Report

	Assembly_with_MEGAHIT_on_data_36_and_data_35
# contigs (>= 0 bp)	324
# contigs (>= 1000 bp)	276
Total length (>= 0 bp)	6558711
Total length (>= 1000 bp)	6537235
# contigs	292
Largest contig	166668
Total length	6548927
Reference length	4176973
GC (%)	45.80
Reference GC (%)	34.93
N50	44433
NG50	63437
N90	11471
NG90	38090
auN	51713.0
auNG	81079.0
L50	46
LG50	25
L90	151
LG90	58
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	289 + 3 part
Unaligned length	6548713
Genome fraction (%)	0.009
Duplication ratio	1.734
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3271.03
# indels per 100 kbp	0.00
# genomic features	12 + 0 part
Complete BUSCO (%)	89.86
Partial BUSCO (%)	2.70
# predicted rRNA genes	2 + 0 part
Largest alignment	76
Total aligned length	214
NA50	-
NGA50	-
NA90	-
NGA90	-
auNA	0.0
auNGA	0.0
LA50	-
LGA50	-
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

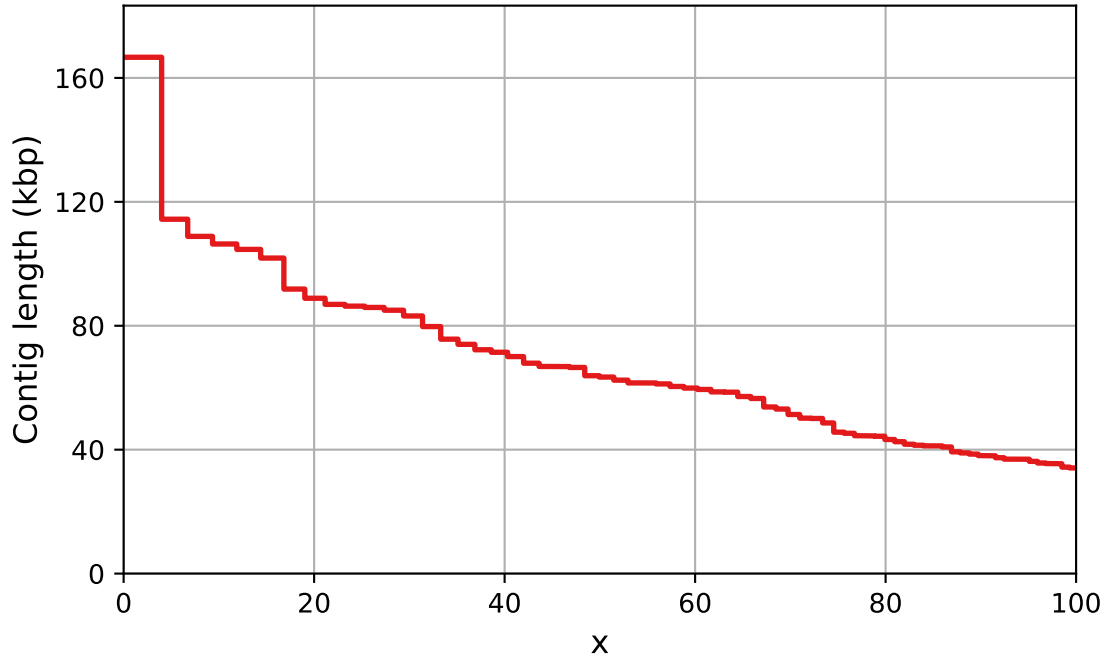|	Assembly_with_MEGAHIT_on_data_36_and_data_35
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	7
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	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).

