

Cell Line TGFb CXCL12: (/projects/33550562) FASTQ Toolkit
11/22/2016 10:21:22

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ANALYSIS INFO

(/analyses/39352173/info?projectId=33550562)

INPUTS

(/analyses/39352173/inputs?projectId=33550562)

OUTPUT FILES

(/analyses/39352173/files?projectId=33550562)

ANALYSIS REPORTS

JRN008CGATGL002
(/analyses/39352173/results/36215215?projectId=33550562)

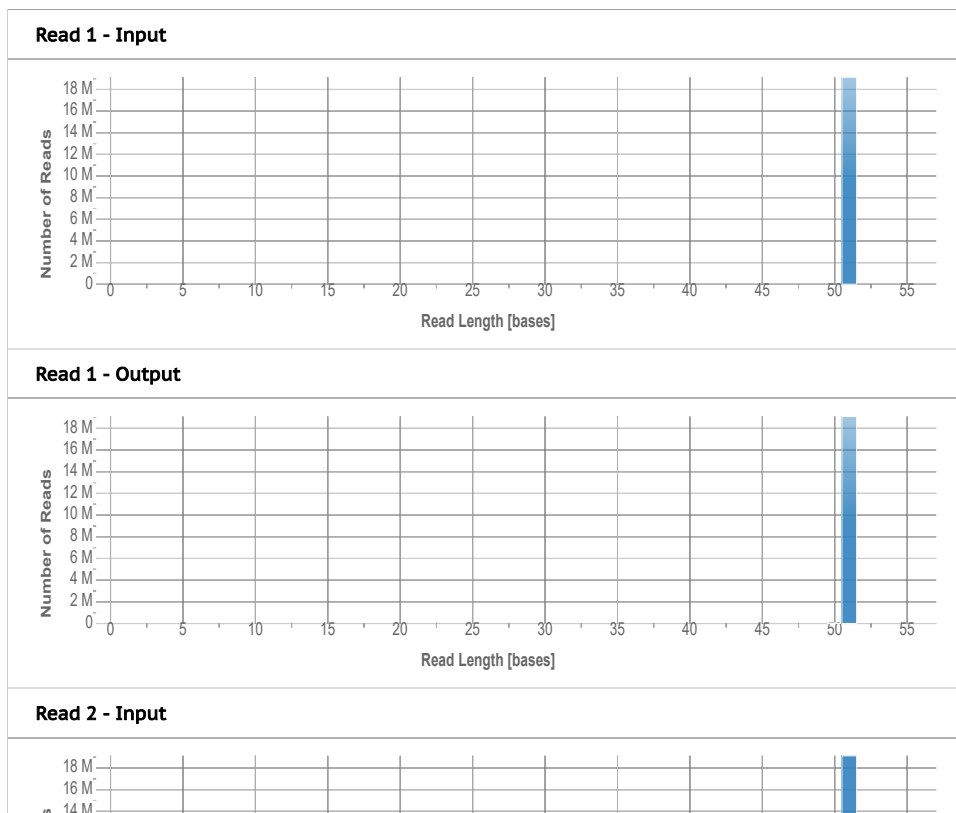
RESULTS FOR INPUT SAMPLE JRN008CGATGL002 (/SAMPLE/41135114/JRN008CGATGL002)

INPUT AND OUTPUT SAMPLE SUMMARY

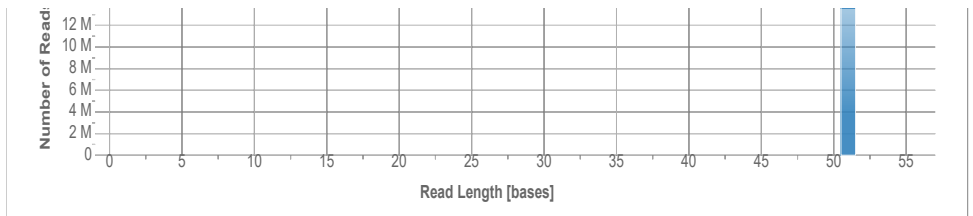
	Input Sample	Output Sample	
Sample Name	JRN008CGATGL002 (/sample/41135114/JRN008CGATGL002)	JRN008CGATGL002-R1, JRN008CGATGL002-R2	
Number of FASTQ Entries	19,134,586	19,130,187	99.98%
Number of Reads Read1	19,134,586	19,130,187	99.98%
Number of Reads Read2	19,134,586	19,130,187	99.98%
Number of Bases Read1	975,863,886	975,608,380	99.97%
Number of Bases Read2	975,863,886	975,578,163	99.97%
Maximum Read Length	51	51	100%
Read Pairs (Not Counting Singletons)	19,134,586	19,130,187	99.98%

Note: The number of reads for Read1 and Read2 in the Output column in the table above do not include N-reads. N-reads contain only no-calls (Ns) and are used for singletons in paired-end data to conserve the order and number of FASTQ entries.

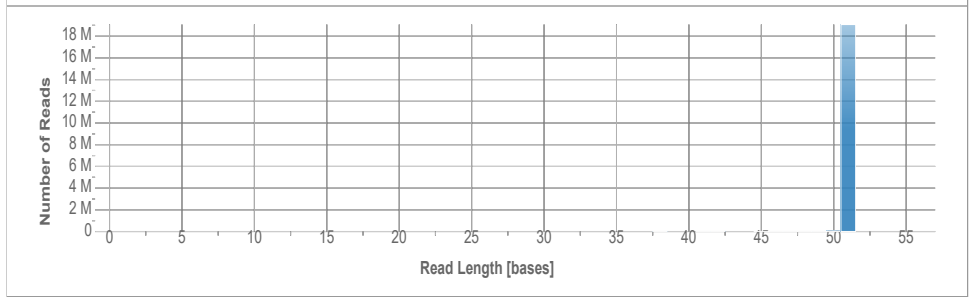
Read Length Distributions



Analyses - BaseSpace Sequence Hub



Read 2 - Output



Note: Reads that only contain Ns (no-calls) in the output sample are represented with length zero in the charts above.

READ FILTER SUMMARY

Filter	Reads Filtered Read1		Reads Filtered Read2	
Read Length	0	0%	4,399	0.02%
Mean Quality	0	0%	0	0%
G/C Content	0	0%	0	0%