Report

|	final.contigs
# contigs (>= 0 bp)	1565
# contigs (>= 1000 bp)	408
Total length (>= 0 bp)	1297276
Total length (>= 1000 bp)	641890
# contigs	1079
Largest contig	4490
Total length	1119941
Reference length	1283598
GC (%)	26.35
Reference GC (%)	26.30
N50	1130
NG50	1002
N75	781
NG75	655
L50	331
LG50	408
L75	635
LG75	807
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	86.860
Duplication ratio	1.062
# N's per 100 kbp	0.00
# mismatches per 100 kbp	128.89
# indels per 100 kbp	0.18
Largest alignment	4490
NA50	1129
NGA50	1002
NA75	781
NGA75	655
LA50	331
LGA50	408
LA75	635
LGA75	807

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	1437
# indels	2
# short indels	2
# long indels	0
Indels length	2

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).
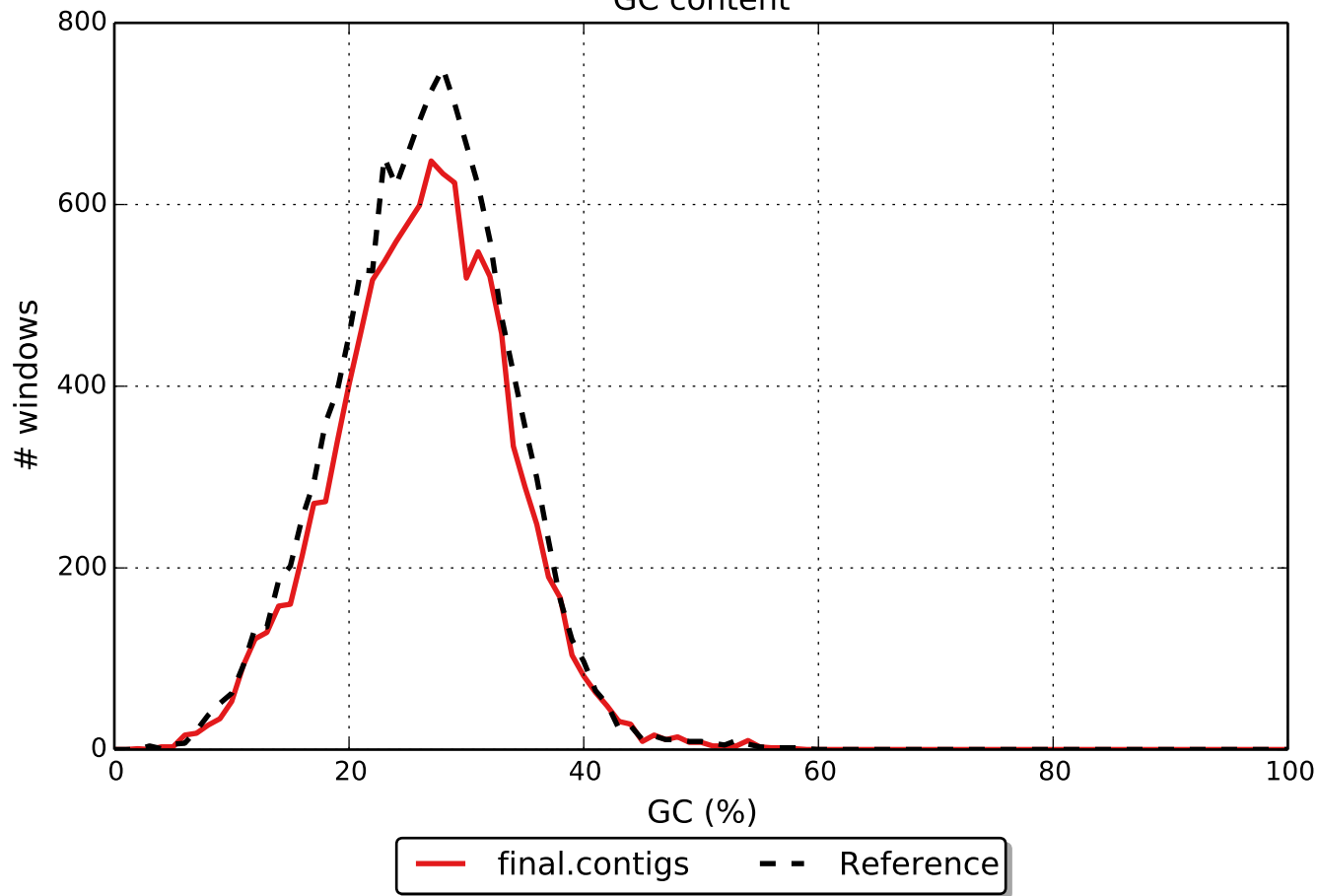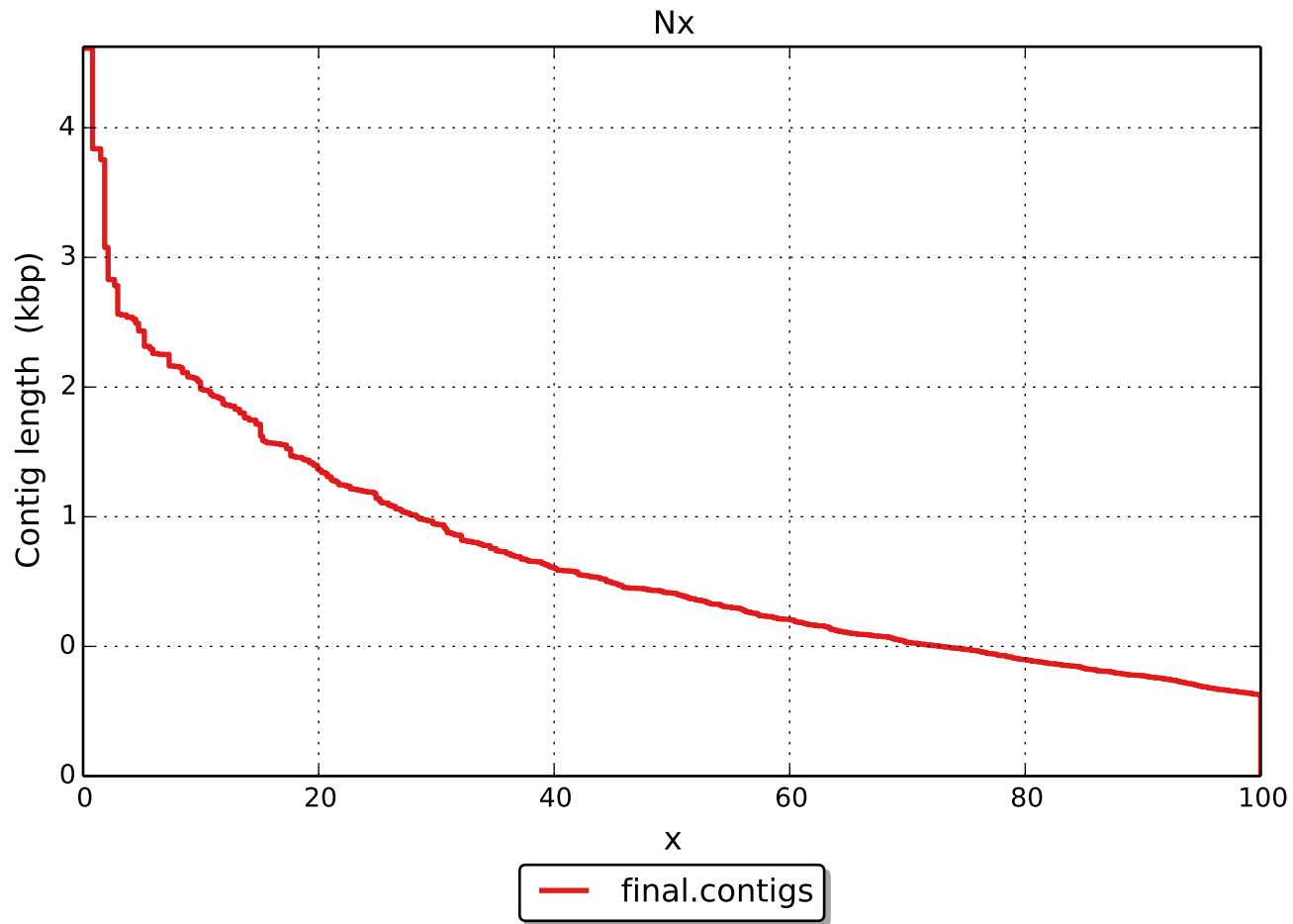
Unaligned report

	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).
