

Report

	final_contigs
# contigs (>= 0 bp)	195
# contigs (>= 1000 bp)	73
# contigs (>= 5000 bp)	56
# contigs (>= 10000 bp)	51
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	27
Total length (>= 0 bp)	4583272
Total length (>= 1000 bp)	4544757
Total length (>= 5000 bp)	4508882
Total length (>= 10000 bp)	4469853
Total length (>= 25000 bp)	4299141
Total length (>= 50000 bp)	3790466
# contigs	83
Largest contig	414033
Total length	4551166
Reference length	4091782
GC (%)	50.74
Reference GC (%)	51.83
N50	148541
NG50	173413
N75	66400
NG75	95078
L50	10
LG50	9
L75	21
LG75	17
# misassemblies	3865
# misassembled contigs	66
Misassembled contigs length	4524077
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	3 + 51 part
Unaligned length	550840
Genome fraction (%)	96.731
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.20
# indels per 100 kbp	0.30
Largest alignment	7077
Total aligned length	3957212
NA50	1068
NGA50	1167
NA75	648
NGA75	786
LA50	1400
LGA50	1194
LA75	2738
LGA75	2257

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

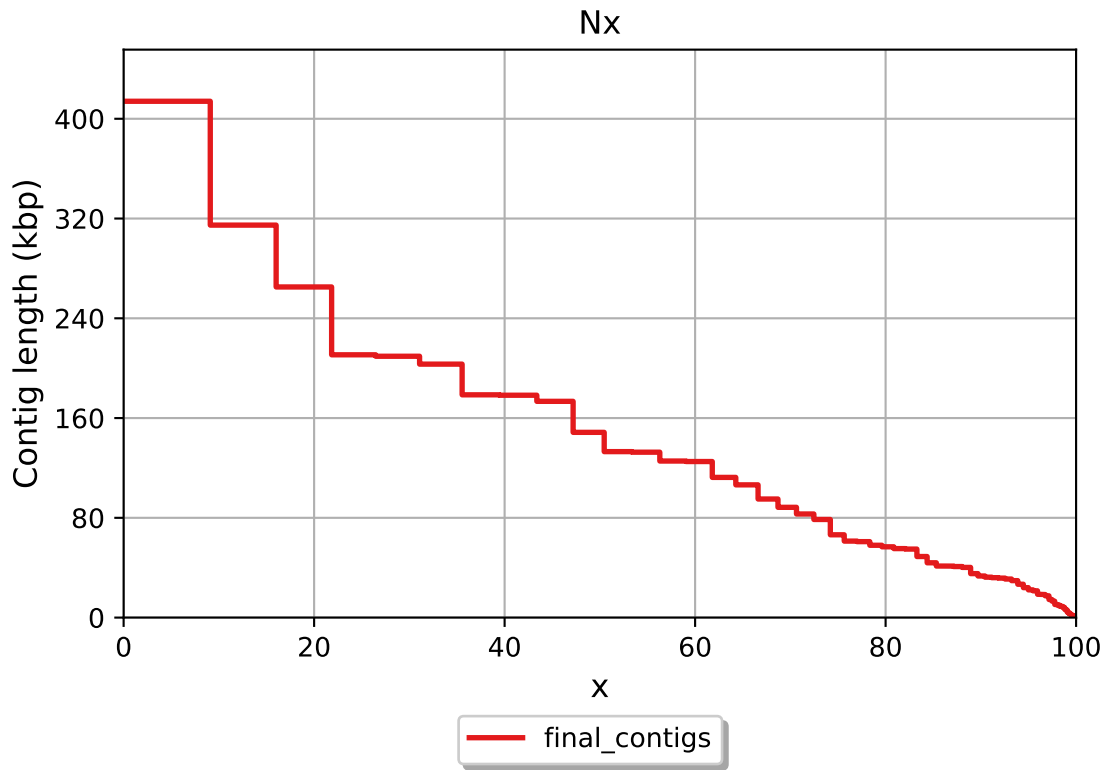
	final_contigs
# misassemblies	3865
# contig misassemblies	3865
# c. relocations	0
# c. translocations	3865
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	66
Misassembled contigs length	4524077
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	87
# indels	12
# indels (<= 5 bp)	12
# indels (> 5 bp)	0
Indels length	13

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).

