

Report

	final.contigs
# contigs (≥ 0 bp)	962
# contigs (≥ 1000 bp)	797
# contigs (≥ 5000 bp)	544
# contigs (≥ 10000 bp)	342
# contigs (≥ 25000 bp)	102
# contigs (≥ 50000 bp)	13
Total length (≥ 0 bp)	9744433
Total length (≥ 1000 bp)	9670015
Total length (≥ 5000 bp)	8978208
Total length (≥ 10000 bp)	7495850
Total length (≥ 25000 bp)	3759221
Total length (≥ 50000 bp)	742484
# contigs	857
Largest contig	66131
Total length	9713900
Reference length	9714864
N50	19088
N75	10567
L50	153
L75	322
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	99.305
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.53
# indels per 100 kbp	0.00
Largest alignment	66131
NA50	19088
NA75	10567
LA50	153
LA75	322

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

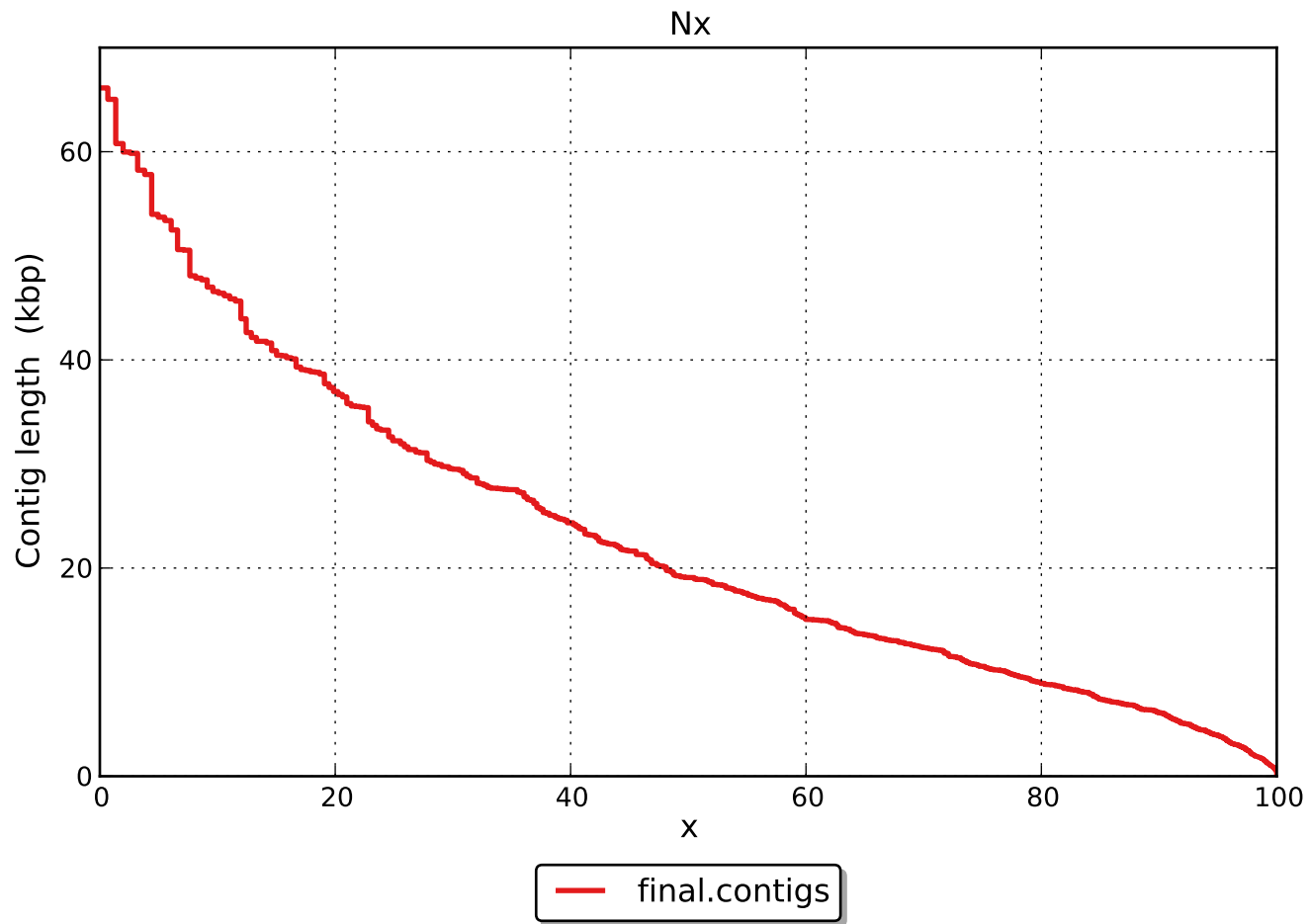
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	51
# indels	0
# short indels	0
# long indels	0
Indels length	0

