Report

	HP126
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	8772056
Total length (>= 1000 bp)	8772056
Total length (>= 5000 bp)	8772056
Total length (>= 10000 bp)	8772056
Total length (>= 25000 bp)	8772056
Total length (>= 50000 bp)	8772056
# contigs	4
Largest contig	6996028
Total length	8772056
Reference length	9619655
GC (%)	72.00
Reference GC (%)	71.93
N50	6996028
NG50	6996028
N75	6996028
NG75	1054438
L50	1
LG50	1
L75	1
LG75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.953
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.23
# indels per 100 kbp	0.69
Largest alignment	6996028
Total aligned length	8771911
NA50	6996028
NGA50	6996028
NA75	6996028
NGA75	1054438
LA50	1
LGA50	1
LA75	1
LGA75	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).

Misassemblies report

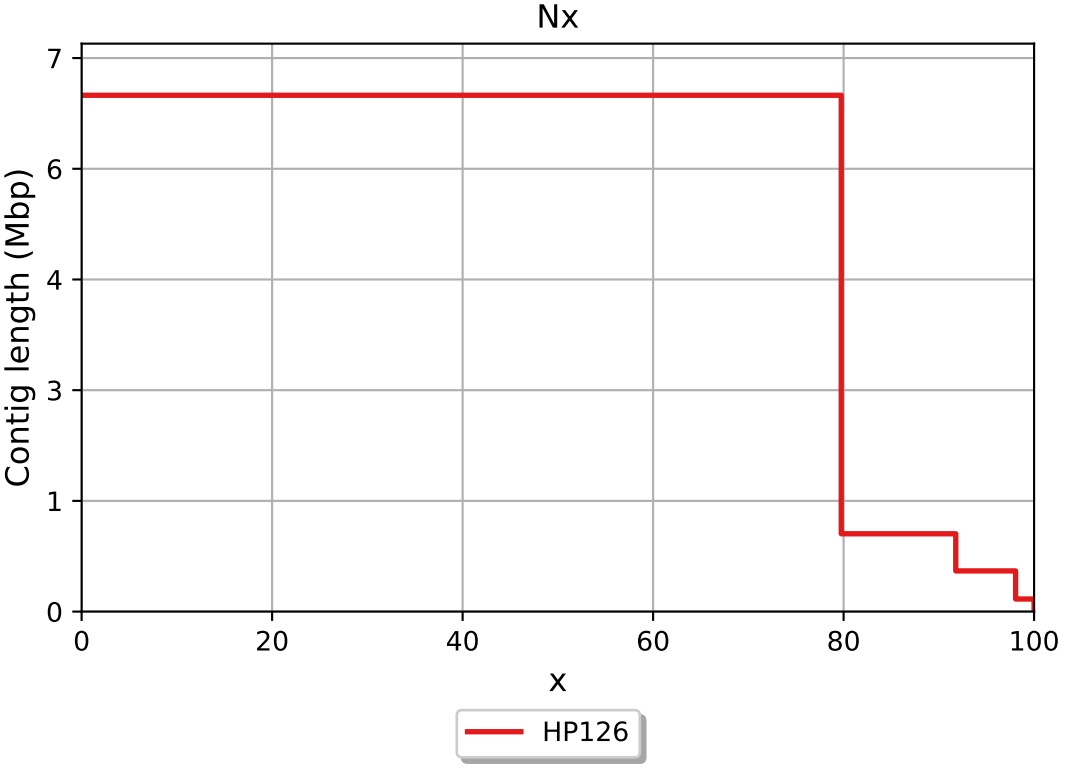
	HP126
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	20
# indels	60
# indels (<= 5 bp)	59
# indels (> 5 bp)	1
Indels length	88

