## Report

| # contigs (>= 1000 bp)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                          | final.contigs |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------|---------------|
| # contigs (>= 5000 bp)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | # contigs (>= 1000 hp)   |               |
| # contigs (>= 10000 bp)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | •                        |               |
| # contigs (>= 25000 bp)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                          |               |
| # contigs (>= 50000 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp)  # contigs Largest contig Total length 4243543 Reference length 4857432 GC (%) 52.21 Reference GC (%) N50 977 NG50 898 N75 718 NG75 1630 1497 LG50 1824 L75 LG75 3451 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs length 10 Genome fraction (%) Buplication ratio 10 de 10 de 10 de 10 de 10 de 10 de 11 de 10 de 11 | , ,                      |               |
| Total length (>= 1000 bp)         2055609           Total length (>= 5000 bp)         0           Total length (>= 10000 bp)         0           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         4523           Largest contig         3778           Total length         4243543           Reference length         4857432           GC (%)         52.21           Reference GC (%)         52.22           N50         977           NG50         898           N75         718           NG75         623           L50         1497           LG50         1824           L75         2765           LG75         3451           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # unaligned length         0           Genome fraction (%)         81.968           Duplication ratio         1.066           # N's per 100 kbp         0.05           Largest alignment         3778           NA50         898                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | -                        |               |
| Total length (>= 5000 bp)     Total length (>= 10000 bp)     Total length (>= 25000 bp)     Total length (>= 50000 bp)     Total length (>= 50000 bp)     Total length (>= 50000 bp)     # contigs     Largest contig     Total length                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | _                        |               |
| Total length (>= 10000 bp)         0           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         4523           Largest contig         3778           Total length         4243543           Reference length         4857432           GC (%)         52.21           Reference GC (%)         52.22           N50         977           NG50         898           N75         718           NG75         623           L50         1497           LG50         1824           L75         2765           LG75         3451           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         81.968           Duplication ratio         1.066           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.05           Largest alignment         3778           NA50         977           NGA50 <td></td> <td>_</td>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                          | _             |
| Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         4523           Largest contig         3778           Total length         4243543           Reference length         4857432           GC (%)         52.21           Reference GC (%)         52.22           N50         977           NG50         898           N75         718           NG75         623           L50         1497           LG50         1824           L75         2765           LG75         3451           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         81.968           Duplication ratio         1.066           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.05           Largest alignment         3778           NA50         977           NGA50         898           NA75         718 <td></td> <td></td>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                          |               |
| Total length (>= 50000 bp)       0         # contigs       4523         Largest contig       3778         Total length       4243543         Reference length       4857432         GC (%)       52.21         Reference GC (%)       52.22         N50       977         NG50       898         N75       718         NG75       623         L50       1497         LG50       1824         L75       2765         LG75       3451         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned length       0         Genome fraction (%)       81.968         Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                          | _             |
| # contigs       4523         Largest contig       3778         Total length       4243543         Reference length       4857432         GC (%)       52.21         Reference GC (%)       52.22         N50       977         NG50       898         N75       718         NG75       623         L50       1497         LG50       1824         L75       2765         LG75       3451         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.968         Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                          |               |
| Largest contig       3778         Total length       4243543         Reference length       4857432         GC (%)       52.21         Reference GC (%)       52.22         N50       977         NG50       898         N75       718         NG75       623         L50       1497         LG50       1824         L75       2765         LG75       3451         # misassemblies       0         # sassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.968         Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                          |               |
| Total length         4243543           Reference length         4857432           GC (%)         52.21           Reference GC (%)         52.22           N50         977           NG50         898           N75         718           NG75         623           L50         1497           LG50         1824           L75         2765           LG75         3451           # misassemblies         0           # local misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         81.968           Duplication ratio         1.066           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.05           Largest alignment         3778           NA50         977           NGA50         898           NA75         718           NGA75         623           LA50         1497           LGA50         1824                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                          |               |
| Reference length       4857432         GC (%)       52.21         Reference GC (%)       52.22         N50       977         NG50       898         N75       718         NG75       623         L50       1497         LG50       1824         L75       2765         LG75       3451         # misassemblies       0         # local misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.968         Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | _                        |               |
| GC (%)       52.21         Reference GC (%)       52.22         N50       977         NG50       898         N75       718         NG75       623         L50       1497         LG50       1824         L75       2765         LG75       3451         # misassemblies       0         # misassembled contigs       0         Misassembled contigs       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.968         Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                          |               |
| Reference GC (%)       52.22         N50       977         NG50       898         N75       718         NG75       623         L50       1497         LG50       1824         L75       2765         LG75       3451         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.968         Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                          |               |
