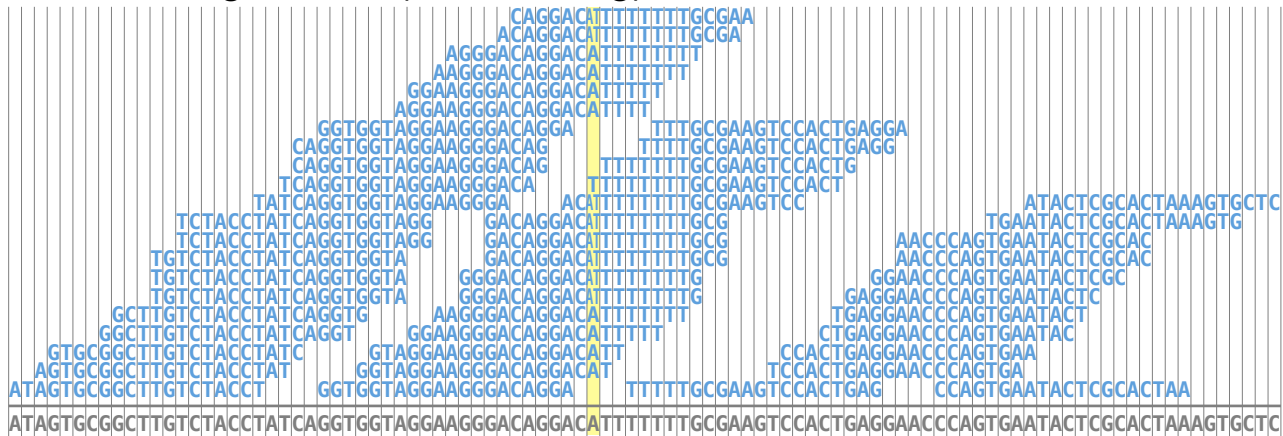
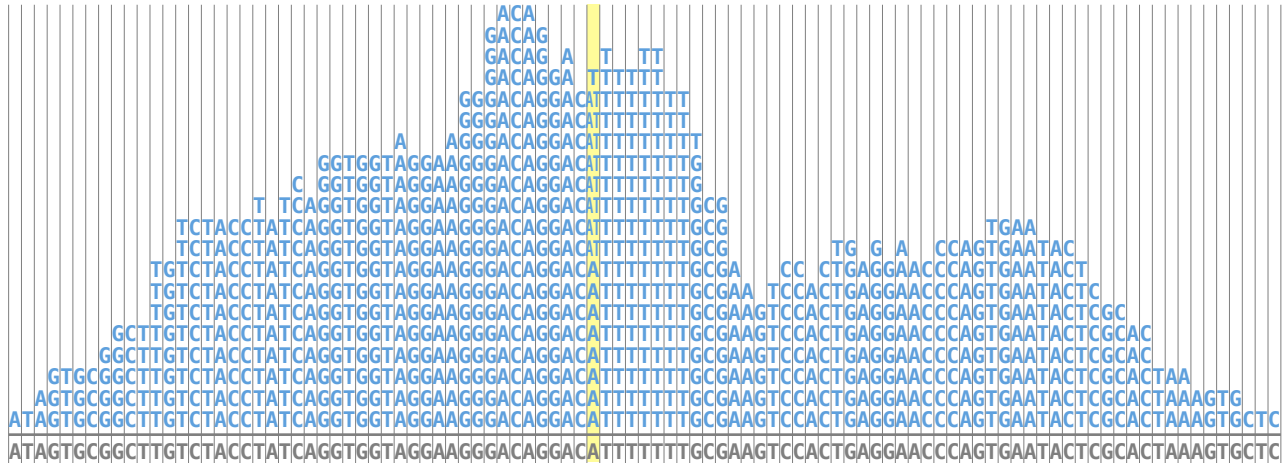


