

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	7
# misassembled contigs	7
Misassembled contigs length	33782
# local misassemblies	9
# unaligned contigs	0 + 3 part
Unaligned length	256
Genome fraction (%)	96.961
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	255.12
# indels per 100 kbp	0.24
Largest alignment	22627
NA50	3811
NGA50	3808
NA75	2290
NGA75	2290
LA50	372
LGA50	373
LA75	759
LGA75	759

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

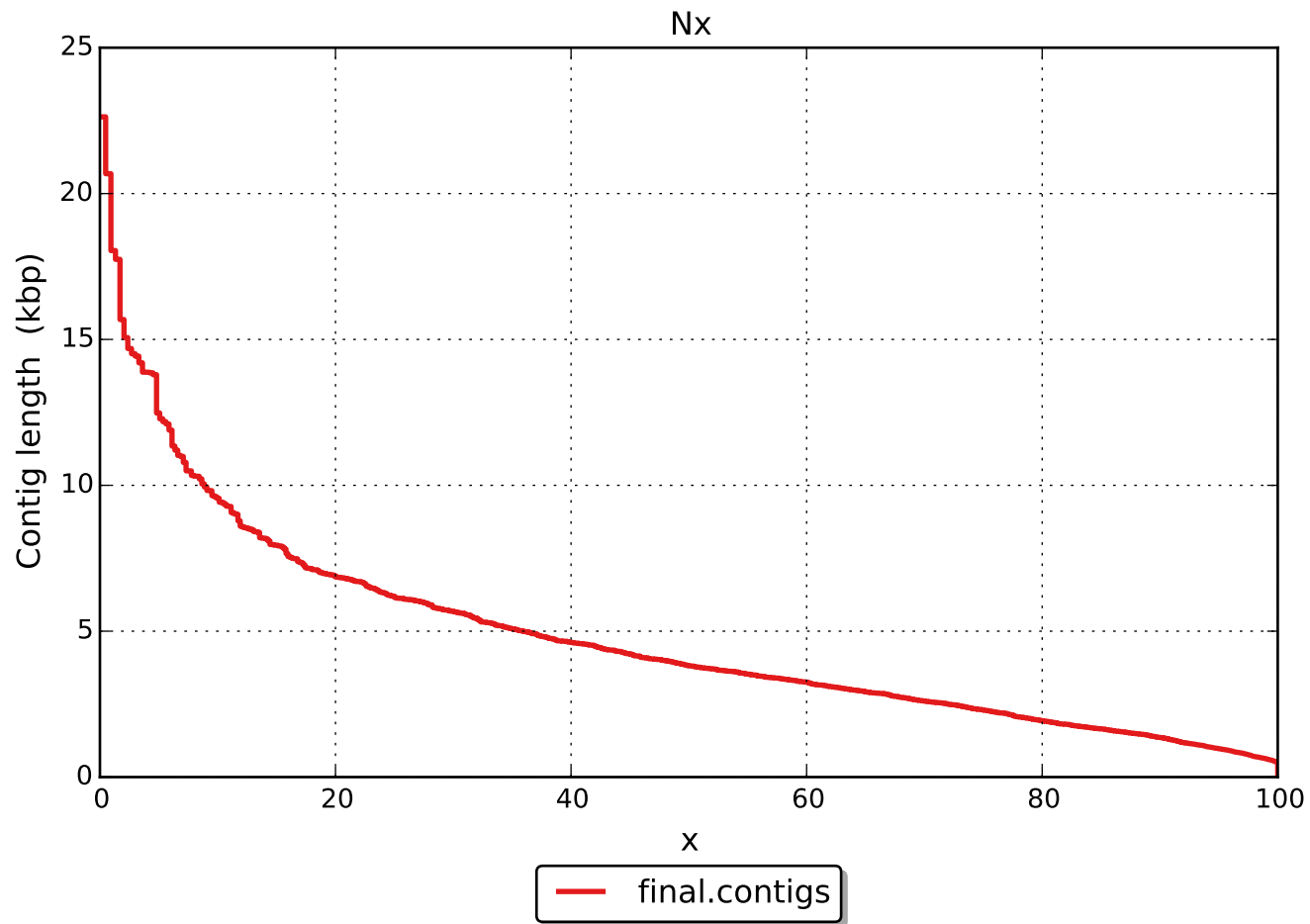
	final.contigs
# misassemblies	7
# relocations	6
# translocations	0
# inversions	1
# misassembled contigs	7
Misassembled contigs length	33782
# local misassemblies	9
# mismatches	11482
# indels	11
# short indels	5
# long indels	6
Indels length	110

