Report

	final.contigs
# contigs (>= 0 bp)	657
# contigs (>= 1000 bp)	558
# contigs (>= 5000 bp)	305
# contigs (>= 10000 bp)	166
# contigs (>= 25000 bp)	20
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	4606781
Total length (>= 1000 bp)	4557313
Total length (>= 5000 bp)	3876277
Total length (>= 10000 bp)	2886212
Total length (>= 25000 bp)	646507
Total length (>= 50000 bp)	54626
# contigs	599
Largest contig	54626
Total length	4587033
Reference length	4641652
N50	12933
N75	6998
L50	113
L75	233
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	51334
# local misassemblies	14
# unaligned contigs	0 + 2 part
Unaligned length	447
Genome fraction (%)	97.896
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	147.56
# indels per 100 kbp	9.79
Largest alignment	54626
NA50	12897
NA75	6981
LA50	114
LA75	234

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).
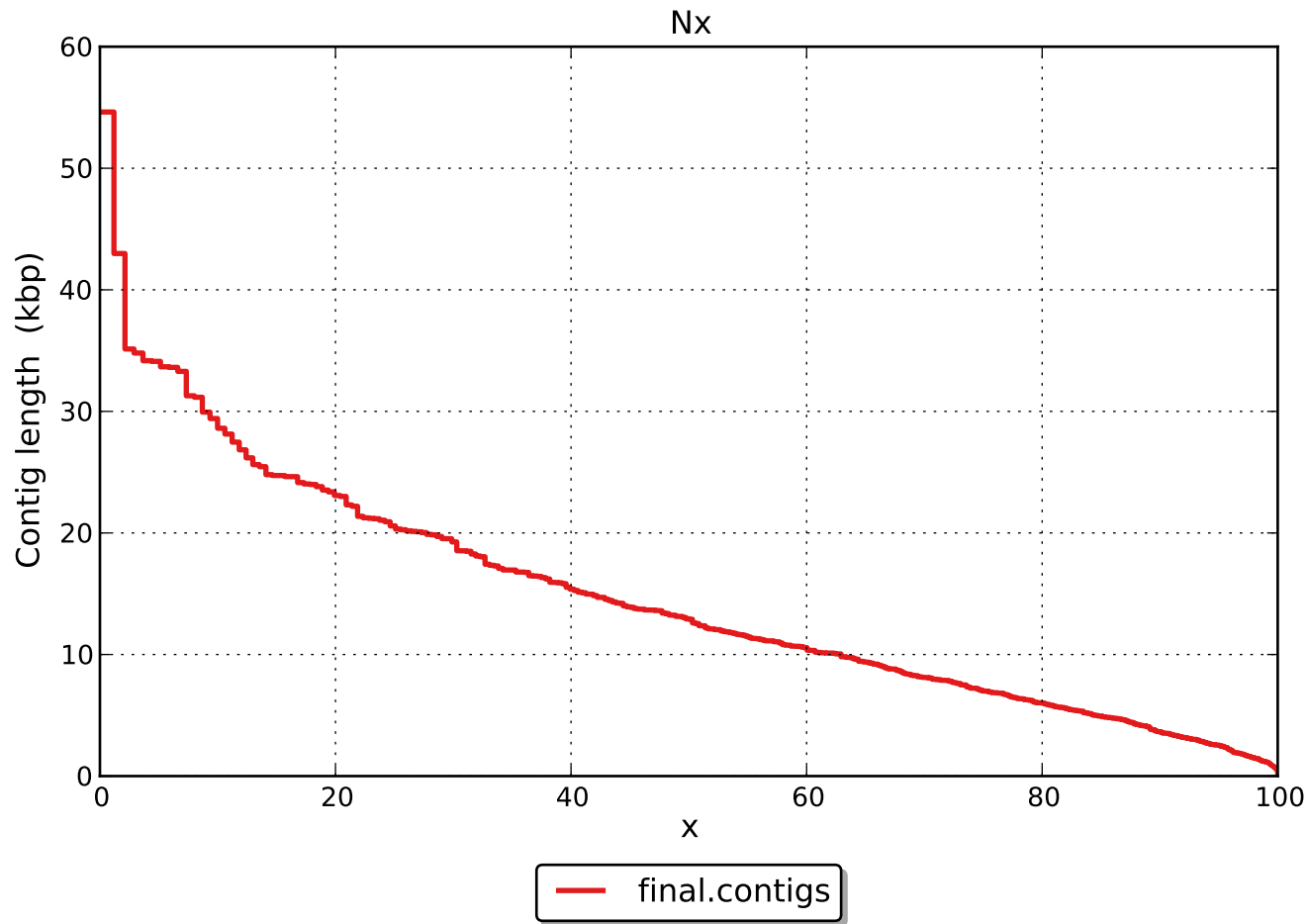
Misassemblies report

