Report

	soapdenovoK49_result
# contigs (>= 0 bp)	743727
# contigs (>= 1000 bp)	671
# contigs (>= 5000 bp)	74
# contigs (>= 10000 bp)	10
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	59895070
Total length (>= 1000 bp)	1845154
Total length (>= 5000 bp)	546987
Total length (>= 10000 bp)	117931
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1052
Largest contig	16421
Total length	2103624
Reference length	2366763
GC (%)	49.27
Reference GC (%)	49.44
N50	2916
NG50	2500
N75	1549
NG75	1149
L50	208
LG50	257
L75	459
LG75	606
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1121
# local misassemblies	30
# unaligned mis. contigs	0
# unaligned contigs	103 + 0 part
Unaligned length	56719
Genome fraction (%)	85.932
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	30.09
# indels per 100 kbp	3.05
Largest alignment	16421
Total aligned length	2037999
NA50	2896
NGA50	2494
NA75	1533
NGA75	1145
LA50	208
LGA50	257
LA75	461
LGA75	610

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

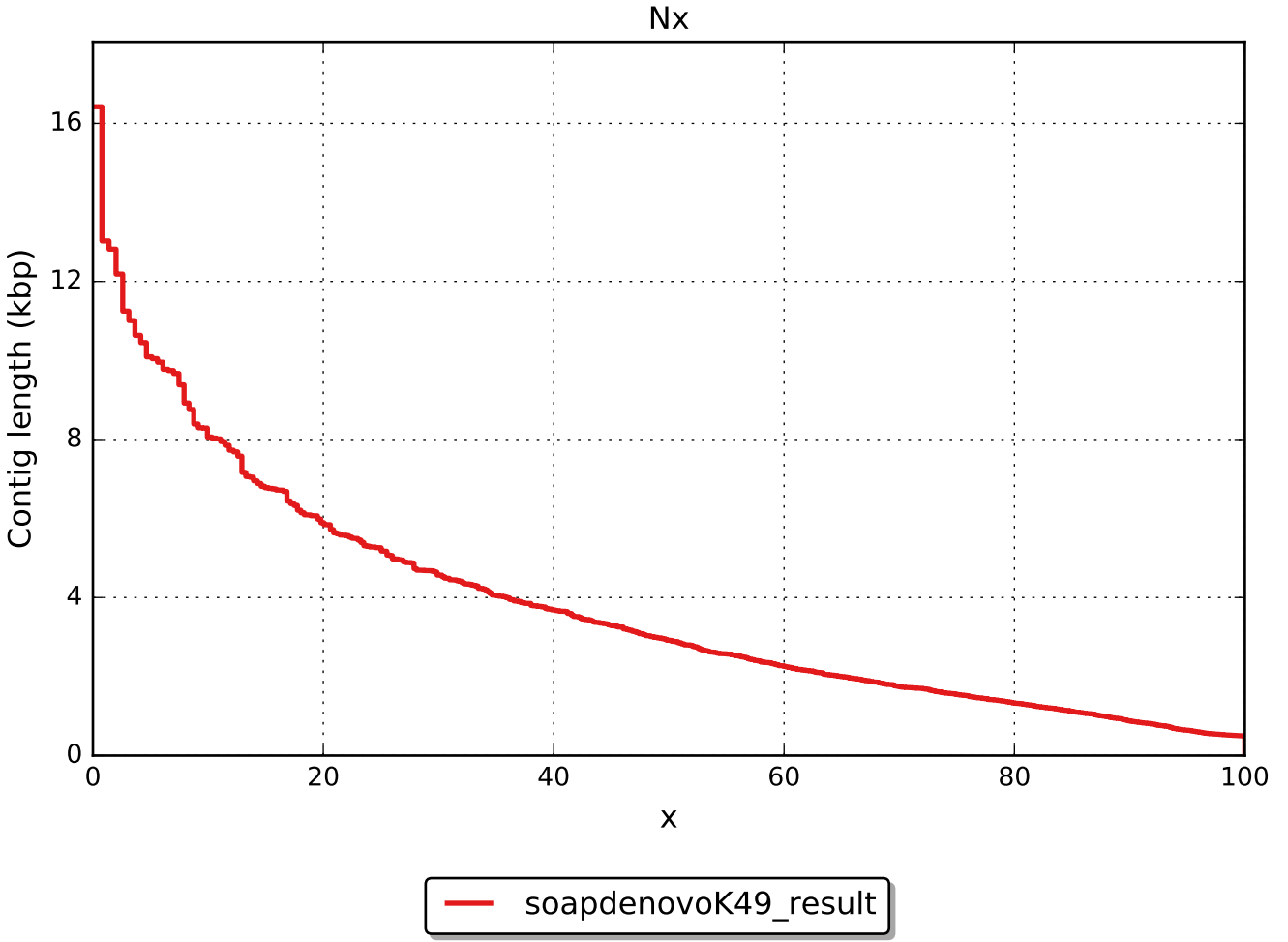
	soapdenovoK49_result
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	1121
# local misassemblies	30
# unaligned mis. contigs	0
# mismatches	612
# indels	62
# indels (<= 5 bp)	39
# indels (> 5 bp)	23
Indels length	878

