

Report

	final.contigs
# contigs (>= 1000 bp)	537
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	707149
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1415
Largest contig	3132
Total length	1419809
Reference length	4641652
GC (%)	50.57
Reference GC (%)	50.79
N50	999
N75	857
L50	540
L75	922
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	9071
# local misassemblies	1
# unaligned contigs	0 + 19 part
Unaligned length	1201
Genome fraction (%)	30.303
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	405.88
# indels per 100 kbp	10.10
Largest alignment	3127
NA50	998
NGA50	-
NA75	854
LA50	543
LA75	926

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	6
# relocations	3
# translocations	0
# inversions	3
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	6
Misassembled contigs length	9071
# local misassemblies	1
# mismatches	5709
# indels	142
# short indels	142
# long indels	0
Indels length	205

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	19
# with misassembly	0
# both parts are significant	0
Partially unaligned length	1201
# 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).

Report

	final.contigs
# contigs (≥ 0 bp)	1589
# contigs (≥ 1000 bp)	537
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	1482456
Total length (≥ 1000 bp)	707149
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	1415
Largest contig	3132
Total length	1419809
Reference length	4641652
N50	999
N75	857
L50	540
L75	922
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	9071
# local misassemblies	1
# unaligned contigs	0 + 19 part
Unaligned length	1201
Genome fraction (%)	30.303
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	405.88
# indels per 100 kbp	10.10
Largest alignment	3127
NA50	998
NA75	854
LA50	543
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Misassemblies report

	final.contigs
# misassemblies	6
# relocations	3
# translocations	0
# inversions	3
# possibly misassembled contigs	0
# misassembled contigs	6
Misassembled contigs length	9071
# local misassemblies	1
# mismatches	5709
# indels	142
# short indels	142
# long indels	0
Indels length	205

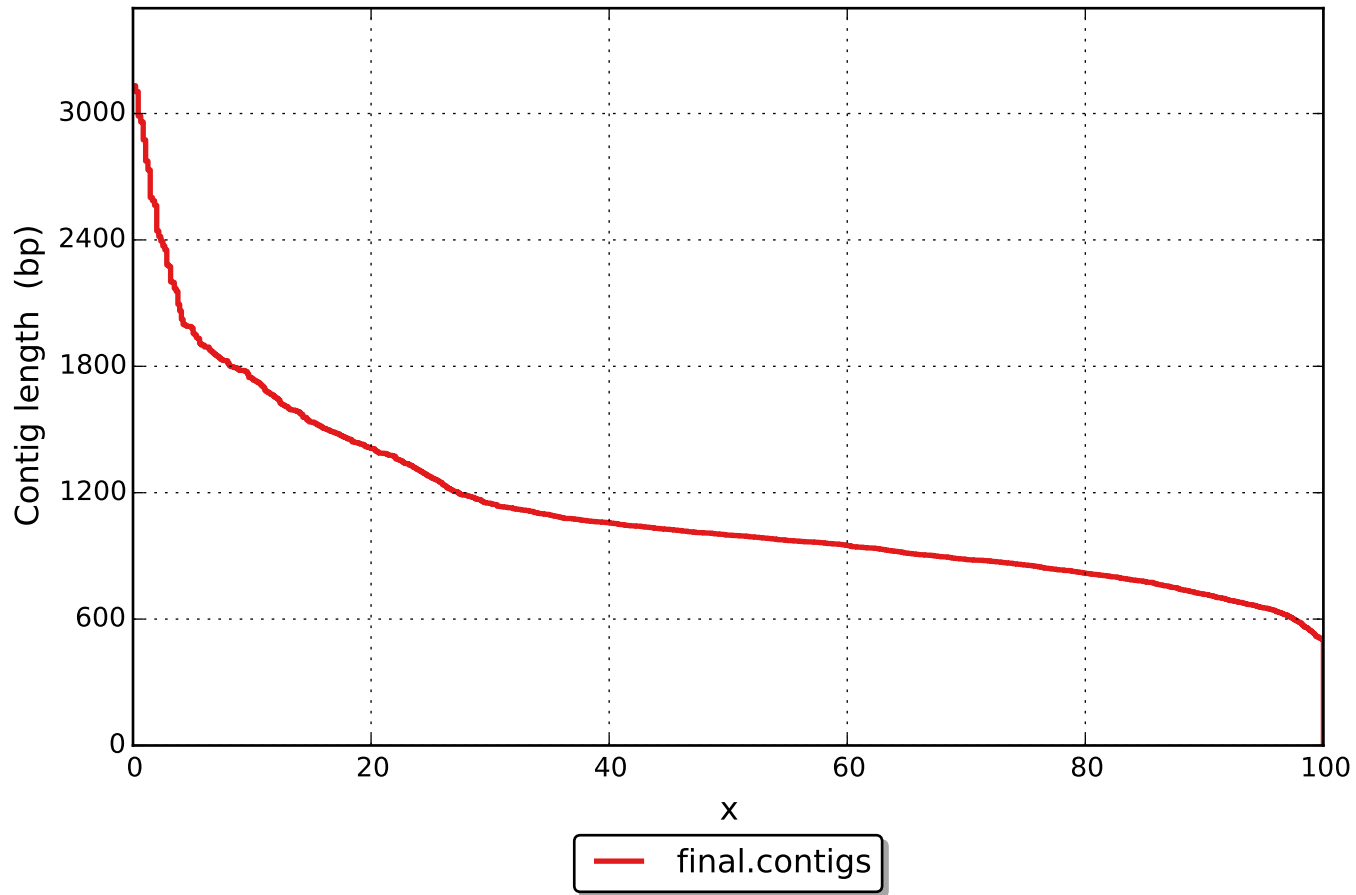
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