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).

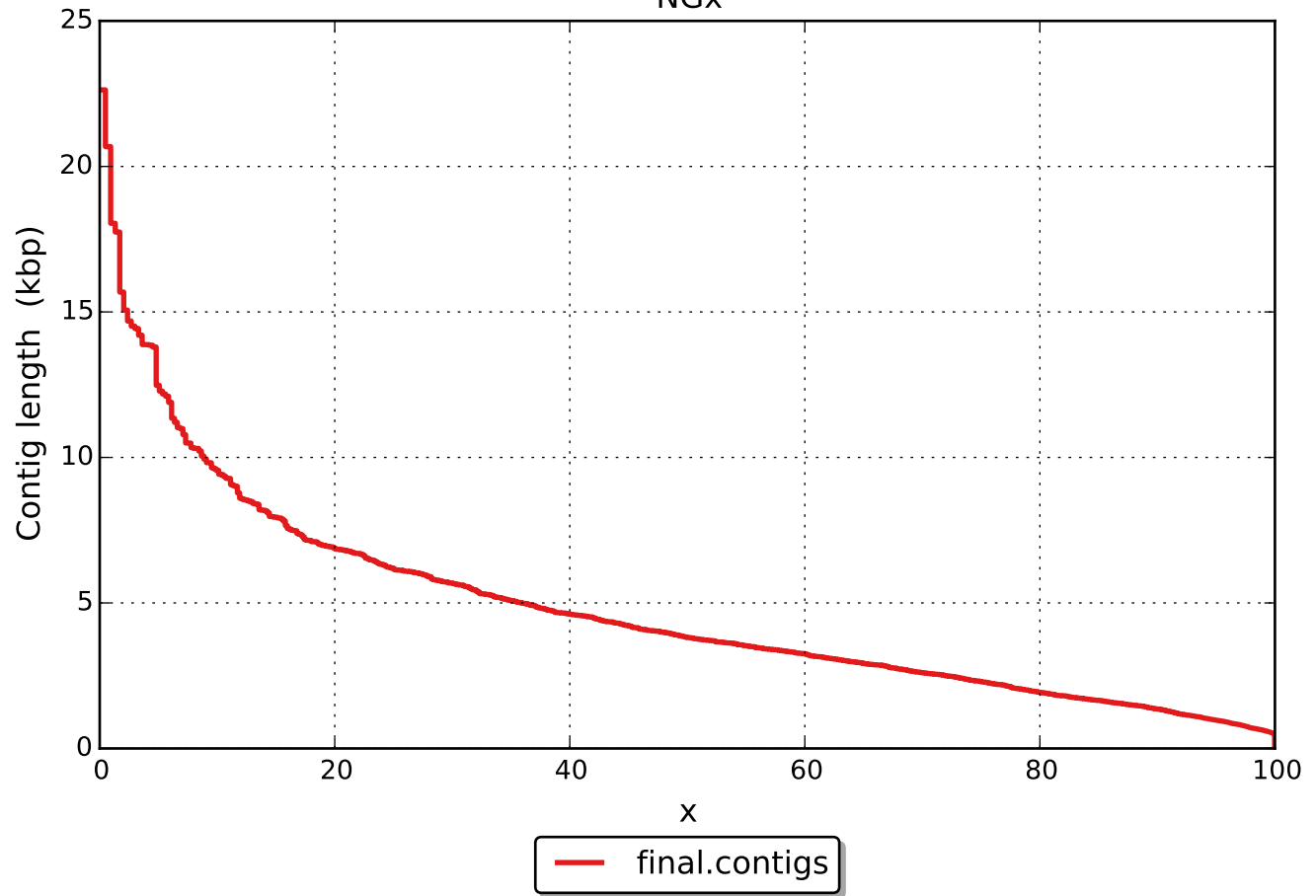
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	256
# N's	0

