

Report

	contigs
# contigs (≥ 0 bp)	8552
# contigs (≥ 1000 bp)	10
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	2748013
Total length (≥ 1000 bp)	16592
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	632
Largest contig	3178
Total length	394862
Reference length	4641652
GC (%)	50.71
Reference GC (%)	50.79
N50	604
N75	540
L50	268
L75	442
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	8133
# local misassemblies	0
# unaligned contigs	0 + 5 part
Unaligned length	204
Genome fraction (%)	8.462
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1403.88
# indels per 100 kbp	1.78
Largest alignment	3178
NA50	602
NGA50	-
NA75	539
LA50	270
LA75	444

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

	contigs
# misassemblies	6
# relocations	6
# translocations	0
# inversions	0
# misassembled contigs	6
Misassembled contigs length	8133
# local misassemblies	0
# mismatches	5514
# indels	7
# short indels	7
# long indels	0
Indels length	7

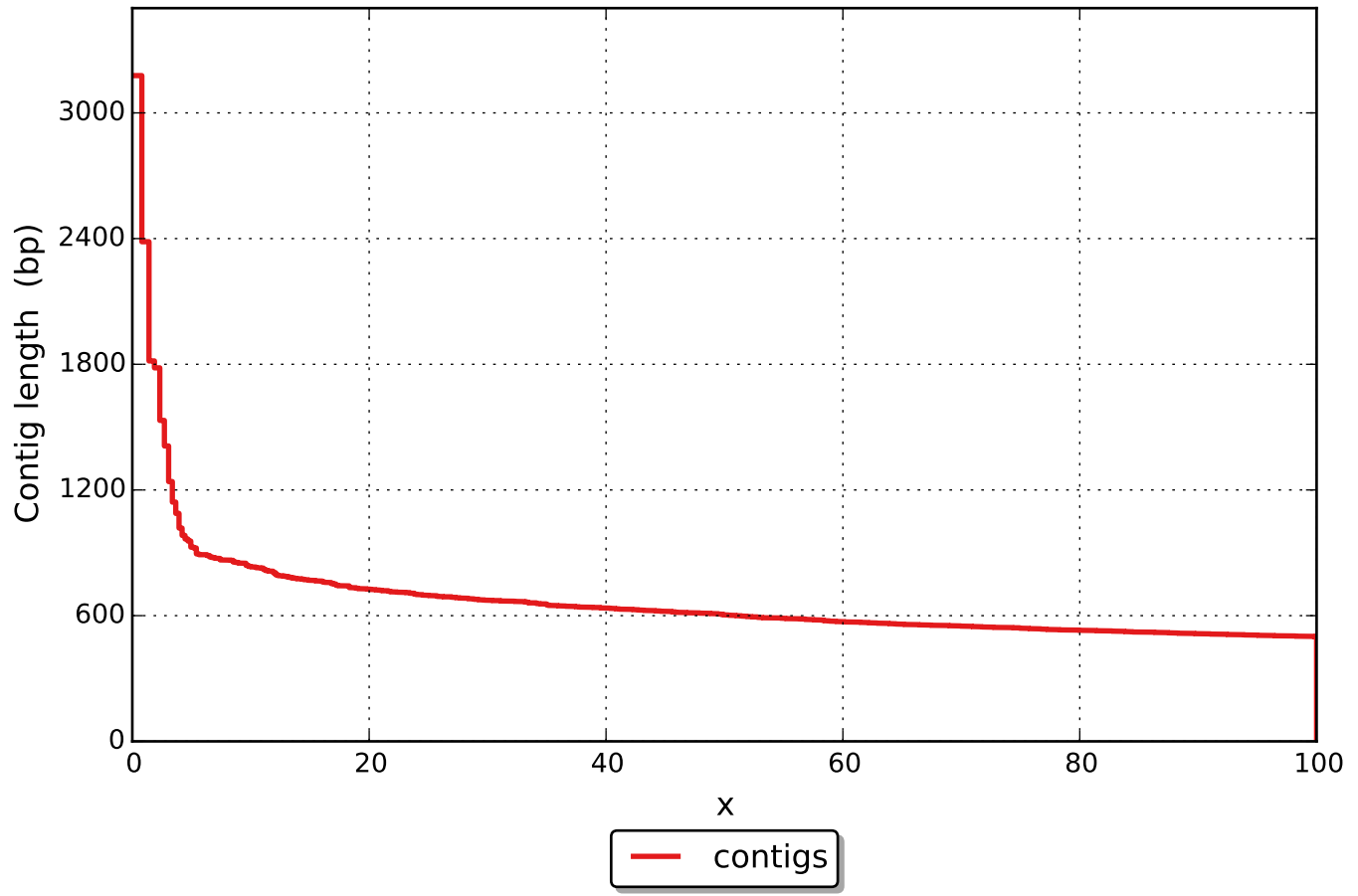
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

