

Report

	PTA123.scaffolds	PTA111.scaffolds
# contigs (>= 0 bp)	105	20
# contigs (>= 1000 bp)	9	10
# contigs (>= 5000 bp)	0	0
# contigs (>= 10000 bp)	0	0
# contigs (>= 25000 bp)	0	0
# contigs (>= 50000 bp)	0	0
Total length (>= 0 bp)	49184	25675
Total length (>= 1000 bp)	17140	21870
Total length (>= 5000 bp)	0	0
Total length (>= 10000 bp)	0	0
Total length (>= 25000 bp)	0	0
Total length (>= 50000 bp)	0	0
# contigs	22	12
Largest contig	3315	4389
Total length	25580	23573
Reference length	34064	34064
GC (%)	36.85	36.52
Reference GC (%)	51.01	51.01
N50	1190	2589
NG50	1080	1455
N75	717	1455
NG75	538	-
L50	6	4
LG50	9	7
L75	12	7
LG75	22	-
# 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	11 + 0 part	12 + 0 part
Unaligned length	18503	23573
Genome fraction (%)	20.649	-
Duplication ratio	1.006	-
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	156.41	-
# indels per 100 kbp	42.66	-
# genomic features	1 + 13 part	-
Largest alignment	893	-
Total aligned length	7050	-
NGA50	-	-

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

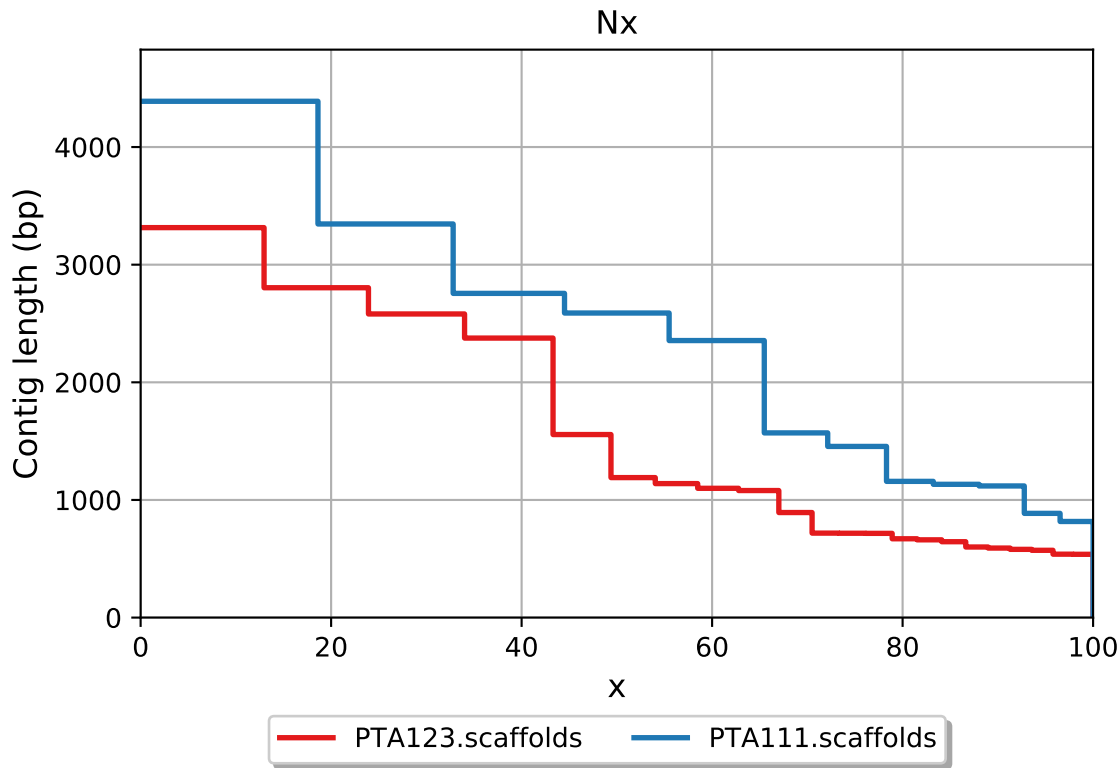
	PTA123.scaffolds	PTA111.scaffolds
# misassemblies	0	-
# contig misassemblies	0	-
# c. relocations	0	-
# c. translocations	0	-
# c. inversions	0	-
# scaffold misassemblies	0	-
# s. relocations	0	-
# s. translocations	0	-
# s. inversions	0	-
# misassembled contigs	0	-
Misassembled contigs length	0	-
# local misassemblies	0	-
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	-
# mismatches	11	-
# indels	3	-
# indels (<= 5 bp)	2	-
# indels (> 5 bp)	1	-
Indels length	16	-

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).

