

Report

	final.contigs
# contigs (≥ 0 bp)	1313
# contigs (≥ 1000 bp)	1056
Total length (≥ 0 bp)	3741570
Total length (≥ 1000 bp)	3549057
# contigs	1313
Largest contig	15927
Total length	3741570
Reference length	1892775
GC (%)	32.25
Reference GC (%)	32.26
N50	4207
NG50	6601
N75	2277
NG75	5172
L50	284
LG50	103
L75	584
LG75	185
# misassemblies	56
# misassembled contigs	53
Misassembled contigs length	216160
# local misassemblies	0
# unaligned contigs	99 + 72 part
Unaligned length	513008
Genome fraction (%)	99.328
Duplication ratio	1.717
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1358.68
# indels per 100 kbp	1.60
Largest alignment	15927
NA50	3242
NGA50	5553
NA75	1347
NGA75	4241
LA50	336
LGA50	116
LA75	780
LGA75	215

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

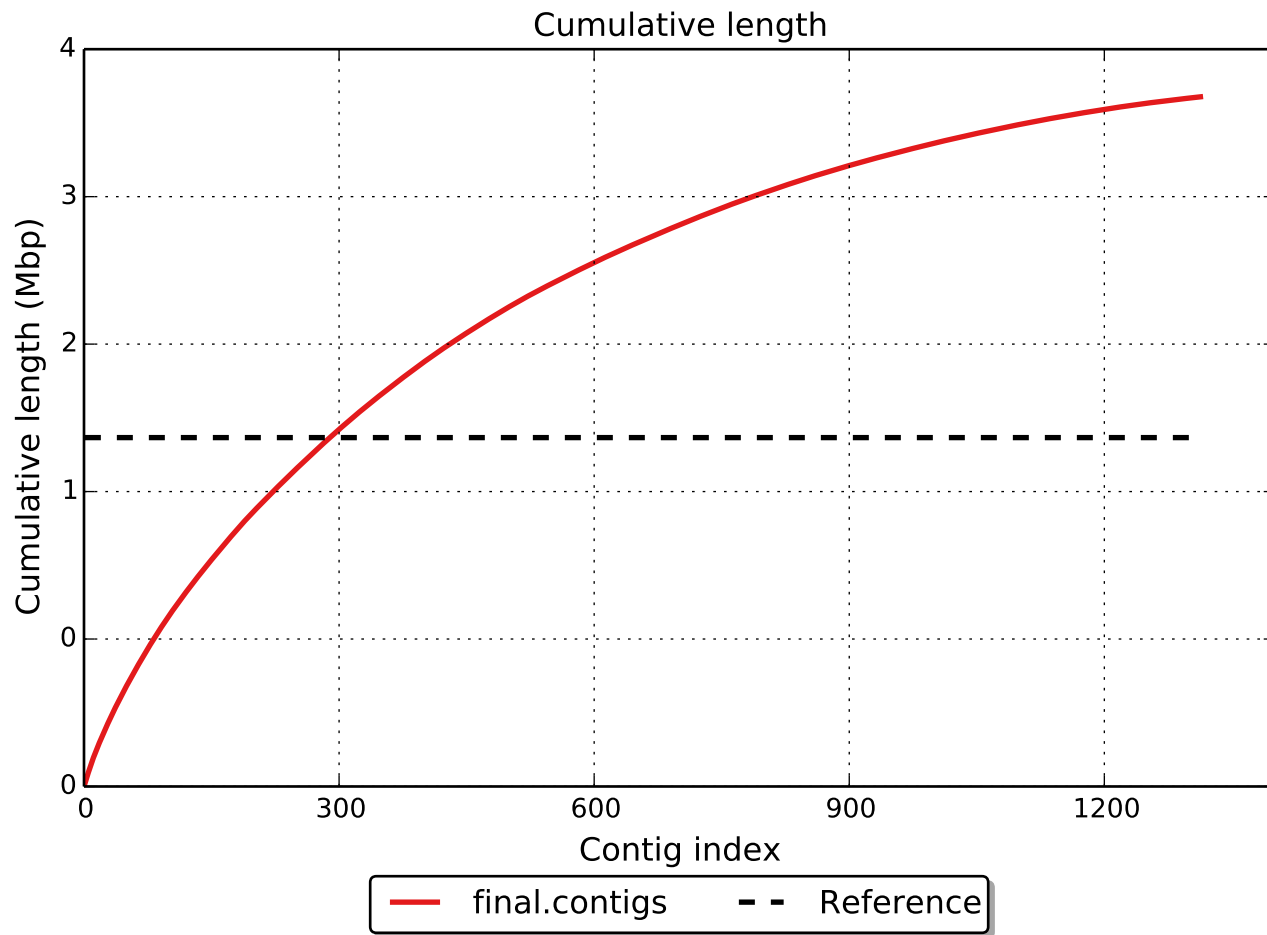
	final.contigs
# misassemblies	56
# relocations	53
# translocations	0
# inversions	3
# possibly misassembled contigs	46
# misassembled contigs	53
Misassembled contigs length	216160
# local misassemblies	0
# mismatches	25544
# indels	30
# short indels	30
# long indels	0
Indels length	30