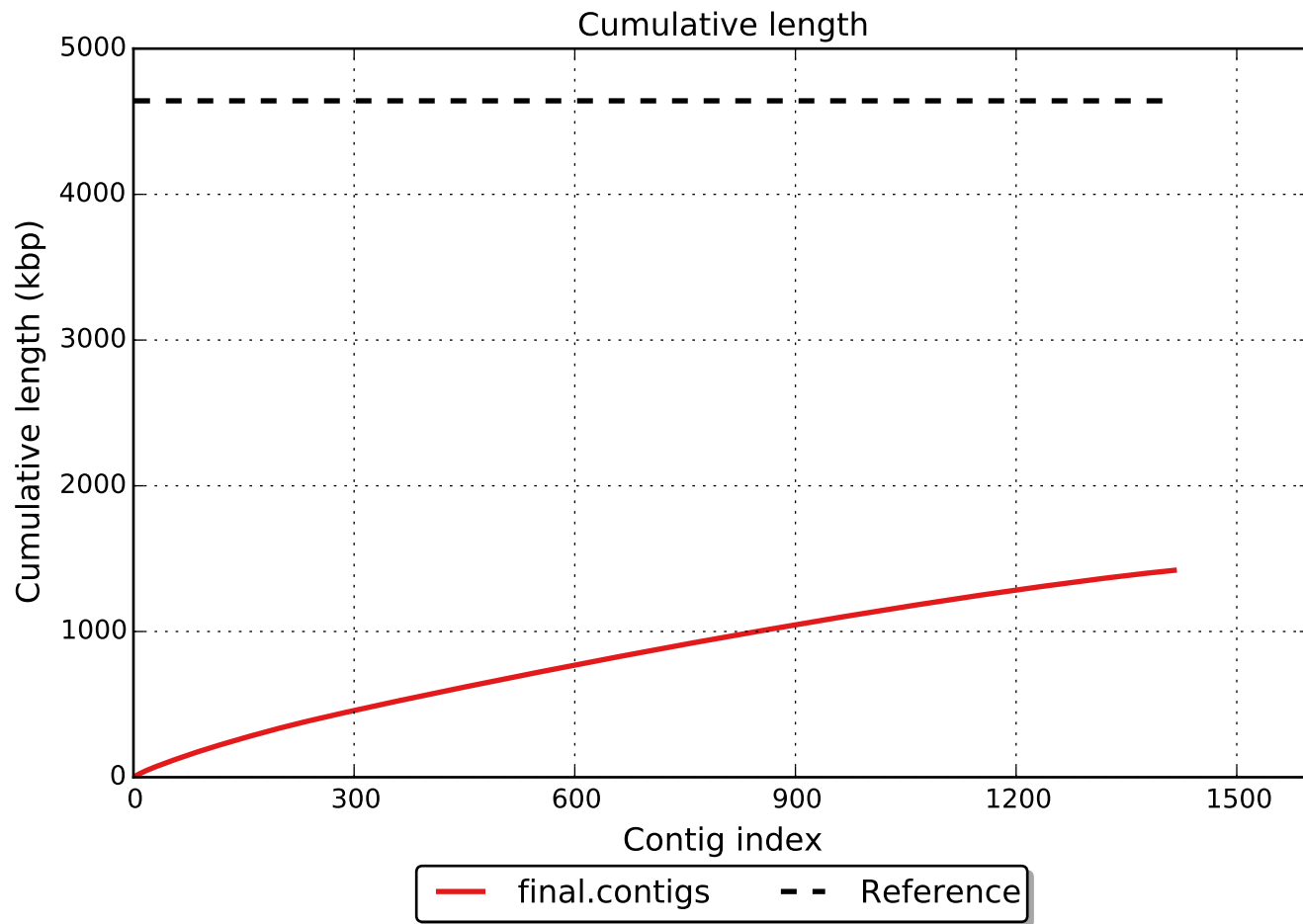
Unaligned report

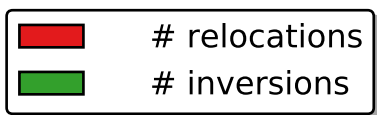
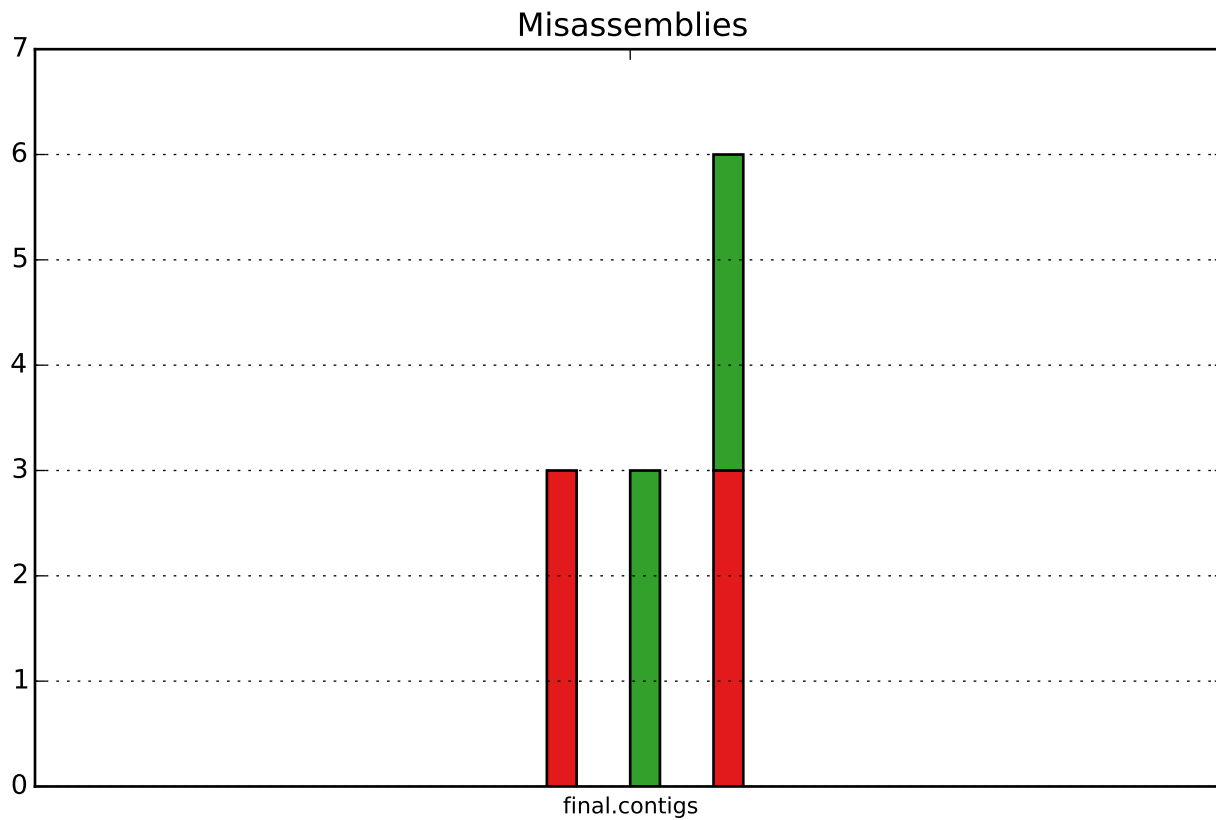
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	19
# with misassembly	0
# both parts are significant	0
Partially unaligned length	1201
# N's	0