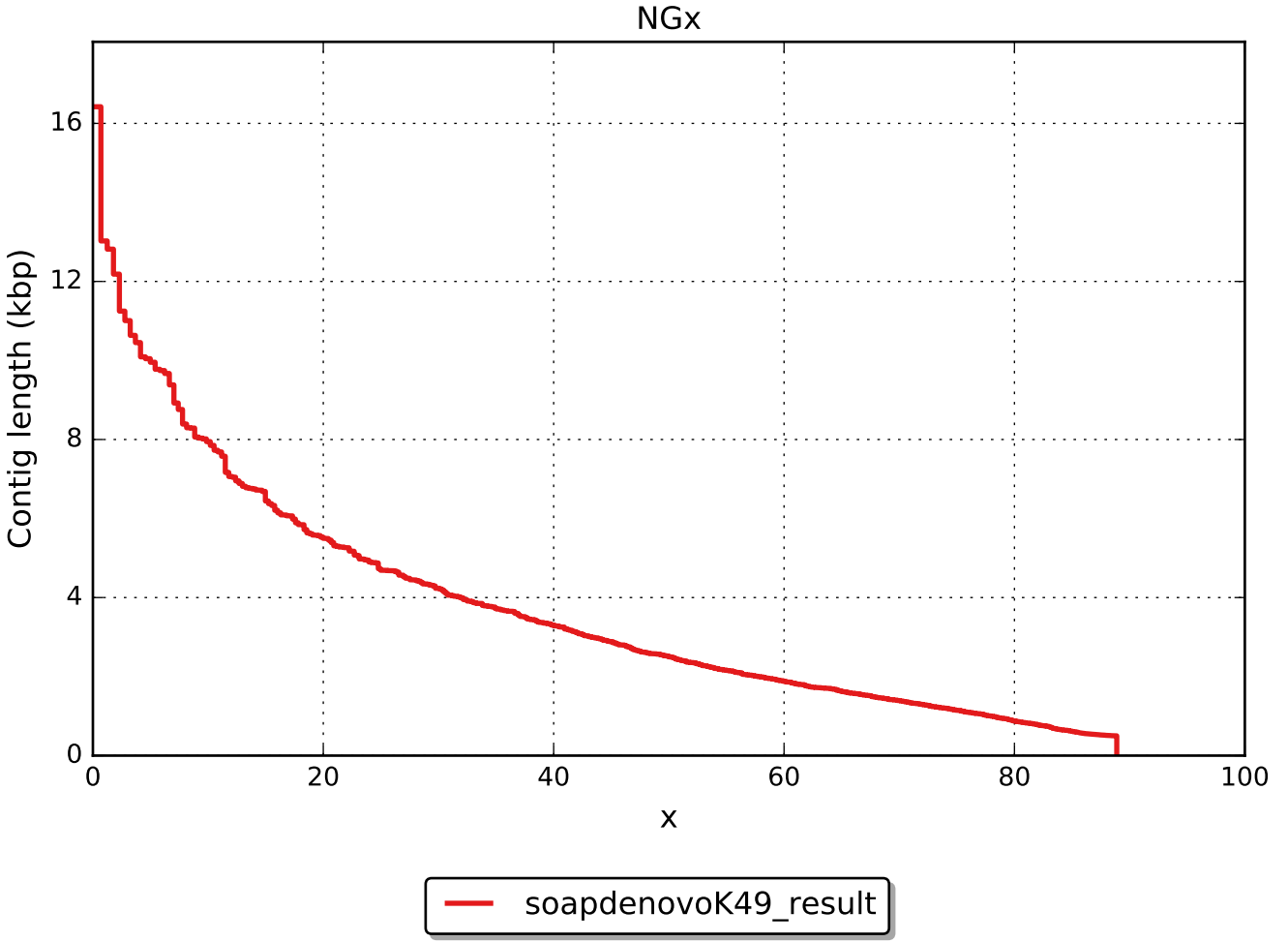
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

