

Report

	final.contigs
# contigs (>= 0 bp)	1852
# contigs (>= 1000 bp)	1334
# contigs (>= 5000 bp)	221
# contigs (>= 10000 bp)	31
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4710811
Total length (>= 1000 bp)	4390205
Total length (>= 5000 bp)	1665674
Total length (>= 10000 bp)	411577
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1668
Largest contig	22629
Total length	4640501
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	3816
NG50	3814
N75	2300
NG75	2300
L50	371
LG50	372
L75	757
LG75	757
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	31226
# local misassemblies	3
# unaligned contigs	106 + 14 part
Unaligned length	88689
Genome fraction (%)	95.535
Duplication ratio	1.026
# N's per 100 kbp	0.00
# mismatches per 100 kbp	243.15
# indels per 100 kbp	0.02
Largest alignment	22627
NA50	3804
NGA50	3804
NA75	2285
NGA75	2285
LA50	373
LGA50	373
LA75	760
LGA75	760

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

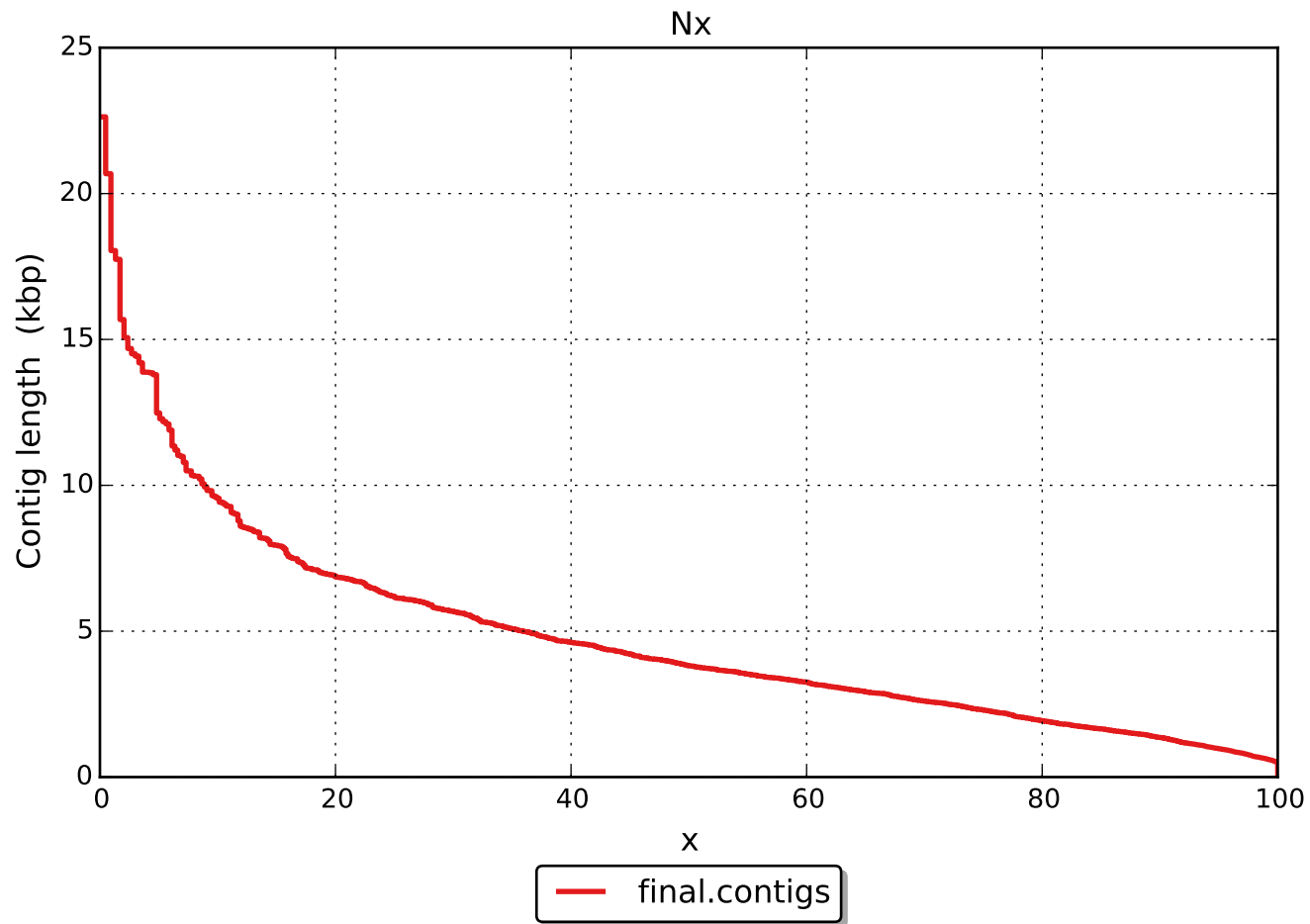
	final.contigs
# misassemblies	5
# relocations	5
# translocations	0
# inversions	0
# misassembled contigs	5
Misassembled contigs length	31226
# local misassemblies	3
# mismatches	10782
# indels	1
# short indels	0
# long indels	1
Indels length	24

