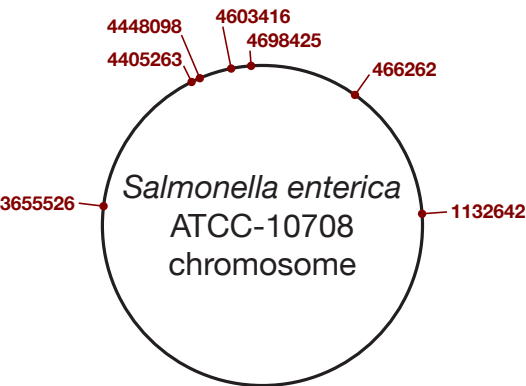


## A. rRNA operons



## B. error counts

**before polishing:** 35

pypolca-defaults: 33

pypolca-careful: 33

Polypolish-defaults: 1

Polypolish-careful: 35

FMLRC2: 0

HyPo: 35

NextPolish: 30

Pilon: 32

**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. Five random substitution errors were added to each operon, creating 35 total errors, all in repeat sequences.

**B:** Each polishing tool was run on the error-containing genome and the remaining 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.