

Report

	final_contigs
# contigs (>= 0 bp)	562
# contigs (>= 1000 bp)	141
# contigs (>= 5000 bp)	106
# contigs (>= 10000 bp)	89
# contigs (>= 25000 bp)	59
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	4585926
Total length (>= 1000 bp)	4514581
Total length (>= 5000 bp)	4428472
Total length (>= 10000 bp)	4290665
Total length (>= 25000 bp)	3803506
Total length (>= 50000 bp)	2819989
# contigs	162
Largest contig	169244
Total length	4529468
Reference length	4091782
GC (%)	50.74
Reference GC (%)	51.83
N50	60350
NG50	73698
N75	35580
NG75	42739
L50	23
LG50	19
L75	46
LG75	38
# misassemblies	3793
# misassembled contigs	136
Misassembled contigs length	4493543
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	4 + 81 part
Unaligned length	503889
Genome fraction (%)	96.467
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.46
# indels per 100 kbp	0.13
Largest alignment	7077
Total aligned length	3945872
NA50	1066
NGA50	1161
NA75	648
NGA75	780
LA50	1396
LGA50	1200
LA75	2729
LGA75	2269

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

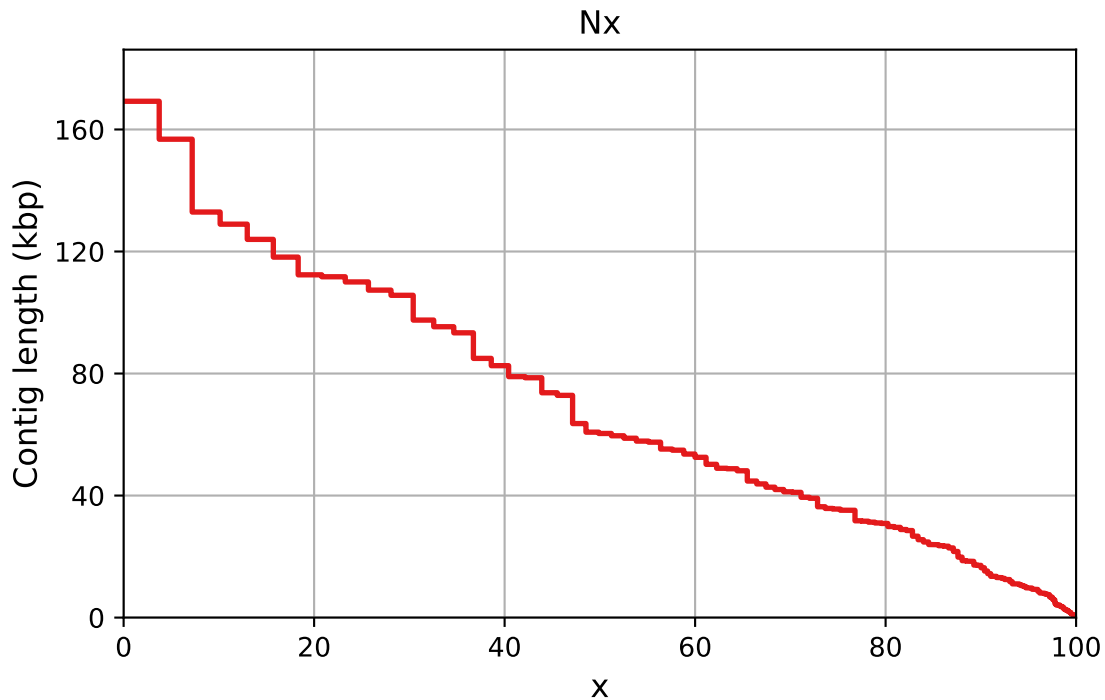
	final_contigs
# misassemblies	3793
# contig misassemblies	3793
# c. relocations	0
# c. translocations	3793
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	136
Misassembled contigs length	4493543
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	18
# indels	5
# indels (<= 5 bp)	5
# indels (> 5 bp)	0
Indels length	6