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).

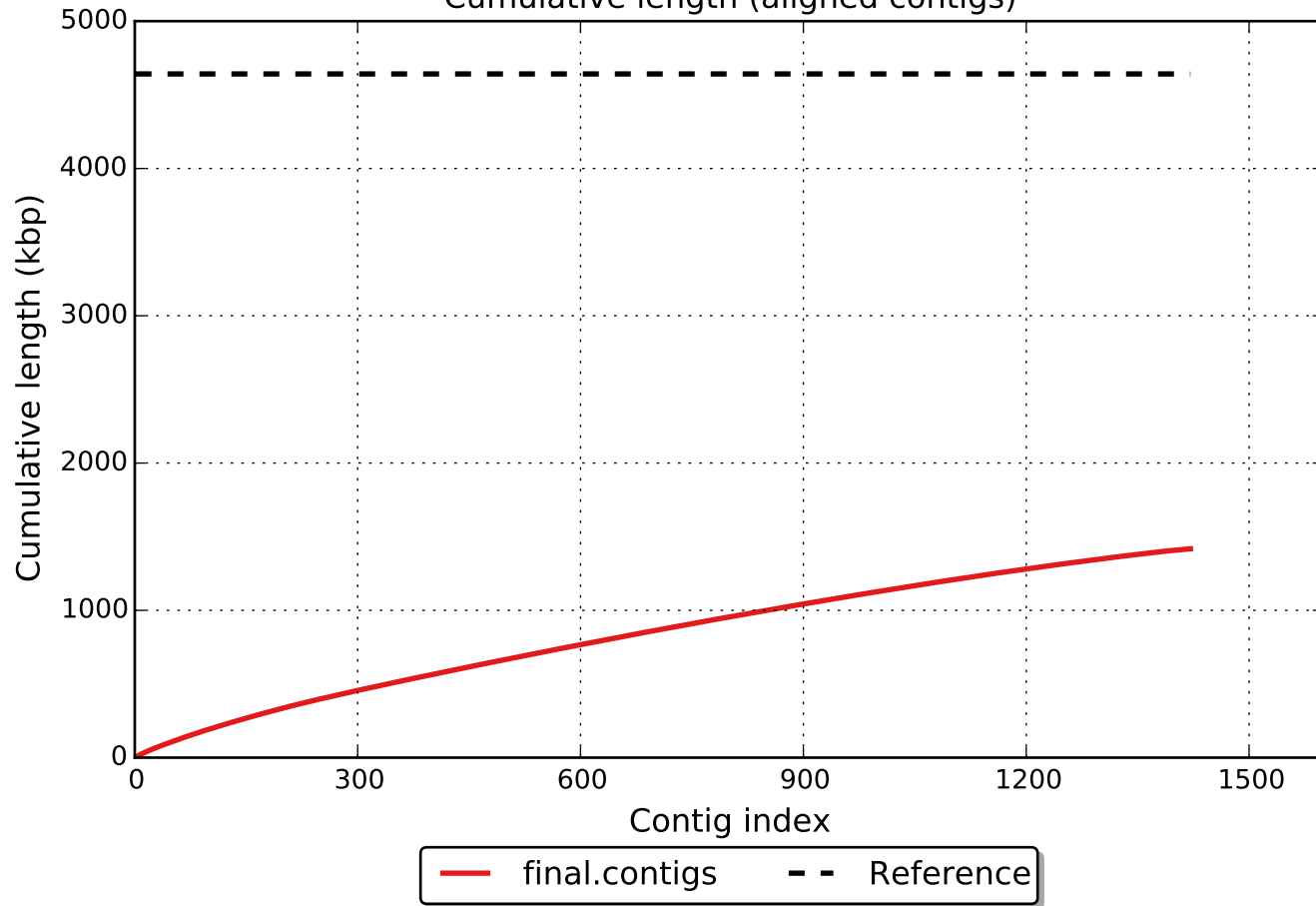
Nx