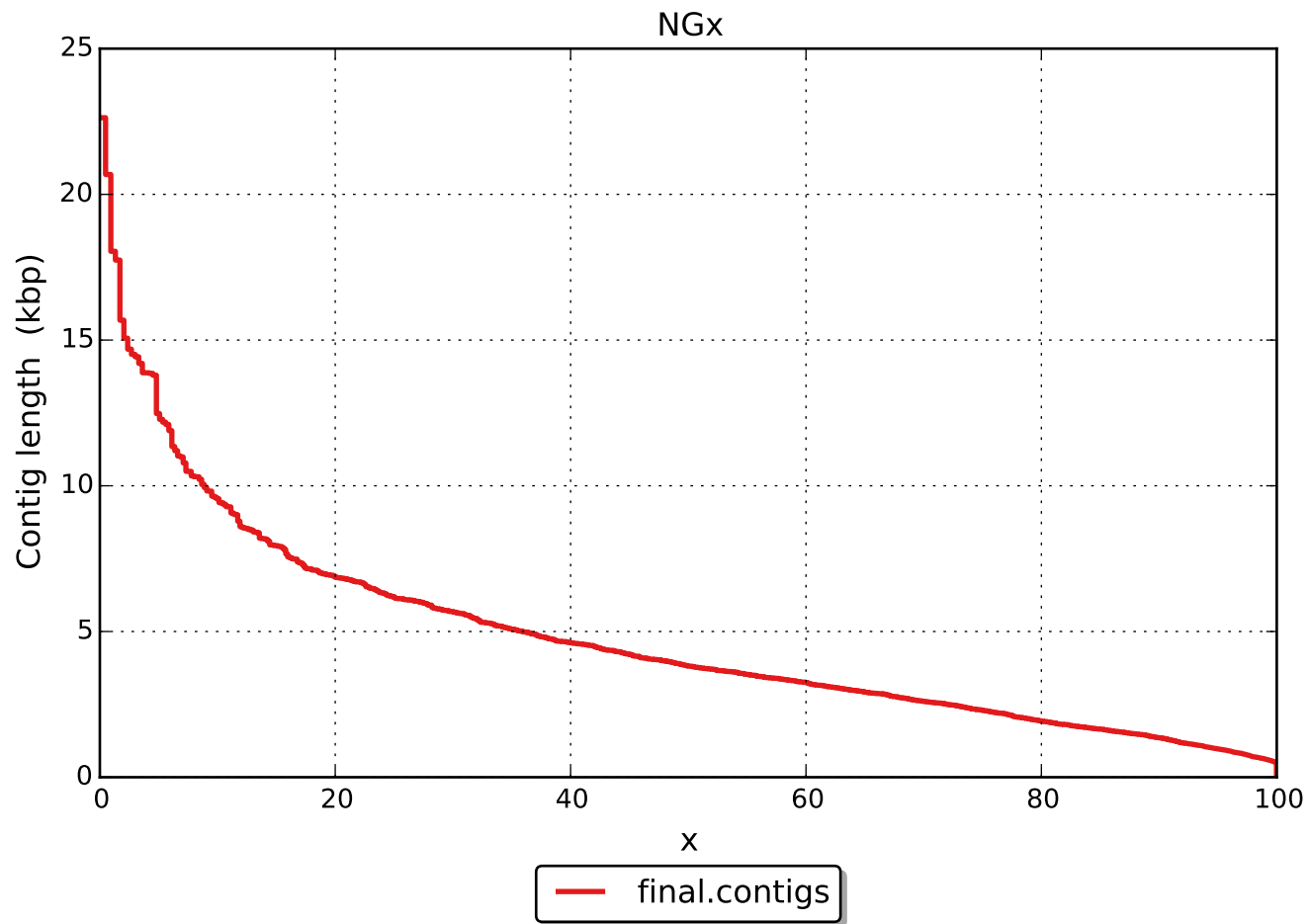
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