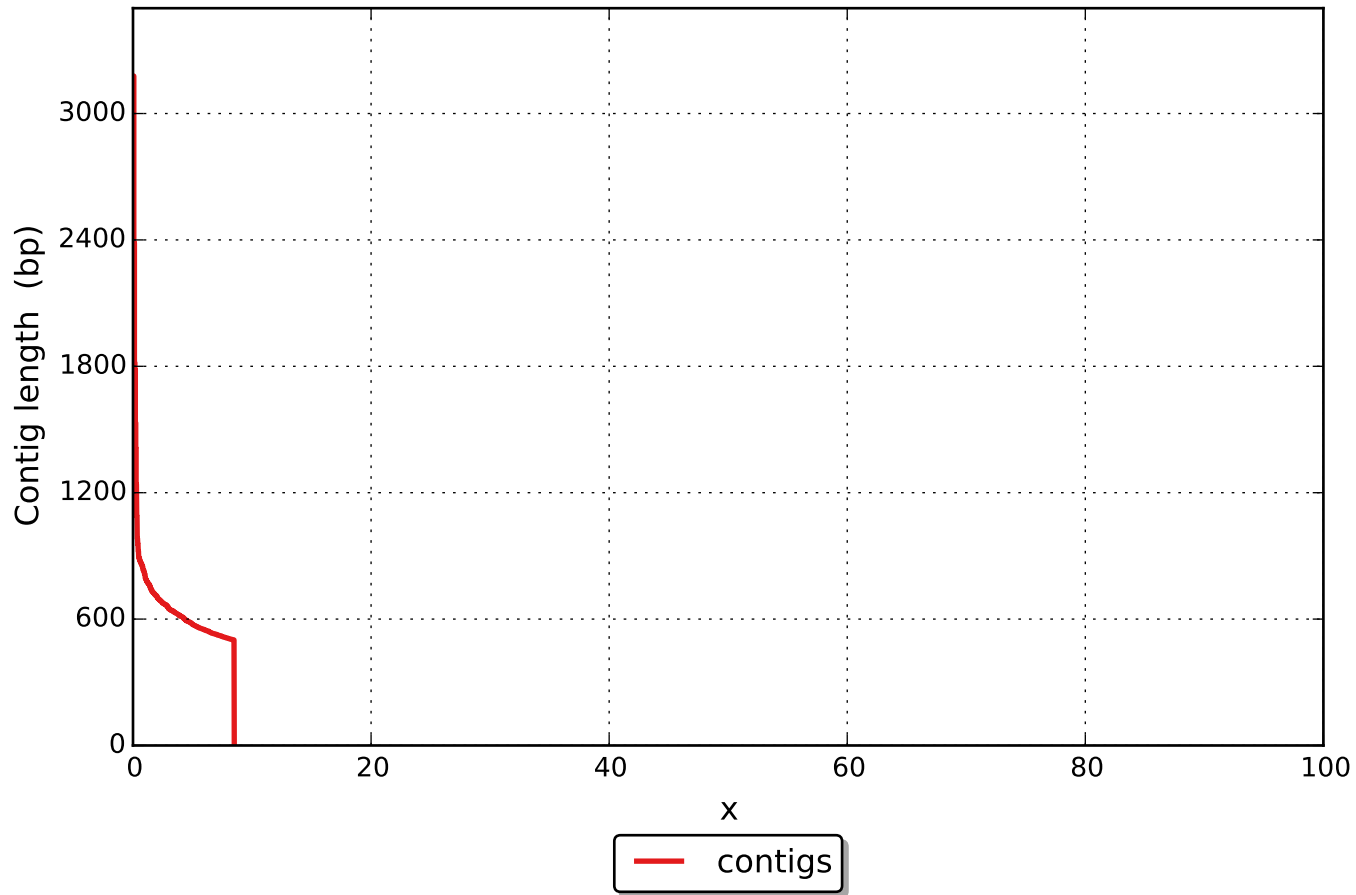
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	0
Partially unaligned length	204
# N's	0

