

Report

	P_cali_8
# contigs (>= 0 bp)	1851769
# contigs (>= 1000 bp)	131899
# contigs (>= 5000 bp)	39026
# contigs (>= 10000 bp)	8852
# contigs (>= 25000 bp)	328
# contigs (>= 50000 bp)	11
Total length (>= 0 bp)	1007051673
Total length (>= 1000 bp)	584516010
Total length (>= 5000 bp)	332013941
Total length (>= 10000 bp)	125745248
Total length (>= 25000 bp)	10357409
Total length (>= 50000 bp)	656503
# contigs	74045
Largest contig	103765
Total length	468431423
Reference length	804620767
GC (%)	36.89
Reference GC (%)	37.01
N50	6822
NG50	3937
N75	4694
L50	22207
LG50	54864
L75	43012
# misassemblies	41
# misassembled contigs	39
Misassembled contigs length	266331
# local misassemblies	191
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	17
# possible TEs	4
# unaligned mis. contigs	2173
# unaligned contigs	61729 + 12262 part
Unaligned length	451104938
Genome fraction (%)	1.638
Duplication ratio	1.324
# N's per 100 kbp	208.89
# mismatches per 100 kbp	3762.96
# indels per 100 kbp	506.62
# genomic features	0 + 0 part
Complete BUSCO (%)	40.92
Partial BUSCO (%)	29.37
Largest alignment	14876
Total aligned length	16328463
NGA50	-
K-mer-based compl. (%)	0.29

All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Kmers report

	P_cali_8
K-mer-based compl. (%)	0.29

All statistics are based on contigs of size ≥ 3000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Misassemblies report

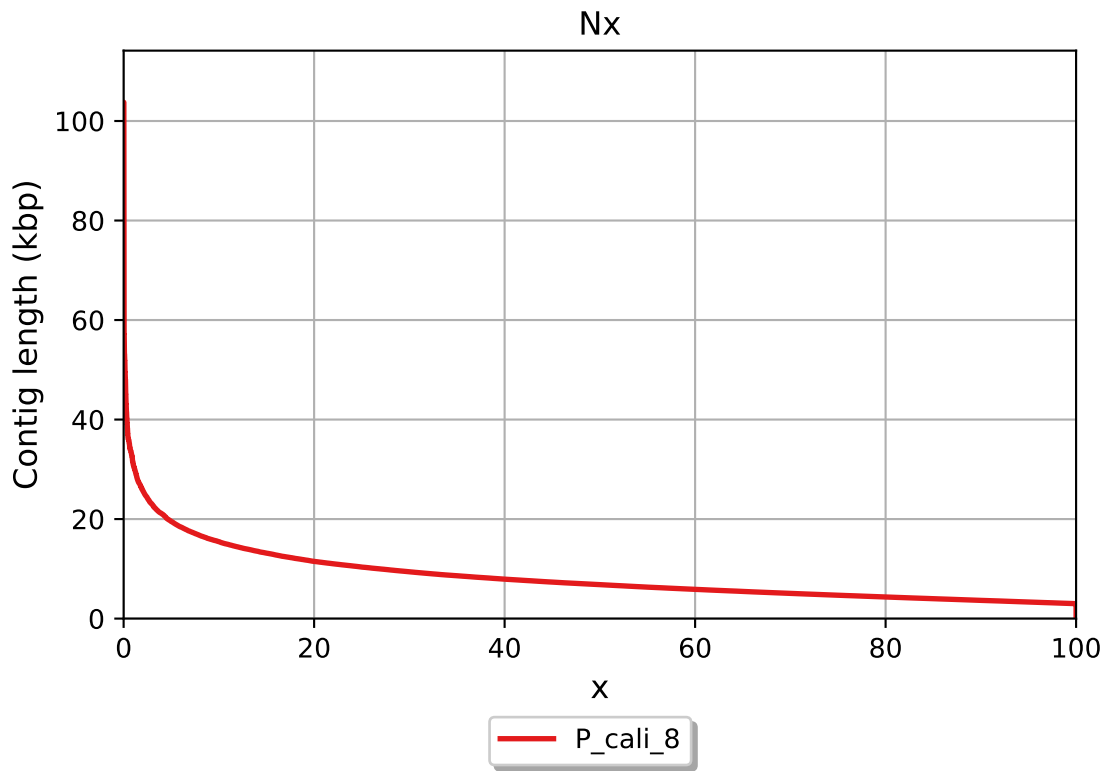
	P_cali_8
# misassemblies	41
# contig misassemblies	38
# c. relocations	7
# c. translocations	31
# c. inversions	0
# scaffold misassemblies	3
# s. relocations	0
# s. translocations	3
# s. inversions	0
# misassembled contigs	39
Misassembled contigs length	266331
# local misassemblies	191
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	17
# possible TEs	4
# unaligned mis. contigs	2173
# mismatches	492349
# indels	66287
# indels (<= 5 bp)	60855
# indels (> 5 bp)	5432
Indels length	152676

