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 (%)	57.702
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	312.29
# indels per 100 kbp	0.00
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).
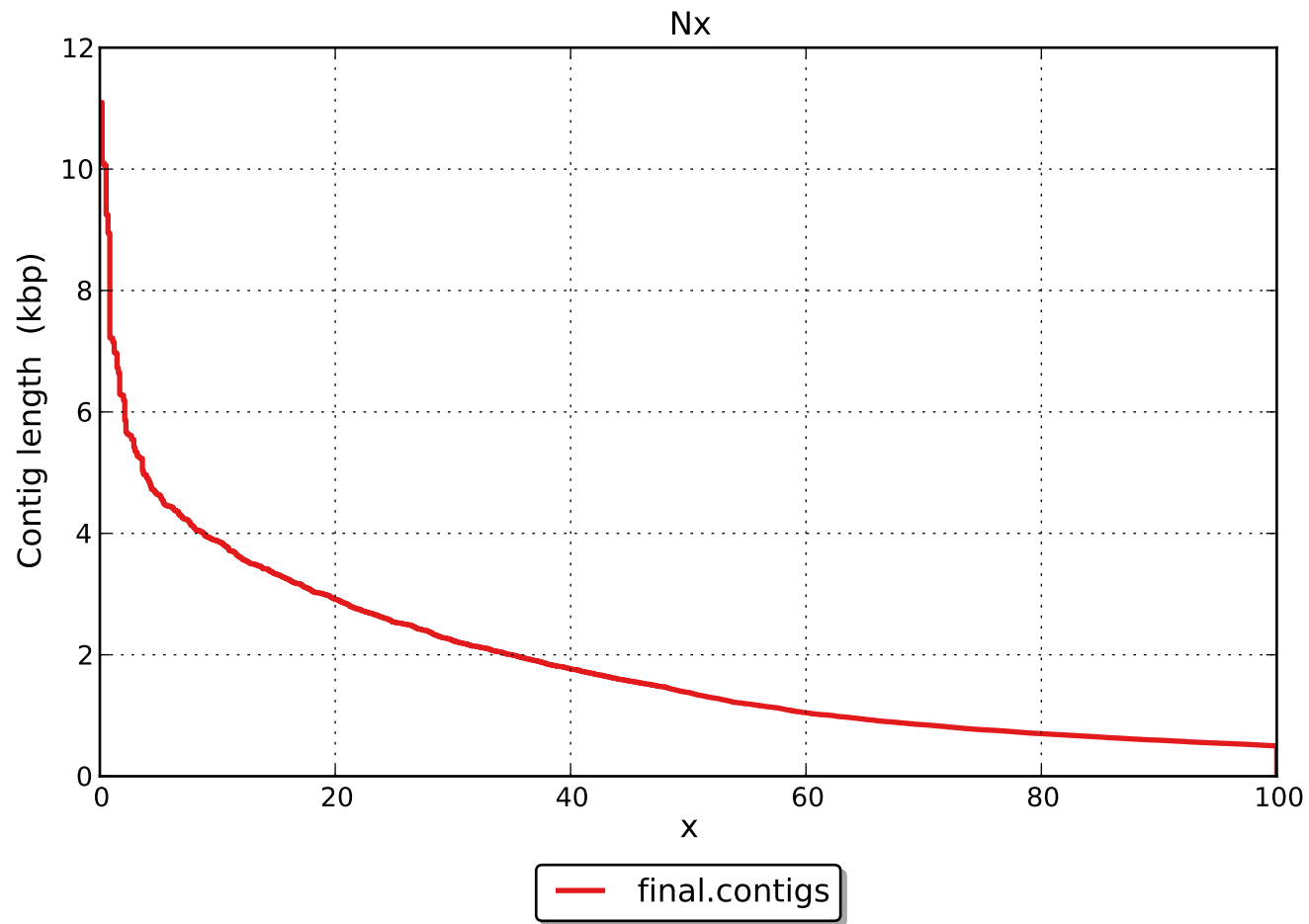
Misassemblies report

