

Report

	contigs
# contigs (≥ 0 bp)	4854
# contigs (≥ 1000 bp)	1006
# contigs (≥ 5000 bp)	3
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	3510794
Total length (≥ 1000 bp)	1514829
Total length (≥ 5000 bp)	18221
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	2772
Largest contig	6520
Total length	2765684
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	1067
NG50	659
N75	760
L50	879
LG50	1998
L75	1651
# misassemblies	26
# misassembled contigs	26
Misassembled contigs length	54456
# local misassemblies	3
# unaligned contigs	1 + 14 part
Unaligned length	3708
Genome fraction (%)	59.377
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	771.72
# indels per 100 kbp	1.16
Largest alignment	6021
NA50	1061
NGA50	655
NA75	753
LA50	887
LGA50	2017
LA75	1666

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
# misassemblies	26
# relocations	26
# translocations	0
# inversions	0
# misassembled contigs	26
Misassembled contigs length	54456
# local misassemblies	3
# mismatches	21269
# indels	32
# short indels	31
# long indels	1
Indels length	124

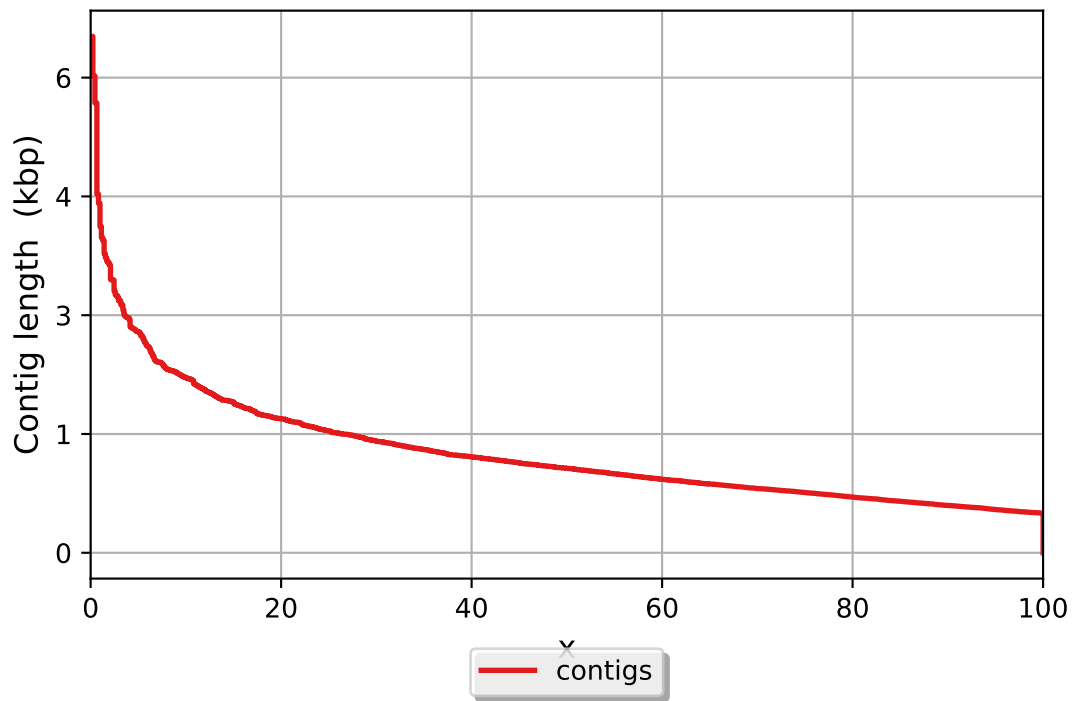
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

