

Report

	final.contigs
# contigs (≥ 0 bp)	2782
# contigs (≥ 1000 bp)	1445
Total length (≥ 0 bp)	3448070
Total length (≥ 1000 bp)	2486531
# contigs	2782
Largest contig	7759
Total length	3448070
Reference length	1892775
GC (%)	32.28
Reference GC (%)	32.26
N50	1437
NG50	2032
N75	956
NG75	1638
L50	807
LG50	347
L75	1547
LG75	609
# misassemblies	76
# misassembled contigs	75
Misassembled contigs length	124917
# local misassemblies	0
# unaligned contigs	2 + 3 part
Unaligned length	2977
Genome fraction (%)	92.772
Duplication ratio	1.962
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1745.66
# indels per 100 kbp	1.25
Largest alignment	7759
NA50	1411
NGA50	1991
NA75	934
NGA75	1603
LA50	820
LGA50	352
LA75	1573
LGA75	618

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

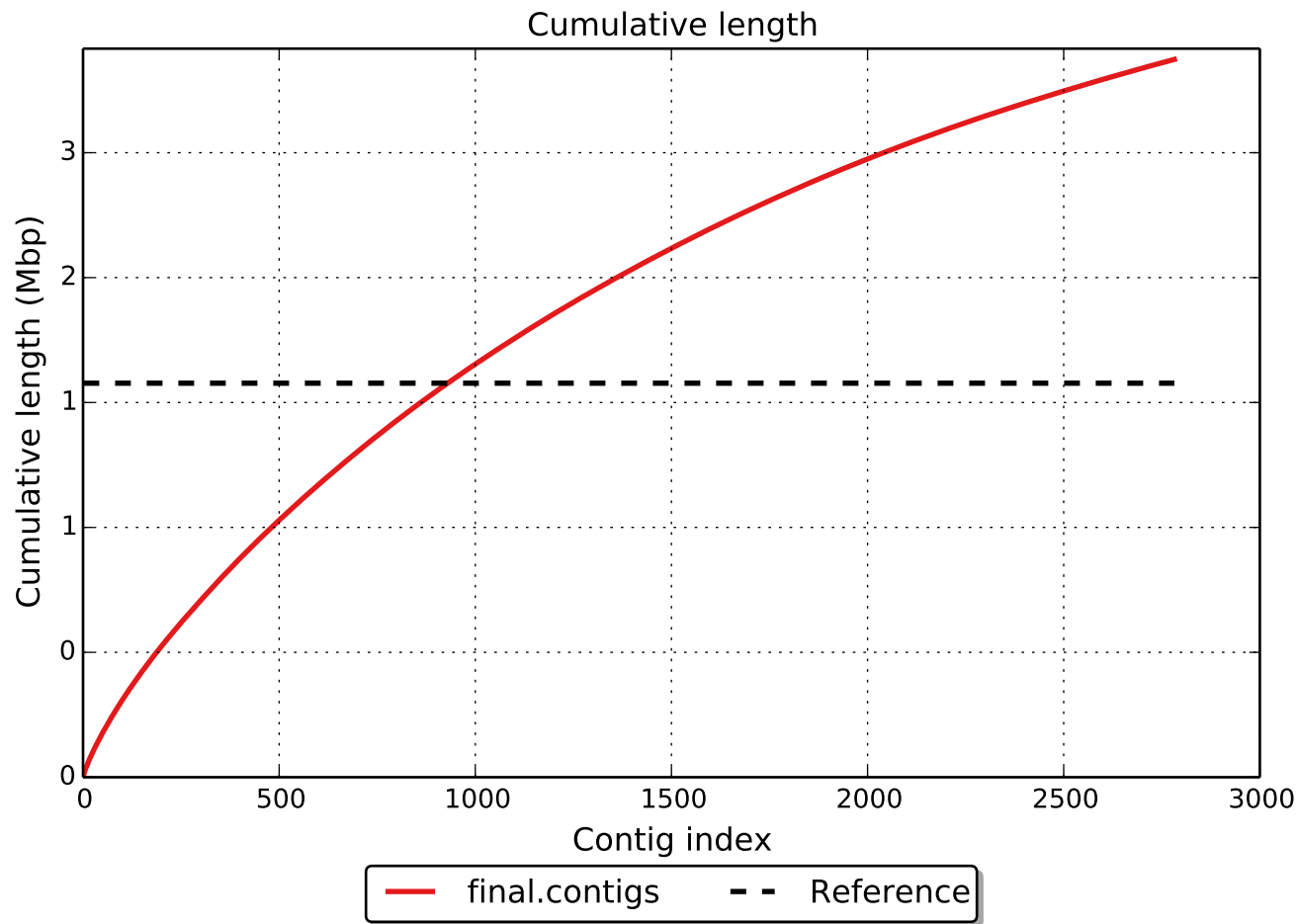
	final.contigs
# misassemblies	76
# relocations	76
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	75
Misassembled contigs length	124917
# local misassemblies	0
# mismatches	30653
# indels	22
# short indels	22
# long indels	0
Indels length	22