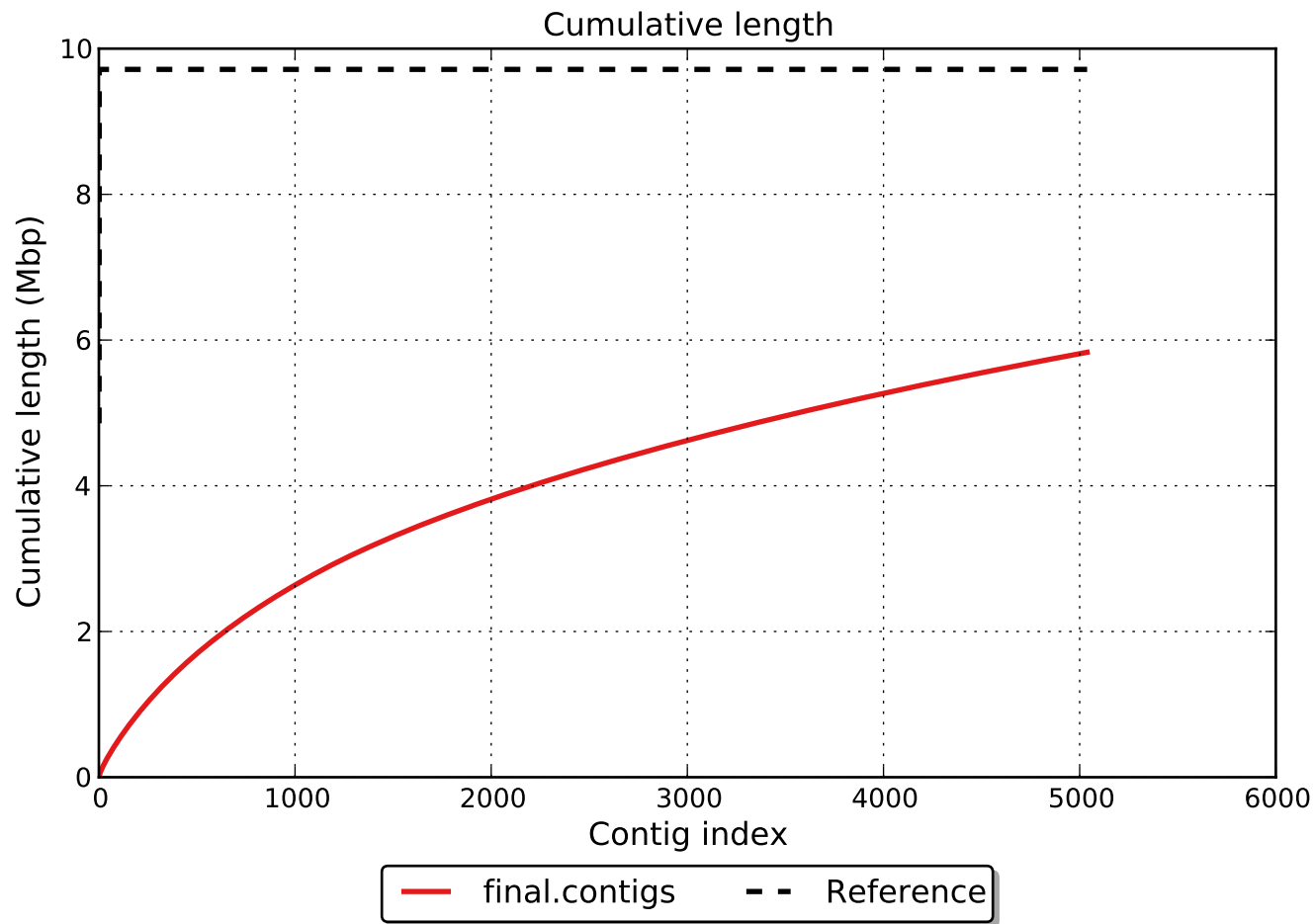|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	17506
# indels	0
# short indels	0
# long indels	0
Indels length	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).

Cumulative length

Misassemblies

final.contigs

Cumulative length (aligned contigs)