

Correction: Telomere Length as a Quantitative Trait: Genome-Wide Survey and Genetic Mapping of Telomere Length-Control Genes in Yeast

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Table 1 was incomplete. The full table is printed below.

Table 1. Genes Whose Deletion Affects Telomere Length and Their Interaction with Telomerase Pathway

Category	Gene	L/S	Score	Function	Synthetic Phenotypes with <i>tlc1Δ</i>		
					Doublings	Telomere	
Telomerase and telomere cap complex	<i>EST1</i>	S	1	Telomerase component			
	<i>EST2</i>	S	1	Telomerase component			
	<i>EST3</i>	S	1	Telomerase component			
	<i>YKU70</i>	S	1	Telomere binding protein	< 20	< <i>tlc1Δ</i>	
	<i>YKU80</i>	S	1	Telomere binding protein	< 20	< <i>tlc1Δ</i>	
	<i>EBS1</i>	S	3	<i>EST1</i> homologue			
	<i>SIR4</i>	S	3	Telomere binding protein			
	<i>RIF1</i>	L	1	Telomere binding protein			
	<i>RIF2</i>	L	1	Telomere binding protein			
	DNA metabolism	<i>RAD50</i>	S	1	DNA repair (<i>Rad50, Mre11, Xrs2</i> complex)		< <i>tlc1Δ</i>
<i>XRS2</i>		S	1	DNA repair (<i>Rad50, Mre11, Xrs2</i> complex)		< <i>tlc1Δ</i>	
<i>TEL1</i>		S	1	<i>PIK</i> homologue		< <i>tlc1Δ</i>	
<i>MRC1</i>		S	3	DNA damage response			
<i>DUN1</i>		S	3	DNA damage response		< <i>tlc1Δ</i>	
<i>DCC1</i>		S	3	Sister chromatid cohesion	< 20	< <i>tlc1Δ</i>	
<i>CTF8</i>		S	3	Sister chromatid cohesion	< 20	< <i>tlc1Δ</i>	
<i>DOA4</i>		S	2	Ubiquitin-specific protease	< 20	< <i>tlc1Δ</i>	
<i>PIF1</i>		L	1	DNA helicase			
<i>RAD27</i>		L	1	Flap-endonuclease	< 40		
<i>APN1</i>		L	2	DNA repair, apurinic endonuclease			
<i>ELG1</i>		L	2	RFC complex	< 40		
<i>POL32</i>		L	3	Polymerase delta subunit			
<i>RAD5</i>		L	3	DNA repair, DNA helicase			
<i>SLX8</i>		L	3	Synthetic lethal with Sgs1	< 20		
RNA metabolism		<i>NAM7</i>	S	1	Nonsense-mediated decay		< <i>tlc1Δ</i>
		<i>UPF3</i>	S	2	Nonsense-mediated decay		< <i>tlc1Δ</i>
	<i>NMD2</i>	S	2	Nonsense-mediated decay		< <i>tlc1Δ</i>	
	<i>KEM1</i>	S	2	RNA degradation	< 40	< <i>tlc1Δ</i>	
	<i>SOL2</i>	L	2	tRNA synthesis and function			
	<i>STO1</i>	L	2	mRNA cap binding protein			
	<i>CBC2</i>	L	2	Nuclear cap binding complex subunit			
	<i>LEA1</i>	L	2	RNA splicing			
	<i>LSM7</i>	L	3	mRNA decay complex with Kem1p			
	<i>NRP1^a</i>	L	3	RNA binding protein			
	<i>REF2</i>	L	3	RNA processing			
	<i>TIF1</i>	L	3	RNA helicase			
	Nucleotide metabolism	<i>PRS3</i>	S	1	Phosphoribosylpyrophosphate synthase		< <i>tlc1Δ</i>
<i>RNR1</i>		S	1	Ribonucleotide reductase large subunit	< 20	< <i>tlc1Δ</i>	
<i>MET7</i>		S	2	Folylpolyglutamate synthase	< 20	< <i>tlc1Δ</i>	
<i>PRS5</i>		S	3	Phosphoribosylpyrophosphate synthase		< <i>tlc1Δ</i>	
<i>YBR284W</i>		L	2	Similar to Amd1 adenosine deaminase			
Transcription		<i>AHC2</i>	L	2	ADA acetyltransferase component		
	<i>SIG1</i>	S	2	CCR4-NOT transcription complex			
	<i>DIG1</i>	L	4	MAP kinase transcriptional regulator	< 40		
	<i>PGD1</i>	S	3	Mediator complex component			
	<i>SRB2</i>	S	3	Mediator complex component	< 40	< <i>tlc1Δ</i>	
	<i>SRB5</i>	S	3	Mediator complex component	< 40	< <i>tlc1Δ</i>	
	<i>GAL11</i>	S	2	Mediator complex component			
	<i>MED1</i>	L	3	Mediator complex component			

