

Report

	PTA102.scaffolds	PTA103.scaffolds	PTA128.scaffolds	PTA127.scaffolds	PTA132.scaffolds
# contigs (>= 0 bp)	19	28	25	137	92
# contigs (>= 1000 bp)	3	2	8	3	8
# contigs (>= 5000 bp)	1	1	1	0	2
# contigs (>= 10000 bp)	0	0	0	0	0
# contigs (>= 25000 bp)	0	0	0	0	0
# contigs (>= 50000 bp)	0	0	0	0	0
Total length (>= 0 bp)	14790	16669	25968	44456	49156
Total length (>= 1000 bp)	10361	9028	20259	10101	19976
Total length (>= 5000 bp)	7338	7449	7315	0	12698
Total length (>= 10000 bp)	0	0	0	0	0
Total length (>= 25000 bp)	0	0	0	0	0
Total length (>= 50000 bp)	0	0	0	0	0
# contigs	3	4	10	5	22
Largest contig	7338	7449	7315	4536	7320
Total length	10361	10497	21687	11516	29322
Reference length	7428	7428	7428	7428	7428
GC (%)	42.47	47.09	39.25	44.95	45.73
Reference GC (%)	42.02	42.02	42.02	42.02	42.02
N50	7338	7449	2337	2798	1278
NG50	7338	7449	7315	4536	7320
N75	1537	1579	1786	2767	876
NG75	7338	7449	7315	2798	7320
L50	1	1	3	2	4
LG50	1	1	1	1	1
L75	2	2	6	3	11
LG75	1	1	1	2	1
# misassemblies	-	-	0	0	0
# misassembled contigs	-	-	0	0	0
Misassembled contigs length	-	-	0	0	0
# local misassemblies	-	-	0	0	0
# scaffold gap ext. mis.	-	-	0	0	0
# scaffold gap loc. mis.	-	-	0	0	0
# unaligned mis. contigs	-	-	0	0	0
# unaligned contigs	3 + 0 part	4 + 0 part	9 + 0 part	3 + 0 part	21 + 0 part
Unaligned length	10361	10497	14362	4172	22002
Genome fraction (%)	-	-	99.754	99.741	99.768
Duplication ratio	-	-	1.002	1.005	1.001
# N's per 100 kbp	0.00	0.00	46.11	86.84	0.00
# mismatches per 100 kbp	-	-	300.92	273.60	3925.05
# indels per 100 kbp	-	-	0.00	0.00	27.35
Largest alignment	-	-	7311	4536	7314
Total aligned length	-	-	7311	7330	7314
NA50	-	-	-	2794	-
NGA50	-	-	7311	4536	7314
NGA75	-	-	7311	2794	7314
LA50	-	-	-	2	-
LGA50	-	-	1	1	1
LGA75	-	-	1	2	1

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

	PTA102.scaffolds	PTA103.scaffolds	PTA128.scaffolds	PTA127.scaffolds	PTA132.scaffolds
# misassemblies	-	-	0	0	0
# contig misassemblies	-	-	0	0	0
# c. relocations	-	-	0	0	0
# c. translocations	-	-	0	0	0
# c. inversions	-	-	0	0	0
# scaffold misassemblies	-	-	0	0	0
# s. relocations	-	-	0	0	0
# s. translocations	-	-	0	0	0
# s. inversions	-	-	0	0	0
# misassembled contigs	-	-	0	0	0
Misassembled contigs length	-	-	0	0	0
# local misassemblies	-	-	0	0	0
# scaffold gap ext. mis.	-	-	0	0	0
# scaffold gap loc. mis.	-	-	0	0	0
# unaligned mis. contigs	-	-	0	0	0
# mismatches	-	-	22	20	287
# indels	-	-	0	0	2
# indels (<= 5 bp)	-	-	0	0	2
# indels (> 5 bp)	-	-	0	0	0
Indels length	-	-	0	0	4

