R P S L L E O H L R T -H S N E R F F V C D Y T G C S R A F Y R K S H L K T H K R C H N V : 80
C C H H C C H H H

* 200 * 220 * 240 * 260 *
SACE : -K F F Q C S Y --- C G K G V T T R O O L K R H E V T H --- T K S F I C P E E G C N L R F Y K H P O L R A H I L S V H L H K I --- T C --- P H C N K S F O R P Y L R N H I S K H : 185
CAGL : -R E F Y C S F --- C G K G I T T R O O L K R H E V T H --- T K S F N C E Y E G C N E S F Y K H P O L R A H I L A V H L Q S I --- K C --- H E C N K S F O R P Y L R N H I S K H : 172
VAPO : -K F F T C A V --- C N K G I T T R O O L K R H E I T H --- T K S F V C P H D C S S E S F Y K H P O L R S H I L A V H L O K I --- R C --- Q H C S D F O R P Y L R L R L H I A K H : 178
KLLA : -K F F T C S I --- C G K G V T T R O O L K R H E I T H --- T K S F H C S Y E G C N E S F Y K H P O L R S H I L S V H E K K I --- T C --- P H C N K T F O R P Y L R N K N H I D K H : 242
ERGO : -K F F S C T V --- C G K G V T T R O O L R R H E I T H --- T K S F K C P H C C G E A F Y K H P O L R S H V L A V H E Q K I --- T C --- T H C D R F O R P Y L R K T H I A K H : 255
DEHA : E S K F F O C A T --- C G K G V N L O H L K R H E I T H --- T K S F I C P F E C C N E S F Y K H Q S I R H H T S V H E K K I --- L C --- N K C N S E N P R Y S L A O H N I K Y : 162
CAAL : -K F F H C S V --- C G K G V N S R O H L K R H E I T H --- T K S F K C T F F E C C N E S F Y K H Q S I R H H L S V H E K T I --- T C --- K C N K V T T R P S L A O H K L A H : 162
YALI : -K R Y H C S F --- C A K G F N T R O H L L R H E V T H --- K S I K H C P H O D C S Q C R T E V O L D E H C V A D H A T W K -H Q C T Y P E C G R A I G S E R O M Q Y H W E R D : 227
SCPO : -K F F S C H Y D G C D A Q F Y T O O L E R H I E V H R K P P V A C T W E C C D C E S K H Q O L R S H I S A C H T H L P Y P C T Y Q D C E L R A T K O L Q N E V N R A : 168
C C H H C C H H C C H H C C H H

280 * 300 * 320 * 340 * 360
SACE : H D P E V E N P Y O C T F A G C C --- K E F R I W S A L Q S H I K N D H P K L K C P I C S K P C V G E N G L Q M H I I -H D D S L --- I T K N W K C H I --- C : 258
CAGL : H N P D V N V A Y O C T F S V C S --- K S E K T W S A L R L H V K N D H P K L K C P I C S K P C V G E D G L N M H I K -L H D E N L --- V S R N W K C H I --- C : 245
VAPO : H N P D V E N P Y O C T F G G C S --- L S E K T W A L O T H T K N D H P K L K A I C D K P C V G E A G L Q M H I E -V H N E F L --- V A K N W K C S K --- C D : 252
KLLA : H N P E S T G M Y C D F L S C T --- D V E S W S L Q O H I K Q C H P L K P C I C K P C V A E S L R N H M -L H D E S L --- I T K N W K C S S --- C : 315
ERGO : H G P A S Q R F Y O C T N A G C V --- Q C F E T W S A L Q O H I H T D H P K L P G C V C G K L C V G E T G L Q M H I T -V H D E S R --- I L K N W K C S V --- C : 328
DEHA : H S D S P --- A Y O C D H Q G C F --- G N E M T W S A L O L H I K T E H P K I K C P I C G K G C V G K K G L R S H N -H H D E E K --- I V K L W N C N Y --- C : 233
CAAL : H G G S P --- A Y O C D H P G C F --- K N F Q T W S V L O F H I K Q S H P L K C P K C G K G C V G K K C S S H L -S H D D S T --- I K I T A T C D Y --- C : 233
YALI : H N Q T P --- Q Y K C P H D E C E --- E V A S O W I K L O K H V S K A H N W L C H H C E G I F D D V O S M Y E H E K S V H G L S V L Y R G G H R T P G Y R O L T W C P E E S --- C : 312
SCPO : H E K I I --- S V S C P H E S C V G H E G E K E W S O L O N H I R E A H V P -S S I C G R O F K T A A H L R H H V -L H O T T L E --- E R T V H C P M E G C --- C : 243
H C C H H C C H H C C H H C C H H