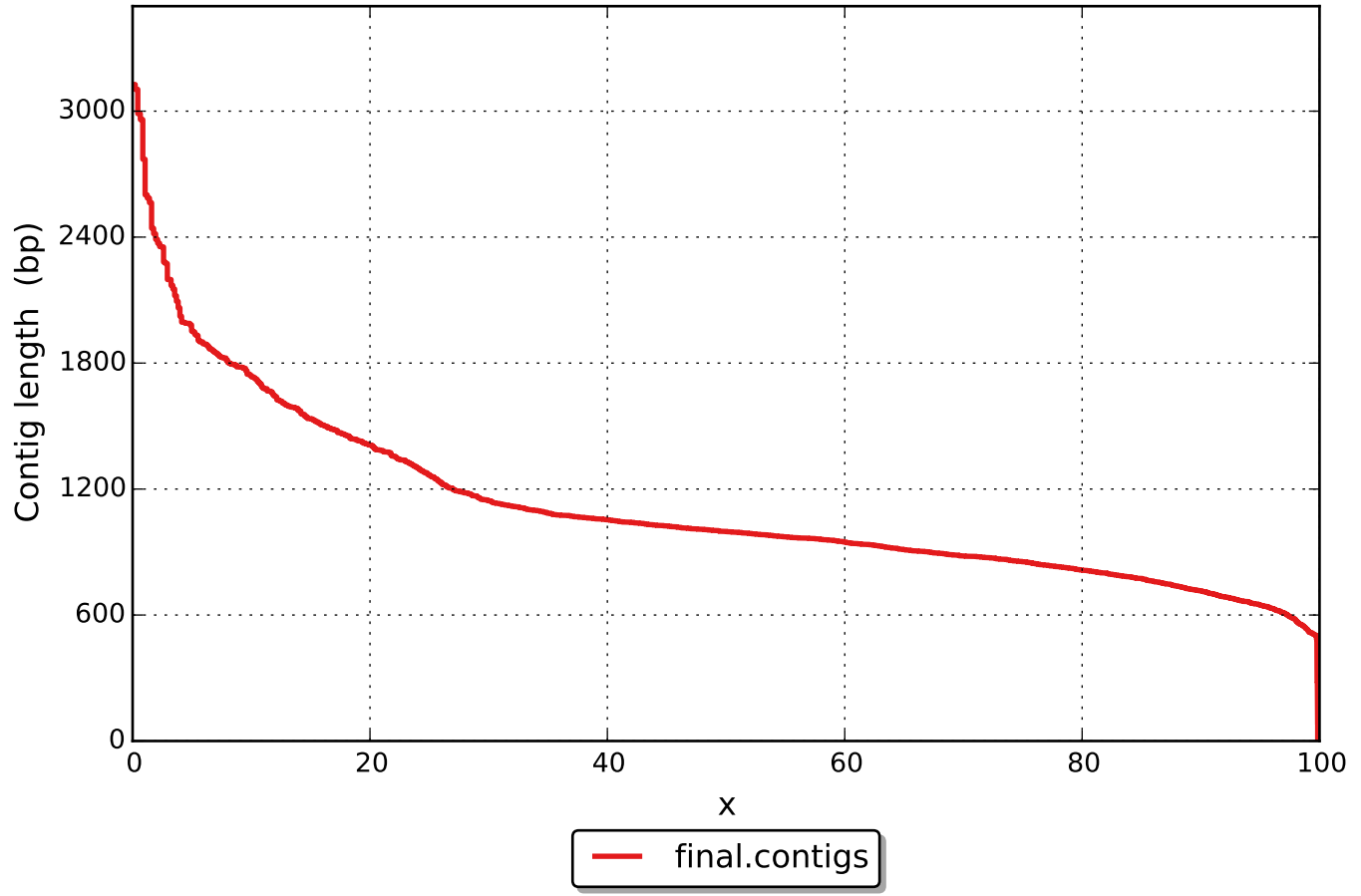




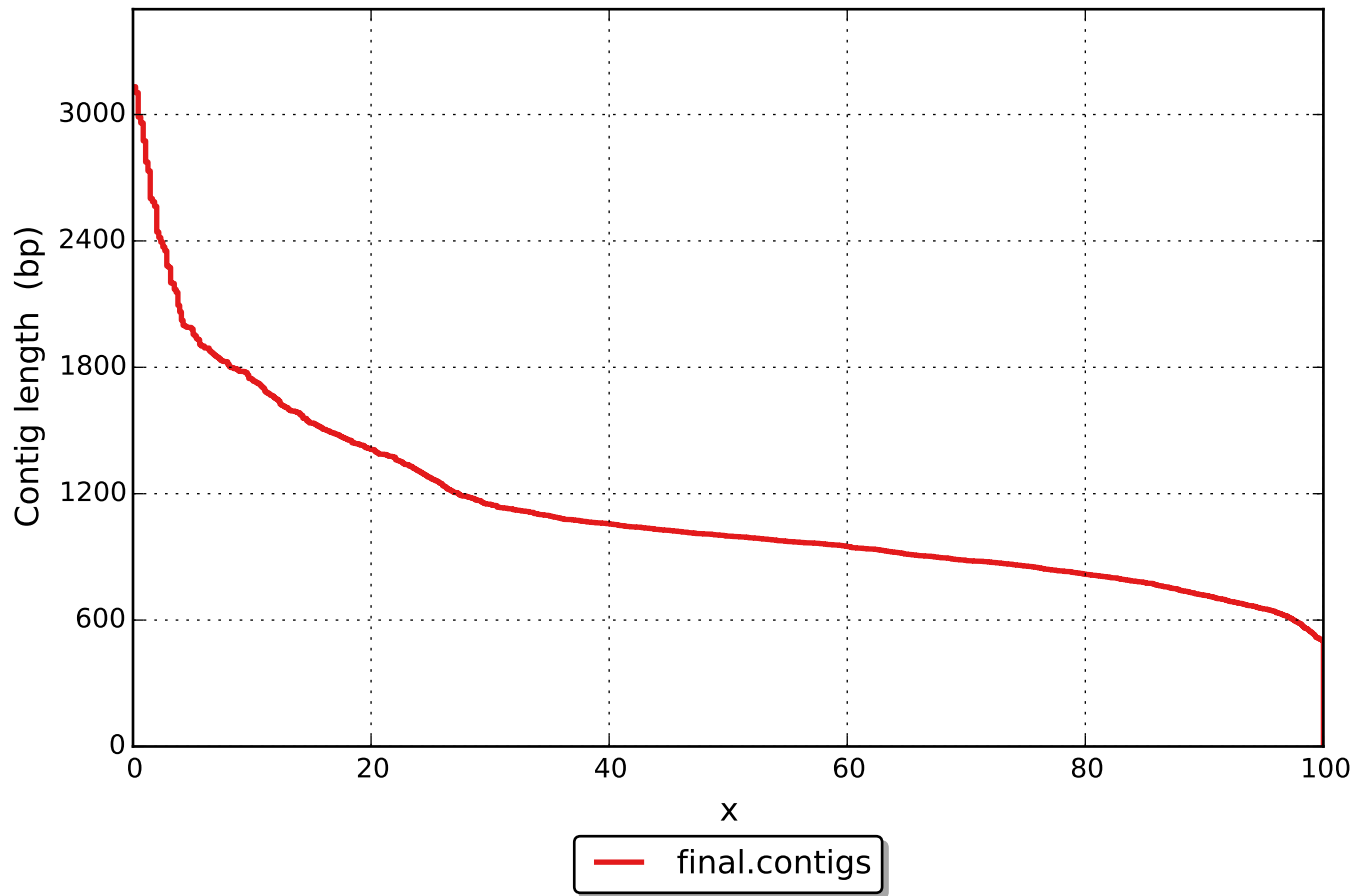
Cumulative length (aligned contigs)



