

Report

	final.contigs
# contigs (≥ 0 bp)	3406
# contigs (≥ 1000 bp)	958
Total length (≥ 0 bp)	3116837
Total length (≥ 1000 bp)	1396686
# contigs	3406
Largest contig	3974
Total length	3116837
Reference length	1892775
GC (%)	32.32
Reference GC (%)	32.26
N50	940
NG50	1246
N75	694
NG75	987
L50	1126
LG50	551
L75	2090
LG75	982
# misassemblies	38
# misassembled contigs	37
Misassembled contigs length	39714
# local misassemblies	0
# unaligned contigs	1 + 1 part
Unaligned length	915
Genome fraction (%)	85.819
Duplication ratio	1.918
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1157.44
# indels per 100 kbp	0.37
Largest alignment	3974
NA50	831
NGA50	1082
NA75	594
NGA75	882
LA50	1271
LGA50	622
LA75	2390
LGA75	1109

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

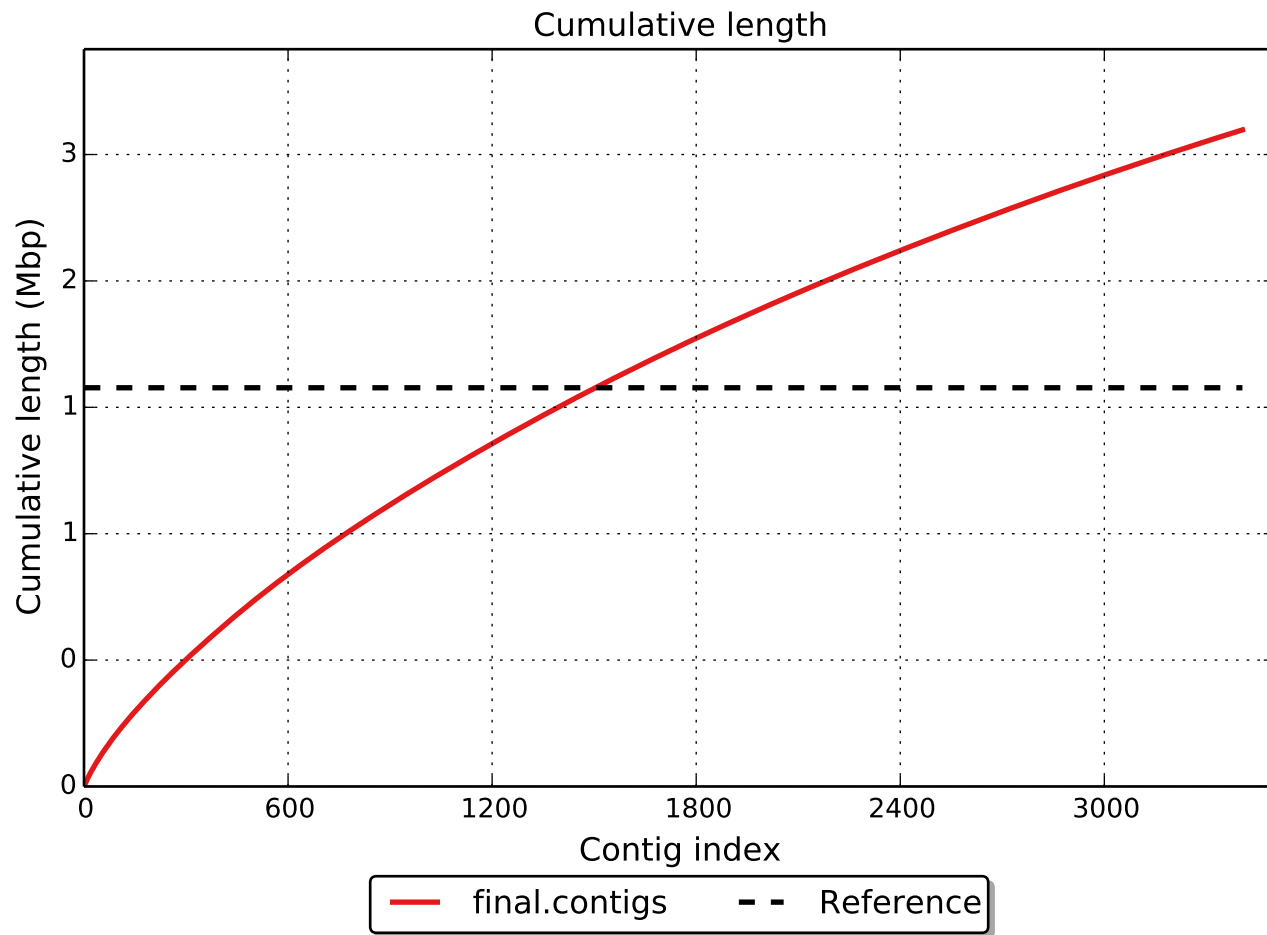
	final.contigs
# misassemblies	38
# relocations	38
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	37
Misassembled contigs length	39714
# local misassemblies	0
# mismatches	18801
# indels	6
# short indels	6
# long indels	0
Indels length	6