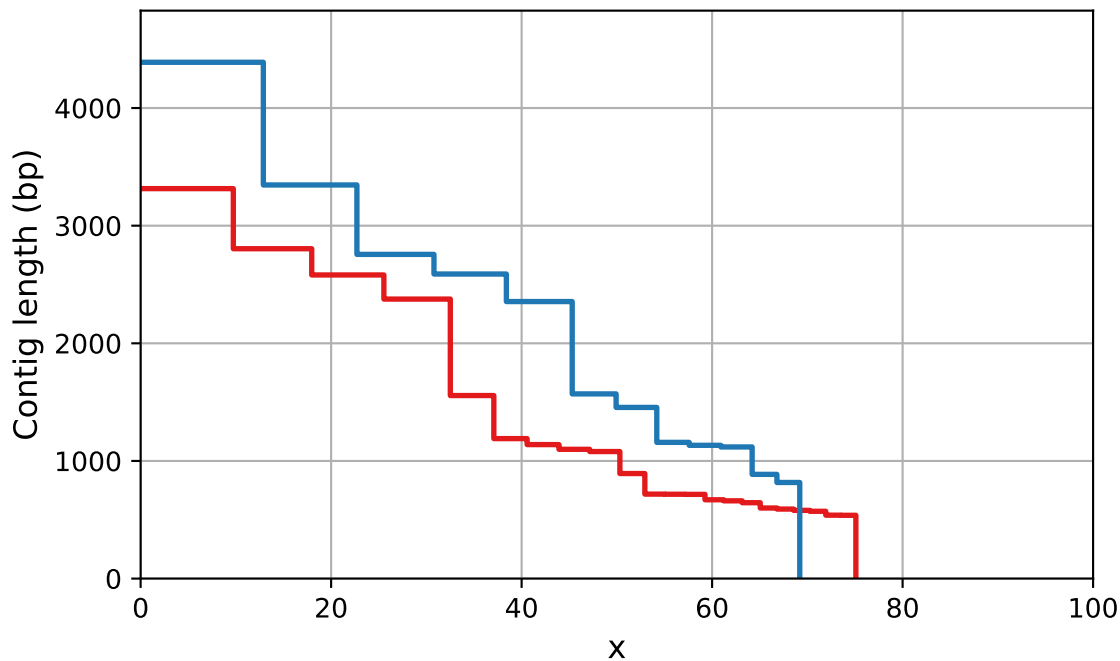
Unaligned report

	PTA123.scaffolds	PTA111.scaffolds
# fully unaligned contigs	11	12
Fully unaligned length	18503	23573
# partially unaligned contigs	0	-
Partially unaligned length	0	-
# 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).



