Report

| | APPLdM_assembly.bp.p_ctg |
|---|---|
| # contigs (>= 0 bp) | 235 |
| # contigs (>= 1000 bp) | 235 |
| # contigs (>= 5000 bp) | 235 |
| # contigs (>= 10000 bp) | 235 |
| # contigs (>= 25000 bp) | 207 |
| # contigs (>= 50000 bp) | 159 |
| Total length (>= 0 bp) | 172613046 |
| Total length (>= 1000 bp) | 172613046 |
| Total length (>= 5000 bp) | 172613046 |
| Total length (>= 10000 bp) | 172613046 |
| Total length (>= 25000 bp) | 172057282 |
| Total length (>= 50000 bp) | 170309106 |
| # contigs | 235 |
| Largest contig | 28074898 |
| Total length | 172613046 |
| Reference length | 143726002 |
| GC (%) | 41.28 |
| Reference GC (%) | 42.01 |
| N50 | 15651427 |
| NG50 | 15651427 |
| N90 | 418484 |
| NG90 | 1674018 |
| auN | 13353182.8 |
| auNG | 16036997.6 |
| L50 | 4 |
| LG50 | 4 |
| L90 | 46 |
| LG90 | 14 |
| # misassemblies | 9260 |
| # misassembled contigs | 124 |
| Misassembled contigs length | 165303916 |
| # local misassemblies | 2243 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 49 |
| # unaligned contigs | 26 + 172 part |
| Unaligned length | 10199698 |
| Genome fraction (%) | 93.400 |
| Duplication ratio | 1.210 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 567.60 |
| # indels per 100 kbp | 124.39 |
| Largest alignment | 1088857 |
| Total aligned length | 161185225 |
| NA50 | 86983 |
| NGA50 | 111560 |
| NA90 | 2734 |
| NGA90 | 20147 |
| auNA | 129681.6 |
| auNGA | 155745.9 |
| LA50 | 495 |
| LGA50 | 348 |
| LA90 | 5337 |
| LGA90 | 1450 |

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

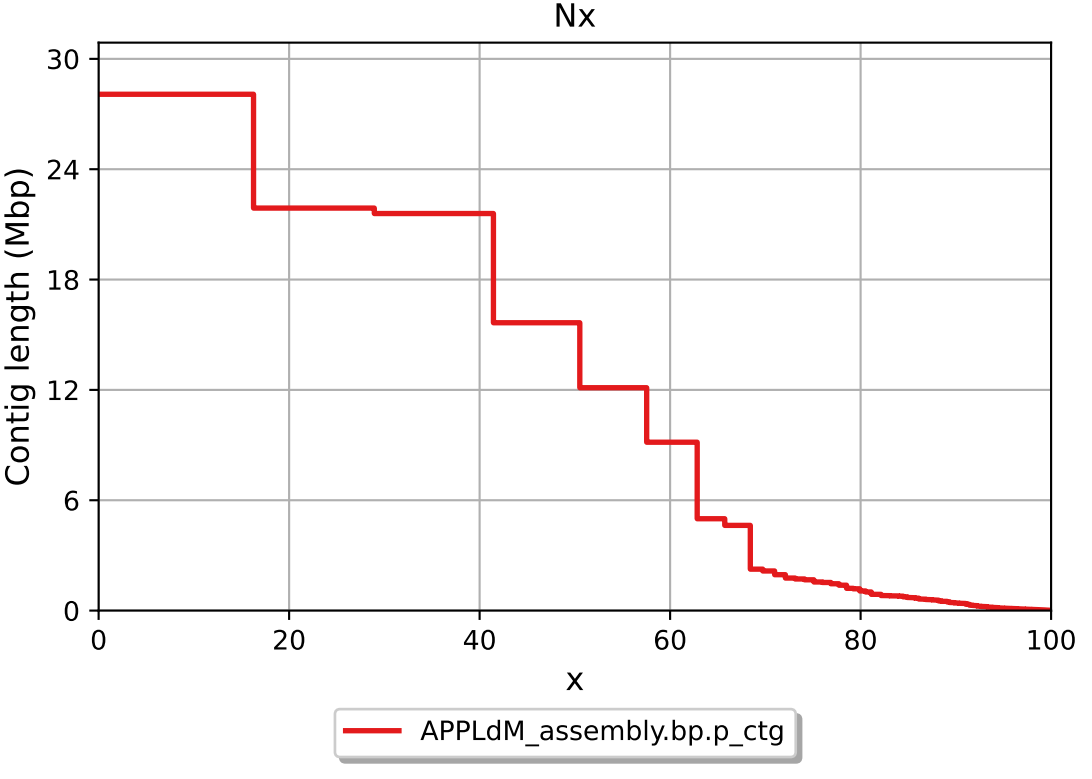
| | APPLdM_assembly.bp.p_ctg |
|---|---|
| # misassemblies | 9260 |
| # contig misassemblies | 9260 |
| # c. relocations | 3486 |
| # c. translocations | 5724 |
| # c. inversions | 50 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 124 |
| Misassembled contigs length | 165303916 |
| # local misassemblies | 2243 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 49 |
| # mismatches | 914888 |
| # indels | 200492 |
| # indels (<= 5 bp) | 148863 |
| # indels (> 5 bp) | 51629 |
| Indels length | 1372597 |

