

Report

	contigs
# contigs (≥ 0 bp)	2530
# contigs (≥ 1000 bp)	1513
# contigs (≥ 5000 bp)	124
# contigs (≥ 10000 bp)	6
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	4432408
Total length (≥ 1000 bp)	3857209
Total length (≥ 5000 bp)	801163
Total length (≥ 10000 bp)	64961
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	2091
Largest contig	11817
Total length	4281904
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	2697
NG50	2512
N75	1584
NG75	1353
L50	499
LG50	568
L75	1011
LG75	1194
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	26612
# local misassemblies	7
# unaligned contigs	0 + 1 part
Unaligned length	178
Genome fraction (%)	92.058
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.20
# indels per 100 kbp	0.21
Largest alignment	11817
NA50	2686
NGA50	2510
NA75	1584
NGA75	1352
LA50	502
LGA50	571
LA75	1014
LGA75	1198

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	6
# relocations	6
# translocations	0
# inversions	0
# misassembled contigs	6
Misassembled contigs length	26612
# local misassemblies	7
# mismatches	222
# indels	9
# short indels	8
# long indels	1
Indels length	94

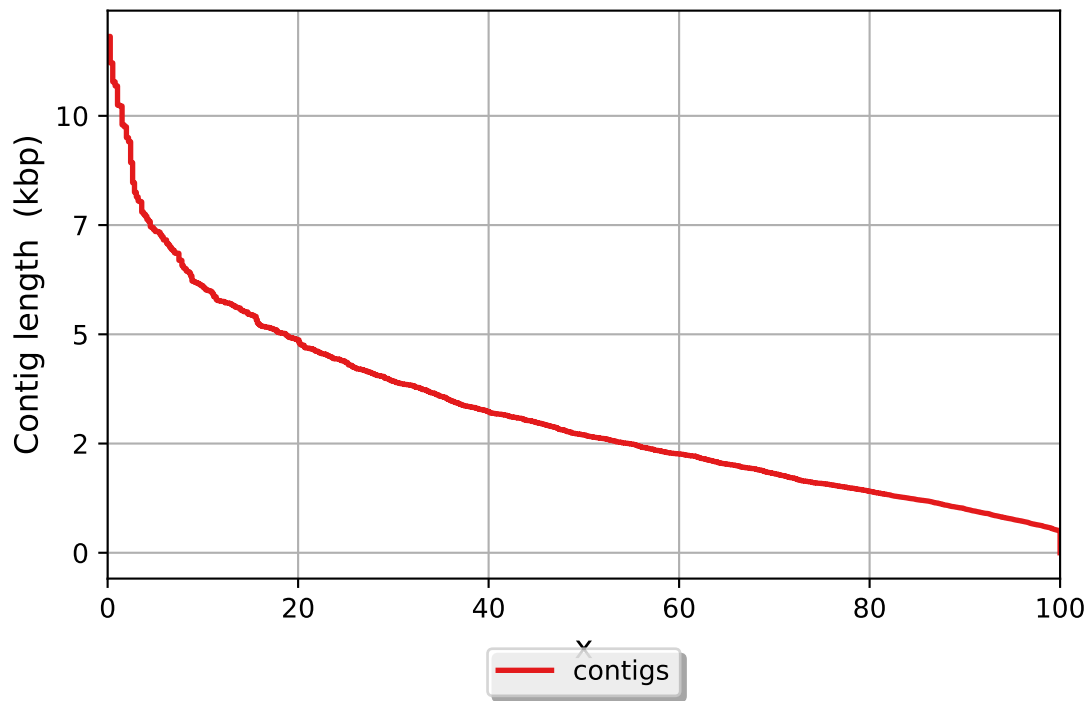
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