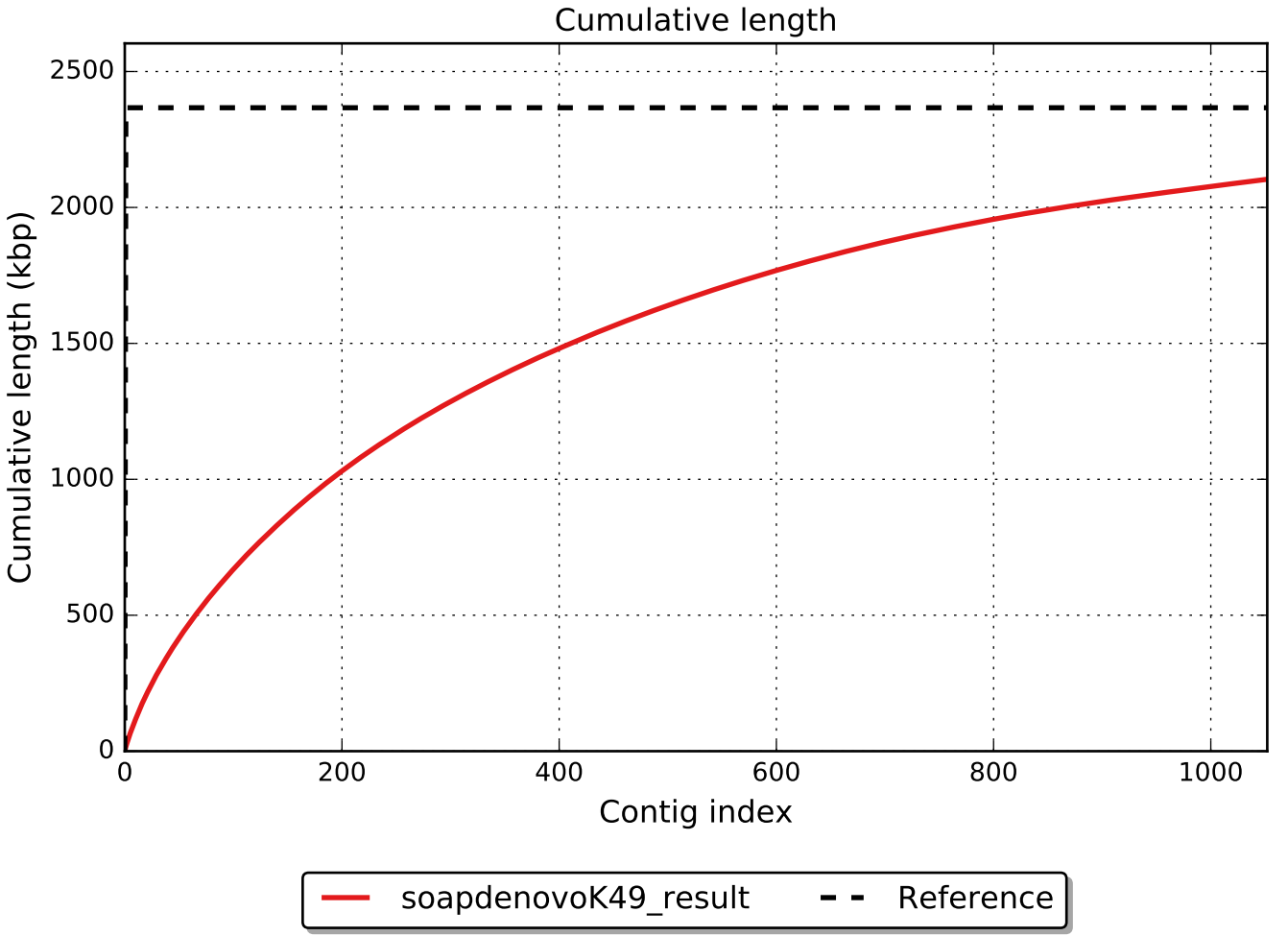
Unaligned report

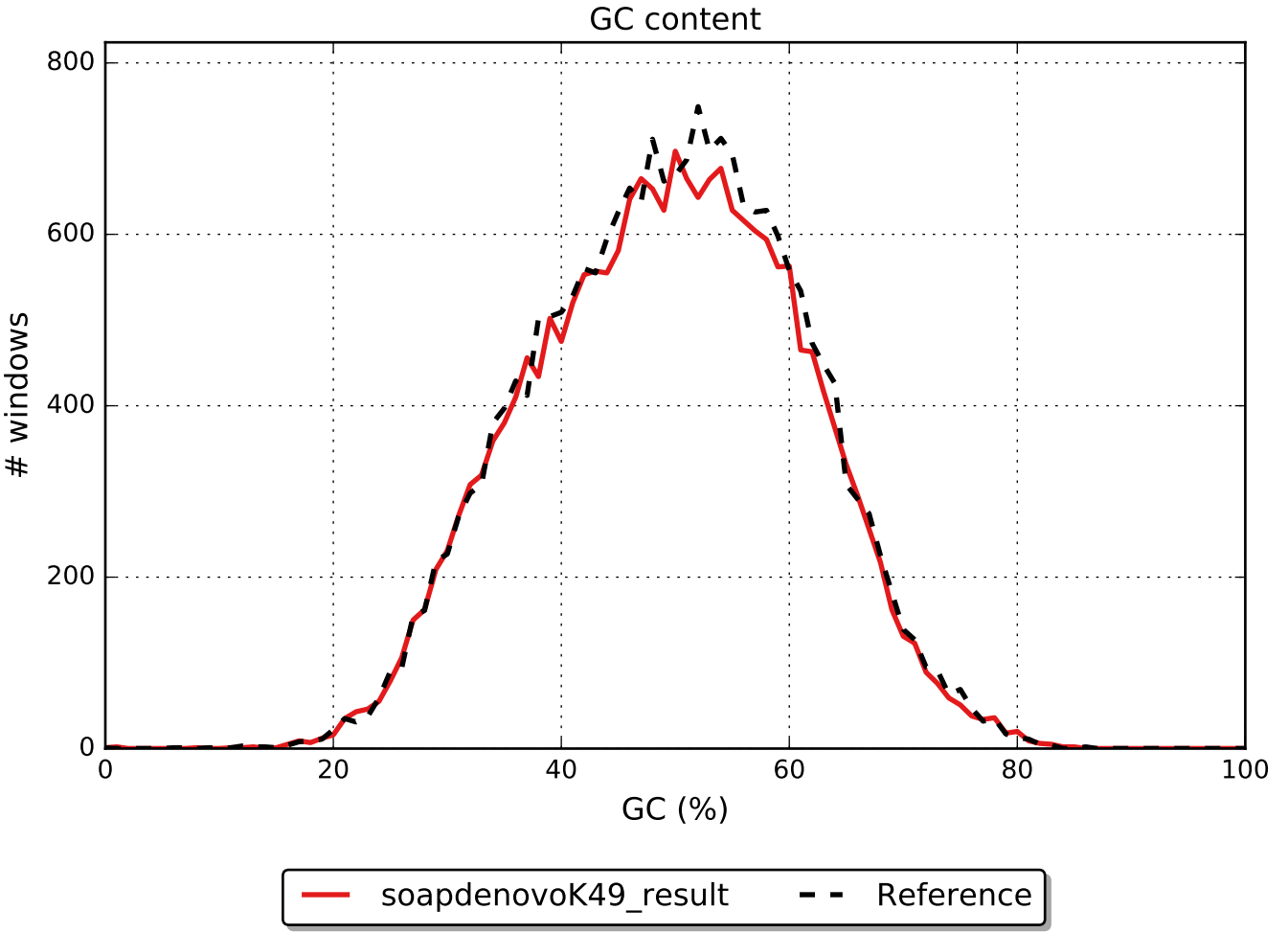
	soapdenovoK49_result
# fully unaligned contigs	103
Fully unaligned length	56719
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

