Report

	contigs_1	contigs_2
# contigs (>= 0 bp)	3	4
# contigs (>= 1000 bp)	3	2
Total length (>= 0 bp)	6710	5870
Total length (>= 1000 bp)	6710	5460
# contigs	3	2
Largest contig	3980	3360
Total length	6710	5460
Reference length	10000	10000
GC (%)	51.28	52.44
Reference GC (%)	52.07	52.07
N50	3980	3360
NG50	1610	2100
N75	1610	2100
L50	1	1
LG50	2	2
L75	2	2
# misassemblies	1	2
# misassembled contigs	1	1
Misassembled contigs length	3980	3360
# local misassemblies	0	0
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	67.120	54.610
Duplication ratio	1.000	1.000
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	0.00	0.00
# indels per 100 kbp	0.00	0.00
# genes	5 + 4 part	1 + 6 part
# operons	1 + 1 part	0 + 2 part
# predicted genes (unique)	7	6
# predicted genes (>= 0 bp)	7	6
# predicted genes (>= 300 bp)	6	5
# predicted genes (>= 1500 bp)	1	1
# predicted genes (>= 3000 bp)	0	0
Largest alignment	2030	2100
NA50	1950	1470
NGA50	1610	700
NA75	1610	1190
LA50	2	2
LGA50	3	4
LA75	3	3

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

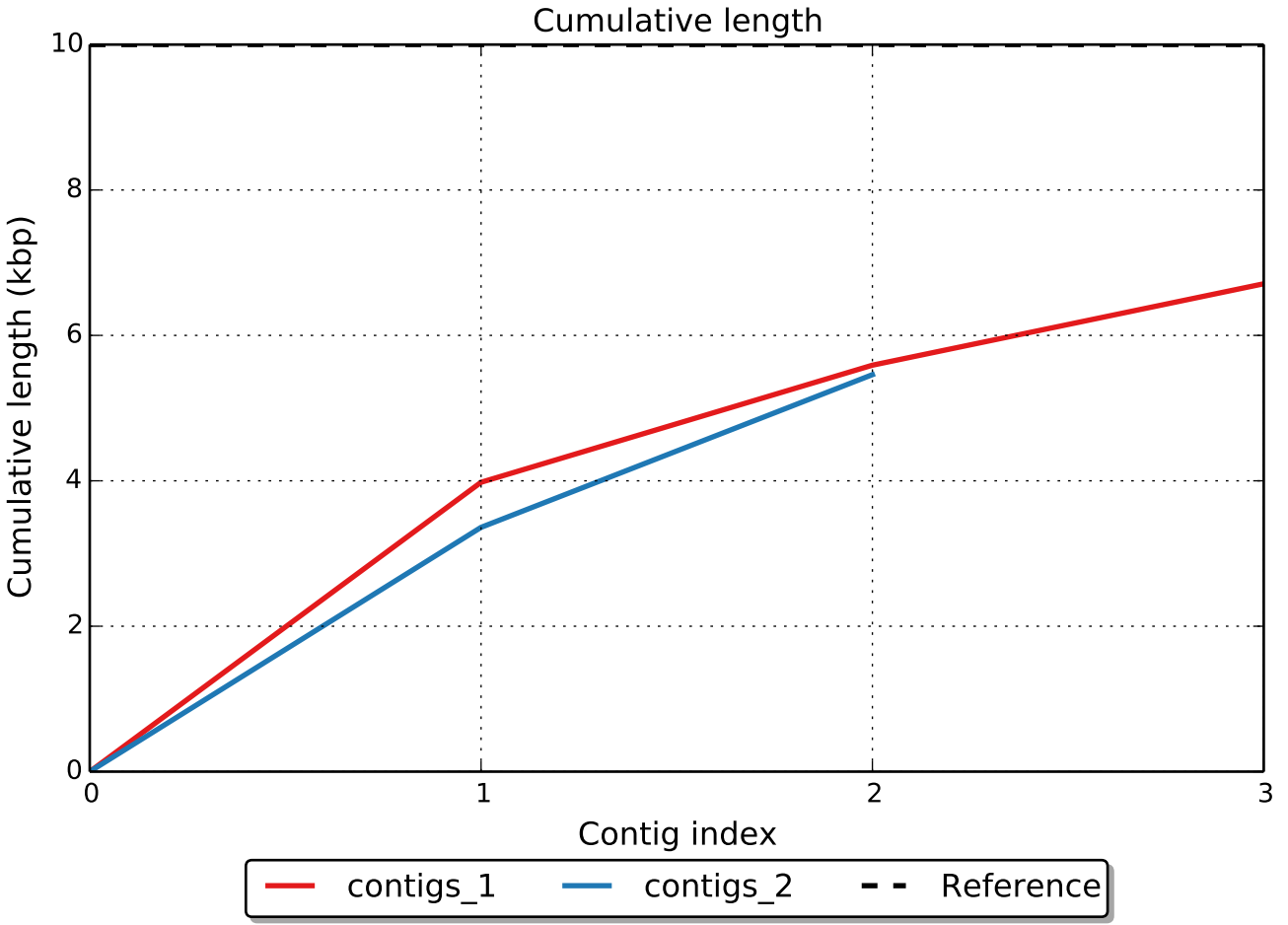
	contigs_1	contigs_2
# misassemblies	1	2
# relocations	1	2
# translocations	0	0
# inversions	0	0
# misassembled contigs	1	1
Misassembled contigs length	3980	3360
# local misassemblies	0	0
# mismatches	0	0
# indels	0	0
# short indels	0	0
# long indels	0	0
Indels length	0	0

