

Report

	final.contigs
# contigs (≥ 0 bp)	5424
# contigs (≥ 1000 bp)	1459
# contigs (≥ 5000 bp)	204
# contigs (≥ 10000 bp)	18
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	5965847
Total length (≥ 1000 bp)	4390270
Total length (≥ 5000 bp)	1414964
Total length (≥ 10000 bp)	203284
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	2192
Largest contig	15182
Total length	4889604
Reference length	9714864
N50	3297
N75	1882
L50	461
L75	946
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	8223
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	49.468
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	376.32
# indels per 100 kbp	0.12
Largest alignment	15182
NA50	3297
NA75	1876
LA50	461
LA75	947

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

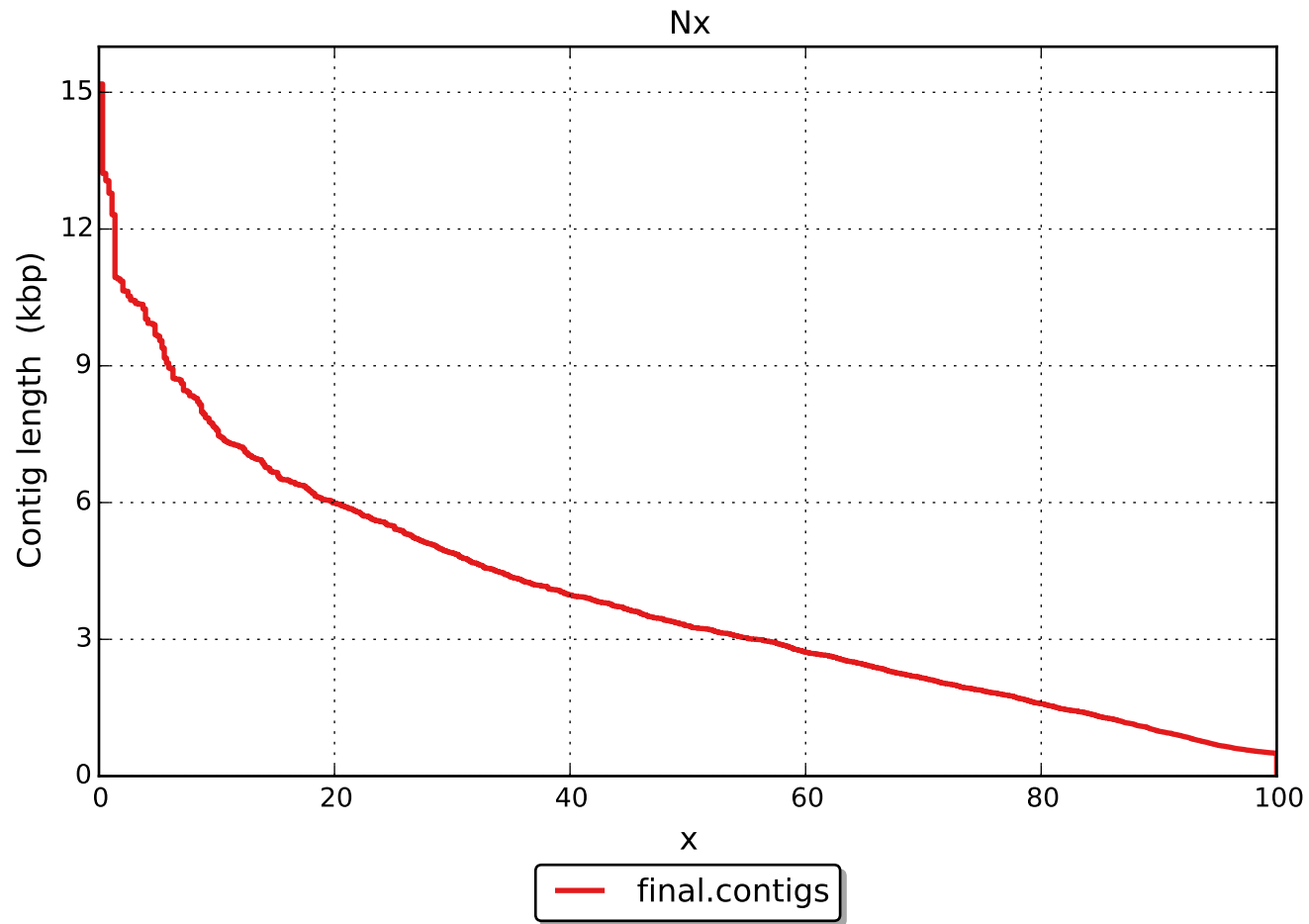
	final.contigs
# misassemblies	2
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	8223
# local misassemblies	2
# mismatches	18085
# indels	6
# short indels	6
# long indels	0
Indels length	9

