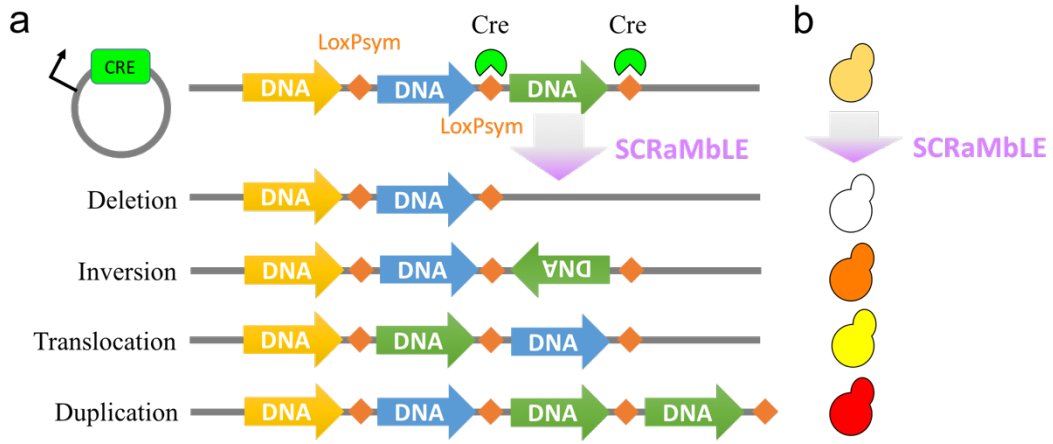
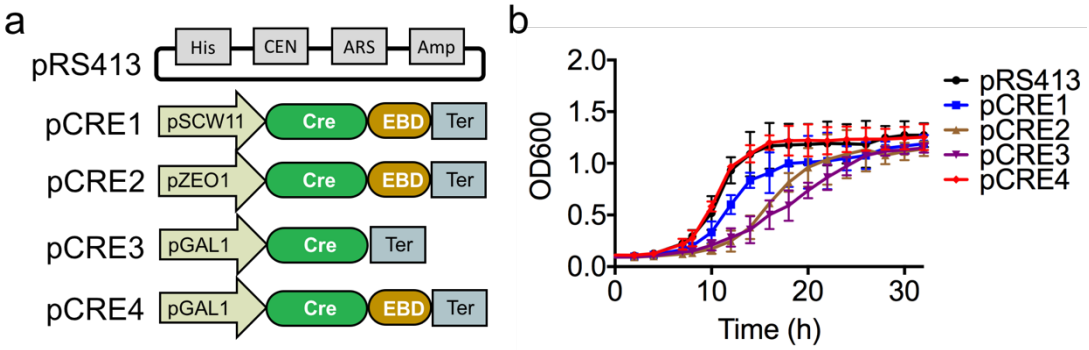
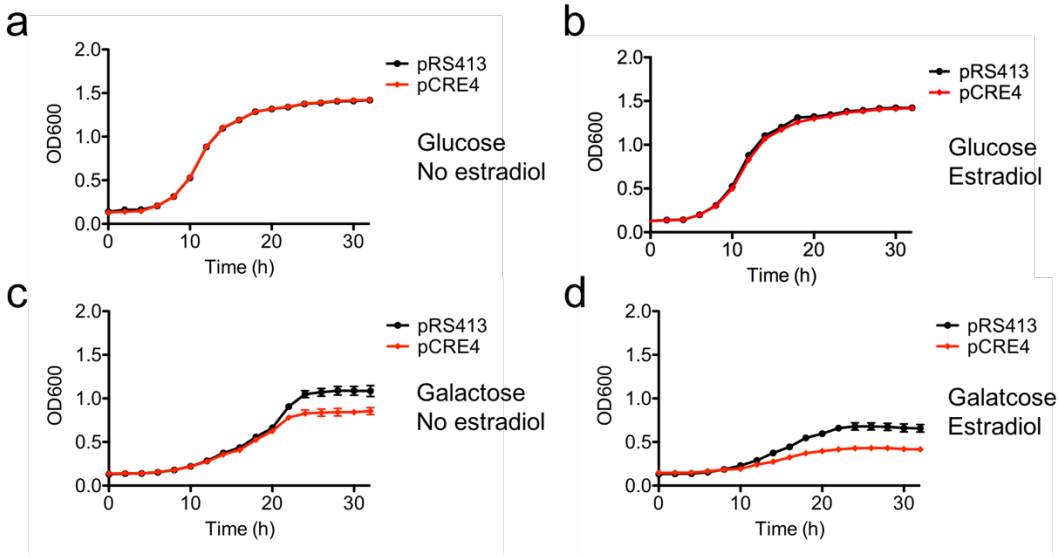


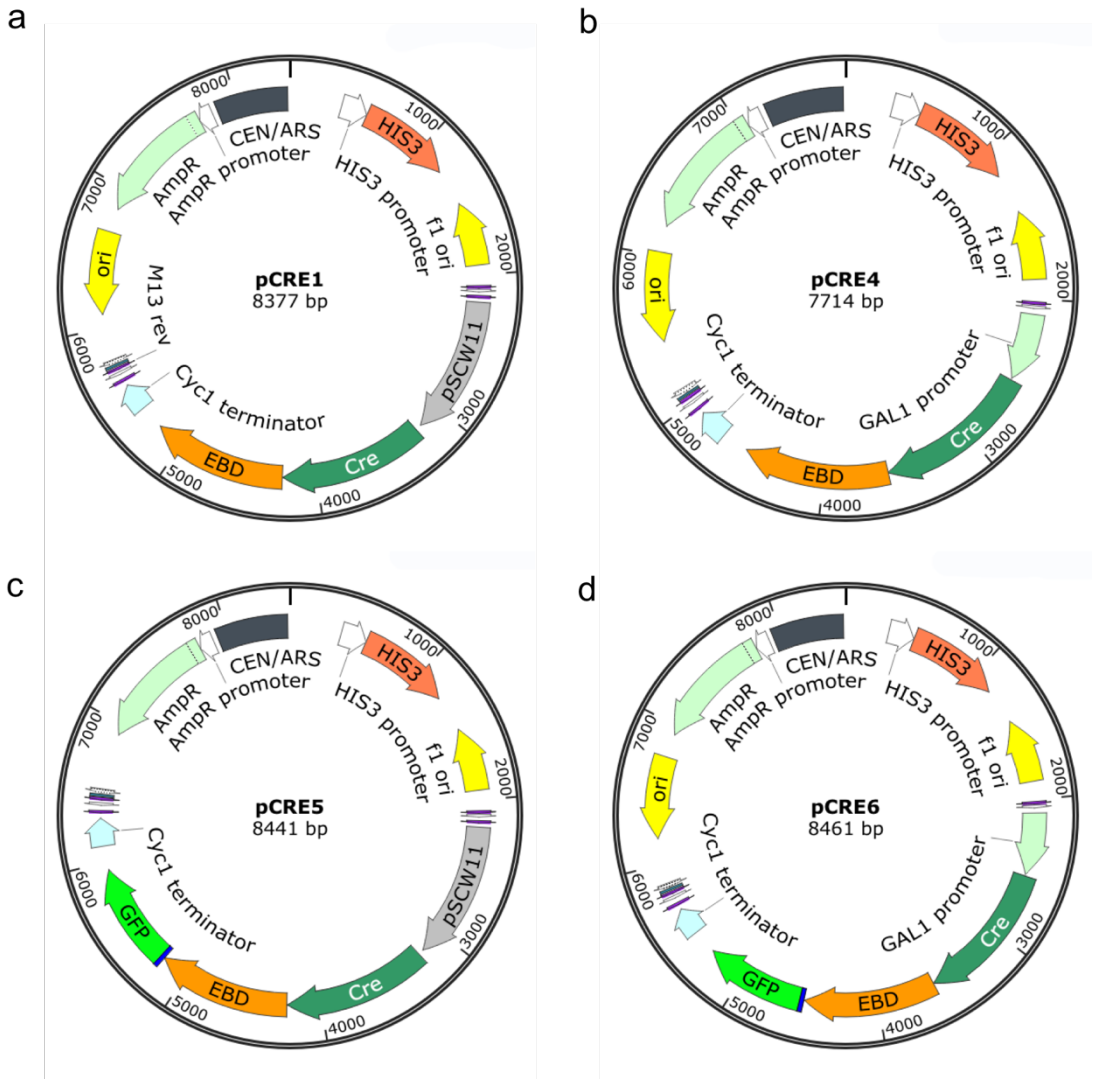

**Supplementary Figure 1. SCRaMbLE leads to diversity generating desired phenotypes.** (a) LoxPsym sites (orange diamonds) are inserted in the 3'UTR of each non-essential gene. The symmetry of loxPsym sites result in deletion, inversion, translocation and duplication, simultaneously. (b) Induction of SCRaMbLE in a synthetic strain results in a significant increase in diversity, generating desired phenotypes. SCRaMbLE events can be analyzed by deep sequencing and long-read sequencing.



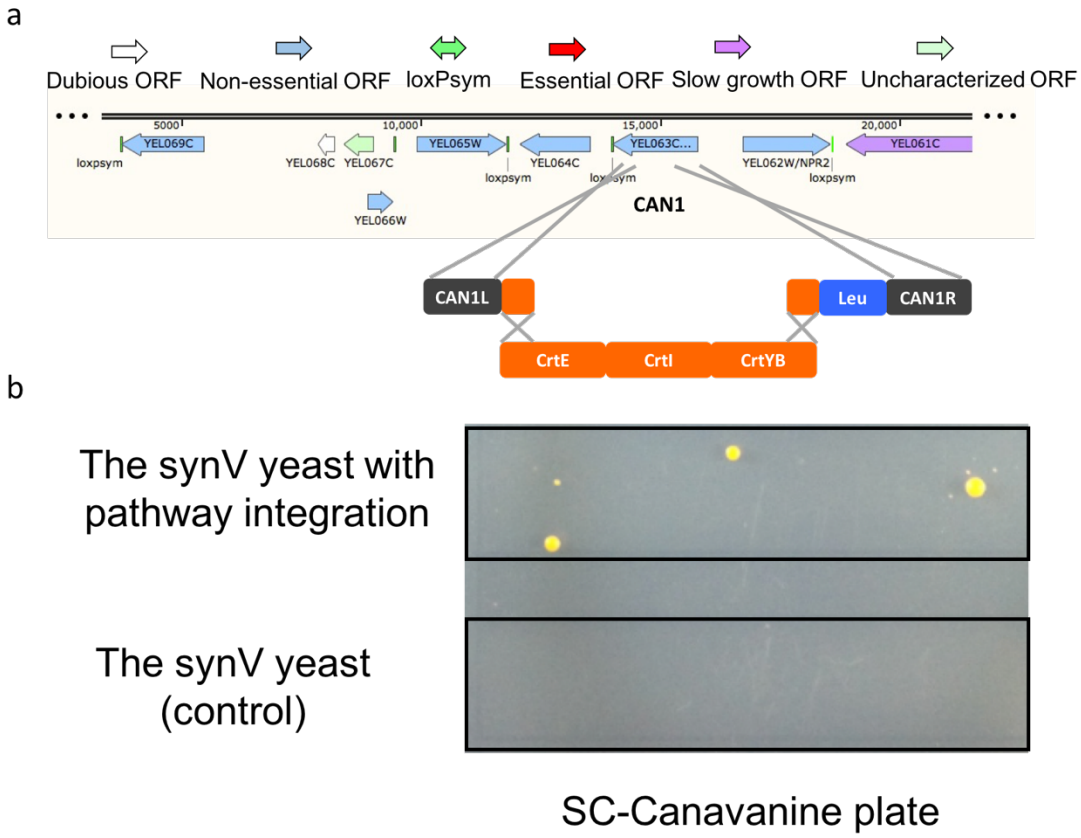

**Supplementary Figure 2. Design of Cre switches for tightly regulation of Cre activity.** (a) Design of different CRE switches and fitness assays in the synV yeast; pSCW11 is a daughter-cell-specific promoter； pZEO1 is a weak constitutive yeast promoter; The pGAL1 promoter is galactose inducible promoter; The Cre-EBD is a fusion protein of Cre recombinase and estrogen binding domain (EBD); The Ter is the CYC1 transcription terminator. (b) Growth curve of synV strains containing pCRE1, pCRE2, pCRE3, pCRE4 and pRS413, respectively. Growth of strains was assessed at 30℃ on SC-His medium for 32 hours. Error bars represent s.d. from three independent experiments.



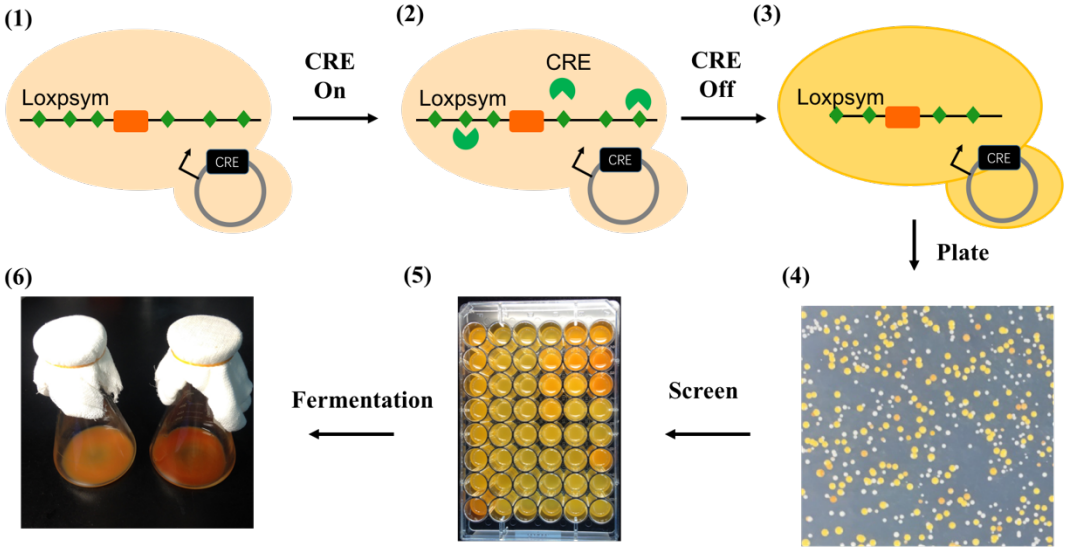

**Supplementary Figure 3. Growth curve of synthetic strains contained pRS413 (control) and pCRE4 at different medium.** (**a**) SC-His glucose medium without estradiol; (**b**) SC-His glucose medium with 1 μM estradiol; (**c**) SGal-His medium without estradiol; (**d**) SGal-His medium with 1 μM estradiol. Error bars represent s.d. from three independent experiments.



