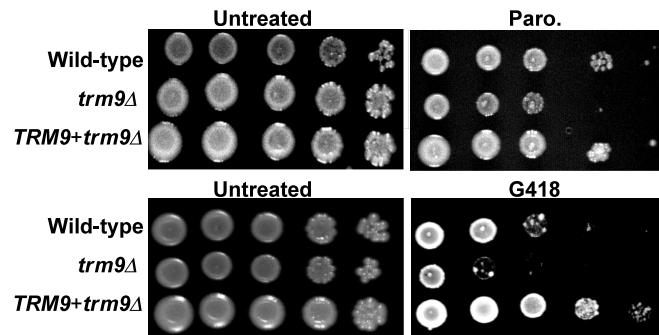


Supplemental Material to: Ashish Patil, Clement Chan, Madhu Dyavaiah, John Rooney, Peter Dedon and Thomas Begley. Translational infidelity-induced protein stress results from a deficiency in Trm9-catalyzed tRNA modifications. *RNA Biology* 2012; 9(7); DOI: 10.4161/rna.20531;
<http://www.landesbioscience.com/journals/rnabiology/article/20531/>

Supplemental Figure S1. Viability phenotypes associated with translational infidelity identified in *trm9Δ* cells.



(A) Wild-type (CEN.PK2-1C) and *trm9Δ* cells were grown overnight in YPD at 30°C. Cultures were serially (10-fold) diluted and plated on YPD, YPD + paromomycin (350 $\mu\text{g/ml}$) or YPD + G418 (20 $\mu\text{g/ml}$).

Supplemental Table S1

W_RNR1	ATG	TAC	GTT	TAT	AAA	AGA	GAC	GGT	CGT	AAA
O_RNR1	ATG	TAT	GTT	TAT	AAA	CGT	GAT	GGT	CGT	AAA
Rnr1 (1-10)	M	Y	V	Y	K	R	D	G	R	K
W_RNR1	GAA	CCT	GTC	CAA	TTC	GAT	AAG	ATT	ACC	GCT
O_RNR1	GAA	CCA	GTT	CAA	TTC	GAT	AAA	ATT	ACT	GCT
Rnr1 (11-20)	E	P	V	Q	F	D	K	I	T	A
W_RNR1	CGT	ATA	TCA	CGC	TTA	TGC	TAT	GGT	TTA	GAT
O_RNR1	CGT	ATT	TCT	CGT	CTA	TGT	TAT	GGT	CTA	GAT
Rnr1 (21-30)	R	I	S	R	L	C	Y	G	L	D
W_RNR1	CCA	AAA	CAT	ATC	GAC	GCC	GTT	AAG	GTC	ACC
O_RNR1	CCA	AAA	CAT	ATT	GAT	GCT	GTT	AAA	GTT	ACT
Rnr1 (31-40)	P	K	H	I	D	A	V	K	V	T
W_RNR1	CAA	CGT	ATC	ATT	TCT	GGT	GTC	TAT	GAA	GGT
O_RNR1	CAA	CGT	ATT	ATT	TCT	GGT	GTT	TAT	GAA	GGT
Rnr1 (41-50)	Q	R	I	I	S	G	V	Y	E	G
W_RNR1	GTC	ACA	ACA	ATC	GAA	CTA	GAC	AAC	TTA	GCC
O_RNR1	GTT	ACT	ACT	ATT	GAA	CTA	GAT	AAT	CTA	GCT
Rnr1 (51-60)	V	T	T	I	E	L	D	N	L	A
W_RNR1	GCT	GAA	ACA	TGC	GCT	TAT	ATG	ACT	ACT	GTT
O_RNR1	GCT	GAA	ACT	TGT	GCT	TAT	ATG	ACT	ACT	GTT
Rnr1 (61-70)	A	E	T	C	A	Y	M	T	T	V
W_RNR1	CAT	CCA	GAT	TAC	GCC	ACC	CTA	GCG	GCC	AGA
O_RNR1	CAT	CCA	GAT	TAT	GCT	ACT	CTA	GCT	GCT	CGT
Rnr1 (71-80)	H	P	D	Y	A	T	L	A	A	R
W_RNR1	ATT	GCC	ATT	TCT	AAT	TTA	CAT	AAA	CAA	ACC
O_RNR1	ATT	GCT	ATT	TCT	AAT	CTA	CAT	AAA	CAA	ACT
Rnr1 (81-90)	I	A	I	S	N	L	H	K	Q	T
W_RNR1	ACA	AAA	CAA	TTT	TCT	AAG	GTT	GTC	GAA	GAT