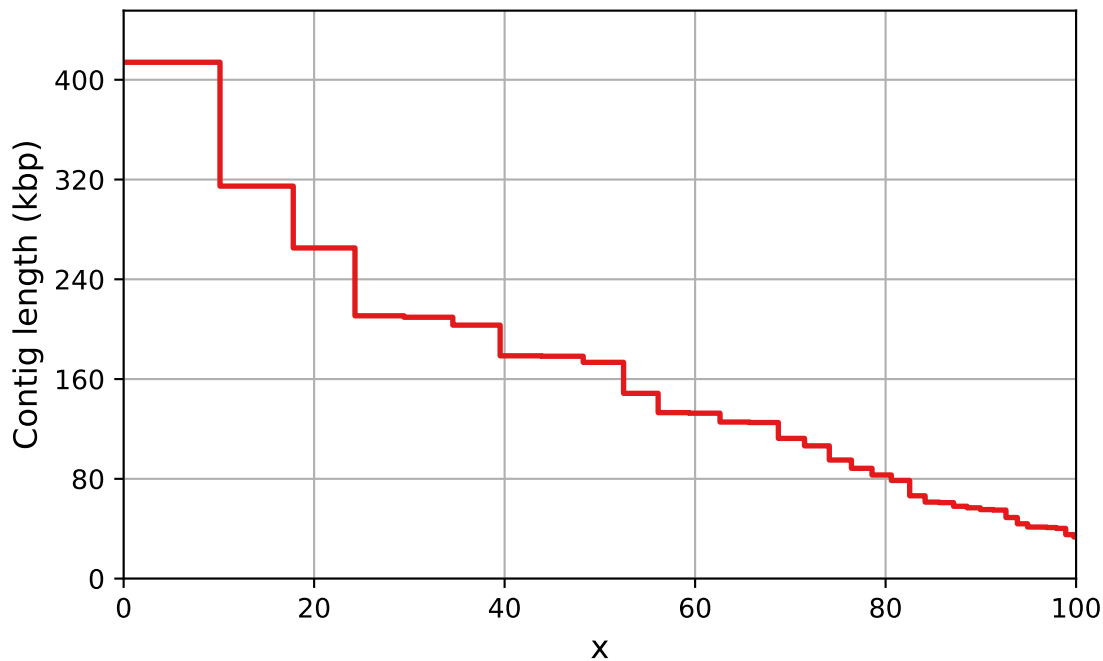
Unaligned report

	final_contigs
# fully unaligned contigs	3
Fully unaligned length	5246
# partially unaligned contigs	51
Partially unaligned length	545594
# N's	0

