

Report

	final.contigs
# contigs (≥ 1000 bp)	3
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	4612
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	9
Largest contig	2250
Total length	8896
Reference length	4610381
GC (%)	53.07
Reference GC (%)	59.05
N50	1123
N75	731
L50	3
L75	6
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 6 part
Unaligned length	5039
Genome fraction (%)	0.064
Duplication ratio	1.304
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2670.72
# indels per 100 kbp	304.26
Largest alignment	1387
Total aligned length	2961
NGA50	-

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

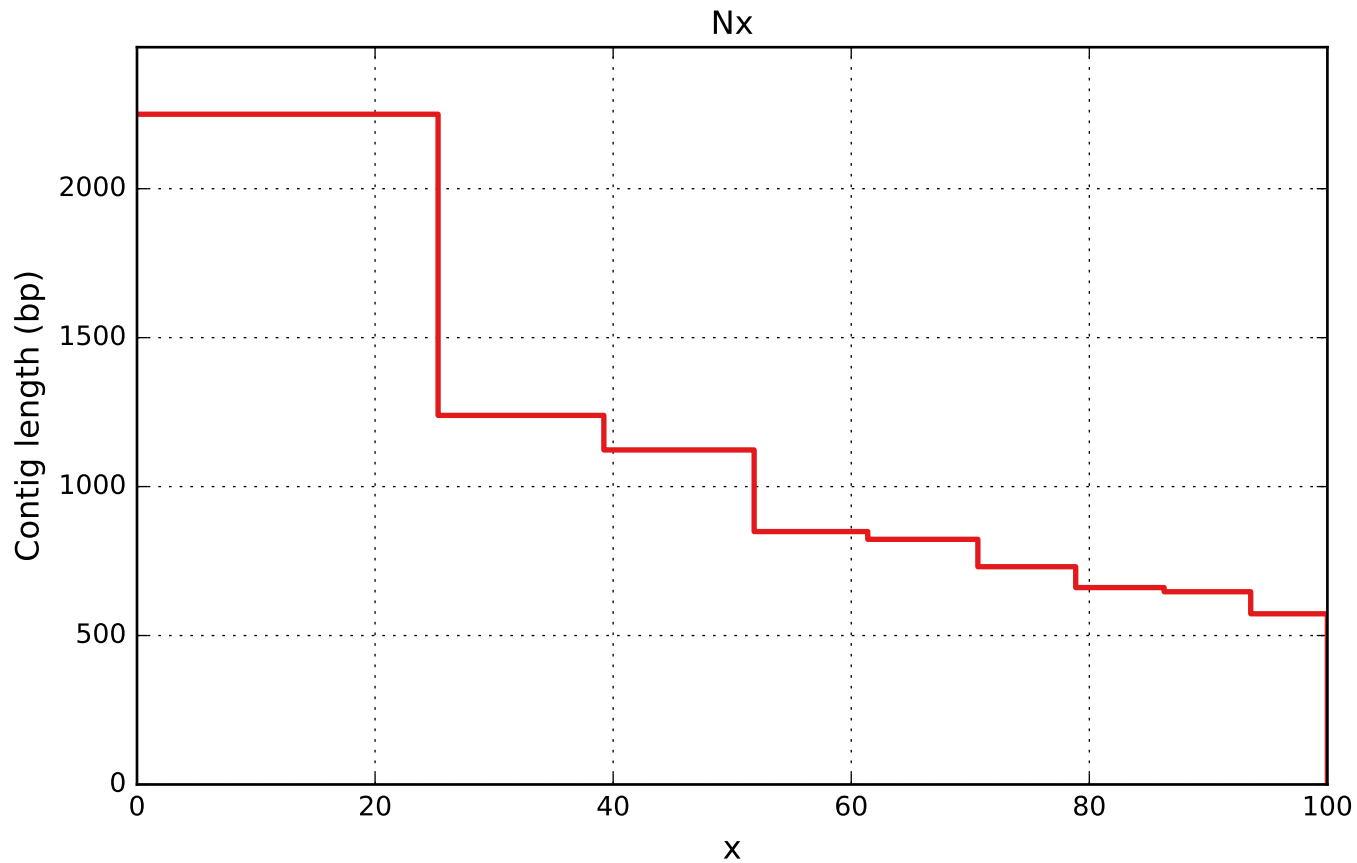
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	1
# possible misassemblies	1
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	1
# mismatches	79
# indels	9
# indels (≤ 5 bp)	9
# indels (> 5 bp)	0
Indels length	9

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).

