

Report

	assembly_output_graph
# contigs (≥ 0 bp)	1864045
# contigs (≥ 1000 bp)	913
# contigs (≥ 5000 bp)	112
# contigs (≥ 10000 bp)	12
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	140745671
Total length (≥ 1000 bp)	2643778
Total length (≥ 5000 bp)	817295
Total length (≥ 10000 bp)	157909
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	1573
Largest contig	21249
Total length	3086744
Reference length	3380749
GC (%)	45.23
Reference GC (%)	45.32
N50	3087
NG50	2755
N75	1535
NG75	1180
L50	299
LG50	349
L75	652
LG75	814
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	11980
# local misassemblies	9
# unaligned mis. contigs	0
# unaligned contigs	252 + 0 part
Unaligned length	149071
Genome fraction (%)	86.558
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	27.78
# indels per 100 kbp	1.30
Largest alignment	21234
Total aligned length	2933300
NA50	3087
NGA50	2712
NA75	1519
NGA75	1151
LA50	299
LGA50	350
LA75	655
LGA75	820

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

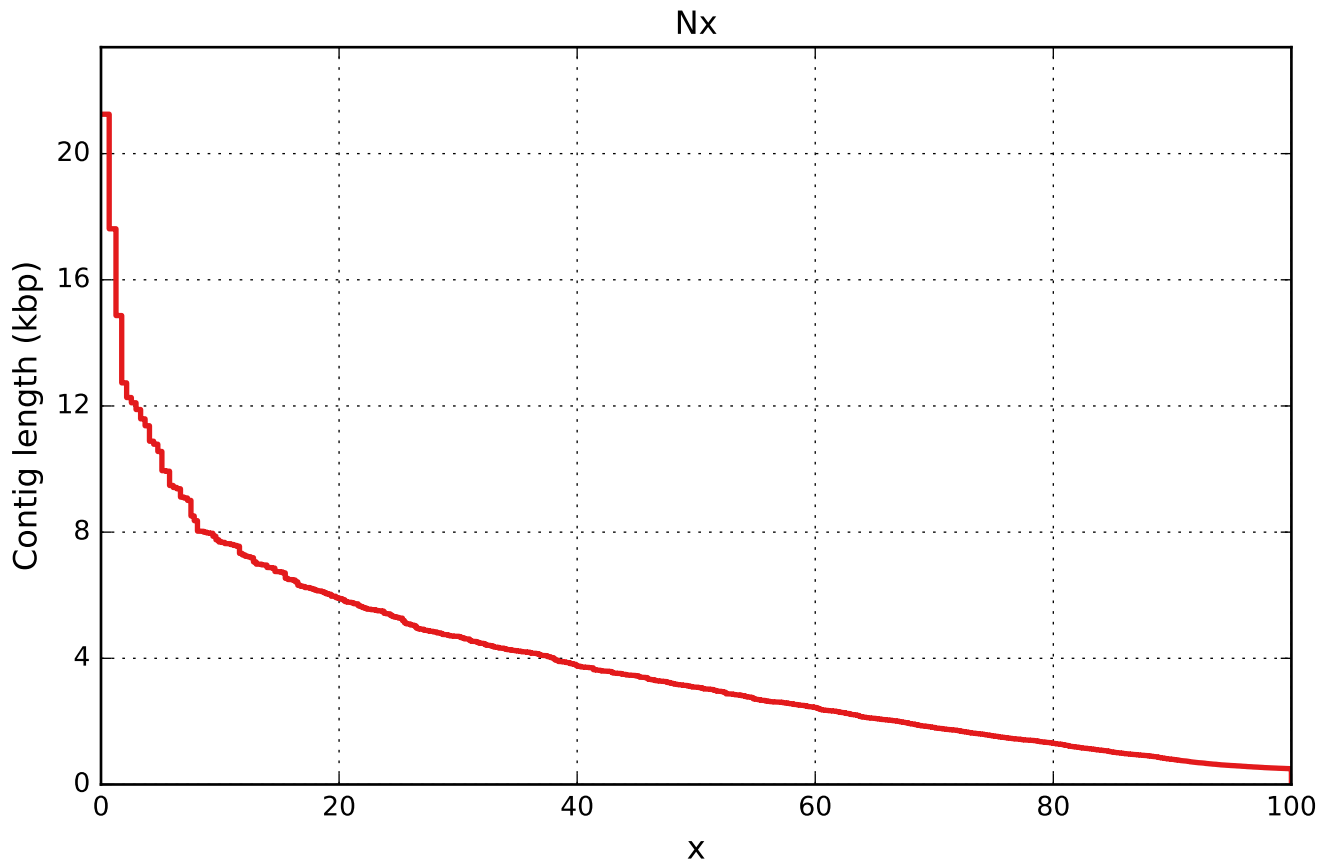
	assembly_output_graph
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	11980
# local misassemblies	9
# unaligned mis. contigs	0
# mismatches	813
# indels	38
# indels (≤ 5 bp)	30
# indels (> 5 bp)	8
Indels length	452

