

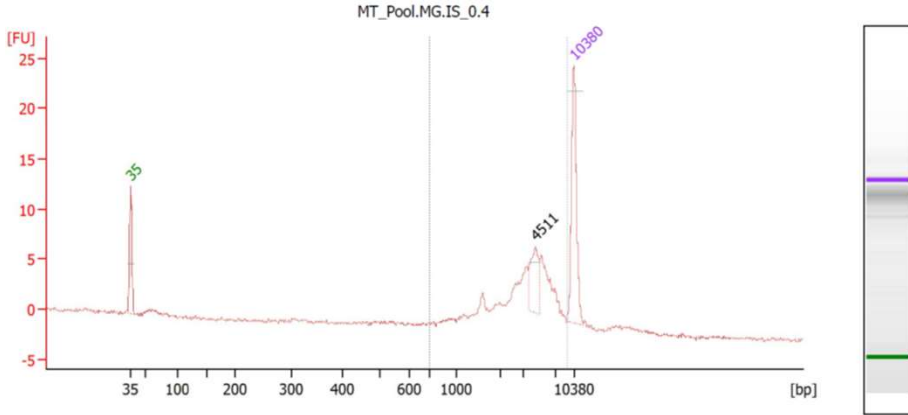
UW PacBio Sequencing Report



Requester: Matthew George
 Requester's email: mngeorge@uw.edu
 Date Submitted: 12/14/2022

Library Statistics:

MT_Pool.MG.IS
 Library prep: Iso-Seq Express
 Library size range (bp): 1,500-9,000



Sequencing Run Parameters

Total Sequencing run: 1 Number of SMRT cells: 1

Run Name	Sample	Chemistry	SMRT Cell Type	Movie Time (hrs)	Pre-Extension Time (hrs)	Total Bases (Gb)
20230426_SQ2_PCB-CC_eee	MT_Pool.MG.IS	Sequel II v3.1	SMRT Cell 8M	30	2	461.5

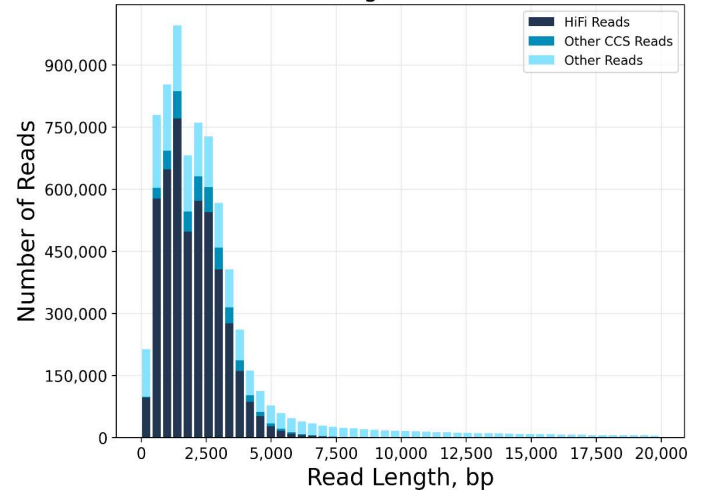
Sequencing Run Statistics

Run Name	Sample	Unique Molecular Yield (Gb)	P1 Total	Polymerase RL (bp)	Longest Subread (bp)	Longest Subread N50 (bp)
20230426_SQ2_PCB-CC_eee	MT_Pool.MG.IS	32.1	7,446,997	62,150	5,807	11,911

CCS Analysis Results

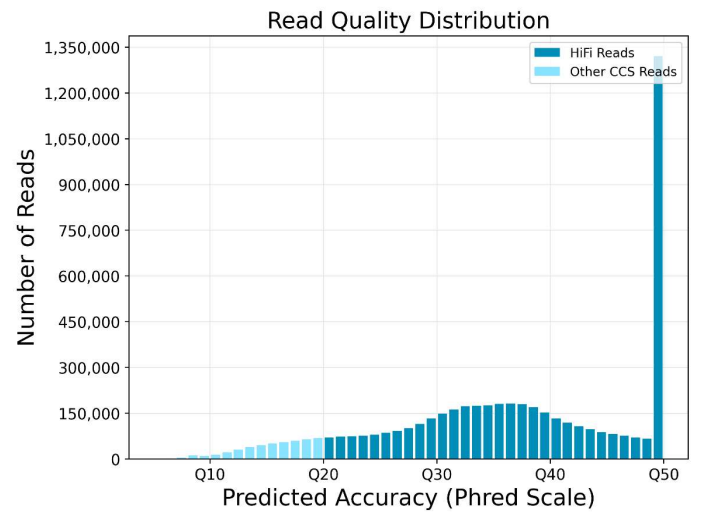
Sample Name	MT_Pool.MG.IS
Status	SUCCESSFUL
HiFi Reads	4,757,587
HiFi Yield (bp)	9,361,595,057
HiFi Read Length (mean, bp)	1,967
HiFi Read Length (median, bp)	1,809
HiFi Read Length N50 (bp)	2,529
HiFi Read Quality (median)	Q39
HiFi Number of Passes (mean)	20
<Q20 Reads	475,292
<Q20 Yield (bp)	1,200,565,758
<Q20 Read Length (mean, bp)	2,525
<Q20 Read Quality (median)	Q16

Read Length Distribution



Iso-Seq Analysis Read Classification

Sample Name	MT_Pool.MG.IS
Reads	7,426,132
Reads with 5' and 3' Primers	5,012,206
Non-Concatamer Reads with 5' and 3' Primers	4,849,473
Non-Concatamer Reads with 5' and 3' Primers and Poly-A Tail	4,844,793
Mean Length of Full-Length Non-Concatamer Reads	1,899
Unique Primers	6
Mean Reads per Primer	835,367
Max. Reads per Primer	2,542,894
Min. Reads per Primer	11,955
Reads without Primers	2,413,926
Percent Bases in Reads with Primers	31%
Percent Reads with Primers	67%



Primer Data

Bio Sample Name	Primer Name	CCS Reads	Mean Primer Quality	Reads with 5' and 3' Primers	Non-Concatamer Reads with 5' and 3' Primers	Reads with 5' and 3' Primers and Poly-A Tail
MTF_rep2	bc1012_MTF_2_5p--bc1012_MTF_2_3p	1,393,520	94	1,393,520	1,298,206	1,297,327
MTG	bc1020_MTG_5p--bc1020_MTG_3p	2,542,894	95	2,542,894	2,530,035	2,527,226
MTF	bc1023_MTF_5p--bc1023_MTF_3p	1,004,737	94	1,004,737	963,640	962,715

Transcript Clustering

Sample Name	Number of High-Quality Isoforms	Number of Low-Quality Isoforms
MTF_rep2	188,270	1,646
MTG	327,736	3,428
MTF	159,632	1,513

