


AZENTA NGS PACBIO DATA REPORT

1. PROJECT

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Email	
Quote	
Configuration	Revio

2. WORKFLOW

2.1 PacBio sequel sequencing workflow

The quantity and quality of DNA were assessed. DNA was sheared with Megaruptor 3 system into desired size, PacBio library was prepared using SMRTbell prep kit with bead size selection per the manufacturer’s protocol. Follow the run design guidelines for sequencing. Figure 2.1 outlines the PacBio library preparation and sequencing workflow.

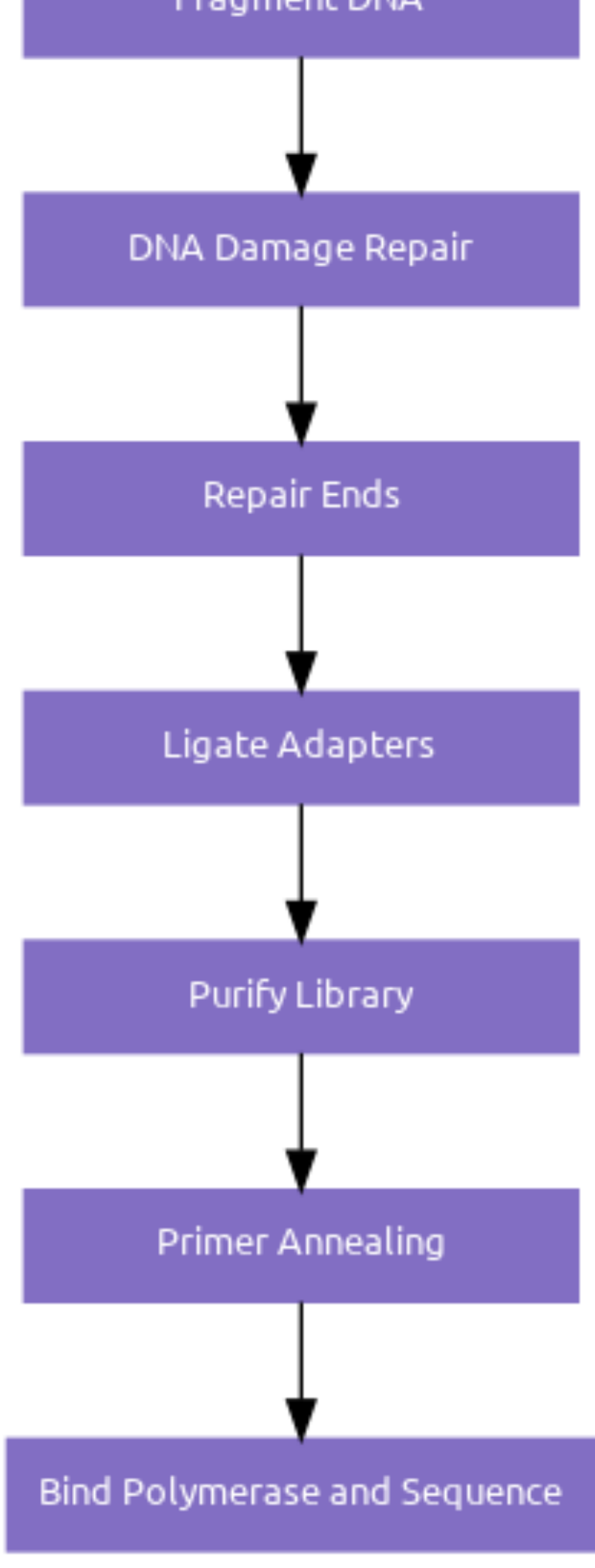


Figure 2.1 Pacbio library preparation and sequencing workflow

3. CCS ANALYSIS

PacBio SMRTbell libraries were prepared per the manufacturer’s instructions. SMRTbell libraries were then sequenced on the PacBio Revio platform with v3.0 chemistry. Then, hifi_reads.bam were generated by SQIle running SMRTLINK v.12.0.