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).

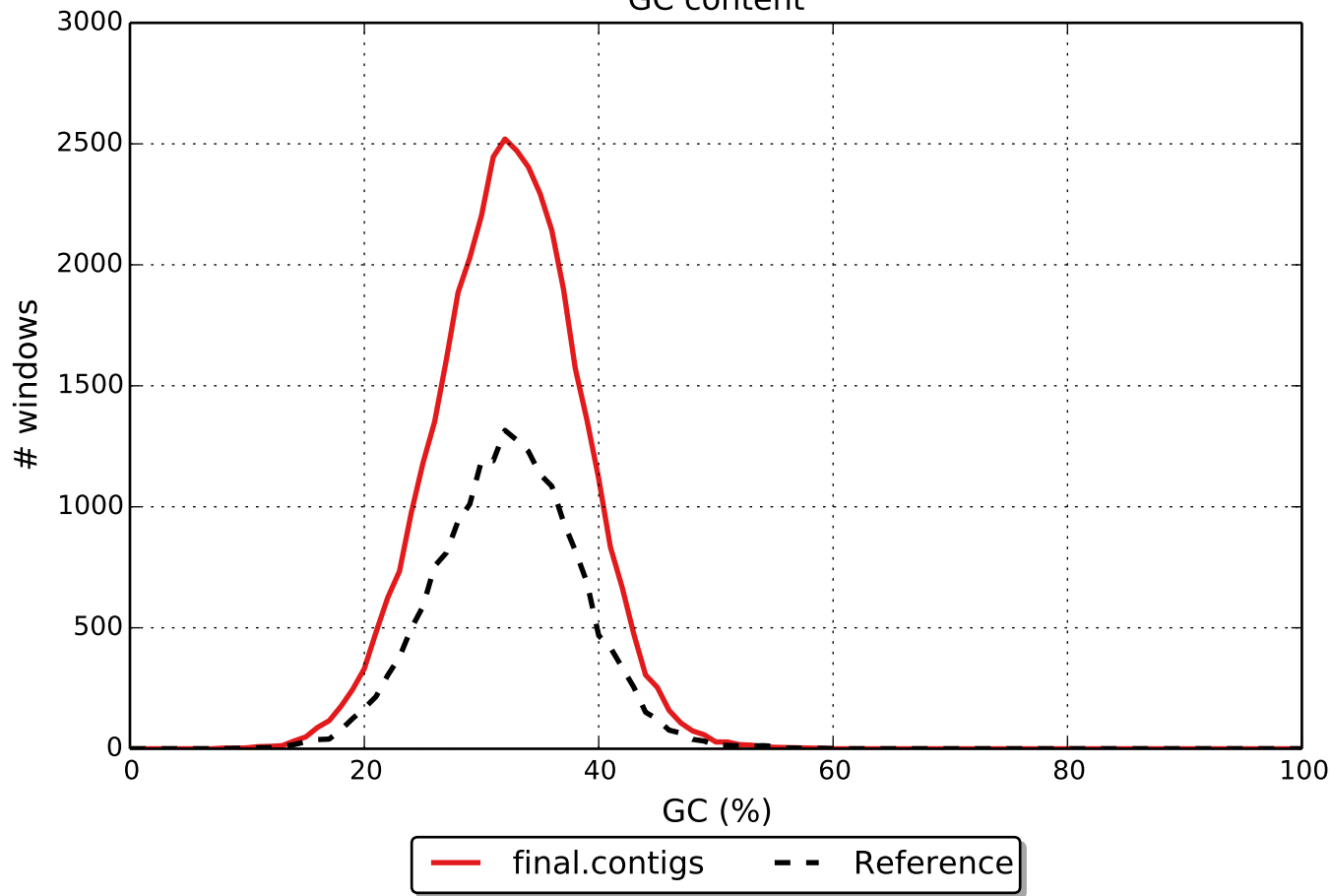
Unaligned report

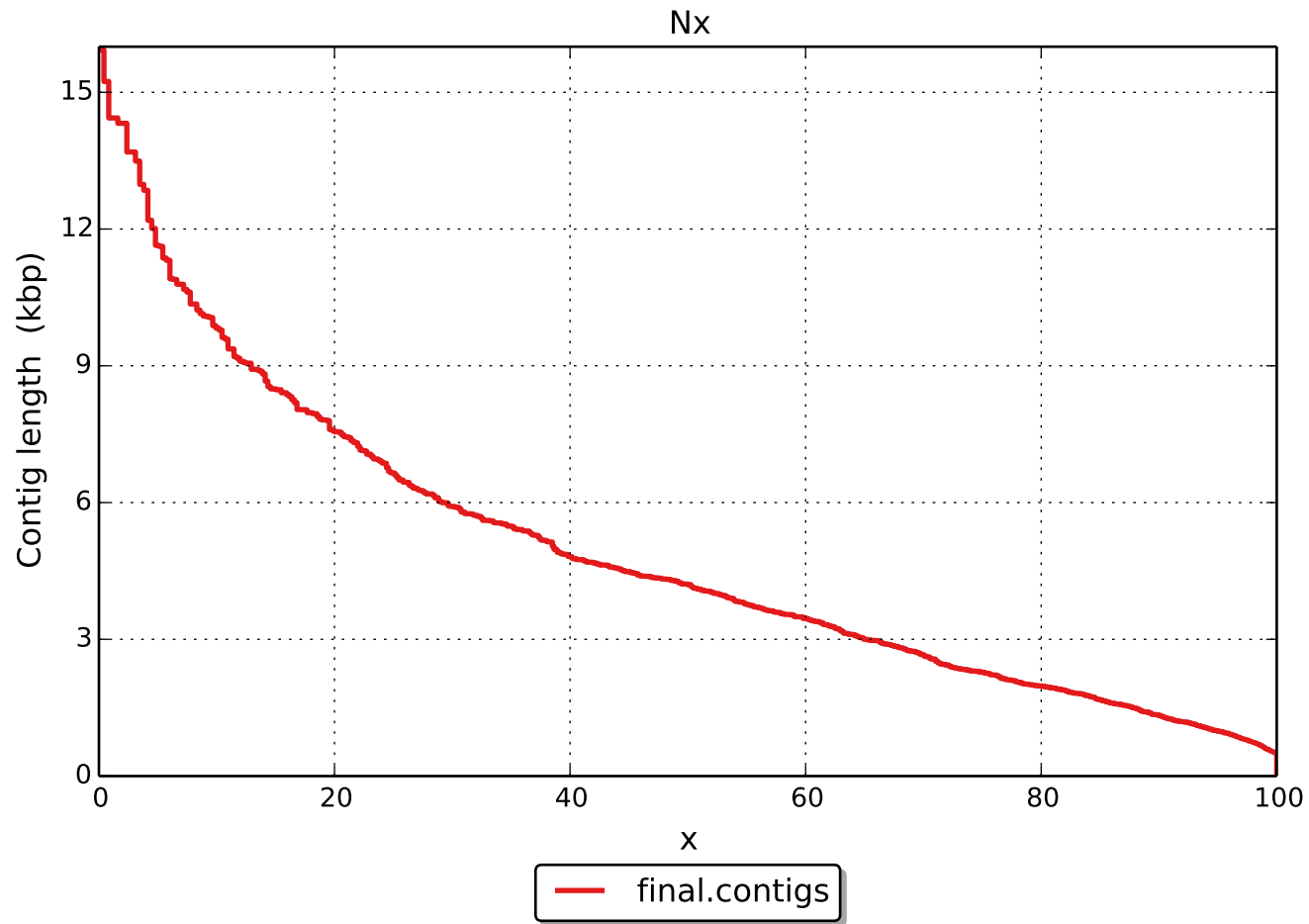
	final.contigs
# fully unaligned contigs	99
Fully unaligned length	311955
# partially unaligned contigs	72
# with misassembly	9
# both parts are significant	38
Partially unaligned length	201053
# N's	0

