

# Report

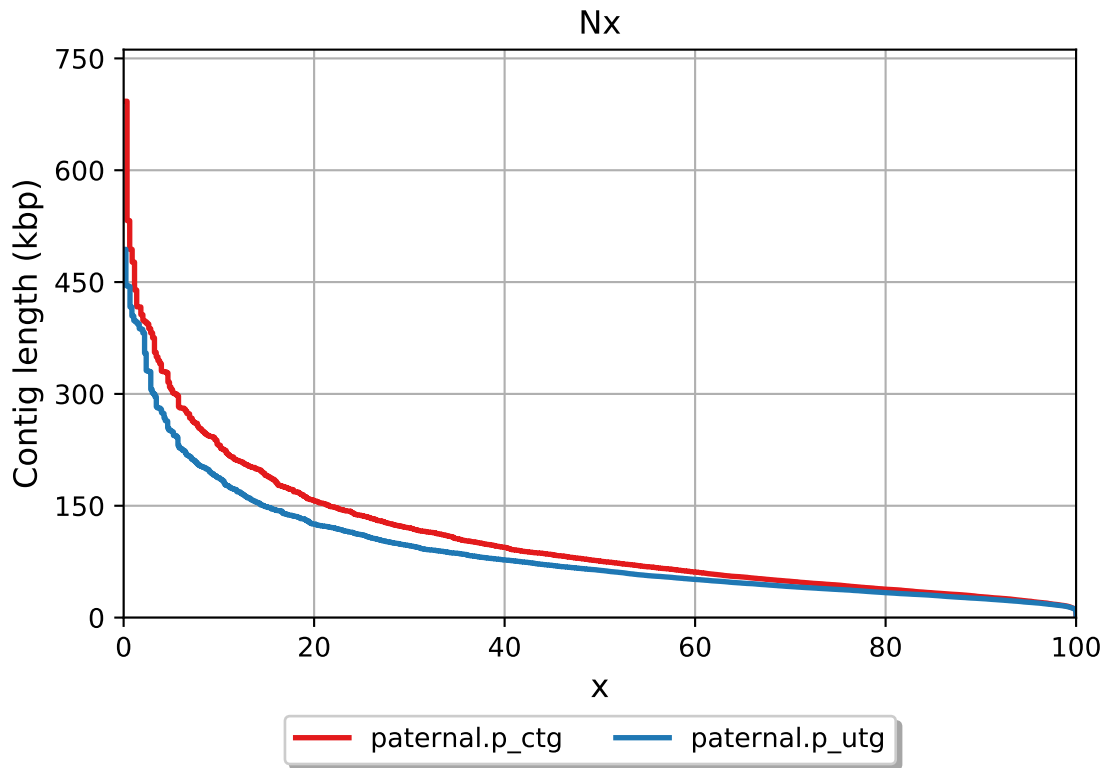
|                             | paternal.p_ctg      | paternal.p_utg      |
|-----------------------------|---------------------|---------------------|
| # contigs (>= 0 bp)         | 3308                | 4085                |
| # contigs (>= 1000 bp)      | 3308                | 4085                |
| # contigs (>= 5000 bp)      | 3308                | 4085                |
| # contigs (>= 10000 bp)     | 3297                | 4072                |
| # contigs (>= 25000 bp)     | 2585                | 3064                |
| # contigs (>= 50000 bp)     | 1297                | 1358                |
| Total length (>= 0 bp)      | 191715854           | 206788730           |
| Total length (>= 1000 bp)   | 191715854           | 206788730           |
| Total length (>= 5000 bp)   | 191715854           | 206788730           |
| Total length (>= 10000 bp)  | 191615729           | 206673518           |
| Total length (>= 25000 bp)  | 178170427           | 187435231           |
| Total length (>= 50000 bp)  | 131724718           | 126589739           |
| # contigs                   | 3308                | 4085                |
| Largest contig              | 692509              | 493847              |
| Total length                | 191715854           | 206788730           |
| Reference length            | 152958180           | 152958180           |
| GC (%)                      | 35.87               | 35.87               |
| Reference GC (%)            | 35.92               | 35.92               |
| N50                         | 75820               | 63373               |
| NG50                        | 94370               | 82091               |
| N75                         | 43648               | 37711               |
| NG75                        | 61322               | 55893               |
| L50                         | 713                 | 944                 |
| LG50                        | 482                 | 569                 |
| L75                         | 1556                | 2018                |
| LG75                        | 989                 | 1134                |
| # misassemblies             | 23091               | 24687               |
| # misassembled contigs      | 2657                | 3275                |
| Misassembled contigs length | 170605021           | 181738293           |
| # local misassemblies       | 57791               | 61821               |
| # scaffold gap ext. mis.    | 0                   | 0                   |
| # scaffold gap loc. mis.    | 0                   | 0                   |
| # unaligned mis. contigs    | 185                 | 234                 |
| # unaligned contigs         | 299 + 2764 part     | 309 + 3399 part     |
| Unaligned length            | 50142911            | 53377641            |
| Genome fraction (%)         | 58.179              | 58.974              |
| Duplication ratio           | 1.591               | 1.701               |
| # N's per 100 kbp           | 0.00                | 0.00                |
| # mismatches per 100 kbp    | 4401.88             | 4675.03             |
| # indels per 100 kbp        | 511.30              | 545.75              |
| # genomic features          | 409992 + 34458 part | 414995 + 33967 part |
| Largest alignment           | 125973              | 109690              |
| Total aligned length        | 141037715           | 152781737           |
| NA50                        | 7748                | 7711                |
| NGA50                       | 11855               | 12984               |
| NGA75                       | 4313                | 5780                |
| LA50                        | 5472                | 6039                |
| LGA50                       | 3457                | 3356                |
| LGA75                       | 8708                | 7728                |