|	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	51334
# local misassemblies	14
# mismatches	6705
# indels	445
# short indels	443
# long indels	2
Indels length	696

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).
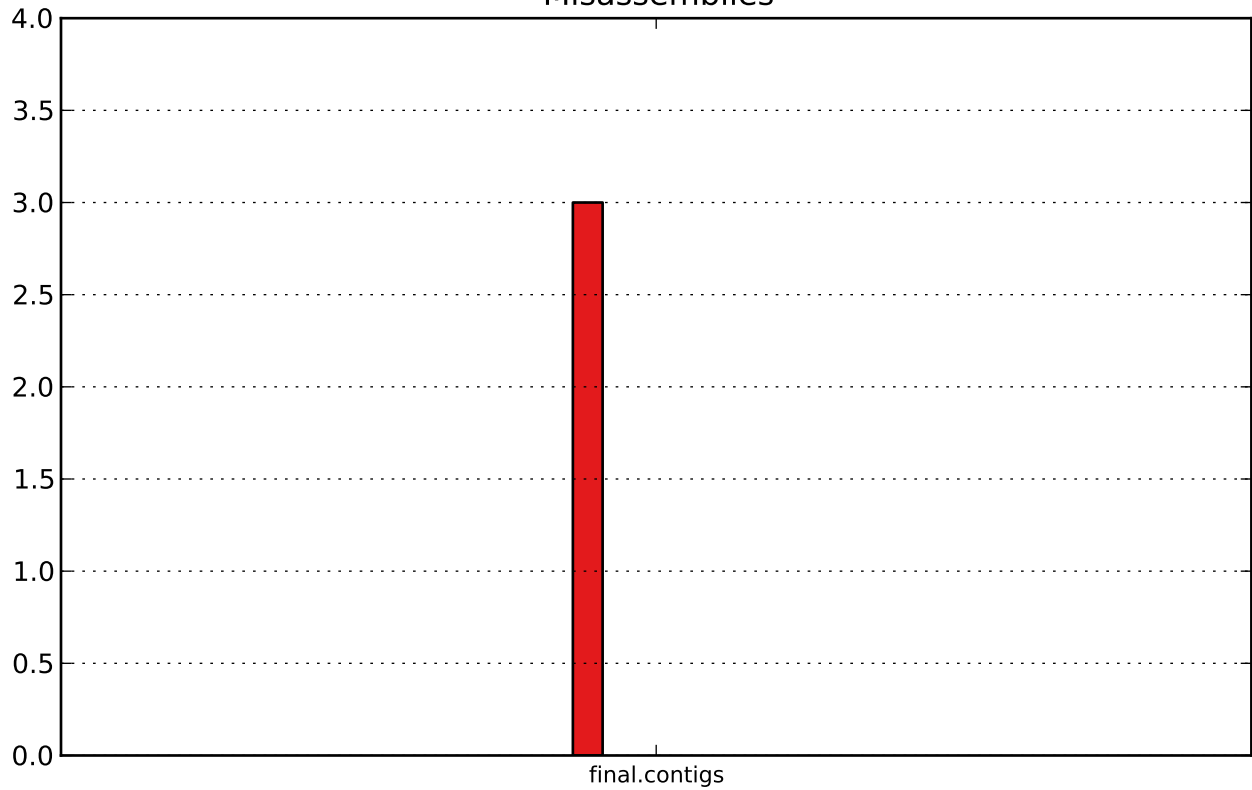
Unaligned report