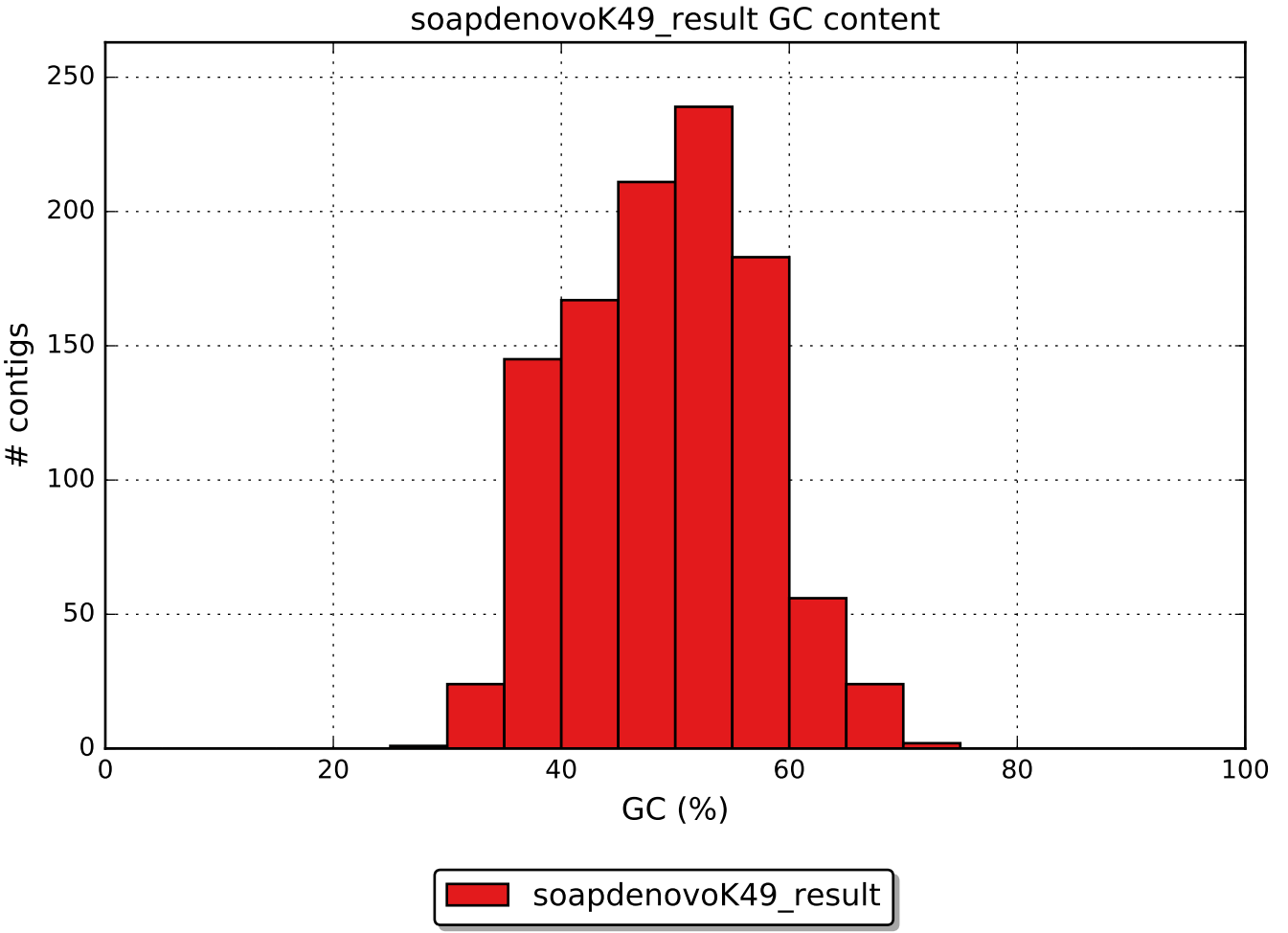
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

