Report

	ERR1795072.contigs	ERR1795073.contigs
# contigs (>= 0 bp)	413	557
# contigs (>= 1000 bp)	119	150
# contigs (>= 5000 bp)	77	86
# contigs (>= 10000 bp)	61	67
# contigs (>= 25000 bp)	41	44
# contigs (>= 50000 bp)	31	33
Total length (>= 0 bp)	5827273	5881752
Total length (>= 1000 bp)	5720389	5730301
Total length (>= 5000 bp)	5621715	5571890
Total length (>= 10000 bp)	5507342	5432736
Total length (>= 25000 bp)	5157139	5053531
Total length (>= 50000 bp)	4827153	4661625
# contigs	143	187
Largest contig	429580	329050
Total length	5735957	5755059
Reference length	16883701	16883701
N50	149488	134791
N75	95965	84908
L50	11	15
L75	23	28
# misassemblies	53	50
# misassembled contigs	30	35
Misassembled contigs length	3409372	3276731
# local misassemblies	41	48
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	13	16
# unaligned contigs	35 + 50 part	55 + 60 part
Unaligned length	645774	635327
Genome fraction (%)	67.410	65.921
Duplication ratio	1.027	1.018
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	1585.29	1477.80
# indels per 100 kbp	30.32	27.31
Largest alignment	256214	231458
Total aligned length	5060348	5111498
NA50	81632	77715
NA75	33557	31521
LA50	21	23
LA75	46	50

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

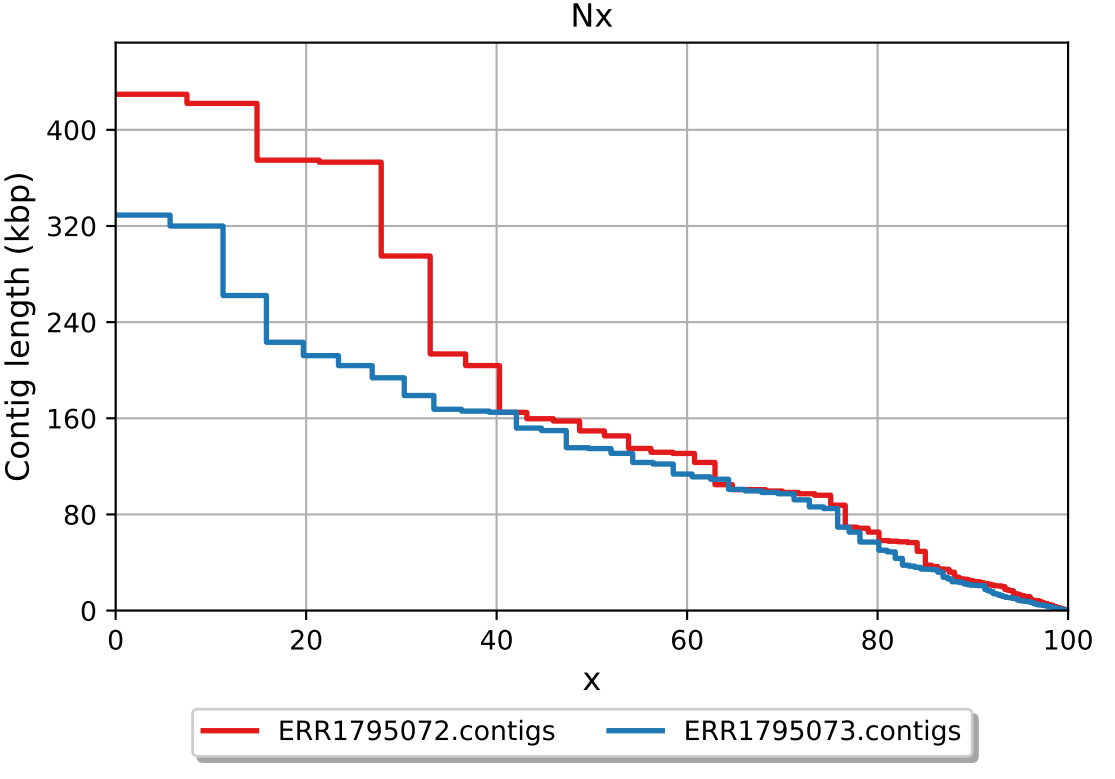
	ERR1795072.contigs	ERR1795073.contigs
# misassemblies	53	50
# contig misassemblies	53	50
# c. relocations	23	28
# c. translocations	0	0
# c. inversions	4	1
# c. interspecies translocations	26	21
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# s. interspecies translocations	0	0
# misassembled contigs	30	35
Misassembled contigs length	3409372	3276731
# possibly misassembled contigs	38	45
# possible misassemblies	63	66
# local misassemblies	41	48
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	13	16
# mismatches	180268	164334
# indels	3448	3037
# indels (<= 5 bp)	3158	2763
# indels (> 5 bp)	290	274
Indels length	11939	10502

