

Report

	ESI26H
# contigs (>= 0 bp)	64
# contigs (>= 1000 bp)	19
# contigs (>= 5000 bp)	12
# contigs (>= 10000 bp)	12
# contigs (>= 25000 bp)	9
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1276481
Total length (>= 1000 bp)	1261812
Total length (>= 5000 bp)	1250609
Total length (>= 10000 bp)	1250609
Total length (>= 25000 bp)	1195814
Total length (>= 50000 bp)	1022869
# contigs	26
Largest contig	910396
Total length	1266427
Reference length	1521208
GC (%)	28.49
Reference GC (%)	28.18
N50	910396
NG50	910396
N90	26979
NG90	-
auN	664340.0
auNG	553072.4
L50	1
LG50	1
L90	7
LG90	-
# misassemblies	14
# misassembled contigs	6
Misassembled contigs length	157202
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	3 + 5 part
Unaligned length	140199
Genome fraction (%)	72.915
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	488.39
# indels per 100 kbp	31.81
# genomic features	1159 + 41 part
Largest alignment	910396
Total aligned length	1125333
NA50	910396
NGA50	910396
NA90	-
NGA90	-
auNA	657497.0
auNGA	547375.5
LA50	1
LGA50	1
LA90	-
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

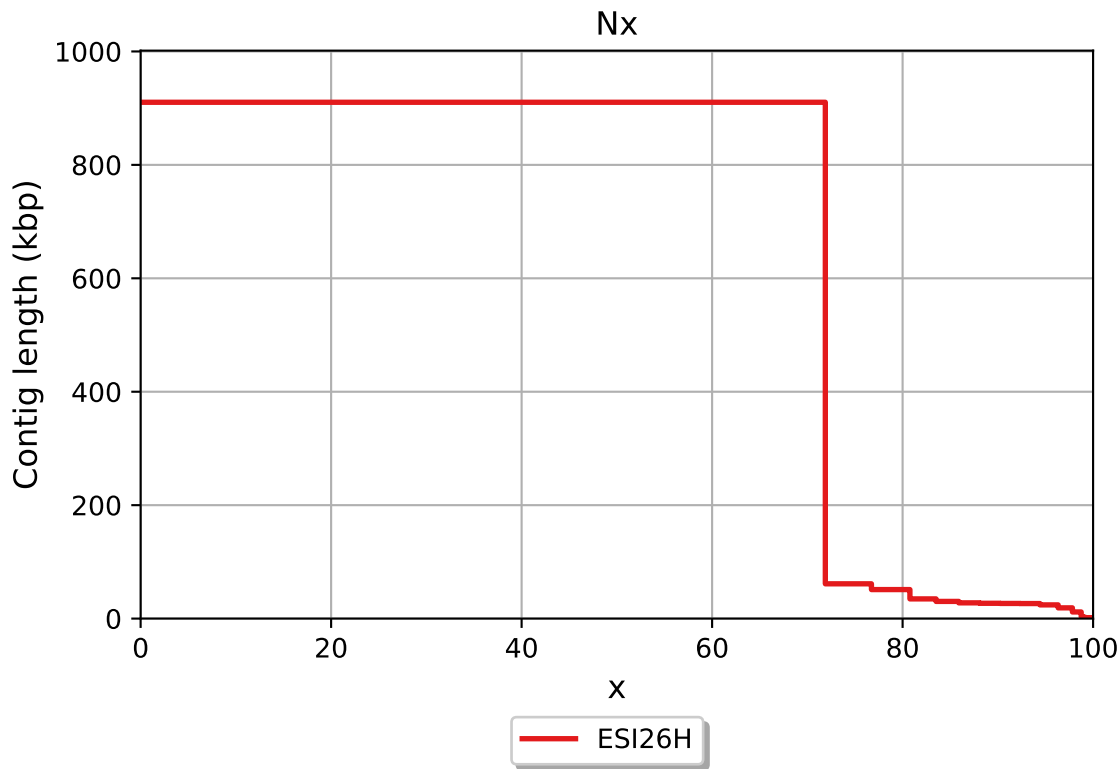
	ESI26H
# misassemblies	14
# contig misassemblies	14
# c. relocations	4
# c. translocations	10
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	6
Misassembled contigs length	157202
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	5496
# indels	358
# indels (<= 5 bp)	320
# indels (> 5 bp)	38
Indels length	1826

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).