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).

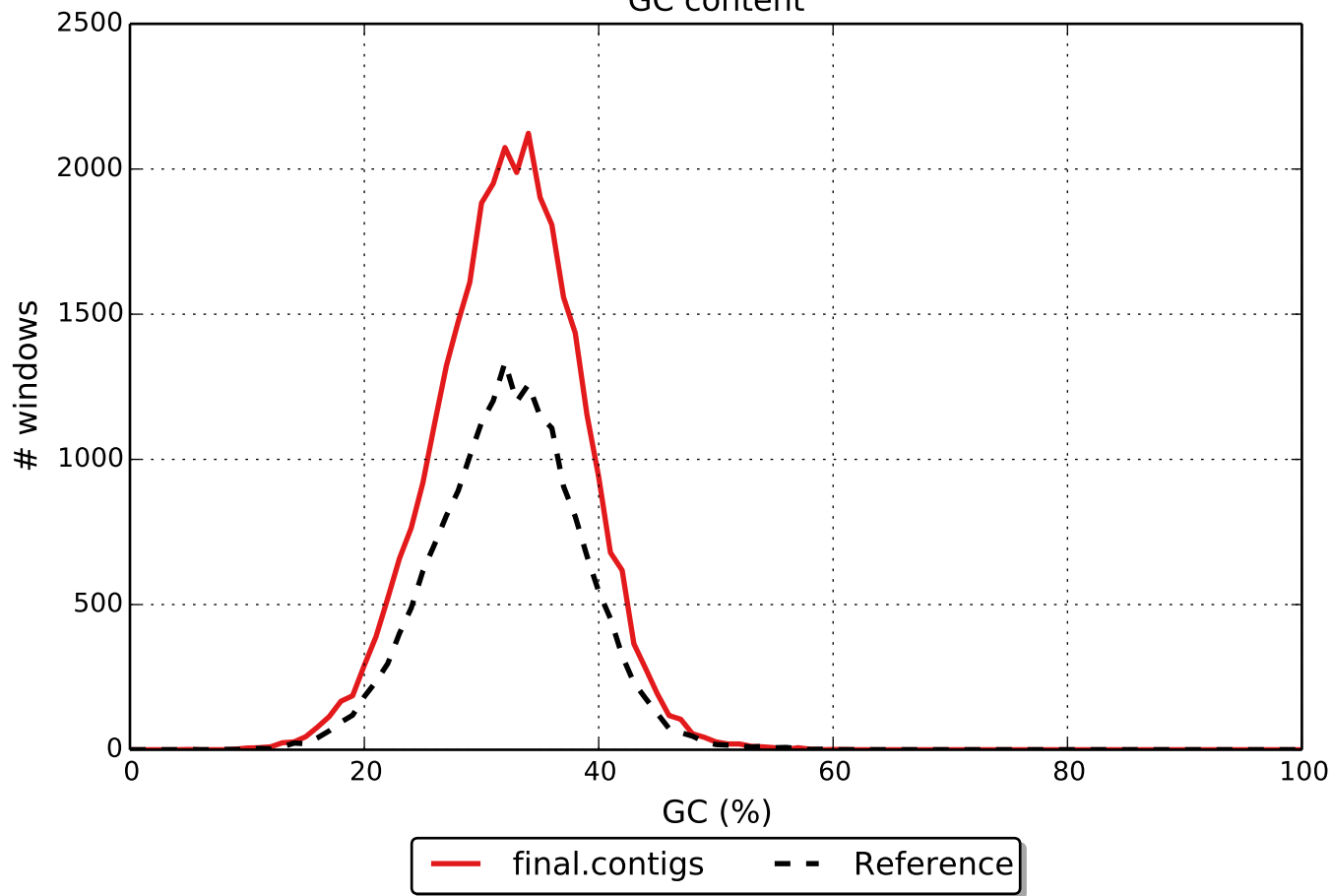
Unaligned report

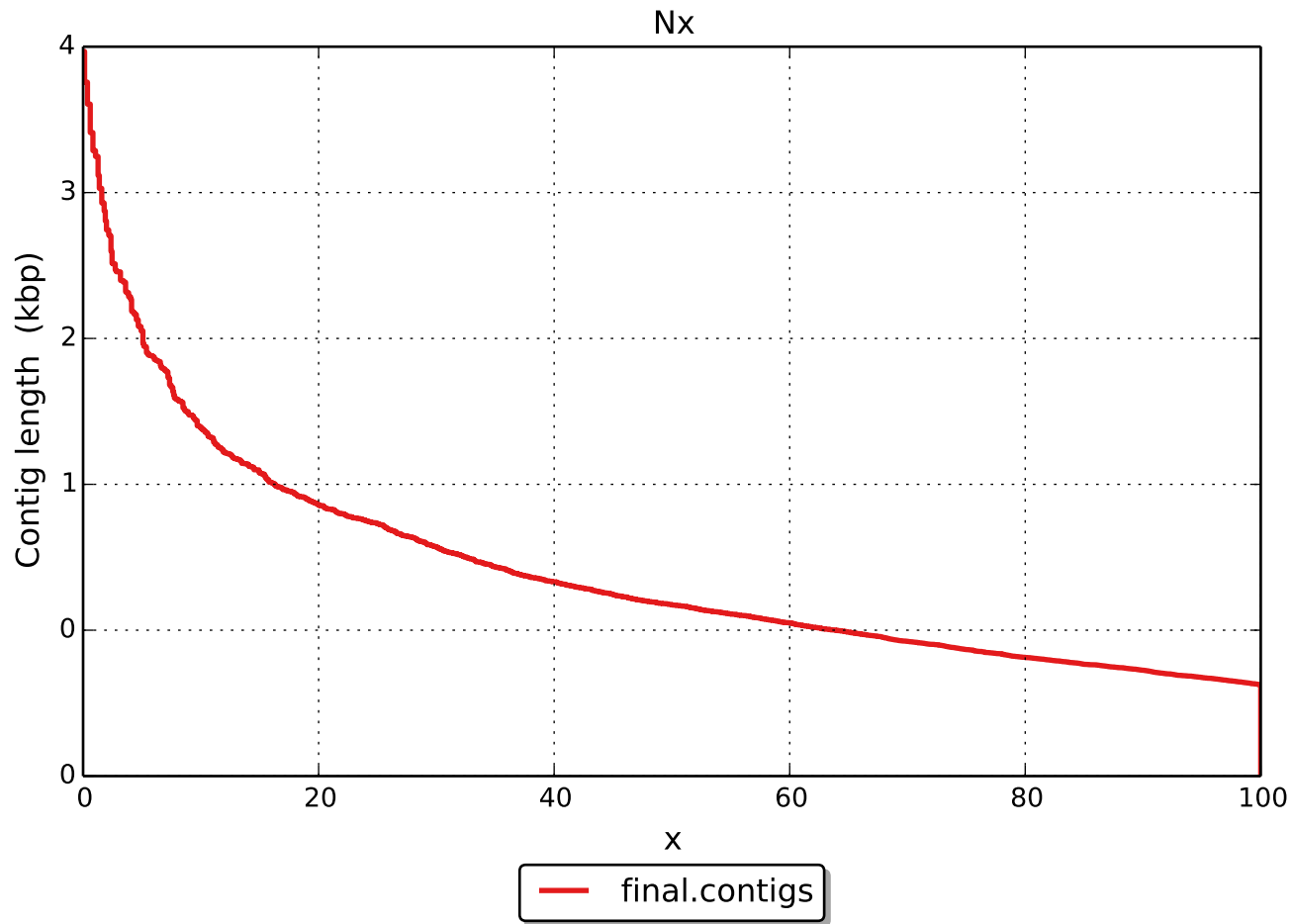
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	529
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	386
# N's	0

