

Report

	ESI425H
# contigs (>= 0 bp)	21
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	15
# contigs (>= 10000 bp)	15
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	5
Total length (>= 0 bp)	1260215
Total length (>= 1000 bp)	1258483
Total length (>= 5000 bp)	1251728
Total length (>= 10000 bp)	1251728
Total length (>= 25000 bp)	1194982
Total length (>= 50000 bp)	995150
# contigs	18
Largest contig	434789
Total length	1259311
Reference length	1521208
GC (%)	28.24
Reference GC (%)	28.18
N50	342816
NG50	342816
N90	27761
NG90	-
auN	262972.6
auNG	217698.3
L50	2
LG50	2
L90	10
LG90	-
# misassemblies	12
# misassembled contigs	4
Misassembled contigs length	145460
# local misassemblies	13
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	1 + 10 part
Unaligned length	120708
Genome fraction (%)	73.825
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	813.35
# indels per 100 kbp	39.89
# genomic features	1159 + 40 part
Largest alignment	434789
Total aligned length	1138005
NA50	342816
NGA50	342816
NA90	1204
NGA90	-
auNA	257501.5
auNGA	213169.1
LA50	2
LGA50	2
LA90	25
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

	ESI425H
# misassemblies	12
# contig misassemblies	12
# c. relocations	3
# c. translocations	9
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	4
Misassembled contigs length	145460
# local misassemblies	13
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	9256
# indels	454
# indels (≤ 5 bp)	411
# indels (> 5 bp)	43
Indels length	1948

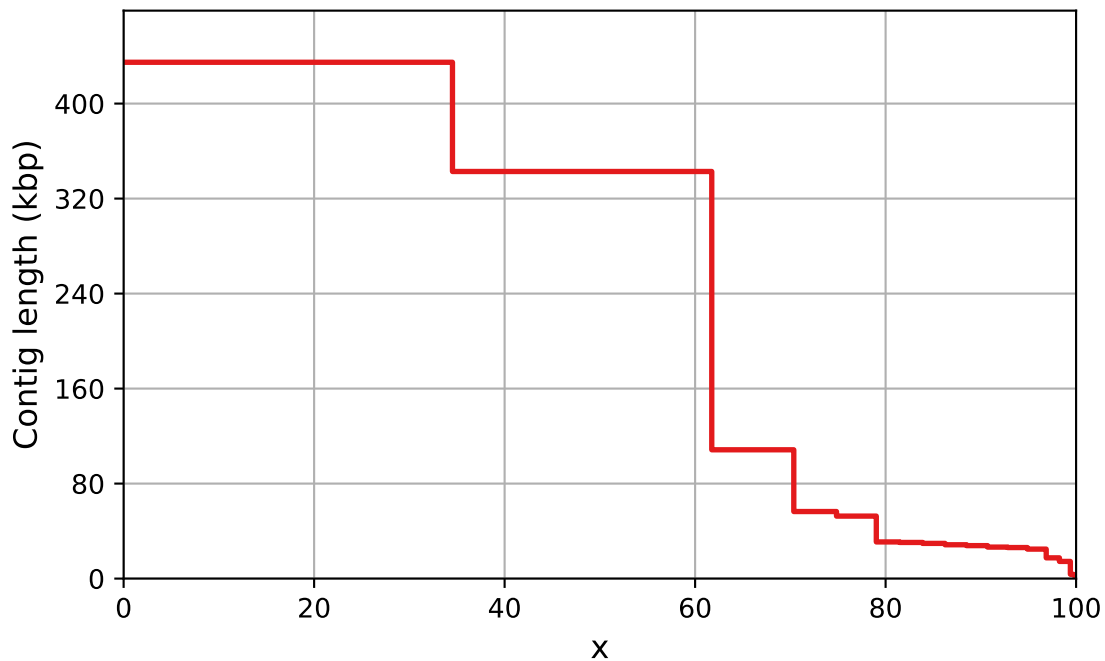
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	ESI425H
# fully unaligned contigs	1
Fully unaligned length	828
# partially unaligned contigs	10
Partially unaligned length	119880
# N's	0