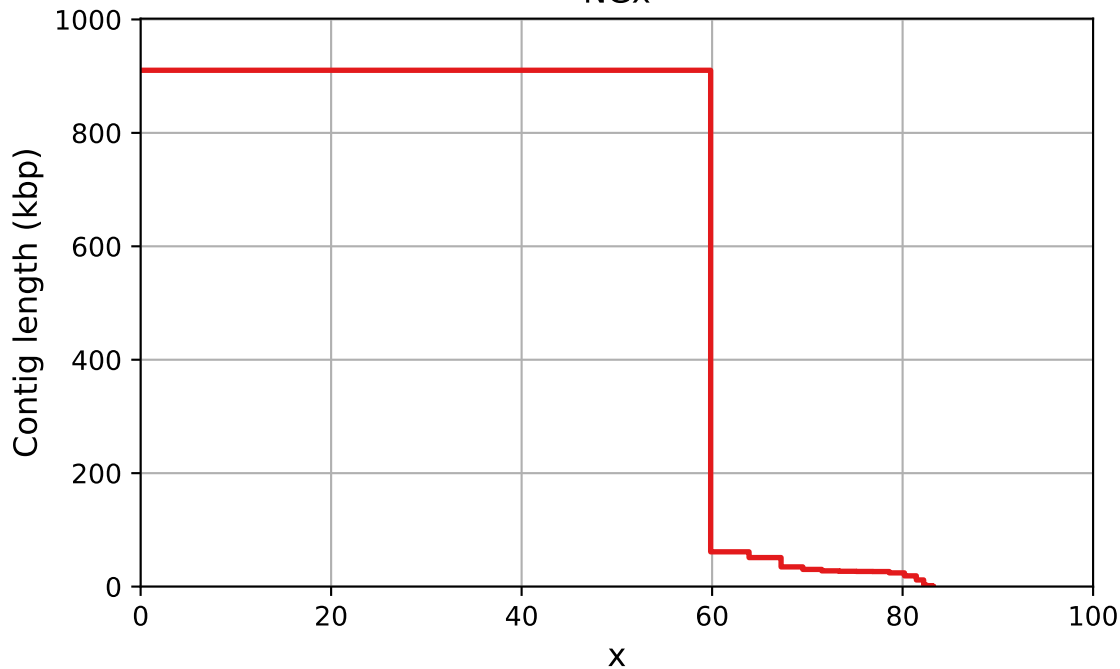
Unaligned report

	ESI26H
# fully unaligned contigs	3
Fully unaligned length	55532
# partially unaligned contigs	5
Partially unaligned length	84667
# N's	0

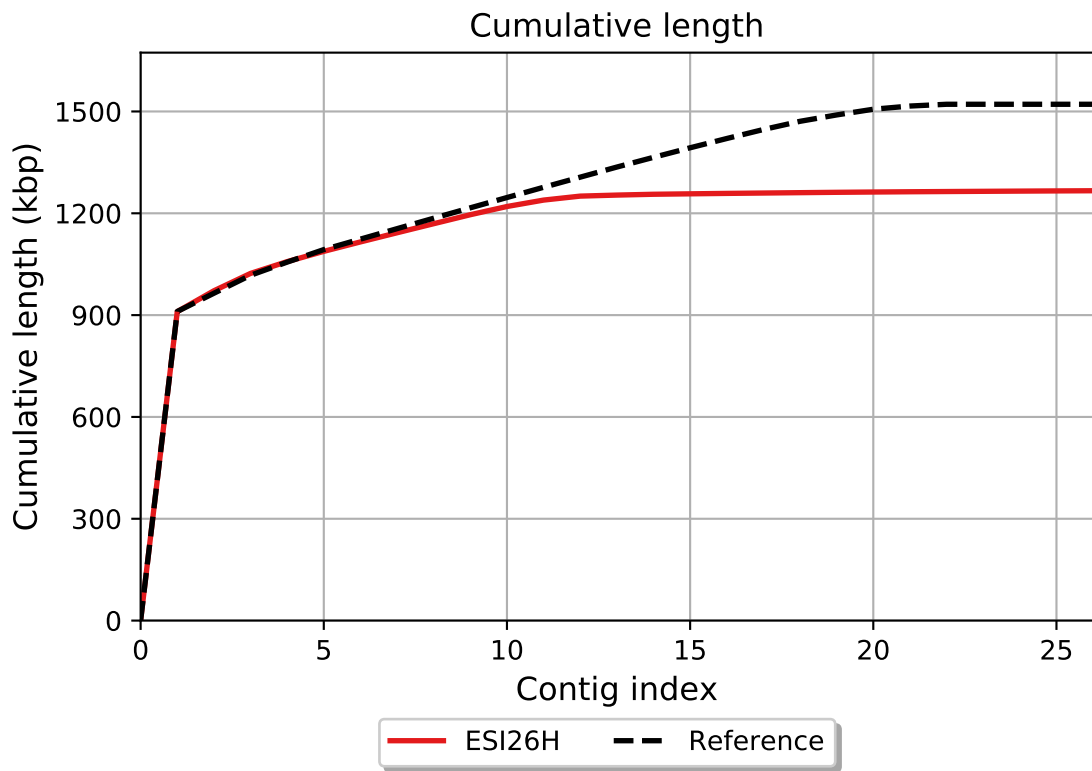
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



