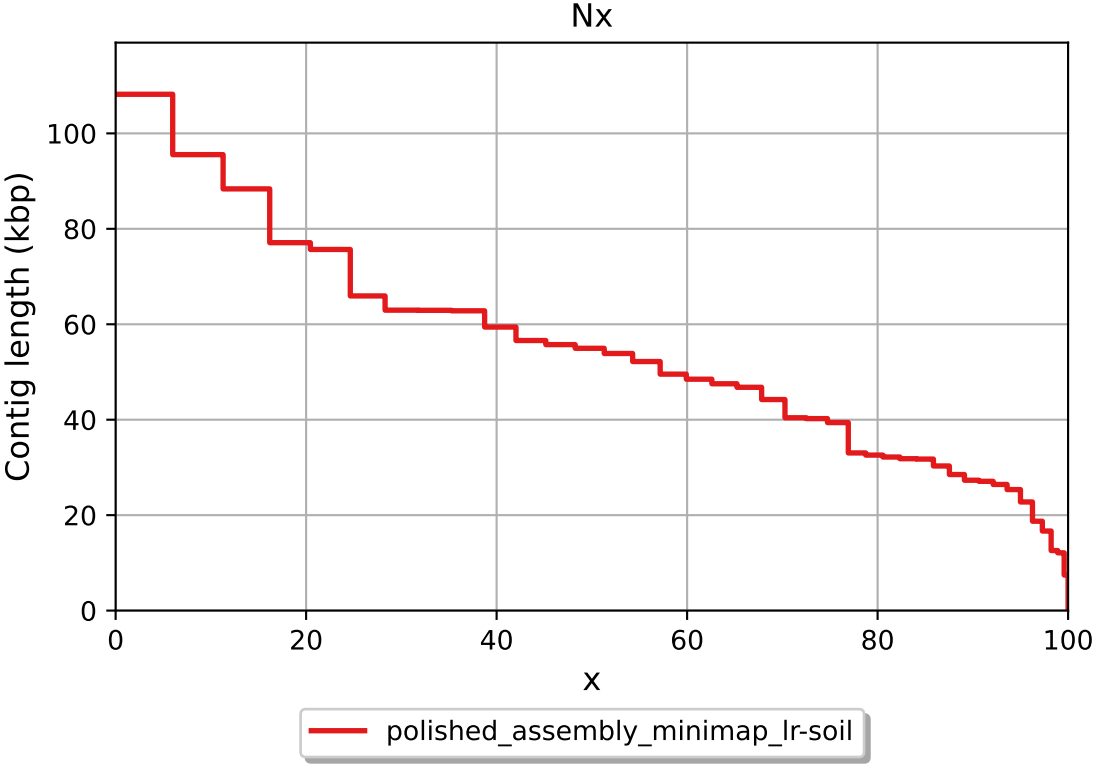
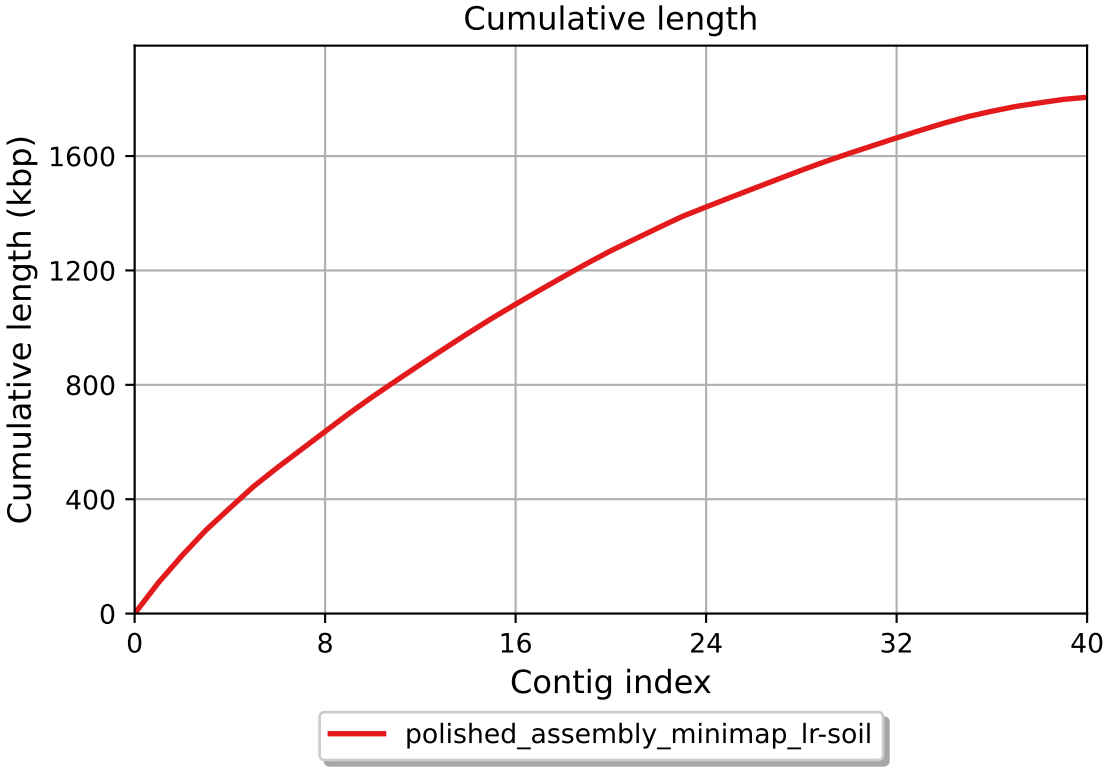
