

Report

	ESI403H
# contigs (>= 0 bp)	34
# contigs (>= 1000 bp)	20
# contigs (>= 5000 bp)	16
# contigs (>= 10000 bp)	15
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1364813
Total length (>= 1000 bp)	1360620
Total length (>= 5000 bp)	1350272
Total length (>= 10000 bp)	1341177
Total length (>= 25000 bp)	1281323
Total length (>= 50000 bp)	1014244
# contigs	23
Largest contig	910442
Total length	1362461
Reference length	1521208
GC (%)	28.26
Reference GC (%)	28.18
N50	910442
NG50	910442
N90	29808
NG90	-
auN	619229.7
auNG	554609.4
L50	1
LG50	1
L90	10
LG90	-
# misassemblies	10
# misassembled contigs	5
Misassembled contigs length	140010
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	1 + 9 part
Unaligned length	72536
Genome fraction (%)	83.085
Duplication ratio	1.019
# N's per 100 kbp	0.00
# mismatches per 100 kbp	541.99
# indels per 100 kbp	35.63
# genomic features	1339 + 43 part
Largest alignment	909795
Total aligned length	1288209
NA50	909795
NGA50	909795
NA90	15315
NGA90	-
auNA	614837.8
auNGA	550675.8
LA50	1
LGA50	1
LA90	14
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

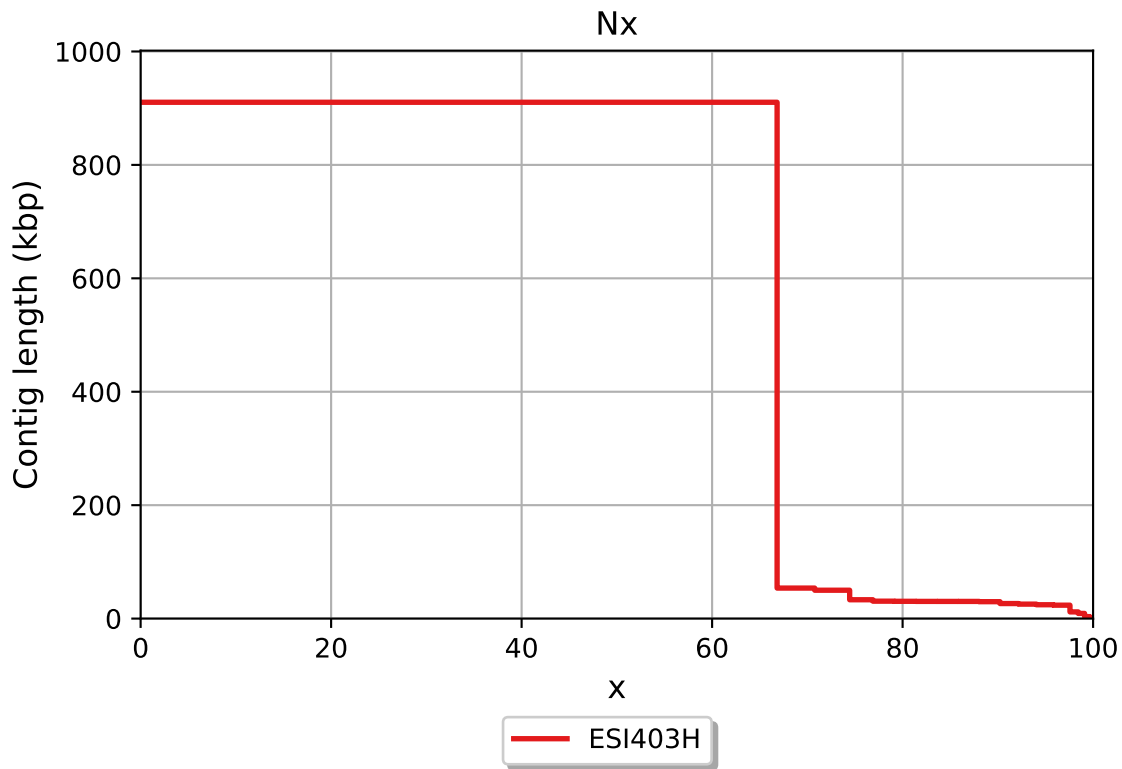
	ESI403H
# misassemblies	10
# contig misassemblies	10
# c. relocations	3
# c. translocations	7
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	5
Misassembled contigs length	140010
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	6982
# indels	459
# indels (<= 5 bp)	398
# indels (> 5 bp)	61
Indels length	2803

