

Report

	contigs
# contigs (≥ 0 bp)	240
# contigs (≥ 1000 bp)	105
# contigs (≥ 5000 bp)	77
# contigs (≥ 10000 bp)	74
# contigs (≥ 25000 bp)	66
# contigs (≥ 50000 bp)	48
Total length (≥ 0 bp)	9123427
Total length (≥ 1000 bp)	9068952
Total length (≥ 5000 bp)	9023066
Total length (≥ 10000 bp)	9000541
Total length (≥ 25000 bp)	8856332
Total length (≥ 50000 bp)	8233238
# contigs	142
Largest contig	600951
Total length	9093038
Reference length	9283304
N50	200817
N75	110783
L50	16
L75	31
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.558
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	550.65
# indels per 100 kbp	1.08
Largest alignment	600951
NA50	200817
NA75	110783
LA50	16
LA75	31

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
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	50381
# indels	99
# short indels	99
# long indels	0
Indels length	100

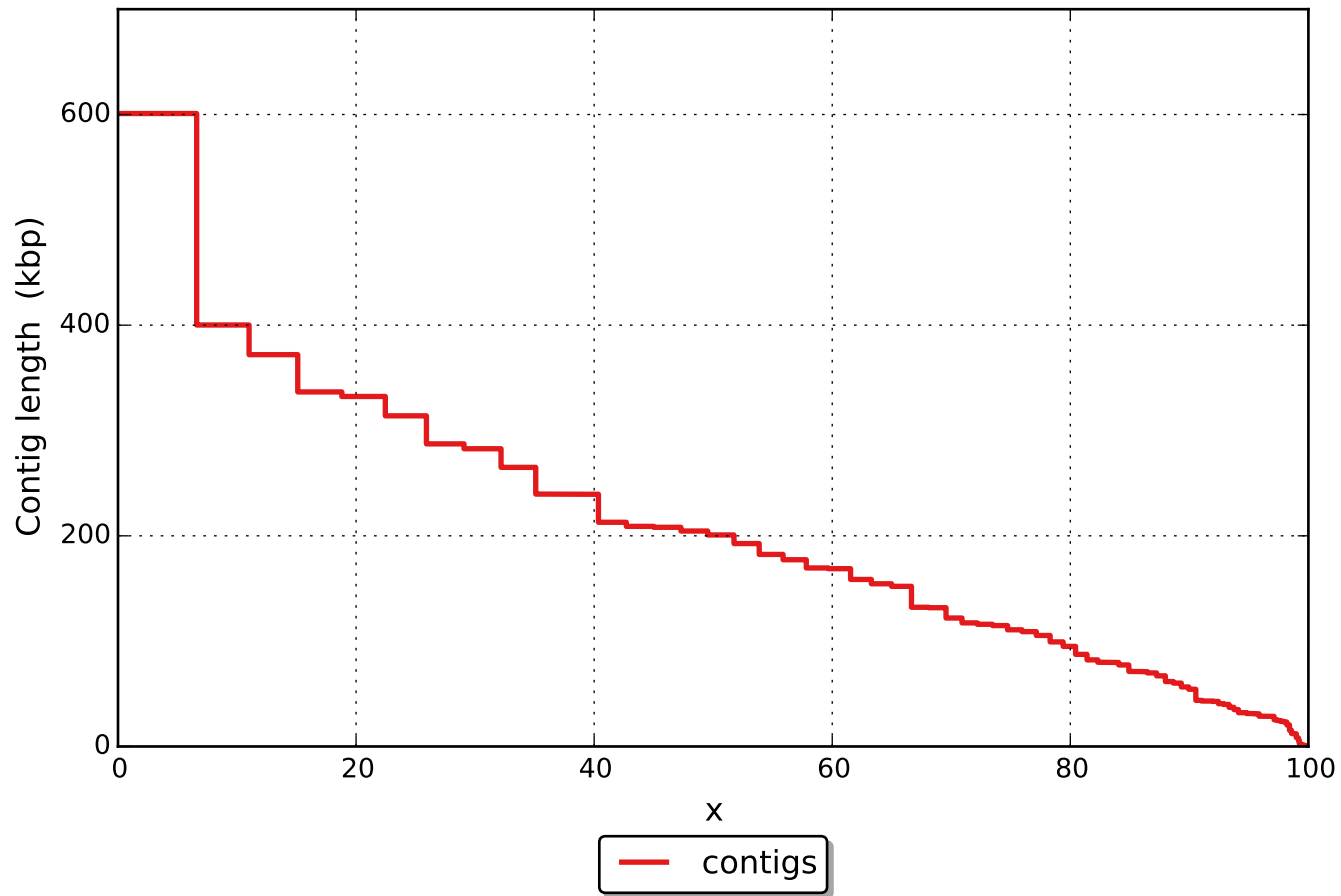
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