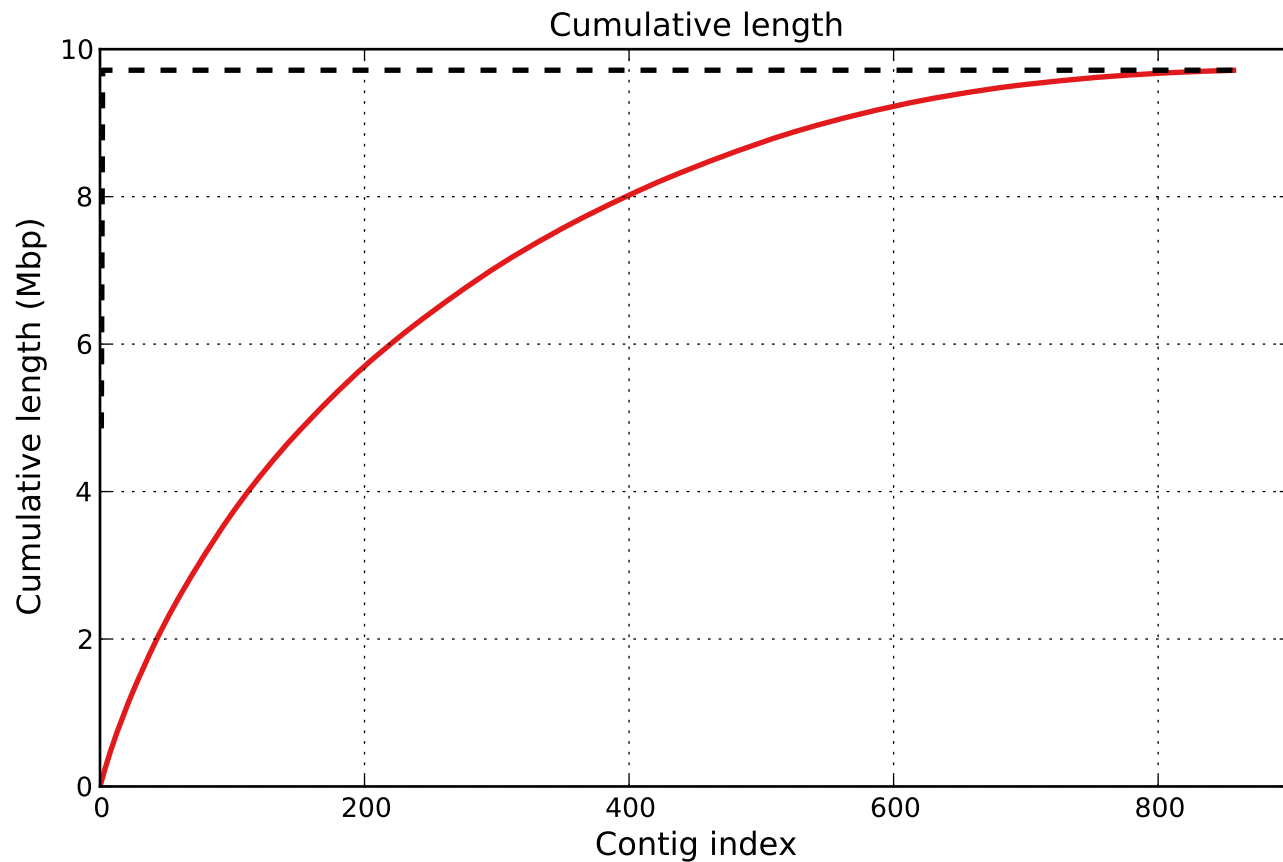
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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).