Unaligned report

	Assembly_with_MEGAHIT_on_data_36_and_data_35
# fully unaligned contigs	289
Fully unaligned length	6471429
# partially unaligned contigs	3
Partially unaligned length	77284
# 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).
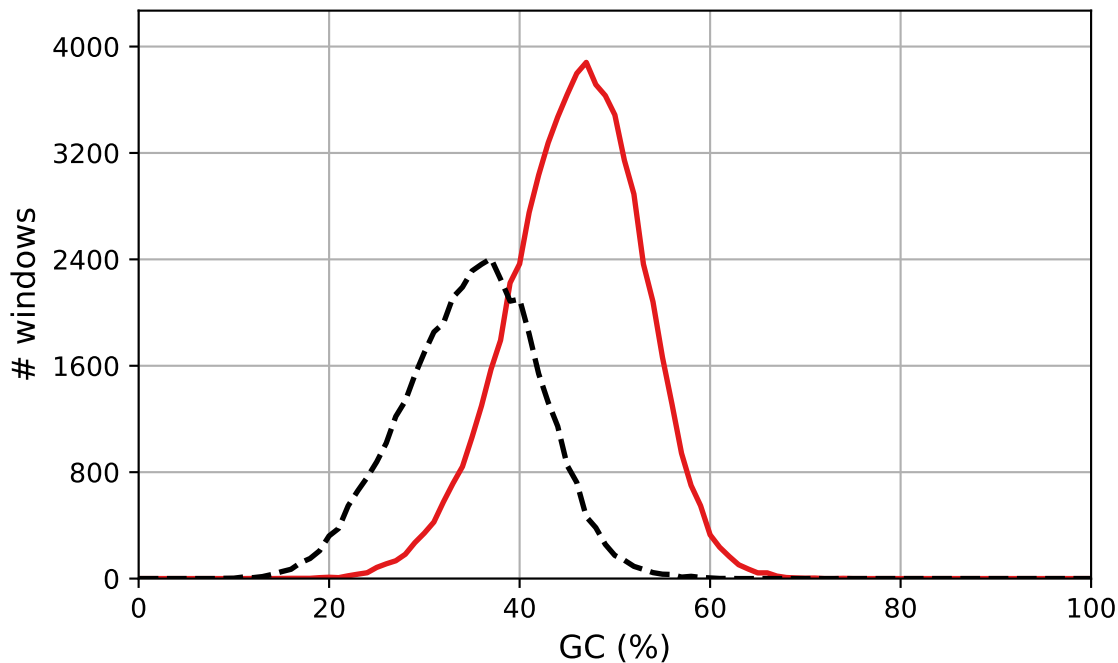
Nx
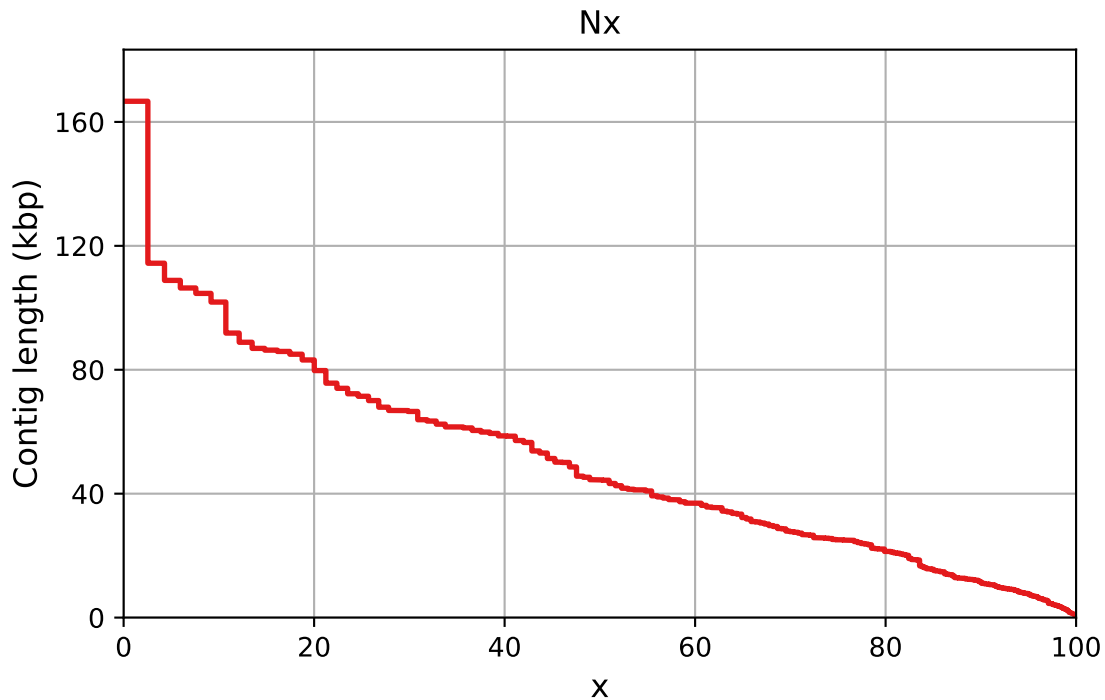
Assembly_with_MEGAHIT_on_data_36_and_data_35

