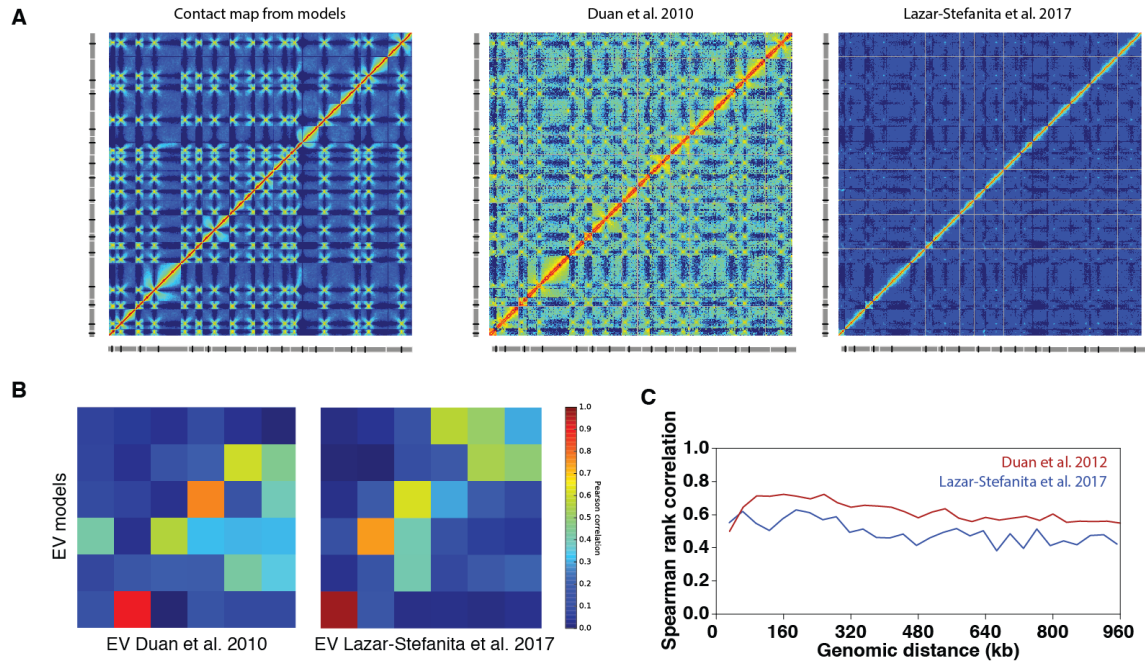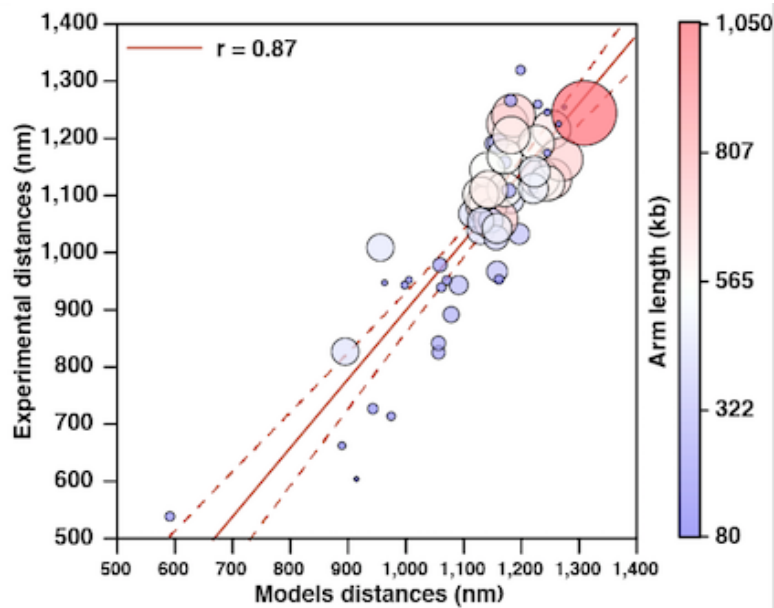