Report

	ERR1795072.contigs	ERR1795073.contigs
# contigs (>= 1000 bp)	26	22
# contigs (>= 5000 bp)	19	15
# contigs (>= 10000 bp)	17	13
# contigs (>= 25000 bp)	14	8
# contigs (>= 50000 bp)	10	6
Total length (>= 1000 bp)	1904522	976276
Total length (>= 5000 bp)	1894122	965107
Total length (>= 10000 bp)	1876128	953525
Total length (>= 25000 bp)	1822759	875469
Total length (>= 50000 bp)	1694690	809210
# contigs	30	27
Largest contig	373091	193699
Total length	1907337	980209
Reference length	324283	324283
GC (%)	56.60	56.68
Reference GC (%)	50.67	50.67
N50	164908	149771
NG50	373091	193699
N75	123259	98269
NG75	373091	178947
L50	4	3
LG50	1	1
L75	7	5
LG75	1	2
# misassemblies	4	2
# misassembled contigs	3	1
Misassembled contigs length	3318	634
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	5	7
# unaligned contigs	0 + 23 part	0 + 22 part
Unaligned length	1882713	954181
Genome fraction (%)	6.756	7.337
Duplication ratio	1.124	1.094
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	821.58	954.10
# indels per 100 kbp	82.16	75.66
Largest alignment	4157	4157
Total aligned length	23678	25766
NGA50	-	-

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

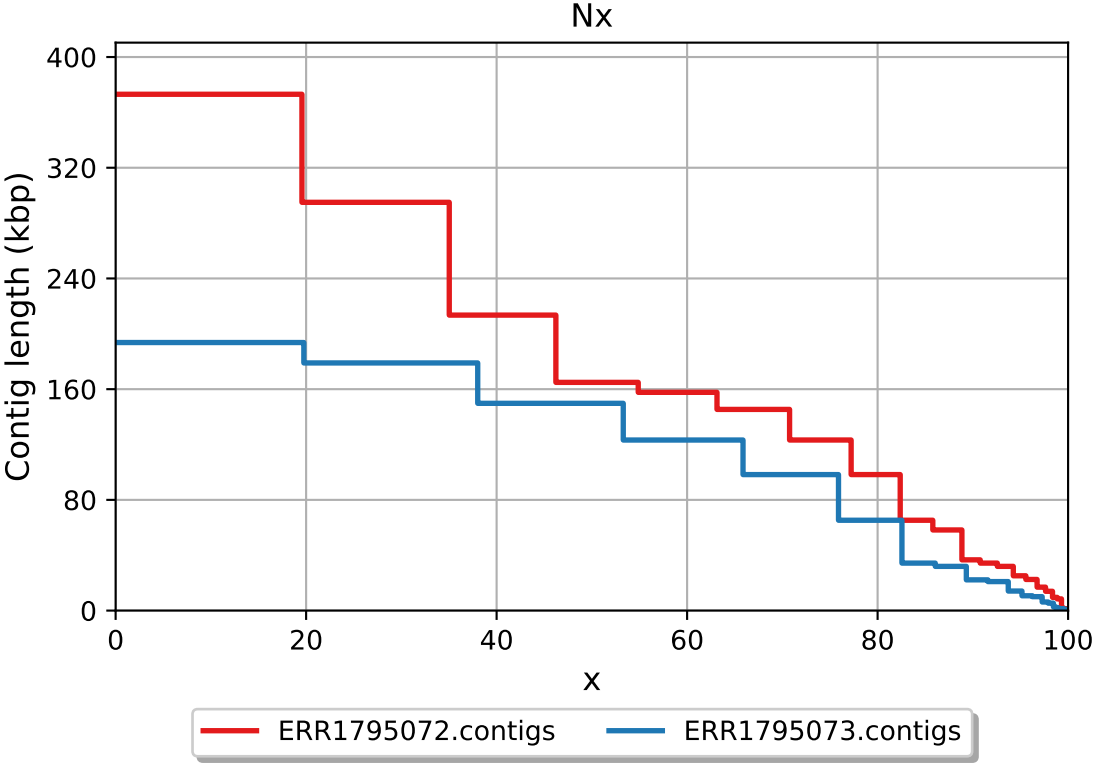
	ERR1795072.contigs	ERR1795073.contigs
# misassemblies	4	2
# contig misassemblies	4	2
# c. relocations	2	2
# c. translocations	0	0
# c. inversions	2	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	3	1
Misassembled contigs length	3318	634
# possibly misassembled contigs	3	6
# possible misassemblies	3	6
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	5	7
# mismatches	180	227
# indels	18	18
# indels (<= 5 bp)	15	16
# indels (> 5 bp)	3	2
Indels length	93	70

