multiqc

v1.17

- General Stats
- STAR

![multiqc logo]

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

Report generated on 2024-03-24, 03:24 EDT based on data in:

- `/athena/cayuga_0019/scratch/shp4022/project/Alignment/E16_retina_rep1_Log.final.out`
- `/athena/cayuga_0019/scratch/shp4022/project/Alignment/E16_retina_rep2_Log.final.out`

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

General Statistics

[📋 Copy table] [▦ Configure Columns] [📊 Plot]   Showing ⁸/₈ rows and ²/₂ columns.

Sample Name	% Aligned	M Aligned
E16_retina_rep1	84.7%	33.3
E16_retina_rep2	84.1%	42.6
E18_cornea_rep1	80.6%	23.2
E18_cornea_rep2	90.0%	38.3
E18_retina_rep1	92.0%	31.2
E18_retina_rep2	92.4%	51.2
E8_retina_rep1	92.5%	66.8
E8_retina_rep2	90.7%	39.8

STAR

STAR is an ultrafast universal RNA-seq aligner. *DOI: 10.1093/bioinformatics/bts635.*

Alignment Scores

[Number of Reads] [Percentages]

STAR: Alignment Scores

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

Created with MultiQC

seqera