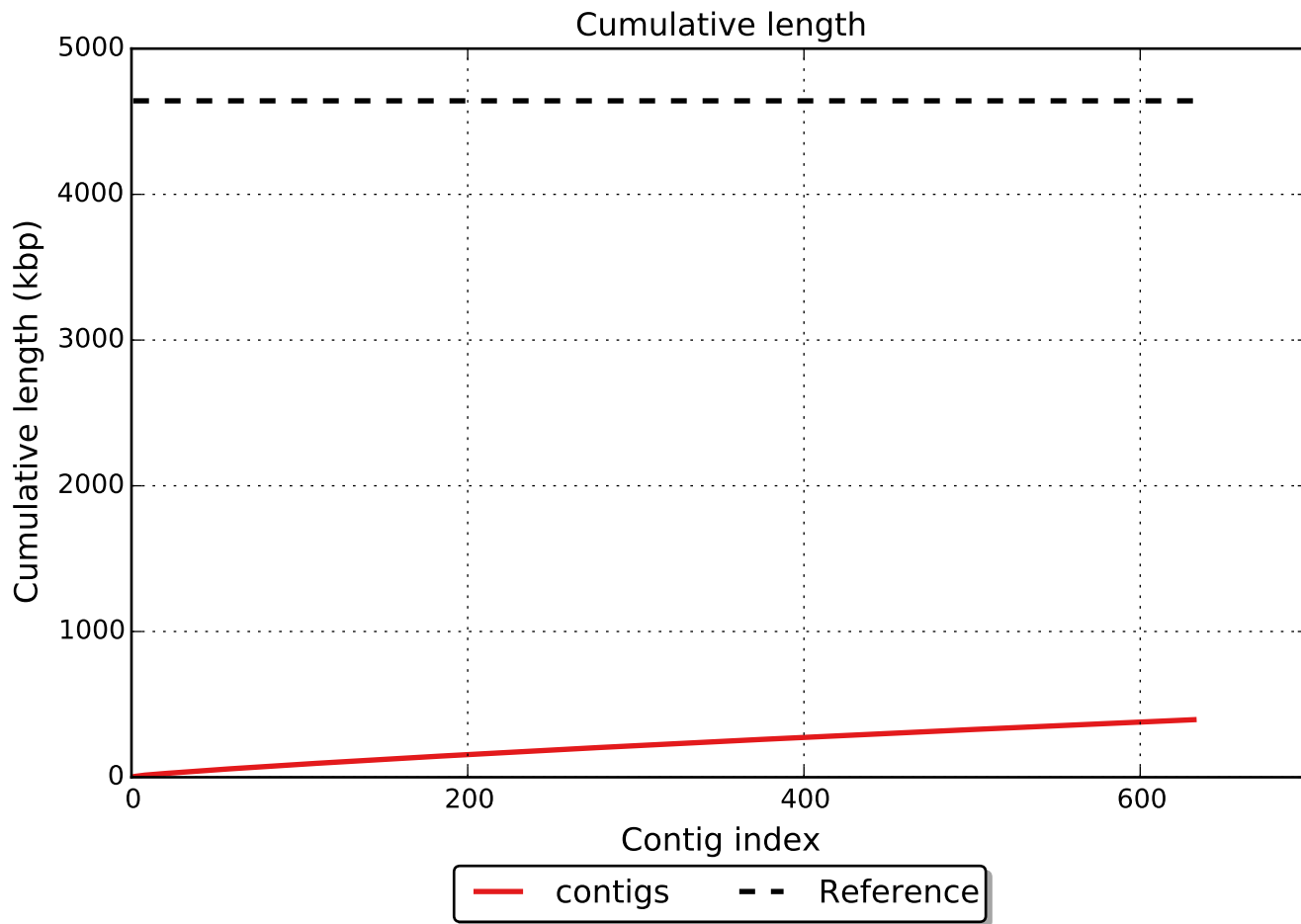
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