## Misassemblies report

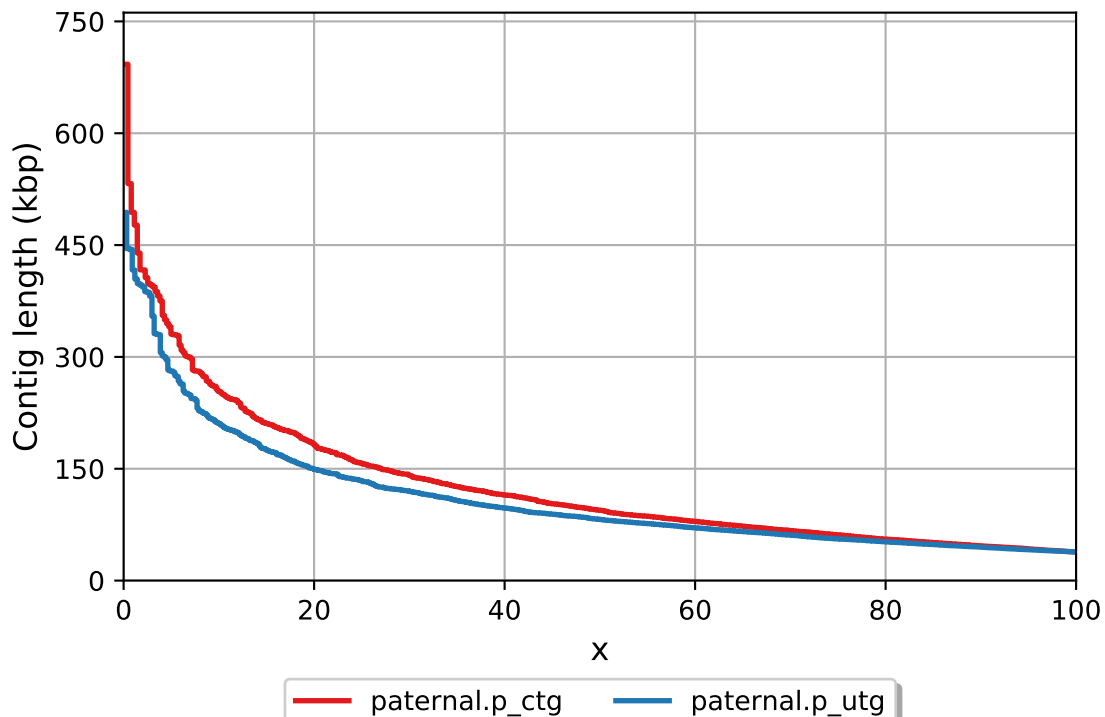
|                             | paternal.p_ctg | paternal.p_utg |
|-----------------------------|----------------|----------------|
| # misassemblies             | 23091          | 24687          |
| # contig misassemblies      | 23091          | 24687          |
| # c. relocations            | 9581           | 10231          |
| # c. translocations         | 13442          | 14382          |
| # c. inversions             | 68             | 74             |
| # scaffold misassemblies    | 0              | 0              |
| # s. relocations            | 0              | 0              |
| # s. translocations         | 0              | 0              |
| # s. inversions             | 0              | 0              |
| # misassembled contigs      | 2657           | 3275           |
| Misassembled contigs length | 170605021      | 181738293      |
| # local misassemblies       | 57791          | 61821          |
| # scaffold gap ext. mis.    | 0              | 0              |
| # scaffold gap loc. mis.    | 0              | 0              |
| # unaligned mis. contigs    | 185            | 234            |
| # mismatches                | 3916849        | 4216734        |
| # indels                    | 454959         | 492253         |
| # indels (<= 5 bp)          | 350207         | 379611         |
| # indels (> 5 bp)           | 104752         | 112642         |
| Indels length               | 2385624        | 2566594        |

