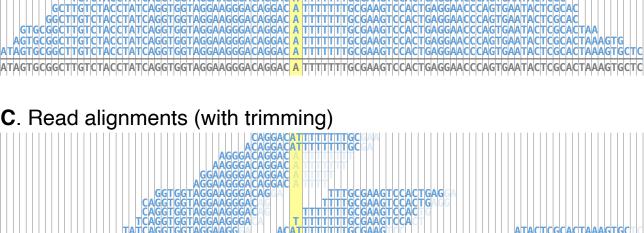
A. Read alignments (no trimming) GTGCGGCTTGTCTACCTATCAGGTGGTAGGAAGGGACAGGAC<mark>A T</mark>TTTTTTTGCGAAGTCCACTGAGGGAACCCAGTGAATACTCGCACTAAAGTGCT **B**. Pileup (no trimming)



D. Pileup (with trimming)

ITAGTIGCGGCTTGTCTACCTATCAGGTGGTAGGAAGGGACAGGAC<mark>A</mark> TTTTTTTTTGCGAAGTCCACTGAGGAACCCAGTGAATACTCGCACTAAAGTGCTC

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 call) and 'A' (an incorrect call).
- 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 call 'A'.