

Report

	B500PP
# contigs (>= 0 bp)	19
# contigs (>= 1000 bp)	19
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	19
# contigs (>= 25000 bp)	15
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1429303
Total length (>= 1000 bp)	1429303
Total length (>= 5000 bp)	1429303
Total length (>= 10000 bp)	1429303
Total length (>= 25000 bp)	1346823
Total length (>= 50000 bp)	957418
# contigs	19
Largest contig	903660
Total length	1429303
Reference length	1521208
GC (%)	28.21
Reference GC (%)	28.18
N50	903660
NG50	903660
N90	27715
NG90	24387
auN	582816.5
auNG	547605.2
L50	1
LG50	1
L90	13
LG90	16
# misassemblies	36
# misassembled contigs	15
Misassembled contigs length	445637
# local misassemblies	17
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 13 part
Unaligned length	91974
Genome fraction (%)	82.511
Duplication ratio	1.059
# N's per 100 kbp	0.00
# mismatches per 100 kbp	988.31
# indels per 100 kbp	69.57
# genomic features	1304 + 49 part
Largest alignment	903470
Total aligned length	1329549
NA50	903470
NGA50	903470
NA90	4162
NGA90	-
auNA	577097.1
auNGA	542231.3
LA50	1
LGA50	1
LA90	28
LGA90	-

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

	B500PP
# misassemblies	36
# contig misassemblies	36
# c. relocations	3
# c. translocations	29
# c. inversions	4
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	15
Misassembled contigs length	445637
# local misassemblies	17
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	13140
# indels	925
# indels (<= 5 bp)	817
# indels (> 5 bp)	108
Indels length	6527

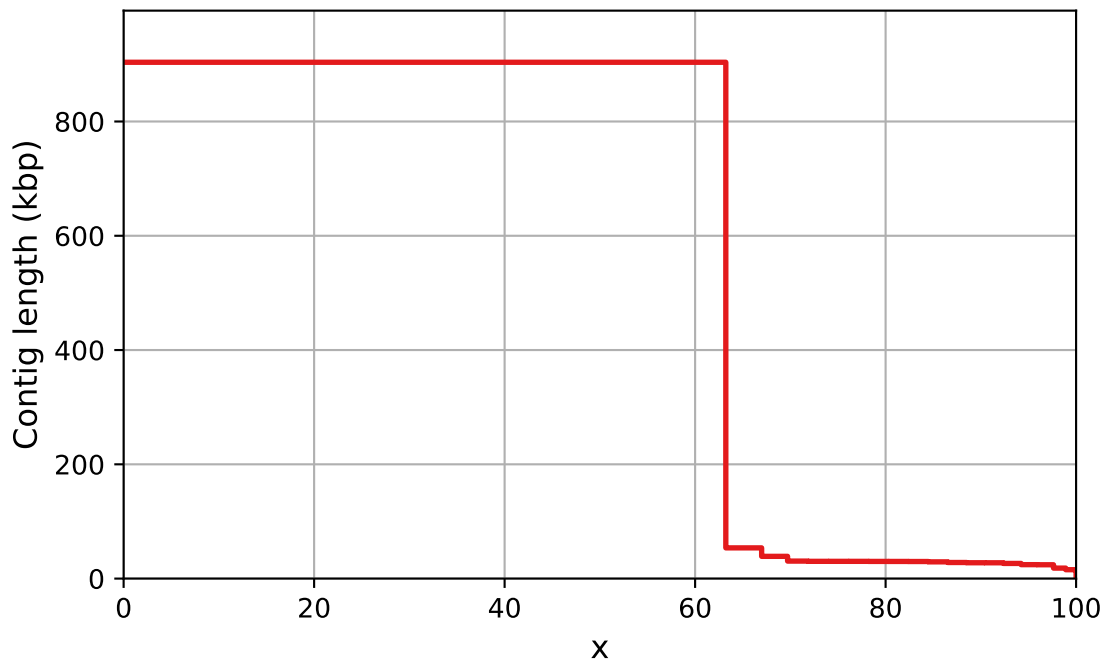
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	B500PP
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	13
Partially unaligned length	91974
# N's	0