## Unaligned report

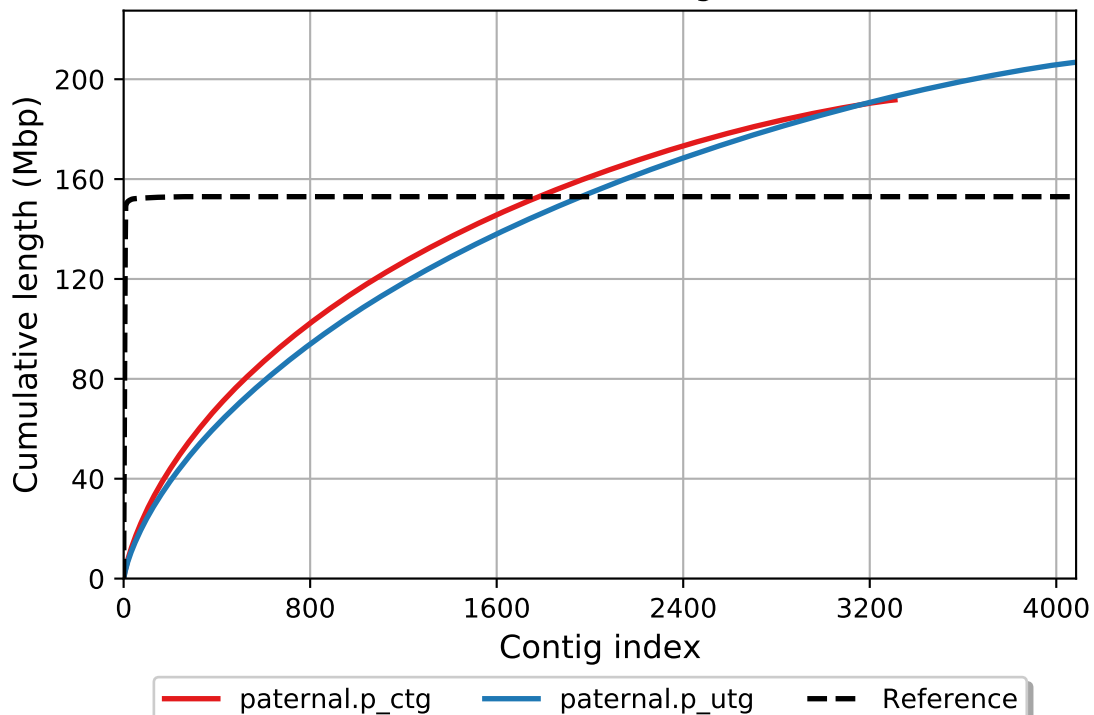
|                               | paternal.p_ctg | paternal.p_utg |
|-------------------------------|----------------|----------------|
| # fully unaligned contigs     | 299            | 309            |
| Fully unaligned length        | 9678305        | 9941277        |
| # partially unaligned contigs | 2764           | 3399           |
| Partially unaligned length    | 40464606       | 43436364       |
| # N's                         | 0              | 0              |