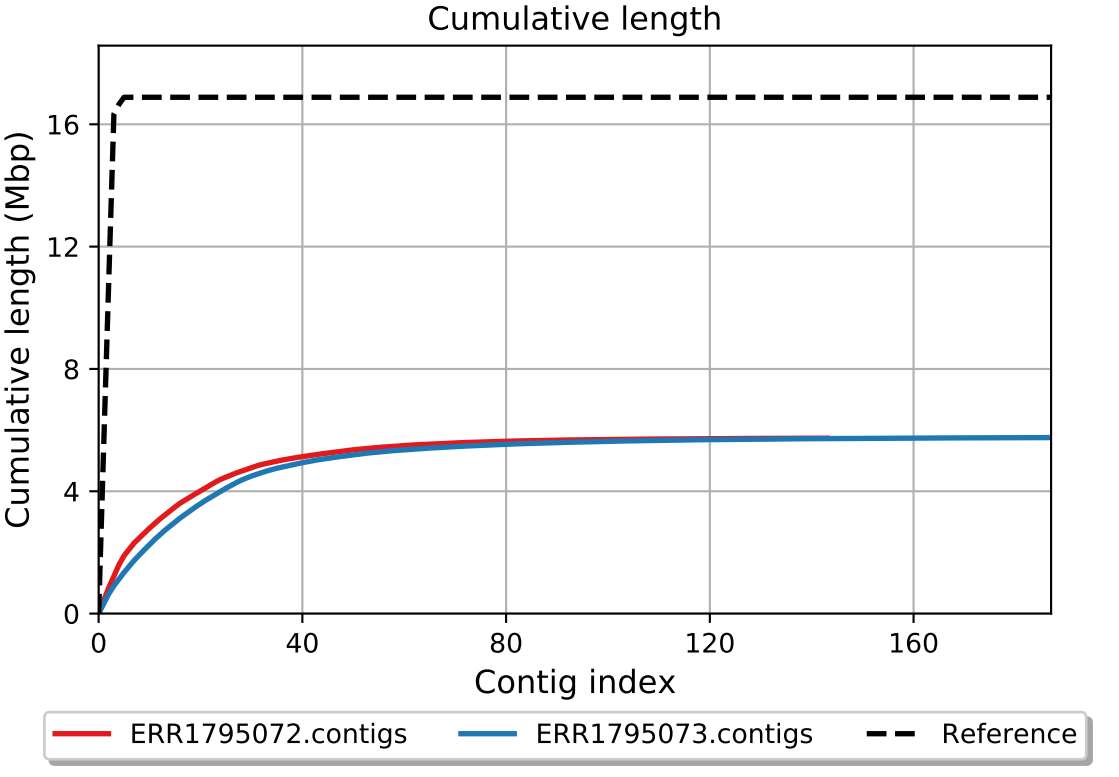
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