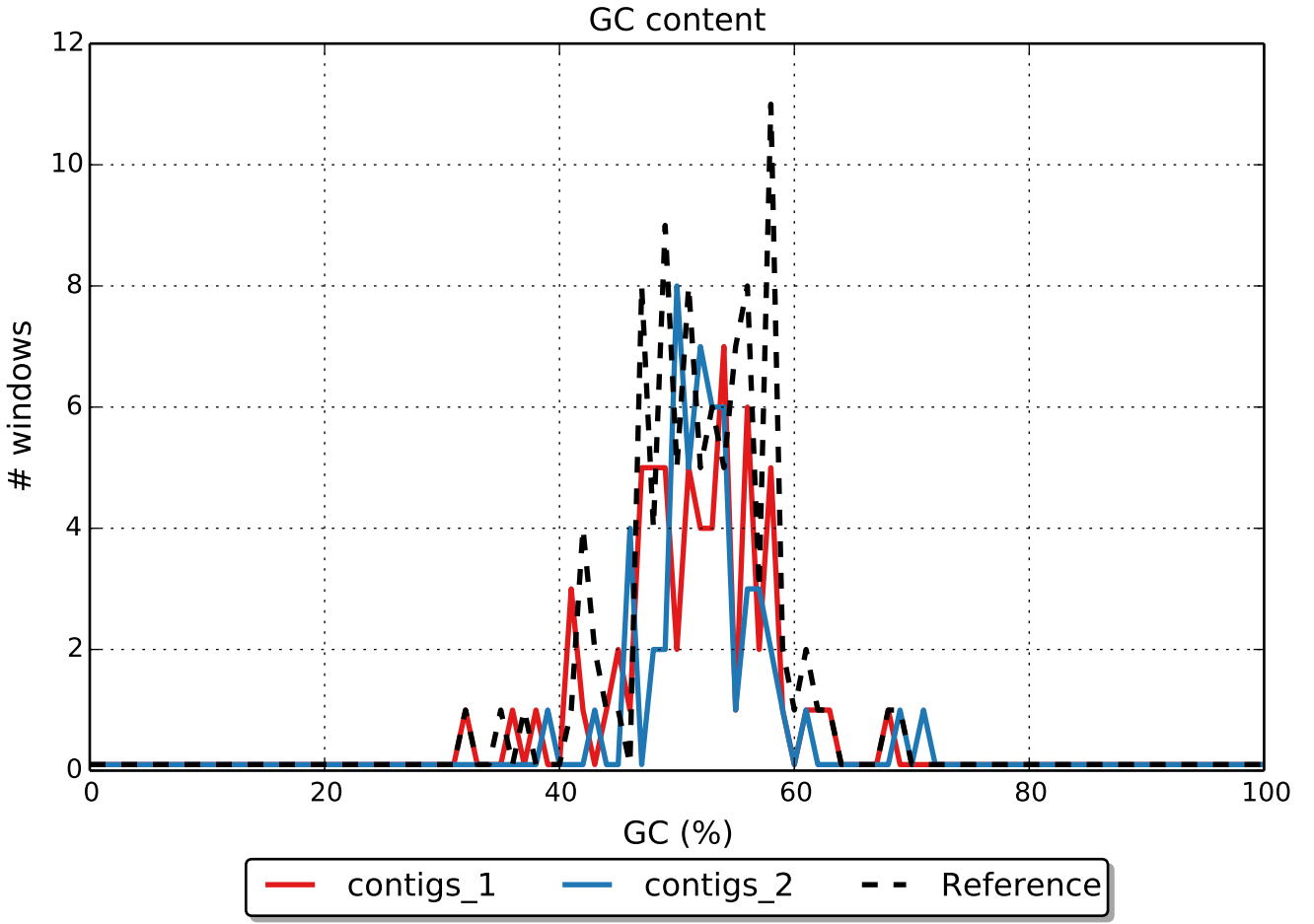
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