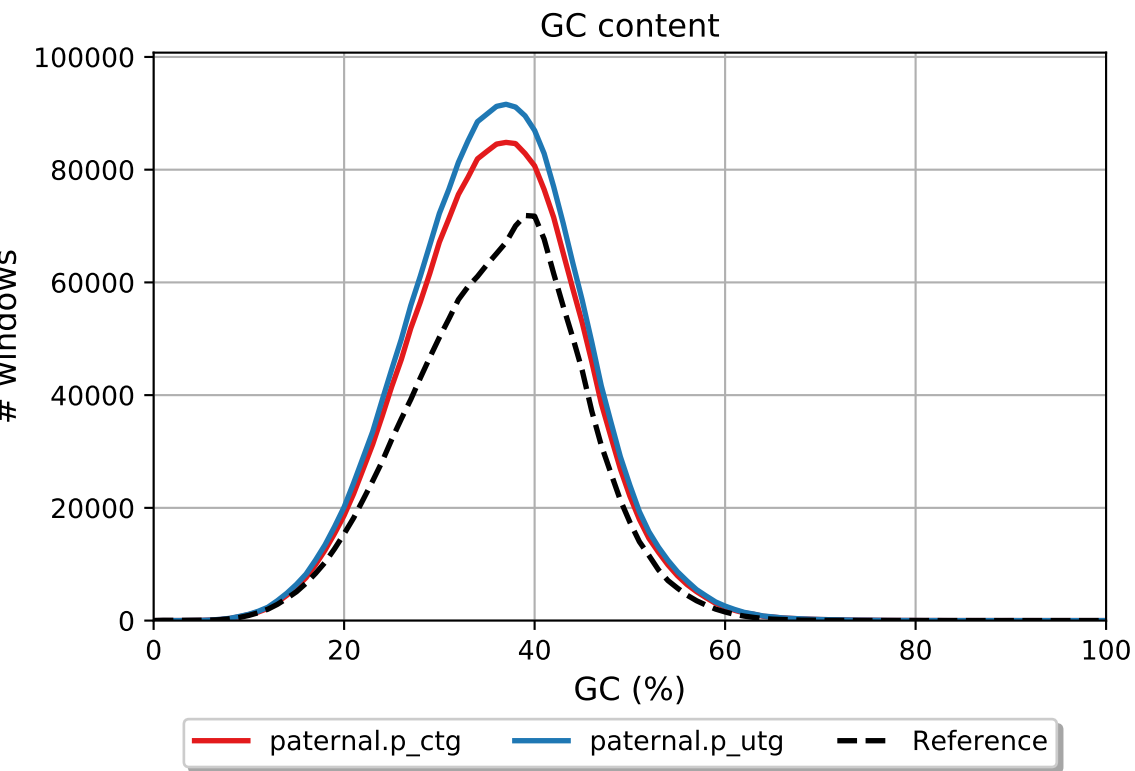


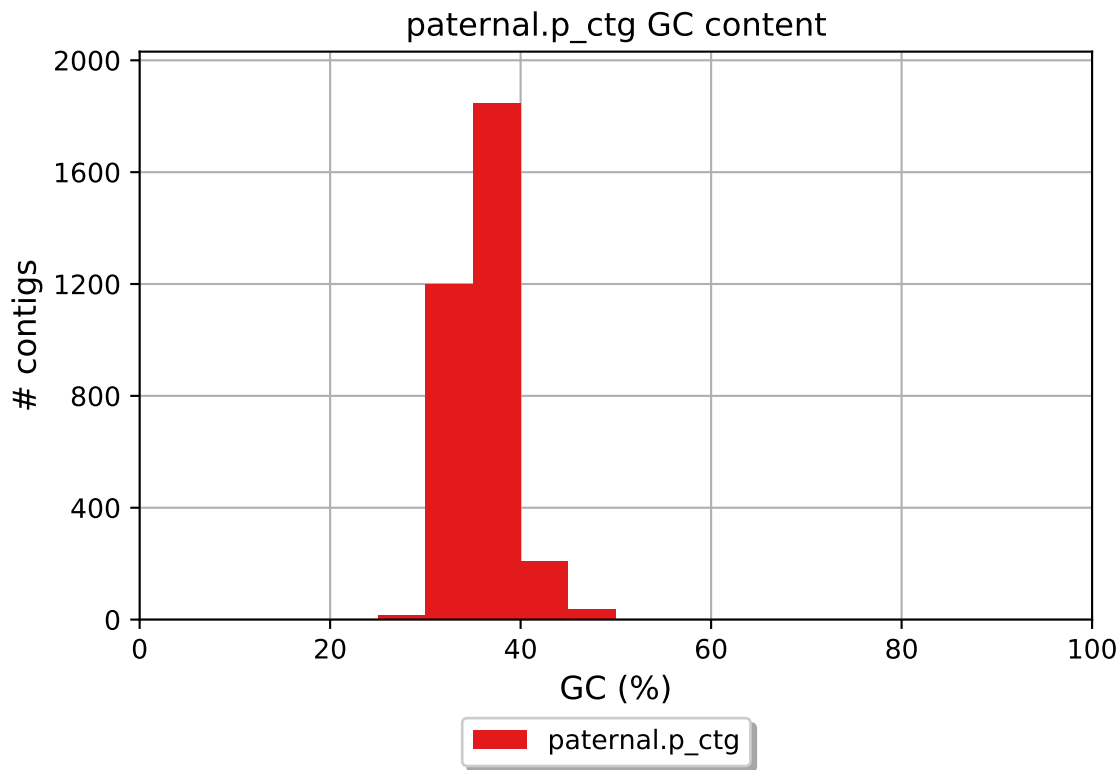
# NGx



Cumulative length

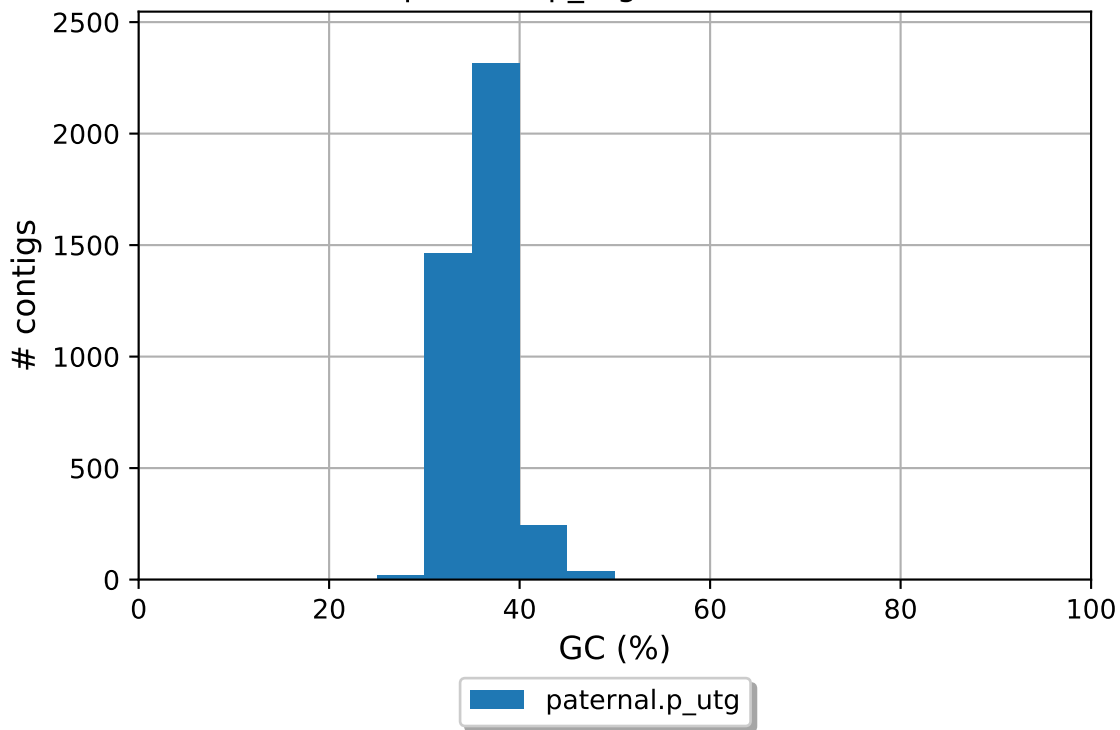




