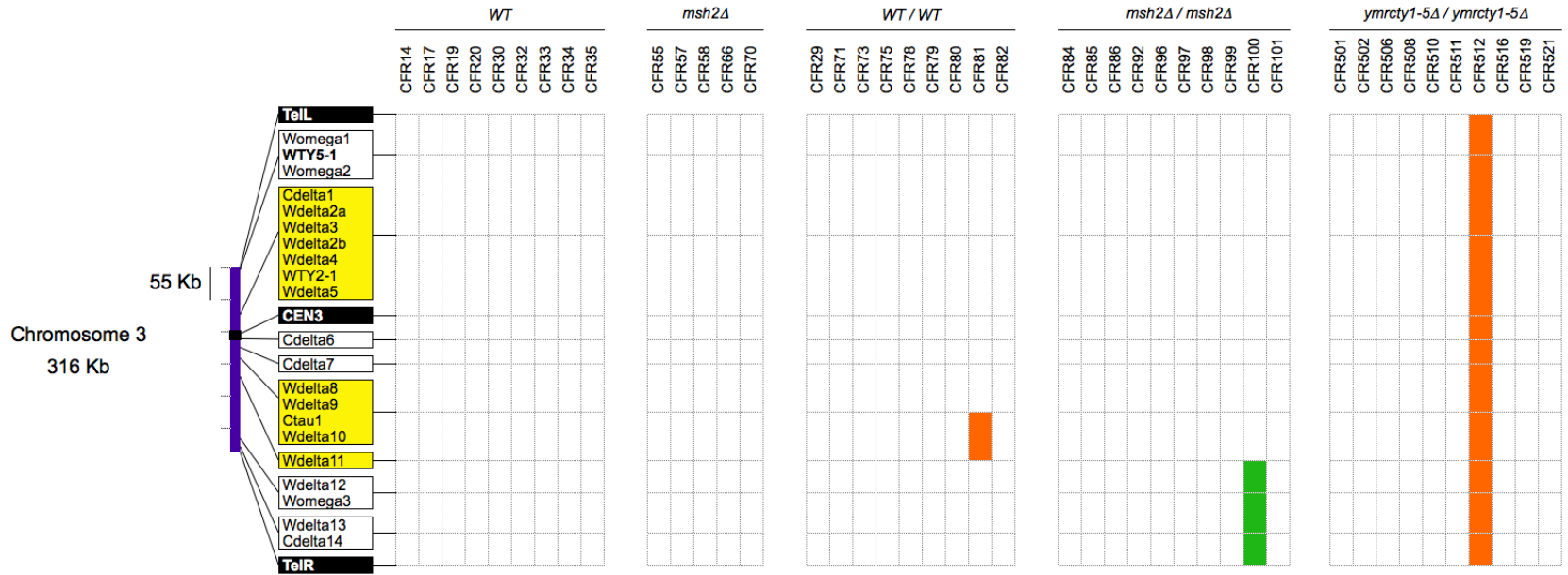
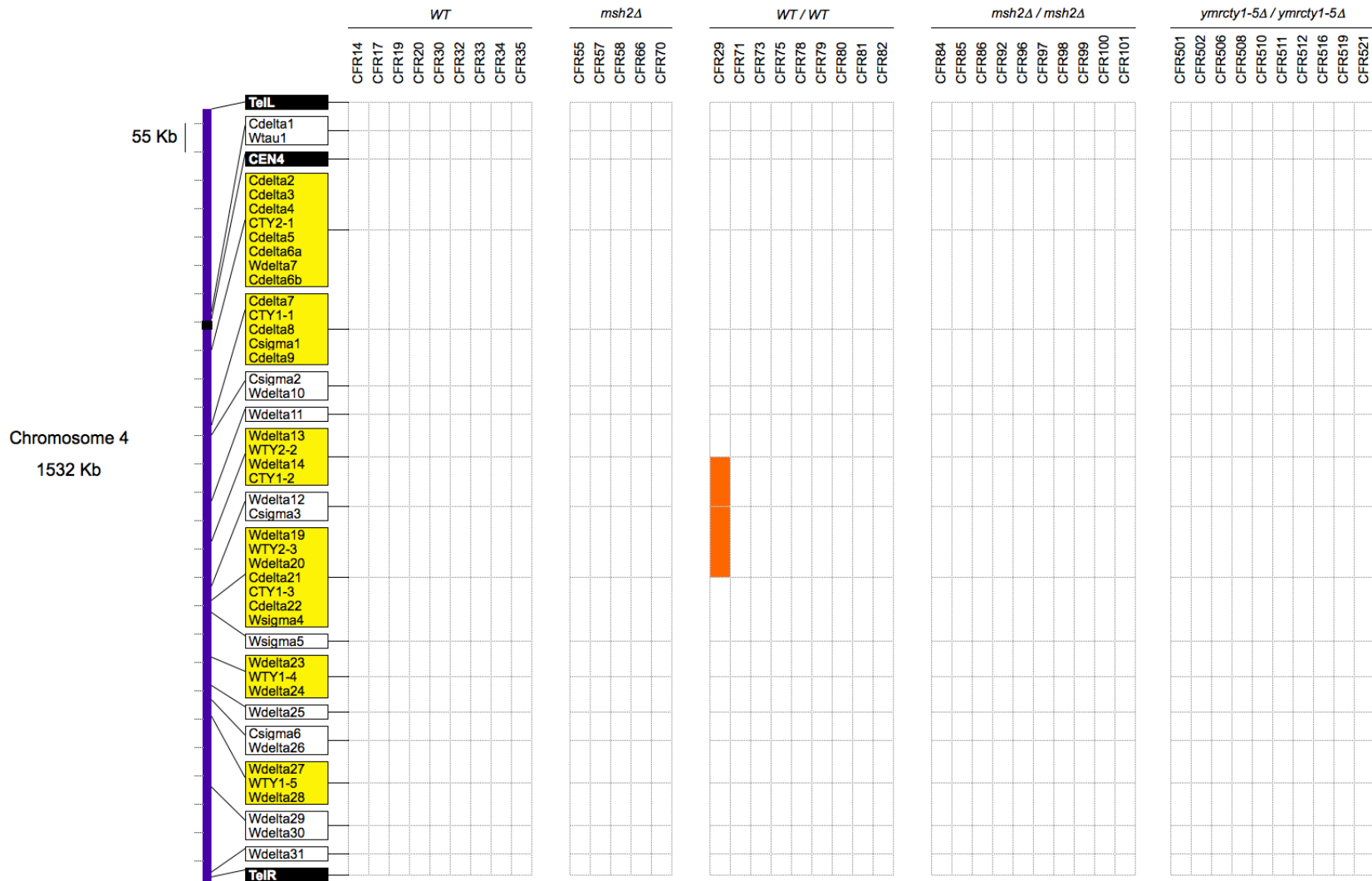


**Figure S1** Graphical summary of the array-CGH data for the CFR clones (part 1 of 8).

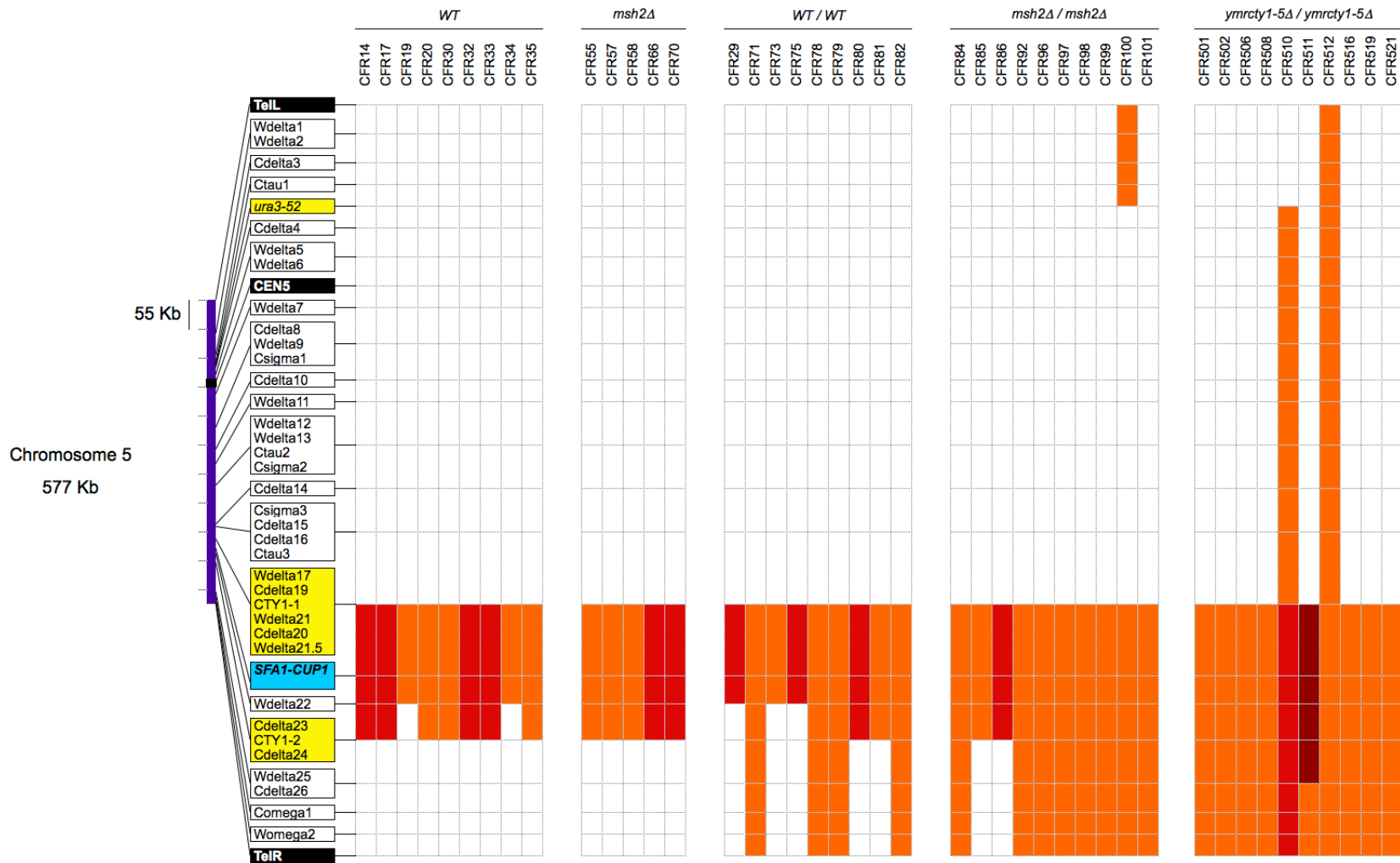
The panels show a graphical representation of the deletion and amplification events detected by array-CGH for each chromosome. Only the chromosomes for which CNVs were detected are shown. The columns correspond to individual FA/Cu resistant isolates, the corresponding genotype of haploids or diploids is also indicated. Each row in the tables corresponds to a Ty-containing site or an LTR-containing site that is annotated in the S288c reference genome sequence available at the Saccharomyces Genome Database (SGD). Tys and LTRs are frequently clustered and in this analysis they appear as a groups since our microarrays do not have the resolution to discriminate the hybridization signal from each individual part of the cluster. A cluster means that there are no probes of non-repetitive DNA between each feature. Sites containing full-length Ty1 and/or Ty2 insertions are highlighted in yellow. Sites containing solo LTRs and/or full length Ty3, Ty4 and Ty5 insertions are not highlighted. The site containing the *SFA1-CUP1* CNV reporter genes on Chr5 is highlighted in blue. The columns are colored to indicate that an alteration of gene dosage was detected by the array-CGH in the corresponding interval. The gene dosage changes are color-coded according to the legend above, and specifically: Bright green = -1 copy relative to parent haploid or diploid; White (or no color) = no dose change; Orange = +1 copy relative to parent (2 copies in haploids, and 3 copies in diploids); Red = +2 copies relative to parent (3 copies in haploids, and 4 copies in diploids); Brown = +3 or more copies relative to parent (4 or more copies in haploids, and 5 or more copies in diploids). The extent of the colored bars corresponds to the chromosomal region where the dose change occurred, and it indicates the specific boundaries for dosage change (breakpoints). Aneuploidy events are shown as the entire chromosome colored from telomere to telomere.