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).

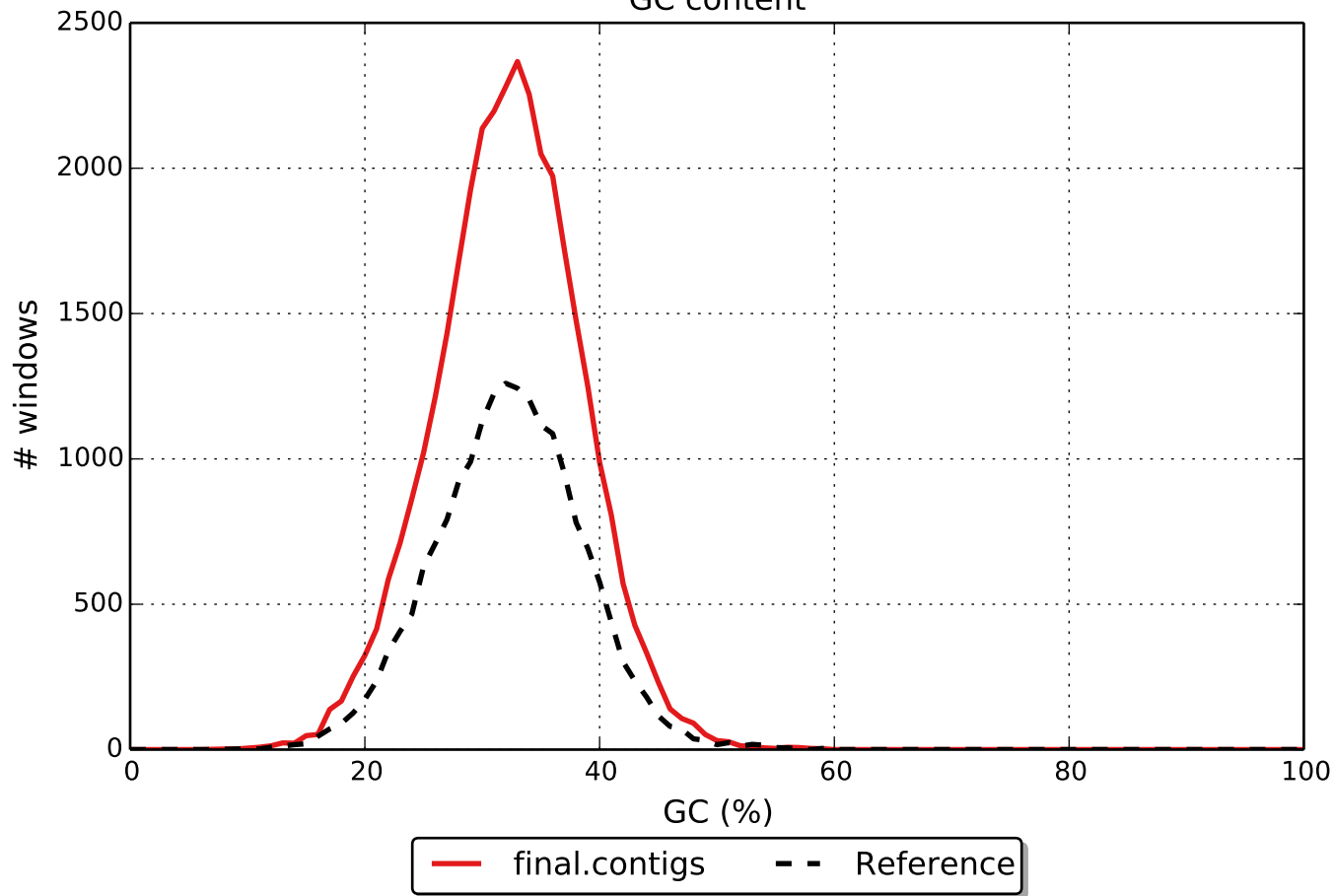
Unaligned report

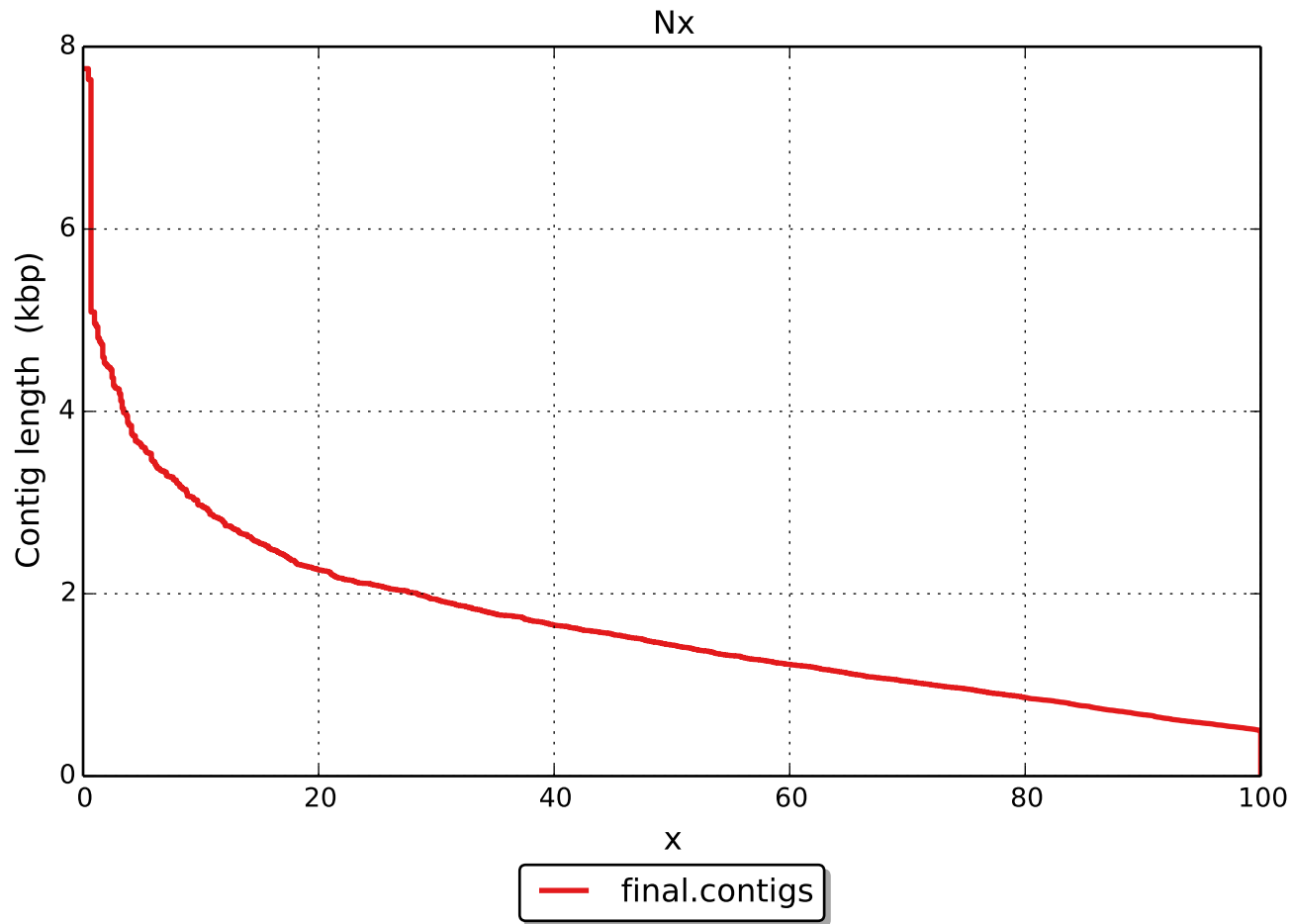
	final.contigs
# fully unaligned contigs	2
Fully unaligned length	2263
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	714
# N's	0