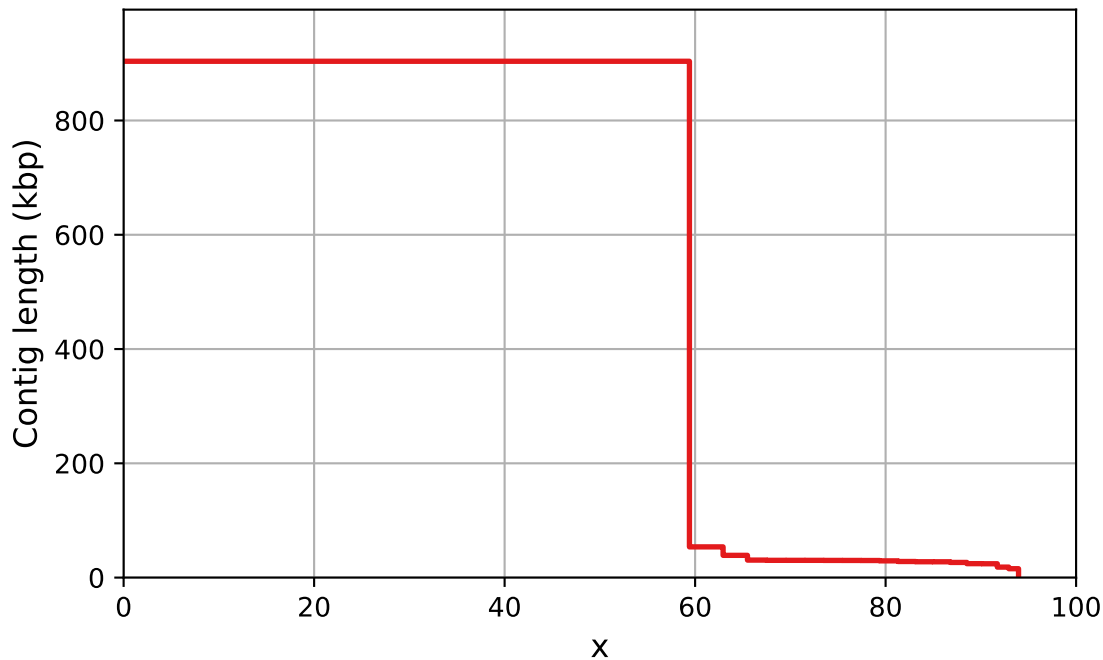
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

