

Report

	contigs
# contigs (≥ 0 bp)	175
# contigs (≥ 1000 bp)	104
# contigs (≥ 5000 bp)	78
# contigs (≥ 10000 bp)	67
# contigs (≥ 25000 bp)	51
# contigs (≥ 50000 bp)	30
Total length (≥ 0 bp)	4567170
Total length (≥ 1000 bp)	4549416
Total length (≥ 5000 bp)	4495762
Total length (≥ 10000 bp)	4408131
Total length (≥ 25000 bp)	4149250
Total length (≥ 50000 bp)	3409655
# contigs	110
Largest contig	327399
Total length	4553707
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	105830
NG50	105830
N75	48829
NG75	45329
L50	15
LG50	15
L75	31
LG75	32
# misassemblies	4
# misassembled contigs	3
Misassembled contigs length	236556
# local misassemblies	7
# unaligned contigs	0 + 1 part
Unaligned length	24
Genome fraction (%)	98.061
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13.67
# indels per 100 kbp	0.44
Largest alignment	327399
NA50	105830
NGA50	95495
NA75	48829
NGA75	45329
LA50	15
LGA50	16
LA75	32
LGA75	33

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

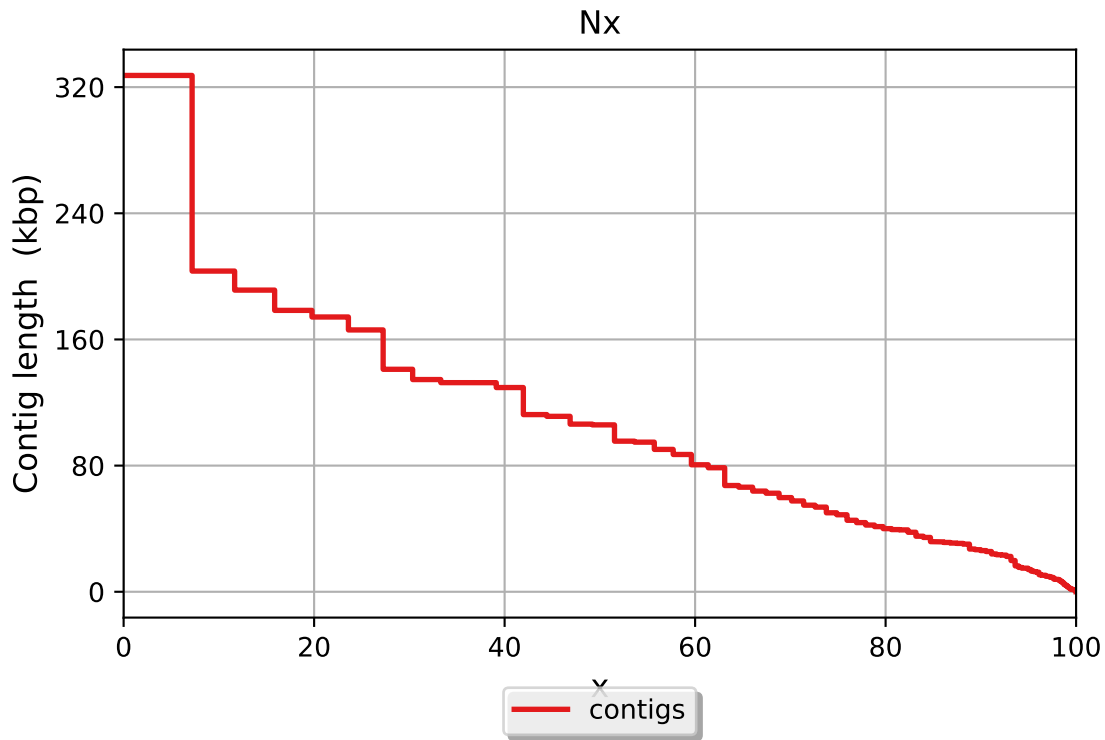
	contigs
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	236556
# local misassemblies	7
# mismatches	622
# indels	20
# short indels	18
# long indels	2
Indels length	102

