

Report

	transcripts
# contigs (>= 0 bp)	5278
# contigs (>= 1000 bp)	7
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	1011955
Total length (>= 1000 bp)	10430
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	5278
Largest contig	2247
Total length	1011955
Reference length	3990777
GC (%)	41.56
Reference GC (%)	36.99
N50	182
N75	156
L50	2004
L75	3509
# misassemblies	27
# misassembled contigs	17
Misassembled contigs length	8597
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	11
# unaligned contigs	4021 + 3 part
Unaligned length	737252
Genome fraction (%)	4.710
Duplication ratio	1.486
# N's per 100 kbp	63.24
# mismatches per 100 kbp	1172.44
# indels per 100 kbp	68.71
Largest alignment	2247
Total aligned length	213394
NGA50	-

All statistics are based on contigs of size >= 50 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	transcripts
# misassemblies	27
# contig misassemblies	27
# c. relocations	27
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	17
Misassembled contigs length	8597
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	11
# mismatches	2167
# indels	127
# indels (<= 5 bp)	114
# indels (> 5 bp)	13
Indels length	441

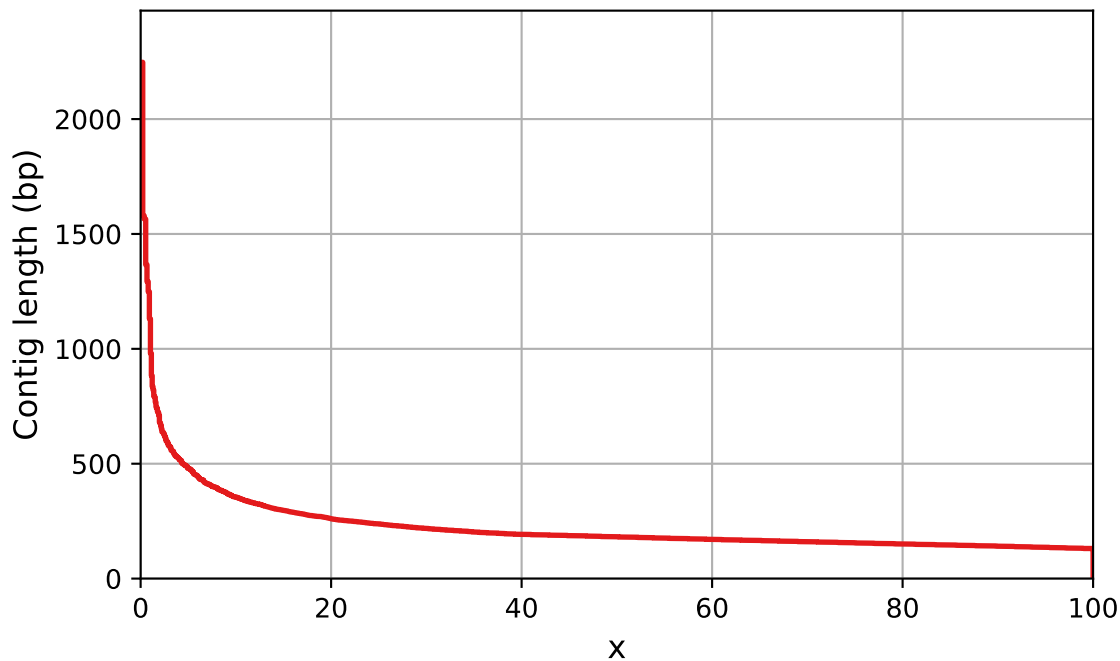
All statistics are based on contigs of size ≥ 50 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	transcripts
# fully unaligned contigs	4021
Fully unaligned length	734343
# partially unaligned contigs	3
Partially unaligned length	2909
# N's	640