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

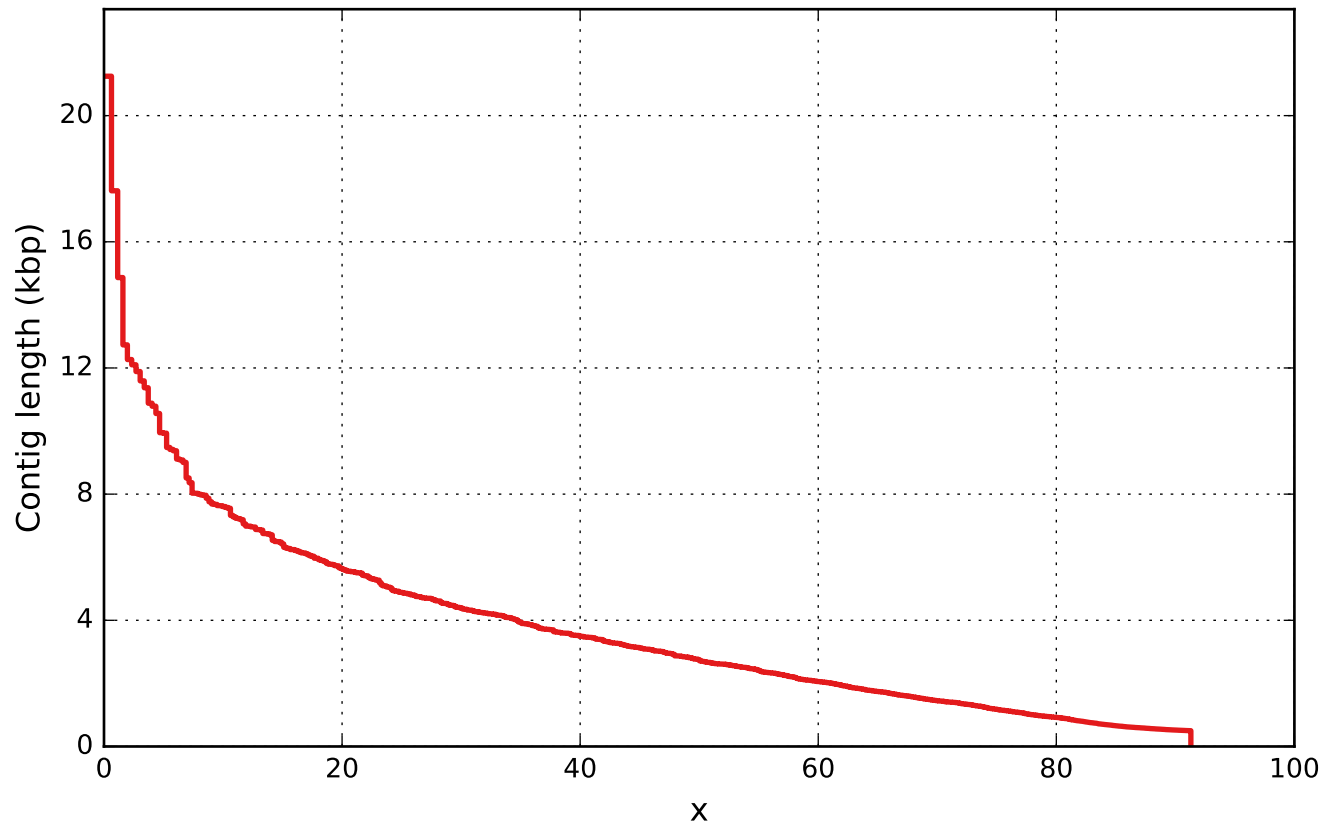
	assembly_output_graph
# fully unaligned contigs	252
Fully unaligned length	149071
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