O_RNR1	ACT	AAA	CAA	TTC	TCT	AAA	GTT	GTT	GAA	GAT
Rnr1 (91-100)	T	K	Q	F	S	K	V	V	E	D
W_RNR1	CTT	TAT	AGA	TAC	GTC	AAT	GCT	GCT	ACT	GGT
O_RNR1	CTA	TAT	CGT	TAT	GTT	AAT	GCT	GCT	ACT	GGT
Rnr1 (101-110)	L	Y	R	Y	V	N	A	A	T	G
W_RNR1	AAG	CCC	GCT	CCC	ATG	ATC	TCT	GAT	GAT	GTC
O_RNR1	AAA	CCA	GCT	CCA	ATG	ATT	TCT	GAT	GAT	GTT
Rnr1 (111-120)	K	P	A	P	M	I	S	D	D	V
W_RNR1	TAC	AAT	ATT	GTC	ATG	GAA	AAC	AAG	GAT	AAA
O_RNR1	TAT	AAT	ATT	GTT	ATG	GAA	AAT	AAA	GAT	AAA
Rnr1 (121-130)	Y	N	I	V	M	E	N	K	D	K
W_RNR1	TTG	AAC	TCC	GCA	ATT	GTC	TAT	GAC	AGA	GAT
O_RNR1	CTA	AAT	TCT	GCT	ATT	GTT	TAT	GAT	CGT	GAT
Rnr1 (131-140)	L	N	S	A	I	V	Y	D	R	D
W_RNR1	TTT	CAG	TAC	AGT	TAT	TTT	GGT	TTT	AAA	ACT
O_RNR1	TTC	CAG	TAT	TCT	TAT	TTC	GGT	TTC	AAA	ACT
Rnr1 (141-150)	F	Q	Y	S	Y	F	G	F	K	T
W_RNR1	TTG	GAA	CGT	TCT	TAT	TTA	CTA	AGA	ATC	AAC
O_RNR1	CTA	GAA	CGT	TCT	TAT	CTA	CTA	CGT	ATT	AAT
Rnr1 (151-160)	L	E	R	S	Y	L	L	R	I	N
W_RNR1	GGT	CAA	GTG	GCC	GAA	CGT	CCA	CAA	CAT	TTA
O_RNR1	GGT	CAA	GTT	GCT	GAA	CGT	CCA	CAA	CAT	CTA
Rnr1 (161-170)	G	Q	V	A	E	R	P	Q	H	L
W_RNR1	ATT	ATG	AGA	GTC	GCA	CTA	GGC	ATC	CAC	GGT
O_RNR1	ATT	ATG	CGT	GTT	GCT	CTA	GGT	ATT	CAT	GGT
Rnr1 (171-180)	I	M	R	V	A	L	G	I	H	G
W_RNR1	AGA	GAT	ATC	GAG	GCT	GCT	TTA	GAA	ACG	TAT
O_RNR1	CGT	GAT	ATT	GAA	GCT	GCT	CTA	GAA	ACT	TAT
Rnr1 (181-190)	R	D	I	E	A	A	L	E	T	Y
W_RNR1	AAC	TTG	ATG	TCT	CTA	AAA	TAT	TTT	ACT	CAC
O_RNR1	AAT	CTA	ATG	TCT	CTA	AAA	TAT	TTC	ACT	CAT

