



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

Report generated on 2022-12-15, 21:24 EST based on data in:

/mnt/d/LanboData/12.11.2022_data/alignments

General Statistics

Copy table

Configure Columns

Plot

Showing 48/48 rows and 2/2 columns.

Sample Name	% Aligned	M Aligned
C0-1_noninfection_time_0	96.1%	29.9
C0-2_noninfection_time_0	95.6%	28.1
C0-3_noninfection_time_0	96.1%	29.7
C0-4_noninfection_time_0	95.8%	28.7
C1-10_infection_D25+_glutamine	95.1%	24.1
C1-11_Infection_D55+glutamine	94.4%	24.9
C1-12_Infection_D55+glutamine	94.8%	26.8
C1-14_Infection_D55+glutamine	94.9%	24.2
C1-15_Infection_D55+glutamine	94.7%	23.7
C1-6_infection_D25+_glutamine	94.8%	24.9
C1-8_infection_D25+_glutamine	94.9%	25.5
C1-9_infection_D25+_glutamine	94.9%	24.2
C24-1_infection-24h	95.5%	26.9
C24-2_infection-24h	95.5%	25.8
C24-3_infection-24h	95.6%	29.3
C24-4_infection-24h	95.5%	27.6
C4-1_infection-4h	95.9%	31.1
C4-2_infection-4h	95.7%	24.6
C4-3_infection-4h	95.7%	24.6
C4-4_infection-4h	95.9%	28.1
R0-1_noninfection+inhibitor_time_0	95.4%	29.7