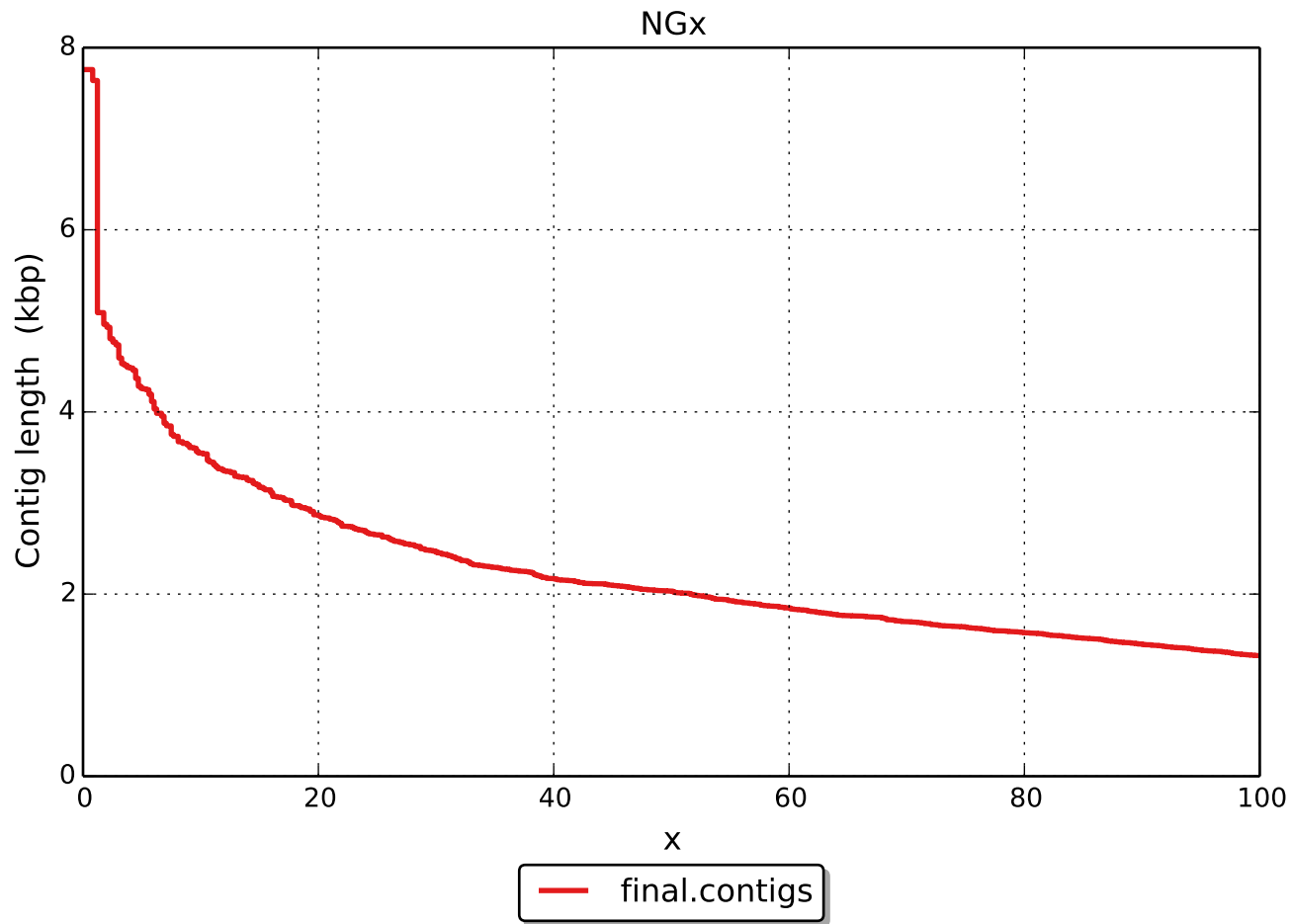
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