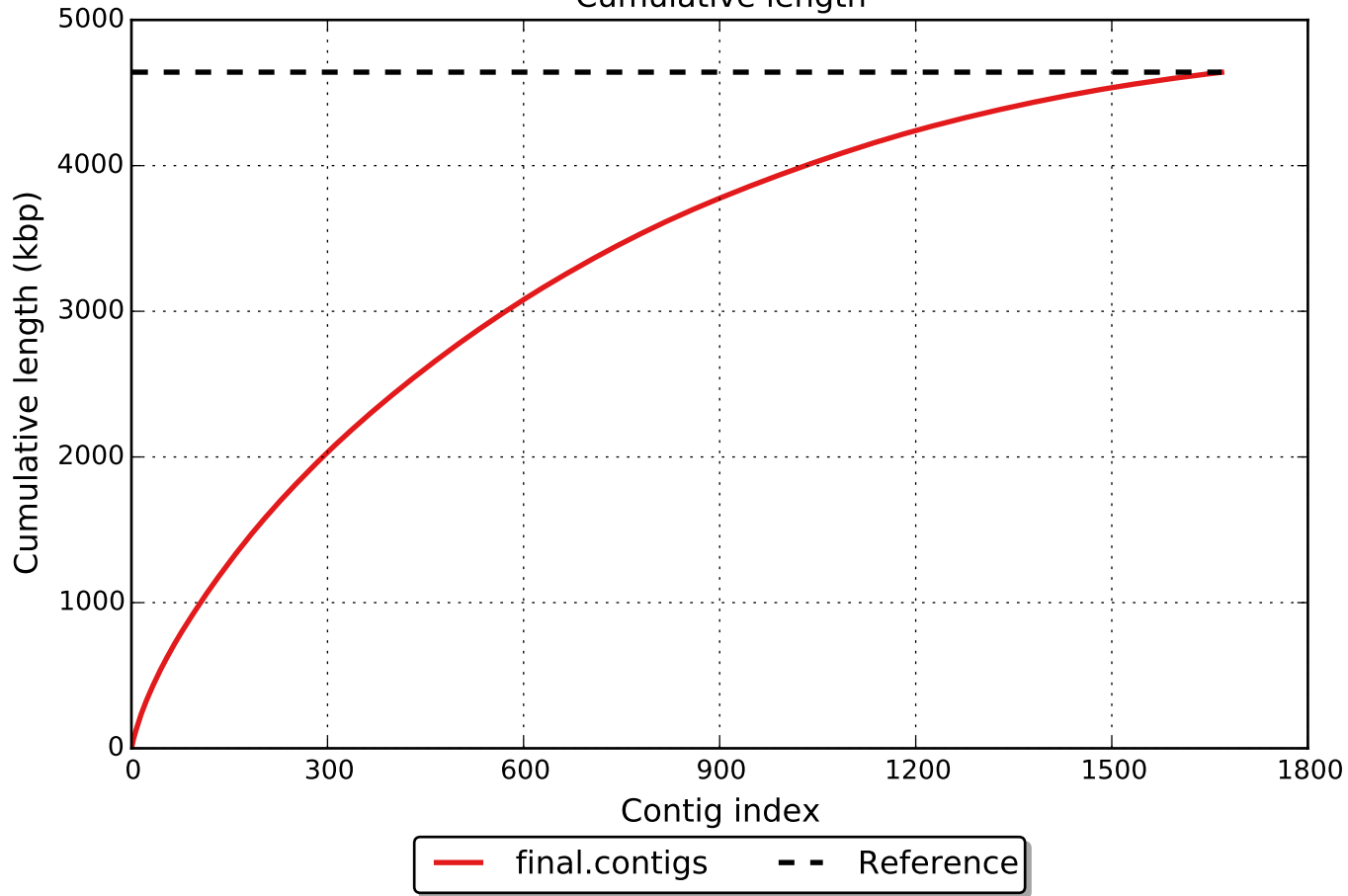
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



