

## RNA STAR OUTPUT FOR GSM461177

Galaxy31-[RNA\_STAR\_on\_data\_24,\_data\_19,\_and\_data\_18\_log] - Notepad

File Edit Format View Help

Started job on	Oct 28 22:23:46
Started mapping on	Oct 28 22:24:45
Finished on	Oct 28 22:32:17
Mapping speed, Million of reads per hour	83.05
Number of input reads	10428011
Average input read length	73
UNIQUE READS:	
Uniquely mapped reads number	8666702
Uniquely mapped reads %	83.11%
Average mapped length	72.87
Number of splices: Total	952323
Number of splices: Annotated (sjdb)	943181
Number of splices: GT/AG	942946
Number of splices: GC/AG	7149
Number of splices: AT/AC	288
Number of splices: Non-canonical	1940
Mismatch rate per base, %	0.77%
Deletion rate per base	0.00%
Deletion average length	1.48
Insertion rate per base	0.00%
Insertion average length	1.39
MULTI-MAPPING READS:	
Number of reads mapped to multiple loci	571324
% of reads mapped to multiple loci	5.48%
Number of reads mapped to too many loci	574223
% of reads mapped to too many loci	5.51%
UNMAPPED READS:	
Number of reads unmapped: too many mismatches	0
% of reads unmapped: too many mismatches	0.00%
Number of reads unmapped: too short	599120
% of reads unmapped: too short	5.75%
Number of reads unmapped: other	16642
% of reads unmapped: other	0.16%
CHIMERIC READS:	
Number of chimeric reads	0
% of chimeric reads	0.00%

# RNA STAR OUTPUT FOR GSM461180

Galaxy34-[RNA\_STAR\_on\_data\_24,\_data\_22,\_and\_data\_21\_log] - Notepad

File Edit Format View Help

Started job on	Oct 29 03:23:49
Started mapping on	Oct 29 03:27:00
Finished on	Oct 29 03:33:31
Mapping speed, Million of reads per hour	102.77
Number of input reads	11161595
Average input read length	71
UNIQUE READS:	
Uniquely mapped reads number	8818168
Uniquely mapped reads %	79.00%
Average mapped length	70.52
Number of splices: Total	946755
Number of splices: Annotated (sjdb)	929256
Number of splices: GT/AG	938411
Number of splices: GC/AG	5295
Number of splices: AT/AC	385
Number of splices: Non-canonical	2664
Mismatch rate per base, %	1.73%
Deletion rate per base	0.00%
Deletion average length	1.44
Insertion rate per base	0.00%
Insertion average length	1.34
MULTI-MAPPING READS:	
Number of reads mapped to multiple loci	507492
% of reads mapped to multiple loci	4.55%
Number of reads mapped to too many loci	587775
% of reads mapped to too many loci	5.27%
UNMAPPED READS:	
Number of reads unmapped: too many mismatches	0
% of reads unmapped: too many mismatches	0.00%
Number of reads unmapped: too short	1239790
% of reads unmapped: too short	11.11%
Number of reads unmapped: other	8370
% of reads unmapped: other	0.07%
CHIMERIC READS:	
Number of chimeric reads	0
% of chimeric reads	0.00%

## MULTI QC REPORTS



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

Report generated on 2021-10-28, 22:39 based on data in: /corral4/main/jobs/038/733/38733800/working/multiqc\_wDir

Welcome! Not sure where to start? [Watch a tutorial video](#) (6:06)

[don't show again](#) ✕

### General Statistics

[Copy table](#) [Configure Columns](#) [Plot](#) Showing 2 rows and 2 columns.

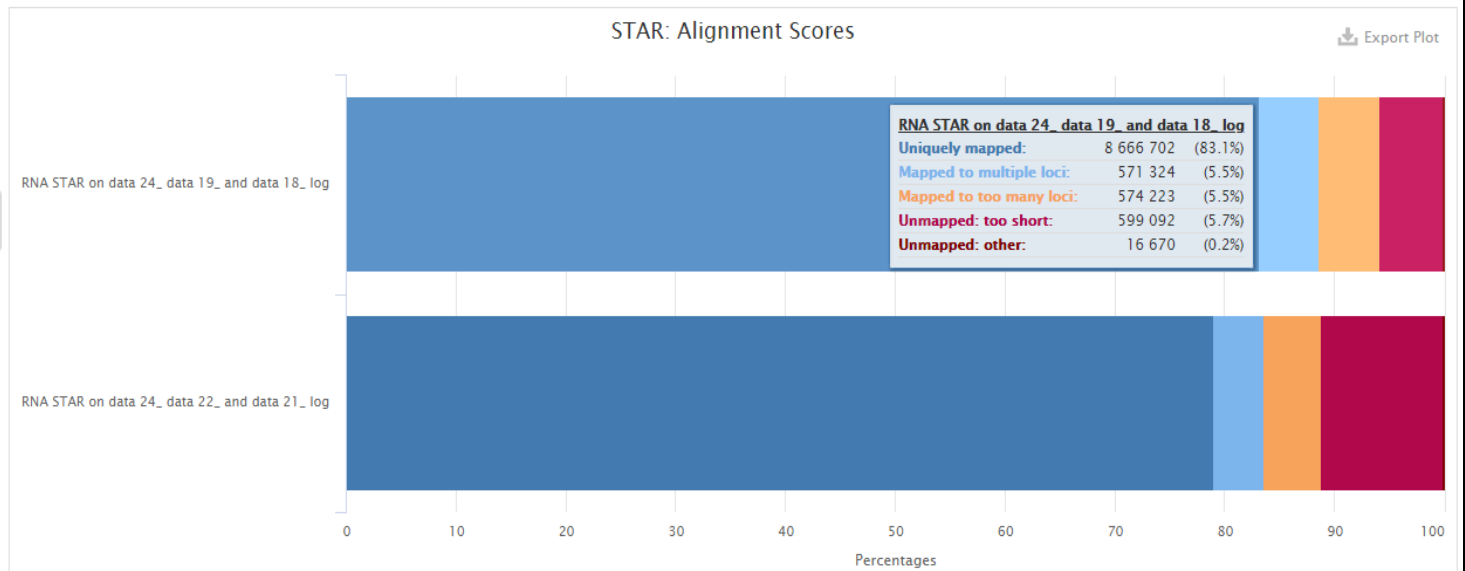
Sample Name	% Aligned	M Aligned
RNA STAR on data 24_ data 19_ and data 18_ log	83.1%	8.7
RNA STAR on data 24_ data 22_ and data 21_ log	79.0%	8.8

### STAR

STAR is an ultrafast universal RNA-seq aligner.

#### Alignment Scores

[Number of Reads](#) [Percentages](#)



# STAR

STAR is an ultrafast universal RNA-seq aligner.

## Alignment Scores

Number of Reads Percentages