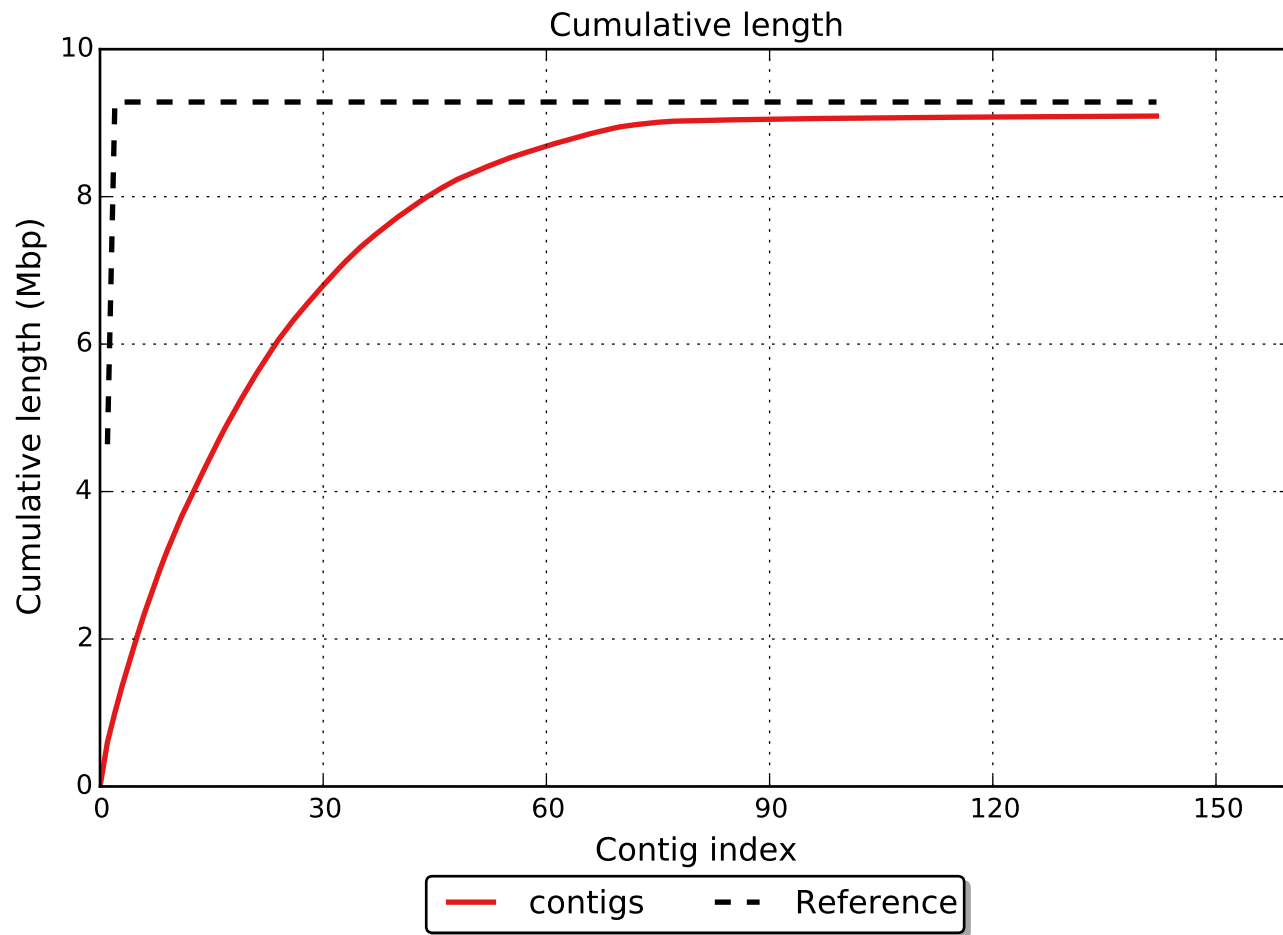
Unaligned report

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