All statistics are based on contigs of size ≥ 3000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

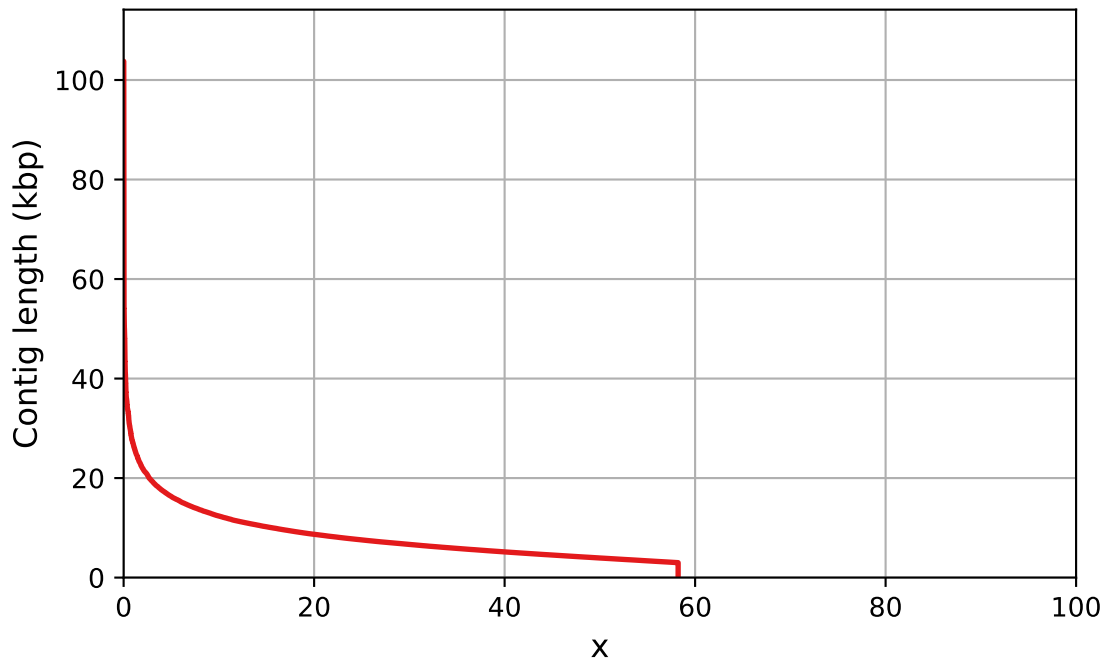
Unaligned report

	P_cali_8
# fully unaligned contigs	61729
Fully unaligned length	369514091
# partially unaligned contigs	12262
Partially unaligned length	81590847
# N's	978495

All statistics are based on contigs of size ≥ 3000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