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

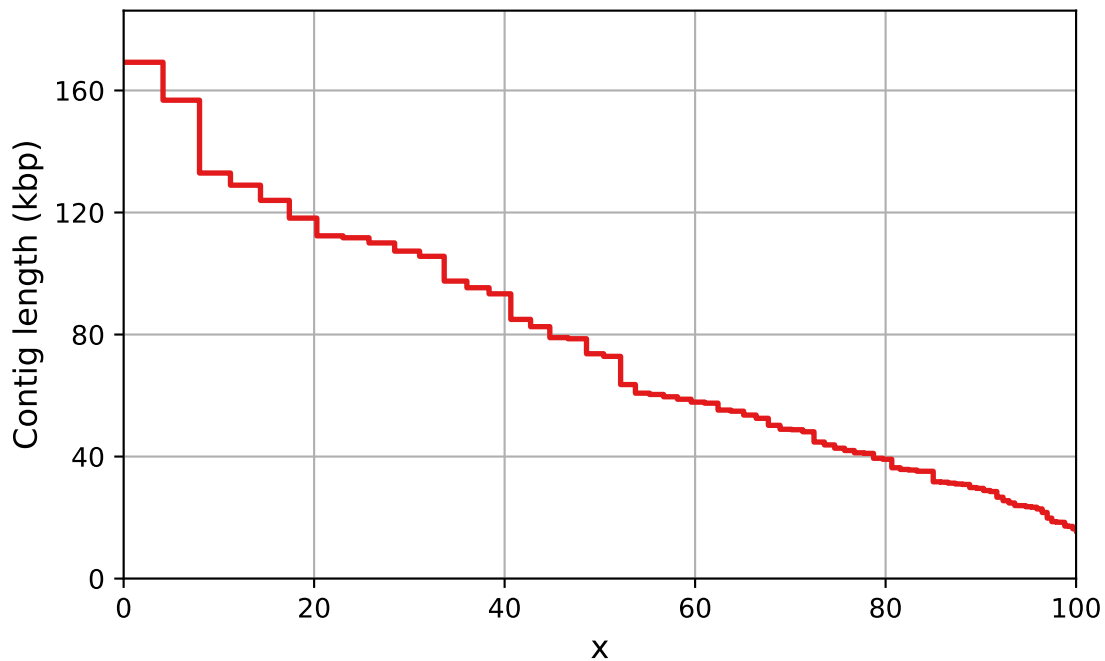
	final_contigs
# fully unaligned contigs	4
Fully unaligned length	5348
# partially unaligned contigs	81
Partially unaligned length	498541
# N's	0

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).