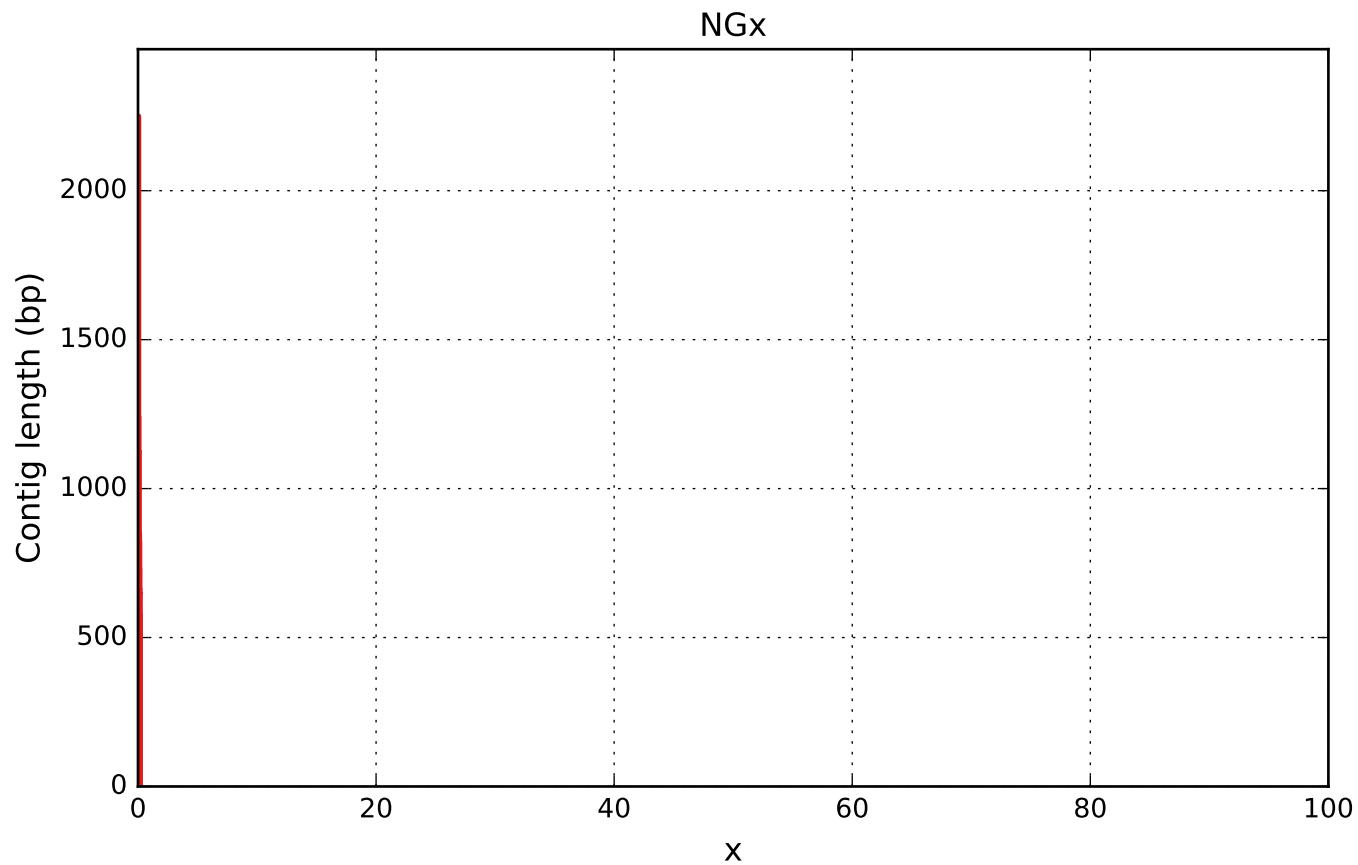
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
Partially unaligned length	5039
# N's	0