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

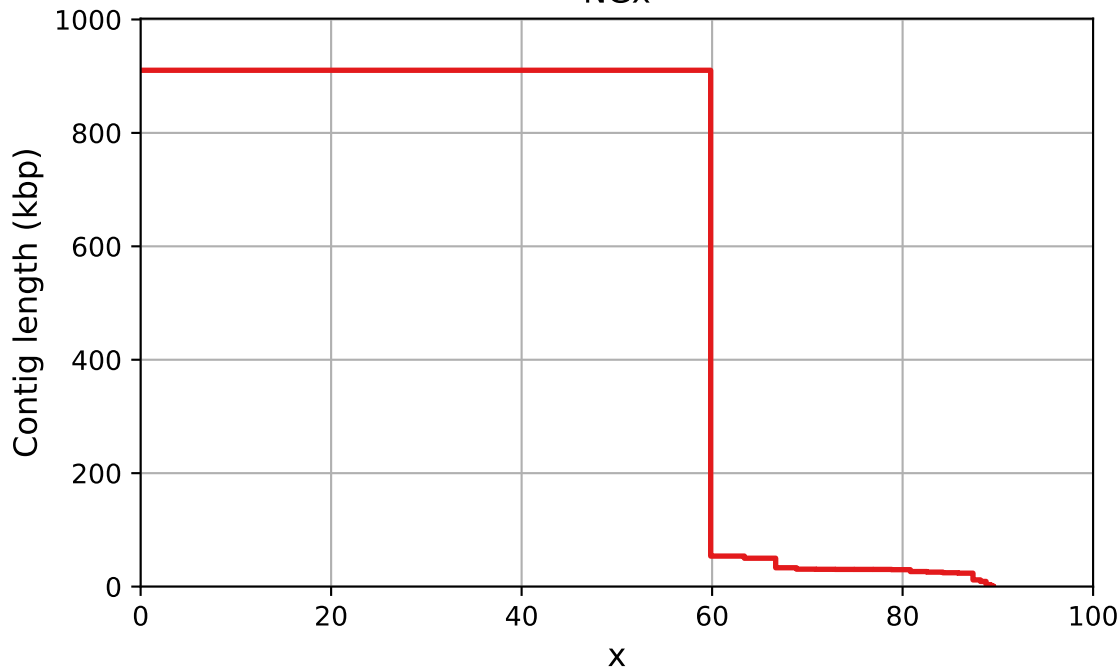
## Unaligned report

	ESI403H
# fully unaligned contigs	1
Fully unaligned length	9095
# partially unaligned contigs	9
Partially unaligned length	63441
# N's	0

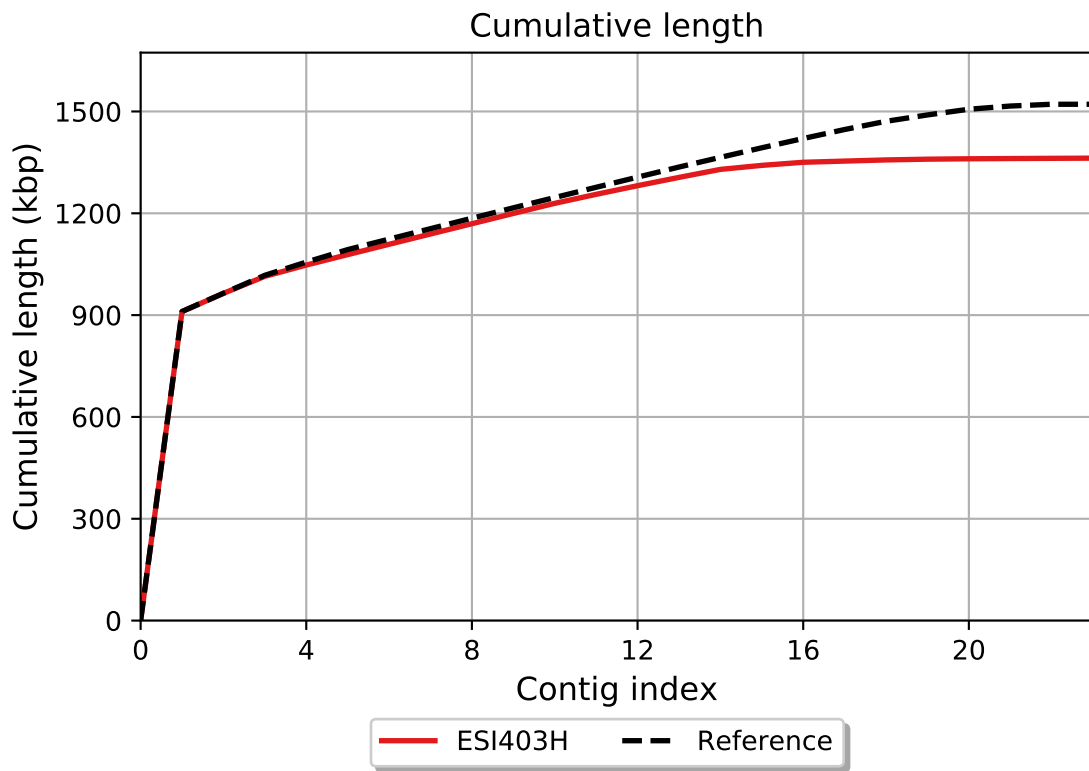
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