Rnr1 (191-200)	N	L	M	S	L	K	Y	F	T	H
W_RNR1	GCC	TCT	CCA	ACG	TTG	TTC	AAT	GCC	GGT	ACT
O_RNR1	GCT	TCT	CCA	ACT	CTA	TTC	AAT	GCT	GGT	ACT
Rnr1 (201-210)	A	S	P	T	L	F	N	A	G	T
W_RNR1	CCA	AAA	CCT	CAA	ATG	TCC	TCT	TGT	TTC	TTG
O_RNR1	CCA	AAA	CCA	CAA	ATG	TCT	TCT	TGT	TTC	CTA
Rnr1 (211-220)	P	K	P	Q	M	S	S	C	F	L
W_RNR1	GTT	GCC	ATG	AAG	GAG	GAC	TCT	ATC	GAG	GGG
O_RNR1	GTT	GCT	ATG	AAA	GAA	GAT	TCT	ATT	GAA	GGT
Rnr1 (221-230)	V	A	M	K	E	D	S	I	E	G
W_RNR1	ATT	TAC	GAC	ACC	TTG	AAG	GAA	TGT	GCT	TTG
O_RNR1	ATT	TAT	GAT	ACT	CTA	AAA	GAA	TGT	GCT	CTA
Rnr1 (231-240)	I	Y	D	T	L	K	E	C	A	L
W_RNR1	ATT	TCC	AAA	ACT	GCT	GGT	GGT	ATT	GGT	CTA
O_RNR1	ATT	TCT	AAA	ACT	GCT	GGT	GGT	ATT	GGT	CTA
Rnr1 (241-250)	I	S	K	T	A	G	G	I	G	L
W_RNR1	CAT	ATC	CAT	AAC	ATT	CGT	TCA	ACT	GGT	TCT
O_RNR1	CAT	ATT	CAT	AAT	ATT	CGT	TCT	ACT	GGT	TCT
Rnr1 (251-260)	H	I	H	N	I	R	S	T	G	S
W_RNR1	TAC	ATT	GCT	GGT	ACA	AAC	GGT	ACT	TCT	AAC
O_RNR1	TAT	ATT	GCT	GGT	ACT	AAT	GGT	ACT	TCT	AAT
Rnr1 (261-270)	Y	I	A	G	T	N	G	T	S	N
W_RNR1	GGT	TTA	ATT	CCT	ATG	ATT	CGT	GTT	TTC	AAT
O_RNR1	GGT	CTA	ATT	CCA	ATG	ATT	CGT	GTT	TTC	AAT
Rnr1 (271-280)	G	L	I	P	M	I	R	V	F	N
W_RNR1	AAC	ACT	GCC	CGT	TAT	GTT	GAC	CAG	GGT	GGT
O_RNR1	AAT	ACT	GCT	CGT	TAT	GTT	GAT	CAG	GGT	GGT
Rnr1 (281-290)	N	T	A	R	Y	V	D	Q	G	G
W_RNR1	AAT	AAA	AGA	CCT	GGT	GCG	TTT	GCC	CTT	TAC
O_RNR1	AAT	AAA	CGT	CCA	GGT	GCT	TTC	GCT	CTA	TAT
Rnr1 (291-300)	N	K	R	P	G	A	F	A	L	Y

