This is the Supplementary Information for 'Identification of dosage-sensitive genes in *Saccharomyces cerevisiae* using the genetic tug-of-war method' by Koji Makanae, Reiko Kintaka, Takashi Makino, Hiroaki Kitano, Moriya Hisao

Table of contents

Additional files provided as separate files.

Supplementary tables below provides as one Excel file with multiple worksheets.

- **Table S1**: Original gTOW6000 data
- **Table S4**: Copy number data for frameshift analysis
- **Table S5**: yeast DSGs
- **Table S6**: DSGs in Jones clones
- **Table S8**: Primers to construct gTOW6000
- **Table S9**: Additional primers to construct gTOW6000

Supplementary Figures

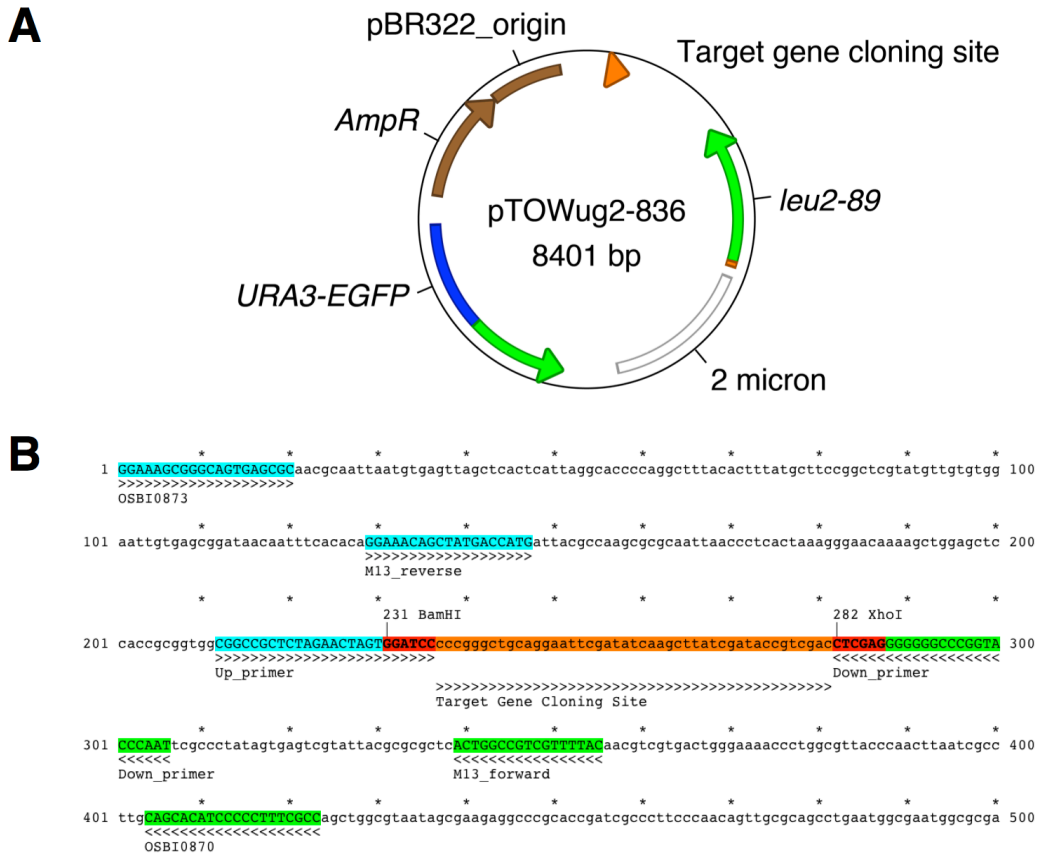


Figure S1. Structure of the pTOWug2-836 plasmid used in gTOW experiments in this study.

(*A*) A map of pTOWug2-836. (*B*) The nucleotide sequence of the target-gene cloning site of pTOWug2-836 (5′ to 3′ direction). The target gene cloning site, the *Bam*HI and *Xho*I sites used to prepare the host vector and the locations of primers used to check the inserts are indicated.

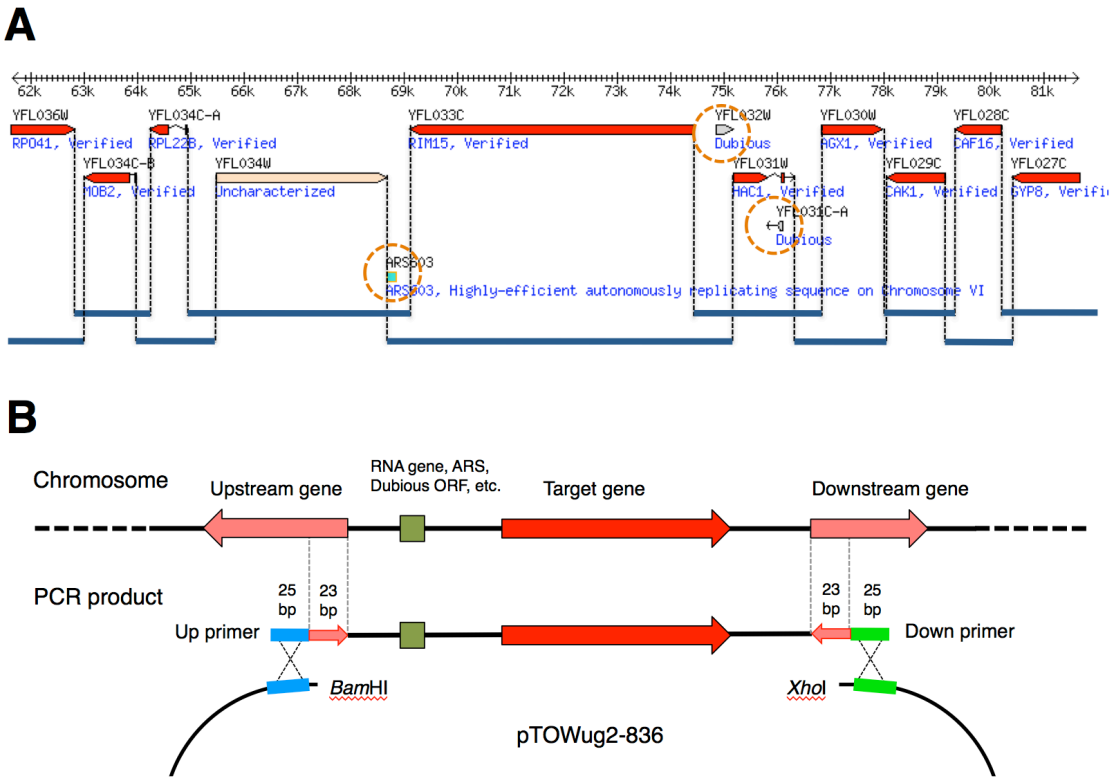


Figure S2. Cloning of the target gene into pTOWug2-836.

A part of chromosome VI is shown as an example. The details of this figure are explained in the Method section of the main text.

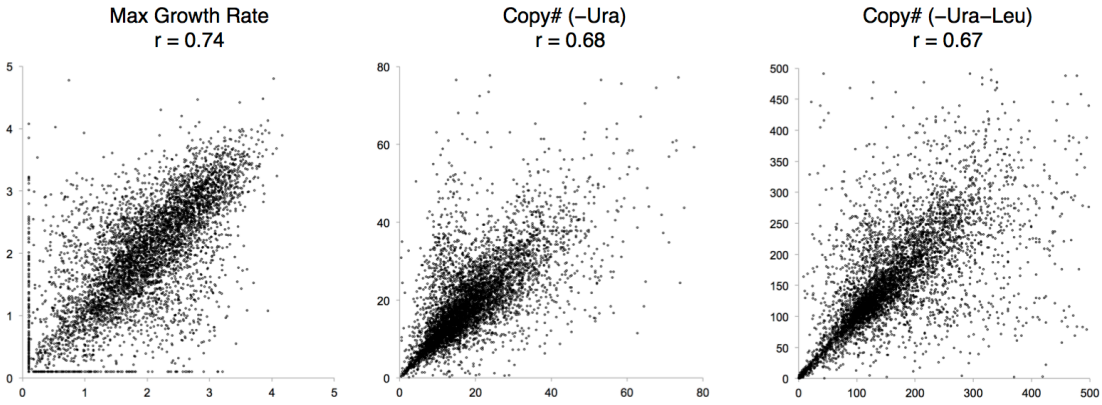


Figure S3. Reproducibility of the gTOW6000 data.

The data from two independent experiments were compared. Pearson's correlation coefficients (r) are shown.

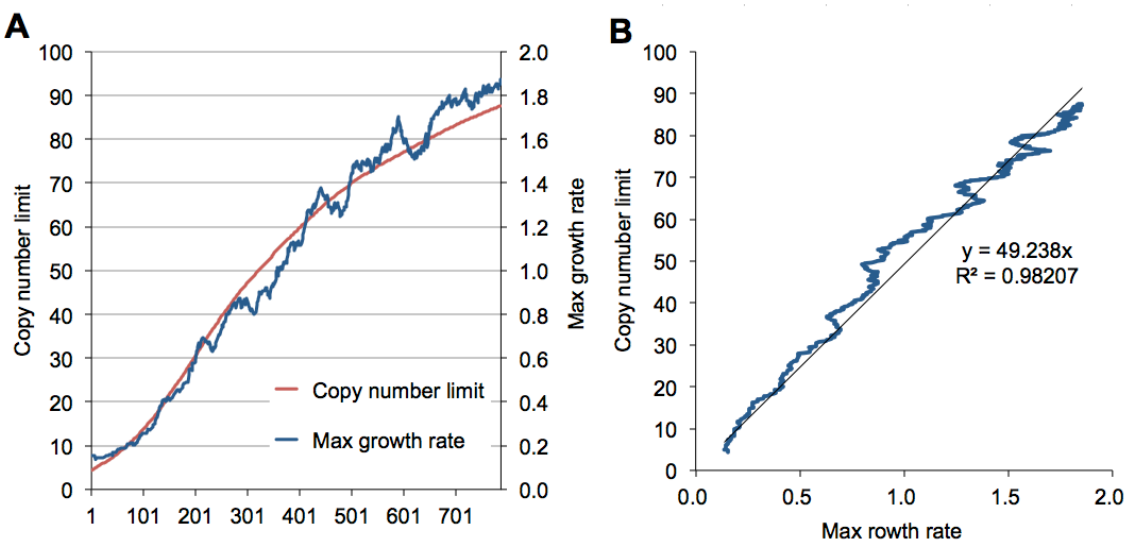


Figure S4. Relationship between CNL and max growth rate.
(*A*) Moving average of the CNL and the max growth rate of each 100 genes. X-axis shows the number of bin ordered by the CNL. (*B*) Relationship between the CNL and the max growth rate shown in ***A***. Approximated curve is shown in black line.

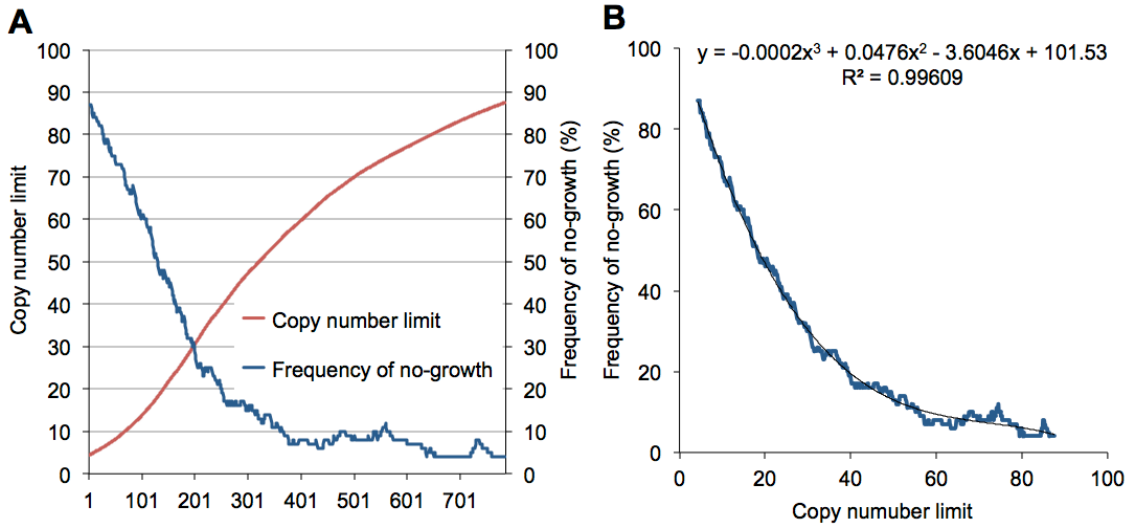


Figure S5. Relationship between CNL and frequency of no-growth.
(*A*) Moving average of the CNL and the frequency of no-growth of each 100 genes. X-axis shows the number of bin ordered by CNL. (*B*) Relationship between CNL and frequency of no-growth shown in *A*. Approximated curve is shown in black line.

