

Report

	contigs
# contigs (≥ 0 bp)	722
# contigs (≥ 1000 bp)	610
# contigs (≥ 5000 bp)	318
# contigs (≥ 10000 bp)	156
# contigs (≥ 25000 bp)	18
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	4527903
Total length (≥ 1000 bp)	4479169
Total length (≥ 5000 bp)	3693561
Total length (≥ 10000 bp)	2526281
Total length (≥ 25000 bp)	502507
Total length (≥ 50000 bp)	0
# contigs	650
Largest contig	37456
Total length	4508689
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	11147
NG50	10879
N75	6478
NG75	5891
L50	131
LG50	137
L75	263
LG75	279
# misassemblies	15
# misassembled contigs	15
Misassembled contigs length	222467
# local misassemblies	15
# unaligned contigs	0 + 1 part
Unaligned length	18
Genome fraction (%)	96.907
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	226.32
# indels per 100 kbp	2.00
Largest alignment	37450
NA50	10879
NGA50	10574
NA75	6256
NGA75	5693
LA50	134
LGA50	140
LA75	271
LGA75	288

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	15
# relocations	15
# translocations	0
# inversions	0
# misassembled contigs	15
Misassembled contigs length	222467
# local misassemblies	15
# mismatches	10180
# indels	90
# short indels	84
# long indels	6
Indels length	212

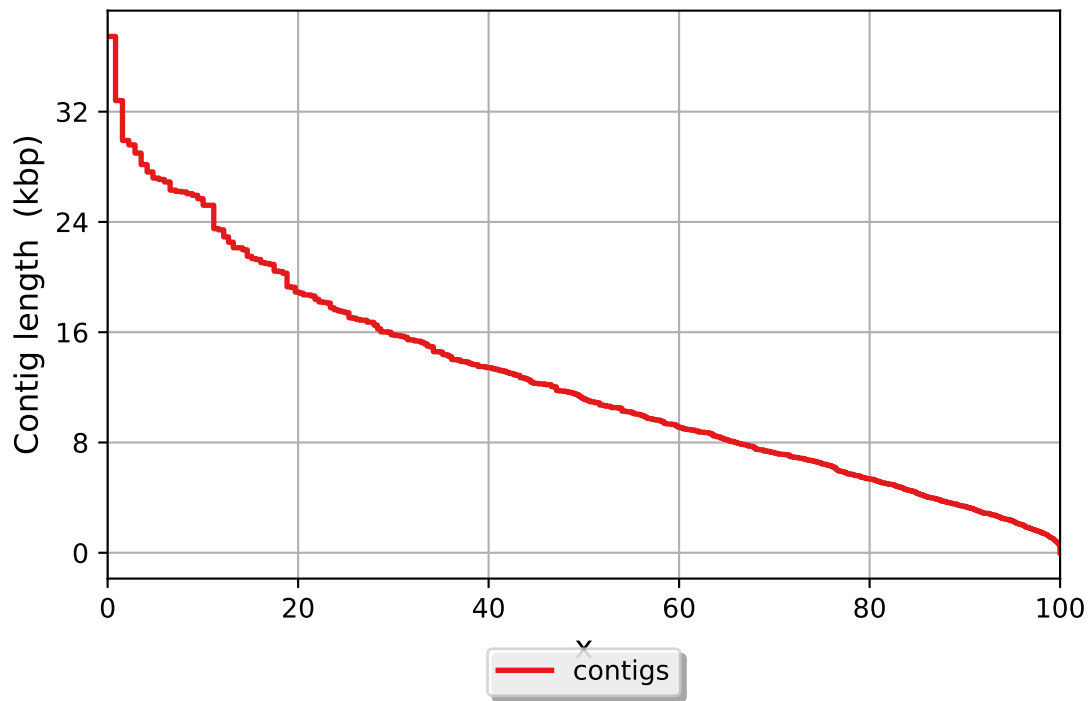
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

