

Report

	final.contigs
# contigs (≥ 0 bp)	1445
# contigs (≥ 1000 bp)	775
Total length (≥ 0 bp)	2941392
Total length (≥ 1000 bp)	2498648
# contigs	1445
Largest contig	17983
Total length	2941392
Reference length	5478683
GC (%)	50.19
Reference GC (%)	50.49
N50	3515
NG50	644
N75	1608
L50	240
LG50	1088
L75	545
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	52.683
Duplication ratio	1.019
# N's per 100 kbp	0.00
# mismatches per 100 kbp	440.63
# indels per 100 kbp	0.07
Largest alignment	17983
NA50	3515
NGA50	643
NA75	1608
LA50	240
LGA50	1088
LA75	545

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

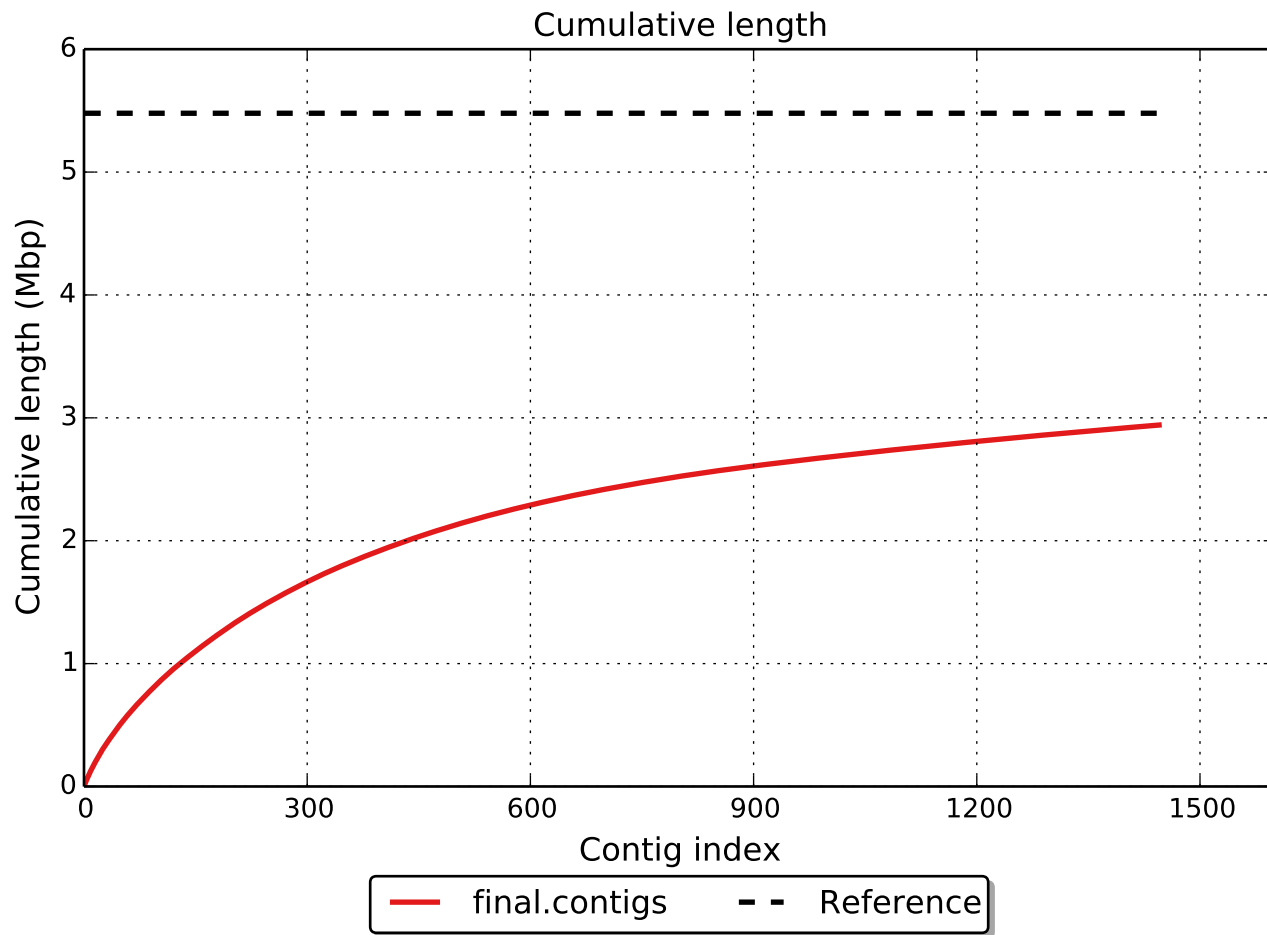
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	12718
# indels	2
# short indels	0
# long indels	2
Indels length	24