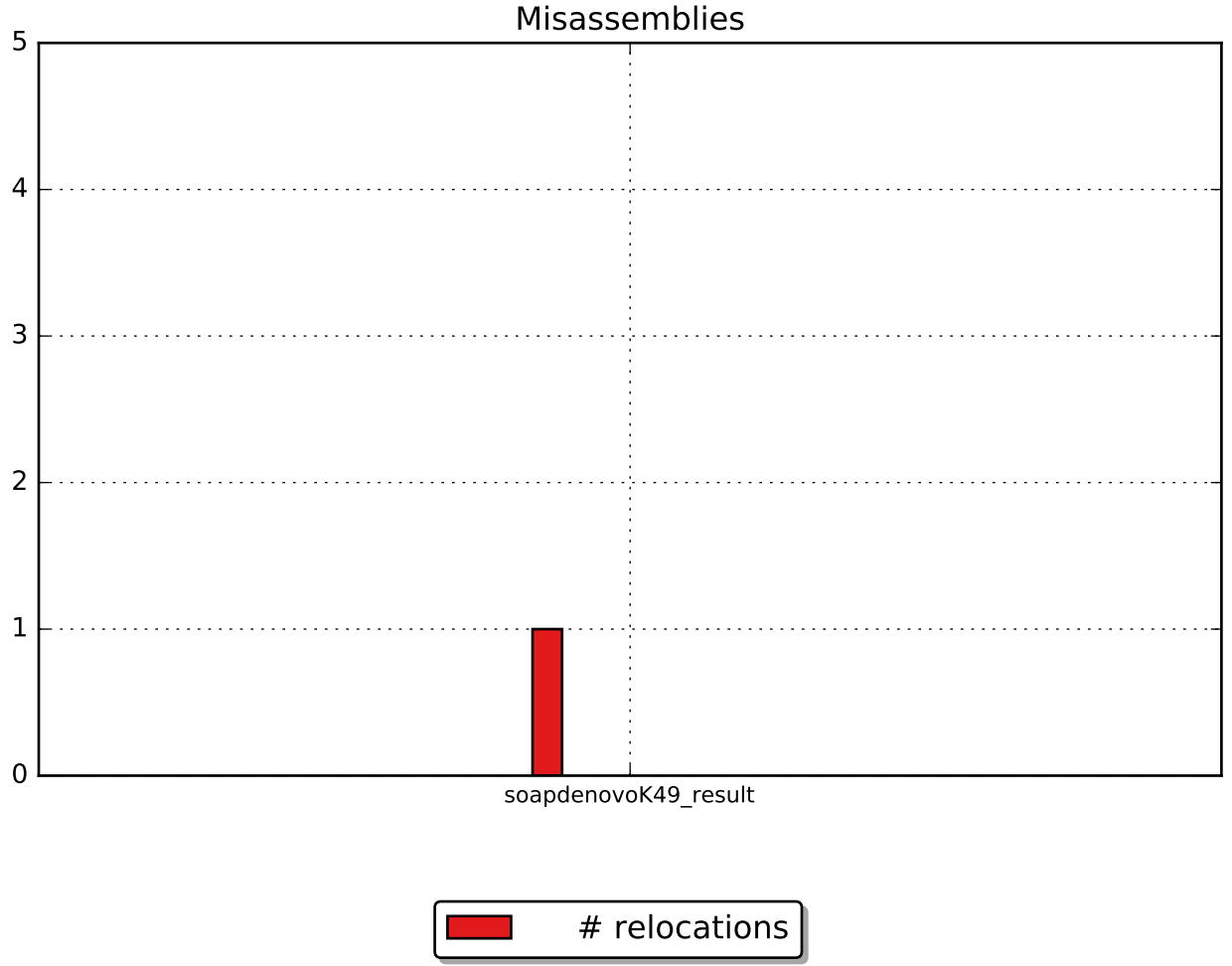

Nx
Contig length (kbp)
16
12
8
4
0
0
20
40
60
80
100
x
soapdenovoK49_result

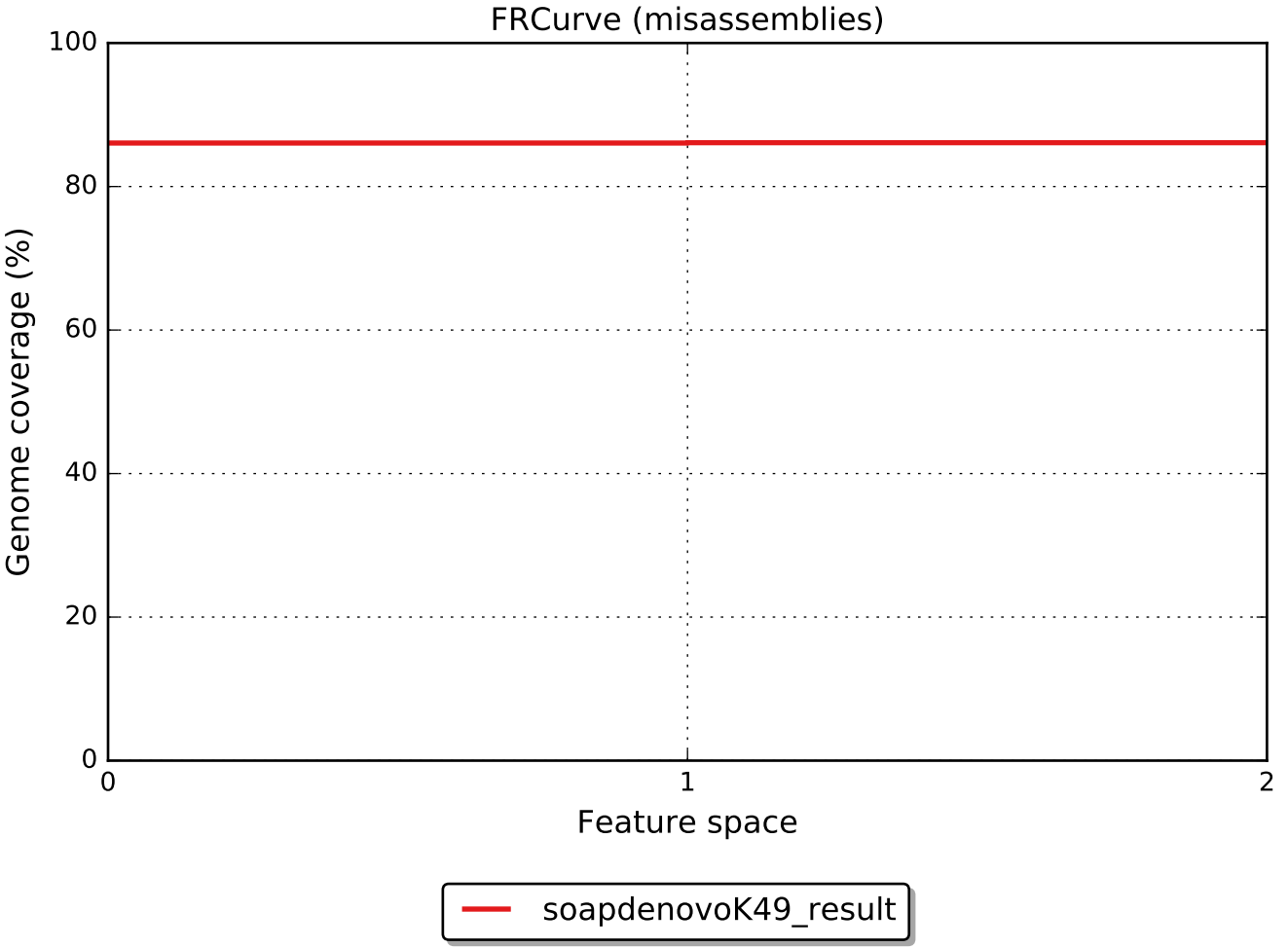

NGx
Contig length (kbp)
