

Report

	contigs
# contigs (≥ 0 bp)	311
# contigs (≥ 1000 bp)	220
# contigs (≥ 5000 bp)	172
# contigs (≥ 10000 bp)	141
# contigs (≥ 25000 bp)	64
# contigs (≥ 50000 bp)	19
Total length (≥ 0 bp)	4571416
Total length (≥ 1000 bp)	4544705
Total length (≥ 5000 bp)	4415622
Total length (≥ 10000 bp)	4179616
Total length (≥ 25000 bp)	2910119
Total length (≥ 50000 bp)	1334270
# contigs	235
Largest contig	118259
Total length	4555775
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	34552
NG50	32452
N75	19042
NG75	18834
L50	43
LG50	44
L75	88
LG75	91
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.103
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.75
# indels per 100 kbp	0.29
Largest alignment	118259
NA50	34552
NGA50	32452
NA75	19042
NGA75	18834
LA50	43
LGA50	44
LA75	88
LGA75	91

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

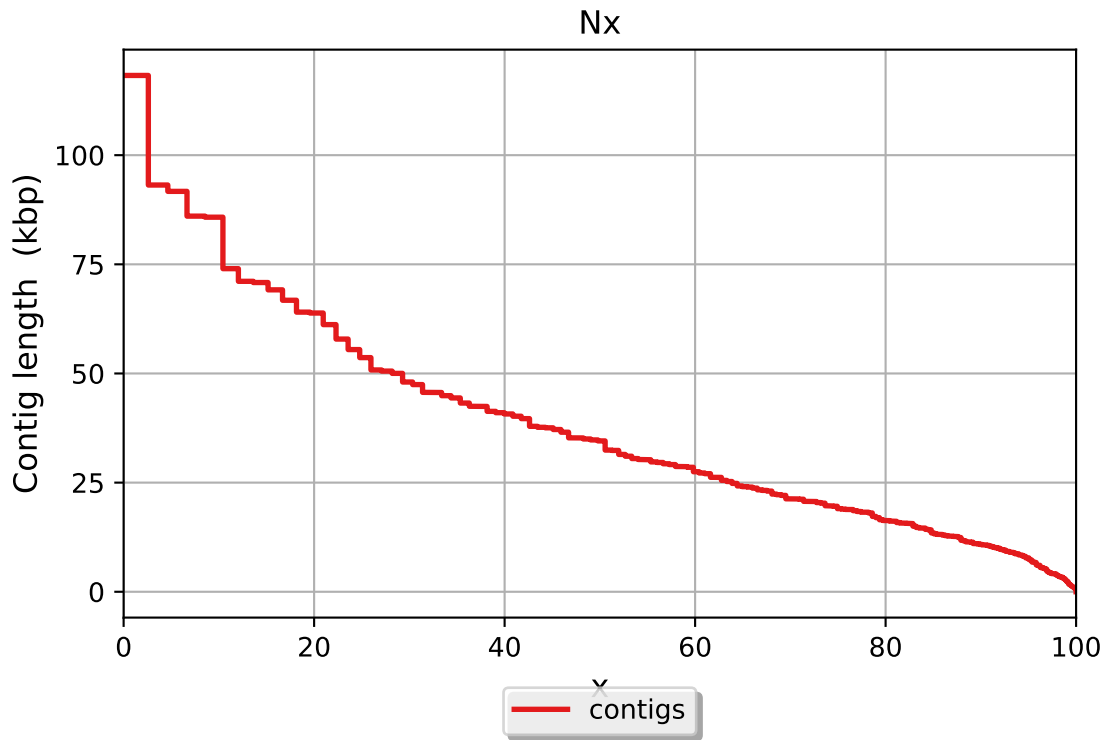
	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# mismatches	125
# indels	13
# short indels	11
# long indels	2
Indels length	178