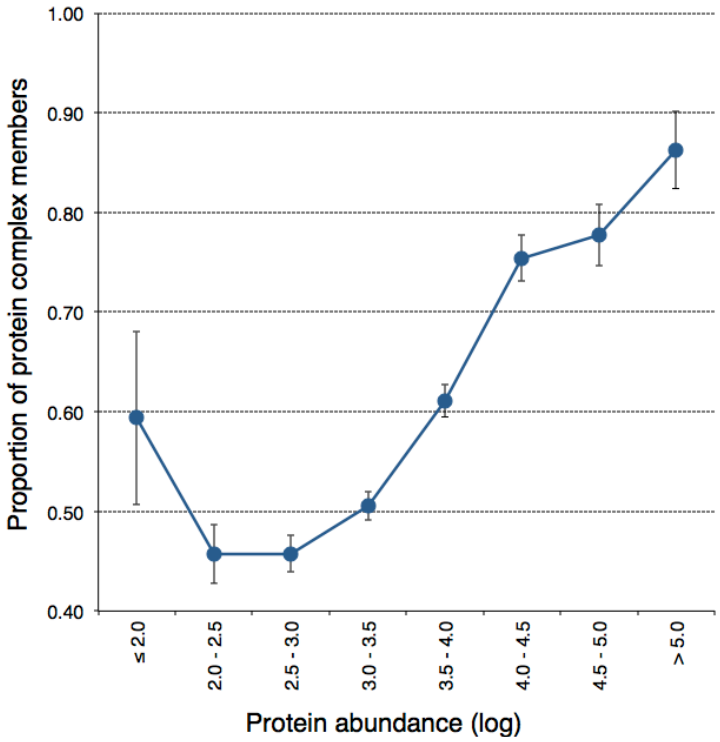


Figure S6. Protein complex components tend to be highly expressed.

The protein abundance data were obtained from Ghaemmaghami *et al.* (2003), and the data for protein complex members were obtained from MIPs (mips; ftp://ftpmips.gsf.de/yeast/catalogues/complexcat/complexcat_data_18052006). The protein abundance unit is molecules per cell. The error bars indicate the standard error of the mean (SEM).

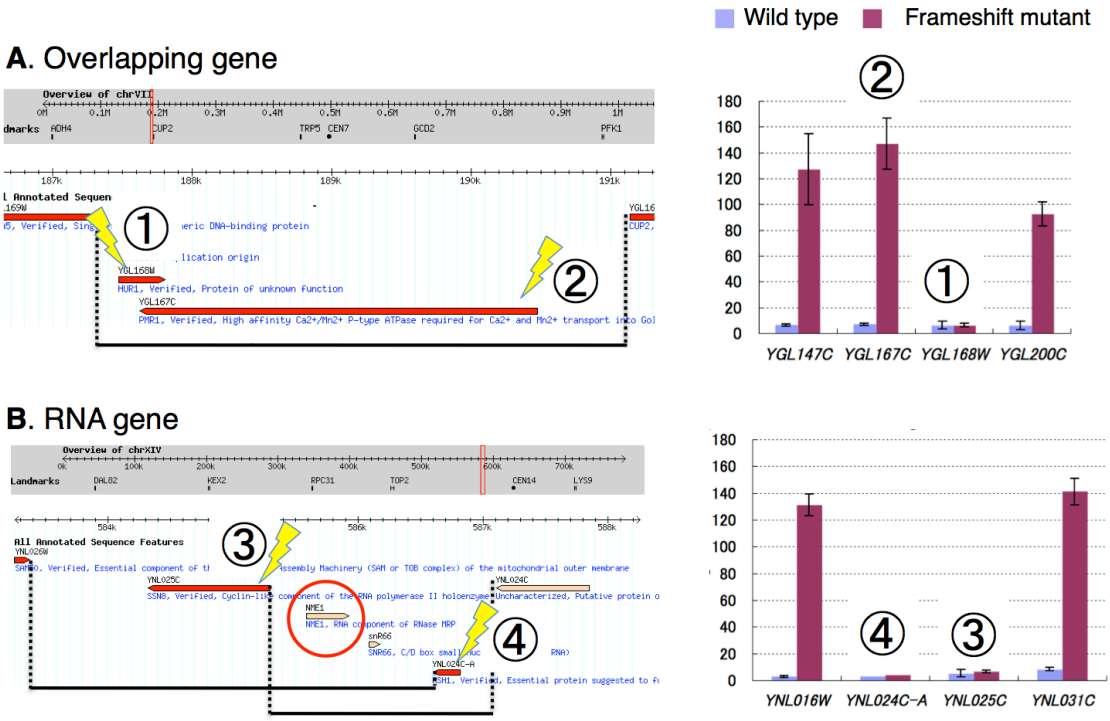


Figure S7. An example of genes that were not affected by the frameshift mutation.

The charts on the left show the chromosomal regions containing the target genes. The sites of frameshift mutations are shown in yellow arcs. A red circle indicates an RNA gene (*NME1*). The graphs on the right show the CNLs of wild-type genes and the frameshift mutants of the target genes. The average results for two independent experiments are shown with the standard deviations, excluding *YNL024C-A/KSH1*, for which only one experiment each was performed for the wild-type and frameshift mutant. The case of overlapping genes (*YGL167C*/*PMR1* and *YGL168W*/*HUR1*) (*A*), and the case of an RNA gene (*NME1*) (*B*) are shown.

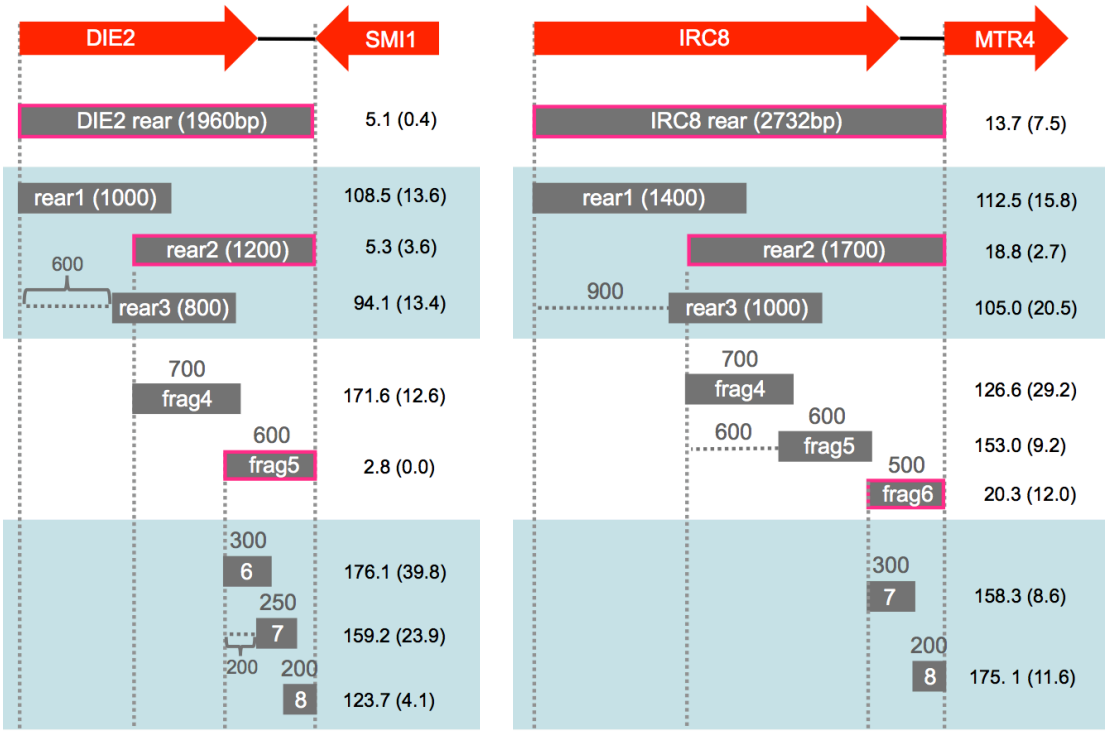


Figure S8. Unknown DNA elements are the determinants of the low CNLs within the locus of *DIE2* and *IRC8*.

The fragments that we analysed are shown in grey boxes with their names, and the size of each fragment is shown above the box. The number on the right side of the box indicates the copy number limit of the individual fragment. Fragments causing the low limit are enclosed with red boxes. Each fragment was amplified by PCR and cloned into pTOWug2-836. The average copy number and the standard deviation (within parentheses) of more than two independent experiments are shown.

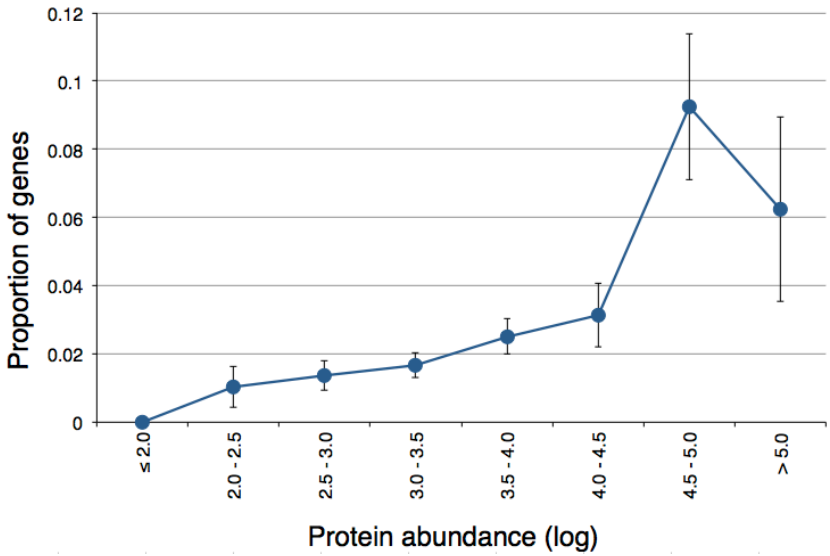


Figure S9. Yeast DSGs tend to be highly expressed.

The distribution of 115 DGSs ordered by their native protein levels. Each bin contains genes ordered by their native protein level (Ghaemmaghami *et al.*, 2003). The protein abundance unit is molecules per cell. The error bars indicate the standard error of the mean (SEM).

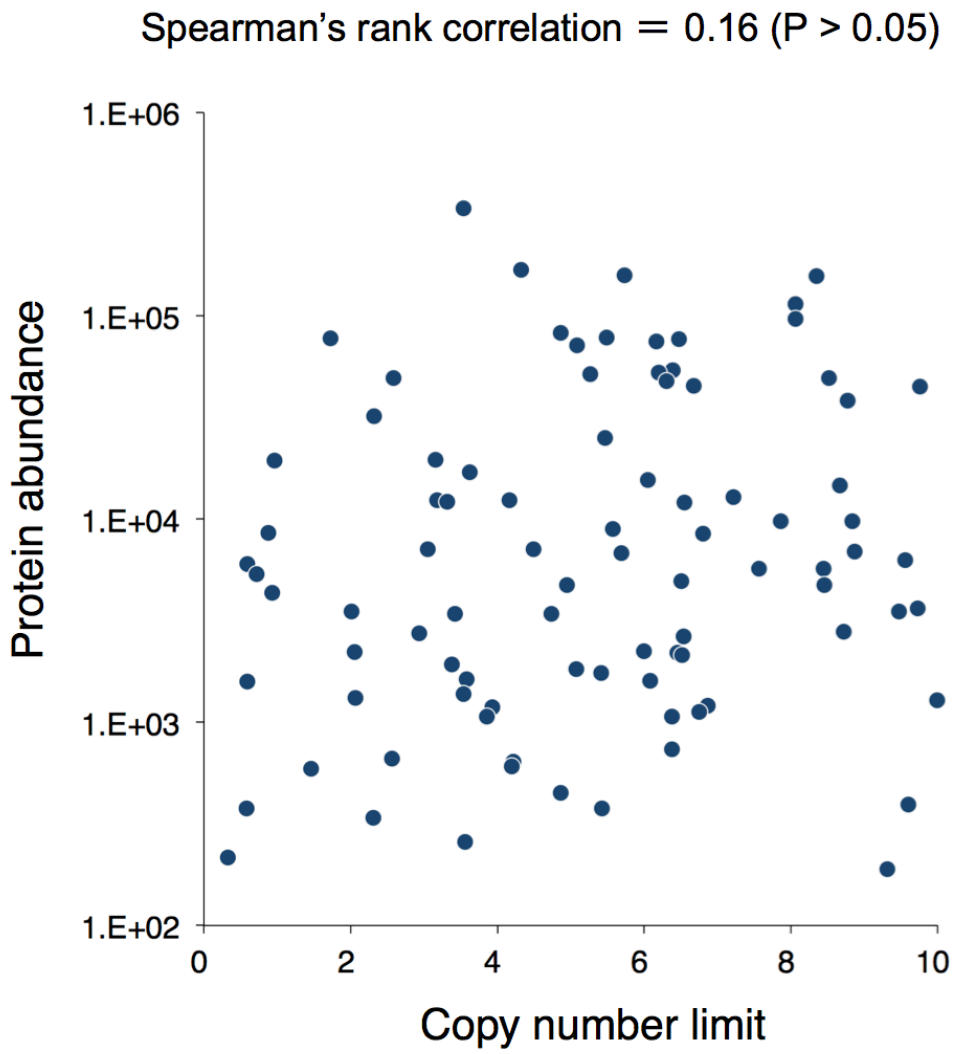


Figure S10. Correlation between the copy number limit and protein abundance. Genes with upper copy number limits ≤10. The protein abundance data were obtained from Ghaemmaghami *et al.* (2003). The protein abundance unit is molecule per cell.