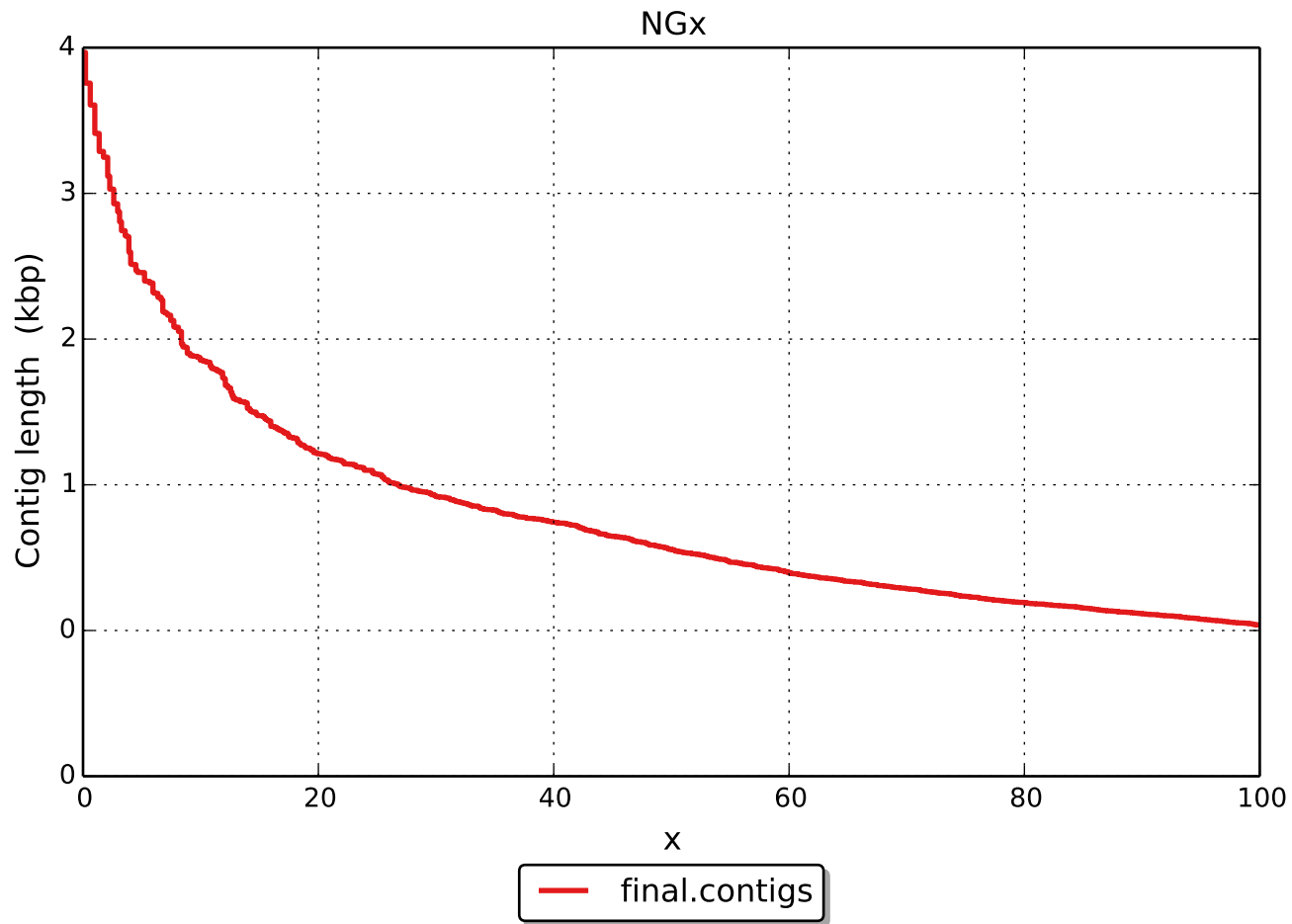
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