| N50       977         NG50       898         N75       718         NG75       623         L50       1497         LG50       1824         L75       2765         LG75       3451         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.968         Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                          |               |
| NG50       898         N75       718         NG75       623         L50       1497         LG50       1824         L75       2765         LG75       3451         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.968         Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                          |               |
| N75       718         NG75       623         L50       1497         LG50       1824         L75       2765         LG75       3451         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.968         Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                          |               |
| NG75       623         L50       1497         LG50       1824         L75       2765         LG75       3451         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.968         Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       182.42         # indels per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                          |               |
| L50       1497         LG50       1824         L75       2765         LG75       3451         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.968         Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       182.42         # indels per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                          |               |
| LG50       1824         L75       2765         LG75       3451         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.968         Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       182.42         # indels per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                          |               |
| L75       2765         LG75       3451         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.968         Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       182.42         # indels per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                          |               |
| LG75       3451         # misassemblies       0         # misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.968         Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       182.42         # indels per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                          |               |
| # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.968 Duplication ratio 1.066 # N's per 100 kbp 0.00 # mismatches per 100 kbp 182.42 # indels per 100 kbp 0.05 Largest alignment 3778 NA50 977 NGA50 898 NA75 718 NGA75 623 LA50 1497 LGA50 1824 LA75                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                          |               |
| # misassembled contigs                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | # misassemblies          | _             |
| Misassembled contigs length         0           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         81.968           Duplication ratio         1.066           # N's per 100 kbp         0.00           # mismatches per 100 kbp         182.42           # indels per 100 kbp         0.05           Largest alignment         3778           NA50         977           NGA50         898           NA75         718           NGA75         623           LA50         1497           LGA50         1824           LA75         2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                          | 0             |
| # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.968 Duplication ratio 1.066 # N's per 100 kbp 0.00 # mismatches per 100 kbp 182.42 # indels per 100 kbp 0.05 Largest alignment 3778 NA50 977 NGA50 898 NA75 718 NGA75 623 LA50 1497 LGA50 1824 LA75 2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                          | _             |
| # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.968 Duplication ratio 1.066 # N's per 100 kbp 0.00 # mismatches per 100 kbp 182.42 # indels per 100 kbp 0.05 Largest alignment 3778 NA50 977 NGA50 898 NA75 718 NGA75 623 LA50 1497 LGA50 1824 LA75 2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                          | 0             |
| Unaligned length       0         Genome fraction (%)       81.968         Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       182.42         # indels per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                          | 0 + 0 part    |
| Genome fraction (%)       81.968         Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       182.42         # indels per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                          |               |
| Duplication ratio       1.066         # N's per 100 kbp       0.00         # mismatches per 100 kbp       182.42         # indels per 100 kbp       0.05         Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                          | 81.968        |
| # N's per 100 kbp 0.00 # mismatches per 100 kbp 182.42 # indels per 100 kbp 0.05 Largest alignment 3778 NA50 977 NGA50 898 NA75 718 NGA75 623 LA50 1497 LGA50 1824 LA75 2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                          |               |
| # indels per 100 kbp 0.05 Largest alignment 3778 NA50 977 NGA50 898 NA75 718 NGA75 623 LA50 1497 LGA50 1824 LA75 2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ,                        |               |
| Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | # mismatches per 100 kbp | 182.42        |
| Largest alignment       3778         NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                          |               |
| NA50       977         NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                          |               |
| NGA50       898         NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                          |               |
| NA75       718         NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                          | 898           |
| NGA75       623         LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | NA75                     |               |
| LA50       1497         LGA50       1824         LA75       2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | NGA75                    |               |
| LGA50 1824<br>LA75 2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | LA50                     |               |
| LA75 2765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                          | 1824          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                          |               |
| LGA/5   3452                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | LGA75                    | 3452          |

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

|                                 | final.contigs |
|---------------------------------|---------------|
| # misassemblies                 | 0             |
| # relocations                   | 0             |
| # translocations                | 0             |
| # inversions                    | 0             |
| # possibly misassembled contigs | 0             |
| # misassembled contigs          | 0             |
| Misassembled contigs length     | 0             |
| # local misassemblies           | 0             |
| # mismatches                    | 7263          |
| # indels                        | 2             |
| # short indels                  | 2             |
| # long indels                   | 0             |
| Indels length                   | 2             |

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Unaligned report

|                               | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs     | 0             |
| Fully unaligned length        | 0             |
| # partially unaligned contigs | 0             |
| # with misassembly            | 0             |
| # both parts are significant  | 0             |
| Partially unaligned length    | 0             |
| # N's                         | 0             |

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).