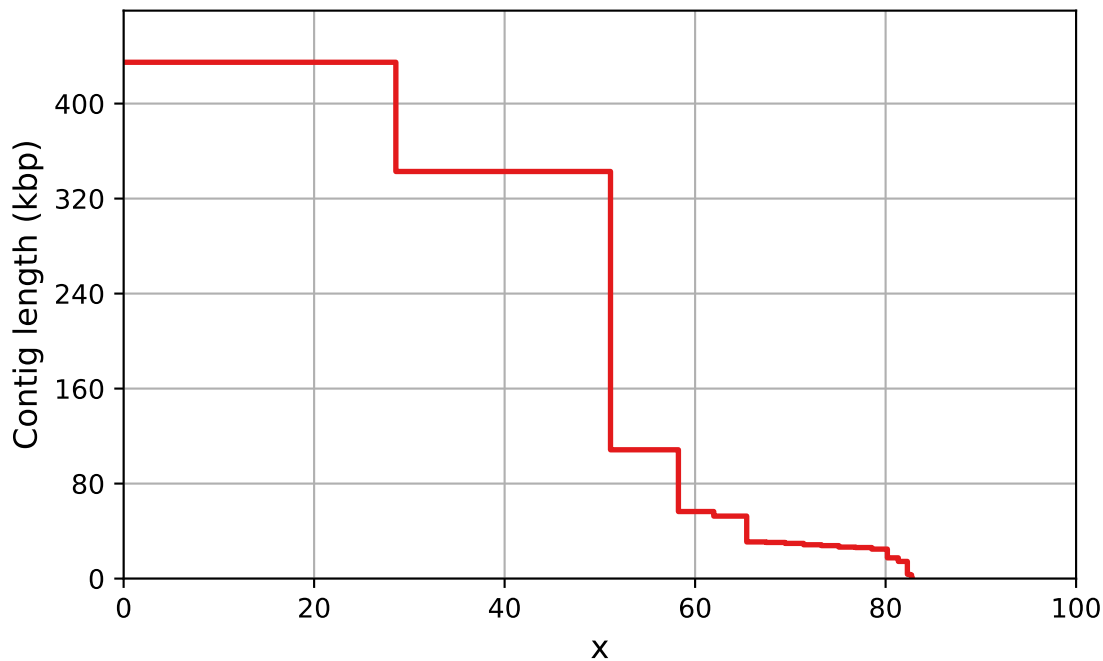
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