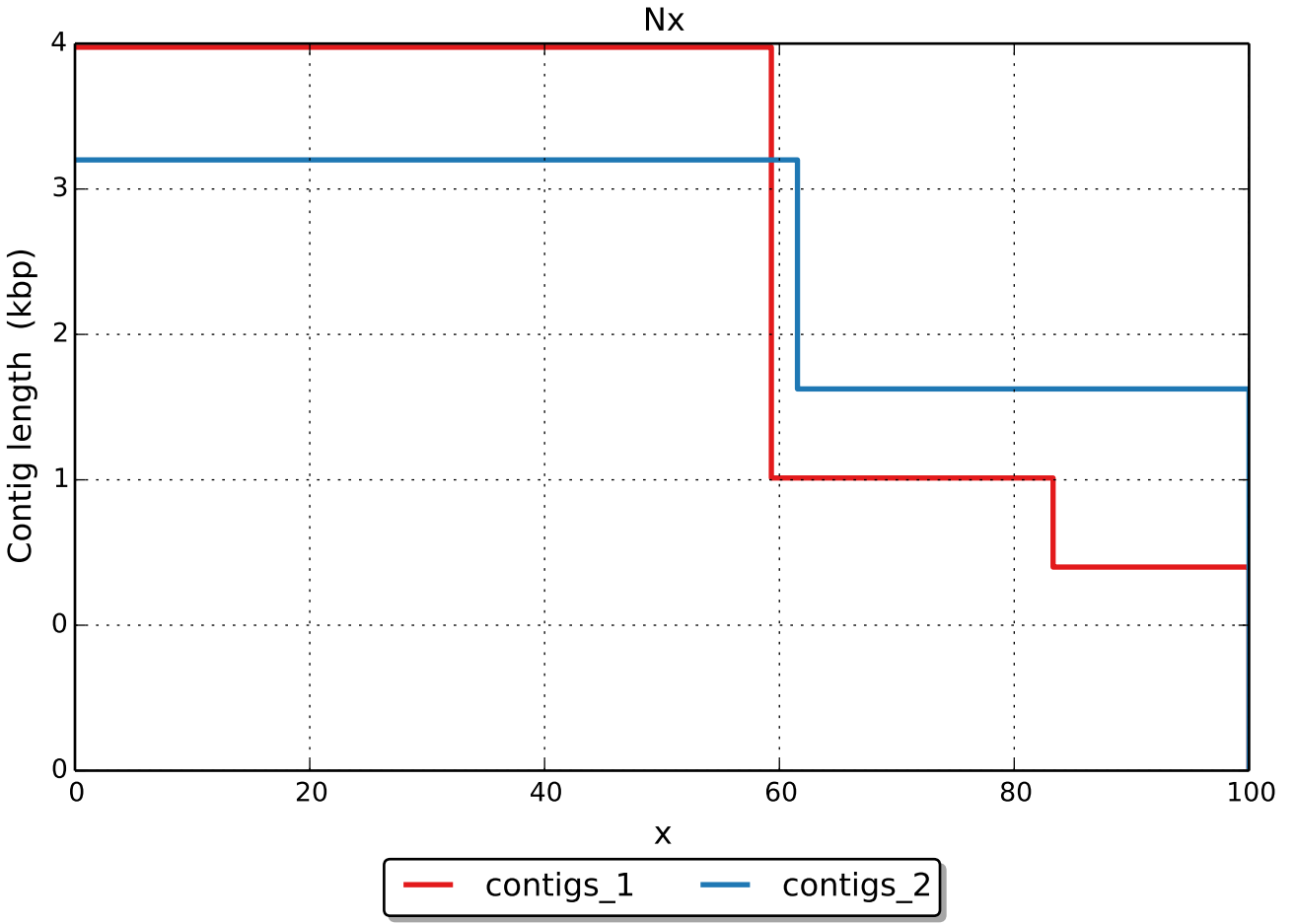
Unaligned report

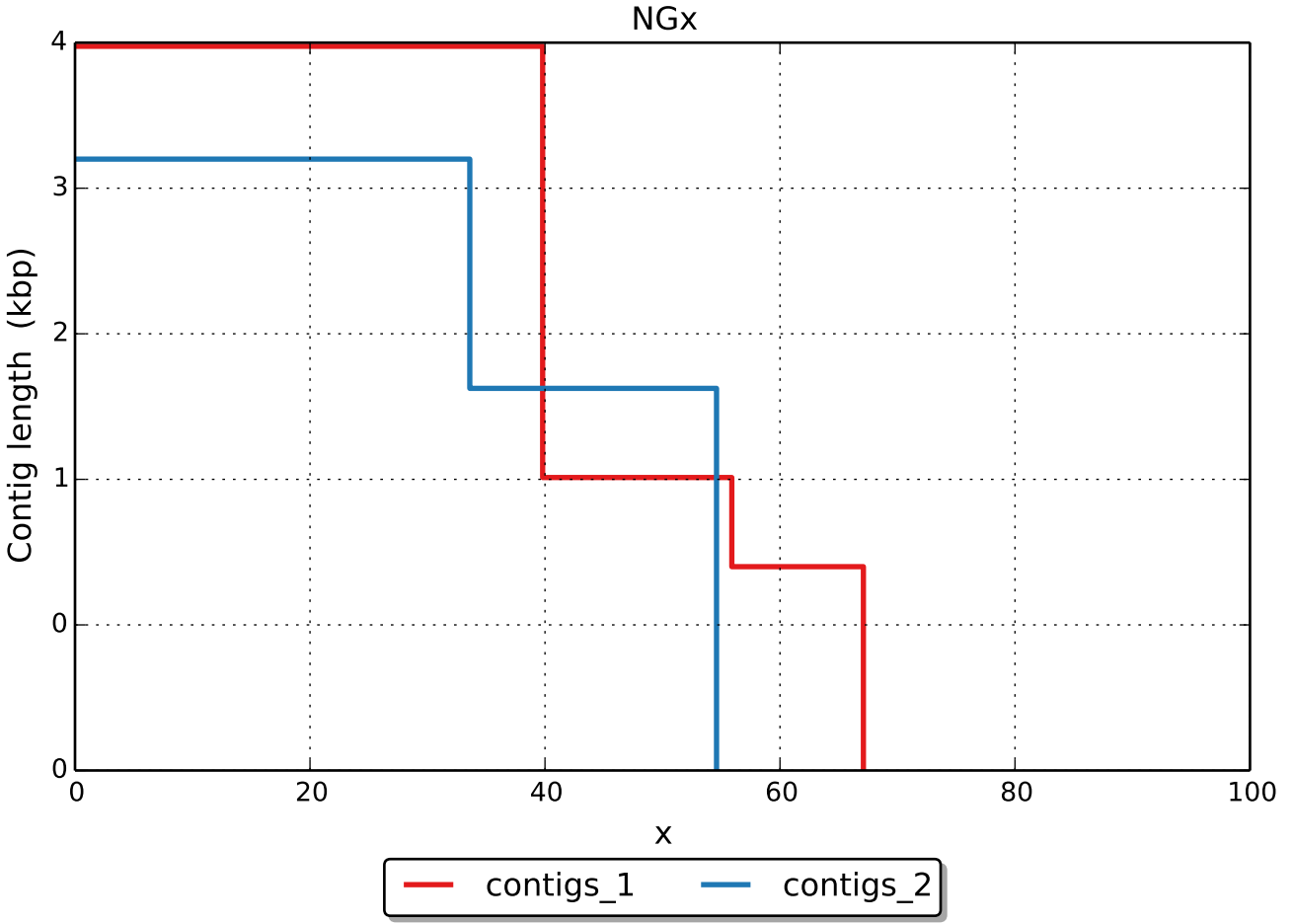
	contigs_1	contigs_2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
# with misassembly	0	0
# both parts are significant	0	0
Partially unaligned length	0	0
# N's	0	0