16
12
8
4
0
0
20
40
60
80
100
x
soapdenovoK49_result

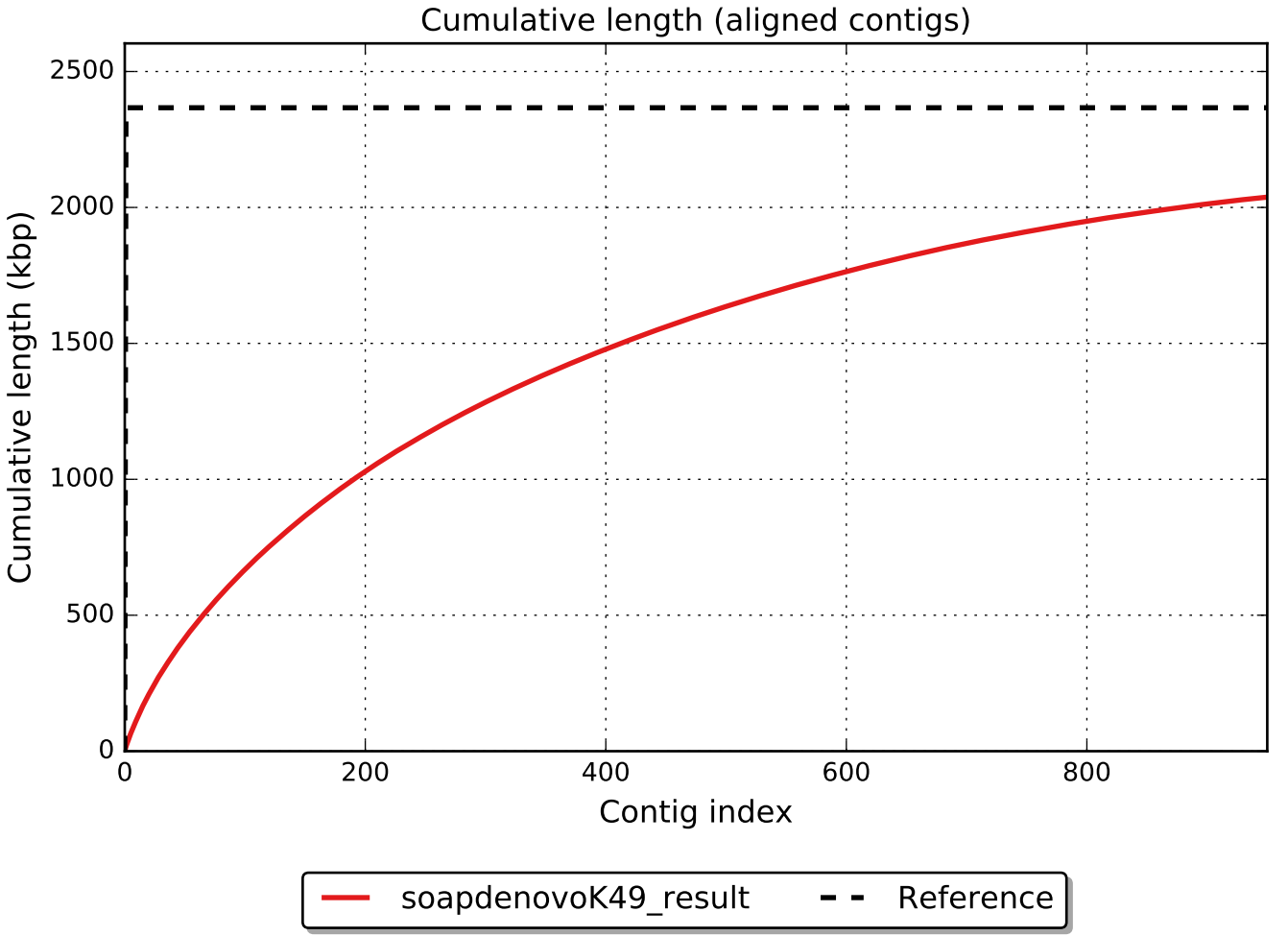

Cumulative length
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
200
400
600
