

Report

	final.contigs
# contigs (≥ 0 bp)	13917
# contigs (≥ 1000 bp)	2993
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	10292436
Total length (≥ 1000 bp)	4497321
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	8414
Largest contig	4818
Total length	8325679
Reference length	9714864
N50	1052
N75	748
L50	2668
L75	5009
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	3459
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	112
Genome fraction (%)	83.949
Duplication ratio	1.068
# N's per 100 kbp	0.00
# mismatches per 100 kbp	182.74
# indels per 100 kbp	0.27
Largest alignment	4818
NA50	1052
NA75	748
LA50	2668
LA75	5010

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	4
# relocations	2
# translocations	0
# inversions	1
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	3459
# local misassemblies	0
# mismatches	14903
# indels	22
# short indels	22
# long indels	0
Indels length	22

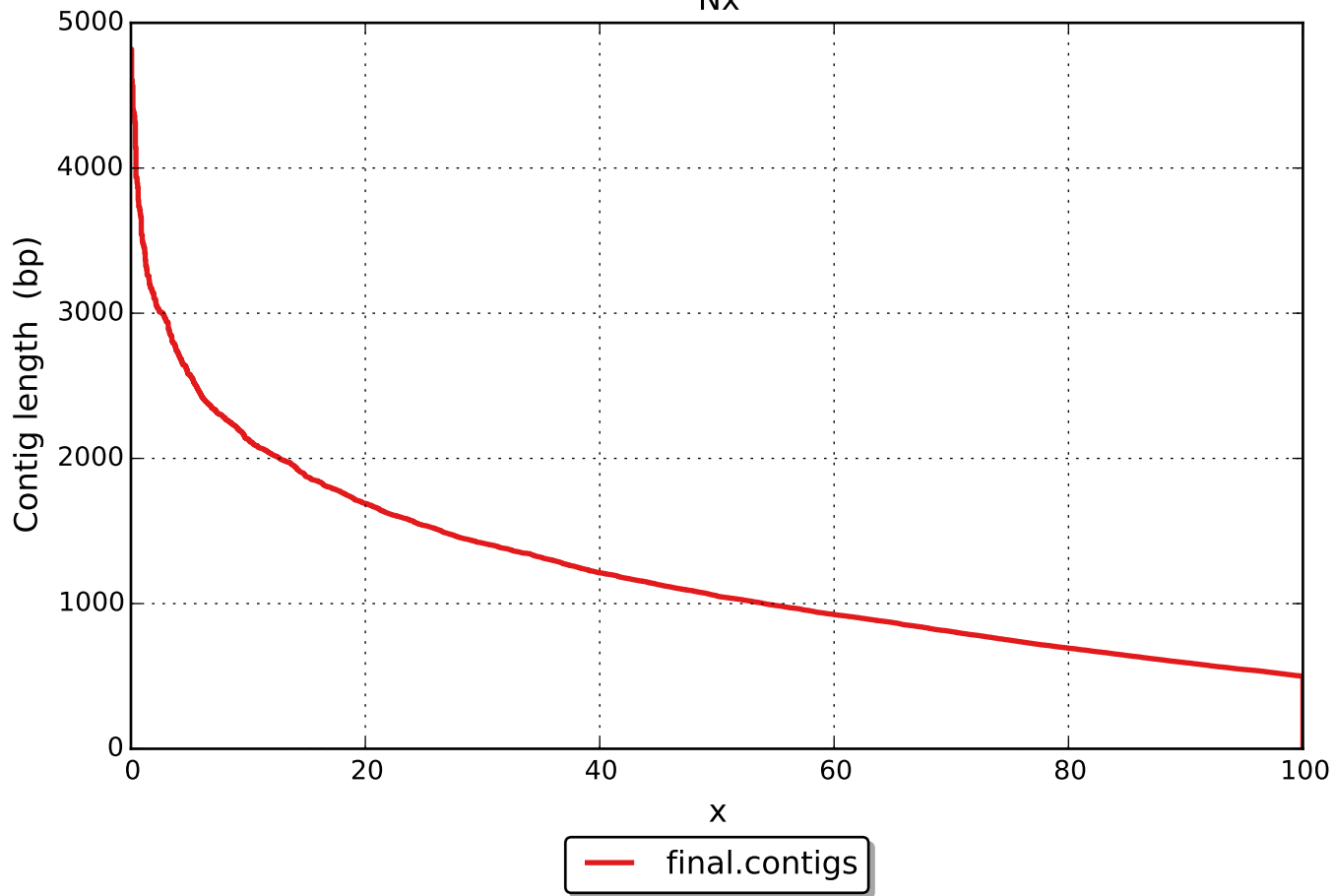
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

