

## **Additional materials**

**UGDR: A generic pipeline to detect recombined regions in polyploid and complex hybrid yeast genomes.**

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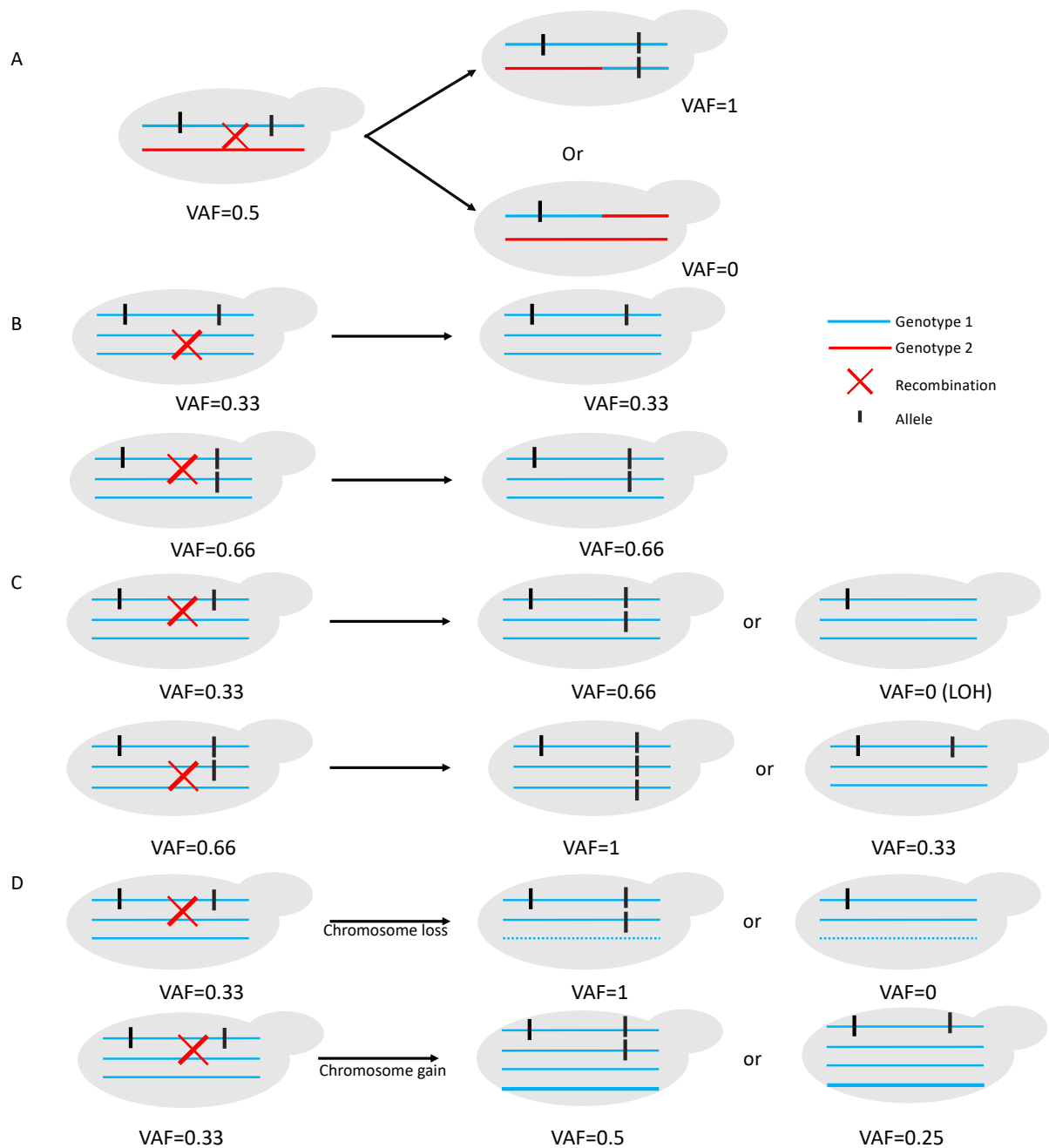


**Figure S1: Summary of different allelic frequency variation during recombination upon yeast ploidy.** (A) In diploids, heterozygous alleles recombine to form homozygous regions (LOH) toward one genotype or to another. (B) Masked recombination: in triploids the allelic frequency did not vary when recombination involves chromosome copies that did not carry the alleles (B-top:  $1/3 \rightarrow 1/3$ ) or both carry same allele (B-bottom:  $2/3 \rightarrow 2/3$ ). (C) When recombination involves chromatids that one has an allele and the other one does not have the allele, the allelic frequency varies ( $1/3 \rightarrow 0$  (LOH) or  $1/3 \rightarrow 2/3$  and  $2/3 \rightarrow 1/3$  or  $2/3 \rightarrow 1$  (LOH)). (D) Recombination and chromosomal rearrangement followed by ploidy changes. LOH: Lost of heterozygosity. VAF: variant allele frequency.