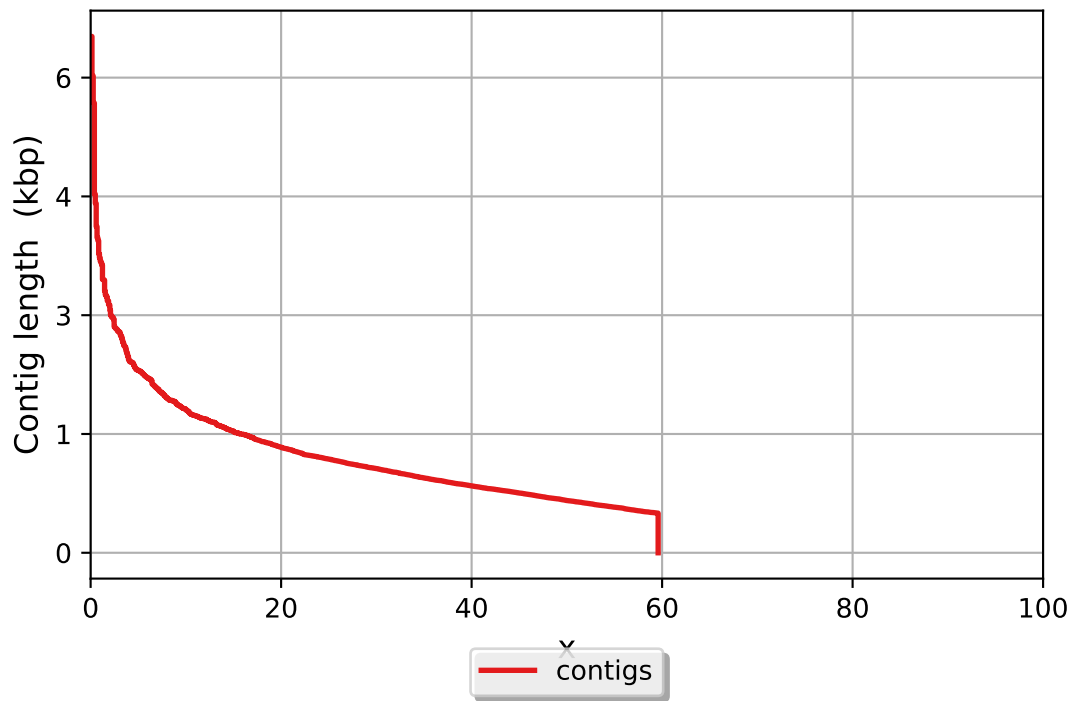
	contigs
# fully unaligned contigs	1
Fully unaligned length	989
# partially unaligned contigs	14
# with misassembly	0
# both parts are significant	1
Partially unaligned length	2719
# N's	0

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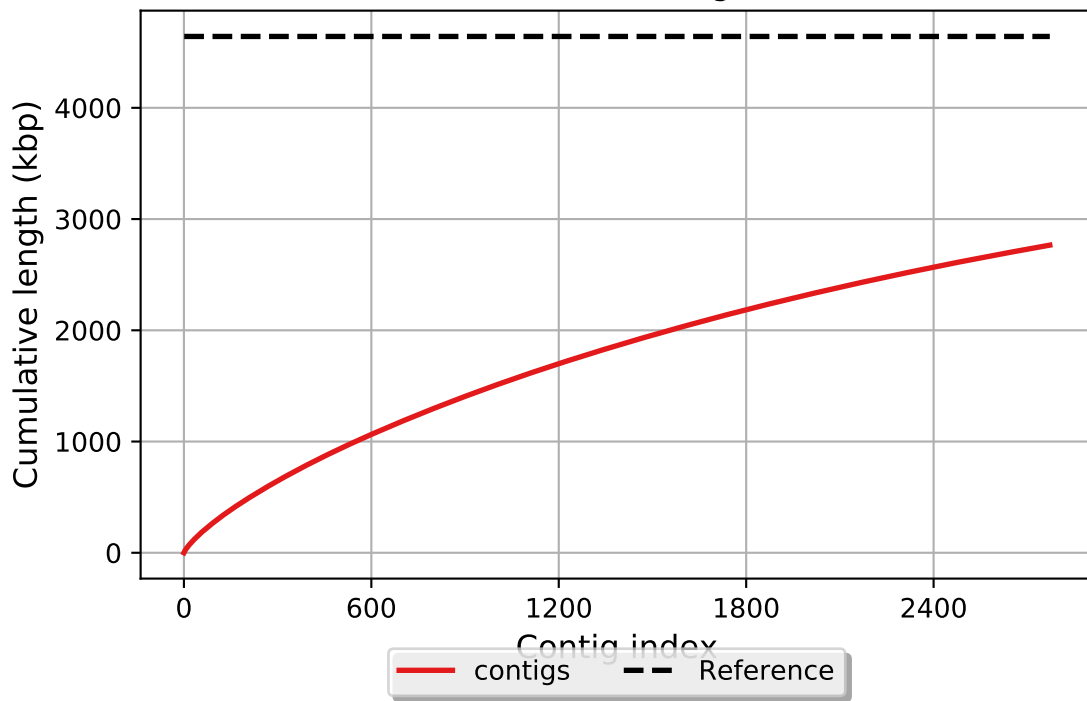
Nx