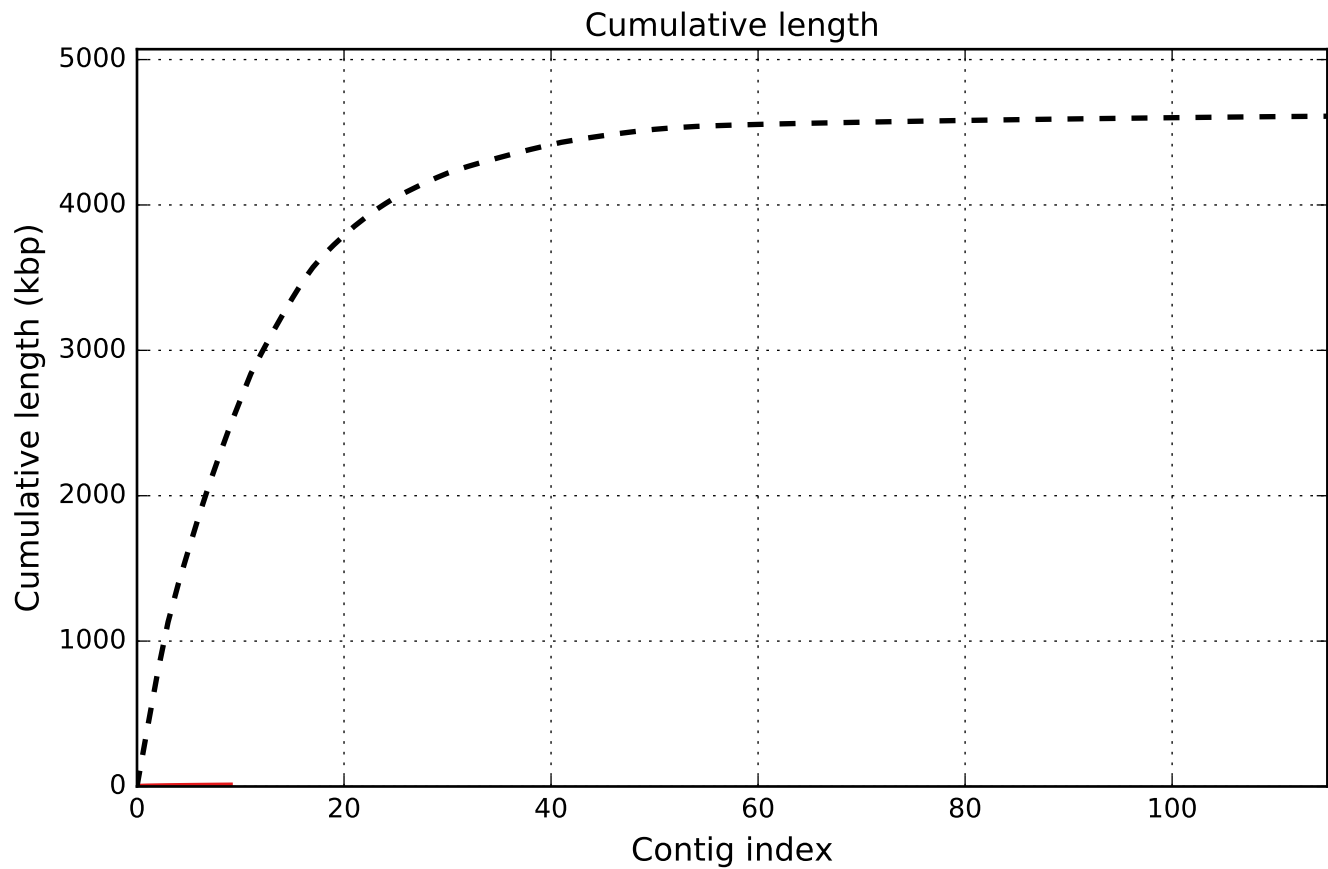
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