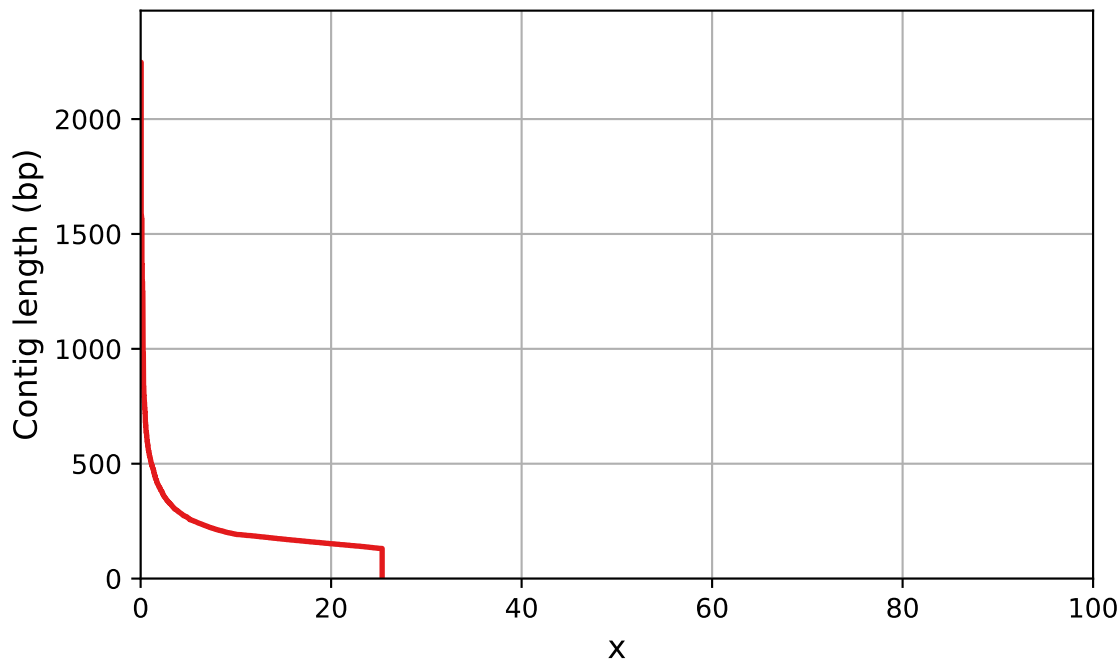
All statistics are based on contigs of size ≥ 50 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

