

Report	assembly_b
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	1041
Total length (>= 1000 bp)	1041
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	1041
Total length	1041
Reference length	1000
GC (%)	51.97
Reference GC (%)	52.00
N50	1041
NG50	1041
N90	1041
NG90	1041
auN	1041.0
auNG	1083.7
L50	1
LG50	1
L90	1
LG90	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	100.000
Duplication ratio	1.041
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	96.06
Largest alignment	1041
Total aligned length	1041
NA50	1041
NGA50	1041
NA90	1041
NGA90	1041
auNA	1041.0
auNGA	1083.7
LA50	1
LGA50	1
LA90	1
LGA90	1

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

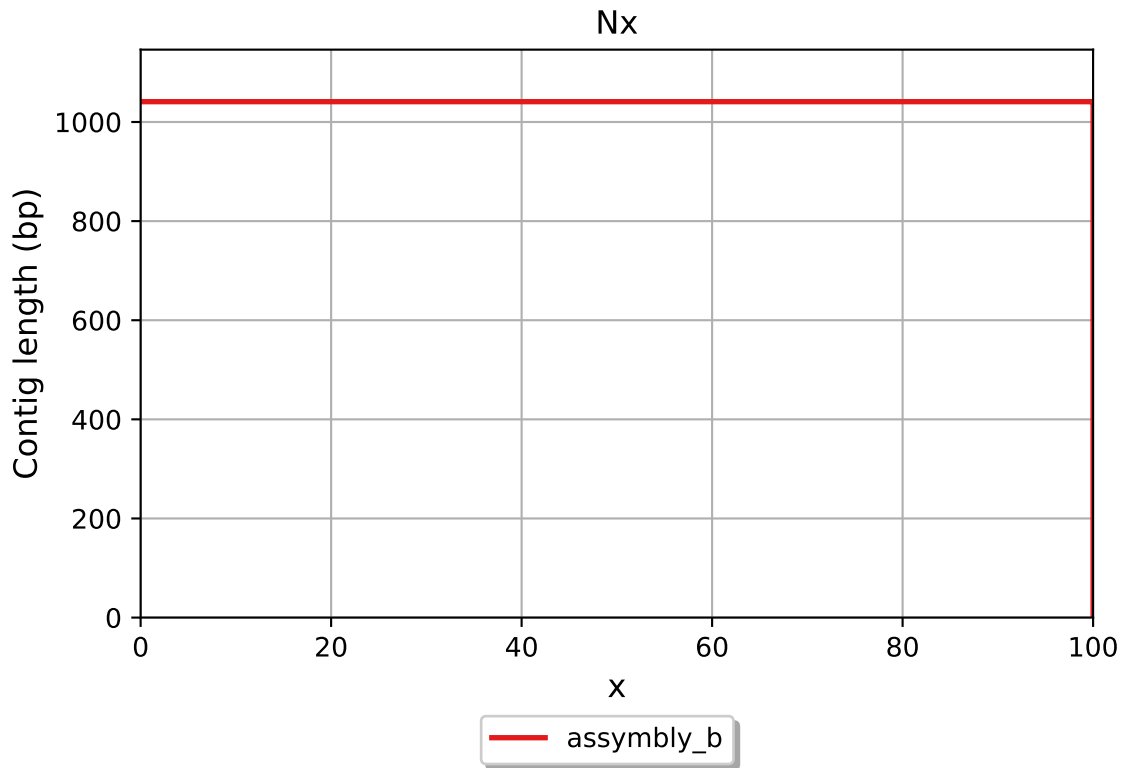
	assembly_b
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	1
# indels (<= 5 bp)	0
# indels (> 5 bp)	1
Indels length	41

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).