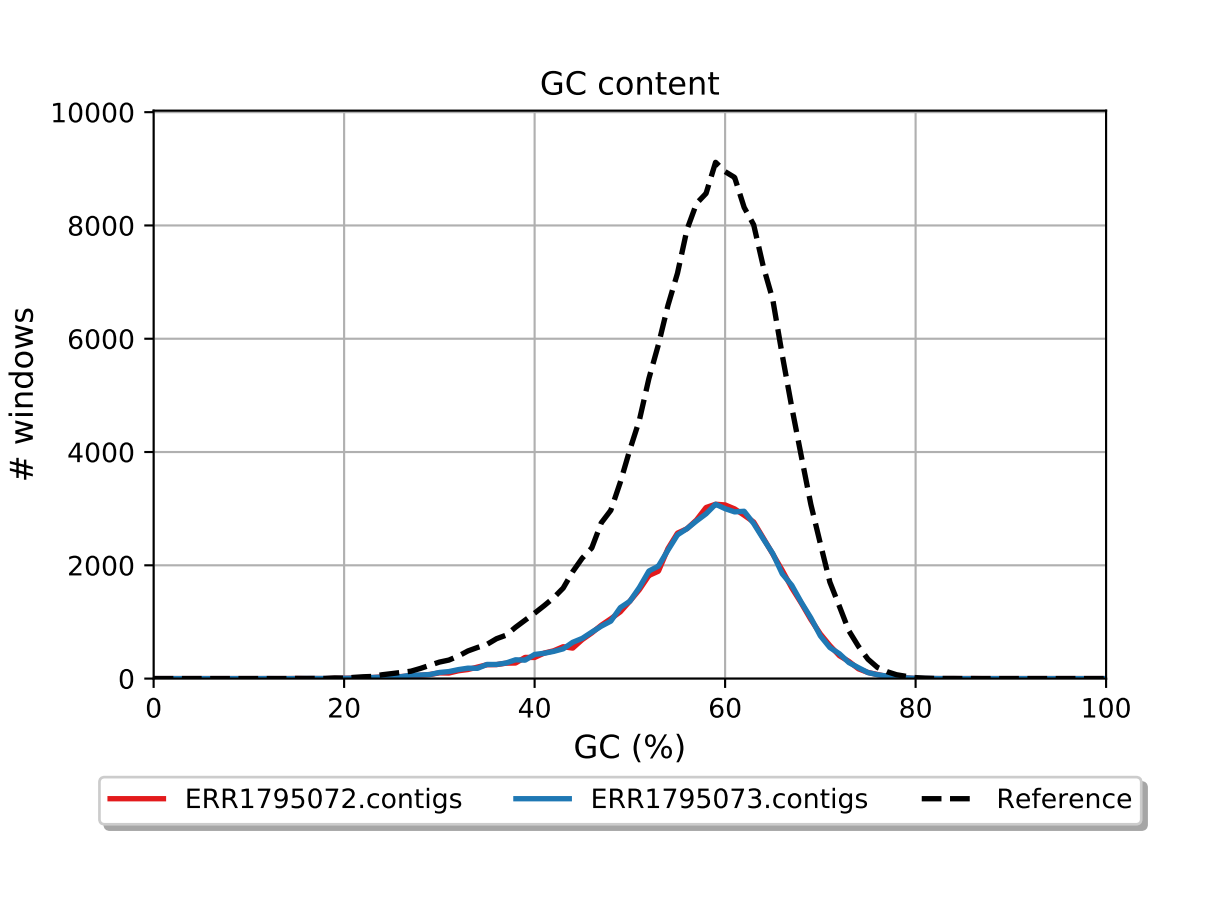
Unaligned report

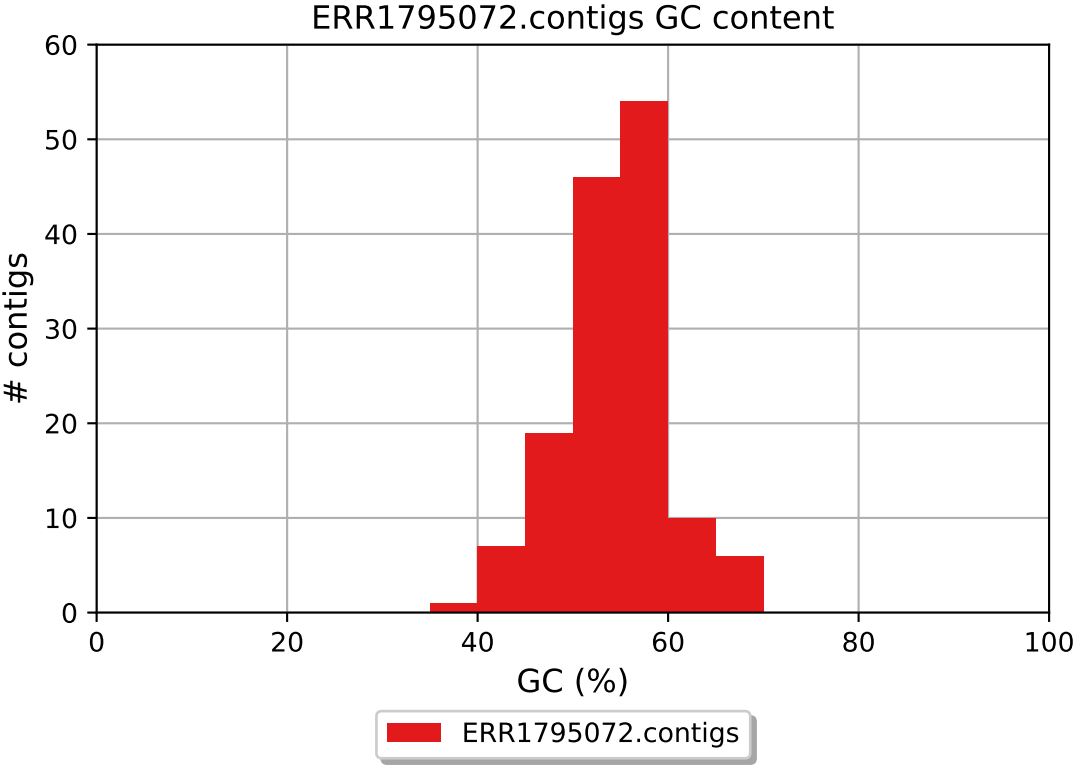
	ERR1795072.contigs	ERR1795073.contigs
# fully unaligned contigs	35	55
Fully unaligned length	142240	164727