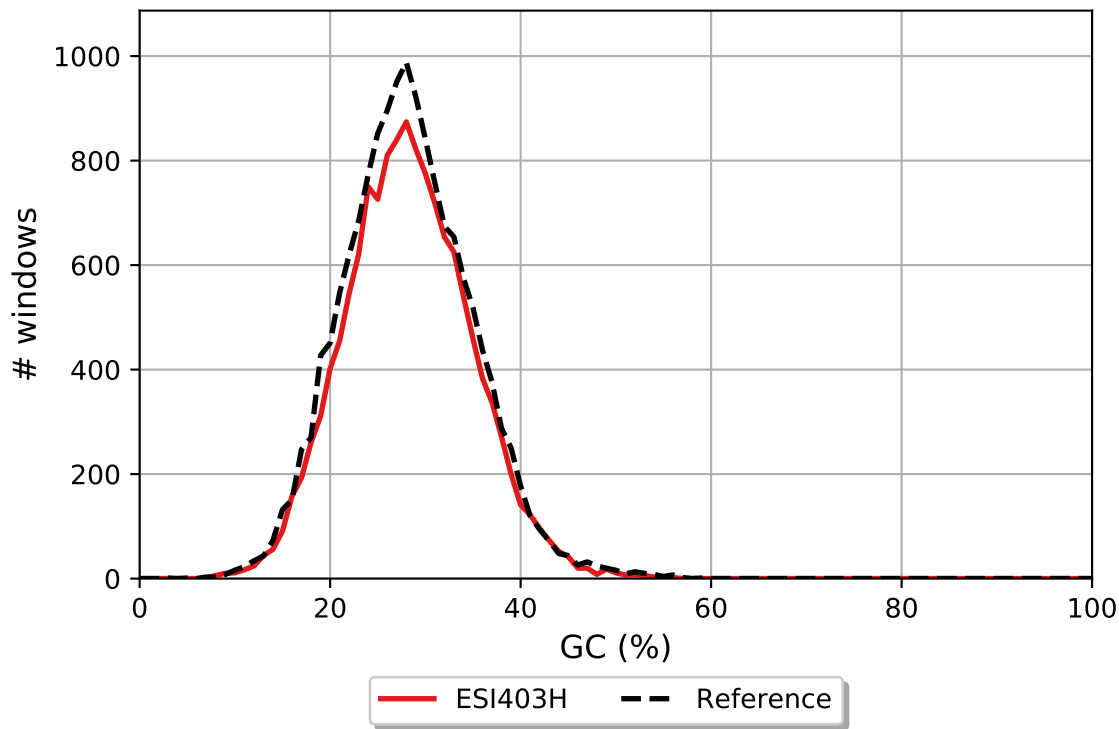
NGx



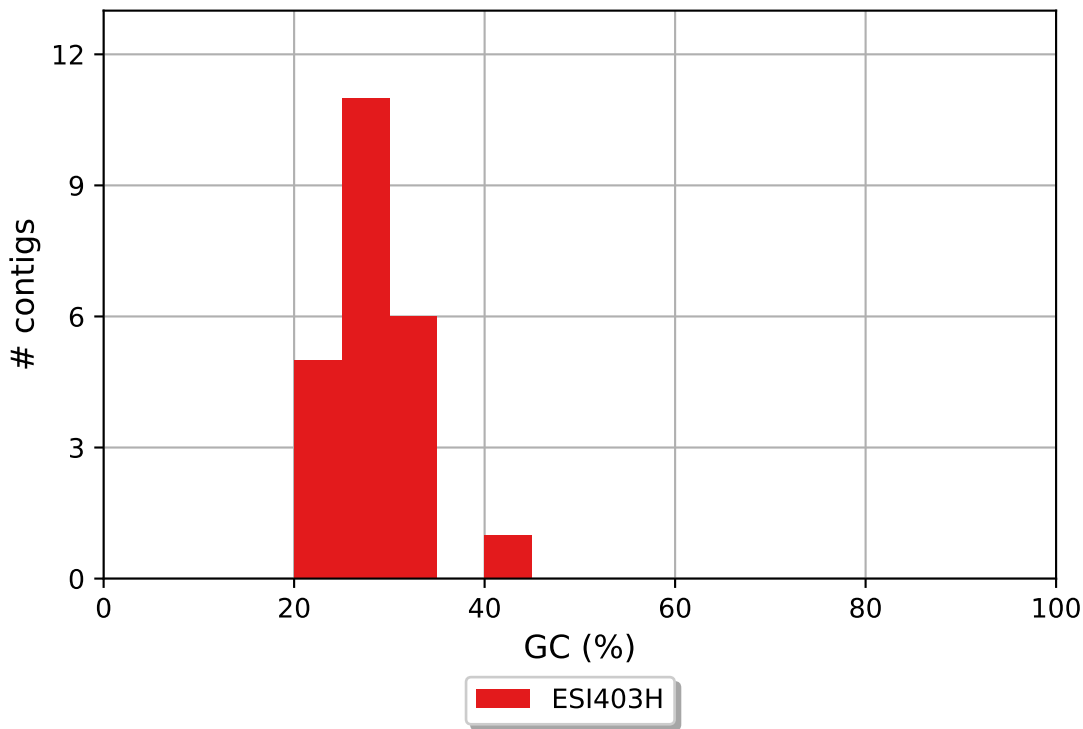
ESI403H