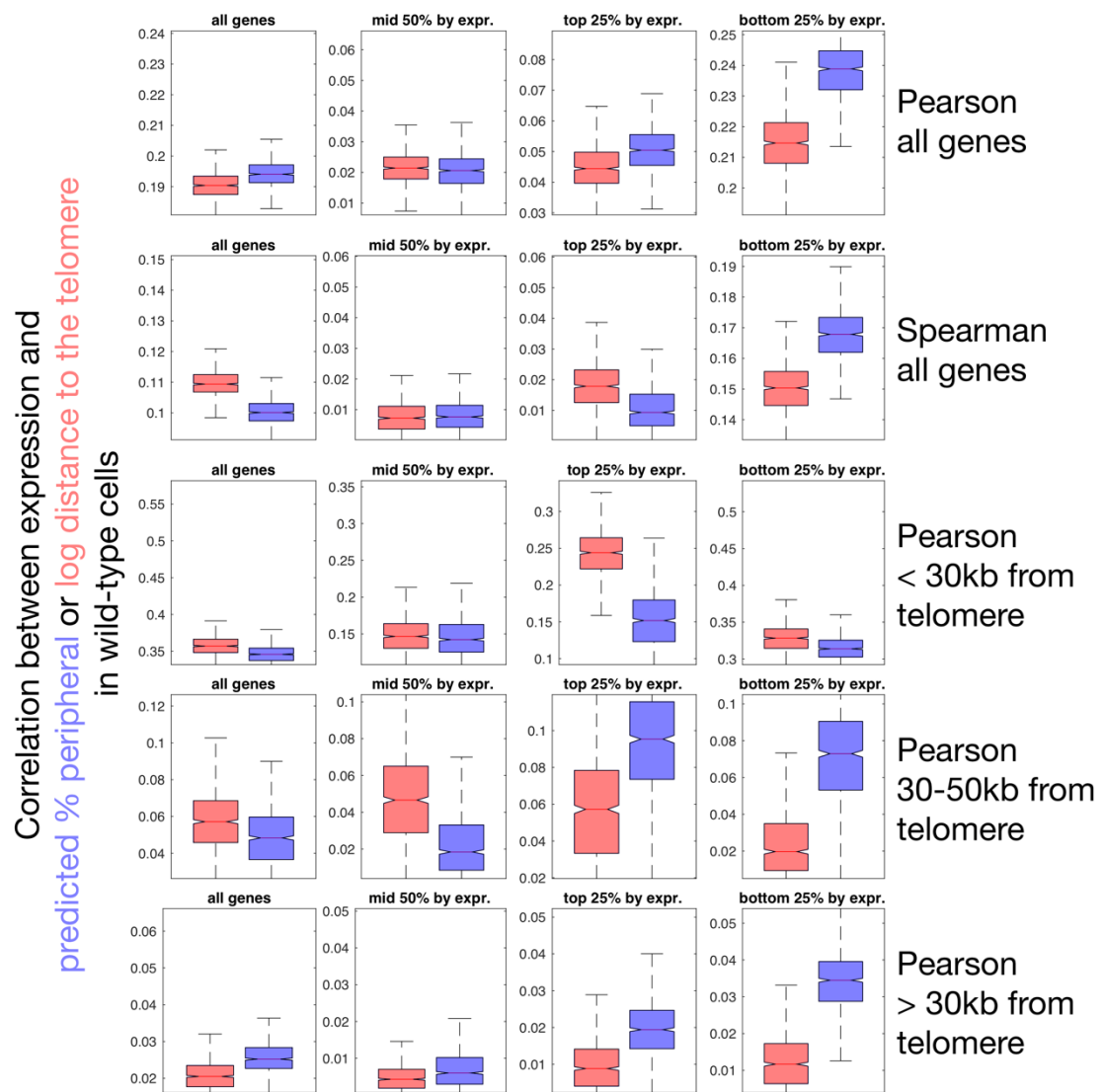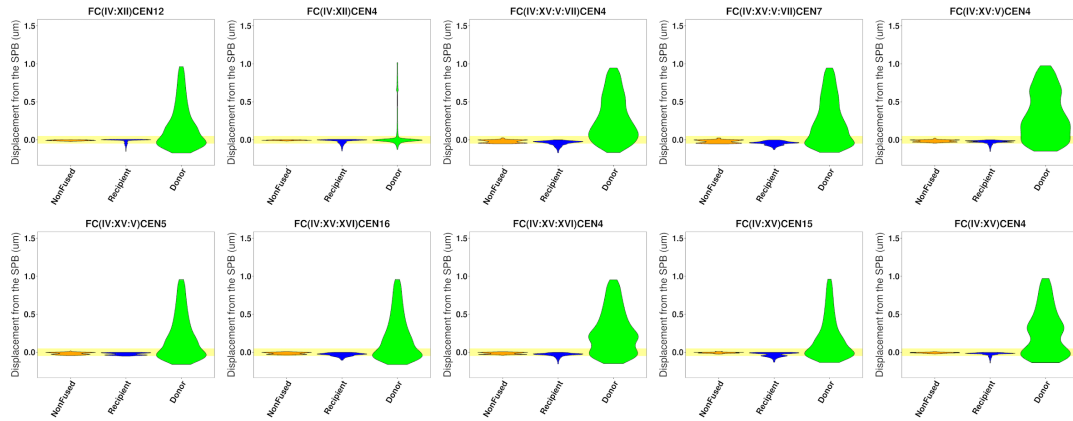# SUPPLEMENTARY FIGURES