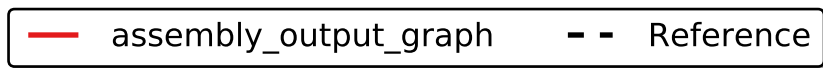
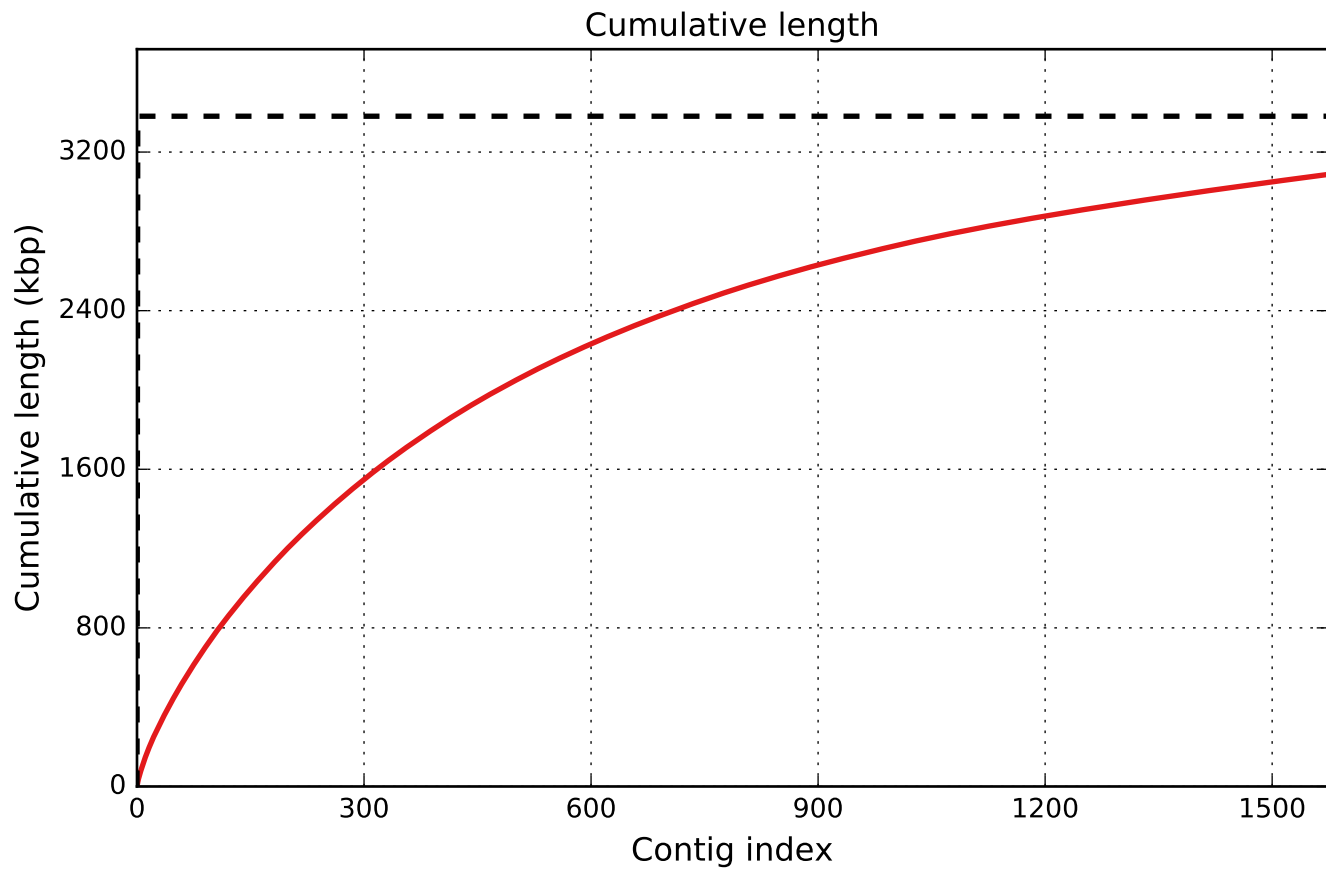