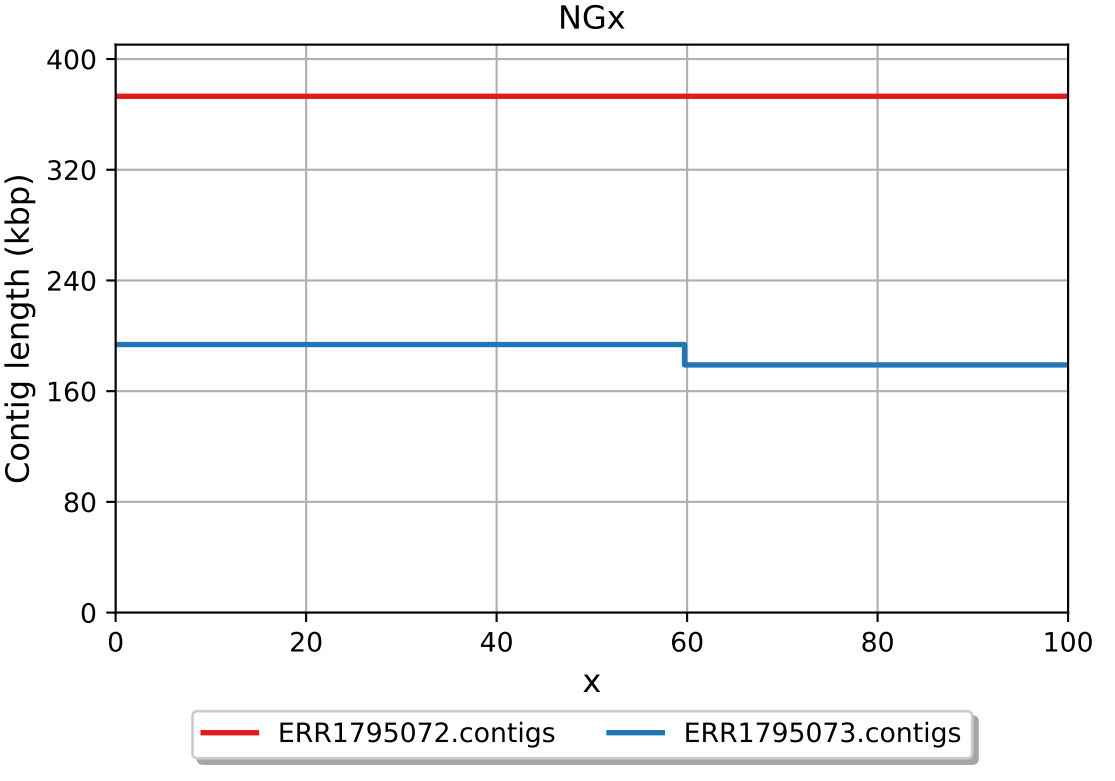
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