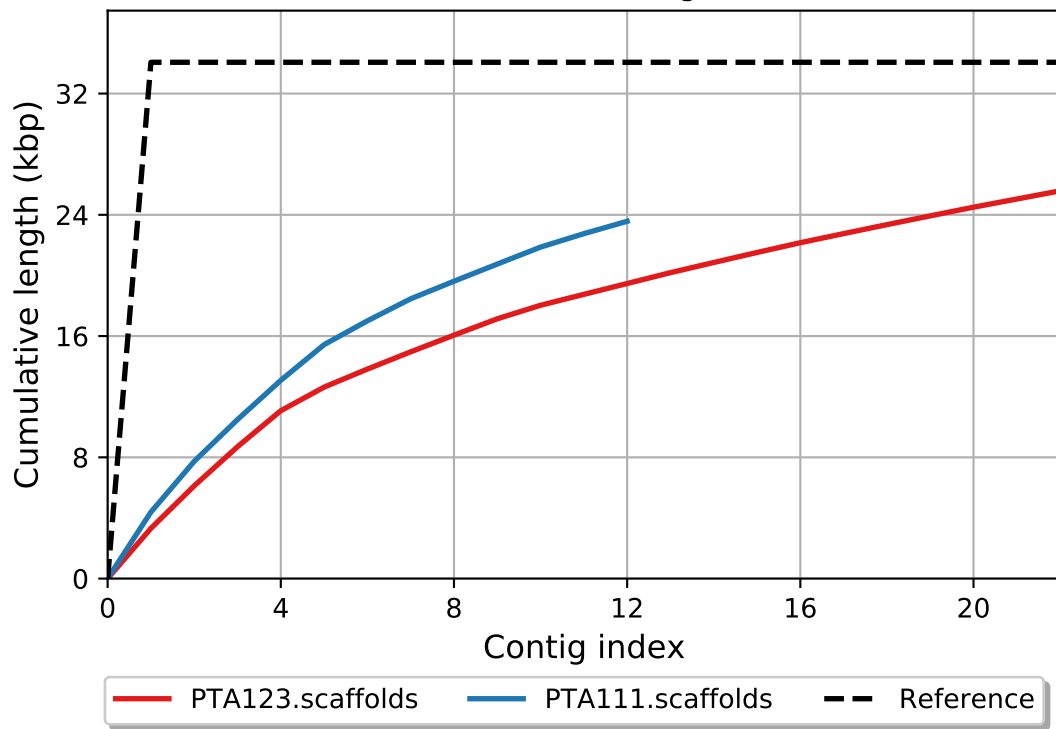
NGx



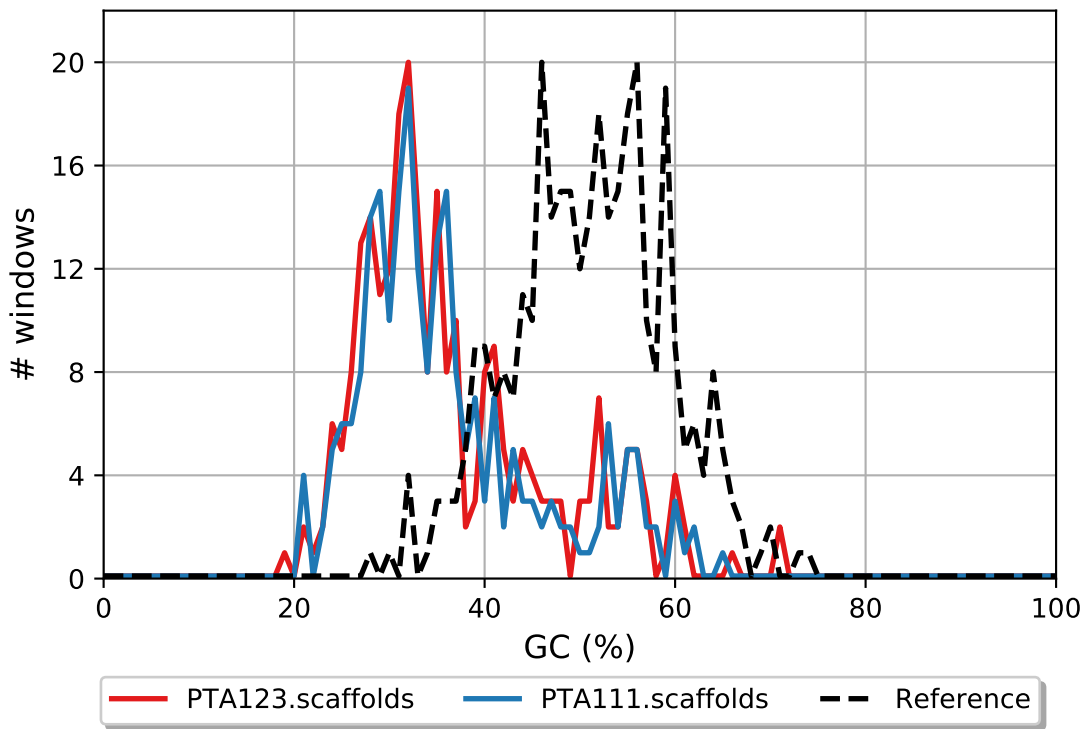
PTA123.scaffolds

PTA111.scaffolds

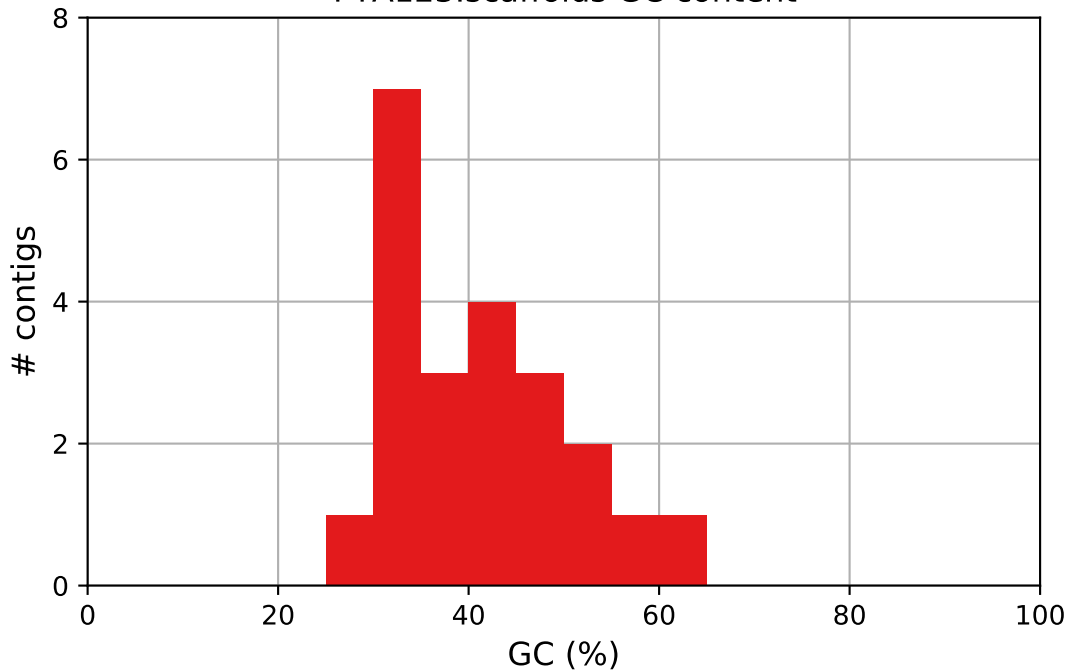