800
1000
Contig index
soapdenovoK49_result
Reference

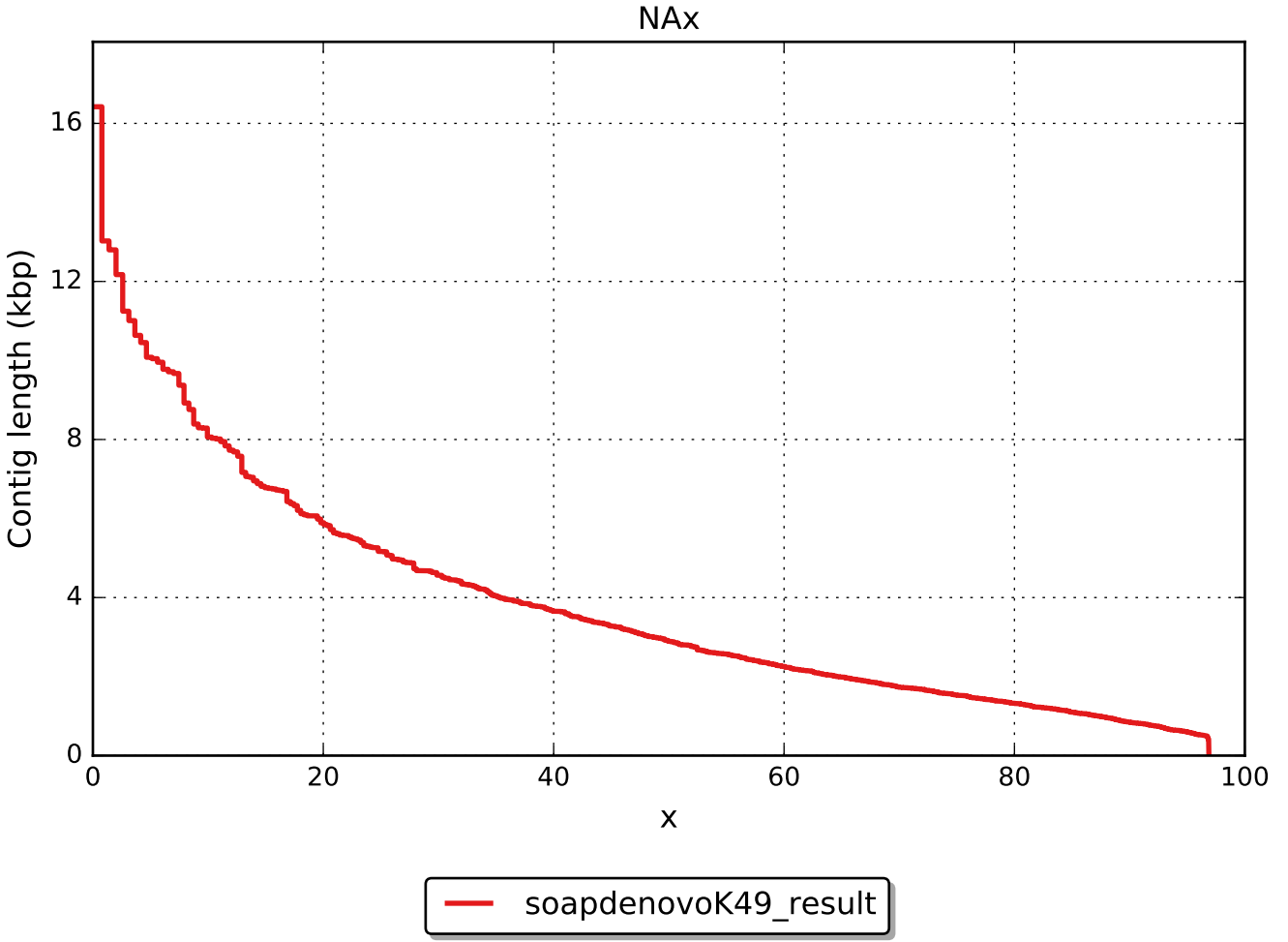

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
soapdenovoK49_result
Reference

