Report

	final.contigs
# contigs (>= 0 bp)	3865
# contigs (>= 1000 bp)	1445
Total length (>= 0 bp)	3833713
Total length (>= 1000 bp)	2486531
# contigs	2782
Largest contig	7759
Total length	3448070
Reference length	3785550
GC (%)	32.28
Reference GC (%)	32.25
N50	1437
NG50	1324
N75	956
NG75	824
L50	807
LG50	930
L75	1547
LG75	1833
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	87.312
Duplication ratio	1.043
# N's per 100 kbp	0.00
# mismatches per 100 kbp	42.78
# indels per 100 kbp	0.00
Largest alignment	7759
NA50	1437
NGA50	1324
NA75	956
NGA75	824
LA50	807
LGA50	930
LA75	1547
LGA75	1833

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).
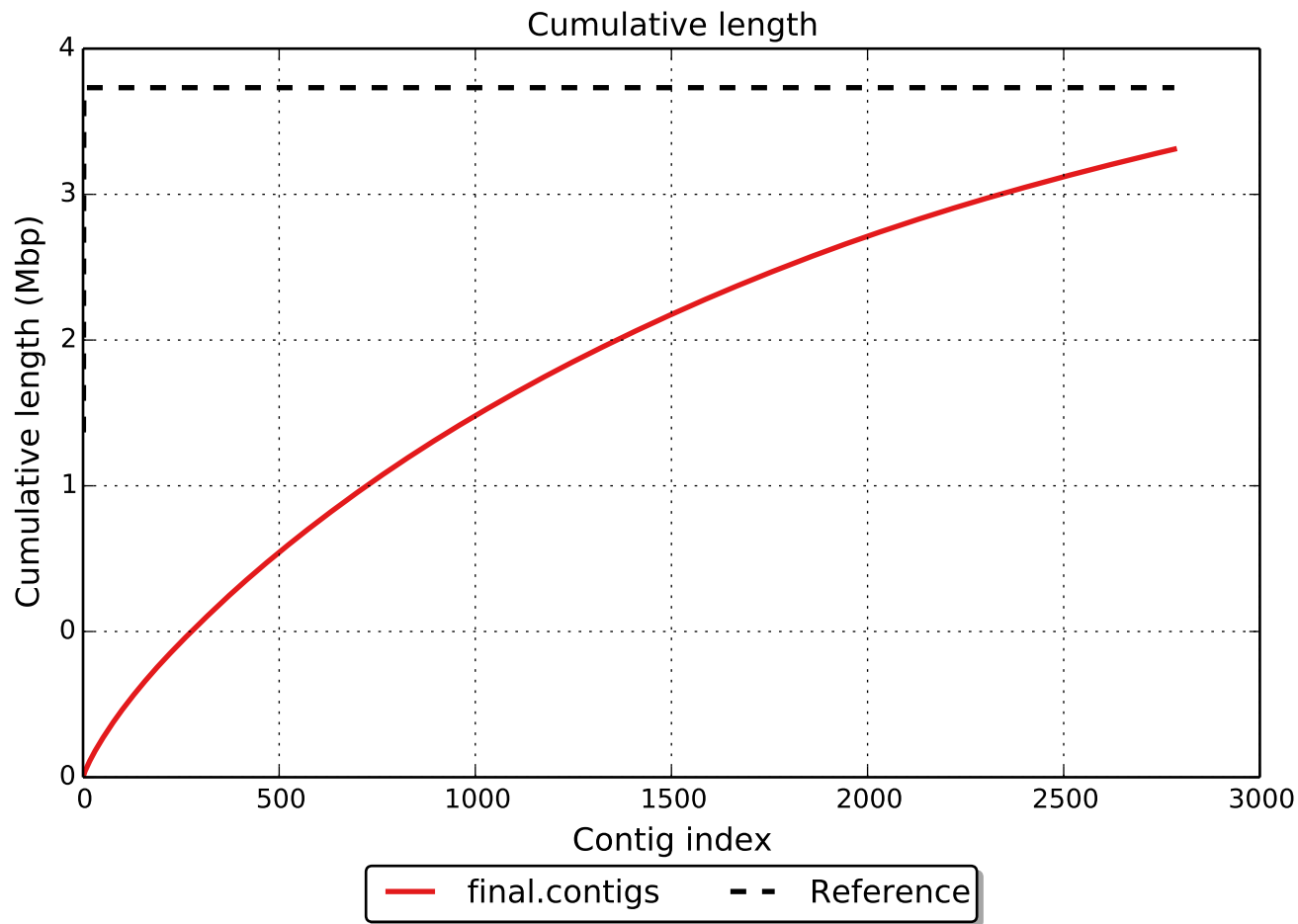
Misassemblies report