Cumulative length



GC content

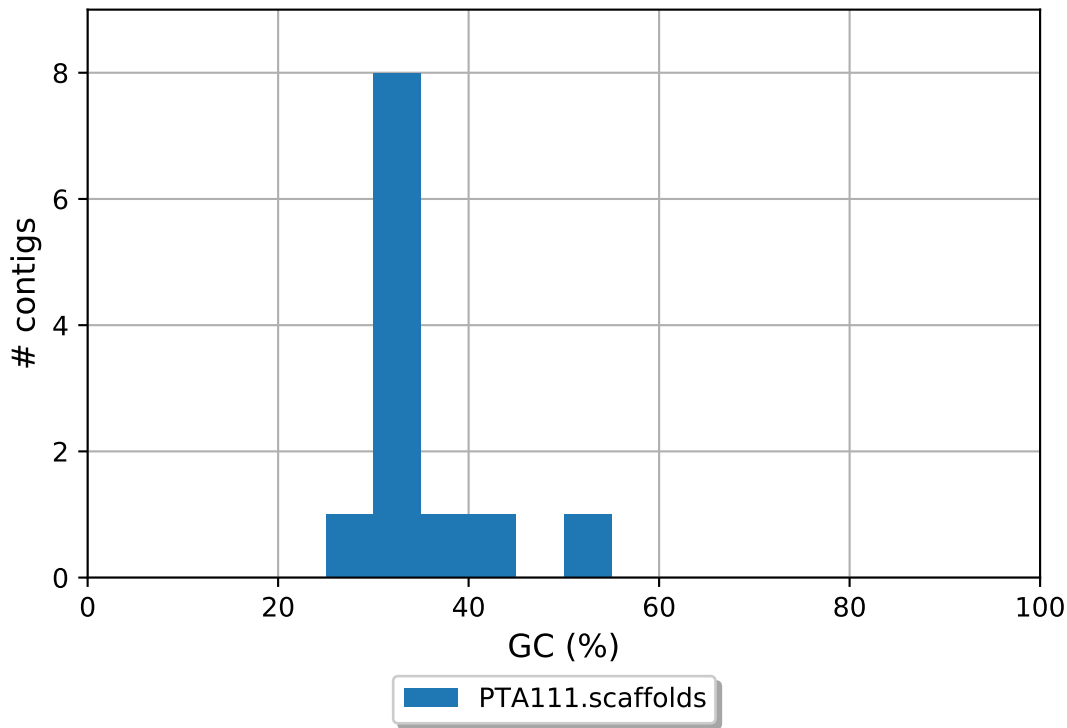


PTA123.scaffolds GC content

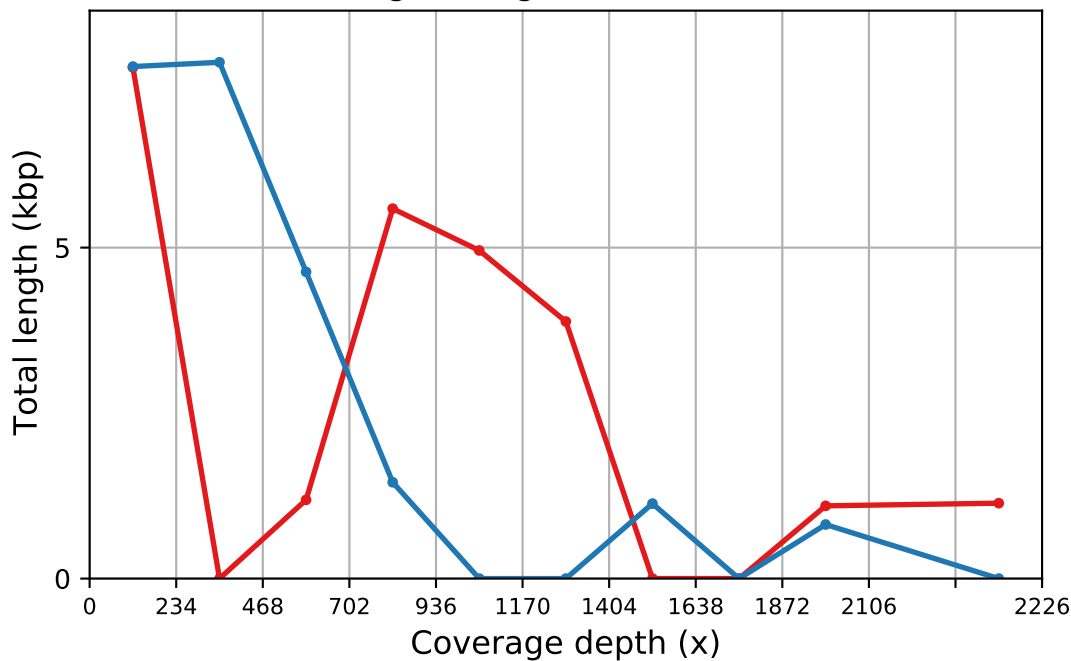


