1. **Raw FastQ File**

Number of packages: 27520546

Number of packages that would passQual: 26380808

Number of packages in outfile: 25800361

Number of packages in triagefile: 580447

1. **Bowtie, n = 0**

# reads processed: 25800361

# reads with at least one reported alignment: 7168789 (27.79%)

# reads that failed to align: 16239234 (62.94%)

# reads with alignments suppressed due to -m: 2392338 (9.27%)

Reported 7168789 alignments to 1 output stream(s)

1. **Bowtie, n = 1**

# reads processed: 18631572

# reads with at least one reported alignment: 4501925 (24.16%)

# reads that failed to align: 10111060 (54.27%)

# reads with alignments suppressed due to -m: 4018587 (21.57%)

Reported 4501925 alignments to 1 output stream(s)

1. **Bowtie, n = 2**

# reads processed: 14129647

# reads with at least one reported alignment: 1485214 (10.51%)

# reads that failed to align: 7927012 (56.10%)

# reads with alignments suppressed due to -m: 4717421 (33.39%)

Reported 1485214 alignments to 1 output stream(s)

1. **Generate BL files**

Number of lines in part 0: 7168789

Number of lines in part 1: 4501925

Number of lines in part 2: 1485214

Number of lines in total: 13155928

Length of collatedKeyToReadNum before output length files: 5495260

Number of lengths in lengthToKeys: 18

Number of linesWritten to file 24: 339

====== Last line written ======

==============================================

Number of linesWritten to file 25: 444

====== Last line written ======

==============================================

Number of linesWritten to file 26: 617

====== Last line written ======

==============================================

Number of linesWritten to file 27: 965

====== Last line written ======

==============================================

Number of linesWritten to file 20: 257

====== Last line written ======

==============================================

Number of linesWritten to file 21: 262

====== Last line written ======

==============================================

Number of linesWritten to file 22: 293

====== Last line written ======

==============================================

Number of linesWritten to file 23: 348

====== Last line written ======

==============================================

Number of linesWritten to file 33: 307754

====== Last line written ======

==============================================

Number of linesWritten to file 32: 109821

====== Last line written ======

==============================================

Number of linesWritten to file 31: 22924

====== Last line written ======

==============================================

Number of linesWritten to file 30: 6302

====== Last line written ======

==============================================

Number of linesWritten to file 28: 1577

====== Last line written ======

==============================================

Number of linesWritten to file 36: 4547147

====== Last line written ======

==============================================

Number of linesWritten to file 34: 492913

====== Last line written ======

==============================================

Number of linesWritten to file 19: 221

====== Last line written ======

==============================================

Number of linesWritten to file 18: 164

====== Last line written ======

==============================================

Number of linesWritten to file 29: 2912

====== Last line written ======

1. **Convert BL to FA**

======= Data/CGATGT-s\_6\_1\_seed29\_genome.18.fa ============

Number of linesWritten: 328

======= Data/CGATGT-s\_6\_1\_seed29\_genome.19.fa ============

Number of linesWritten: 442

======= Data/CGATGT-s\_6\_1\_seed29\_genome.20.fa ============

Number of linesWritten: 514

======= Data/CGATGT-s\_6\_1\_seed29\_genome.21.fa ============

Number of linesWritten: 524

======= Data/CGATGT-s\_6\_1\_seed29\_genome.22.fa ============

Number of linesWritten: 586

======= Data/CGATGT-s\_6\_1\_seed29\_genome.23.fa ============

Number of linesWritten: 696

======= Data/CGATGT-s\_6\_1\_seed29\_genome.24.fa ============

Number of linesWritten: 678

======= Data/CGATGT-s\_6\_1\_seed29\_genome.25.fa ============

Number of linesWritten: 888

======= Data/CGATGT-s\_6\_1\_seed29\_genome.26.fa ============

Number of linesWritten: 1234

======= Data/CGATGT-s\_6\_1\_seed29\_genome.27.fa ============

Number of linesWritten: 1930

======= Data/CGATGT-s\_6\_1\_seed29\_genome.28.fa ============

Number of linesWritten: 3154

======= Data/CGATGT-s\_6\_1\_seed29\_genome.29.fa ============

Number of linesWritten: 5824

======= Data/CGATGT-s\_6\_1\_seed29\_genome.30.fa ============

Number of linesWritten: 12604

======= Data/CGATGT-s\_6\_1\_seed29\_genome.31.fa ============

======= needs splitting ==============

Number of splitBLfiles made: 2

======= Data/CGATGT-s\_6\_1\_seed29\_genome.31.fa ============

Number of outlinesWritten: 45848

======= Data/CGATGT-s\_6\_1\_seed29\_genome.32.fa ============

======= needs splitting ==============

Number of splitBLfiles made: 6

======= Data/CGATGT-s\_6\_1\_seed29\_genome.32.fa ============

Number of outlinesWritten: 219642

======= Data/CGATGT-s\_6\_1\_seed29\_genome.33.fa ============

======= needs splitting ==============

Number of splitBLfiles made: 16

======= Data/CGATGT-s\_6\_1\_seed29\_genome.33.fa ============

Number of outlinesWritten: 615508

======= Data/CGATGT-s\_6\_1\_seed29\_genome.34.fa ============

======= needs splitting ==============

Number of splitBLfiles made: 25

======= Data/CGATGT-s\_6\_1\_seed29\_genome.34.fa ============

Number of outlinesWritten: 985826

======= Data/CGATGT-s\_6\_1\_seed29\_genome.36.fa ============

======= needs splitting ==============

Number of splitBLfiles made: 228

======= Data/CGATGT-s\_6\_1\_seed29\_genome.36.fa ============

Number of outlinesWritten: 9094294

1. **Convert FA to RLL (rRNA)**
2. **Convert RLL to OLL (tRNA)**
3. **Check stats**