Figure S6. Split mapping of long reads fails to detect the translocation between chromosomes XI and II in the Jean-Talon strain. Heatmaps show the number of reads which have supplementary mappings to exactly two chromosomes in windows of 20 kb. Color maps correspond to the approximate genome-wide coverage depth equivalent of the supporting reads (the upper bound corresponds to coverage depth equal or higher than two). Simulated translocations (bottom right) show that breakpoints at Ty1 elements are difficult to detect with the split mapping approach (coverage depth equivalent <1), while the genic breakpoint is correctly detected (coverage depth equivalent around 1). Mapping of the S288C dataset against the S288C assembly (bottom left) illustrates some artefacts of the split mapping approach, where signal is detected in many other strains. Although we cannot exclude that some of the signal from the Jean-Talon strain (top) and other beer strains (middle) might not be artefactual, there is no signal corresponding to the translocation detected in the Jean-Talon assembly.