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).

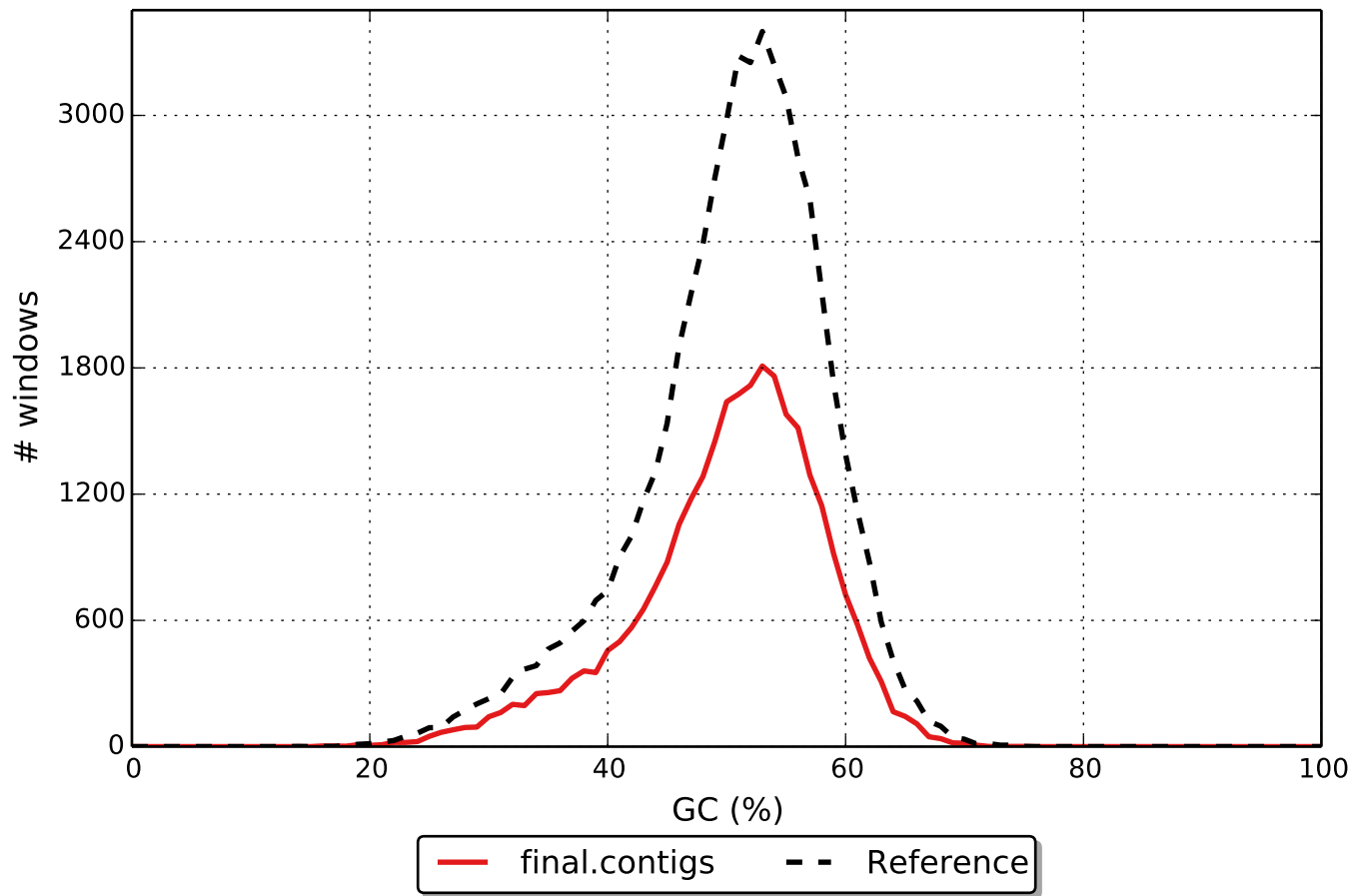
