

Report

	final.contigs
# contigs (≥ 0 bp)	1271
# contigs (≥ 1000 bp)	1074
# contigs (≥ 5000 bp)	668
# contigs (≥ 10000 bp)	337
# contigs (≥ 25000 bp)	63
# contigs (≥ 50000 bp)	2
Total length (≥ 0 bp)	9768521
Total length (≥ 1000 bp)	9680258
Total length (≥ 5000 bp)	8599122
Total length (≥ 10000 bp)	6259300
Total length (≥ 25000 bp)	2132651
Total length (≥ 50000 bp)	101589
# contigs	1139
Largest contig	51551
Total length	9727747
Reference length	9714864
N50	13432
N75	7496
L50	215
L75	458
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	99.404
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.48
# indels per 100 kbp	0.00
Largest alignment	51551
NA50	13432
NA75	7496
LA50	215
LA75	458

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

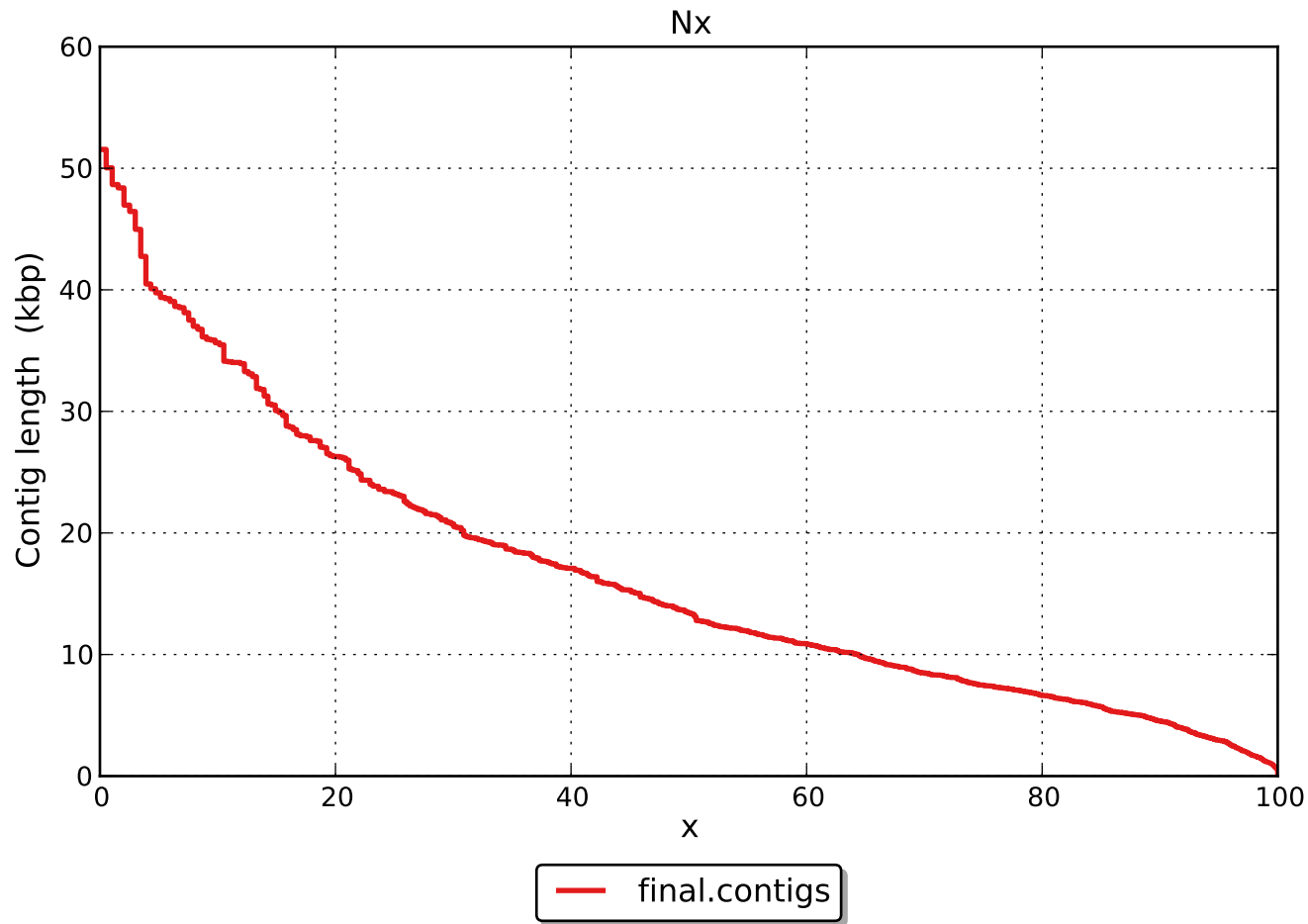
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	143
# indels	0
# short indels	0
# long indels	0
Indels length	0

