

Supplementary Table S1 Telomere length correction factors (telomere/rDNA) for dot blot-based ChIP

Tagged protein	Genetic background	Correction factor ^a	Tagged protein	Genetic background	Correction factor ^a
Trt1-myc	wt	1.000±0.011 (n=23)	Rad11-FLAG	wt	1.000±0.026 (n=17)
	<i>poz1Δ</i>	7.523±0.235 (n=22)		<i>poz1Δ</i>	2.950±0.063 (n=17)
	<i>rap1Δ</i>	7.576±0.133 (n=23)		<i>rap1Δ</i>	6.281±0.152 (n=17)
	<i>taz1Δ</i>	6.507±0.085 (n=22)		<i>taz1Δ</i>	4.407±0.093 (n=15)
	<i>trt1-D743A</i>	1.277±0.158 (n=9)			
	<i>trt1-D743A rap1Δ</i>	2.409±0.190 (n=7)			
Pol1-FLAG	wt	1.000±0.013 (n=18)	Tpz1-myc	wt	1.000±0.014 (n=18)
	<i>poz1Δ</i>	2.474±0.044 (n=18)		<i>poz1Δ</i>	5.671±0.107 (n=18)
	<i>rap1Δ</i>	1.802±0.032 (n=18)		<i>rap1Δ</i>	6.229±0.154 (n=18)
	<i>taz1Δ</i>	1.001±0.027 (n=18)		<i>taz1Δ</i>	5.420±0.194 (n=18)
	<i>trt1Δ</i>	0.669±0.035 (n=9)			
	<i>trt1-D743A rap1Δ trt1Δ</i>	0.146±0.009 (n=9)			
Pol2-FLAG	wt	1.000±0.020 (n=18)	Ccq1-myc	wt	1.000±0.020 (n=36)
	<i>poz1Δ</i>	5.389±0.146 (n=18)		<i>poz1Δ</i>	3.544±0.140 (n=33)
	<i>rap1Δ</i>	6.362±0.151 (n=15)		<i>rap1Δ</i>	5.061±0.216 (n=35)
	<i>taz1Δ</i>	5.008±0.087 (n=15)		<i>taz1Δ</i>	4.975±0.258 (n=35)
	<i>trt1Δ</i>	0.632±0.015 (n=9)			
	<i>trt1-D743A rap1Δ trt1Δ</i>	0.832±0.016 (n=9)			
myc-Rad3	wt	1.000±0.019 (n=9)	Poz1-myc	wt	1.000±0.025 (n=26)
	<i>poz1Δ</i>	3.730±0.097 (n=9)		<i>rap1Δ</i>	4.773±0.311 (n=24)
	<i>rap1Δ</i>	4.790±0.114 (n=9)		<i>taz1Δ</i>	3.892±0.282 (n=27)
	<i>taz1Δ</i>	2.750±0.101 (n=9)			
myc-Rad26	wt	1.000±0.017 (n=18)	Stn1-myc	wt	1.000±0.021 (n=25)
	<i>poz1Δ</i>	6.842±0.132 (n=18)		<i>poz1Δ</i>	3.624±0.237 (n=27)
	<i>rap1Δ</i>	9.516±0.165 (n=18)		<i>rap1Δ</i>	5.416±0.364 (n=27)
	<i>taz1Δ</i>	6.105±0.124 (n=16)		<i>taz1Δ</i>	4.497±0.260 (n=26)
				<i>rap1Δ trt1Δ</i>	0.666±0.013 (n=9)

^aMean ± standard error of the mean. Values are normalized to wt cells with indicated tagged proteins. Number of samples used to determine correction factors are also indicated as (n=#).