

Report

	final.contigs
# contigs (≥ 0 bp)	8615
# contigs (≥ 1000 bp)	1807
# contigs (≥ 5000 bp)	33
# contigs (≥ 10000 bp)	3
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	7141500
Total length (≥ 1000 bp)	3630565
Total length (≥ 5000 bp)	215889
Total length (≥ 10000 bp)	31260
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	5038
Largest contig	11097
Total length	5832055
Reference length	9714864
N50	1379
N75	765
L50	1190
L75	2664
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	85.433
Duplication ratio	1.065
# N's per 100 kbp	0.00
# mismatches per 100 kbp	545.06
# indels per 100 kbp	0.05
Largest alignment	11097
NA50	1379
NA75	765
LA50	1190
LA75	2664

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

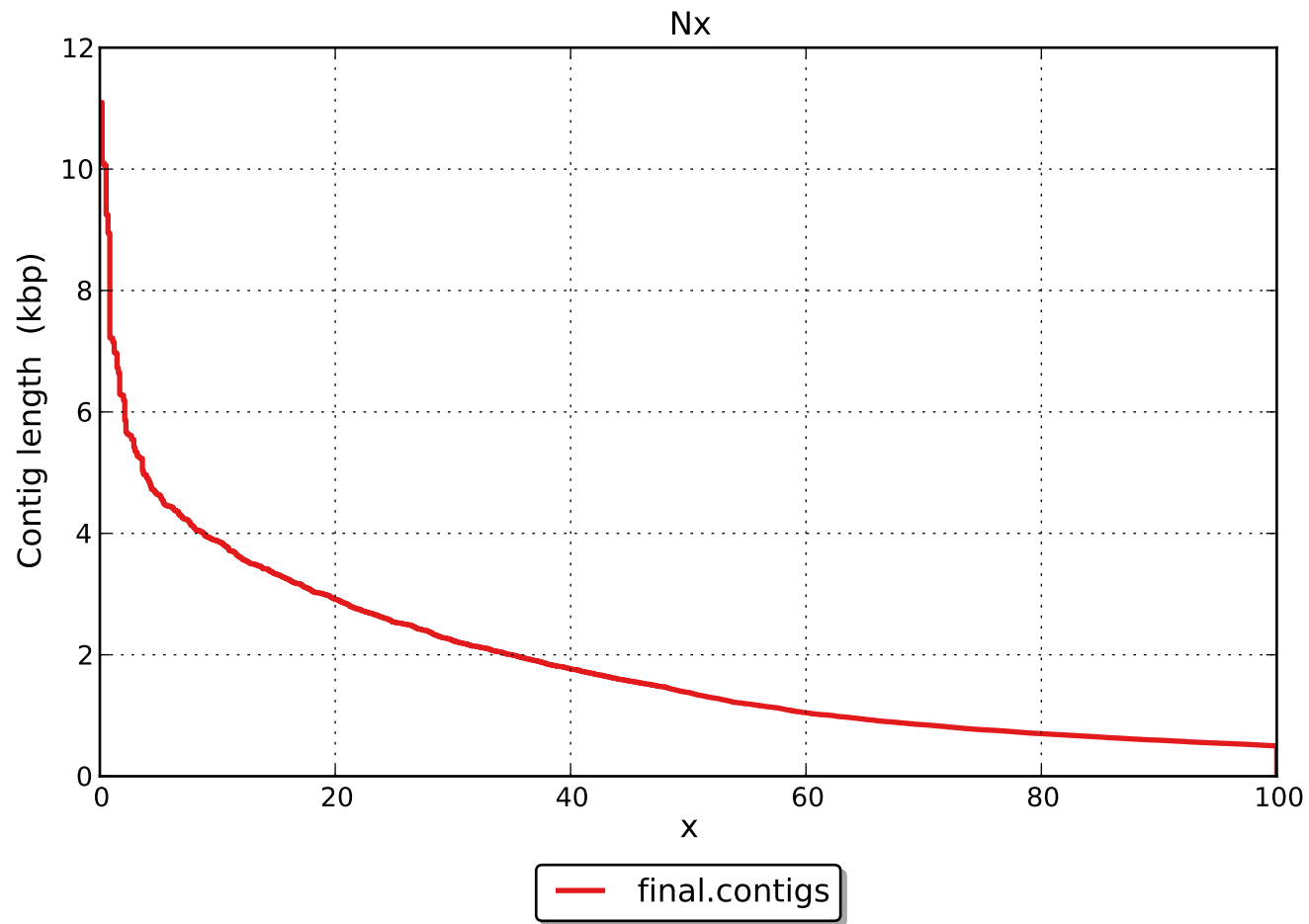
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	45238
# indels	4
# short indels	4
# long indels	0
Indels length	4