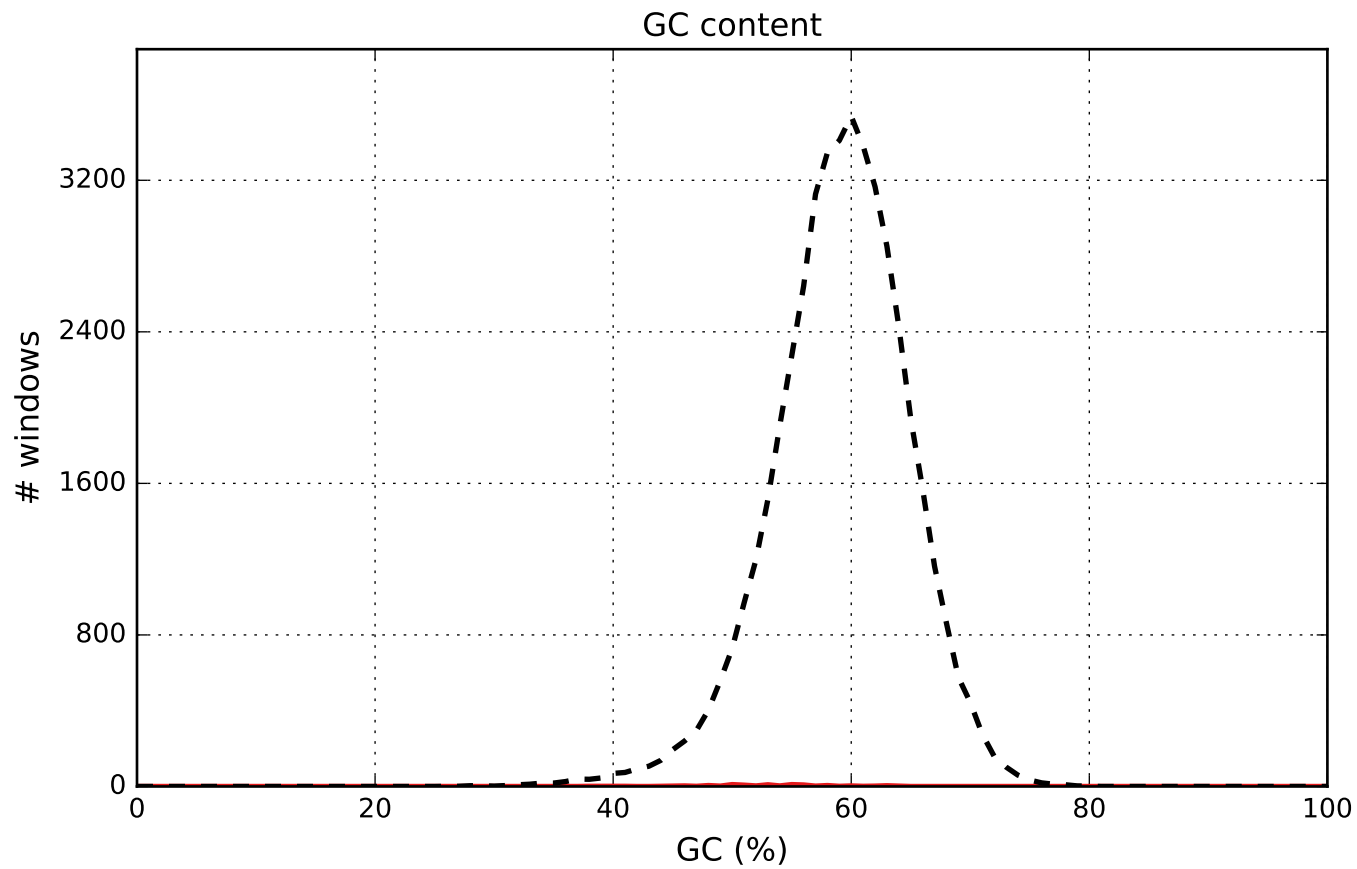


— final.contigs



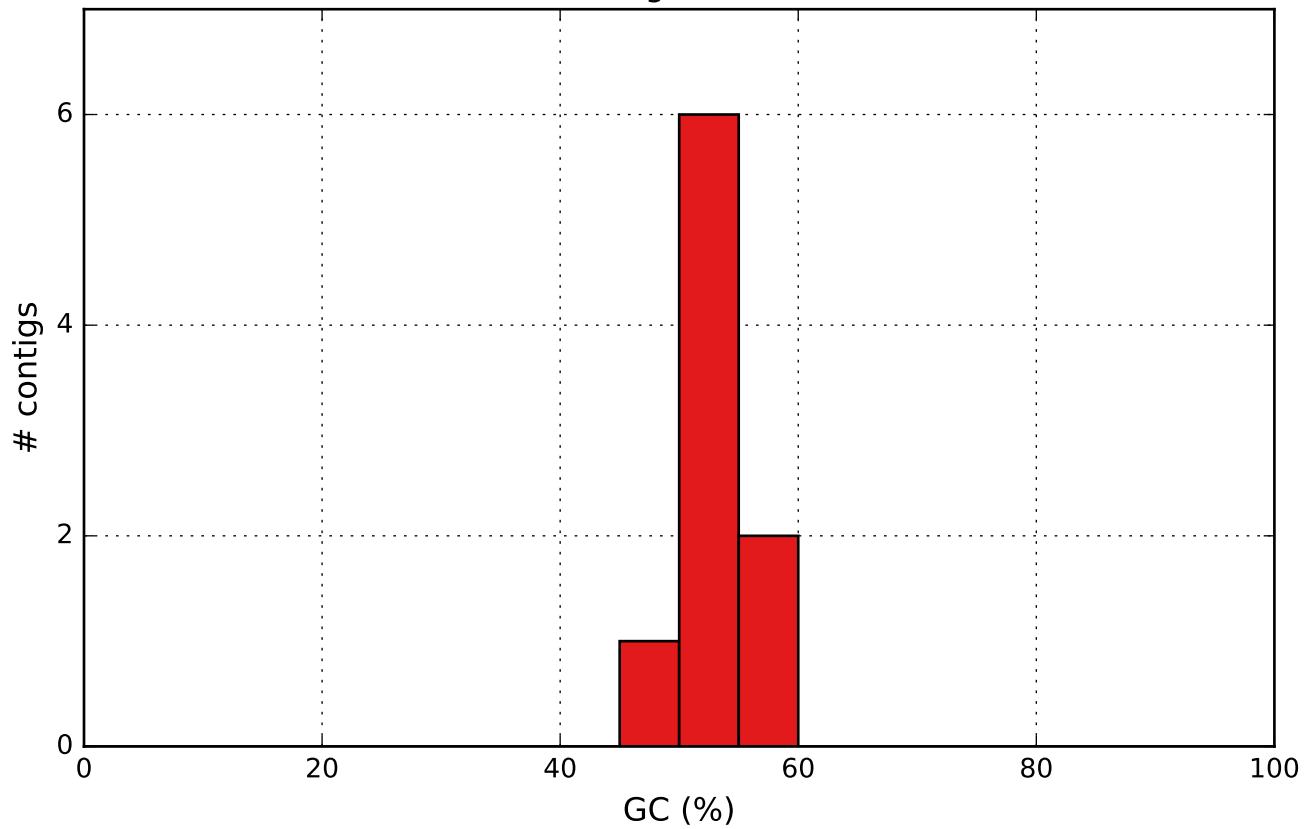