Table 1. Continued.

Category	Gene	L/S	Score	Function	Synthetic Phenotypes with <i>tlc1Δ</i>	
					Doublings	Telomere
	SRB10	L	2	Mediator complex component		
	SRB9	L	2	Mediator complex component		
	SRB8	L	1	Mediator complex component		
	<i>CDC73</i>	S	2	PAF1 complex		< <i>tlc1Δ</i>
	LEO1	S	3	PAF1 complex		
	PAF1	S	2	PAF1 complex		
	<i>RTF1</i>	S	3	PAF1 complex		
	<i>HMO1</i>	L	2	HMG-box protein		
	<i>MOT3</i>	S	3	POLII transcription		
	HF11	S	3	POLII transcription		
	<i>RPB4</i>	S	3	POLII transcription		
	<i>SPT21</i>	S	3	Regulator of histone gene transcription		
	SSN6	S	3	Repressor in complex TUP1		< <i>tlc1Δ</i>
	<i>HIT1</i>	L	3	RSC complex component		
	<i>HTL1</i>	L	2	RSC complex interacting protein		
	<i>RFM1</i>	S	2	SUM1/RFM1 repressor complex		
	<i>SUM1</i>	S	2	SUM1/RFM1 repressor complex		
	RAD6	S	2	Ubiquitin ligase (E2) for histone H2B		
	<i>BRE1</i>	S	3	Ubiquitin ligase (E3) required for <i>Rad6</i> function		
Protein modifications	ARD1	L	1	N-terminal acetyltransferase complex		
	<i>MAK31</i>	L	2	N-terminal acetyltransferase complex		
	<i>MAK10</i>	L	2	N-terminal acetyltransferase complex		
	<i>MAK3</i>	L	2	N-terminal acetyltransferase complex		
	NAT3	L	2	N-terminal acetyltransferase complex		
	PF1	L	3	Protein chaperone		
Vesicular transport	ERG2	S	3	Ergosterol biosynthesis		
	ARF1	S	3	GTP-binding protein		
	SSH1	L	2	Protein translocation into ER		
	<i>VPS15</i>	S	2	Vesicular transport	< 20	< <i>tlc1Δ</i>
	VPS54	S	3	Vesicular transport		< <i>tlc1Δ</i>
	SWA2	S	3	Vesicular transport		
	SEM1	S	3	Vesicular transport		
	<i>VPS34</i>	S	2	Vesicular transport		< <i>tlc1Δ</i>
	YPT7	S	3	Vesicular transport		
	SLA2	S	3	Vesicular transport		
	SNC2	S	3	Vesicular transport		
	<i>VPS22</i>	S	3	Vesicular transport		< <i>tlc1Δ</i>
	<i>VPS28</i>	S	3	Vesicular transport	< 40	
	APG17	L	2	Vesicular transport		
	<i>VPS23</i>	S	3	Vesicular transport	< 40	< <i>tlc1Δ</i>
Ribosome	RPL34B	S	2	Ribosomal protein L34B		
	<i>RPL13B</i>	S	3	Ribosomal protein L13		
	HCR1	S	3	Pre-20S rRNA processing		< <i>tlc1Δ</i>
	<i>NSR1^a</i>	L	2	Ribosome biogenesis		< <i>tlc1Δ</i>
	RPS4A	L	2	Ribosomal protein S4A		
	RPS30B	L	3	Ribosomal protein S30B		
	RPS28B	L	3	Ribosomal protein S28B		
	RPS27B	L	3	Ribosomal protein S27B		
	RPS23A	L	3	Ribosomal protein S23A		
	RPS23B	L	2	Ribosomal protein S23		
	RPS22A	L	3	Ribosomal protein S22A		
	RPS21A	L	3	Ribosomal protein S21A		
	RPS19A	L	3	Ribosomal protein S19A		
	RPS18A	L	3	Ribosomal protein S18A		
	RPS17B	L	3	Ribosomal protein S17B		
	<i>RPS16B</i>	L	3	Ribosomal protein S16B		
	<i>RPS16A</i>	L	3	Ribosomal protein S16A		
	RPS11B	L	3	Ribosomal protein S11B		
	RSA1	L	1	Ribosomal large subunit assembly		
	<i>RRP8</i>	L	2	Pre-rRNA processing, methyltransferase		
	BUD21	L	3	Pre-20S rRNA processing		
	RPA14	L	3	POL1 transcription		
Mitochondria	<i>MRPL44</i>	S	3	Mitochondrial ribosomal protein		
	GLO4	L	3	Mitochondrial glyoxylase II	< 40	
	MDM10	L	3	Mitochondrial membrane protein		

