

Report

	final.contigs
# contigs (≥ 0 bp)	1674
# contigs (≥ 1000 bp)	351
Total length (≥ 0 bp)	1243657
Total length (≥ 1000 bp)	503853
# contigs	1101
Largest contig	2937
Total length	1035241
Reference length	1283598
GC (%)	26.39
Reference GC (%)	26.30
N50	984
NG50	849
N75	720
NG75	568
L50	365
LG50	502
L75	674
LG75	966
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	76.950
Duplication ratio	1.048
# N's per 100 kbp	0.00
# mismatches per 100 kbp	109.95
# indels per 100 kbp	0.00
Largest alignment	2937
NA50	984
NGA50	849
NA75	720
NGA75	568
LA50	365
LGA50	502
LA75	674
LGA75	966

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	1086
# indels	0
# short indels	0
# long indels	0
Indels length	0

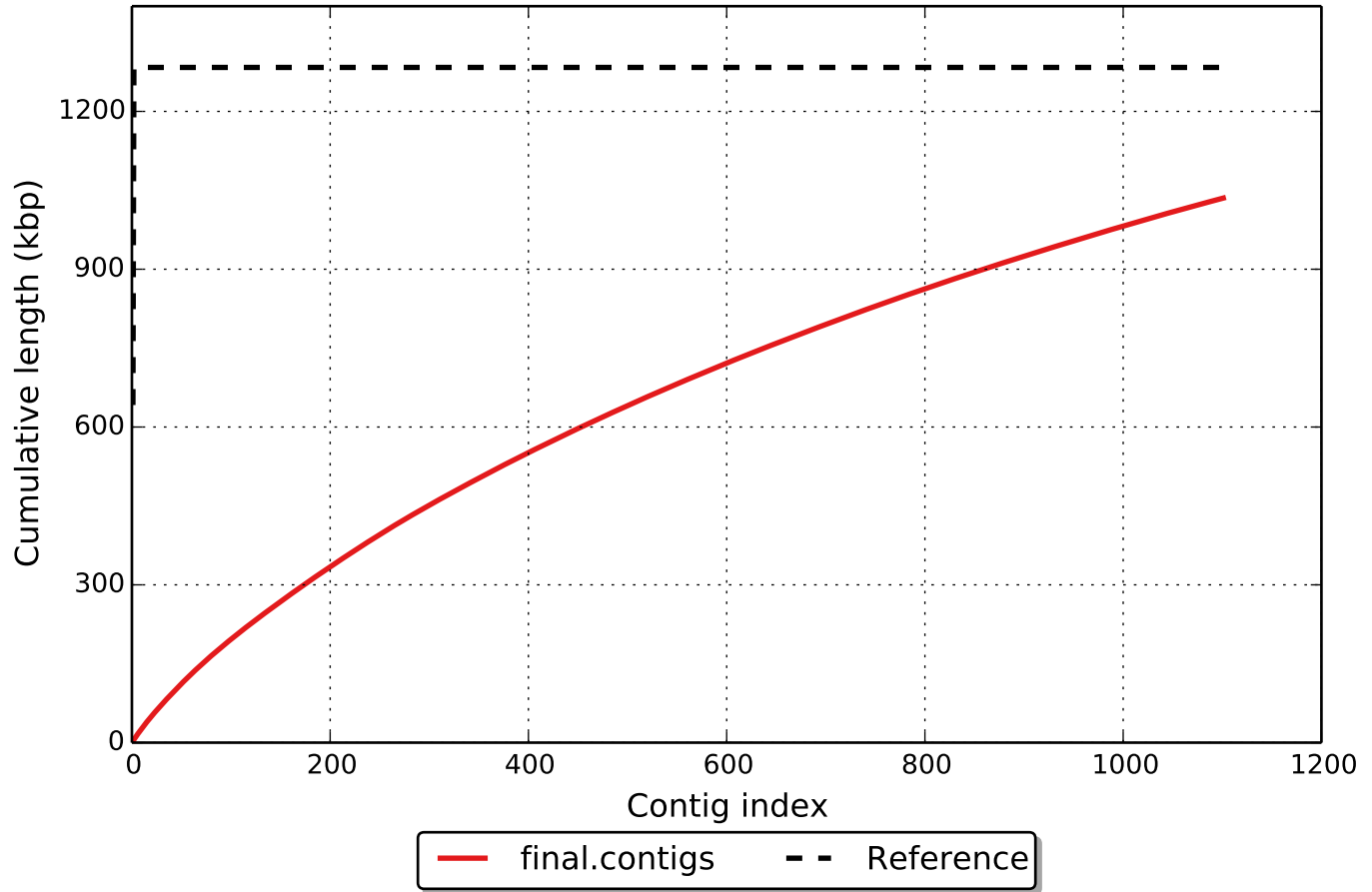
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