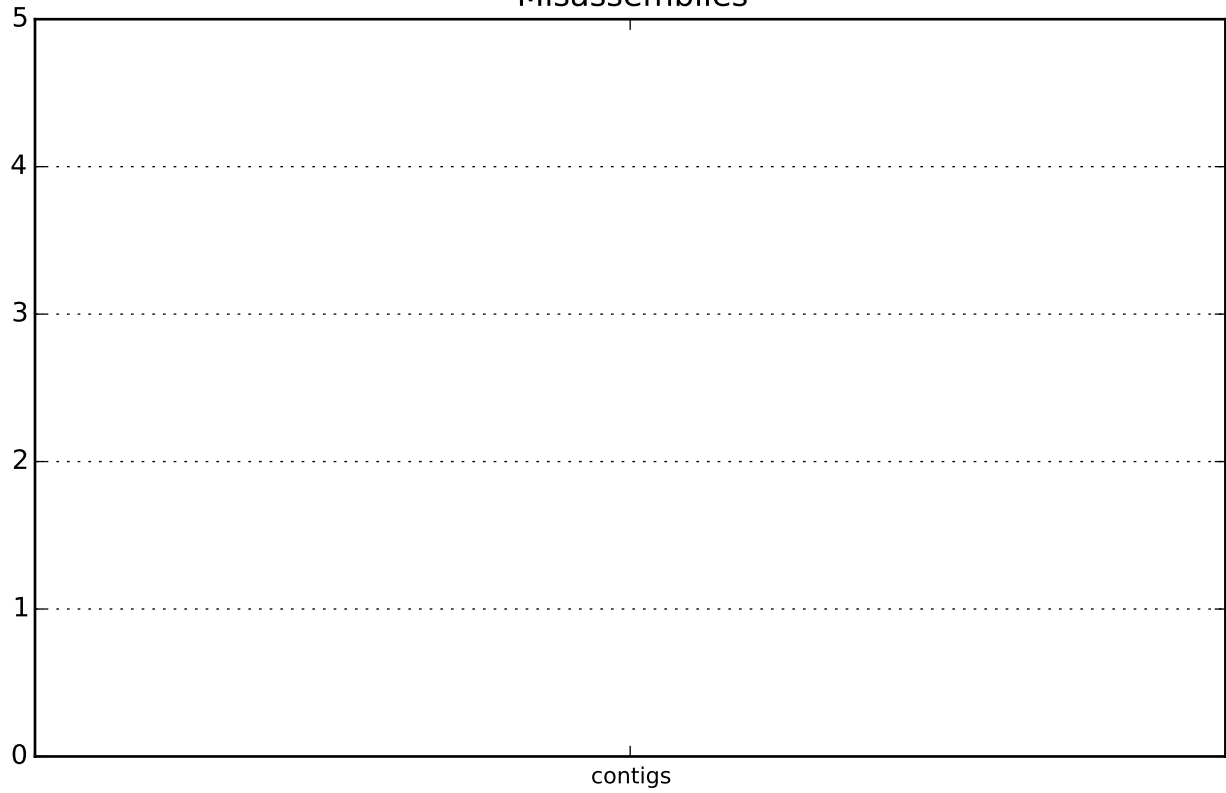
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

