

Report

	final.contigs
# contigs (>= 1000 bp)	1210
# contigs (>= 5000 bp)	243
# contigs (>= 10000 bp)	28
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4178600
Total length (>= 5000 bp)	1803177
Total length (>= 10000 bp)	365081
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1528
Largest contig	18143
Total length	4411595
Reference length	4641652
GC (℥)	50.75
Reference GC (℥)	50.79
N50	4124
NG50	3930
N75	2443
NG75	2134
L50	332
LG50	360
L75	674
LG75	749
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	12922
# local misassemblies	8
# unaligned contigs	0 + 5 part
Unaligned length	1111
Genome fraction (℥)	94.725
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	108.99
# indels per 100 kbp	10.33
Largest alignment	18143
NA50	4124
NGA50	3930
NA75	2429
NGA75	2124
LA50	332
LGA50	360
LA75	674
LGA75	750

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

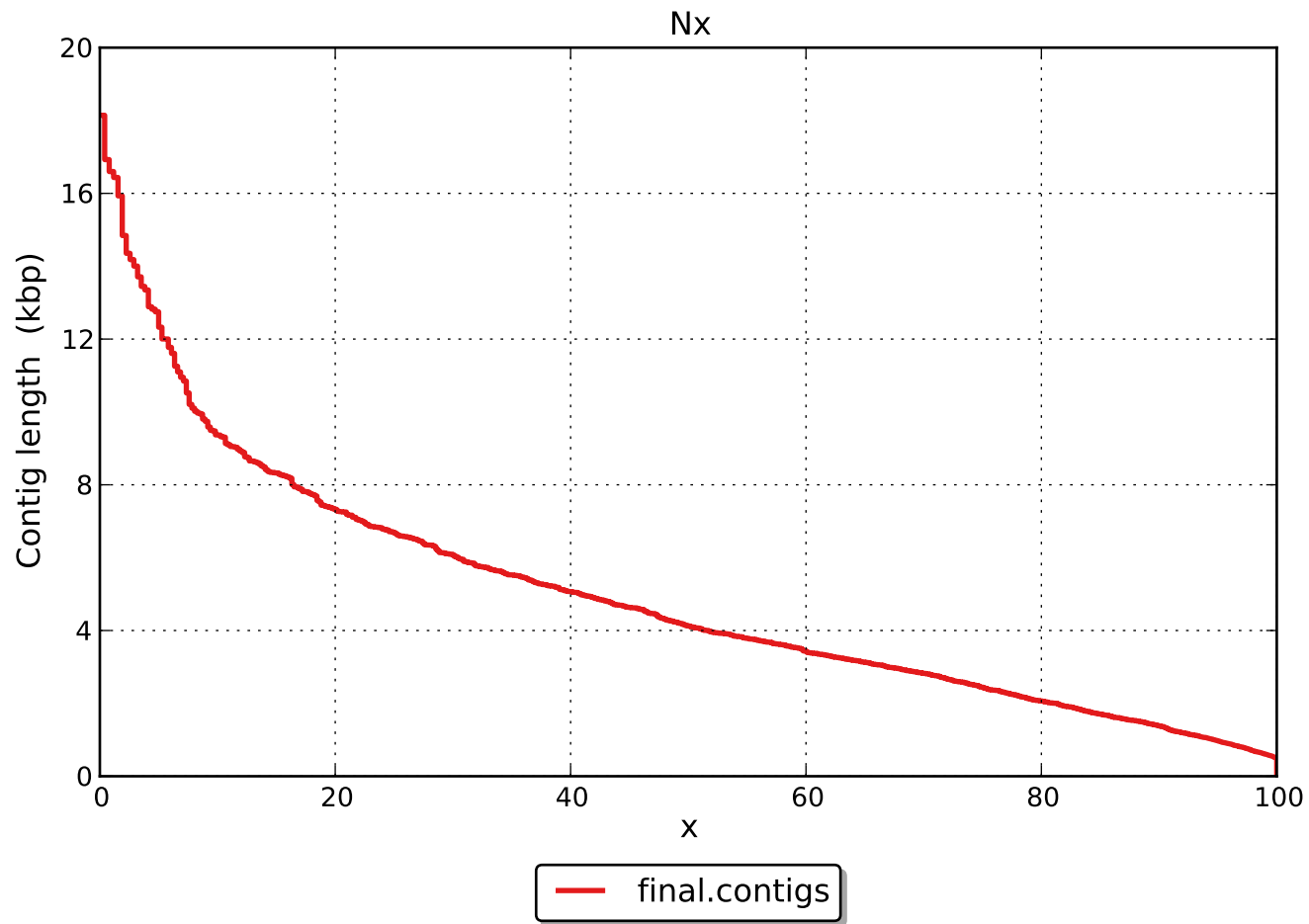
	final.contigs
# misassemblies	4
# relocations	3
# translocations	0