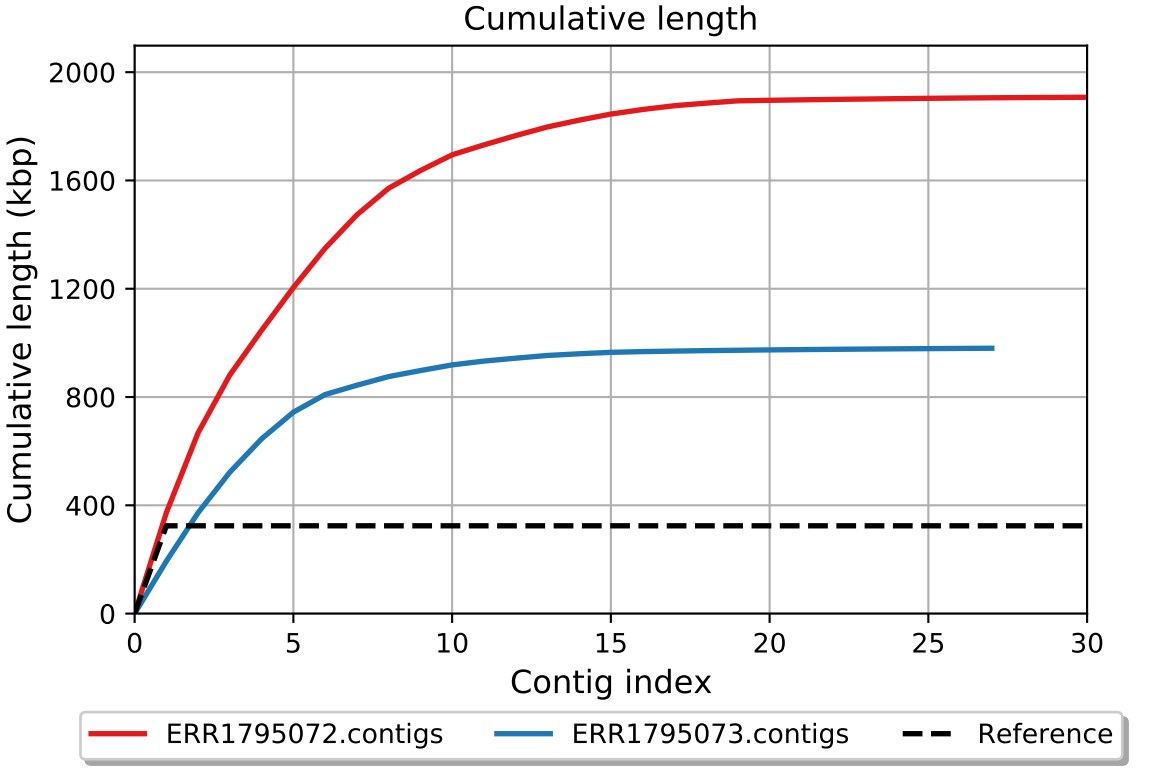
Unaligned report

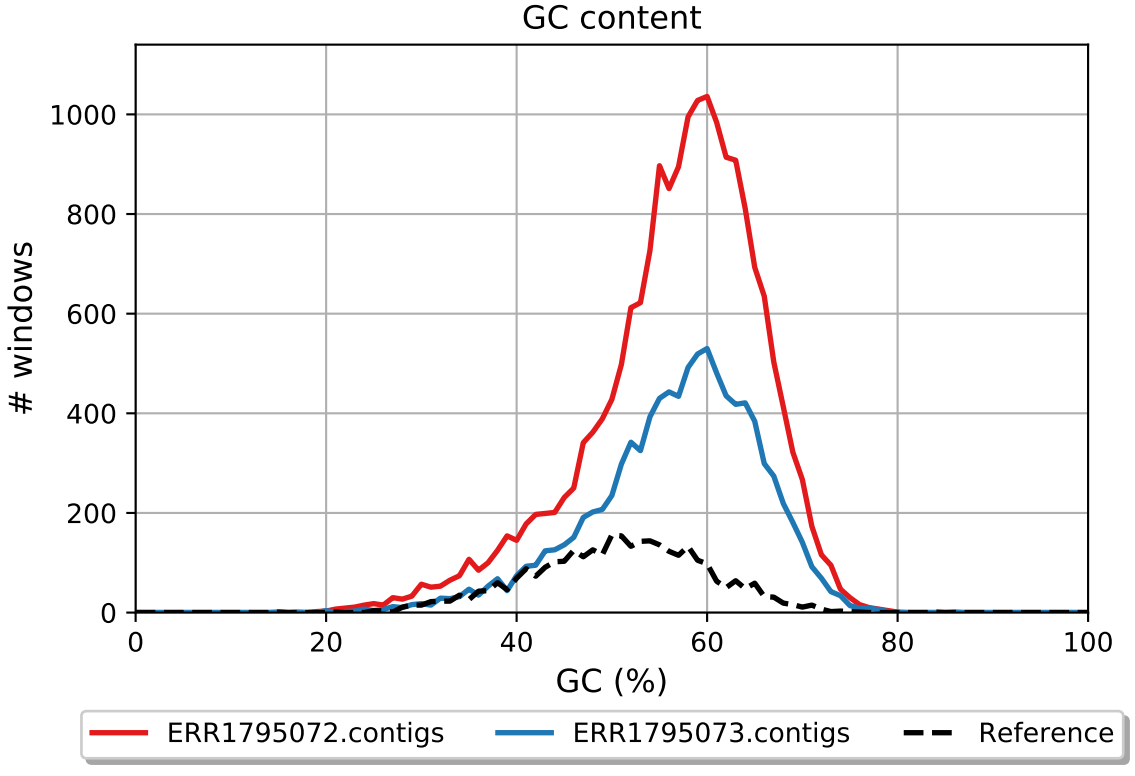
	ERR1795072.contigs	ERR1795073.contigs
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	23	22
Partially unaligned length	1882713	954181
# N's	0	0