# partially unaligned contigs	50	60
Partially unaligned length	503534	470600
# N's	0	0

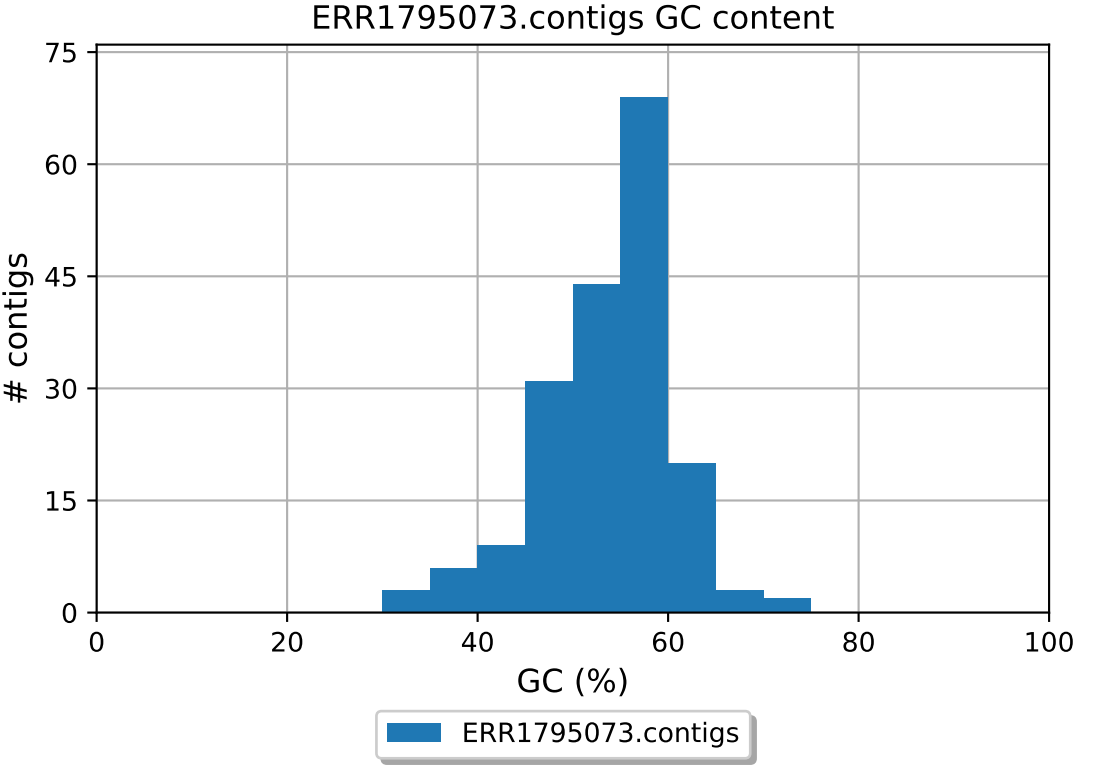
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