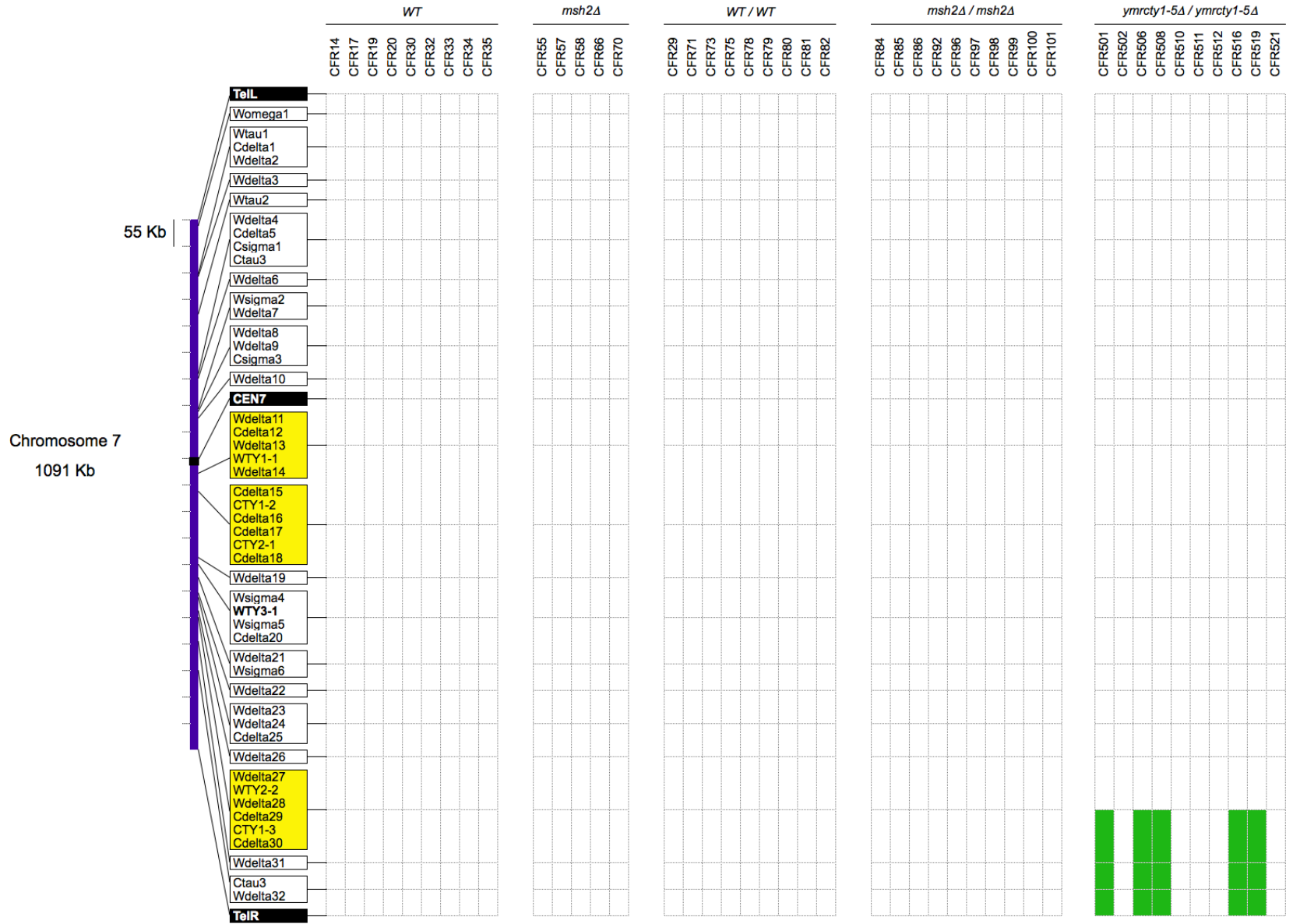
**Figure S1** Graphical summary of the array-CGH data for the CFR clones (continued; part 2 of 8).