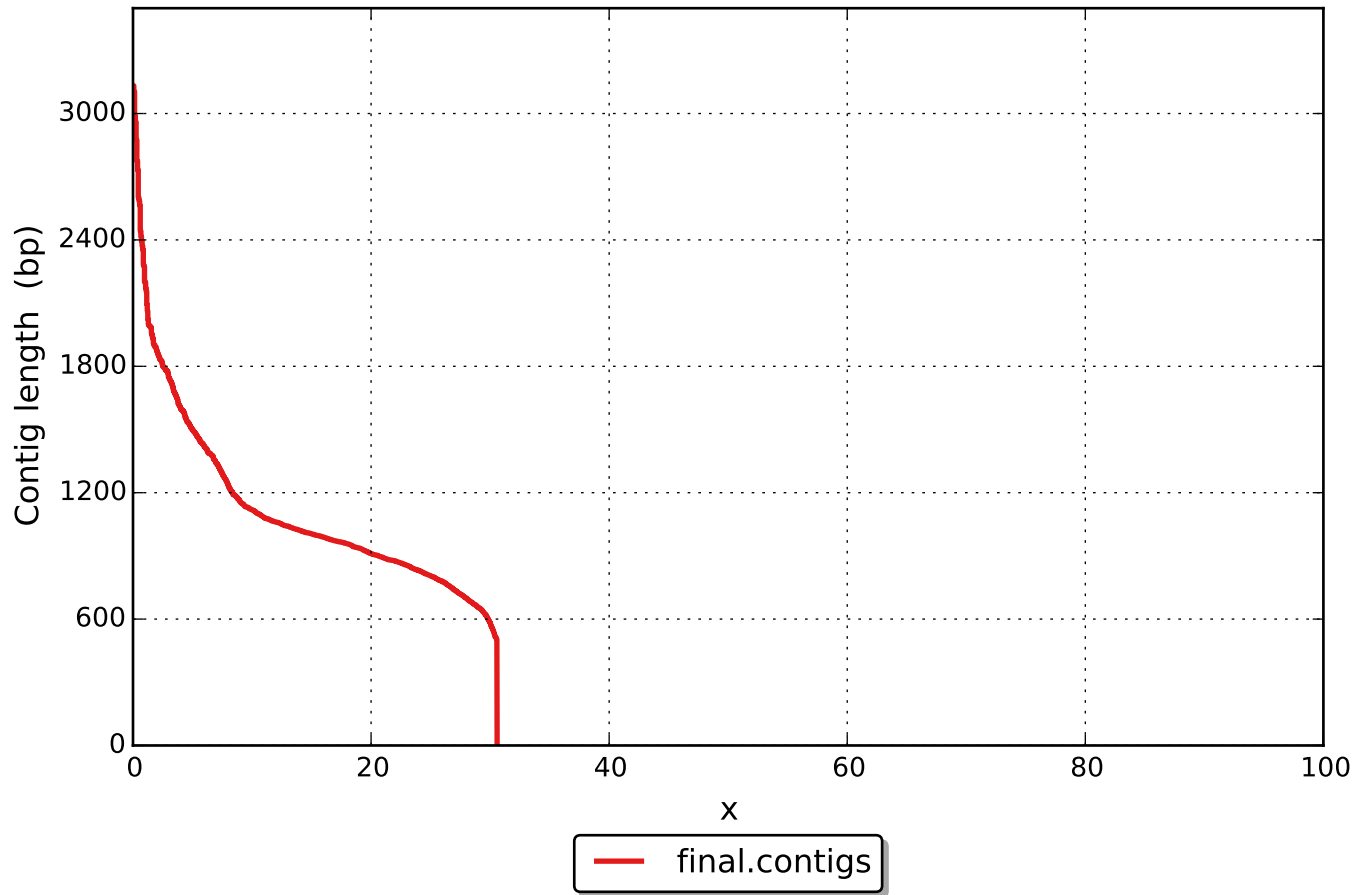
NAx

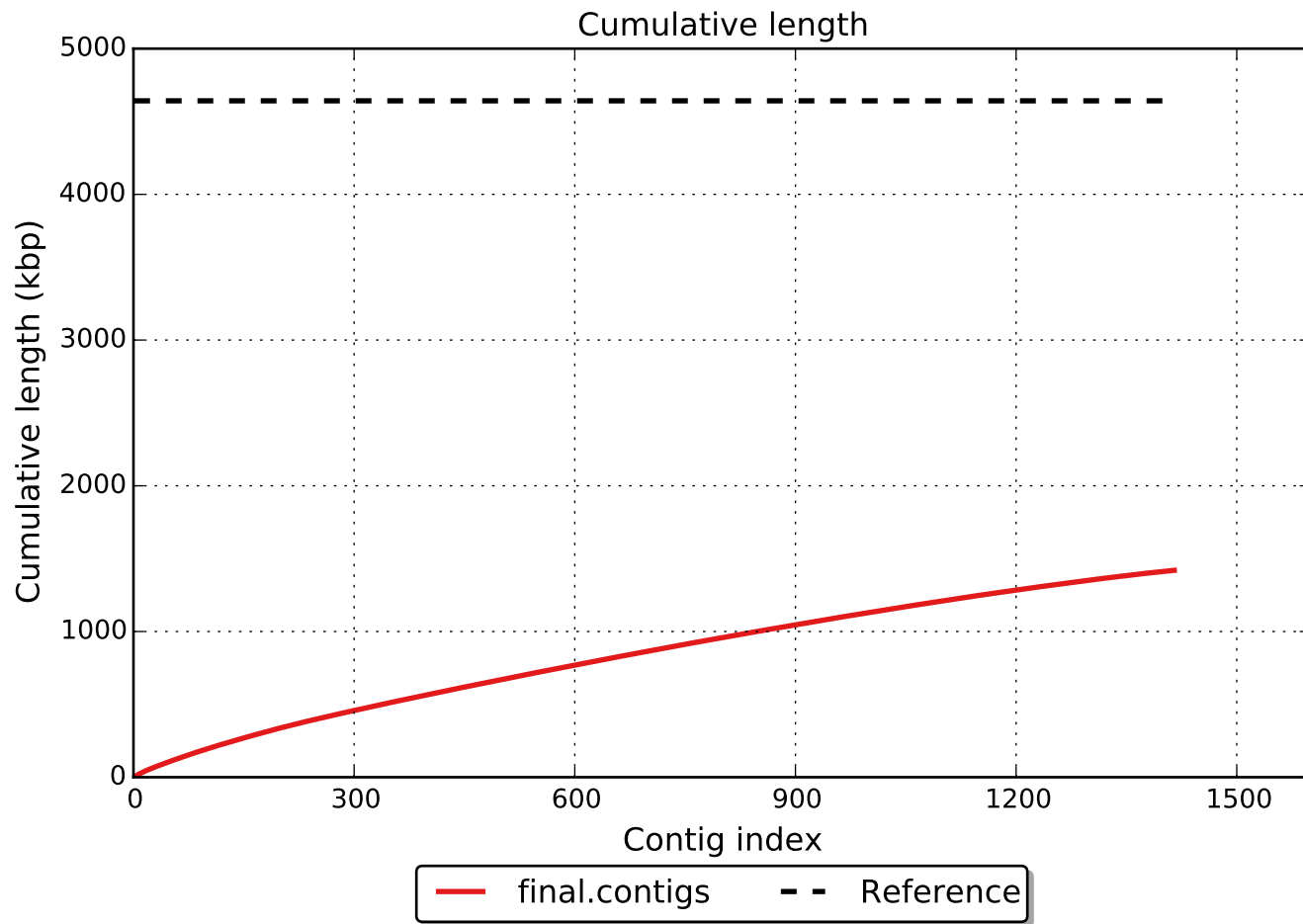