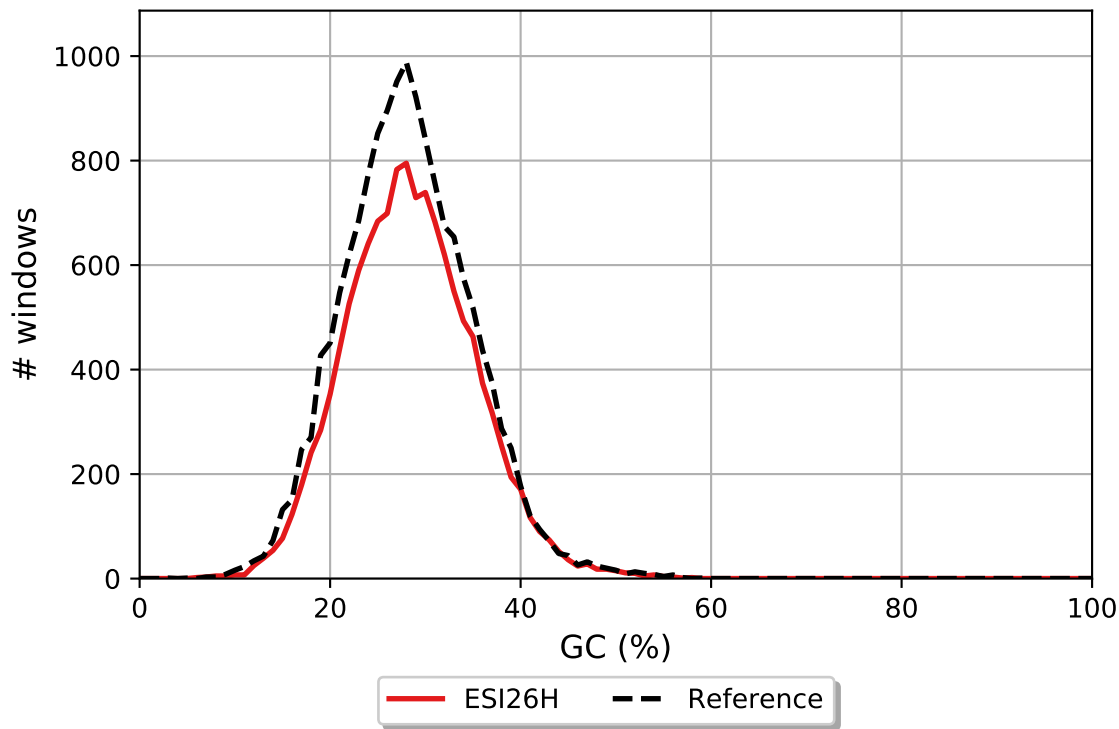
NGx



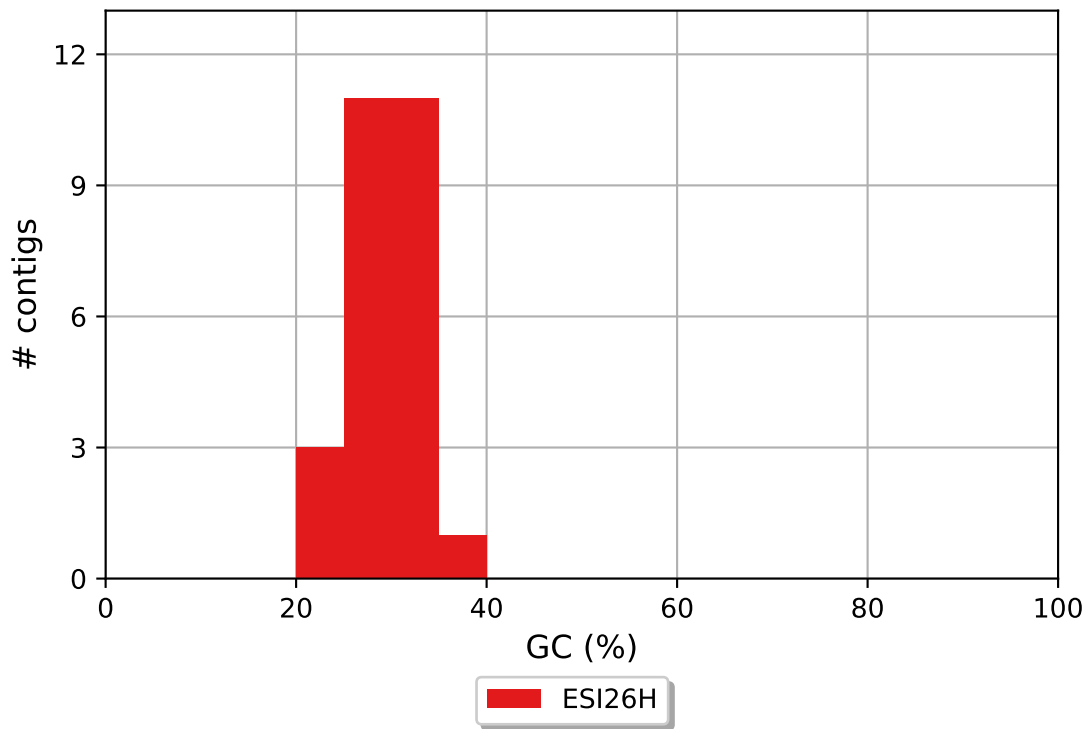
ESI26H