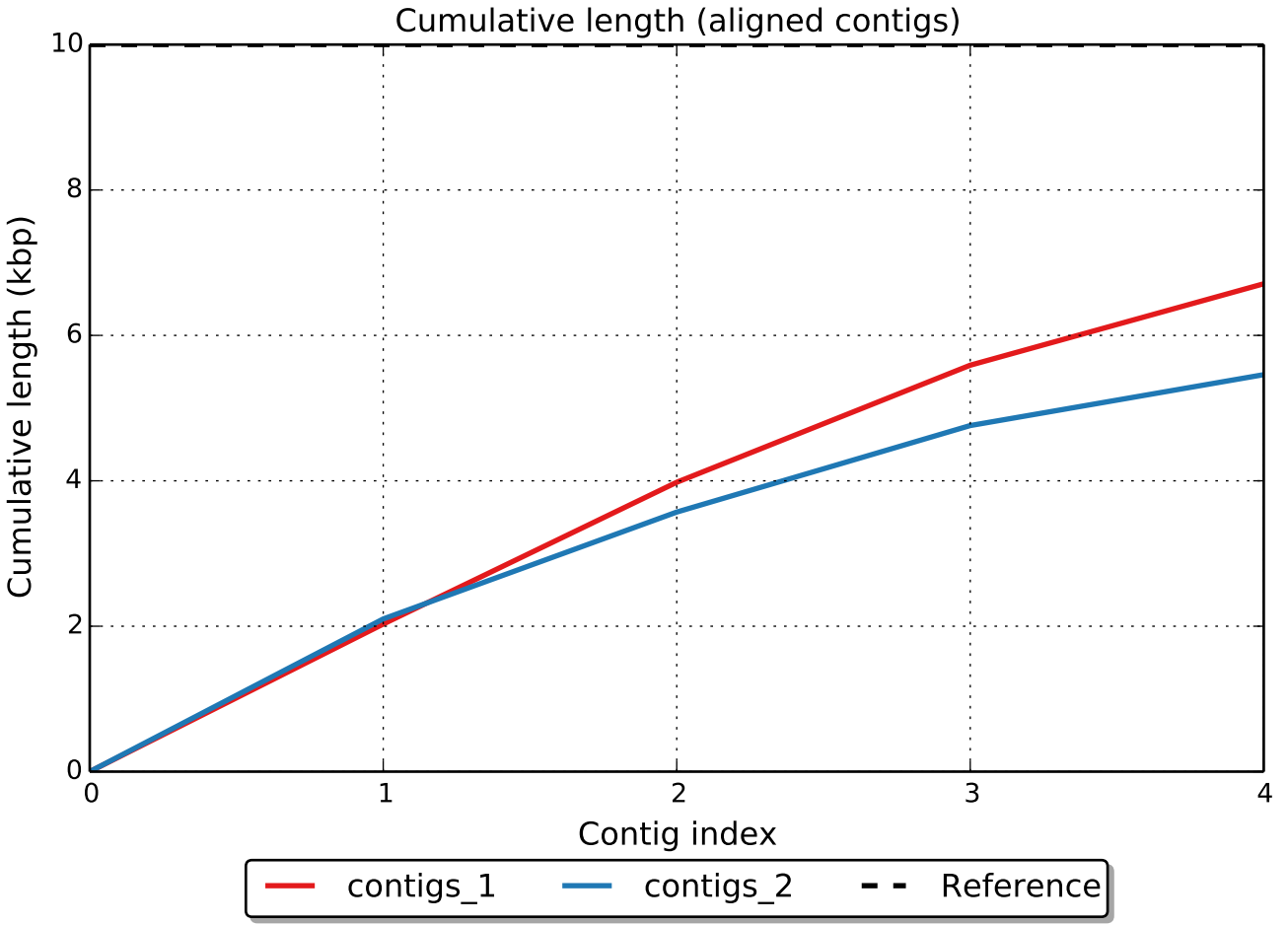
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

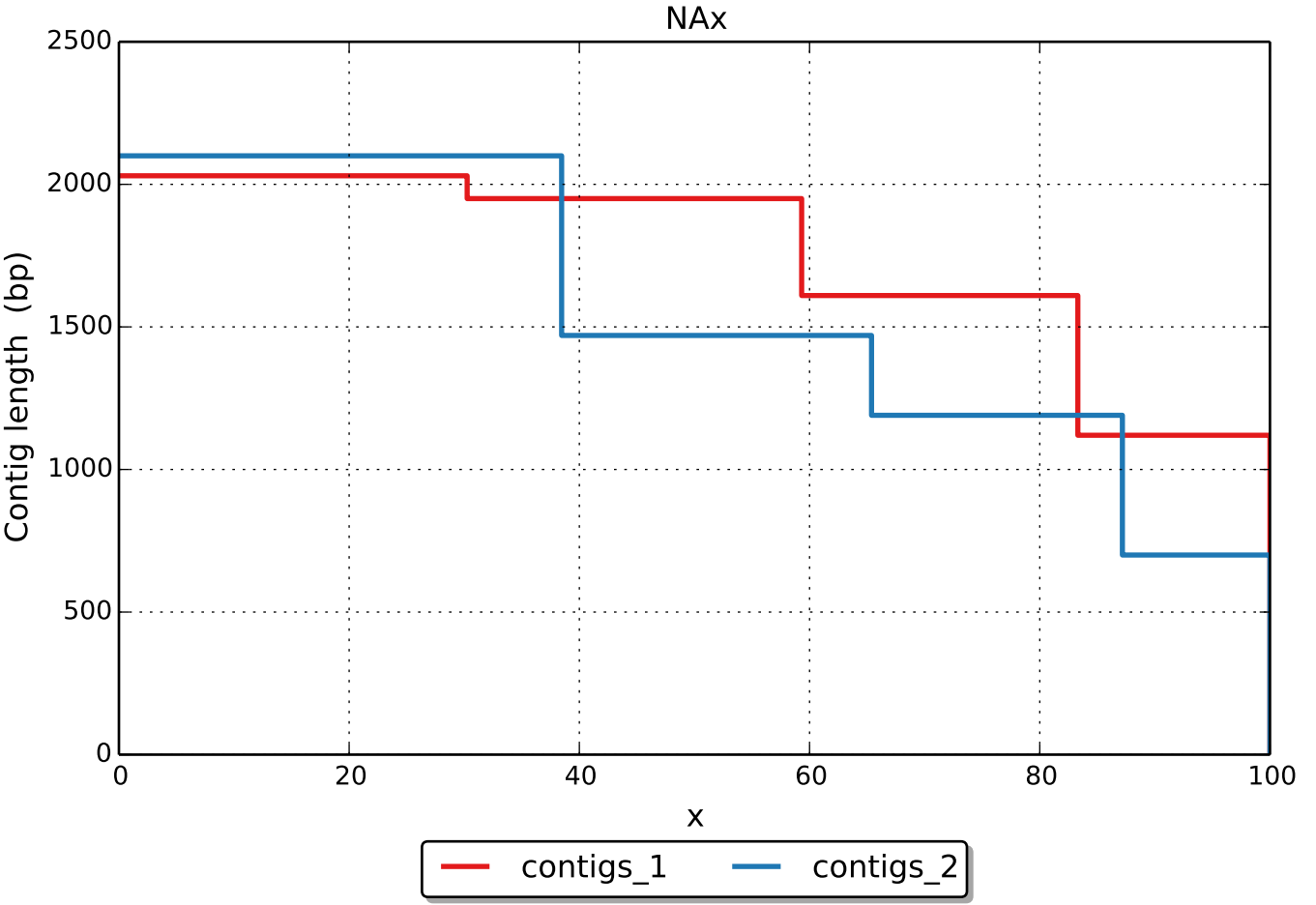

Cumulative length
Cumulative length (kbp)
10
8
6
4
2
0
0
1
2
3
Contig index
contigs_1
contigs_2
Reference