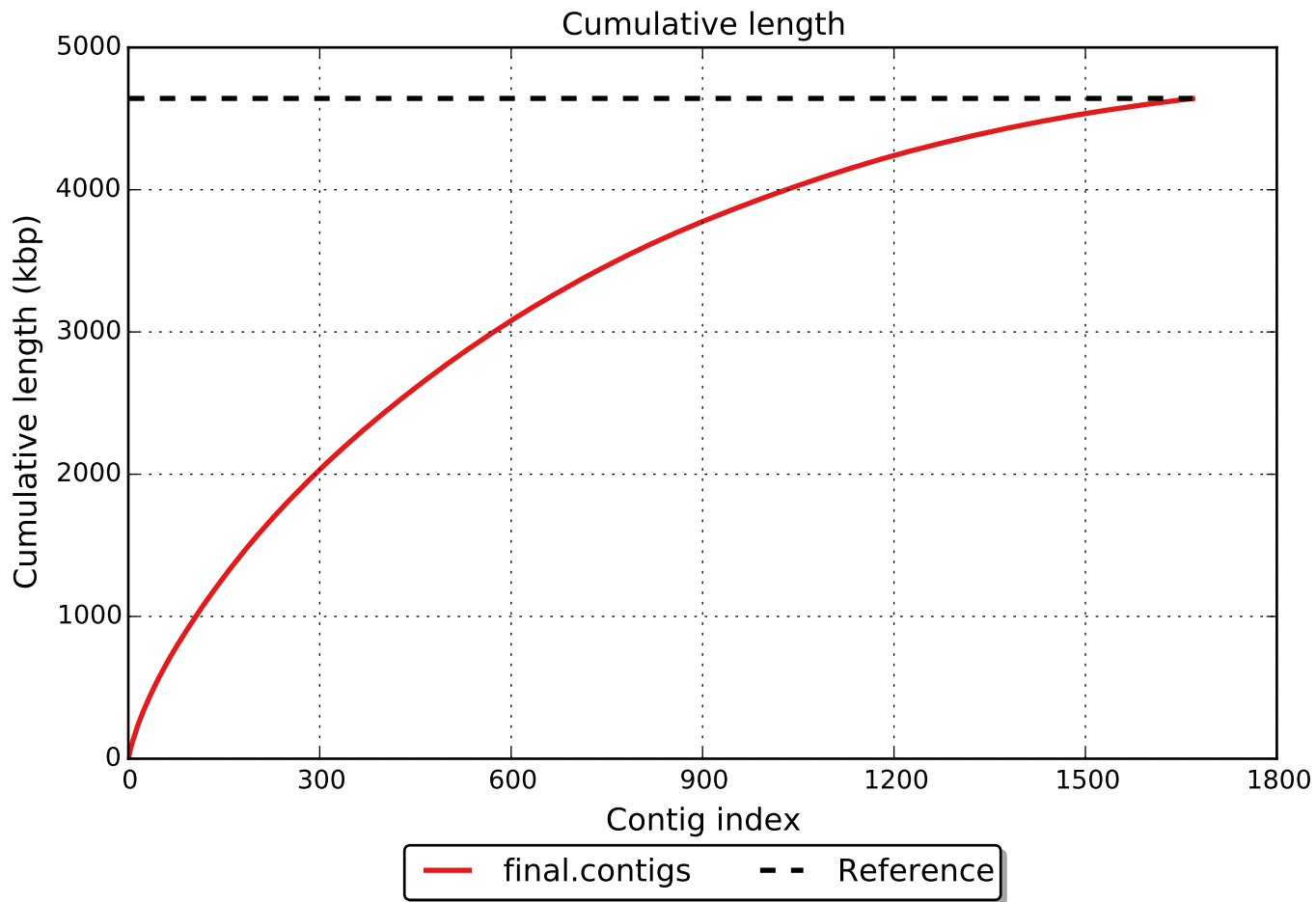
Unaligned report

	final.contigs
# fully unaligned contigs	106
Fully unaligned length	84459
# partially unaligned contigs	14
# with