

Report

	final.contigs
# contigs (≥ 0 bp)	1079
# contigs (≥ 1000 bp)	621
# contigs (≥ 5000 bp)	460
# contigs (≥ 10000 bp)	326
# contigs (≥ 25000 bp)	125
# contigs (≥ 50000 bp)	26
Total length (≥ 0 bp)	9845565
Total length (≥ 1000 bp)	9680546
Total length (≥ 5000 bp)	9210191
Total length (≥ 10000 bp)	8266302
Total length (≥ 25000 bp)	5057686
Total length (≥ 50000 bp)	1702123
# contigs	660
Largest contig	88870
Total length	9707665
Reference length	9714864
N50	25875
N75	14236
L50	118
L75	245
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.416
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	33.10
# indels per 100 kbp	0.10
Largest alignment	88870
NA50	25875
NA75	14236
LA50	118
LA75	245

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

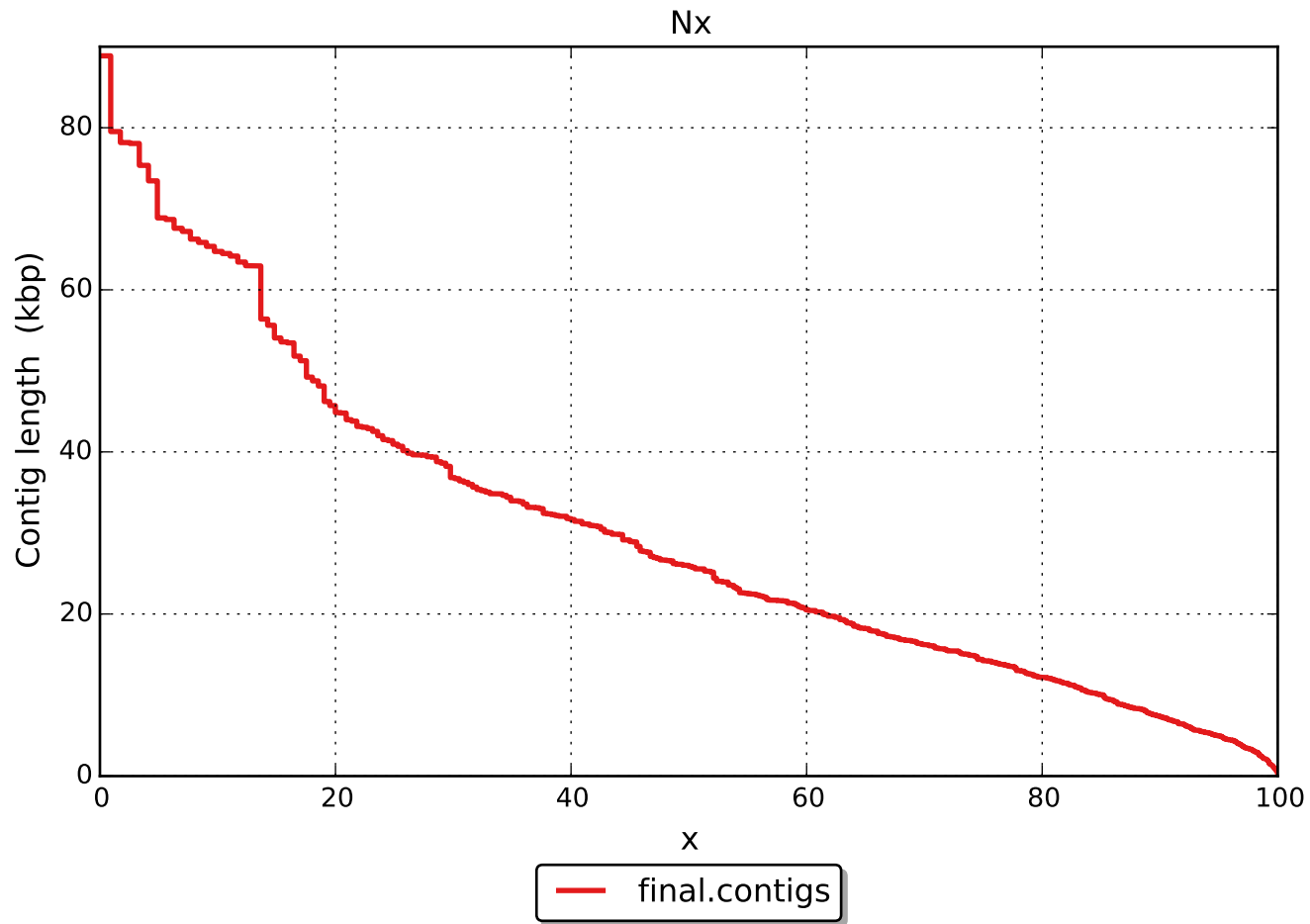
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	3197
# indels	10
# short indels	9
# long indels	1
Indels length	18