# inversions	1
# possibly misassembled contigs	1
# misassembled contigs	4
Misassembled contigs length	12922
# local misassemblies	8
# mismatches	4792
# indels	454
# short indels	449
# long indels	5
Indels length	785

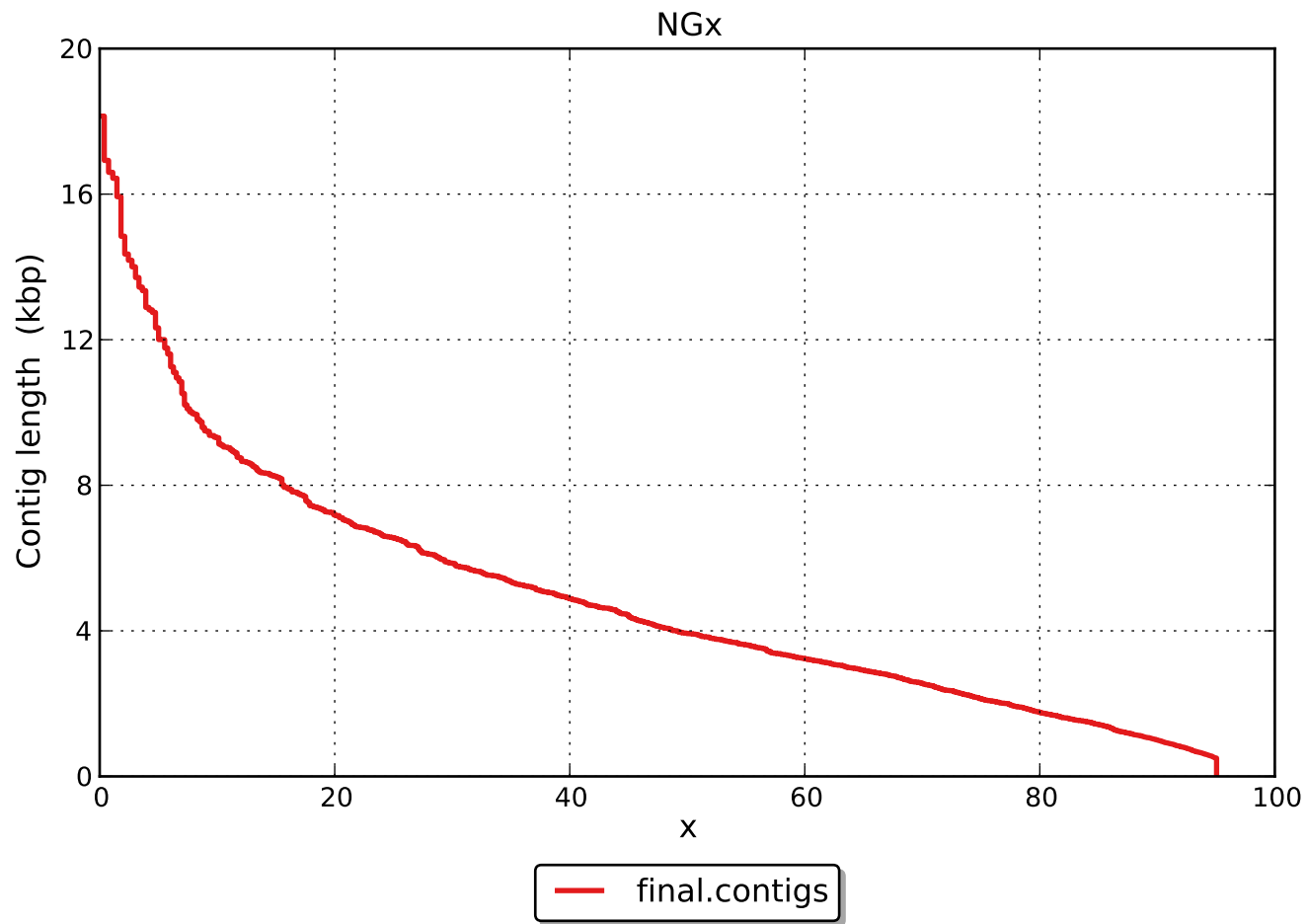