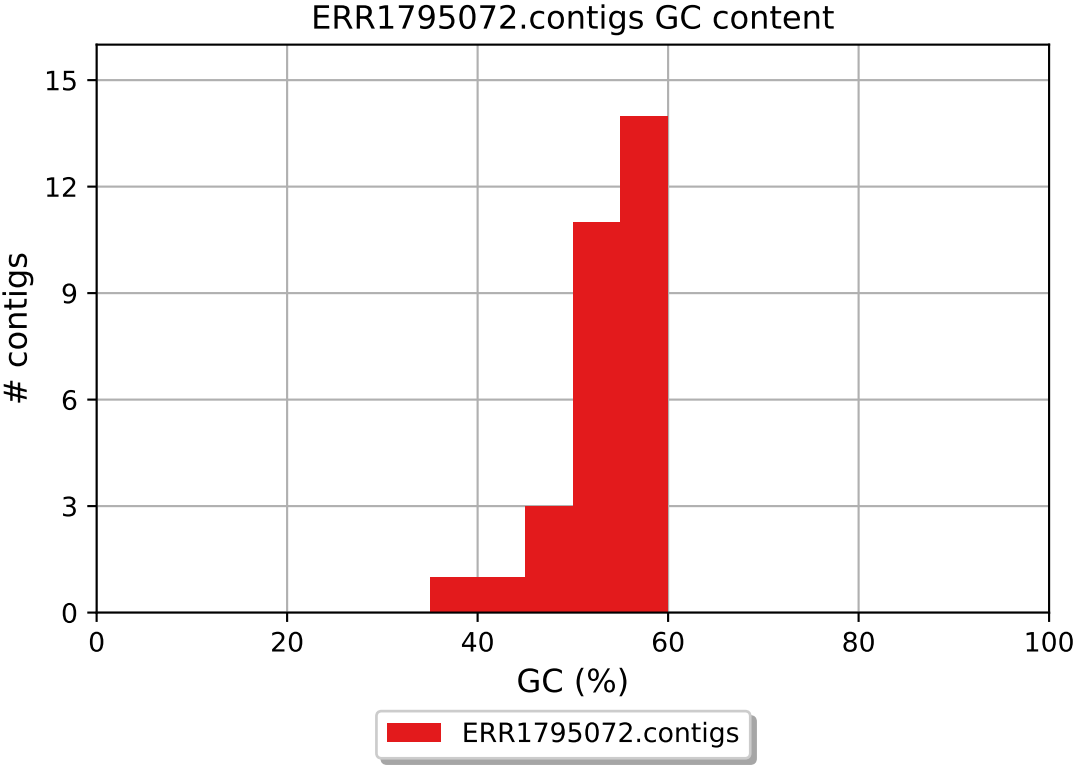
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

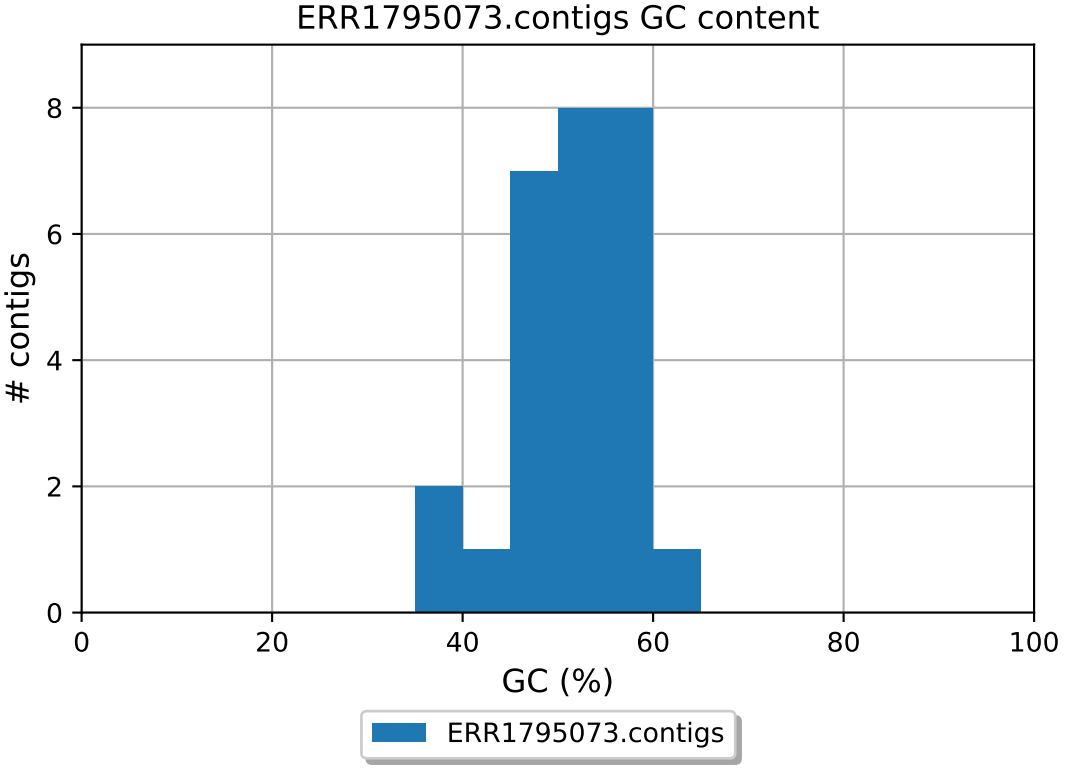

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
ERR1795072.contigs
ERR1795073.contigs

