**Phage Genomics and Bioinformatics Assembly Report**

PHATCAT

**«Phage\_Name»**

|  |  |
| --- | --- |
| Sequencing Run Name | «Sequencing\_Run\_Name» |
| Date Data Received | «Date\_Data\_Received» |
| Date Pipeline Ran | «DateAnalysisRan» |
| Data location | «OutputLocation» |

Sequencing Reads Statistics

|  |  |  |
| --- | --- | --- |
| Total # of reads | «TotalNumReads» | |
| Average Quality Score | «AvgQual» | |
| # Reads Passed QC | **EDGE** | **CLCbio** |
| «NumQCReadsEDGE» | «NumQCReadsCLC» |
| % reads that passed QC | «PercentQCReadsEDGE» | «PercentQCReadsCLC» |

Genome Assembly Statistics

|  |  |  |
| --- | --- | --- |
| ***Original Assembly***  # of contigs (>700 bp) | **SPAdes** | **CLCbio** |
| «NumSPAdesContigs» | «NumCLCContigs» |
| Largest Contig Size (bp) | «SPAdesLargestContigSize» | «CLCLargestContigSize» |
| Largest Contig Coverage | «SPAdesLargestContigCov» | «CLCLargestContigCov» |
| N50 | «SPAdesN50» | «CLCN50» |
| Total Assembly Size (bp) | «SPAdesAssemblySize» | «CLCAssemblySize» |
| # Overlap Bases | «SPAdesOverlap» | «CLCOverlap» |
| ***Subassembly*** | **SPAdes** | **CLCbio** |
| # Reads Subsampled | «SSNumReads» | |
| # of Contigs (>700 bp) | «NumSPAdesSSContigs» | «NumCLCSSContigs» |
| Largest Contig Size (bp) | «SPAdesSSLargestContigSize» | «CLCSSLargestContigSize» |
| Largest Contig Coverage | «SPAdesSSLargestContigCov» | «CLCSSLargestContigCov» |
| N50 | «SPAdesSSN50» | «CLCSSN50» |
| Total Assembly Size (bp) | «SPAdesSSAssemblySize» | «CLCSSAssemblySize» |
| # Overlap Bases | «SPAdesSSOverlap» | «CLCSSOverlap» |
| Comparison of Largest Contigs | «AssemblyComparison» | |