

| <b>Alignment-based statistics</b>   |  | <b>Minia_on_data_28</b> |
|-------------------------------------|--|-------------------------|
| Genome fraction (%)                 |  | 90.061                  |
| Duplication ratio                   |  | 1.004                   |
| Largest alignment                   |  | 40 450                  |
| Total aligned length                |  | 4 168 496               |
| NGA50                               |  | 6536                    |
| LGA50                               |  | 206                     |
| <b>Misassemblies</b>                |  |                         |
| # misassemblies                     |  | 2                       |
| Misassembled contigs length         |  | 19 630                  |
| <b>Per base quality</b>             |  |                         |
| # mismatches per 100 kbp            |  | 16.34                   |
| # indels per 100 kbp                |  | 2.28                    |
| # N's per 100 kbp                   |  | 0                       |
| <b>Statistics without reference</b> |  |                         |
| # contigs                           |  | 886                     |
| Largest contig                      |  | 40 450                  |
| Total length                        |  | 4 170 116               |
| Total length ( $\geq$ 1000 bp)      |  | 4 081 154               |
| Total length ( $\geq$ 10000 bp)     |  | 1 418 544               |
| Total length ( $\geq$ 50000 bp)     |  | 0                       |