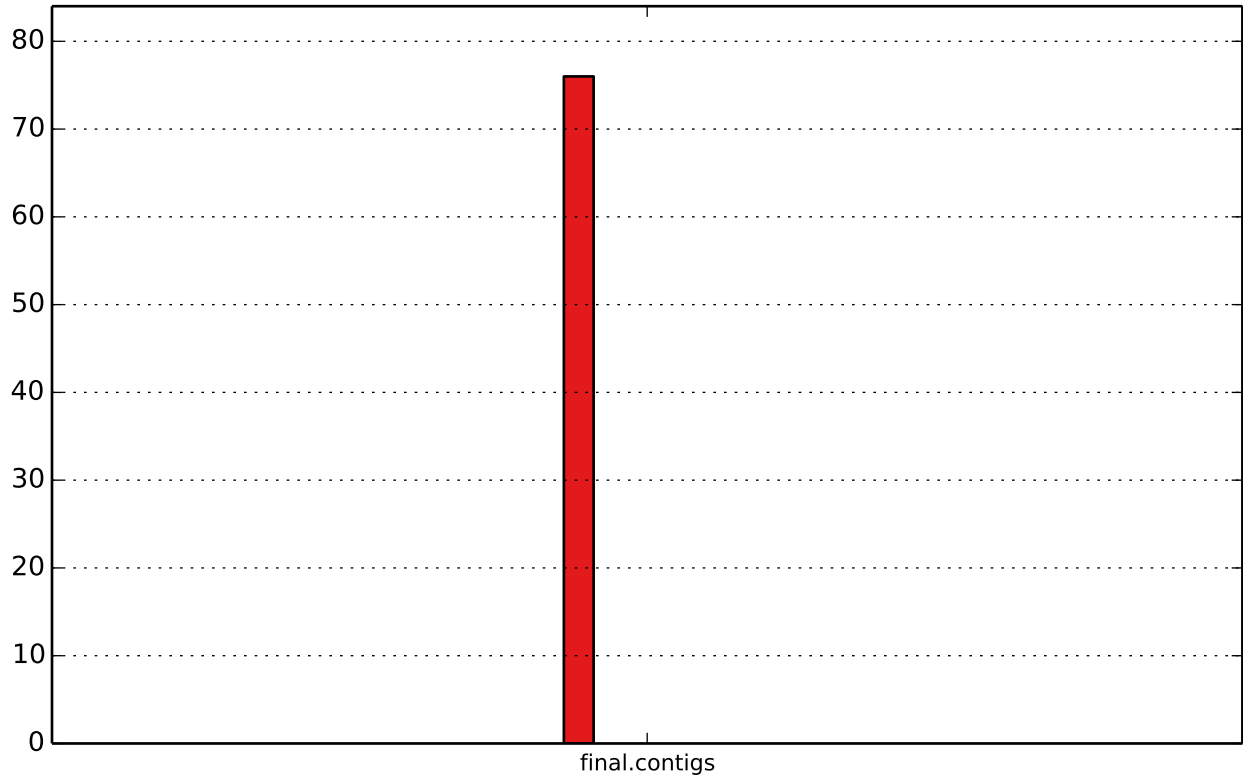
GC content