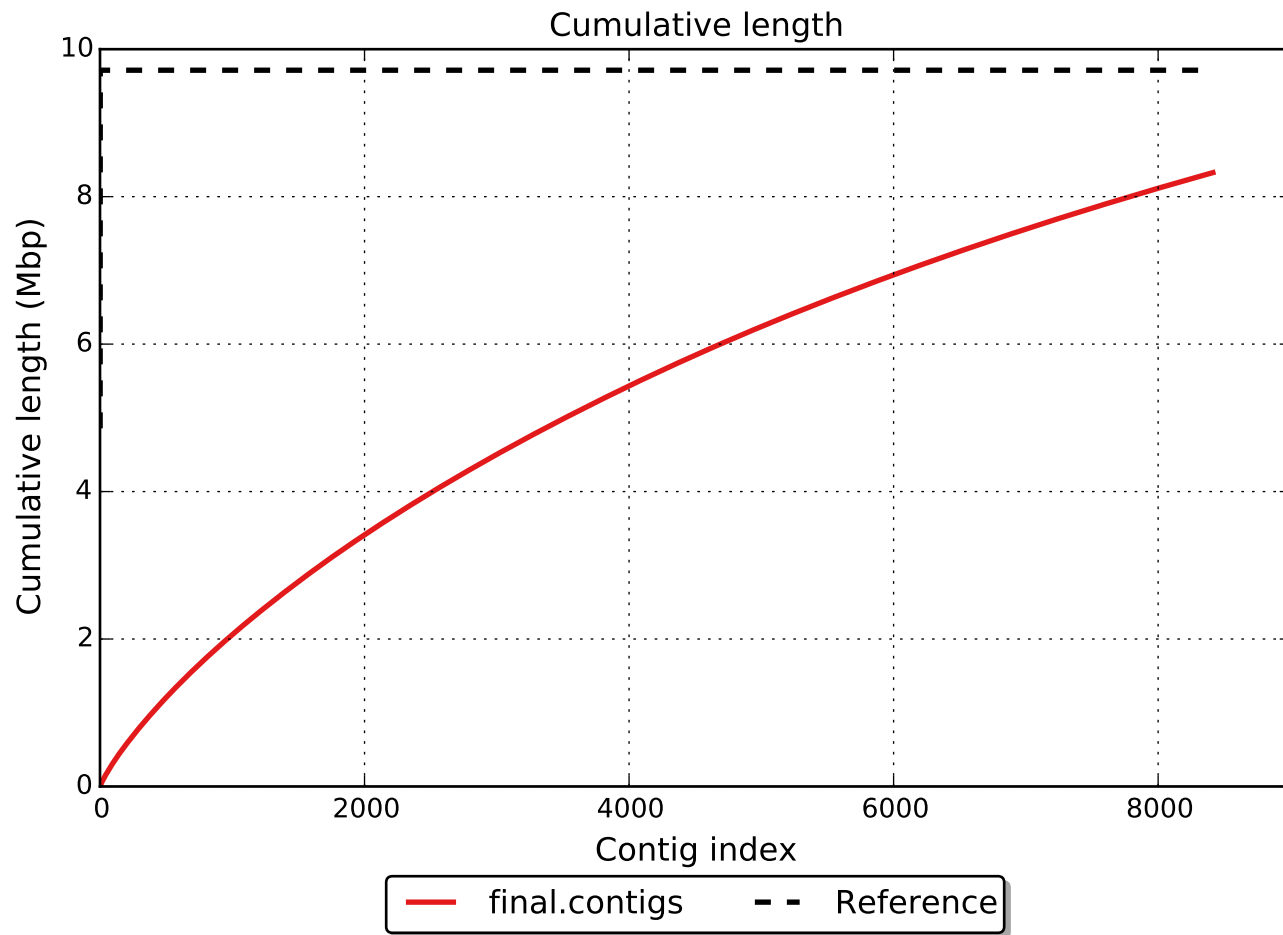
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	112
# N's	0