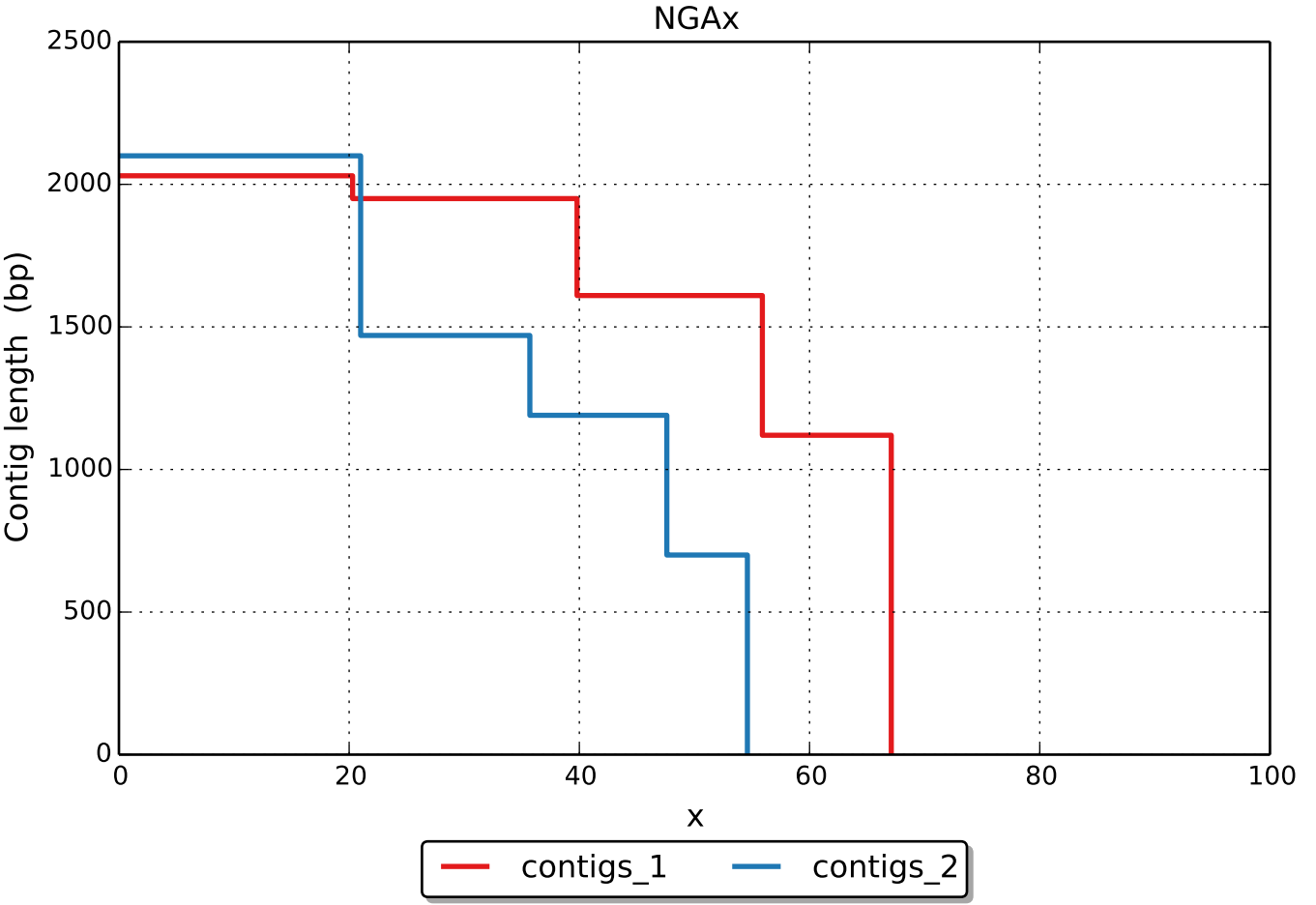

GC content
windows
GC (%)
0
2
4
6
8
10
12
0
20
40
60
80
100
contigs_1
contigs_2
Reference