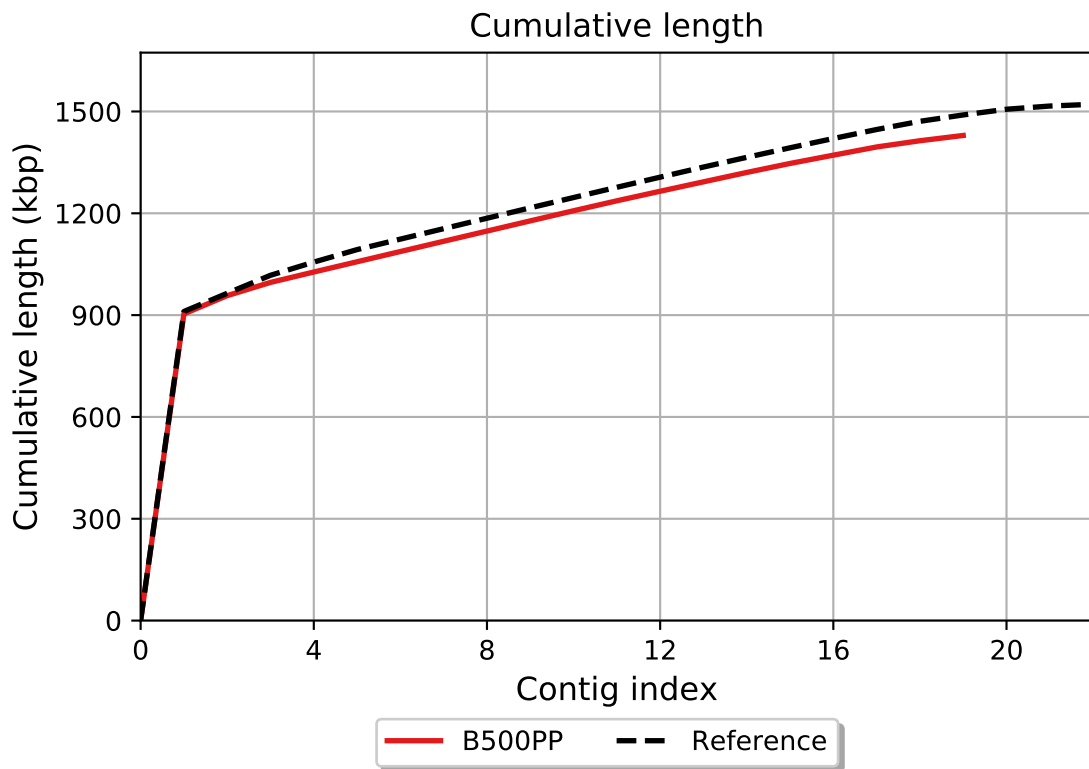


B500PP

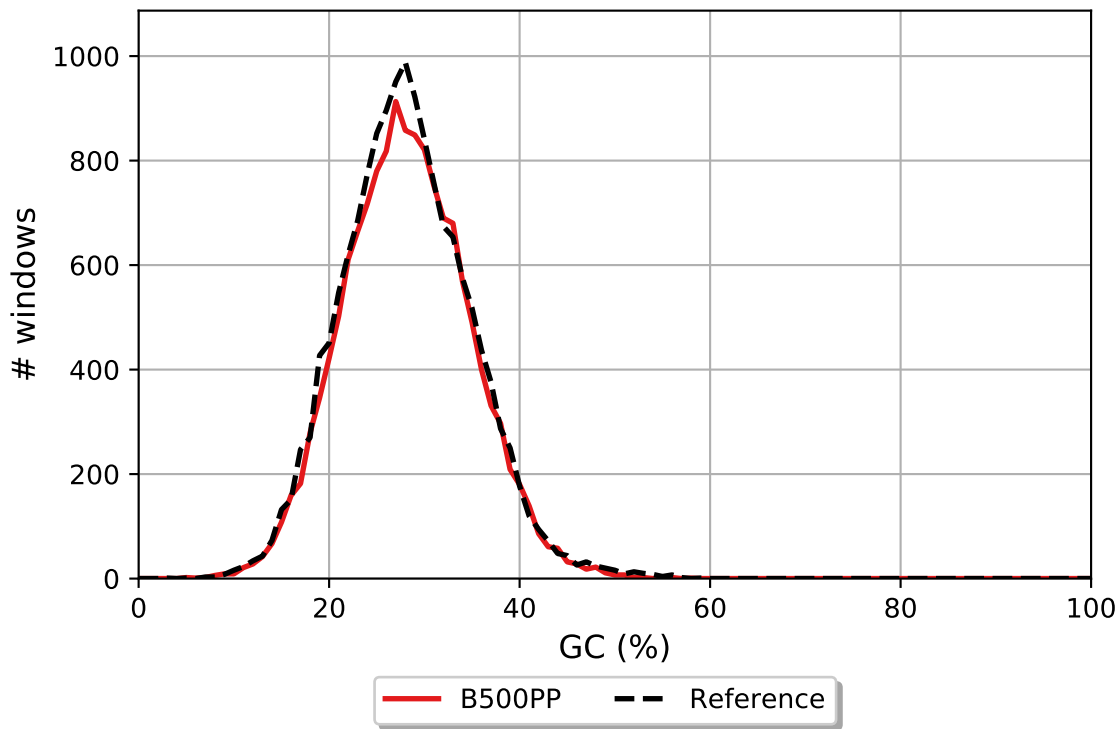
NGx