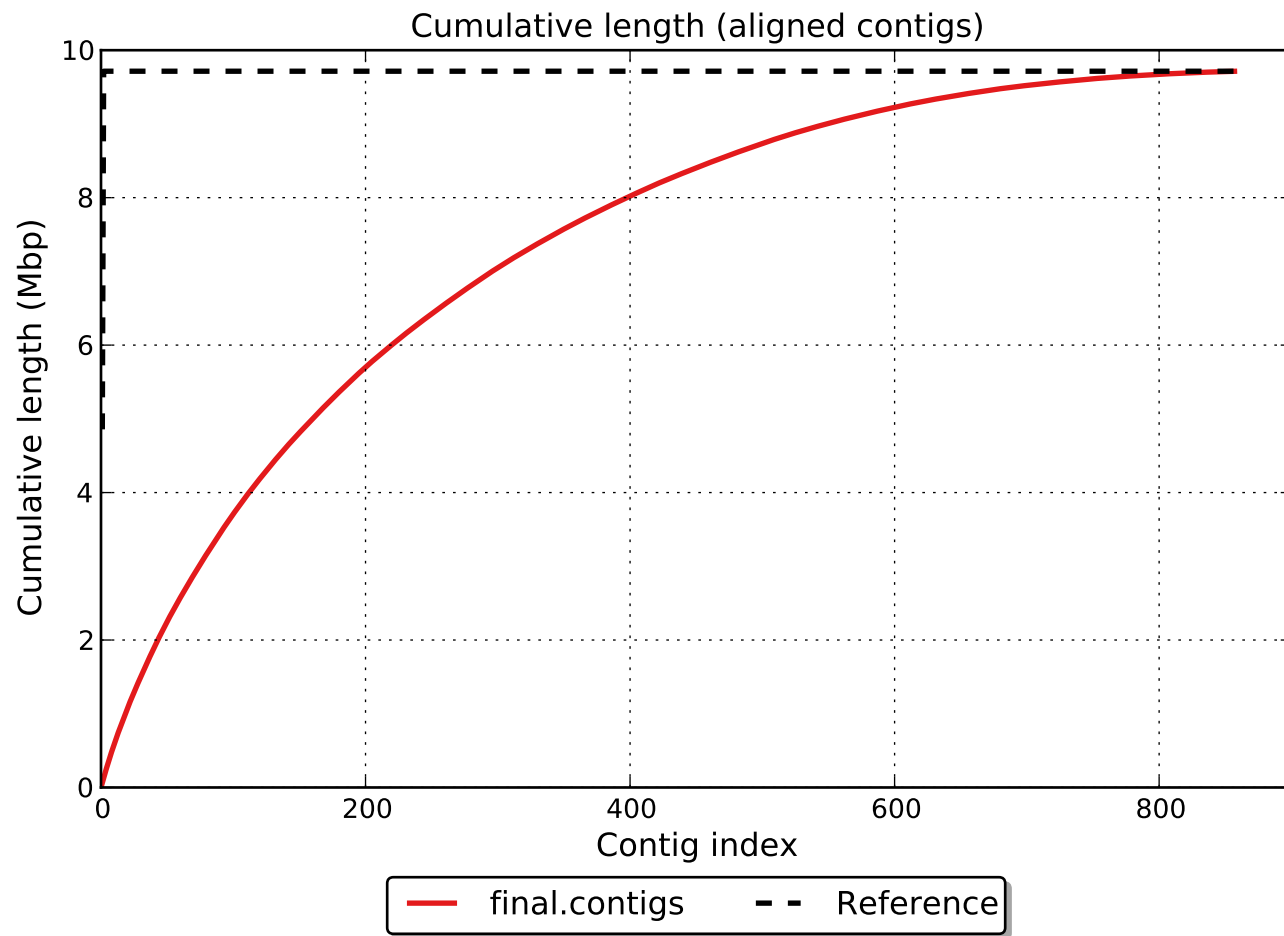




— final.contigs - - Reference

Misassemblies





NAx