— final.contigs



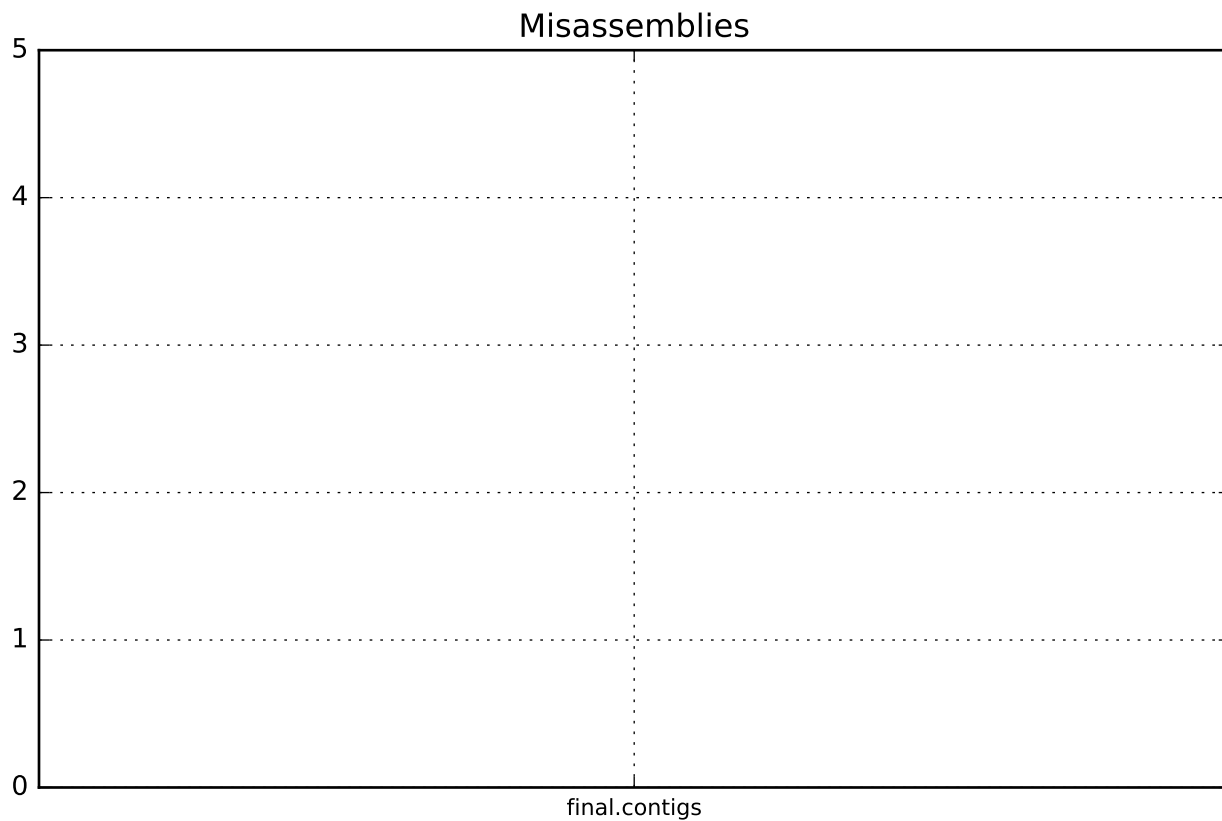