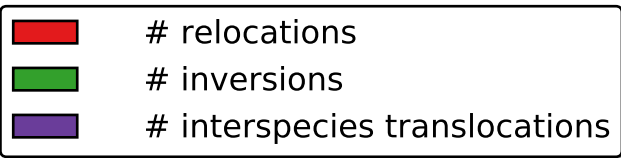
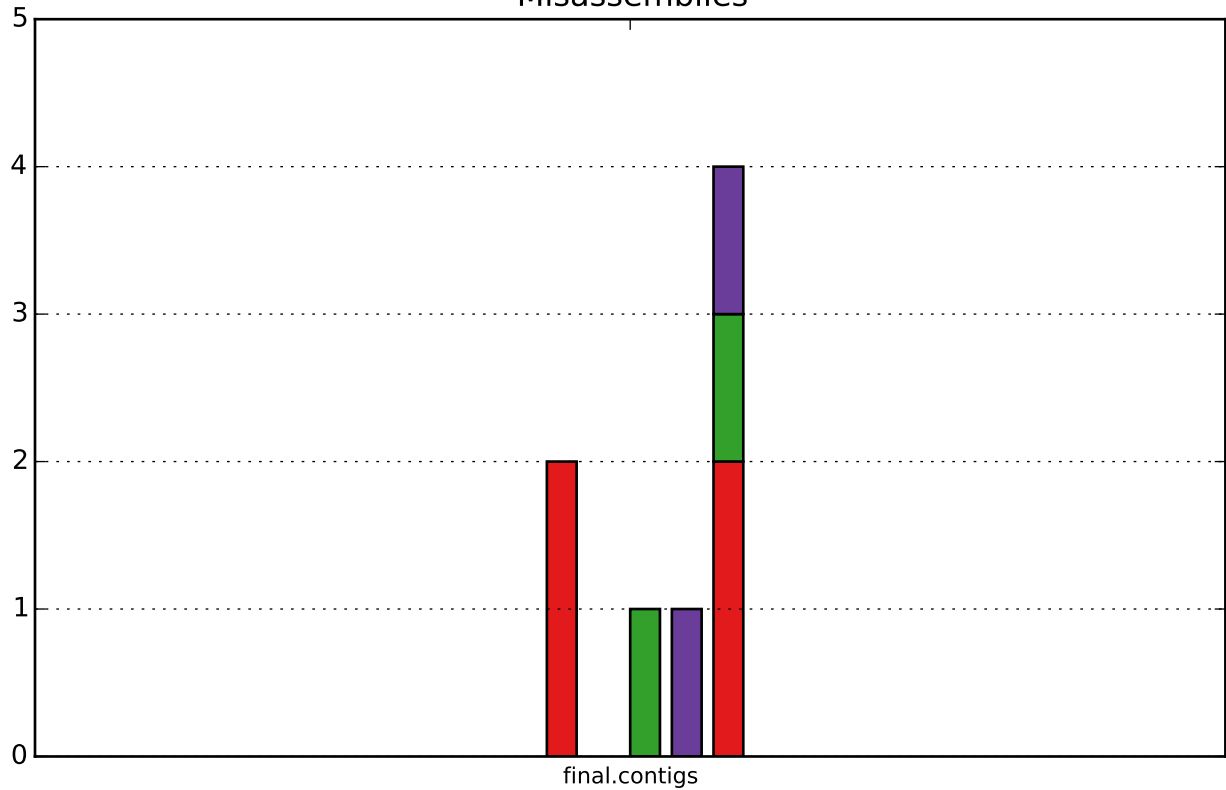
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