NGx

Assembly_with_MEGAHIT_on_data_36_and_data_35
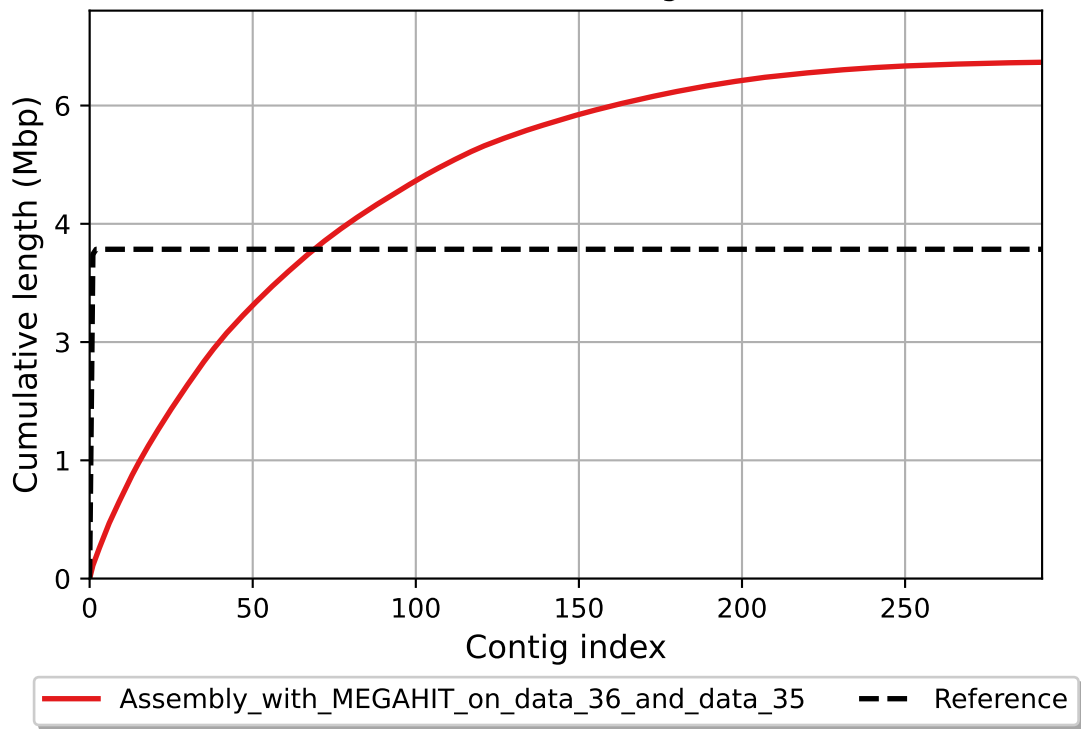
Cumulative length