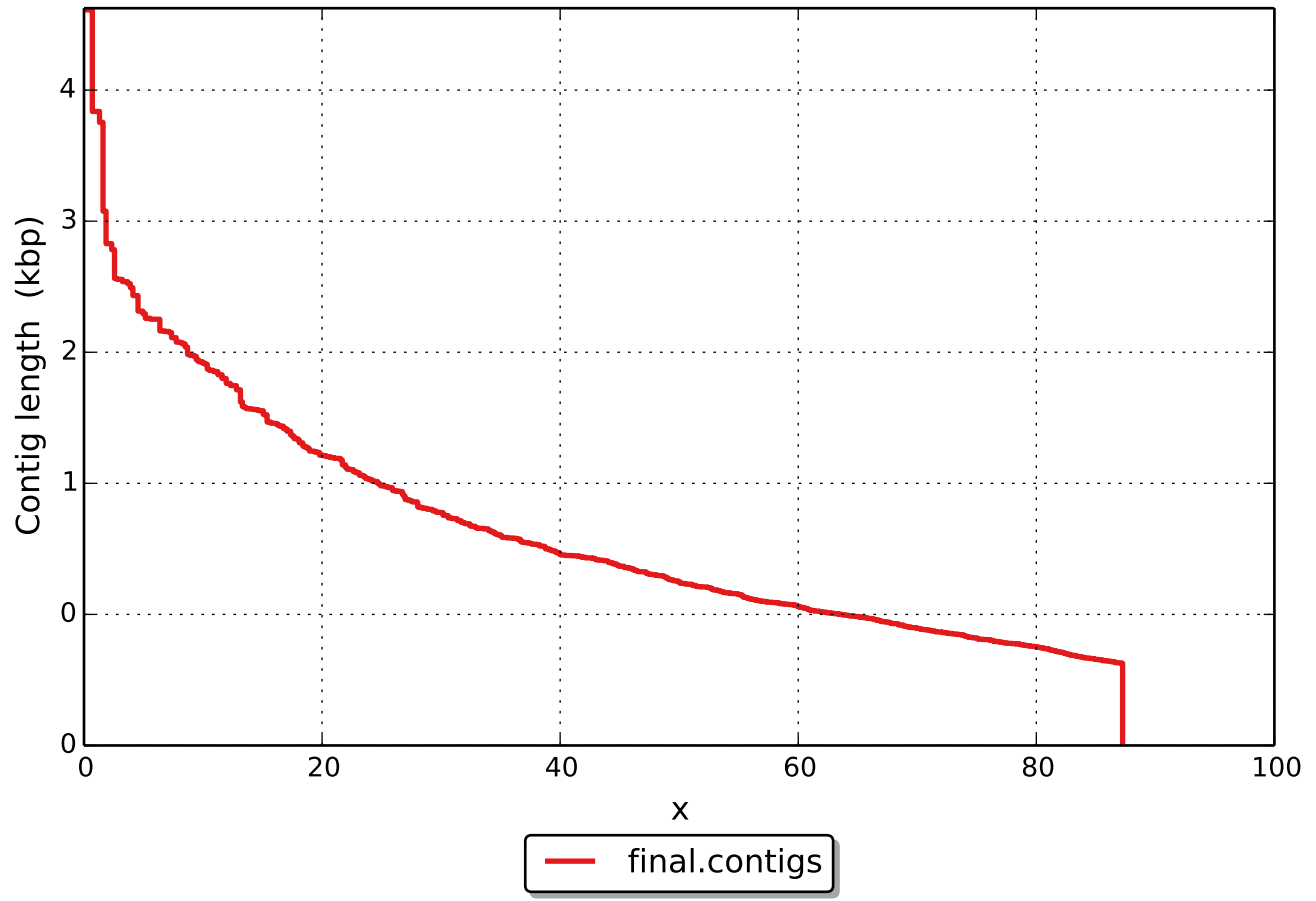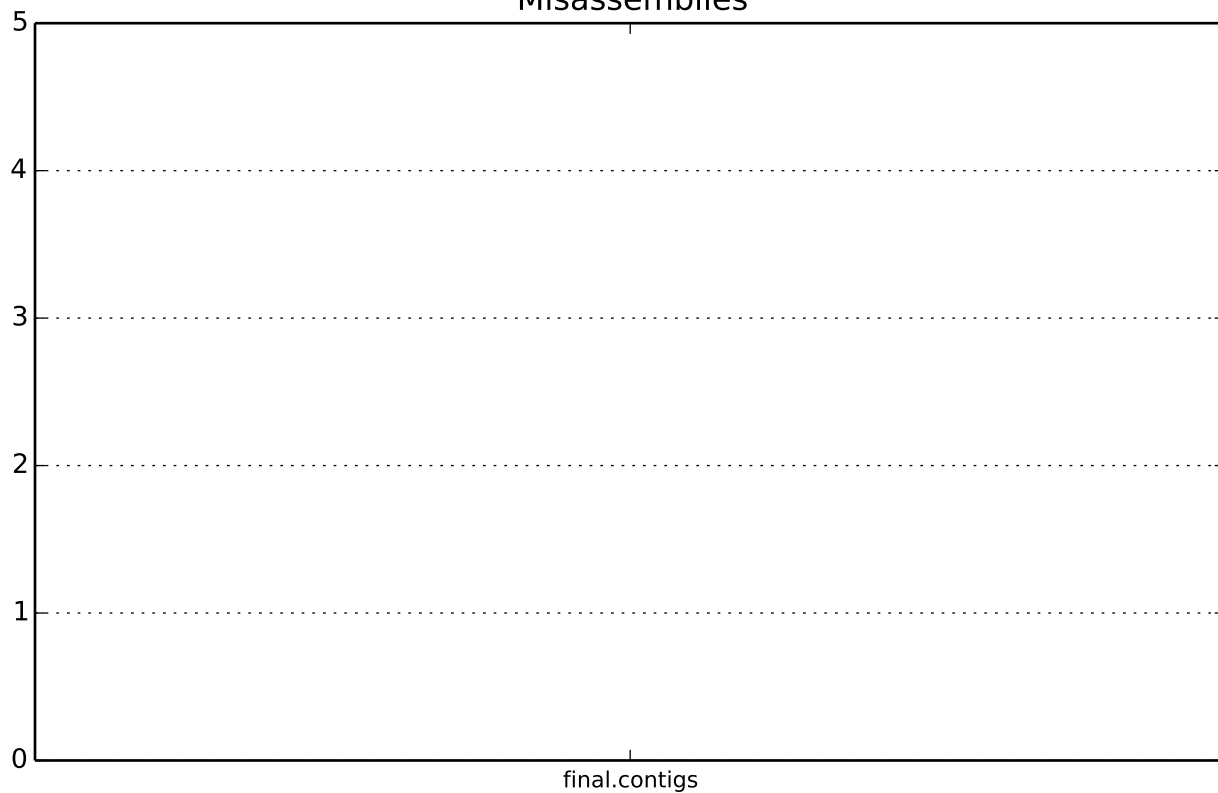