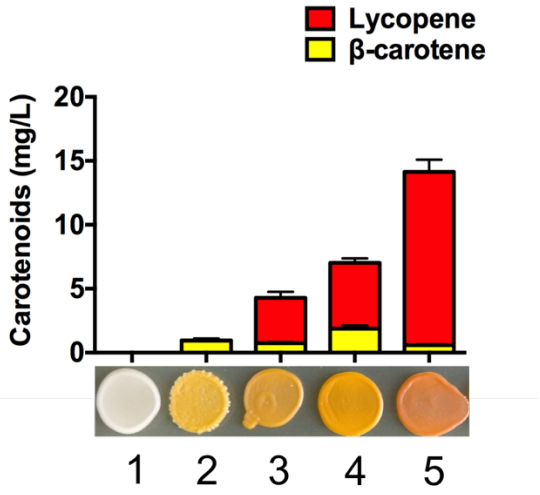

**Supplementary Figure 4. Plasmids map of four CRE switches used in this study.** (a) Plasmid map of the pCRE1: pSCW11-Cre-EBD-CYC1t; (b) Plasmid map of the pCRE4: pGAL1-Cre-EBD-CYC1t; (c) Plasmid map of the pCRE5: pSCW11-Cre-EBD-GFP-CYC1t; (d) Plasmid map of the pCRE6: pSCW11-Cre-EBD-GFP-CYC1t;



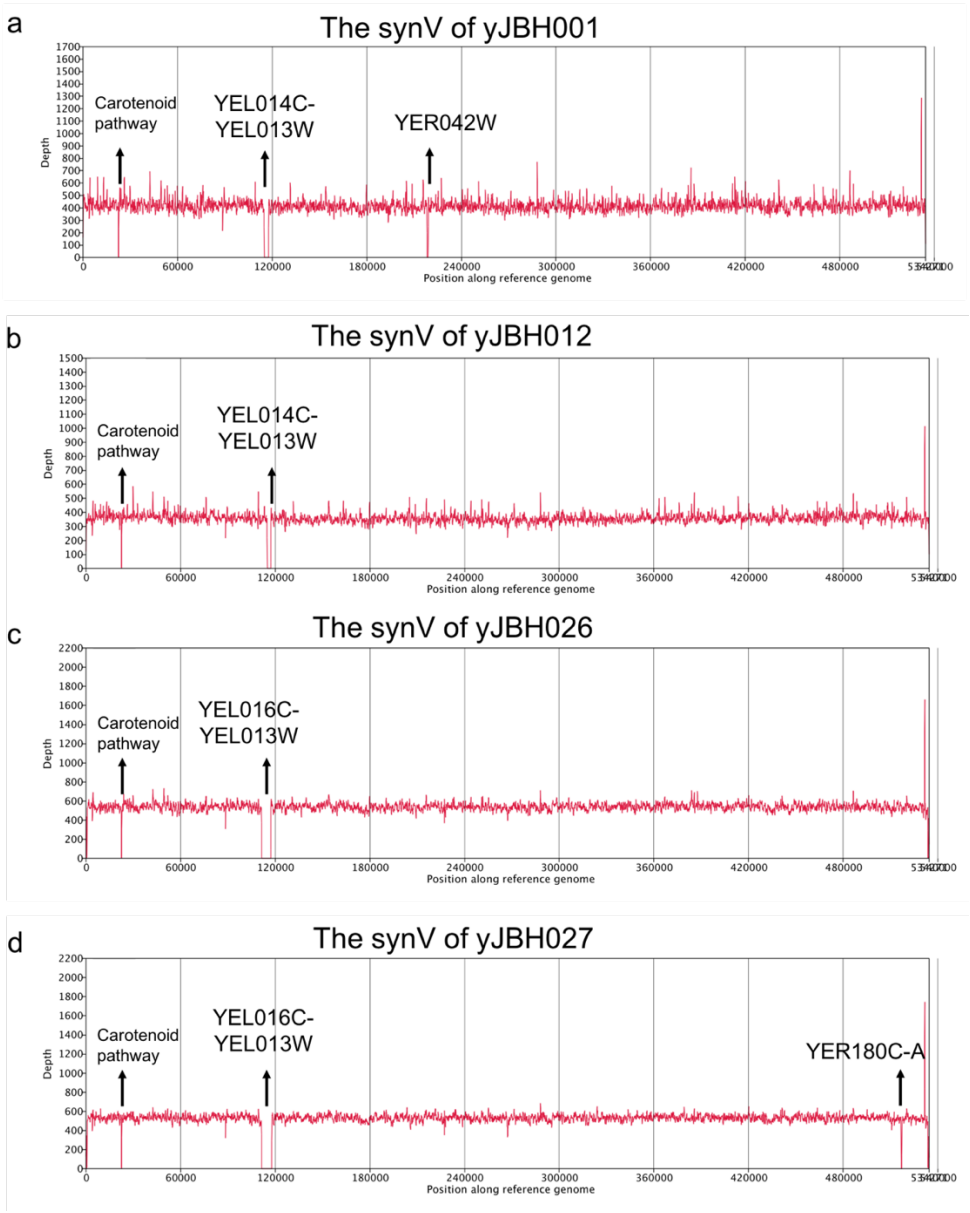

**Supplementary Figure 5. Integration of the carotenoid pathway into the synV chromosome.** (a) The carotenoid pathway was integrated into the YEL063C/CAN1 site with auxotrophic marker Leu2. The YEL066W, YEL065W, YEL064C, YEL063C and the YEL062W are all non-essential genes. (b) The SC-Canavanine plate was used for selection of the carotenoids pathway integration. The orange color colonies were the synV haploid yeast with carotenoid pathway integration (yJBH000) in the SC-Canavanine plate, while no colonies appear in the control group. The endogenous negative selectable gene CAN1, encoding plasma membrane arginine permease. The disruption mutant of CAN1 can grow in the presence of toxic arginine analogue L-Canavanine.



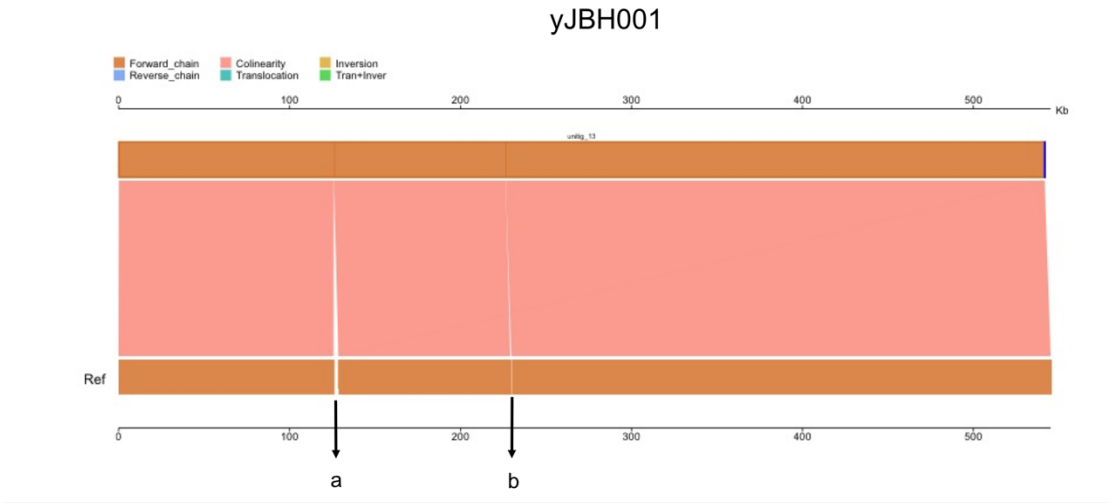

**Supplementary Figure 6. Schematic diagram of the SCRaMbLE and screen system**. (1) the carotenoid pathway was integrated into the chromosome synV. The parent synV strains were transformed using the tight switch pCRE4 and plated onto SC-His agar. The plates were incubated at 30°C for 72 h. (2) Single colonies were inoculated into 5 mL SC-His overnight. The cultures were washed twice with dd$H_2O$ and re-inoculated to obtain an OD600 of 1.0 in 2% galactose SGal-His medium containing 1μM estradiol (Sigma-Aldrich). The cultures were incubated at 30°C for 8 h to turn on Cre activity in the cells and begin the SCRaMbLE progress. (3) The yeast pellet from 1 mL of culture was washed twice with dd$H_2O$ and resuspended in 1 mL of SC-His glucose medium. (4) The SCRaMbLE library was plated on SC-His glucose agar and the strains incubated at 30°C until clear differences in carotenoid pigmentation were observed (72 h to 120 h). (5) Colonies colored darker than the wild-type parent strains were inoculated into a 48-well plate on SC-His glucose medium and dropped on SC-His glucose agar plates at 30°C for 48 h. (6) Strains colored darker than the wild-type parent strain in the 48-well plate were prepared for fermentation. Three independent colonies of each were inoculated into 5 mL of YPD medium for 24 h, then re-inoculated to obtain an OD600 of 0.1 in 40 mL YPD with 40 g/L glucose medium in 250 mL flasks, which were then incubated for 60 h at 30°C.




**Supplementary Figure 7. Color-base screen method for high throughput screening from the SCRaMbLE library.** Five scrambled colonies exhibited different colors were resuspended in 10 μL of water and dropped on an SC-His glucose plate at 30°C for 48 h. These five colonies were also inoculated in 40 mL YPD with 40 g/L glucose medium in 250 mL flasks for 60 h. Error bars represent s.d. from three independent experiments.

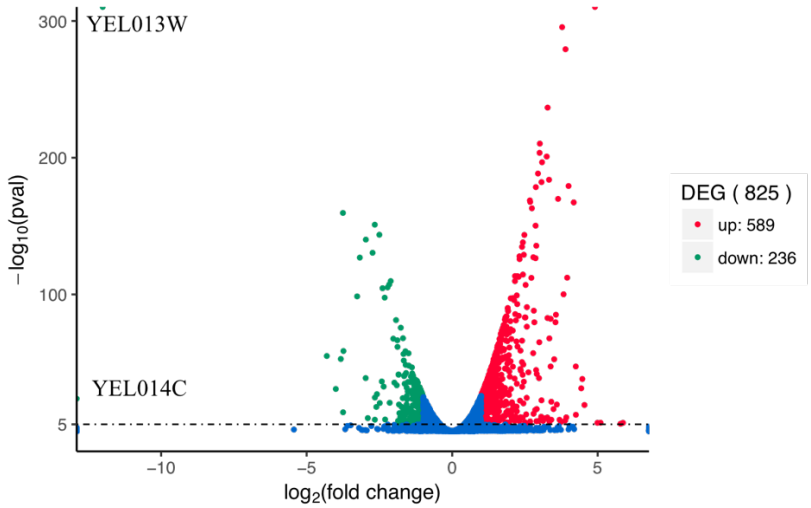



**Supplementary Figure 8. Deep sequencing analysis of four haploids with high production of carotenoids.** **(a)** Deep sequencing coverage of yJBH001 strain revealed two deletions of synthetic fragments (the YEL014C-YEL013W and the YER042W). (b) Deep sequencing coverage of yJBH012 strain revealed a deletions of synthetic fragments (YEL014C-YEL013W). (c) Deep sequencing coverage of yJBH026 strain revealed a deletions of synthetic fragments (YEL016C-YEL013W). (d) Deep sequencing coverage of yJBH027 strain revealed a deletions of synthetic fragments (YEL016C-YEL013W and YER180C-A). The first deletion is the YEL063C disrupted by integration of the carotenoid pathway.