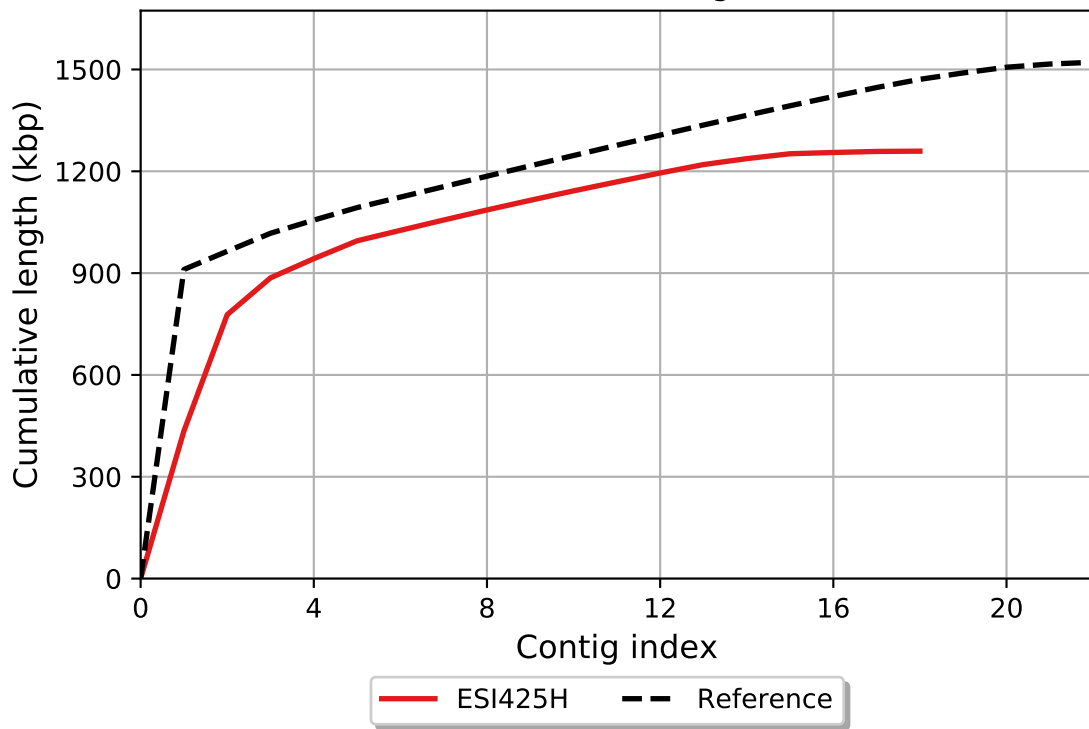
ESI425H

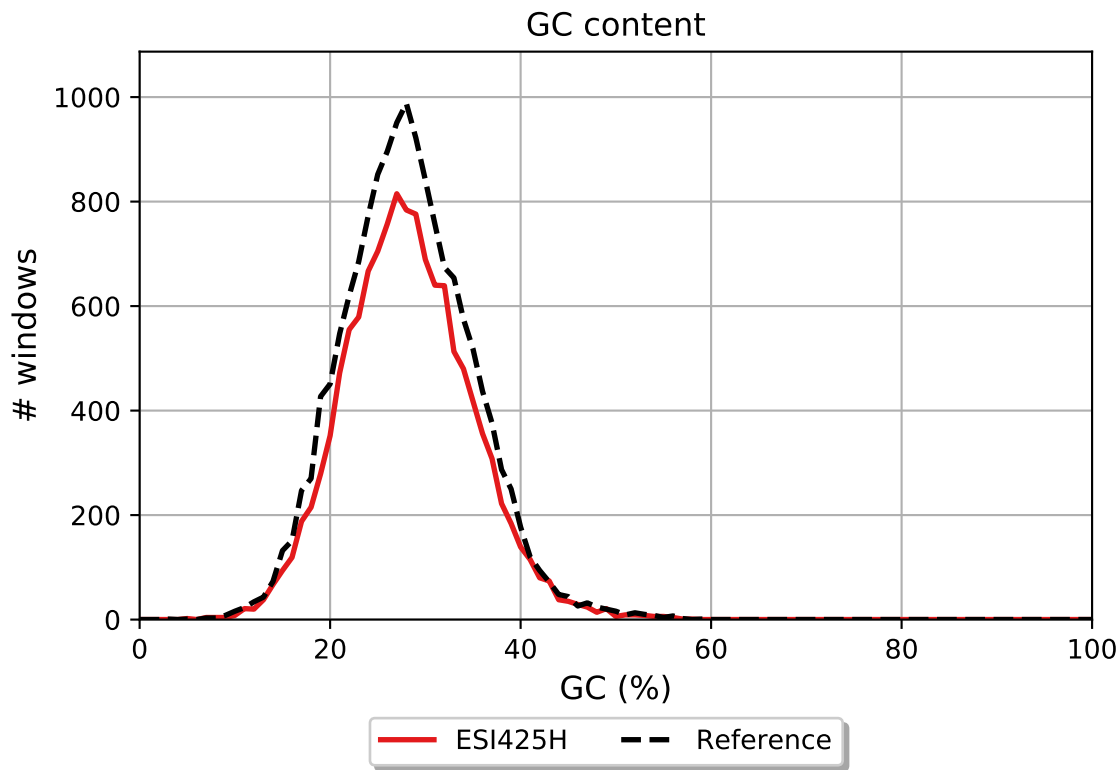
NGx