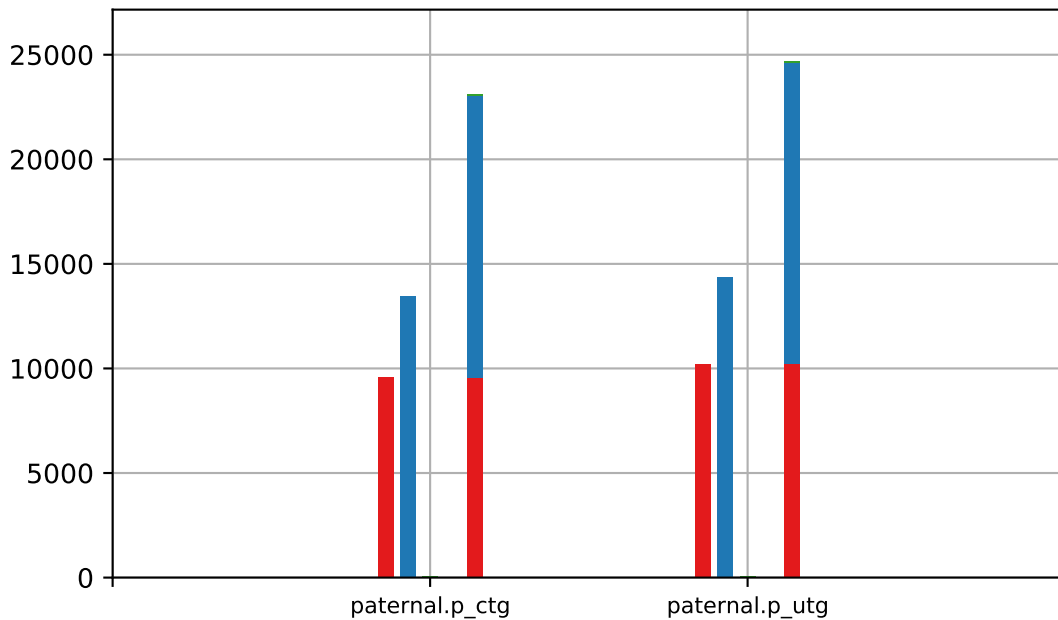




paternal.p\_utg GC content



## Misassemblies



# relocations

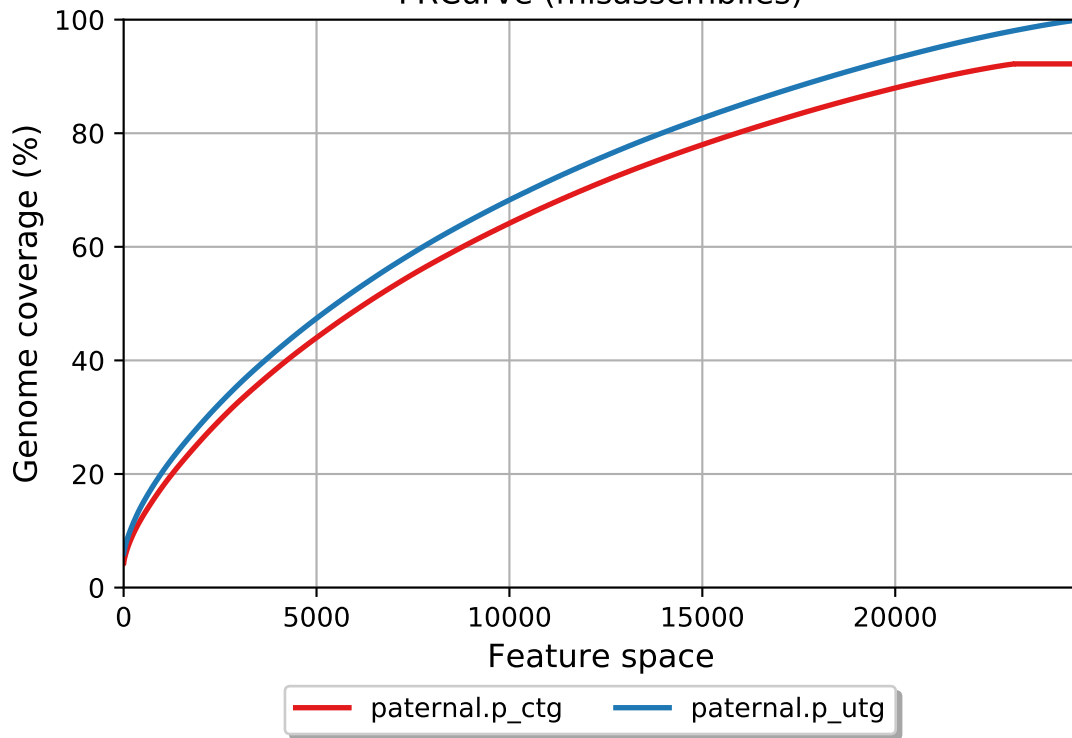