Nx

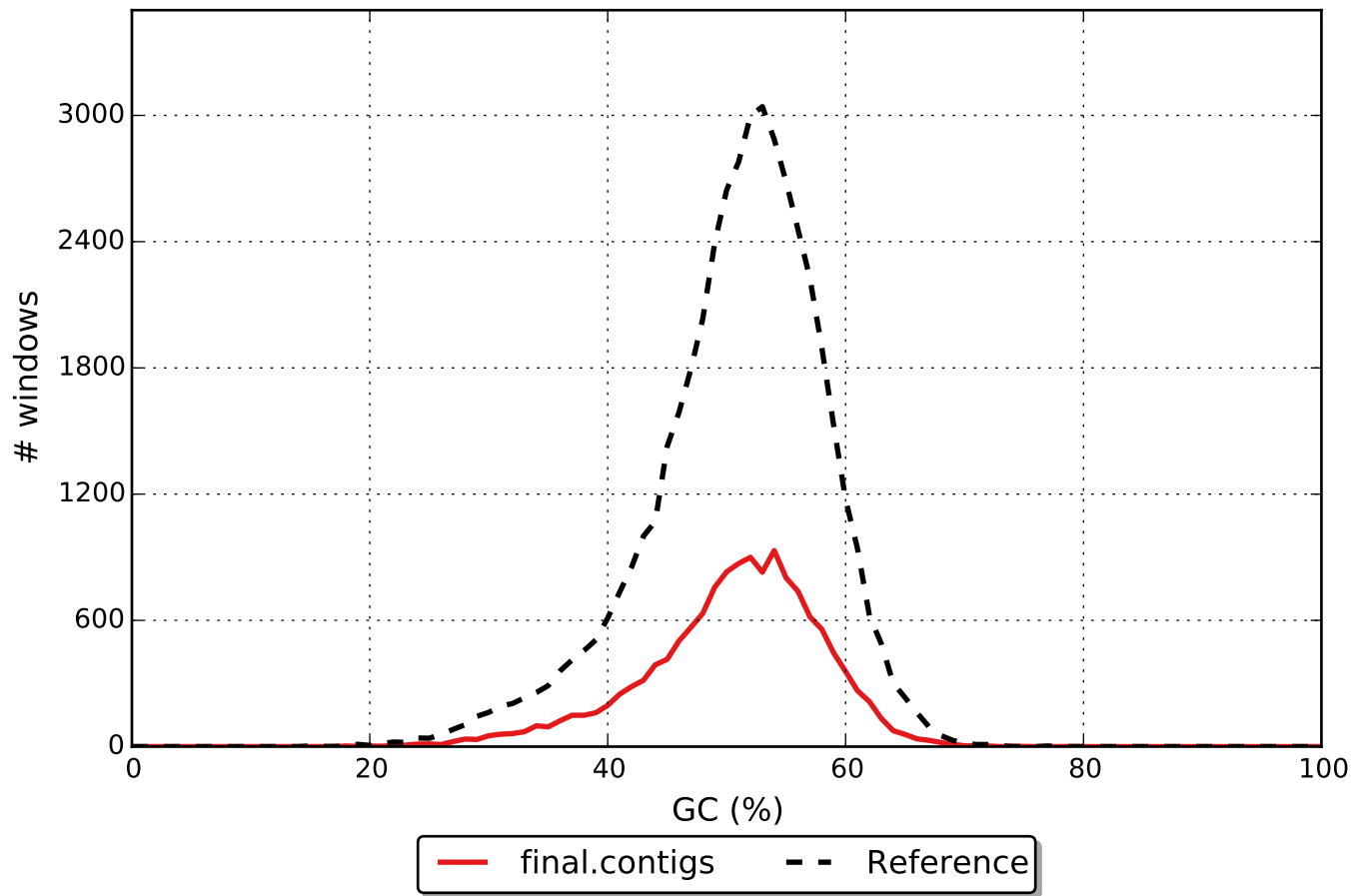