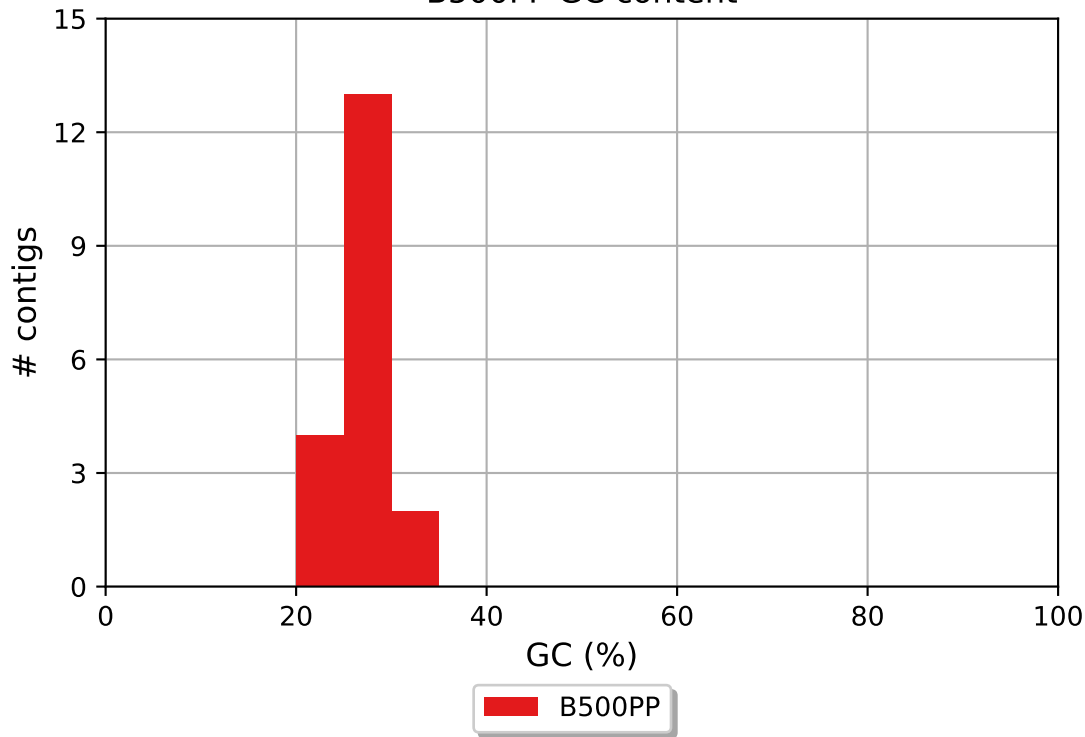
B500PP



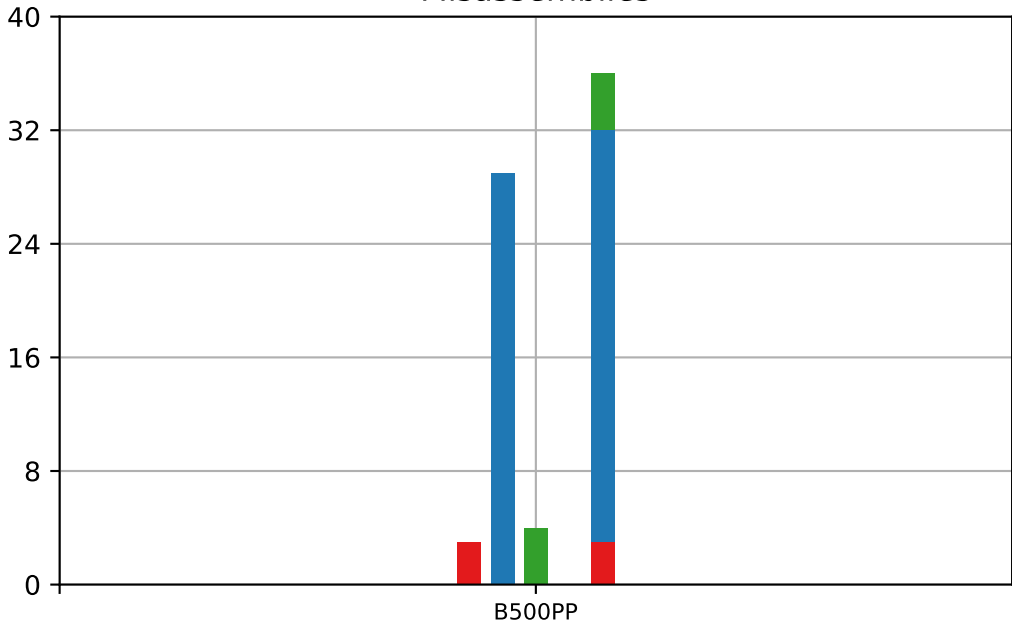
GC content



B500PP GC content



Misassemblies