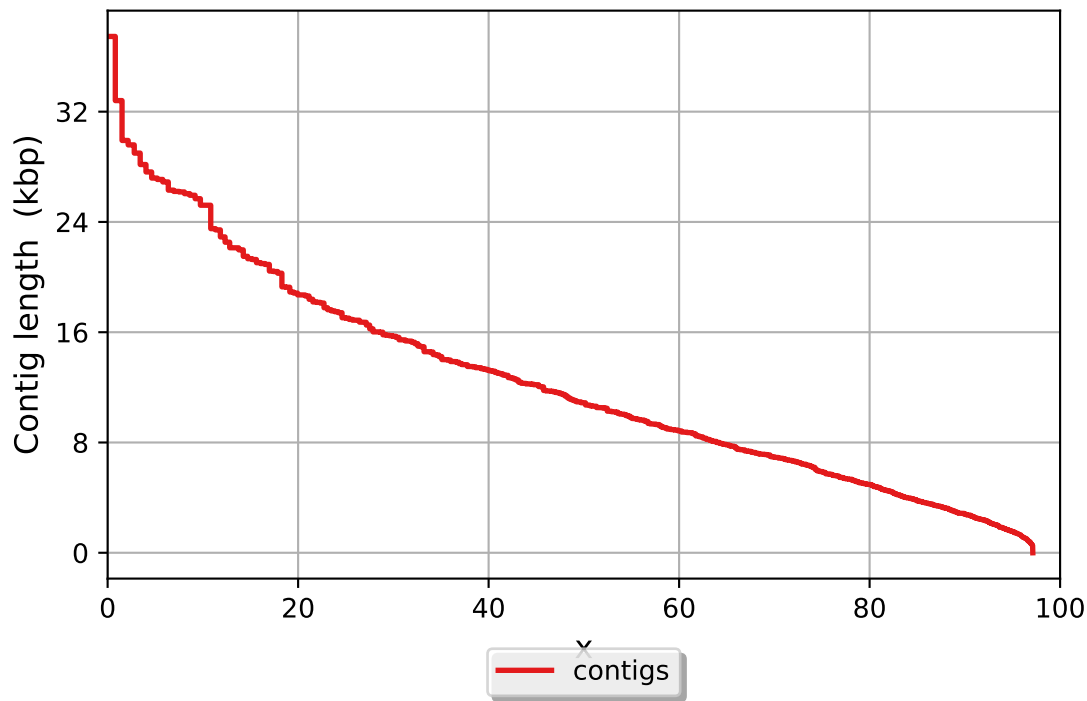
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	18
# N's	0

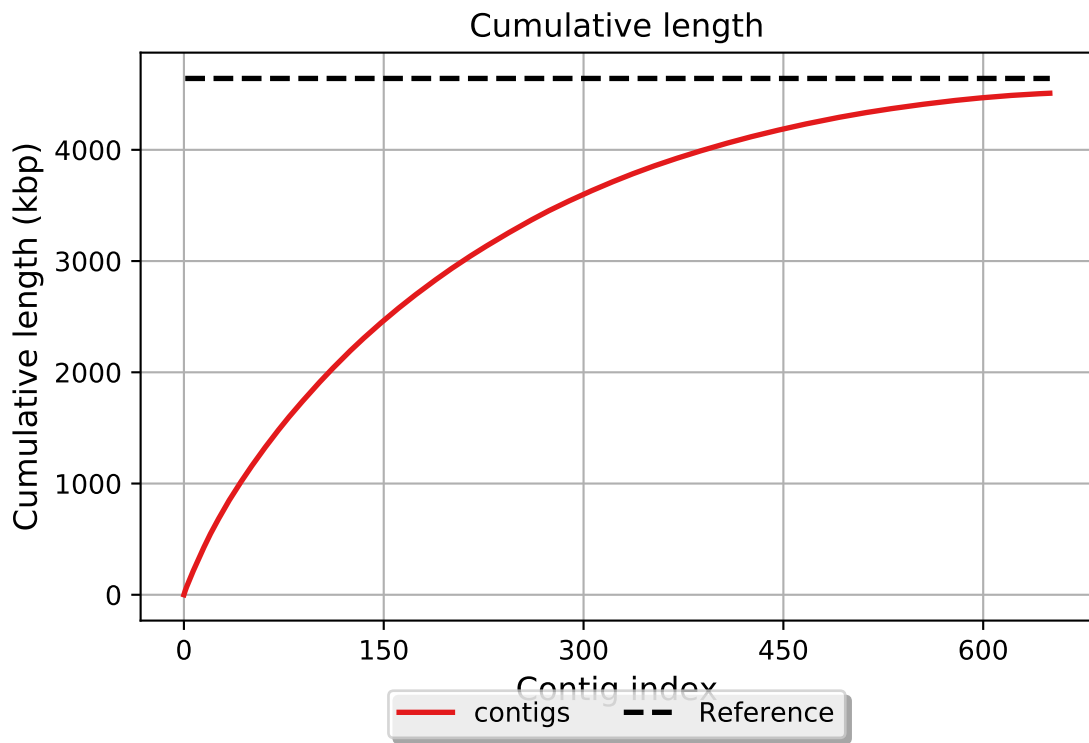
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

