

Report

	contigs_1	contigs_2
# contigs (≥ 0 bp)	3	4
# contigs (≥ 1000 bp)	3	2
# contigs (≥ 5000 bp)	0	0
# contigs (≥ 10000 bp)	0	0
# contigs (≥ 25000 bp)	0	0
# contigs (≥ 50000 bp)	0	0
Total length (≥ 0 bp)	6710	5870
Total length (≥ 1000 bp)	6710	5460
Total length (≥ 5000 bp)	0	0
Total length (≥ 10000 bp)	0	0
Total length (≥ 25000 bp)	0	0
Total length (≥ 50000 bp)	0	0
# 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 mis. contigs	0	0
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	67.100	54.600
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
Largest alignment	2030	2100
Total aligned length	6710	5460
NA50	1950	1471
NGA50	1610	700
NA75	1610	1189
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

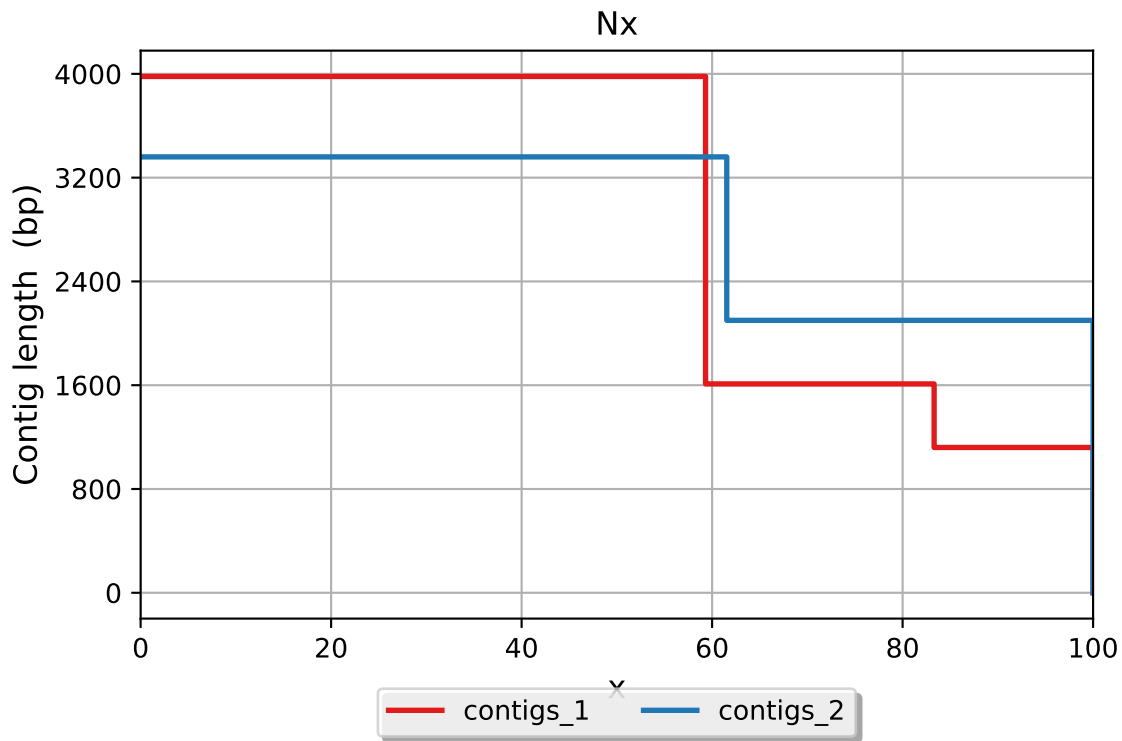
	contigs_1	contigs_2
# misassemblies	1	2
# relocations	1	2
# translocations	0	0
# inversions	0	0
# misassembled contigs	1	1
Misassembled contigs length	3980	3360
# local misassemblies	0	0
# unaligned mis. contigs	0	0
# mismatches	0	0
# indels	0	0
# indels (≤ 5 bp)	0	0
# indels (> 5 bp)	0	0
Indels length	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).