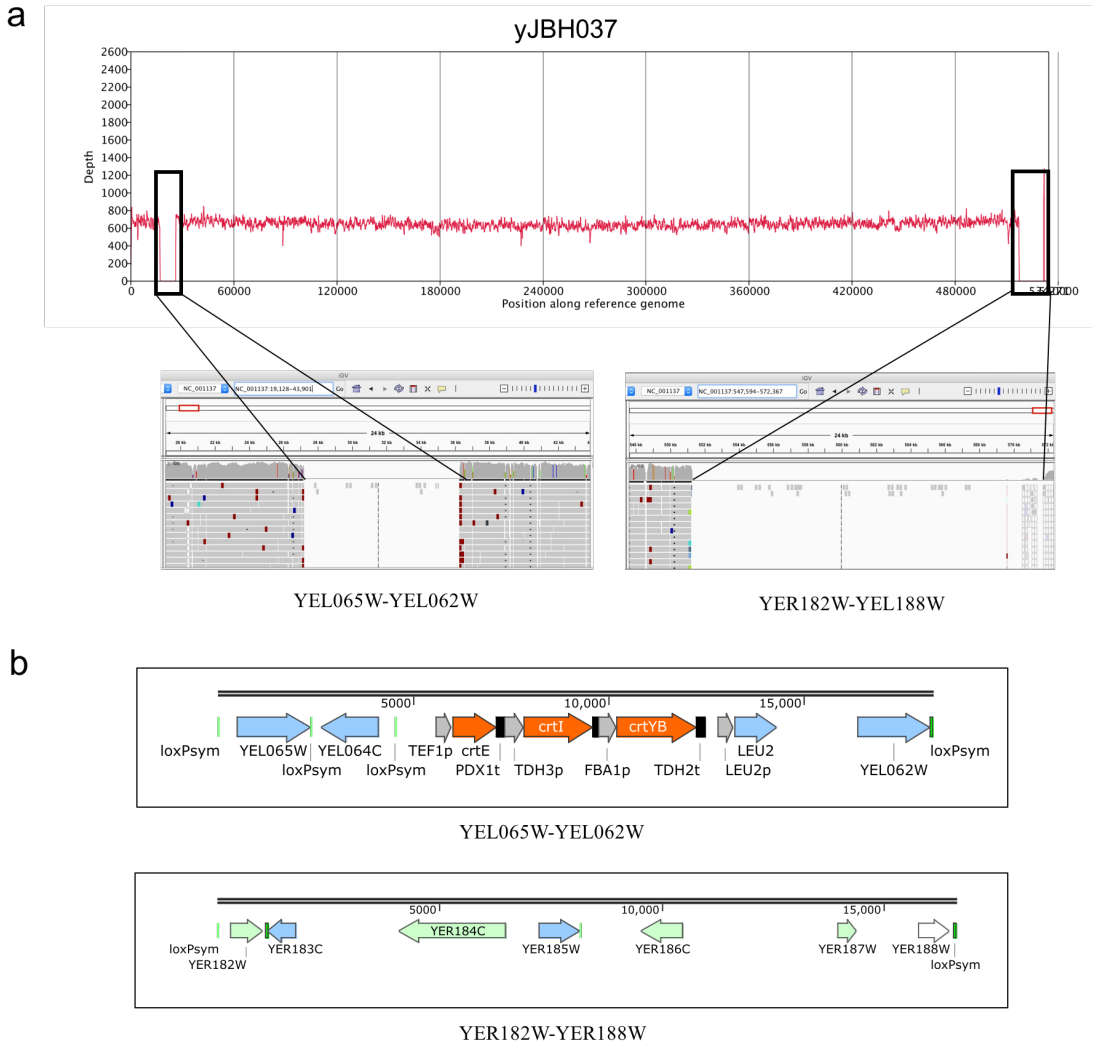



| Numbers | Structure Variety | Copy Variety | Range | Size bp |
|---|---|---|---|---|
| a | Deletion | -1 | YEL014C-YEL013W | 2345 |
| b | Deletion | -1 | YER042W | 819 |

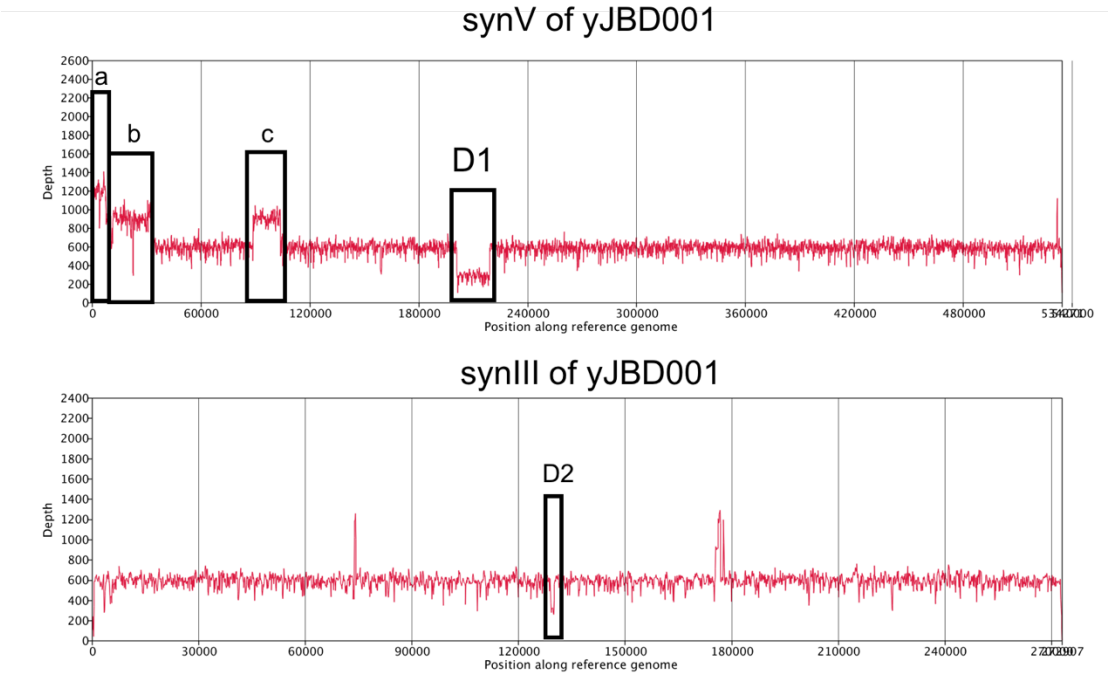
**Supplementary Figure 9. Long-Read sequencing analysis of the synV of the yJBH001.** Long-Read sequencing the synV rearrangement of the haploid yJBH001 revealed two deletions of synthetic fragments: the YEL014C-YEL013W and the YER042W. The Ref represents the chromosome sequence of synV with carotenoid pathway integration. The uniting 73 represents the assembled sequence data of the yJBH001. The “a” represents the deletion of YEL014C-YEL013W, the “b” represents the deletion of YEL042W.




**Supplementary Figure 10. Transcript profiling of ancestor (yJBH000) and scrambled yeast (yJBH012) using a volcano plot.** All the strains were grown in YPD media supplemented with 40 g/L glucose at 30 °C until late-exponential phase. Three biological replicates were performed per strain. The dashed line identifies the Family Wise Error Rate (FWER) threshold at 5% (threshold = 7.02E-6). The genes significantly (Log2FoldChange > 1-fold) differentially expressed were analyzed further to identify potential mechanisms for increased carotenoids production. The YEL013W and YEL014C were deleted in the post-SCRaMbLE haploid yJBH012. Triplicate samples were used for transcriptional analysis.

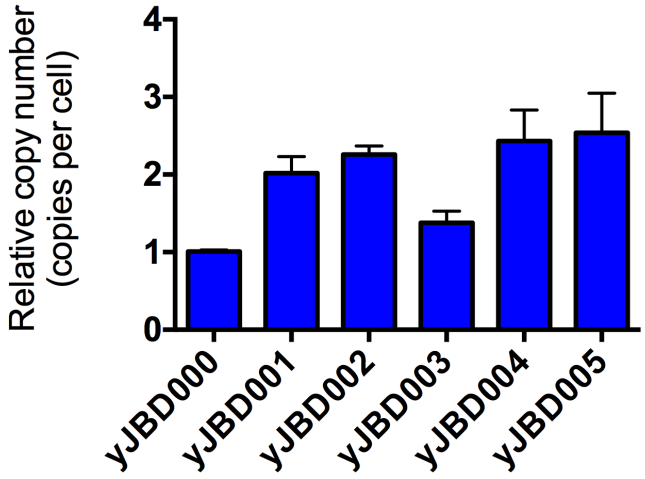



**Supplementary Figure 11. Large deletion of nonessential genes.** (**a**) Sequence analysis of yJBH010. Sequence data were aligned to synV. (**b**) Two larger deletion of synV were observed in yJBH010. Deletion from YEL065W to YEL062W was a 15908 bp fragments containing the carotene pathway. Deletion from YER182W to YEL188W was a 16612 bp fragments at the end of right arm of synV.

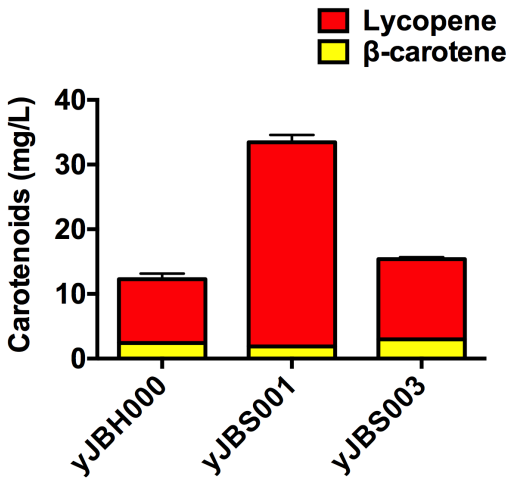



| Numbers | Structure Variety | Copy Variety | Range | Size (bp) |
|---|---|---|---|---|
| a | Duplication | +2 | YEL072W-YEL071W | 6970 |
| b | Duplication | +1 | YEL070W-YEL060C | 24820 |
| c | Duplication | +1 | YEL027W-YEL022W | 16700 |
| D1 | Deletion | -1 | YER033C-YER042W | 17611 |
| D2 | Deletion | -1 | YCR018C | 1315 |

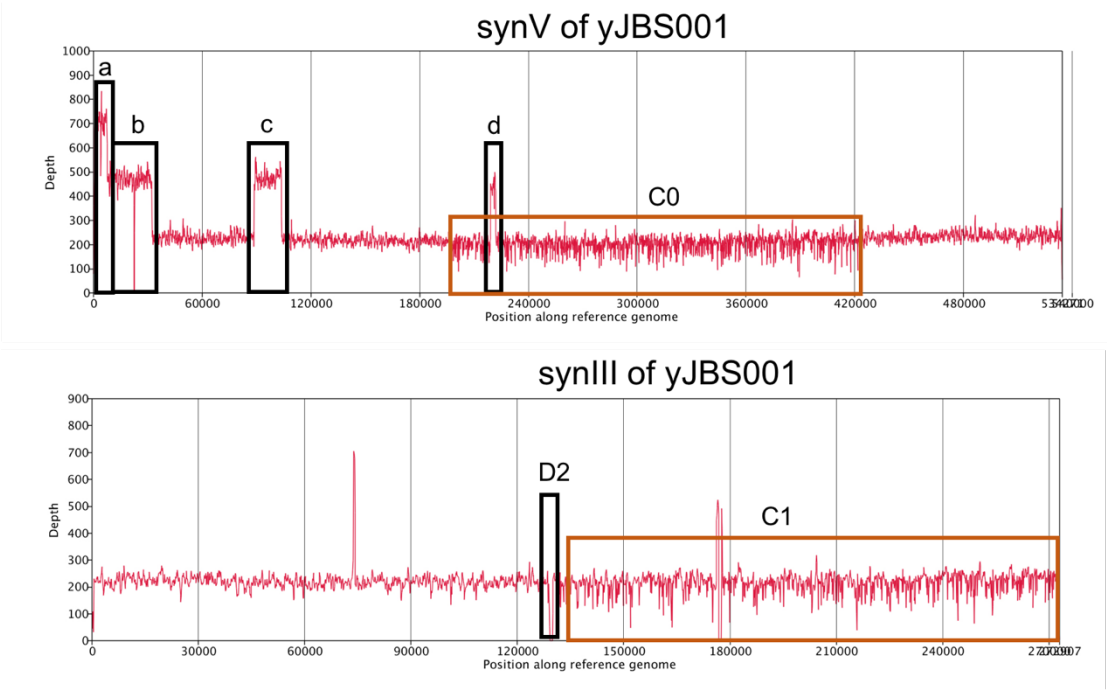
**Supplementary Figure 12. Deep sequencing analysis of the synV of the yJBD001.** Deep sequencing coverage of yJBD001 strain revealed three duplications (YEL072W-YEL071W, YEL070W-YEL060C and YEL027W-YEL022W) and two deletions (YER033C-YER042W and YCR018C).




**Supplementary Figure 13. Relative copy numbers assay of the carotenoids pathway in diploids.** The yJBD000 were used as control. Copy numbers of carotenoids pathway of yJBD001, yJBD002, yJBD003, yJBD004 and yJBD005 were verified by qPCR. The *ALG9* gene and the *CrtE* gene were chosen as the reference gene and target genes, respectively. Error bars represent s.d. from three independent experiments.

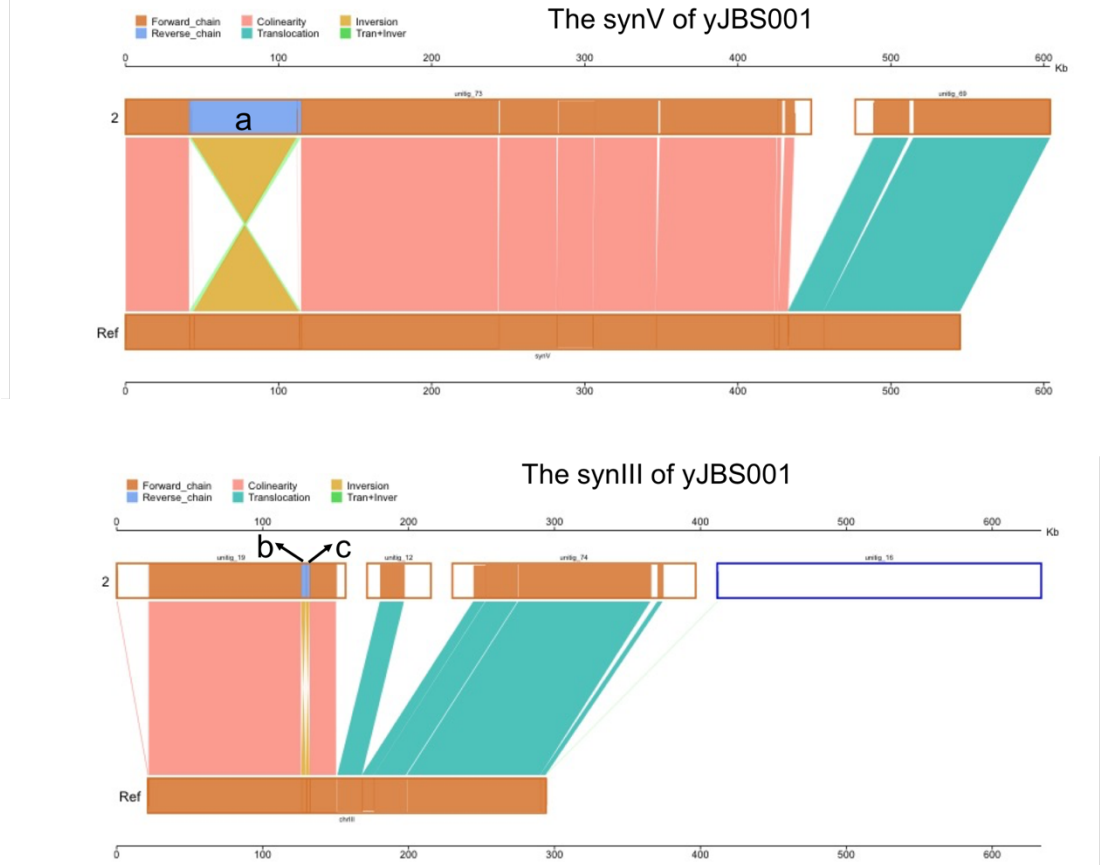



**Supplementary Figure 14. HPLC analysis of extracted carotenoids from cultures of the two spores.** The yJBS001 is a darker color spore and yJBS003 is a normal color spore compared with the yJBH000. Both of yJBS001 and yJBS003 were spores of the yJBD001. the yJBH000, yJBS001 and yJBS003 were 12.38 mg/L, 33.46 mg/L and 15.38 mg/L, respectively. Error bars represent s.d. from three independent experiments.