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

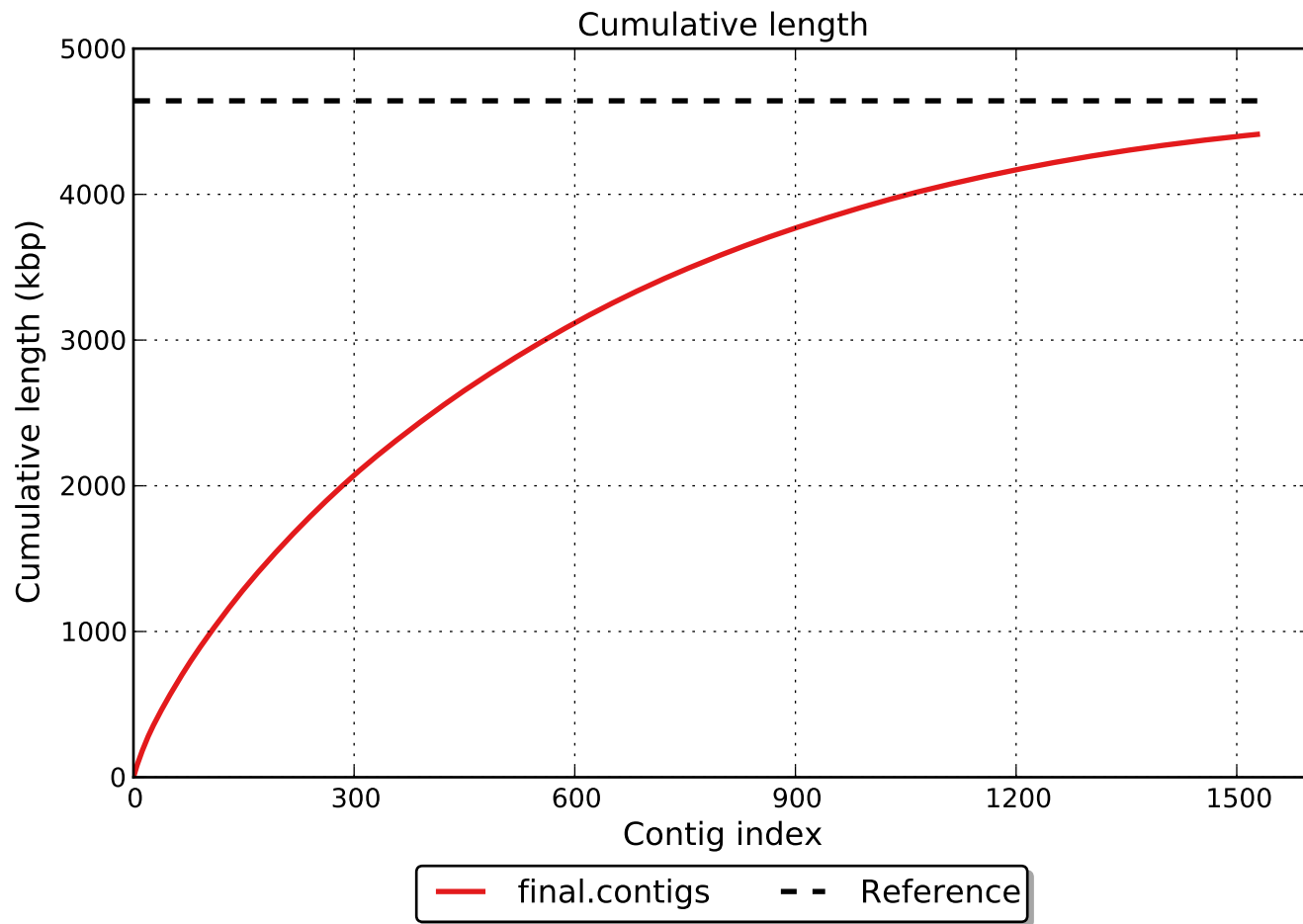
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1111
# N's	0

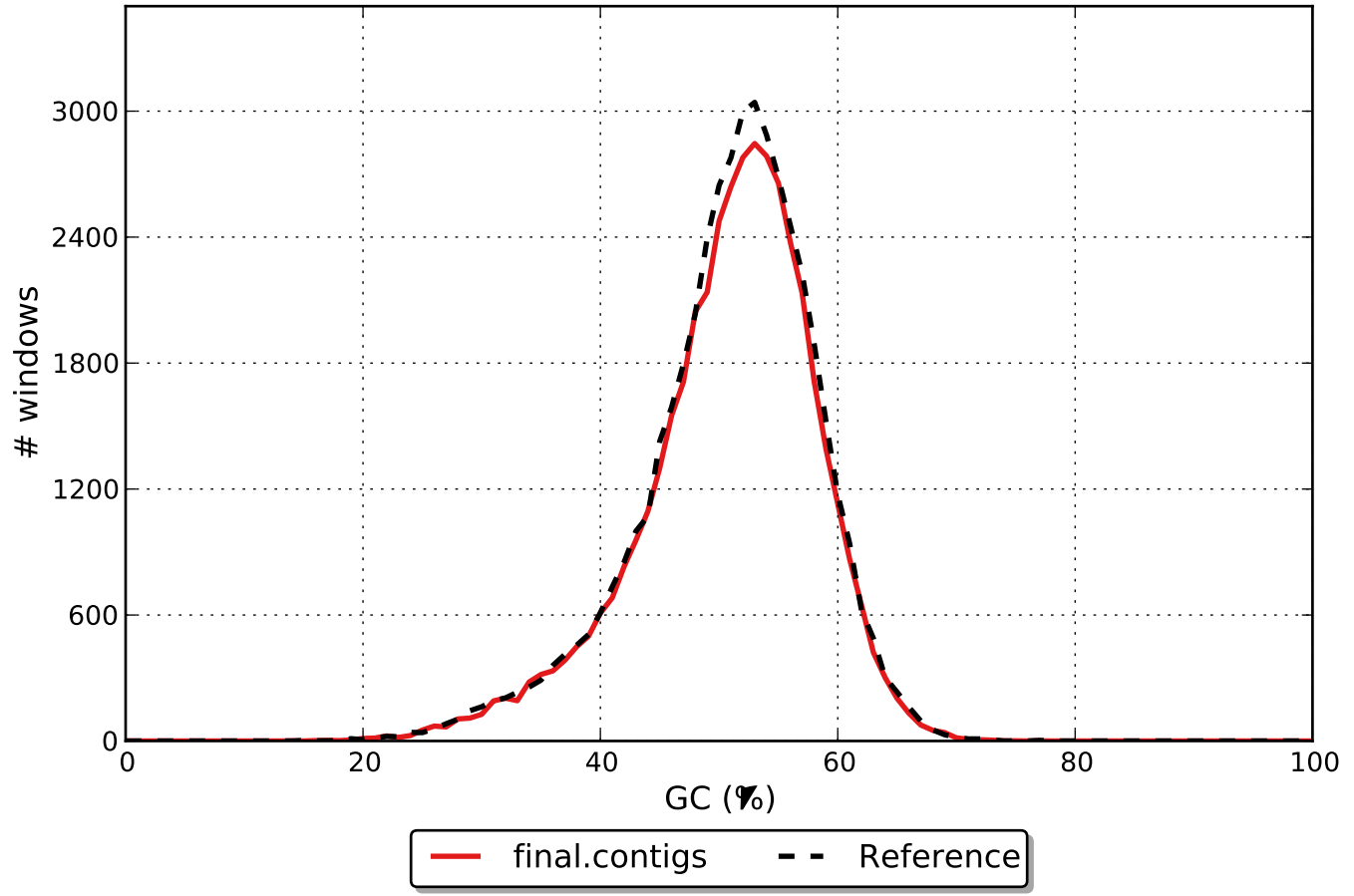
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

