Figure S1

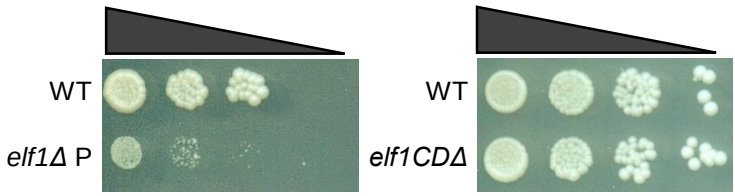


Figure S2

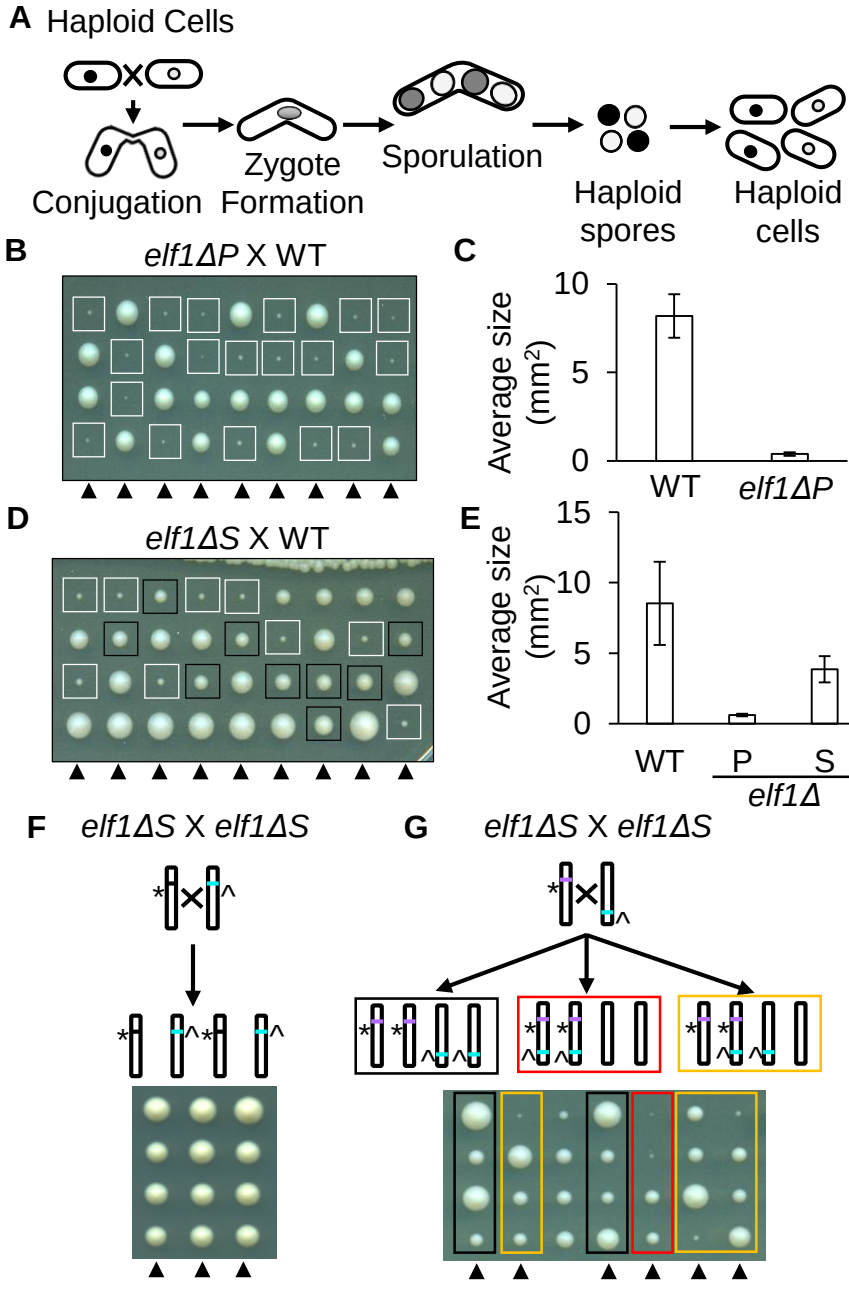

A Haploid Cells
Conjugation
Zygote Formation
Sporulation
Haploid spores
Haploid cells
B
elf1ΔP X WT
C
Average size (mm²)
10
5
0
WT
elf1ΔP
D
elf1ΔS X WT
E
Average size (mm²)
15
10
5
0
WT
P
S
elf1Δ
F
elf1ΔS X elf1ΔS
G
elf1ΔS X elf1ΔS