Table 1. Continued.

Category	Gene	L/S	Score	Function	Synthetic Phenotypes with <i>tlc1Δ</i>	
					Doublings	Telomere
	IMG2	L	2	Mitochondrial ribosomal protein	< 20	
	MRM2	L	3	Mitochondrial rRNA methyl transferase		
Mitosis	<i>KRE28</i>	S	3	Spindle pole protein		
	SLI15	L	3	Mitotic spindle protein S.L. with <i>ipl1</i>		
Cell wall	<i>LDB7</i>	L	2	Maturation of N-linked oligosaccharides		
	CHO2	L	3	Phospholipid biosynthesis		
	ZEO1	L	3	Plasma membrane protein		
	ATC1	L	3	Bipolar budding		
	YHL012W	L	3	UTP-glucose-1-phosphate uridylyltransferase		
Killer toxin-related	FYV4	S	3	K1 killer toxin sensitive		
	FYV13	L	3	K1 killer toxin sensitive		
	FYV6	L	3	K1 killer toxin sensitive		
Growth control	WHI2	S	3	Whi mutant (small cell size)		
	SIW14	S	3	Phosphatase, synthetic lethal with <i>Whi2</i>		
Nucleocytoplasmic transport	<i>GTR2</i>	S	3	Small GTPase		
	<i>NPL6</i>	L	3	Import of proteins into nucleus		
Phosphatase	SHP1	S	3	Carbohydrate metabolism	< 40	< <i>tlc1Δ</i>
Phosphate metabolism	PHO88	S	3	Phosphate transport		
Amino-acid biosynthesis	PRO1	S	3	Proline biosynthesis		
Unknown	YJL184W	S	2	unknown		
	<i>YDL118W</i>	S	3	unknown		< <i>tlc1Δ</i>
	YDL119C	S	3	unknown	< 40	
	YGL024W	S	3	unknown		
	YBL046W	S	3	unknown		
	YIL077C	S	3	unknown		
	YCR026C	L	2	unknown		
	YBR300C	L	2	unknown		
	YDR442W	L	3	unknown		
	YPL017C	L	3	unknown	< 40	
	YBR134W	L	3	unknown		
	YBR292C	L	3	unknown		
	YLR322W	L	3	unknown		
	YOR066W	L	3	unknown		
	YJL182C	L	3	unknown		
	YJR079W	L	3	unknown		
	YOR235W	L	3	unknown		
	YPL068C	L	3	unknown		
	YPL068C	L	3	unknown		

Genes in bold were not previously implicated in telomere length regulation.

^aGenes previously reported not to have telomere length alteration [19].

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