PTA123.scaffolds

PTA111.scaffolds GC content

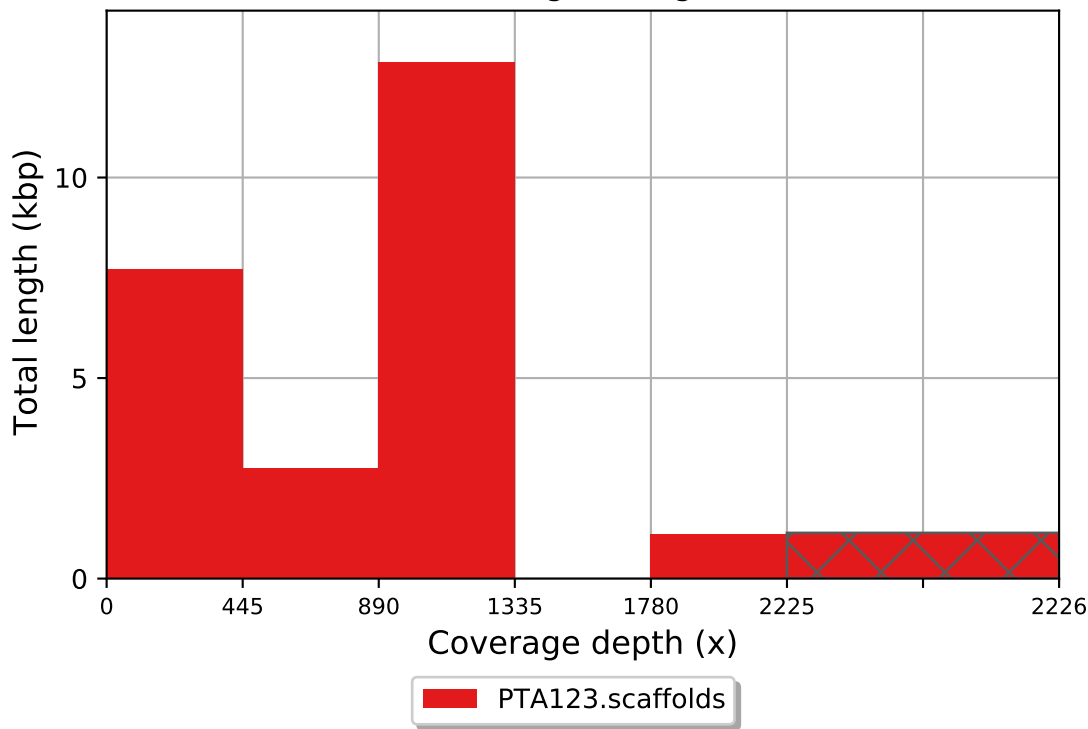


Coverage histogram (bin size: 234x)