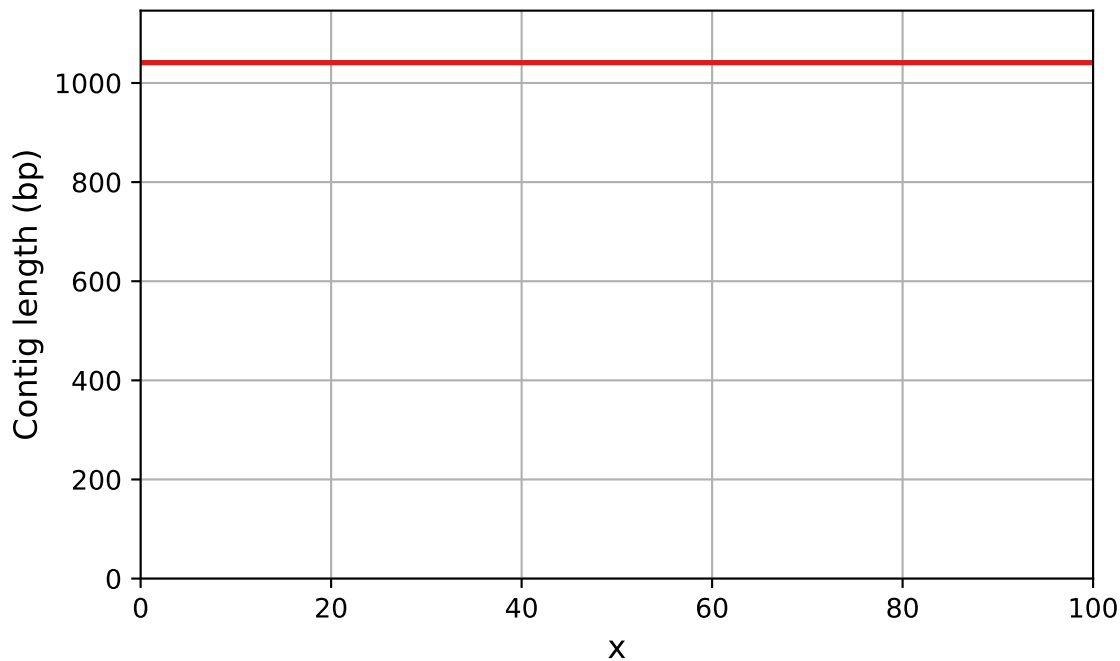
Unaligned report

	assembly_b
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

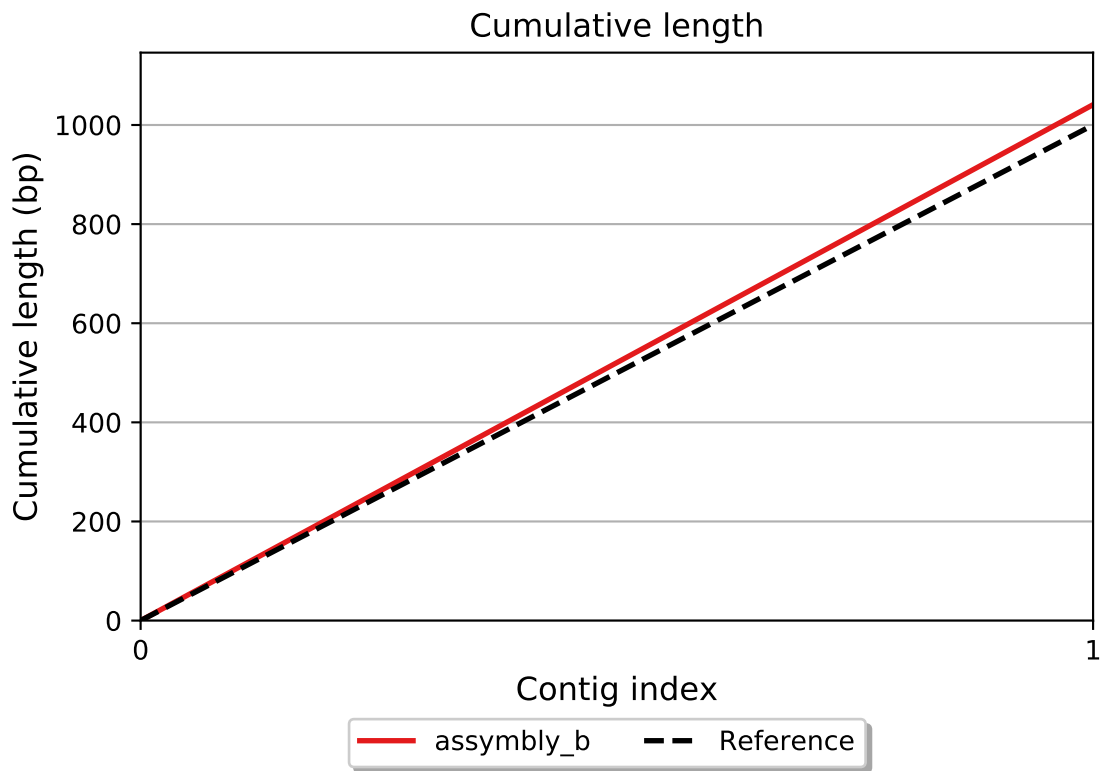
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