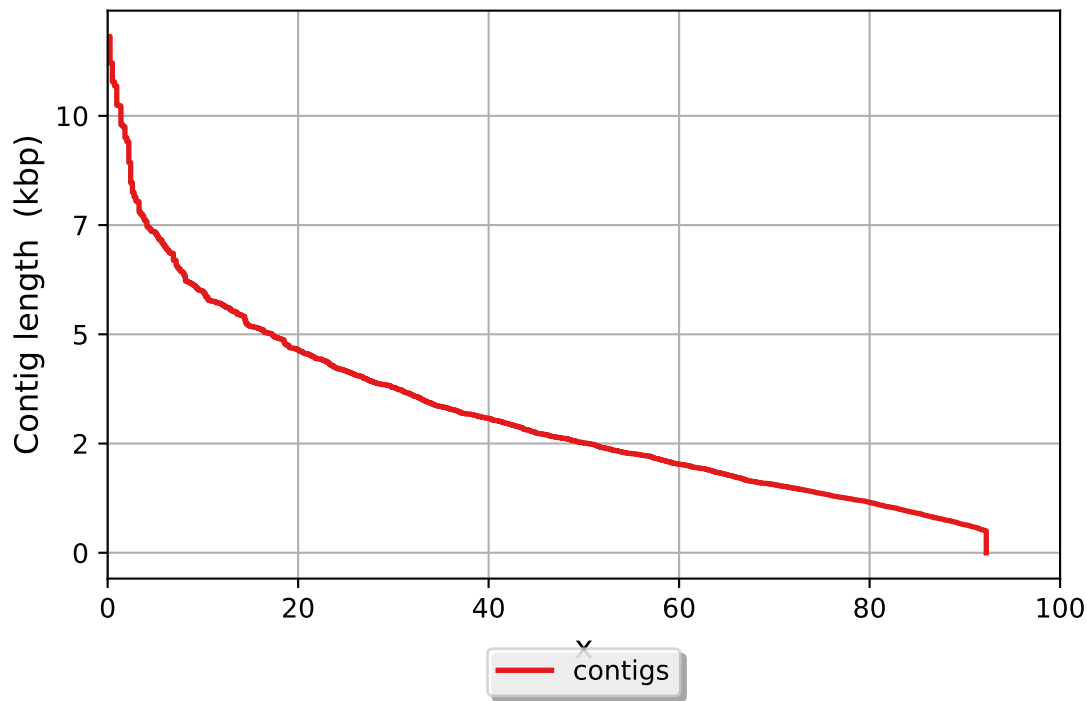
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	178
# N's	0

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).