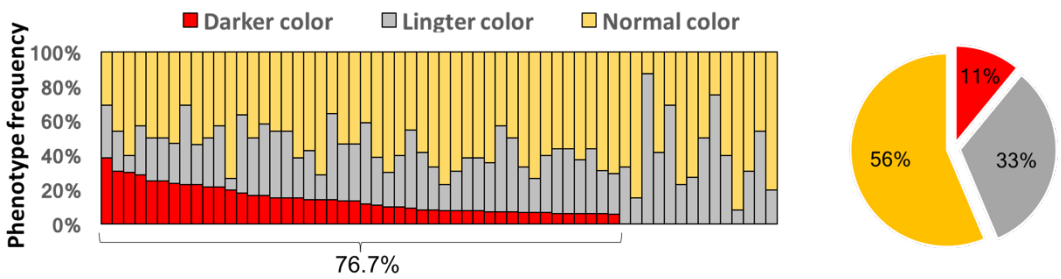

| Numbers | Structure Variety | Copy Variety | Range | Size (bp) |
|---|---|---|---|---|
| a | Duplication | +2 | YEL072W-YEL071W | 6970 |
| b | Duplication | +1 | YEL070W-YEL060C | 24820 |
| c | Duplication | +1 | YEL027W-YEL022W | 16700 |
| d | Duplication | +1 | YER043C-YER044C | 3064 |
| C0 | Crossing-over | 0 | YER032W-YER139C | 225048 |
| C1 | Crossing-over | 0 | YCR018C-YCR098C | 168382 |
| D2 | Deletion | -1 | YCR018C | 1315 |

**Supplementary Figure 15. Deep sequencing analysis of the synV and synIII of the yJBS001.** Deep sequencing coverage of synV revealed four duplications of synthetic fragments (YEL072W-YEL071W, YEL070W-YEL060C, YEL027W-YEL022W and the YER043C-YER044W) and a larger crossing-over fragment between synV and wildtype V chromosome (YER032W-YER139C). Deep sequencing coverage of synIII strain revealed a larger crossing-over fragment between synIII and wildtype III chromosome (YCR018C-YCR098C) and. Reads mapping of the right arm of the yJBS001 to wild-type chromosome III was rough while reads mapping of the right arm of the yJBS001 to synIII was smooth, which was caused by the PCR tag in the synIII.

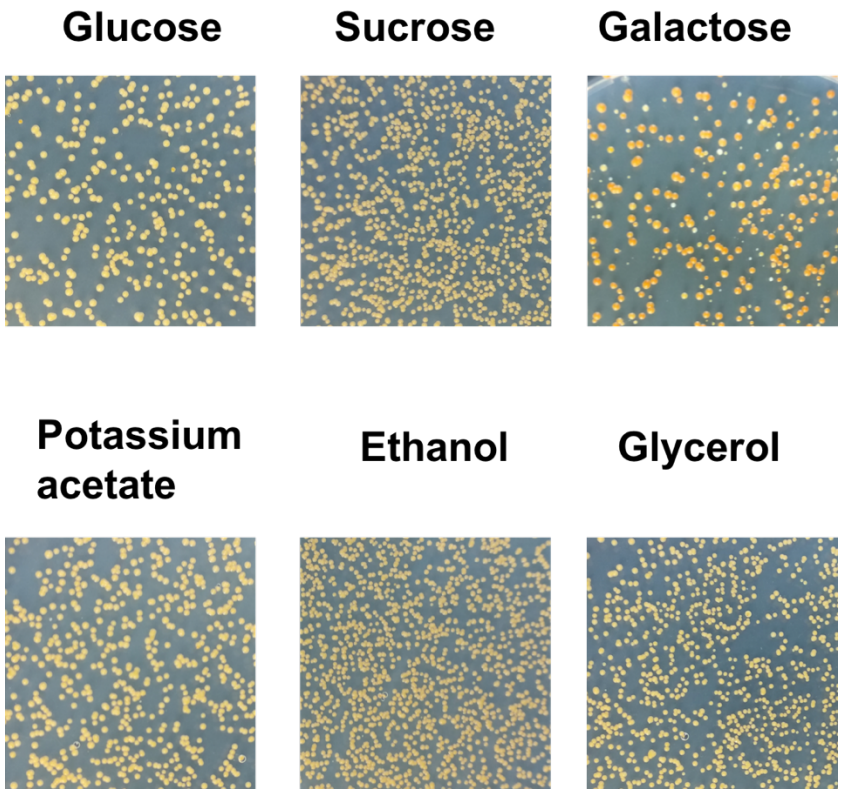



| Numbers | Structure Variety | Copy Variety | Range | Size bp |
|---|---|---|---|---|
| a | Inversion | 0 | YEL059W-YEL022W | 73201 |
| b | Inversion | 0 | YCR007C | 3284 |
| c | Inversion | 0 | YCR008W | 2529 |

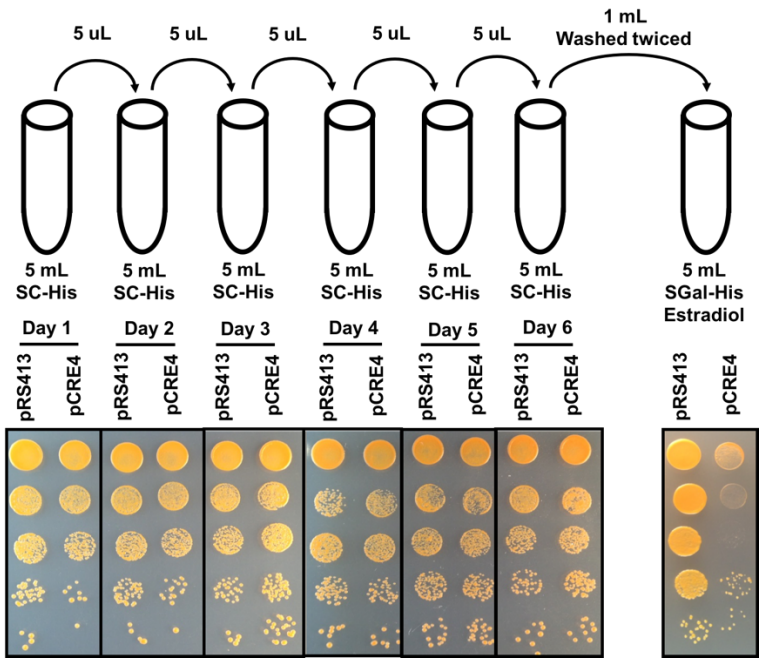
**Supplementary Figure 16. Long-Read sequencing analysis of the synV and the synIII of the yJBH001.** Long-Read sequencing of the yJBS001 revealed one inversion on the synV (YEL059W-YEL022W) and two inversions on the synIII (YCR007C and YCR008W)



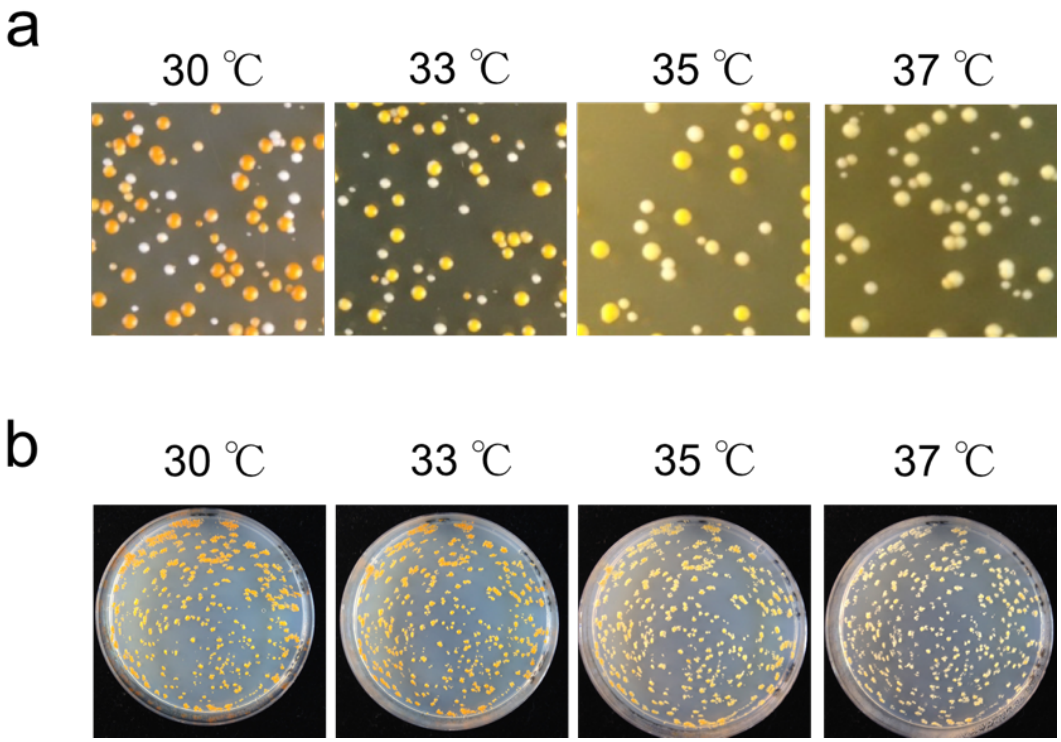

**Supplementary Figure 17. Spores phenotype frequency were analyzed from counting 60 sporulation plates.** Red represents darker color spores. Grey represents white color or lighter spores. Orange represents normal orange color spores. Darker color spores could be screened from 46 plates (76.7%) of the total 60 plates, and the darker color phenotype ranged from 0% to 38.5% in single plate. In sum 86 red spores (11%), 256 white spores (33%) and 442 orange spores (56%) were observed in the total 784 spores on the 60 plates, which is in accord with the law of linkage and crossing-over.



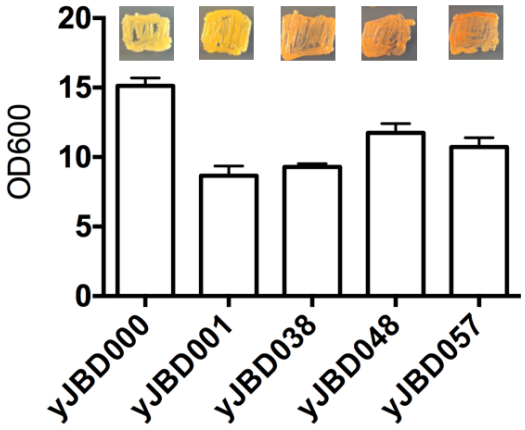

**Supplementary Figure 18. Assay the leakiness of the GAL promotor in medias with different carbon source.** The yJBD000 strains containing the pCRE4 were cultured for 24 hours in S-His medium containing 2% of glucose, sucrose, galactose, potassium acetate, ethanol and glycerol, respectively. white colonies appeared on the galactose medium plate.



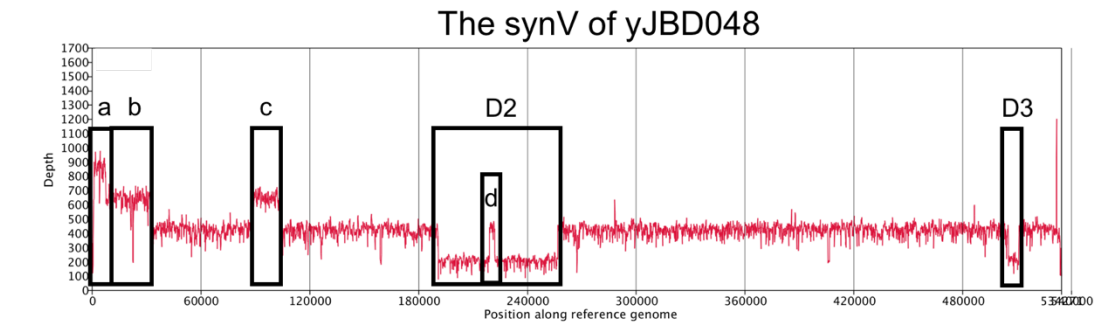

**Supplementary Figure 19. Stability analysis of pCRE4 was carried out in synV haploid strains.** One fresh single colony was picked up from SC-His and inoculated in 5 mL of SC-His medium at 30℃ for 24 hours, and then 5 μL of overnight culture was transferred to 5 mL of fresh SC-His medium. This experiment was continued for 5 days to get ~48 generations. Then 1 mL cells were washed twice by ddH2O and re-inoculated to an OD600 of 1.0 in 2% galactose SGal-His medium contained 1μM Estradiol (Sigma-Aldrich). Strains were incubated at 30˚C for 8 h to turn CRE activity on in cells and implement the SCRaMbLE. Ten-fold serial dilutions were carried out in water, and the dilutions corresponding to $10^{-1}$ to $10^{-5}$ spotted on the appropriate agar plates.

