Report

	Haslr	Unicycler_hybrid
# contigs (>= 0 bp)	1	21
# contigs (>= 1000 bp)	1	13
# contigs (>= 5000 bp)	1	10
# contigs (>= 10000 bp)	1	8
# contigs (>= 25000 bp)	1	7
# contigs (>= 50000 bp)	1	4
Total length (>= 0 bp)	88302	5546142
Total length (>= 1000 bp)	88302	5542773
Total length (>= 5000 bp)	88302	5535794
Total length (>= 10000 bp)	88302	5522779
Total length (>= 25000 bp)	88302	5511681
Total length (>= 50000 bp)	88302	5405332
# contigs	1	16
Largest contig	88302	4721566
Total length	88302	5544454
Reference length	5694894	5694894
GC (%)	48.32	57.21
Reference GC (%)	57.15	57.15
N50	88302	4721566
NG50	-	4721566
N75	88302	4721566
NG75	-	4721566
L50	1	1
LG50	-	1
L75	1	1
LG75	-	1
# total reads	3095801	2965872
# left	1495775	1424418
# right	1495795	1424443
Mapped (%)	0.43	99.25
Reference mapped (%)	88.76	88.76
Properly paired (%)	0.26	94.87
Reference properly paired (%)	83.98	83.98
Avg. coverage depth	300	407
Reference avg. coverage depth	379	379
Coverage >= 1x (%)	99.11	100.0
Reference coverage >= 1x (%)	93.24	93.24
# misassemblies	0	49
# misassembled contigs	0	6
Misassembled contigs length	0	5423105
# local misassemblies	0	52
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# structural variations	0	5
# unaligned mis. contigs	1	2
# unaligned contigs	0 + 1 part	4 + 5 part
Unaligned length	81536	500044
Genome fraction (%)	0.119	88.163
Duplication ratio	1.000	1.005
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	1212.30	584.81
# indels per 100 kbp	325.25	22.67
Largest alignment	2969	425815
Total aligned length	6766	5042287
NA50	-	178774
NGA50	-	153469
NA75	-	73303
NGA75	-	69678
LA50	-	11
LGA50	-	12
LA75	-	23
LGA75	-	25

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).

Reads report

	Haslr	Unicycler_hybrid
# total reads	3095801	2965872
# left	1495775	1424418
# right	1495795	1424443
# mapped	13344	2943646
Mapped (%)	0.43	99.25
# properly paired	8028	2813838
Properly paired (%)	0.26	94.87
# singletons	1038	5056
Singletons (%)	0.03	0.17
# misjoint mates	0	4926
Misjoint mates (%)	0.0	0.17
Avg. coverage depth	300	407
Coverage >= 1x (%)	99.11	100.0
Coverage >= 5x (%)	94.58	100.0
Coverage >= 10x (%)	94.39	100.0
# reference mapped	2652539	2652539
Reference mapped (%)	88.76	88.76
# reference properly paired	2509736	2509736
Reference properly paired (%)	83.98	83.98
# reference singletons	9100	9100
Reference singletons (%)	0.3	0.3
# reference misjoint mates	1866	1866
Reference misjoint mates (%)	0.06	0.06
Reference avg. coverage depth	379	379
Reference coverage >= 1x (%)	93.24	93.24
Reference coverage >= 5x (%)	92.88	92.88
Reference coverage >= 10x (%)	92.8	92.8