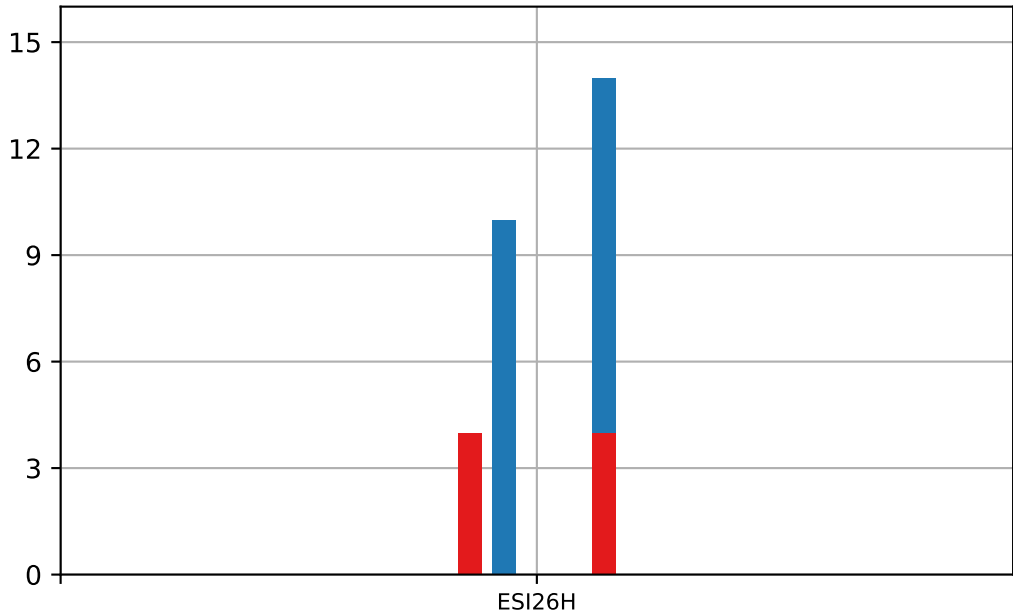
GC content



ESI26H GC content



Misassemblies