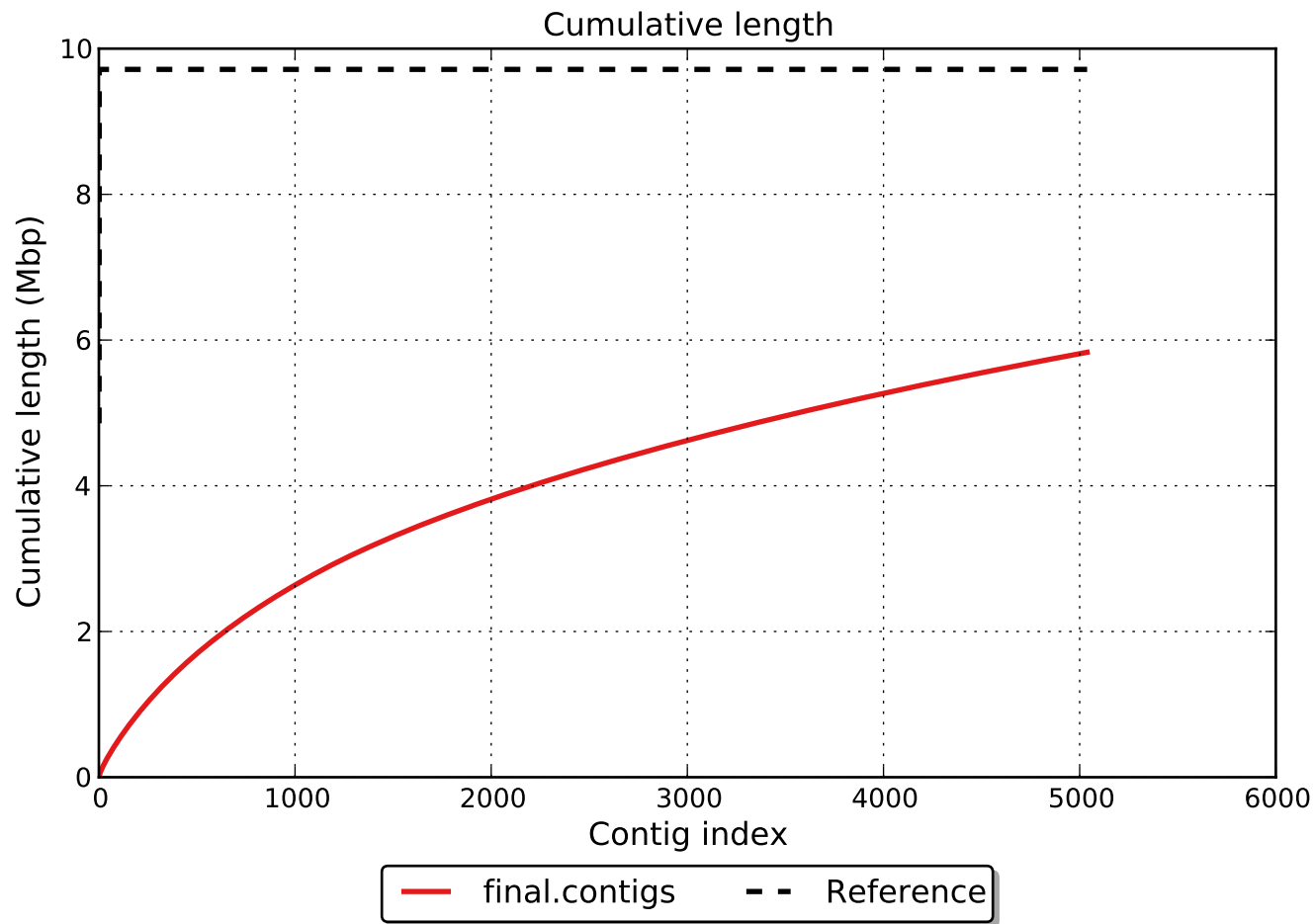
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Unaligned report

	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