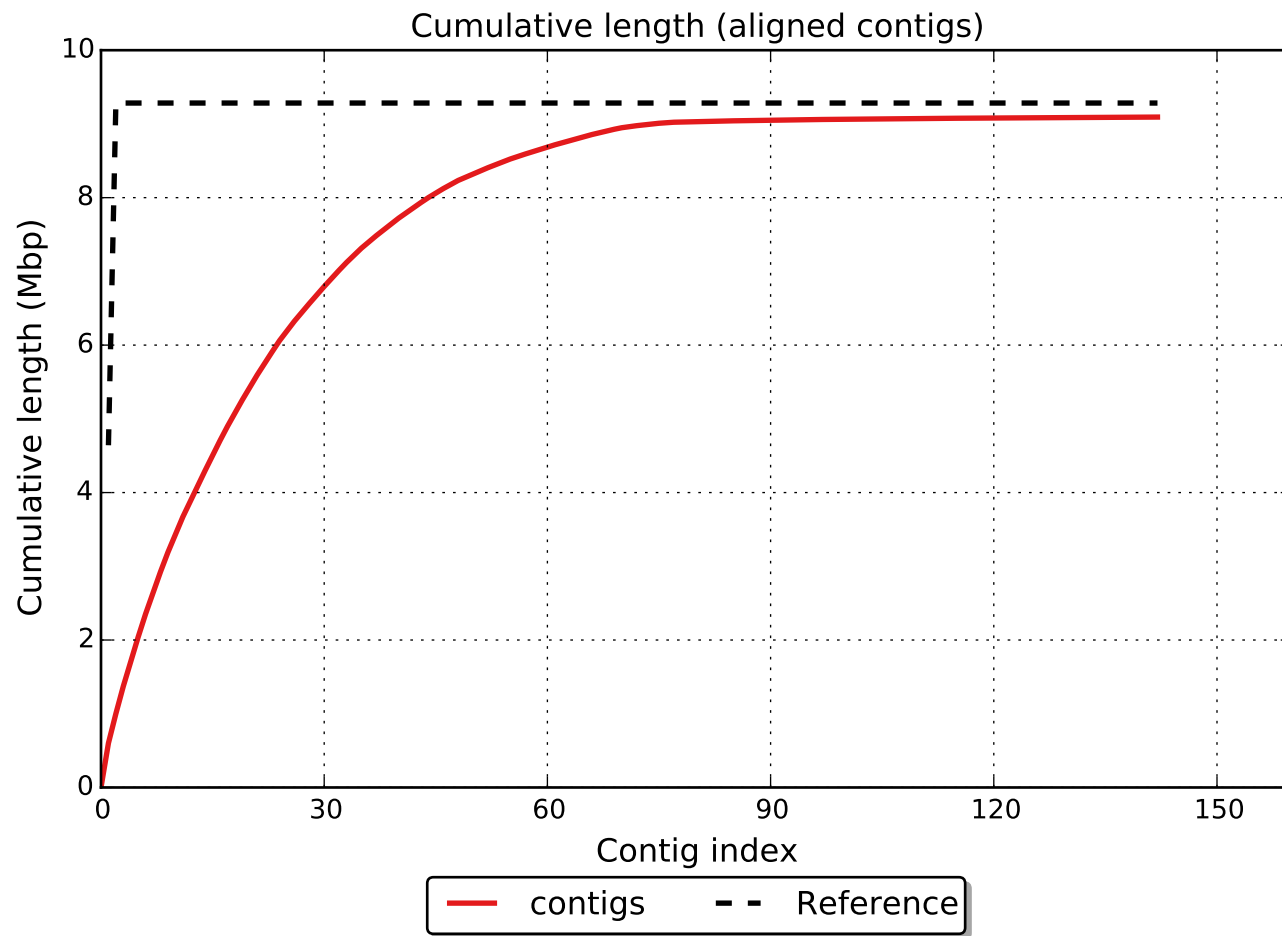
Nx





Misassemblies





NAx