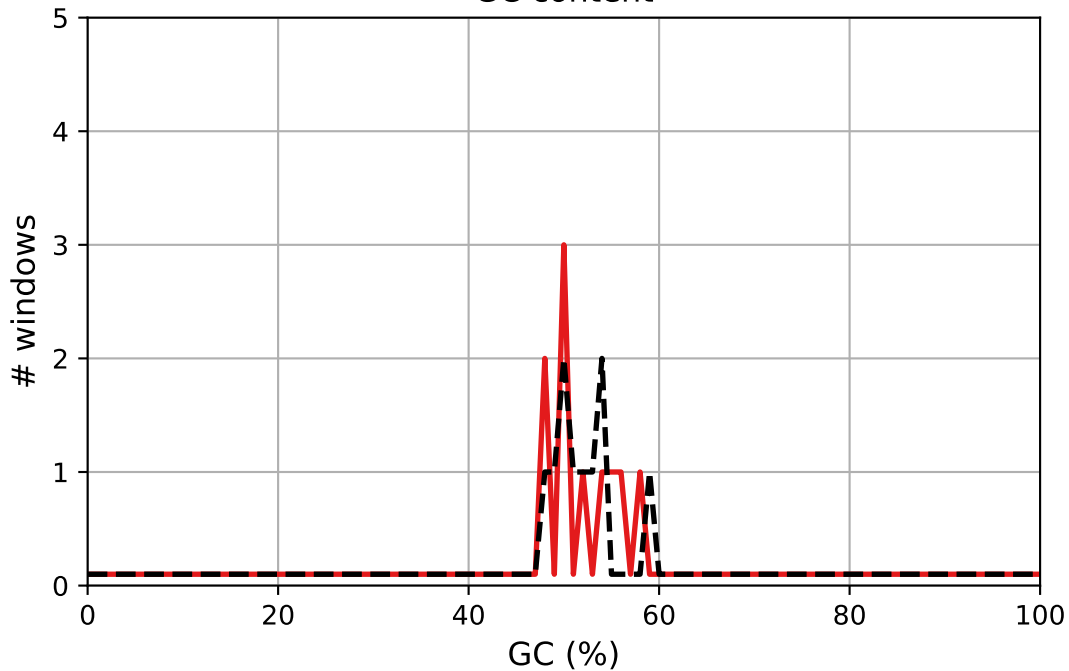
NGx



— assembly_b

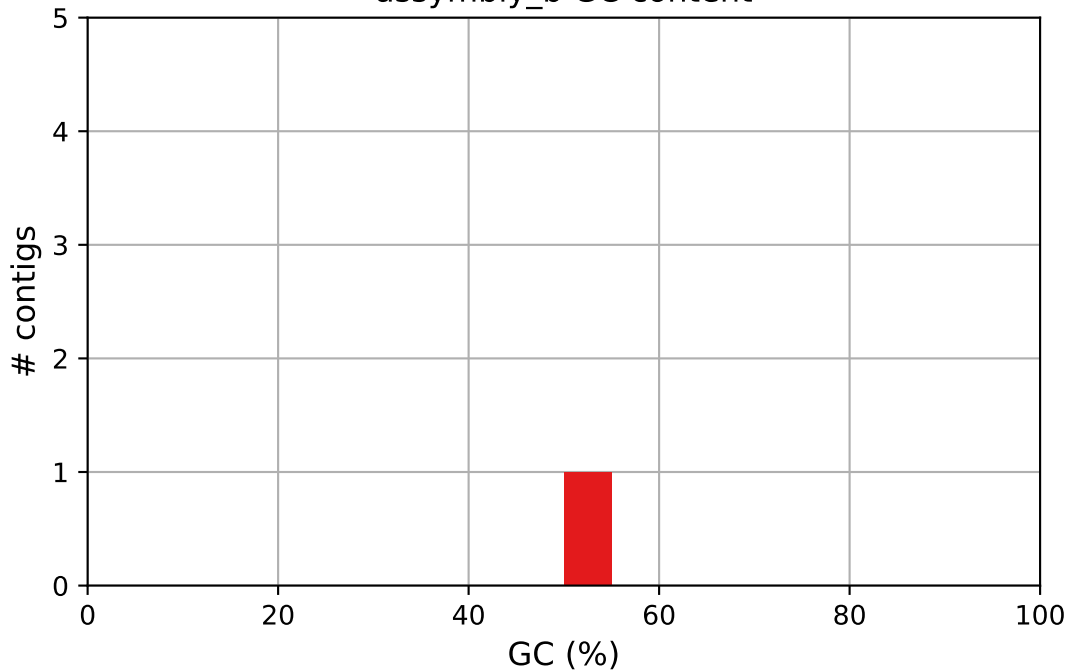


GC content