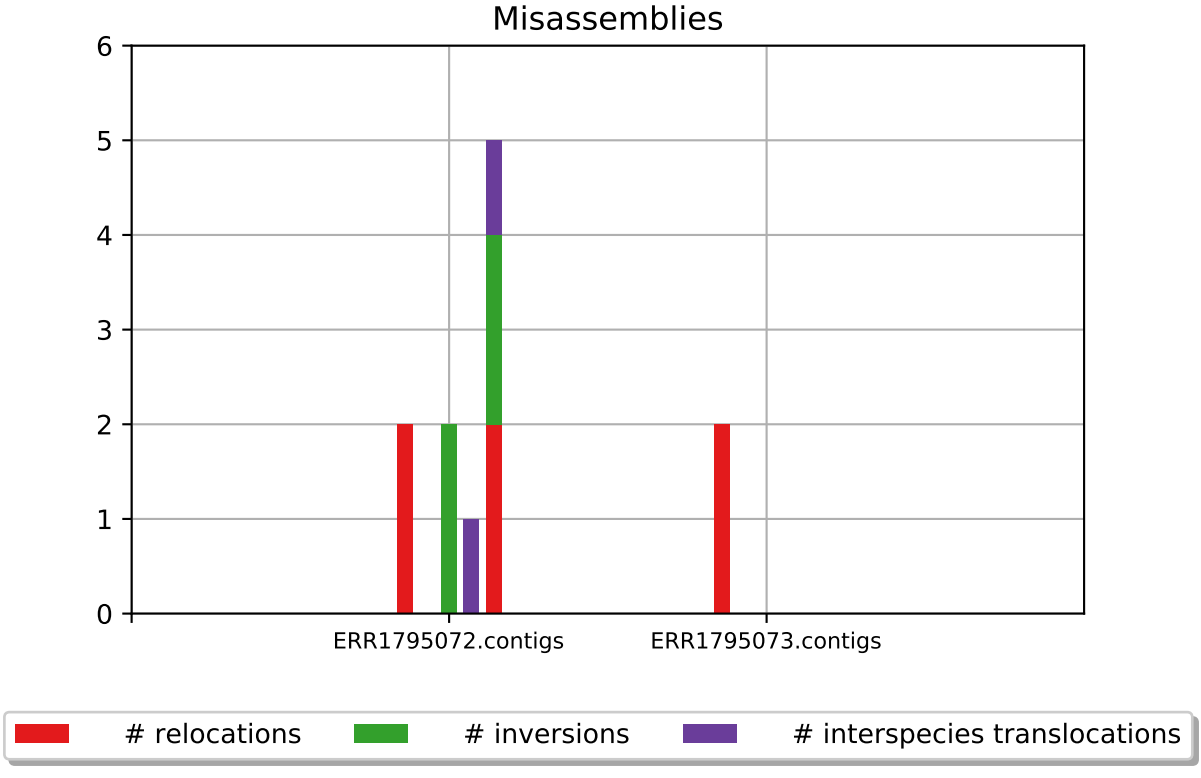

NGx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
ERR1795072.contigs
ERR1795073.contigs