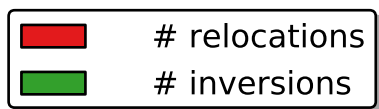
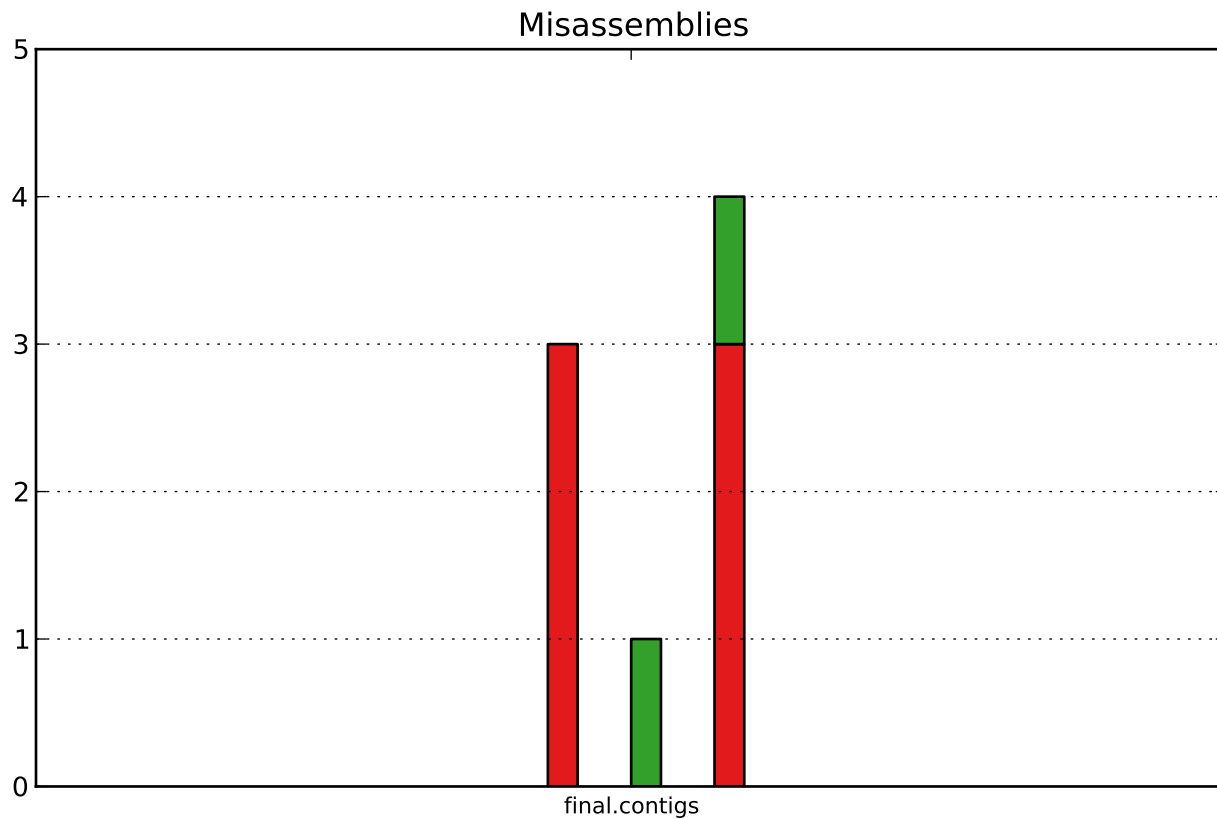




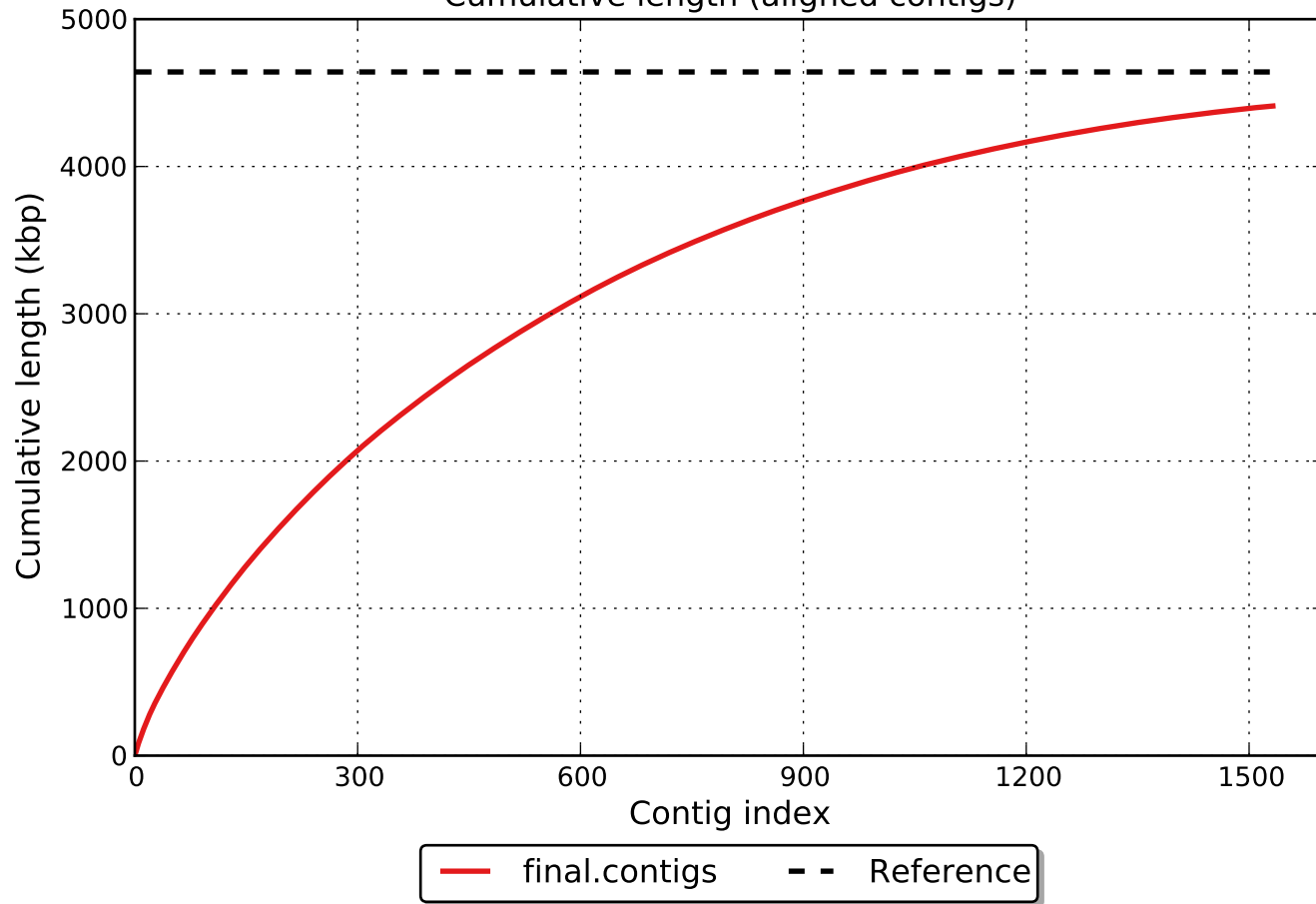


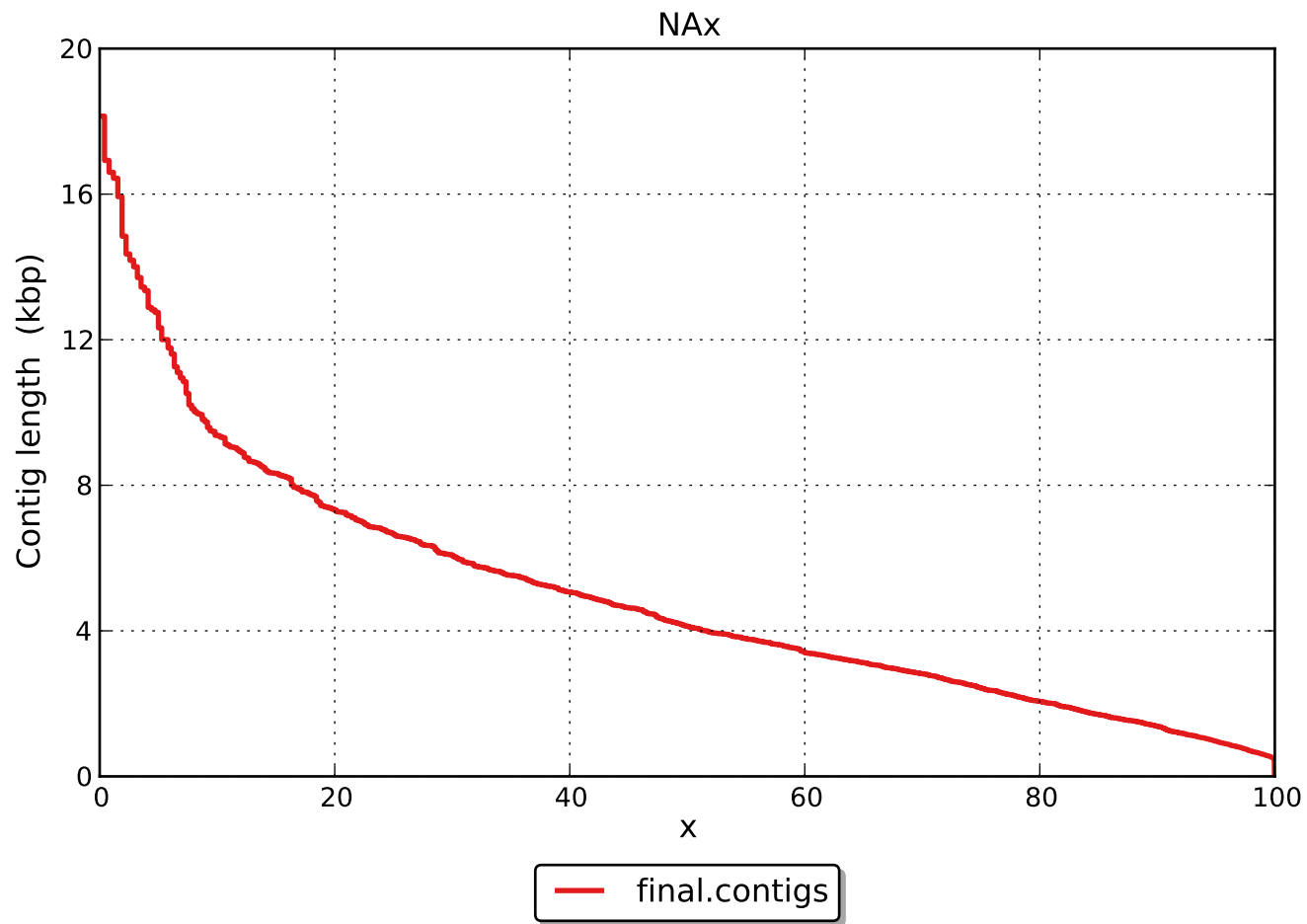
GC content





Cumulative length (aligned contigs)





NGAx