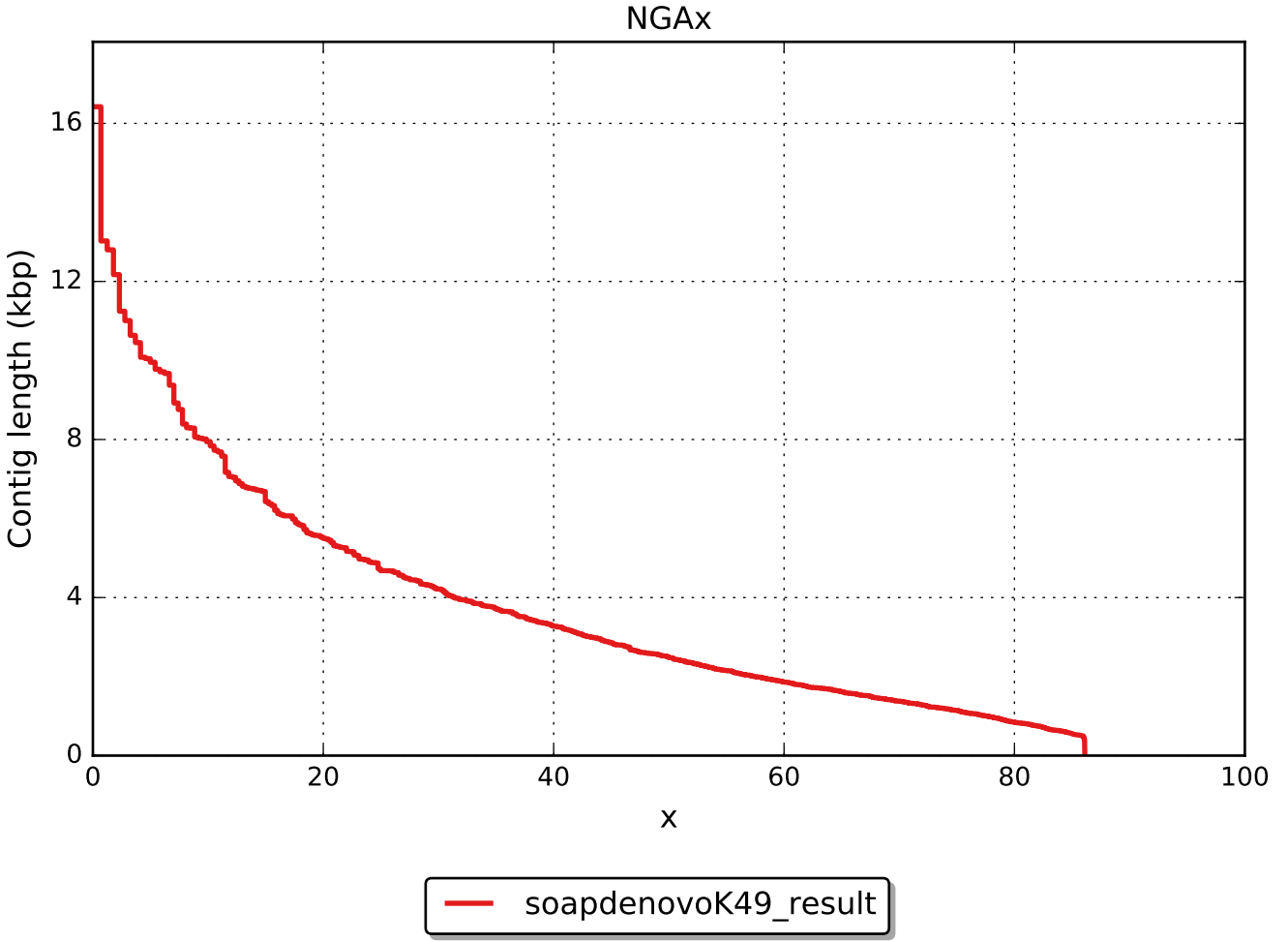

soapdenovoK49_result GC content
contigs
GC (%)
0
50
100
150
200
250
0
20
40
60
80
100
soapdenovoK49_result


Misassemblies
5
4
3
2
1
0
soapdenovoK49_result
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
Feature space
soapdenovoK49_result


Cumulative length (aligned contigs)
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
200
400
600
800
Contig index
soapdenovoK49_result
Reference


NAx
Contig length (kbp)
16
12
8
4
0
0
20
40
60
80
100
x
soapdenovoK49_result


NGAx
Contig length (kbp)
16
12
8
4
0
0
20
40
60
80
100
x
soapdenovoK49_result