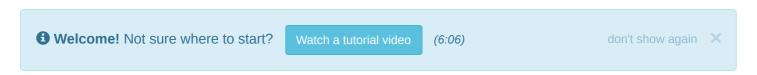# multiqc

A modular tool to aggregate results from bioinformatics analyses across many samples into a single report.

Report generated on 2024-03-28, 12:46 EDT based on data in:
`/athena/cayuga_0019/scratch/mij4011/homework/project/alignments`

ℹ Welcome! Not sure where to start? [Watch a tutorial video] *(6:06)*   don't show again ✕

General Statistics

[⧉ Copy table] [▦ Configure columns] [⊞ Scatter plot] [≡ Violin plot]   Showing [40]/[40] rows and [2]/[2] columns.

Sample Name	% Aligned	M Aligned
SRR21190736	92.8 %	28.9 M
SRR21190737	92.1 %	29.5 M
SRR21190738	89.6 %	27.9 M
SRR21190739	88.0 %	26.2 M
SRR21190740	89.3 %	30.1 M
SRR21190741	86.1 %	31.8 M
SRR21190742	90.9 %	25.9 M
SRR21190743	92.5 %	27.7 M
SRR21190744	91.1 %	26.3 M
SRR21190745	91.1 %	27.2 M
SRR21190746	93.2 %	34.2 M
SRR21190747	94.5 %	30.0 M
SRR21190748	93.2 %	30.8 M
SRR21190749	94.0 %	31.3 M
SRR21190750	94.0 %	32.9 M

⌄

STAR

[STAR](#) is an ultrafast universal RNA-seq aligner.   *DOI:* [10.1093/bioinformatics/bts635.](#)

Alignment Scores

[Percentages]   [Export Plot]

STAR: Alignment Scores

Legend: Uniquely mapped · Mapped to multiple loci · Mapped to too many loci · Unmapped: too short · Unmapped: other

Reads

Created with MultiQC

seqera