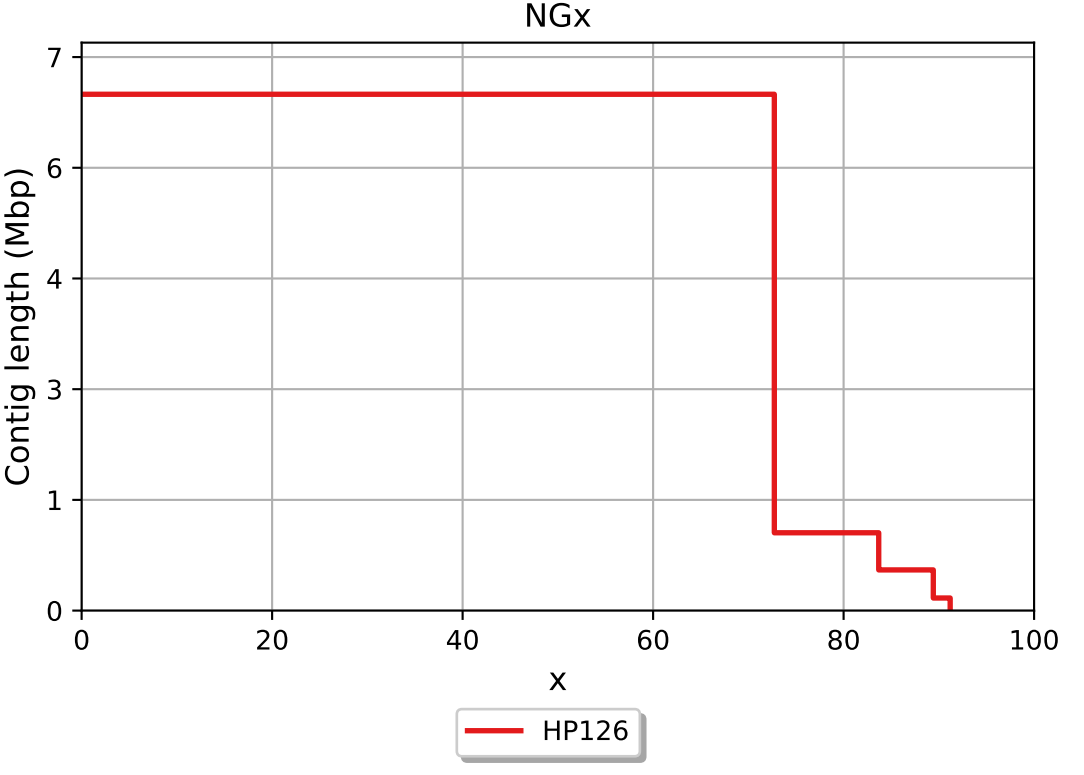
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