Figure S3

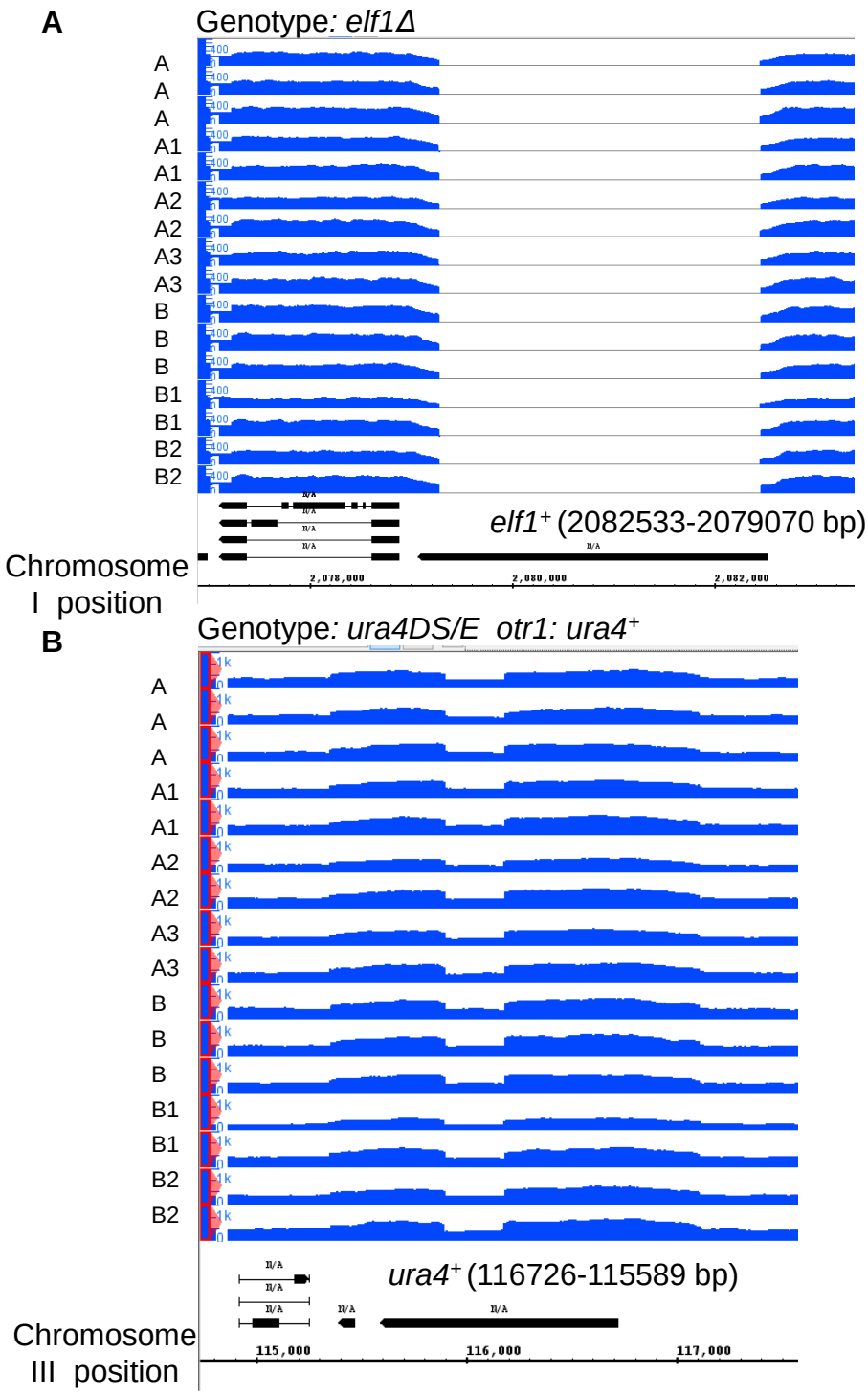
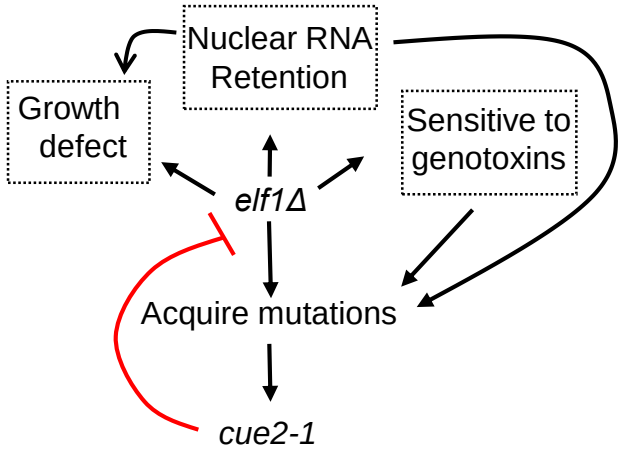