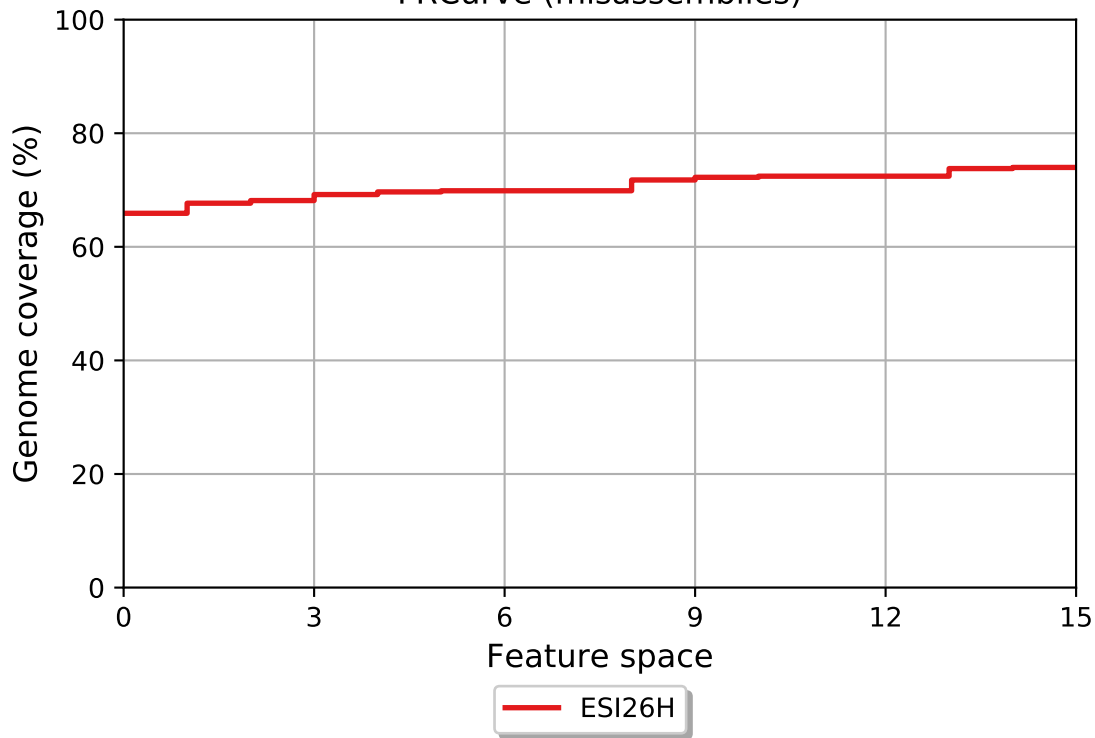


relocations

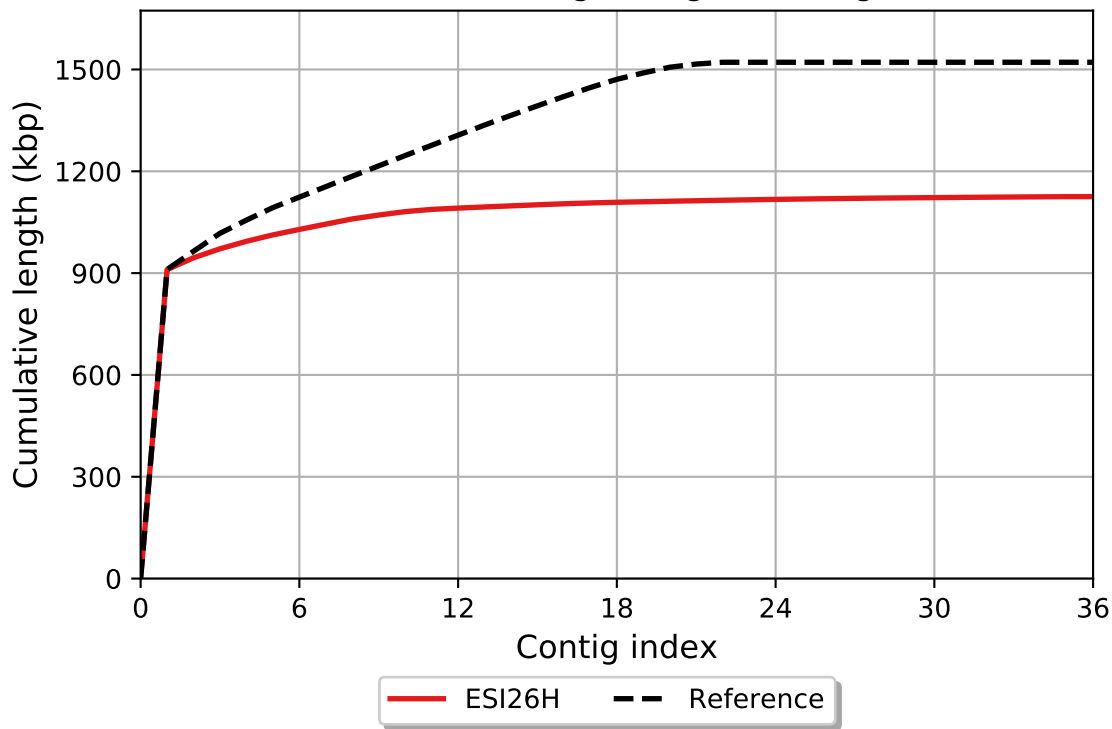


translocations