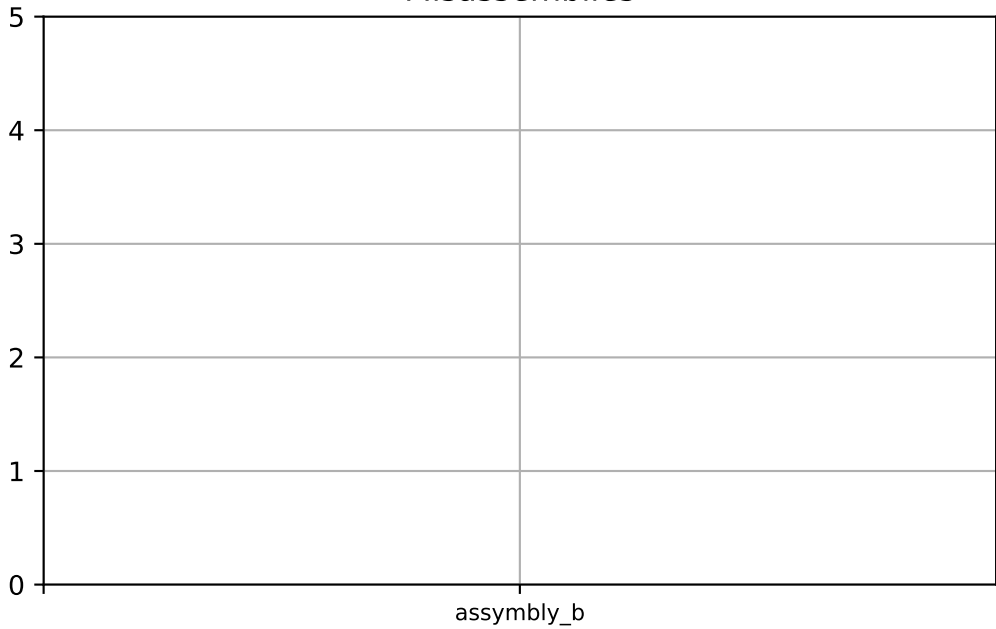
— assembly_b - - Reference

assembly_b GC content

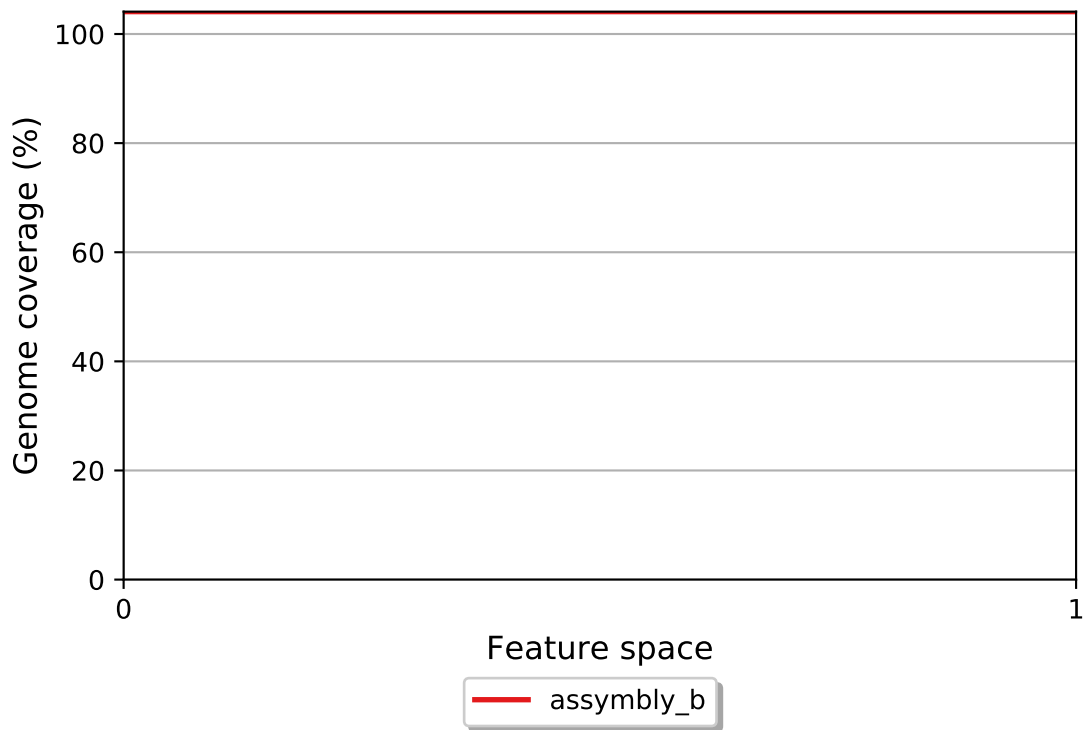


