**Nanopore Full-Length Sequencing Report**

1. **Clean Data QC**

The raw data obtained from Nanopore sequencing undergoes quality control processes, such as trimming residual adapter sequences, length filtering, and sequencing quality filtering to generate clean data. This clean data is used for further data analysis.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Vector/Sample ID** | **Clone ID** | **Total Reads** | **Total Bases** | **Read Length N50** | **Mean Read Length** | **Mean Read Quality** |
| {{vector\_id}} | {{clone\_id}} | {{total\_reads}} | {{total\_base}} | {{read\_len\_n50}} | {{mean\_read\_len}} | {{mean\_read\_qual}} |

1. **Distribution of Read Length**

A distribution plot of read lengths in sequencing results. The x-axis represents the read lengths, while the y-axis represents the number of reads. The bins represent the length intervals of the histogram.

{{image1}}

1. **Clean Data Mapping Results**

The clean data is aligned to a reference sequence using minimap2, and the results are analyzed to obtain information such as coverage and depth.The pattern diagram of the sequencing results aligned to the reference sequence is shown below. The X-axis represents the position of bases in the reference sequence, and the Y-axis represents the sequencing depth at each position.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Vector/Sample ID** | **Ref Length** | **Map Ratio** | **Avg Depth** | **Median Depth** | **Coverage** | **Cov 30x** | **Cov 100x** | **Mutation Counts** | **Result** |
| {{vector\_id}} | {{ref\_len}} | {{map\_ratio}} | {{avg\_depth}} | {{median\_depth}} | {{cov}} | {{cov\_30x}} | {{cov\_100x}} | {{mutation\_counts}} | {{is\_map\_pass}} |

{{image2}}

1. **Mutations and Structure Variation**

This section displays the differences between the actual sequencing results and the reference sequence. If the table contains only a "-", it indicates that no credible variations were detected in sample.

**4.1 High-confidence Results**

These are confident mutations as there are no specific structures near these types of mutations, and the allele frequency is higher.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Vector/Sample ID** | **POS** | **REF/SV Type** | **ALT/SV Length** | **AF (%)** |
| {%tr for k,d in hi\_mutation\_list.items() %} | | | | |
| {{vector\_id}} | {{d.pos}} | {{d.ref}} | {{d.alt}} | {{d.af}} |
| {%tr endfor %} | | | | |
| {% if hi\_mutation\_list|length ==0 %}-{% else %}{% endif %} | | | | |

**4.2 Low-confidence Results**

These types of mutations occur in low complexity regions of nucleic acids, such as oligonucleotide regions, and have a low allele frequency. Consequently, these sites have a low level of confidence.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Vector/Sample ID** | **POS** | **REF (SV Type)** | **ALT (SV Len)** | **AF (%)** |
| {%tr for k,d in low\_mutation\_list.items() %} | | | | |
| {{vector\_id}} | {{d.pos}} | {{d.ref}} | {{d.alt}} | {{d.af}} |
| {%tr endfor %} | | | | |
| {% if low\_mutation\_list|length ==0 %}-{% else %}{% endif %} | | | | |