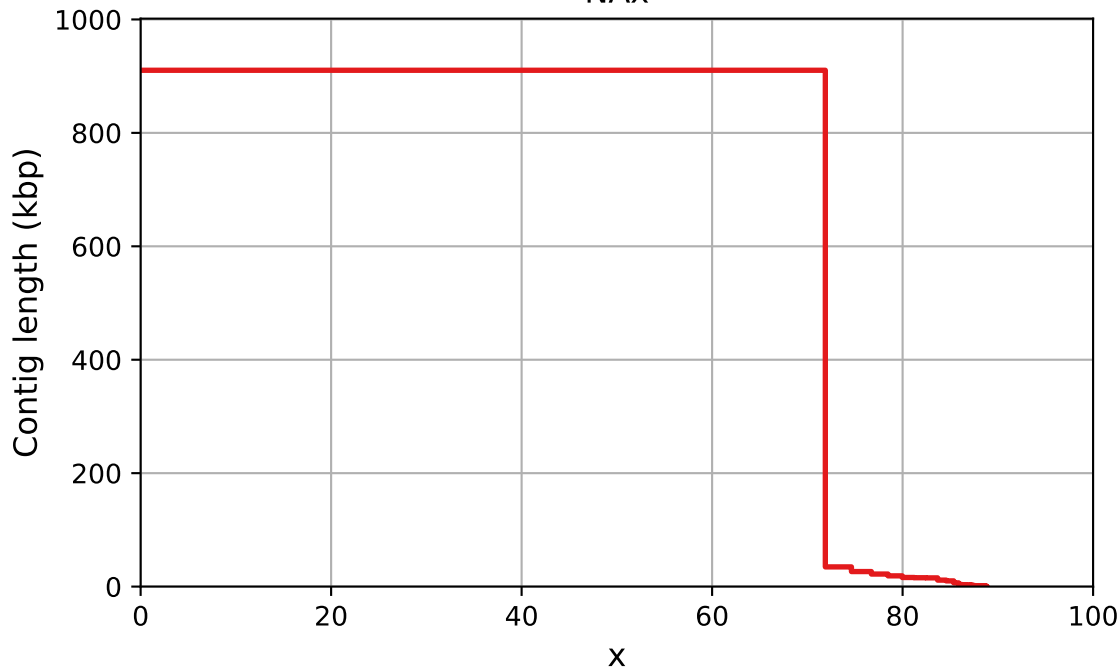
FRCurve (misassemblies)



Cumulative length (aligned contigs)