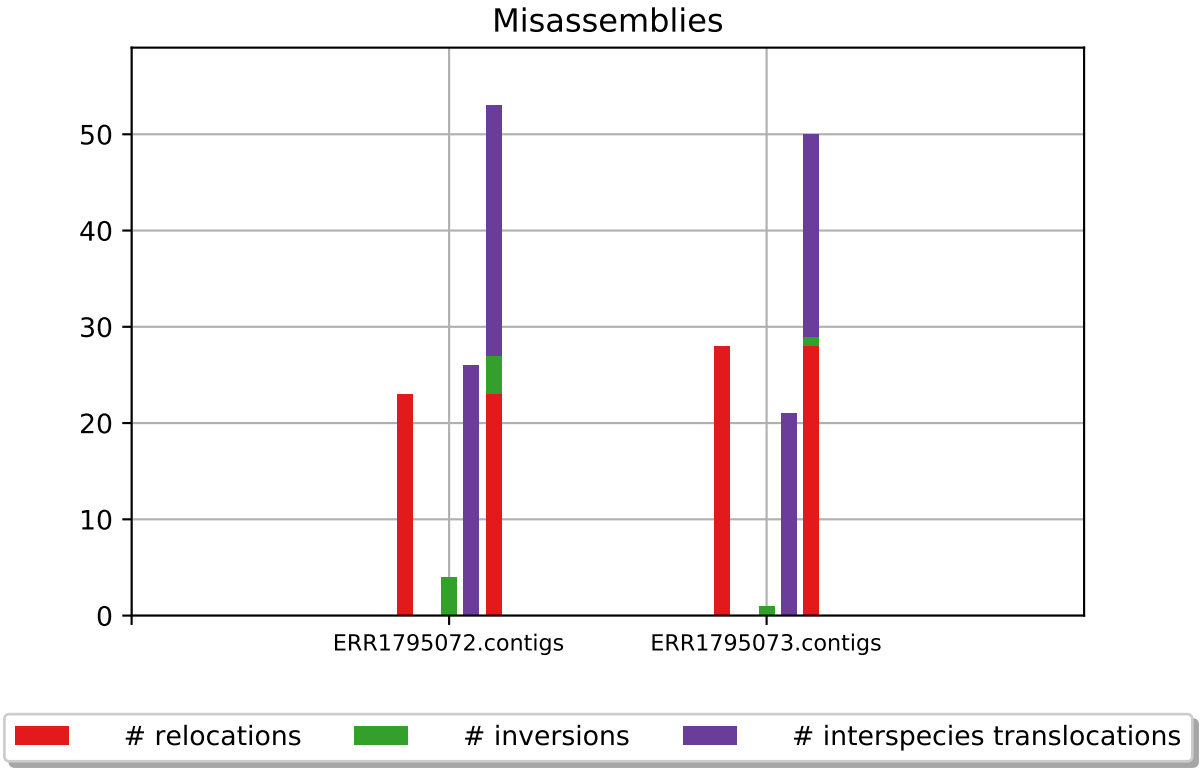

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
ERR1795072.contigs
ERR1795073.contigs