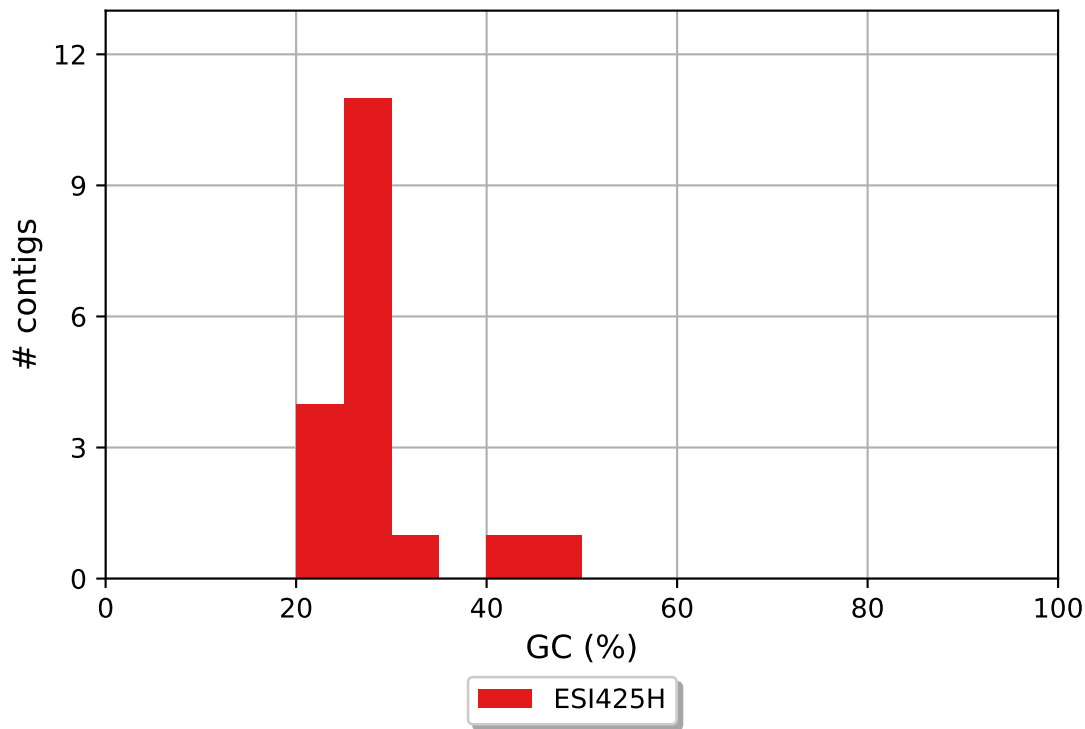
ESI425H

Cumulative length

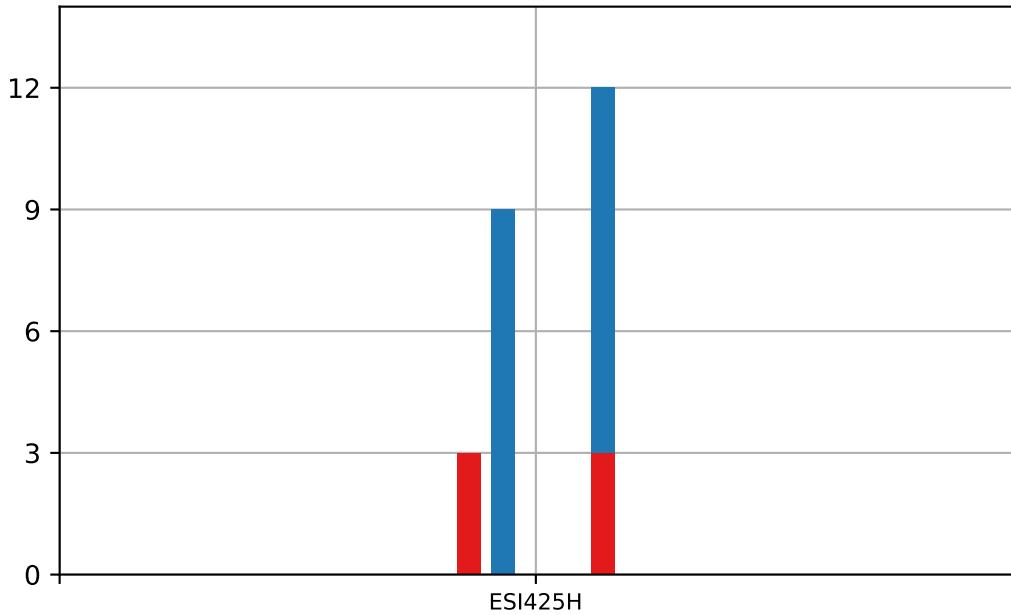




ESI425H GC content