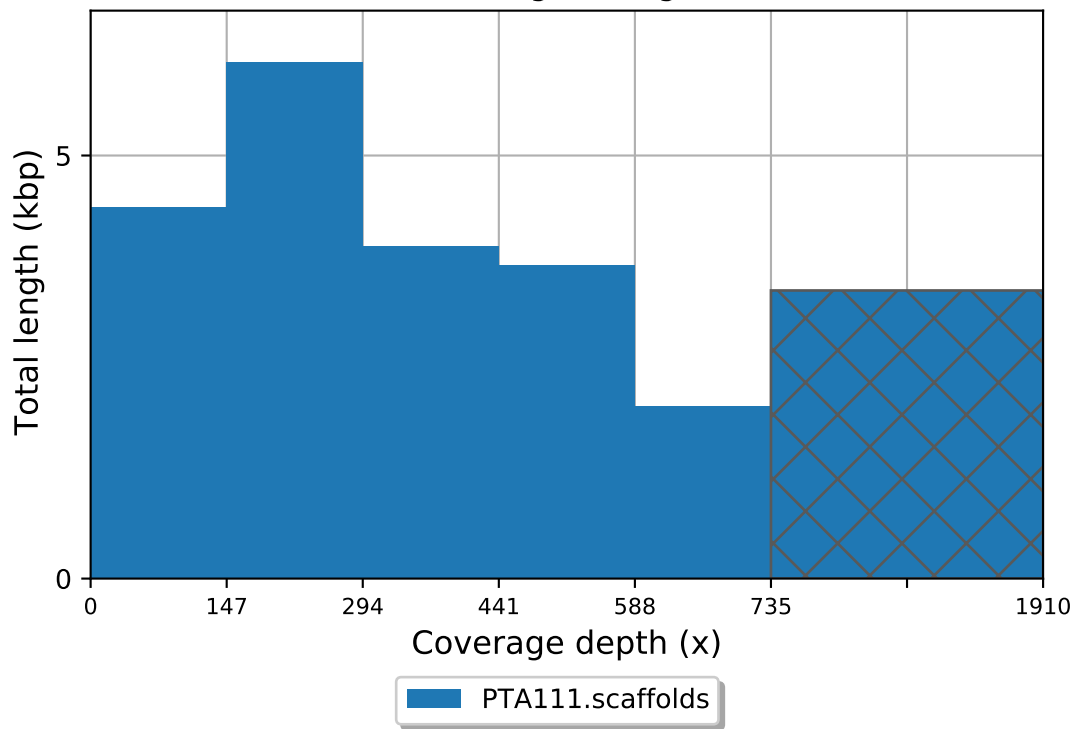


PTA123.scaffolds PTA111.scaffolds

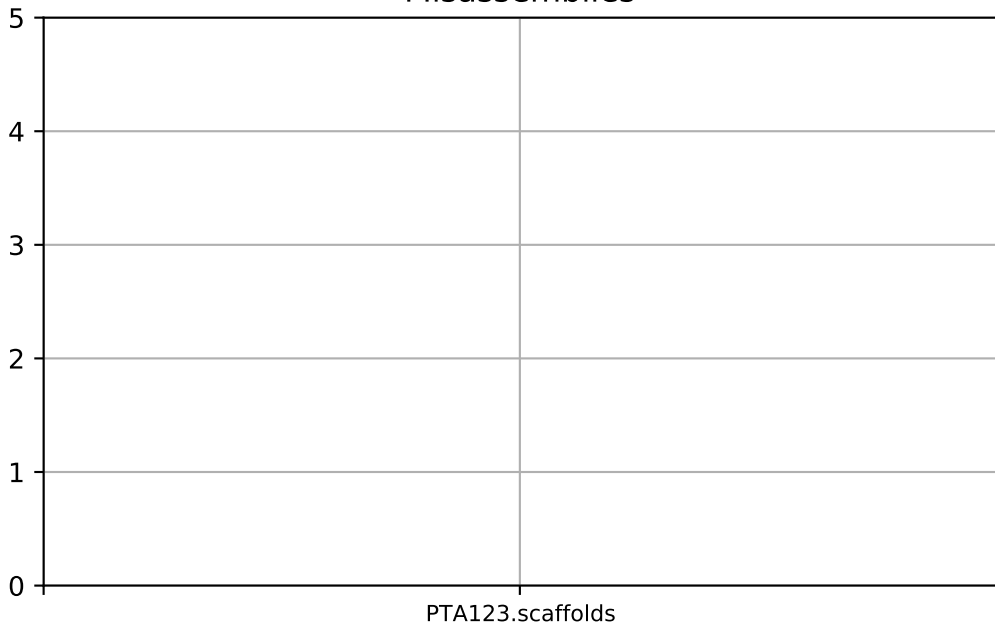
PTA123.scaffolds coverage histogram (bin size: 445x)



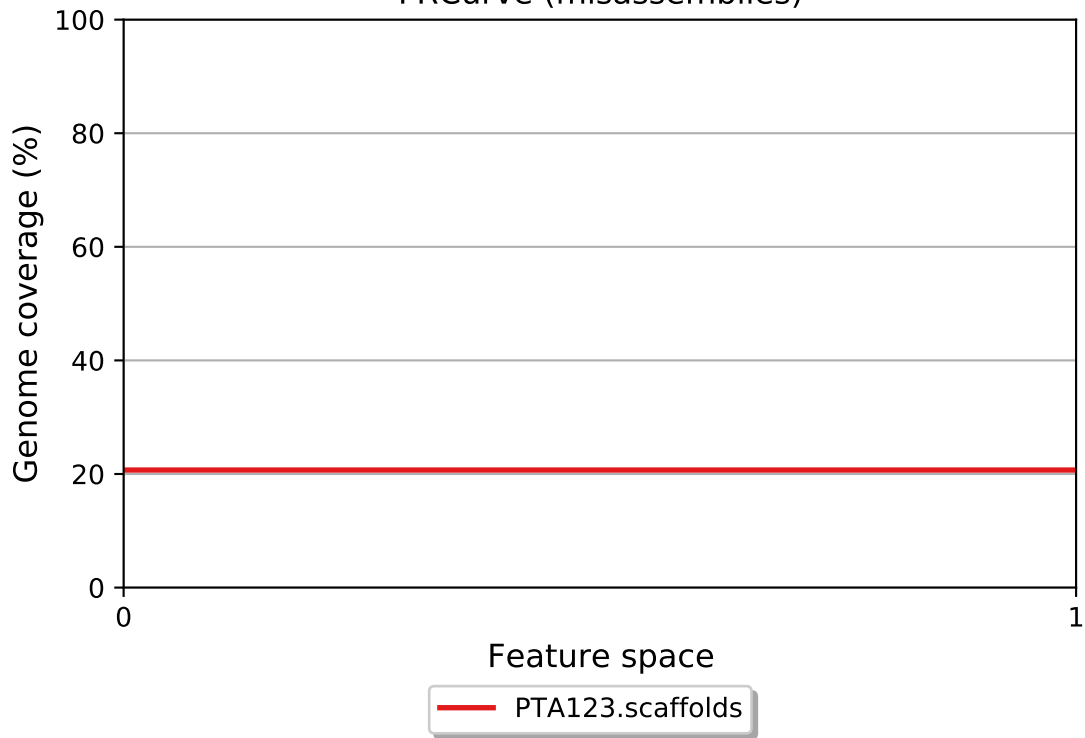
PTA111.scaffolds coverage histogram (bin size: 147x)