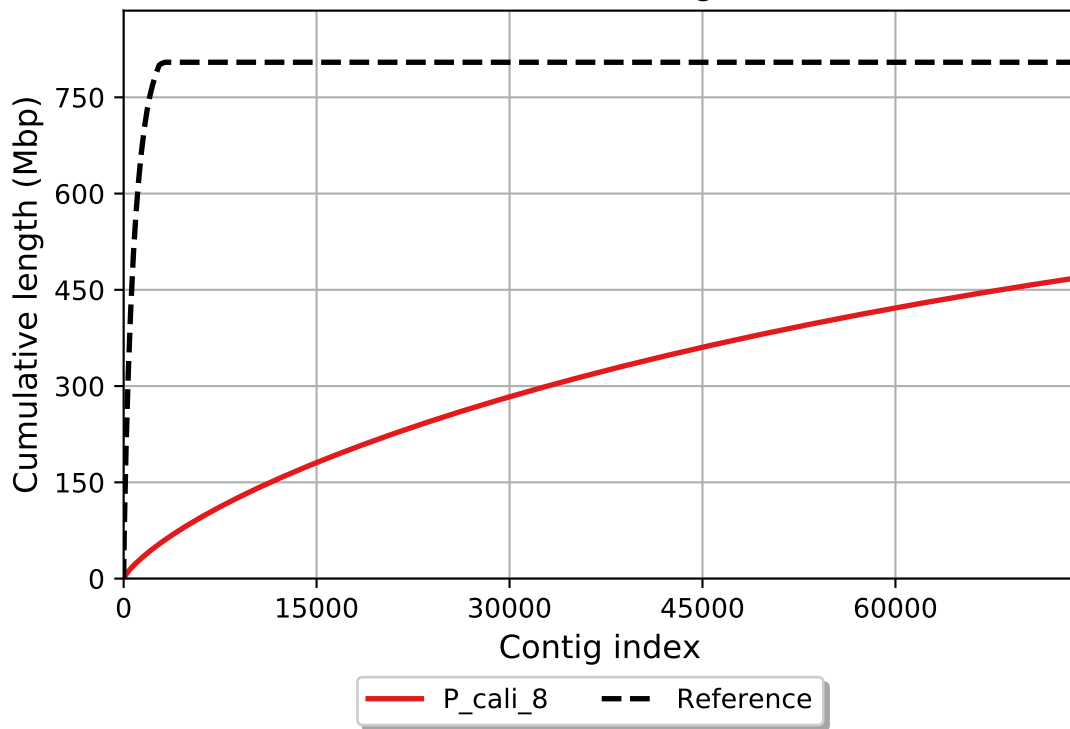


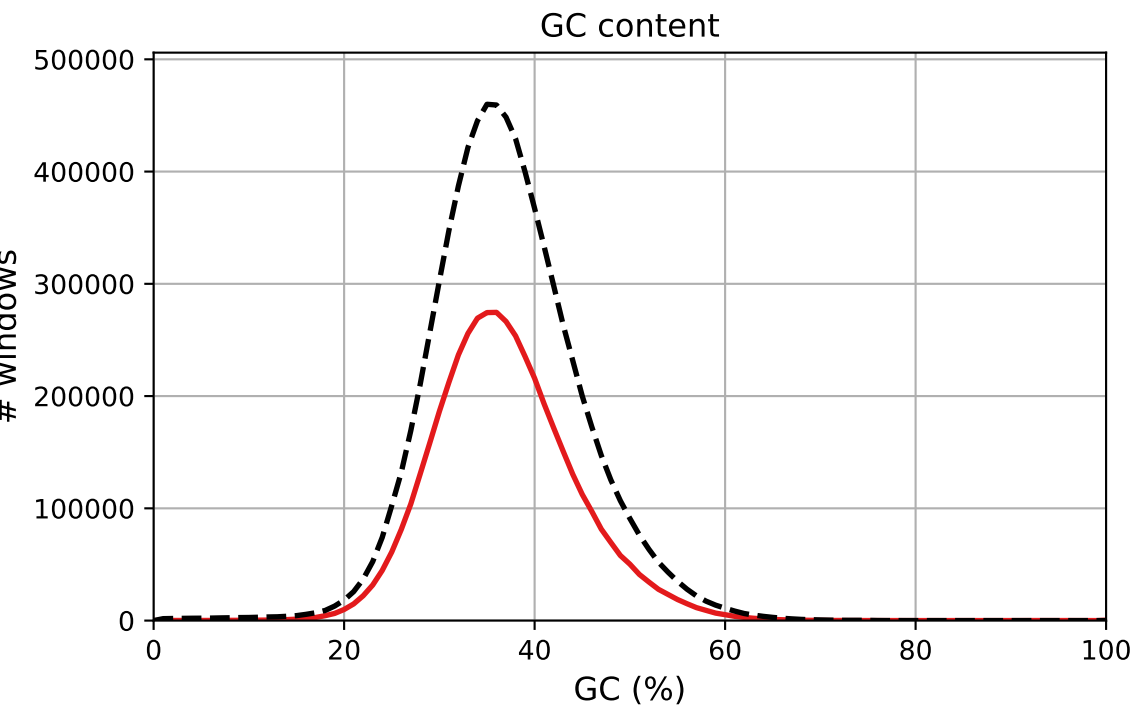
NGx



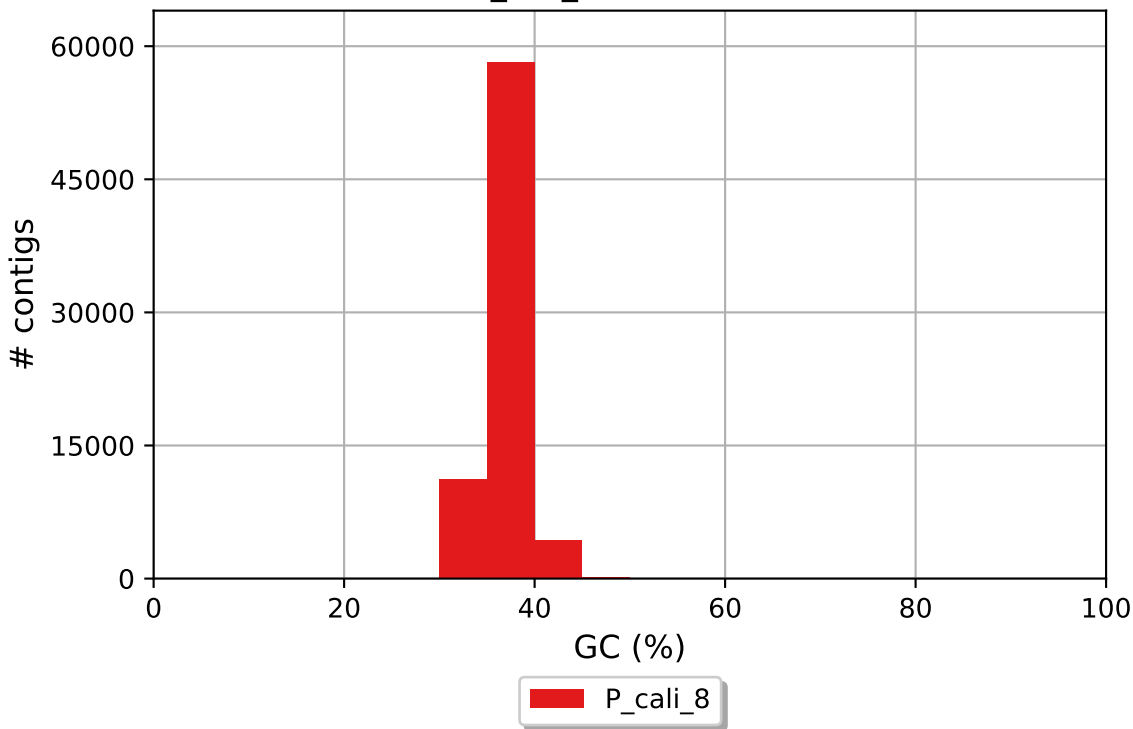