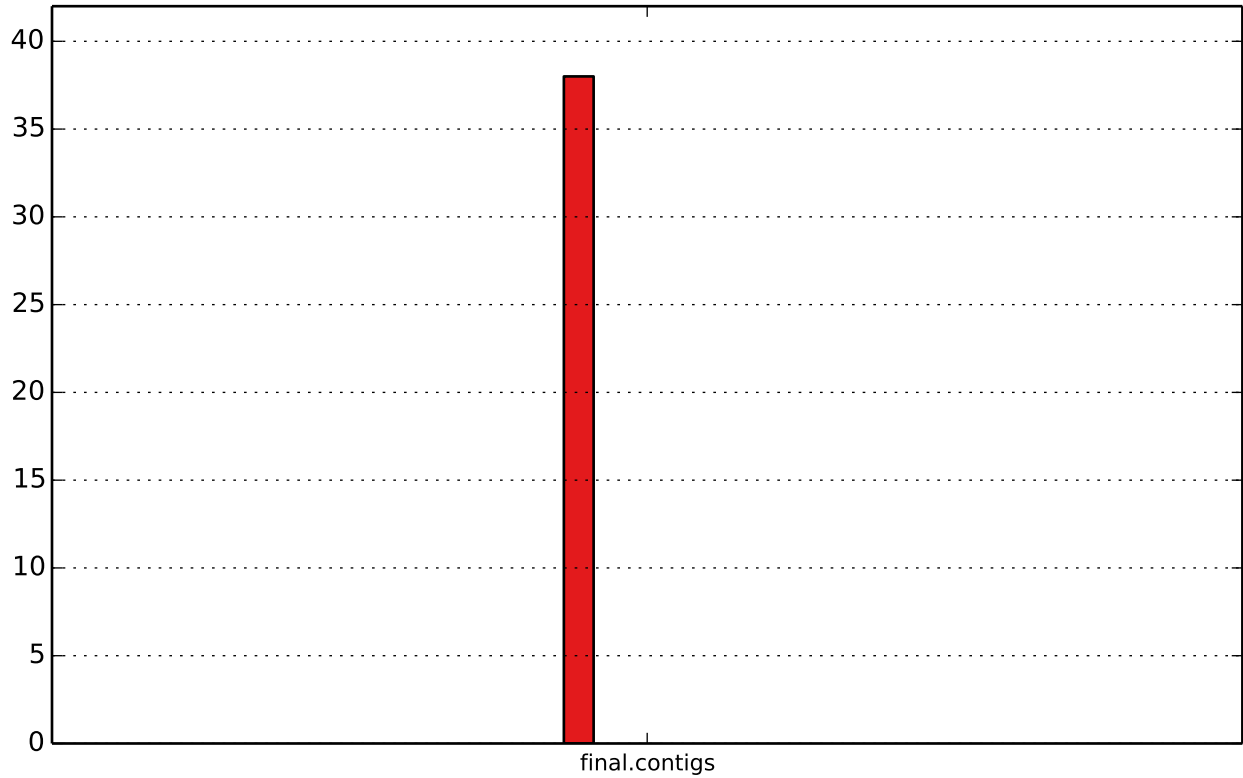
GC content