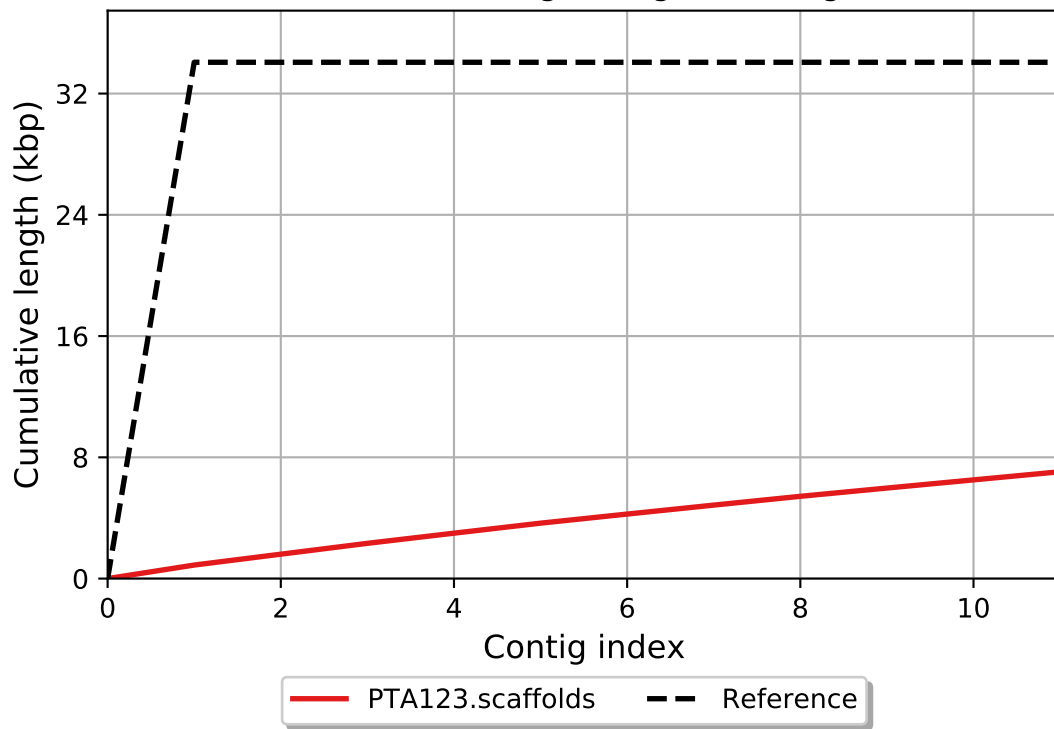
Misassemblies



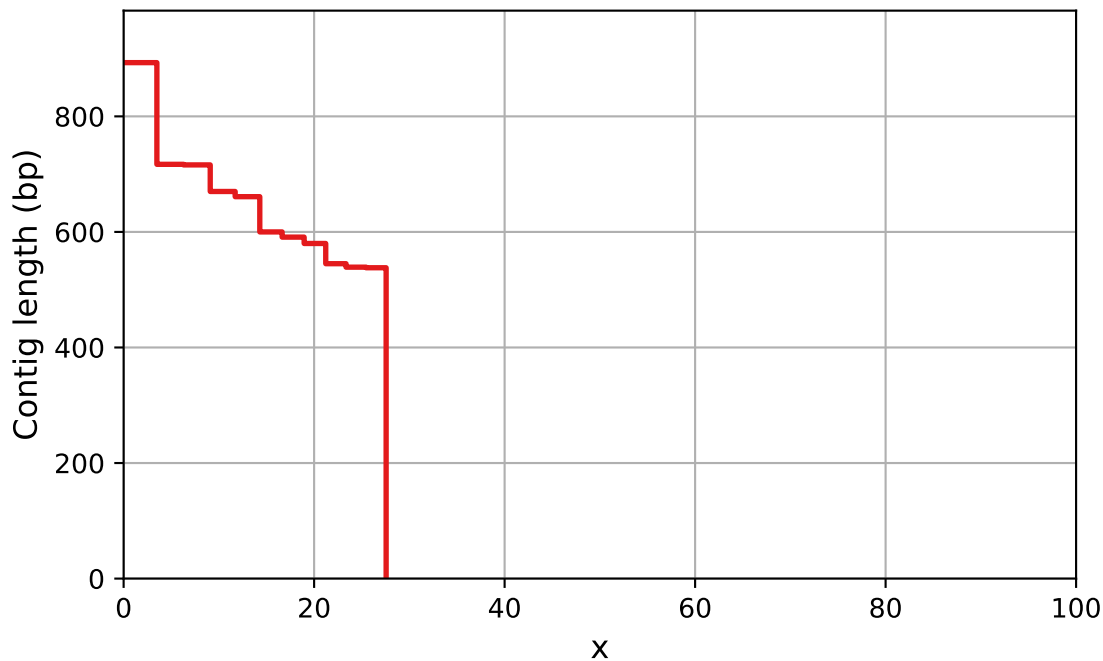
FRCurve (misassemblies)



Cumulative length (aligned contigs)