Figure S11. Results of 2D-gTOW experiments (plate assay).

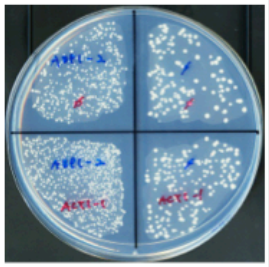
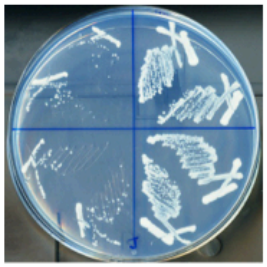
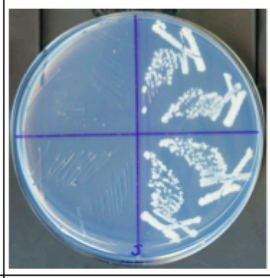
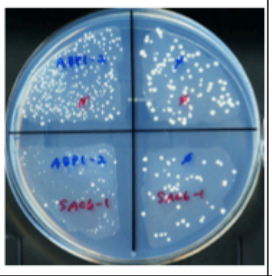
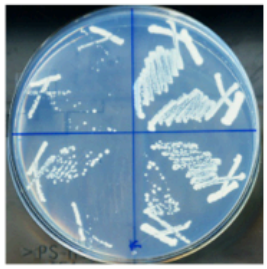
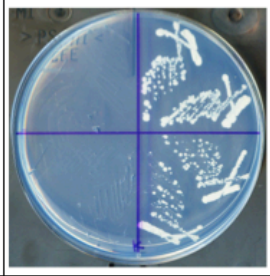
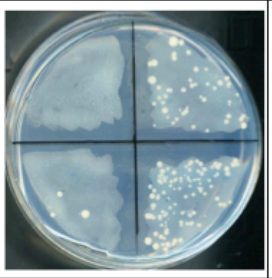
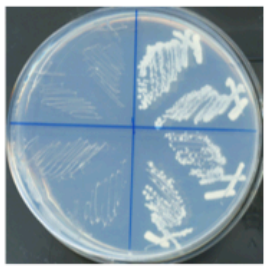
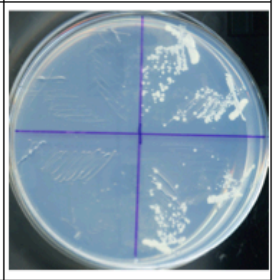
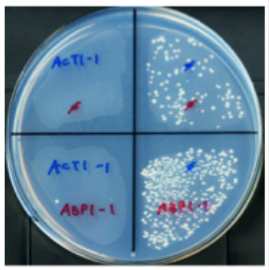
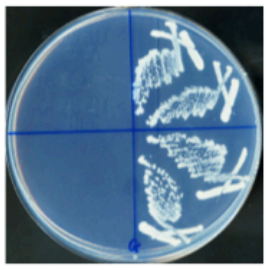
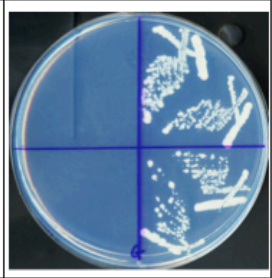
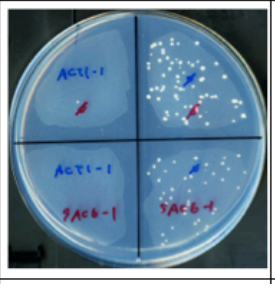
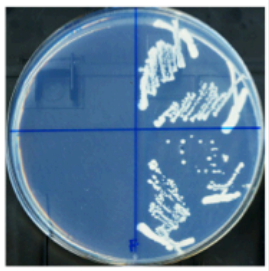
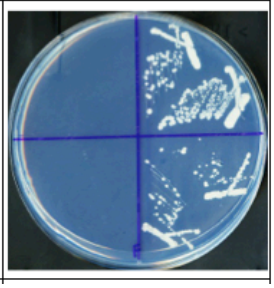
DSG (pTOW)	Partnere candidate (pRS423)	Co-transform	Streaked (−His −Ura)	Streaked (−His −Leu −Ura)
ABP1	*ACT1*			
ABP1	*SAC6*			
ACT1	*COF1*			
ACT1	*ABP1*			
ACT1	*SAC6*			