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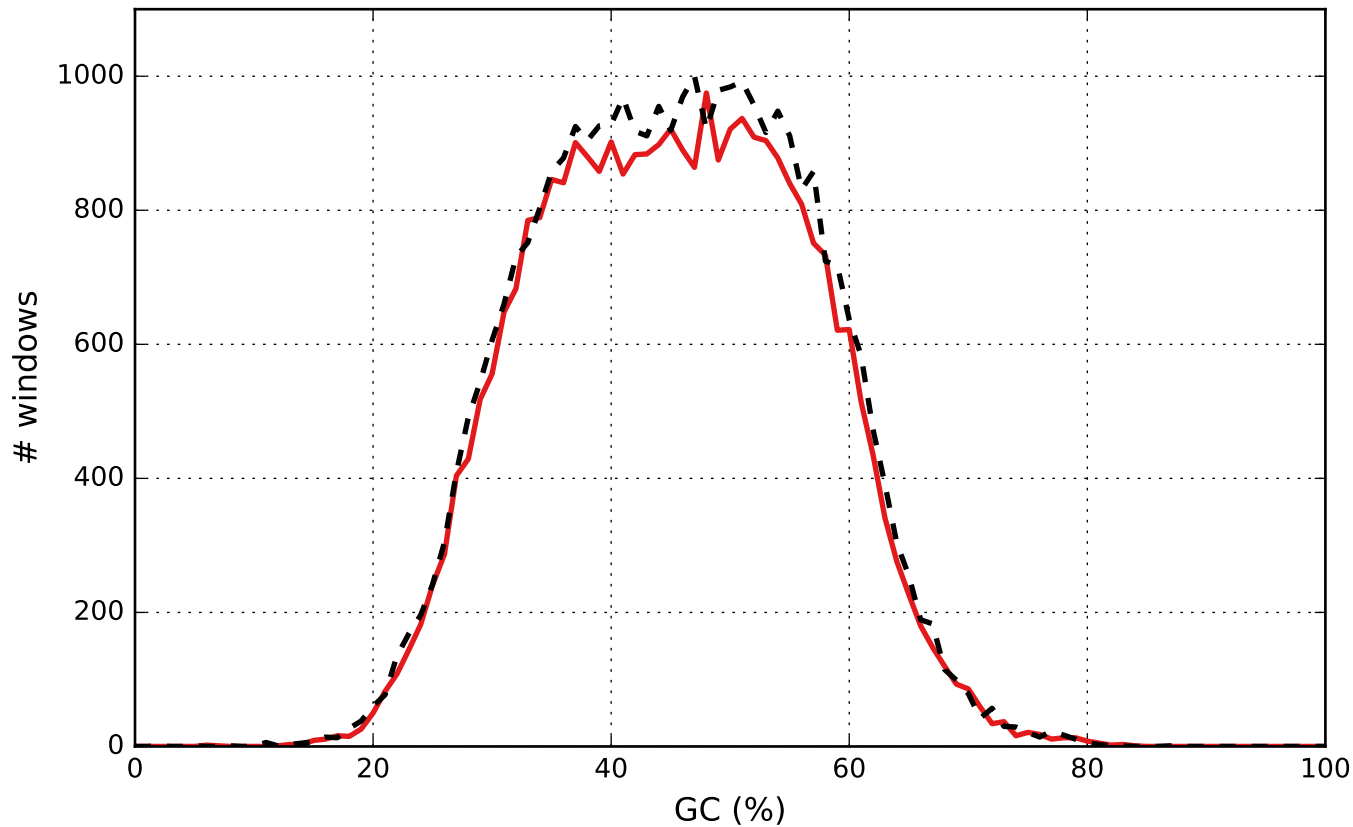
NGx



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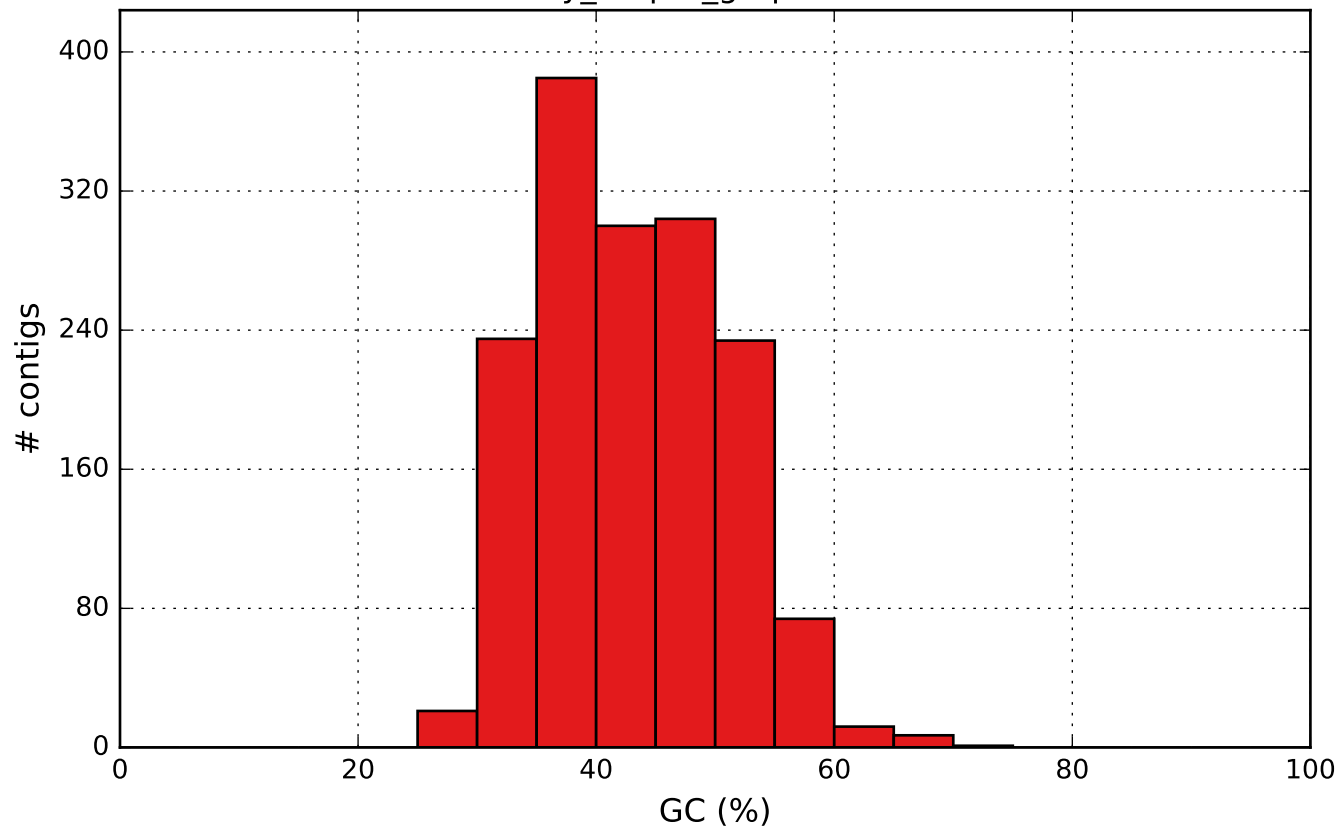