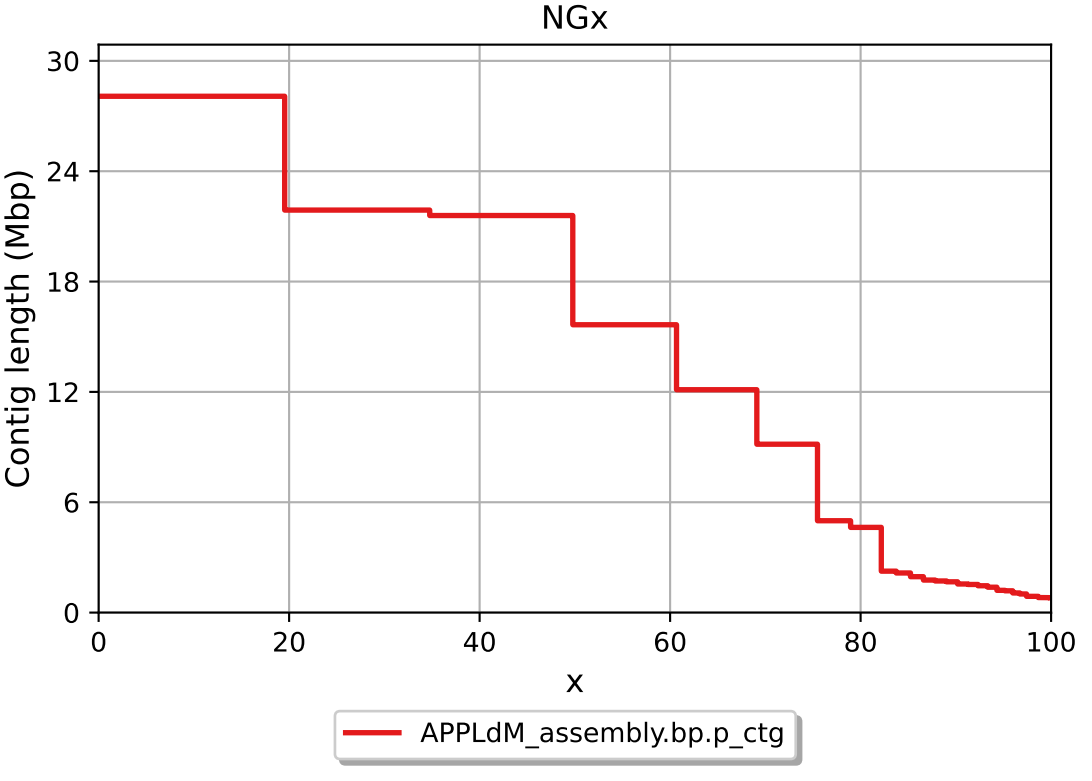
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