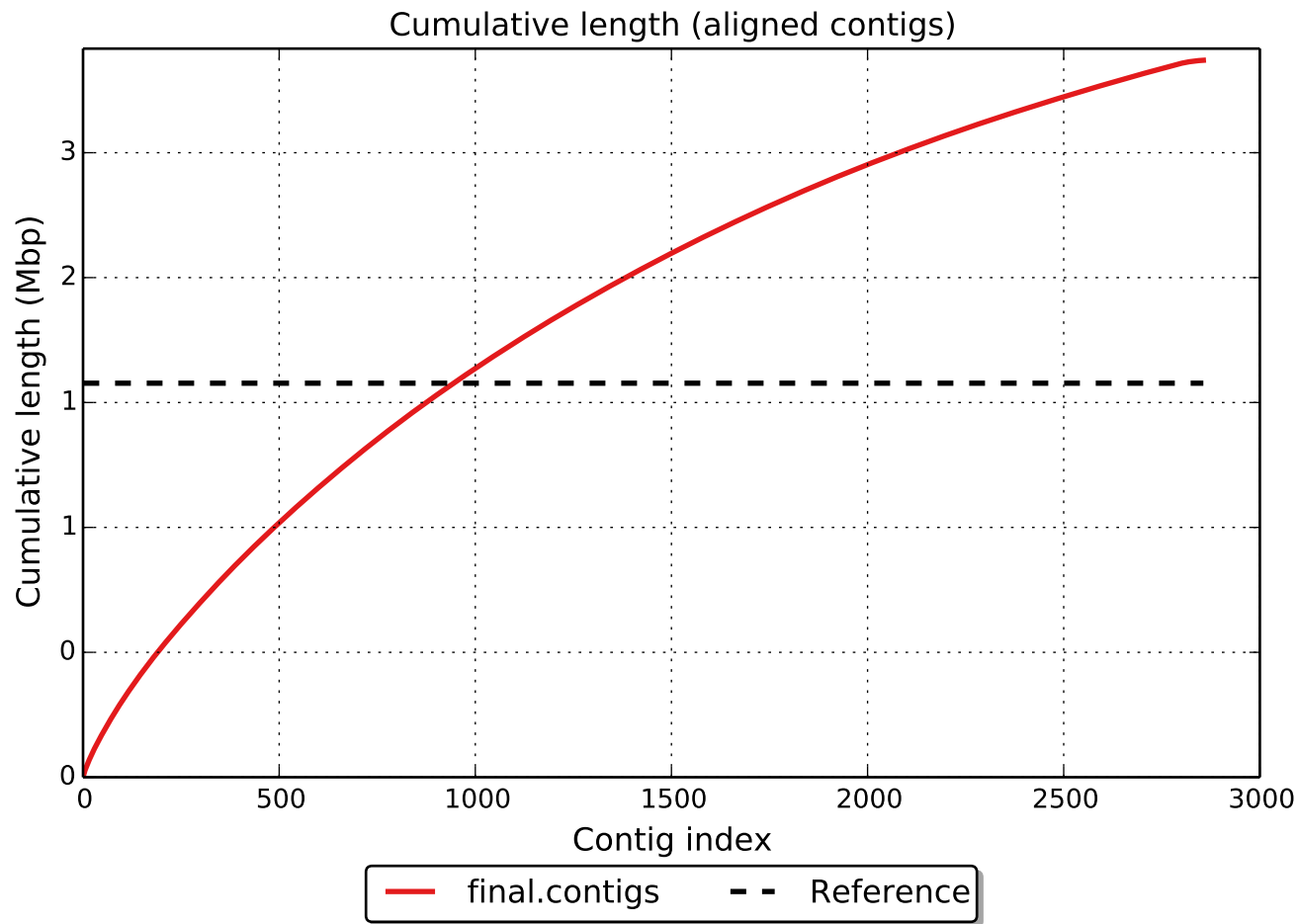