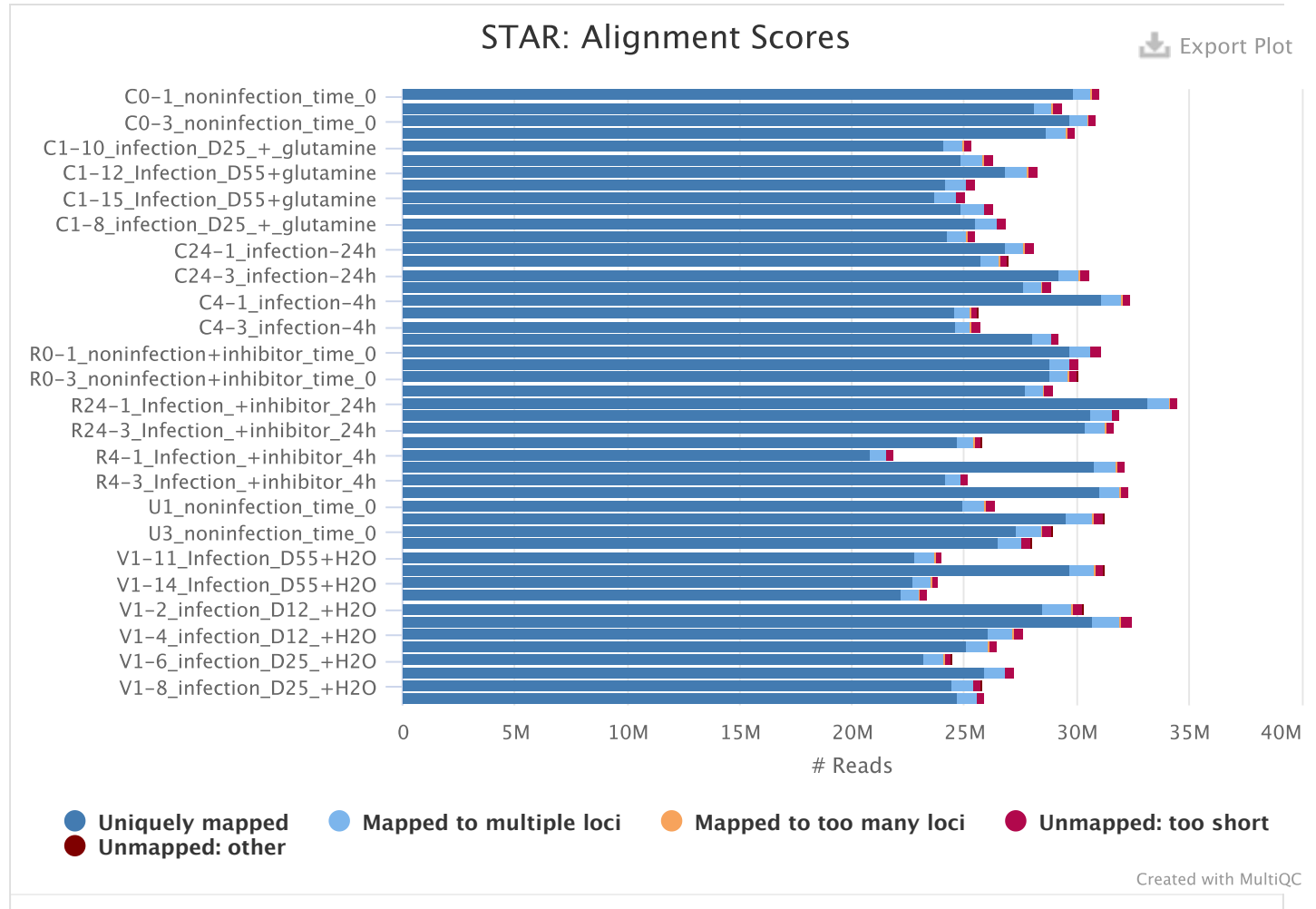
Sample Name	% Aligned	M Aligned
R0-2_noninfection+inhibitor_time_0	95.8%	28.9
R0-3_noninfection+inhibitor_time_0	95.8%	28.8
R0-4_noninfection+inhibitor_time_0	95.7%	27.8
R24-1_Infection_+inhibitor_24h	96.1%	33.2
R24-2_Infection_+inhibitor_24h	96.0%	30.7
R24-3_Infection_+inhibitor_24h	96.0%	30.4
R24-4_Infection_+inhibitor_24h	95.9%	24.8
R4-1_Infection_+inhibitor_4h	95.4%	20.9
R4-2_Infection_+inhibitor_4h	95.9%	30.9
R4-3_Infection_+inhibitor_4h	95.7%	24.2
R4-4_Infection_+inhibitor_4h	96.1%	31.1
U1_noninfection_time_0	94.6%	25.0
U2_noninfection_time_0	94.6%	29.6
U3_noninfection_time_0	94.4%	27.3
U4_noninfection_time_0	94.7%	26.5
V1-11_Infection_D55+H2O	94.9%	22.8
V1-12_Infection_D55+H2O	95.1%	29.8
V1-14_Infection_D55+H2O	95.4%	22.8
V1-15_Infection_D55+H2O	94.9%	22.2
V1-2_infection_D12_+H2O	94.2%	28.6
V1-3_infection_D12_+H2O	94.5%	30.7
V1-4_infection_D12_+H2O	94.2%	26.1
V1-5_infection_D12_+H2O	94.8%	25.1
V1-6_infection_D25_+H2O	95.0%	23.3
V1-7_infection_D25_+H2O	95.1%	25.9
V1-8_infection_D25_+H2O	94.9%	24.5
V1-9_infection_D25_+H2O	95.2%	24.7