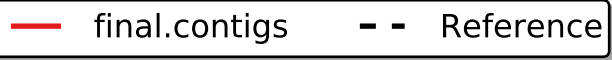
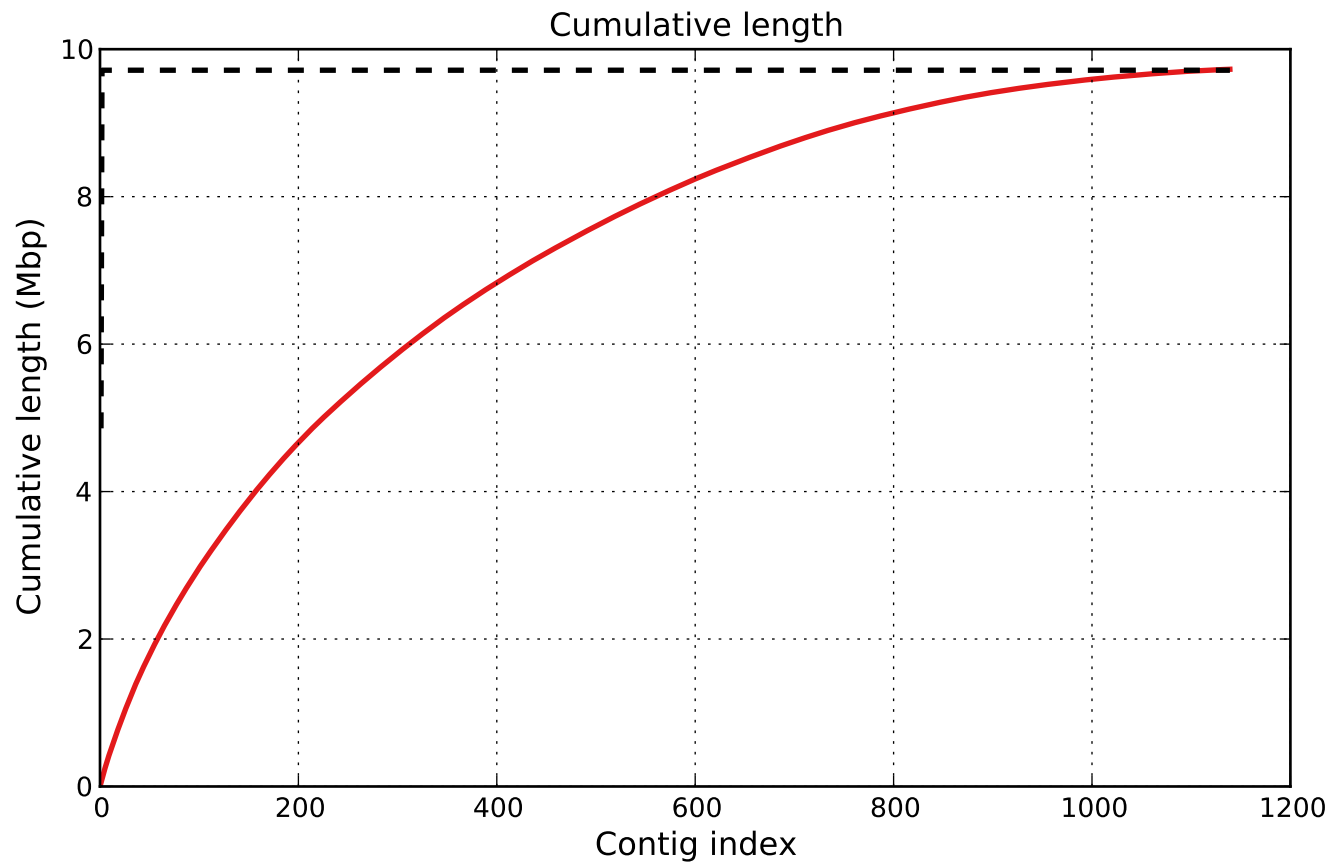
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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



