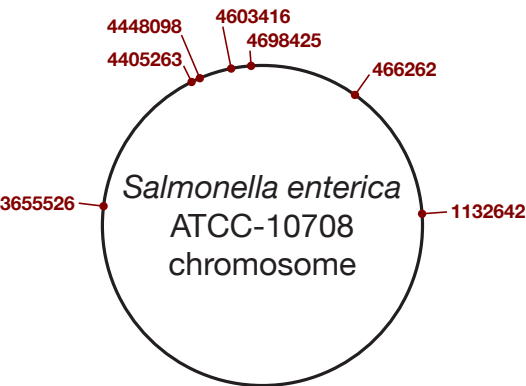


A. rRNA operons



B. error counts

before polishing: 35

Polypolish (defaults): 1

Polypolish --careful: 35

pypolca (defaults): 33

pypolca --careful: 33

FMLRC2: 0

HyPo: 35

NextPolish: 30

Figure SX: short-read polishing of errors in repeats.

A: The chromosome of *Salmonella enterica* ATCC-10708 contains seven copies of the rRNA operon, each ~5.5 kbp in size, with their coordinates (centre position) shown above. Five random substitution errors were added to each, creating 35 total errors, all in repeat sequences.

B: Each polishing tool was run on the error-containing genome and the resulting errors were counted. Polypolish (defaults) was the only alignment-based tool able to fix most errors in repeats. FMLRC2, a non-alignment-based approach, was able to fix all errors in repeats.