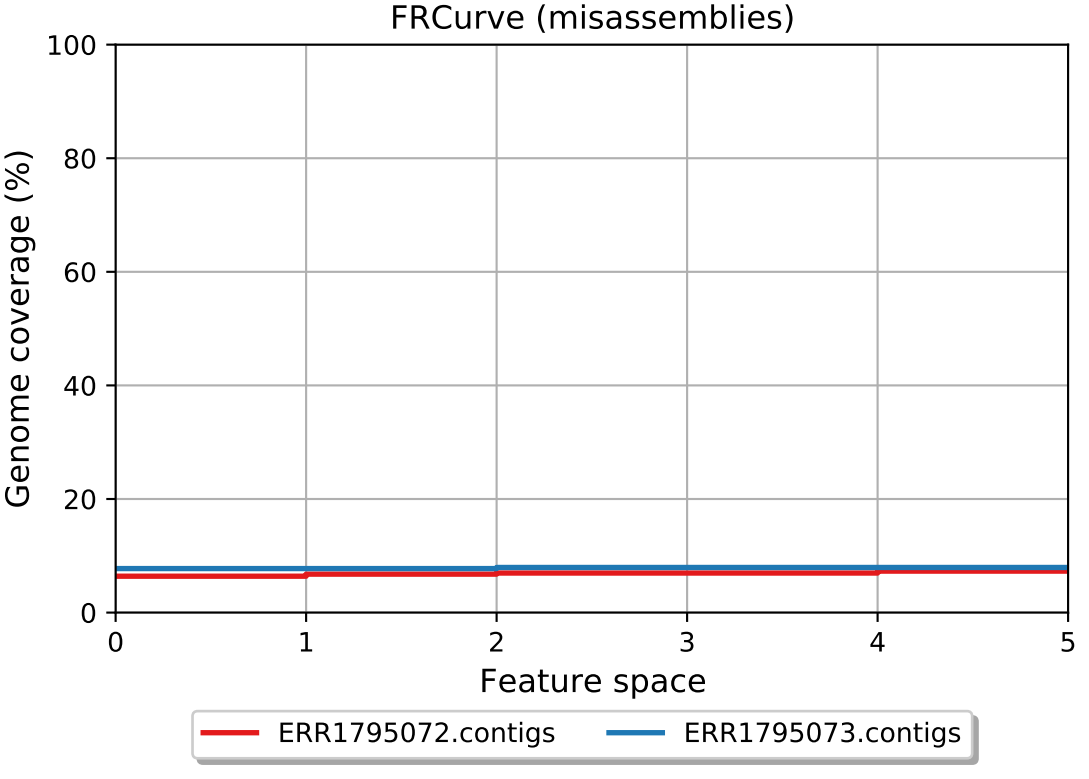

Cumulative length
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
5
10
15
20
25
30
Contig index
ERR1795072.contigs
ERR1795073.contigs
Reference

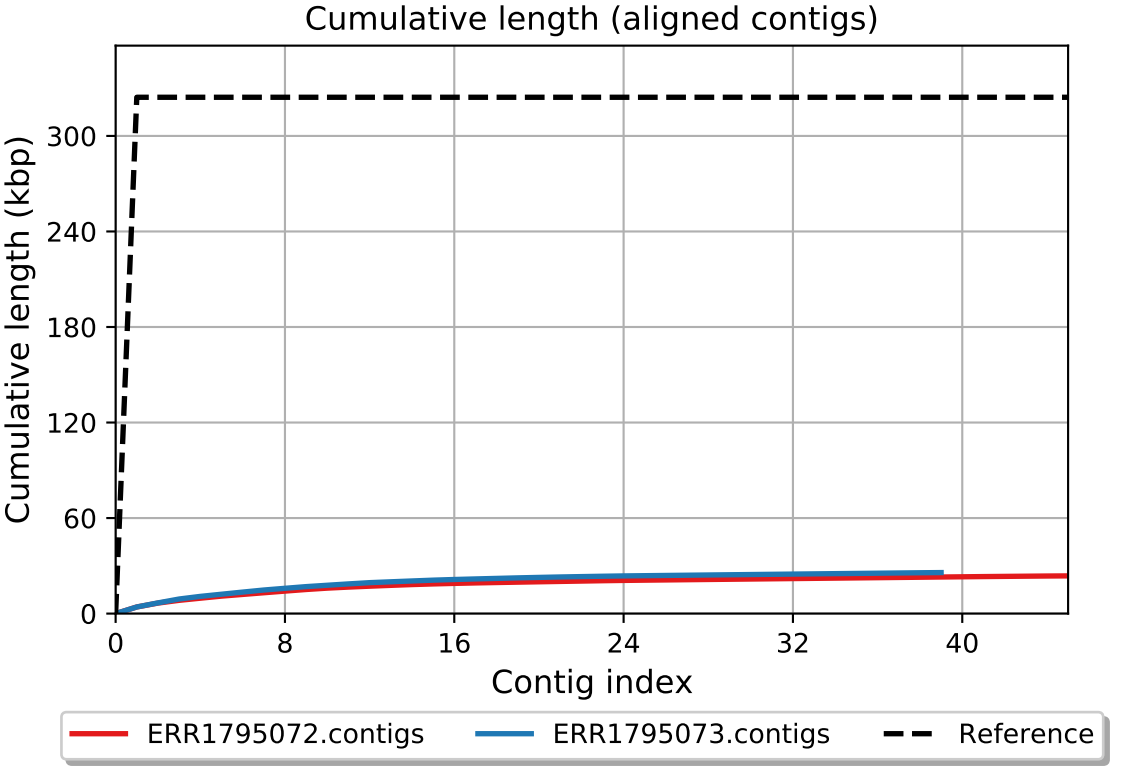

GC content
windows
GC (%)
0
200
400
600
800
1000
0
20
40
60
80
100
ERR1795072.contigs
ERR1795073.contigs
Reference