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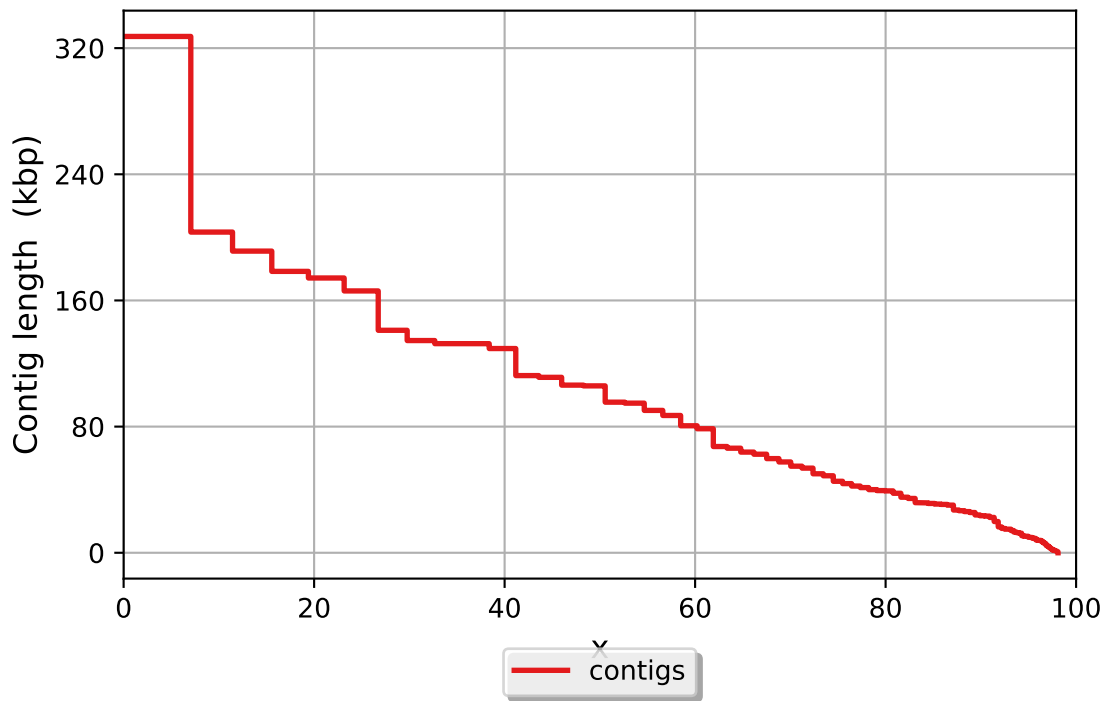
Unaligned report