assembly_b

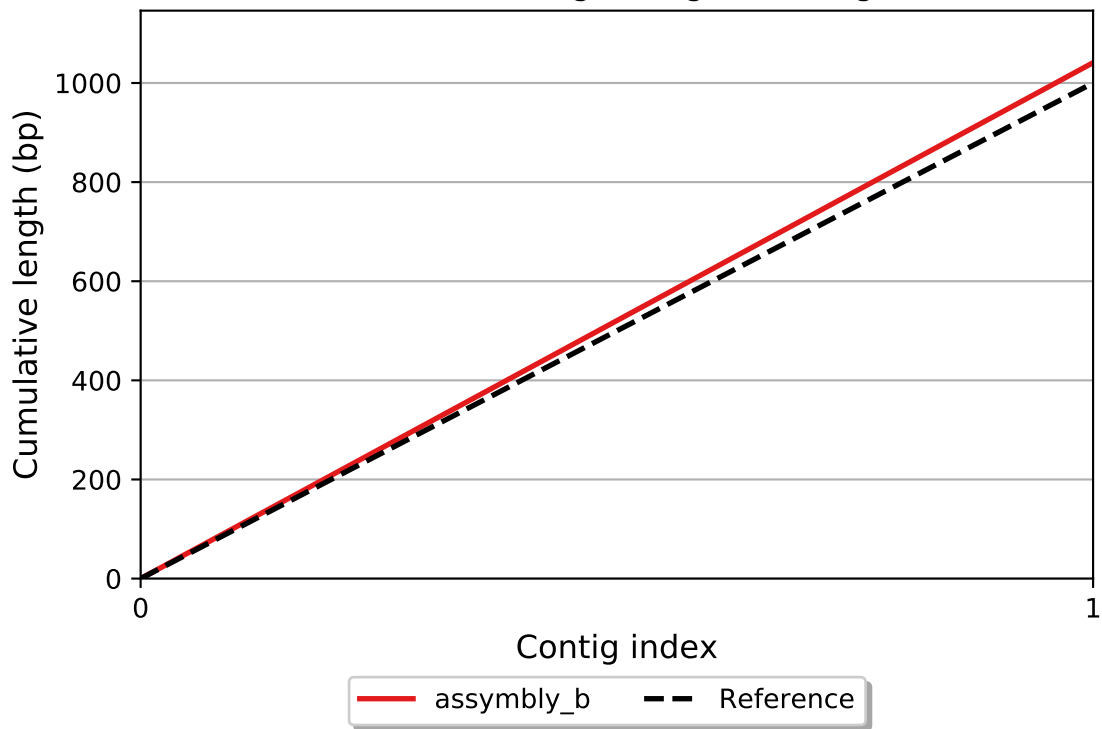
Misassemblies



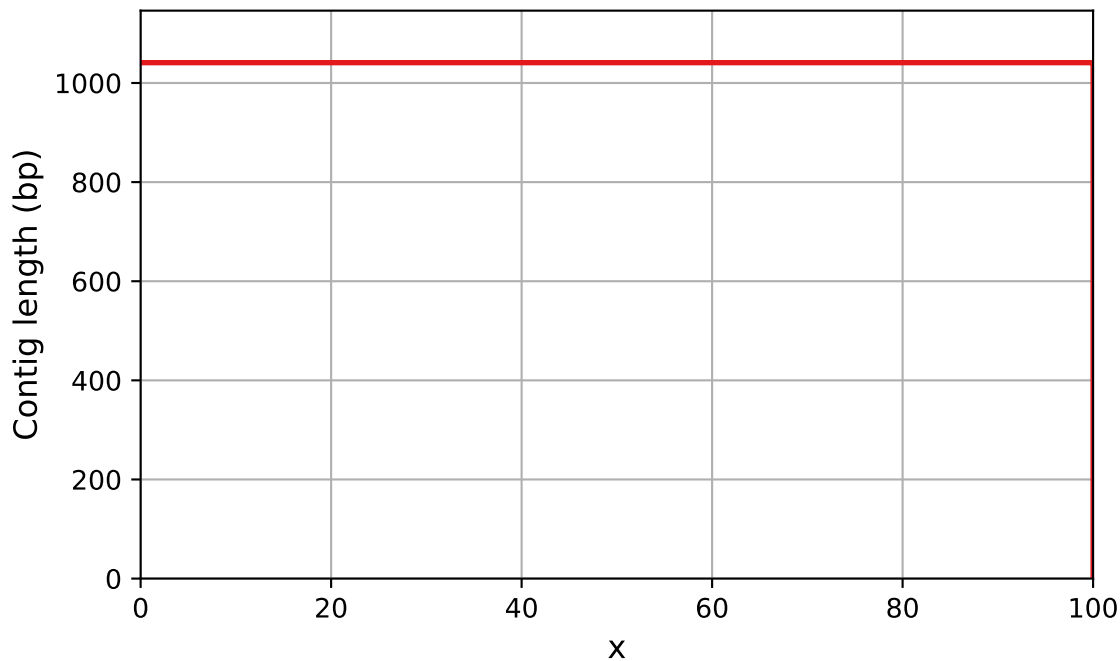
FRCurve (misassemblies)



