

The following Questions and Answers are regarding RFSO# 01R11-22-S009 for High Throughput Sequencing Services, Lacombe, AB

Question 11:

The sequencing quantity for 16S rRNA Gene Sequencing will not give the requested coverage of 50,000 reads per sample (1 run MiSeq PE 250bp or PE 300bp). Can we change the quantity indicated for the one that will give the coverage requested?

Response: Yes.

Question 12:

For the Shotgun Metagenomic Sequencing, it is indicated NovaSeq6000 SP 2x150bp) flowcell, meaning Paired End 150bp, and for the other sequencing options it is indicated 1 x 150bp, meaning Single End 150bp. There are no available kits for Single End 150bp sequencing. Was Paired End 150bp meant to be written for all the sequencing options?

Response: If single end 150 bp sequencing is not available then it can be paired-end 150 bp sequencing.

Question 13:

For the Whole Genome Sequencing of bacterial Genome-Short read, can we offer the sequencing option that will best fit the shotgun library size (PE 300bp is not ideal, PE 250bp is better suited)?

Response: Yes