

Cell Line TGFb CXCL12: (/projects/33550562) FASTQ Toolkit  
11/22/2016 8:31:31

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ANALYSIS INFO

(/analyses/39353963/info?projectId=33550562)

INPUTS

(/analyses/39353963/inputs?projectId=33550562)

OUTPUT FILES

(/analyses/39353963/files?projectId=33550562)

ANALYSIS REPORTS

**JRN008CGATGT**  
(/analyses/39353963/results/36219184?projectId=33550562)

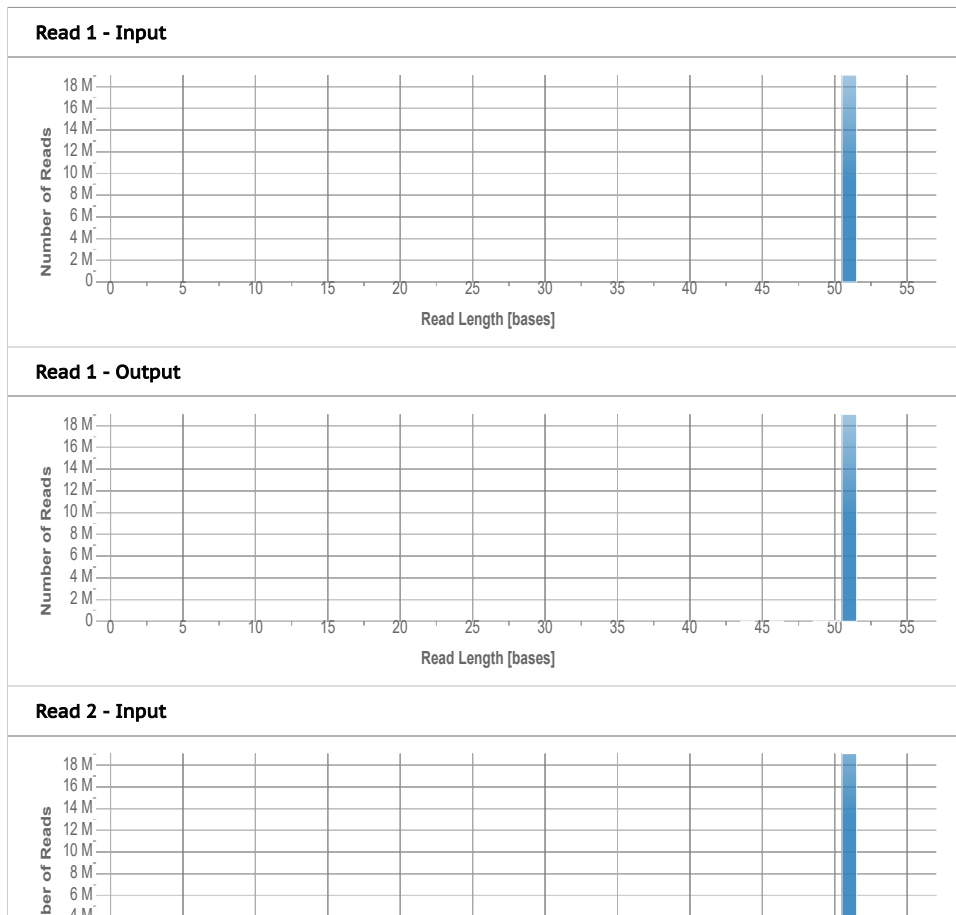
**RESULTS FOR INPUT SAMPLE JRN008CGATGT (/SAMPLE/41118406/JRN008CGATGT)**

**INPUT AND OUTPUT SAMPLE SUMMARY**

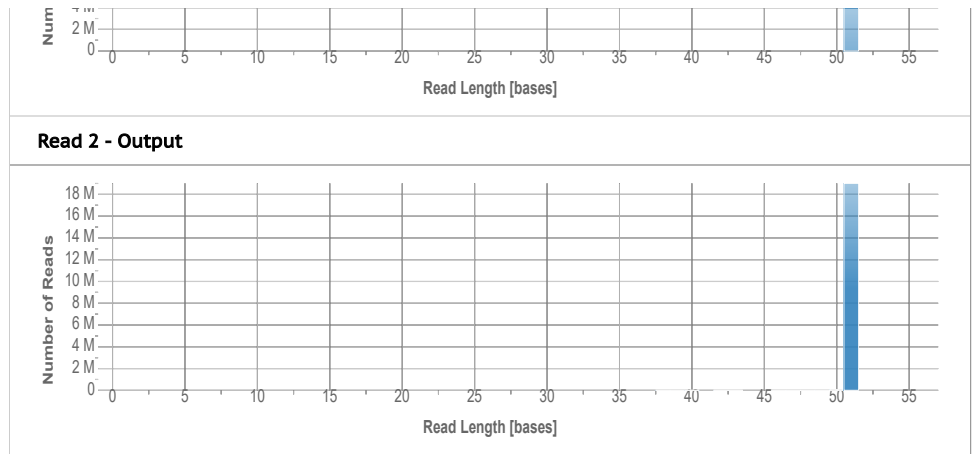
	Input Sample	Output Sample	
Sample Name	JRN008CGATGT (/sample/41118406/JRN008CGATGT)	JRN008CGATGT-R1, JRN008CGATGT-R2	
Number of FASTQ Entries	19,074,141	19,070,383	99.98%
Number of Reads Read1	19,074,141	19,070,383	99.98%
Number of Reads Read2	19,074,141	19,070,383	99.98%
Number of Bases Read1	972,781,191	972,565,509	99.98%
Number of Bases Read2	972,781,191	972,524,721	99.97%
Maximum Read Length	51	51	100%
Read Pairs (Not Counting Singletons)	19,074,141	19,070,383	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



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%	3,758	0.02%
Mean Quality	0	0%	0	0%
G/C Content	0	0%	0	0%
Complexity	0	0%	0	0%
Not Passing Filters Flag	0	0%	0	0%