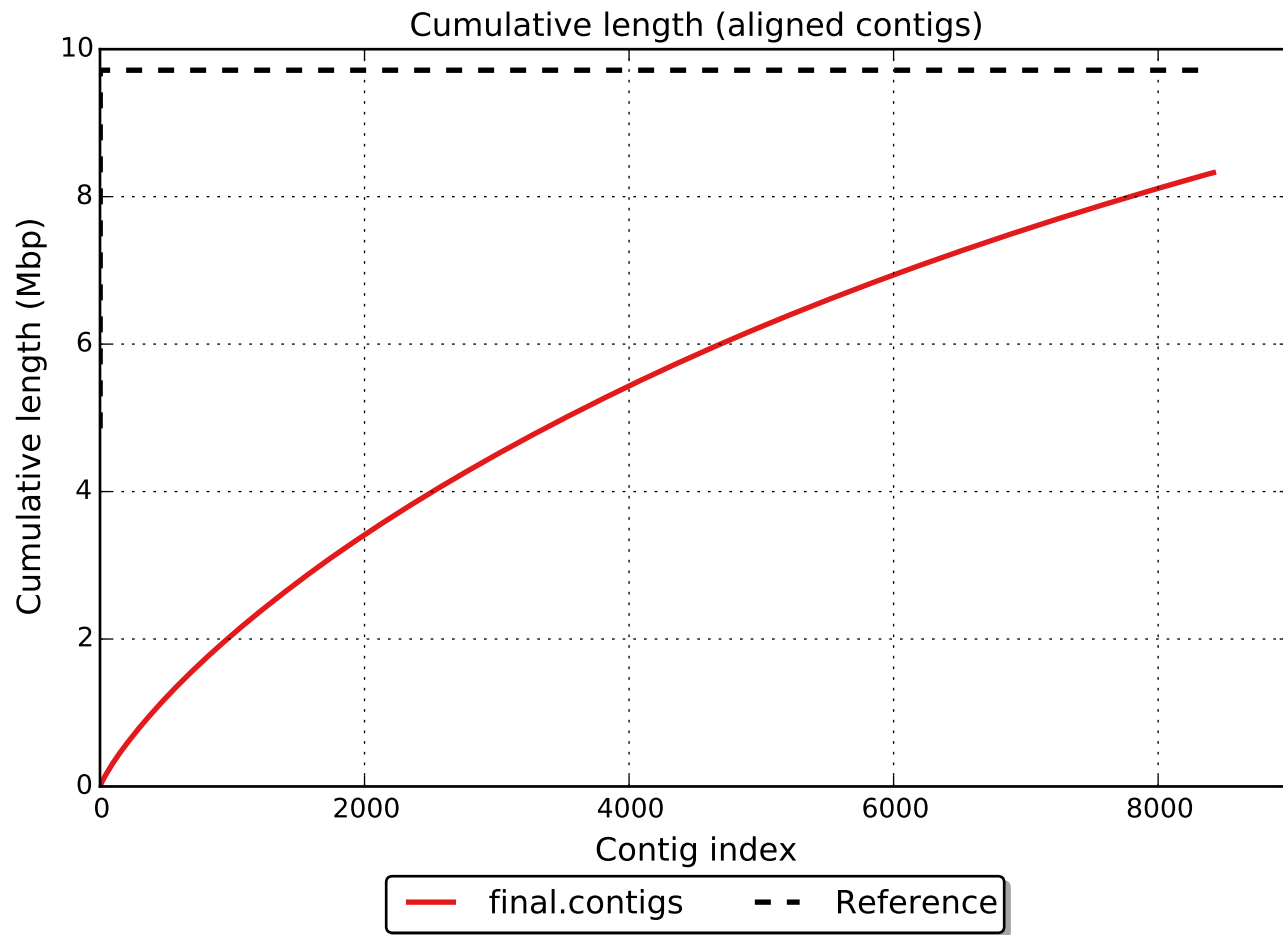
Nx





Misassemblies





NAx