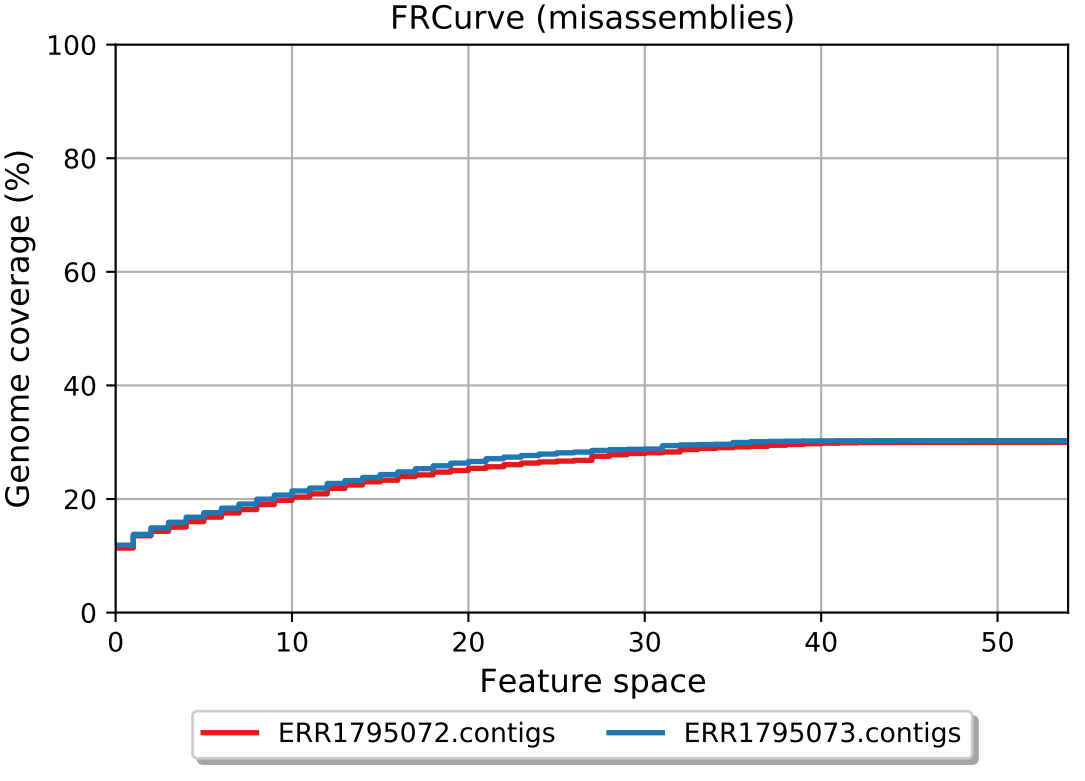

Cumulative length
Cumulative length (Mbp)
0
4
8
12
16
0
40
80
120
160
Contig index
ERR1795072.contigs
ERR1795073.contigs
Reference

