iSeq\_report\_test

Patrick Mitchell

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## R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

## Read Metrics

The table below gives quality metrics for the reads produced by this run. Targets are average forward and reverse quality scores for both the forward and reverse reads and coverage depth X for *E. coli* and X for *L. monocytogenes*. Coverage is estimated by multiplying the number of reads by the average read length and dividing by the expected genome length (5 Mbp for *E. coli* and 3 Mbp for *L. monocytogenes*).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Isolate | Reads | F.Length | R.Length | F.Q | R.Q | Est..Coverage |
| 804-002-iSeq-EC-11\_FS10000375 | 1010607 | 148.29 | 148.28 | 35.08 | 34.50 | 60X |
| 804-002-iSeq-EC-12\_FS10000375 | 811051 | 147.79 | 147.77 | 35.08 | 34.55 | 48X |
| 804-002-iSeq-EC-13\_FS10000375 | 1006291 | 147.93 | 147.92 | 35.16 | 34.54 | 60X |
| 804-002-iSeq-EC-14\_FS10000375 | 763342 | 148.26 | 148.23 | 35.12 | 34.75 | 45X |
| 804-002-iSeq-LM-19\_FS10000375 | 606247 | 148.26 | 148.25 | 35.16 | 34.80 | 60X |
| 804-002-iSeq-LM-20\_FS10000375 | 817280 | 147.77 | 147.76 | 35.21 | 34.60 | 81X |

## Assembly Metrics

The table below describes the *de novo* assemblies generated for each isolate by SKESA. Target values for the number of contigs and total assembly length are are 264 600 and 4.2013 5.9 Mbp for *E. coli* and 264 200 and 2.8265 3.1 Mbp for *L. monocytogenes*. The

You can also embed plots, for example:



Note that the echo = FALSE parameter was added to the code chunk to prevent printing of the R code that generated the plot.