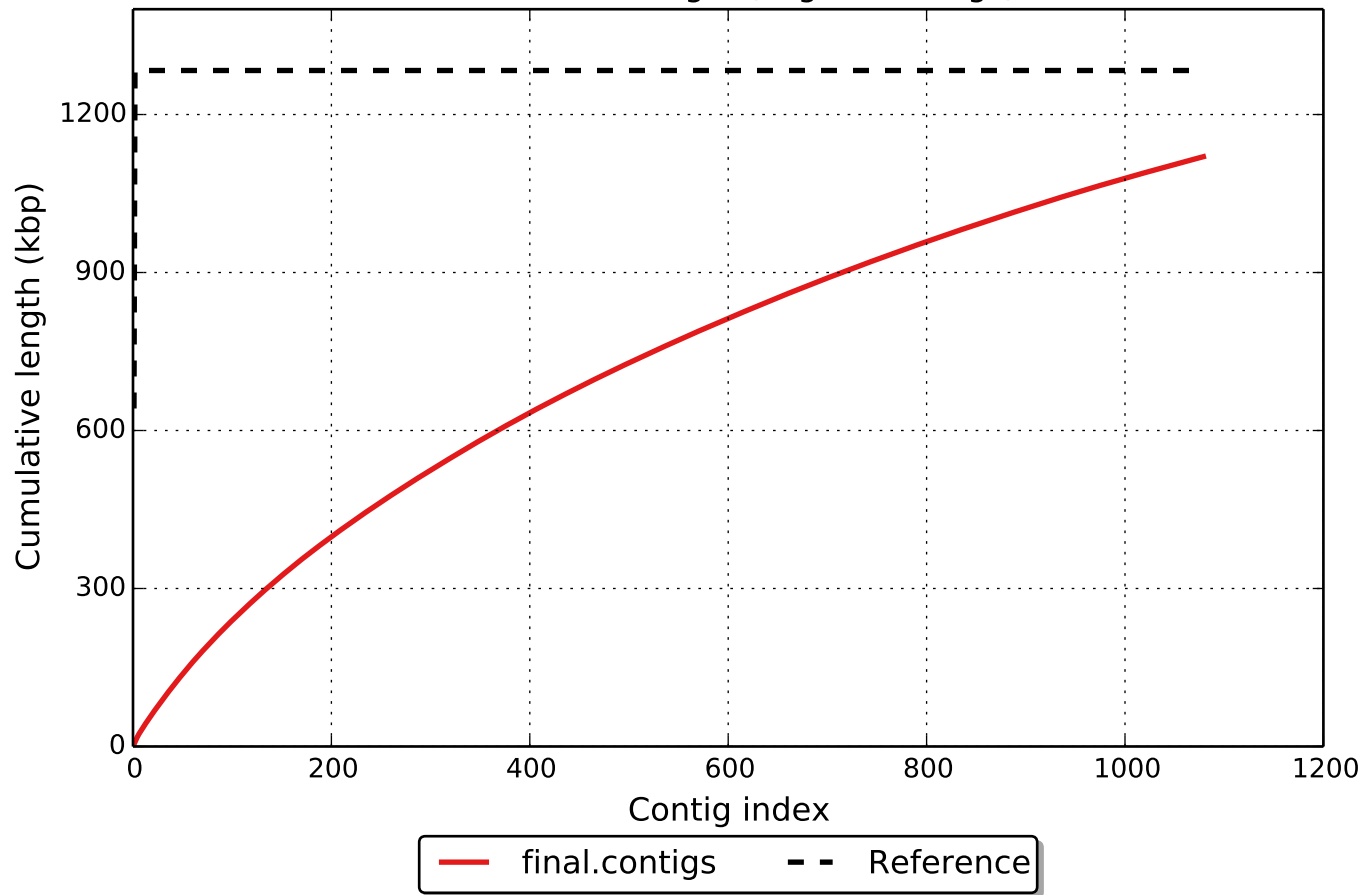