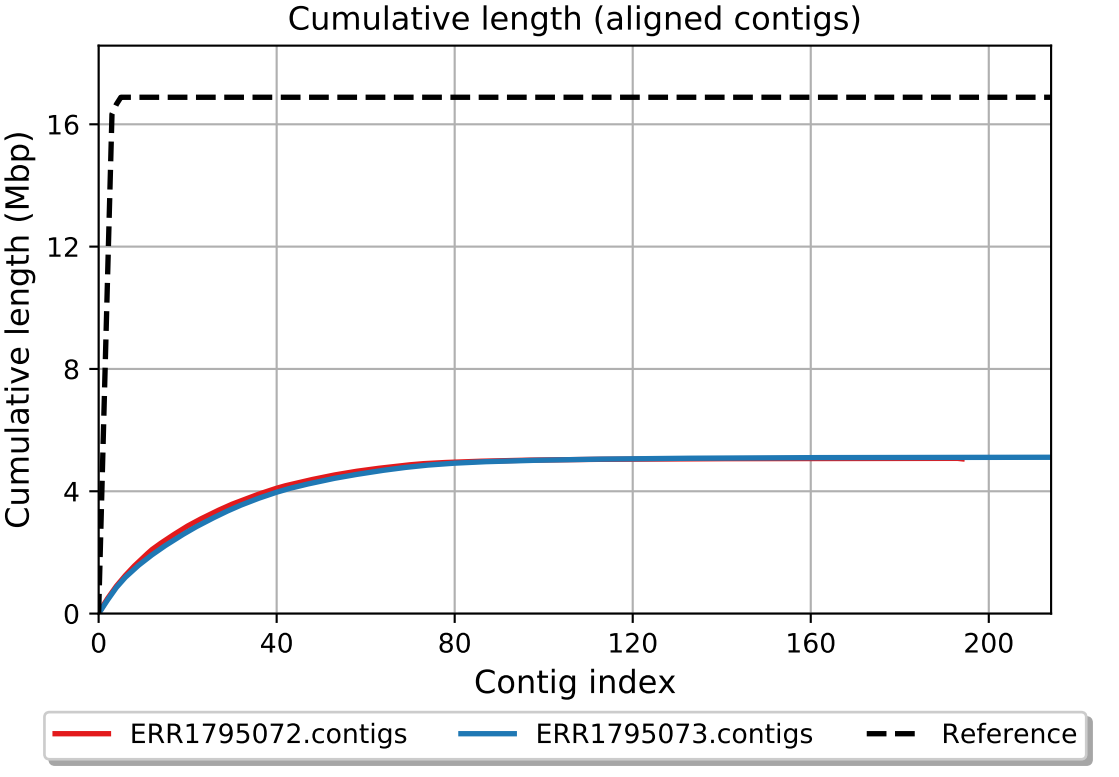

GC content
10000
8000
6000
4000
2000
0
windows
0
20
40
60
80
100
GC (%)
ERR1795072.contigs
ERR1795073.contigs
Reference