— final.contigs - - Reference

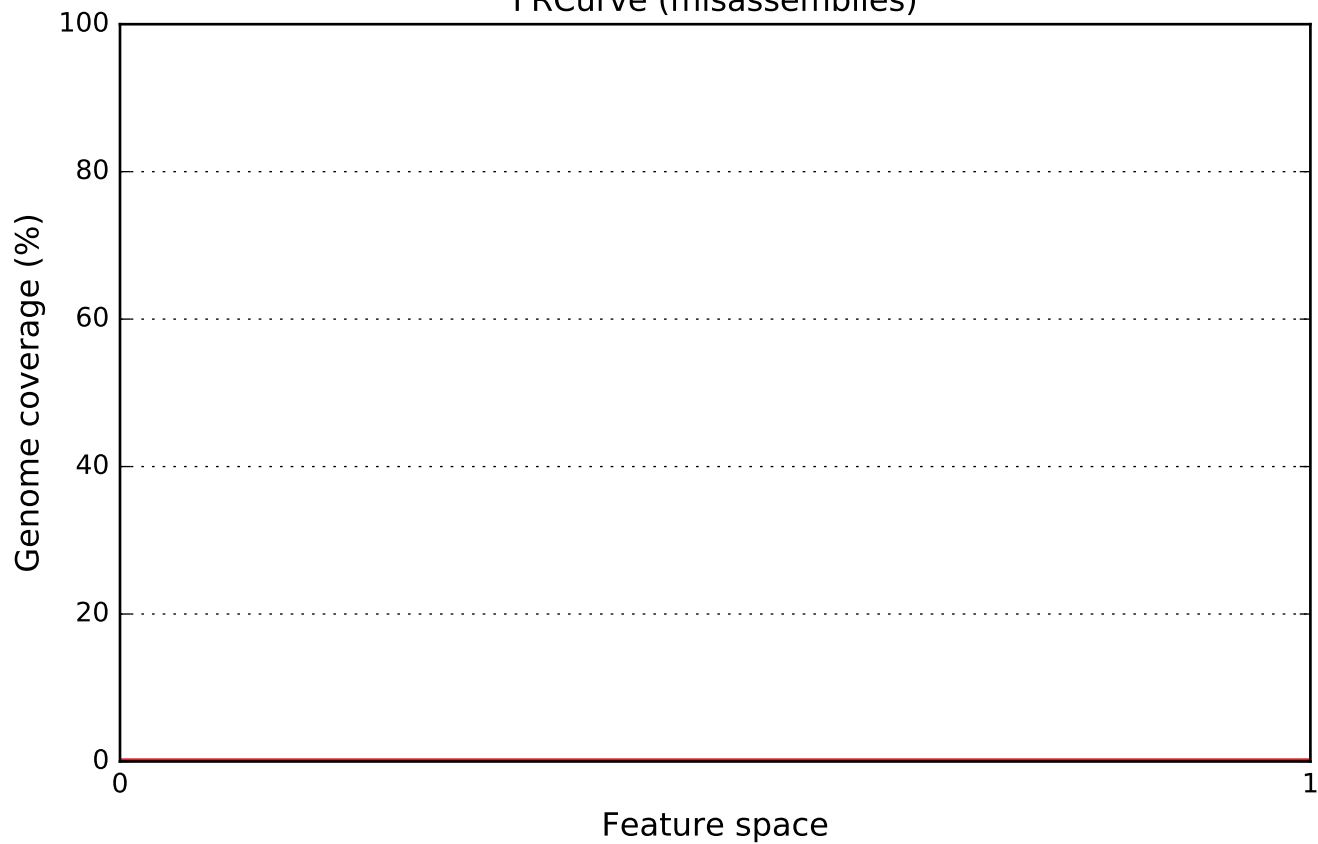
final.contigs GC content