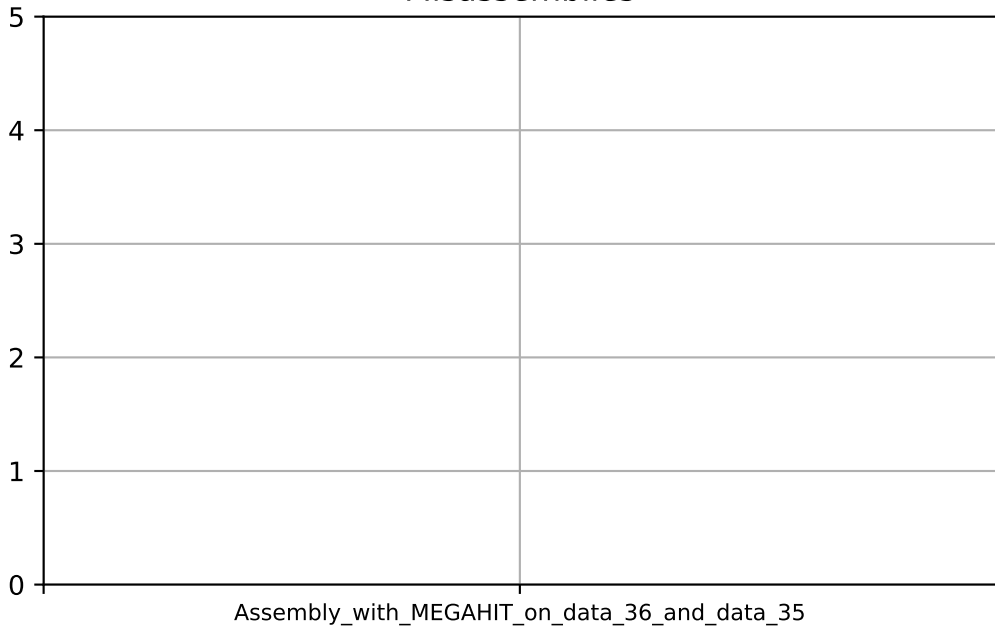GC content

Assembly_with_MEGAHIT_on_data_36_and_data_35 GC content

Misassemblies

Assembly_with_MEGAHIT_on_data_36_and_data_35

FRCurve (misassemblies)