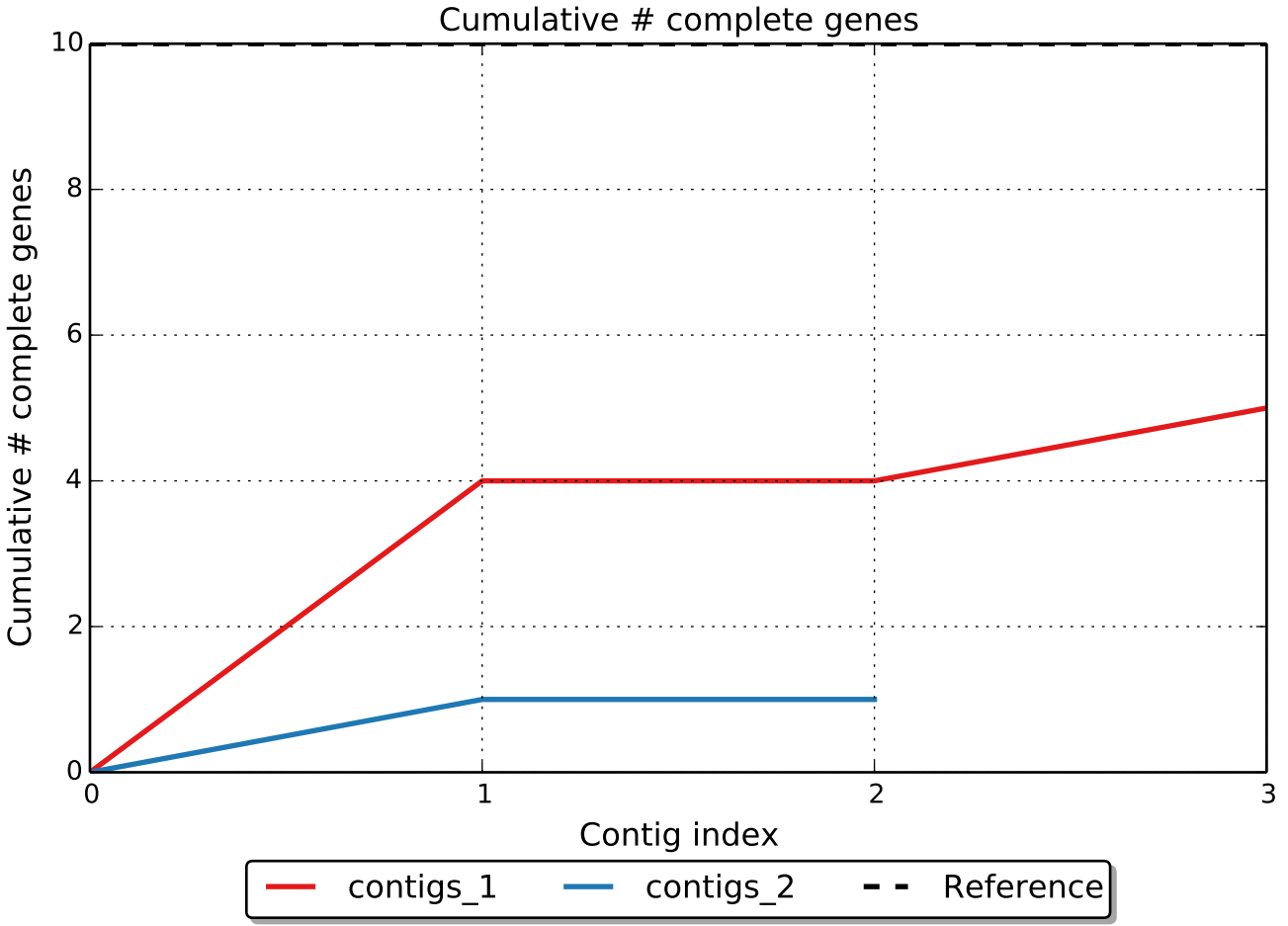

Nx
Contig length (kbp)
4
3
2
1
0
0
0
20
40
60
80
100
x
contigs_1
contigs_2

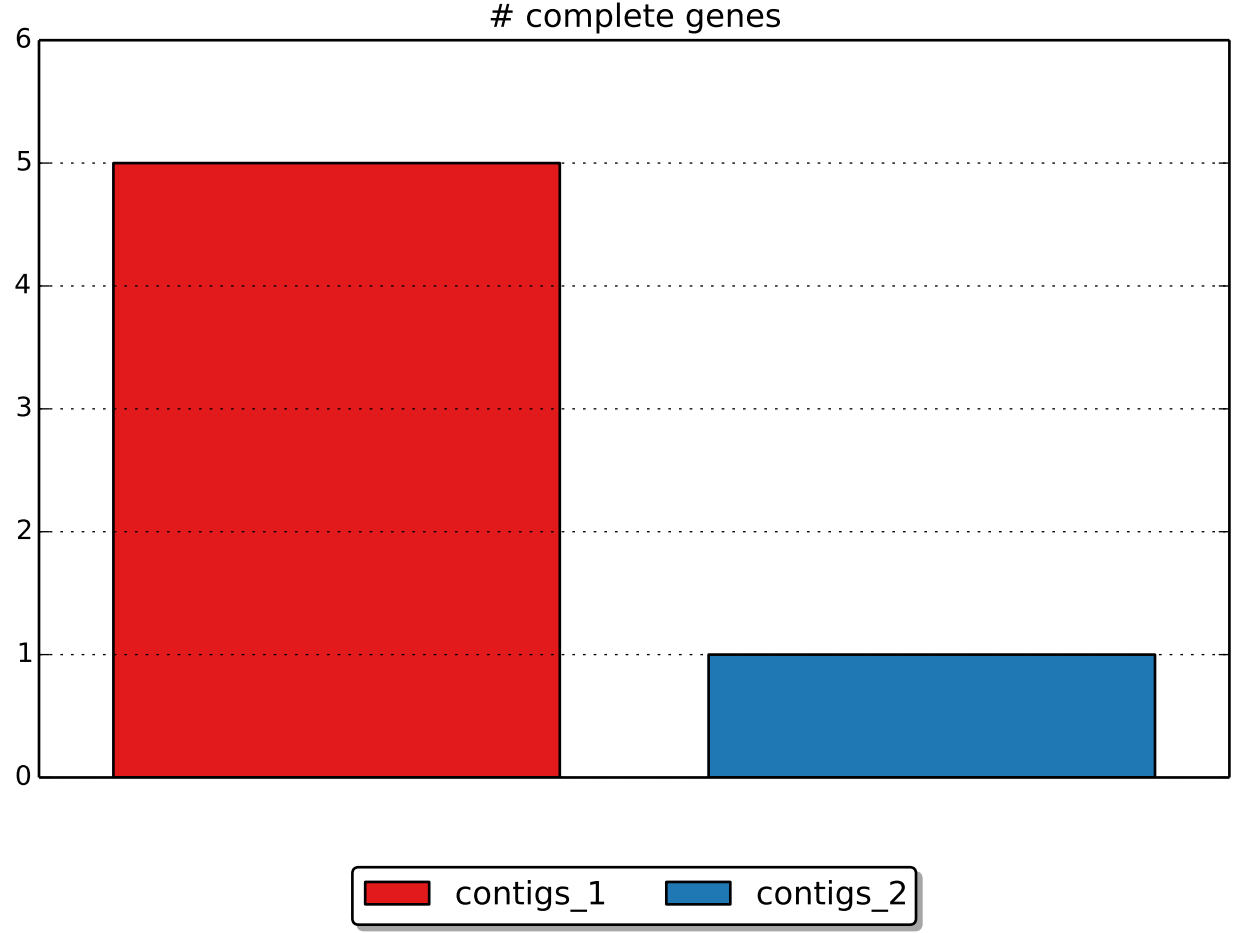

NGx
Contig length (kbp)
4
3
2
1
0
0
20
40