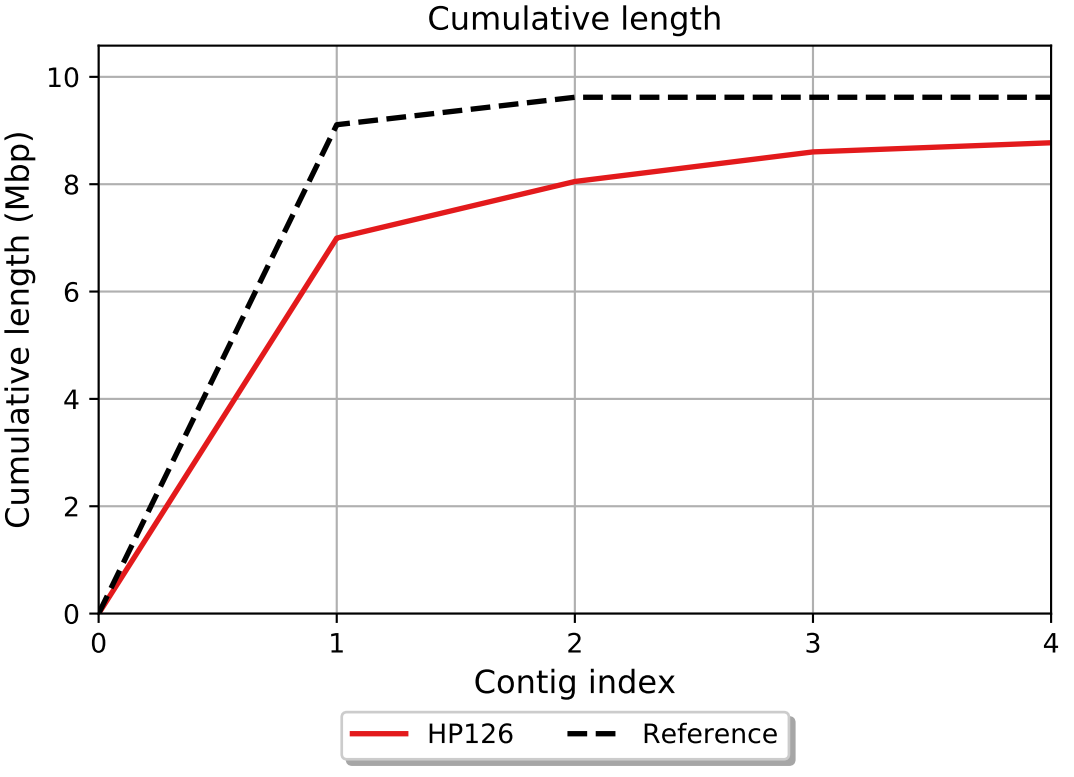
Unaligned report

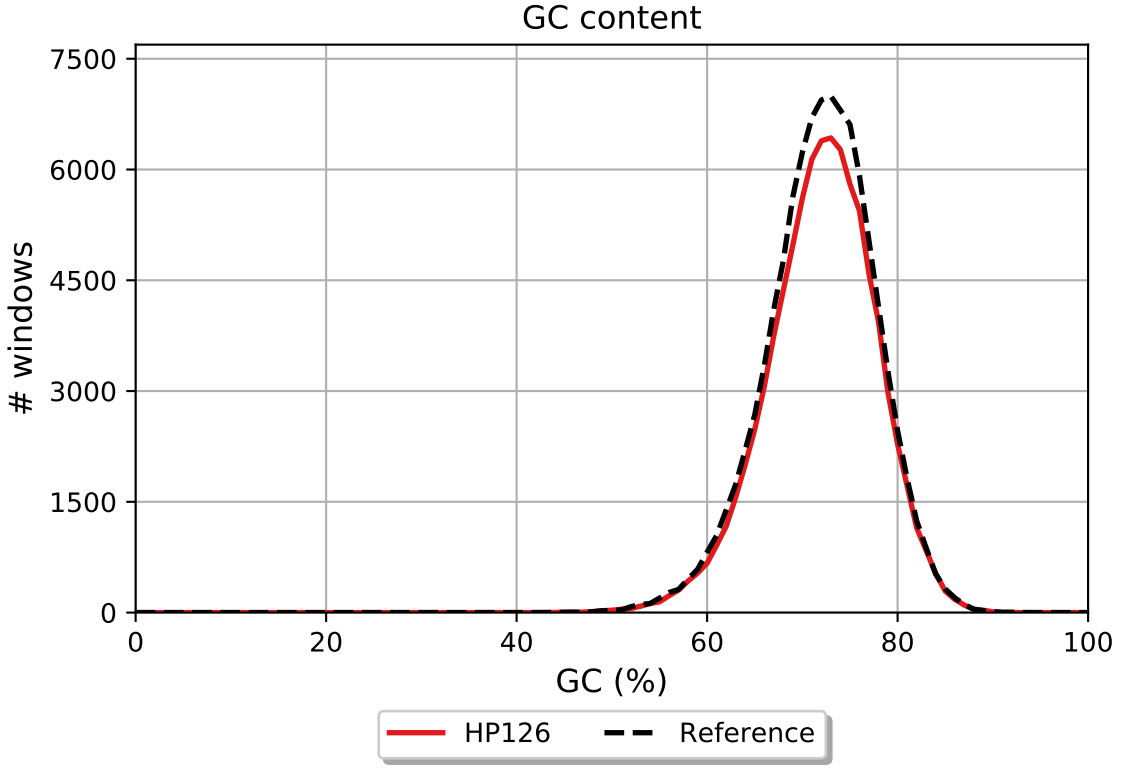
	HP126
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