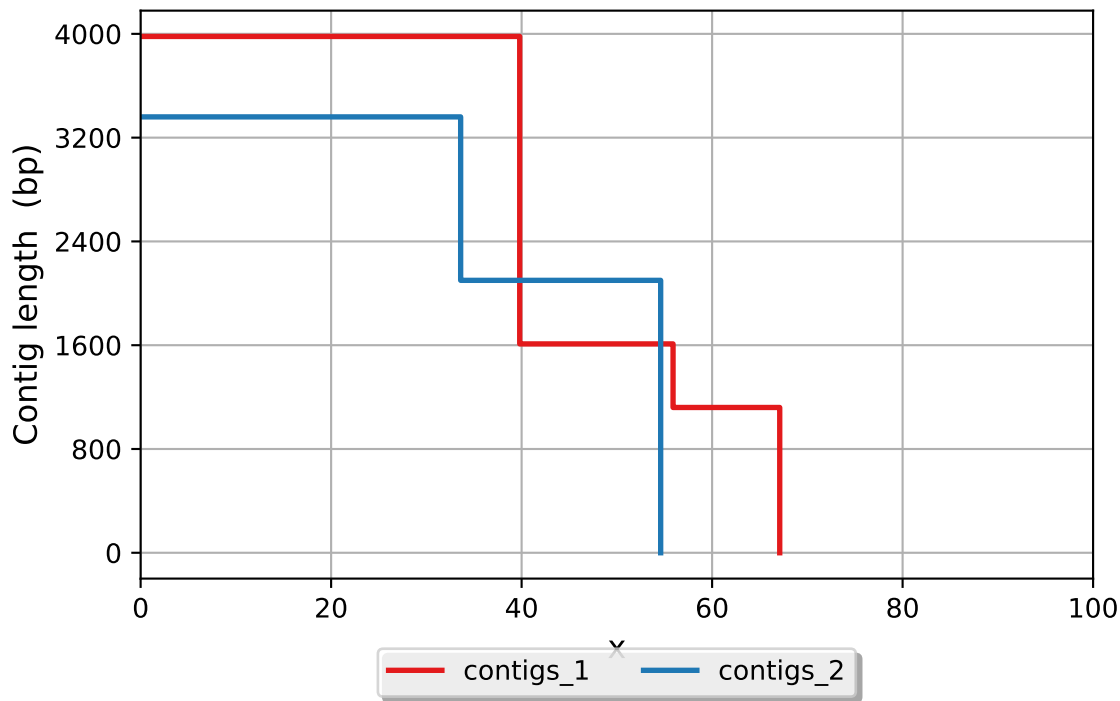
Unaligned report

	contigs_1	contigs_2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	0	0

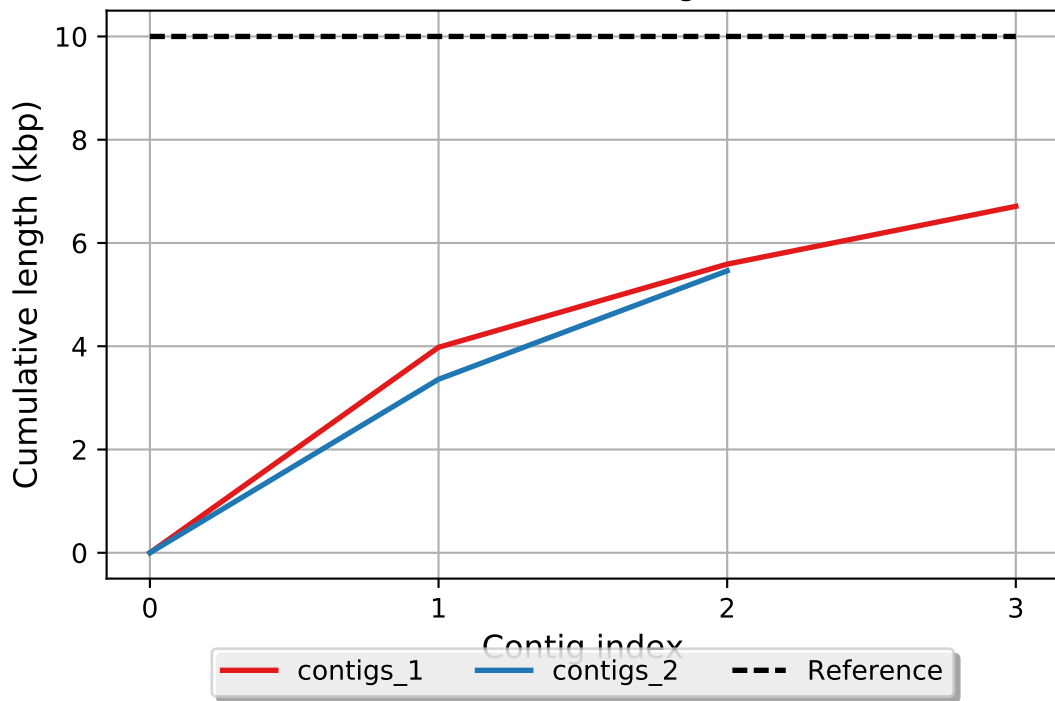
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