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).
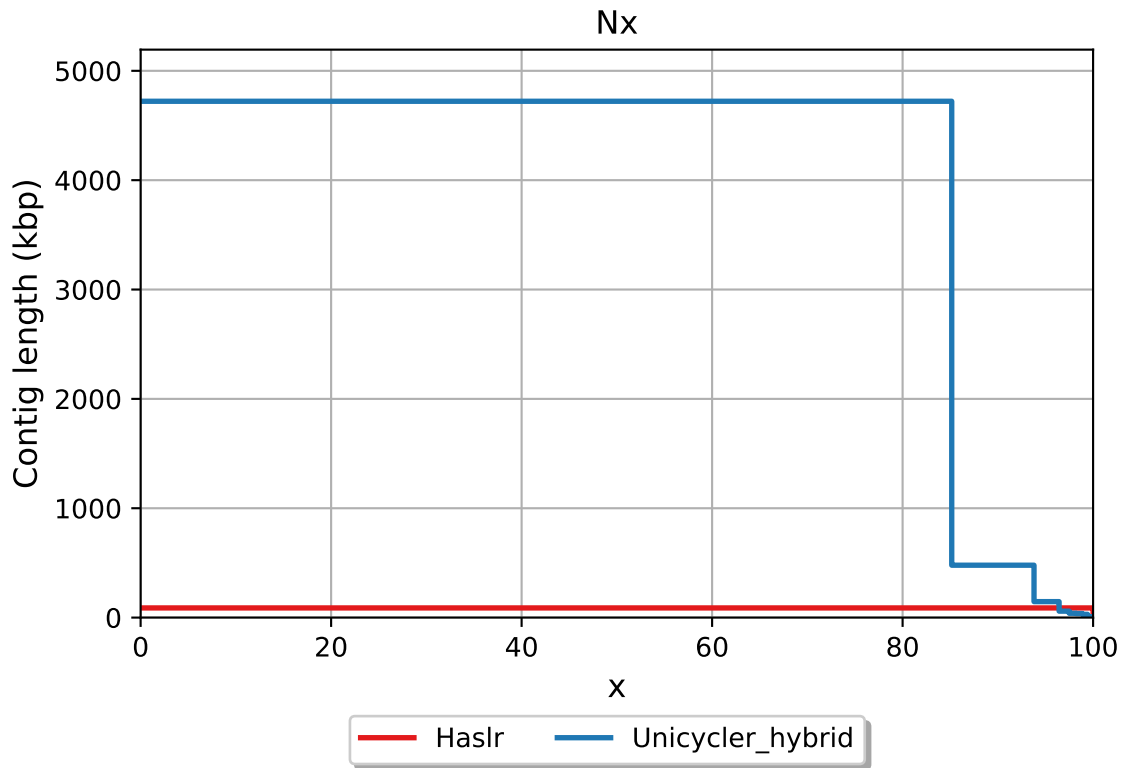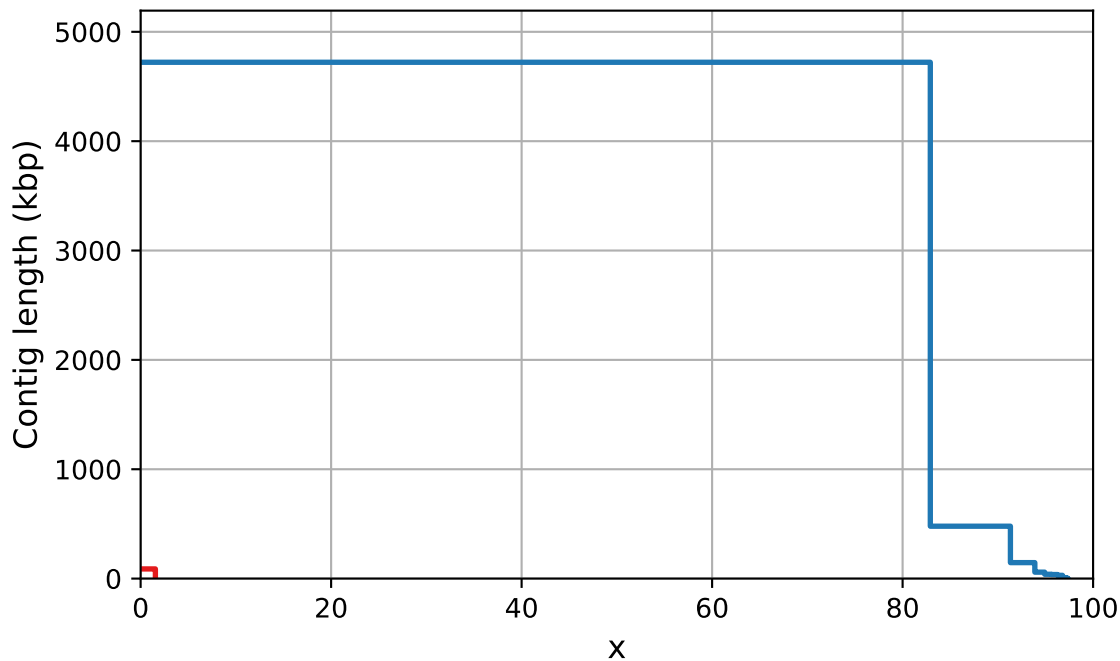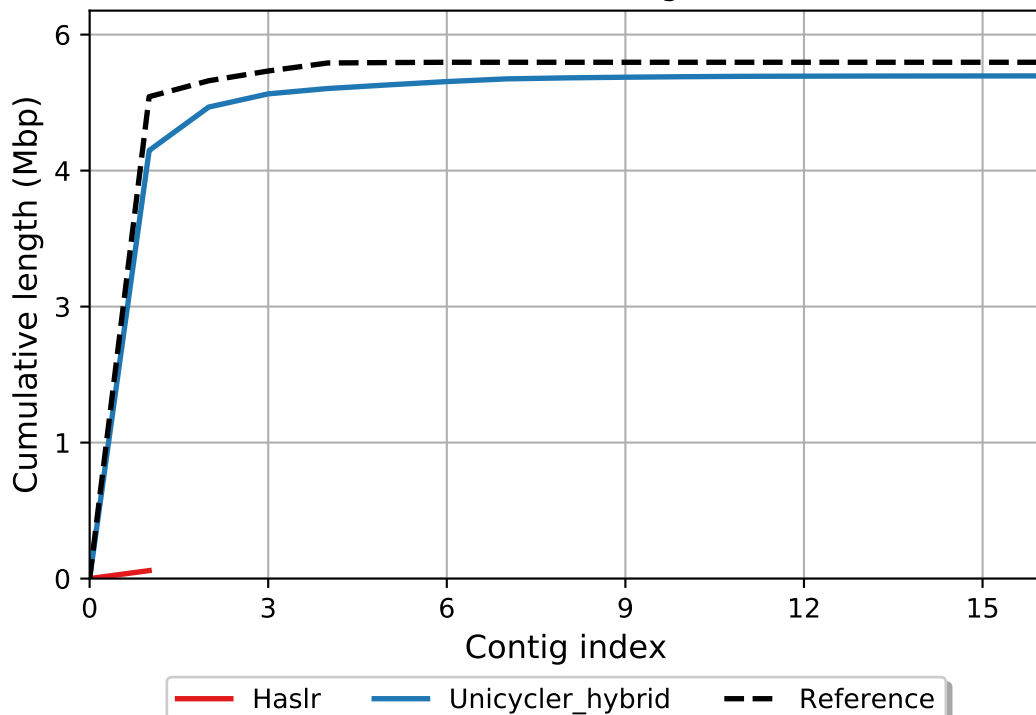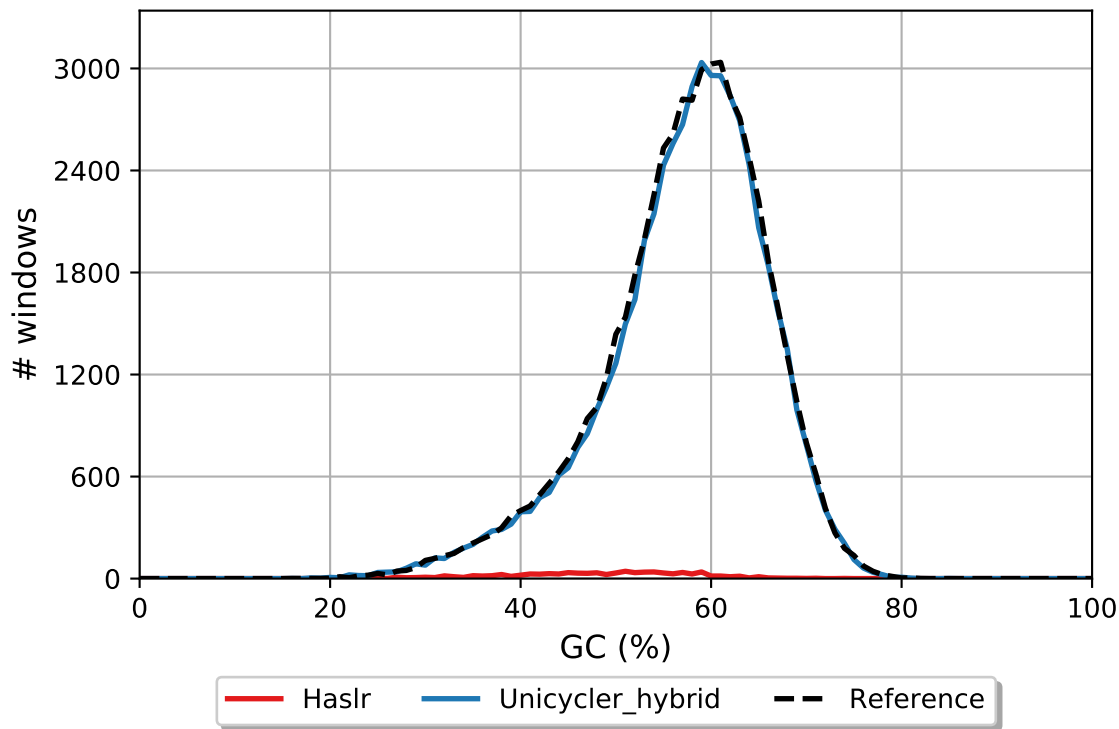