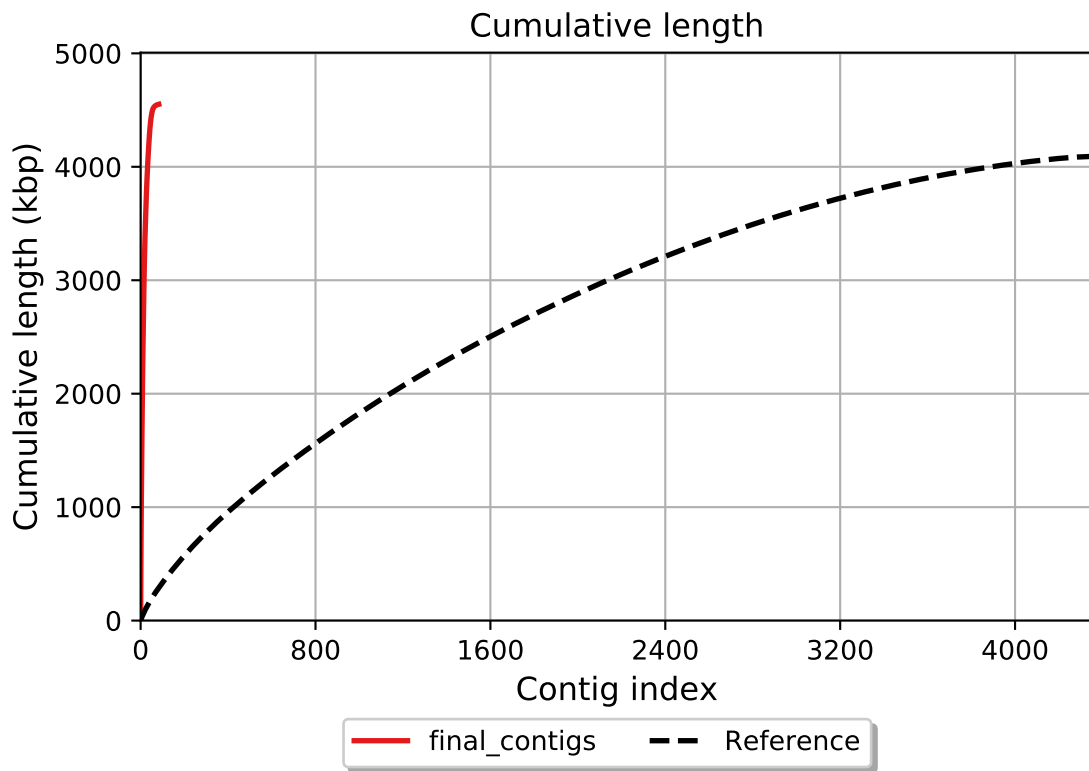
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