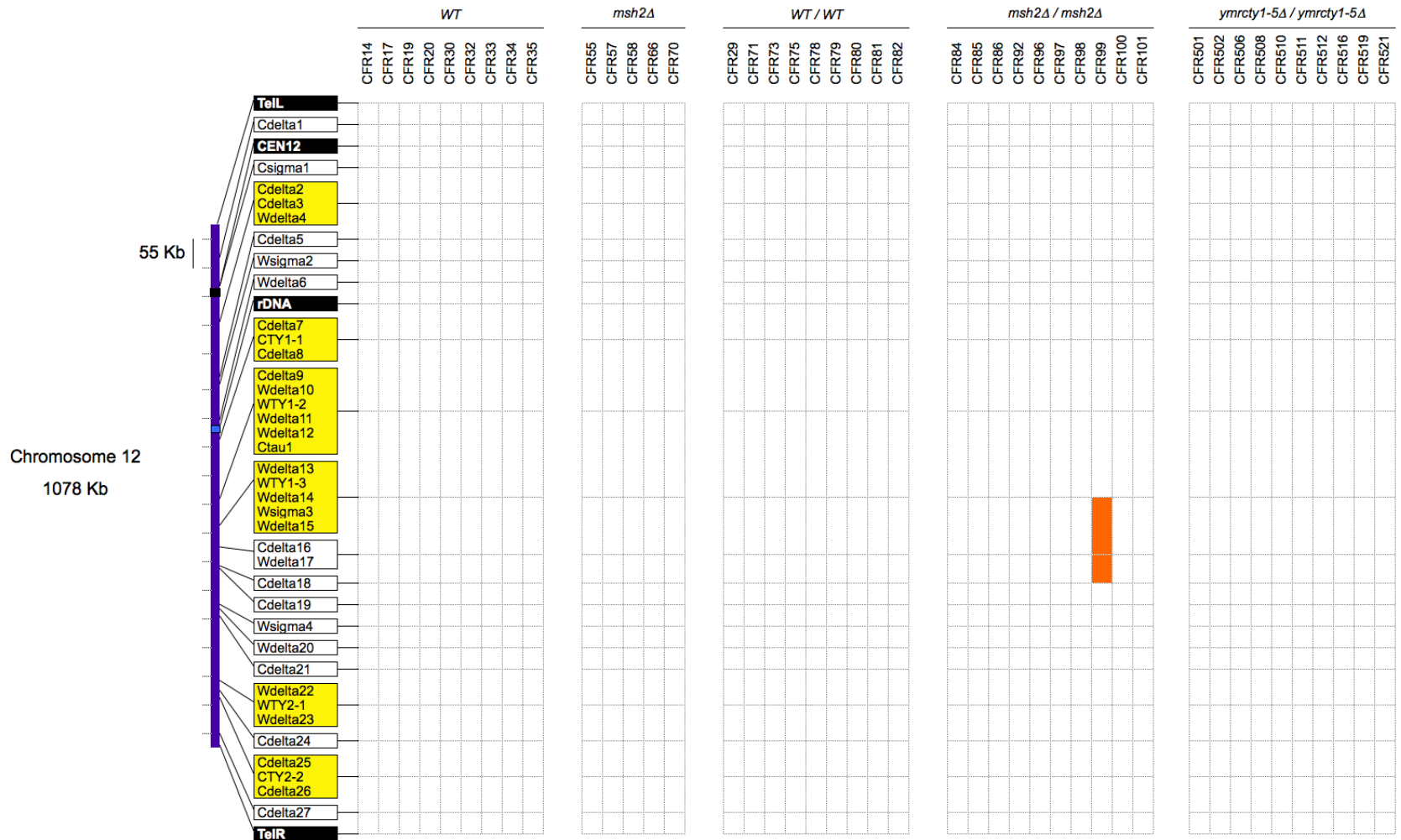
**Figure S1** Graphical summary of the array-CGH data for the CFR clones (continued; part 3 of 8).