3.1 CCS read Statistics

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Table 3.1 CCS data summary statistics by sample

Sample ID	CCS Reads	Number of CCS Bases	CCS Read Length (mean)	CCS Read Score (mean)	Number of Passes (mean)
APPLdM	333,998	3,460,557,768	10,360	0.999	16

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3.2 CCS Read Length

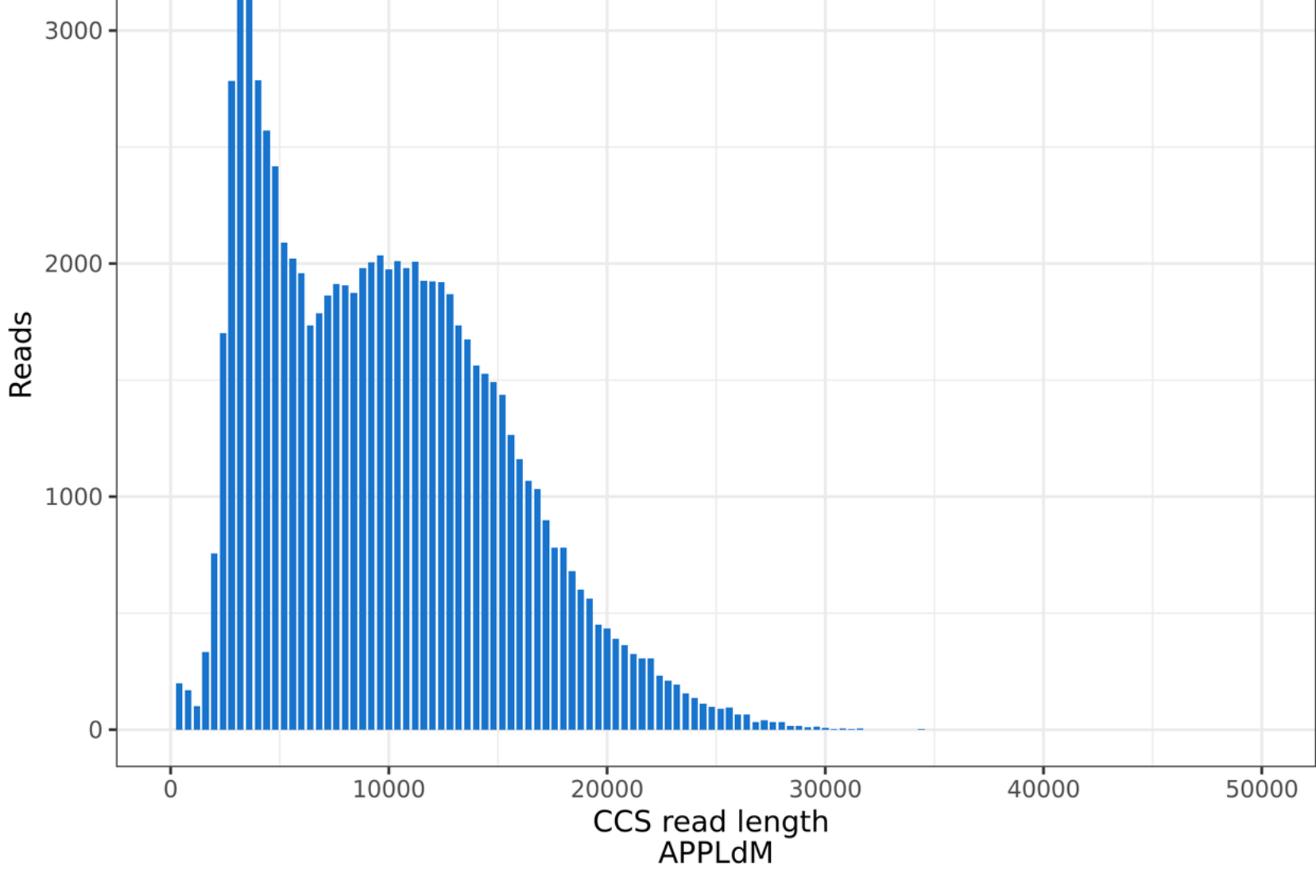


Figure 3.2 CCS data read length distribution

3.3 CCS Read Score