60
80
100
x
contigs_1
contigs_2

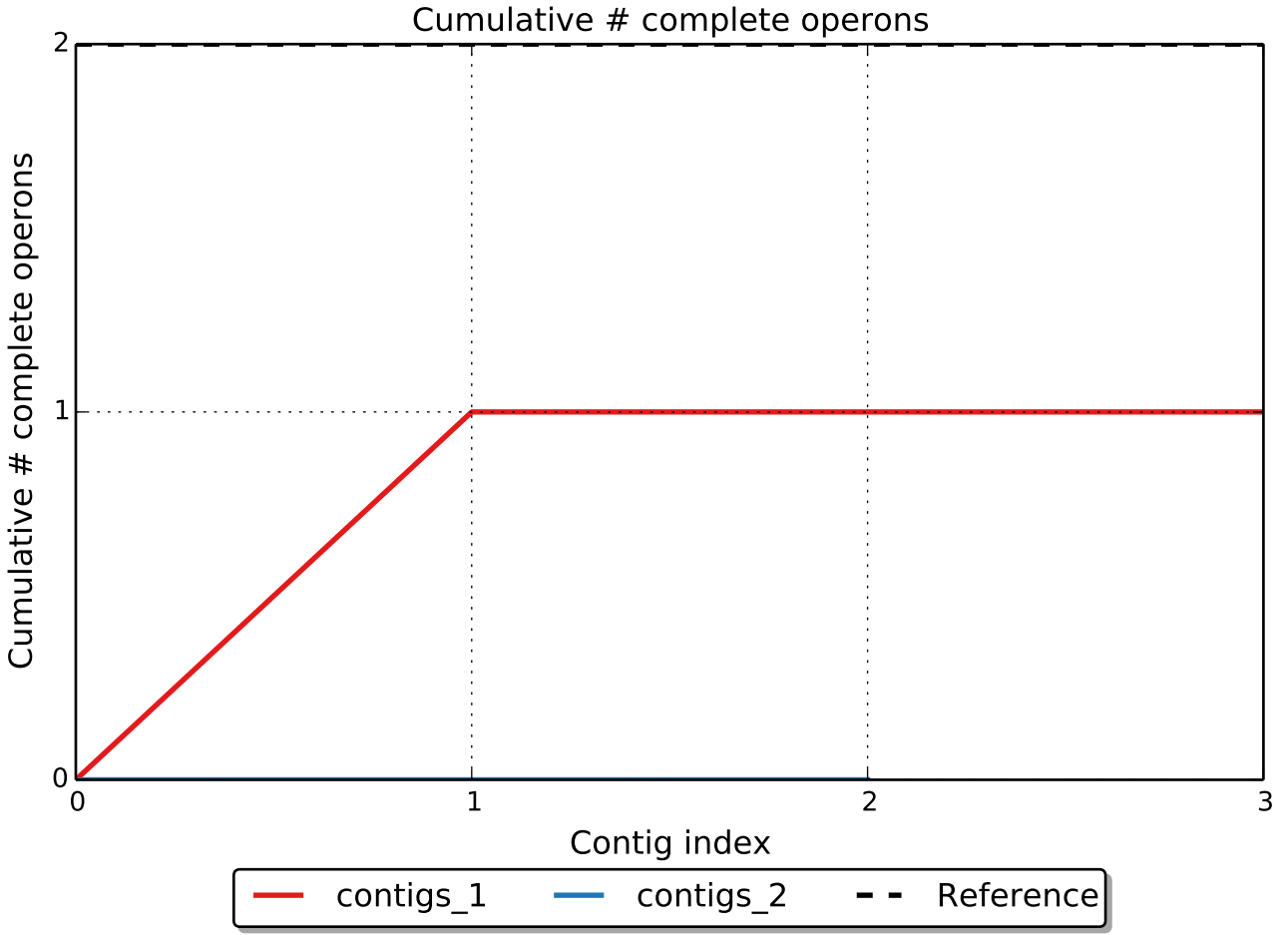

Cumulative length (aligned contigs)
Cumulative length (kbp)
Contig index
0
2
4
6
8
10
0
1
2
3
4
contigs_1
contigs_2
Reference