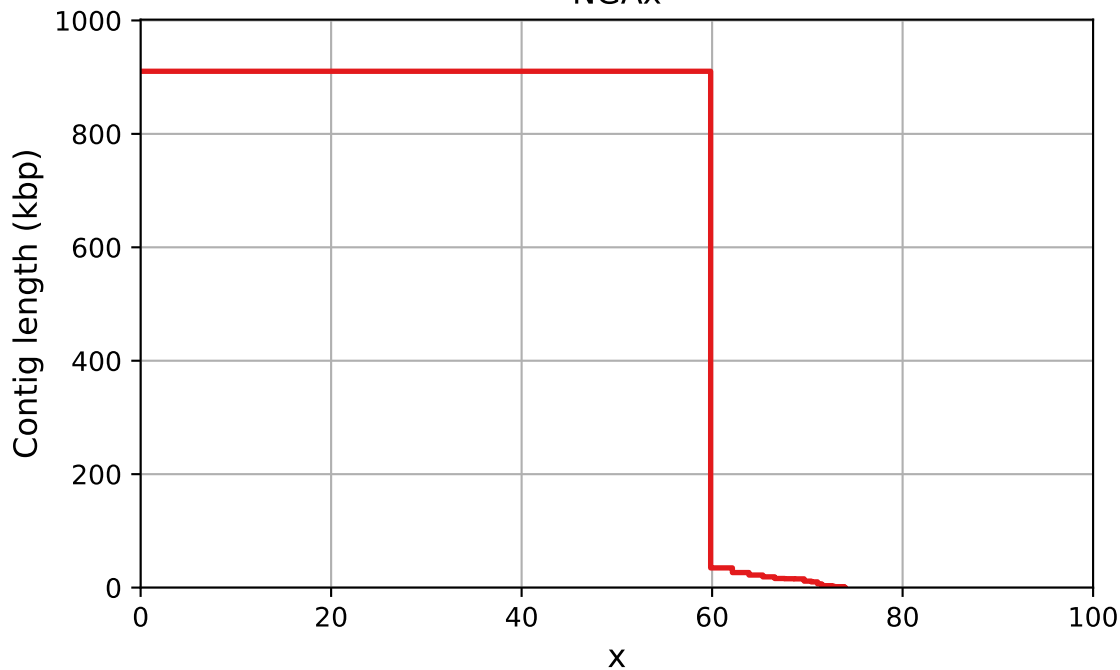


NAx

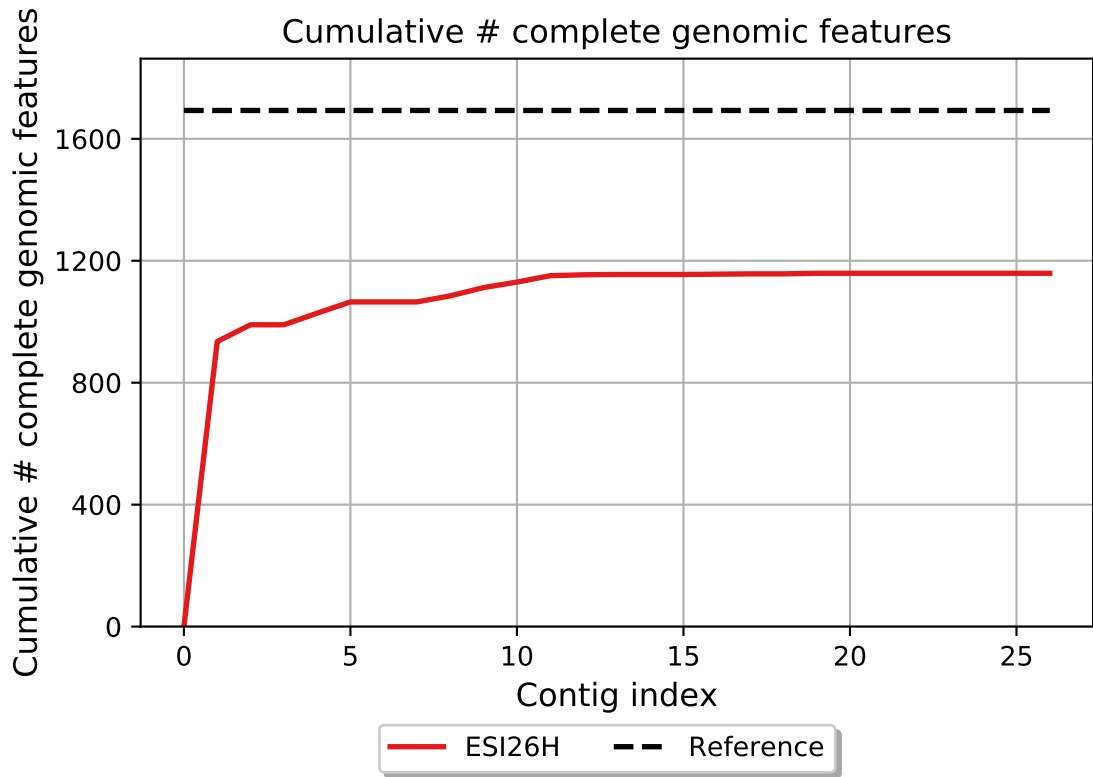


ESI26H

NGAx



ESI26H



FRCurve (genomic features)