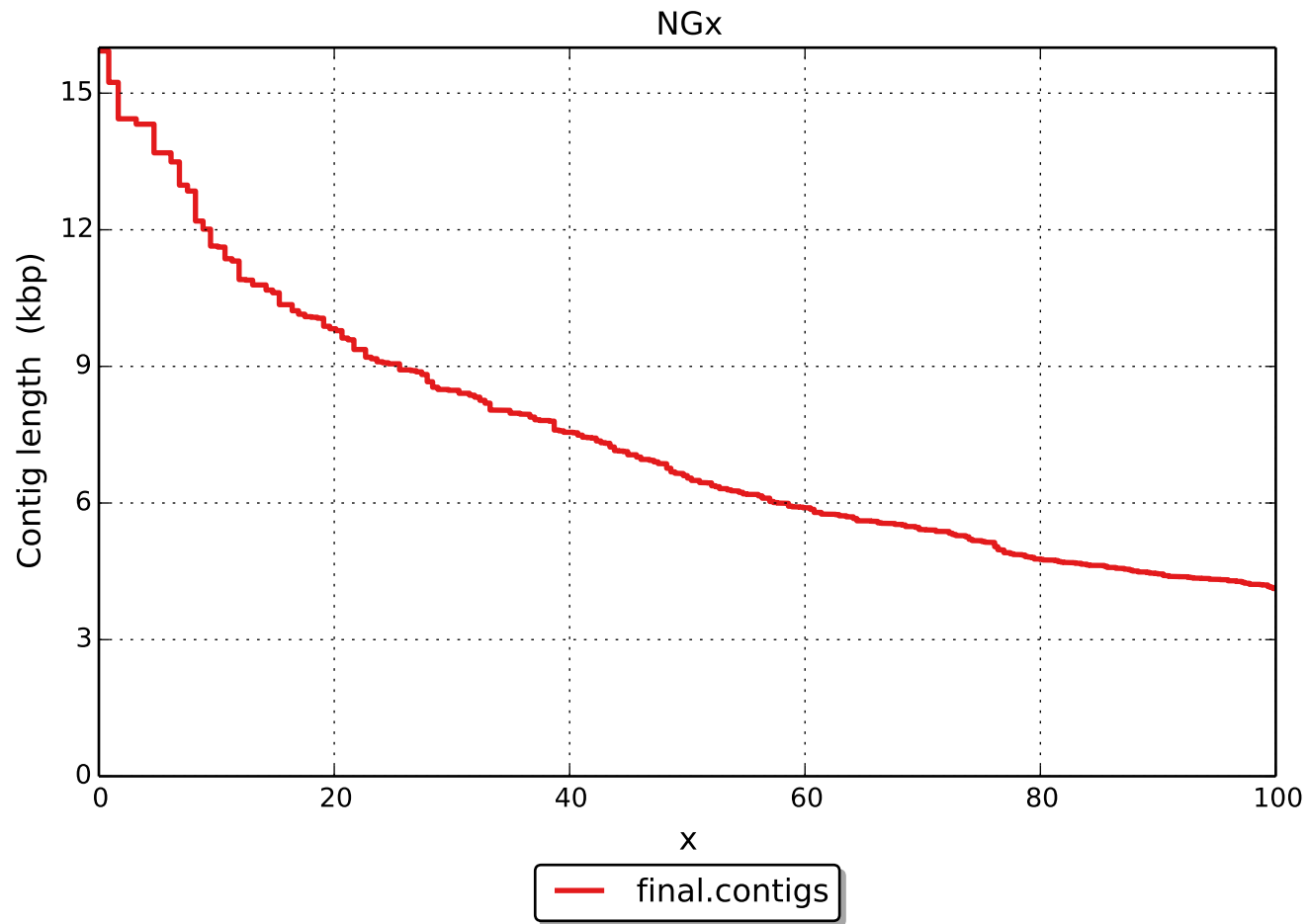
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