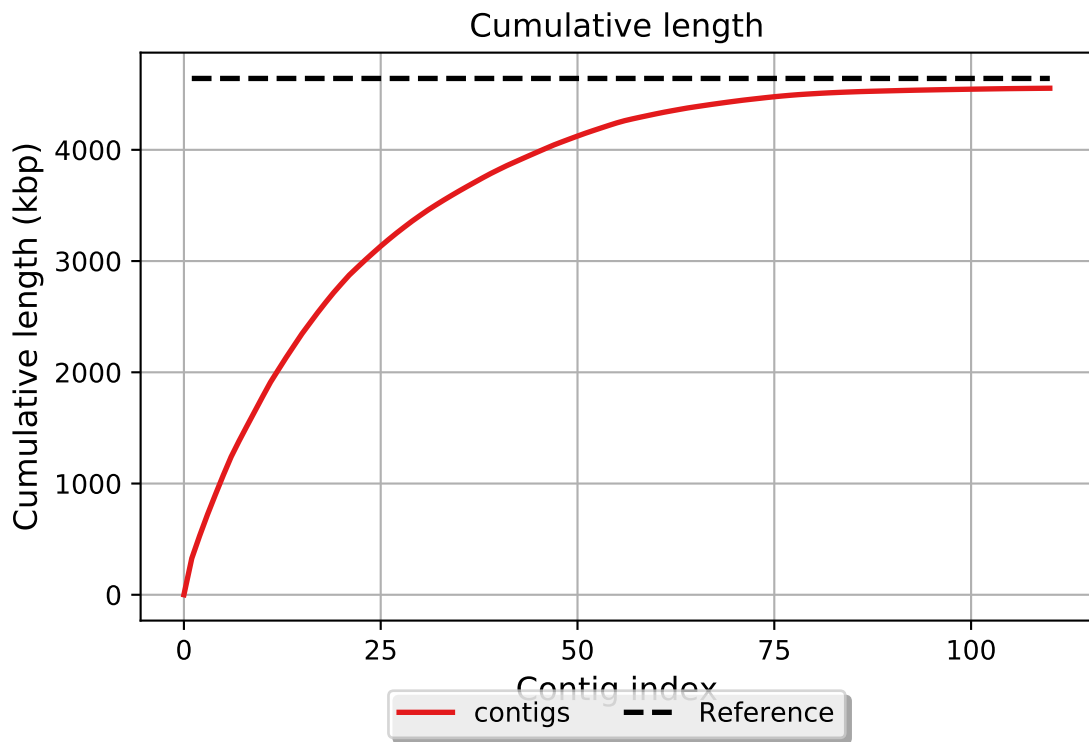
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	24
# N's	0

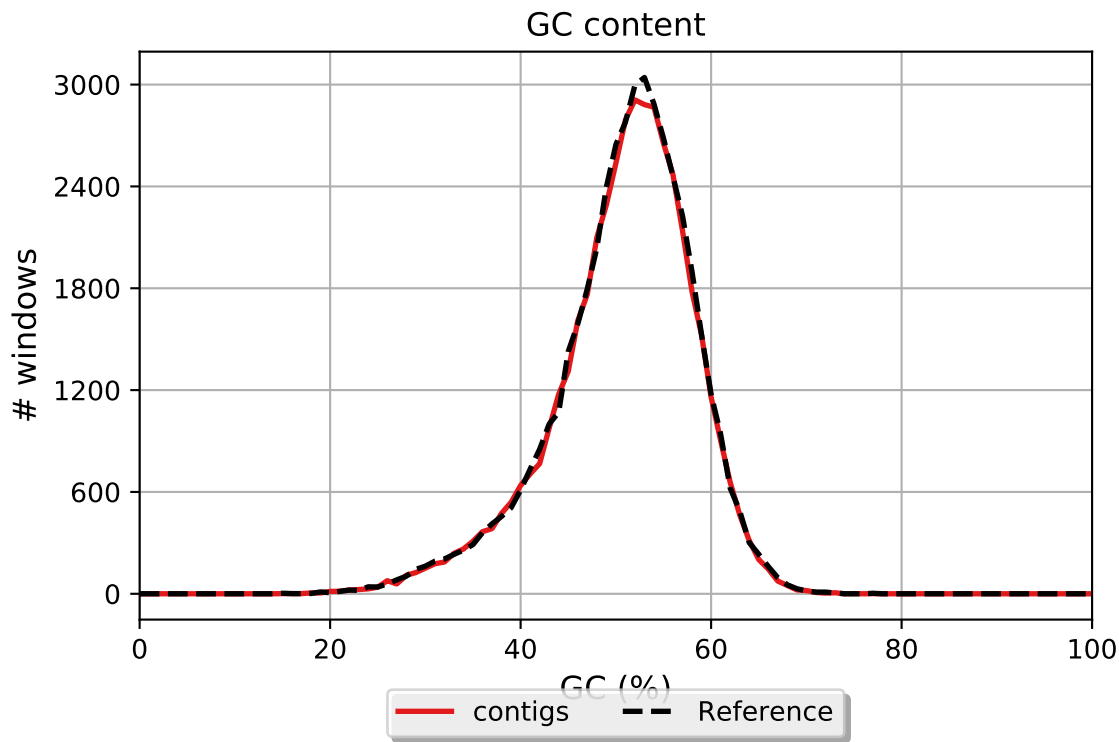
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