final.contigs

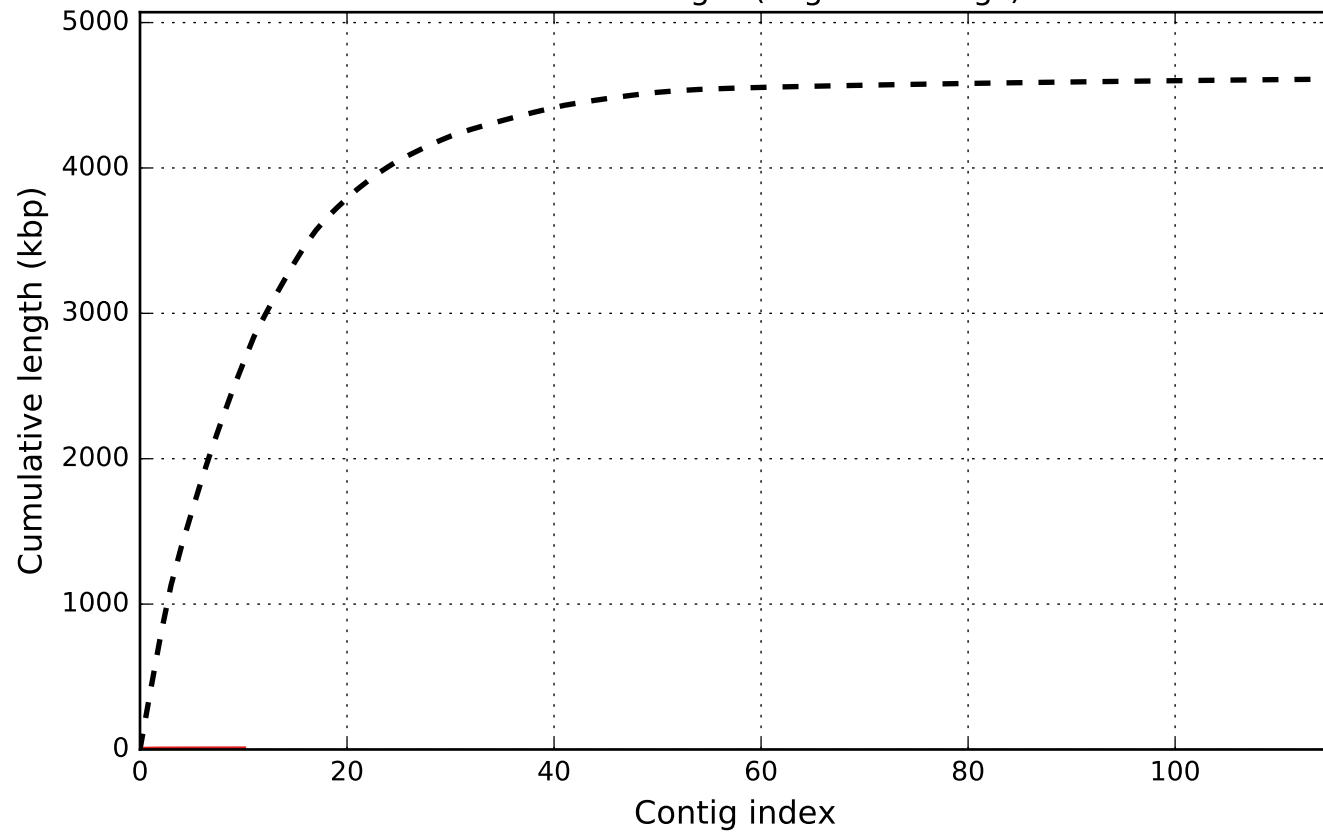


FRCurve (misassemblies)