W_RNR1	ACA	CCT	TTC	GTT	GTT	TAC	AAG	GAT	GCT	TGT
O_RNR1	ACT	CCA	TTC	GTT	GTT	TAT	AAA	GAT	GCT	TGT
Rnr1 (401-410)	T	P	F	V	V	Y	K	D	A	C
W_RNR1	AAC	AGA	AAA	TCT	AAT	CAA	AAA	AAC	TTA	GGT
O_RNR1	AAT	CGT	AAA	TCT	AAT	CAA	AAA	AAT	CTA	GGT
Rnr1 (411-420)	N	R	K	S	N	Q	K	N	L	G
W_RNR1	GTC	ATC	AAG	TCA	TCA	AAC	TTA	TGC	TGT	GAA
O_RNR1	GTT	ATT	AAA	TCT	TCT	AAT	CTA	TGT	TGT	GAA
Rnr1 (421-430)	V	I	K	S	S	N	L	C	C	E
W_RNR1	ATT	GTT	GAA	TAC	TCA	GCT	CCA	GAT	GAA	ACT
O_RNR1	ATT	GTT	GAA	TAT	TCT	GCT	CCA	GAT	GAA	ACT
Rnr1 (431-440)	I	V	E	Y	S	A	P	D	E	T
W_RNR1	GCT	GTT	TGT	AAC	TTG	GCT	TCC	GTT	GCC	TTA
O_RNR1	GCT	GTT	TGT	AAT	CTA	GCT	TCT	GTT	GCT	CTA
Rnr1 (441-450)	A	V	C	N	L	A	S	V	A	L
W_RNR1	CCA	GCA	TTC	ATT	GAA	ACT	TCT	GAG	GAT	GGT
O_RNR1	CCA	GCT	TTC	ATT	GAA	ACT	TCT	GAA	GAT	GGT
Rnr1 (451-460)	P	A	F	I	E	T	S	E	D	G
W_RNR1	AAG	ACT	TCC	ACA	TAC	AAC	TTC	AAA	AAA	TTA
O_RNR1	AAA	ACT	TCT	ACT	TAT	AAT	TTC	AAA	AAA	CTA
Rnr1 (461-470)	K	T	S	T	Y	N	F	K	K	L
W_RNR1	CAT	GAA	ATT	GCT	AAA	GTT	GTT	ACT	CGT	AAT
O_RNR1	CAT	GAA	ATT	GCT	AAA	GTT	GTT	ACT	CGT	AAT
Rnr1 (471-480)	H	E	I	A	K	V	V	T	R	N
W_RNR1	TTA	AAC	AGA	GTC	ATT	GAT	CGT	AAT	TAC	TAC
O_RNR1	CTA	AAT	CGT	GTT	ATT	GAT	CGT	AAT	TAT	TAT
Rnr1 (481-490)	L	N	R	V	I	D	R	N	Y	Y
W_RNR1	CCT	GTT	GAA	GAA	GCG	AGA	AAA	TCC	AAT	ATG
O_RNR1	CCA	GTT	GAA	GAA	GCT	CGT	AAA	TCT	AAT	ATG
Rnr1 (491-500)	P	V	E	E	A	R	K	S	N	M
W_RNR1	AGA	CAT	AGA	CCA	ATT	GCT	TTG	GGT	GTT	CAA

O_RNR1	CGT	CAT	CGT	CCA	ATT	GCT	CTA	GGT	GTT	CAA
Rnr1 (501-510)	R	H	R	P	I	A	L	G	V	Q
W_RNR1	GGT	CTC	GCT	GAC	ACT	TTC	ATG	CTG	TTA	CGT
O_RNR1	GGT	CTA	GCT	GAT	ACT	TTC	ATG	CTA	CTA	CGT
Rnr1 (511-520)	G	L	A	D	T	F	M	L	L	R
W_RNR1	TTG	CCA	TTT	GAT	TCT	GAG	GAA	GCC	CGT	TTG
O_RNR1	CTA	CCA	TTC	GAT	TCT	GAA	GAA	GCT	CGT	CTA
Rnr1 (521-530)	L	P	F	D	S	E	E	A	R	L
W_RNR1	CTA	AAT	ATC	CAA	ATC	TTT	GAA	ACT	ATT	TAT
O_RNR1	CTA	AAT	ATT	CAA	ATT	TTC	GAA	ACT	ATT	TAT
Rnr1 (531-540)	L	N	I	Q	I	F	E	T	I	Y
W_RNR1	CAT	GCC	TCC	ATG	GAA	GCT	TCT	TGT	GAA	CTA
O_RNR1	CAT	GCT	TCT	ATG	GAA	GCT	TCT	TGT	GAA	CTA
Rnr1 (541-550)	H	A	S	M	E	A	S	C	E	L
W_RNR1	GCT	CAG	AAG	GAC	GGT	CCA	TAC	GAA	ACT	TTC
O_RNR1	GCT	CAG	AAA	GAT	GGT	CCA	TAT	GAA	ACT	TTC
Rnr1 (551-560)	A	Q	K	D	G	P	Y	E	T	F
W_RNR1	CAA	GGA	TCT	CCT	GCT	TCT	CAA	GGT	ATA	CTA
O_RNR1	CAA	GGT	TCT	CCA	GCT	TCT	CAA	GGT	ATT	CTA
Rnr1 (561-570)	Q	G	S	P	A	S	Q	G	I	L
W_RNR1	CAG	TTT	GAT	ATG	TGG	GAC	CAA	AAA	CCC	TAC
O_RNR1	CAG	TTC	GAT	ATG	TGG	GAT	CAA	AAA	CCA	TAT
Rnr1 (571-580)	Q	F	D	M	W	D	Q	K	P	Y
W_RNR1	GGC	ATG	TGG	GAT	TGG	GAC	ACC	TTA	AGA	AAA
O_RNR1	GGT	ATG	TGG	GAT	TGG	GAT	ACT	CTA	CGT	AAA
Rnr1 (581-590)	G	M	W	D	W	D	T	L	R	K
W_RNR1	GAT	ATC	ATG	AAG	CAT	GGT	GTT	AGA	AAT	TCC
O_RNR1	GAT	ATT	ATG	AAA	CAT	GGT	GTT	CGT	AAT	TCT
Rnr1 (591-600)	D	I	M	K	H	G	V	R	N	S
W_RNR1	TTG	ACC	ATG	GCA	CCA	ATG	CCT	ACT	GCA	TCC
O_RNR1	CTA	ACT	ATG	GCT	CCA	ATG	CCA	ACT	GCT	TCT