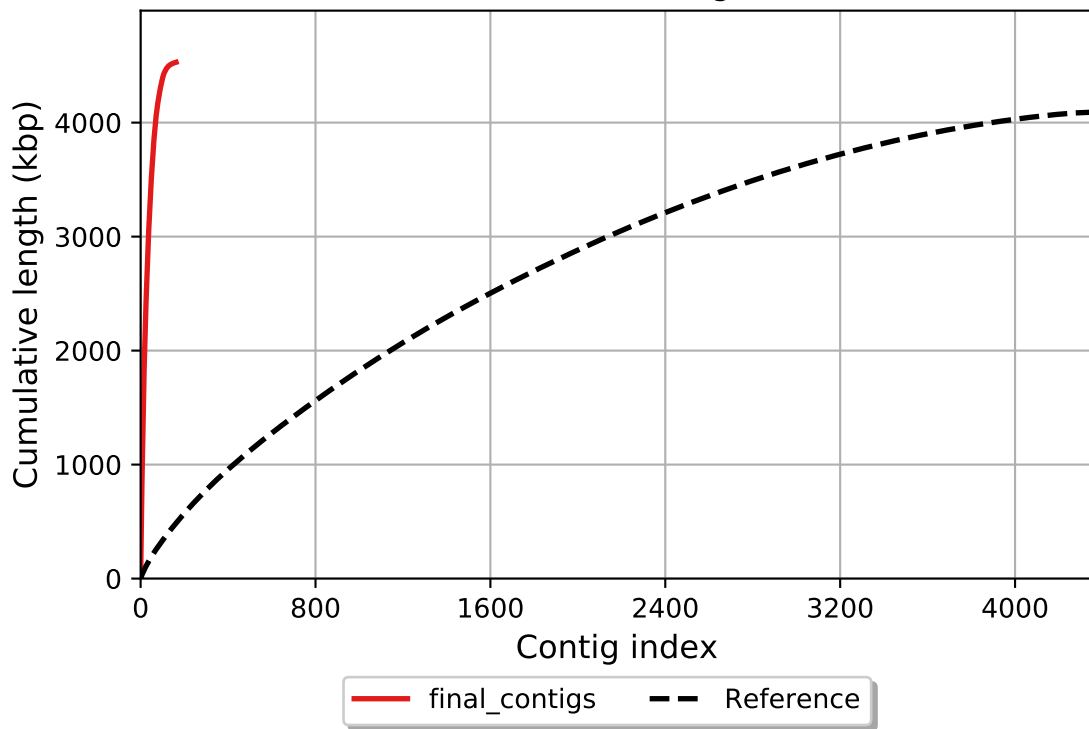
— final_contigs

NGx

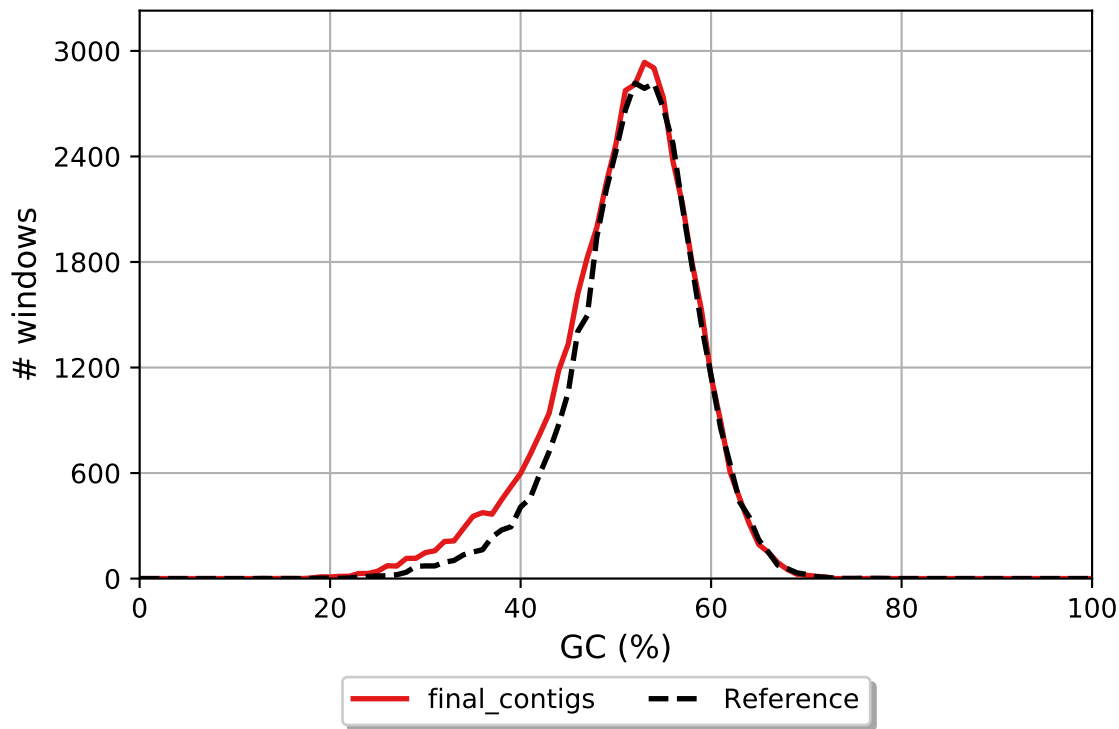