relocations

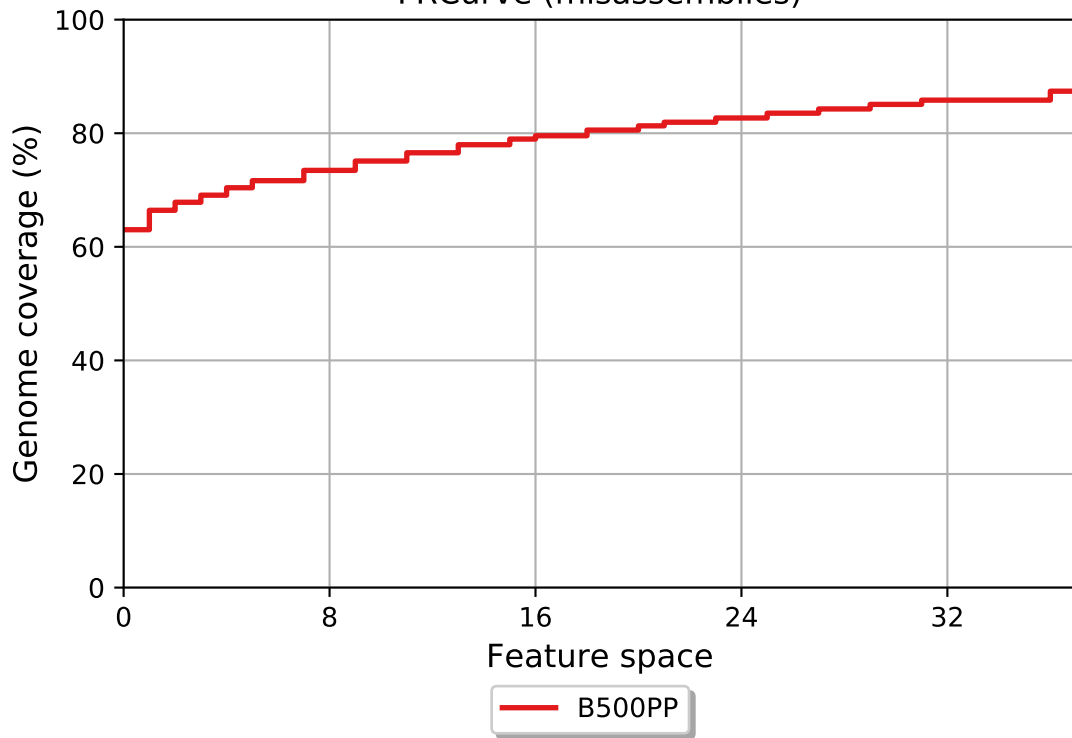


translocations

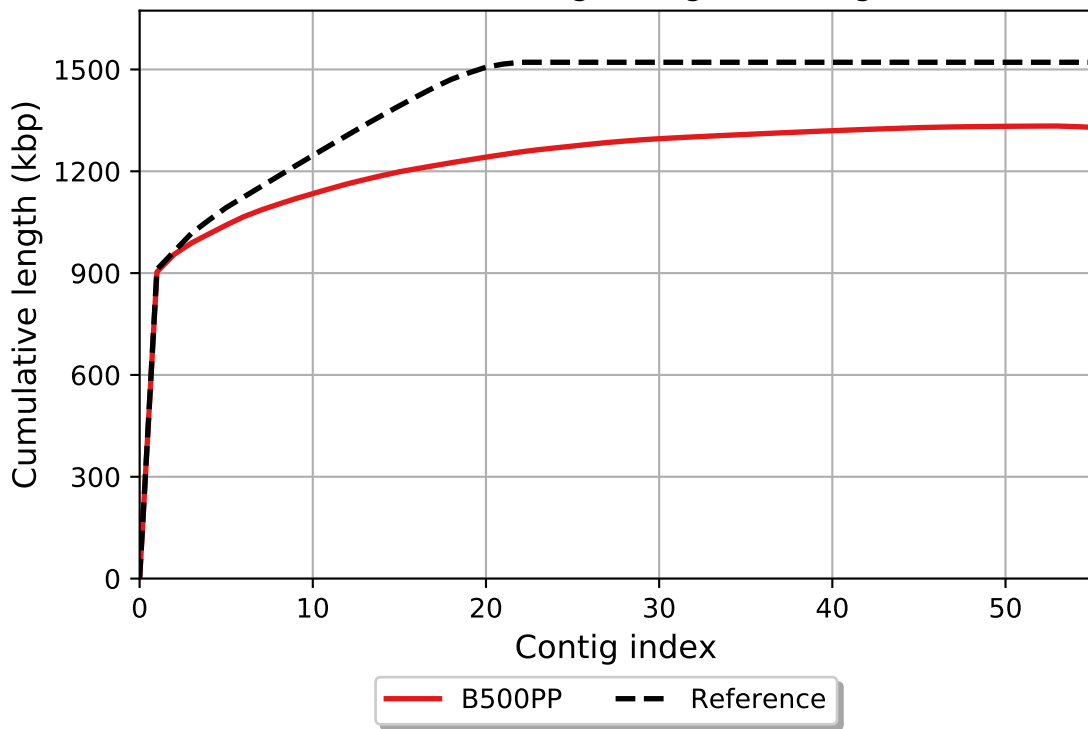


