Report

	final.contigs
# contigs (>= 0 bp)	1655
# contigs (>= 1000 bp)	1210
# contigs (>= 5000 bp)	243
# contigs (>= 10000 bp)	28
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4462752
Total length (>= 1000 bp)	4178600
Total length (>= 5000 bp)	1803177
Total length (>= 10000 bp)	365081
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1528
Largest contig	18143
Total length	4411595
Reference length	4641652
N50	4124
N75	2443
L50	332
L75	674
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	12922
# local misassemblies	8
# unaligned contigs	0 + 5 part
Unaligned length	1111
Genome fraction (%)	94.725
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	108.99
# indels per 100 kbp	10.33
Largest alignment	18143
NA50	4124
NA75	2429
LA50	332
LA75	674

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	3
# translocations	0
# inversions	1
# interspecies translocations	0
# possibly misassembled contigs	1
# misassembled contigs	4
Misassembled contigs length	12922
# local misassemblies	8
# mismatches	4792
# indels	454
# short indels	449
# long indels	5
Indels length	785

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	5
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1111
# 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

Cumulative length

Misassemblies
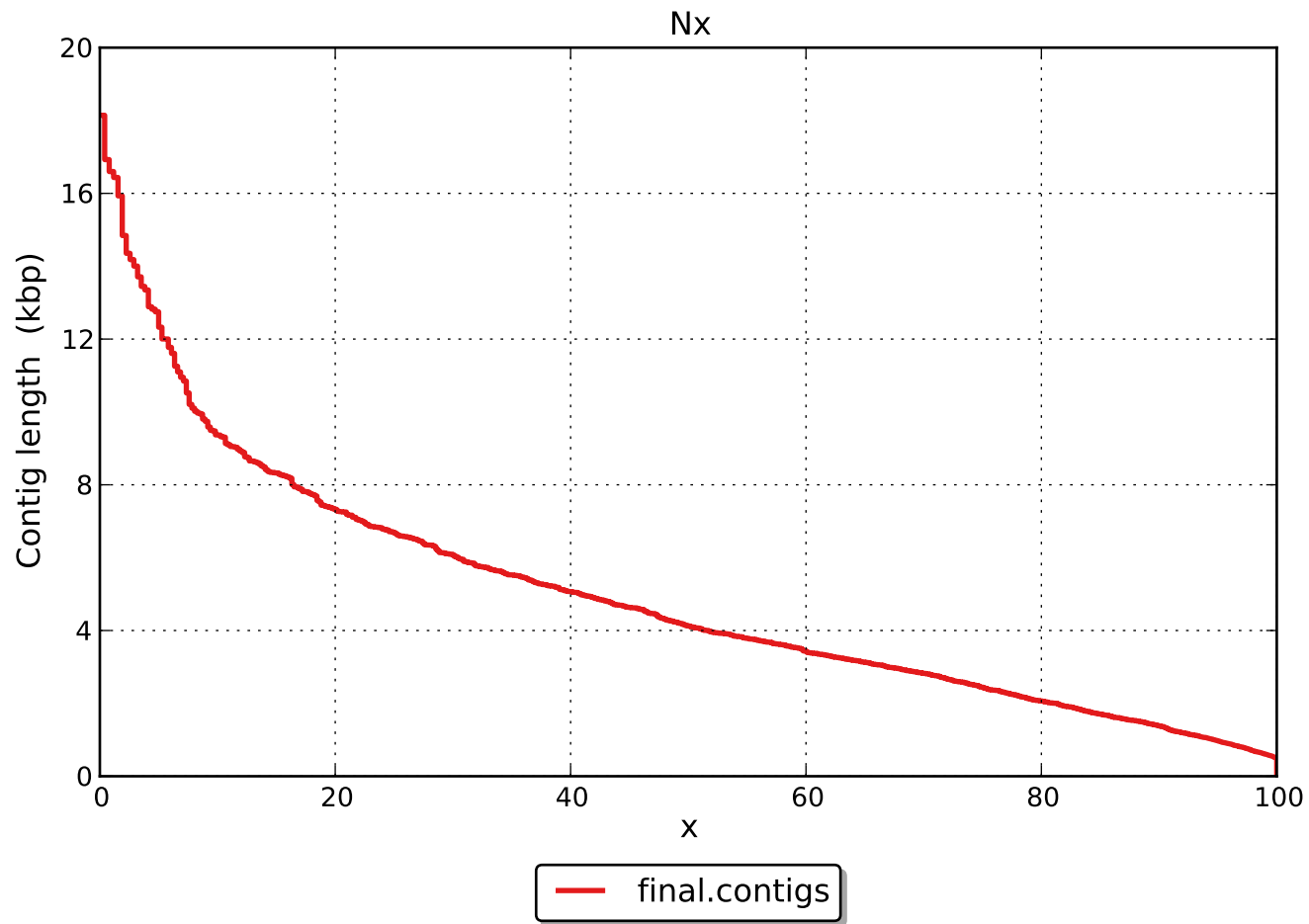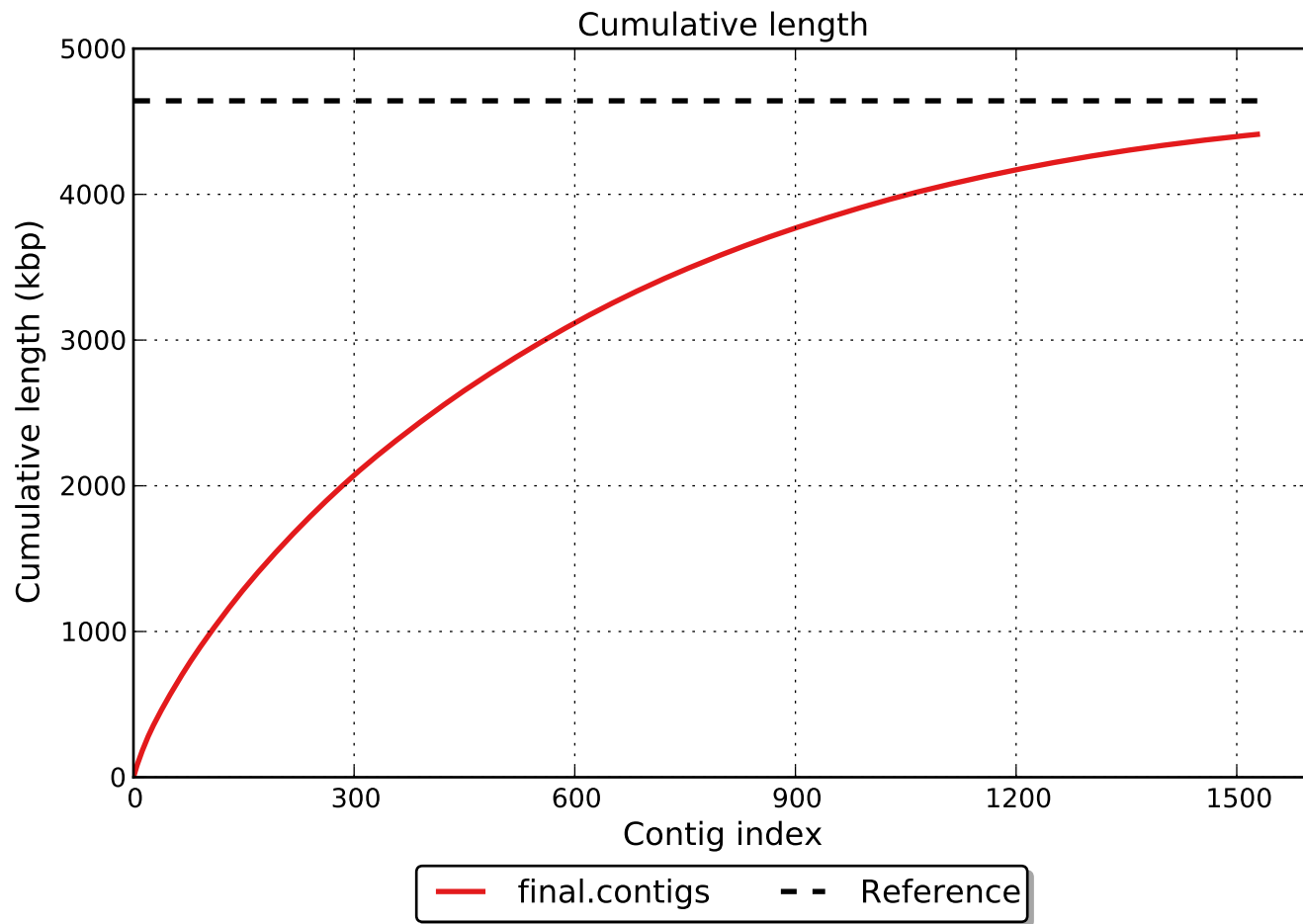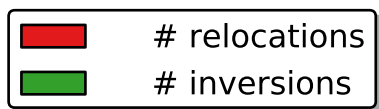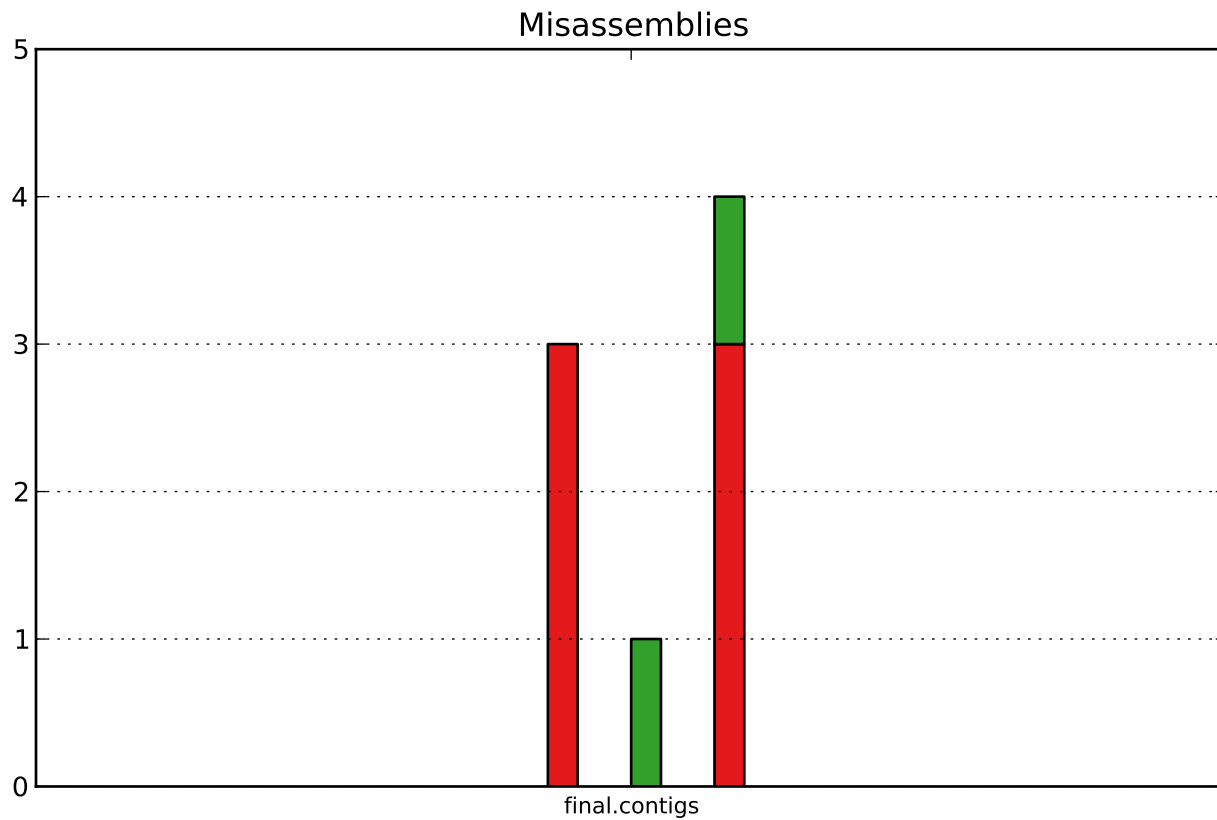
Cumulative length (aligned contigs)