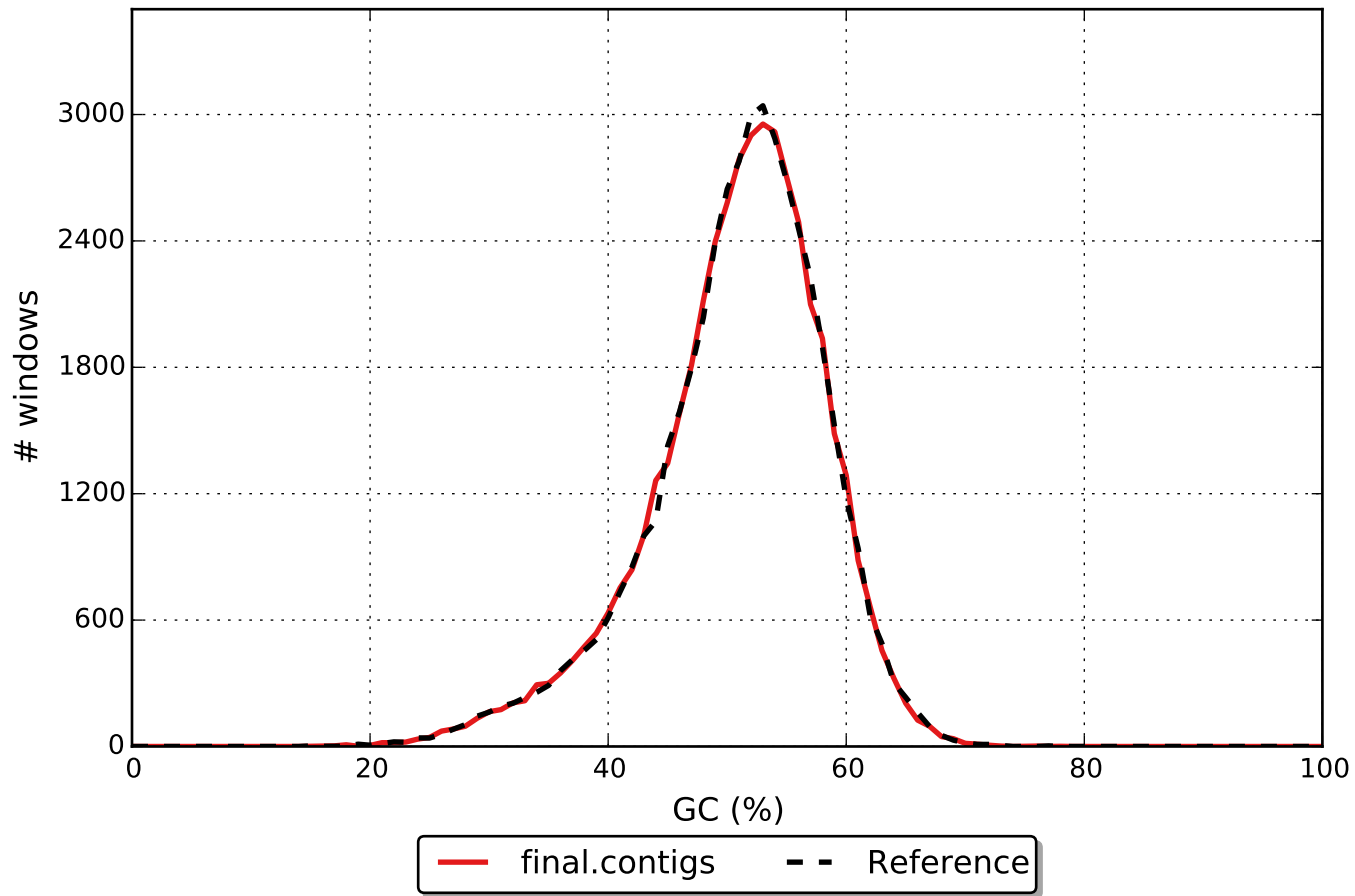
NGx