STAR

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

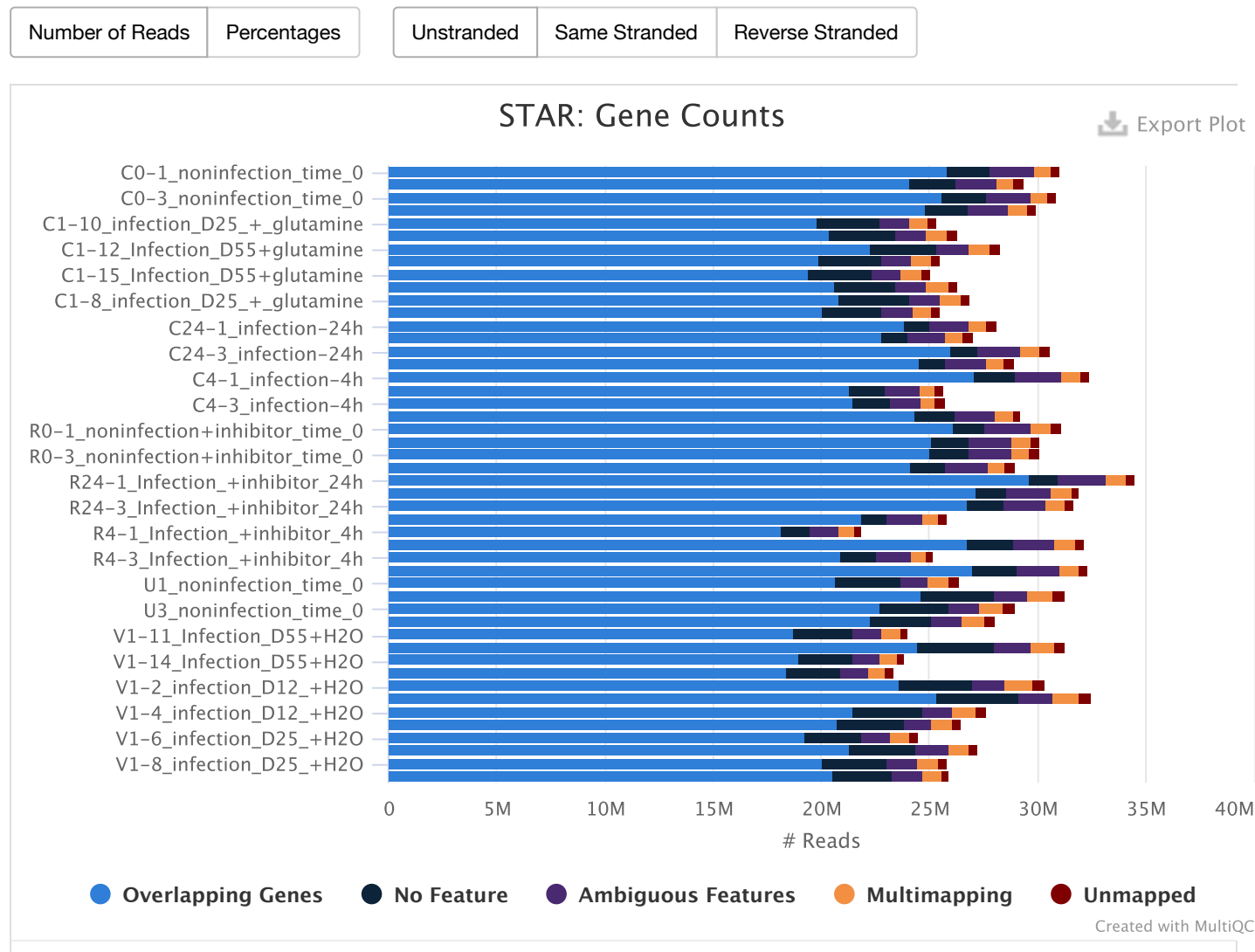
Alignment Scores

Number of Reads Percentages



Gene Counts

Statistics from results generated using `--quantMode GeneCounts`. The three tabs show counts for unstranded RNA-seq, counts for the 1st read strand aligned with RNA and counts for the 2nd read strand aligned with RNA.



MultiQC v1.13 - Written by [Phil Ewels](#), available on [GitHub](#).

This report uses [HighCharts](#), [jQuery](#), [jQuery UI](#), [Bootstrap](#), [FileSaver.js](#) and [clipboard.js](#).