Assembly_with_MEGAHIT_on_data_36_and_data_35
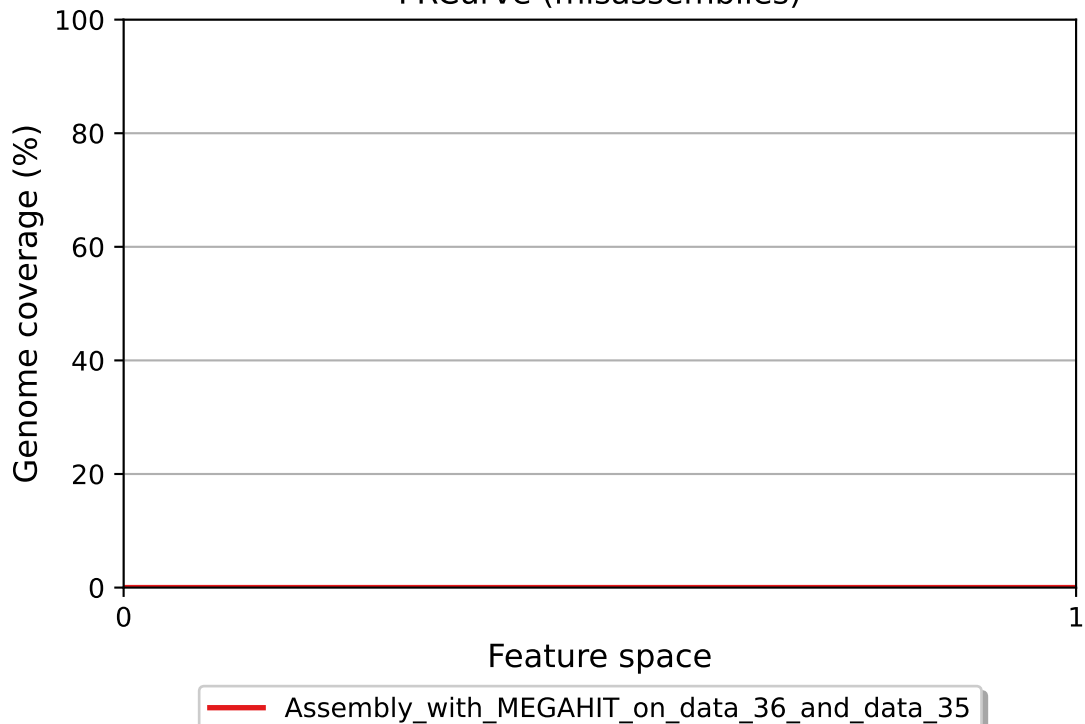
Cumulative length (aligned contigs)
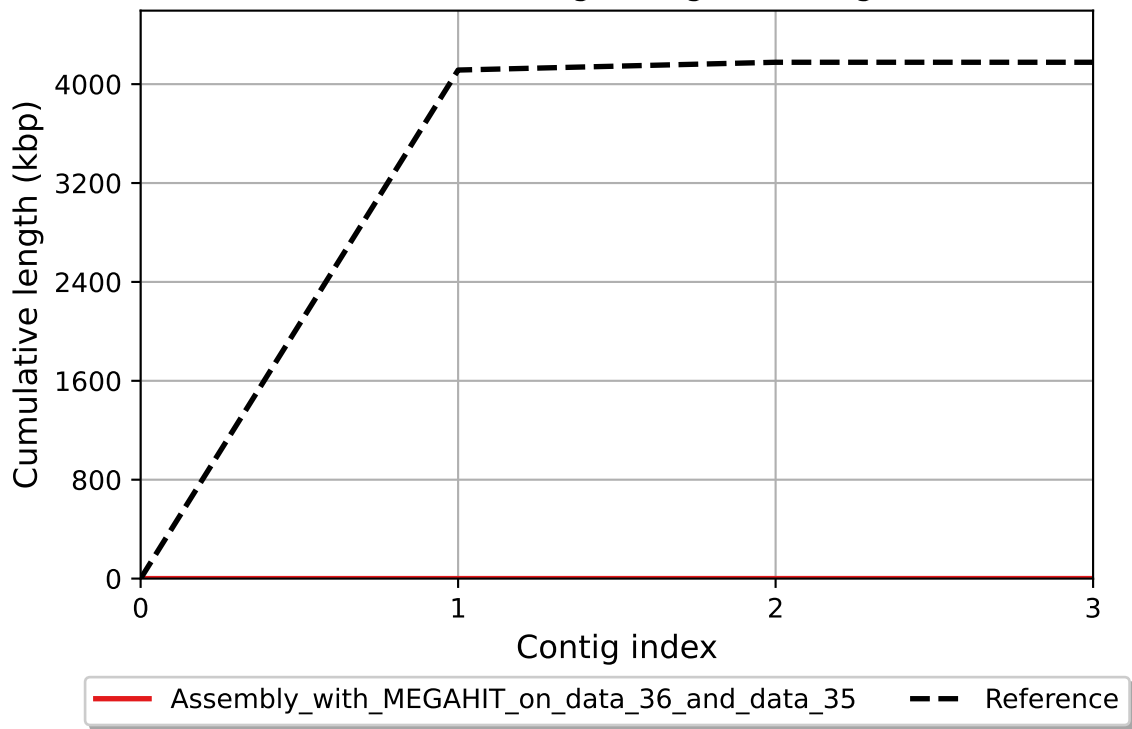
NAx
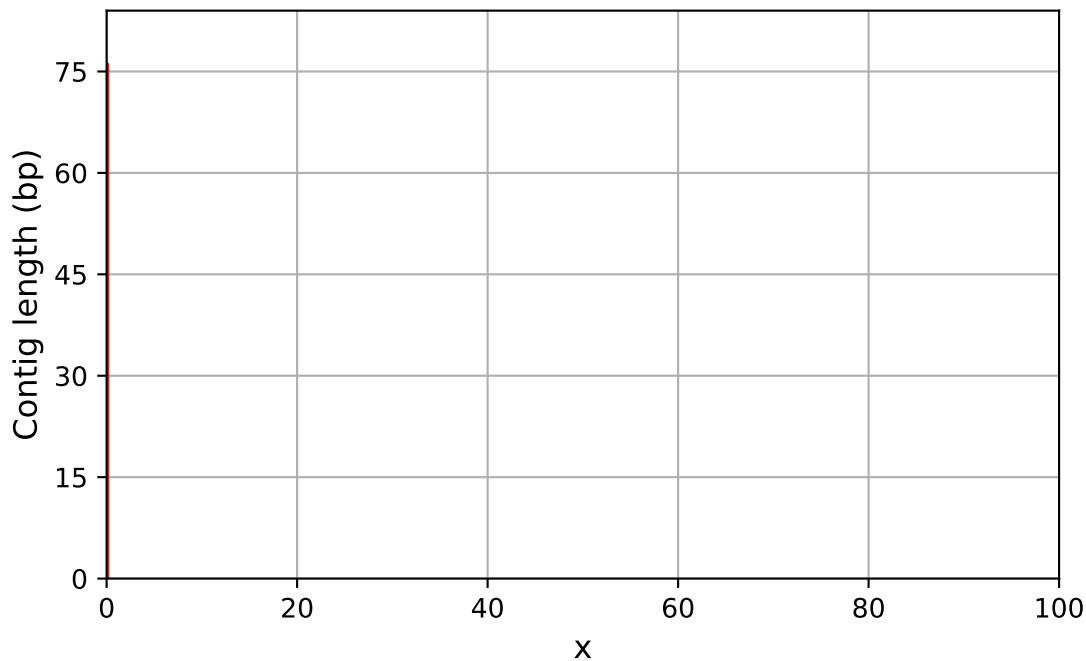
Assembly_with_MEGAHIT_on_data_36_and_data_35