Figure S11 continued

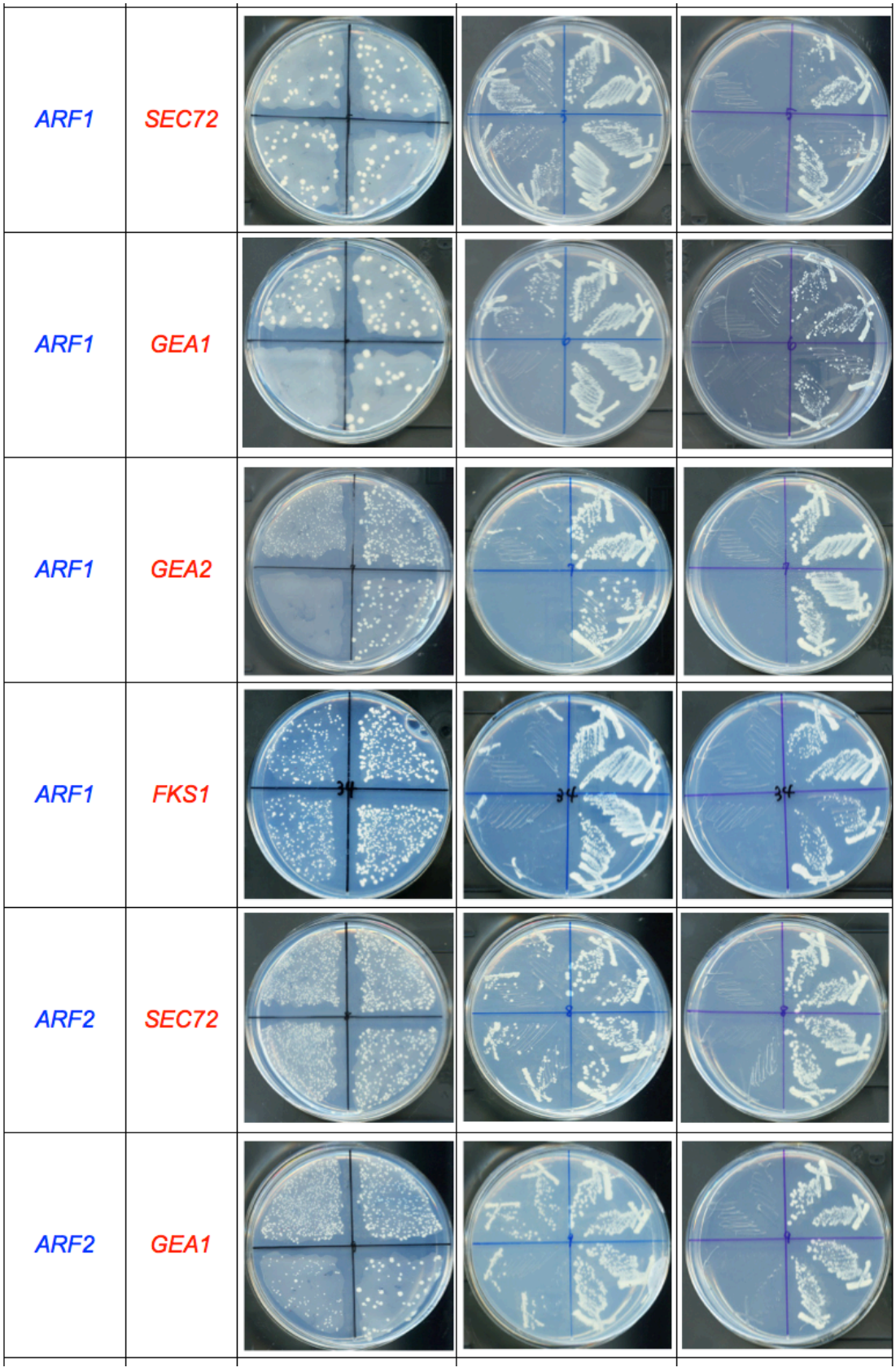


Figure S11 continued

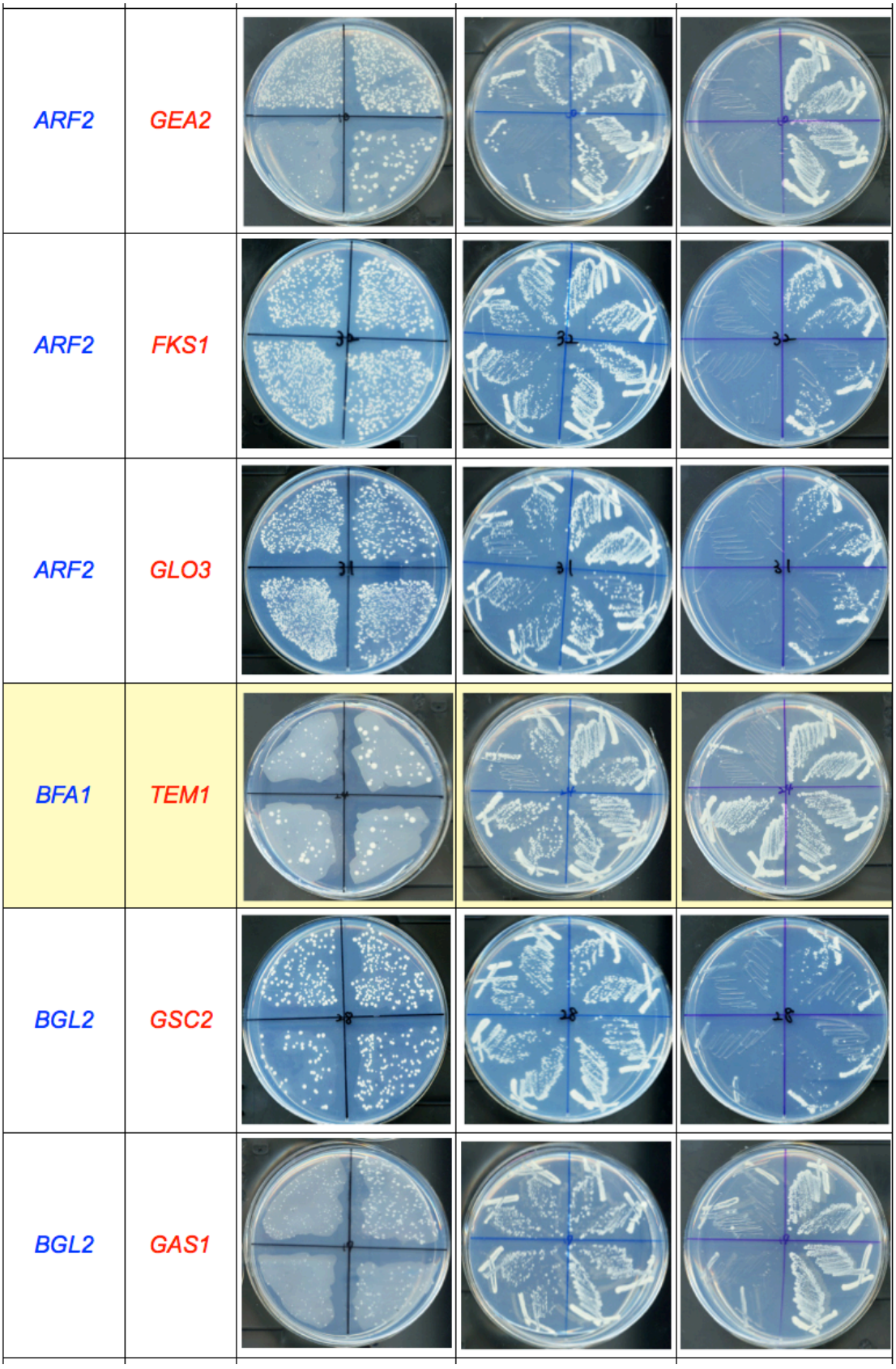


Figure S11 continued

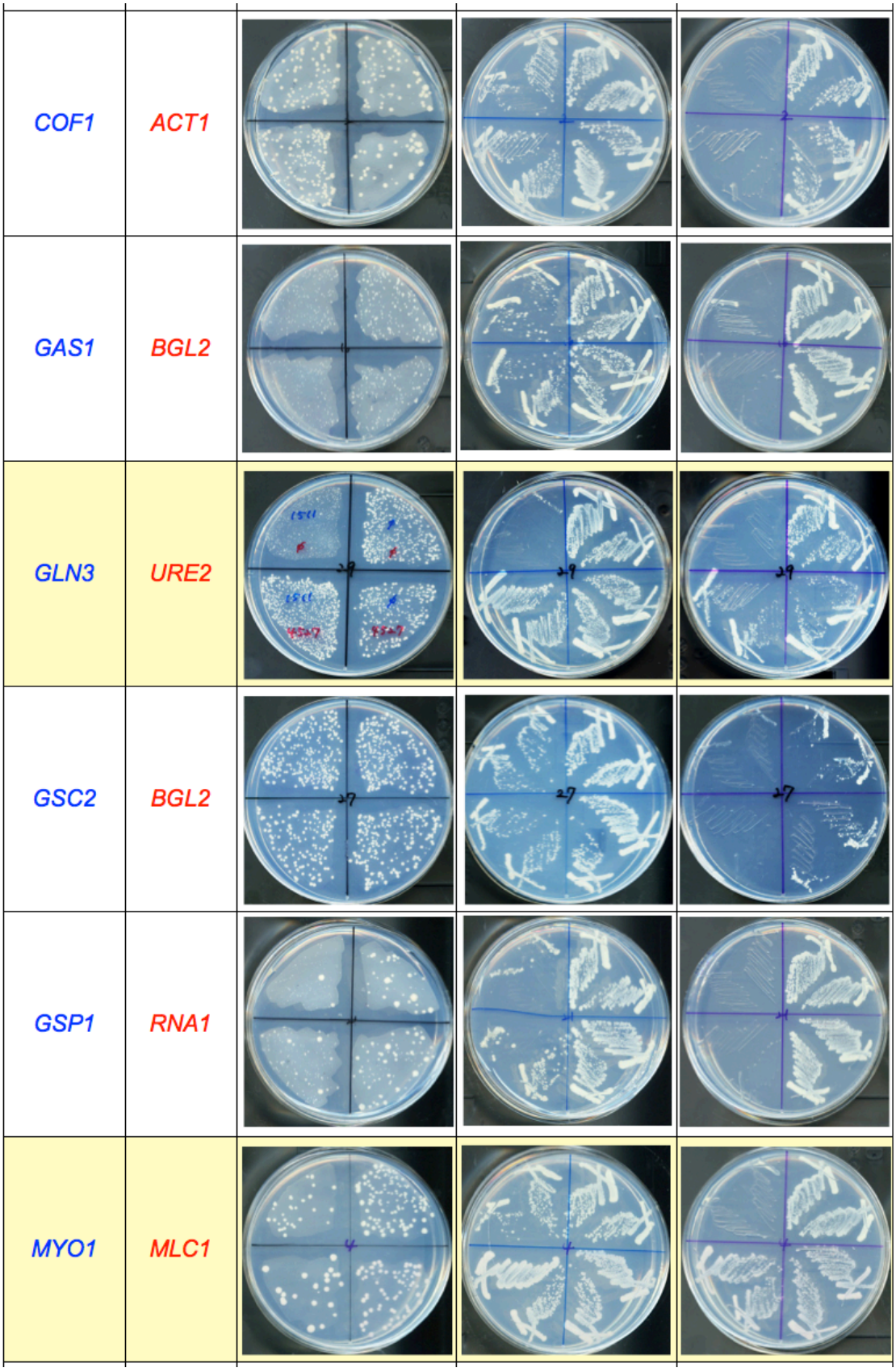


Figure S11 continued

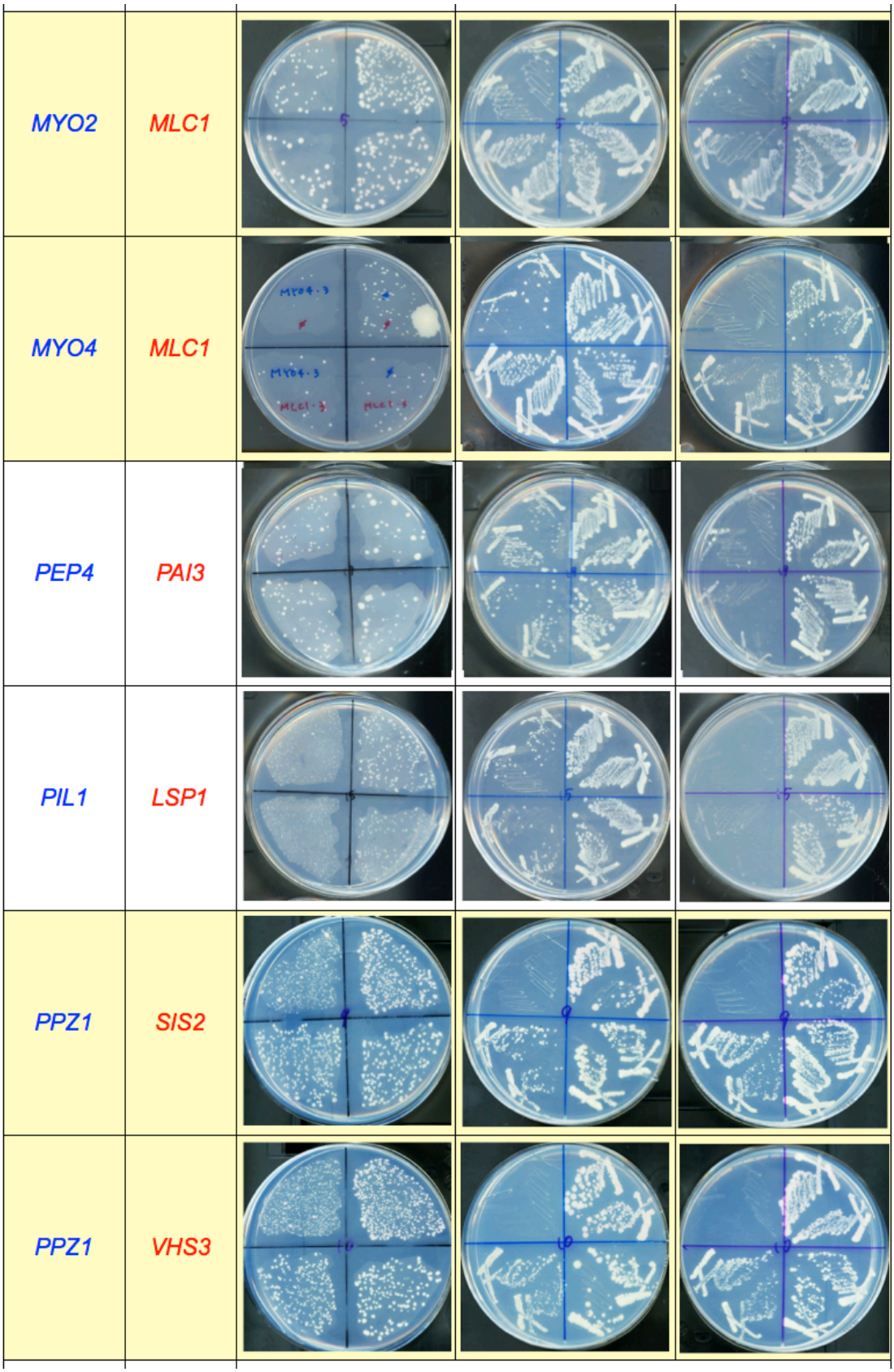


Figure S11 continued

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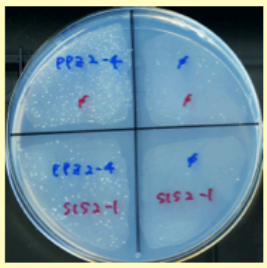
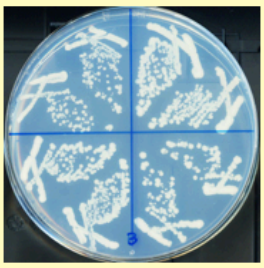
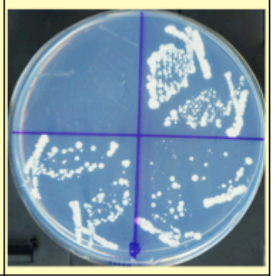
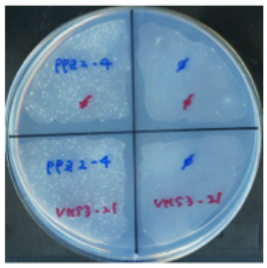
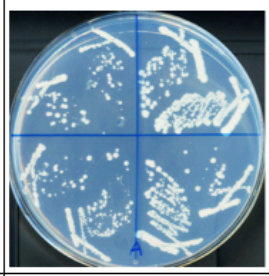
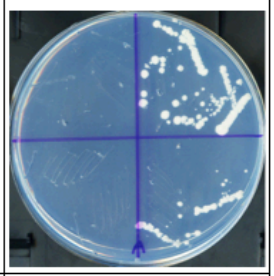
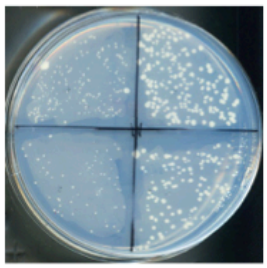
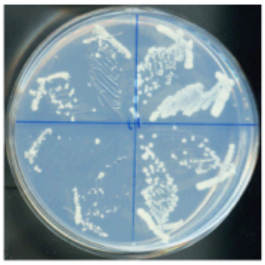
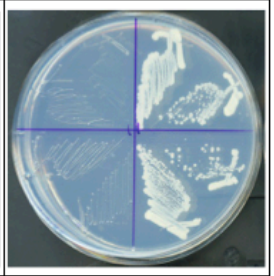
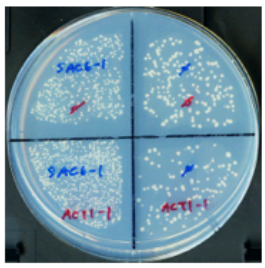
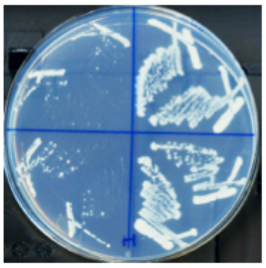
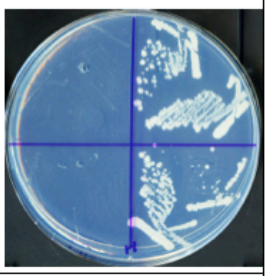
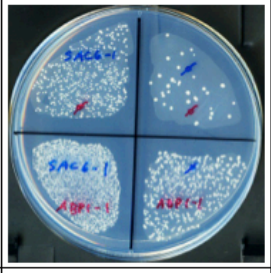
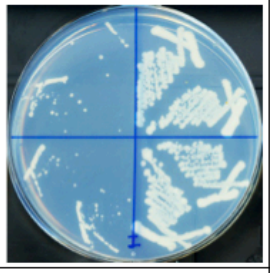
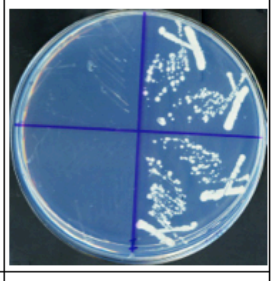
PPZ2	*SIS2*			
PPZ2	*VHS3*			
RTN1	*YOP1*			
SAC6	*ACT1*			
SAC6	*ABP1*			