Misassemblies report
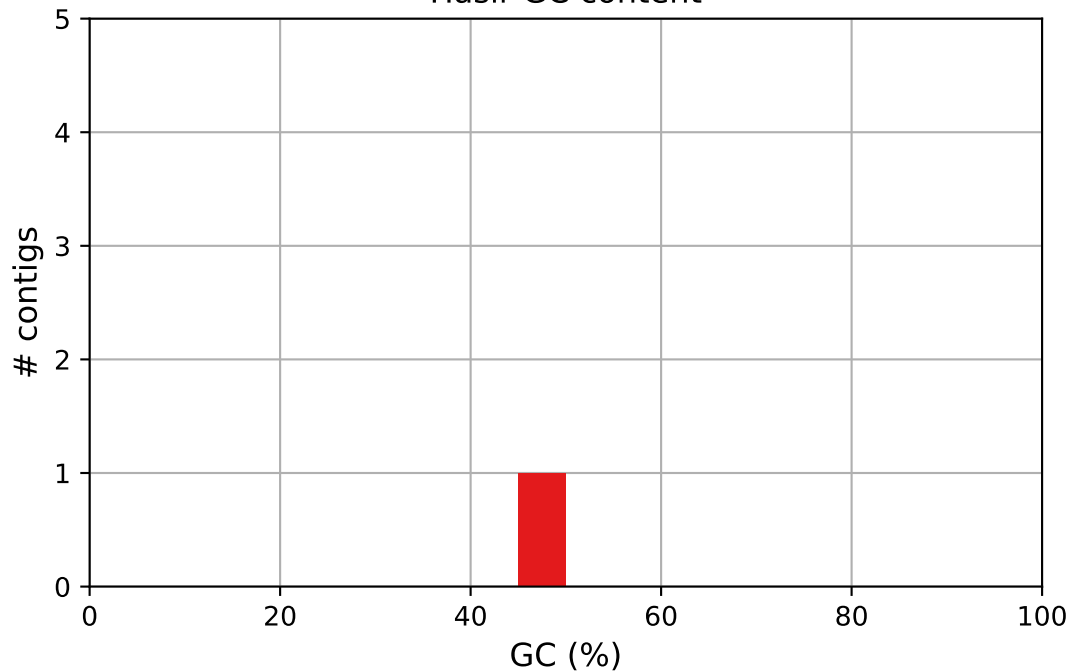
	Haslr	Unicycler_hybrid
# misassemblies	0	49
# contig misassemblies	0	49
# c. relocations	0	46
# c. translocations	0	1
# c. inversions	0	2
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	6
Misassembled contigs length	0	5423105
# local misassemblies	0	52
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# structural variations	0	5
# unaligned mis. contigs	1	2
# mismatches	82	29362
# indels	22	1138
# indels (<= 5 bp)	22	1046
# indels (> 5 bp)	0	92
Indels length	28	3453