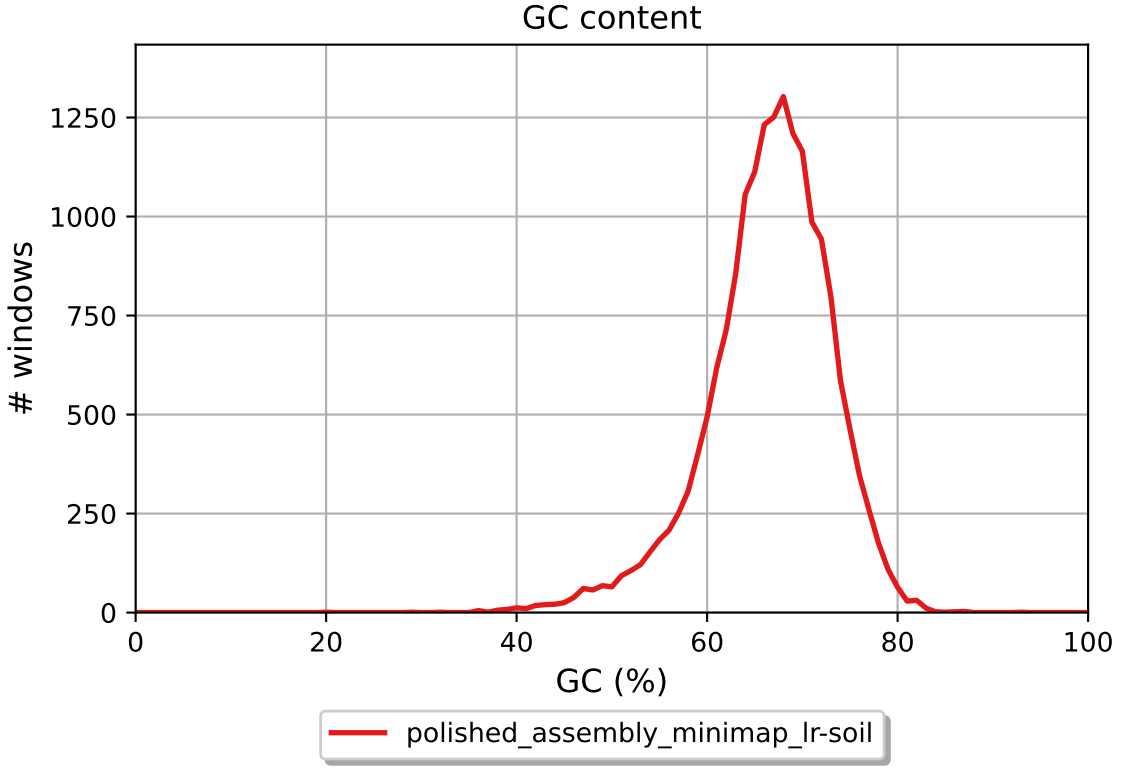
# Report