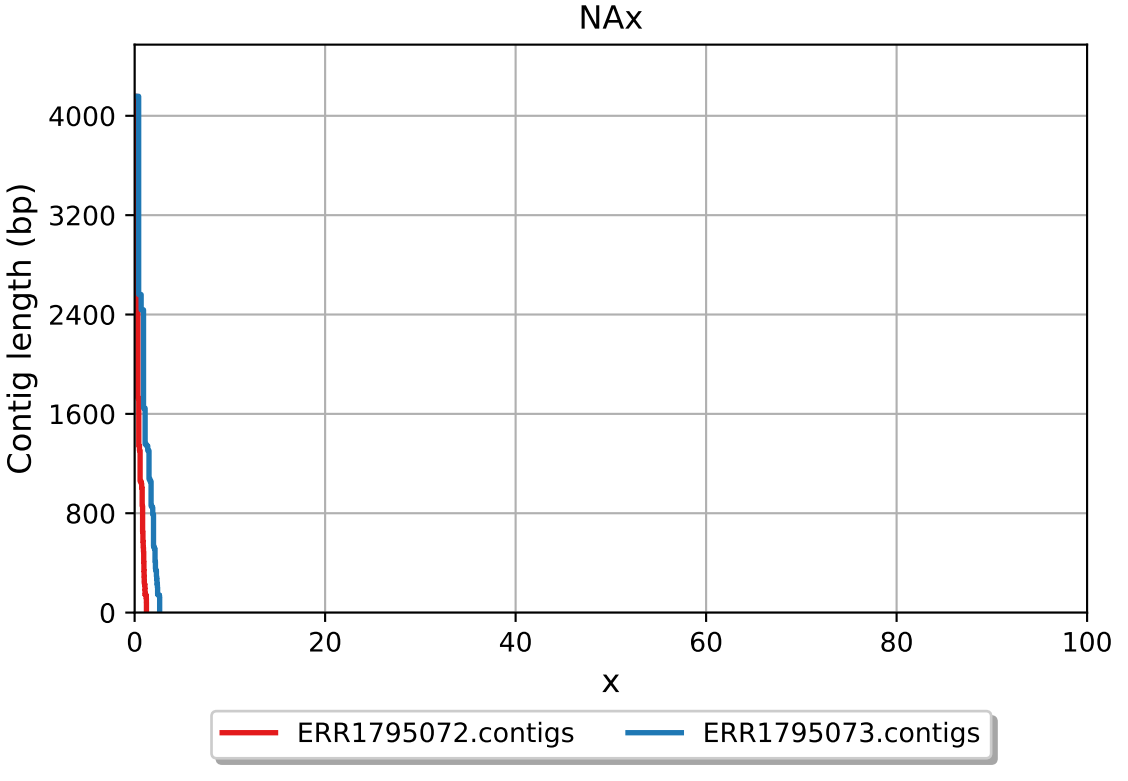

ERR1795072.contigs GC content
contigs
GC (%)
0
3
6
9
12
15
0
20
40
60
80
100
ERR1795072.contigs

