WGS Competency Assessment Report

Example Report

August 26, 2019

1 Overview

This report provides an analytical evaluation of sequencing metrics for bacterial whole genome sequencing data comprising a sequencing competency assessment exercise. Sequence metrics have been compared to expected values based on recommended data submission thresholds or derived from the distribution of isolates sequenced during the 2018 PulseNet-GenomeTrakr harmonized Proficiency Testing (PT) exercise as part of a 16-sample 2X250 run on an Illumina MiSeq machine (V2 chemistry) using the Nextera XT DNA Library Prep Kit.

	Isolate ID	Organism
1	SAP18-0432	Salmonella enterica subsp. enterica serovar Enteritidis
2	SAP18-H9654	Salmonella enterica subsp. enterica serovar Enteritidis
3	SAP18-6199	Salmonella enterica subsp. enterica serovar Typhimurium
4	SAP18-8729	Salmonella enterica subsp. enterica serovar Newport
5	LMP18-H2446	Listeria monocytogenes
6	LMP18-H8393	Listeria monocytogenes

Table 1: The 2018 PT isolates.

	Sample ID	Isolate ID	Machine	Flowcell
1	SEQ000070739	SAP18-H9654	M04590	BKRCT
2	SEQ000070740	SAP18-8729	M04590	BKRCT
3	SEQ000070741	SAP18-6199	M04590	BKRCT
4	SEQ000070742	SAP18-0432	M04590	BKRCT
5	SEQ000070743	LMP18-H8393	M04590	BKRCT
6	SEQ000070744	LMP18-H2446	M04590	BKRCT

Table 2: Isolates submitted for analysis.

2 Results

Of the 6 isolates submitted as part of this exercise, 6 (100%) were determined to be correctly annotated and to have fully met the analytical expectations of this exercise.

2.1 Competency Assessment Metrics

The following metrics are under evaluation in this competency assessment -

- **Taxonomy Check** - was the correct organism sequenced?
- **MeanDepth** - the mean depth of coverage.
- **MeanInsert** - the mean length of the sequence between the adapters.
- **MeanR1Qual** - the mean R1 read quality scores (forward reads).
- **MeanR2Qual** - the mean R2 read quality scores (reverse reads).
- **NG50** - a metric describing the distribution of contig lengths.
- **Contigs** - the total number of contigs in the assembly.

SampleID	Isolate ID	Metric	Threshold	Value
SEQ000070739	SAP18-H9654	Taxonomy Check	PASS	**PASS**
SEQ000070739	SAP18-H9654	MeanR1Qual	≥ 30	**35.2**
SEQ000070739	SAP18-H9654	MeanR2Qual	≥ 30	**33**
SEQ000070739	SAP18-H9654	MeanDepth	≥ 20	**141.98**
SEQ000070739	SAP18-H9654	MeanInsert	≥ 203.3	**467.16**
SEQ000070739	SAP18-H9654	NG50	≥ 259138.5	**401093**
SEQ000070739	SAP18-H9654	Contigs	≤ 97.25	**68**
SEQ000070740	SAP18-8729	Taxonomy Check	PASS	**PASS**
SEQ000070740	SAP18-8729	MeanR1Qual	≥ 30	**35.1**
SEQ000070740	SAP18-8729	MeanR2Qual	≥ 30	**32.7**
SEQ000070740	SAP18-8729	MeanDepth	≥ 20	**100.07**
SEQ000070740	SAP18-8729	MeanInsert	≥ 203.1	**480.47**
SEQ000070740	SAP18-8729	NG50	≥ 0	**498666**
SEQ000070740	SAP18-8729	Contigs	≤ 132	**103**
SEQ000070741	SAP18-6199	Taxonomy Check	PASS	**PASS**
SEQ000070741	SAP18-6199	MeanR1Qual	≥ 30	**35.1**
SEQ000070741	SAP18-6199	MeanR2Qual	≥ 30	**32.7**
SEQ000070741	SAP18-6199	MeanDepth	≥ 20	**103.15**
SEQ000070741	SAP18-6199	MeanInsert	≥ 144.9	**478.79**
SEQ000070741	SAP18-6199	NG50	≥ 76894.5	**325078**
SEQ000070741	SAP18-6199	Contigs	≤ 116.5	**69**
SEQ000070742	SAP18-0432	Taxonomy Check	PASS	**PASS**
SEQ000070742	SAP18-0432	MeanR1Qual	≥ 30	**35**
SEQ000070742	SAP18-0432	MeanR2Qual	≥ 30	**32.3**
SEQ000070742	SAP18-0432	MeanDepth	≥ 20	**88.05**
SEQ000070742	SAP18-0432	MeanInsert	≥ 180.65	**467.6**
SEQ000070742	SAP18-0432	NG50	≥ 38077.5	**479246**
SEQ000070742	SAP18-0432	Contigs	≤ 102.5	**66**
SEQ000070743	LMP18-H8393	Taxonomy Check	PASS	**PASS**
SEQ000070743	LMP18-H8393	MeanR1Qual	≥ 30	**36.5**
SEQ000070743	LMP18-H8393	MeanR2Qual	≥ 30	**34**
SEQ000070743	LMP18-H8393	MeanDepth	≥ 20	**130.35**
SEQ000070743	LMP18-H8393	MeanInsert	≥ 160.25	**428.81**
SEQ000070743	LMP18-H8393	NG50	≥ 67986.5	**523238**
SEQ000070743	LMP18-H8393	Contigs	≤ 159	**53**
SEQ000070744	LMP18-H2446	Taxonomy Check	PASS	**PASS**
SEQ000070744	LMP18-H2446	MeanR1Qual	≥ 30	**36.5**
SEQ000070744	LMP18-H2446	MeanR2Qual	≥ 30	**33.9**
SEQ000070744	LMP18-H2446	MeanDepth	≥ 20	**96.87**
SEQ000070744	LMP18-H2446	MeanInsert	≥ 172.6	**434.23**
SEQ000070744	LMP18-H2446	NG50	≥ 347436.5	**497410**
SEQ000070744	LMP18-H2446	Contigs	≤ 128.5	**64**

Table 3: Competency Assessment Metrics - Quantitative Results.