

UWBC Service Request Summary

Submission: M005172

Project:

Submitter: Gilbert Loiseau

loiseau@wisc.edu

Account: Senes Lab

Funding Source/PO: 144-073000-AAH2728-4

Submission Created Date: Oct 16, 2023

Sample Drop off Date

(Requester Must Enter when Dropping off Samples): _____

Mailing Address:

Room 1250
Biotechnology Center
425 Henry Mall
Madison WI 53706
Email: nextgen-seq@biotech.wisc.edu
Phone: (608) 262-4657

Type of Submission	Library Preparation and Sequencing (Includes applicable QC)
Submission Summary	<p>Library Preparation Services: -Index PCR (TruSeq) Library Preparation</p> <p>Sequencing Services: -Illumina (NovaSeq) Sequencing [2x150 Shared (10M read increments)]</p> <p>QC Services: -None</p> <p>Additional Services: -None</p>
Sample Type	DNA, Amplified or Enriched DNA
General Sample Information	<p>Organism/Sample Type: E. coli (purified DNA)</p> <p>Biosafety Level: Unknown</p> <p>Collection Date Unknown</p>
Number of Samples or Libraries	36
Number of Pools	
Sequencing Run Type	<p>Platform: Illumina (NovaSeq)</p> <p>Flow Cell: 2x150 Shared (10M read increments)</p> <p>Read Length: 2x150 (Paired-End Sequencing)</p>
Total Number of Lanes/Flow Cells	
Total Ordered Reads (Millions)	36.0
Index Type/Length	
Custom Primer Information	
Sample Buffer	Qiagen EB Buffer
Sequencing Special Instructions	Quick question: Since I have 36 samples that I typically would want 1M reads for, will I instead be able to get 40M reads total making it ~1.11M reads for each sample?

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Customer Plate/Container Name

GJL-CHIP2