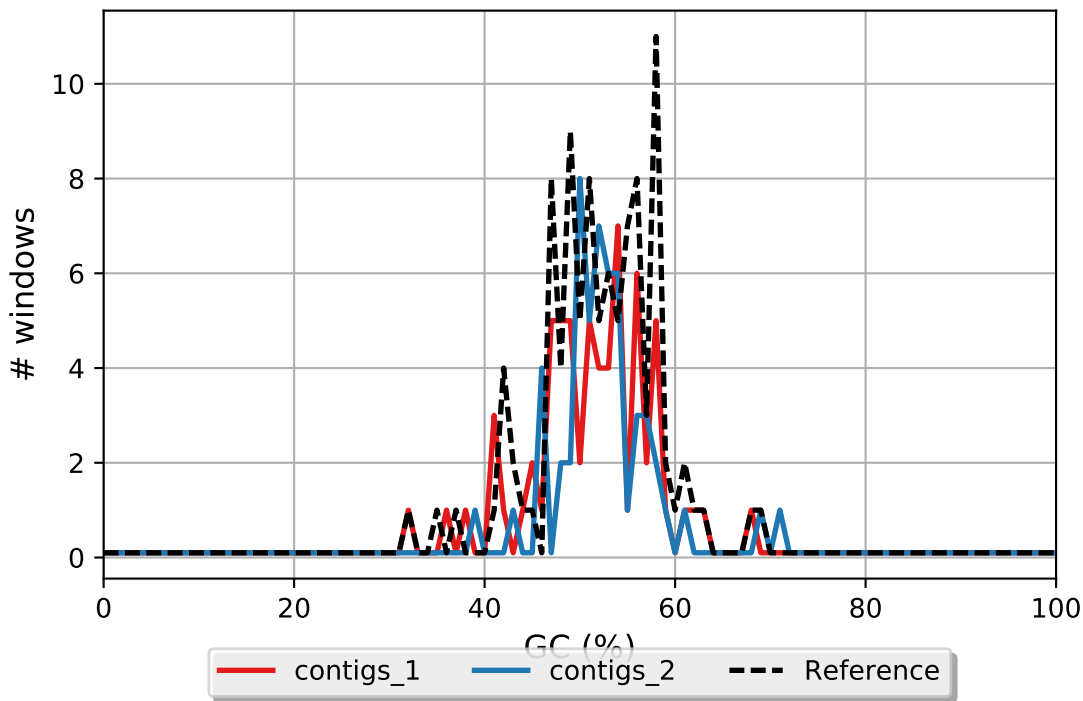
NGx



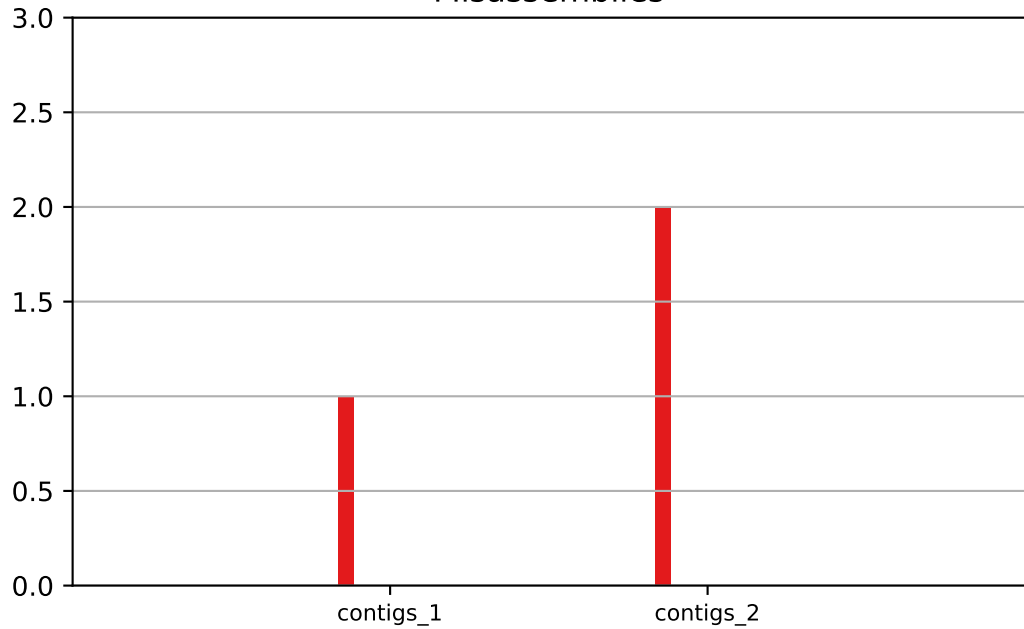
Cumulative length



GC content