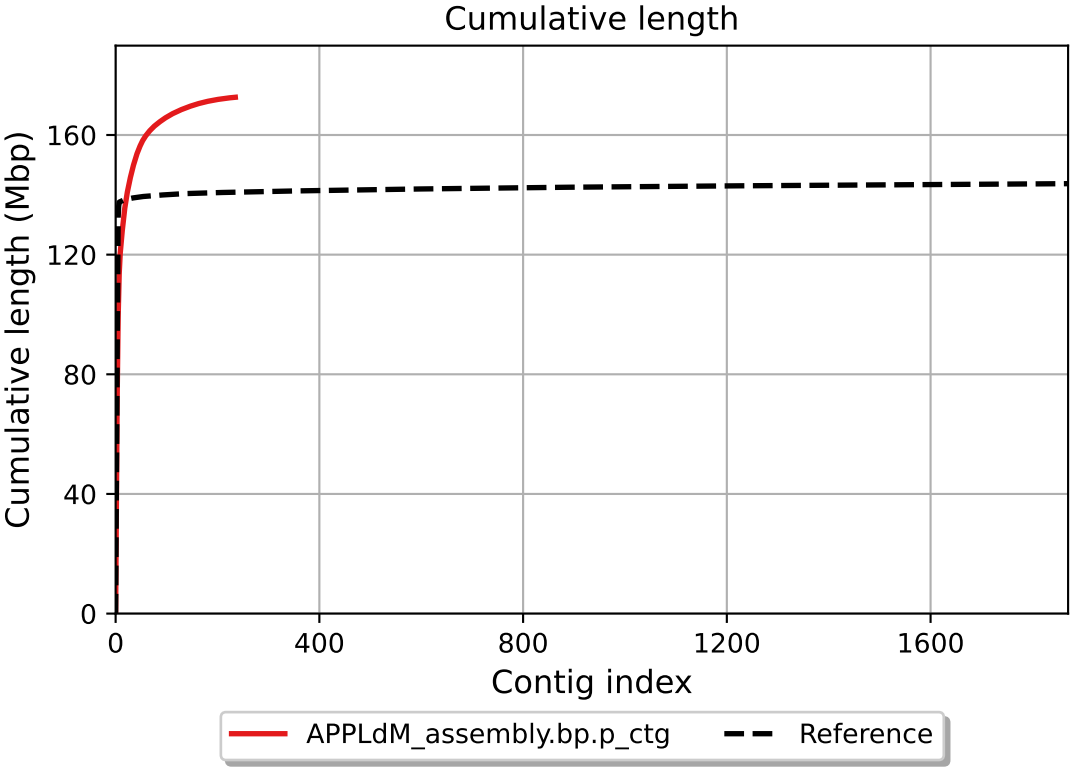
## Unaligned report

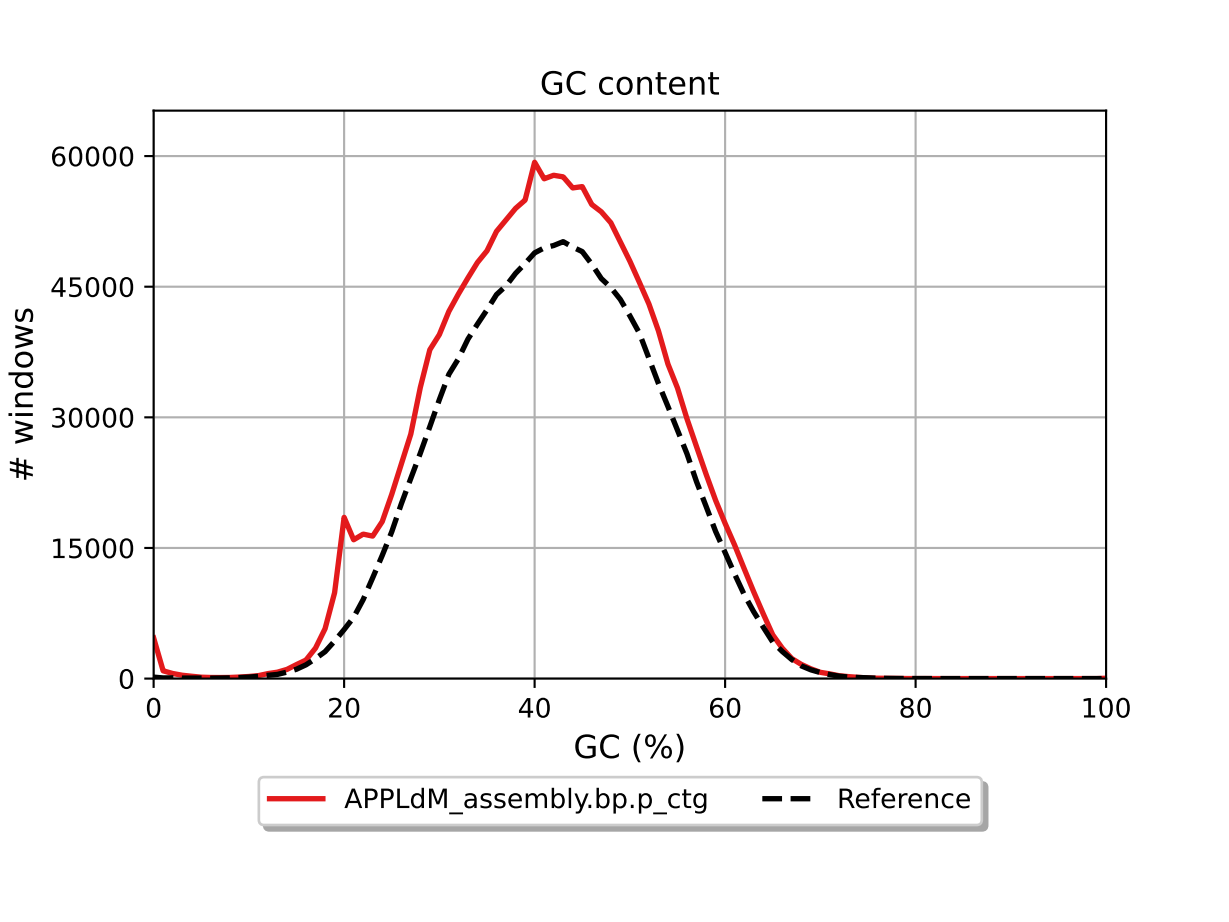
| | APPLdM_assembly.bp.p_ctg |
|---|---|
| # fully unaligned contigs | 26 |
| Fully unaligned length | 1070438 |