# translocations

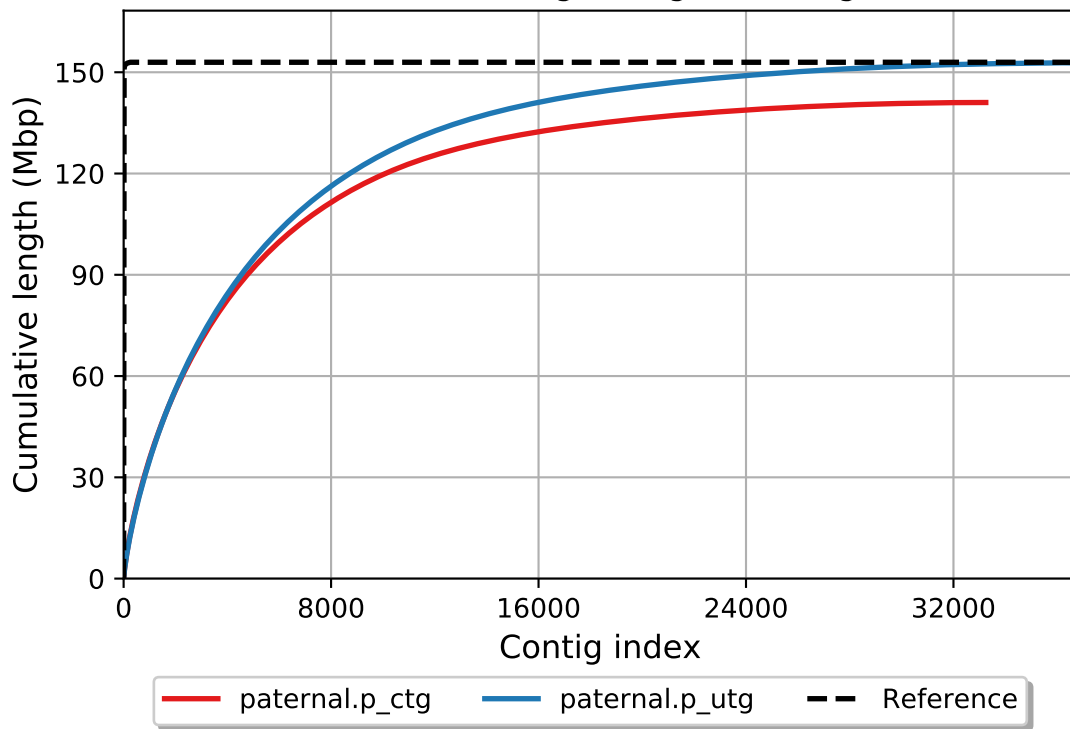


# inversions

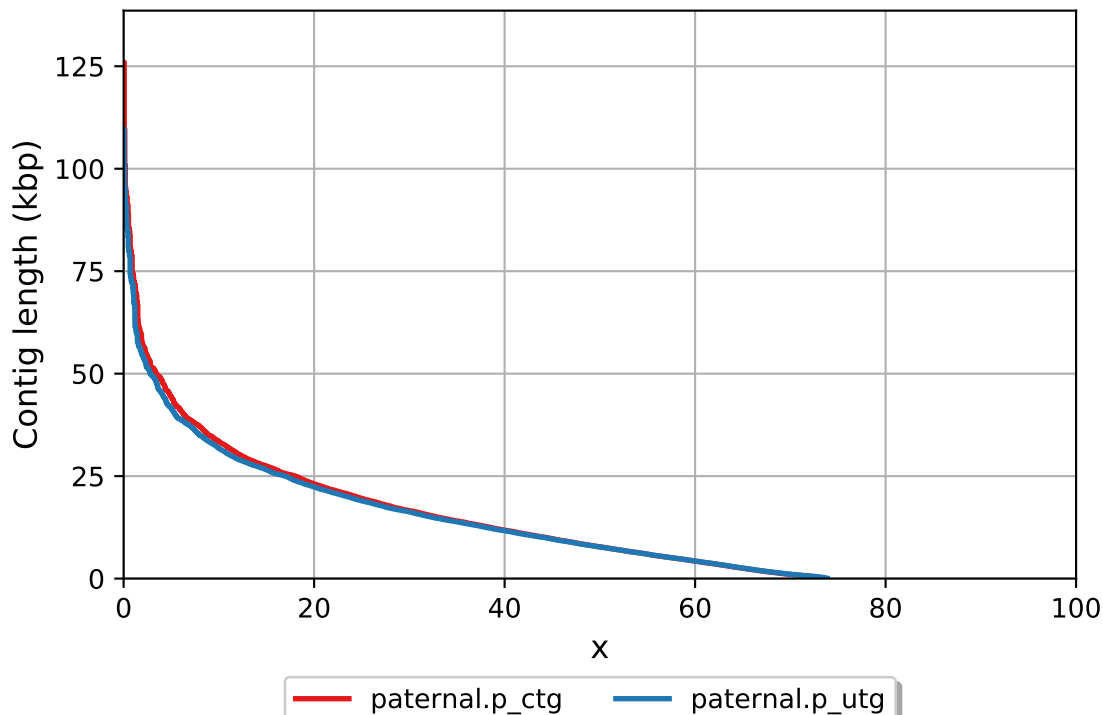
FRCurve (misassemblies)