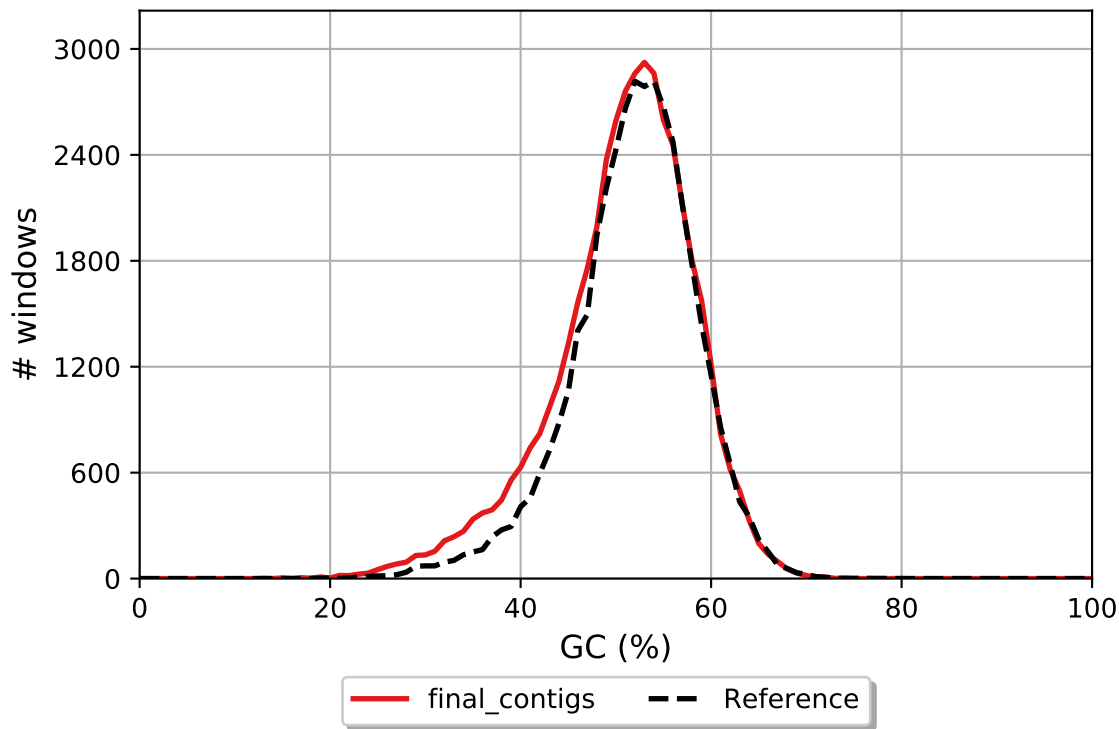
NGx



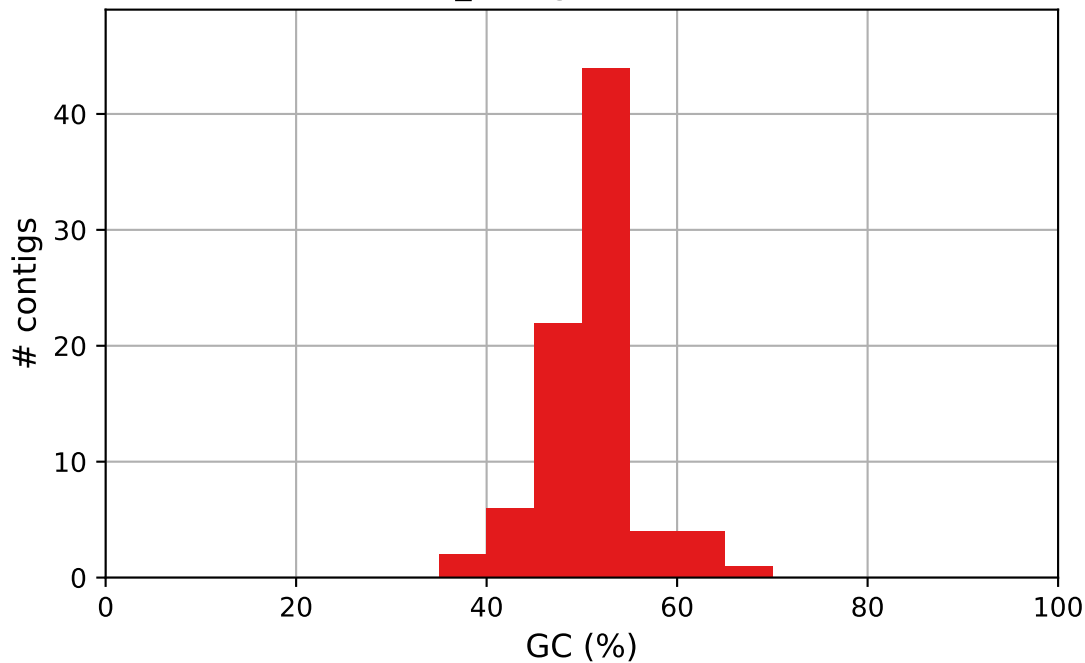
— final_contigs



GC content