P_cali_8

Cumulative length

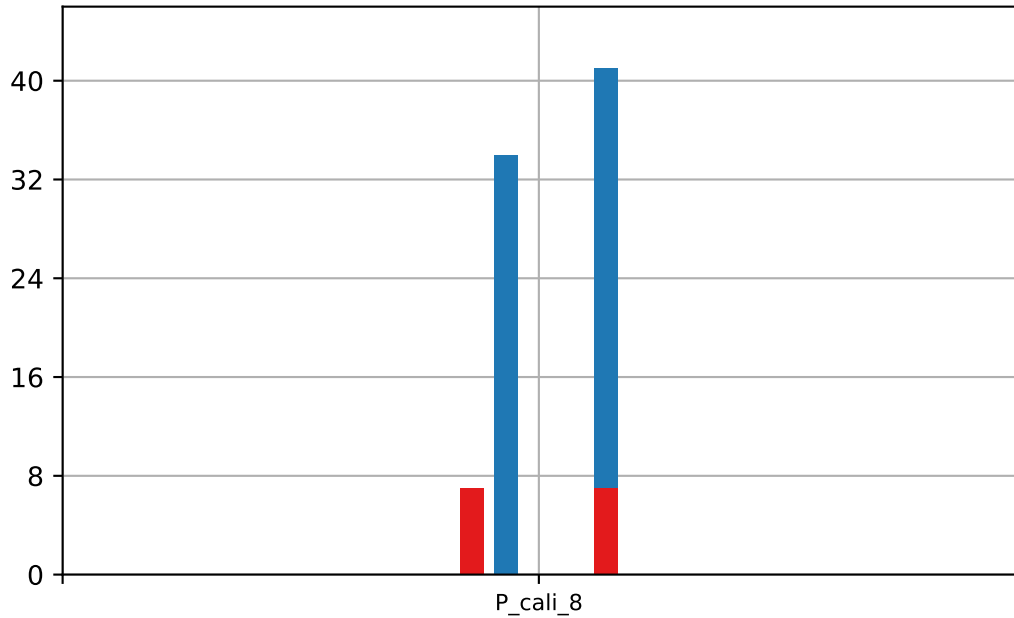




P_cali_8 GC content