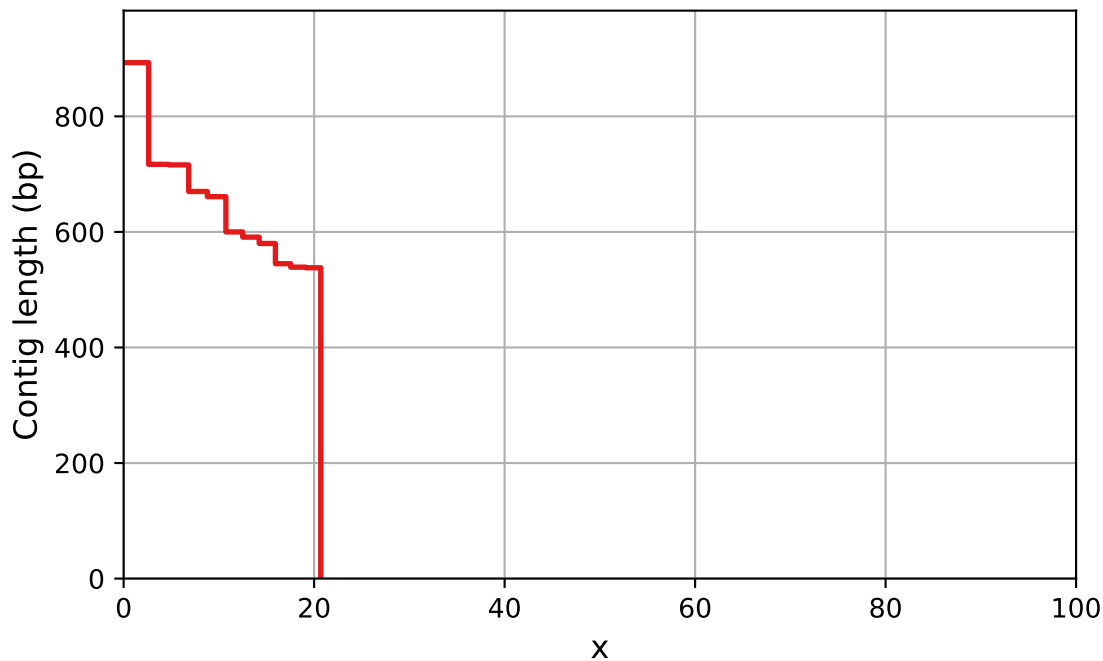


NAx

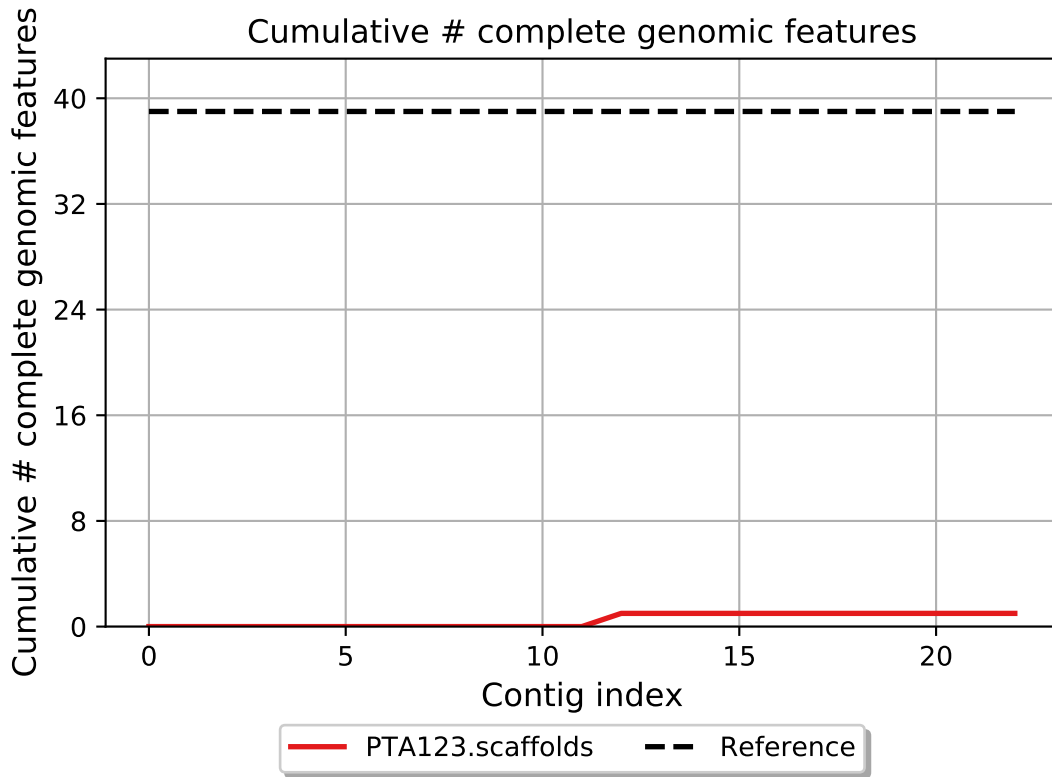


— PTA123.scaffolds

NGAx



— PTA123.scaffolds



FRCurve (genomic features)