Misassemblies

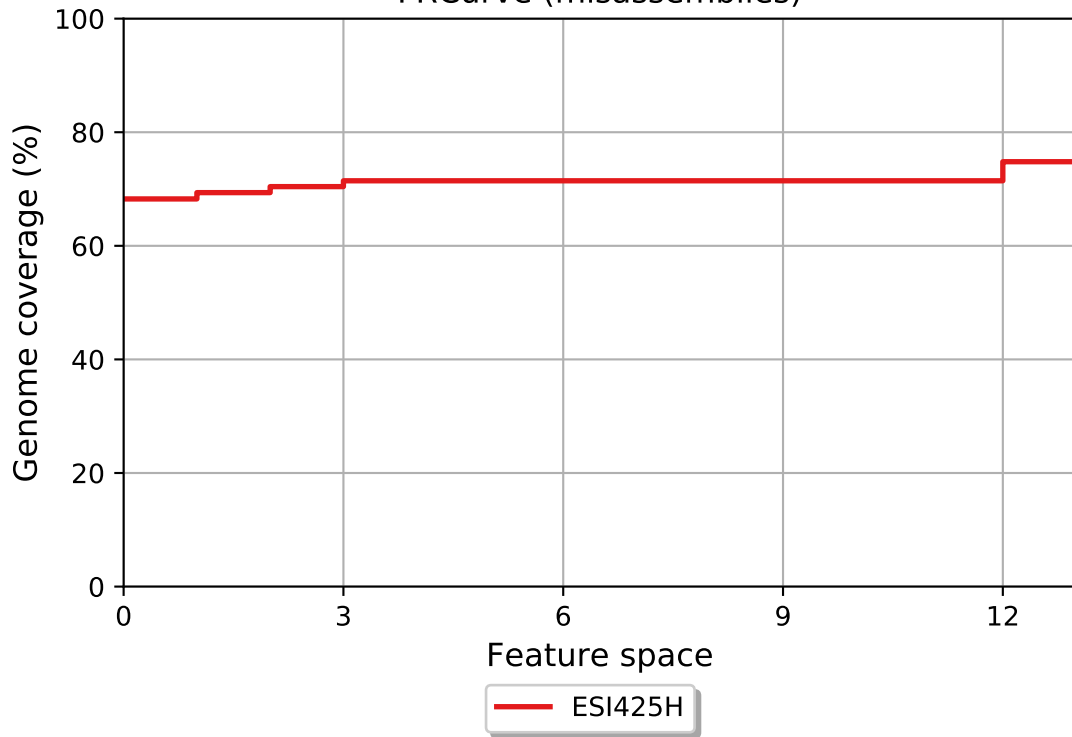


relocations

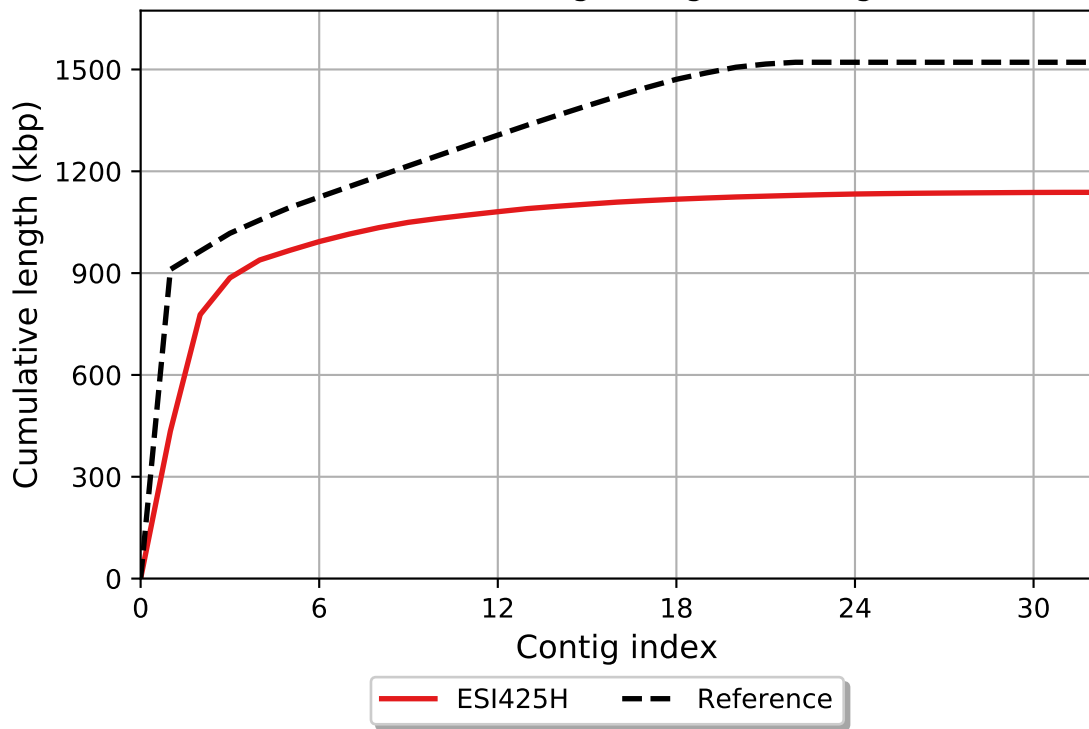