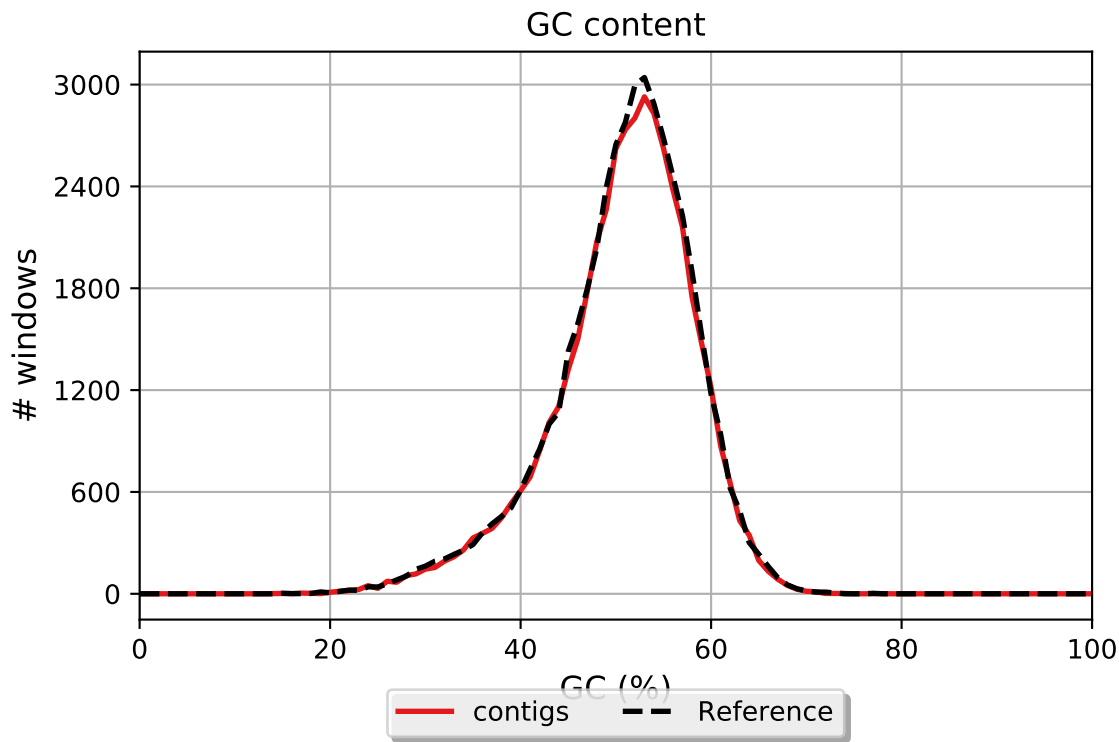
Nx



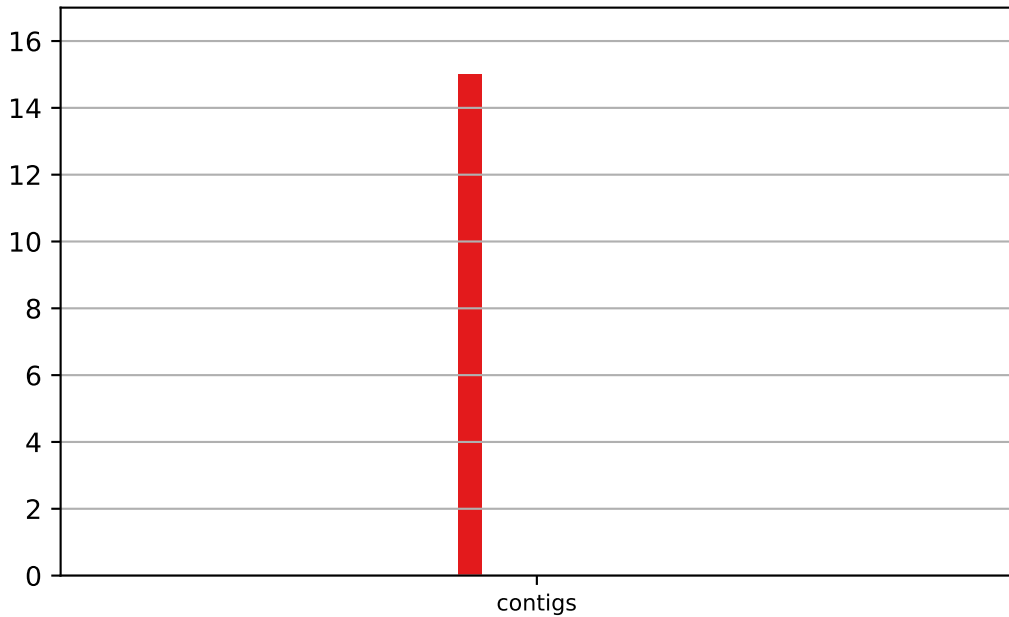
NGx



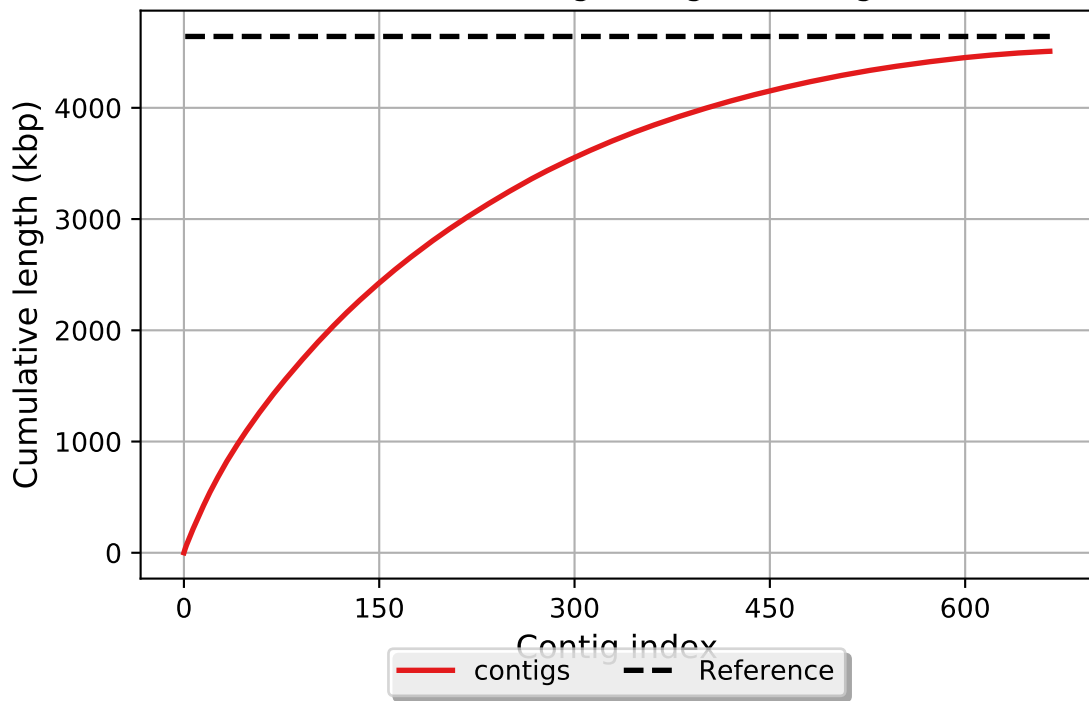