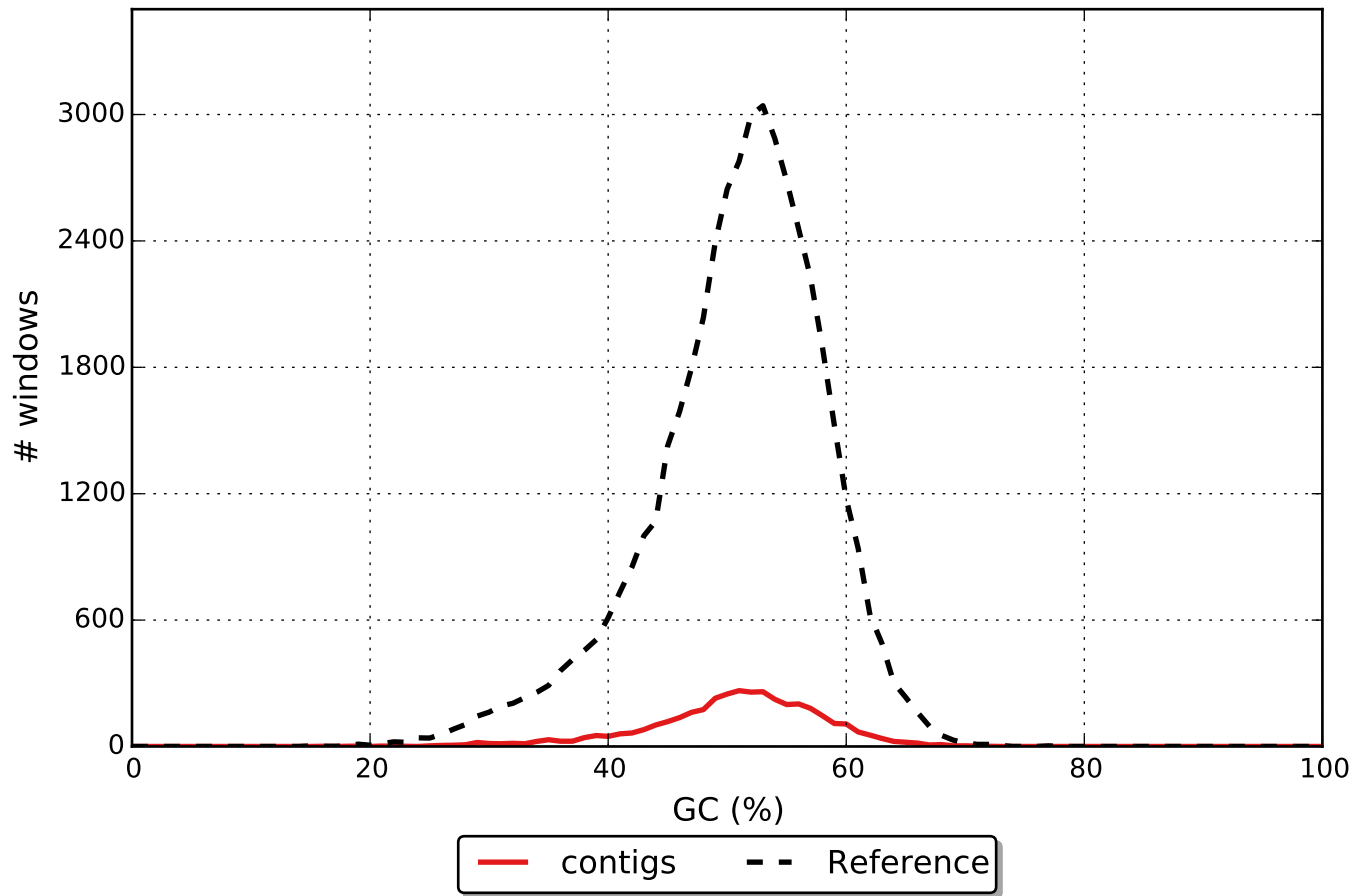