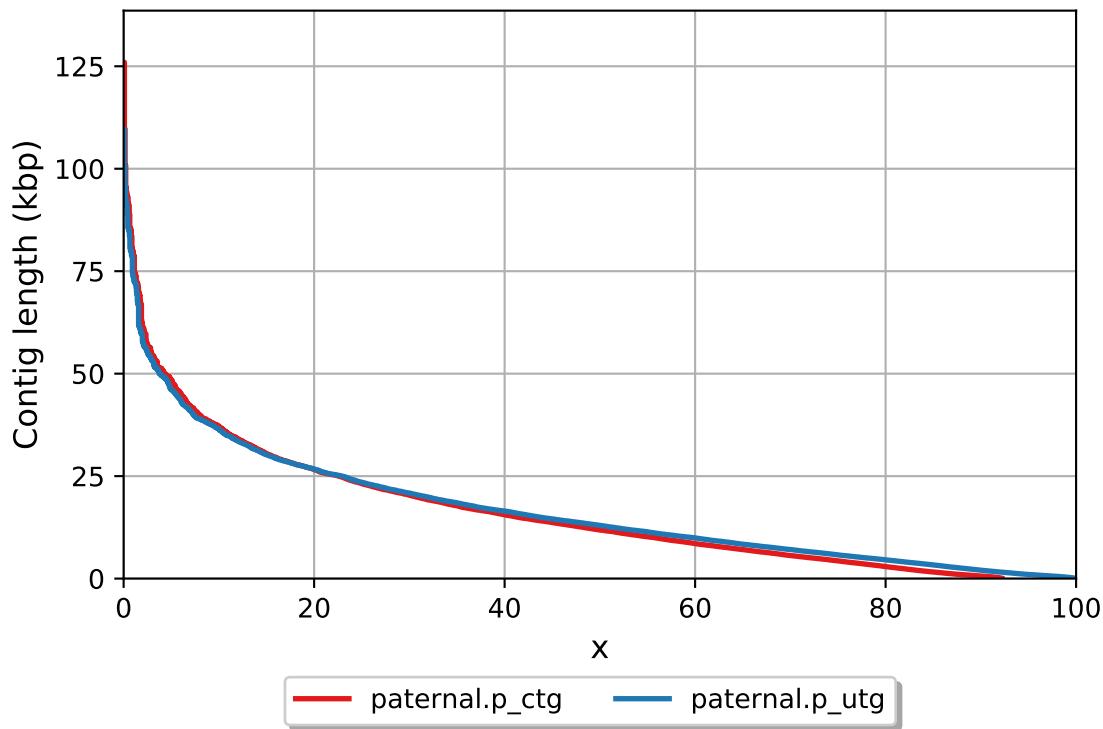
Cumulative length (aligned contigs)