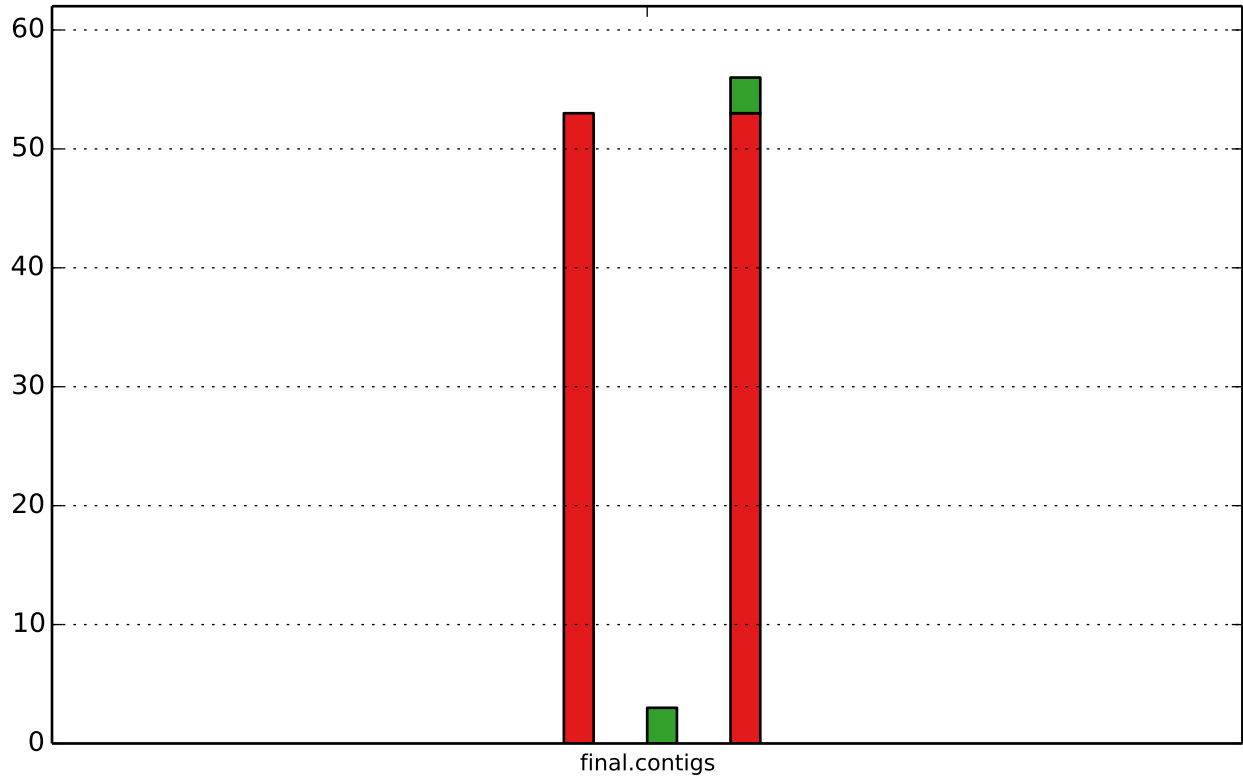
GC content