inversions

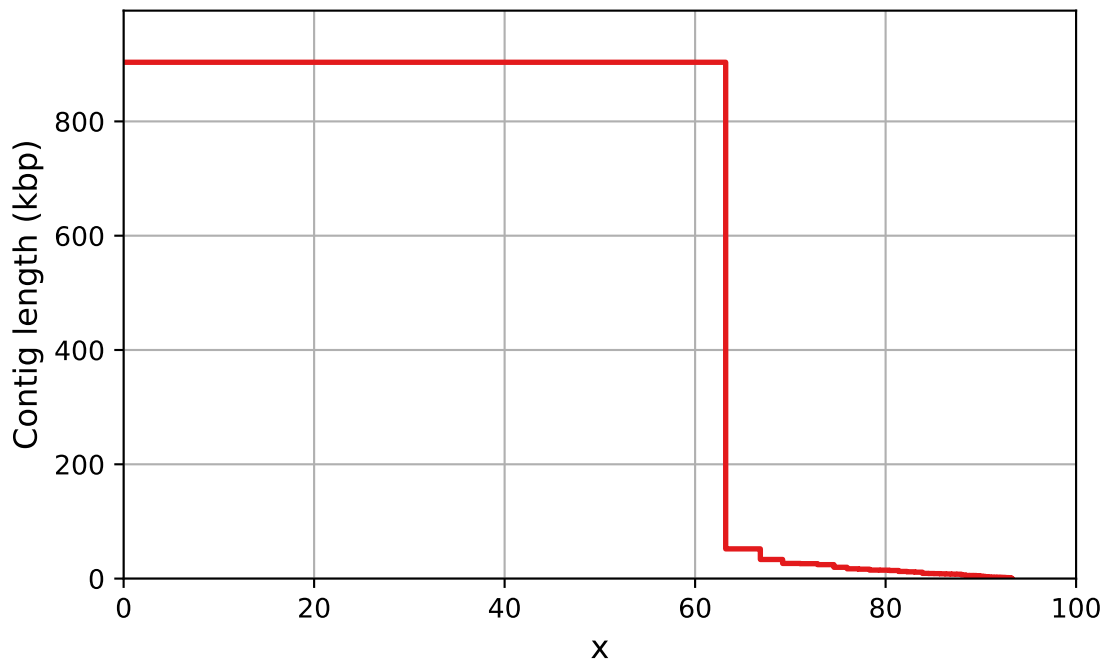
FRCurve (misassemblies)



Cumulative length (aligned contigs)