NAx

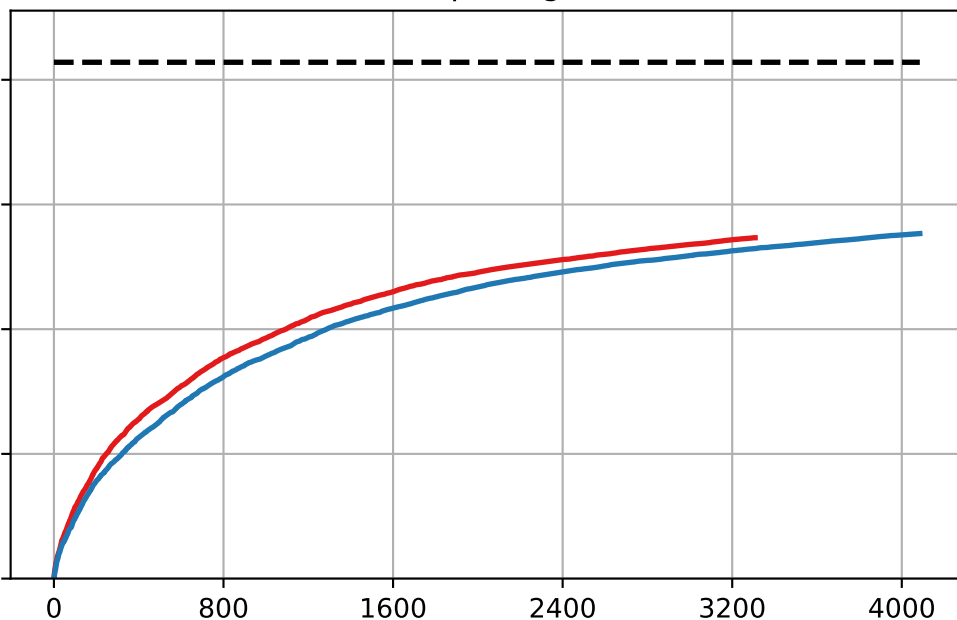


## NGAx



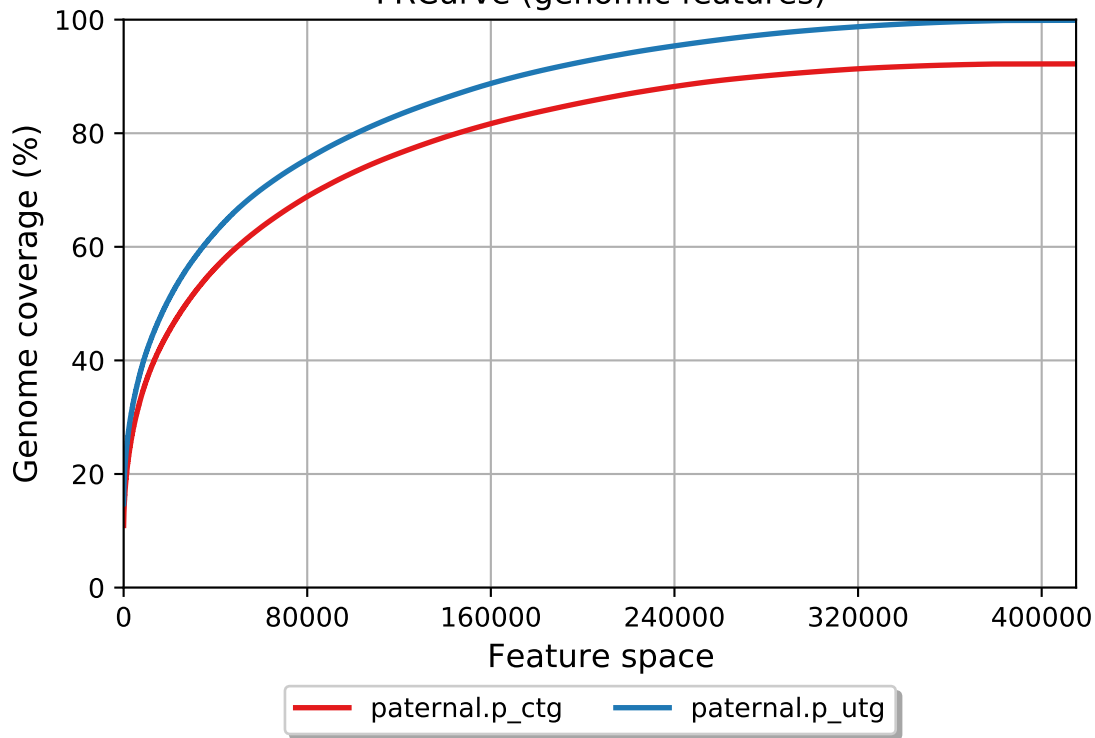
Cumulative # complete genomic features

Cumulative # complete genomic features



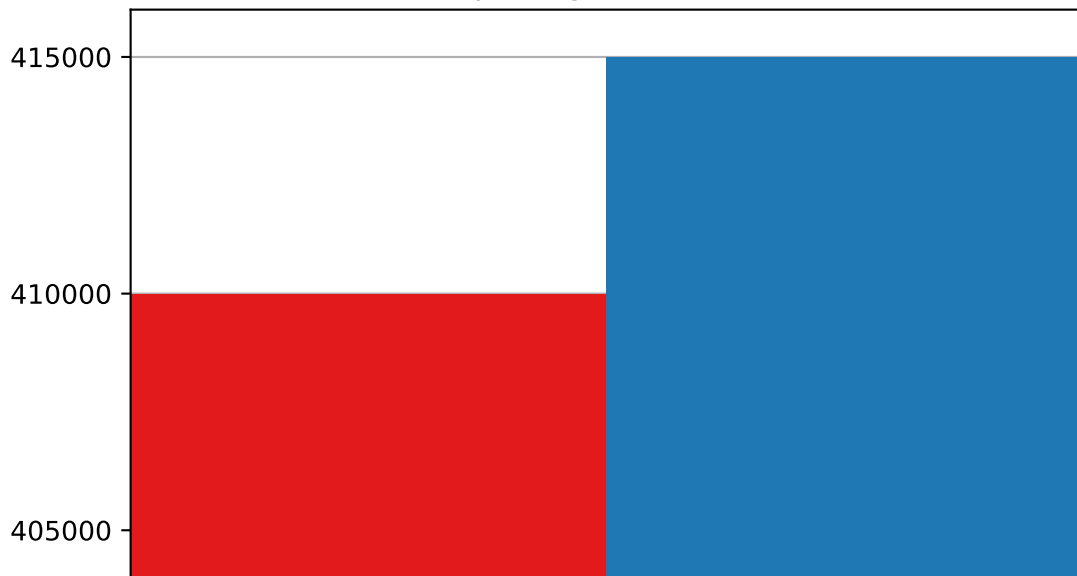
paternal.p\_ctg paternal.p\_utg Reference

FRCurve (genomic features)





# complete genomic features

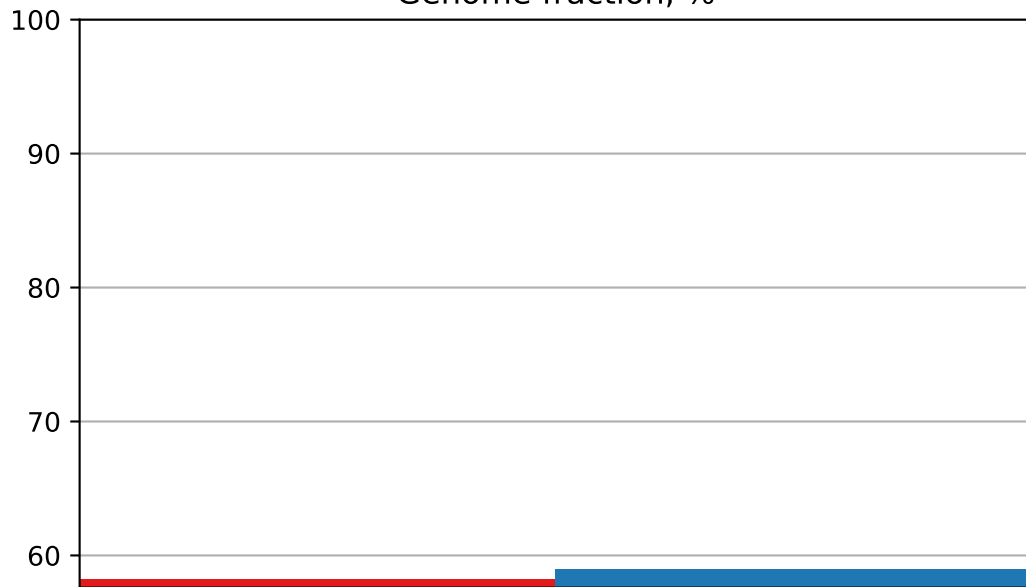


paternal.p\_ctg



paternal.p\_utg

Genome fraction, %



paternal.p\_ctg



paternal.p\_utg