— final_contigs

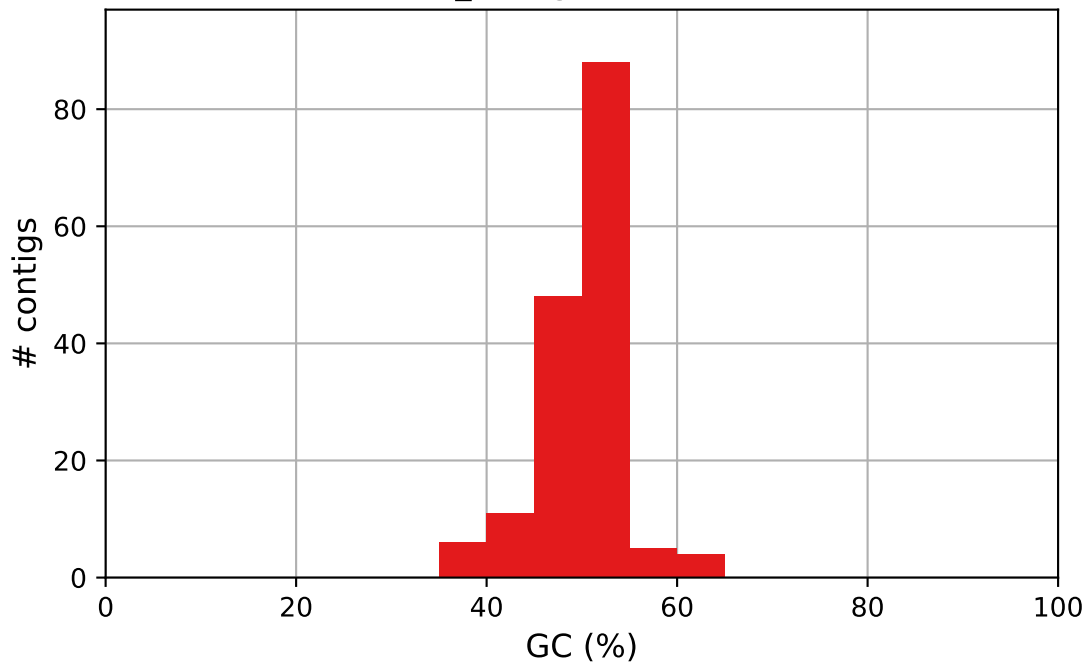
Cumulative length



GC content