| # partially unaligned contigs | 172 |
| Partially unaligned length | 9129260 |
| # N's | 0 |

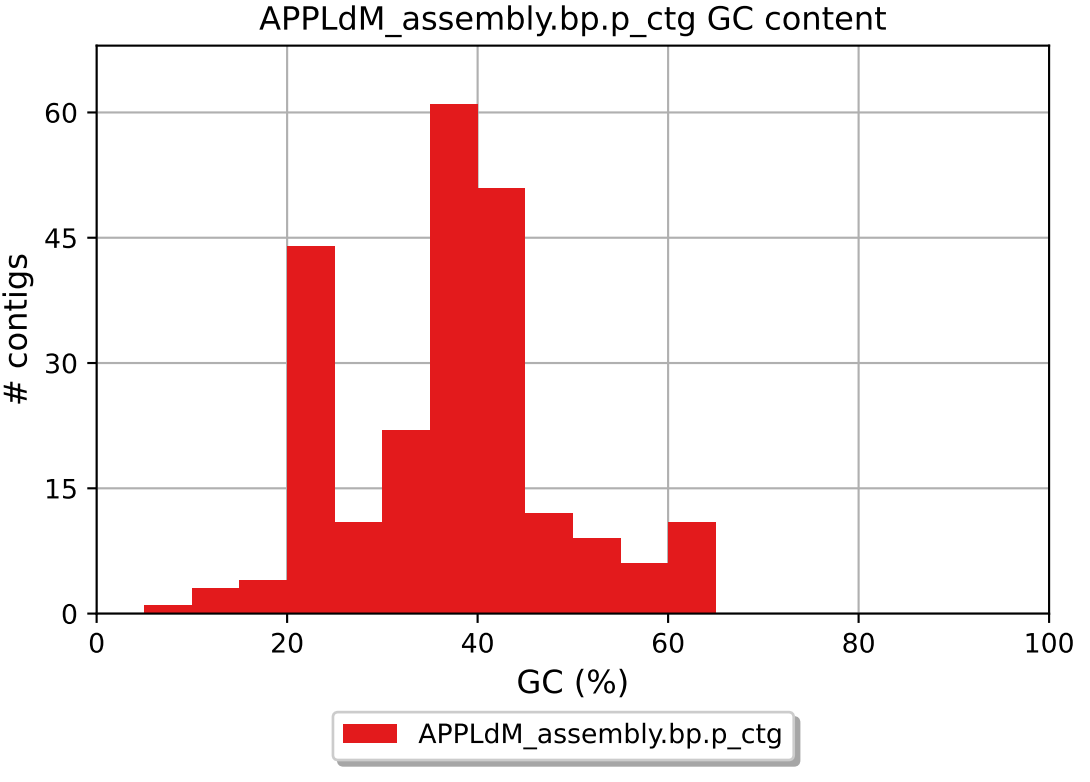
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