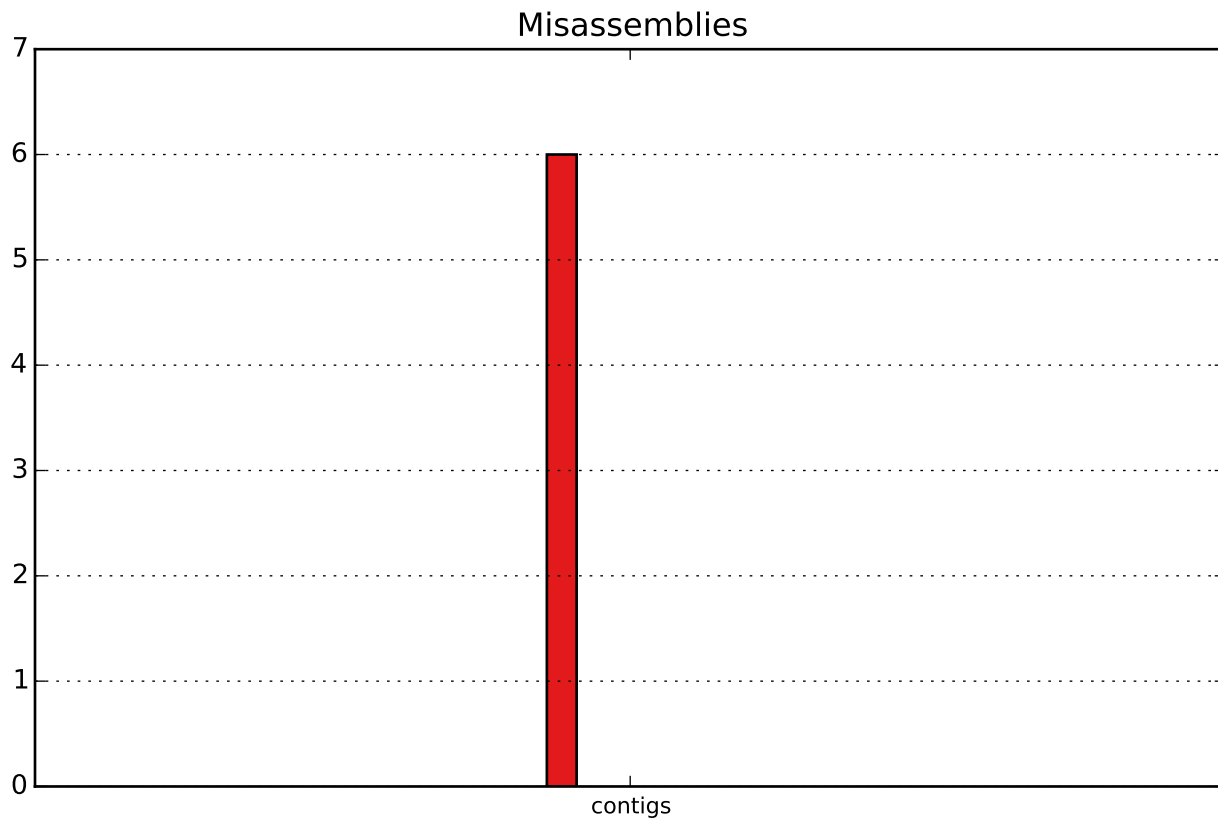
NGx



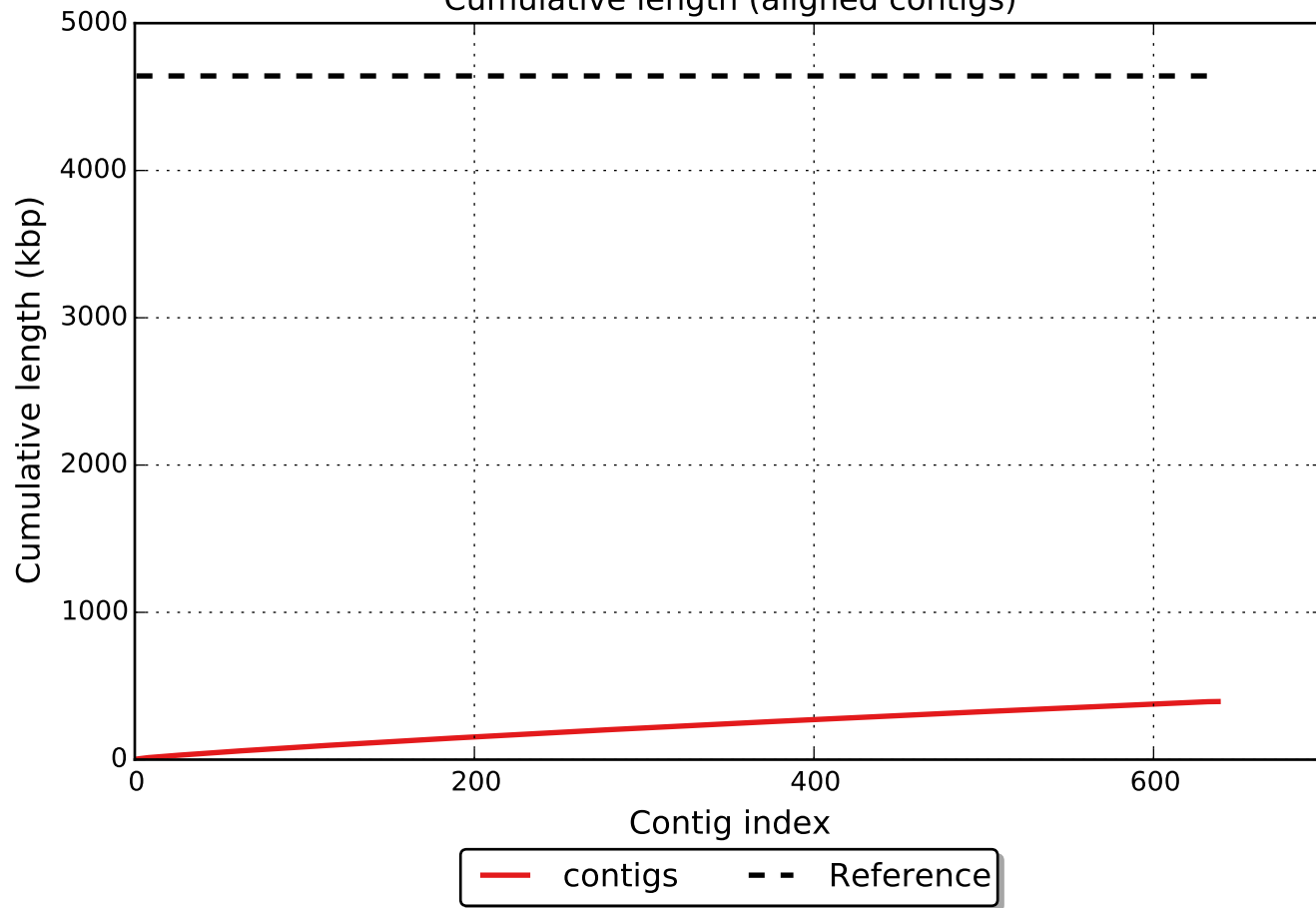


