

Report

	final.contigs
# contigs (≥ 0 bp)	3280
# contigs (≥ 1000 bp)	2237
Total length (≥ 0 bp)	10998794
Total length (≥ 1000 bp)	10499566
# contigs	2646
Largest contig	31841
Total length	10795490
Reference length	10957366
GC (%)	50.38
Reference GC (%)	50.49
N50	6333
NG50	6121
N75	3532
NG75	3414
L50	527
LG50	540
L75	1099
LG75	1134
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	29757
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	13
Genome fraction (%)	96.500
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	23.08
# indels per 100 kbp	0.03
Largest alignment	31841
NA50	6330
NGA50	6106
NA75	3532
NGA75	3414
LA50	528
LGA50	541
LA75	1100
LGA75	1135

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

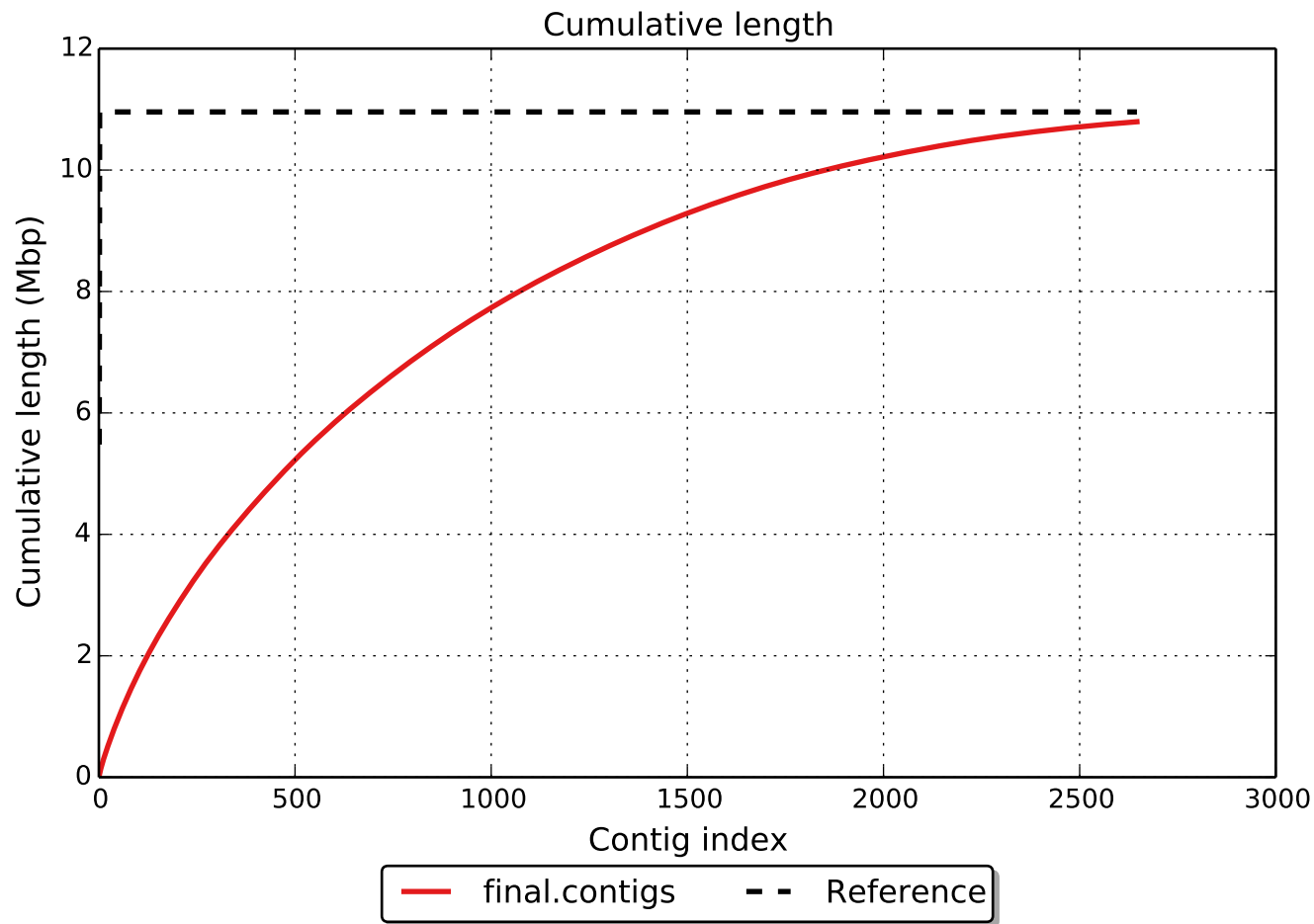
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	29757