	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	1414
# indels	0
# short indels	0
# long indels	0
Indels length	0

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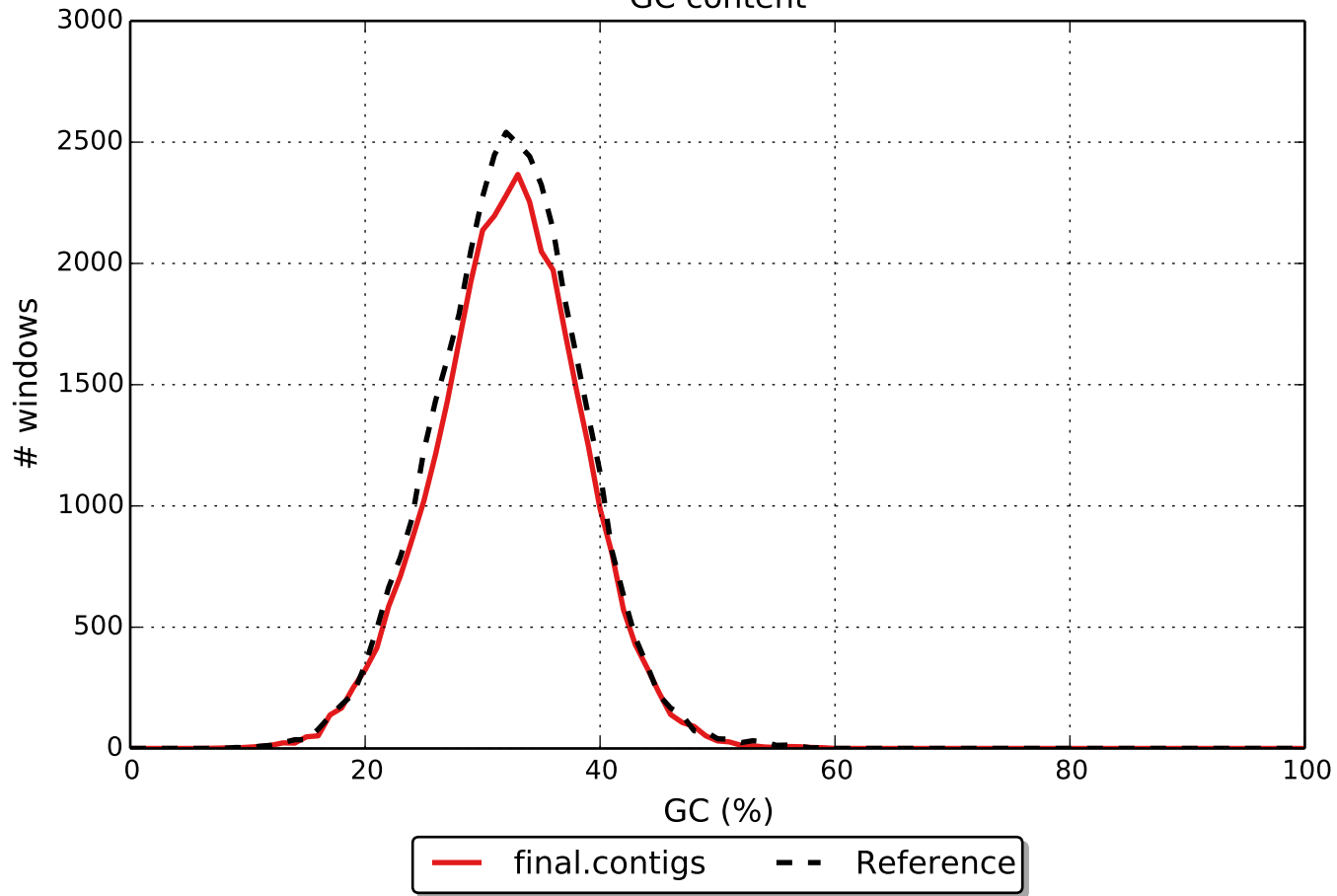(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