## GC content

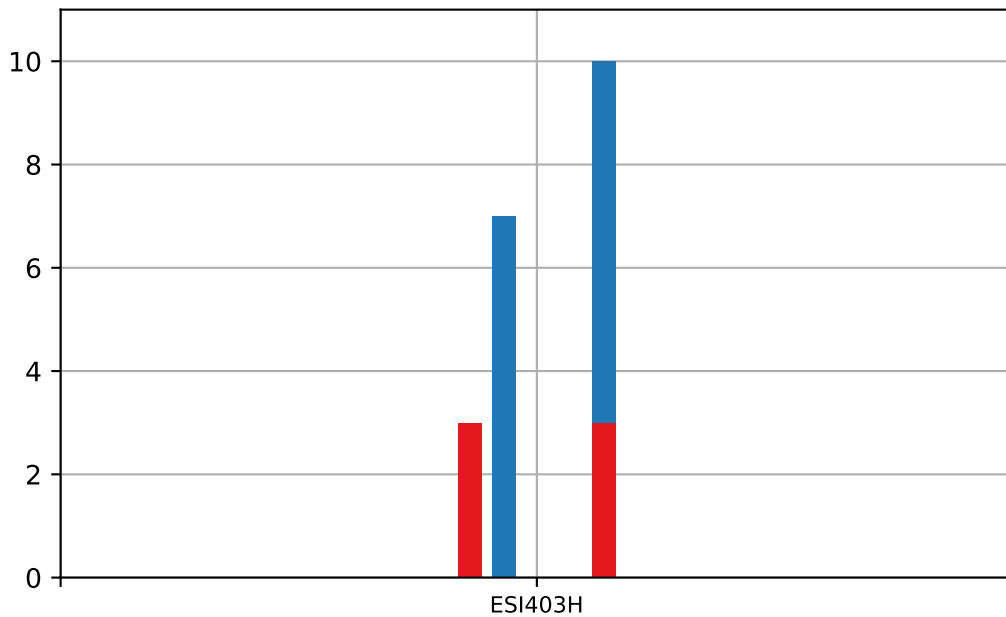


ESI403H GC content





## Misassemblies