# local misassemblies	2
# mismatches	2440
# indels	3
# short indels	1
# long indels	2
Indels length	31

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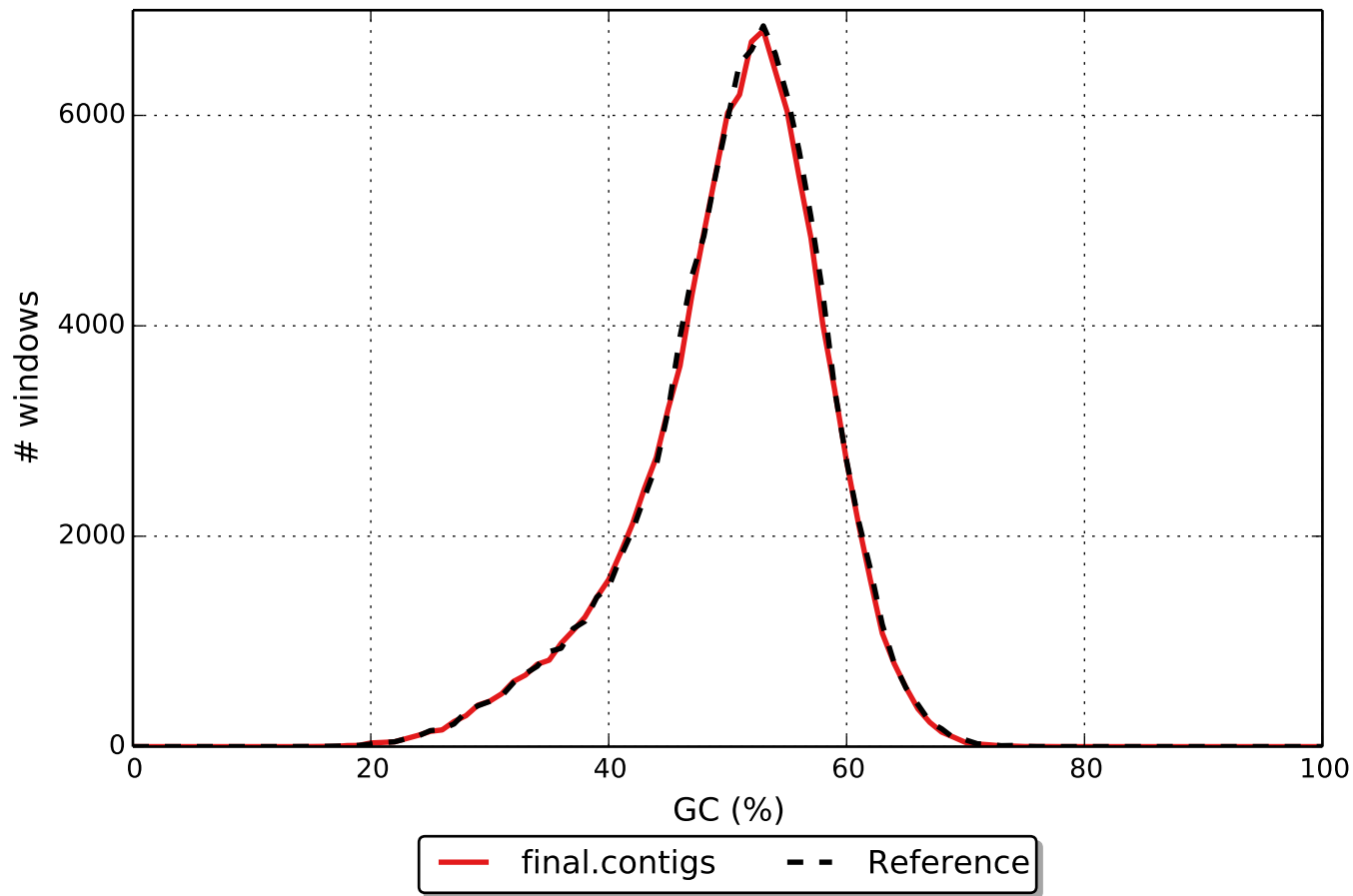
Unaligned report