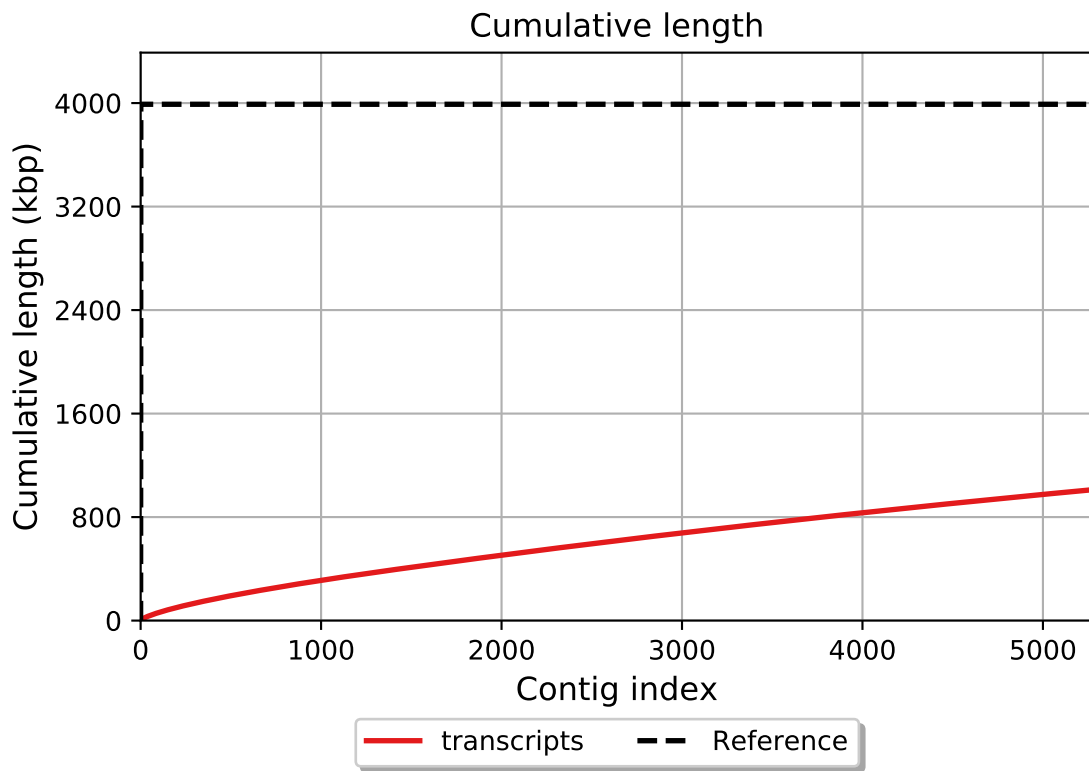


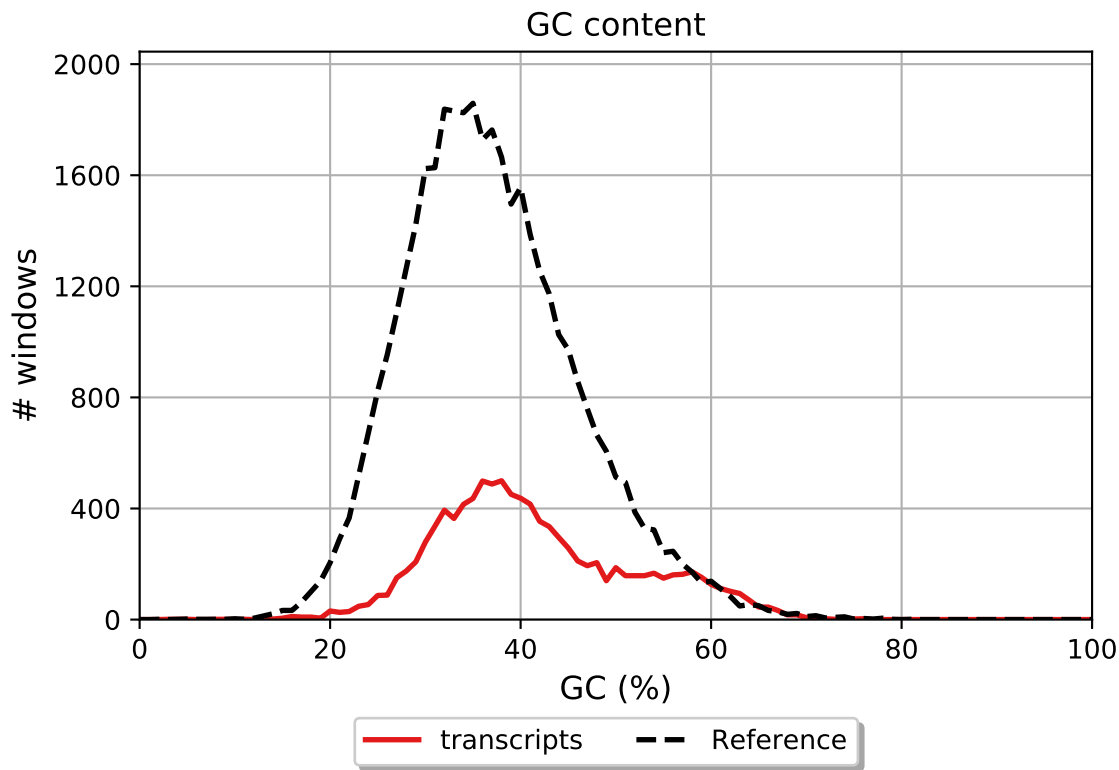
transcripts

NGx