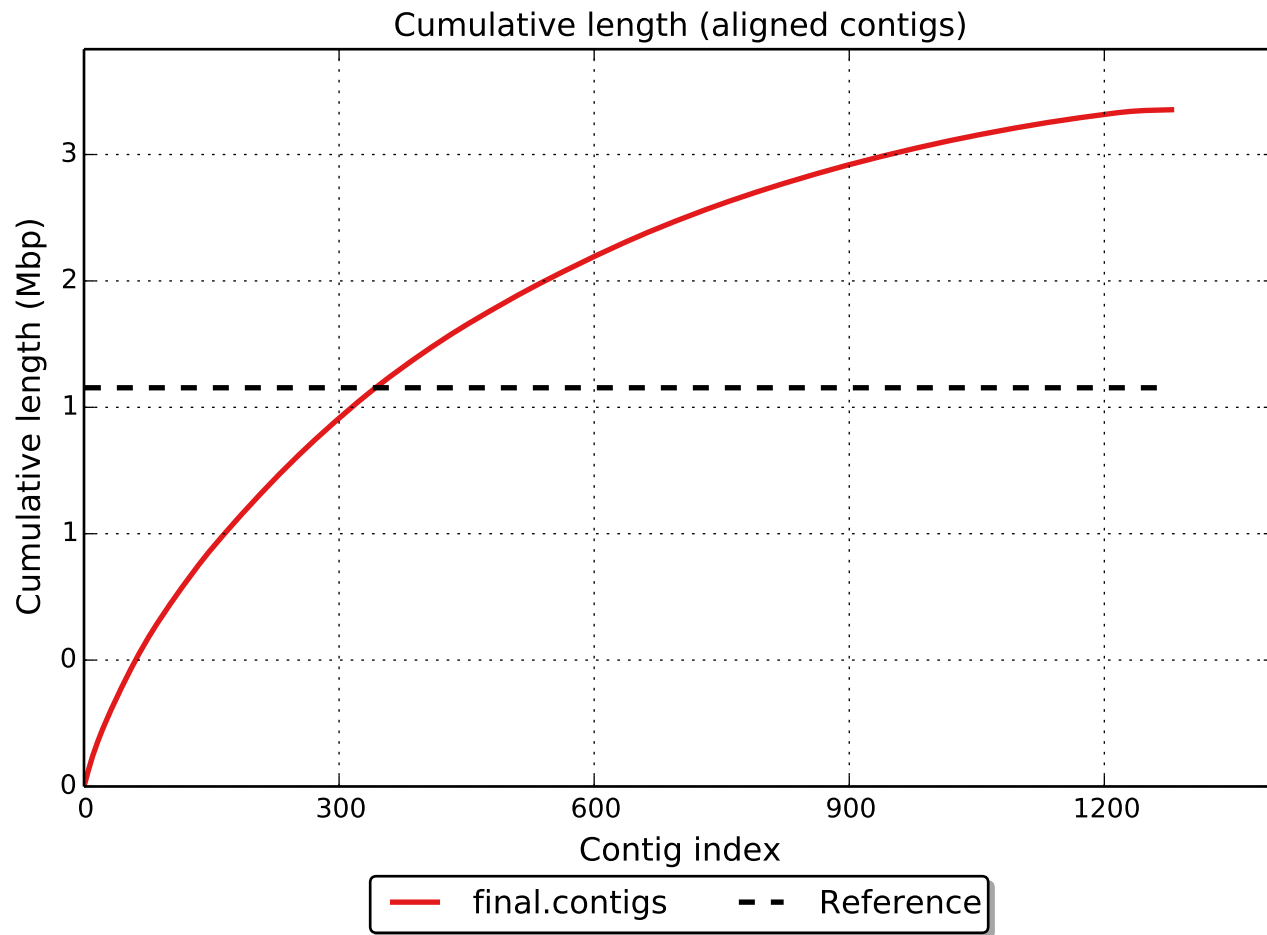