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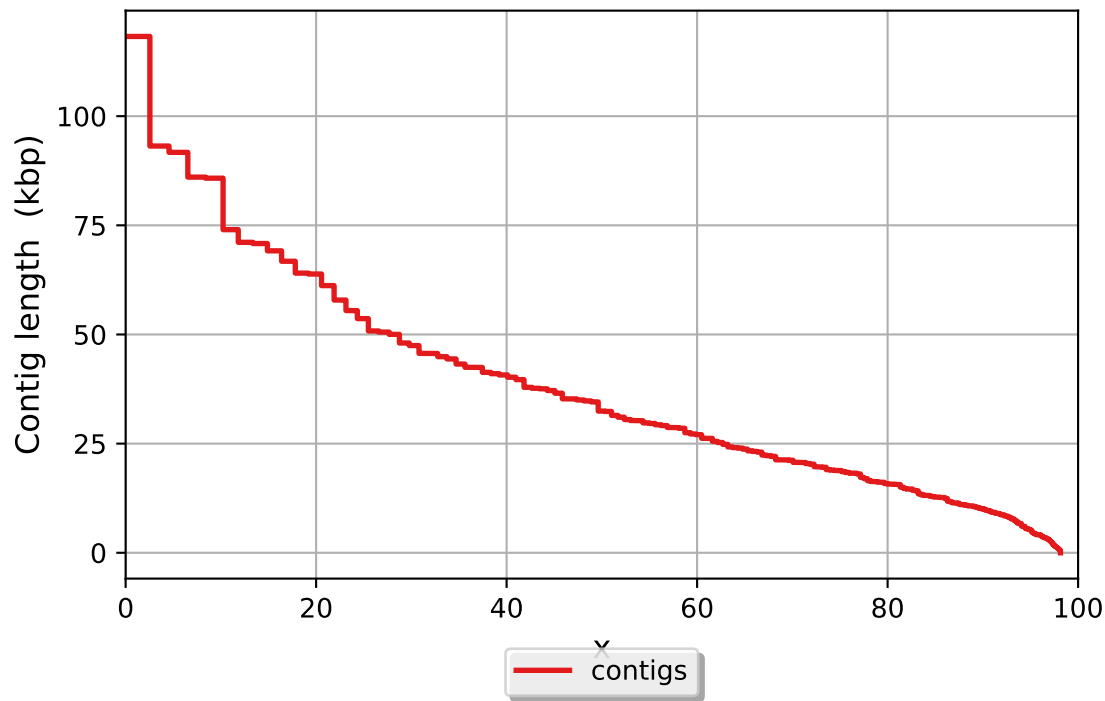
Unaligned report

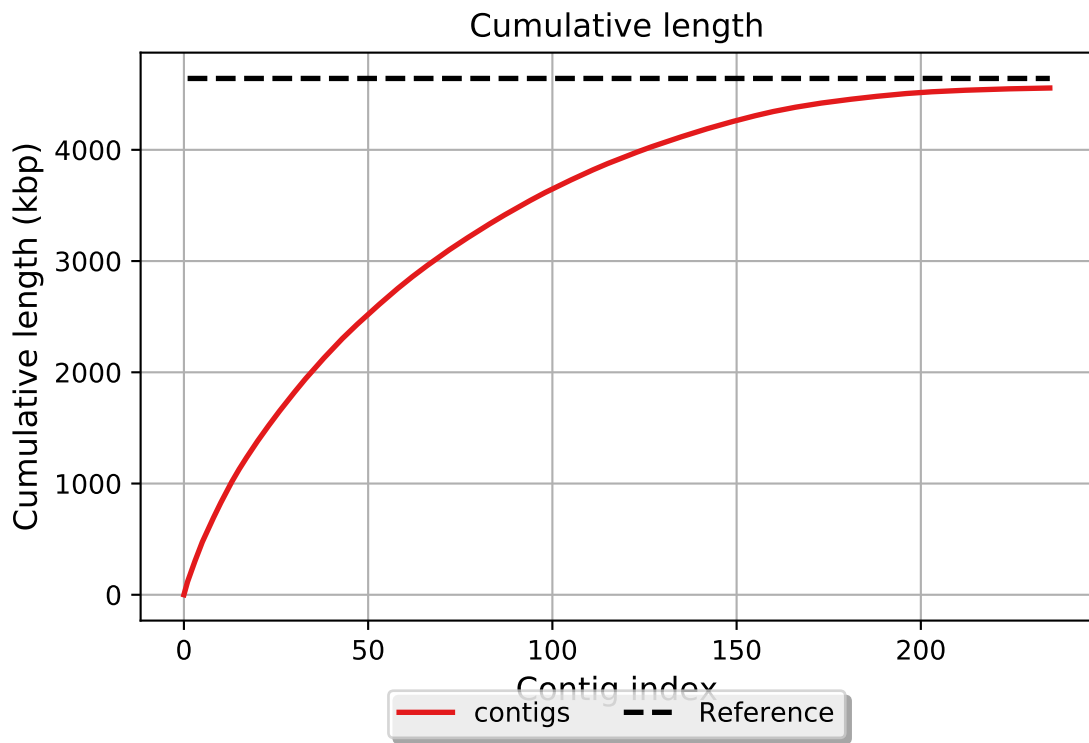
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