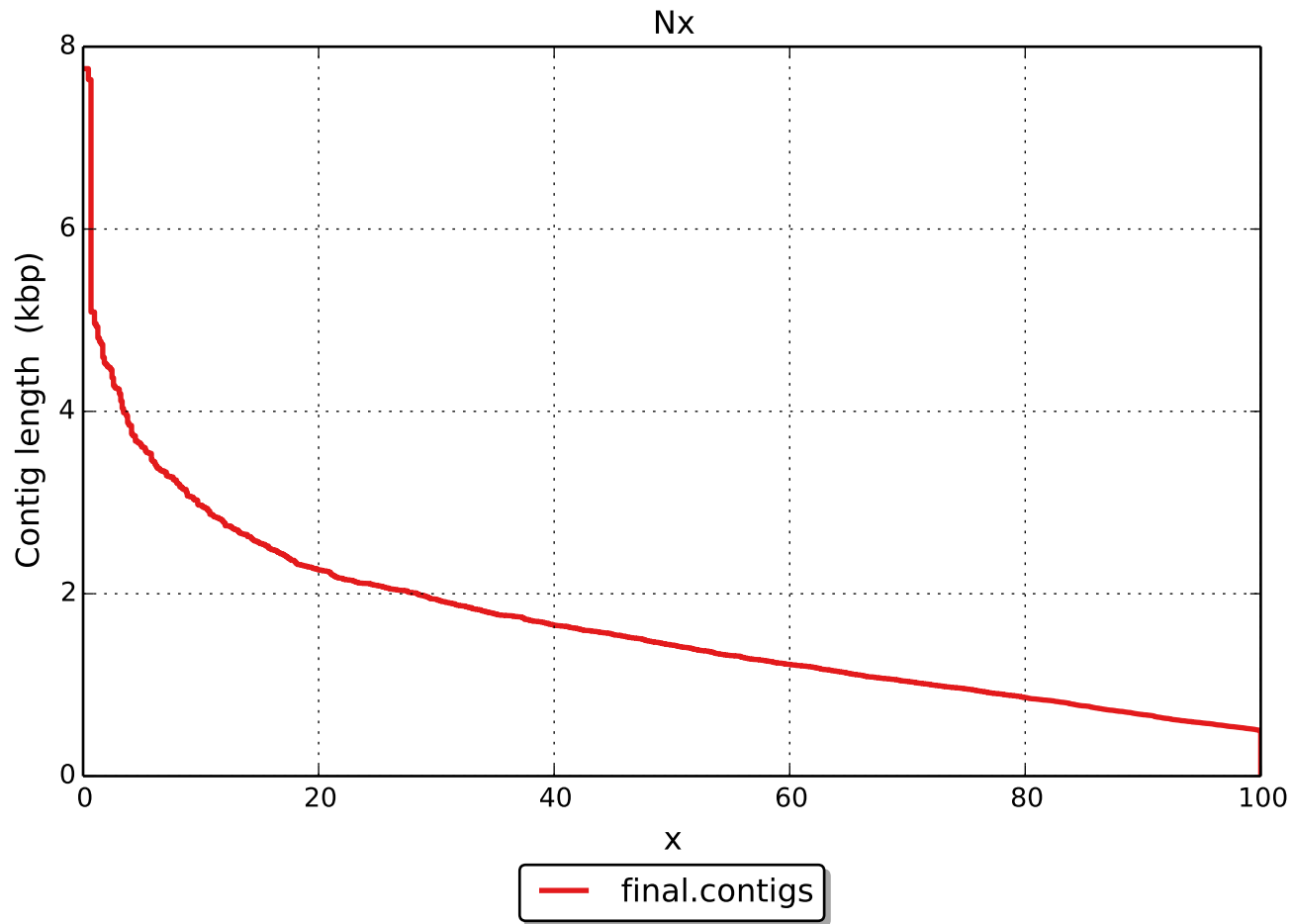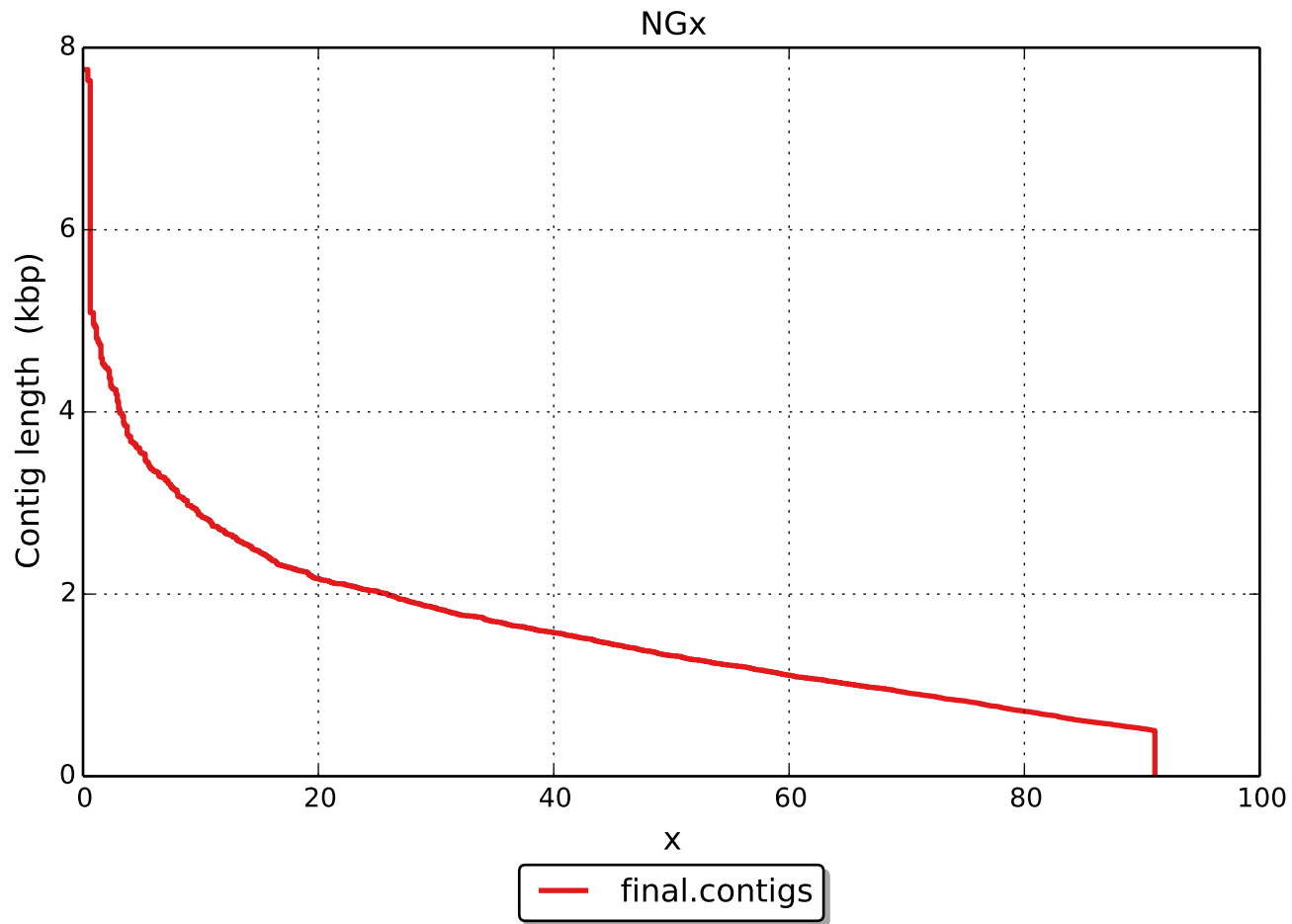
Unaligned report