Supplementary Figure 1. Comparison of the experimental and predicted contact maps. (A) DNA contact maps obtained from computational models and from experimental approaches. **(B)** Spectral decompositions of the maps show significant internal correlations up the first 6th eigenvalues (Imakaev *et al.* 2012). **(C)** Correlations between elements grouped by genomic distance are significant up to the typical length of a budding yeast chromosome arm.

Supplementary Figure 2. Correlation between measured median telomere-telomere distances in (Therizols *et al.* 2010). *vs.* the model prediction in the wild-type strain. The scatter plot of the 60 median telomere-telomere distances measured in (Therizols *et al.* 2010) considering Tel10R, Tel6R and Tel4R *vs.* most of the 32 telomeres is shown together with the correspondent linear regression analysis. The points are colored (from blue to red) and sized proportionally to the length of the corresponding chromosome-arm. The Spearman rank correlation between experimental data and model predictions indicates a significant agreement.
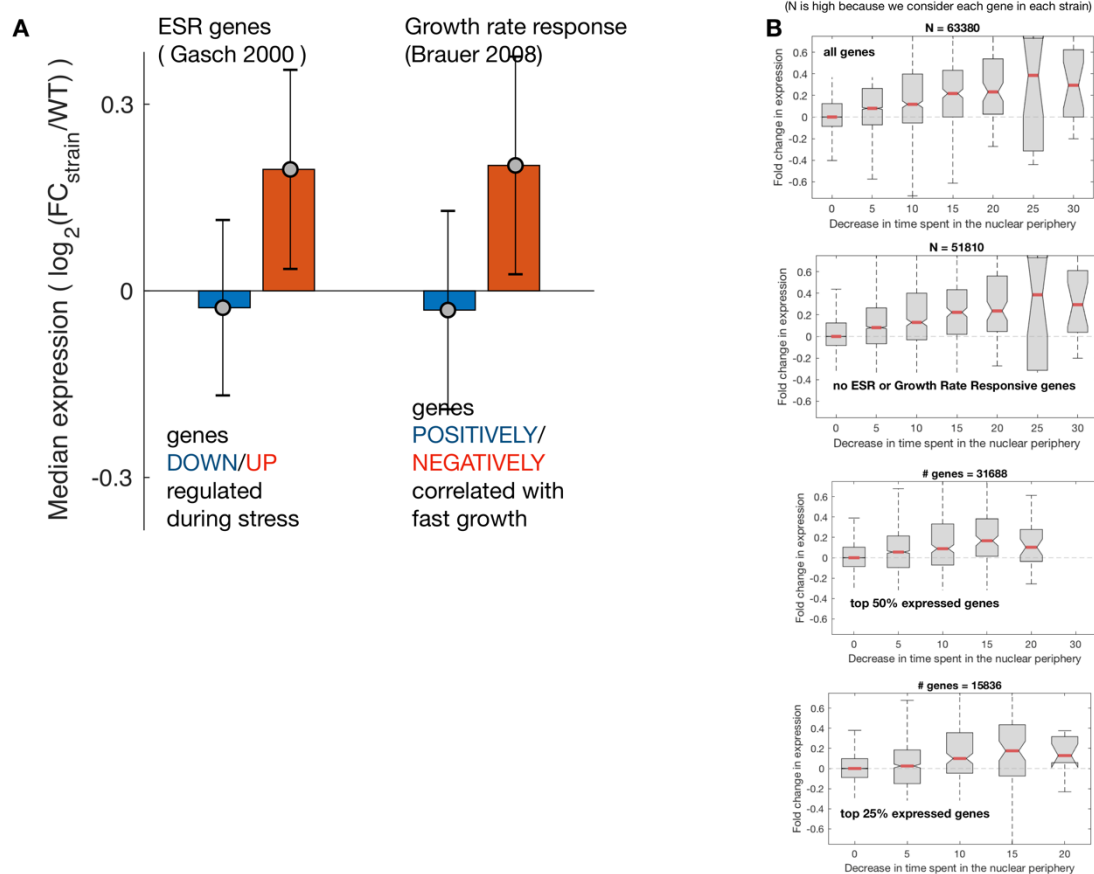
Supplementary Figure 3. Correlation between expression and either predicted % peripheral and distance to the telomere in wild-type cells. Identical to Figure 2D, but for different subsets of genes, and different methods of calculating correlation. The results are robust to how the data are analyzed.