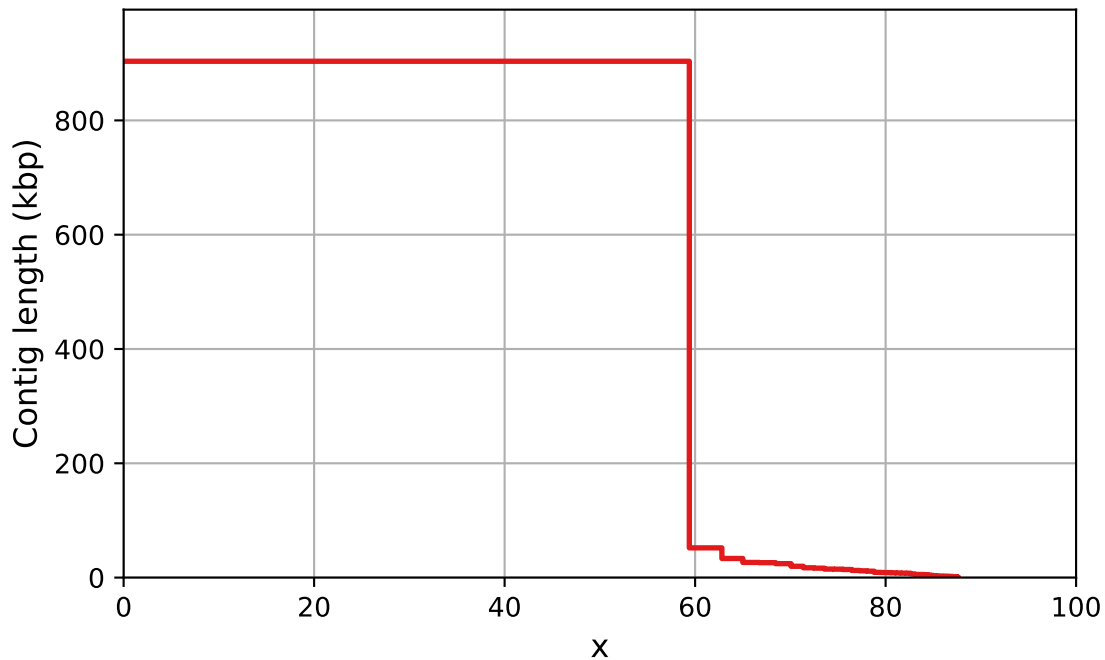


NAx



B500PP

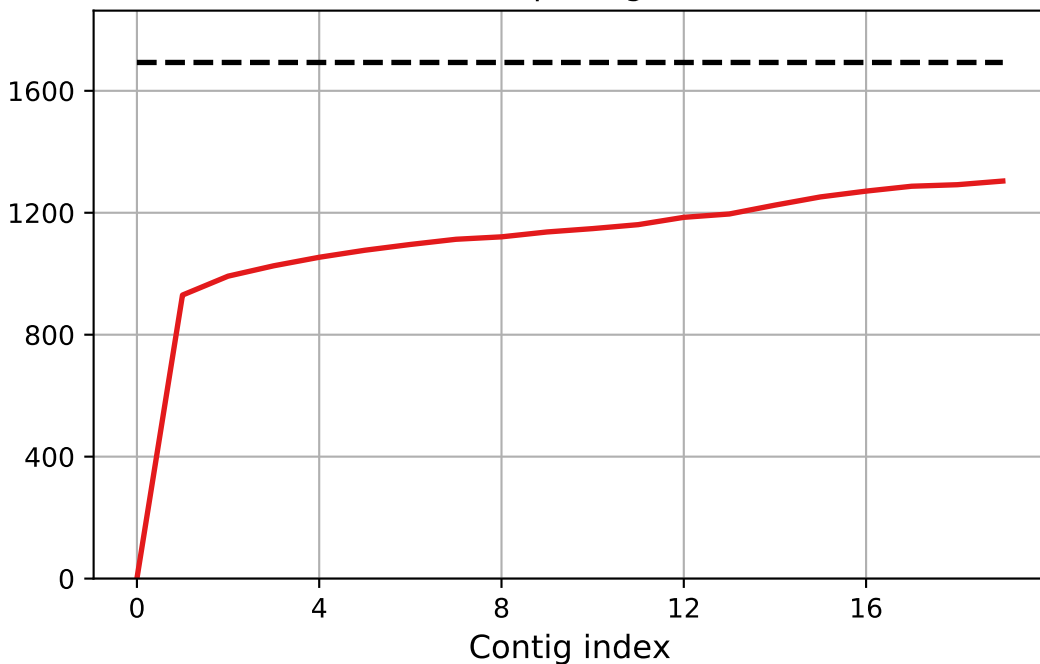
NGAx



B500PP

Cumulative # complete genomic features

Cumulative # complete genomic features



— B500PP - - Reference

FRCurve (genomic features)