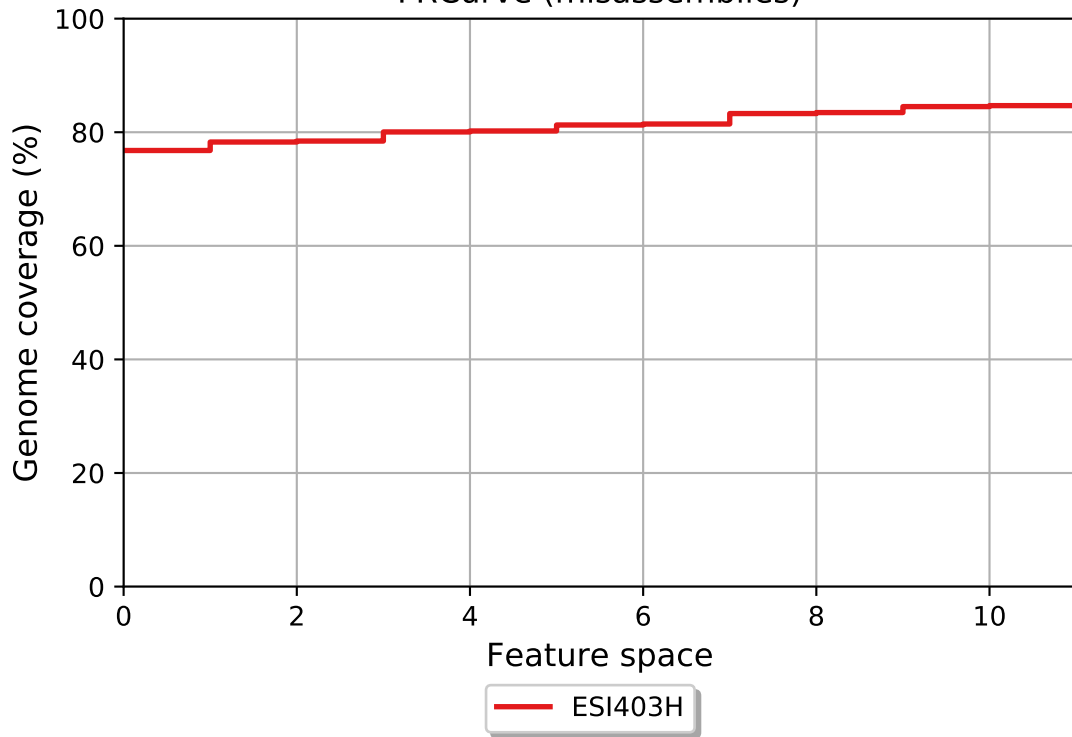


# relocations

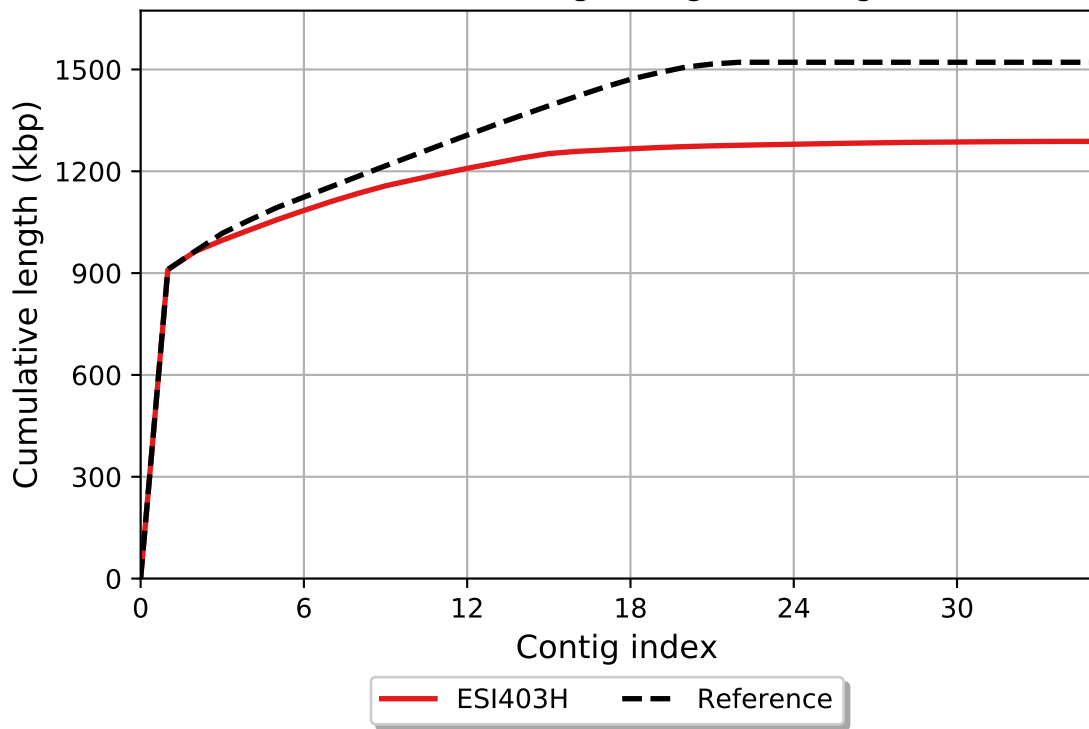


# translocations