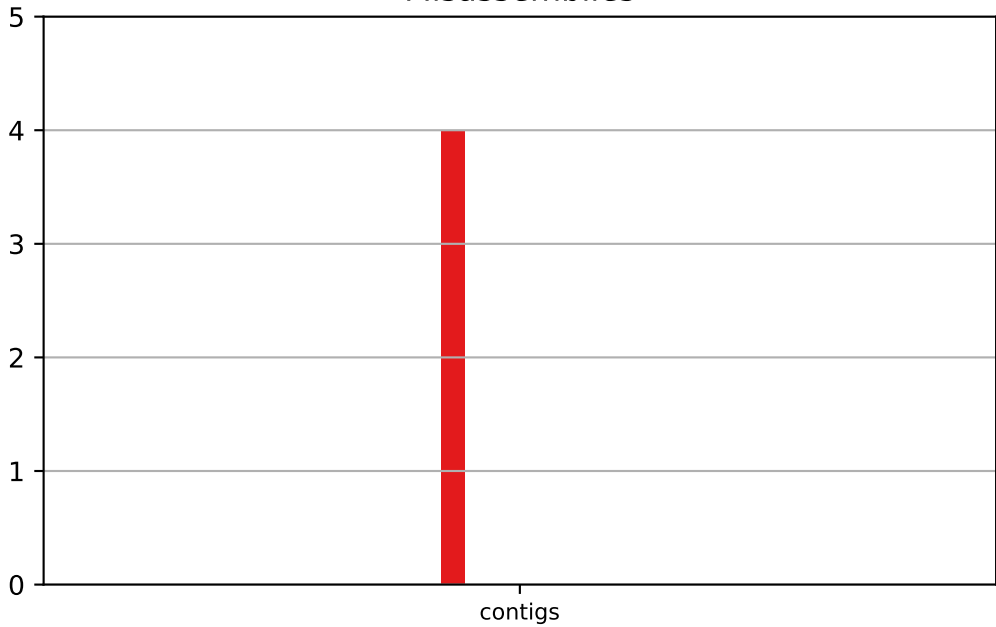
NGx



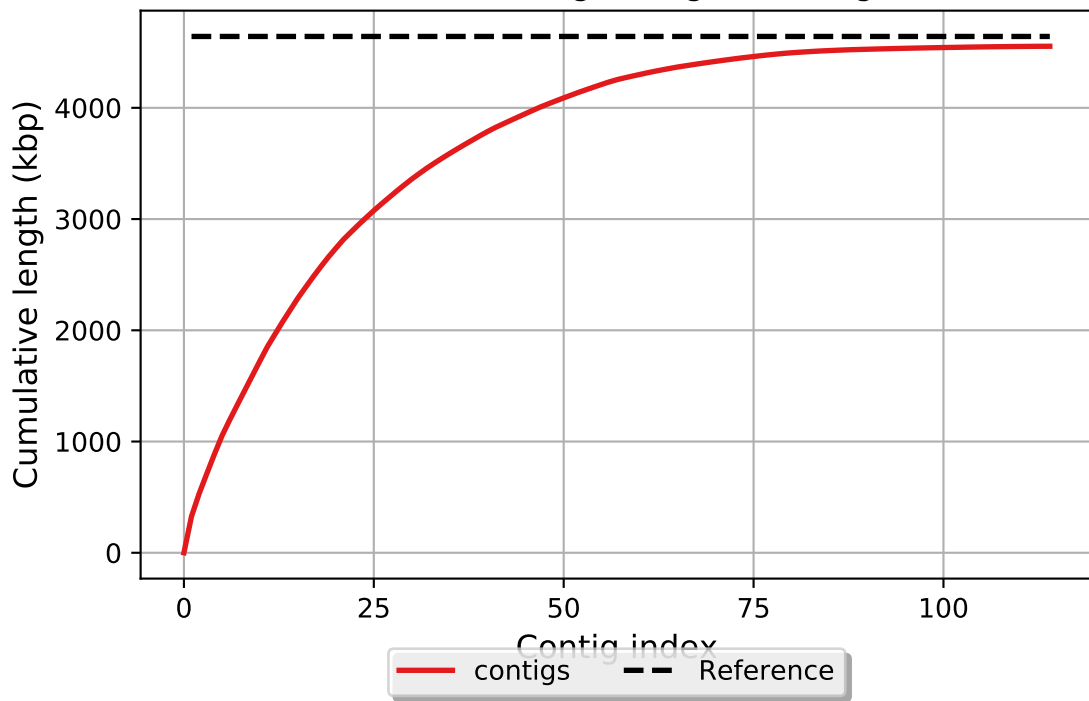