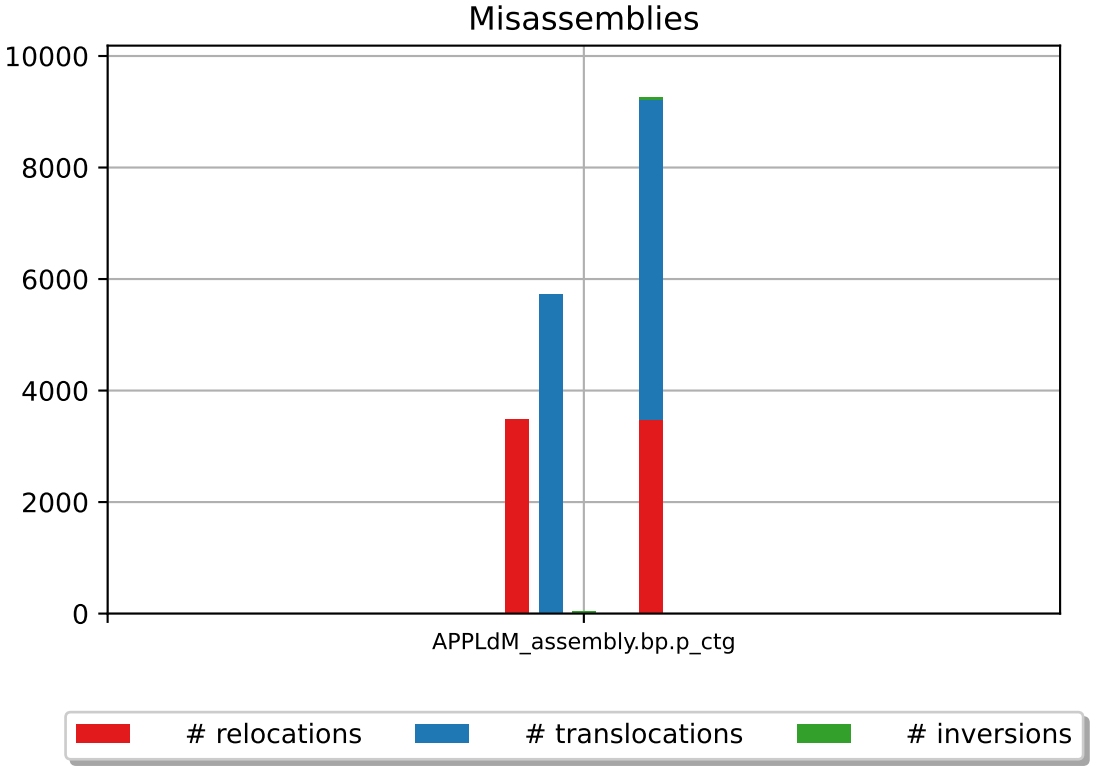

Nx
Contig length (Mbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
APPLdM_assembly.bp.p_ctg