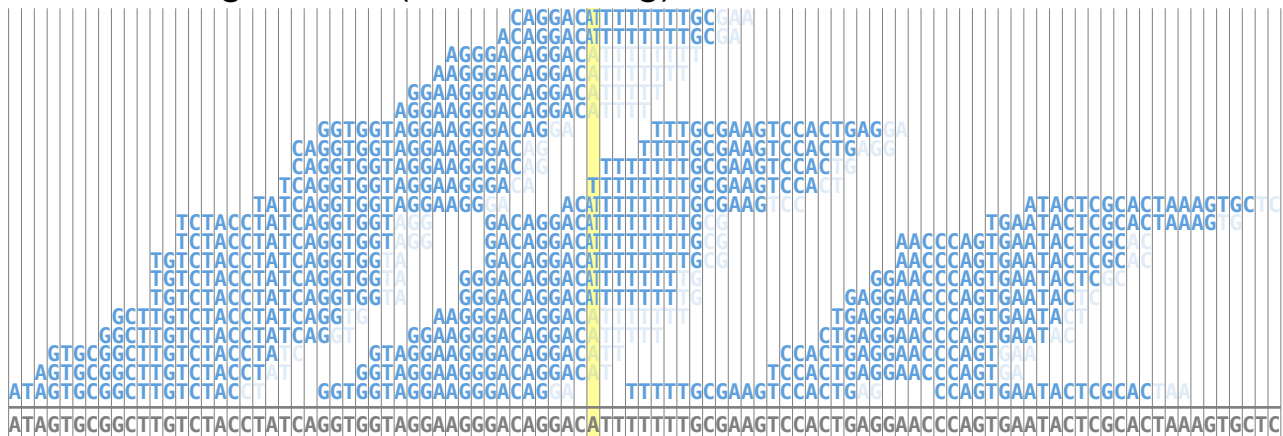
## A. Read alignments (no trimming)



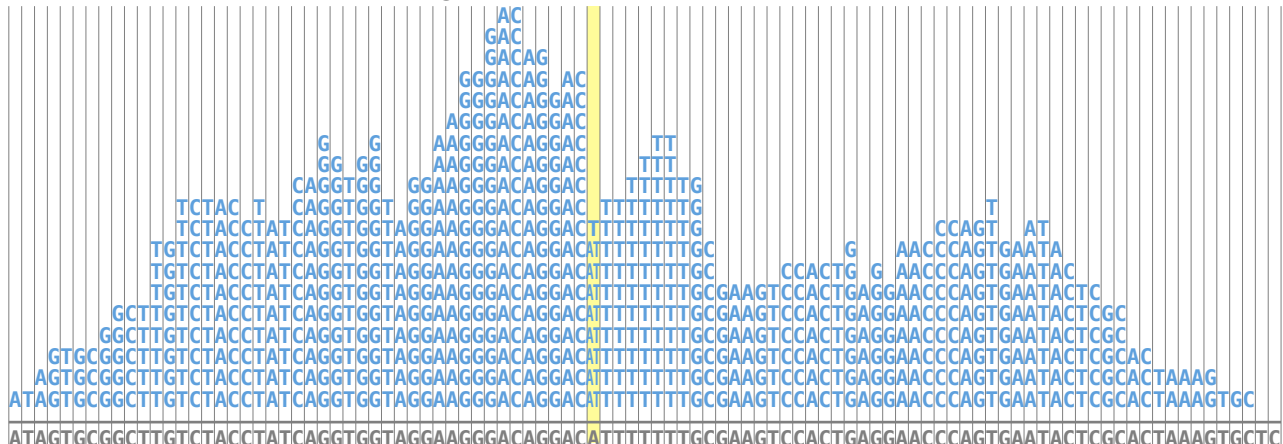
## B. Pileup (no trimming)



## C. Read alignments (with trimming)



## D. Pileup (with trimming)



**Figure S2:** alignment trimming in the Polypolish algorithm. The assembly sequence contains a homopolymer-length error, the position of which is highlighted in yellow.

**A:** short-read alignments to the assembly sequence, without any alignment trimming.

**B:** pileup generated from the untrimmed alignments. The error-containing position contains multiple instances of both 'AT' (the correct sequence) and 'A' (an incorrect sequence).

**C:** short-read alignments to the assembly sequence, where bases have been trimmed from the end of each alignment: the last base has been trimmed (however many times it occurs) and one additional base. Trimmed bases are shown in dimmed type.

**D:** pileup generated from the trimmed alignments. The error-containing position no longer contains any instances of the incorrect sequence 'A'.