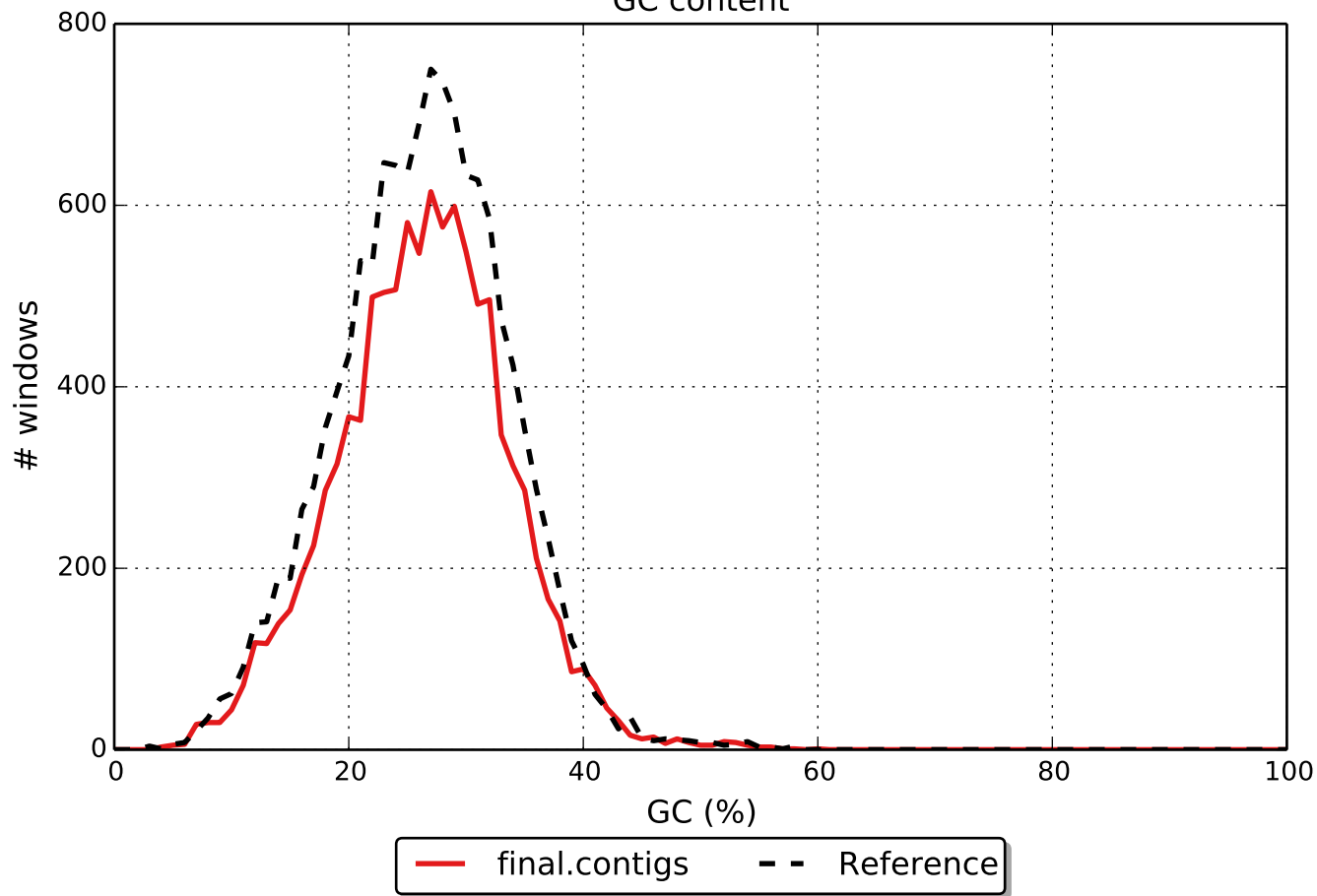
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

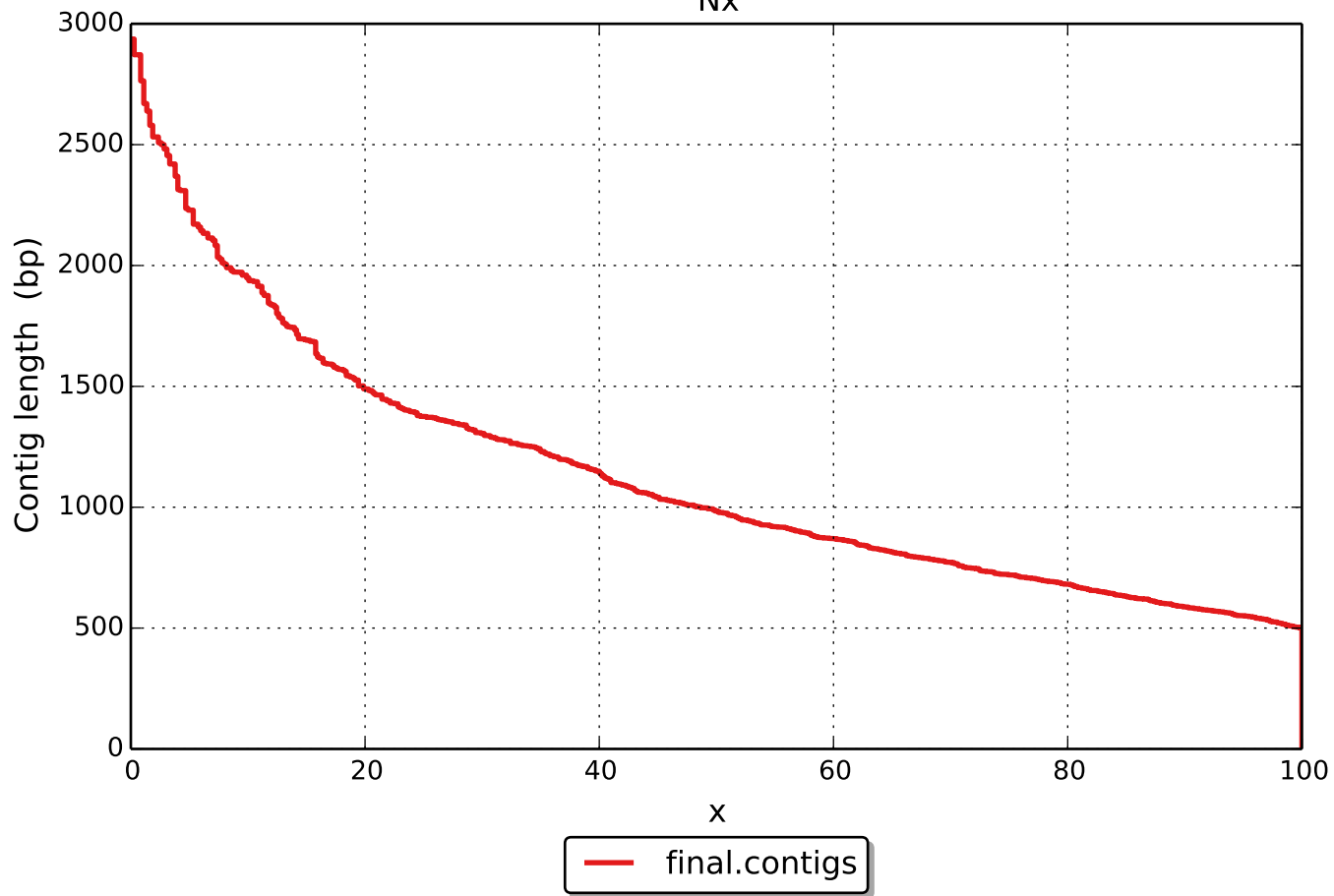
Cumulative length



