**Mapped to the Yeast Rna Genome. Fasta file acquired from: http://downloads.yeastgenome.org/sequence/S288C\_reference/rna/**

# reads processed: 250000

# reads with at least one reported alignment: 1513 (0.61%)

# reads that failed to align: 248487 (99.39%)

Reported 1513 alignments to 1 output stream(s)