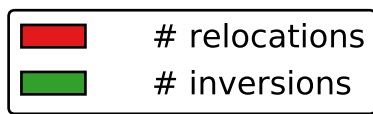
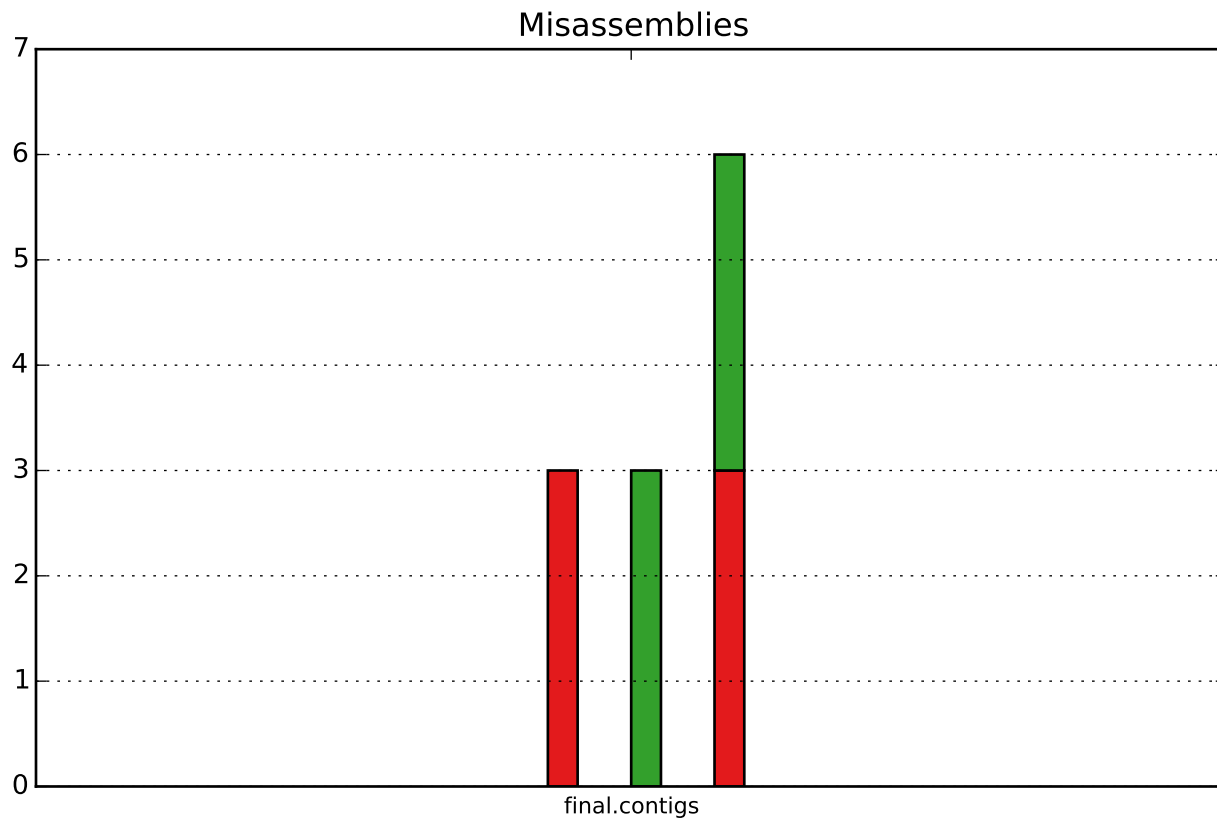
NGx



