

Report

	final.contigs
# contigs (≥ 0 bp)	4844
# contigs (≥ 1000 bp)	1322
# contigs (≥ 5000 bp)	213
# contigs (≥ 10000 bp)	21
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	5746513
Total length (≥ 1000 bp)	4125554
Total length (≥ 5000 bp)	1529024
Total length (≥ 10000 bp)	254666
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	2528
Largest contig	21375
Total length	4928247
Reference length	9283304
N50	3228
N75	1573
L50	448
L75	983
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	51.860
Duplication ratio	1.024
# N's per 100 kbp	0.00
# mismatches per 100 kbp	415.03
# indels per 100 kbp	0.04
Largest alignment	21375
NA50	3228
NA75	1573
LA50	448
LA75	983

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

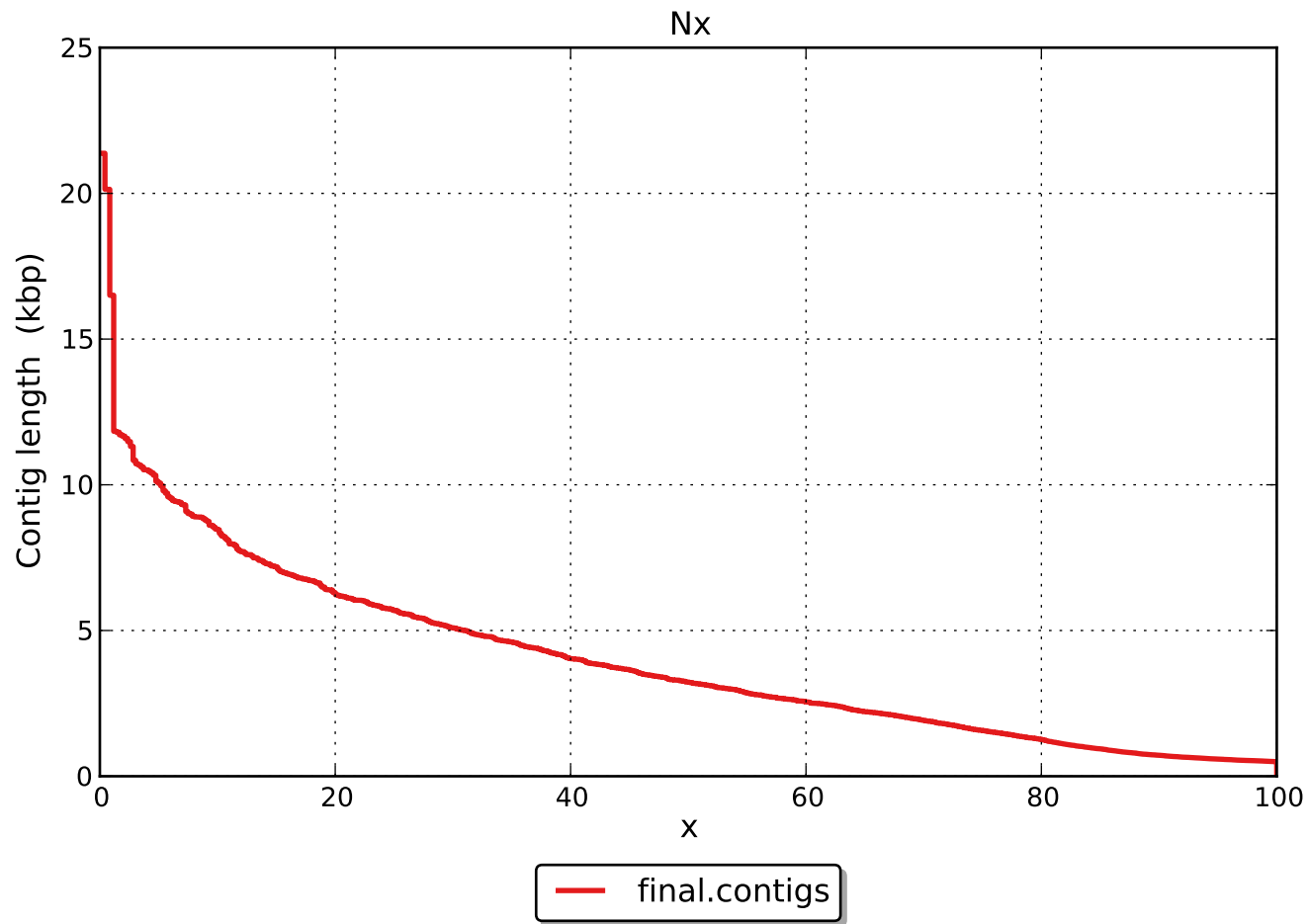
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	19981
# indels	2
# short indels	2
# long indels	0
Indels length	2