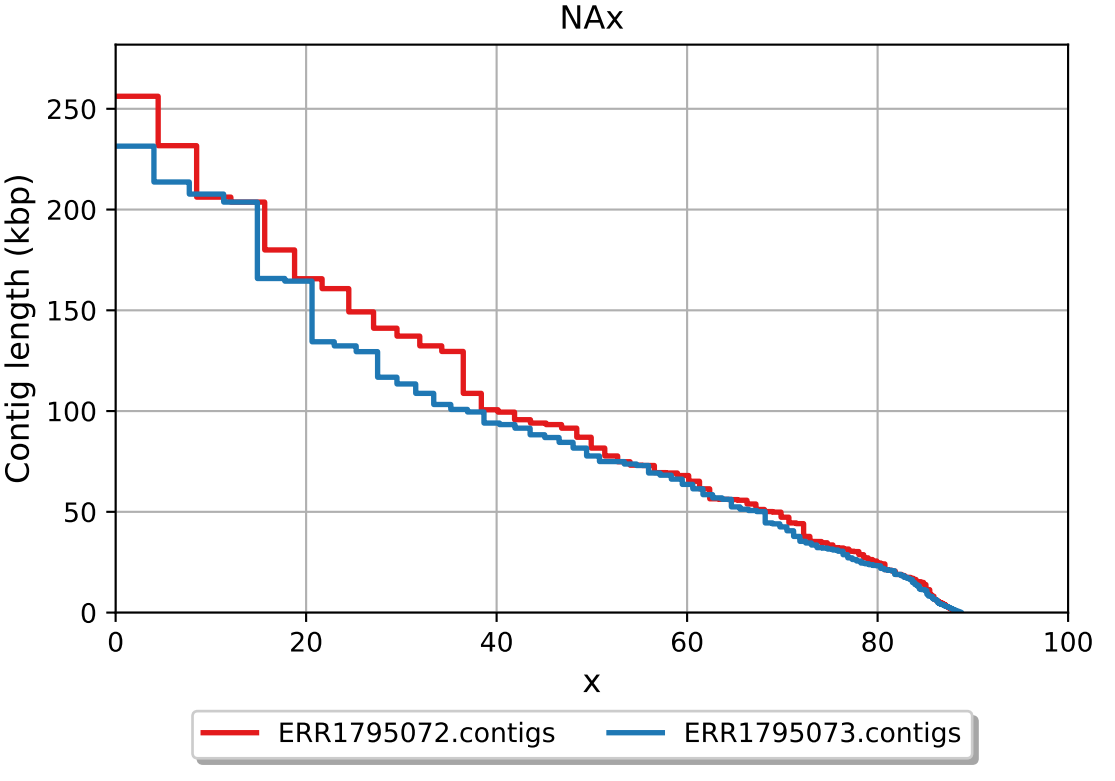

ERR1795072.contigs GC content
contigs
GC (%)
0
10
20
30
40
50
60
0
20
40
60
80
100
ERR1795072.contigs

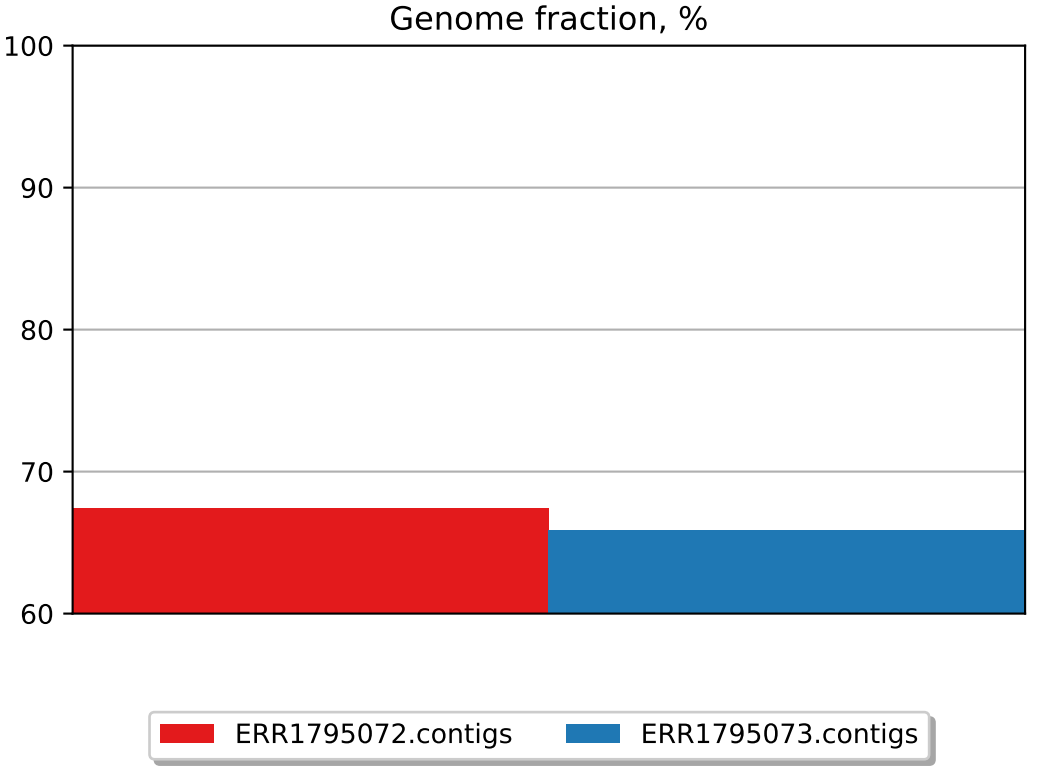

ERR1795073.contigs GC content
contigs
GC (%)
0
15
30
45
60
75
0
20
40
60
80
100
ERR1795073.contigs


Misassemblies
50
40
30
20
10
0
ERR1795072.contigs
ERR1795073.contigs
relocations
inversions
interspecies translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
10
20
30
40
50
Feature space
ERR1795072.contigs
ERR1795073.contigs


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
4
8
12
16
0
40
80
120
160
200
Contig index
ERR1795072.contigs
ERR1795073.contigs
Reference


NAx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
ERR1795072.contigs
ERR1795073.contigs


Genome fraction, %
100
90
80
70
60
ERR1795072.contigs
ERR1795073.contigs