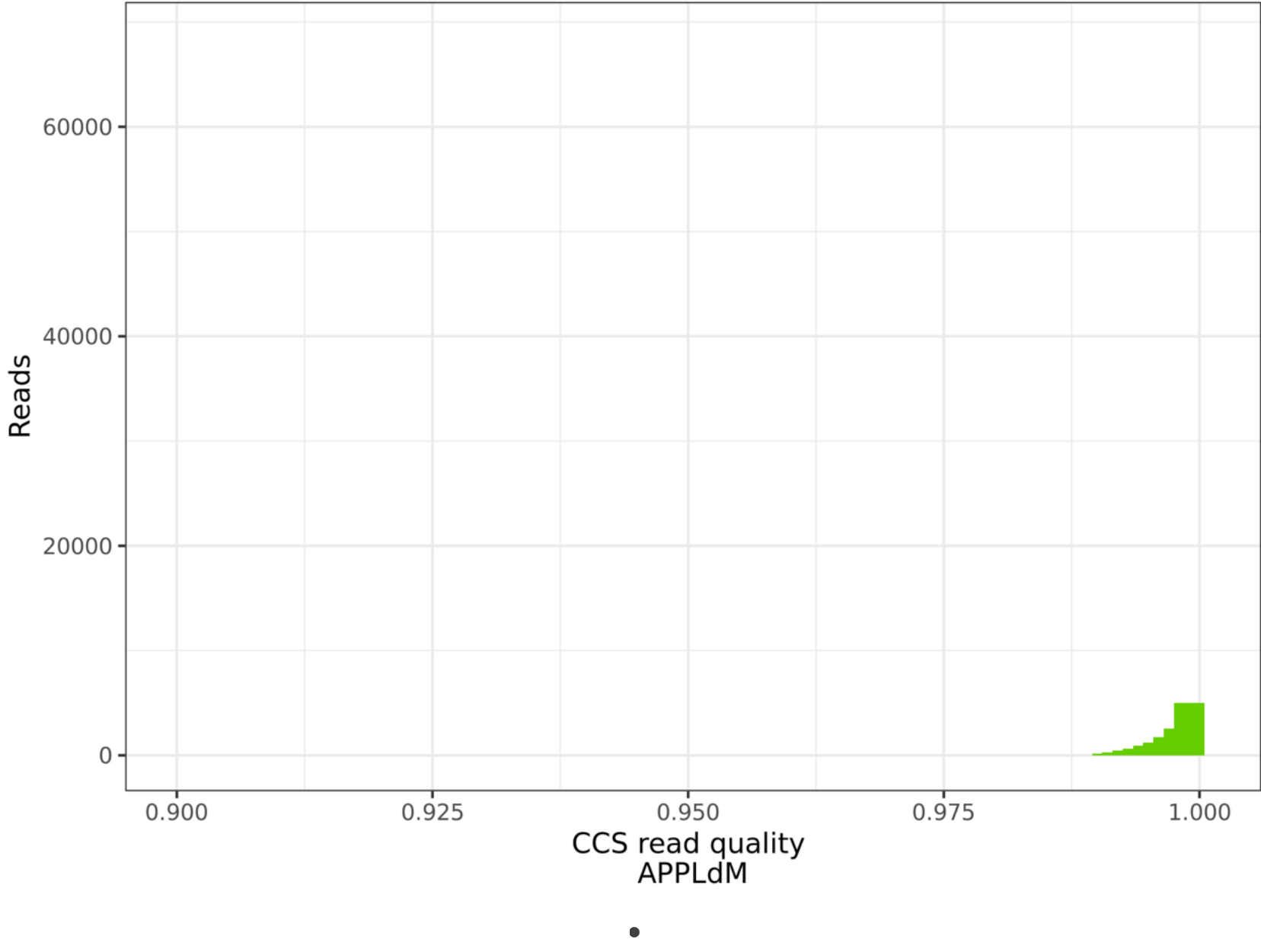


Figure 3.3 CCS data read score distribution

3.4 Number of Passes

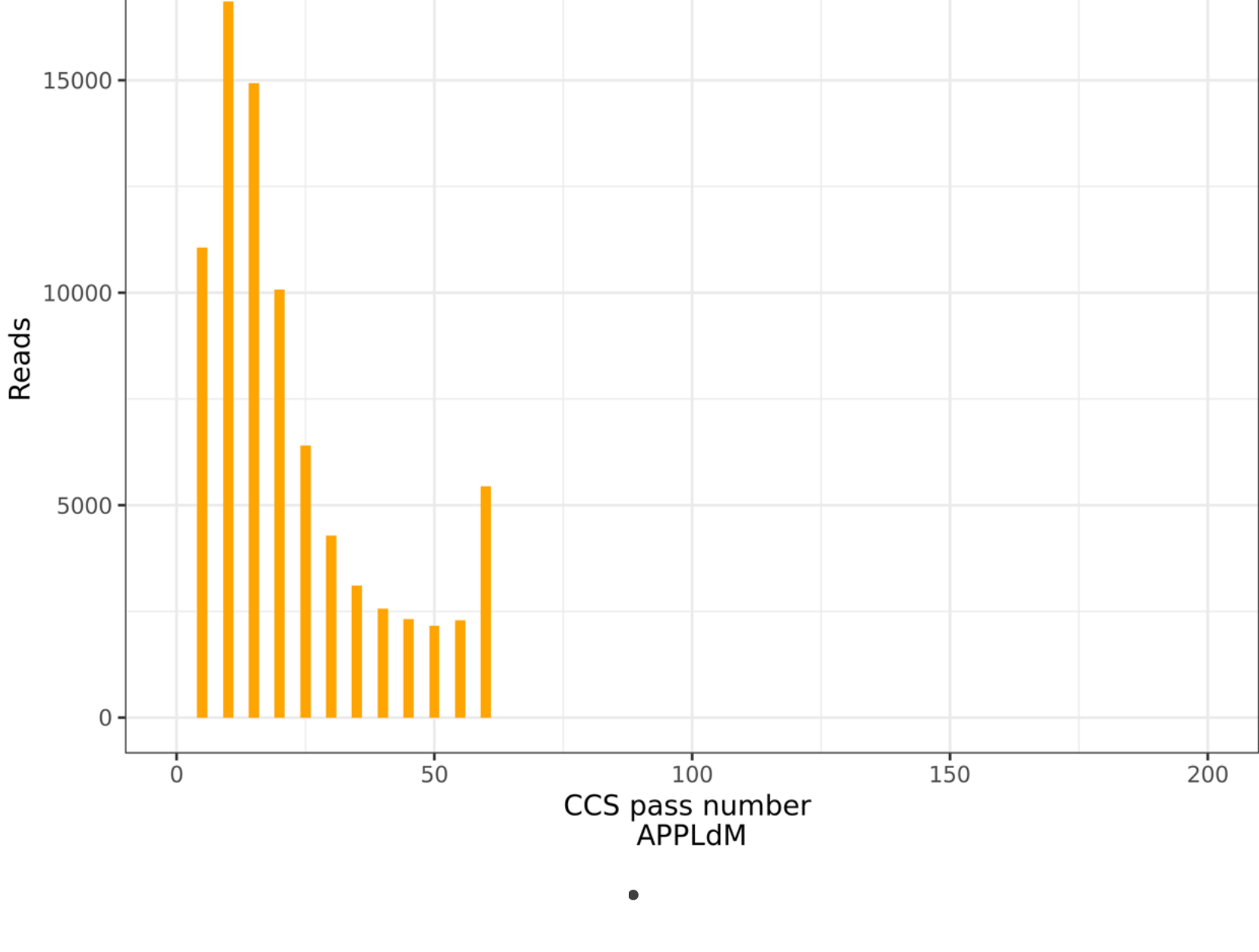


Figure 3.4 CCS data pass number distribution

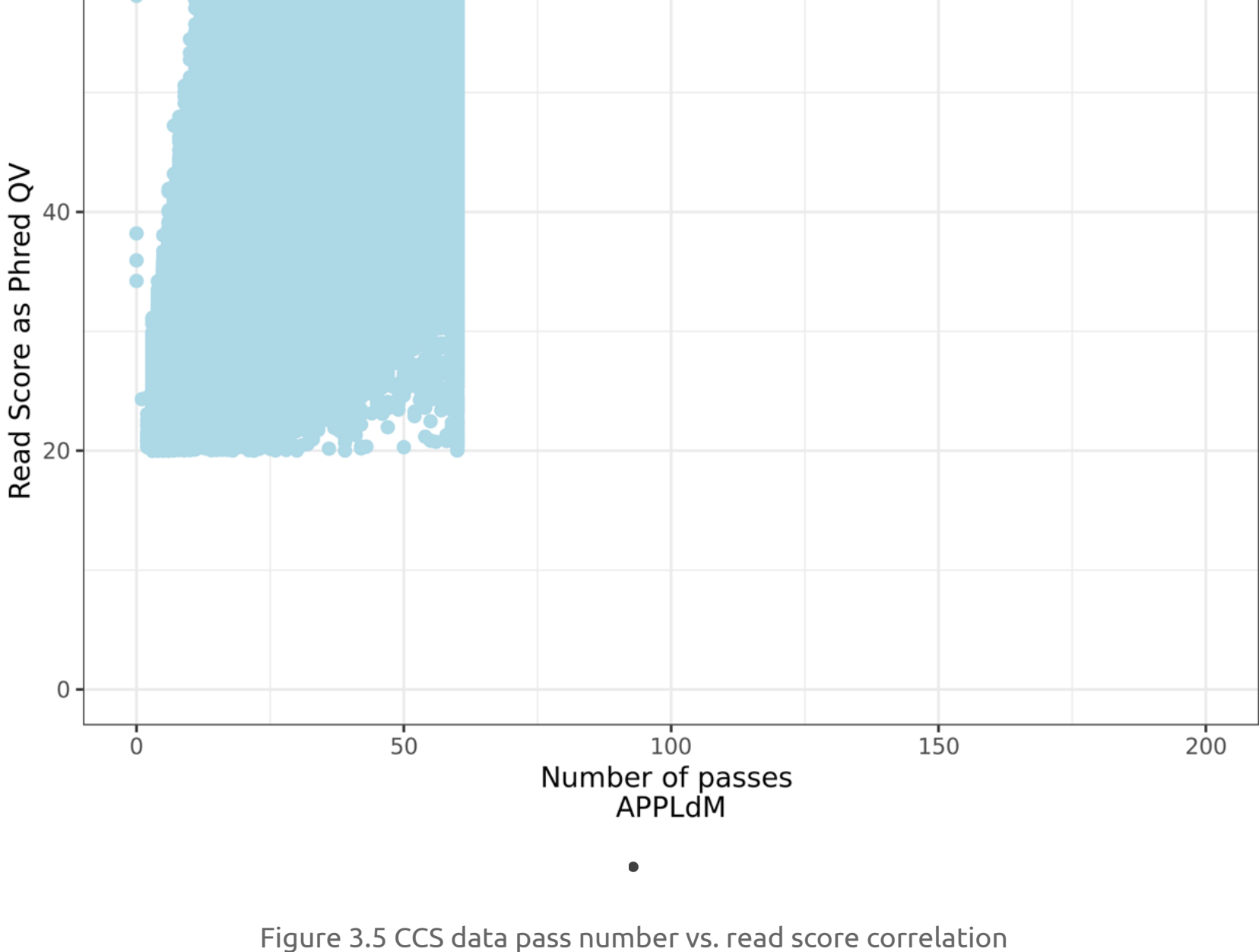


Figure 3.5 CCS data pass number vs. read score correlation

4. DELIVERABLES

- Data Analysis Report.
- Raw reads.bam output and supporting files.
- Demultiplexed output and supporting files (if applicable).
- Fastq files with CCS reads for each sample.