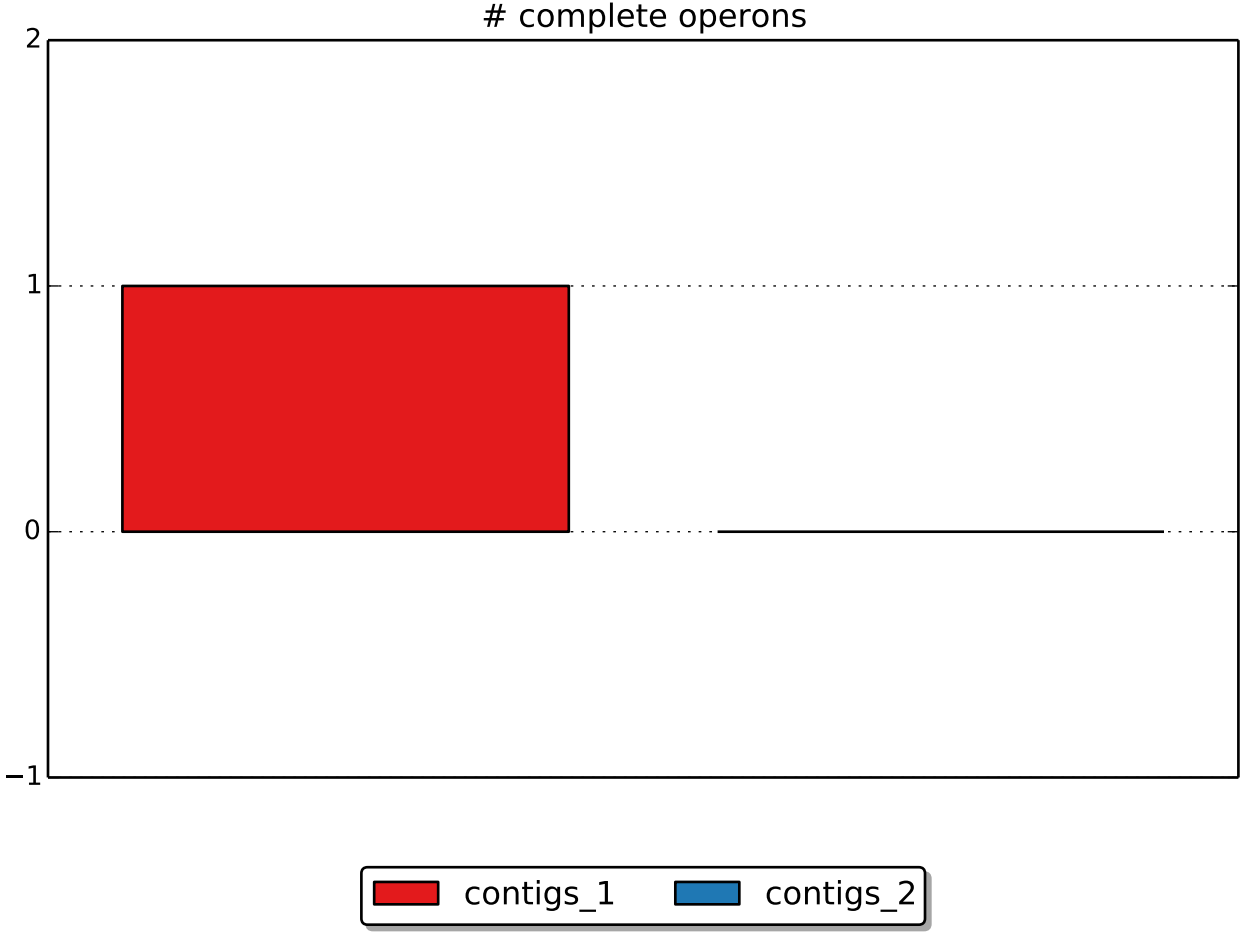

NAx
2500
2000
1500
1000
500
0
Contig length (bp)
0
20
40
60
80
100
x
contigs_1
contigs_2

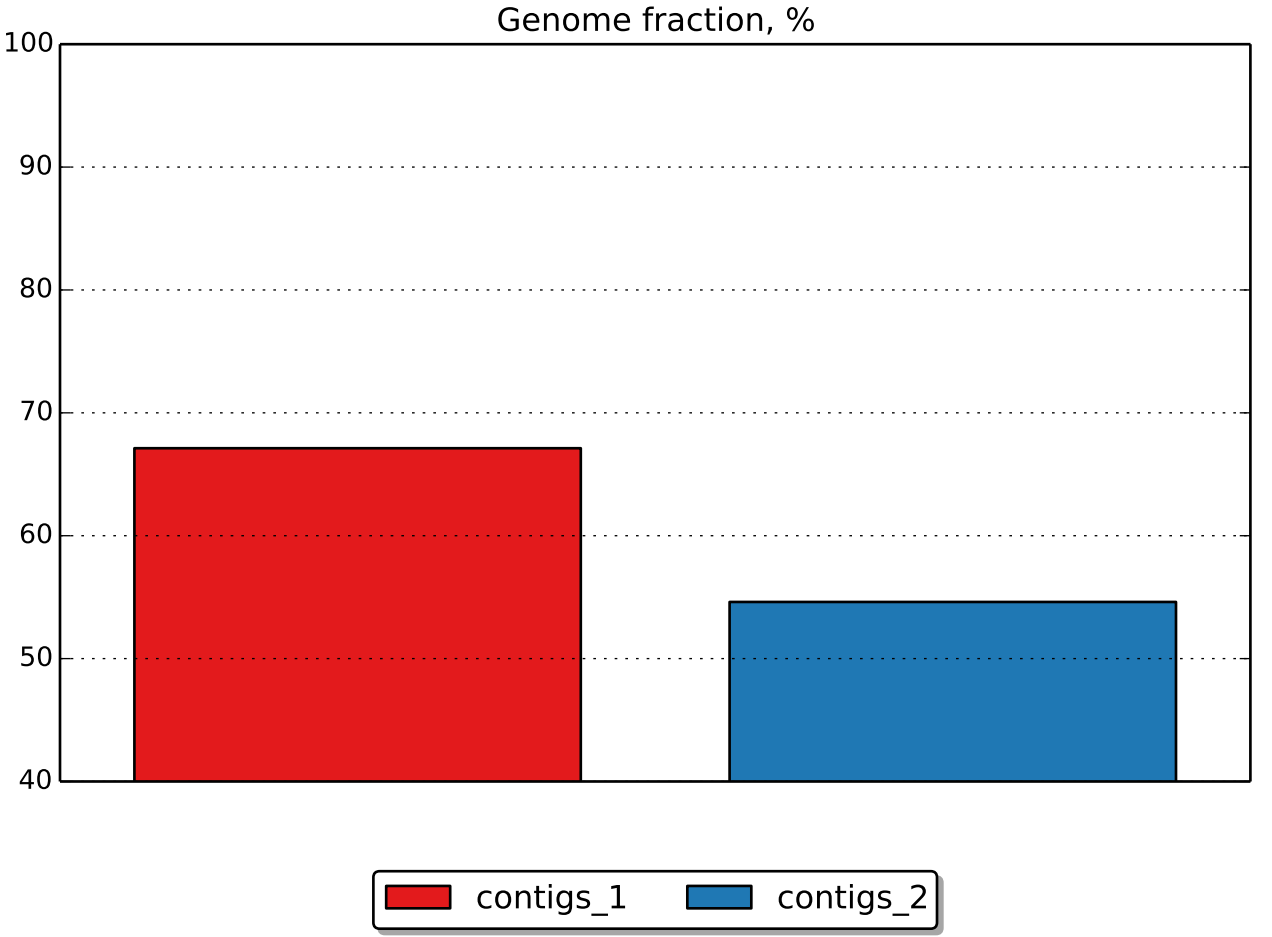

NGAx
Contig length (bp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
contigs_1
contigs_2


Cumulative # complete genes
Cumulative # complete genes
10
8
6
4
2
0
0
1
2
3
Contig index
contigs_1
contigs_2
Reference


complete genes
6
5
4
3
2
1
0
contigs_1
contigs_2


Cumulative # complete operons
Cumulative # complete operons
2
1
0
0
1
2
3
Contig index
contigs_1
contigs_2
Reference


complete operons
2
1
0
−1
contigs_1
contigs_2


Genome fraction, %
100
90
80
70
60
50
40
contigs_1
contigs_2