* 380 * 400 * 420 * 440 *
SACE : P D M S F S R K H D L L T H Y G S I H -T E E D I P L E L --- K Y K I S D I Q --- Q V Q D H G V Q L G N S K H S N E Q D E E K I S N R L R K R R K L T E N N N V E F L Q N : 339
CAGL : N D Q S F A K K L E L D D H Y S N S H -S E E P A Y L L --- E Q K V V P Y V --- E T N V -T G K T E C E K S P T --- K R Y V K A T M L A I R --- T : 310
VAPO : P P I S F V K K N E L I T H Y L E I H -K E E P P G L V --- E S A S E P T S --- K V A E --- S P A N E I L T R --- A K R R K L N N A S A V L --- N : 315
KLLA : P D T S F A K K T O L V Q H Y E E S H -K D V D P E L L L L P T D A D E D T N I --- K V N T D I K I S E T E D S F S S G K K T L L D F P S F S K R K V D E L G S V E --- A : 396
ERGO : S D T T Y A K M A D I A H Y M K T H -G D S I P K E L E H V N A E S P A V V --- H V D E Q Q R E D P E I V R P --- Q K R R N S D N T I M G S L T : 399
DEHA : N I G F V K K A D I D H Y N T Y H -D R N P D D L K P I E R E Q L D K L L S E K D S T N I D F N T L E G L Q S K G F V E V P S D E E K E E N D Y M S N G L Q A S H K --- S : 319
CAAL : D V G F A K K N E L V E H Y N I F H -D G N P D D L K E T E V K K L E N L L D Q G S K I N N L H E L E T --- E K L K V E E D E E D E S L D E K R S D V R S D S M A Q R S : 320
YALI : G H O S F D K D L -Y A K H V S -H N K A P V R D M F E S V A E Y D I T P --- E I P Y F E K P E K L T R K G R S E R T S L E G K S G E E Y Q L P S E R P A K --- R Q : 391
SCPO : -K K S F T R S S A K K I S V I H -E G N I -A F H C D S C G P K F G Y K H --- M L Q R H L E R G T C K K A H K P Y I N E C G I K H D G I E G V A I H D Q K E --- K : 320
H H H C C H H C C H H C C H H

460 * 480 * 500 * 520 * 540
SACE : E V D I E K R L E S G E -N G I N L L L N T V --- G R K Y R C F Y N N C S R T E K T K E K Y E K H I -D K E K V H --- : 392
CAGL : E T N N R F F D G G K -D A M T L L L N T V --- G R K F R C P Y S K Y R S E K T E E K Y N I H I -E K E R I H --- : 363
VAPO : E E K L E E Y L E S G N -S G I S L L L N T V --- G R R L K C K Y L G C S R T E K T E E R Y D K H I -H R E K I H --- : 368
KLLA : E I K K K Y I E S G K -T T K S L L L N T V --- G Q R R K C P Y T N C N R T E K S K E K F D T H I -E K E K I H --- : 449
ERGO : E E K R K L I E S G R -T G I S L L L N T A --- G R K K R C P Y L G C S R V E K T E D K Y D L H I -S K E K I N --- : 452
DEHA : L N S N L T L E S G K A S I V D I L L N Y L --- K R K V P C P K K N C D R M S R D Y D L E R H L -K W H E S H --- : 374
CAAL : I K S F T A S L E G S K -S V S K I S N S --- G K I N C P K N N C D R M S R B Y D L R H H -K W H D D N --- : 372
YALI : R R E V S K P T N T A A -S I V D K I T G A G Y S D S T I P C V V E T C M H R E N R K Y D L D R H V A A N A T N C A V C P F G S H I L T E V R D H M S D E H R T E W P A E C Y Q : 480
SCPO : E L S N L V S D V A K -K I I N E V T G H G Y K E A E Y S C S F P E C N Y R E K R L Y D M H R H L -N S H I --- : 374
C C H H C C H H C C H H C C H H

* 560 * 580 * 600 * 620 *
SACE : -----E L K I K I L Q E K E E N K T L-----V D Q N H K E P F I I Q K E T Q S A G D K----- : 429
CAGL : -----E Q N K E L E T S G Q L Q-----M A D I E P D R Q S T A L E K E E----- : 394
VAPO : -----E L K I K I A I T K E D T D K E----- : 384
KLLA : -----E L K K I L E D E N Q K-----S S K N D H A R K I----- : 472
ERGO : -----D L K V K L L E D K L K T E A-----A A G K D P A C G----- : 476
DEHA : -----L K K I E A F L K S L E L E K V P D S N M H D K R L F P E N D E P V M A T K R H H A M E S S D D D F E L D D L I D E E L K S I Q A G Q T A S N N T T N V K----- : 452
CAAL : -----L Q R I E S F L N S I E K E E-----T P E G E P L V K A R M D L L P N E T S V I S R----- : 412
YALI : A S P D A H I K I H L A Y L R G E T P E V E P V N T T S Q N --- M Y K N L H Y P T P G L R R N A P R Q S N S S Y N S P L H S P I I Q V P Q R A H S E S P M H M Y G N S Y Q P I Q : 567
SCPO : ----- : -

640 * 660 * 680 * 700 *
SACE : ----- : -
CAGL : ----- : -
VAPO : ----- : -
KLLA : ----- : -
ERGO : ----- : -
DEHA : ----- : -
CAAL : ----- : -
YALI : H T S P I S V T S Y P T Q T P T P G S I G S P A P L Q Q L N E A V E Y A P F D S I P L S A M S A Y Y S P A L S H I L A G G H D M E Y S S N E E V N F T K D S I D P E L F R Q : 655
SCPO : ----- : -