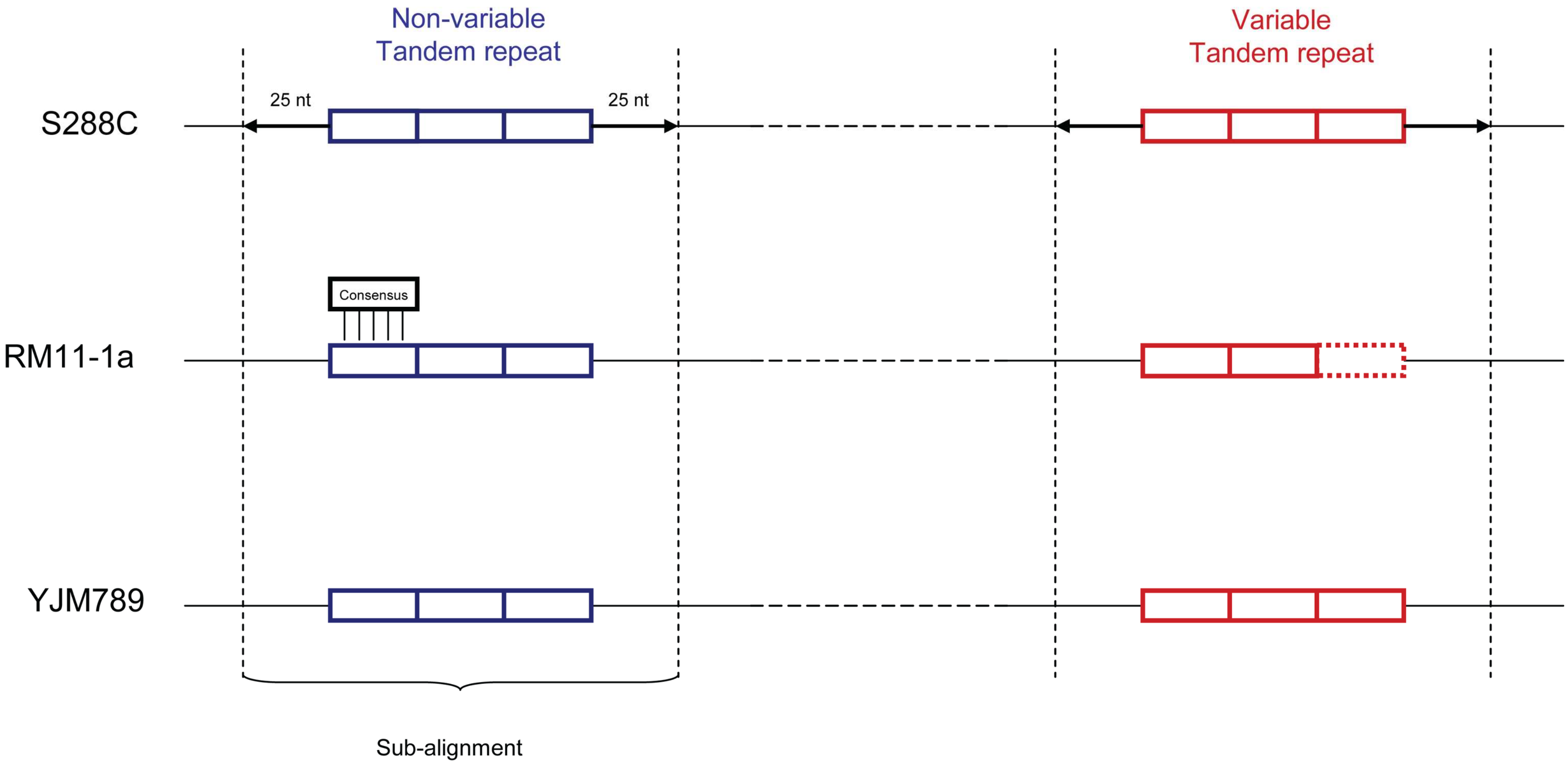

***Supplemental Fig. 4. Automated detection of variation in repeats between different yeast strains.***
Detected tandem repeats are mapped onto whole genome alignment between 3 *S. cerevisiae* strains (S288C, RM11-1a and YJM789). Each position is sliced (plus 25 nt. on each side) into a "sub-alignment". Consensus pattern is re-aligned on each "sub-sequence". Tandem repeats are then categorized as variable (in red) or non-variable (in blue).