GC content

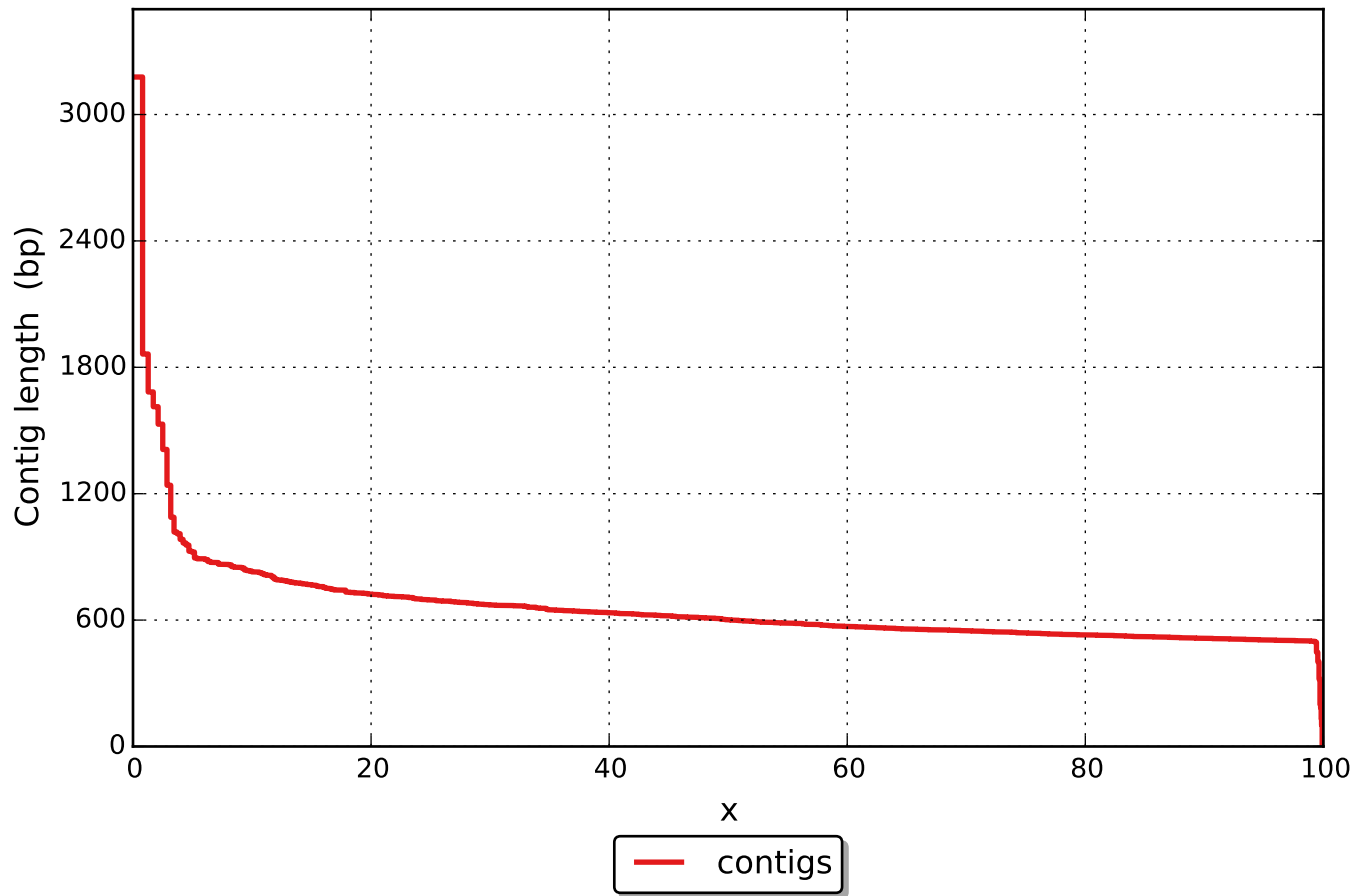




Cumulative length (aligned contigs)



NAx



NGAx