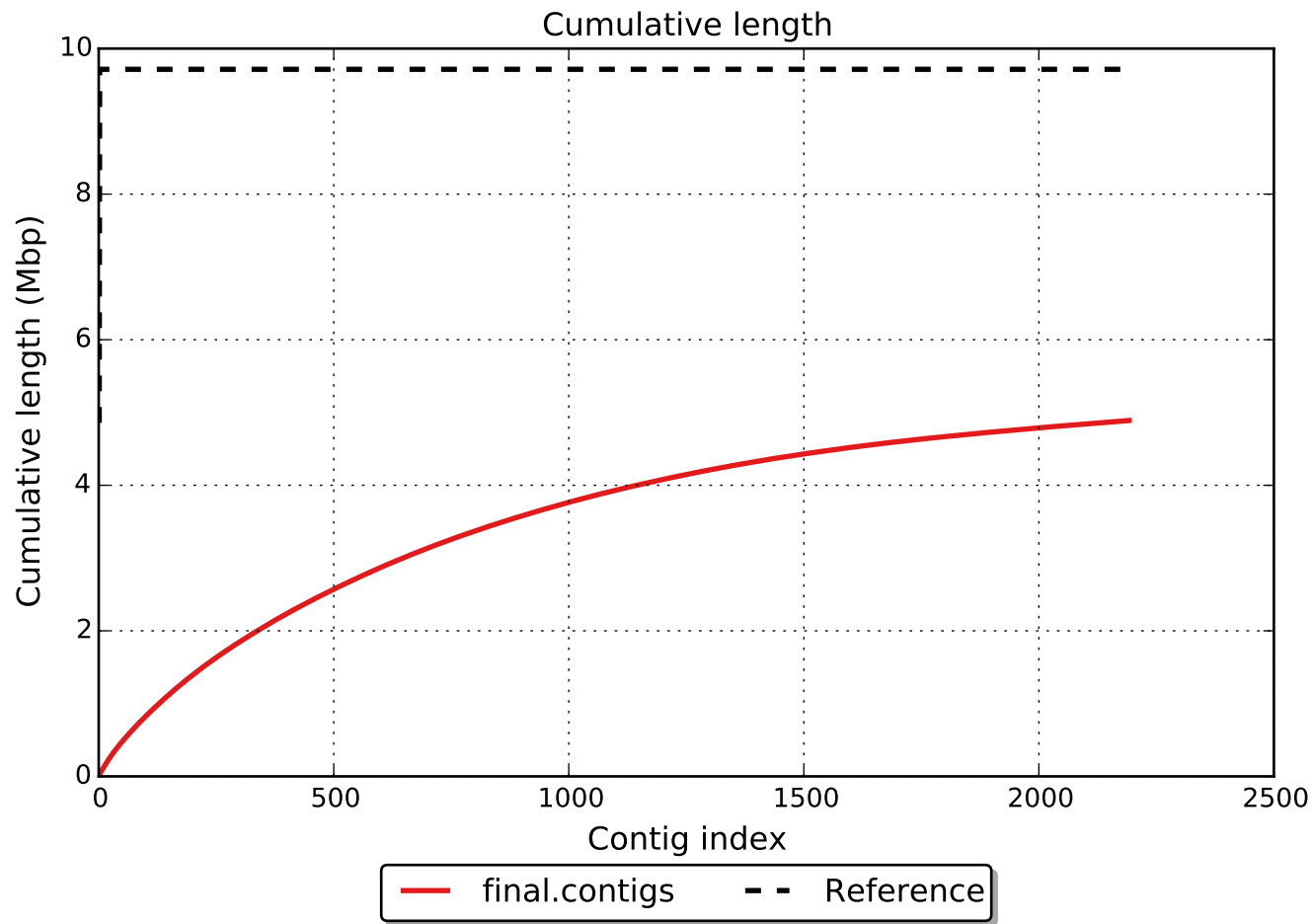
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