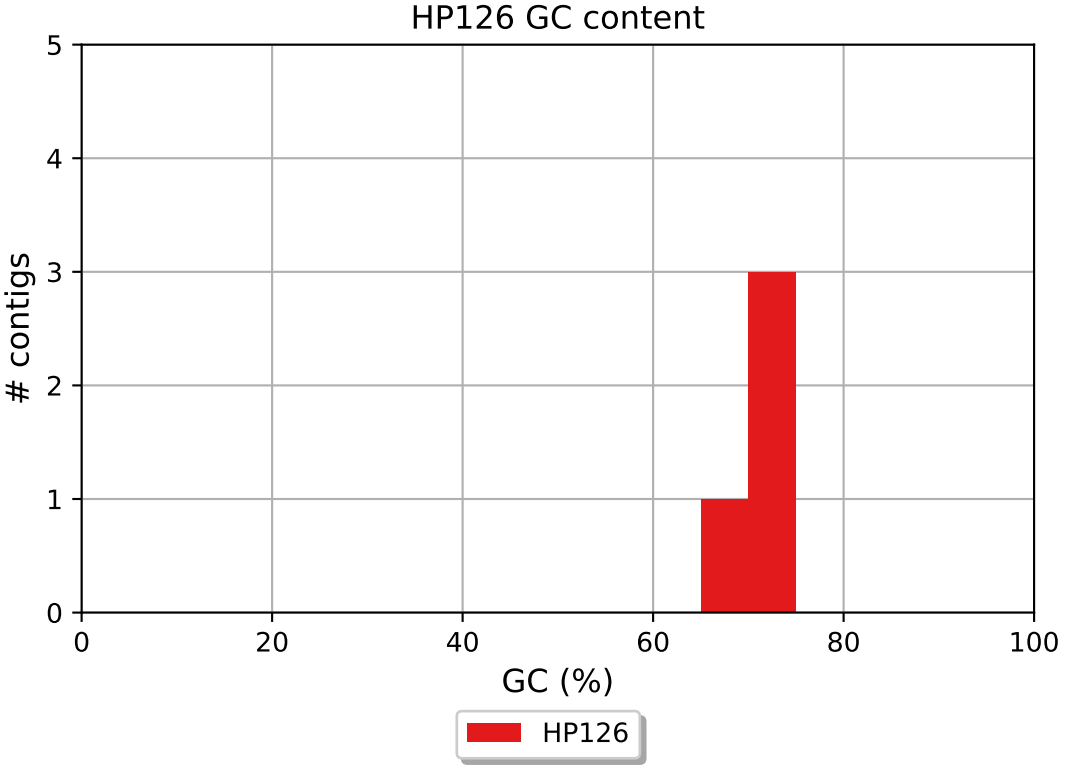
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

