# CLR (Continuous Long Read) Result

1. Loading

|  |  |  |  |
| --- | --- | --- | --- |
| **Productive ZMWs** | **Productivity 0** | **Productivity 1** | **Productivity 2** |
| {{zmw\_count}} | {{p0\_count}} | {{p1\_count}} | {{p2\_count}} |
| {{zmw\_percent}} | {{p0\_percent}} | {{p1\_percent}} | {{p2\_percent}} |

Productivity 0: Empty ZMW, no signal detected.

Productivity 1: ZMW with a high quality read detected.

Productivity 2: Other, signal detected but no high quality read.

1. Adapter

|  |  |
| --- | --- |
| **Adapter Dimers (0-10bp) %** | **Short Inserts (11-100bp) %** |
| {{adapter\_dimer}} | {{short\_inserts}} |

Adapter Dimer: The % of pre-filter ZMWs which have observed inserts of 0-10 bp. These are likely adapter dimers.

Short Insert: The % of pre-filter ZMWs which have observed inserts of 11-100 bp. These are likely short fragment contamination.

1. Polymerase Reads

|  |  |  |  |
| --- | --- | --- | --- |
| **Polymerase Read Bases** | **Polymerase Reads** | **Polymerase Read Length (Mean)** | **Polymerase Read N50** |
| {{polymerase\_bases}} | {{polymerase\_reads}} | {{polymerase\_length}} | {{polymerase\_n50}} |

Polymerase Read Length Mean: The mean high-quality read length of all polymerase reads. The value includes bases from adapters as well as multiple passes around a circular template.

Polymerase Read Length N50: 50% of all read bases came from polymerase reads longer than this value.

1. Subreads

|  |  |  |
| --- | --- | --- |
| **Longest Subread Length (Mean)** | **Longest Subread N50** | **Unique Molecular Yield** |
| {{longest\_subread\_length}} | {{longest\_subread\_n50}} | {{unique\_my}} |

Longest Subread Mean: The mean subread length, considering only the longest subread from each ZMW.

Longest Subread N50: 50% of all read bases came from subreads longer than this value when considering only the longest subread from each ZMW.

Unique Molecular Yield: The sum total length of unique single molecules that were sequenced. It is calculated as the sum of perZMW median subread lengths.

1. Polymerase Read Length

{{polymerase\_read\_length\_plot}}

Plots the number of reads against the polymerase read length.

{% if subread\_length\_plot == “” %}{% else %}

1. Subread Read Length

{{subread\_length\_plot}}

Plots the number of reads against the subread length.

{% endif %}

{% if base\_yield\_density\_plot==”” %}{% else %}

1. Base Yield Density

{{base\_yield\_density\_plot}}

Displays the number of bases sequenced in the collection, according to the length of the read in which they were observed. Values displayed are per unit of read length (i.e. the base yield density) and are averaged over 2000 bp windows to gently smooth the data. Regions of the graph corresponding to bases found in reads longer than the N50 and N95 values are shaded in medium and dark blue, respectively.

{% endif %}