Supplementary Figure 4. Displacement of model particles from the SPB in FC strains relative to the wild type. This quantity is computed per each particle as the average distance to the SPB in FC strains minus the same quantity in wildtype. Hence, positive difference values indicate a (typical) displacement of the particle away from the SPB, and vice versa, negative values indicate a (typical) displacement towards the SPB in FC strains with respect to the wild type strain. The displacements are grouped in three categories depending on the chromosomes hosting the particle: non-fused, recipient, or donor. Data for each FC strain are shown in 10 separated panels. Three conclusions can be made from these graphs: (i) In non-fused chromosomes, the particles are minimally displaced (<50 nm) with respect to the SPB. The distributions are always contained in the reference yellow area marking in each plot the values between -50 and 50 nm. (ii) In recipient chromosomes, some of the particles are slightly (<100 nm) displaced towards the SBP. The distributions are slightly skewed towards negative values, meaning that the average distance to the SPB is shorter in FC strains. (iii) In donor chromosomes, some particles are displaced away from SPB by larger amounts (>500 nm). This is conveyed by the fact that the distributions have tails in large positive values.
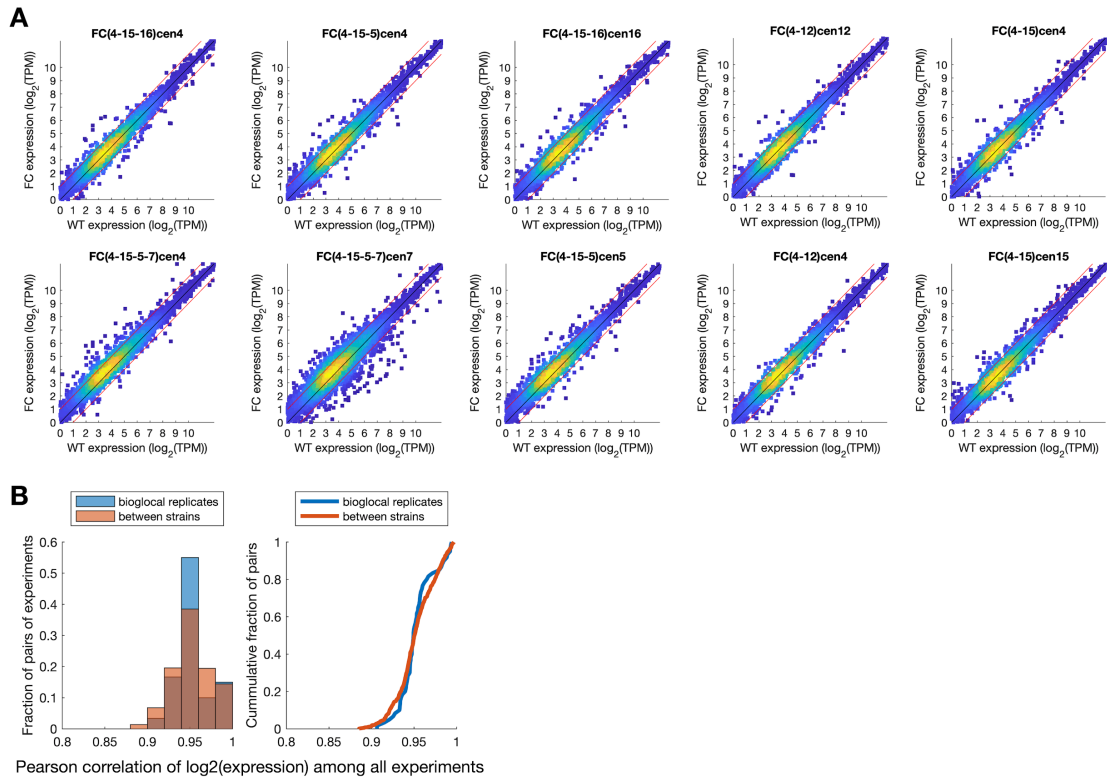
Supplementary Figure 5. *FC* **strains do not exhibit large-scale changes in gene expression across the entire transcriptome.** (**A**) Expression levels in each *FC* strain are compared to expression in the WT-strain. Red lines show a fold change of 2. In this figure, and in all expression analysis we have removed genes that are deleted in the FC strain. (**B**) The pairwise expression correlations between all pairs of biological replicates (blue) or between all strains (red) are identical. Spearman correlation shows the same results. FC strains do not exhibit large transcriptome-wide changes in expression.