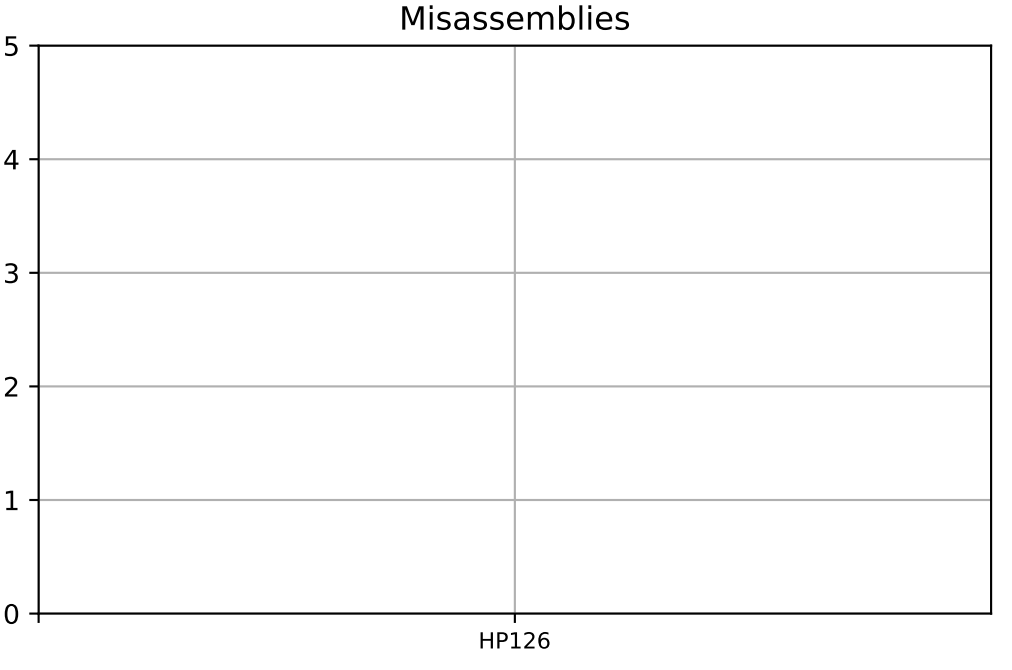

Nx
Contig length (Mbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
HP126

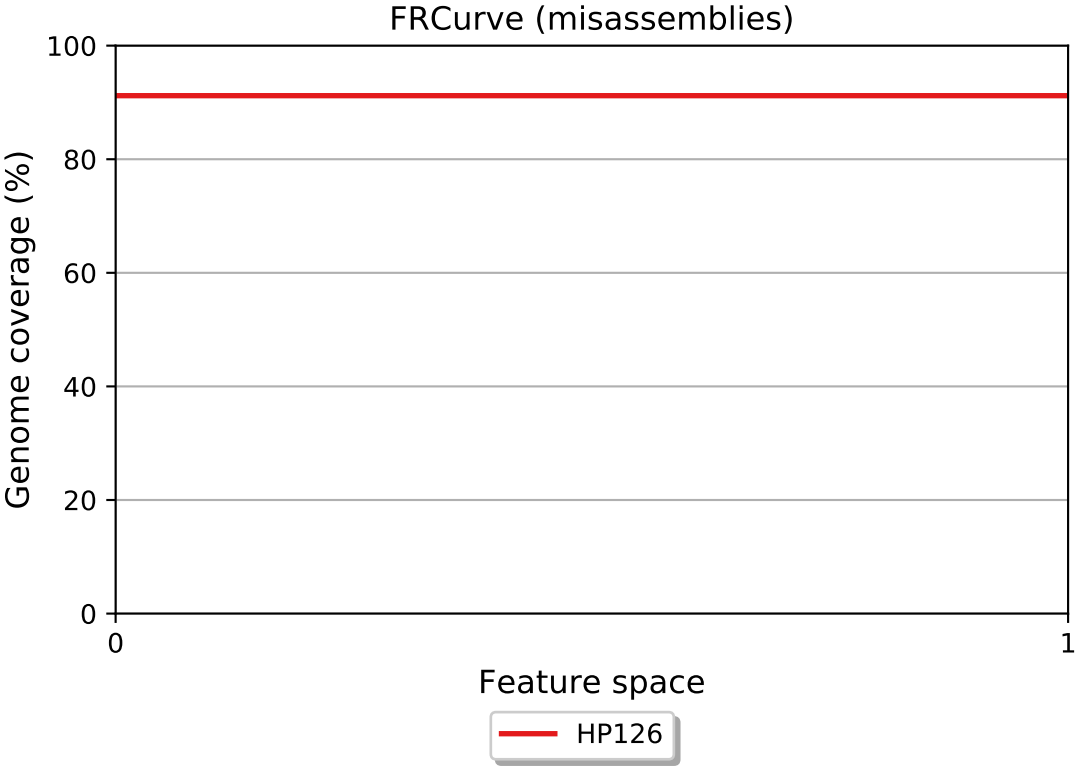

NGx