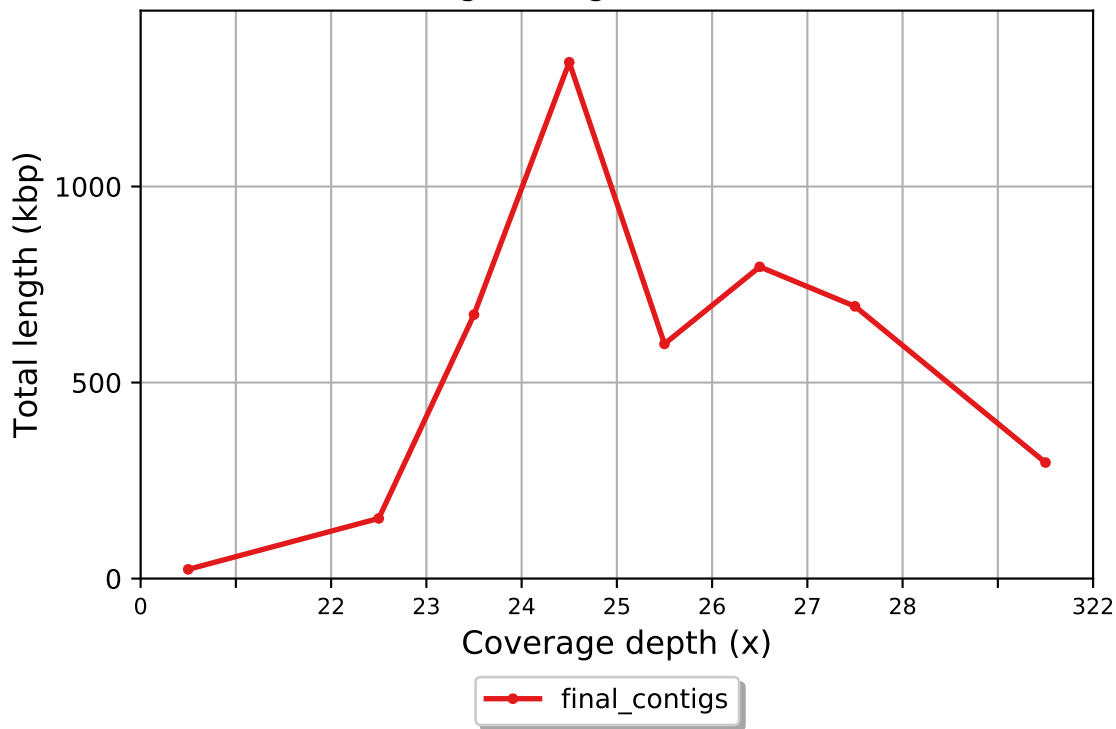


final_contigs GC content

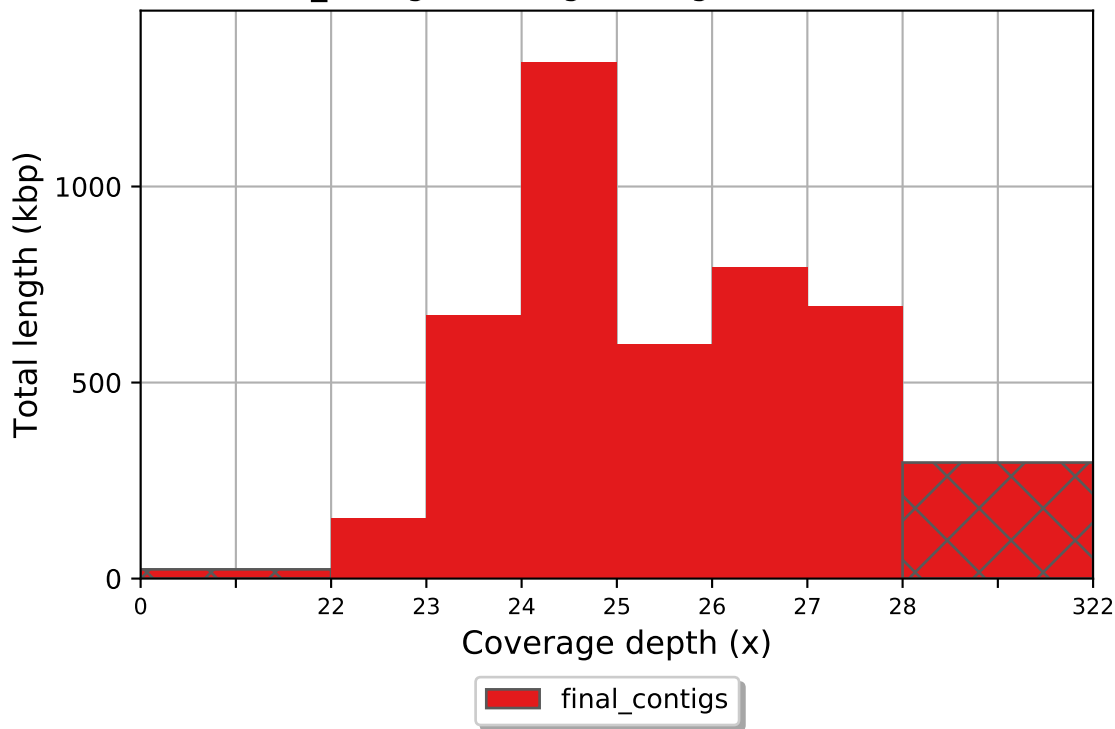


final_contigs

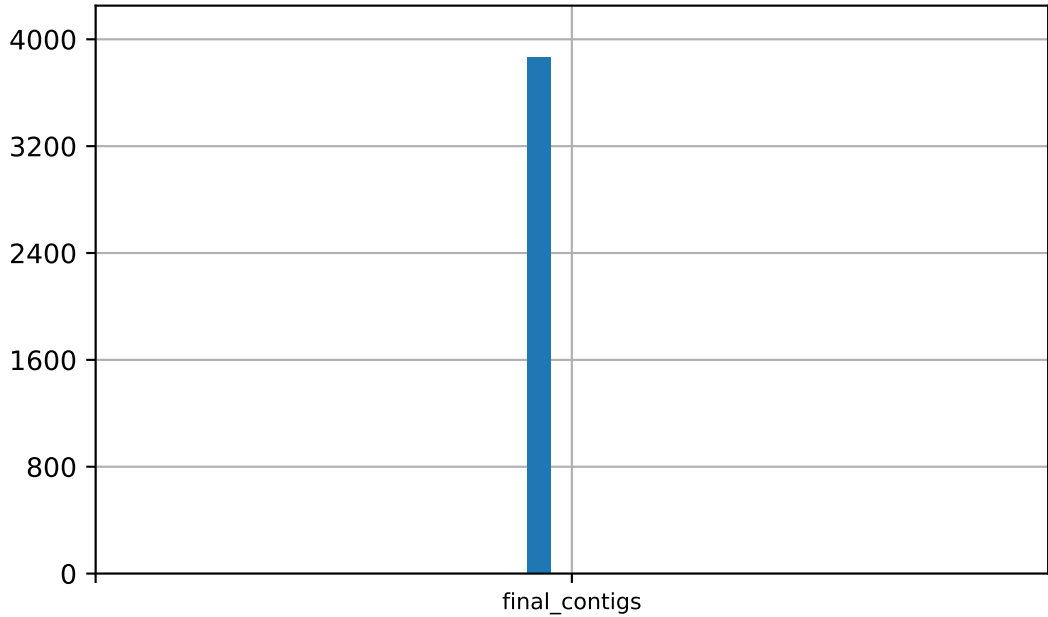