Unaligned report

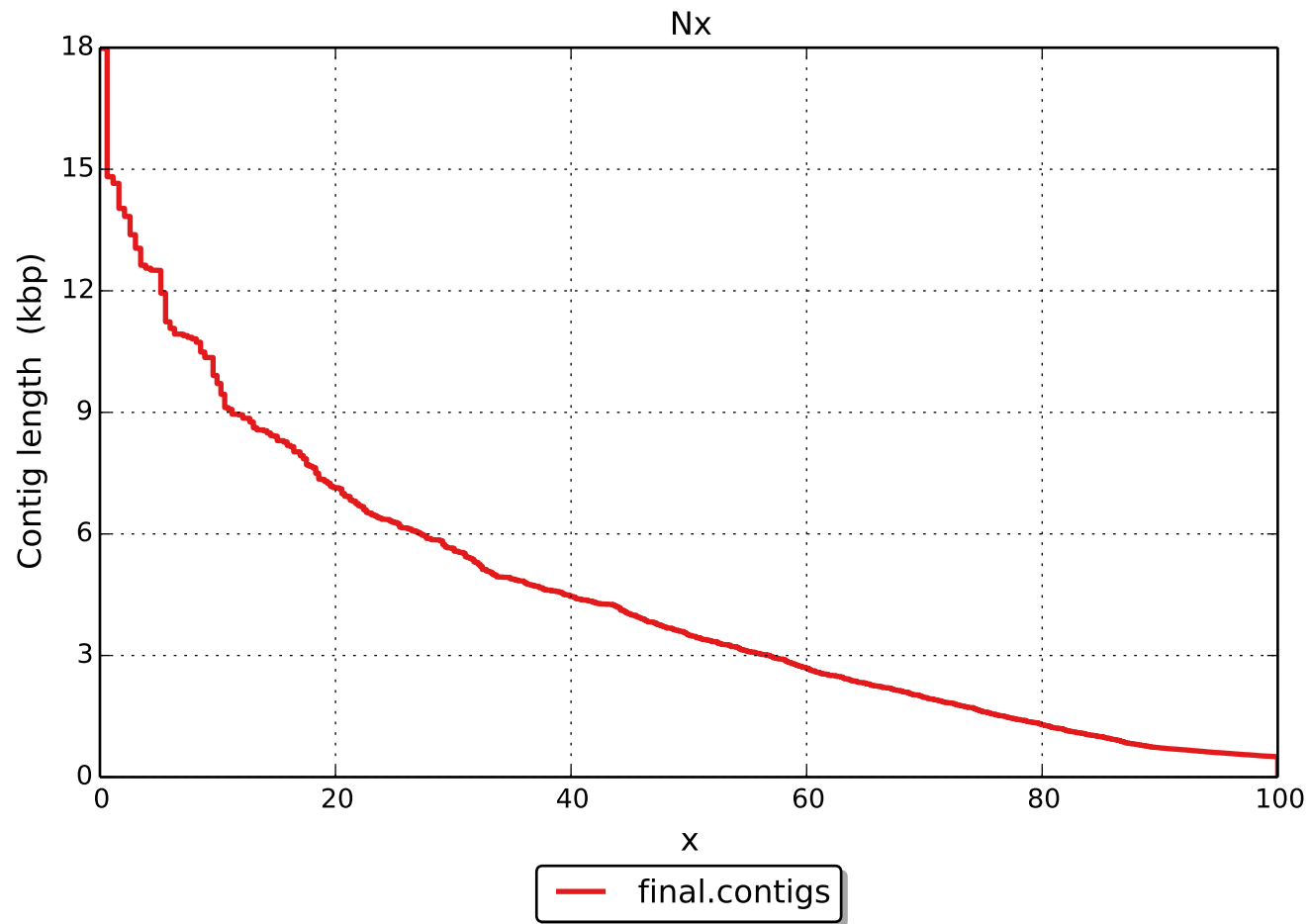
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