Misassemblies

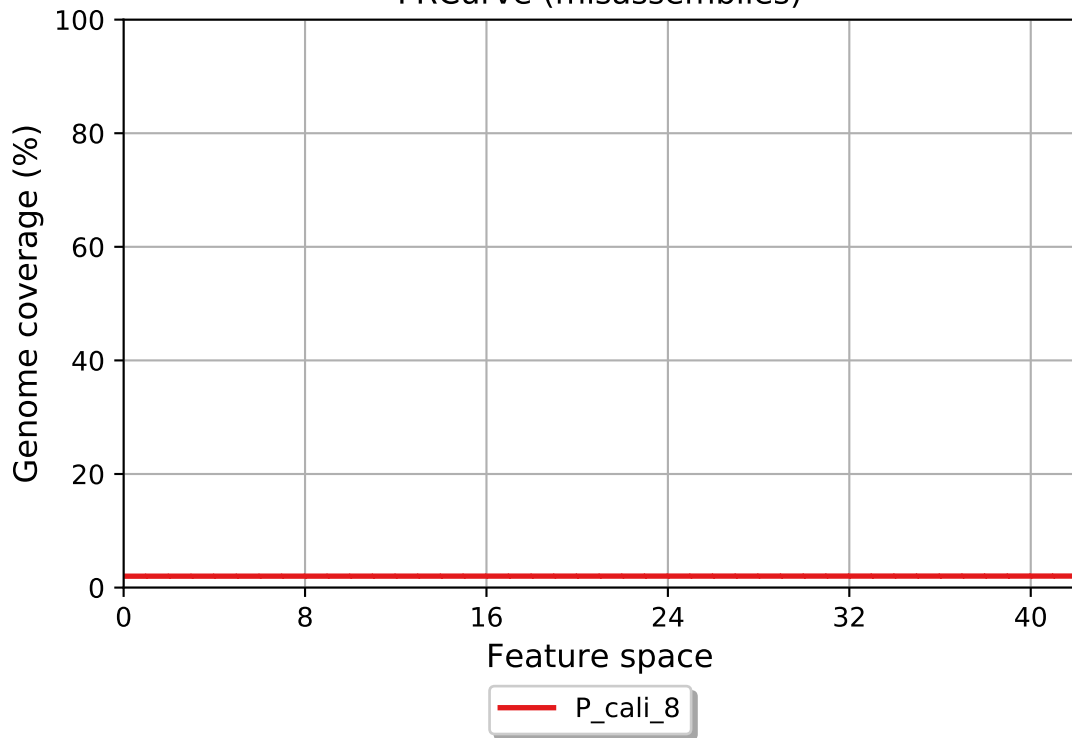


relocations

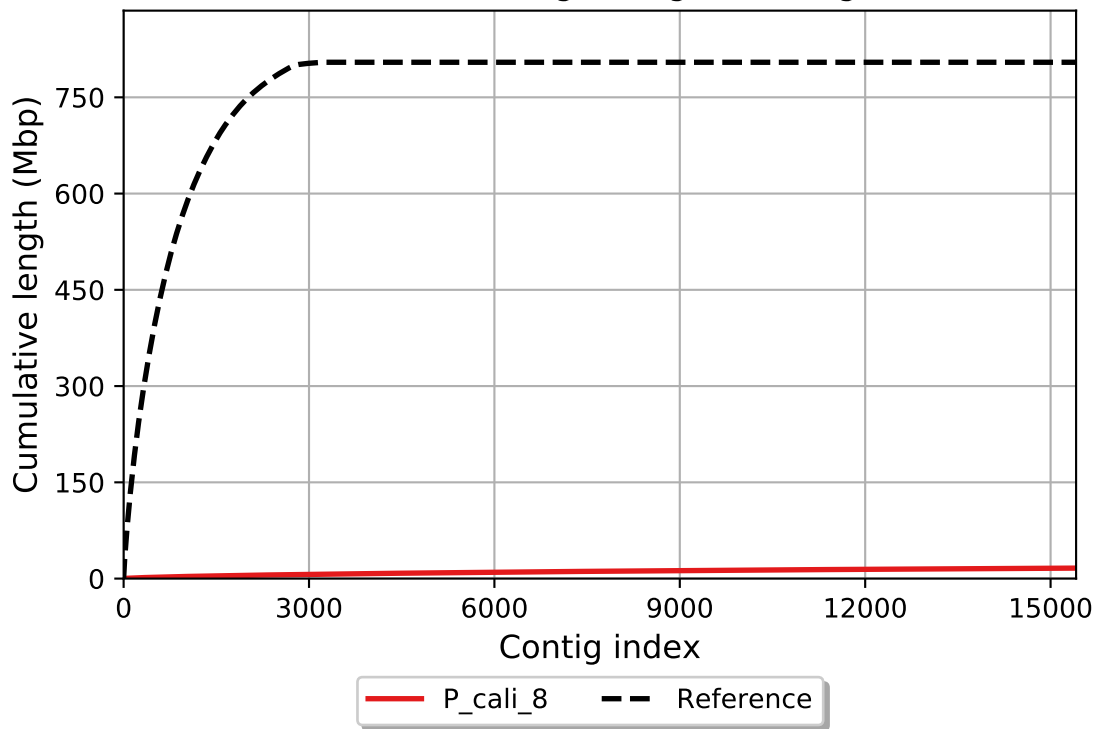