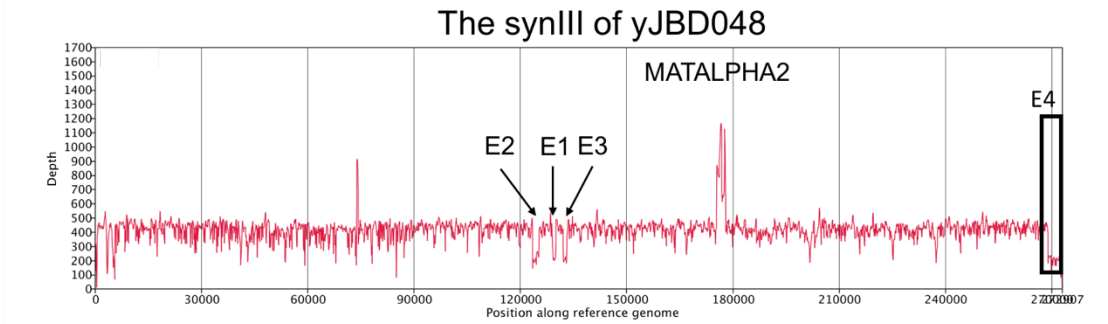



**Supplementary Figure 20. High temperature assist screening.** The yJBD001 were induced to SCRaMbLE. (a) The SCRaMbLEd yeast were plated on SC-His glucose agar and incubated at 30℃, 33℃, 35℃ and 37℃ for 3 days, respectively. (b) yJBD001 colonies were replicated to four plates and incubated at 30℃, 33℃, 35℃ and 37℃ for 3 days, respectively.



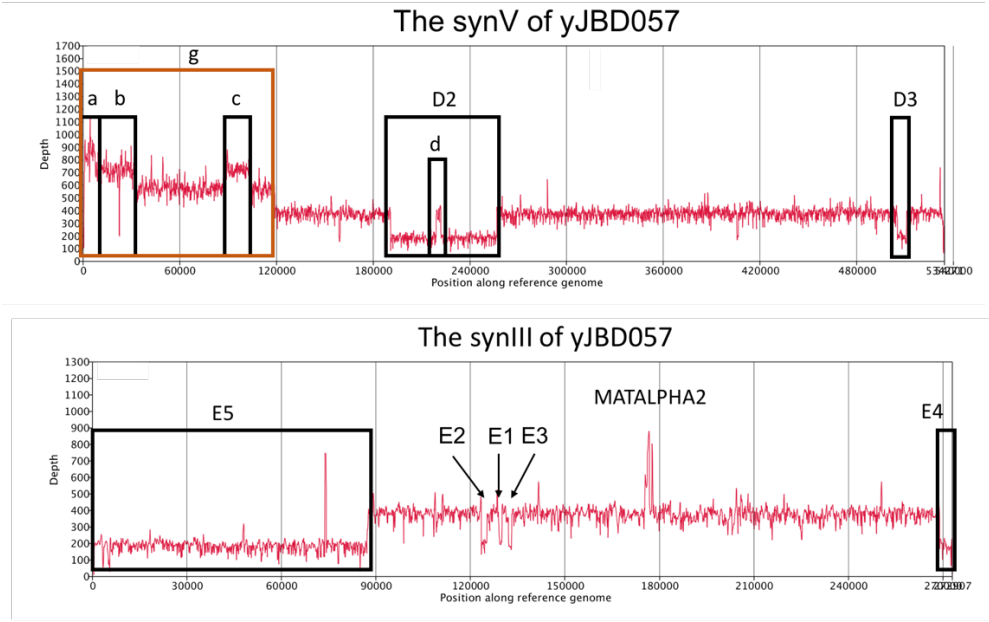

**Supplementary Figure 21. Final culture ODs obtained in shake flask fermentations in YPD medium.** Three independent colonies of each were inoculated into 5 mL YPD medium for 24 h, then re-inoculated to an OD600 of 0.1 in 40 mL YPD with 40 g/L glucose medium in 250 mL flasks which were then incubated for 60 h at 30℃. Error bars represent s.d. from three independent experiments.



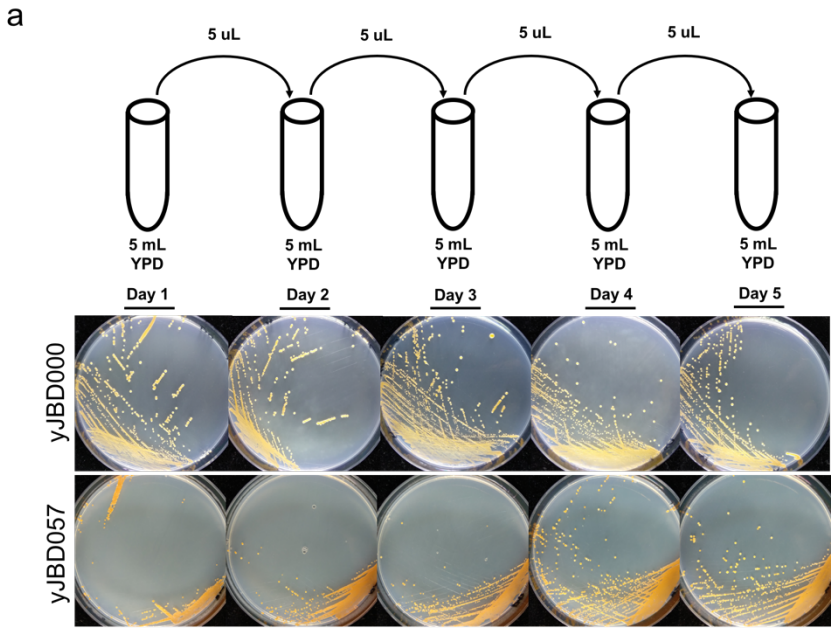

| Numbers | Structure Variety | Copy Variety | Range | Size (bp) |
|---|---|---|---|---|
| a | Duplication | +2 | YEL072W-YEL071W | 6970 |
| b | Duplication | +1 | YEL070W-YEL060C | 24820 |
| c | Duplication | +1 | YEL027W-YEL022W | 16700 |
| d | Translocation | 0 | YER043C-YER044C | 3064 |
| D2 | Deletion | -1 | YER026C-YER059W | 65796 |
| D3 | Deletion | -1 | YER175C-YER176W | 5667 |
| E1 | Deletion | -1 | YCR018C | 1315 |
| E2 | Deletion | -1 | YCR016W | 1757 |
| E3 | Deletion | -1 | YCR020C | 886 |
| E4 | Deletion | -1 | YCR098C | 3682 |

**Supplementary Figure 22. Deep sequencing analysis of the synV and synIII of the yJBD048.** Deep sequencing coverage of synV revealed multiple SCRaMbLE events, including duplications of synthetic fragments (YEL072W-YEL071W, YEL070W-YEL060C, and YEL027W-YEL022W) and deletions of synthetic fragment (YER026C-TER059W and YER175C-YER176W) and a translocation (YER043-YER044C). Deep sequencing coverage of synIII revealed four deletions of synthetic fragments (YCR016W, YCR018C, YCR020C, and YCR098C).




| Numbers | Structure Variety | Copy Variety | Range | Size (bp) |
|---|---|---|---|---|
| a | Duplication | +3 | YEL072W-YEL071W | 6970 |
| b | Duplication | +2 | YEL070W-YEL060C | 24820 |
| c | Duplication | +2 | YEL027W-YEL022W | 16700 |
| d | Translocation | 0 | YER043C-YER044C | 3064 |
| D2 | Deletion | -1 | YER026C-YER059W | 65796 |
| D3 | Deletion | -1 | YER175C-YER176W | 5667 |
| g | Duplication | +1 | YEL072W-YEL012W | 129940 |
| E1 | Deletion | -1 | YCR018C | 1315 |
| E2 | Deletion | -1 | YCR016W | 1757 |
| E3 | Deletion | -1 | YCR020C | 886 |
| E4 | Deletion | -1 | YCR098C | 3682 |
| E5 | Deletion | -1 | YCL073C-YCL009C | 87099 |

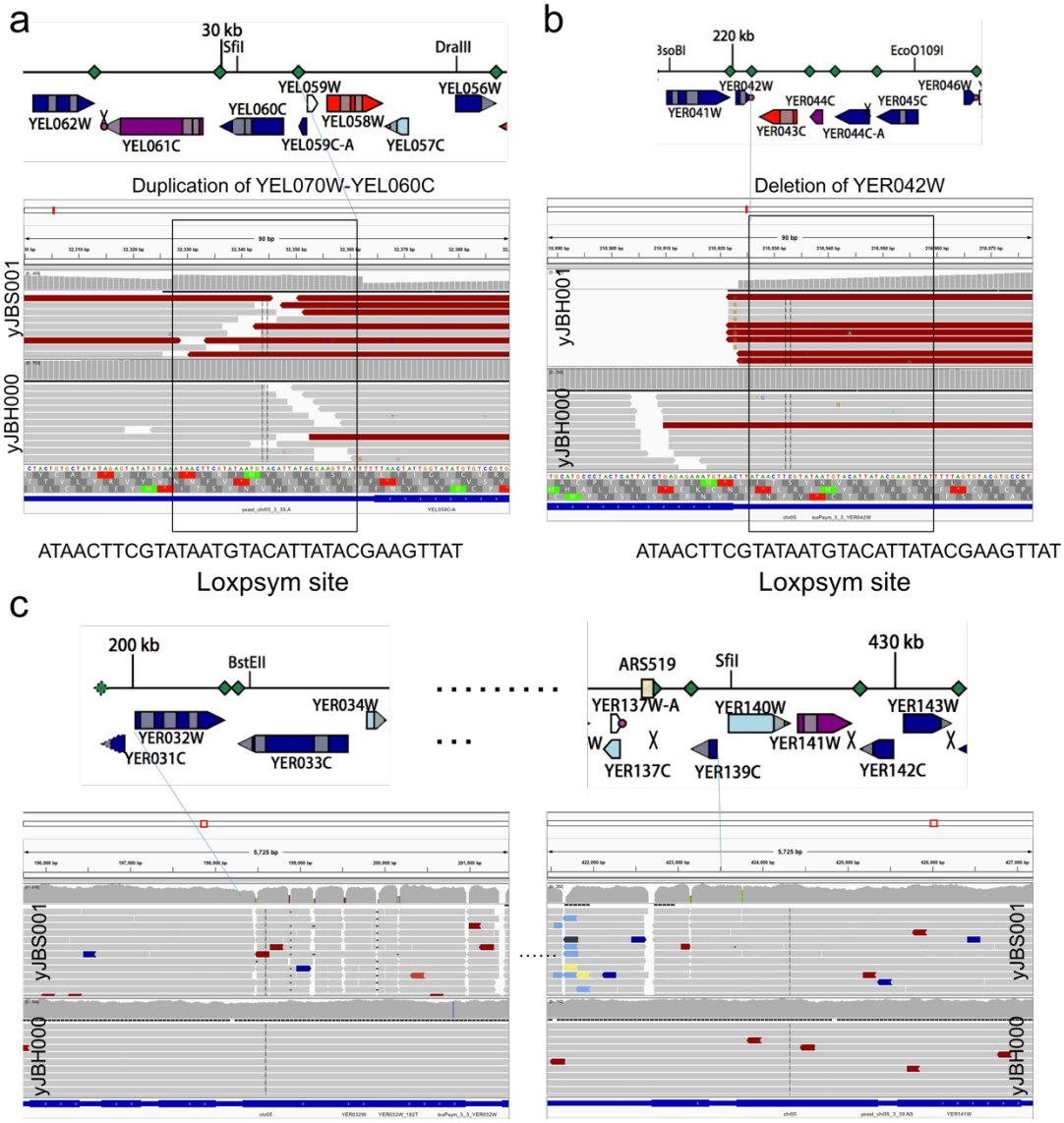
**Supplementary Figure 23. Deep sequencing analysis of the synV of the yJBD057.** Deep sequencing coverage of synV revealed multiple SCRaMbLE events, including a larger duplications of synthetic fragments (YEL072W-YEL071W, YEL070W-YEL060C, YEL059C-A to TEL028W, YEL027W-YEL022W and YEL020C-B to YEL012W) and deletions of synthetic fragment (YER026C-TER059W and YER175C-YER176W) and a translocation (YER043-YER044C). Deep sequencing coverage of synIII strain revealed five deletions of synthetic fragments (YCL073C-YCL009C, YCR016W, YCR018C, YCR020C, and YCR098C).