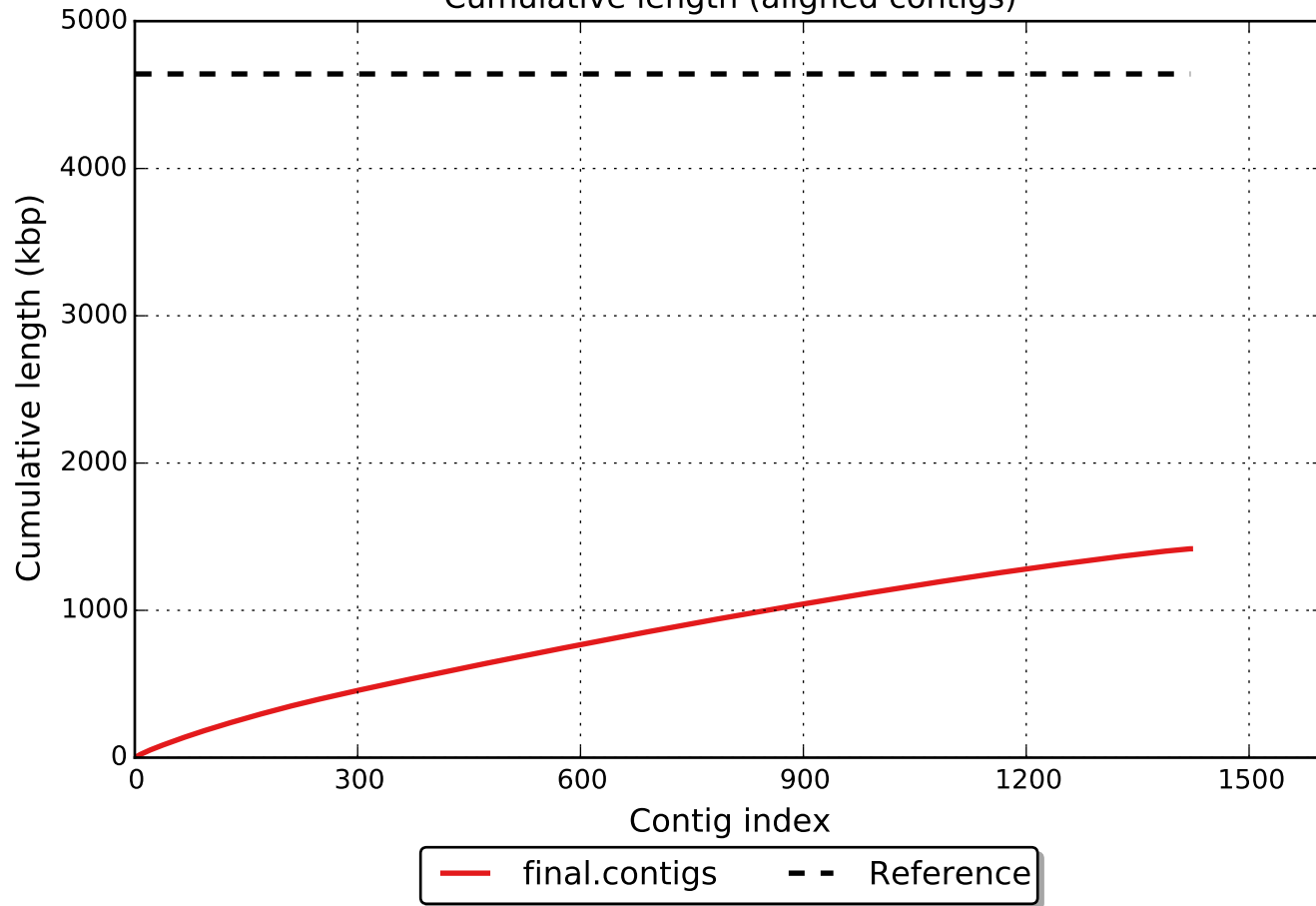


GC content

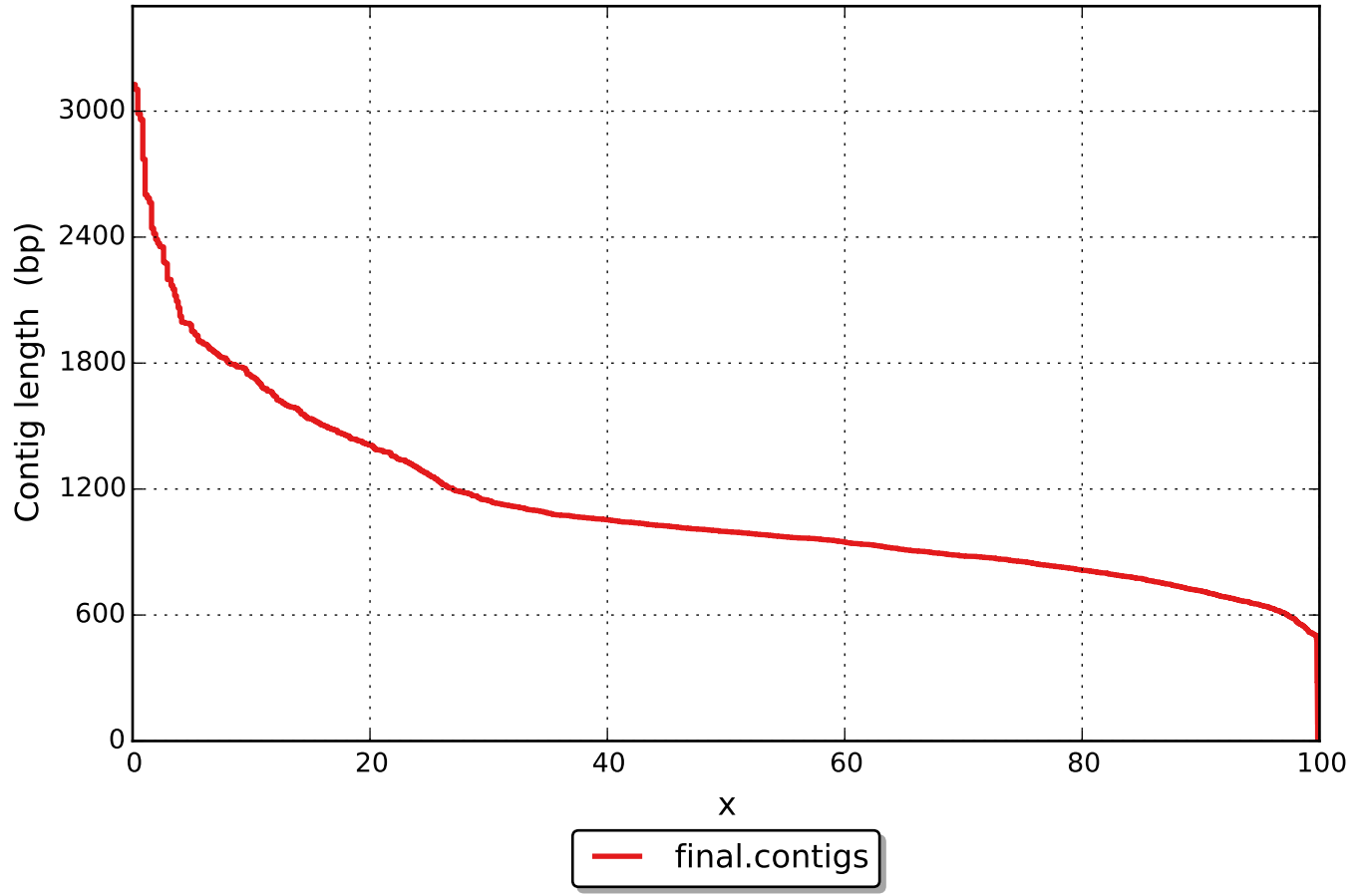




Cumulative length (aligned contigs)



NAx



NGAx