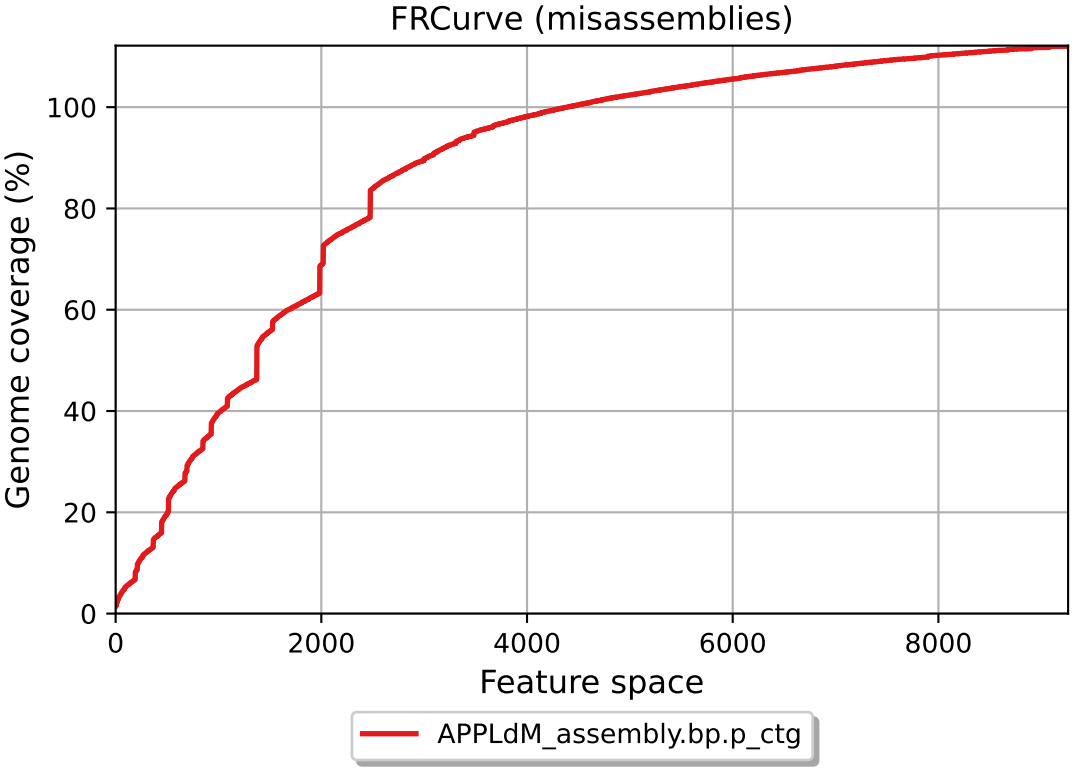

NGx
Contig length (Mbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
APPLdM_assembly.bp.p_ctg

