# Assembly Results

|  |  |
| --- | --- |
| Sample | MS21-02 |
| # of Contigs | 325,092 |
| Total Size of Contigs | 251,871,255 |
| Longest Contig | 383,550 |
| Shortest Contig | 200 |
| Mean Contig Size | 775 |
| Median Contig Size | 366 |
| N50 Contig Length | 1,276 |
| % GC Content | 37.52 |

Around **251Mb** of genome was assembled with ‘**megahit**‘. The longest contig size is apprx. **383kb**, and the shortest contig size is **200bp**. The N50 read length is 1.2kb which is due to the short reads sequenced by Illumina platform.

# Annotation Results

1. Gene Prediction Stats

|  |  |
| --- | --- |
| CDS Count | 372,388 |
| Repeat Region Count | 83 |
| tRNA Count | 3,594 |
| rRNA Count | 867 |

1. Functional Profiles

|  |  |  |  |
| --- | --- | --- | --- |
| **# of GO** | **# of KO** | **# of Pfam** | **# of TIGRFAM** |
| 6,865 | 5,344 | 6,028 | 2,164 |

1. Pathway Profiles

|  |  |
| --- | --- |
| **# of KEGG Pathways** | **# of MetaCyc Pathways** |
| 169 | 46 |

1. Plots

# MAG Results

# MAG Classification Results

# Download Data

# Appendix