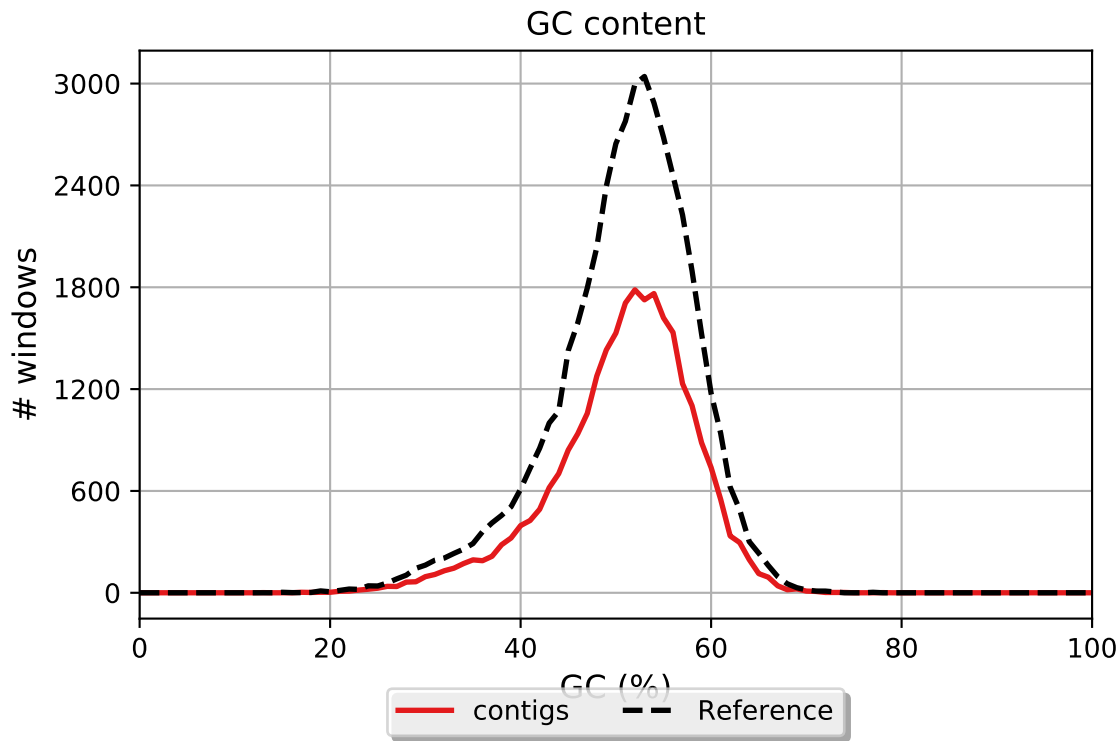


NGx

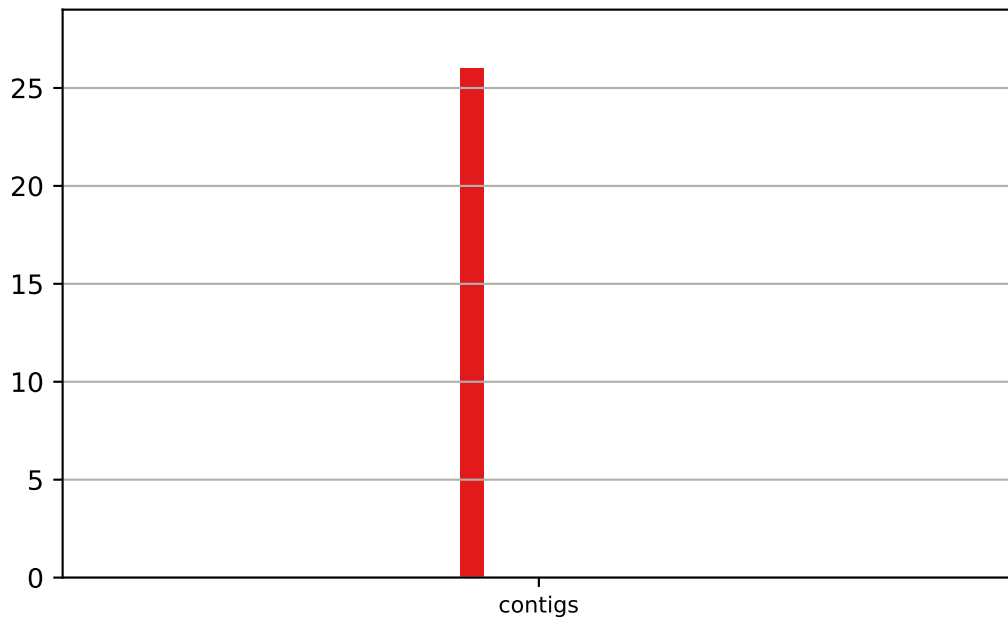


Cumulative length