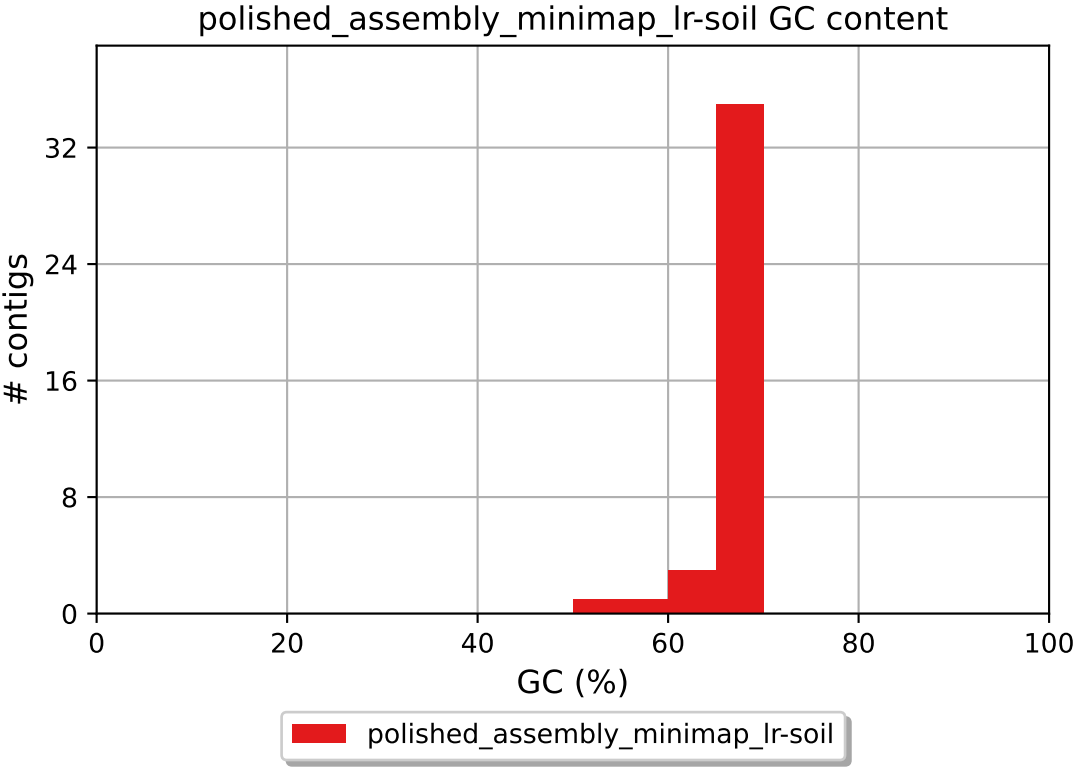
| | polished_assembly_minimap_lr-soil |
|---|---|
| # contigs (>= 0 bp) | 40 |
| # contigs (>= 1000 bp) | 40 |
| # contigs (>= 5000 bp) | 40 |
| # contigs (>= 10000 bp) | 39 |
| # contigs (>= 25000 bp) | 34 |
| # contigs (>= 50000 bp) | 15 |
| Total length (>= 0 bp) | 1805608 |
| Total length (>= 1000 bp) | 1805608 |
| Total length (>= 5000 bp) | 1805608 |
| Total length (>= 10000 bp) | 1798155 |
| Total length (>= 25000 bp) | 1715301 |
| Total length (>= 50000 bp) | 1032301 |
| # contigs | 40 |
| Largest contig | 108196 |
| Total length | 1805608 |
| GC (%) | 66.46 |
| N50 | 54964 |
| N90 | 27317 |
| auN | 56658.6 |
| L50 | 13 |
| L90 | 31 |
| # N's per 100 kbp | 0.00 |
| # predicted genes (unique) | 2217 |
| # predicted genes (>= 0 bp) | 2195 + 24 part |
| # predicted genes (>= 300 bp) | 1839 + 22 part |
| # predicted genes (>= 1500 bp) | 86 + 0 part |
| # predicted genes (>= 3000 bp) | 2 + 0 part |

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 (kbp)
0
20
40
60
80
100
0
20
40
60
80
100
x
polished_assembly_minimap_lr-soil


Cumulative length
Cumulative length (kbp)
1600
1200
800
400
0
0
8
16
24
32
40
Contig index
polished_assembly_minimap_lr-soil


GC content
# windows
1250
1000
750
500
250
0
0
20
40
60
80
100
GC (%)
polished_assembly_minimap_lr-soil


polished_assembly_minimap_lr-soil GC content
# contigs
0
8
16
24
32
0
20
40
60
80
100
GC (%)
polished_assembly_minimap_lr-soil