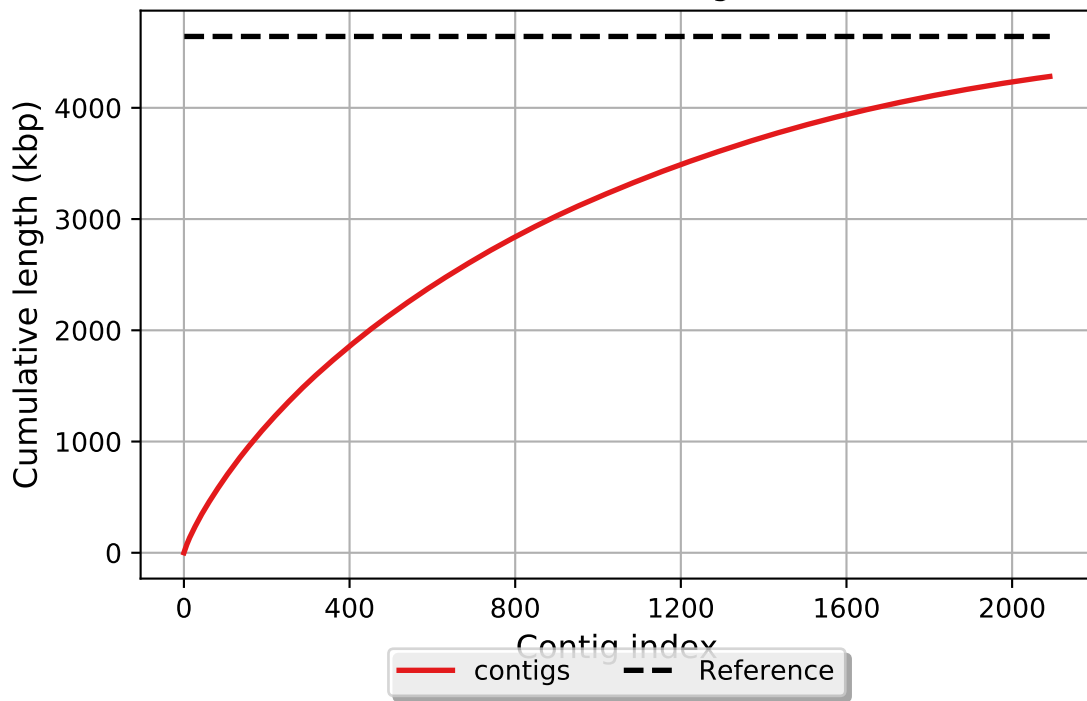
Nx

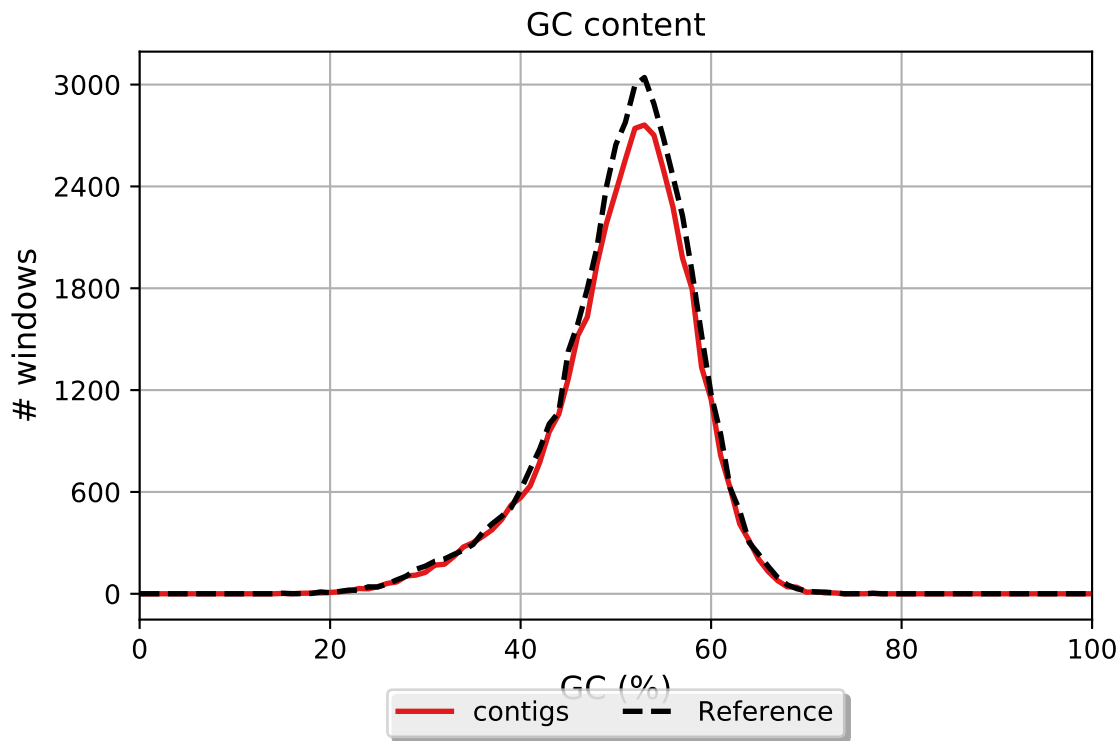


NGx

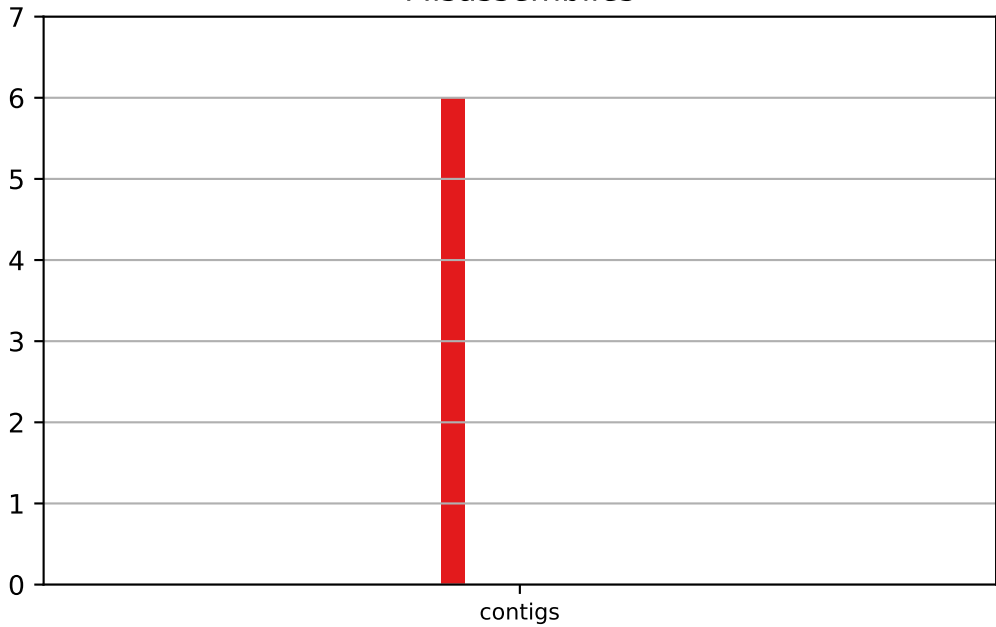


Cumulative length