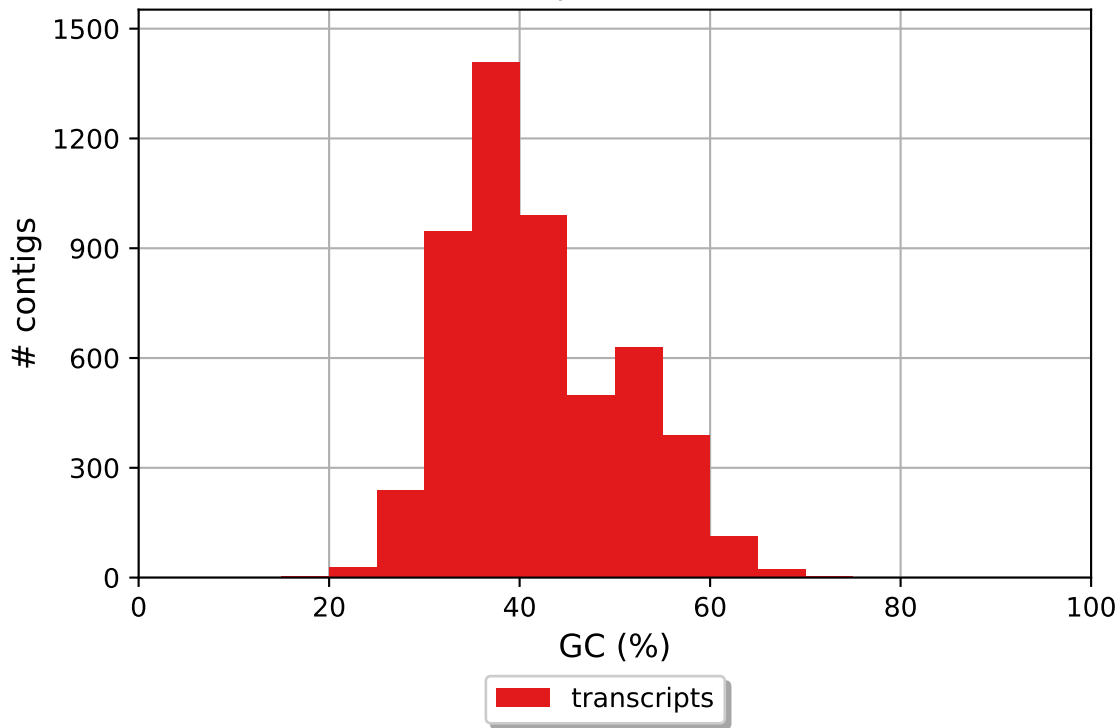


transcripts

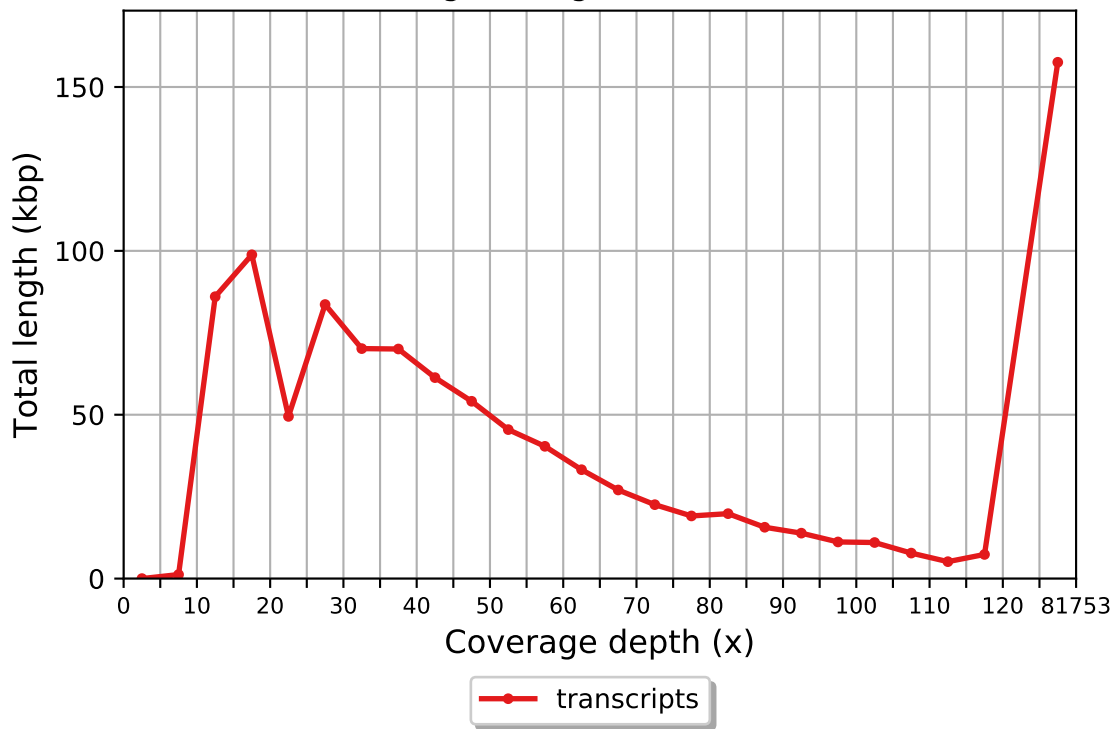