A
Genotype: elf1Δ
A
A
A
A1
A1
A2
A2
A3
A3
B
B
B
B1
B1
B2
B2
elf1+ (2082533-2079070 bp)
Chromosome I position
2,078,000
2,080,000
2,082,000
B
Genotype: ura4DS/E otr1: ura4+
A
A
A
A1
A1
A2
A2
A3
A3
B
B
B
B1
B1
B2
B2
ura4+ (116726-115589 bp)
Chromosome III position
115,000
116,000
117,000

Figure S4


Nuclear RNA Retention
Growth defect
Sensitive to genotoxins
elf1Δ
Acquire mutations
cue2-1

Supporting Figure legends

Figure S1
Although *elf1*Δ cells exhibit severe growth defects, cells without the Elf1 chromodomain (*elf1CD*Δ) do not display an obvious growth defect. A 10-fold serial dilution assay was performed using cells with indicated genotypes. Cells were grown on YEA rich media for 6 days before imaging.

Figure S2
S strains contain heritable genetic alterations that suppress the *elf1Δ* P phenotype and are not in linkage with *elf1*$^+$. (A) Illustration of the process of mating two haploid cells with different mutations, indicated by gray and black nuclei. Resulting spores are separated into vertical tetrads, then allowed to progress into haploid cells forming colonies. (B) Daughter tetrads from wild-type strains were crossed with *elf1Δ* P strains. (C) Average sizes of the resulting colonies from (B) were calculated. (D) Daughter tetrads from wild-type strains crossed with *elf1Δ* S strains. (E) Average sizes of the resulting colonies from (C) were determined. (B & D) Vertical tetrads correspond to colonies grown from the each of the four haploid spores of the mated haploid parental strains, indicated by triangles. Resulting P colonies are outlined with white boxes, and S colonies are outlined with black boxes. (C & E) Error bars indicate ± 1 standard deviation. (F-G) Illustration of possible chromosome segregation outcomes after mating two S strains containing either single suppressor mutation in the same locus (F) or in separate loci (G). Hypothetical mutant loci are indicated by purple or blue lines. The possible combinations of the different segregated suppressors are boxed with different colors and the corresponding tetrads are boxed with the same color (black, red or yellow).

Figure S3
Integrated Genome Browser (IGB) showing the alignment of genome sequencing reads along the chromosome position. (A) *elf1*$^+$ genomic locus is deleted in all observed strains. (B) A truncated *ura4 (ura4DS/E)* and a full length *ura4*$^+$ reporter gene (*otr1: ura4*$^+$*)* are detected.

Figure S4
Genome instability caused by loss of Elf1 may accelerate the acquisition of additional mutations that suppress the *elf1Δ* phenotype, a model.