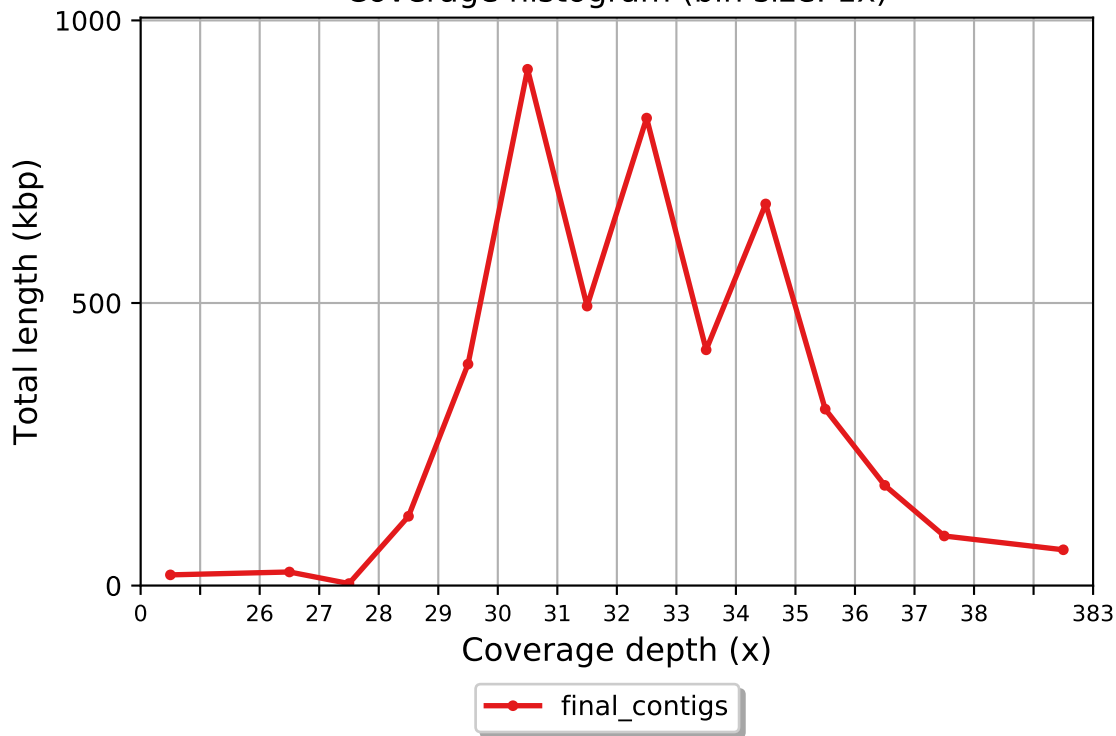


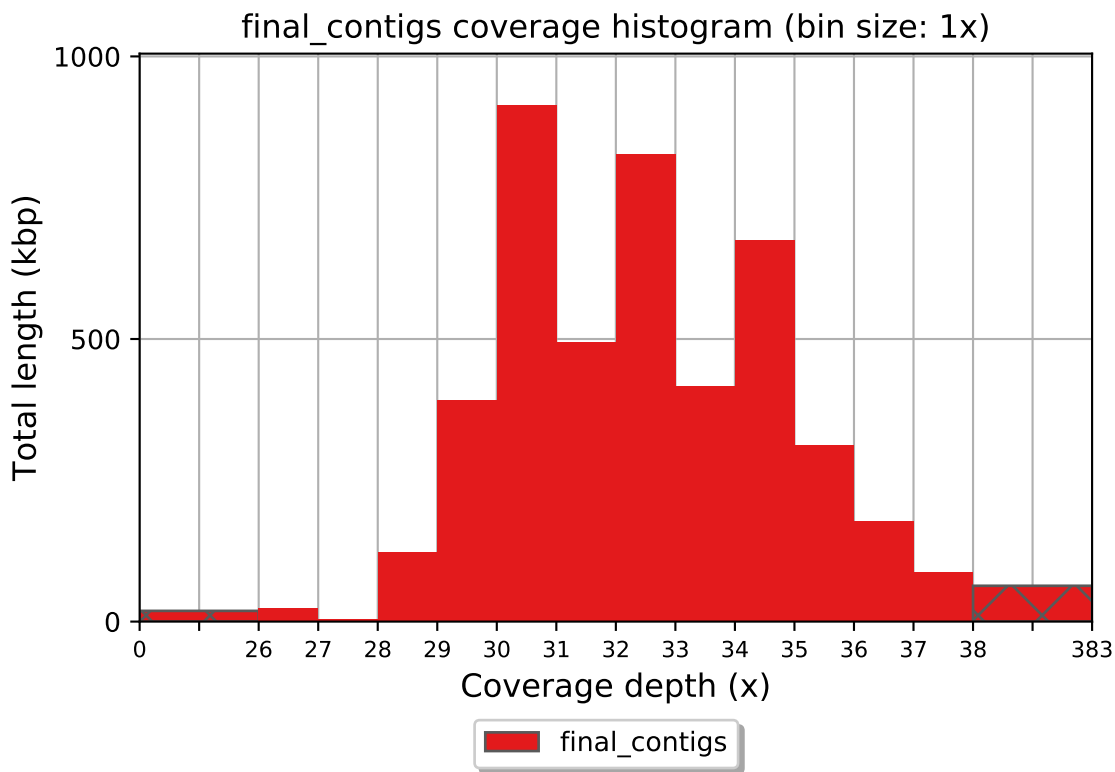
final_contigs GC content