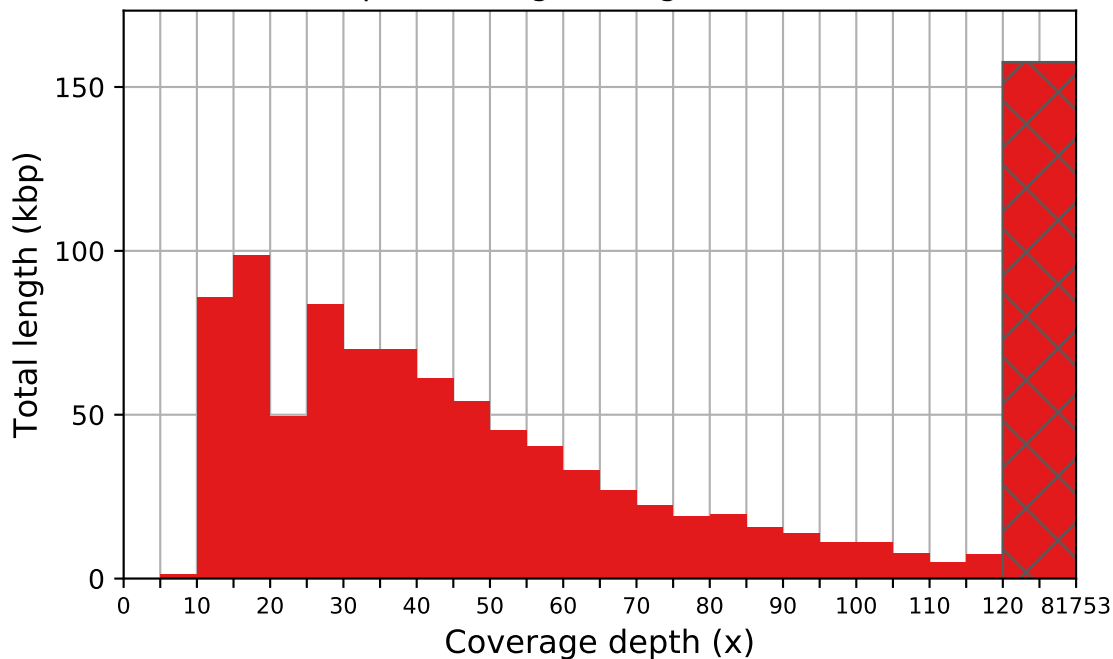
transcripts GC content



Coverage histogram (bin size: 5x)