Coverage histogram (bin size: 1x)



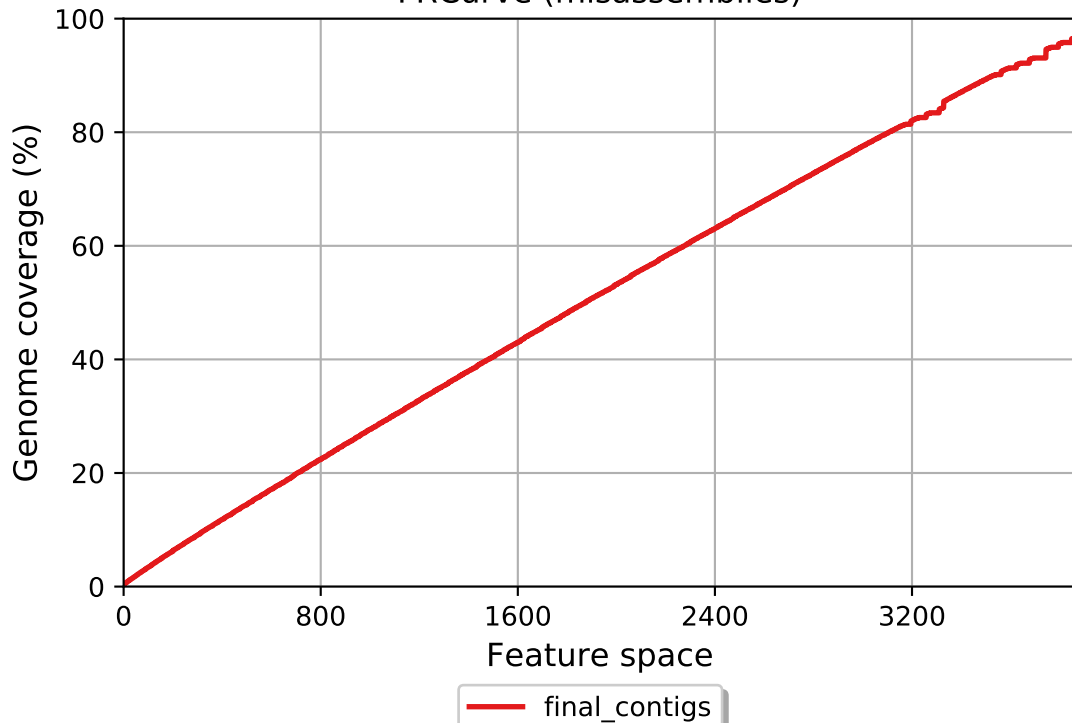
final_contigs coverage histogram (bin size: 1x)