Supplementary Figure 6. The relationship between predicted time in the nuclear periphery and change in expression remains when genes involved in the Environmental Stress Response (Gasch *et al.* 2000) **and Growth Rate Response** (Brauer *et al.* 2008) **are removed. (A)** FC strains exhibit a mild stress response. For each FC strain the genes involved in the growth rate response (right) and the ESR response (right) are differentially expressed in the FC strains, suggesting that FC strains have a minor stress phenotype. Bars show the median, error bars the standard deviation across all FC strains. **(B)** Genes predicted to spend less time in the nuclear periphery (x-axis) exhibit higher expression, even when removing ESR and growth rate responsive genes, or focusing only on highly expressed genes.
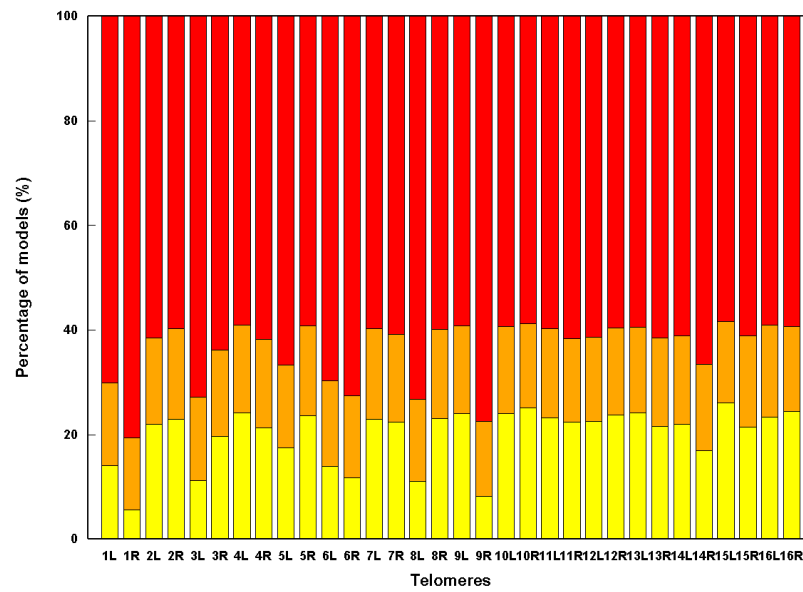
Supplementary Figure 7. Telomere occupancy in 3 pre-defined concentric shells of equal volume in the model nucleus: peripheral (red), middle (orange) and central (yellow). Most telomeres localize outside the perinuclear space in 40% of the models.

SUPPLEMENTARY TABLES

Supplementary Table 1. Predicted % peripheral is a significant feature in a linear model that predicts mRNA expression in wild-type cells from using both zscored predicted %peripheral and zscored log distance to the telomere. Shown are linear models that predict expression from both features independently (bottom) or with an interaction term (top). In the non-interaction model, predicted %peripheral is a stronger predictor of expression than log(distance to the telomere). In the interaction model, the interaction term is the strongest predictor.