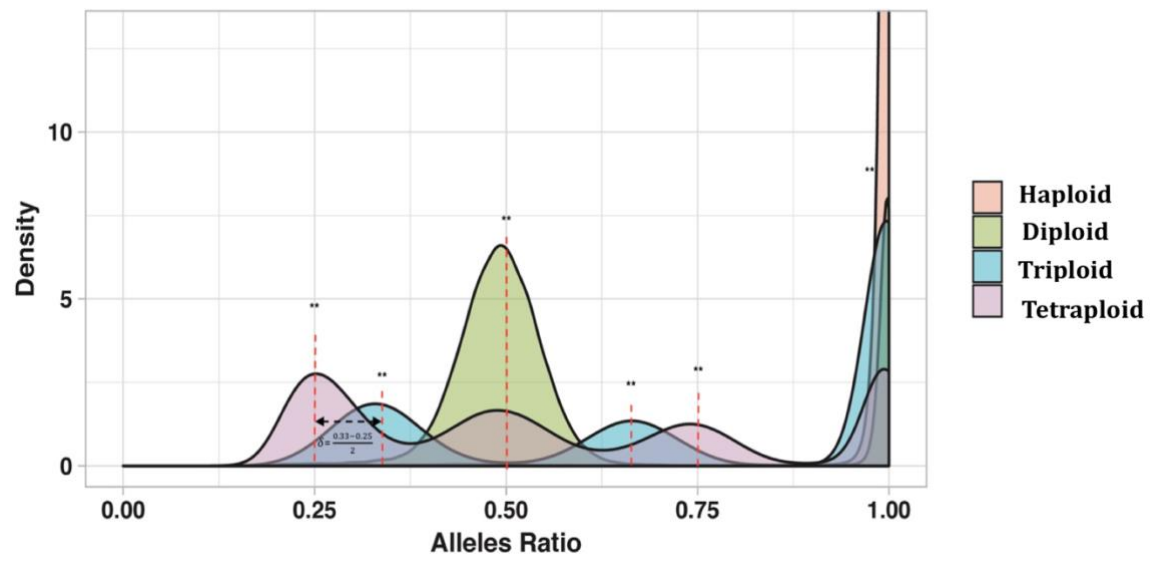


Figure S2: Distribution of the ratio among different ploidies.