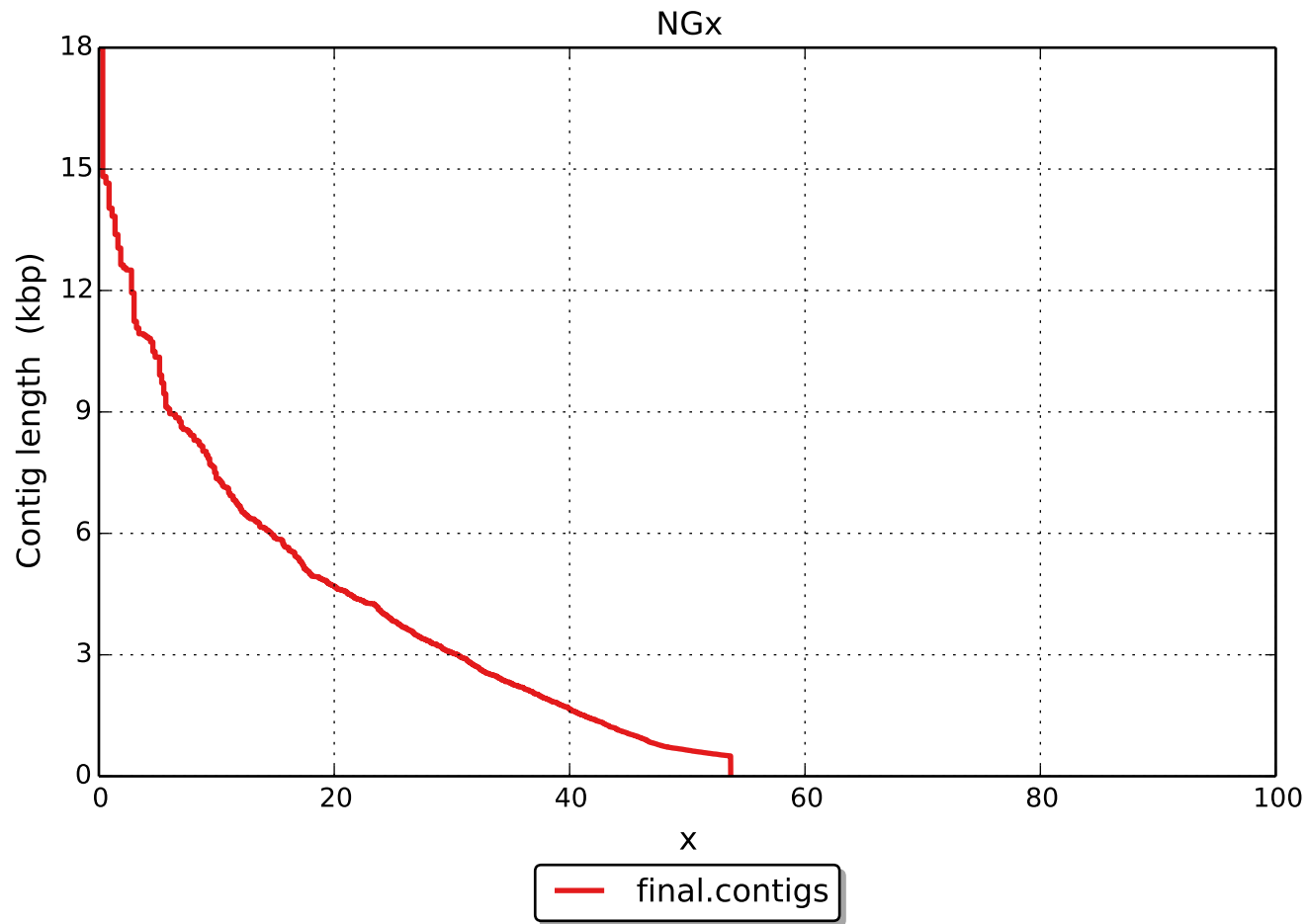
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