Contig length (Mbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
HP126

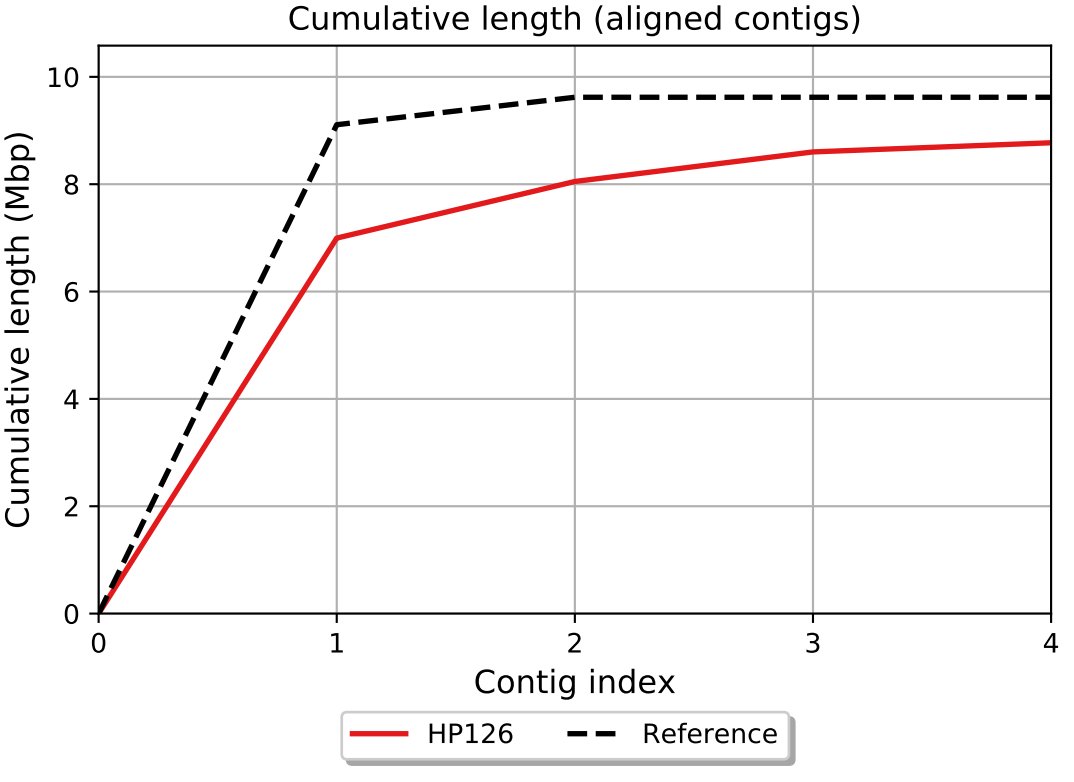

Cumulative length
Cumulative length (Mbp)
10
8
6
4
2
0
0
1
2
3
4
Contig index
HP126
Reference

