M. smegmatis variant calling pipeline - Support #113

QC of files

02/14/2020 01:09 PM - Jon Ambler

Status:	New		**Start date:**	02/14/2020
Priority:	Normal		**Due date:**	
Assignee:	Jon Ambler		**% Done:**	10%
Category:			**Estimated time:**	0.00 hour
Target version:			**Spent time:**	3.00 hours

Description
Running the fastq files through QC to determine if the quality is acceptable.
Using MultiQC pipeline

History

#1 - 02/14/2020 01:14 PM - Jon Ambler

- % Done changed from 0 to 10

After the pipeline was set up, the initial runs failed, and upon inspection of the fastq files it appears that they are using illumina 1.5 encoding for the quality scores, as seen by the use of the "J" character.

The files will need to be converted to 1.9 scores.