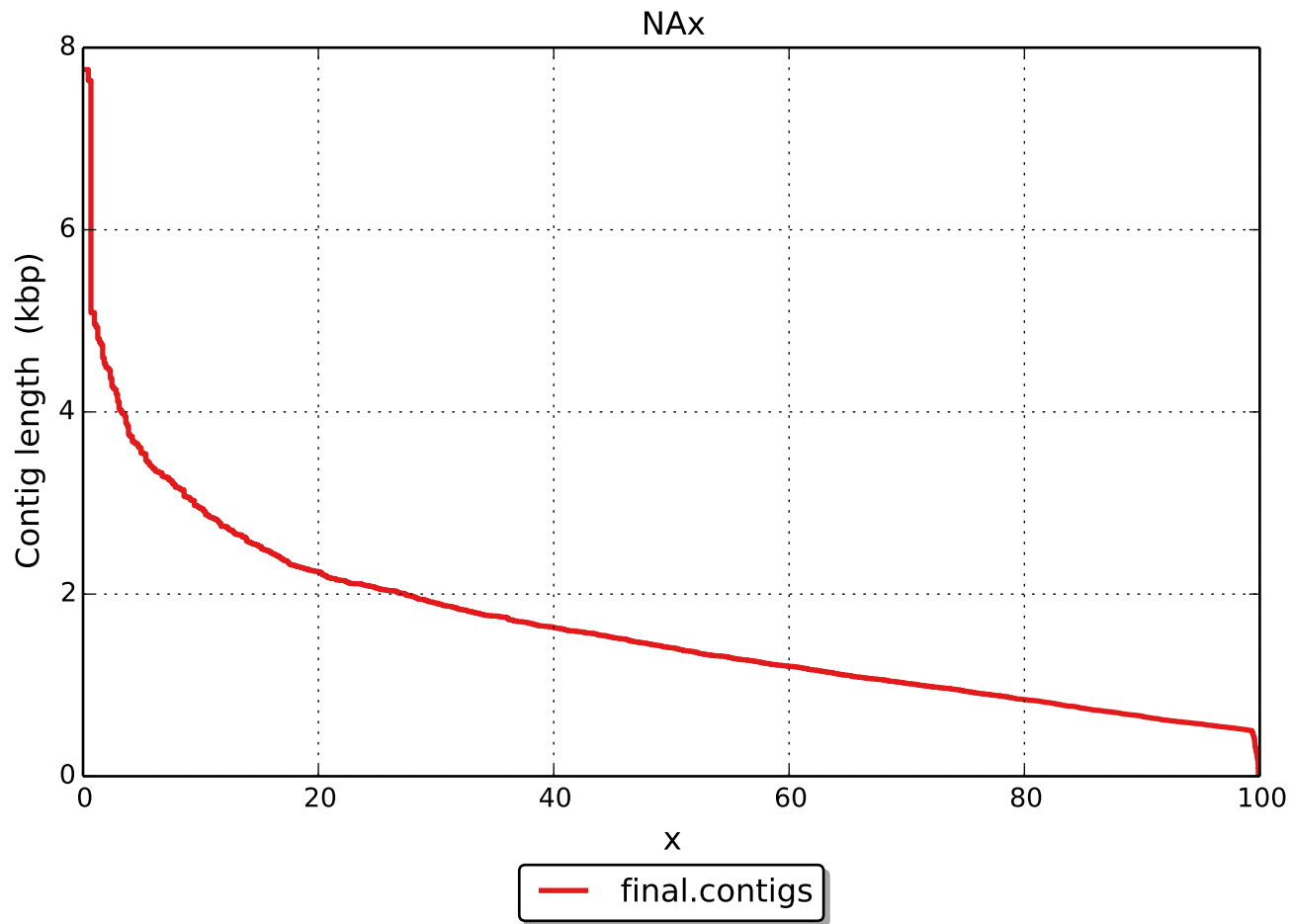




Misassemblies







NGAx