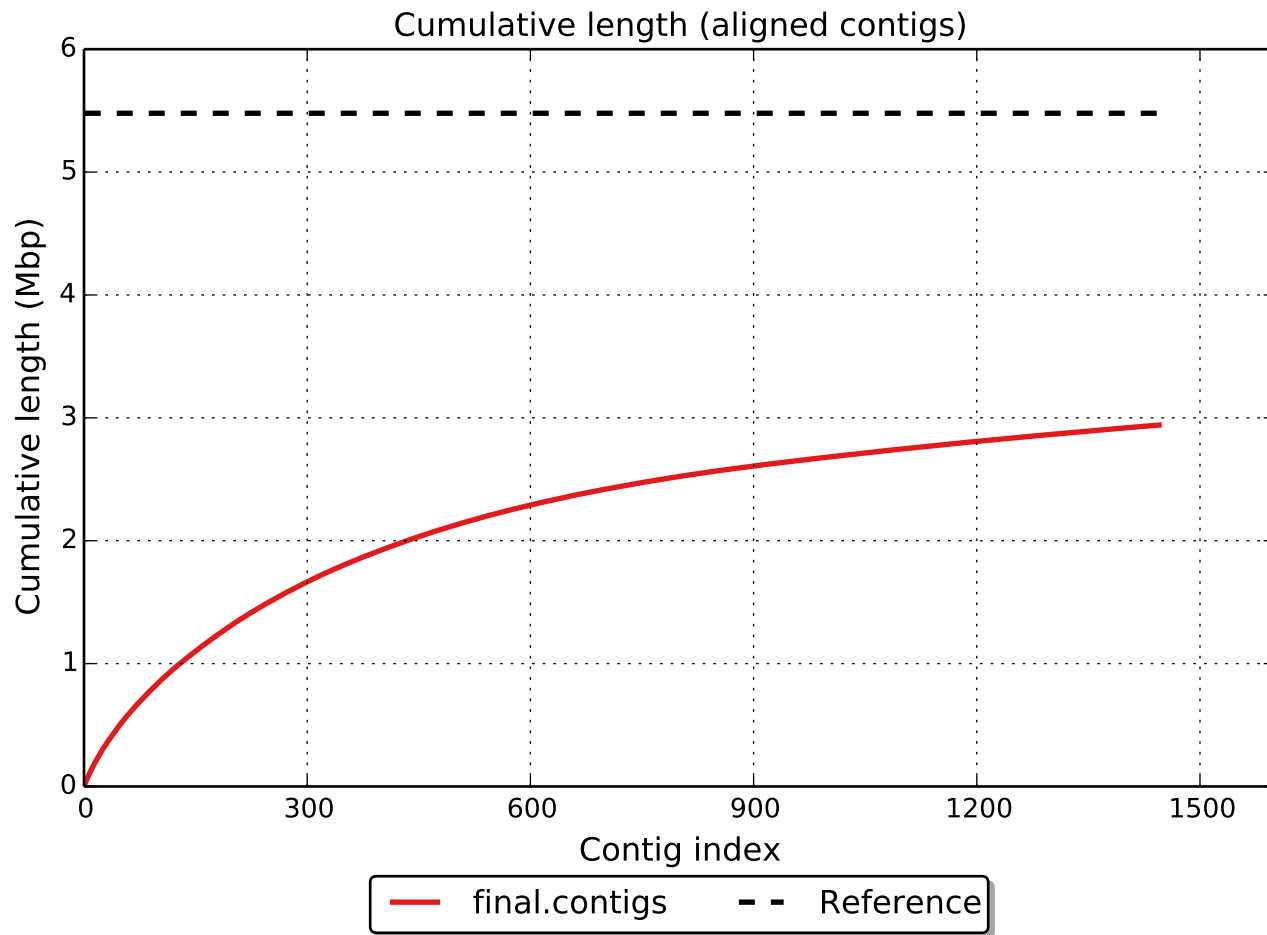