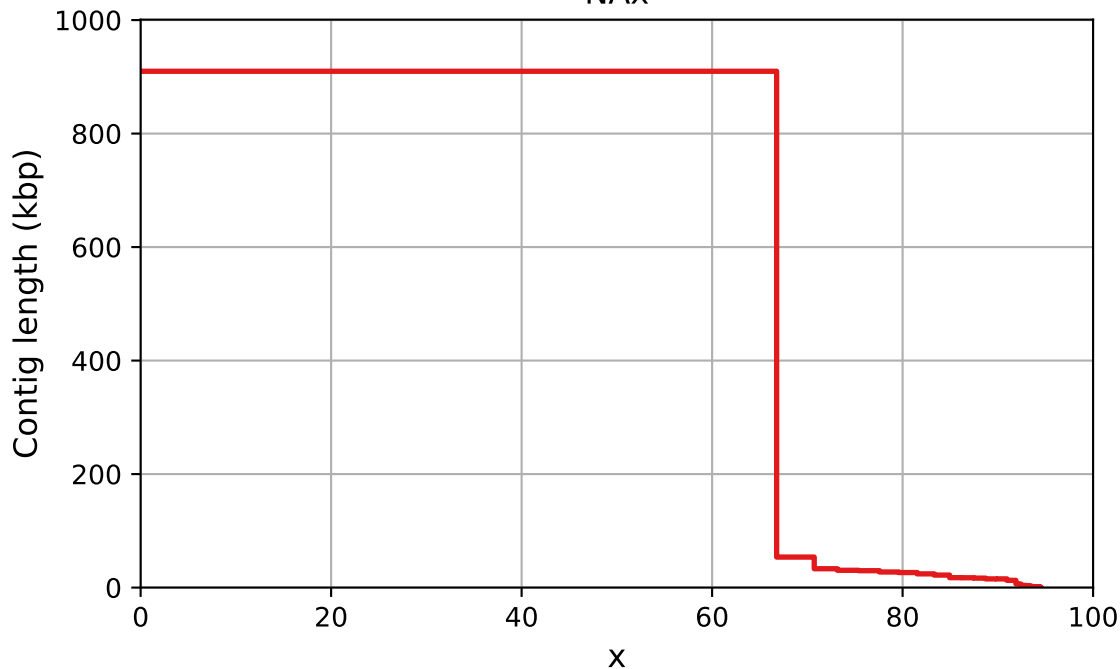
FRCurve (misassemblies)



Cumulative length (aligned contigs)

