# Analysis Results

1. Genome Assembly

|  |  |
| --- | --- |
| Tool | **Count** |
| **# Contigs** | {{contig}} |
| **Total Size of Contigs** | {{size}} |
| **Longest Contig** | {{longest}} |
| **Shortest Contig** | {{shortest}} |
| **# Contigs > 1K nt** | {{K}} |
| **# Contigs > 10K nt** | {{KK}} |
| **# Contigs > 100K nt** | {{KKK}} |
| **# Contigs > 1M nt** | {{M}} |
| **# Contigs > 10M nt** | {{MM}} |
| **Mean Contig Size** | {{mean}} |
| **Median Contig Size** | {{median}} |
| **N50 Contig Length** | {{n50}} |
| **L50 Contig Count** | {{l50}} |
| **% GC Contents** | {{gc}} |

1. Genome Assembly Assessment

|  |  |  |  |
| --- | --- | --- | --- |
| Database – {{db}} | **Count** | | **Percent** |
| **Complete BUSCOs** | | {{complete}} | {{completep}} |
| **Complete & Single-Copy BUSCOs** | | {{completeSC}} | {{completeSCp}} |
| **Complete & Duplicated BUSCOs** | | {{completeD}} | {{completeDp}} |
| **Fragmented BUSCOs** | | {{fragmented}} | {{fragmentedp}} |
| **Missing BUSCOs** | | {{missing}} | {{missingp}} |
| **Total BUSCO Groups Searched** | | {{total}} |  |