GC content

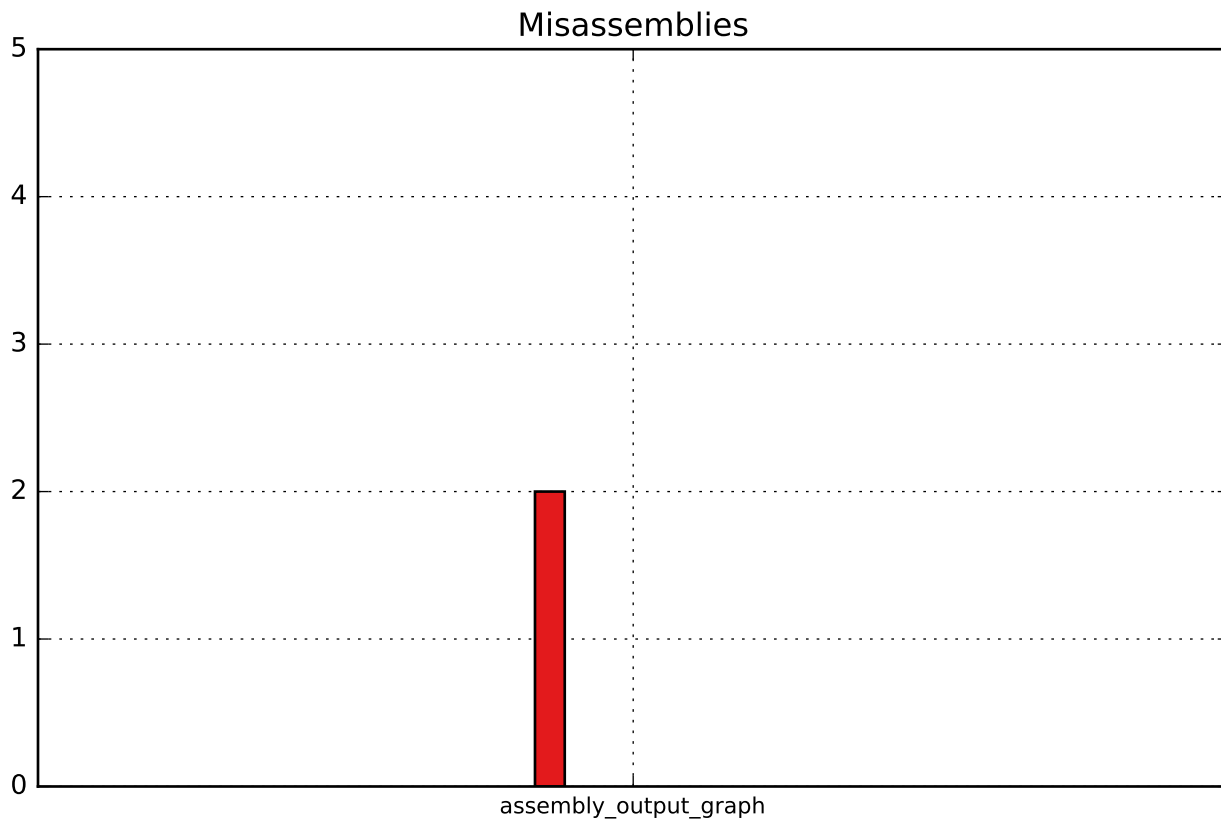


— assembly_output_graph - - Reference

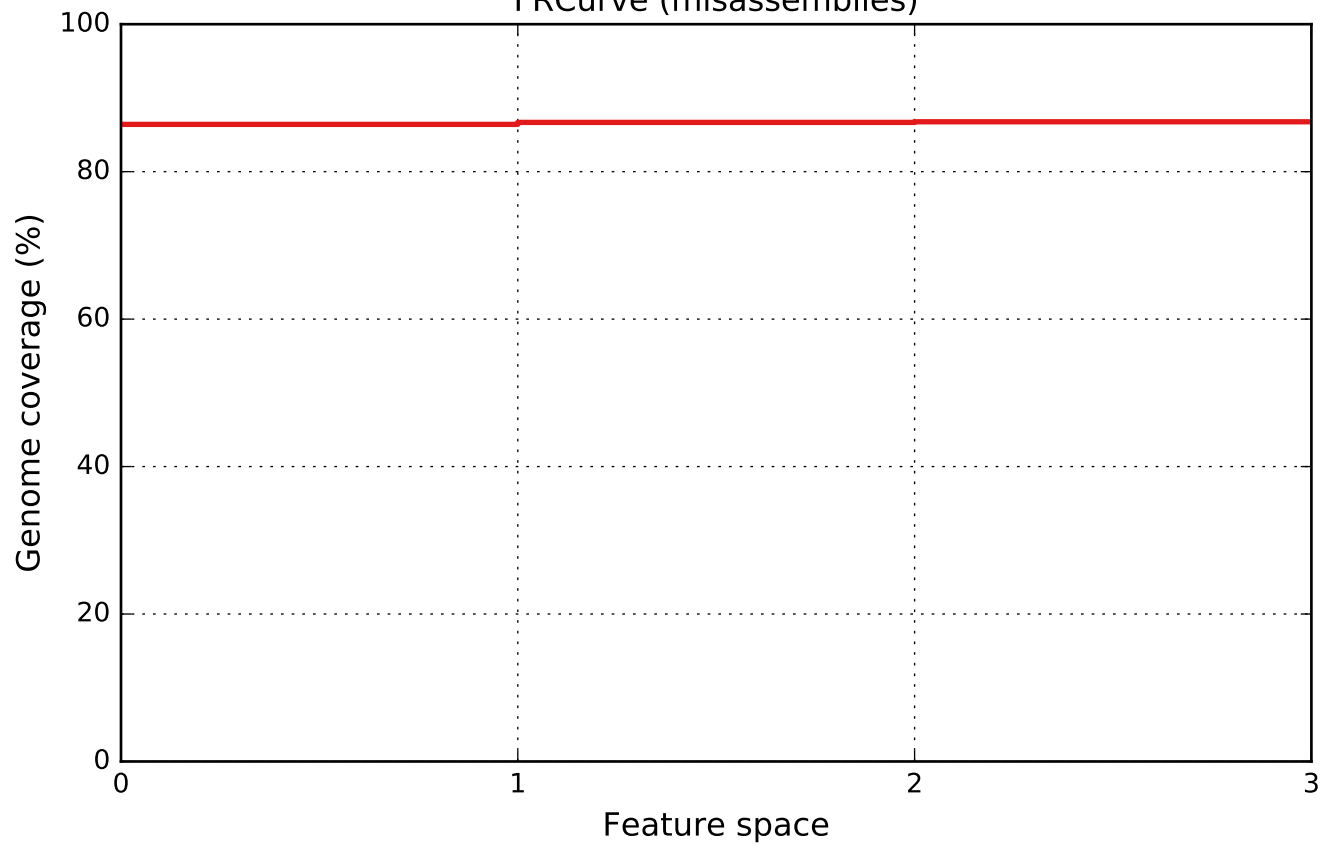