Rnr1 (601-610)	L	T	M	A	P	M	P	T	A	S
W_RNR1	ACA	TCC	CAA	ATA	TTG	GGT	TAT	AAT	GAA	TGT
O_RNR1	ACT	TCT	CAA	ATT	CTA	GGT	TAT	AAT	GAA	TGT
Rnr1 (611-620)	T	S	Q	I	L	G	Y	N	E	C
W_RNR1	TTC	GAA	CCA	GTC	ACT	TCC	AAT	ATG	TAC	TCC
O_RNR1	TTC	GAA	CCA	GTT	ACT	TCT	AAT	ATG	TAT	TCT
Rnr1 (621-630)	F	E	P	V	T	S	N	M	Y	S
W_RNR1	CGT	CGT	GTC	TTA	TCC	GGT	GAA	TTC	CAG	GTT
O_RNR1	CGT	CGT	GTT	CTA	TCT	GGT	GAA	TTC	CAG	GTT
Rnr1 (631-640)	R	R	V	L	S	G	E	F	Q	V
W_RNR1	GTG	AAC	CCT	TAC	TTA	CTG	CGT	GAC	TTG	GTT
O_RNR1	GTT	AAT	CCA	TAT	CTA	CTA	CGT	GAT	CTA	GTT
Rnr1 (641-650)	V	N	P	Y	L	L	R	D	L	V
W_RNR1	GAT	TTA	GGT	ATT	TGG	GAT	GAG	GGT	ATG	AAA
O_RNR1	GAT	CTA	GGT	ATT	TGG	GAT	GAA	GGT	ATG	AAA
Rnr1 (651-660)	D	L	G	I	W	D	E	G	M	K
W_RNR1	CAG	TAT	CTG	ATT	ACA	CAA	AAT	GGC	TCC	ATT
O_RNR1	CAG	TAT	CTA	ATT	ACT	CAA	AAT	GGT	TCT	ATT
Rnr1 (661-670)	Q	Y	L	I	T	Q	N	G	S	I
W_RNR1	CAA	GGC	TTA	CCA	AAC	GTT	CCA	CAA	GAA	TTG
O_RNR1	CAA	GGT	CTA	CCA	AAT	GTT	CCA	CAA	GAA	CTA
Rnr1 (671-680)	Q	G	L	P	N	V	P	Q	E	L
W_RNR1	AAG	GAC	TTA	TAC	AAG	ACT	GTT	TGG	GAA	ATT
O_RNR1	AAA	GAT	CTA	TAT	AAA	ACT	GTT	TGG	GAA	ATT
Rnr1 (681-690)	K	D	L	Y	K	T	V	W	E	I
W_RNR1	TCA	CAA	AAG	ACT	ATC	ATT	AAC	ATG	GCA	GCC
O_RNR1	TCT	CAA	AAA	ACT	ATT	ATT	AAT	ATG	GCT	GCT
Rnr1 (691-700)	S	Q	K	T	I	I	N	M	A	A
W_RNR1	GAT	CGT	TCT	GTC	TAT	ATT	GAT	CAA	TCT	CAT
O_RNR1	GAT	CGT	TCT	GTT	TAT	ATT	GAT	CAA	TCT	CAT
Rnr1 (701-710)	D	R	S	V	Y	I	D	Q	S	H