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

	Haslr	Unicycler_hybrid
# fully unaligned contigs	0	4
Fully unaligned length	0	10852
# partially unaligned contigs	1	5
Partially unaligned length	81536	489192
# N's	0	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

Cumulative length

GC content

Haslr GC content

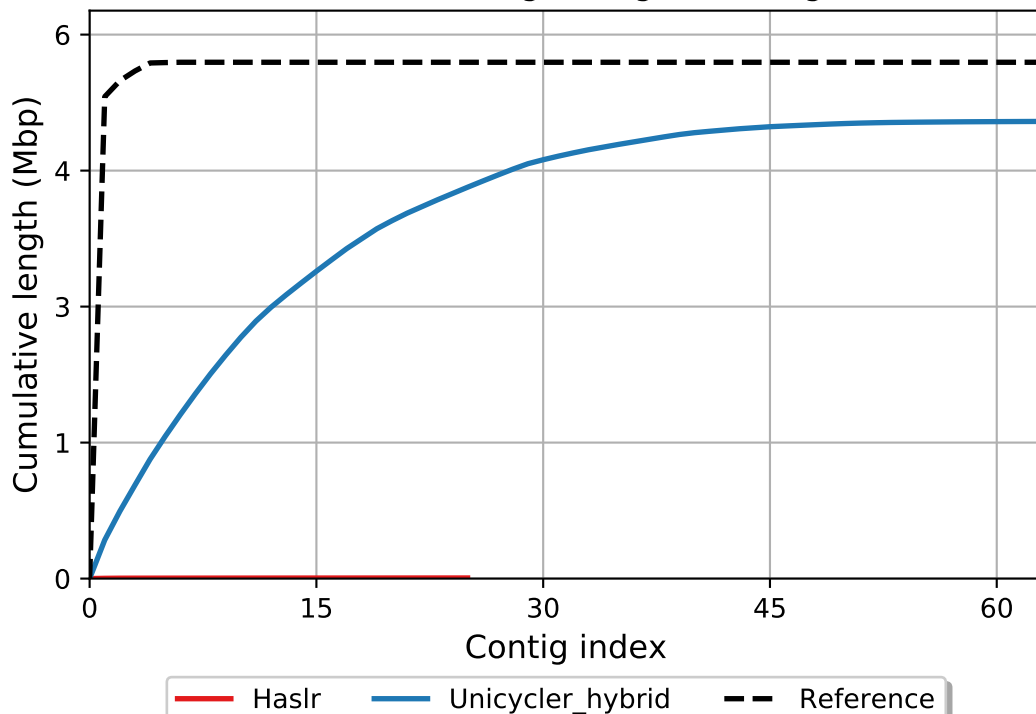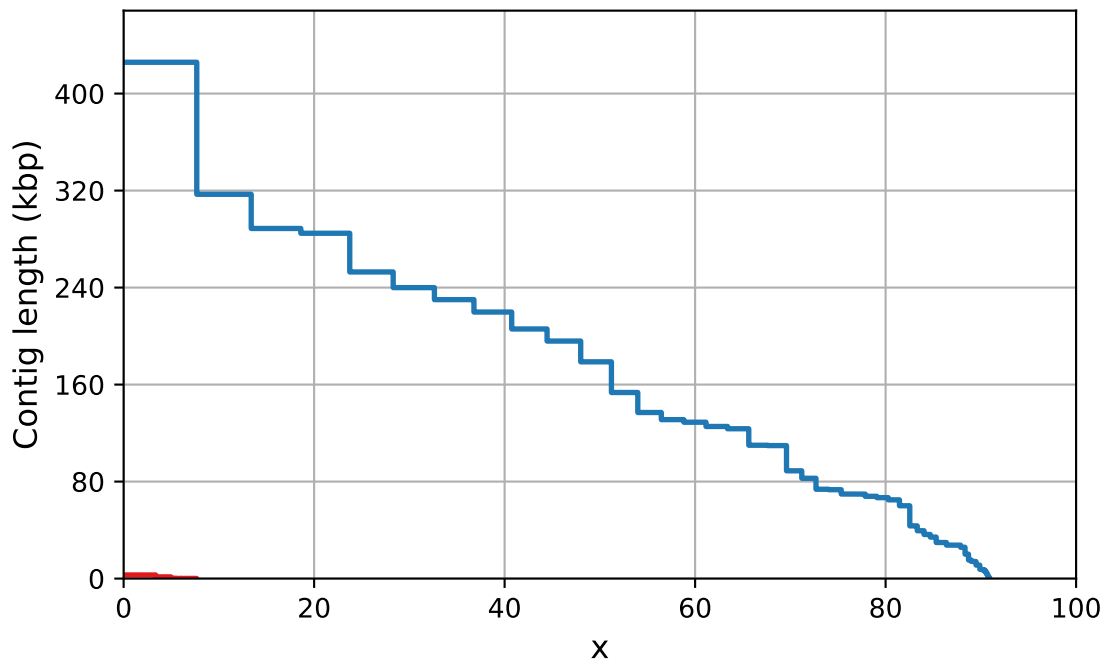Misassemblies