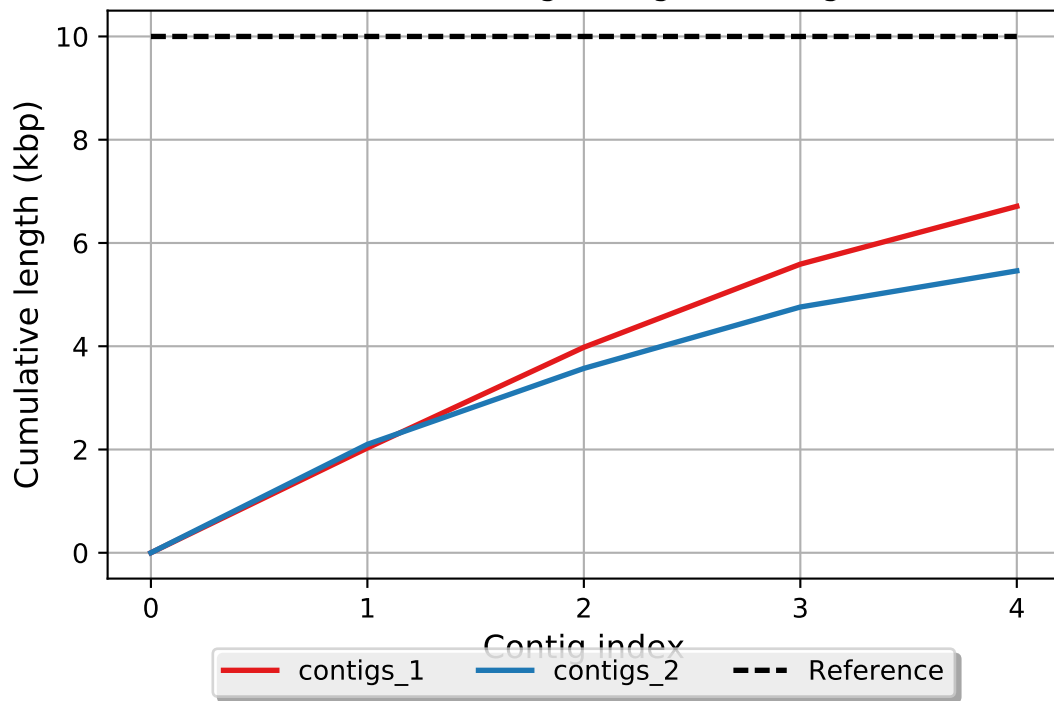


Misassemblies

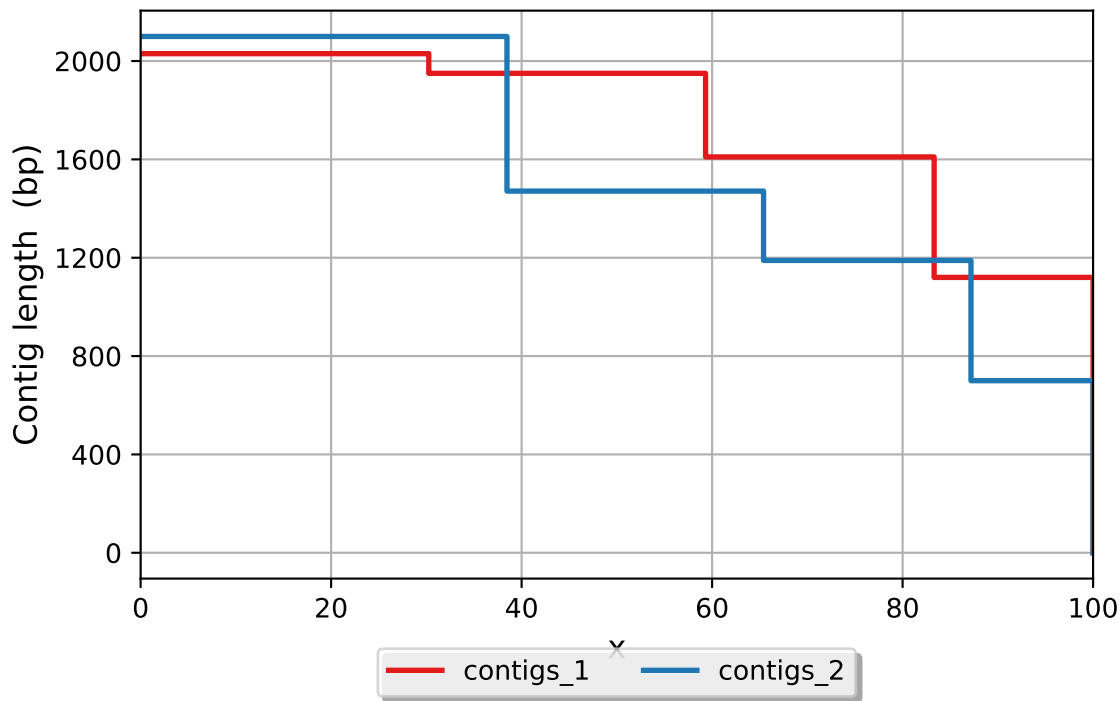