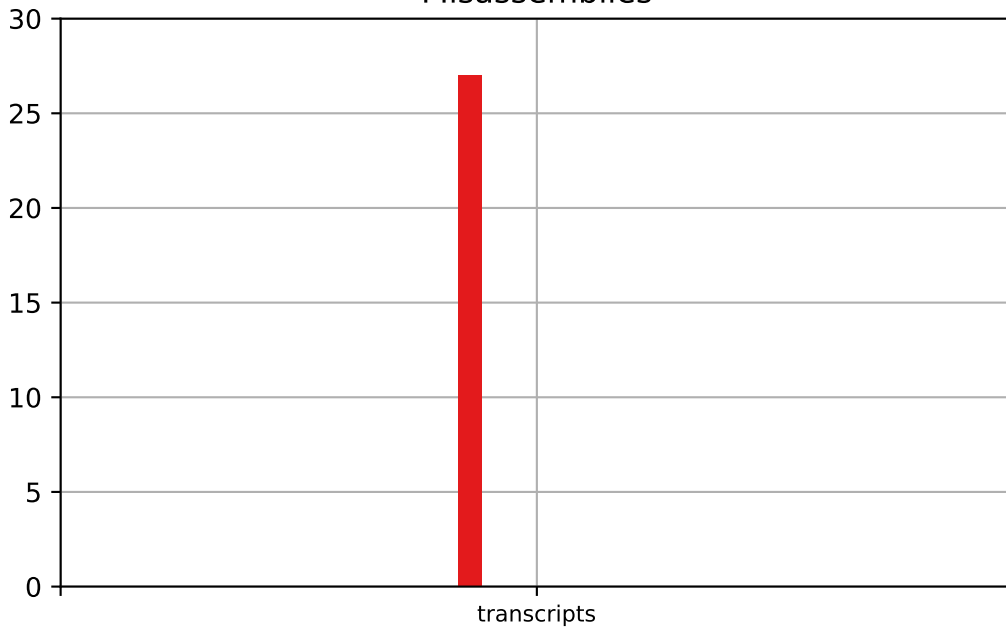


transcripts coverage histogram (bin size: 5x)