Generalized linear regression model with an interaction term:
    Expression ~ 1 + Dist2Tel_log*PercentPeripheral

Estimated Coefficients:

	Estimate	SE	tStat	pValue
Dist2Tel_log	0.056238	0.0156	3.6083	0.00031
PercentPeripheral	-0.016564	0.0180	-0.9225	0.35627
Dist2Tel_log:PercentPeripheral	0.04074	0.0052	7.7097	1.4558e-14

Generalized linear regression model without an interaction term:
    Expression ~ 1 + Dist2Tel_log + PercentPeripheral

Estimated Coefficients:

	Estimate	SE	tStat	pValue
Dist2Tel_log	0.0734	0.0155	4.7359	2.2288e-06
PercentPeripheral	-0.0874	0.0155	-5.6389	1.7857e-08

Supplementary Table 2: Deleted genes in *FC* strains

Fusion	Chromosome arm	Deleted Regions		Deleted genes
		Start (bp)	Stop (bp)	
IV:XII	IVR	1,516,999	END	IRC4, YDR541C, PAU10
	XIIR	1,059,029	END	YLR460C, PAU4
IV:XV	IVR	1,516,999	END	IRC4, YDR541C, PAU10,
	XVR	1,068,611	END	PHR1, YOR385W, FRE5, FIT3, FIT2, YOR381W-A
IV:XV:V	IVR	1,516,999	END	IRC4, YDR541C, PAU10
	XVR	1,068,611	END	PHR1, YOR385W, FRE5, FIT3, FIT2, YOR381W-A
	XVL	BEGIN	5,301	YOL164W-A, YOLWtau1, YOLCdelta1, YOL166C, YOL166C, YOL16
	VR	561,108	END	PUG1, YER184C, SLO1, YERCdelta26, YER181C, FMP10, YERWdelta25, FAU1 /YER183C
IV:XV:XVI	IVR	1,516,999	END	IRC4, YDR541C, PAU10
	XVR	1,068,611	END	PHR1, YOR385W, FRE5, FIT3, FIT2, YOR381W-A
	XVL	BEGIN	5,301	YOL164W-A, YOLWtau1, YOLCdelta1, YOL166C, YOL166C, YOL16
	XVIL	BEGIN	22,026	HSP32, YPL279C, YPL277C,YPL278C, FDH2
IV:XV:V:VII	IVR	1,516,999	END	IRC4, YDR541C, PAU10
	XVR	1,068,611	END	PHR1, YOR385W, FRE5, FIT3, FIT2, YOR381W-A
	XVL	BEGIN	5,301	YOL164W-A, YOLWtau1, YOLCdelta1, YOL166C, YOL166C, YOL16
	VR	561,108	END	PUG1, YER184C, SLO1, YERCdelta26, YER181C, FMP10, YERWdelta25, FAU1 /YER183C
	VL	BEGIN	13,208	YEL077, YEL076, YEL075
	VIIL	BEGIN	2,088	none

Supplementary Table 3. Fold Change in Expression (mean, median and p value) of all genes (see Excel file).

Supplementary Table 4. Fold Change in Expression (mean, median and p value) of genes that are displaced from more than 5% relative to the nuclear periphery, according to the models (see Excel file).

Supplementary Table 5. Parameters of the polymer models.

Parameter	Value	Reference
Number of chromosomes	16	1
Chromosome persistence length	61.7 nm	2
Chromosome persistence length (last 30kb)	195.0 nm	3
Nuclear diameter	2 μm	This study
Particle DNA content	3.2 kb	3
Diameter of euchromatin segments	30 nm	3
Number of repeats of the 9.1kb rDNA region	102	1
Chains can cross each other	No	4

1. Cherry JM, et al. (1997) Genetic and physical maps of Saccharomyces cerevisiae. *Nature* 387 (6632 Suppl):67-73
2. Tjong et al 2012
3. Bystricky et al 2014
4. Rosa and Everaers 2008

Supplementary Table 6. Number of particles per chromosome chain in the polymer models.

Chromosome	# of particles
I	72
II	254
III	99
IV	479
V	180
VI	84
VII	341
VIII	176
IX	138
X	233
XI	208
XII	627
XIII	289
XIV	245
XV	341
XVI	296

Supplementary Table 7. Yeast strains.