	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).
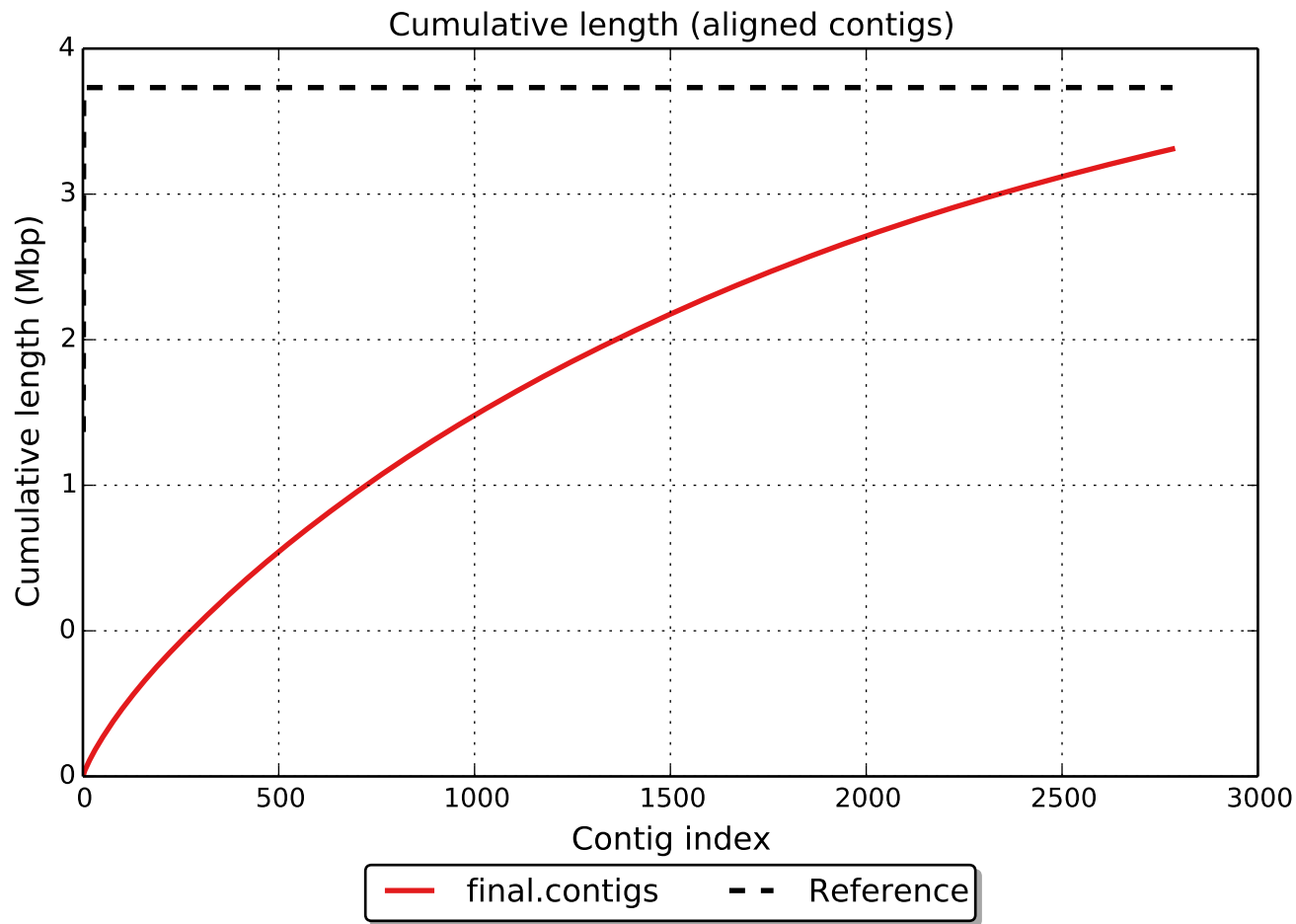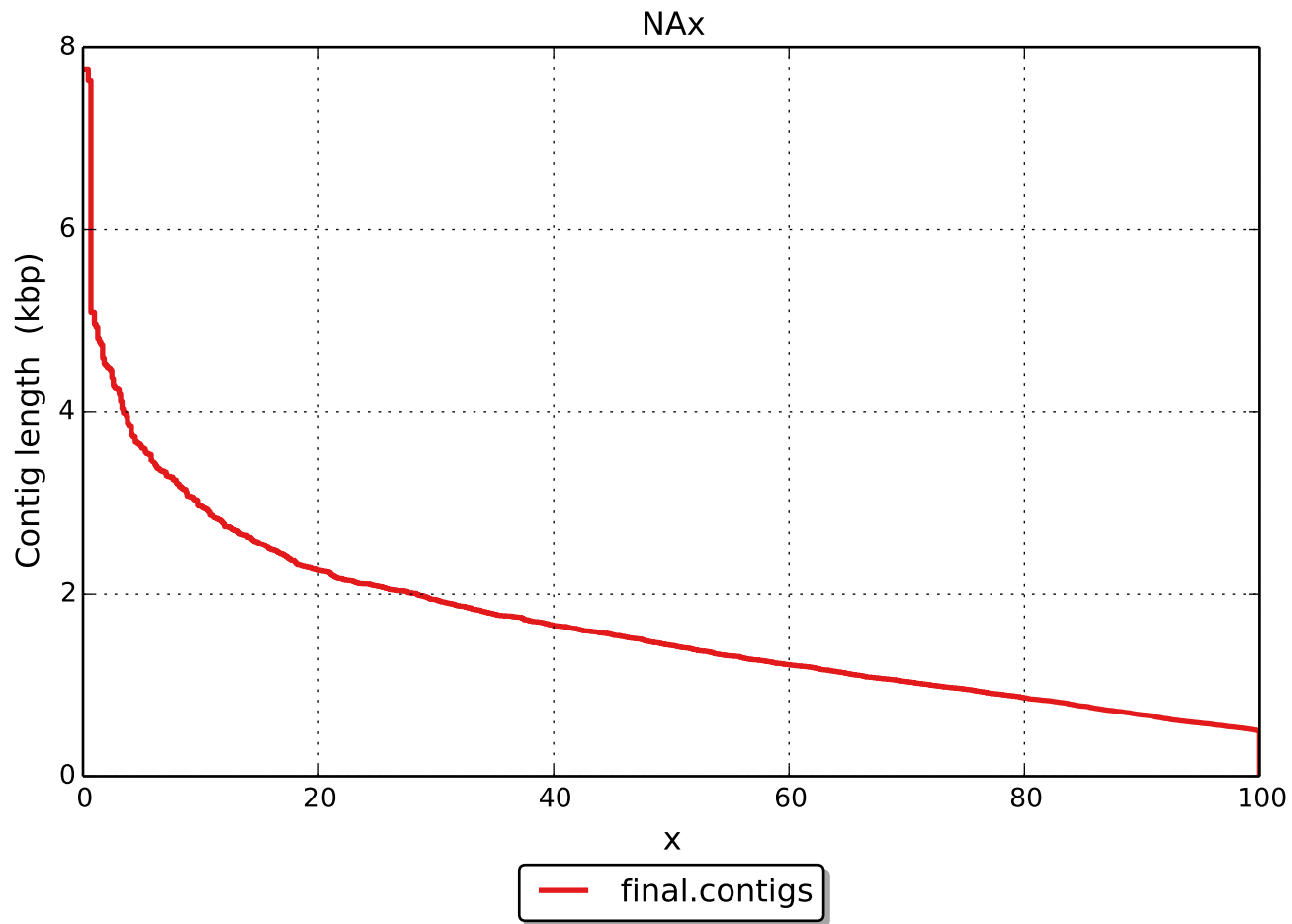
Cumulative length

NGx

Contig length (kbp)

x

final.contigs

Misassemblies

final.contigs

Cumulative length (aligned contigs)