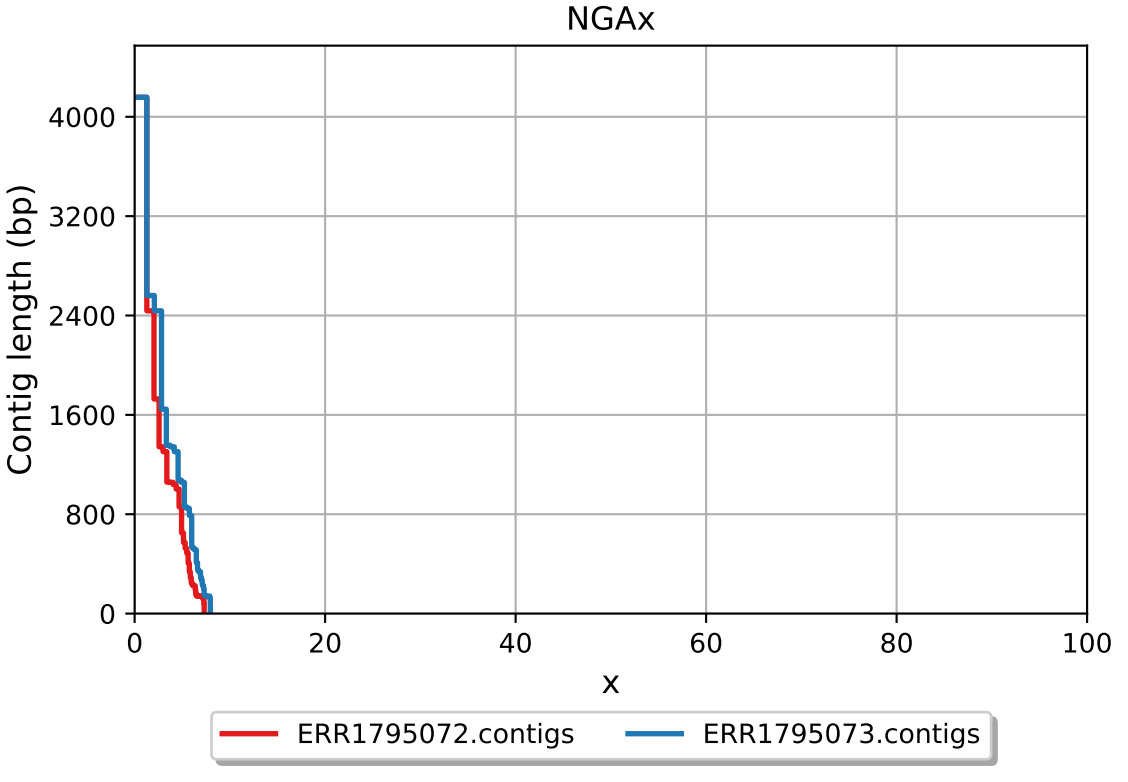

ERR1795073.contigs GC content
contigs
GC (%)
0
2
4
6
8
0
20
40
60
80
100
ERR1795073.contigs

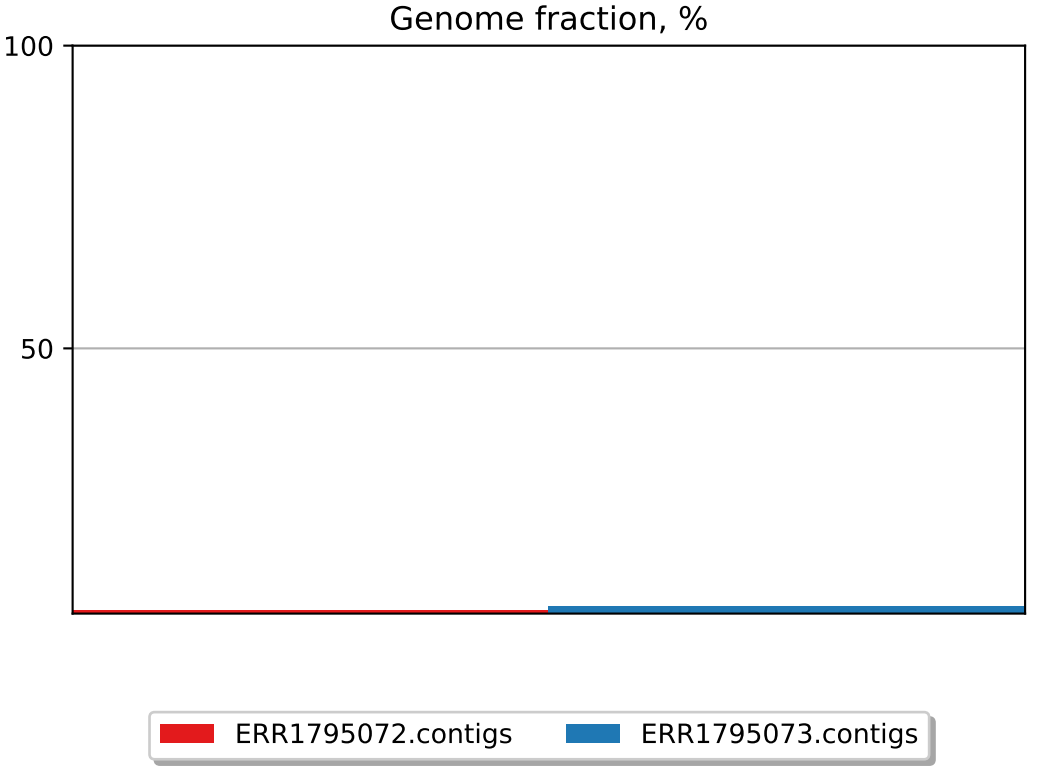

Misassemblies
6
5
4
3
2
1
0
ERR1795072.contigs
ERR1795073.contigs
relocations
inversions
interspecies translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
4
5
Feature space
ERR1795072.contigs
ERR1795073.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
300
240
180
120
60
0
0
8
16
24
32
40
Contig index
ERR1795072.contigs
ERR1795073.contigs
Reference


NAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
ERR1795072.contigs
ERR1795073.contigs


NGAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
ERR1795072.contigs
ERR1795073.contigs


Genome fraction, %
100
50
ERR1795072.contigs
ERR1795073.contigs