translocations

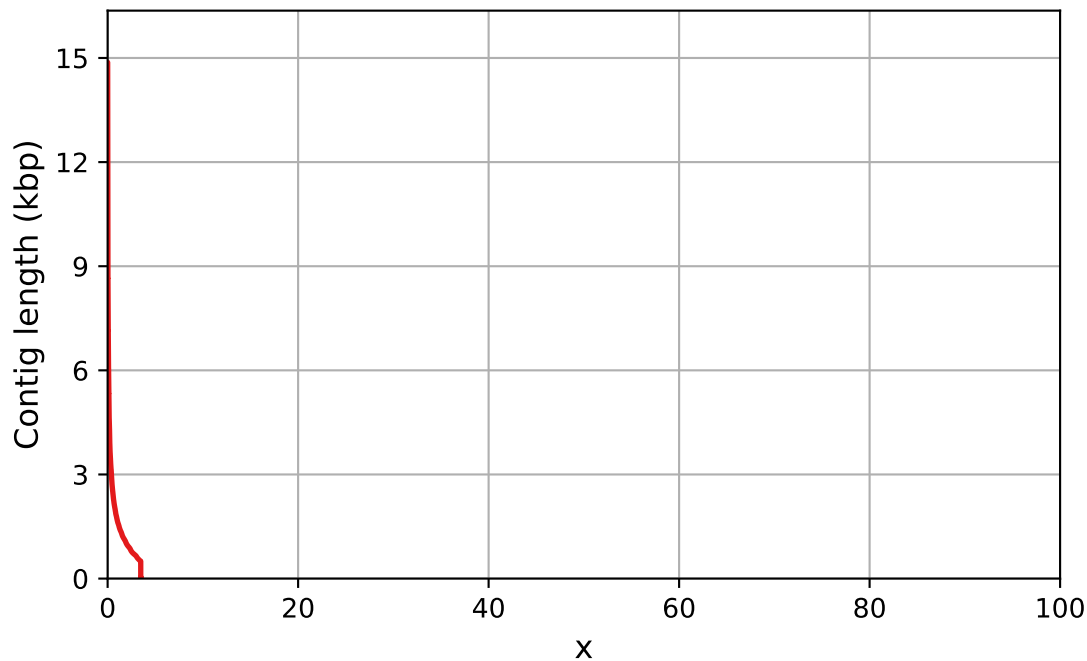
FRCurve (misassemblies)



Cumulative length (aligned contigs)