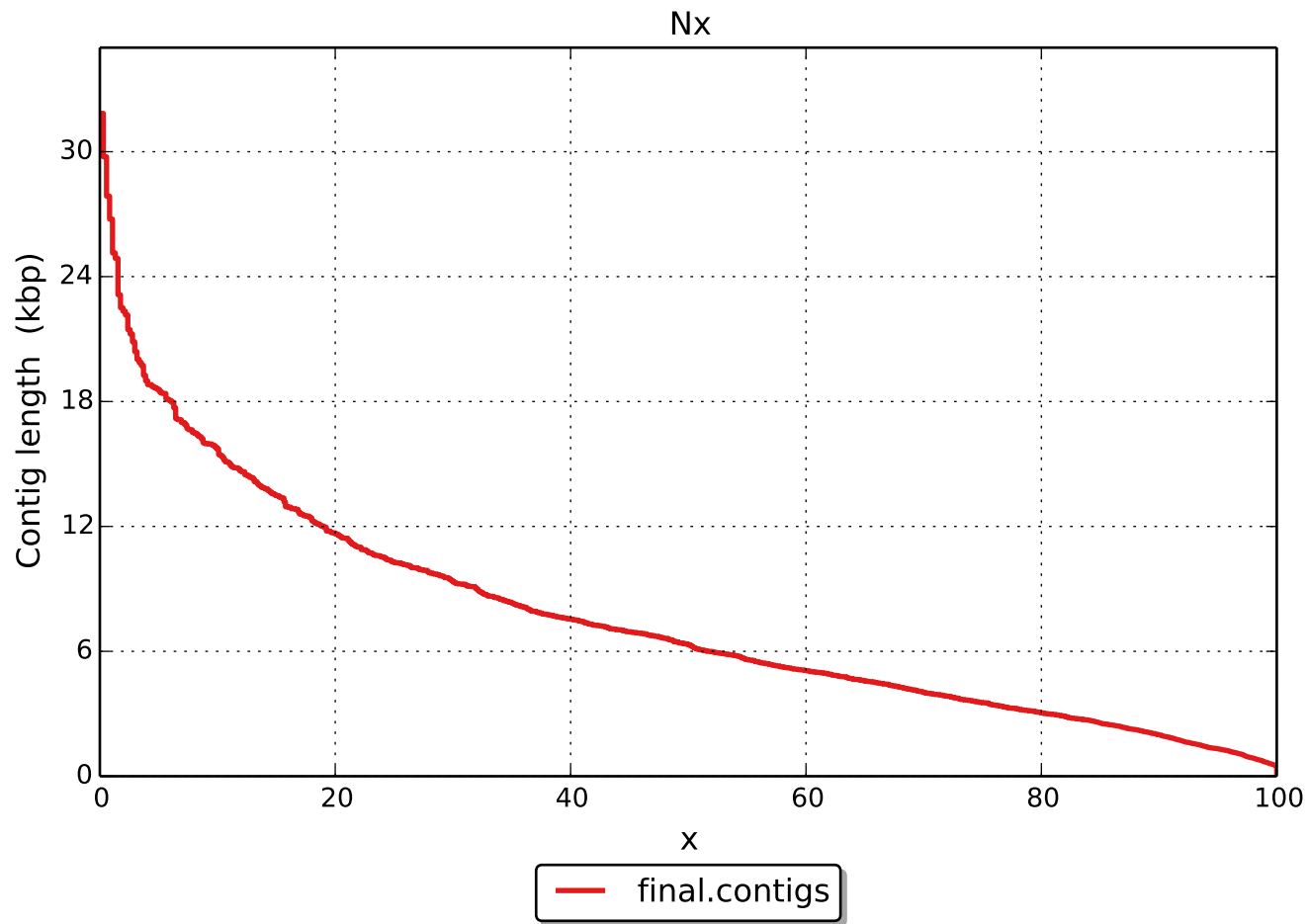
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	13
# N's	0

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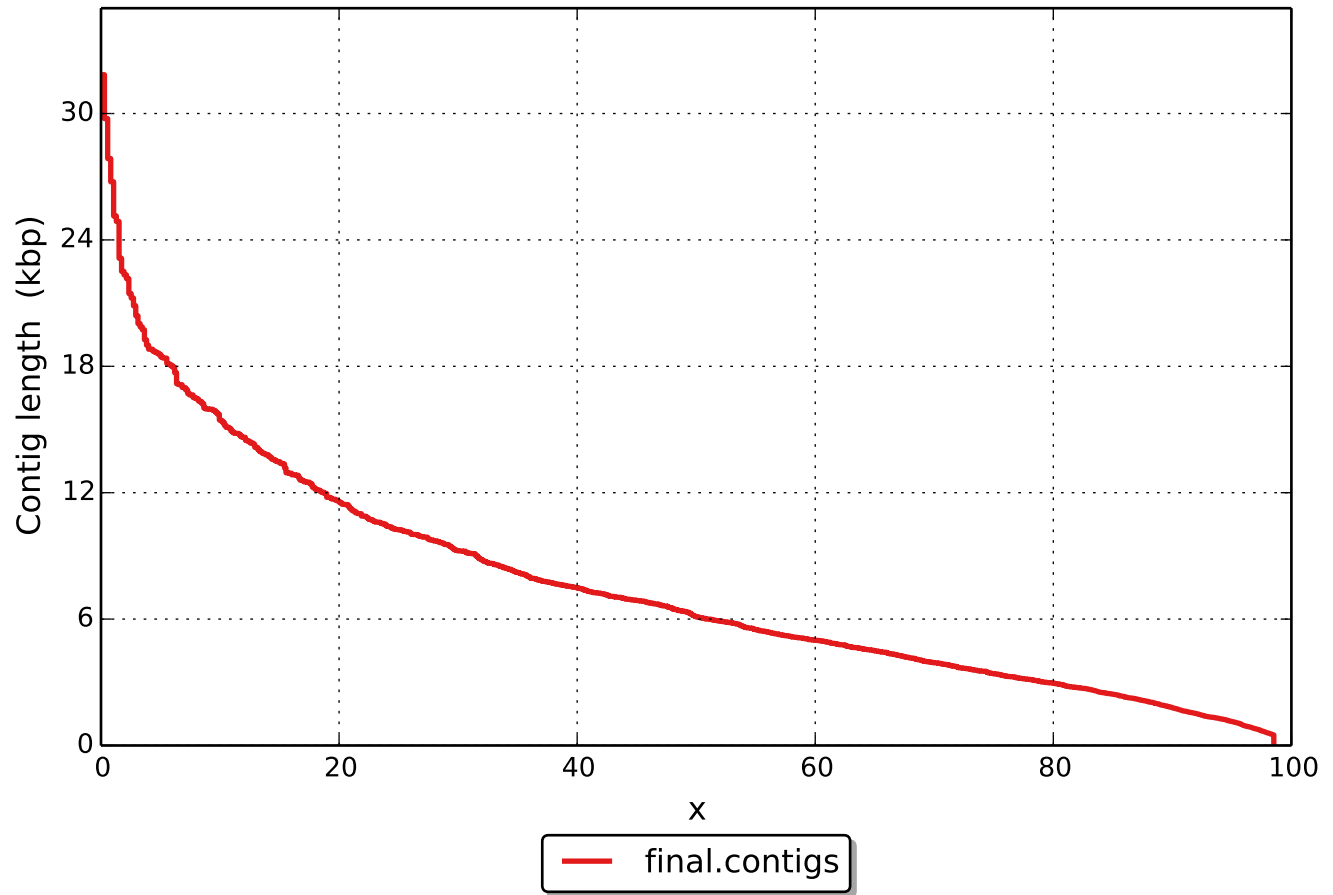