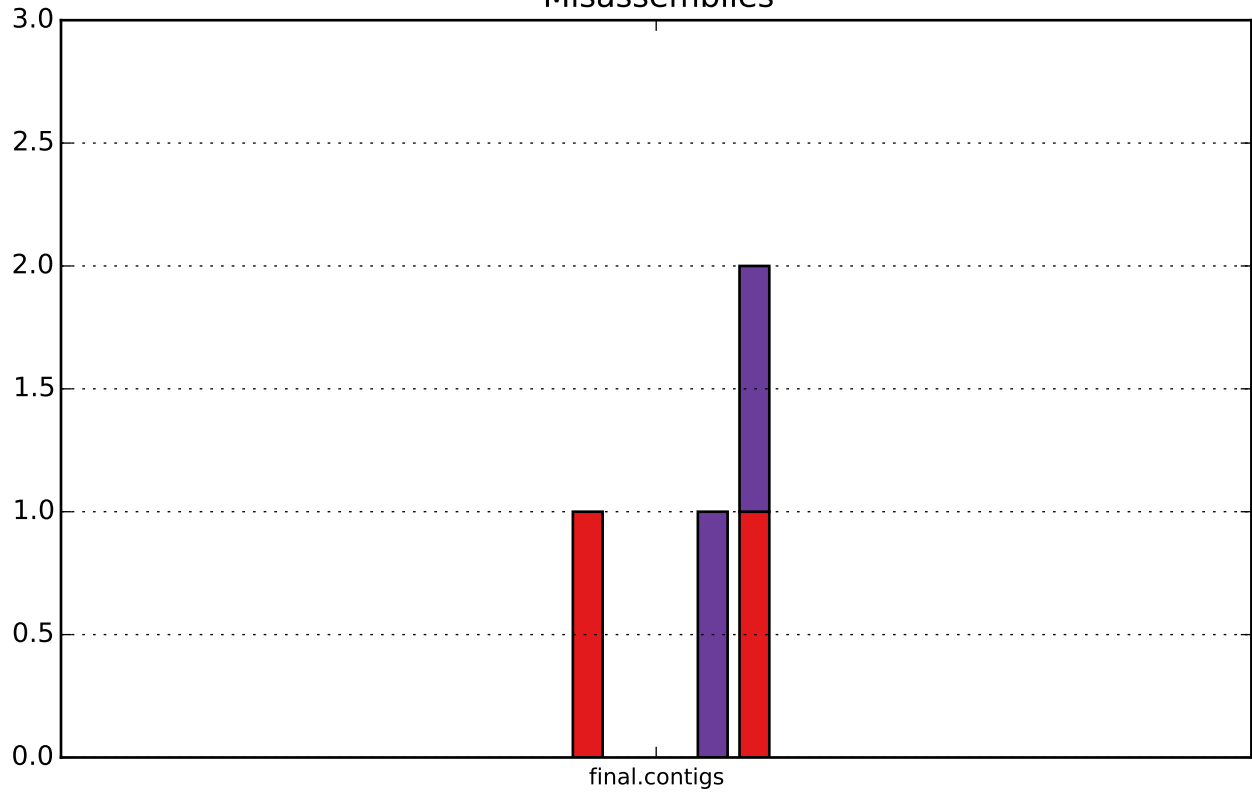
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