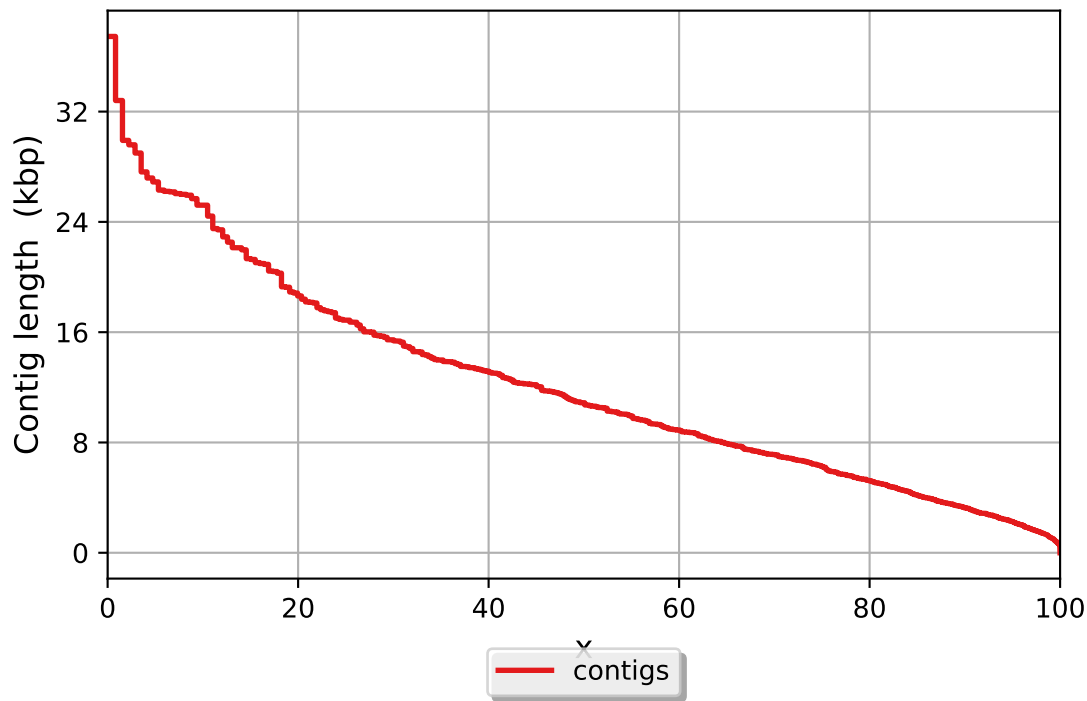
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