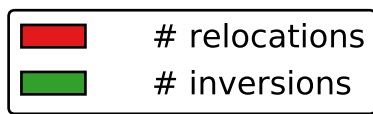
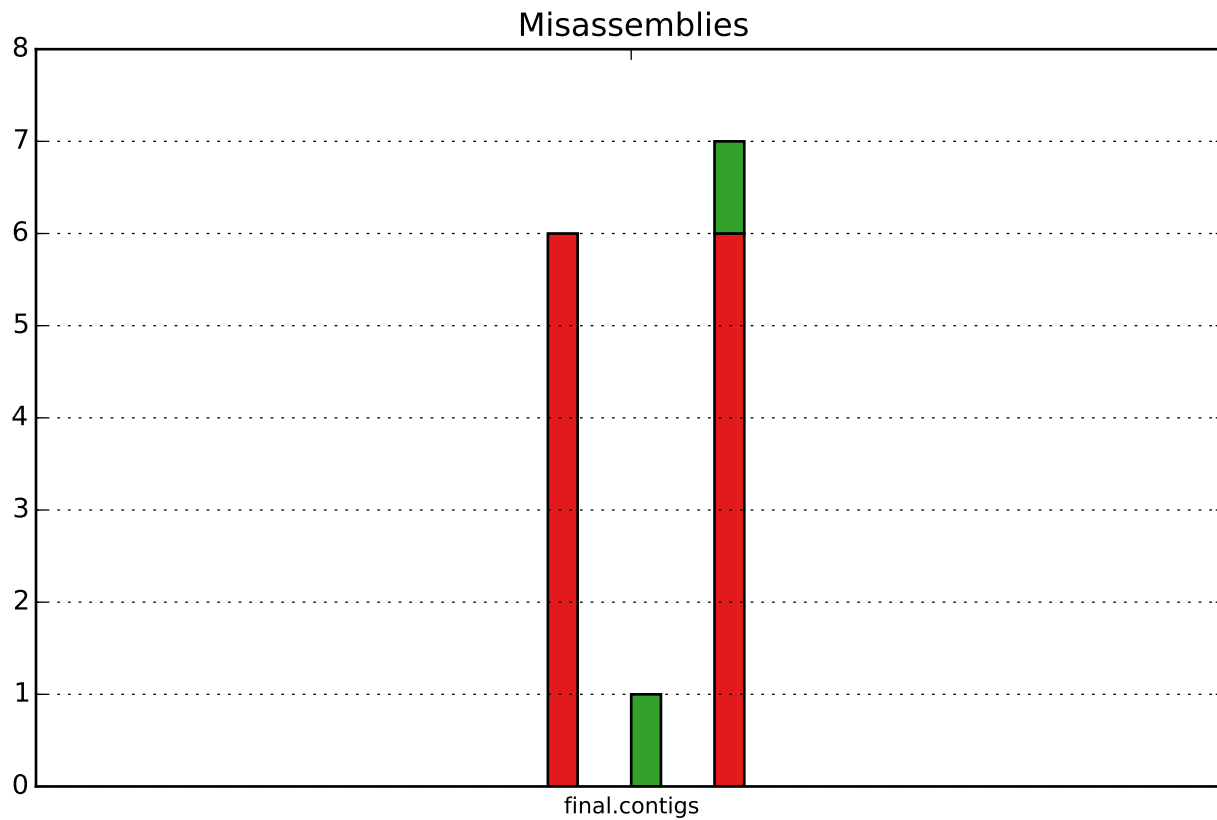