assembly_output_graph GC content



assembly_output_graph

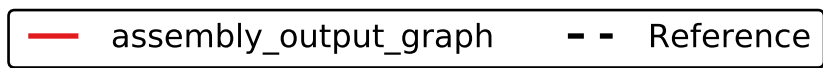
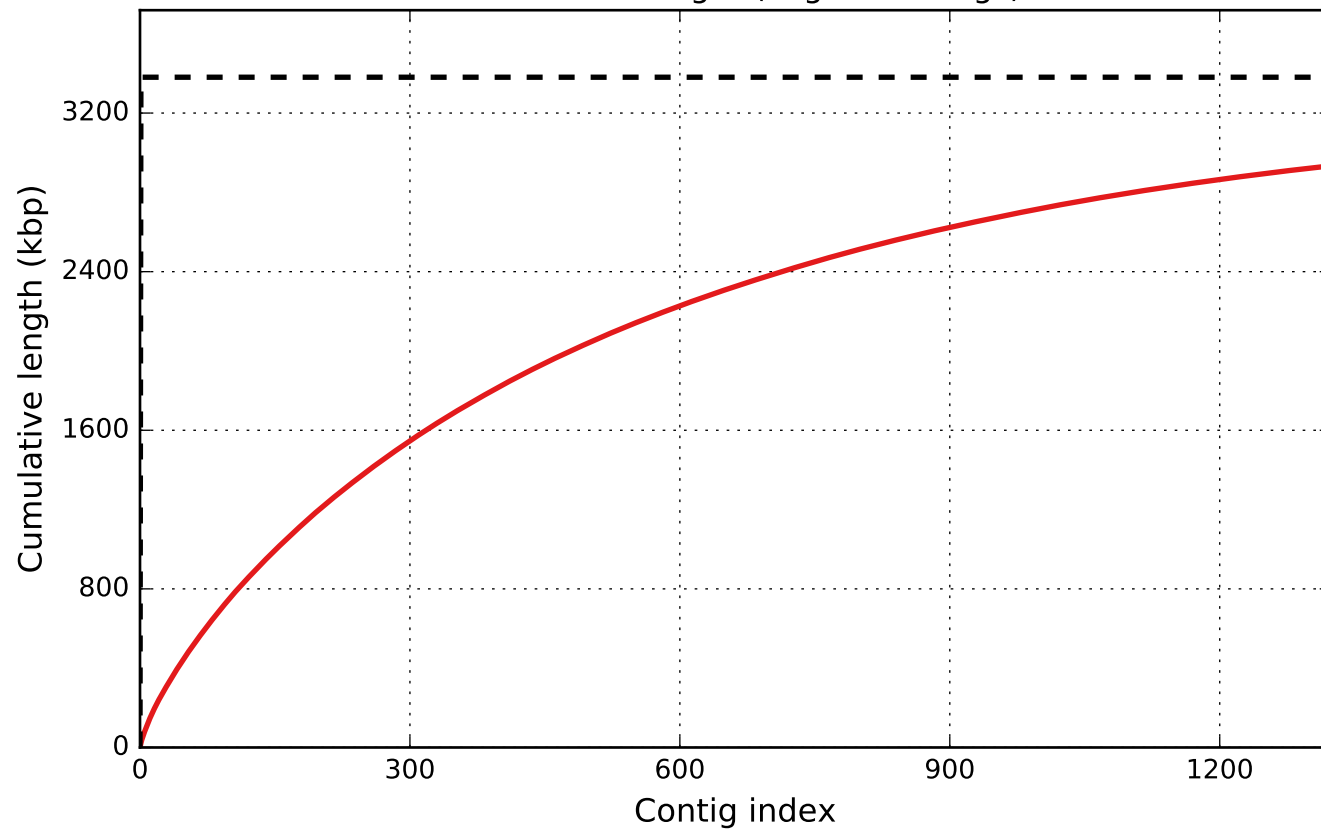


FRCurve (misassemblies)