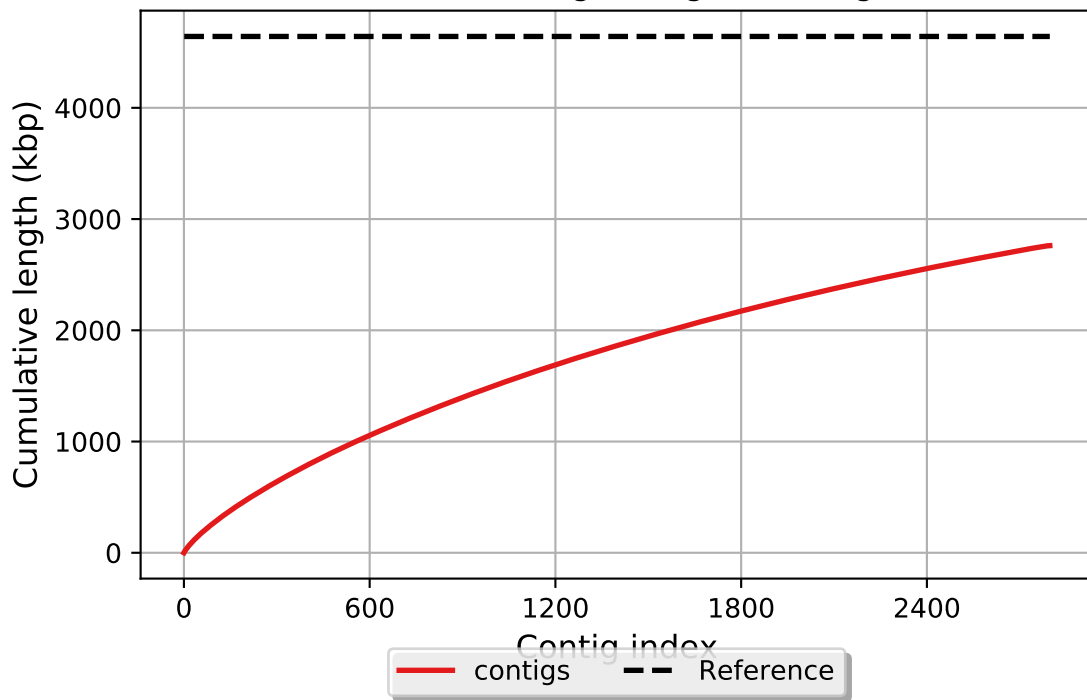




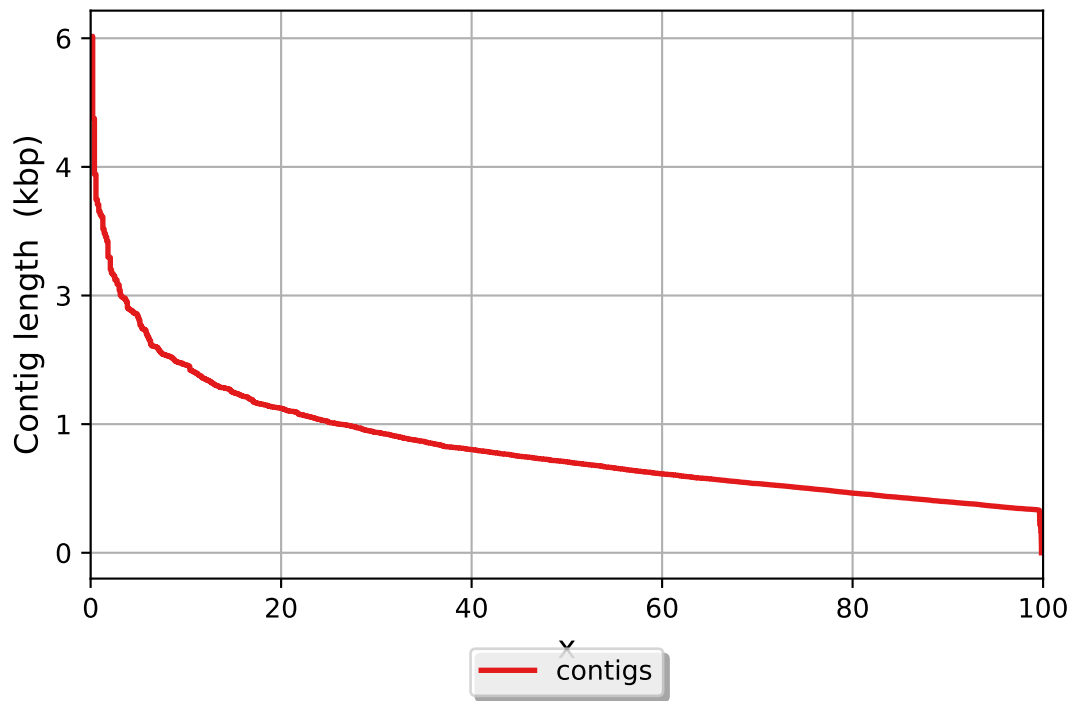
Misassemblies