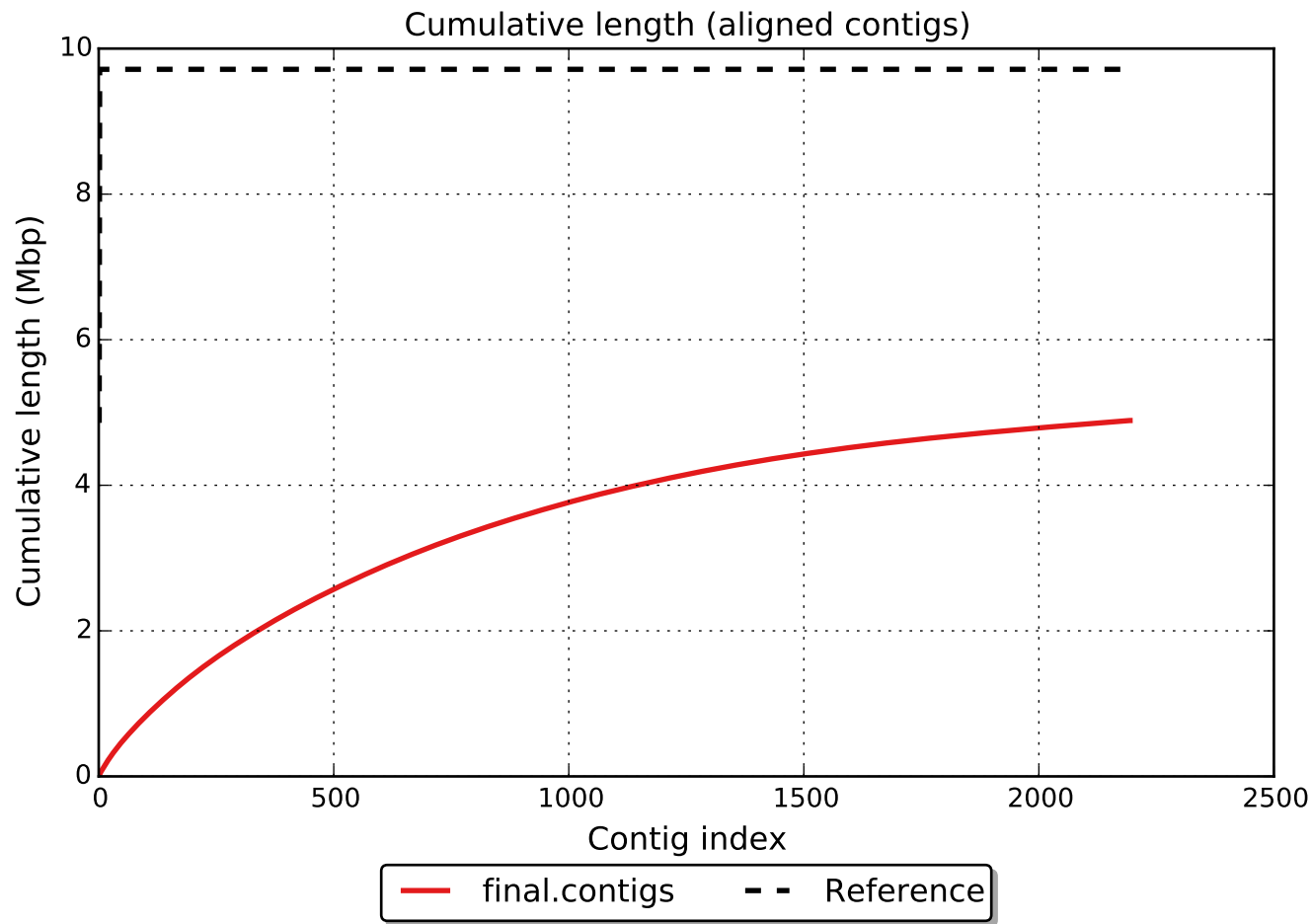
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).





Misassemblies





NAx