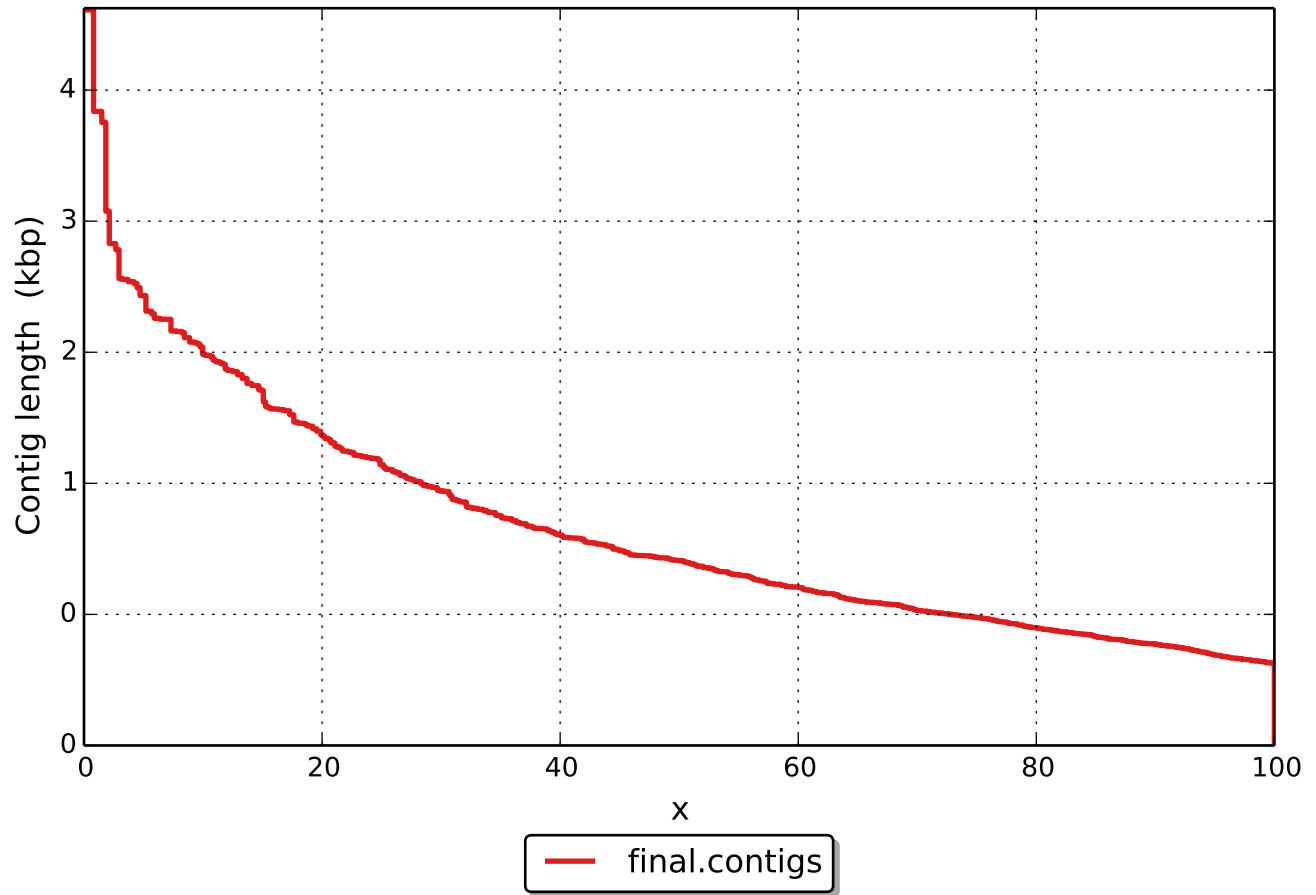
Cumulative length

GC content