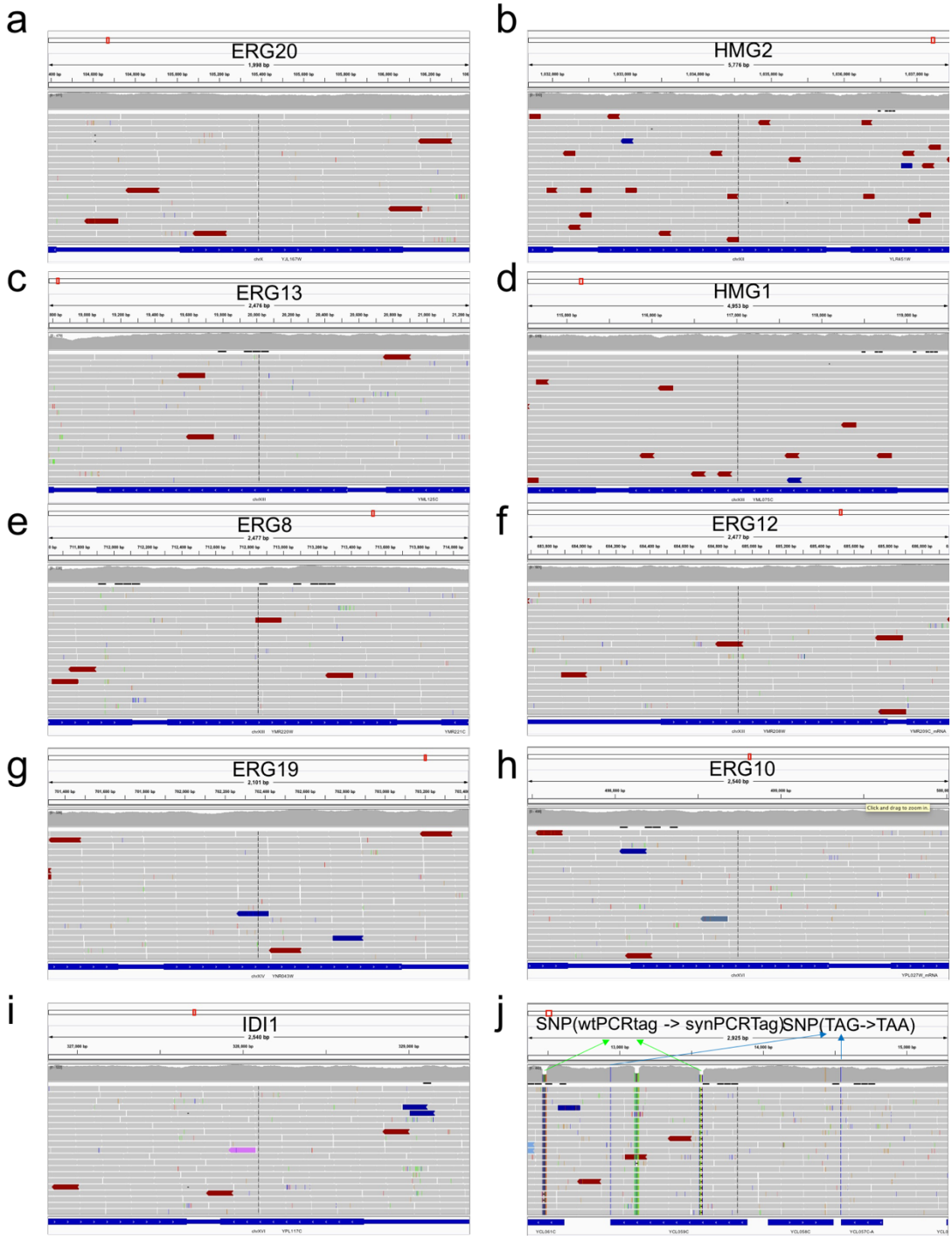

c

| Strains | Number of generation | Number of total colonies | Frequency of white colonies | Deletion observed in PCRtag analysis |
|---|---|---|---|---|
| yJBD000 | 60 | 1784 | 0 | None |
| yJBD057 | 60 | 1904 | 0.0068±0.0031 | YEL072W-YEL060C |

**Supplementary Figure 24. Stability assay of scrambled strains.** (a) The yJBD057 and yJBD000 were serially subcultured for 5 days and streaked on YPD agar each day. Colonies from Day 5 plates were picked for PCRTag analysis. (b) PCRTag analysis of strains after 60 generations of subculture. We assayed for the loss of 96 different segments (**Supplementary Table 8**). No additional deletions were observed in yJBD000 and yJBD057, respectively. Deletions of YEL072W-YEL060C (red line) were observed in white colonies of yJBD057. Blue line indicates the deletion of YER026C-YER059W in yJBD057 as shown in **Supplementary Figure 23**. (c) Yeast cultures after 60 generations were plated on YPD agar ($1:10^5$ dilution) and the number of colonies of each color were counted. 0.68% of colonies observed on the yJBD057 plates were white in color, while no white colonies were observed on the yJBD000 plates.




**Supplementary Figure 25. Deep sequencing analysis of the boundaries of the Recombination events.** (a) The right end of the YEL070W-YEL060C duplication is a loxpsym site. (b) The left end of the YER042W deletion is a loxpsym site. (c) the crossing over (YER032W-YER139C) was not flanked by loxpsym sites.




**Supplementary Figure 26. Deep sequencing analysis of the non-synthetic part of the chromosome.** Deep sequencing data of ERG20, HMG2, ERG13, HMG1, ERG8, ERG12, ERG19, ERG10 and IDI1 in yJBD057 were analyzed (From a to i). No no SNPs or duplications were observed in the 9 genes of the MVA pathway. (j) PCRtag and TAG-TAA switch were observed as SNP in synIII.

**Supplementary Table 1. Significant transcription genes from yJBH001.**

| Gene | Fold Change (log2 value) | P-val | Function |
|---|---|---|---|
| PGM2 | 2.6201 | 9.14E-44 | Glycolysis pathway |
| FBA1 | 1.4215 | 2.42E-53 | |
| TDH1 | 1.6663 | 2.64E-38 | |
| TDH2 | 1.0149 | 3.84E-28 | |
| PGK1 | 1.5461 | 2.68E-56 | |
| ENO1 | 2.6699 | 1.70E-169 | |
| CDC19 | 1.3021 | 3.27E-45 | |
| PDC1 | 1.5558 | 5.35E-63 | |
| ERG10 | 1.3345 | 4.17E-43 | MVA pathway |
| FAS1 | 1.1729 | 3.87E-35 | Fatty acid biosynthesis |
| ACC1 | 1.3621 | 6.11E-45 | |

**Supplementary Table 2. SCRaMbLE colonies counting in this study.**

| Strains used for SCRaMbLE | Lighter & white colonise | Normal colonies | Darker colonies | Total colonies | Darker colonies% |
|---|---|---|---|---|---|
| yJBH000 | 15 | 906 | 2 | 923 | 0.22% |
| yJBH000 | 30 | 765 | 2 | 797 | 0.25% |
| yJBH000 | 39 | 924 | 3 | 966 | 0.31% |
| yJBD000 | 491 | 564 | 8 | 1063 | 0.75% |
| yJBD000 | 821 | 659 | 7 | 1487 | 0.47% |
| yJBD000 | 798 | 521 | 8 | 1327 | 0.6% |
| yJBD001 | 220 | 788 | 6 | 1014 | 0.59% |
| yJBD001 | 208 | 843 | 8 | 1059 | 0.76% |
| yJBD001 | 188 | 860 | 7 | 1055 | 0.66% |
| yJBD038 | 20 | 399 | 3 | 422 | 0.71% |
| yJBD038 | 23 | 569 | 3 | 595 | 0.5% |
| yJBD038 | 28 | 782 | 7 | 817 | 0.86% |
| yJBD048 | 344 | 1032 | 9 | 1385 | 0.65% |
| yJBD048 | 716 | 608 | 7 | 1331 | 0.53% |
| yJBD048 | 370 | 692 | 3 | 1065 | 0.28% |
| yJBD057 | 338 | 673 | 6 | 1017 | 0.59% |
| yJBD057 | 234 | 400 | 5 | 639 | 0.78% |
| yJBD057 | 226 | 346 | 3 | 575 | 0.52% |

**Supplementary Table 3. Chromosome locus of genes involved in MVA pathway**

| Genes of MVA pathway | Chromosome |
|---|---|
| EGR20 | chrX |
| HMG2 | chrXII |
| ERG13, HMG1, ERG12 and ERG8 | chrXIII |
| ERG19 | chrIV |
| ERG10 and IDI1 | chrVI |

**Supplementary Table 4. Yeast strains used in this study.**

| Numbers | *MAT* | Description | Source |
|---|---|---|---|
| **Haploid** | | | |
| synIII | *α* | *his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0* | [1] |
| synV | *a* | *his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* | [2] |
| synX | *a* | *his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* | [3] |
| synX | *α* | *his3Δ1 leu2Δ0 met15Δ0 ura3Δ0* | This study |
| yJBH000 | *a* | Haploid, synV, CAN1:: carotenoids pathway with Leu2 Marker | This study |
| yJBH001 | *a* | SCRaMbLEd strain from the yJBH000 | This study |
| yJBH012 | *a* | SCRaMbLEd strain from the yJBH000 | This study |
| yJBH016 | *a* | SCRaMbLEd strain from the yJBH000 | This study |
| yJBH027 | *a* | SCRaMbLEd strain from the yJBH000 | This study |
| yJBH029 | *a* | SCRaMbLEd strain from the yJBH000 | This study |
| yJBN000 | *a* | yJBH000, his3D1::His3 | This study |
| yJBN006 | *a* | yJBH000, YEL014C-YEL013W:: His3 | This study |
| yJBN007 | *a* | yJBH000, YER042W:: His3 | This study |
| yJBN008 | *a* | yJBN006, YER042W:: KanMX | This study |
| yJBN009 | *a* | yJBH000, YEL013W:: His3 | This study |
| yJBN010 | *a* | yJBH000, YEL014C:: His3 | This study |
| **Diploid** | | | |
| yJBD000 | *a/α* | Diploid, synIII & synV, wildtype III & wildtype V | This study |
| yJBD001 | *a/α* | SCRaMbLEd strain from the yJBD000 | This study |
| yJBD002 | *a/α* | SCRaMbLEd strain from the yJBD000 | This study |
| yJBD003 | *a/α* | SCRaMbLEd strain from the yJBD000 | This study |
| yJBD004 | *a/α* | SCRaMbLEd strain from the yJBD000 | This study |
| yJBD005 | *a/α* | SCRaMbLEd strain from the yJBD000 | This study |

| | | | |
|---|---|---|---|
| yJBN031 | *a/α* | Diploid, synIII & synV, wildtype III & wildtype V, 2 copies carotenoids pathway | This study |
| yJBD038 | *a/α* | SCRaMbLEd strain from the yJBD001 | This study |
| yJBD048 | *a/α* | SCRaMbLEd strain from the yJBD038 | This study |
| yJBD057 | *a/α* | SCRaMbLEd strain from the yJBD048 | This study |
| yJBD069 | *a/α* | SCRaMbLEd strain from the yJBD057 | This study |
| yJBD200 | *a/α* | Diploid, mating synX with yJBS001 (synIII+synV+synX) | This study |
| yJBD201 | *a/α* | SCRaMbLEd strain from the yJBD200 | This study |
| yJBD202 | *a/α* | SCRaMbLEd strain from the yJBD200 | This study |
| yJBD203 | *a/α* | SCRaMbLEd strain from the yJBD200 | This study |
| yJBD204 | *a/α* | SCRaMbLEd strain from the yJBD200 | This study |
| yJBD205 | *a/α* | SCRaMbLEd strain from the yJBD200 | This study |
| **Spores** | | | |
| yJBS001 | *a* | Spore were dissected from the yJBD001 | This study |
| yJBS002 | *a* | Spore were dissected from the yJBD001 | This study |
| yJBS003 | *a* | Spore were dissected from the yJBD001 | This study |

**Supplementary Table 5. Plasmids used in this study.**

| Name | Description | Source |
|---|---|---|
| pRS413 | CEN/ARS with *His3* marker | [4] |
| pRS416 | CEN/ARS with *Ura3* marker | [4] |
| pCRE1 | pRS413, pSCW11-Cre-EBD-tCYC1 | pLM006[1] |
| pCRE2 | pRS413, pZEO1-Cre-EBD-tCYC1 | This study |
| pCRE3 | pRS413, pGAL1-Cre-tCYC1 | pSH62[5] |
| pCRE4 | pRS413, pGal1-Cre-EBD-tCYC1 | pSH62-EBD[5] |
| pCRE5 | pRS413, pSCW11-Cre-EBD-GFP-tCYC1 | This study |
| pCRE6 | pRS413, pGAL1-Cre-EBD-GFP-tCYC1 | This study |
| pCaro | pRS416, pTEF1-crtE-tPDX1-pTDH3-crtI-tMPE1-pFBA1-crtYB-tTDH2 | This study |
| pCAN-A | pUC19, CAN1L(left overlap)-pTEF1 | This study |
| pCAN-B | pUC19, tTDH2-Leu2-CAN1R(right overlap) | This study |

**Supplementary Table 6. Primers used in this study.**

| Numbers | 5'-3' Primer sequence | Comments |
|---|---|---|
| BJ001 | ATAGGGCGAATTGGGTACCGGGCCCCCCCTCGAGGTCGACACGGATTAGAAGCCGCCGA | pCRE4 GAL1p F |
| BJ002 | GGTGTACGGTCAGTAAATTGGACATTATAGTTTTTTCTCCTTGACGTTA | pCRE4 GAL1p F |
| BJ003 | TAACGTCAAGGAGAAAAAACTATAATGTCCAATTTACTGACCGTACACC | pCRE4 Cre-EBD-Cyct F |
| BJ004 | CCCTCACTAAAGGGAACAAAAGCTGGAGCTCCACCGCGGTGGCGGCCGCTCTAG | pCRE4 Cre-EBD-Cyct R |
| BJ005 | CTCACTATAGGGCGAATTGGGTACC | Promoter-Cre-EBD F |
| BJ006 | CATACCTCCTCCGCTTCCACCTCCTCCAGCGCTGACTGTGGCAGGGAAACCCTCT | Promoter-Cre-EBD R |
| BJ007 | GCTGGAGGAGGTGGAAGCGGAGGAGGTATGCGTAAAGGAGAAGAACTTTTCACTG | GFP F |
| BJ008 | ATATTGAGTCAATATCAGGCATTCTACTCATTATTTGTATAGTTCATCCATGCCA | GFP R |
| BJ009 | TGAGTAGAATGCCTGATATTGACTC | CYC1 terminator F |
| BJ010 | CCCTCACTAAAGGGAACAAAAGCTG | CYC1 terminator F |
| Carotenoid | | |
| BJ011 | CCTCGAGGTCGACGGTATCGATAAGCTTGATATCGAATTCACAATGCATACTTTGTACG | TEF1p F |
| BJ012 | ACTCGAGTGGAATTGCTGTGAGGATGTTCGCGTAATCCATTTTGTAATTAAAACTTAGA | TEF1p R |
| BJ013 | ATGGATTACGCGAACATCCTC | CrtE F |
| BJ014 | TCACAGAGGGATATCGGCAAG | CrtE R |
| BJ015 | GGAAGCGATCCTGAAAAAGCTTGCCGATATCCCTCTGTGAATAAAAAACACGCTTTTTC | TDH3p F |
| BJ016 | TGATAGCTGTGGGTTTATCCTGATCTTGTTCTTTTCCCATTTTGTTTGTTTATGTGTGT | TDH3p R |
| BJ017 | ATGGGAAAAGAACAAGATC | CrtI F |
| BJ018 | TTATTCAGAAAGCAAGAACAC | CrtI R |
| BJ019 | GTGATCGCTCGATCCGTTGGTGTTCTTGCTTTCTGAATAACAATACTGACAGTACTAAA | FBA1p F |
| BJ020 | TATAGATCAGATGGATCTGGTAATATGCGAGAGCCGTCATTTTGAATATGTATTACTTG | FBA1p R |
| BJ021 | ATGACGGCTCTCGCATATTAC | CrtYB F |
| BJ022 | TTACTGCCCTTCCCATCCGC | CrtYB R |
| BJ023 | AGTCTTGAGTGTGGTCATGAGCGGATGGGAAGGGCAGTAAATTTAACTCCTTAAGTTAC | TDH2t F |