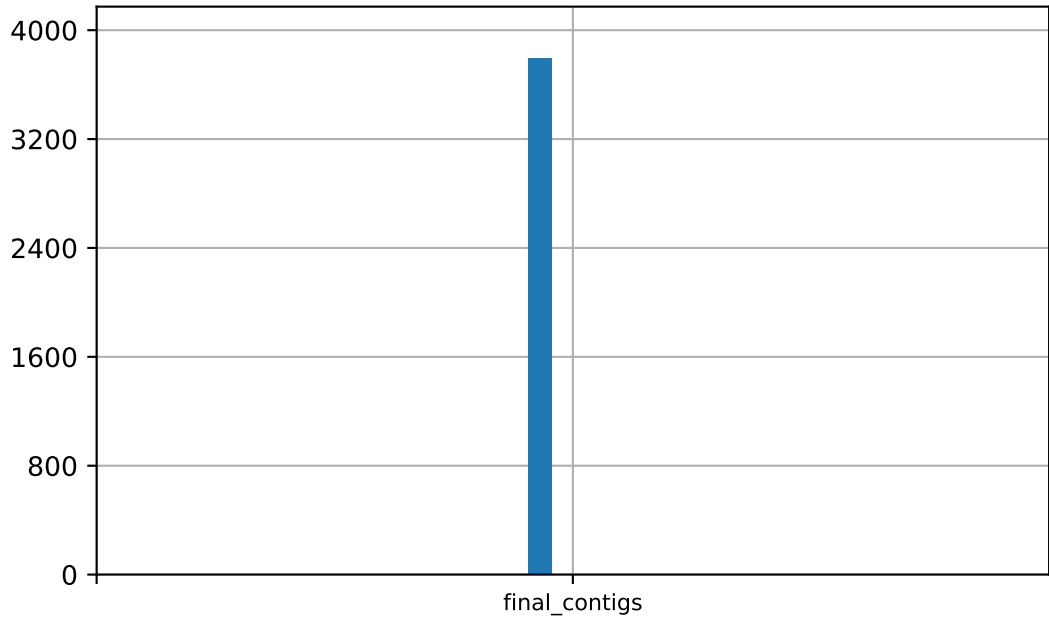
final_contigs

Coverage histogram (bin size: 1x)

