|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Sample** | **M** | **L** | **F** | **1F** | | **2F** | |
| **Sequencing** | Illumina platform | HiSeq2000 | HiSeq2000 | HiSeq2000 | NextSeq500 | | NextSeq500 | |
|  | Number of raw reads | 24,110,256 | 24,330,693 | 23,264,636 | 39,664,366 | | 37,127,852 | |
|  | Number of clean reads | 18,472,374 | 17,435,976 | 15,290,201 | 36,491,216 | | 34,157,623 | |
|  | Average read length (bases) | 2\*100 | 2\*100 | 2\*100 | 2\*80 | | 2\*80 | |
| **Accession number** | NCBI SRA | SRR3995704 | SRR3995705 | SRR3995703 | SRR5965731 | | SRR5965732 | |
|  | NCBI TSA | GEZL00000000 | | | GFWB00000000 | | GFWS00000000 | |
| **Assembly** | **strategy** | **Combined reads for de novo assembly (used as reference)** | | | **de novo** | **ref. guided** | **de novo** | **ref. guided** |
|  | assembler | Trinity | | | Trinity | Bowtie2 | Trinity | Bowtie2 |
|  | total assembled reads | 1,377,646 | | | 20,421,456 | 33,108,438 | 18,032,538 | 30,611,092 |
|  | Number of contigs | 229,116 | | | 109,452 | 147,457 | 97,239 | 141,588 |
|  | Range of contig lenght | 224 -14,368 | | | 201 -8,854 | 210 - 14,375 | 201 -6,882 | 2015 - 14,370 |
|  | N50 lenght | 774 | | | 669.7 | 697.5 | 635 | 626.9 |