Strain number	Strain name	
409	*WT*	*MATa trp1::TetO:TRP1 lys4::LacO:LEU2 his3::LacR-GFP:HIS3 TetR-mRFP Spc42-GFP:hph bar1Δ ura3 ade1 leu2*
681	*FC(IV-XII)CEN4*	*MATa trp1::TetO:TRP1 lys4::LacO:LEU2 his3::LacR-GFP:HIS3 TetR-mRFP Spc42-GFP:hph ChrIV-XII fusion:natNT2 CEN4 cen12::caURA3 bar1Δ ura3 ade1 leu2*
524	*FC(IV-XII)CEN12*	*MATa trp1::TetO:TRP1 lys4::LacO:LEU2 his3::LacR-GFP:HIS3 TetR-mRFP Spc42-GFP:hph ChrIV-XII fusion:natNT2 cen4::caURA3 bar1Δ ura3 ade1 leu2*
1270	*FC(IV-XV)CEN4*	*MATa trp1::TetO:TRP1 lys4::LacO:LEU2 his3::LacR-GFP:HIS3 TetR-mRFP Spc42-GFP:hph ChrIV-XV fusion:natNT2 CEN4 cen15::ble bar1Δ ura3 ade1 leu2*
1138	*FC(IV-XV)CEN15*	*MATa trp1::TetO:TRP1 lys4::LacO:LEU2 his3::LacR-GFP:HIS3 TetR-mRFP Spc42-GFP:hph ChrIV-XV fusion:natNT2 cen4::CaURA3 bar1Δ ura3 ade1 leu2*
1387	*FC(IV-XV-V)CEN4*	*MATa trp1::TetO:TRP1 lys4::LacO:LEU2 his3::LacR-GFP:HIS3 TetR-mRFP Spc42-GFP:hph ChrIV-XV fusion:natNT2 ChrXV-V fusion:CaURA3 CEN4 cen5::ade cen15::ble bar1Δ ura3 ade1 leu2*
1379	*FC(IV-XV-V)CEN5*	*MATa trp1::TetO:TRP1 lys4::LacO:LEU2 his3::LacR-GFP:HIS3 TetR-mRFP Spc42-GFP:hph ChrIV-XV fusion:natNT2 ChrXV-V fusion:CaURA3 cen4::ade cen15::ble bar1Δ ura3 ade1 leu2*
1388	*FC(IV-XV-XVI)CEN4*	*MATa trp1::TetO:TRP1 lys4::LacO:LEU2 his3::LacR-GFP:HIS3 TetR-mRFP Spc42-GFP:hph ChrIV-XV fusion:natNT2 ChrXV-XVI fusion:CaURA3 CEN4 cen15::ble cen16::ade bar1Δ ura3 ade1 leu2*
1380	*FC(IV-XV-XVI)CEN16*	*MATa trp1::TetO:TRP1 lys4::LacO:LEU2 his3::LacR-GFP:HIS3 TetR-mRFP Spc42-GFP:hph ChrIV-XV fusion:natNT2 ChrXV-XVI fusion:CaURA3 cen4::ade cen15::ble bar1Δ ura3 ade1 leu2*
1793	*FC(IV-XV-V-VII)CEN4*	*MATa trp1::TetO:TRP1 lys4::LacO:LEU2 his3::LacR-GFP:HIS3 TetR-mRFP Spc42-GFP:hph ChrIV-XV fusion:natNT2 ChrXV-V fusion:natNT2 ChrV-VII fusion:natNT2 CEN4 cen5::ade cen7::CaURA3 cen15::ble bar1Δ ura3 ade1 leu2*

1788	*FC(IV-XV-V-VII)CEN7*	*MATa trp1::TetO:TRP1 lys4::LacO:LEU2 his3::LacR-GFP:HIS3 TetR-mRFP Spc42-GFP:hph ChrIV-XV fusion:natNT2 ChrXV-V fusion:natNT2 ChrV-VII fusion:natNT2 cen4::CaURA3 cen5::ade cen15::ble bar1Δ ura3 ade1 leu2*
2391	*Nup49-mCherry*	*MATa trp1::TetO:TRP1 lys4::LacO:LEU2 his3::LacR-GFP:HIS3 TetR-mRFP Spc42-GFP:hph bar1Δ ura3 ade1 leu2 Nup49-mCherry:KanMX*
5566	*FC(IV-XII)CEN12 Nup49-mCherry*	*MATa trp1::TetO:TRP1 lys4::LacO:LEU2 his3::LacR-GFP:HIS3 TetR-mRFP Spc42-GFP:hph ChrIV-XII fusion:natNT2 cen4::CaURA3 bar1Δ ura3 ade1 leu2 Nup49-mCherry::KanMX*
5568	*FC(IV-XII)CEN4 Nup49-mCherry*	*MATa trp1::TetO:TRP1 lys4::LacO:LEU2 his3::LacR-GFP:HIS3 TetR-mRFP Spc42-GFP:hph ChrIV-XII fusion:natNT2 CEN4 cen12::CaURA3 bar1Δ ura3 ade1 leu2 Nup49-mCherry::KanMX*