Cumulative length

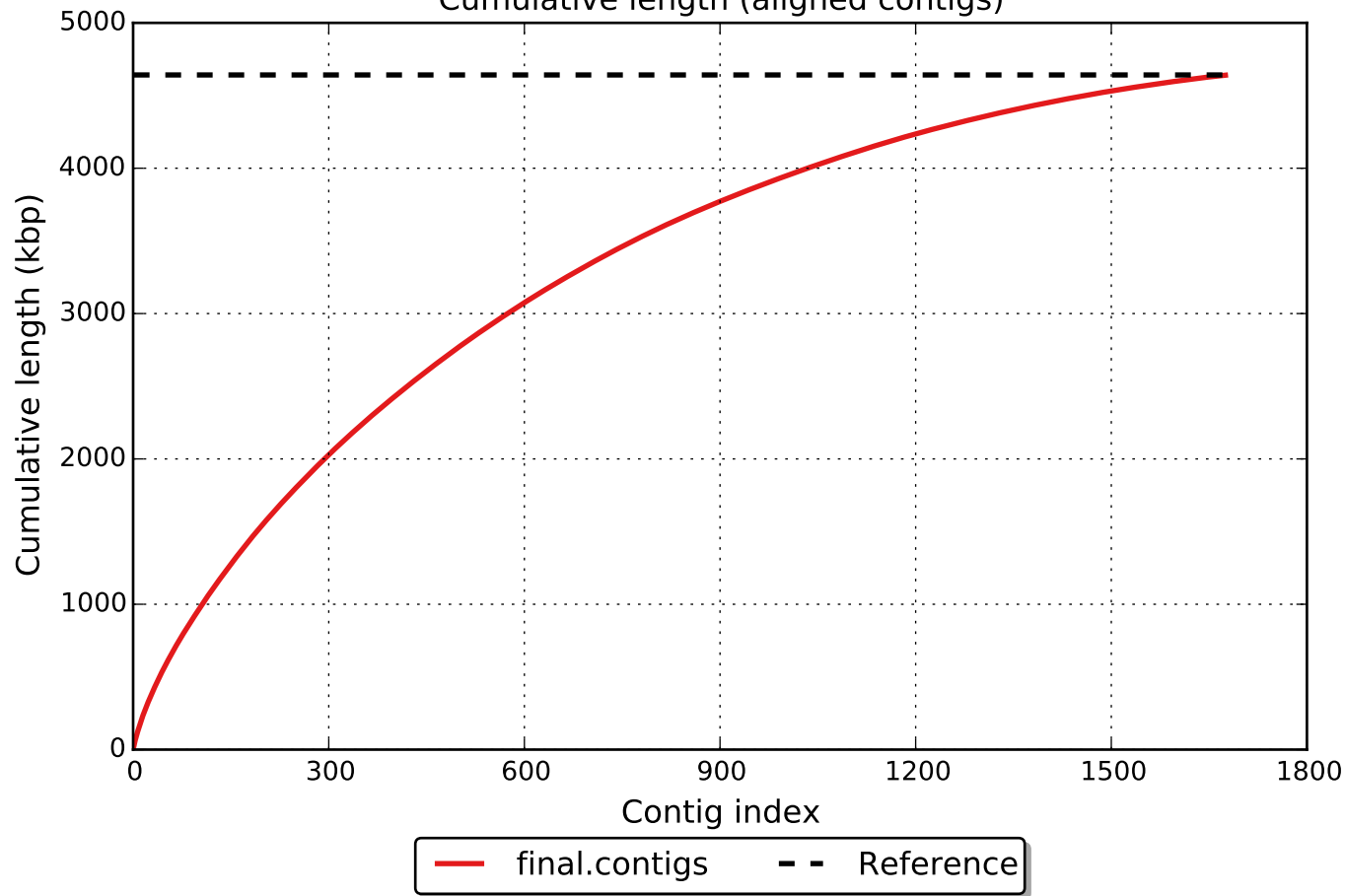


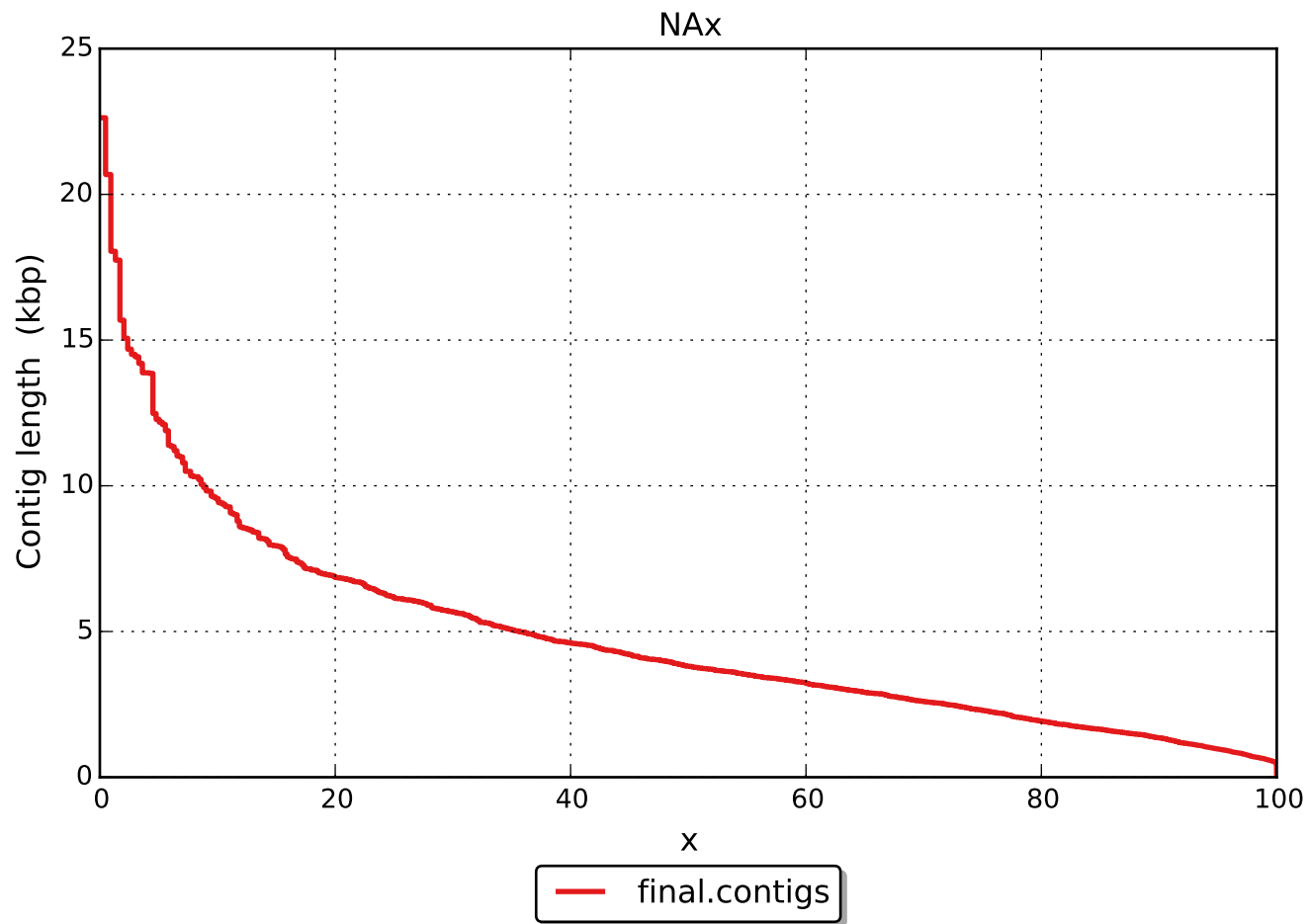
GC content





Cumulative length (aligned contigs)





NGAx