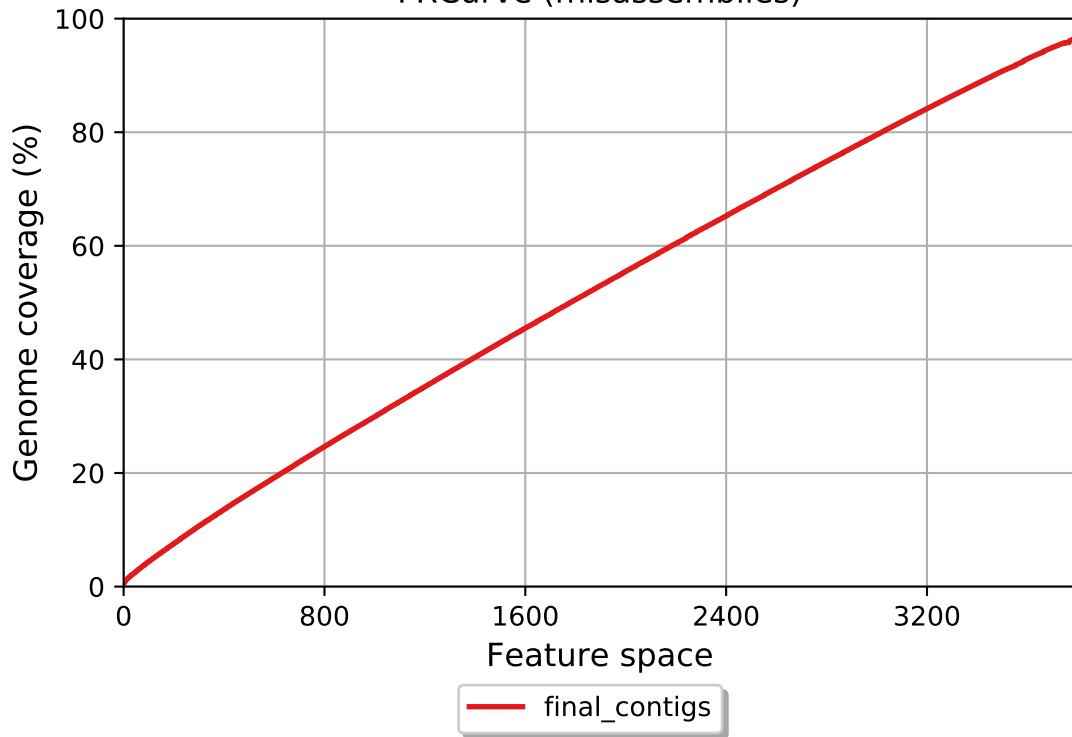




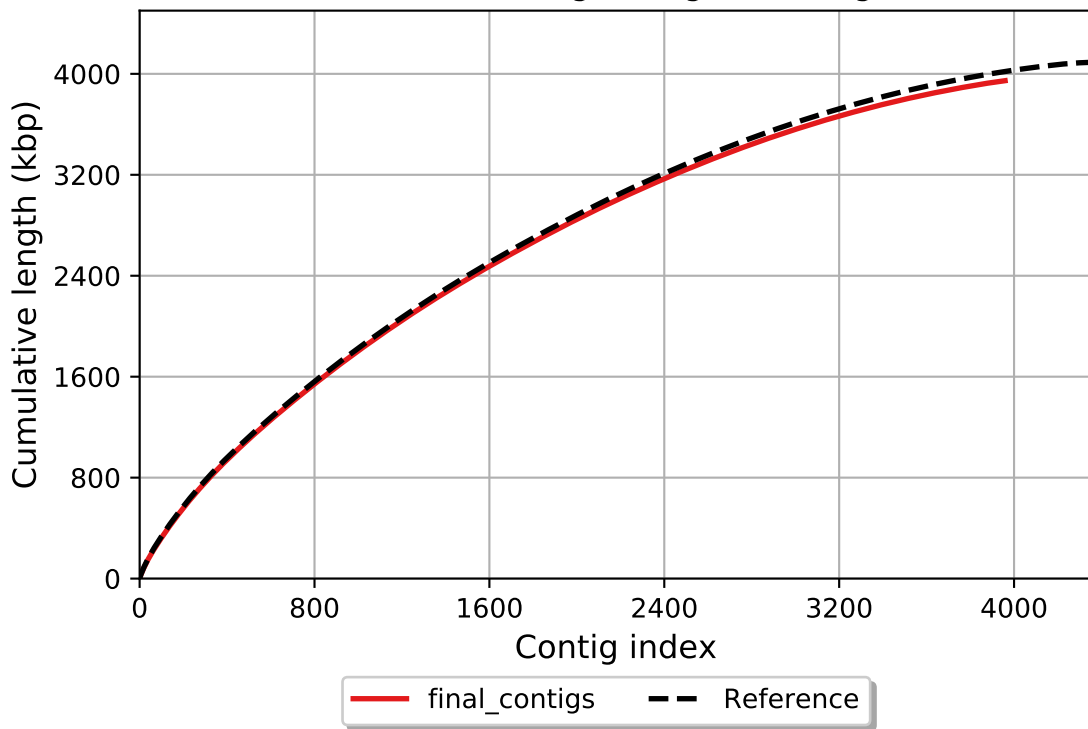
Misassemblies



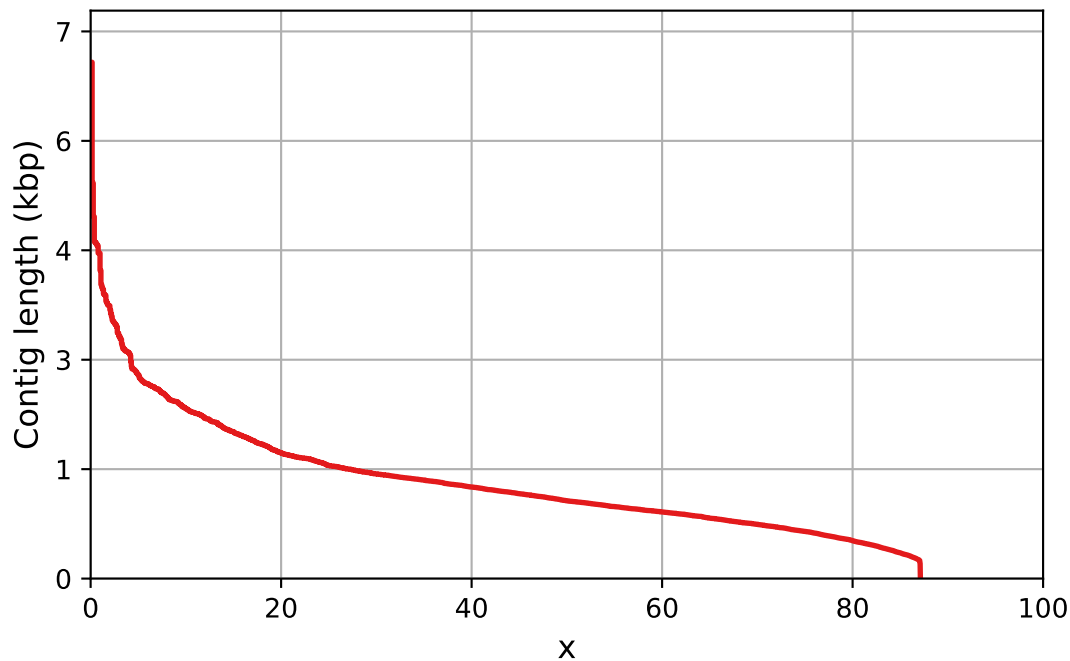