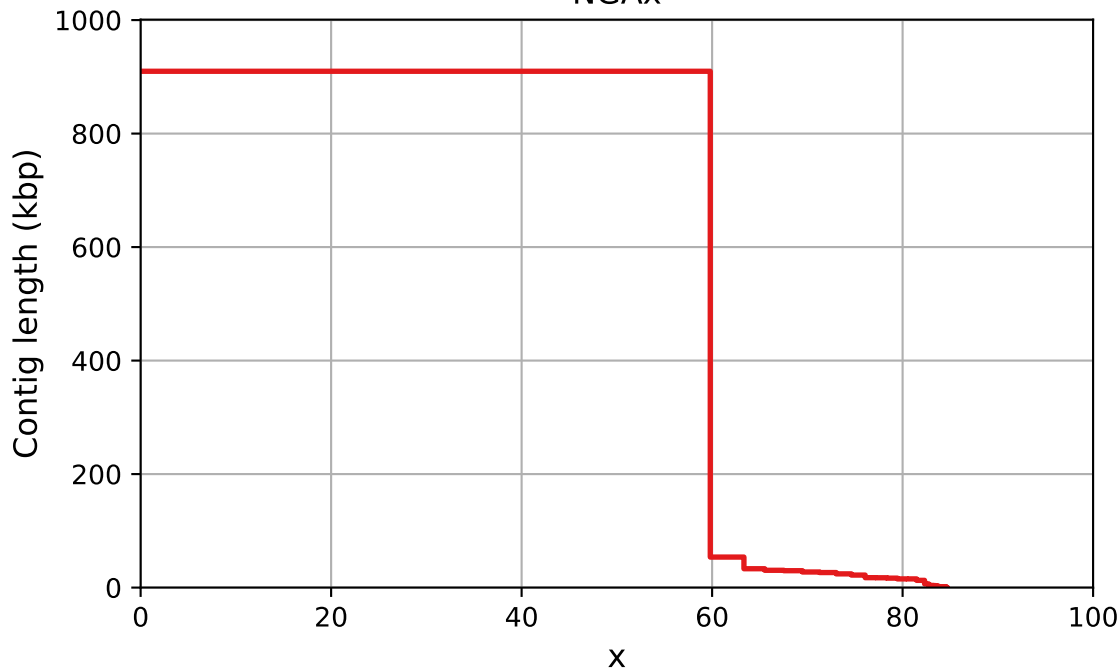


NAx



ESI403H

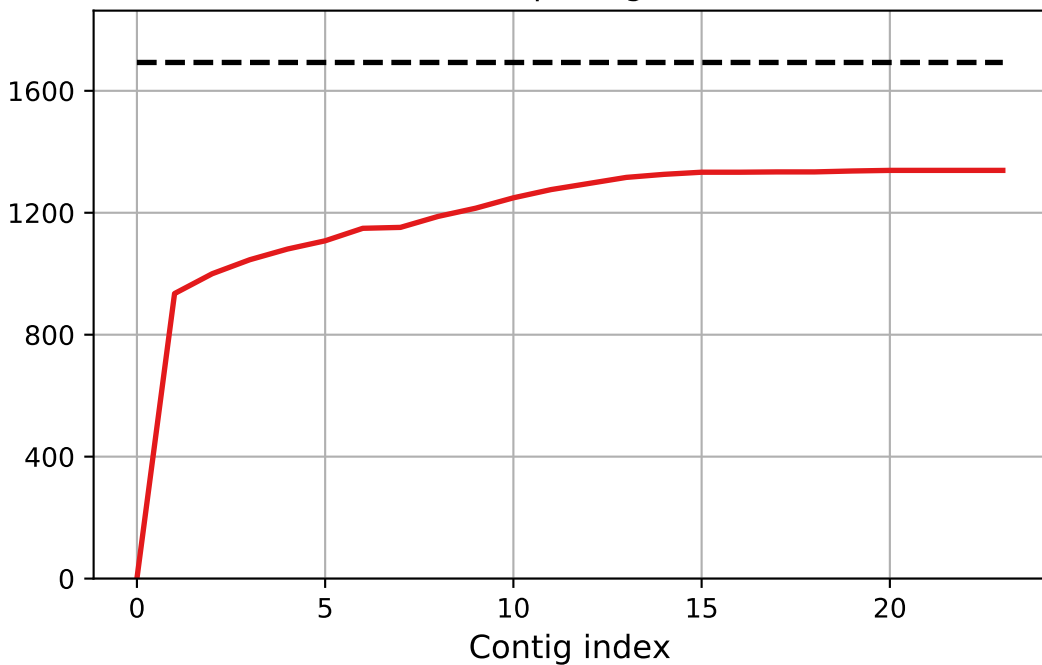
NGAx



ESI403H

Cumulative # complete genomic features

Cumulative # complete genomic features



ESI403H    Reference

FRCurve (genomic features)