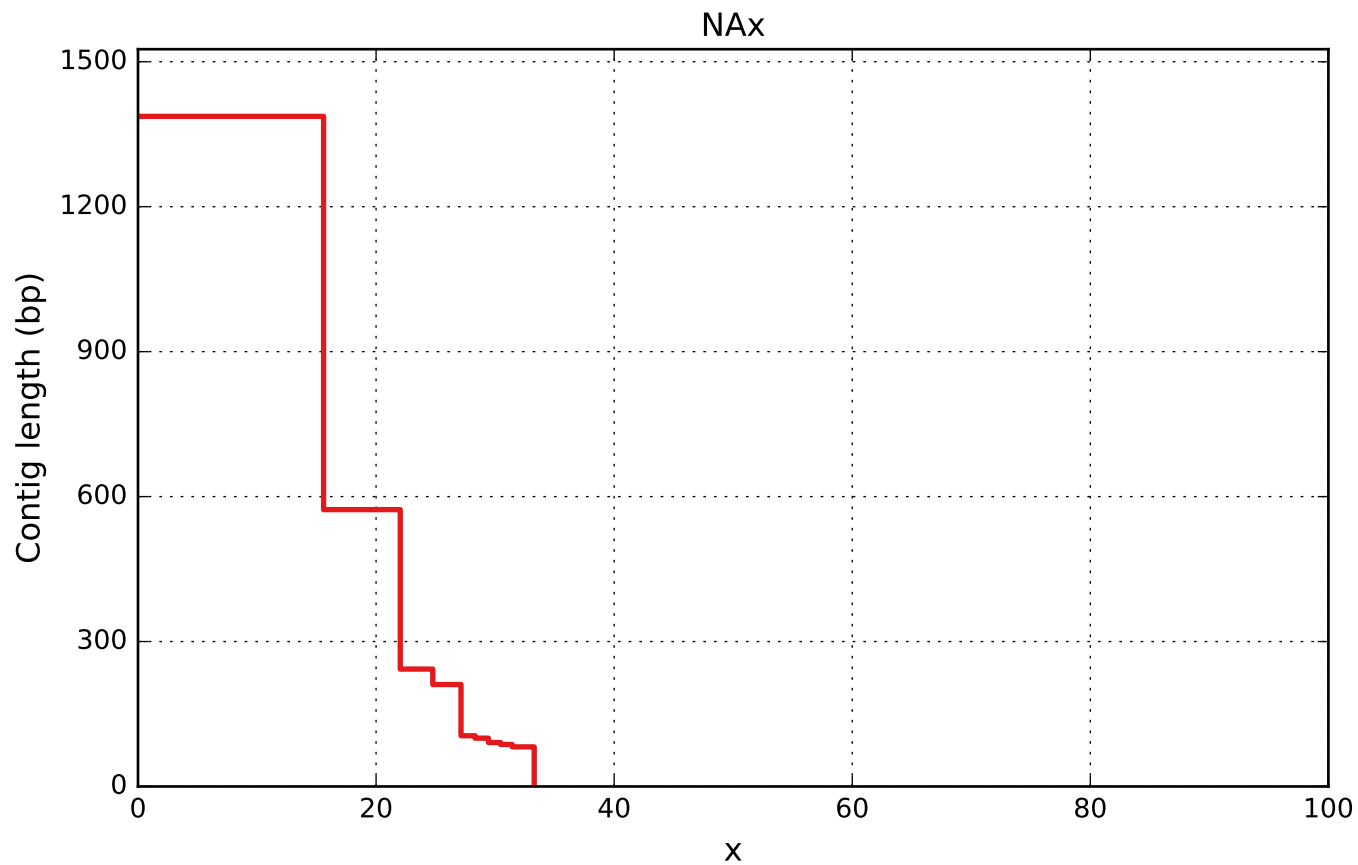


— final.contigs

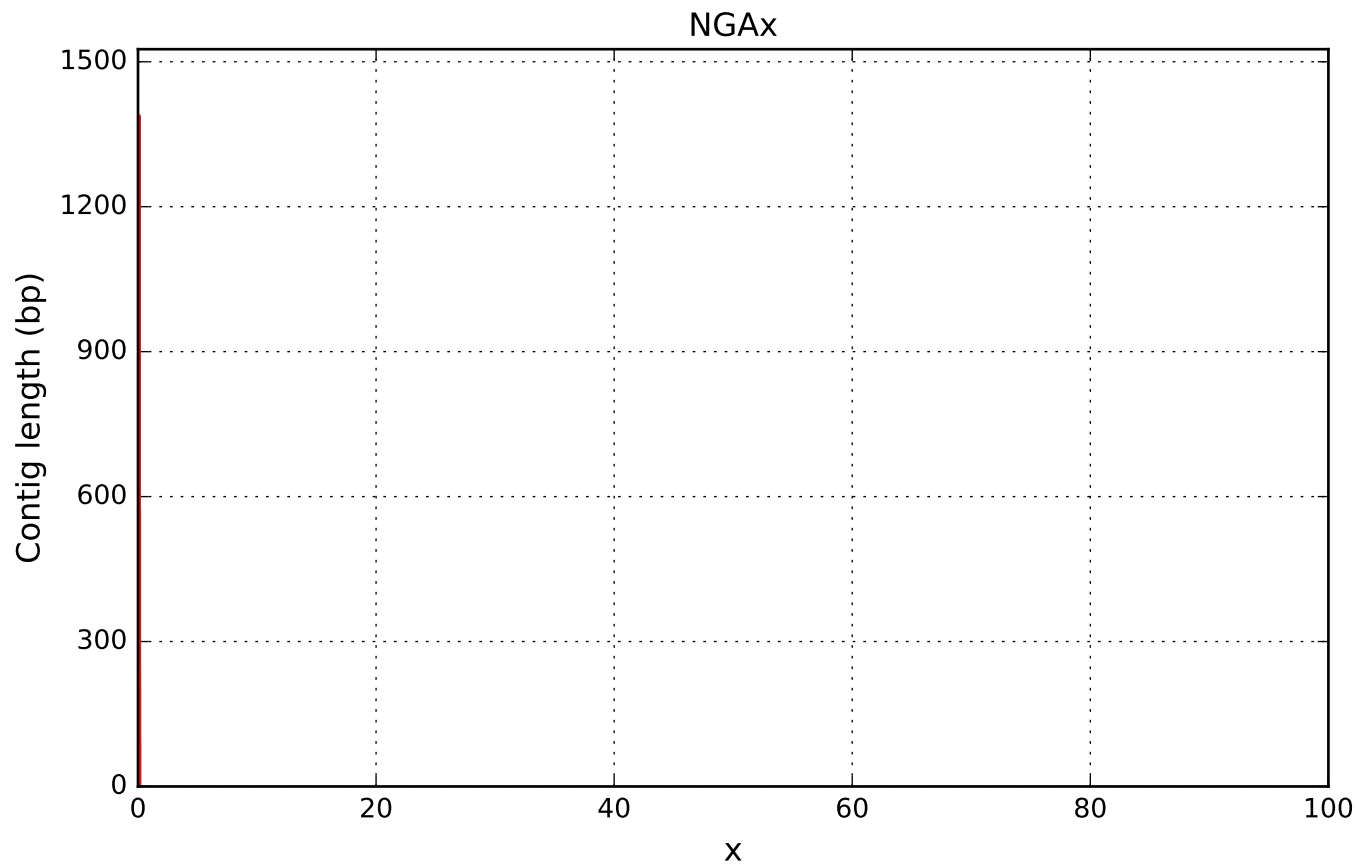
Cumulative length (aligned contigs)



— final.contigs - - Reference



— final.contigs



— final.contigs