Cumulative length (aligned contigs)

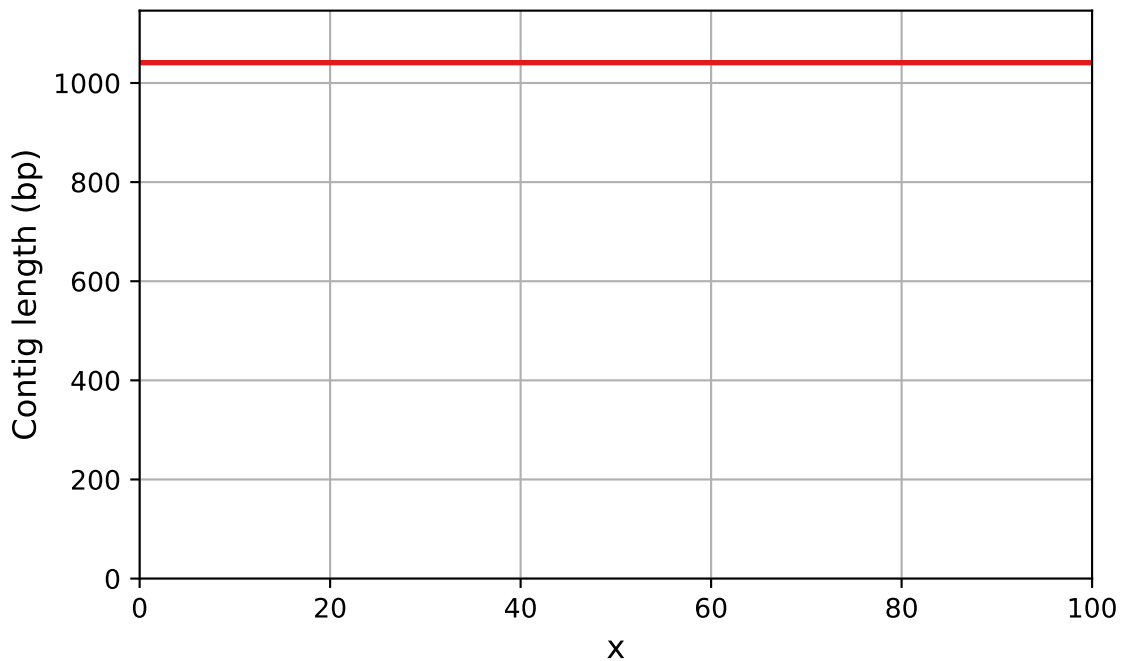


NAx



— assembly_b

NGAx



— assembly_b