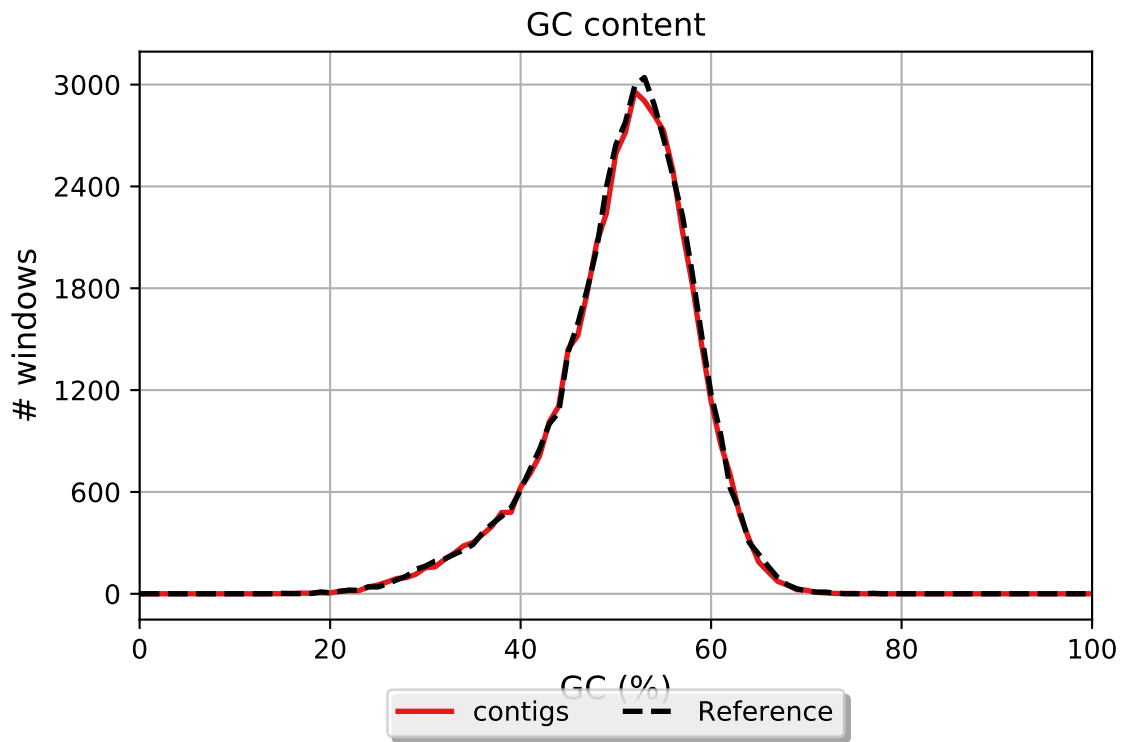
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