misassembly	0
# both parts are significant	1
Partially unaligned length	4230
# N's	0

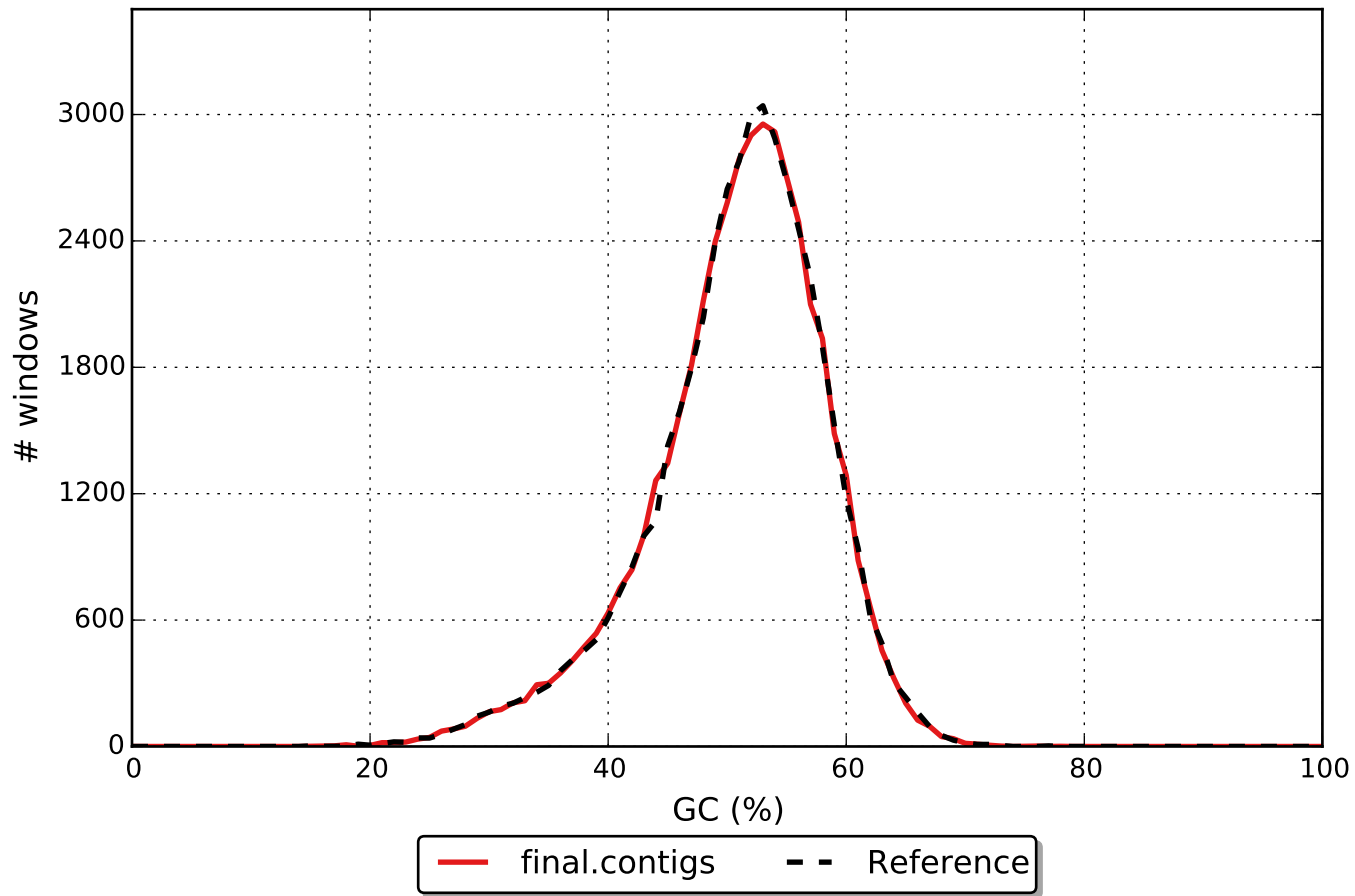
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