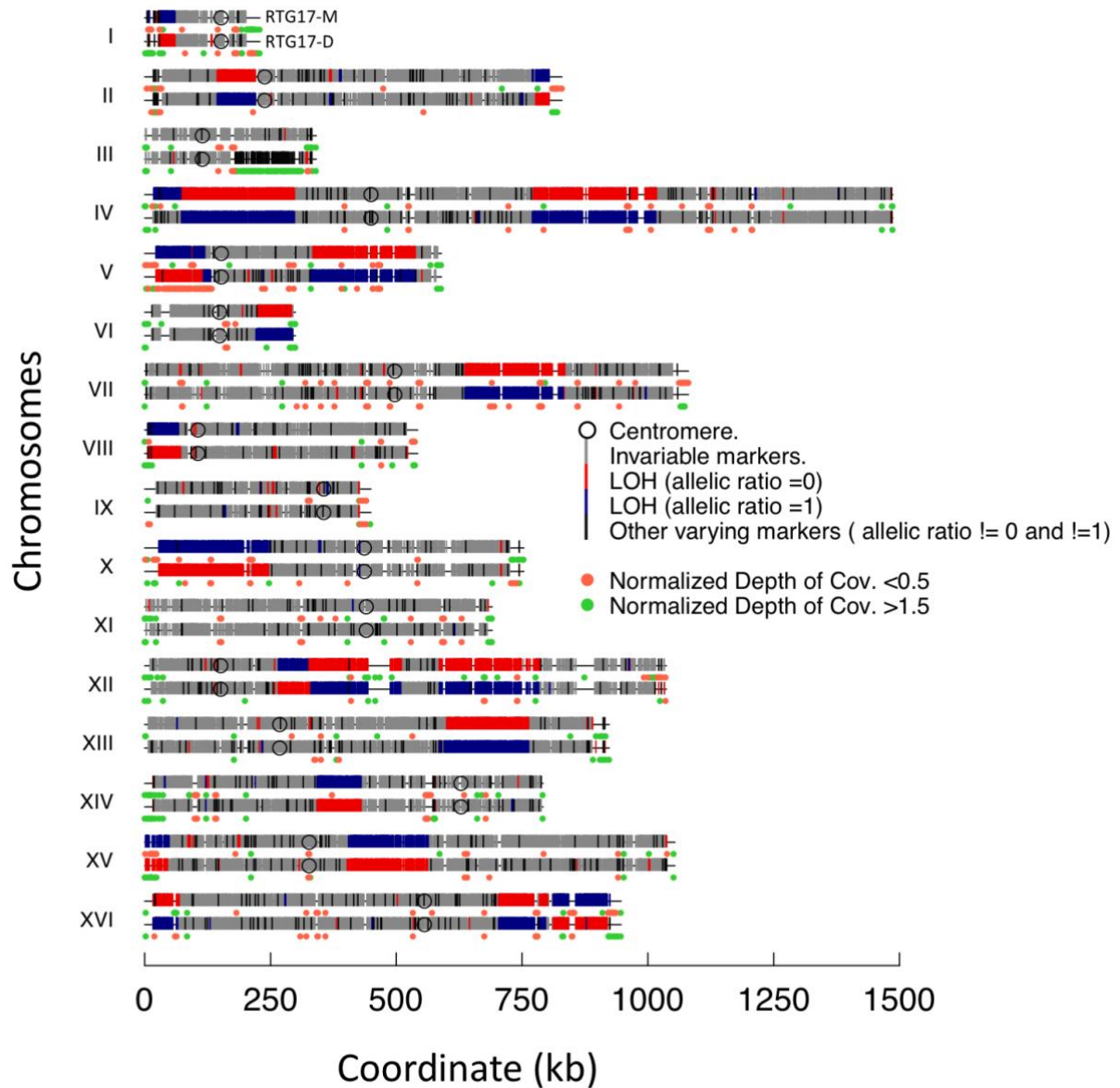


**Figure S3: Genotype of the RTG17M and RTG17D when mapping to SK1.** The genotype of the RTG17M and the RTG17D are shown on the top of each other (names are indicated in chromosome I), separated by dots representing the normalized depth of coverage (NDoC). Orange dots: if deletion occurs (NDoC <0.5) and green dots: if insertion occurs (NDoC >1.5). The genotypes: Invariable, LOH (ratio=0), LOH (ratio=1) and heterozygous recombination are represented by the gray, red, blue and black colored vertical lines.

NDoC: Normalized depth of coverage.

LOH: Lost of heterozygosity.

| SRA Study | Names     | Run        | Sample Name | Unique ID      |                                 |                                |
|-----------|-----------|------------|-------------|----------------|---------------------------------|--------------------------------|
| SRP067222 | SK1/S288C | SRR2984784 | A102R49     | AND1702 *      | Hybrid<br>S288c/SK1             | (Laureau <i>et al.</i> , 2016) |
|           | RTG17-M   | SRR2984813 | A143R13     | AND2612 **     |                                 |                                |
|           | RTG17-D   | SRR2984814 | A143R14     | AND2613 **     |                                 |                                |
|           | RTG10M-1A | SRR2984915 | A102R13     | AND1739-1A *** |                                 |                                |
|           | RTG10M-1B | SRR2984916 | A102R14     | AND1739-1B *** |                                 |                                |
|           | RTG10M-1C | SRR2984917 | A102R15     | AND1739-1C *** |                                 |                                |
|           | RTG10M-1D | SRR2984918 | A102R16     | AND1739-1D *** |                                 |                                |
| SRP072079 | 2-134     | SRR3265371 | SRS1351586  | YJM1138 #      | <i>Saccharomyces cerevisiae</i> | (Zhu <i>et al.</i> , 2016)     |
|           | 2-136     | SRR3265373 | SRS1351584  | YJM1140 #      |                                 |                                |
|           | 2-066     | SRR3265444 | SRS1351640  | YJM958 ¶       |                                 |                                |
|           | 2-067     | SRR3265445 | SRS1351665  | YJM959 ¶       |                                 |                                |

**Table S1: The different yeast used for recombination study.** The 4 spores and the diploid mother and daughter RTGs are compared to the parental strain AND1702. The triploids are compared against each other. Similarly, for the tetraploids.

\*: parental control strain (2n).

\*\*: RTG\_WT (2n).

\*\*\*: Wild type spores.

# : Triploid strains (3n)

¶ : Tetraploid strains (4n)

| Frequency            | Haploid | Diploid | Triploid | Tetraploid |
|----------------------|---------|---------|----------|------------|
| Heterozygous alleles | 1       | 1/2     | 1/3      | 1/4        |
|                      |         |         | 2/3      | 1/2        |
|                      |         |         |          | 3/4        |
| Homozygous alleles   | -       | 1       | 1        | 1          |

**Table S2: Distribution of the allelic ratio following the ploidy.**

| Allelic frequency (ratio) | Diploid | Triploid |     | Tetraploid |     |     | Recombine<br>d cell |
|---------------------------|---------|----------|-----|------------|-----|-----|---------------------|
| Parental ratio            | 1/2     | 1/3      | 2/3 | 1/4        | 1/2 | 3/4 |                     |
| Invariant ratio           | 1/2     | 1/3      | 2/3 | 1/4        | 1/2 | 3/4 |                     |
| Variant ratio             | 0       | 2/3      | 1/3 | 1/2        | 1/4 | 1/2 |                     |
|                           | 1*      | 0*       | 1*  | 0*         | 3/4 | 1*  |                     |
|                           |         |          |     |            | 0*  |     |                     |

**Table S3: potential allelic ratio variation.** e.g.: in the parent/reference, the ratio of an allele x is 2/3, if in the recombined cell the ratio is still 2/3, x is categorized as an invariant allele and if the ratio varies to 1/3 or 1, x is then categorized as a variant allele group. \* represent all the variation that are considered as LOH.