



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’.