	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	447
# 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).
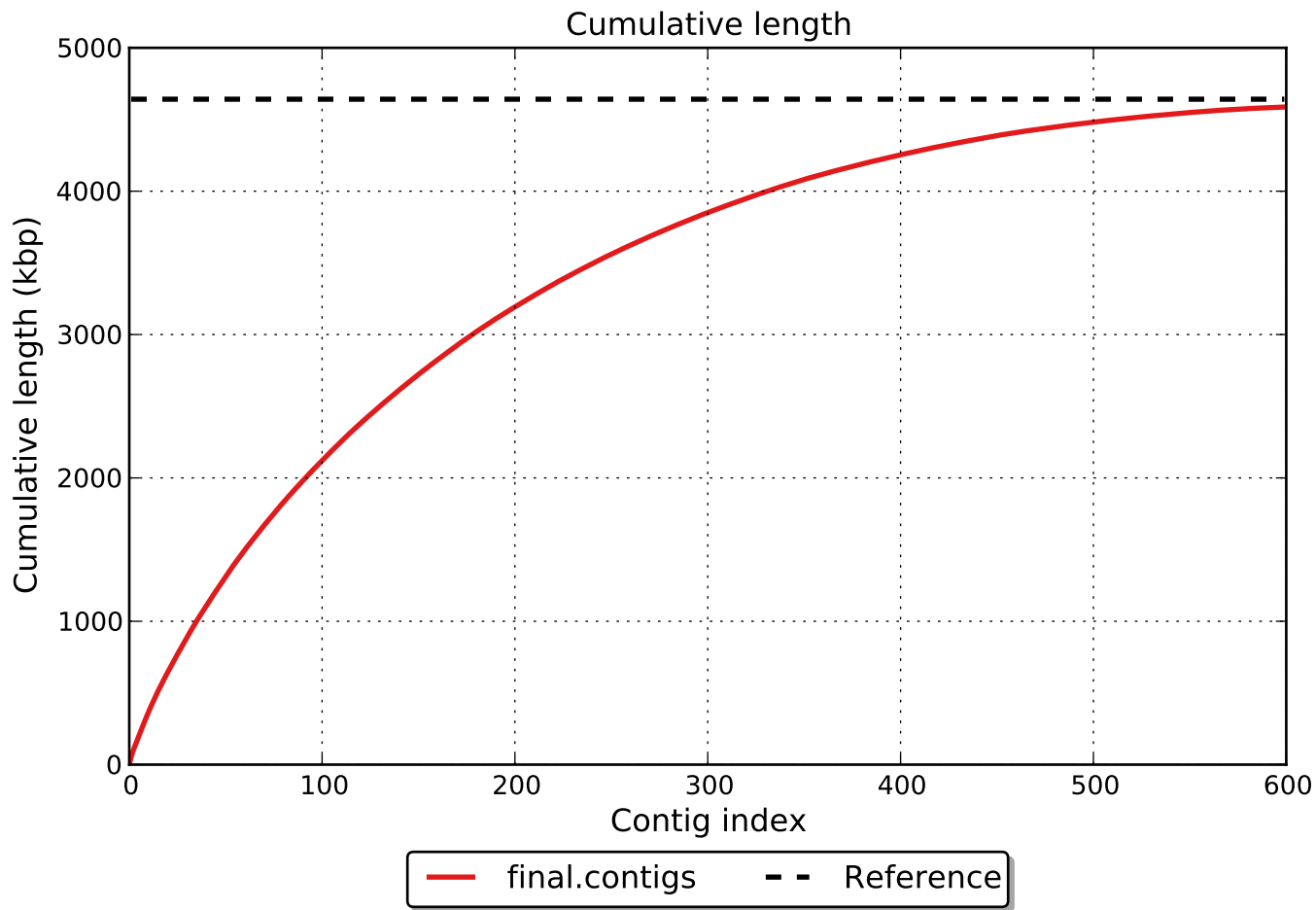
Cumulative length

Misassemblies

Cumulative length (aligned contigs)