NGAx

Assembly_with_MEGAHIT_on_data_36_and_data_35

Cumulative # complete genomic features
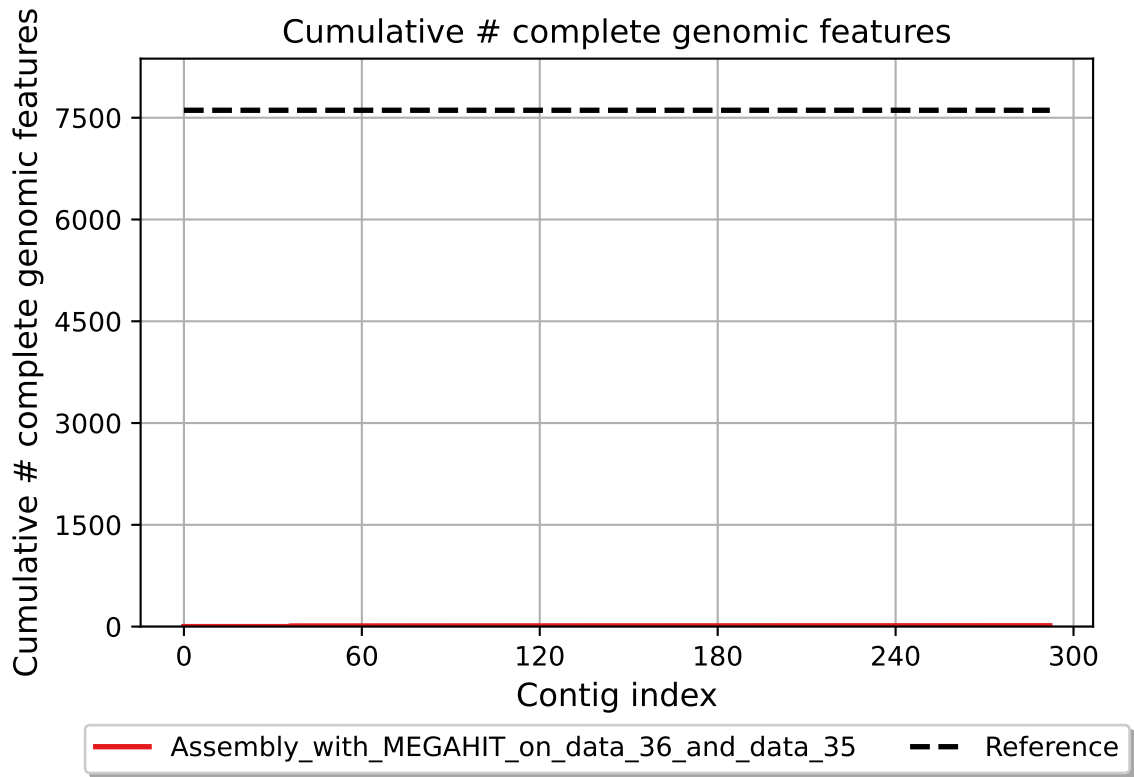
FRCurve (genomic features)

Assembly_with_MEGAHIT_on_data_36_and_data_35