UW PacBio Sequencing Report:

Requester: Sam White
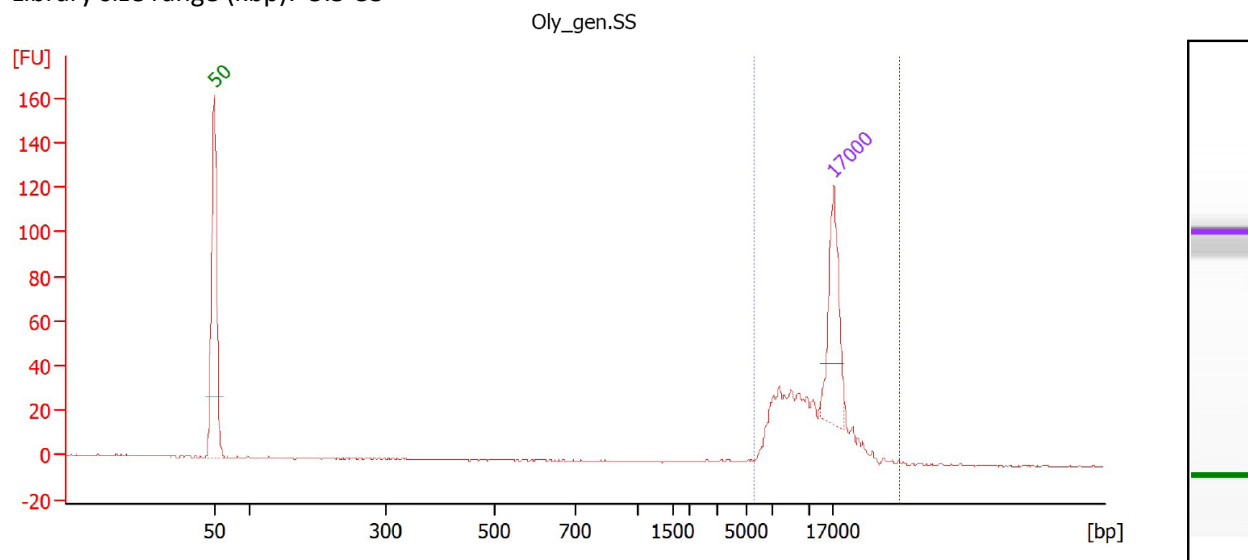Requester's email: samwhite@uw.edu
Date Submitted: 11/14/2016

Library Statistics:
Library prep: 20kb SMRTbell library prep with 5kb cutoff BluePippin size selection and damage repair
Library size range (kbp): 5.5-35

Sequencing Statistics:
Total Sequencing run: 4
Number SMRT cells used: 10

Sample Name	RQ	productive ZMWs	Mean Pol Readlength (bp)	Mean ROI Readlength (bp)
oly_genome_pacbio.SW.SS	0.83	96923	14681	7243
oly_genome_pacbio.SW.SS	0.81	106003	14713	9831
oly_genome_pacbio.SW.SS	0.81	99274	14283	9747
oly_genome_pacbio.SW.SS	0.81	105811	14682	9937
oly_genome_pacbio.SW.SS	0.83	105279	14023	7887
oly_genome_pacbio.SW.SS	0.83	108561	13757	7930
oly_genome_pacbio.SW.SS	0.83	90216	11557	7043
oly_genome_pacbio.SW.SS	0.84	81683	11242	6890
oly_genome_pacbio.SW.SS	0.84	74733	11149	6847
oly_genome_pacbio.SW.SS	0.83	82538	11054	6885

Data download instructions:

1. Install Aspera browser plugin from the Aspera website. Reload the web

http://downloads.asperasoft.com/download_connect/

2. In a web browser, navigate to the UW Genome Science's Aspera server at:

https://aspera.gs.washington.edu/aspera/user/

3. Login to the site with the given username and password.

Username : `pacbio-aspera3`
Password : `vaiC7ciesiec`

4. Select all available files to download and click "Download". From UW's campus we have experienced download speeds of ~40 Mbps. A single SMRT cell's worth of data will take ~10 minutes to download at this rate.

Data are grouped into folders by SMRT cell. Folders are generically named by the position of the cell in the run (A01_1, B01_1, etc.). Reads are available in PacBio's HDF5 format as .bas.h5 files. Metadata for each SMRT cell is available in PacBio's XML format.

PLEASE NOTE THAT DATA WILL BE AVAILABLE ON ASPERA FOR 30 DAYS ONLY. PLEASE DOWNLOAD YOUR FILES BEFORE THIS GRACE PERIOD EXPIRES.

Tools for analysis of .bas.h5 files are available on PacBio's DevNet site (https://github.com/PacificBiosciences/SMRT-Analysis) including the SMRT Analysis toolkit which can perform de novo assembly and resequencing. You will also find documentation for running this analysis tool installed on the Amazon cloud.