**Figure S1** Graphical summary of the array-CGH data for the CFR clones (continued; part 4 of 8).



**Figure S1** Graphical summary of the array-CGH data for the CFR clones (continued; part 5 of 8).



**Figure S1** Graphical summary of the array-CGH data for the CFR clones (continued; part 6 of 8).

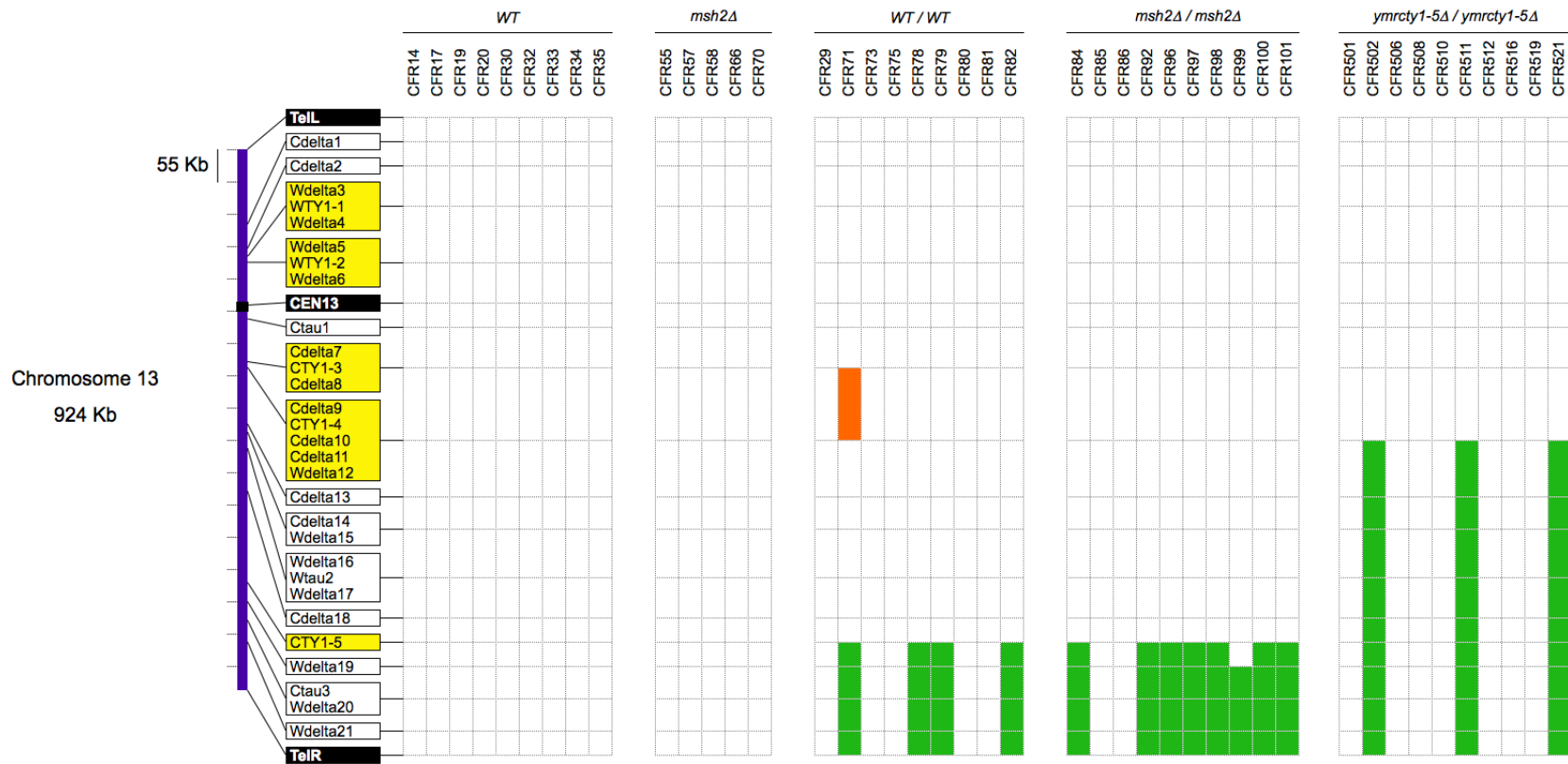
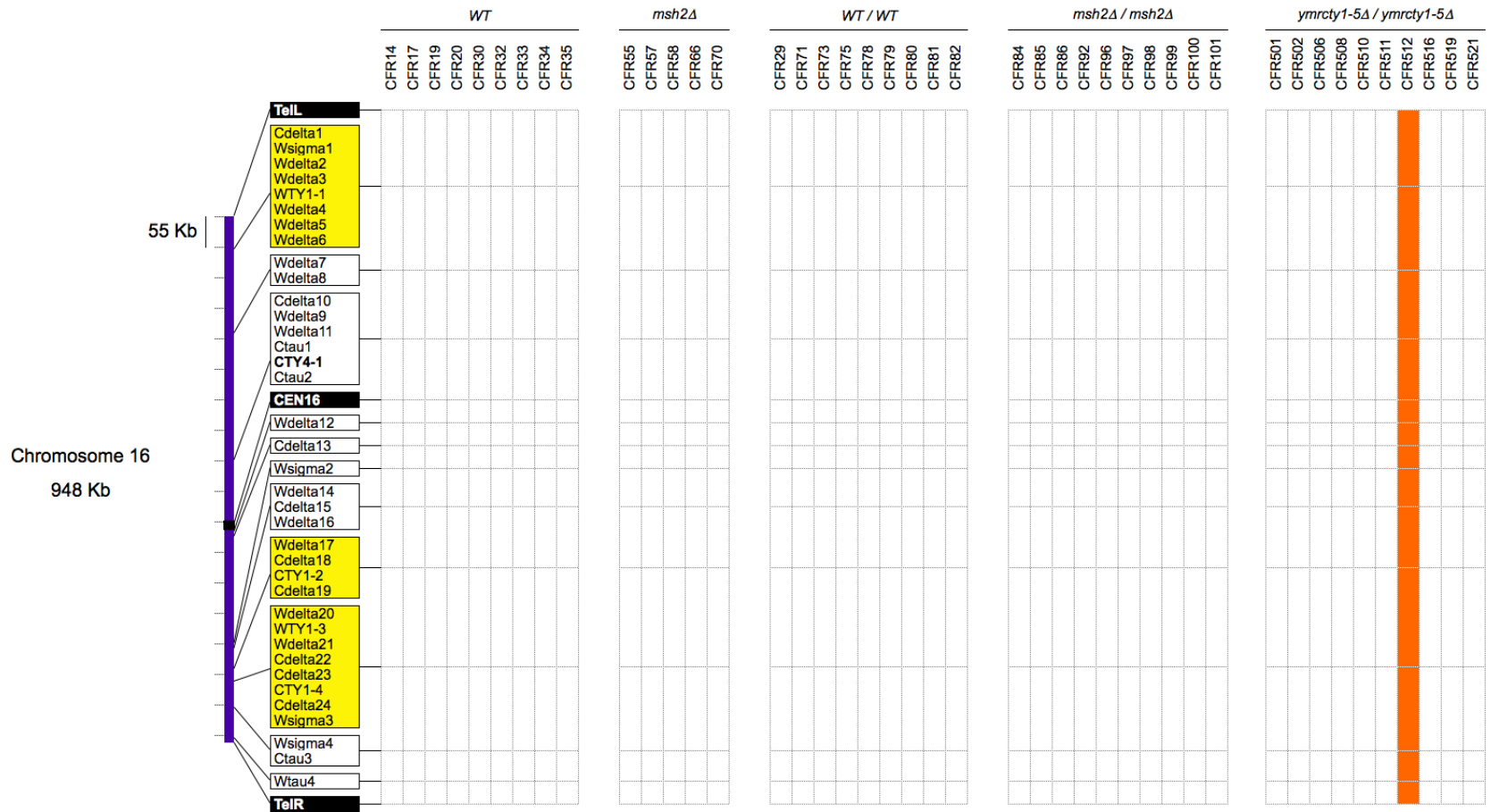


Figure S1 Graphical summary of the array-CGH data for the CFR clones (continued; part 7 of 8).





**Figure S1** Graphical summary of the array-CGH data for the CFR clones (continued; part 8 of 8).