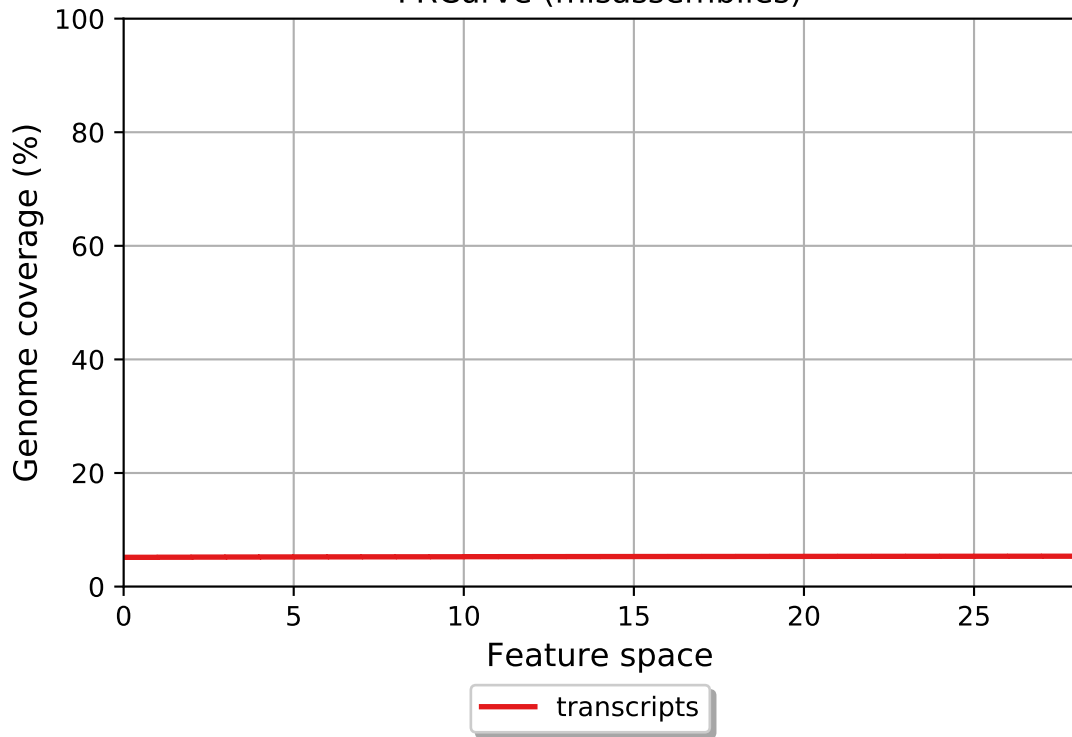


transcripts

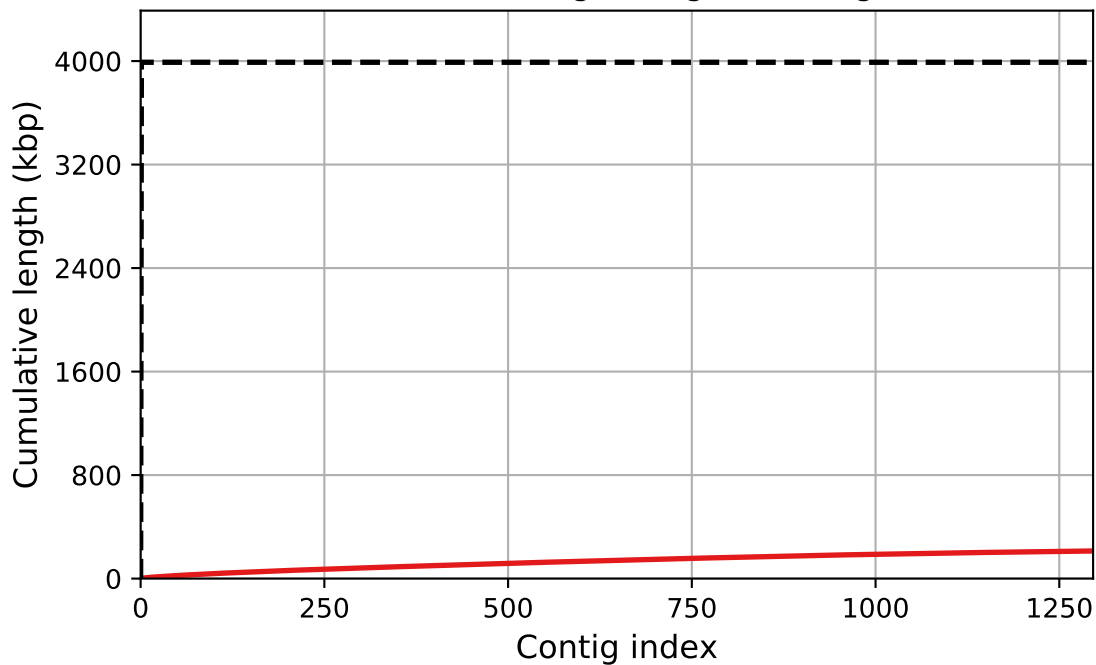
Misassemblies



FRCurve (misassemblies)