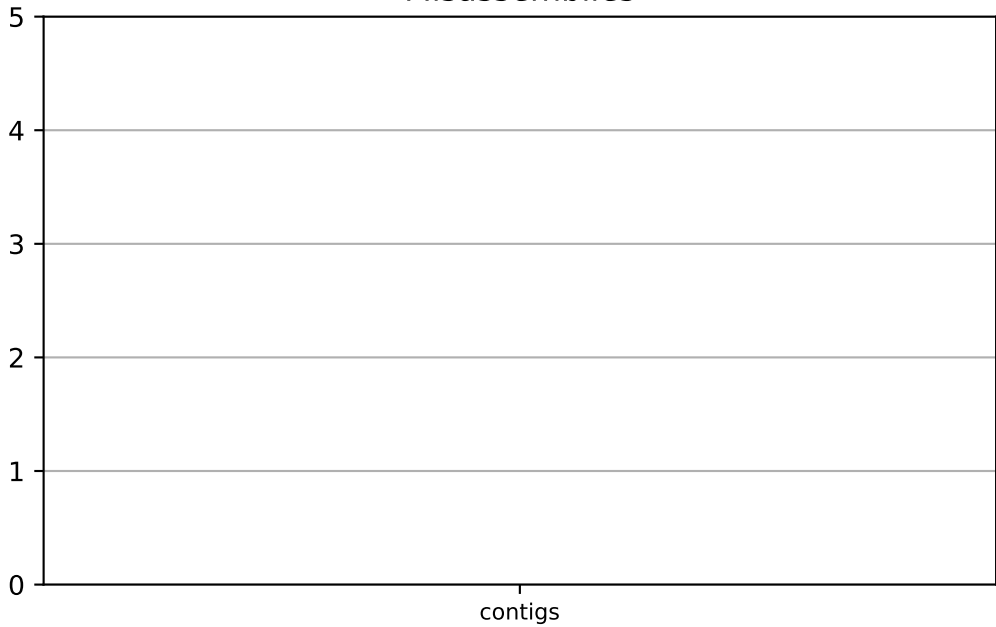
NGx



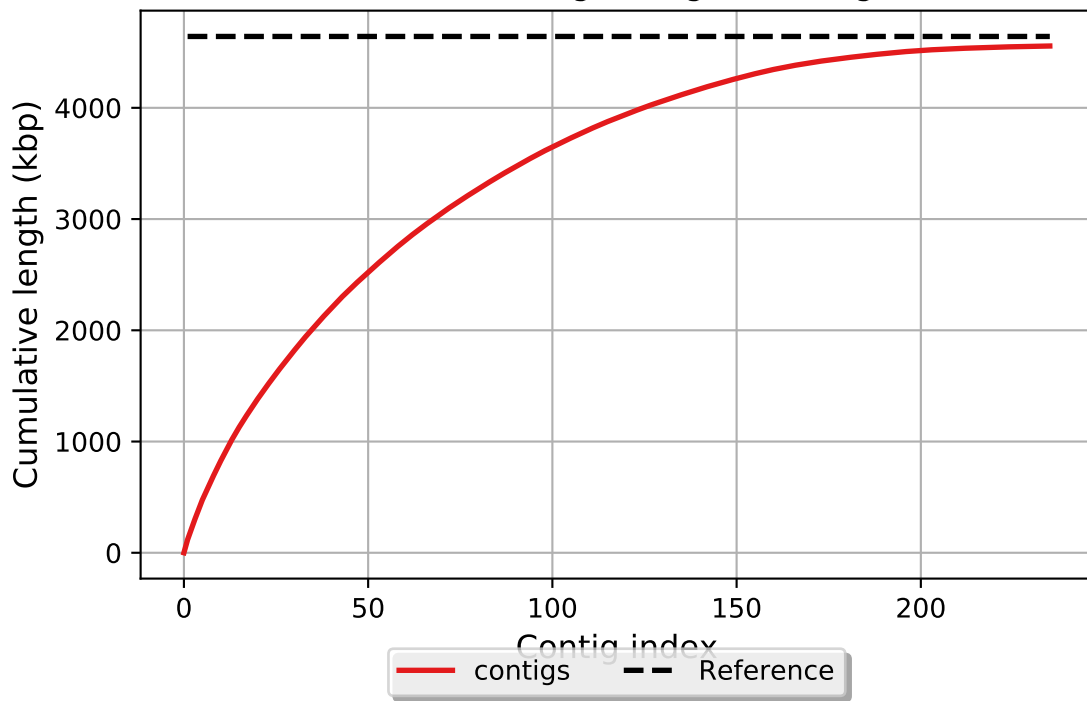




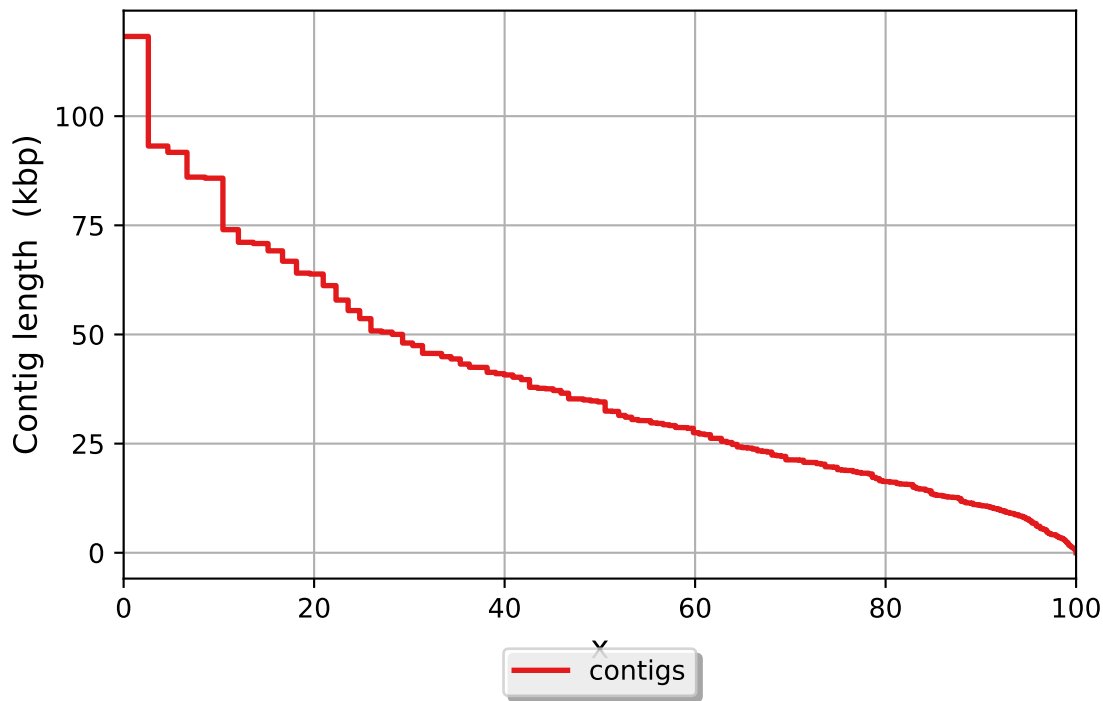
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

