|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GAGE-B Hiseq ctg | Soap Hiseq ctg | GAGE-B Miseq ctg | Soap Miseq ctg | GAGE-B Hiseq scf | Soap Hiseq scf | GAGE-B Miseq scf | Soap Miseq scf |
| Contig ≥ 200 | 139 | 462 | 244 | 439 | - | - | - | - |
| Scaffold ≥ 500 | - | - | - | - | 75 | 77 | 165 | 166 |
| N50 | 135 118 | 21 660 | 71 357 | 29 551 | 200 529 | 200 760 | 91 942 | 92 055 |
| NA50 | 112 904 | 21 657 | 71 357 | 29 551 | 181 115 | 181 222 | 91 942 | 92 054 |
| # misassembly | 15 | 2 | 12 | 2 | 15 | 6 | 14 | 6 |
| # local misassembly | 50 | 0 | 44 | 0 | 76 | 81 | 77 | 111 |
| Unaligned | 1 | 1 | 2 | 2 | 1 | 1 | 2 | 2 |
| Genome fraction | 97.295 | 96.488 | 96.940 | 96.230 | 97.305 | 97.517 | 97.050 | 97.068 |
| # genes | 3479 | 3274 | 3442 | 3336 | 3480 | 3485 | 3443 | 3432 |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GAGE-B Hiseq ctg | SPAdes Hiseq ctg | GAGE-B Miseq ctg | SPAdes Miseq ctg | GAGE-B Hiseq scf | SPAdes Hiseq scf | GAGE-B Miseq scf | SPAdes Miseq scf |
| Contig ≥ 200 | 205 | 158 | 1 475 | 1 480 | - | - | - | - |
| Scaffold ≥ 500 | - | - | - | - | 106 | 106 | 145 | 147 |
| N50 | 83 518 | 137 662 | 262 160 | 262 160 | 98 274 | 225 904 | 262 160 | 262 160 |
| NA50 | 83 518 | 137 656 | 262 160 | 262 160 | 95 858 | 214 751 | 262 160 | 262 160 |
| # misassembly | 4 | 4 | 5 | 5 | 21 | 7 | 5 | 5 |
| # local misassembly | 2 | 9 | 4 | 4 | 17 | 11 | 4 | 4 |
| Unaligned | 1 | 3 | 57 | 57 | 1 | 3 | 57 | 57 |
| Genome fraction | 97.439 | 98.611 | 98.643 | 98.752 | 98.209 | 98.753 | 98.648 | 98.752 |
| # genes | 3 483 | 3 571 | 3 598 | 3597 | 3 544 | 3 586 | 3599 | 3598 |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | GAGE-B Hiseq ctg | Velvet Hiseq ctg | GAGE-B Miseq ctg | Velvet Miseq ctg | GAGE-B Hiseq scf | Velvet Hiseq scf | GAGE-B Miseq scf | Velvet Miseq scf |
| Contig ≥ 200 | 261 | 246 | 201 | 179 | - | - | - | - |
| Scaffold ≥ 500 | - | - | - | - | 85 | 104 | 138 | 133 |
| N50 | 40 877 | 46 346 | 92 036 | 105 176 | 172 545 | 163 386 | 109 996 | 105 176 |
| NA50 | 40 877 | 42 805 | 67 096 | 105 176 | 171 505 | 163 055 | 75 901 | 105 176 |
| # misassembly | 4 | 9 | 14 | 5 | 10 | 10 | 22 | 6 |
| # local misassembly | 8 | 9 | 2 | 3 | 129 | 123 | 13 | 6 |
| Unaligned | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| Genome fraction | 97.038 | 96.34 | 97.563 | 96.234 | 97.14 | 96.251 | 97.598 | 96.242 |
| # genes | 3 386 | 3 392 | 3 491 | 3 460 | 3 400 | 3 379 | 3 492 | 3 459 |