Putative site of selection
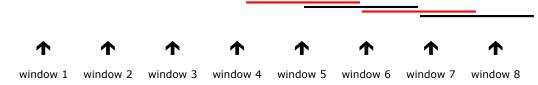
⬇

0010101100100101001001010100101000001010010001001101010010
1001010010100100011100101001010001110100000111001001010010
1101010101010010100100010101001000110101011000111101111111
1101010000110000101001001111100000000000011001010100100000
0000100011011000000010000010011111100010100000101011111111
0101010100101010110010101101010101110101010101010010101010

↑   ↑   ↑   ↑   ↑   ↑   ↑   ↑

window 1   window 2   window 3   window 4   window 5   window 6   window 7   window 8

Figure S33: Schematic illustrating windows for which summary statistics are calculated in our implementation of *SURFDAWave*. Each bold black line underlines one of the eight 10-SNP long windows. Here we show a sample of six haplotypes (rows) across a string of SNPs (columns) for which we calculate summary statistics in $p = 8$ windows. Summary statistics are calculated for each 10-SNP window, with windows overlapping with each neighbor for five SNPs. The central SNP is taken to be the putative selected site and is located in the overlap of windows four and five. Here we have underlined the alternating windows used to calculate the two-dimensional statistics in red.