W_RNR1	GCT	TCA	AGA	GAG	GCA	TCT	CCA	GCT	CCA	ACA
O_RNR1	GCT	TCT	CGT	GAA	GCT	TCT	CCA	GCT	CCA	ACT
Rnr1 (811-820)	A	S	R	E	A	S	P	A	P	T
W_RNR1	GGT	AGC	CAC	TCA	TTA	ACT	AAA	GGA	ATG	GCA
O_RNR1	GGT	TCT	CAT	TCT	CTA	ACT	AAA	GGT	ATG	GCT
Rnr1 (821-830)	G	S	H	S	L	T	K	G	M	A
W_RNR1	GAA	TTA	AAC	GTT	CAA	GAG	TCT	AAG	GTA	GAA
O_RNR1	GAA	CTA	AAT	GTT	CAA	GAA	TCT	AAA	GTT	GAA
Rnr1 (831-840)	E	L	N	V	Q	E	S	K	V	E
W_RNR1	GTT	CCT	GAA	GTA	CCT	GCC	CCA	ACT	AAG	AAT
O_RNR1	GTT	CCA	GAA	GTT	CCA	GCT	CCA	ACT	AAA	AAT
Rnr1 (841-850)	V	P	E	V	P	A	P	T	K	N
W_RNR1	GAA	GAA	AAA	GCT	GCC	CCC	ATC	GTT	GAT	GAT
O_RNR1	GAA	GAA	AAA	GCT	GCT	CCA	ATT	GTT	GAT	GAT
Rnr1 (851-860)	E	E	K	A	A	P	I	V	D	D
W_RNR1	GAG	GAA	ACC	GAG	TTC	GAC	ATT	TAC	AAC	TCT
O_RNR1	GAA	GAA	ACT	GAA	TTC	GAT	ATT	TAT	AAT	TCT
Rnr1 (861-870)	E	E	T	E	F	D	I	Y	N	S
W_RNR1	AAG	GTT	ATA	GCA	TGT	GCT	ATT	GAT	AAC	CCA
O_RNR1	AAA	GTT	ATT	GCT	TGT	GCT	ATT	GAT	AAT	CCA
Rnr1 (871-880)	K	V	I	A	C	A	I	D	N	P
W_RNR1	GAA	GCT	TGT	GAA	ATG	TGT	TCG	GGT	TAA	
O_RNR1	GAA	GCT	TGT	GAA	ATG	TGT	TCT	GGT	TAA	
Rnr1 (881-888)	E	A	C	E	M	C	S	G	*	

Supplemental Table S2 (A)