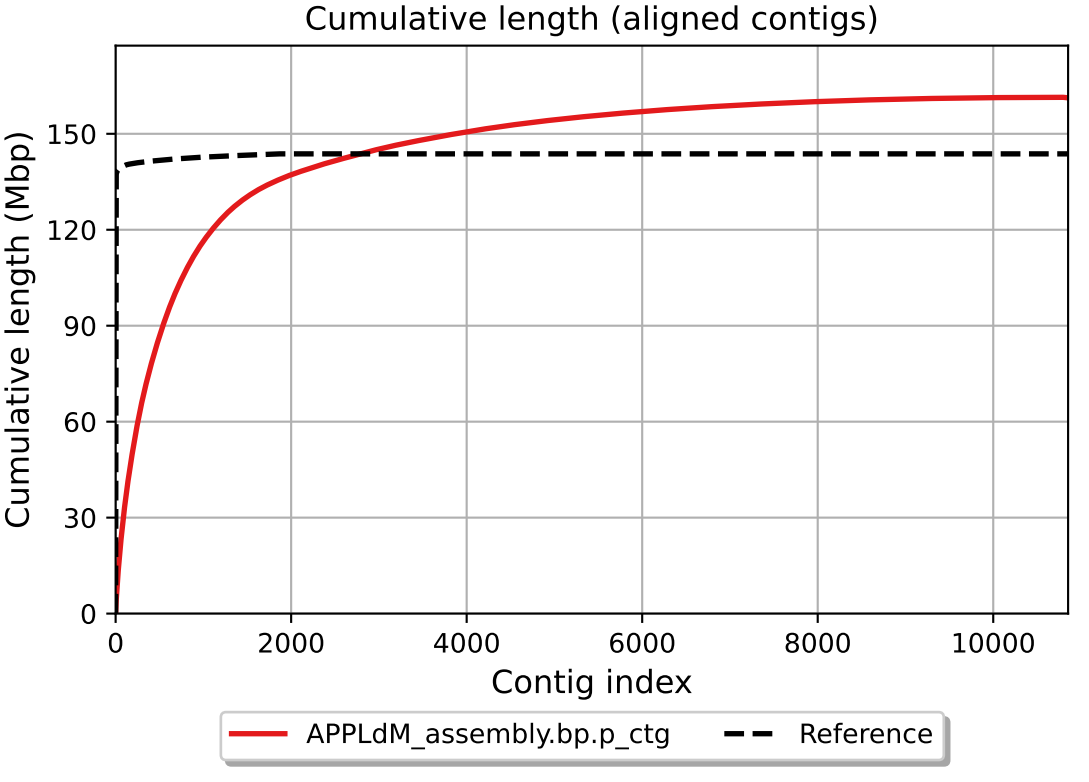

Cumulative length
Cumulative length (Mbp)
160
120
80
40
0
0
400
800
1200
1600
Contig index
APPLdM_assembly.bp.p_ctg
Reference

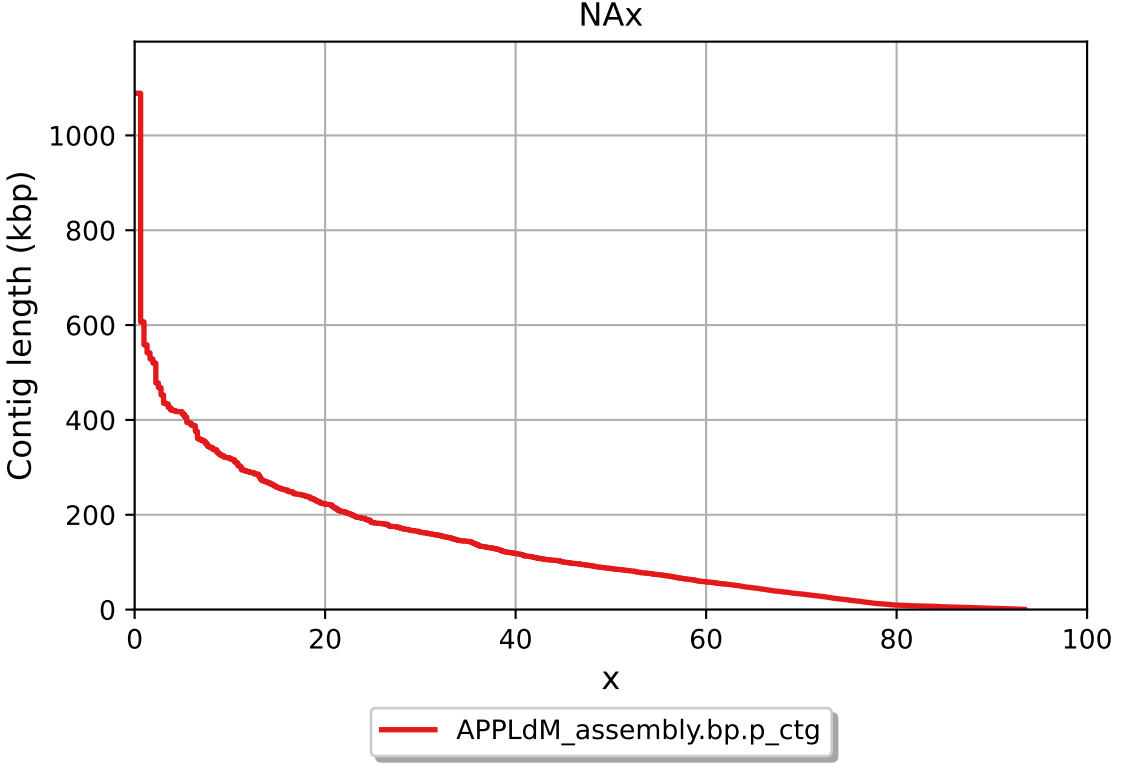

GC content
60000
45000
30000
15000
0
# windows
0
20
40
60
80
100
GC (%)
APPLdM_assembly.bp.p_ctg
Reference