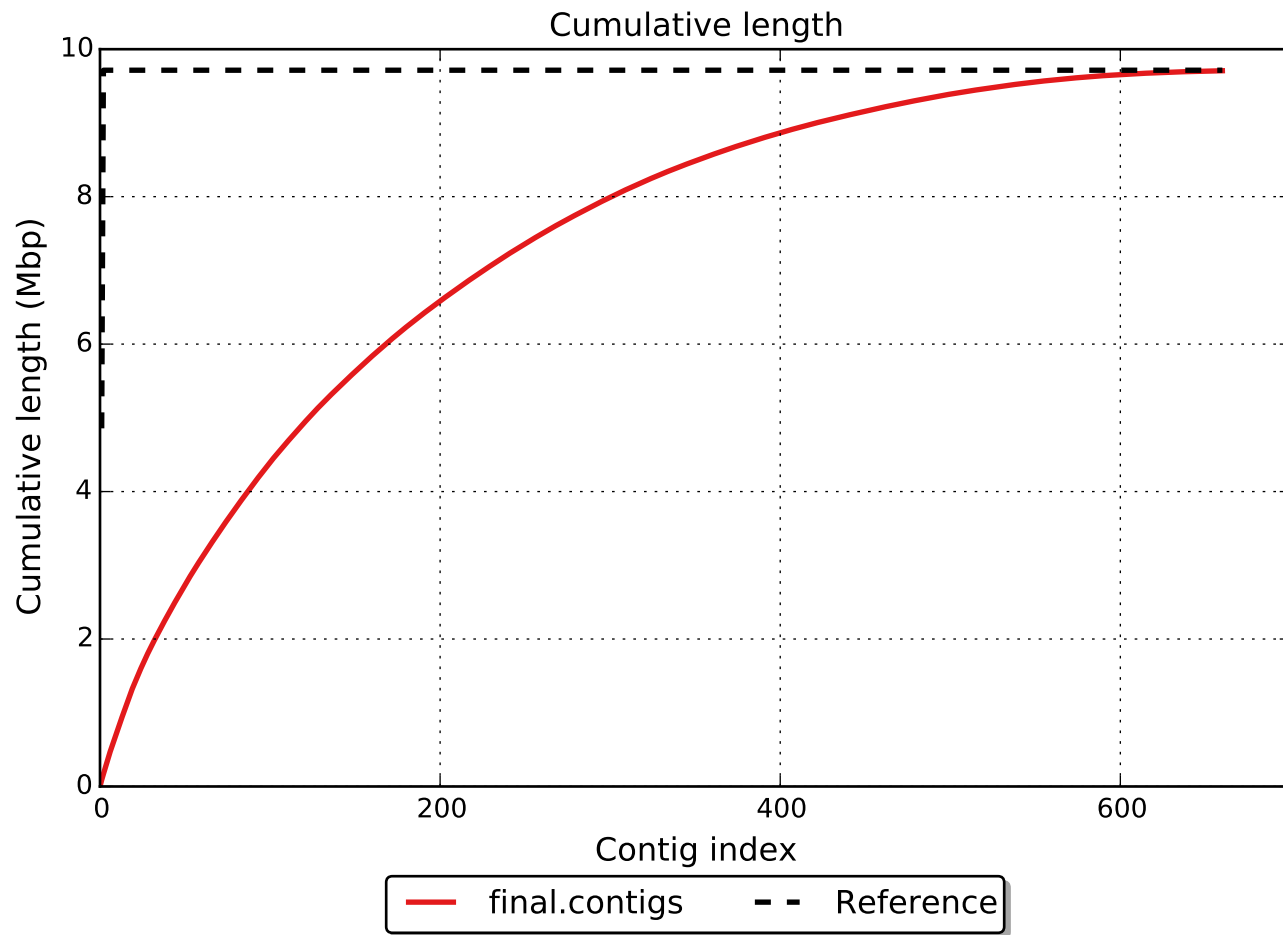
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.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).





Misassemblies