| | # relocations | # translocations | # inversions |

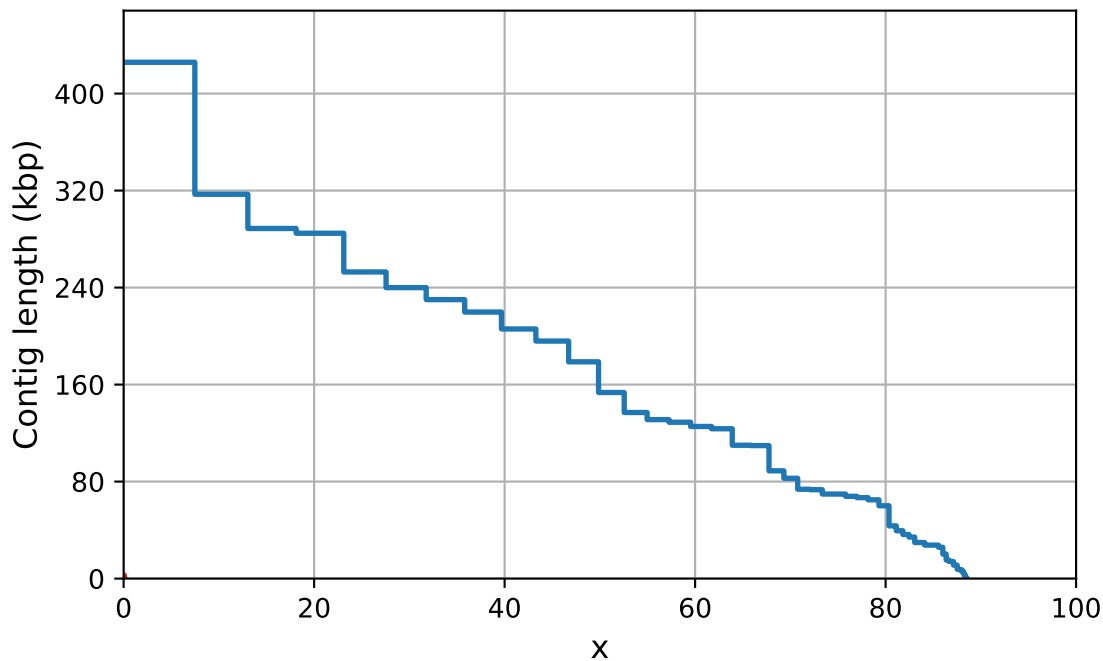FRCurve (misassemblies)
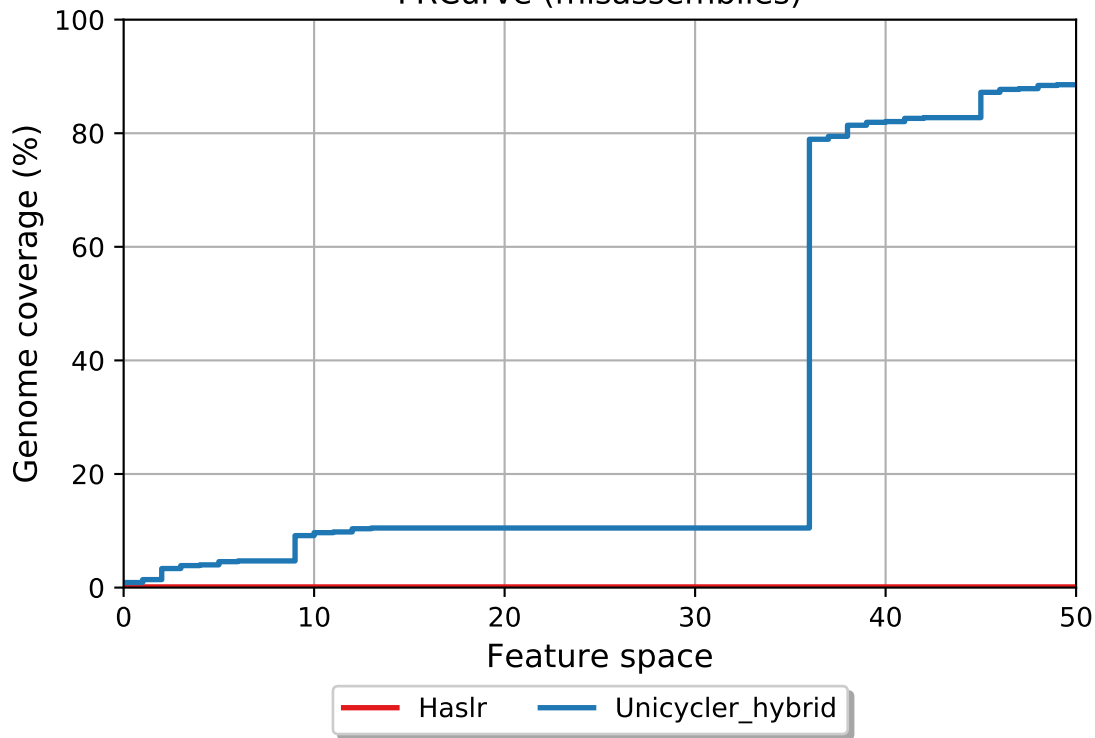
Cumulative length (aligned contigs)

NAx

Legend: Haslr, Unicycler_hybrid

NGAx

Genome fraction, %