 # relocations

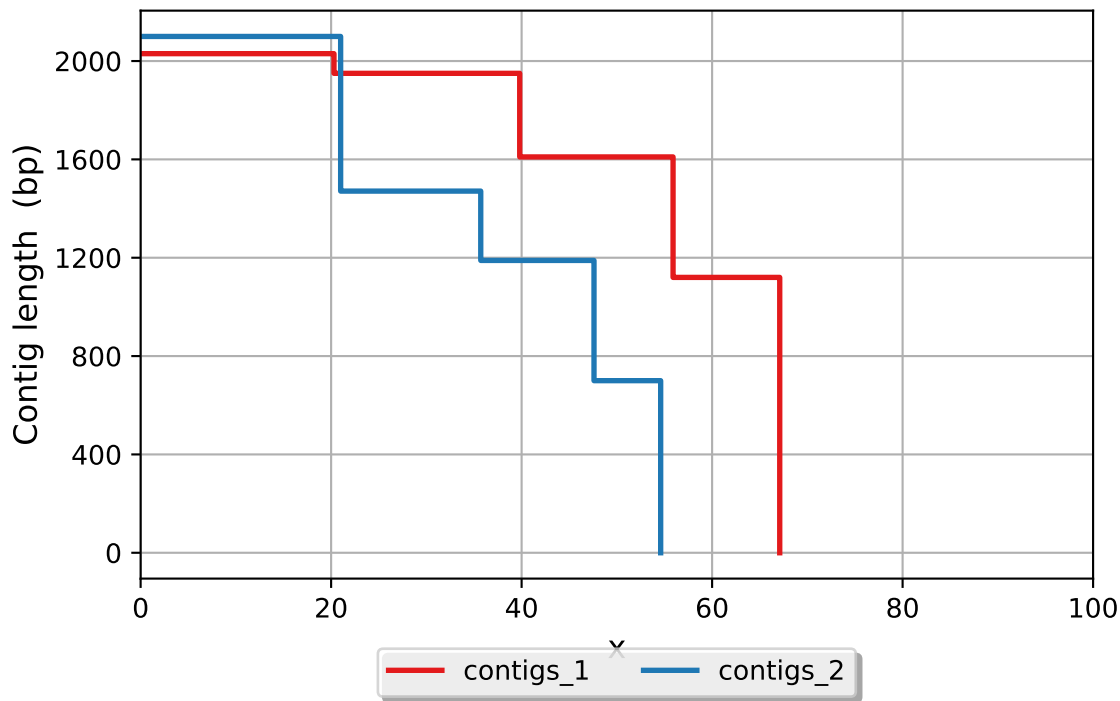
Cumulative length (aligned contigs)



NAx



NGAx



Genome fraction, %