Figure S11 continued

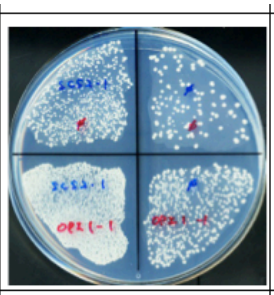
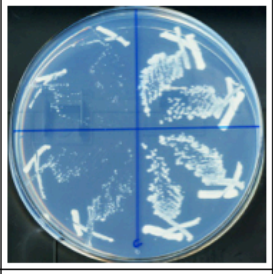
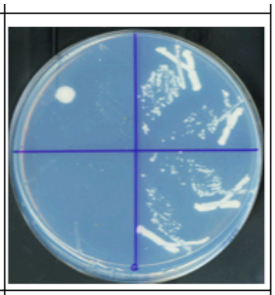
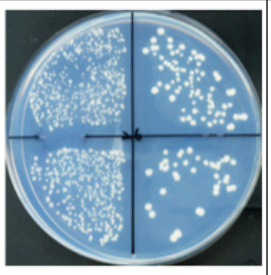
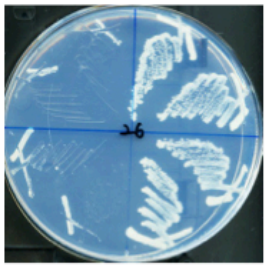
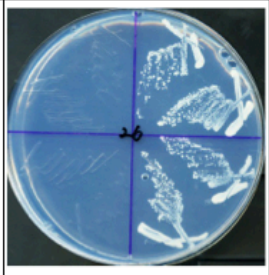
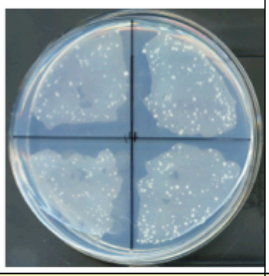
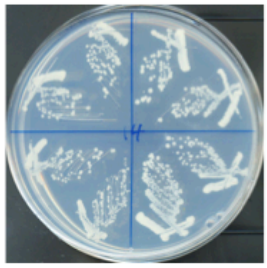
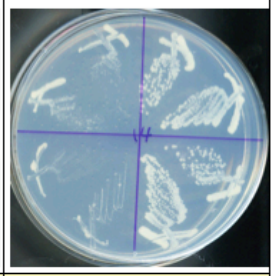
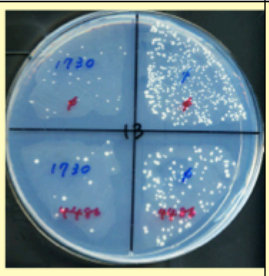
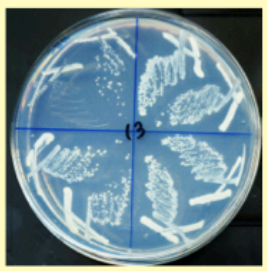
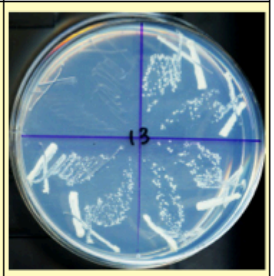
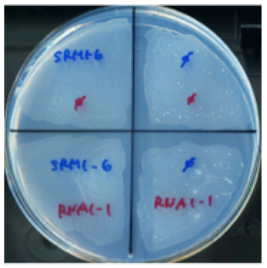
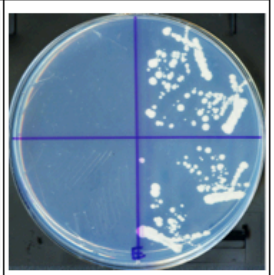
SCS2	*OPI1*			
SEC23	*SAR1*			
SEC31	*SEC13*			
SEC4	*SEC2*			
SRM1	*RNA1*			
TEF1	*EFB1*	Data not shown		

Figure S11 continued

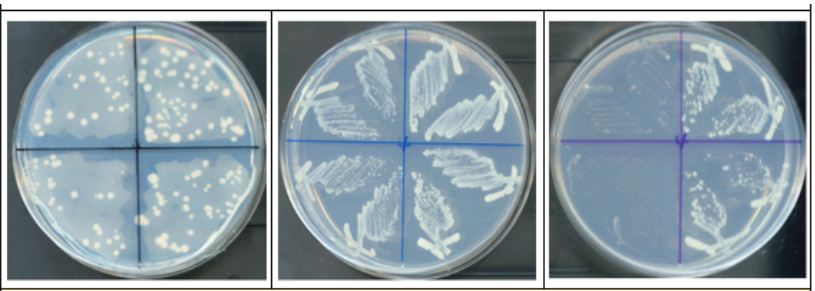
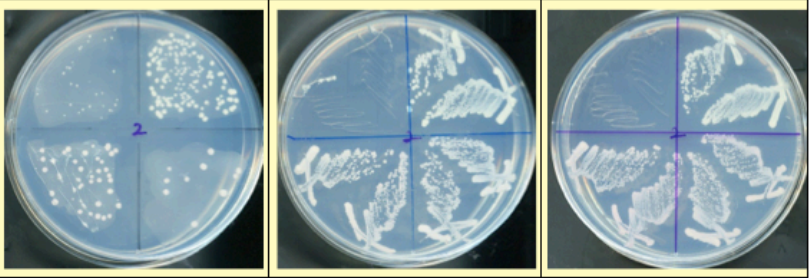
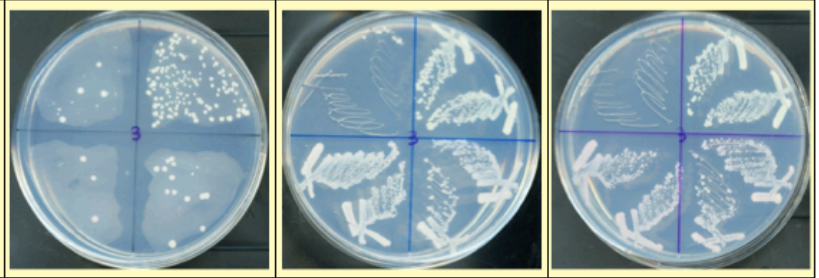
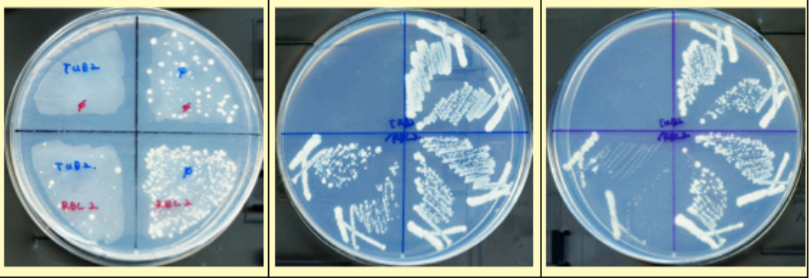
TEF2	*EFB1*	
TPK1	*BCY1*	Data not shown
TPK2	*BCY1*	
TPK3	*BCY1*	
TUB2	*RBL2*	
TUB2	*TUB1*	See Figure S18

Figure S11 continued

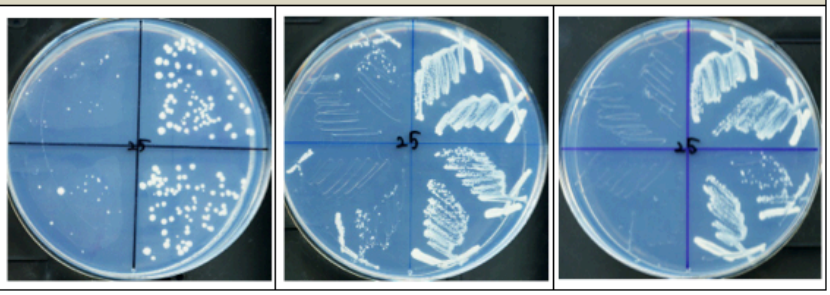
TUB2	*TUB3*	See Figure S18
WWM1	*MCA1*	

Figure S11. Results of 2D-gTOW experiments (plate assay).
In each experiment, yeast strains transformed by the indicated pTOW-DSG and pRS423ks-partner (candidate) were spread onto −His−Ura plates (left plates) and then streaked onto −His−Ura (center plates) and −His−Leu−Ura plates (right plates).

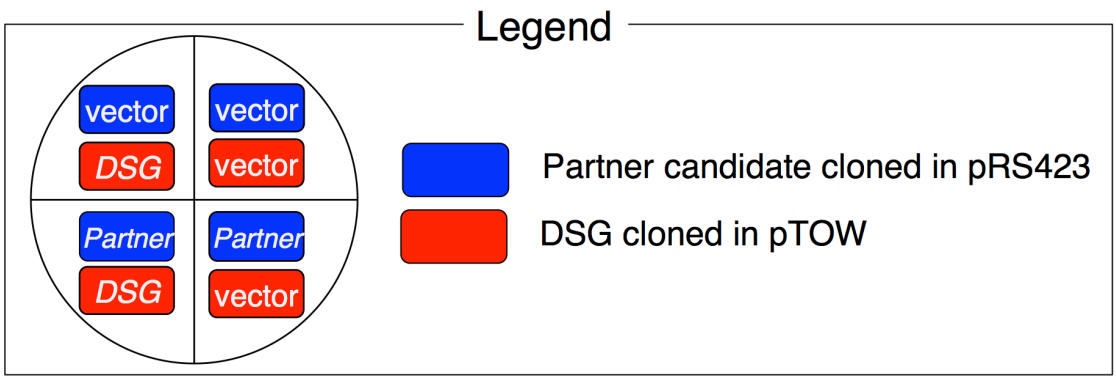


Figure S12. Results of 2D-gTOW experiments (copy number determination)