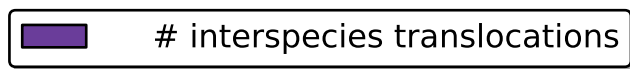
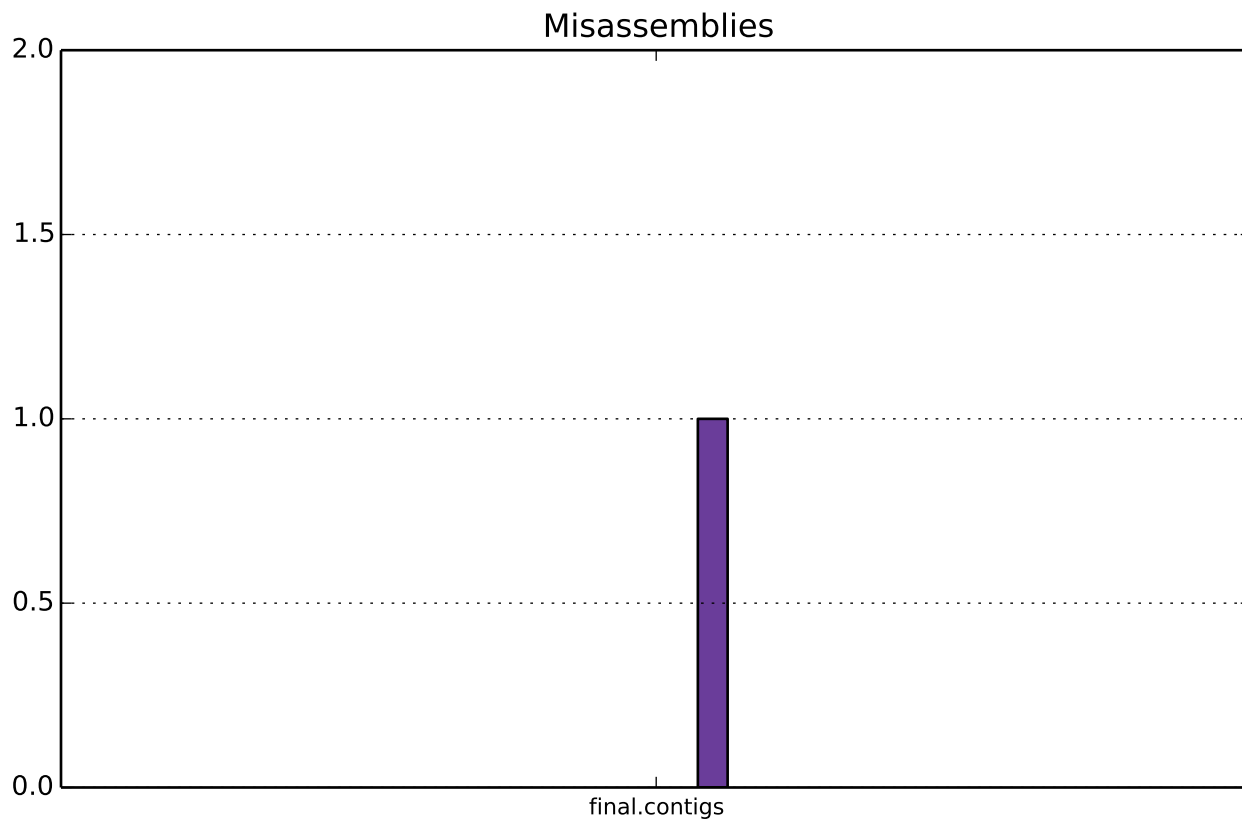
GC content

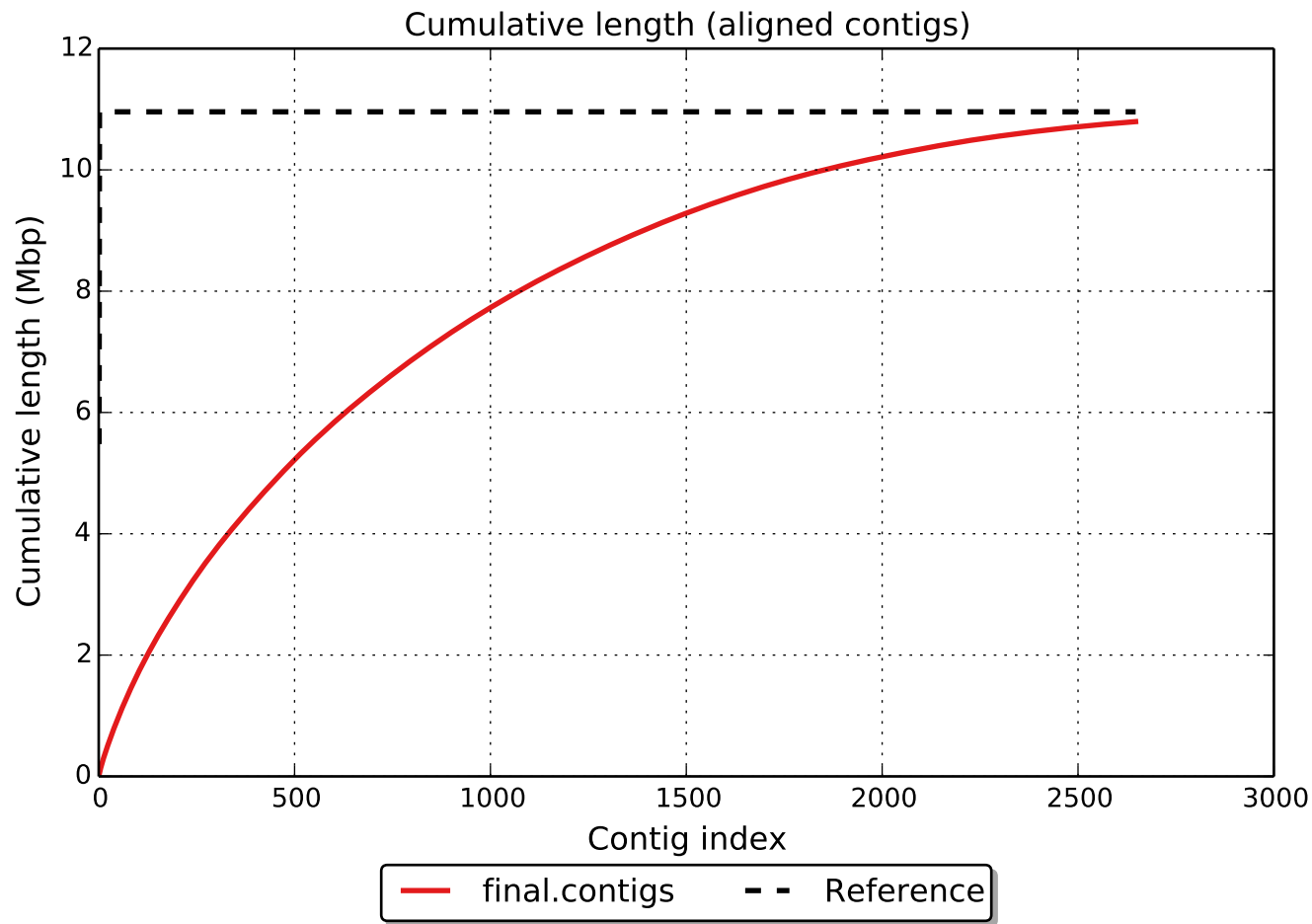




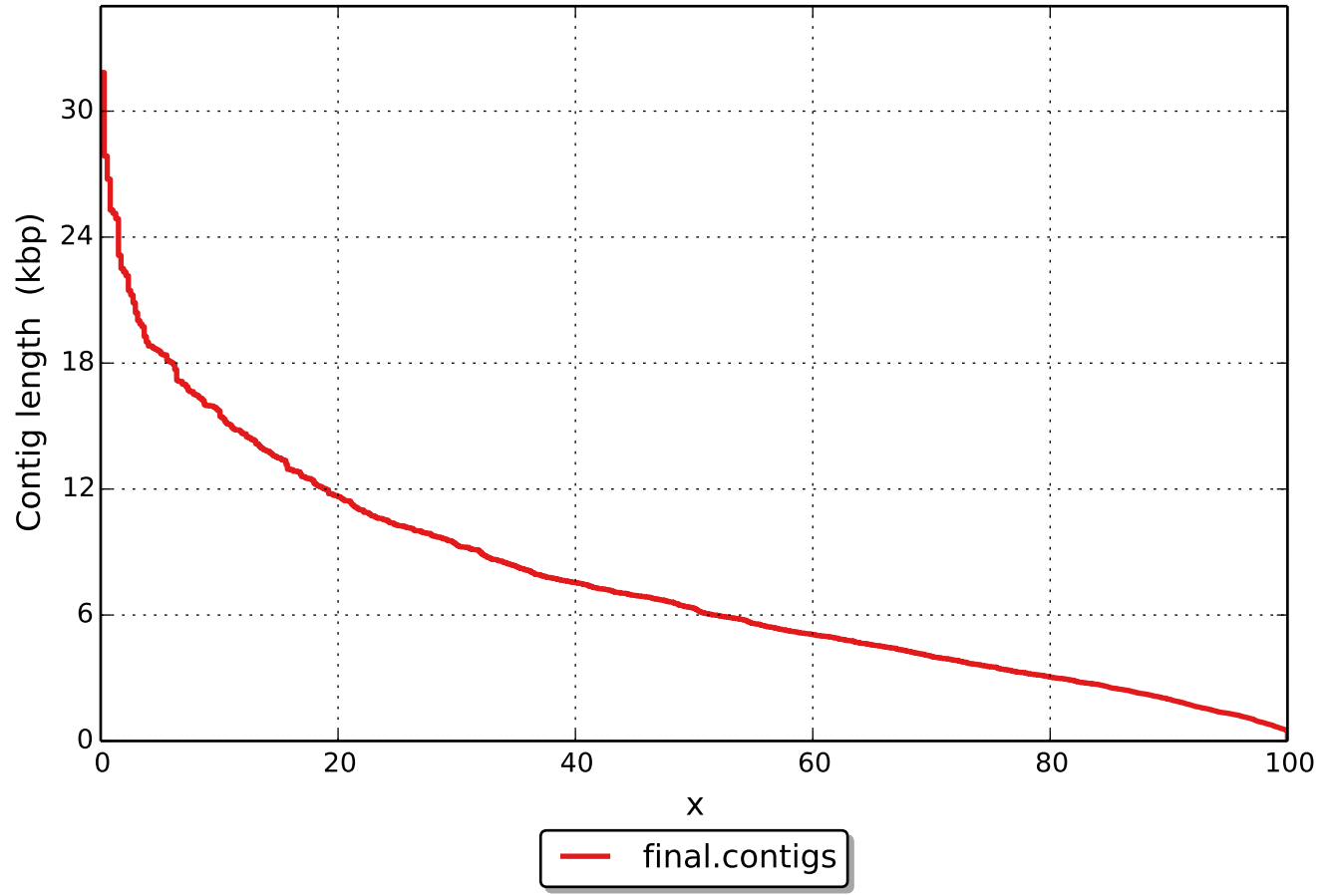
NGx







NAx



NGAx