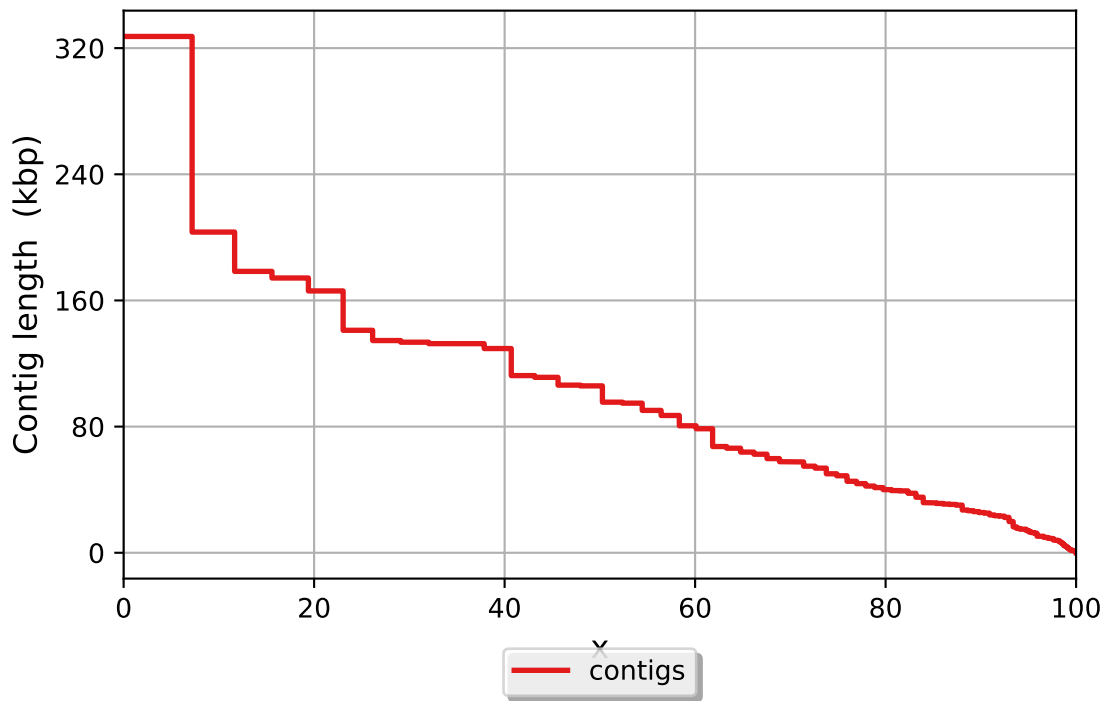
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