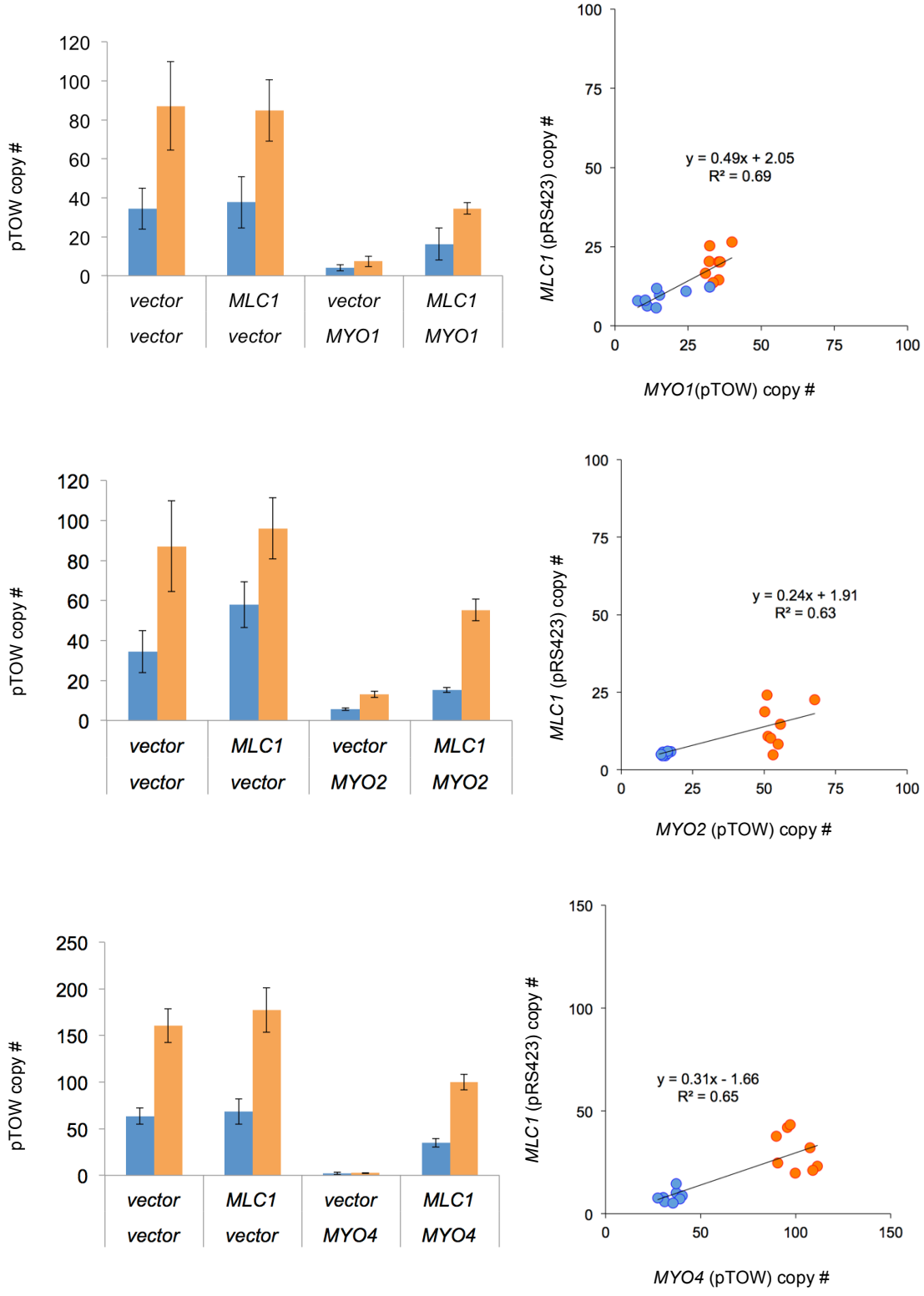


Figure S12 continued

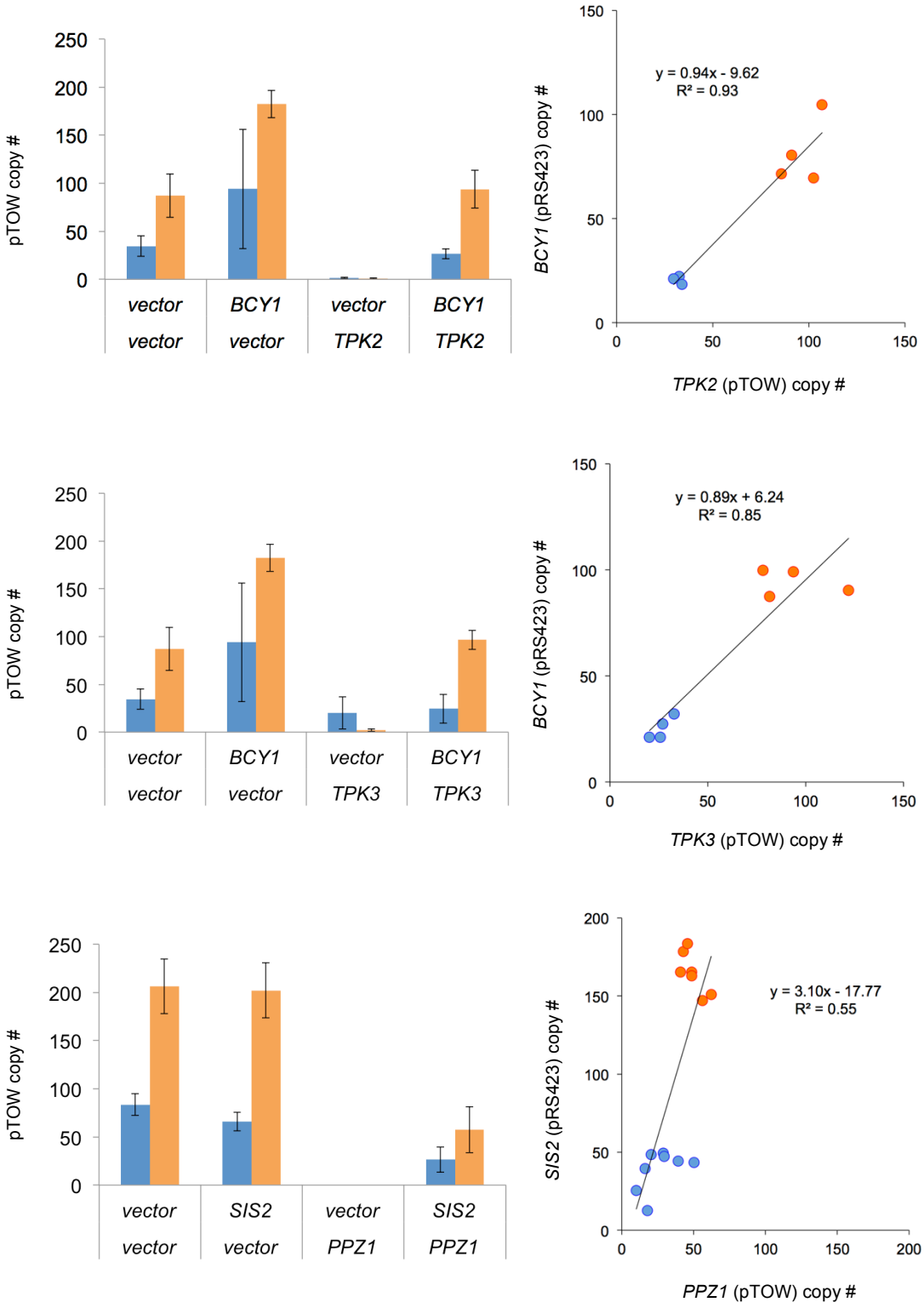


Figure S12 continued

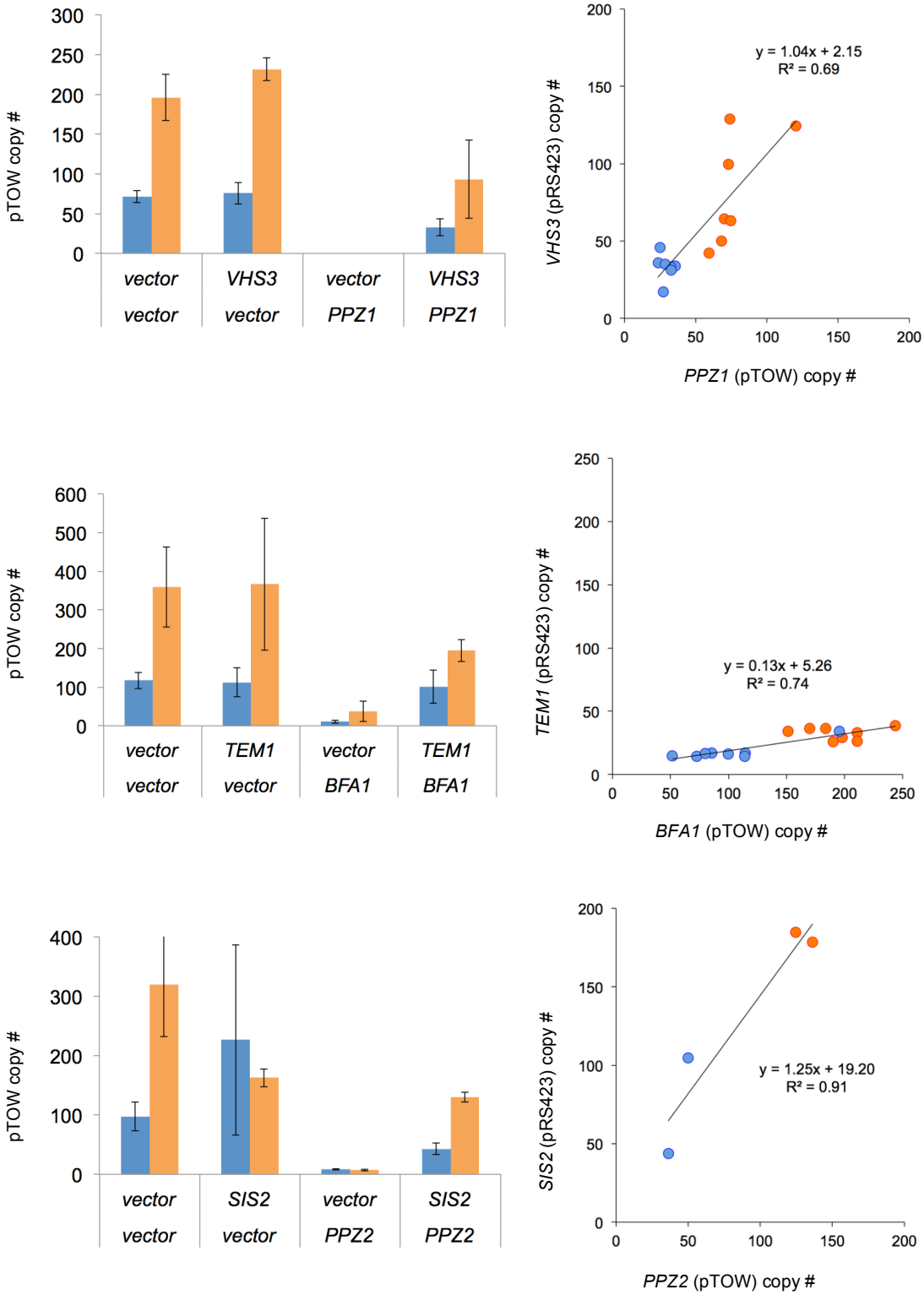


Figure S12 continued

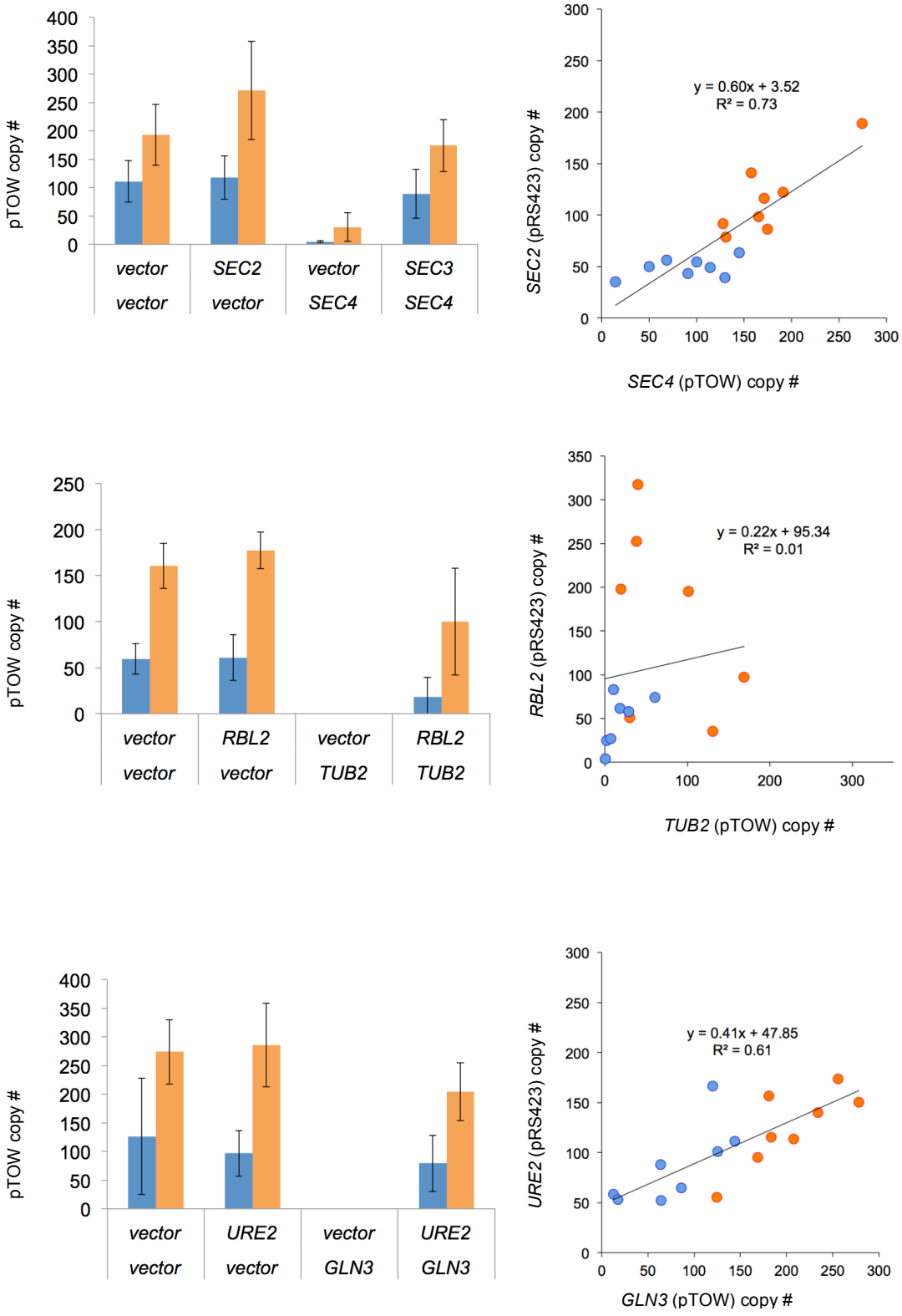


Figure S12 continued

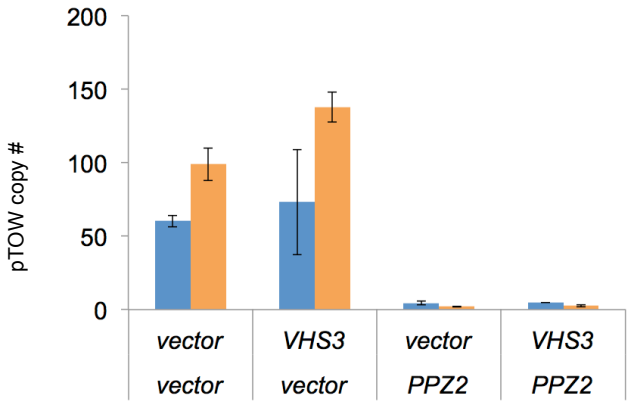


Figure S12. Results of the 2D-gTOW experiments for DSGs and their candidate partners.