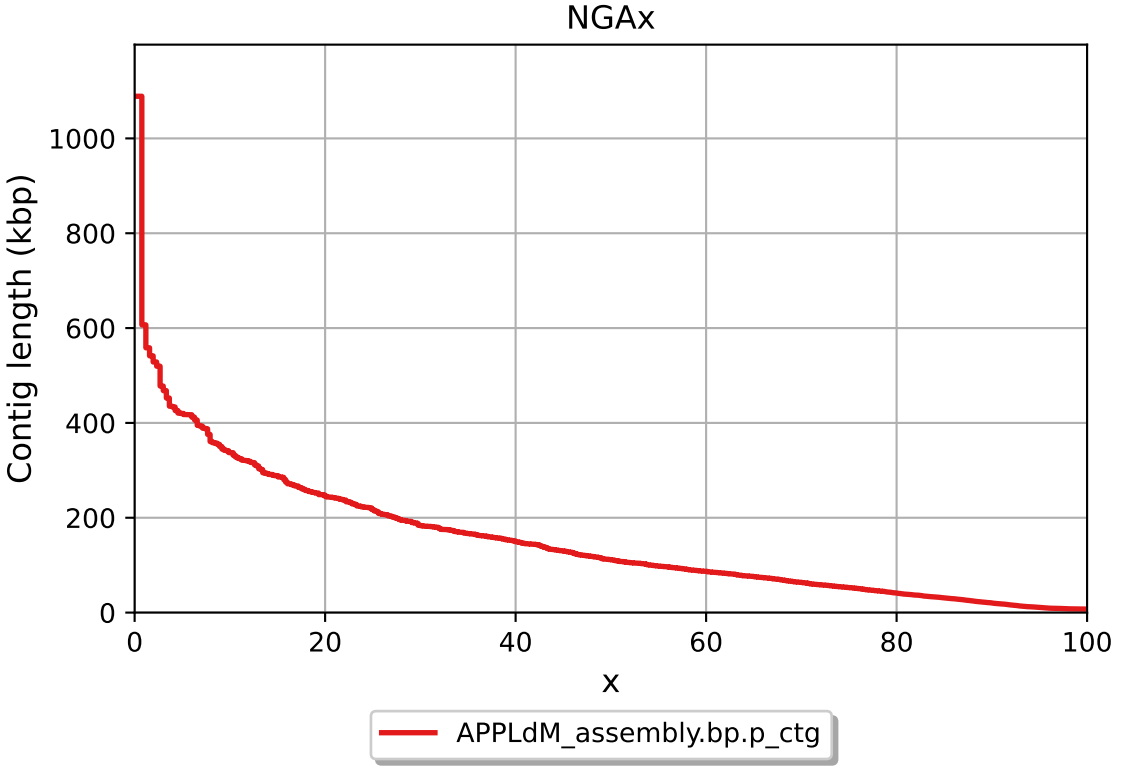

APPLdM_assembly.bp.p_ctg GC content
# contigs
0
15
30
45
60
0
20
40
60
80
100
GC (%)
APPLdM_assembly.bp.p_ctg


Misassemblies
10000
8000
6000
4000
2000
0
APPLdM_assembly.bp.p_ctg
# relocations
# translocations
# inversions


FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
2000
4000
6000
8000
Feature space
APPLdM_assembly.bp.p_ctg


Cumulative length (aligned contigs)
Cumulative length (Mbp)
150
120
90
60
30
0
0
2000
4000
6000
8000
10000
Contig index
APPLdM_assembly.bp.p_ctg
Reference


NAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
APPLdM_assembly.bp.p_ctg


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
APPLdM_assembly.bp.p_ctg