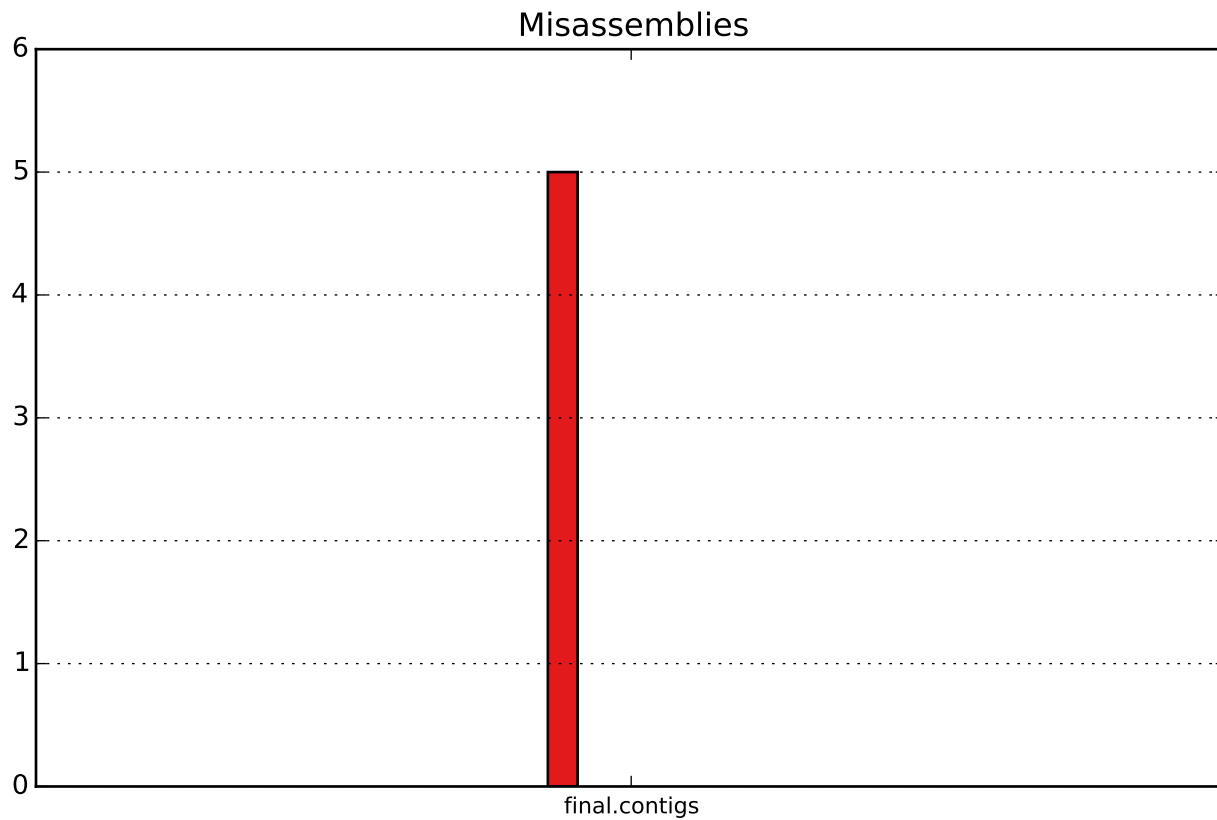