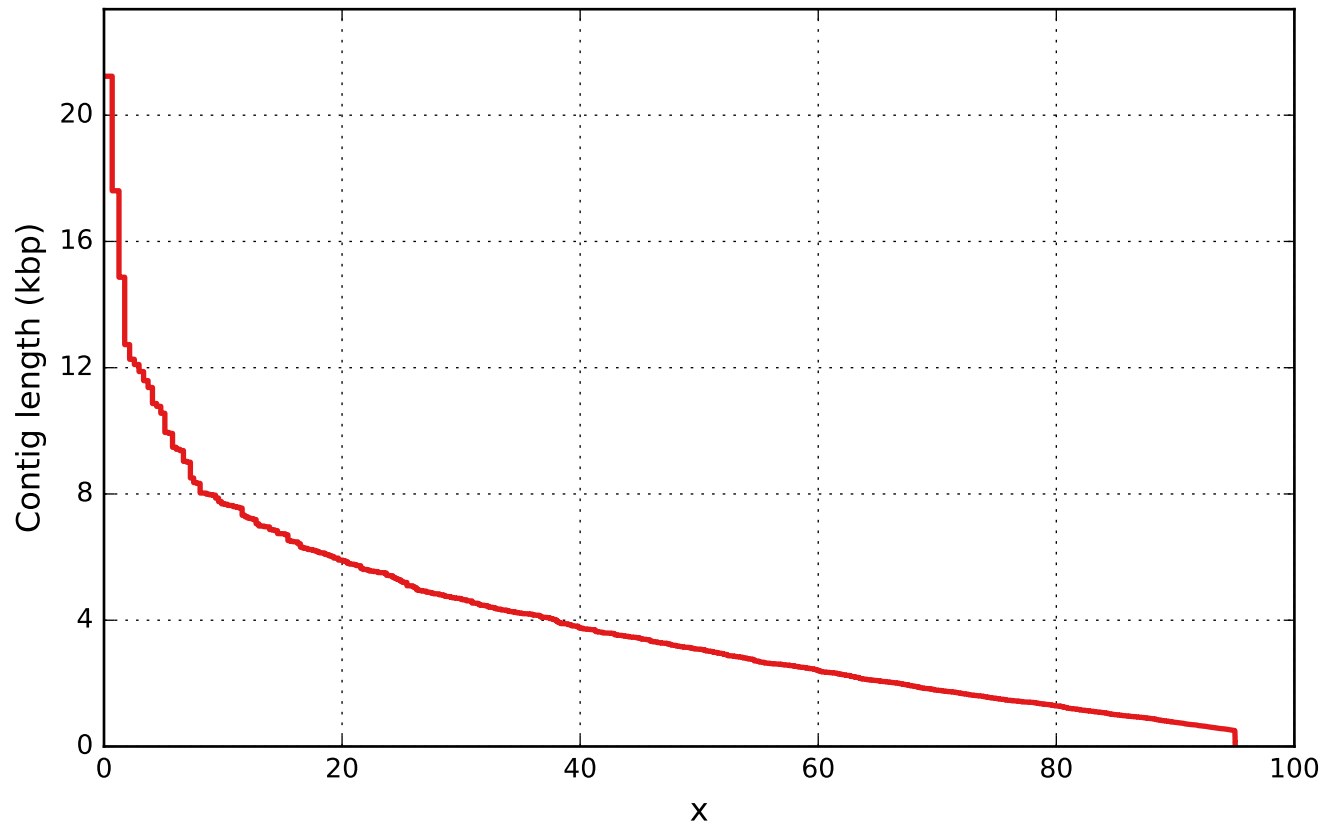


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Cumulative length (aligned contigs)