The legend for the graph is shown below. The copy numbers of pTOW in the low-copy (−His−Ura) and high-copy (−His−Leu−Ura) conditions are shown in the left panel, and the correlation between the copy numbers of pTOW (DSG) and pRS423ks (candidate partner) are shown in the right panel. The result of the *VHS3* vs. *PPZ2* experiment is shown as a negative example.

pRS423-	Vector	Partner	Vector	Partner
pTOW-	Vector	Vector	DSG	DSG

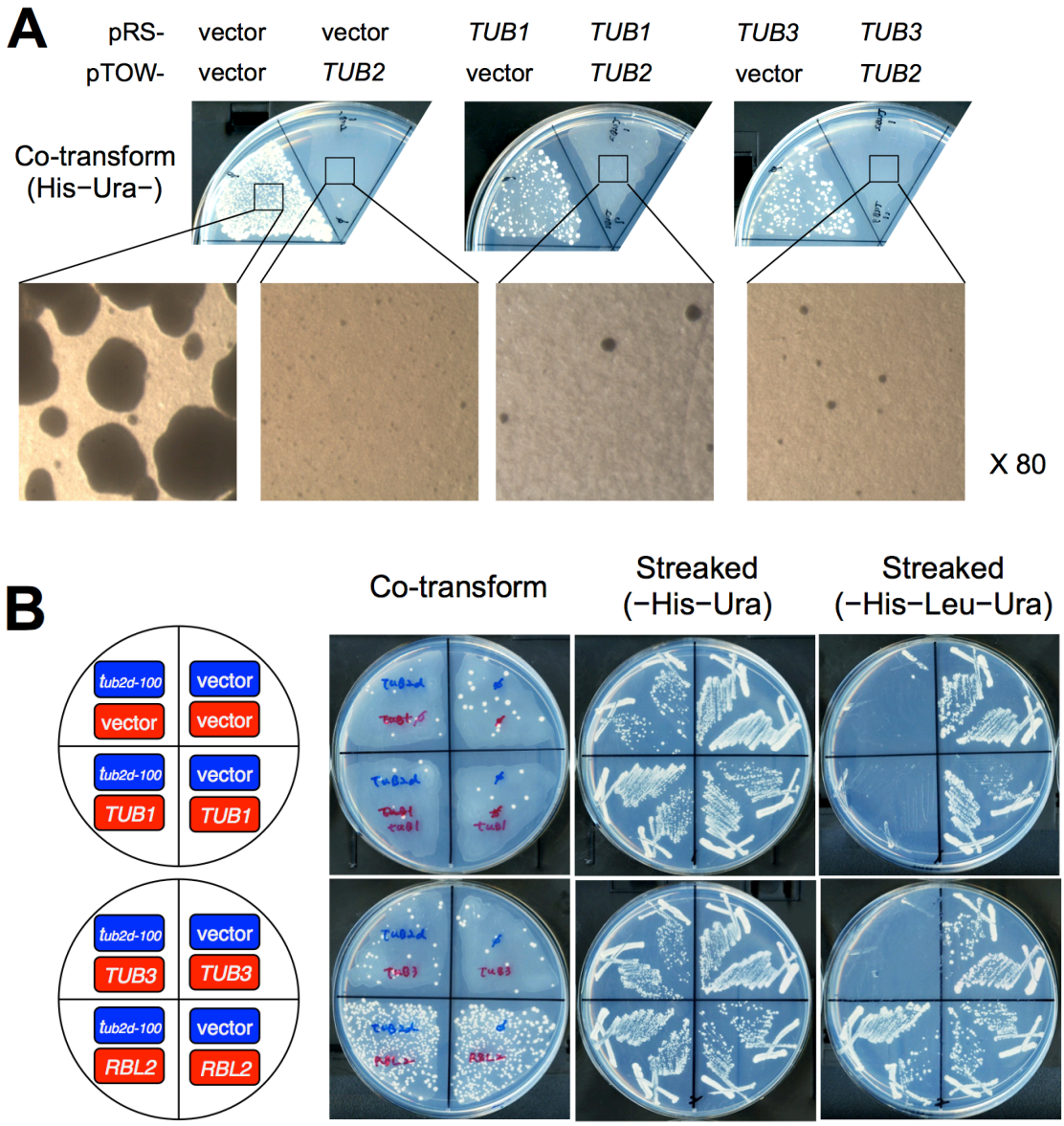


Figure S13. *TUB1* and *TUB3* are weak dosage suppressors (partners) of *TUB2*. *TUB1* and *TUB3* encode α-tubulin; they were suggested to be the partners of *TUB2* (encoding β-tubulin) (Weinstein & Solomon, 1990). However, in our 2D-gTOW experiments, *TUB1* and *TUB3* displayed little suppressive activity (**A** and **B**). By contrast, *RBL2* (encoding a chaperone for a Tub2 monomer) exhibited sufficient suppressive activity (**B**). In **B**, a weakly expressing allele of *TUB2* (*tub2d-100*, see above) was used for 2D-gTOW experiments because *TUB2* is too toxic to obtain any transformant by itself (**A**).

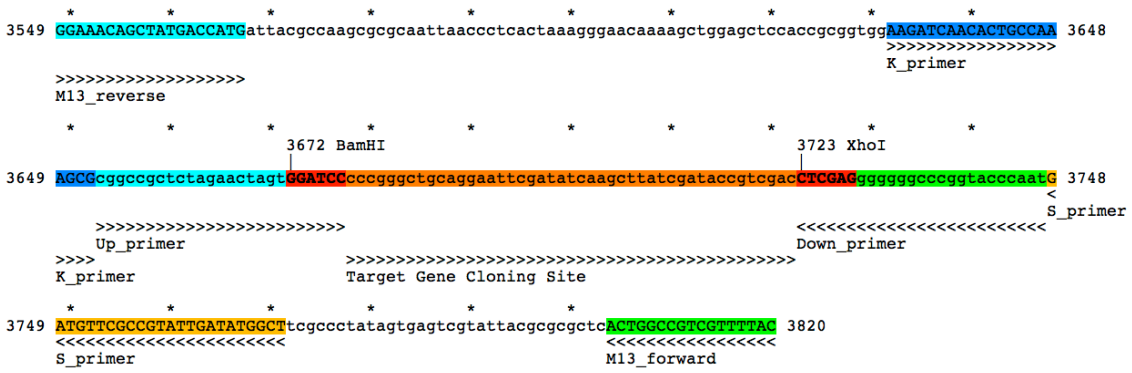


Figure S14. Cloning site of pRS423ks.

The nucleotide sequence is shown in the 5′ to 3′ direction.

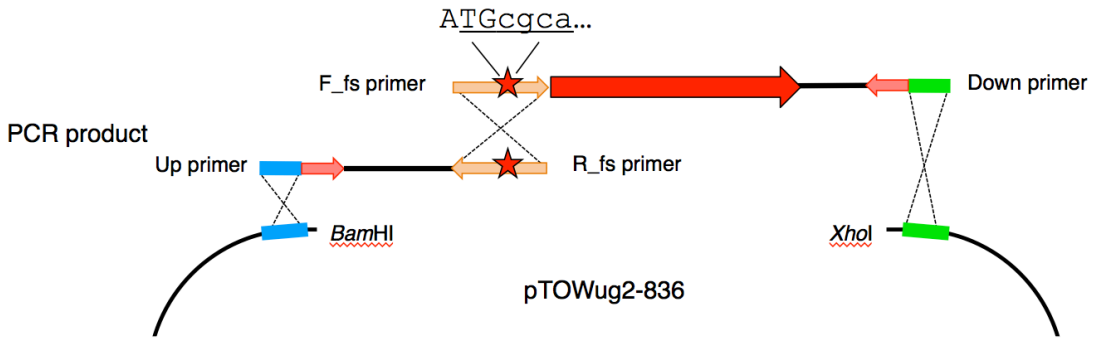


Figure S15. Construction of a frameshift mutant.

The frameshift mutant of each target gene was created by inserting ‘cgca’ immediately after the start codon [a *Fsp*I site (tgcgca) was thus introduced]. Consequently, the correct protein is not produced from the target ORF. To construct the frameshift mutant, F_fs primer and R_fs primer were synthesized for each target gene, and the PCR-amplified fragments were joined and cloned into pTOWug2-836 by the gap-repair method. The information about the start codon of each gene is obtained from the annotation of *Saccharomyces* Genome Database (released on 28 July 2007).

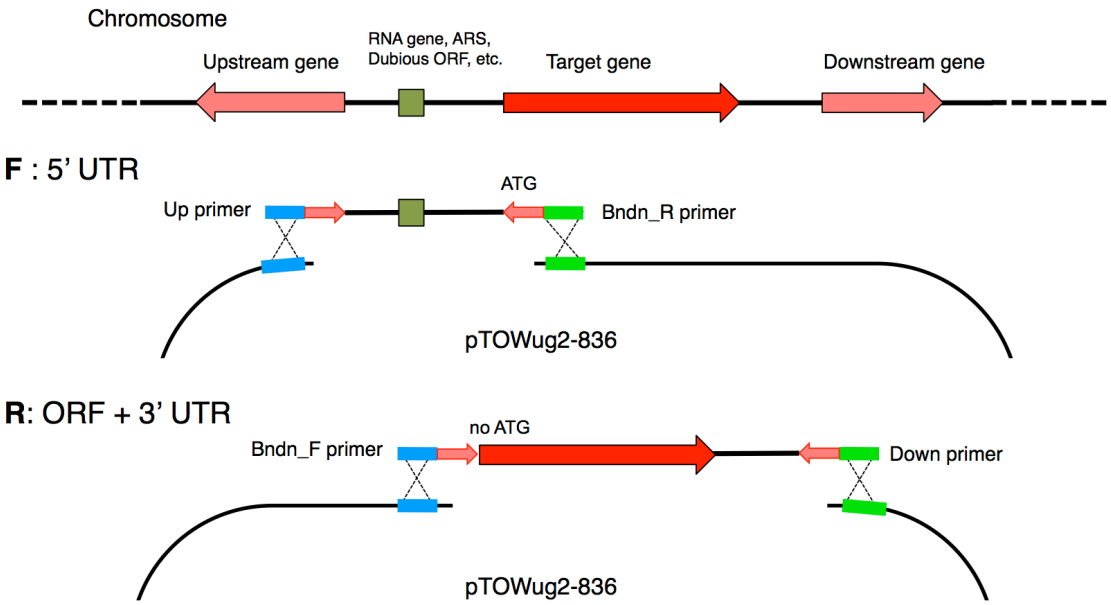
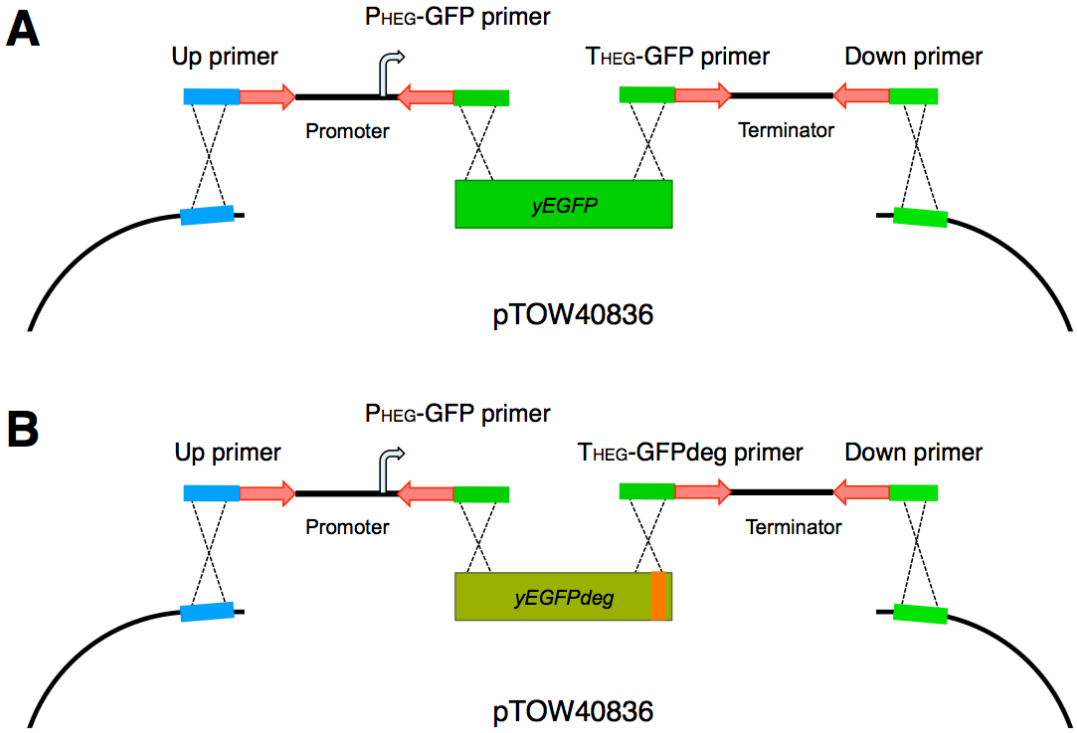


Figure S16. Construction of the segmented genes.