FRCurve (misassemblies)



Cumulative length (aligned contigs)

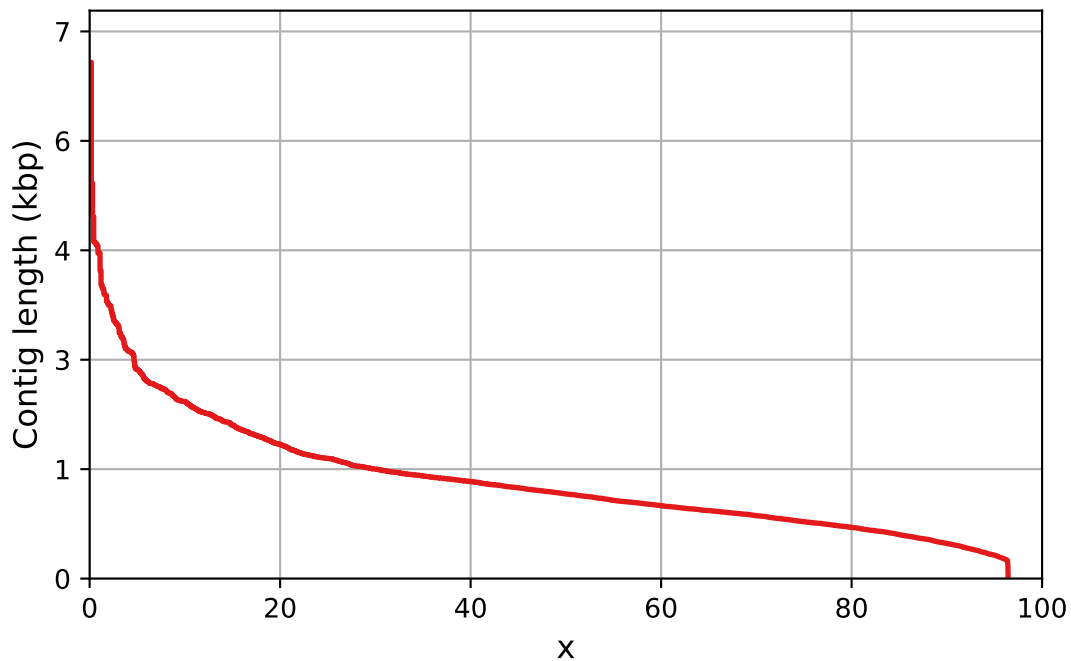


NAx



— final_contigs

NGAx



— final_contigs