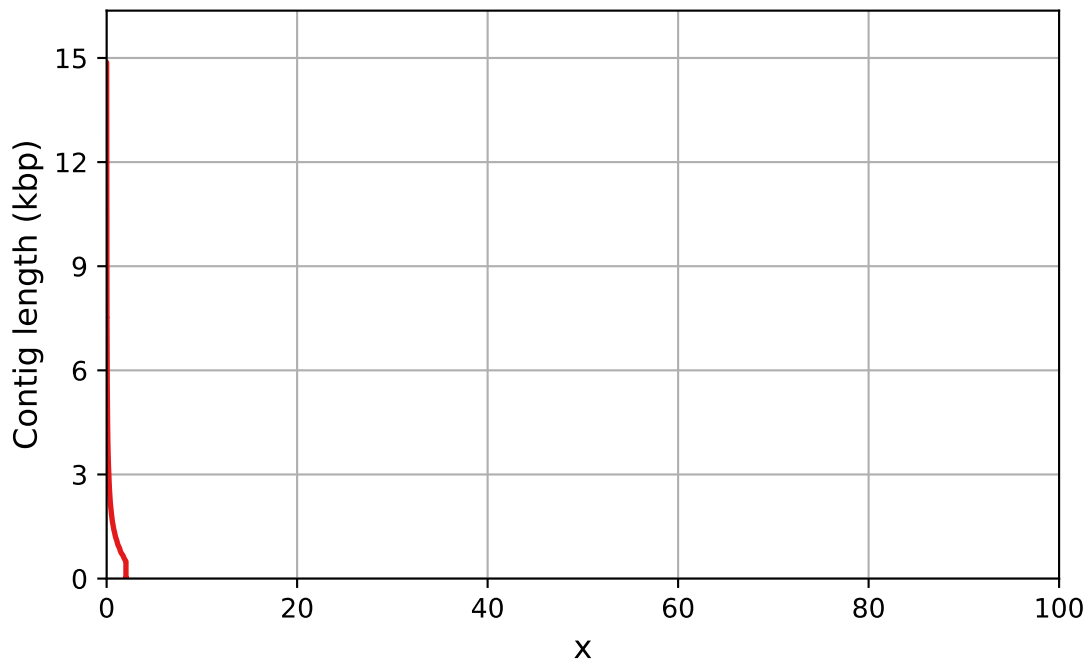


NAx



P_cali_8

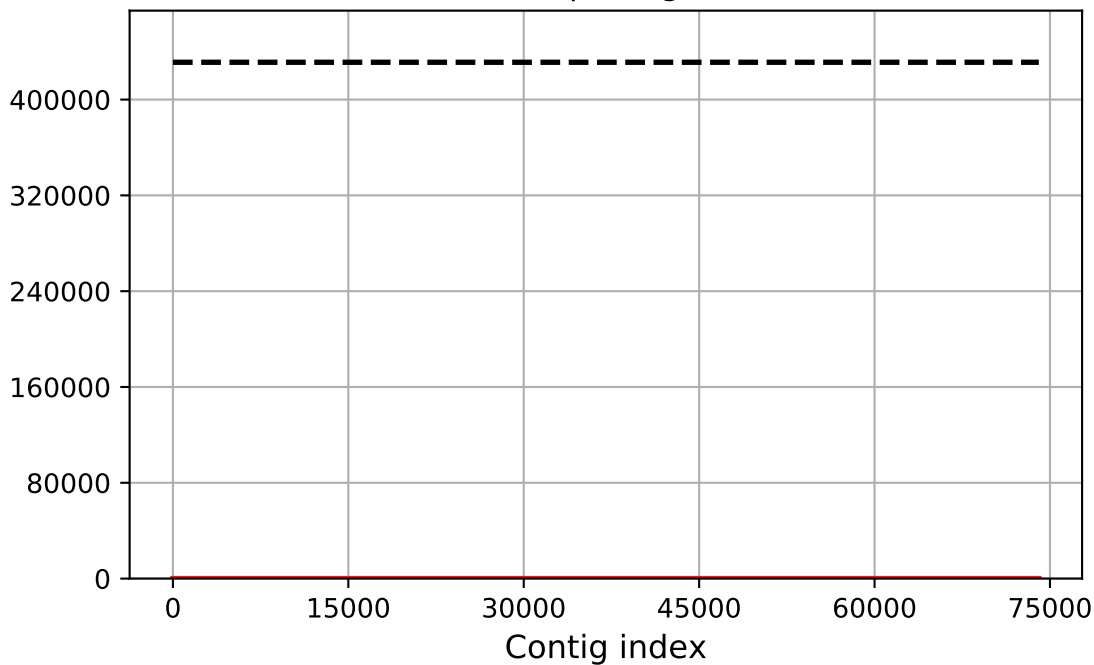
NGAx



P_cali_8

Cumulative # complete genomic features

Cumulative # complete genomic features



FRCurve (genomic features)