Nx
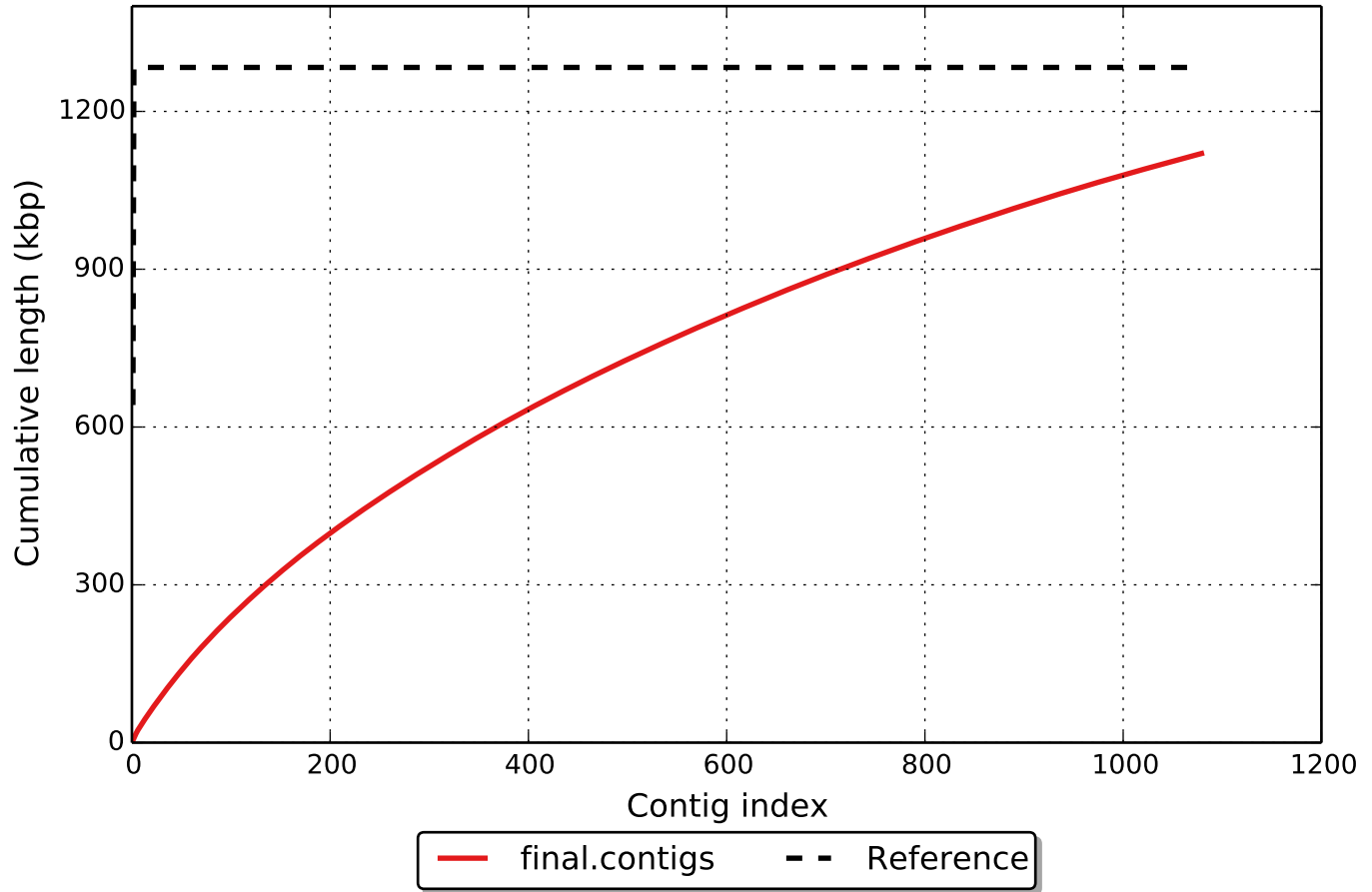
NGx

Misassemblies

final.contigs

Cumulative length (aligned contigs)

NAx

NGAx