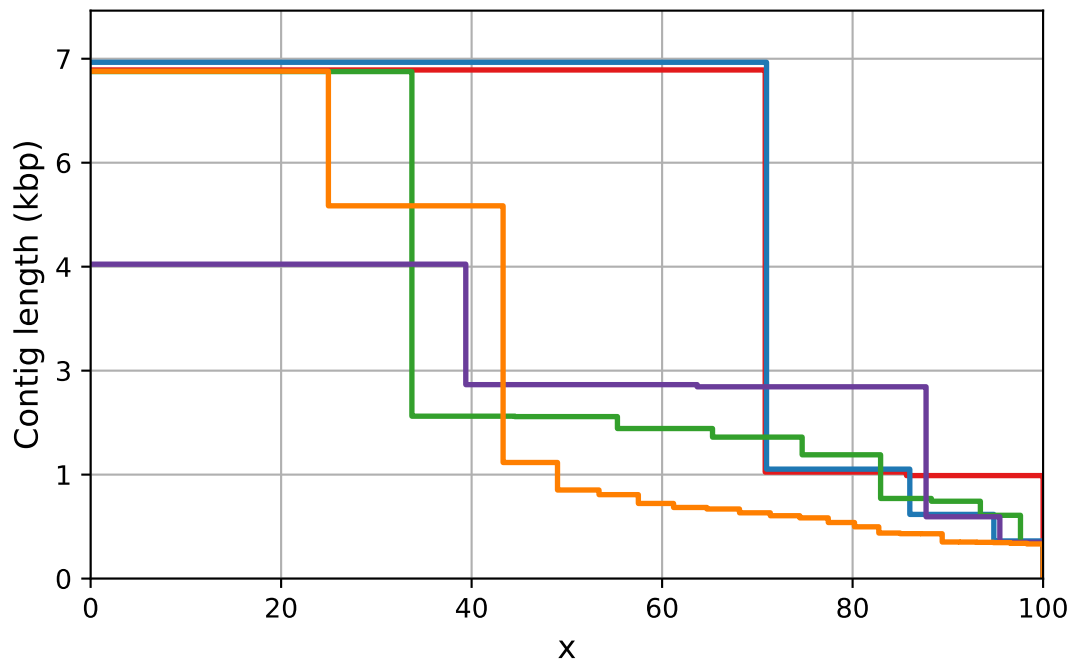
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	PTA102.scaffolds	PTA103.scaffolds	PTA128.scaffolds	PTA127.scaffolds	PTA132.scaffolds
# fully unaligned contigs	3	4	9	3	21
Fully unaligned length	10361	10497	14362	4172	22002
# partially unaligned contigs	-	-	0	0	0
Partially unaligned length	-	-	0	0	0
# N's	0	0	10	10	0

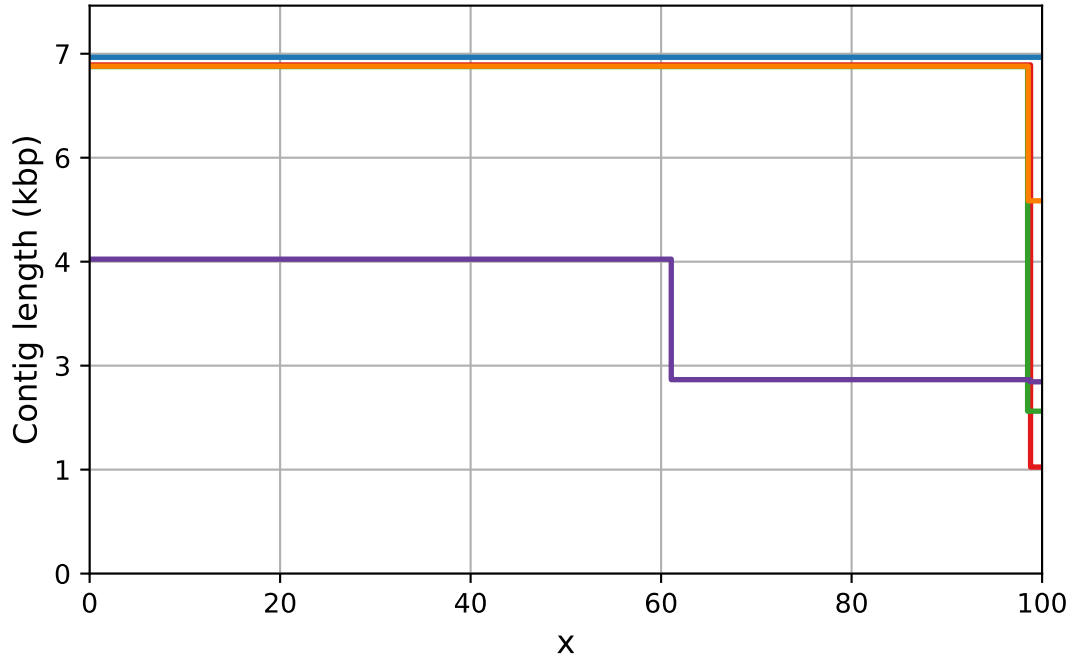
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