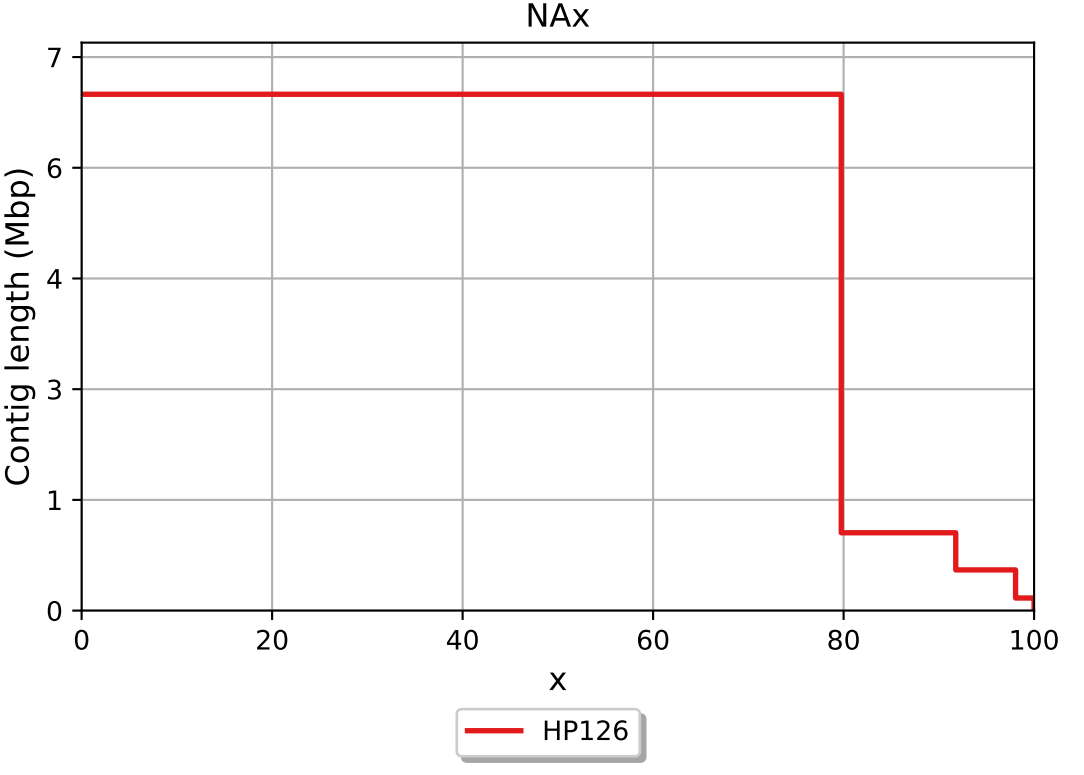

GC content
7500
6000
4500
3000
1500
0
windows
0
20
40
60
80
100
GC (%)
HP126
Reference

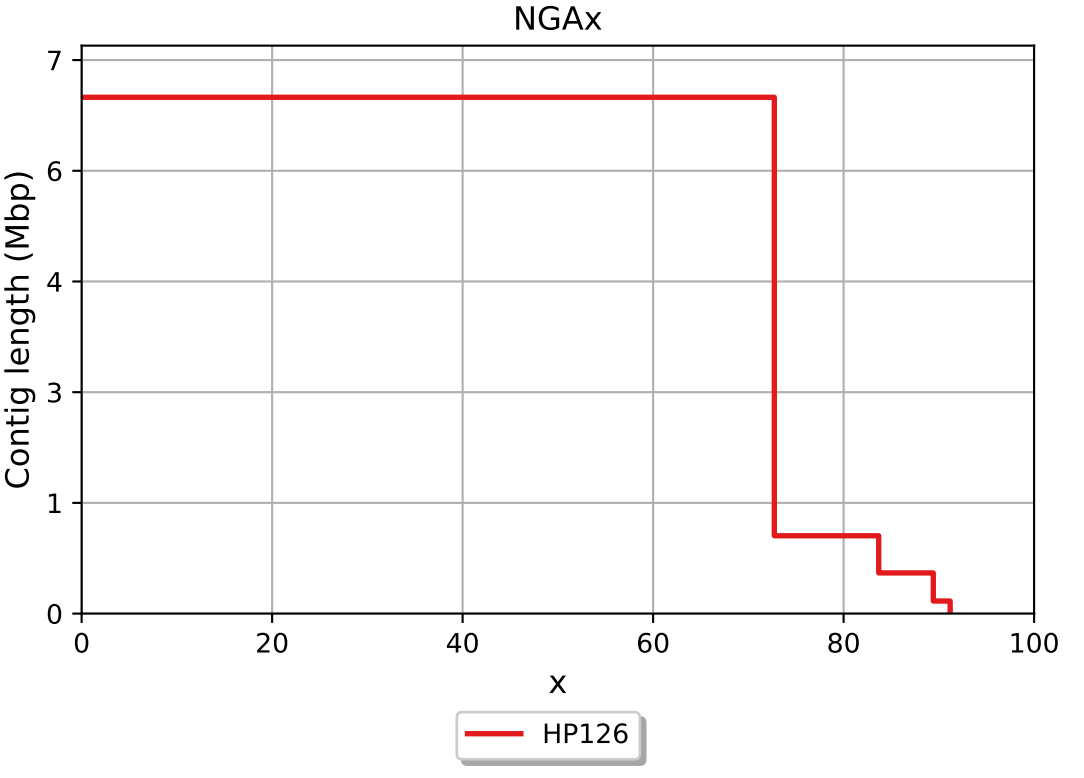

HP126 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
HP126


Misassemblies
5
4
3
2
1
0
HP126


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
HP126


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
2
4
6
8
10
0
1
2
3
4
Contig index
HP126
Reference


NAx
Contig length (Mbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
HP126


NGAx
Contig length (Mbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
HP126