For each target gene, Bndn_R primer and Bndn_F primer were synthesized in order to construct "F" construct that contains 5' region of the target gene, and "R" construct that contains the ORF (without start codon) and 3' UTR. PCR-amplified fragments were joined and cloned into pTOWug2-836 by the gap-repair method. The information about the start codon of each gene is obtained from the annotation of *Saccharomyces* Genome Database (released on 28 July 2007).

Figure S17



C: *yEGFP*

```
ATGTCTAAAGGTGAAGAATTATTCACTGGTGTTGTCCCAATTTTGGTTGAATTAGATGGTGATGTTAATGGTCAC
 M  S  K  G  E  E  L  F  T  G  V  V  P  I  L  V  E  L  D  G  D  V  N  G  H

AAATTTTCTGTCTCCGGTGAAGGTGAAGGTGATGCTACTTACGGTAAATTGACCTTAAAATTTATTTGTACTACT
 K  F  S  V  S  G  E  G  E  G  D  A  T  Y  G  K  L  T  L  K  F  I  C  T  T

GGTAAATTGCCAGTTCCATGGCCAACCTTAGTCACTACTTTAACTTATGGTGTTCAATGTTTTTCTAGATACCCA
 G  K  L  P  V  P  W  P  T  L  V  T  T  L  T  Y  G  V  Q  C  F  S  R  Y  P

GATCATATGAAACAACATGACTTTTTCAAGTCTGCCATGCCAGAAGGTTATGTTCAAGAAAGAACTATTTTTTTC
 D  H  M  K  Q  H  D  F  F  K  S  A  M  P  E  G  Y  V  Q  E  R  T  I  F  F

AAAGATGACGGTAACTACAAGACCAGAGCTGAAGTCAAGTTTGAAGGTGATACCTTAGTTAATAGAATCGAATTA
 K  D  D  G  N  Y  K  T  R  A  E  V  K  F  E  G  D  T  L  V  N  R  I  E  L

AAAGGTATTGATTTTAAAGAAGATGGTAACATTTTAGGTCACAAATTGGAATACAACTATAACTCTCACAATGTT
 K  G  I  D  F  K  E  D  G  N  I  L  G  H  K  L  E  Y  N  Y  N  S  H  N  V

TACATCATGGCTGACAAACAAAAGAATGGTATCAAAGTTAACTTCAAAATTAGACACAACATTGAAGATGGTTCT
 Y  I  M  A  D  K  Q  K  N  G  I  K  V  N  F  K  I  R  H  N  I  E  D  G  S

GTTCAATTAGCTGACCATTATCAACAAAATACTCCAATTGGTGATGGTCCAGTCTTGTTACCAGACAACCATTAC
 V  Q  L  A  D  H  Y  Q  Q  N  T  P  I  G  D  G  P  V  L  L  P  D  N  H  Y

TTATCCACTCAATCTGCCTTATCCAAAGATCCAAACGAAAAGAGAGACCACATGGTCTTGTTAGAATTTGTTACT
 L  S  T  Q  S  A  L  S  K  D  P  N  E  K  R  D  H  M  V  L  L  E  F  V  T

GCTGCTGGTATTACCCATGGTATGGATGAATTGTACAAATAA
 A  A  G  I  T  H  G  M  D  E  L  Y  K  *
```

D: *yEGFPdeg*

```
ATGTCTAAAGGTGAAGAATTATTCACTGGTGTTGTCCCAATTTTGGTTGAATTAGATGGTGATGTTAATGGTCAC
 M  S  K  G  E  E  L  F  T  G  V  V  P  I  L  V  E  L  D  G  D  V  N  G  H

AAATTTTCTGTCTCCGGTGAAGGTGAAGGTGATGCTACTTACGGTAAATTGACCTTAAAATTTATTTGTACTACT
 K  F  S  V  S  G  E  G  E  G  D  A  T  Y  G  K  L  T  L  K  F  I  C  T  T

GGTAAATTGCCAGTTCCATGGCCAACCTTAGTCACTACTTTAACTTATGGTGTTCAATGTTTTTCTAGATACCCA
 G  K  L  P  V  P  W  P  T  L  V  T  T  L  T  Y  G  V  Q  C  F  S  R  Y  P

GATCATATGAAACAACATGACTTTTTCAAGTCTGCCATGCCAGAAGGTTATGTTCAAGAAAGAACTATTTTTTTC
 D  H  M  K  Q  H  D  F  F  K  S  A  M  P  E  G  Y  V  Q  E  R  T  I  F  F

AAAGATGACGGTAACTACAAGACCAGAGCTGAAGTCAAGTTTGAAGGTGATACCTTAGTTAATAGAATCGAATTA
 K  D  D  G  N  Y  K  T  R  A  E  V  K  F  E  G  D  T  L  V  N  R  I  E  L

AAAGGTATTGATTTTAAAGAAGATGGTAACATTTTAGGTCACAAATTGGAATACAACTATAACTCTCACAATGTT
 K  G  I  D  F  K  E  D  G  N  I  L  G  H  K  L  E  Y  N  Y  N  S  H  N  V

TACATCATGGCTGACAAACAAAAGAATGGTATCAAAGTTAACTTCAAAATTAGACACAACATTGAAGATGGTTCT
 Y  I  M  A  D  K  Q  K  N  G  I  K  V  N  F  K  I  R  H  N  I  E  D  G  S

GTTCAATTAGCTGACCATTATCAACAAAATACTCCAATTGGTGATGGTCCAGTCTTGTTACCAGACAACCATTAC
 V  Q  L  A  D  H  Y  Q  Q  N  T  P  I  G  D  G  P  V  L  L  P  D  N  H  Y

TTATCCACTCAATCTGCCTTATCCAAAGATCCAAACGAAAAGAGAGACCACATGGTCTTGTTAGAATTTGTTACT
 L  S  T  Q  S  A  L  S  K  D  P  N  E  K  R  D  H  M  V  L  L  E  F  V  T

GCTGCTGGTATTACCCATGGTATGGATGAATTGTACAAACTGCCCATGTCTTGTGCCCAGGAGtctatcacaagt
 A  A  G  I  T  H  G  M  D  E  L  Y  K  L  P  M  S  C  A  Q  E  S  I  T  S

ttgtacaaaaaagctggttctTAA
 L  Y  K  K  A  G  S  *
```

Figure S17. Construction of GFP and GFPdeg replaced plasmids.

(*A*) Constructions of GFP replaced plasmid. (*B*) Construction of GFPdeg replaced plasmid. The promoter region and the terminator region of each target highly expressed gene and *yEGFP* (or *yEGFPdeg*) were amplified by PCR using indicated primers, and joined and cloned into pTOW40836. (*C*) The nucleotide and amino acid sequences of *yEGFP* used in *A*. (*D*) The nucleotide and amino acid sequences of *yEGFPdeg* used in *B*. The degron sequence from mouse ornithine decarboxylase gene (cODC1) (Jungbluth *et al.*, 2010) is colored with yellow.

Table S2. Statistical data of the 230 empty vector experiments.

	Max growth rate	Copy# (−Ura)	Copy# (−Leu−Ura)
Average	2.2	22.9	205.2
SD[*1]	0.6	12.5	86.6
CV[*2]	29.2	54.9	42.2

*1 Standard deviation

*2 Coefficient of variation

Table S3. Correlations between max growth rates and copy numbers obtained in the gTOW6000 analysis.

	Max growth rate vs. U[*]	Max growth rate vs. L[*]	U vs. LU[*]
ALL	0.18	0.35	0.16
Low-limit top 786	0.32	0.54	0.56

* U and LU indicate the copy number in the −Ura and −Leu−Ura conditions, respectively.

Table S7. Partner-seeking experiment results

DSG	Upper limit	Candidate partner	Reference*	Type of interaction	Verified? (Figures S11 and S12)
ABP1	4.2	*ACT1*	BioGRID	Physical interaction	No
ABP1	4.2	*SAC6*	BioGRID	Physical interaction	No
ACT1	1.2	*COF1*	BioGRID	Physical interaction	No
ACT1	1.2	*ABP1*	BioGRID	Physical interaction	No
ACT1	1.2	*SAC6*	Sandrock *et al.*, 1999	Synthetic rescue	No
ARF1	1.0	*SEC72*	-	-	No
ARF1	1.0	*GEA1*	-	-	No
ARF1	1.0	*GEA2*	BioGRID	Physical interaction	No
ARF1	1.0	*FKS1*	-	-	No
ARF2	5.5	*SEC72*	-	-	No
ARF2	5.5	*GEA1*	BioGRID	Physical interaction	No
ARF2	5.5	*GEA2*	BioGRID	Physical interaction	No
ARF2	5.5	*FKS1*	-	-	No
ARF2	5.5	*GLO3*	-	-	No
BFA1	3.5	*TEM1*	Park *et al.*, 2004	Synthetic rescue	Yes
BGL2	9.8	*GSC2*	-	-	No
BGL2	9.8	*GAS1*	BioGRID	Negative genetic	No

				interaction	
COF1	3.2	*ACT1*	BioGRID	Physical interaction	No
GAS1	4.2	*BGL2*	-	-	No
GLN3	1.5	*URE2*	Palmer *et al.*, 2009	Synthetic rescue	Yes
GSC2	5.1	*BGL2*	-	-	No
GSP1	3.5	*RNA1*	BioGRID	Physical interaction	No
MYO1	6.5	*MLC1*	-	-	Yes
MYO2	12.1	*MLC1*	Stevens & Davis, 1998	Dosage rescue	Yes
MYO4	6.5	*MLC1*	-	-	Yes
PEP4	0.8	*PAI3*	BioGRID	Physical interaction	No
PIL1	8.1	*LSP1*	Deng *et al.*, 2009	Phenotypic enhancement	No
PPZ1	0.3	*SIS2*	Clotet *et al.*, 1999	Dosage rescue	Yes
PPZ1	0.3	*VHS3*	de Nadal *et al.*, 1998	Synthetic rescue	Yes
PPZ1	0.3	*SIS1*	-	-	No
PPZ2	9.3	*SIS2*	BioGRID	Physical interaction	Yes
PPZ2	9.3	*VHS3*	BioGRID	Physical interaction	No
RTN1	15.1	*YOP1*	-	-	No
SAC6	2.0	*ACT1*	Sandrock *et al.*, 1999	Synthetic rescue	No
SAC6	2.0	*ABP1*	BioGRID	Physical interaction	No

SCS2	9.5	*OPI1*	Wilson *et al.*, 2011	Physical interaction	No
SEC23	4.4	*SAR1*	Oka & Nakano, 1994	Dosage rescue	No
SEC31	5.1	*SEC13*	BioGRID	Physical interaction	No Additive
SEC4	5.2	*SEC2*	Ortiz *et al.*, 2002	Dosage rescue	Yes
SRM1	6.5	*RNA1*	-	-	No
TEF1	0.6	*EFB1*	BioGRID	Physical interaction	No
TEF2	4.9	*EFB1*	Kinzy & Woolford, 1995	Dosage rescue	No
TPK1	0.9	*BCY1*	BioGRID	Physical interaction	Yes
TPK2	2.1	*BCY1*	Nehlin *et al.*, 1992	Dosage rescue	Yes
TPK3	0.6	*BCY1*	Mazón *et al.*, 1993	Phenotypic enhancement	Yes
TUB2[#]	2.7	*RBL2*	Abruzzi *et al.*, 2002	Phenotypic suppression	Yes (see also Figure S13)
TUB2[#]	2.7	*TUB1*	Weinstein & Solomon, 1990	Dosage rescue	Weak (Figure S13)
TUB2[#]	2.7	*TUB3*	-	-	Weak (Figure S13)
WWM1	0.6	*MCA1*	Szallies *et al.*, 2002	Synthetic rescue	No

* BioGRID: http://thebiogrid.org/

[#] *tub2-d100* was used in the experiment.

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