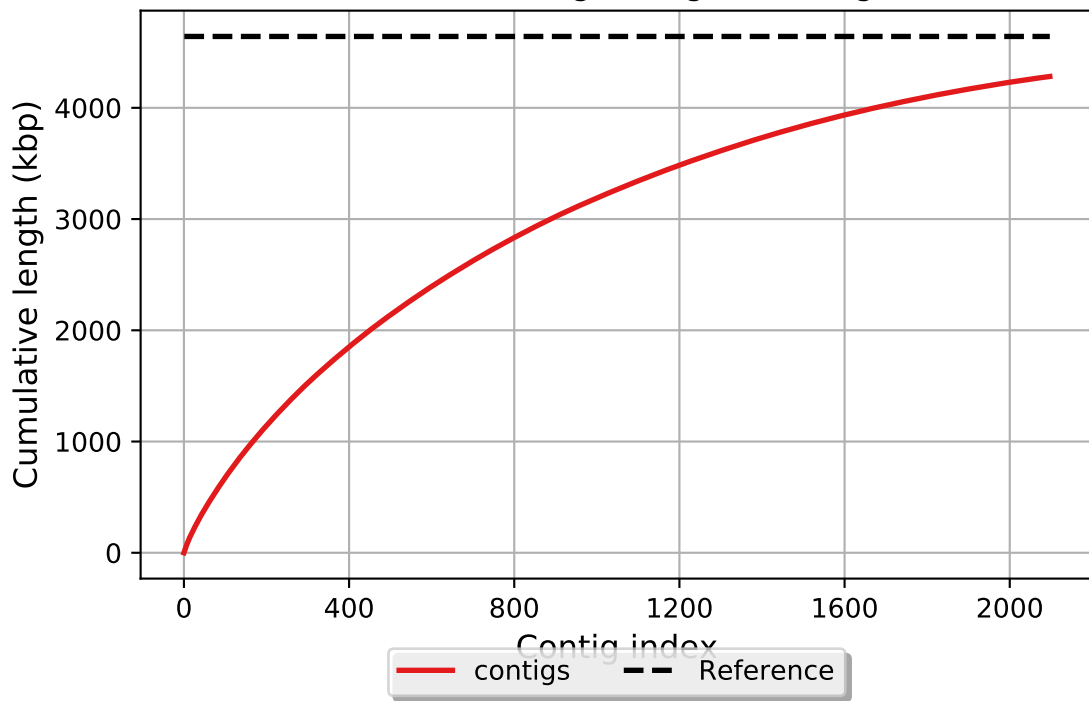




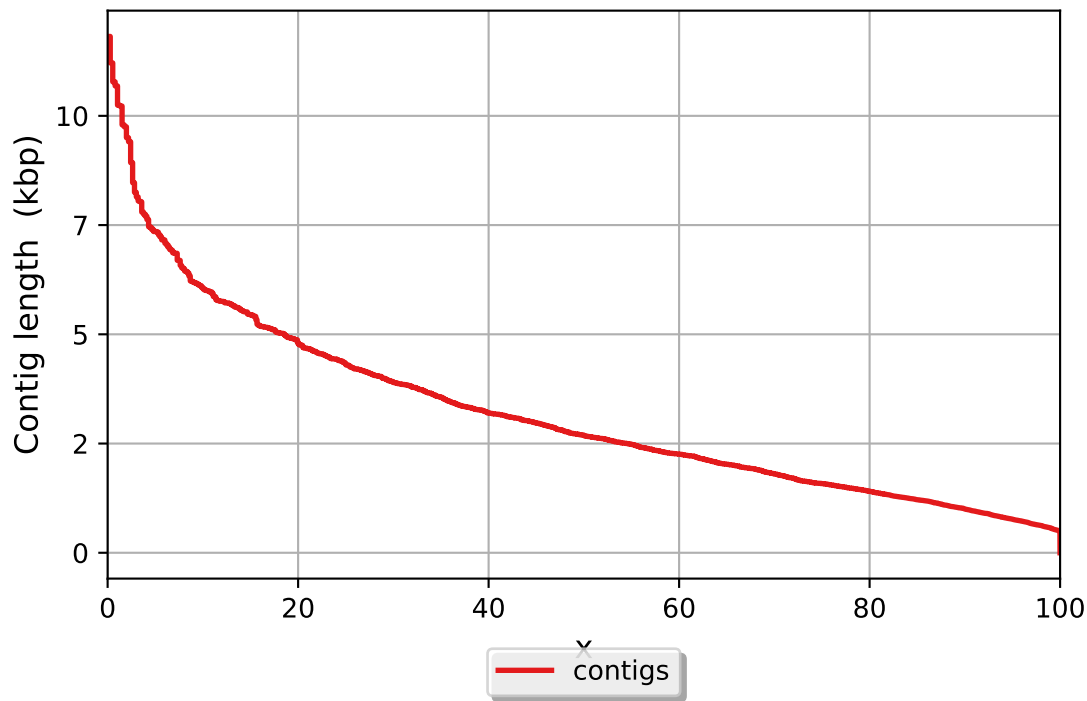
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