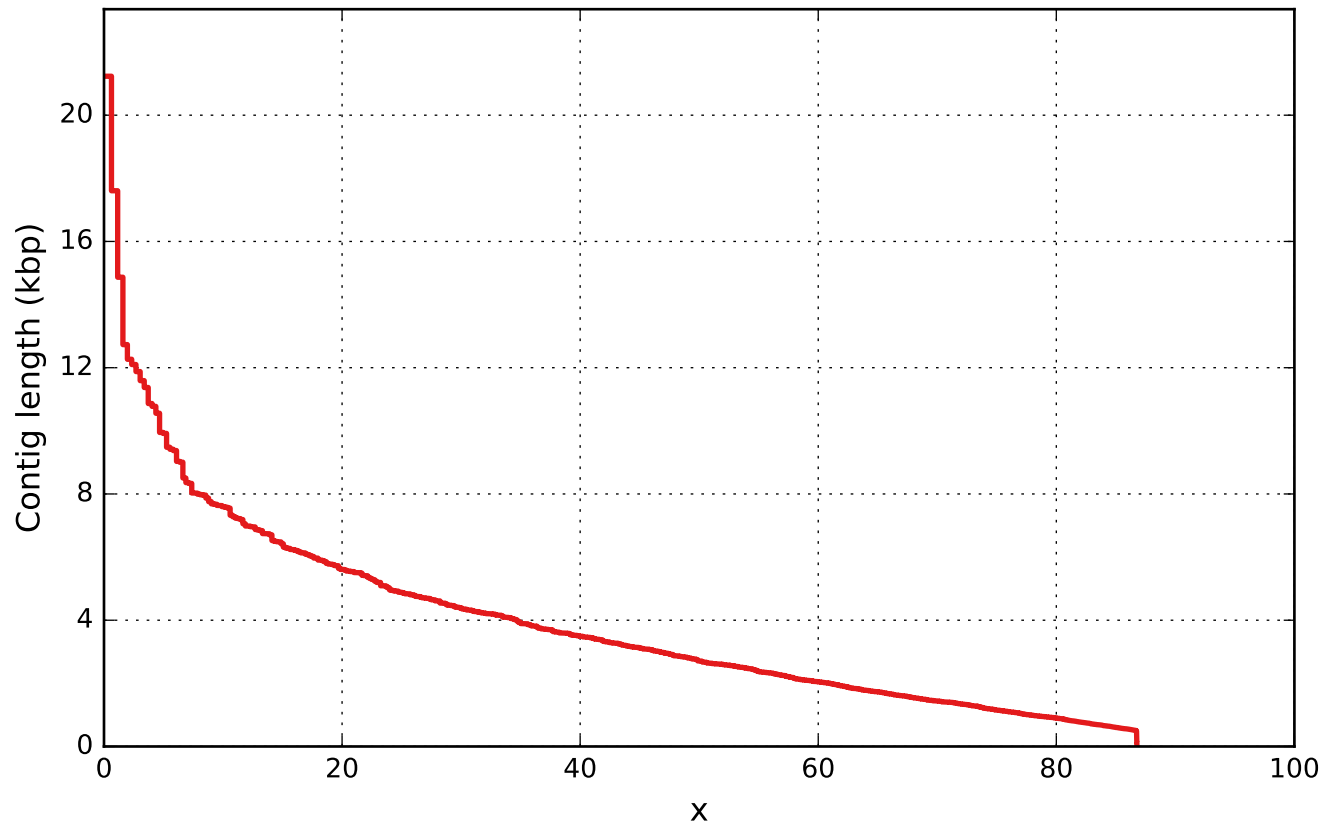


NAx



— assembly_output_graph

NGAx



— assembly_output_graph