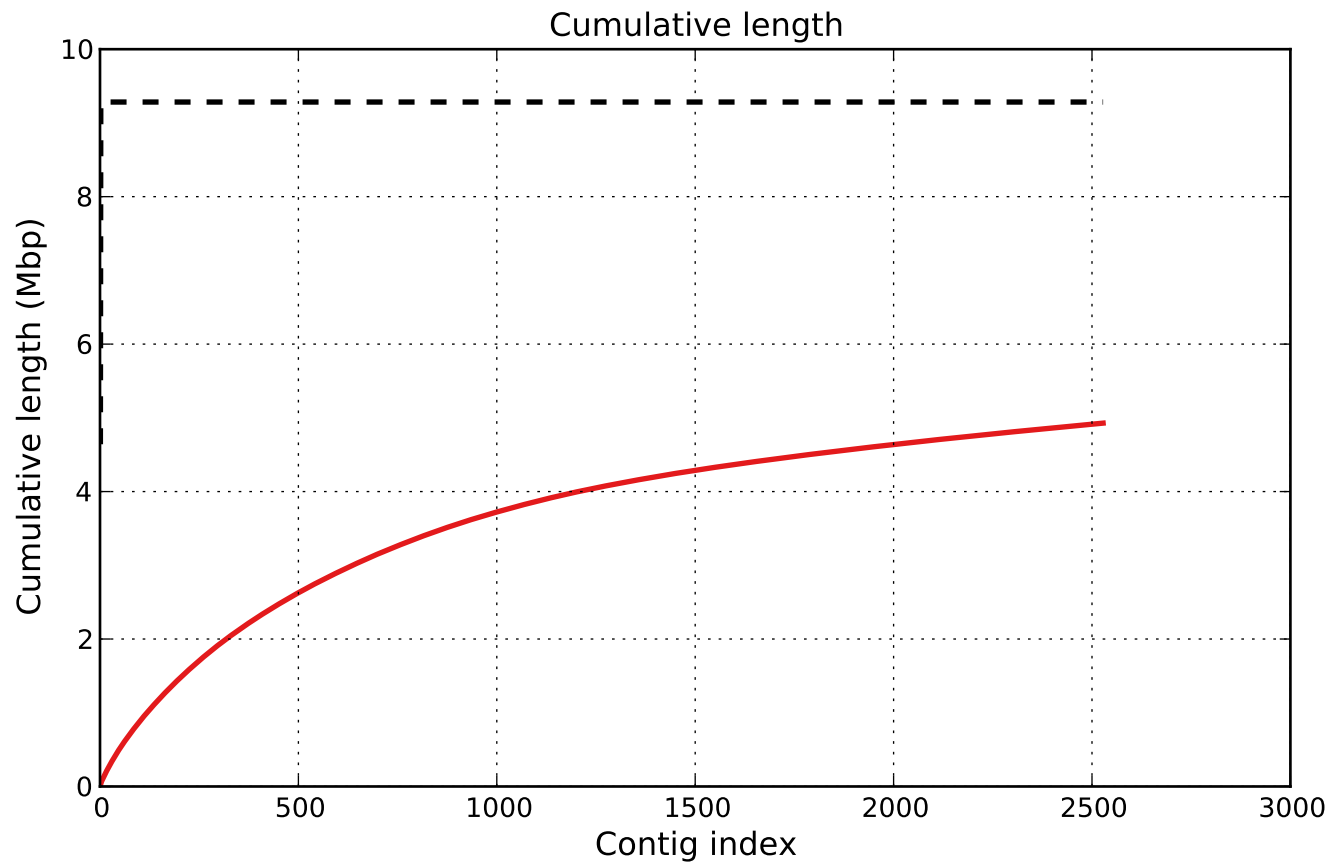
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Unaligned report

	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

