Figure S2A
Karyoscope maps for strain J940047.
For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.
Figure S2B
Karyoscope maps for strain J940557.
For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.
Figure S2C

Karyoscope maps for strain J940915.

For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.
Figure S2D
Karyoscope maps for strain Lalvin EC-1118.

For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.
Figure S2E
For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.
Figure S2F
Karyoscope maps for strain Lalvin ICV D254.

For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.
For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.

Figure S2G
Karyoscope maps for strain AEB Fermol Rouge.

For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.
Karyoscope maps for strain Davis Lalvin 522.

For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.
For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.

Figure S2I
Karyoscope maps for strain 06L3FF02.

CLAC Plot for Sample: 06L3FF02; (FDR=0.251)
For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.
For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.
Figure S2L

Karyoscope maps for strain 06L6FF20.

For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.
Figure S2M
Karyoscope maps for strain BB1235.

For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.
For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.

Figure S2N
Karyoscope maps for strain BB2453.

CLAC Plot for Sample: BB2453; (FDR=0.275)
For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.
For the identification of clusters of ORFs with copy number alterations, the aCGH data was displayed along the chromosomes, using the annotated ORF coordinates of S288C. Vertical bars represent the relative hybridization pattern relatively to the genome of strain S288C. Red bars correspond to amplified ORFs, green bars represent deleted ORFs and grey bars are statistically non-significant alterations. The horizontal lines indicate the hybridization ratios in logarithmic scale. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.
Baseline karyoscope

The karyoscope map for strain S288C shows the baseline noise when deriving karyoscope maps for the other analysed strains. It was obtained with the average of six self-self hybridizations performed with the reference strain S288C. The map was obtained with CGH-Miner, using an averaging moving window of three ORFs.