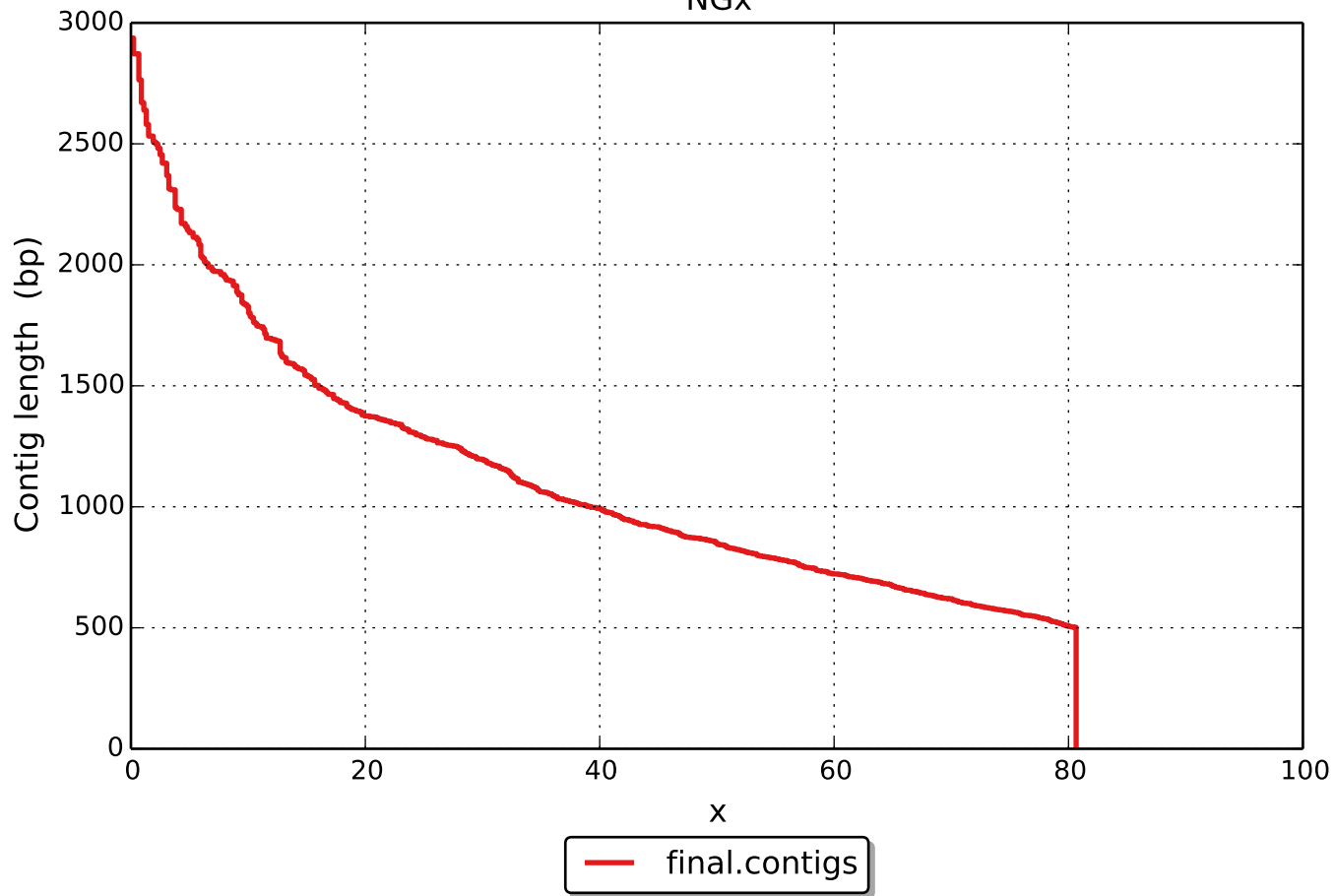
GC content



Nx



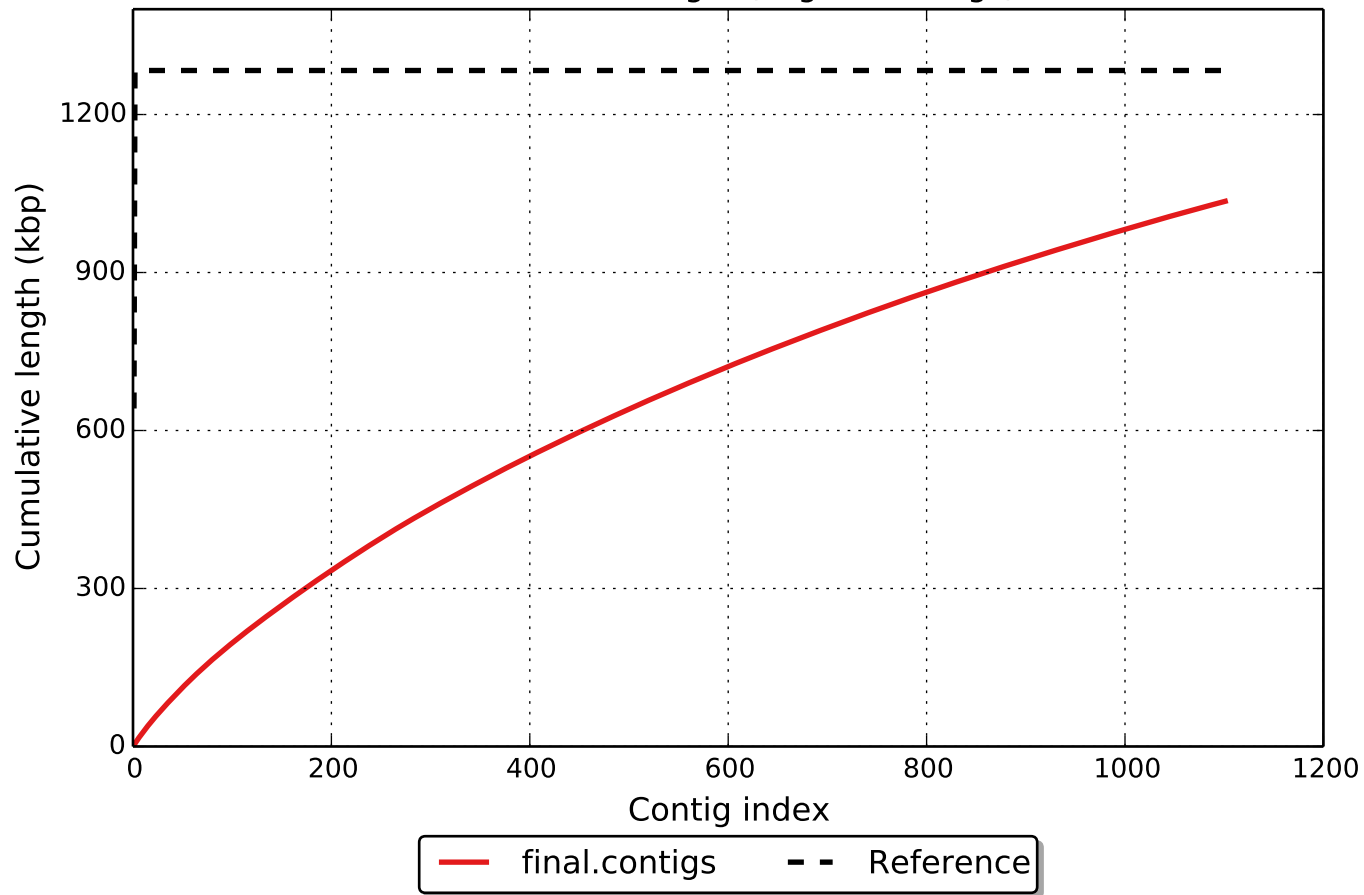
NGx



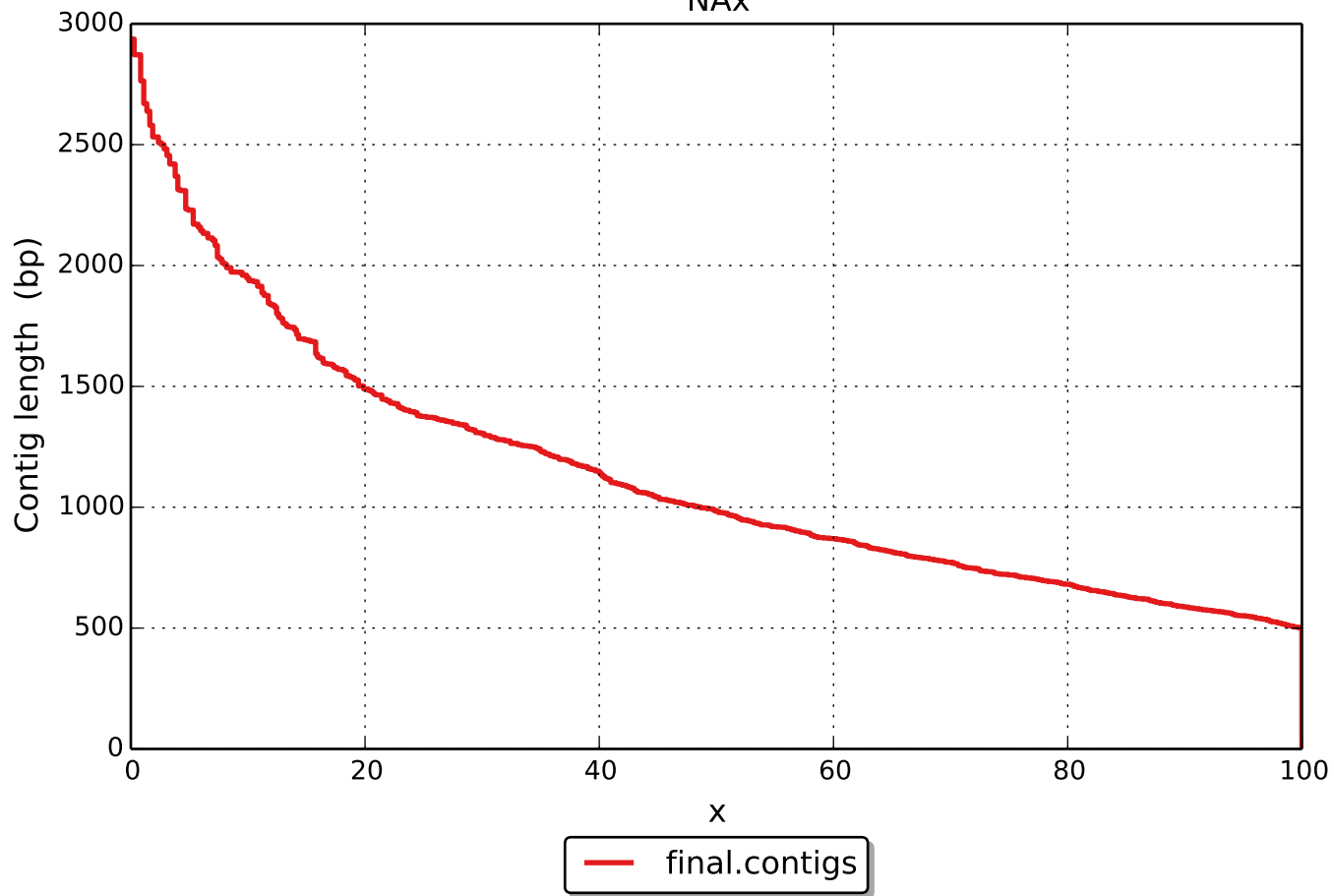
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