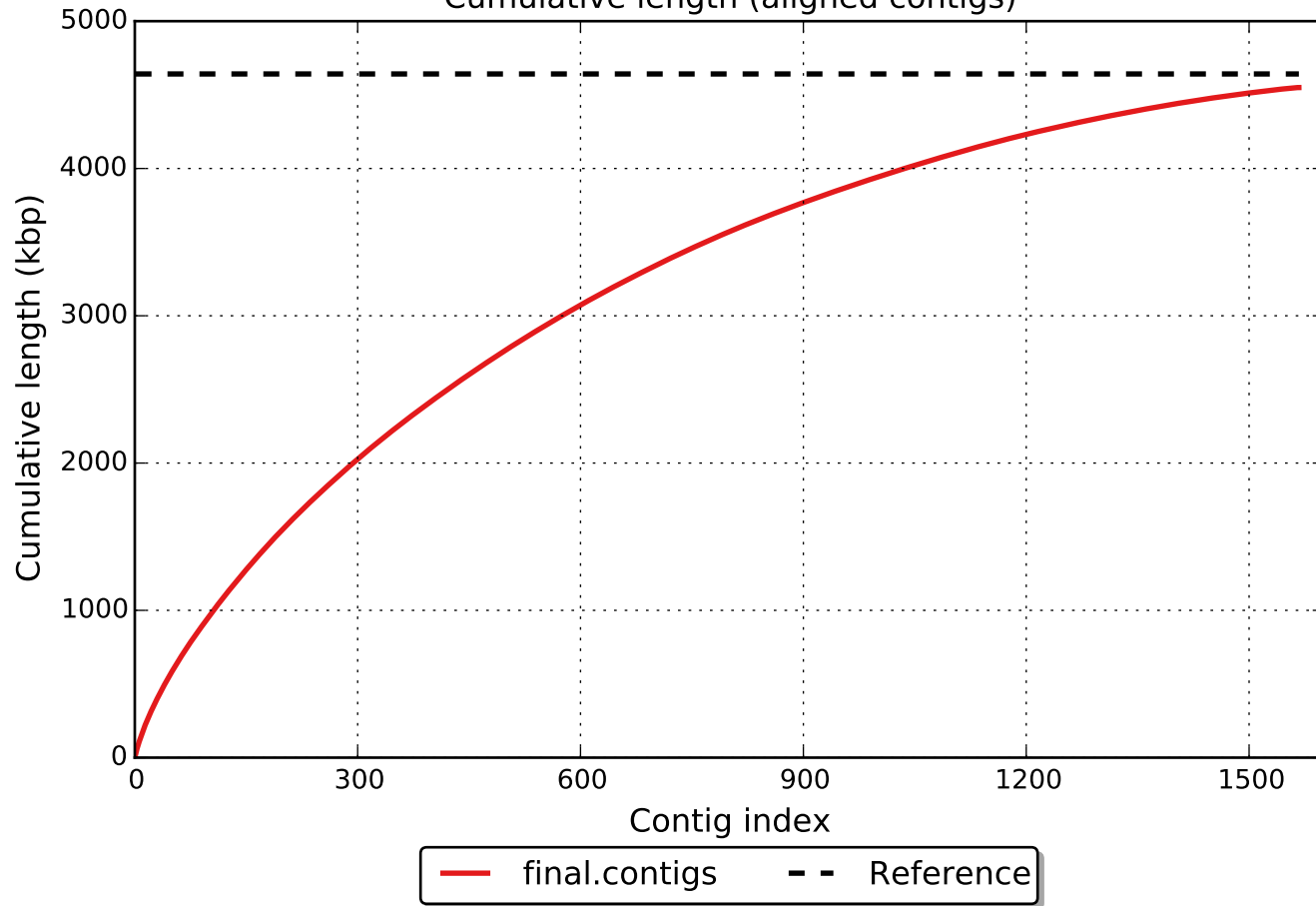


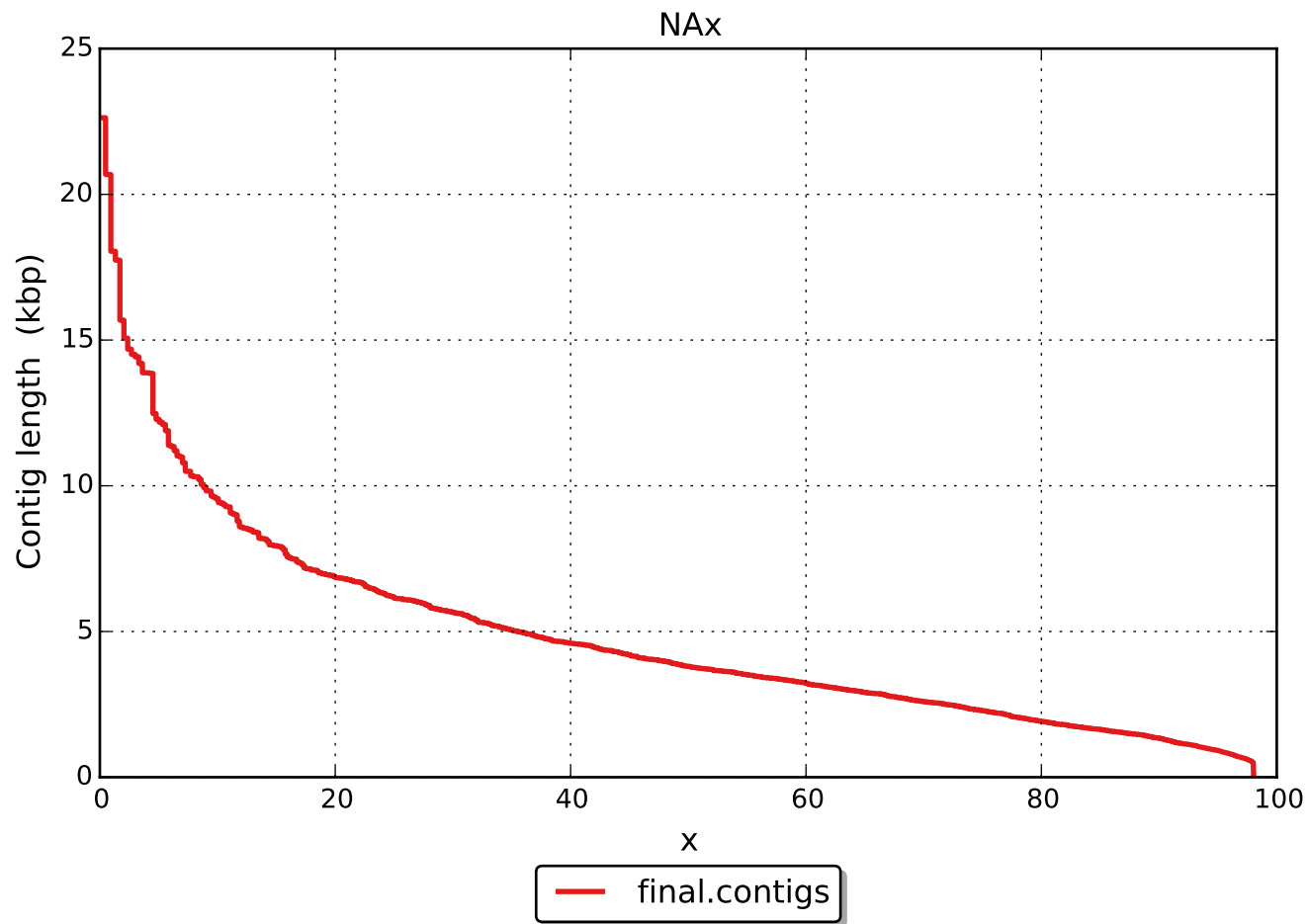
GC content





Cumulative length (aligned contigs)





NGAx