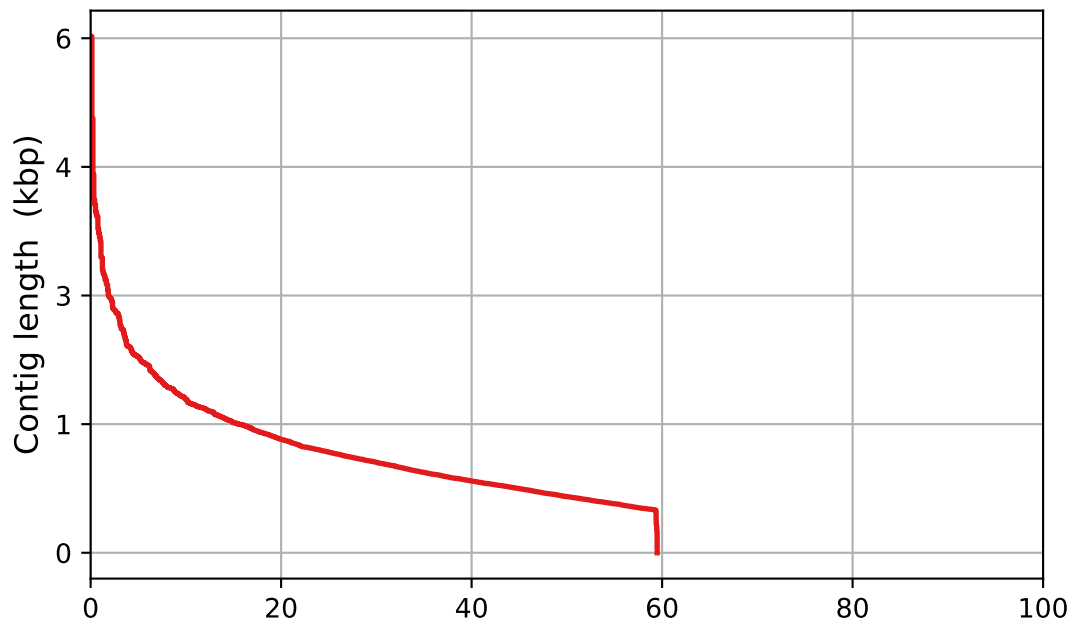
Cumulative length (aligned contigs)



NAx



NGAx



x
contigs