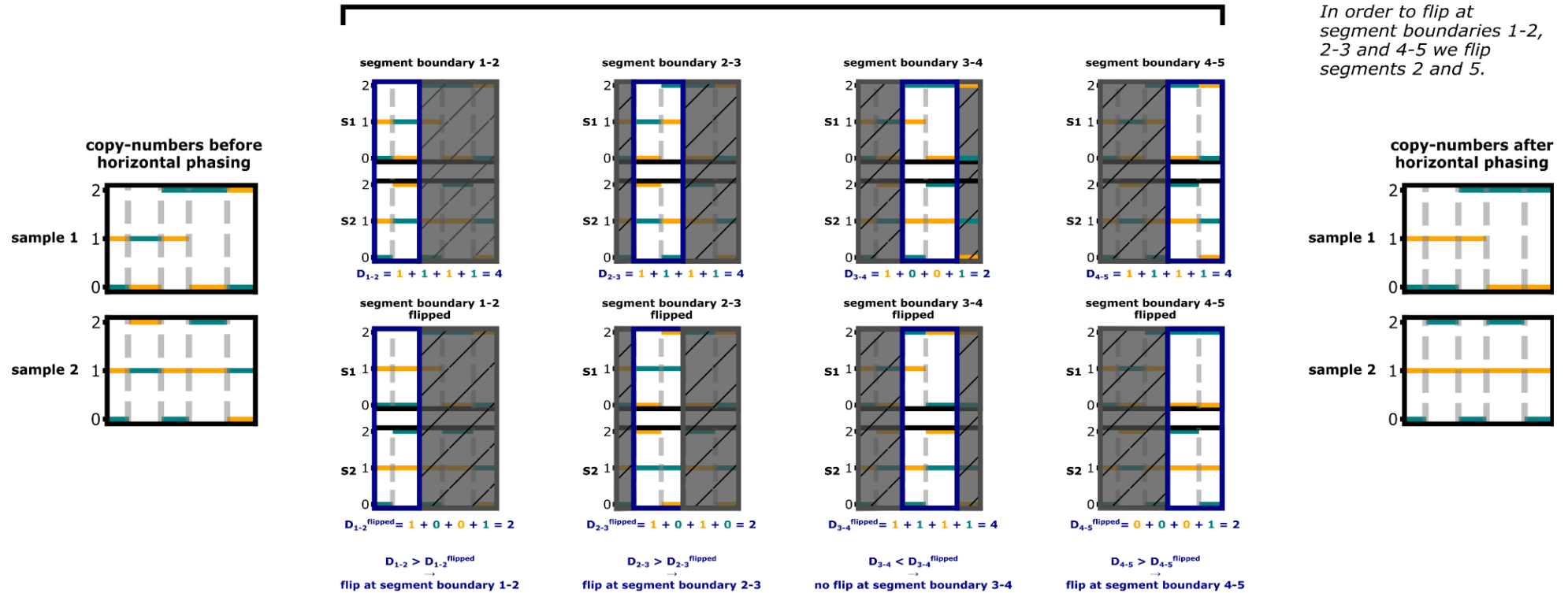# Supplementary Figures

Supplementary Figure 1: Example for the horizontal phasing algorithm. The reference phasing algorithm phases individual segments across all samples but not segments with respect to each other. Therefore we employ a horizontal phasing algorithm which minimises the total number of copy-number breakpoints defined as the total Hamming distance between neighbouring segments (Eq. 6). To this end we compare the Hamming distance between neighbouring segments with a flipped version of those segments (flipping a segment amounts to exchanging the haplotype assignment of that segment for all samples) to determine which segments need to be flipped.