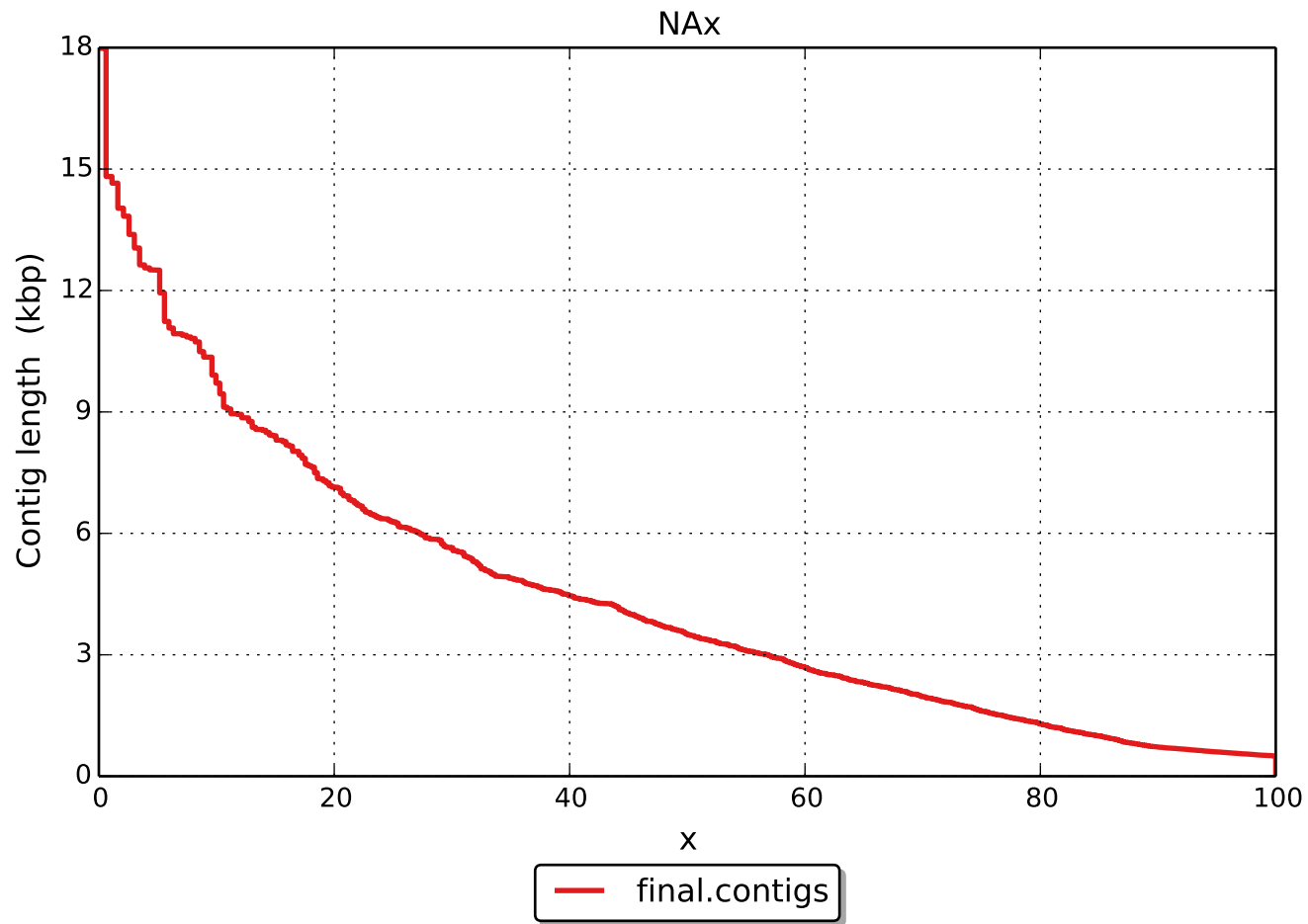




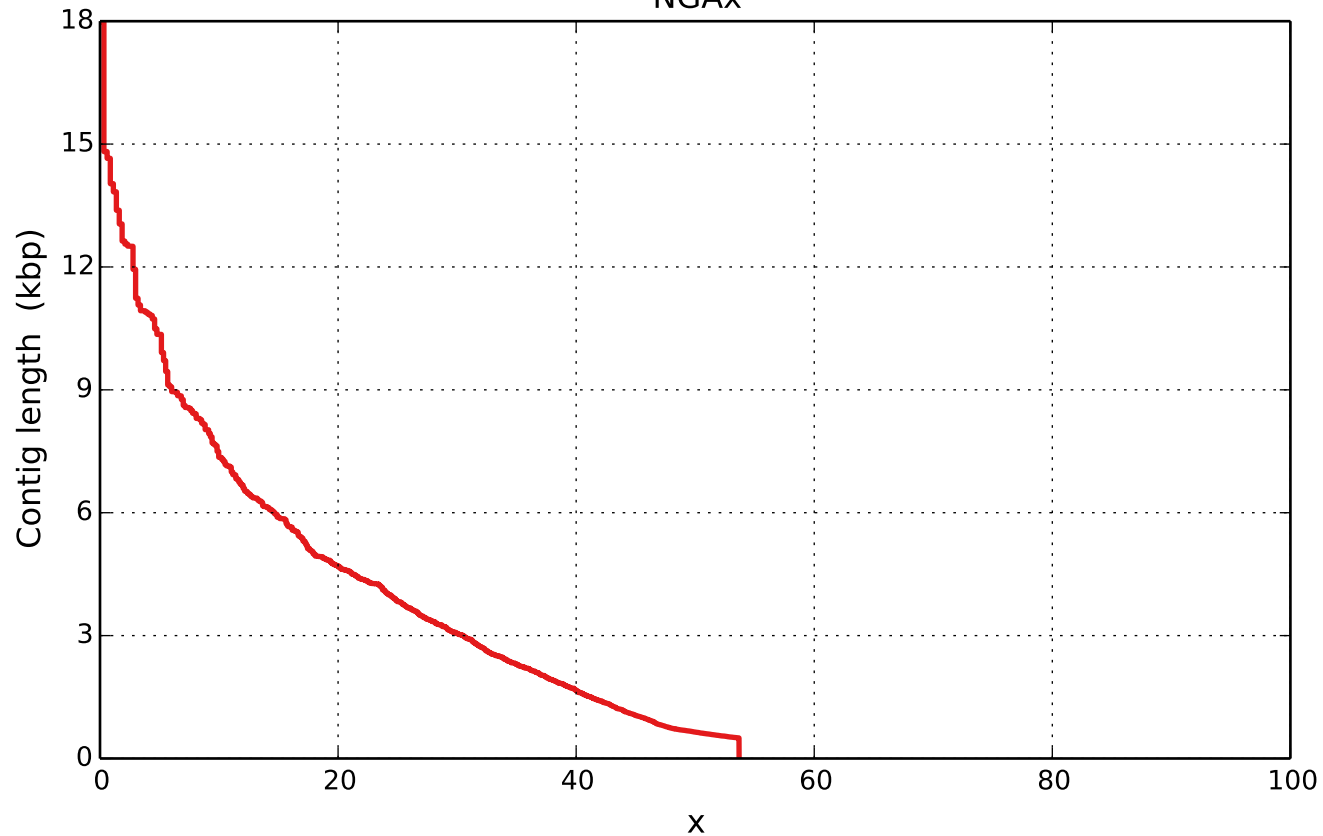
Misassemblies







NGAx



— final.contigs