| | | |
|---|---|---|
| BJ024 | CCGCTCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCTGATCACGGCTAAAACGGT | TDH2t R |
| BJ025 | CAGCTATGACCATGATTACGCCAAGCTTGCATAAATCTGATGTGCGAGATTGAG | CAN1-A F |
| BJ026 | GAACGTACAAAGTATGCATTGTGAATTCAGCTGCAAACCCCAGAAAATCCGTTC | CAN1-A R |
| BJ027 | GAACGGATTTTCTGGGGTTTGCAGCTGAATTCACAATGCATACTTTGTACGTTC | TEF1 F |
| BJ028 | GTTGTAAAACGACGGCCAGTGAATTCGAGCTCTTTGTAATTAAAACTTAGATTAG | TEF1 R |
| BJ029 | AAACAGCTATGACCATGATTACGCCAAGCTTATTTAACTCCTTAAGTTACTTTAATG | TDH2t F |
| BJ030 | TGATCACGGCTAAAACGGTCGAATG | TDH2t R |
| BJ031 | CATTCGACCGTTTTAGCCGTGATCAGAATTCTGCATGCCTGCAG | Leu2 F |
| BJ032 | CCAAGTCATTCAATTTTGGACGTACGCTCGGTACCCGGGGATCCAATACG | Leu2 R |
| BJ033 | CGTATTGGATCCCCGGGTACCGAGCGTACGTCCAAAATTGAATGACTTGG | CAN-B F |
| BJ034 | TTGTAAAACGACGGCCAGTGAATTCGAGCTCCACAAACACACCACAGACGTGGGTC | CAN-B R |
| BJ035-1 | ACTGTGATCTTTTCGTCACTGACGGGTCCCTGCTATTAGATTTGTAAACCTGTGCGGTATTTCACACCGC | Delete YEL014C-His F |
| BJ035-2 | CAGAAAGCAAAGCAGACTCACACAAAAATTTGATCACAATGACAGCACTAGCAGATTGTACTGAGAGTGCACC | Delete YEL014C-His R |
| BJ036-1 | GCAAACTATAAGGGTGTTCTTTCTTCTGTACTATATATACATTTGCAACTTGTGCGGTATTTCACACCGC | Delete YEL013W-His R |
| BJ036-2 | AGAATAGTGTTGATATATGATAAAATTATTGTGGAAATCAATAATTAAGAGCAGATTGTACTGAGAGTGCACC | Delete YEL013W-His R |
| BJ037 | ACCGGTTTGTAGCCTGTGACAGTGATAGCAGTAGCACTATTGAATGAGTTTGTGCGGTATTTCACACCGC | Delete YER042W-His F |
| BJ038 | TCATTCATGCACTTGACTTTTTTTCATAAATAAGGGCACGTACACTAAAAGCAGATTGTACTGAGAGTGCACC | Delete YER042W-His R |
| BJ039 | ACCGGTTTGTAGCCTGTGACAGTGATAGCAGTAGCACTATTGAATGAGTTGACATGGAGGCCCAGAATA | Delete YER042W-G418 F |
| BJ040 | TCATTCATGCACTTGACTTTTTTTCATAAATAAGGGCACGTACACTAAAAAGTATAGCGACCAGCATTC | Delete YER042W-G418 R |
| BJ041 | AATGATAAGGATCAGGTACTAGC | Test YEL014C-YEL013W F |
| BJ042 | CGTAATTGCAATGTGGCAGC | Test YEL014C-YEL013W R |
| BJ043 | GATTCTATGCACGAGATGTTTC | Test YER042W-His F |
| BJ044 | GCCACTGATGTCATGTTGGC | Test YER042W-His R |
| BJ045 | GGTCTCAAAAATGAGCAGTAGGTGTCTCGGG | YER033C3 WT forward |

| | | |
|---|---|---|
| BJ046 | GGTCTCTCAGTGACGCTAGGCCAGTACCTCC | YER033C3 WT reversed |
| BJ047 | GGTCTCAAAAAGTGGTCAGGCCTTGTCAATT | YER033C3 synthetic forward |
| BJ048 | GGTCTCTCAGTCACAGGGCGGGAAATAAGCT | YER033C3 synthetic reversed |
| BJ049 | GCATTCTGCAGTCGCCAATGCAGAGTTG | YER034W1 WT forward |
| BJ050 | ATCGGTCTCTAGTTCTTCCGGTAGATCG | YER034W1 WT reversed |
| BJ051 | TCACAGCGCTGTTGCTAACGCTGAGTTA | YER034W1 synthetic forward |
| BJ052 | GTCAGTCTCCAATTCTTCTGGCAAGTCA | YER034W1 synthetic reversed |
| BJ053 | GGTCTCAAAAACGGACTATGCCCGAGTGGT | YER036C1 WT forward |
| BJ054 | GGTCTCTCAGTGCTCGGCGCGTAGCTTCA | YER036C1 WT reversed |
| BJ055 | GGTCTCAAAAAGTATTTCTGTGAGATGATTATTTTC | YER036C1 synthetic forward |
| BJ056 | GGTCTCTCAGTAGGGAGAAAAGGAACTTATAACGG | YER036C1 synthetic reversed |
| BJ057 | GGTCTCAAAAAAAGTGAGAATGTATCCGGCGAG | YER038C1 WT forward |
| BJ058 | GGTCTCTCAGTAAGTATGGCACCAAACCCTTGG | YER038C1 WT reversed |
| BJ059 | GGTCTCAAAAAAGTAGAAGTTAAAGAAGAACAGGAGG | YER038C1 synthetic forward |
| BJ060 | GGTCTCTCAGTAGCCCGTGAATGAAAGAGGA | YER038C1 synthetic reversed |
| BJ061 | AAGTGCAGGAAATAGTGTCGCATCCTCA | YER040W2 WT forward |
| BJ062 | AGGTCTTGAGACACTCGGTGAATCTACA | YER040W2 WT reversed |
| BJ063 | TTCAGCTGGTAACTCAGTTGCTAGTAGC | YER040W2 synthetic forward |
| BJ064 | TGGACGGCTAACTGATGGGCTGTCAACT | YER040W2 synthetic reversed |
| BJ065 | GGTCTCAAAAATCTCTAGCCTCATCAGCTCCG | YER041W2 WT forward |
| BJ066 | GGTCTCTCAGTAATGTAGATTGGGTGGCTGCT | YER041W2 WT reversed |
| BJ067 | GGTCTCAAAAAGAAAAGCTGCCAACGTGACC | YER041W2 synthetic forward |
| BJ068 | GGTCTCTCAGTGTACGACAACTTACTCTTAATCGG | YER041W2 synthetic reversed |
| BJ069 | GGTCTCAAAAAACTACGGCGAATTCGCTGAC | YER042W1 WT forward |
| BJ070 | GGTCTCTCAGTTCATCATCTTCACGATCTTCAGCATC | YER042W1 WT reversed |
| BJ071 | TTCTAGGTTGGTGCATTGAG | YER042W1 synthetic forward |
| BJ072 | GTGGGCAAATAAACCTGATCTGTACTGG | YER042W1 synthetic reversed |
| BJ073 | GGACAGATAGCGTAGAGA | ALG9 F |
| BJ074 | TGTGGAATTATTGCCTTCT | ALG9 R |
| BJ075 | GAGATTATCAGCAATATCAATG | YEL071W F |
| BJ076 | GTAACGACACCGATAGTA | YEL071W R |
| BJ077 | ATATCGTGCTCCTTGAAC | crtE F |
| BJ078 | TTGACATCCAACCAATAGT | crtE R |
| BJ079 | GACTATTGAGCCTGTTAATGTG | YEL022W F |
| BJ080 | TCTTCTTGACTTCCTTCTTCTT | YEL022W R |
| BJ081 | TACTCTTCTTCAGTTTCA | YER043C F |
| BJ082 | CCTCTTGTAACATCTATTC | YER043C R |
| BJ083 | TCAATATGCTCAGGAATAGGA | YER036C F |
| BJ084 | GCCGTAGATATGGTCTTCT | YER036C R |

**Supplementary Table 7. Deletions/duplications observed in this study**

| Strains | Structure variety | Copy variety | Total copy numbers | Range | Size (bp) |
|---|---|---|---|---|---|
| yJBH001 | Deletion | -1 | 0 | YEL014C-YEL013W | 2345 |
| | Deletion | -1 | 0 | YER042W | 819 |
| yJBH012 | Deletion | -1 | 0 | YEL014C-YEL013W | 2345 |
| yJBH026 | Deletion | -1 | 0 | YEL016C-YEL013W | 5933 |
| yJBH027 | Deletion | -1 | 0 | YEL016C-YEL013W | 5933 |
| | Deletion | -1 | 0 | YER180C-A | 819 |
| yJBH037 | Deletion | -1 | 0 | YEL065W-YEL062W | 18304 |
| | Deletion | -1 | 0 | YER182W-YER188W | 16612 |
| yJBS001 | Duplication | 2 | 3 | YEL072W-YEL071W | 6970 |
| | Duplication | 1 | 2 | YEL070W-YEL060C | 24820 |
| | Duplication | 1 | 2 | YEL027W-YEL022W | 16700 |
| | Duplication | 1 | 2 | YER043C-YER044C | 3064 |
| | Deletion | -1 | 0 | YCR018C | 1315 |
| | crossing-over | 0 | 1 | YER032W-YER139C | 225048 |
| | crossing-over | 0 | 1 | YCR019W-YCR098C | 168382 |
| yJBD001 | Duplication | 1 | 2 | YEL070W-YEL060C | 24820 |
| | Duplication | 1 | 2 | YEL027W-YEL022W | 16700 |
| | Deletion | -1 | 0 | YER033C-YER042W | 17611 |
| | Deletion | -1 | 0 | YCR018C | 1315 |
| yJBD048 | Duplication | 2 | 3 | YEL072W-YEL071W | 6970 |
| | Duplication | 1 | 2 | YEL070W-YEL060C | 24820 |
| | Duplication | 1 | 2 | YEL027W-YEL022W | 16700 |
| | Translocation | 0 | 1 | YER043C-YER044C | 3064 |
| | Deletion | -1 | 0 | YER026C-YER059W | 65796 |
| | Deletion | -1 | 0 | YER175C-YER176W | 5667 |
| yJBD057 | Duplication | 3 | 4 | YEL072W-YEL071W | 6970 |
| | Duplication | 2 | 3 | YEL070W-YEL060C | 24820 |
| | Duplication | 2 | 3 | YEL027W-YEL022W | 16700 |
| | Translocation | 0 | 1 | YER043C-YER044C | 3064 |
| | Deletion | -1 | 0 | YER026C-YER059W | 65796 |
| | Deletion | -1 | 0 | YER175C-YER176W | 5667 |
| | Duplication | 1 | 2 | YEL059C-A-YEL028W | 56536 |
| | Duplication | 1 | 2 | YEL020C-B- YEL012W | 15325 |