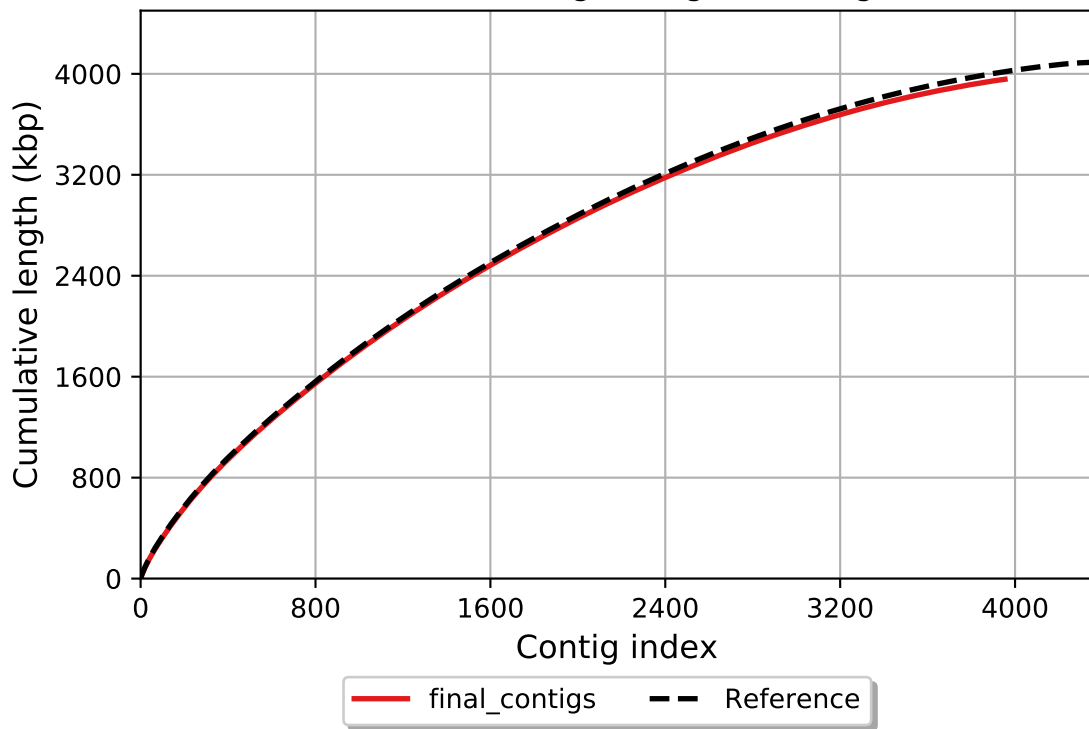
Misassemblies



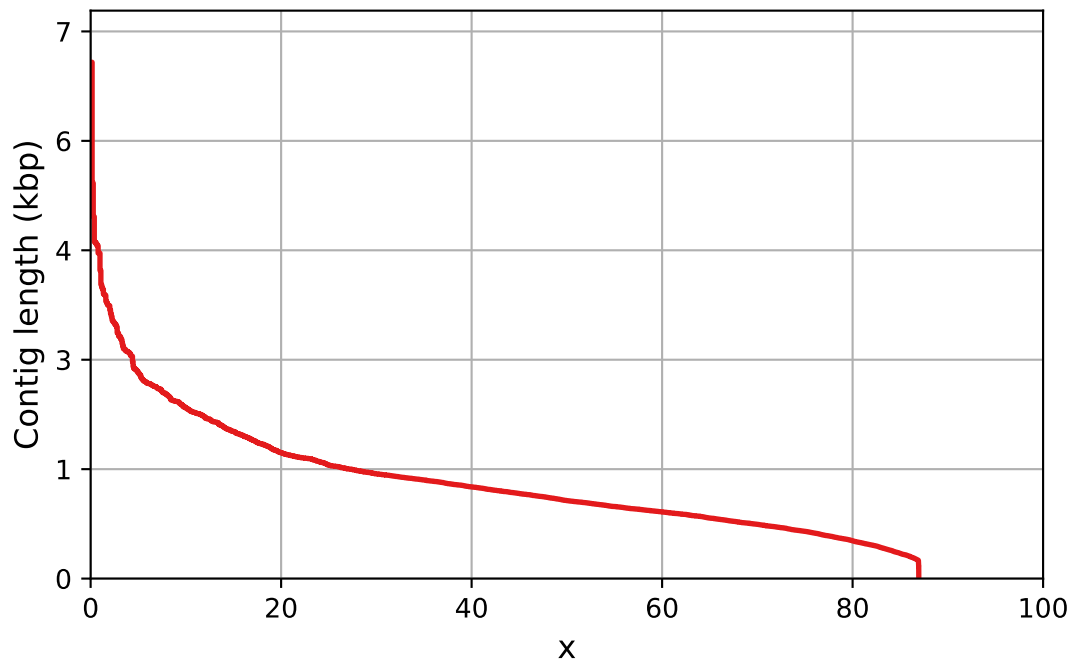
FRCurve (misassemblies)