translocations

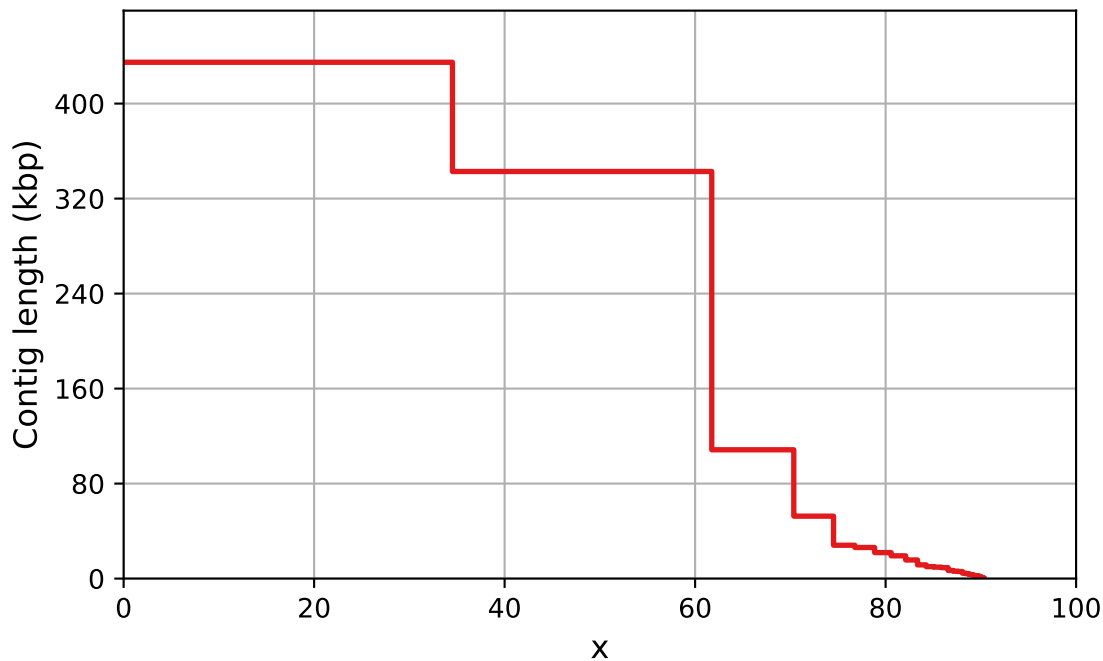
FRCurve (misassemblies)



Cumulative length (aligned contigs)