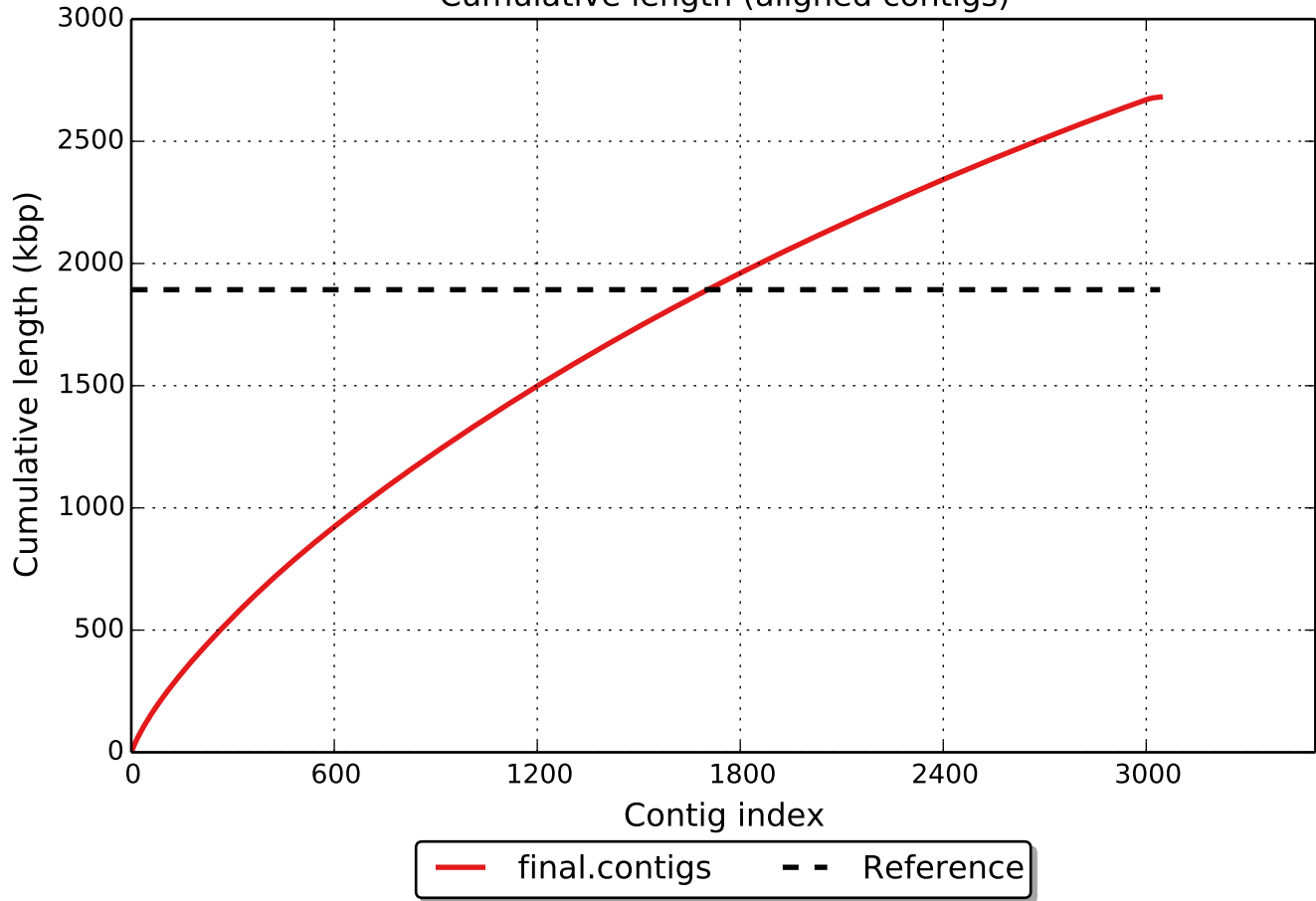


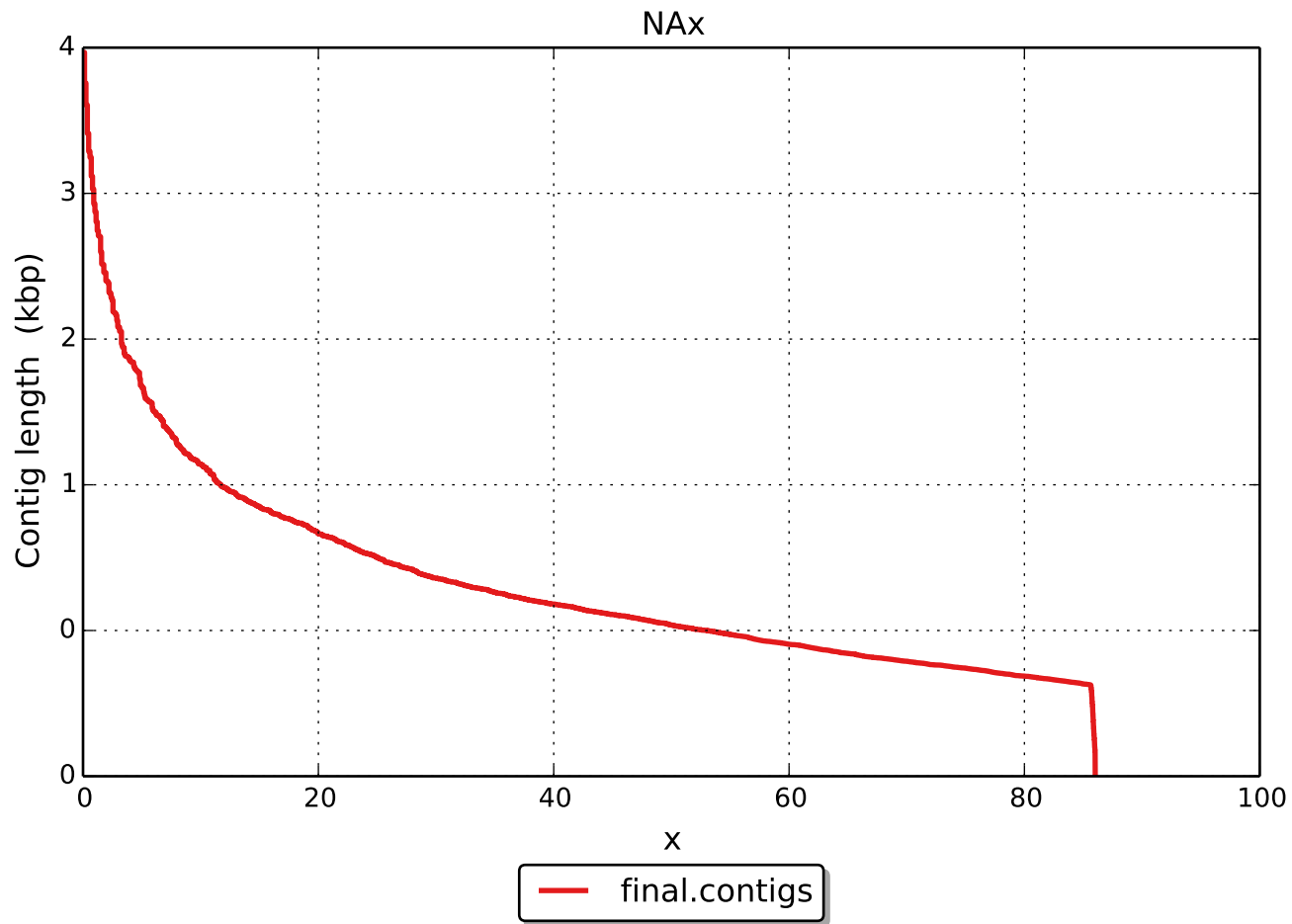


Misassemblies



Cumulative length (aligned contigs)





NGAx