Primer	Sequence
TRM9 +/- 40 BP FORWARD	5'-TGAACAGAGATGAGGTCTCGAA-3'
TRM9 +/- 40 BP REVERSE	5'-TCGTAATACCTGCTGCTACAAAA-3'
TRM9 +/- 500 BP forward	5'-TGACCTGGGTTTTGTTTAGGG-3'
TRM9 +/- 500 BP reverse	5'-TTTCTCTGGTTGGTGCCTTT-3'
TRM9 +500 BP BAMHI Forward	5'-ATGTATCTTCGGGATCCTGACCTGGGTTTTGTTTAGGG-3'
TRM9 -500 BP SACL Reverse in HO plasmid	5'-TAGTGATCAGTCGAGCTCTTTCTCTGGTTGGTGCCTTT-3'
UBI4 Probe forward	5'- CGTTGCATTTGGTGTGAGAT-3'
UBI4 Probe reverse	5'- TCAGTTACCACCCCTCAACC-3'
IRE1 Probe forward	5'- TACTGCCGATCAGCAAACAG-3'
IRE1 Probe reverse	5'-TAGGTTTGGAAAACGCTTGG-3'
KAR2 Probe forward	5'-AACAGACTAAGCGCTGGCAA-3'
KAR2 Probe reverse	5'-CAAACGTTCAAACCAGCGA-3'
HAC1 Probe forward	5'-TCGCACTCGTCGTCTGATAC-3'
HAC1 Probe reverse	5'-AAATGAATTCAAACCTGACTGC-3'
<i>ACT1</i> probe forward	5'-TGGAAAAGATCTGGCATCATA-3'
<i>ACT1</i> probe forward	5'-GGGGCTCTGAATCTTTCGTTA-3'
<i>SSA4</i> probe forward	5'-TGACGAACGATGCTAAGCATT-3'
<i>SSA4</i> probe reverse	5'-CAAATCTTGCCCTTGTAATGG-3'
<i>RNR1</i> Probe forward	5'-TTTCCAAAACGCTGGTGGT-3'
<i>RNR1</i> Probe reverse	5'-TTTCAATGAATGCTGGTAAGG-3'
<i>YEF3</i> Probe forward	5'-AGTACATTGCCGCCATTGGT-3'
<i>YEF3</i> Probe reverse	5'-CATTTTCATCGGTGAAACCGAA-3'

Supplemental Table S2 (B)

Name	Type	Genotype
BY4741	Wild-type	<i>Mata his3Δ leu2Δ met15Δ ura3Δ</i>
YML014W-K	<i>trm9Δ</i> KanMX	<i>Mata his3Δ leu2Δ met15Δ ura3Δ trm9Δ::kanMX4</i>
YML014W-U	<i>trm9Δ</i> Ura3	<i>Mata his3Δ leu2Δ met15Δ ura3Δ trm9Δ::URA3</i>
AWY14W	Wild-type Reporter	<i>MATa UPRE-P_{CYC1(-178)}-LEU2::HIS3 UPRE-P_{CYC1(-178)}-lacZ::TRP1</i>
AWY014WK	AWY14W <i>trm9Δ</i> KanMX	<i>MATa UPRE-P_{CYC1(-178)}-LEU2::HIS3 UPRE-P_{CYC1(-178)}-lacZ::TRP1 trm9Δ::kamMX4</i>
AWY014WU	AWY14W <i>trm9Δ</i> Ura3	<i>MATa UPRE-P_{CYC1(-178)}-LEU2::HIS3 UPRE-P_{CYC1(-178)}-lacZ::TRP1 trm9Δ::URA3</i>
AWY014WKC	AWY14W <i>trm9Δ</i> KanMX + TRM9 complement	<i>MATa UPRE-P_{CYC1(-178)}-LEU2::HIS3 UPRE-P_{CYC1(-178)}-lacZ::TRP1 trm9Δ::kamMX4 HO-hisG-URA3-hisG-TRM9+/-500bp-HO</i>
AWY014WUC	AWY14W <i>trm9Δ</i> KanMX + TRM9 complement	<i>MATa UPRE-P_{CYC1(-178)}-LEU2::HIS3 UPRE-P_{CYC1(-178)}-lacZ::TRP1 trm9Δ::kamMX4 HO-HIS3-TRM9+/-500bp-HO</i>
AWY19		<i>MATa UPRE-P_{CYC1(-178)}-LEU2::HIS3 UPRE-P_{CYC1(-178)}-lacZ::TRP1 ire1Δ</i>
AWY19014WK	AWY19 <i>trm9Δ</i> KanMX	<i>MATa UPRE-P_{CYC1(-178)}-LEU2::HIS3 UPRE-P_{CYC1(-178)}-lacZ::TRP1 ire1Δ trm9Δ::kamMX4</i>
CEN.PK2-1C	Wild-type	<i>MATa; ura3-52; trp1-289; leu2-3,112; his3 Δ1; MAL2-8^C; SUC2</i>
CEN.PK2-1C	CEN.PK2-1C <i>trm9Δ</i> <i>trm9Δ</i>	<i>MATa; ura3-52; trp1-289; leu2-3,112; his3 Δ1; MAL2-8^C; SUC2, trm9Δ::TRP1</i>