## Supplementary Table 8. Synthetic PCRTags used in this study

| Number | Amplicon | Forward Syn | Reverse Syn |
|---|---|---|---|
| 1 | YEL071W_amp1 | CAGCGGTAGTAACAAACGTCATGATGAC | ATTCAAACGCTCGGTAACGGCAGCGCTA |
| 2 | YEL070W_amp1 | TAGTAACCCTGCTATCCAGGATACCGTT | ATGTGGGTCCTTGCCACCTTTGACAGCA |
| 3 | YEL067C_amp1 | GACGGCGCTAACGAAGATAGTGCTACAT | TTGCAGCAGAAGATTCCCACCAGACAAT |
| 4 | YEL065W_amp2 | CATCTTACCATTGGCCTGCATCCCATTG | AACAACGACCCAGCCGATAACTTCTGGA |
| 5 | YEL064C_amp1 | TGAAAAGATGGCACGCAAAACATGTGGG | TGCTTTGGGTTTCATCGTCGACTGGACC |
| 6 | YEL063C_amp1 | ACTCTGGGTAACGCTGTAAGCTAAGCTG | CCGTGTTAACGGTGAGGACACCTTTAGC |
| 7 | YEL061C_amp1 | ACCATCGAAACCGGTGTTTGAGCTACCA | CGAAGTTGCTGGTCCTTTGTTTCAGGAC |
| 8 | YEL060C_amp2 | GCTAGTGCCGCTCAAGGTAGCAGTA | TGGCGTTGCCAAGAACGCTAATGTCGTC |
| 9 | YEL052W_amp1 | CGGCTTGAAGAGTGTTTTCTCAAGAGGT | AGCAACATCGGTAACTTGGAACTCATCG |
| 10 | YEL050C_amp1 | TAACAAAGCAATGTGGCTACTACGGCCA | TAGCCCAGGCTTACGTTGGTATAGAAGT |
| 11 | YEL047C_amp1 | CTTCCATGAGCTTGATCTATCGTTAGGG | CCAATTAGGCGGTCATAGCGTTGCTCGT |
| 12 | YEL044W_amp1 | CGGTTTCCCAAGCCGTTTTAAAAGCGCT | AGCACCACGTAACTTCAAATACTCCTGG |
| 13 | YEL043W_amp2 | TCACGCTAGCAGCCCTCCATTTAATAGT | GTTGGCTGGGCTGCTAGCGCTTTTATGT |
| 14 | YEL042W_amp1 | CAGTGTCGGCGCTGCCAATAGTTTG | ACCCATAATACTGACGCCGTCGCCTTCA |
| 15 | YEL041W_amp1 | CGGTAGTACCGCTTATAGCTTATCAGCT | AACGCTGTATGGTGAAGCGGTGATAACG |
| 16 | YEL040W_amp1 | AAGCACCGCTACTAGCAGTAGTAAGACC | GCCAGCATTGTTGCCTGACATGCTTGAG |
| 17 | YEL038W_amp1 | TCCAGCTCACGACAGCTTAGACTTAAAC | AACTGGAGCGTTGCCTGGTCTACTG |
| 18 | YEL037C_amp1 | GGTCAAACCGATACTGCCAGGTGGA | CGCCCCAGAAGGTAGCCAACCA |
| 19 | YEL030W_amp2 | TGCTCGTATCACTGCTAGCGACATCAGC | AACCAACTCTCTCTCGCCTTGAAAGACC |
| 20 | YEL029C_amp1 | GAATGGAACACGATAGACGATTGGAGTC | AGTCAGATGCATGGGTACCTATTATGCC |
| 21 | YEL022W_amp3 | CCACAGCGAGAAATCAACCAACGGTGCT | AGGATACAACTGTAATCTGTCGCCGCTG |
| 22 | YEL017W_amp1 | CTCAACCGACAATGATAGCAGTACTAGC | GCTGCTGGTAGGCTGACCAGCA |
| 23 | YEL015W_amp2 | AGTCTTGACCGTCGCTAGCCAAAGTGGT | GTCTTGTTGTGGCTGGCTTTGATGGGTA |
| 24 | YEL013W_amp1 | TAGCTTGTTAAGCAGTACTGACCCAGAC | AACTAAGTGTGGTAAACCGCCGGCTCTA |
| 25 | YER010C_amp1 | TCTACCGAAAACAACGGTACCGTTGCTC | CTCAAGTATCGTTGGTACCGCTTATACC |
| 26 | YEL011W_amp2 | CTACGAAGCTCATGTTGGCATCAGCTCA | TAAACCGTCCTCAACATTCTTGCTGGCG |
| 27 | YER016W_amp1 | CAGCAGCTTAGGTATCAATGGCTCACGT | GCCGTTAACCTCACCGTTTGAATTAGCG |
| 28 | YER020W_amp1 | TCAACCTAGCTTAAGCGATGCCAGCTCA | GCTTGGTAAAGCCCATAAGGTGCTGATA |
| 29 | YER026C_amp1 | TGATTTGCTGATCATACCGCAACCGTGA | CGGCAAGCCACACTATGTTCAGAGAGCT |
| 30 | YER027C_amp1 | TGAGCTTGATGAGGCGTCAATGTCGTCG | CAACGAGGCCAGTTTAGCTTATACCTTC |
| 31 | YER028C_amp1 | AGCCAAGCTTGAACCACTGCTGTGAACG | AGTCGCCCAGAACTGTGACGATGTTAAC |
| 32 | YER032W_amp1 | ACGTAGCCCATTGAGATTTACCAGCAGC | CAATGGCTTAAAAGGCTCGATGCTAGGG |
| 33 | YER033C_amp3 | GTTTTTACTACCACCTCTCAATGGGCTC | ACACAGCCAGCAGCCACATTACGCT |
| 34 | YER041W_amp2 | CGGTCCTTCAAGCATCACCAGTCATTCA | ATGCATAATAGCAACGGTGCTAGGCCAA |
| 35 | YER042W_amp1 | CGGTGAAGAGAGCAAGAAAGACTCACCA | GTGGGCAAATAAACCTGATCTGTACTGG |
| 36 | YER045C_amp1 | ACTGTCACCGCTAGGAATGCTTGGG | CCCTTCAGCTGCTATCTATCCTTCATTC |
| 37 | YER047C_amp2 | TGAACTTAAACTGCTCCACTGGACCAAG | TATGTTGTTGTTCGGTCCTCCTGGCACC |
| 38 | YER048C_amp1 | ATCGTGTTTGACCATACCGCCGTCGGTA | CCACCCAGATAAACACCCAGACGATCCT |

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| 39 | YER051W_amp1 | CTCAGGTGTTTACGTTCCAAACGTTGGT | GTTCTCCTCAGCTTTCTCACCGTTAACC |
| 40 | YER053C_amp1 | ACGCTTGCTAGCAACGCTCATACTCTCA | TAAGCAGCAGACCACCATGCCACCATTC |
| 41 | YER054C_amp2 | GCTCTTGCTAGGAGGCATATCAGTTCTA | CAGATCAGGTAACGGCGTTCAAGCTCGT |
| 42 | YER055C_amp1 | GCAGCTAGCCTCAACACTGCCTGAA | TTTCTTACCAGCCGCTGACATCCCTACC |
| 43 | YER056C_amp1 | AAAAGCCAAGCCGGCGACCAAACTAAAG | CGCTTATGAGAAGTGGAGCTGGGTTCCA |
| 44 | YER059W_amp1 | GATCTTGGATGGCGATACCTCAAATAGC | TGGGGTGGTGGTAACTGAGTTACAACGT |
| 45 | YER060C_amp2 | TTTCAGCGTCTTTGGCGCTGAGTTAGGT | AGTGTAATCGGCAGCGTAGGTGGTCCAA |
| 46 | YER060C-A_amp2 | CTTCTTCAGTGTTGTTGCTGGCTTGGCT | GGCAACGGTATACATACCTGGAACGTTG |
| 47 | YER061C_amp1 | ACTACGACCAGGCAACAAAGCGCTAGCA | AACCGCTTGTGCTACCGGCAACAATAGT |
| 48 | YER062C_amp1 | GTCTCTAGTGCCACTGGTAGCAACG | TGACGCCGAACATGTCATTCAAGTTAGC |
| 49 | YER064C_amp2 | GTCAGCGCTGGTTGAGCTTCTGGTA | CGGTTTCGACGCTAGCTTAGCTCCTATT |
| 50 | YER065C_amp1 | TCTGCTAAAATTGTGAACGGCCAAGGCA | TATGAGAGCTAGAGCTTTCGCCCCTTAC |
| 51 | YER066W_amp1 | CCATCGTGCTTTGGTTGGCTTGTTAGGT | GGTGTCGCTTCTAACCAATAAACCTGAG |
| 52 | YER069W_amp1 | CGATACCGCCAGCACTTTGAATAGCAGC | TGGCAAAGCCATGACCCAGAAATCAACG |
| 53 | YER070W_amp3 | GCGTCCAGGCGCTTTCGCTTTGTATTTA | CTTCTCATATCTAGTGTACAAGGCCTCG |
| 54 | YER073W_amp2 | CGGTGGTGCTCGTCACGGTTCA | GATGCCGCTCTGACCAAAACCGCCAAAT |
| 55 | YER075C_amp1 | ACTGTCGCTTTCCAATGACAACATGCTC | TAGTGTCATCCCAGAATGGTTTCAGCAC |
| 56 | YER076C_amp1 | GTCGCATGATGAATTGGTGCTCCAGGTT | CGGCGAAAGCACTTTGTGCCGTGCTAAA |
| 57 | YER081W_amp1 | CGATTTGGATTATGCCACTTCACGTGGC | GTCTTTCATGGCGGCGAATTGAGGAGCT |
| 58 | YER086W_amp1 | TAGCCAAGGCGTTGGCTTAAGCAGTAGA | TCTCTCTTCGGCTAACTTAGCGCATTCG |
| 59 | YER087W_amp1 | TCAATGGCTACCTTTGGGTTTGCGTAGC | GTCAGCCCAAGCTGAGACGAATGGAATC |
| 60 | YER089C_amp1 | ATCAGCGAAGCTTCTAACGCTGGTTCTA | CCCAGATATCTTGGAGCACAGCTTGGAC |
| 61 | YER091C_amp1 | GATAGGAGGACGAACGTAACGACTGCCA | TCCTACCACCACCATCGGCAGTTTTCCA |
| 62 | YER096W_amp1 | CAACCCTTCAGGTAGCGGTAGCAGCAAT | ATAAGCATCGCCCAACAAATACTGAGCG |
| 63 | YER098W_amp1 | TGATCCAAGTATCGCTAAGAGCCCTTCA | AGCTCTGTCTTCGTAGGTGGTGCTACTG |
| 64 | YER099C_amp1 | GACGTCGCCAACCAATAACATTCTGCTG | CGCTAACTTGTTAGAAACCGCTGGCTGC |
| 65 | YER101C_amp1 | GCTATGTGATAAAATGTCGTAGCCGCCA | CGGCGCTGCTGTTTTAAGCGAACACTTT |
| 66 | YER103W_amp1 | CGAAAGAGCTAAACGTACCTTAAGCAGC | GTAGGCGACAGCCTCGTCTGGATTGATA |
| 67 | YER105C_amp1 | TGGAACTGAACCTGATTCACGGCTTGAC | CCCACAAGGCTATGCTAACGTTTTCGCT |
| 68 | YER107C_amp1 | TGACAAGGCATAAGCGAAAACTGAGCCG | TAACCCAAACAGAGCTCCAGGTAGTAAC |
| 69 | YER109C_amp1 | AGCGATTGACAAAGGACTGCTAGCGCTG | AGCCCCACCAACCAAGACCGCT |
| 70 | YER110C_amp1 | ATCGTCAATATGACCGCTCAAGCTGCTA | TTGGAATGCTATCGACGAAAGTACCCGT |
| 71 | YER113C_amp2 | ACCAACGCTGTTAGCCAATGACATCCAG | CCACTGCCCAGGTGCTAGCAAAAATTAT |
| 72 | YER114C_amp2 | ACCACTGGCCAACAAAAATGGTGAACTG | CACCCCAACCGTCAGTTTATCAAAGGCT |
| 73 | YER115C_amp1 | ATCGCATGAGAATCTGGCCAAAGGTGAA | TGCTTGCGATCCTAACAAACAGCAGAAC |
| 74 | YER116C_amp1 | CTTTGAACGGCACAAGGCACAGTGACCA | CATGCACACTGAAGAGCCTGAAGCTTCA |
| 75 | YER118C_amp1 | ACTCAACAAAATAACGCCAGCGCTGGCG | ATTTCCTAGATTCACCTGGTGGGGCATC |
| 76 | YER119C_amp1 | AAAGCTGATGCTGGTACTACCGGTAGCA | CGCCACTGAATCAAGCCCATTAATCAGA |
| 77 | YER122C_amp1 | ACGTGAGGCGGTCAAAATACTTGAACGG | AAGCGATAGCCCATTAGATACTGACAGC |
| 78 | YER129W_amp1 | ATTGGCCGCCTCATCAACCAACTCAAGT | TGGAACATGATCGAAGTCCCAGCTGACG |
| 79 | YER130C_amp1 | AACAACCAAACCGTGGCTGCTGCTACTT | CCAGACTGAAAATAGCAGTAGCCAGAAG |

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| 80 | YER132C_amp1 | TGATGAACGACGGCTTGGAGCCTTAGGA | CAGACGTGCTAGCCATCCATTGCAAAGC |
| 81 | YER141W_amp1 | TAGACCTTTCAGCTTGAGTAGTCCAGTC | ACCAATGGCTCTGCCCCATAAACGG |
| 82 | YER143W_amp1 | CAGCAGCGACAAACCATTGACCCCAACT | AAACAACAAACTAGCGGCGAATTCAGCG |
| 83 | YER144C_amp2 | AGTGCTTGGGGTGTTCAACTTGCTCAAG | CAGCGTTATCAAGCCATTATCAGGTACC |
| 84 | YER151C_amp2 | GCAACTGCTGGTACCAACACGGCTGTTA | CATCGAGCCTTTAGGCAGCATCGCTTTG |
| 85 | YER152C_amp1 | ACTACGTAAGTGAGCGATACAACGCTGA | CTATAGCTTGGAGACTCGTAGACGTTTG |
| 86 | YER161C_amp1 | TGGGCCGTTTGAATGCTTGCTCTTTGAA | AAGAAGCATCGGTGCTTCACACGCTCCT |
| 87 | YER163C_amp1 | GCTGGTCAACAAAACTCTCTTGCCGCTC | AGCTAATCCTGGTCGTGTTGCTACCTTG |
| 88 | YER170W_amp1 | TCGTTACGTCCATGTCCCATCAGGTCGT | GGTTTCACCGCTAACAGTGCCGAAGATA |
| 89 | YER174C_amp1 | GTCGTCACTGCTACCTGATGATTCCTCG | CCCATGTAAGACCATGTCACAGGTTTTG |
| 90 | YER175C_amp1 | CAATTCTGGTCTTCTTCTCAAGCTCTCC | CTGGGGCTACGCTGATCCTATCTTTCCA |
| 91 | YER177W_amp1 | AAATGTCATCGGCGCCAGAAGAGCTAGC | GGTAGCTTTTTCACGGGCGTCACCTGAT |
| 92 | YER178W_amp1 | TGCCAGCCGTAGTAGTGCTATGACC | ATCATAGGCCTTAACTTCGGCTTCGGTA |
| 93 | YER180C_amp1 | TCTTTCAAAGACTGGGTAGGTACCGGCG | TTTGGATTACATCCCAGACAGTCCTAGC |
| 94 | YER182W_amp1 | CGGTGGTTCATTCTTGGGTGGTTGGTAT | AACACCGCCAGGGGTGTTCAAAGCTCTA |
| 95 | YER184C_amp1 | GTGTGAGGCGCTTGAGGCATCCAAGAAT | TGCTAGCTTGCAGAAGGGTTTGGCTAAT |
| 96 | YER188W_amp1 | TCGTAGAAGCGACGCTTTGGGTGTTACC | GTTCCAACACAACATCTGACCAGGTCTG |

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