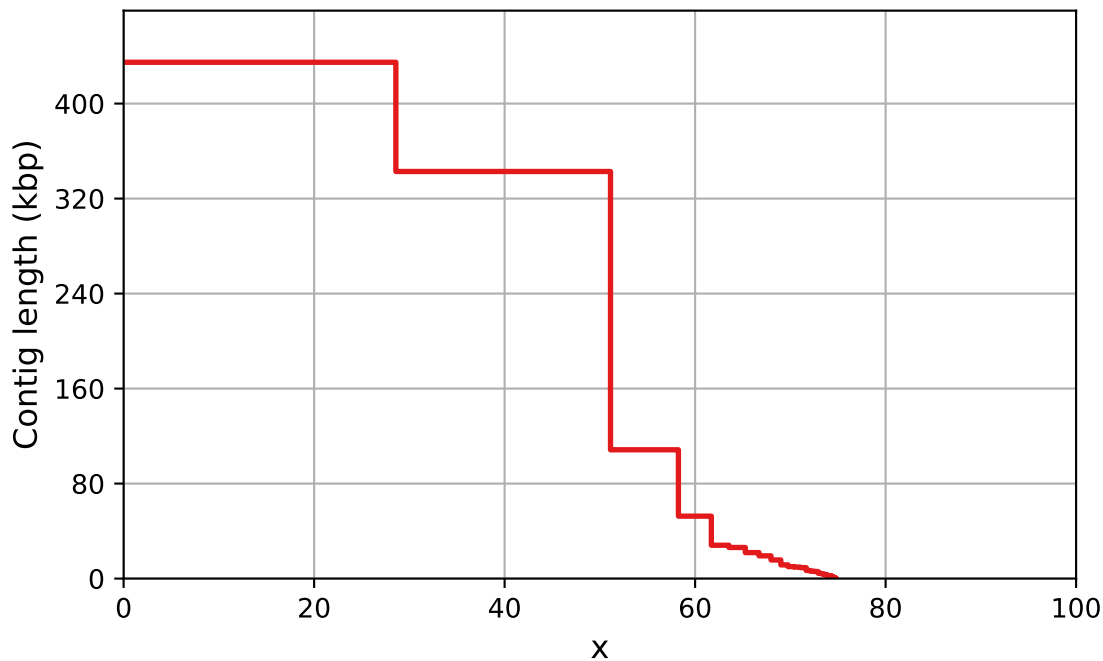


NAx



ESI425H

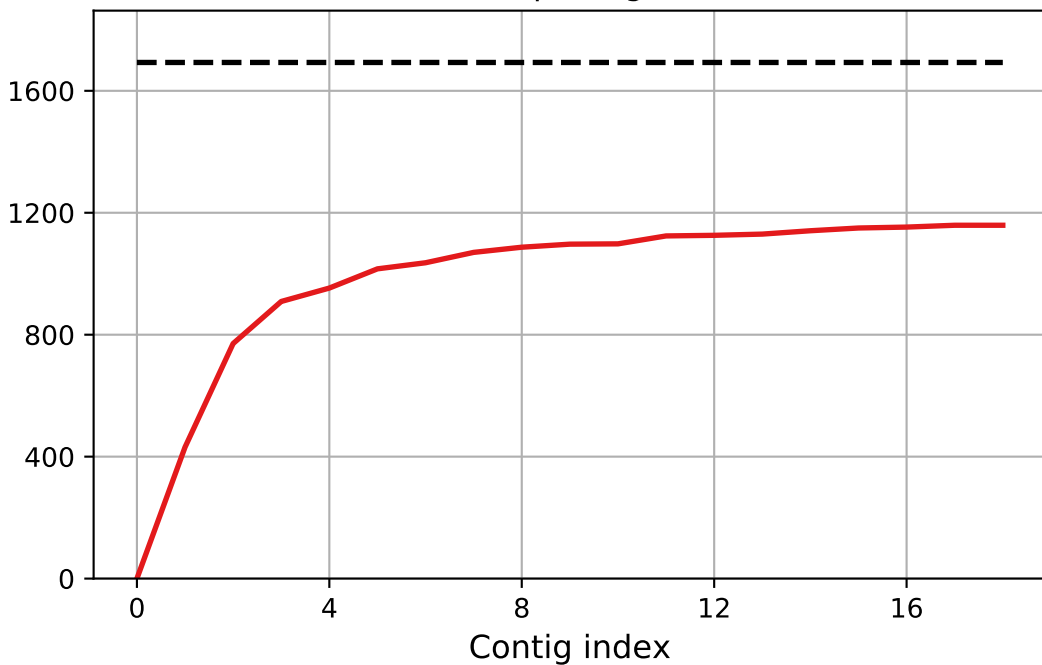
NGAx



ESI425H

Cumulative # complete genomic features

Cumulative # complete genomic features



ESI425H Reference

FRCurve (genomic features)