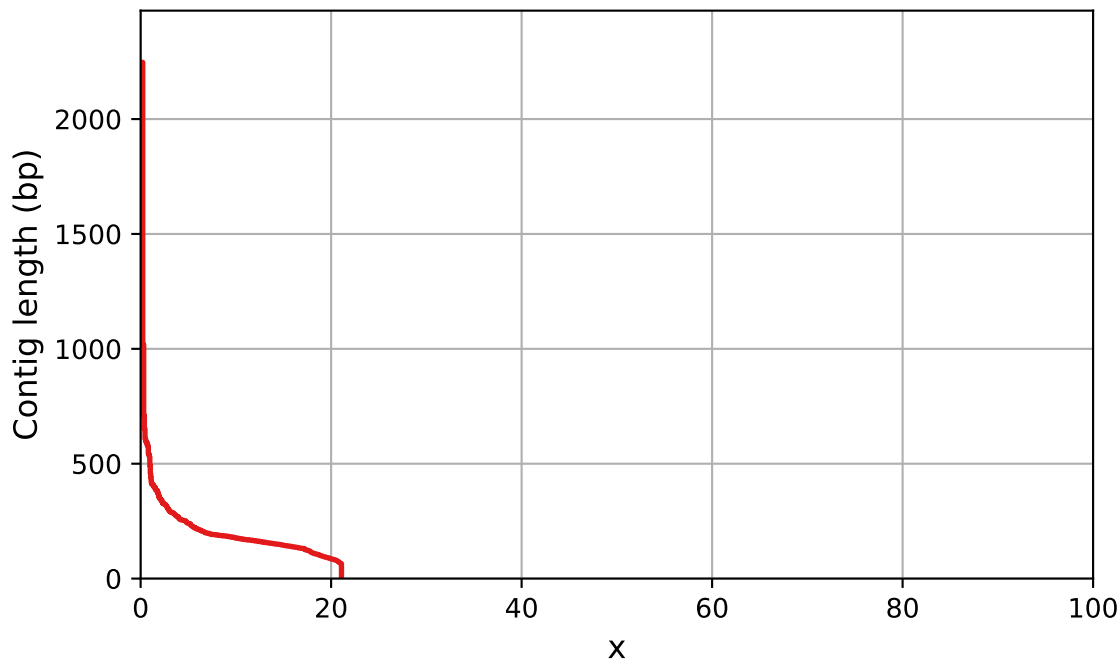


Cumulative length (aligned contigs)



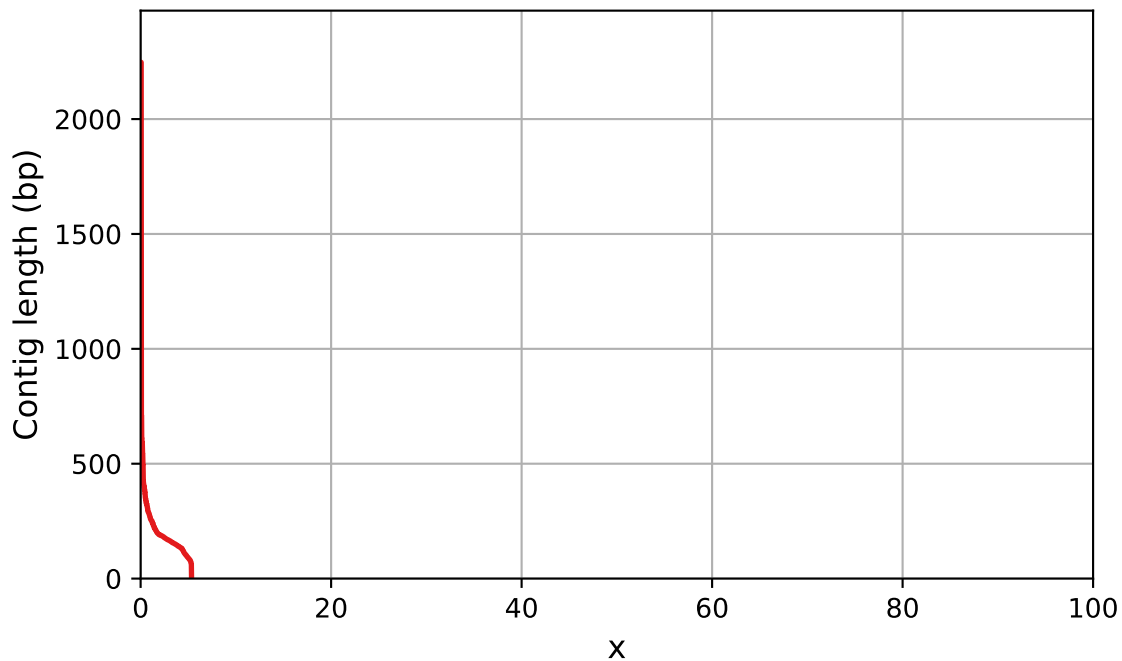
— transcripts - - Reference

NAx



transcripts

NGAx



— transcripts