Cumulative length (aligned contigs)

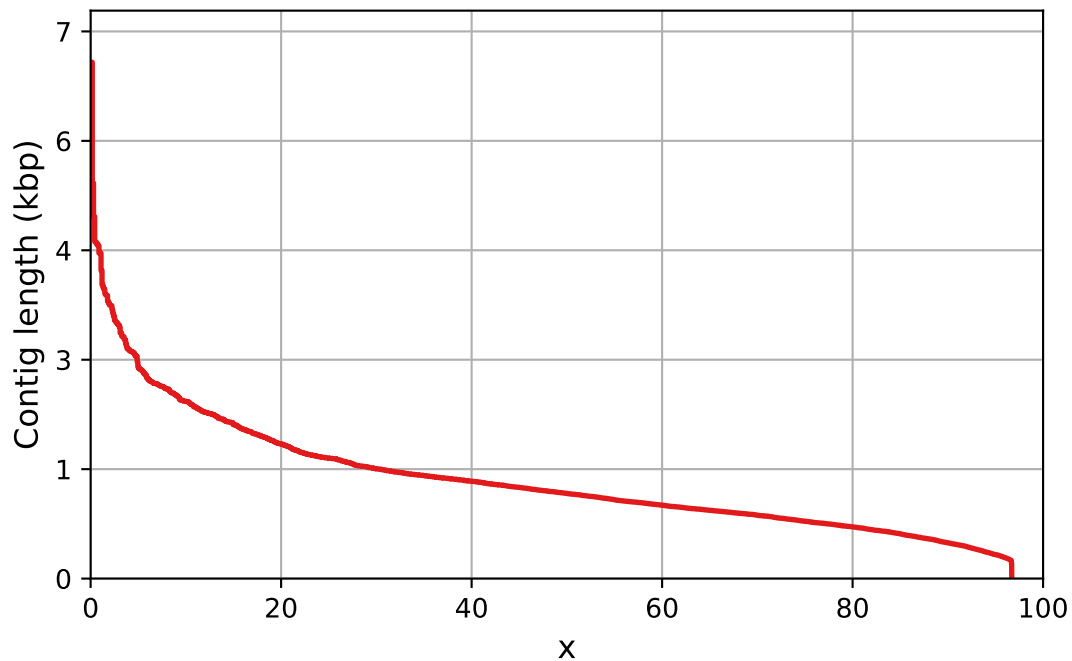


NAx



— final_contigs

NGAx



— final_contigs