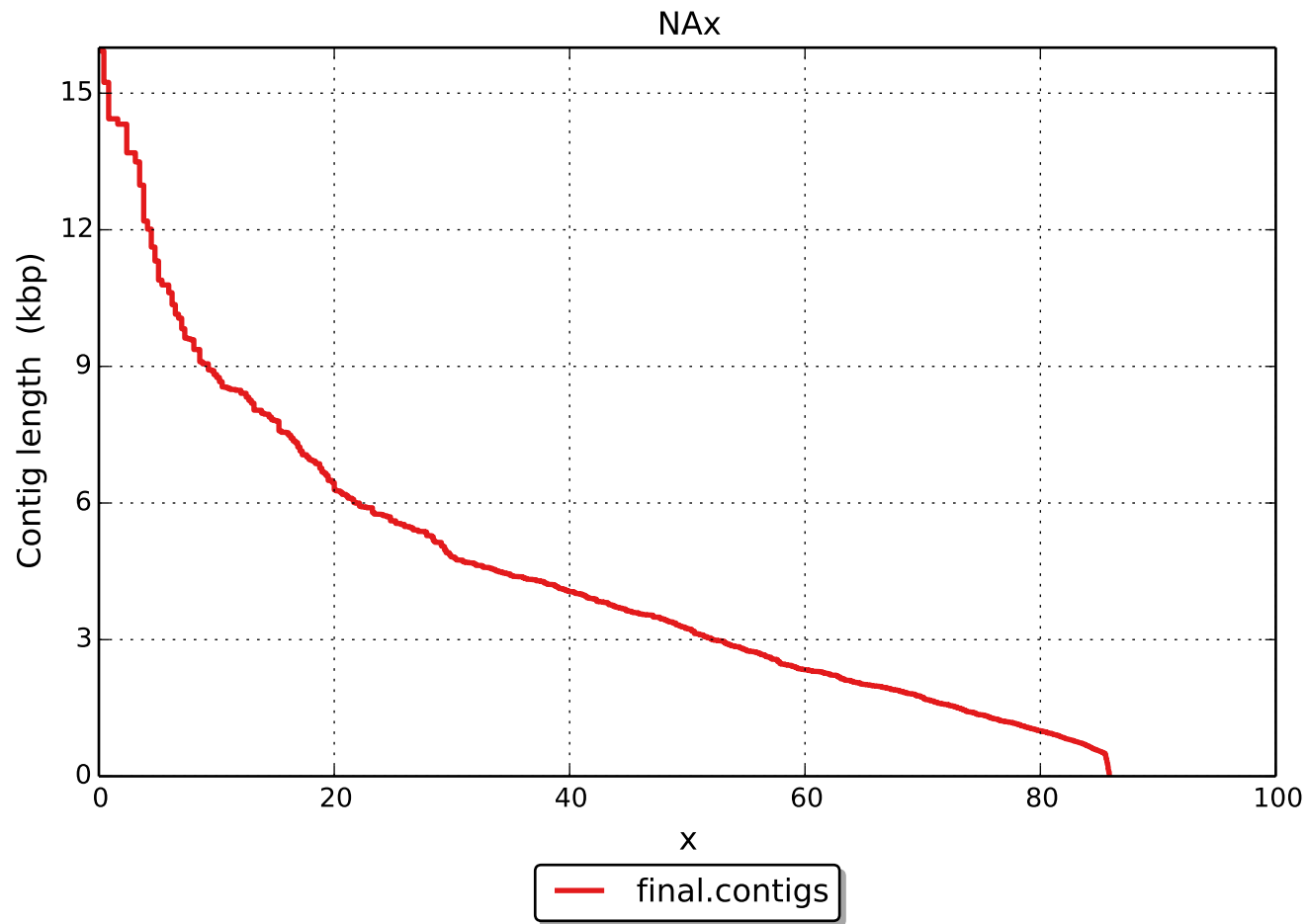




Misassemblies







NGAx