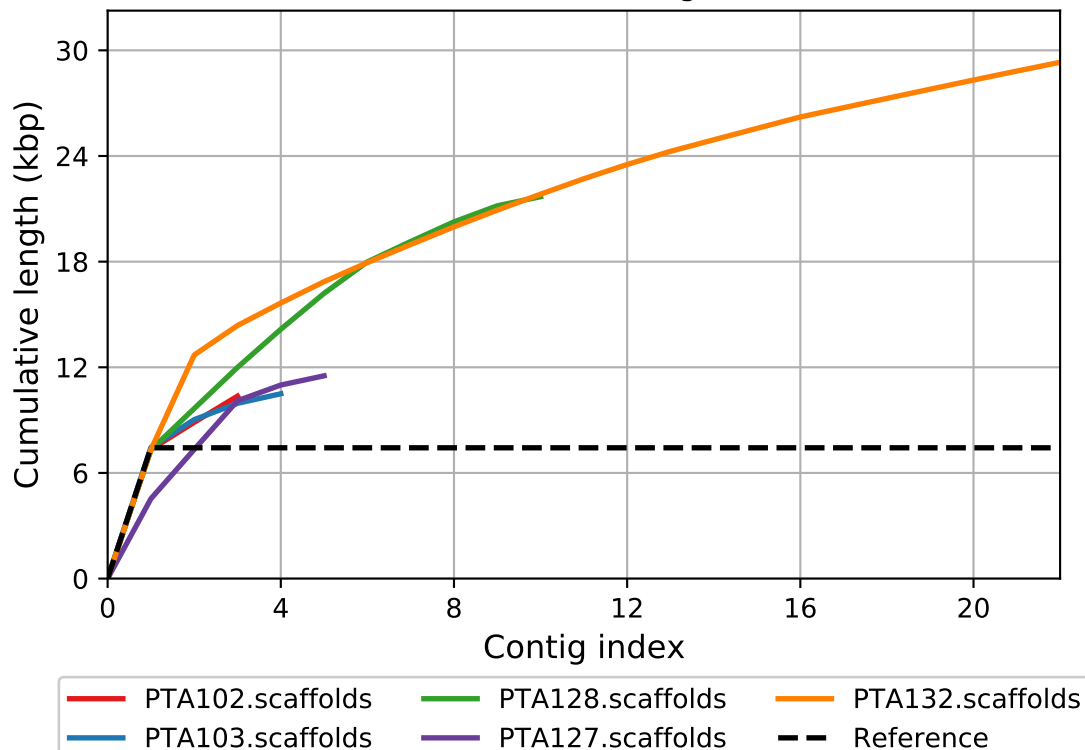
PTA102.scaffolds PTA128.scaffolds PTA132.scaffolds
PTA103.scaffolds PTA127.scaffolds

NGx

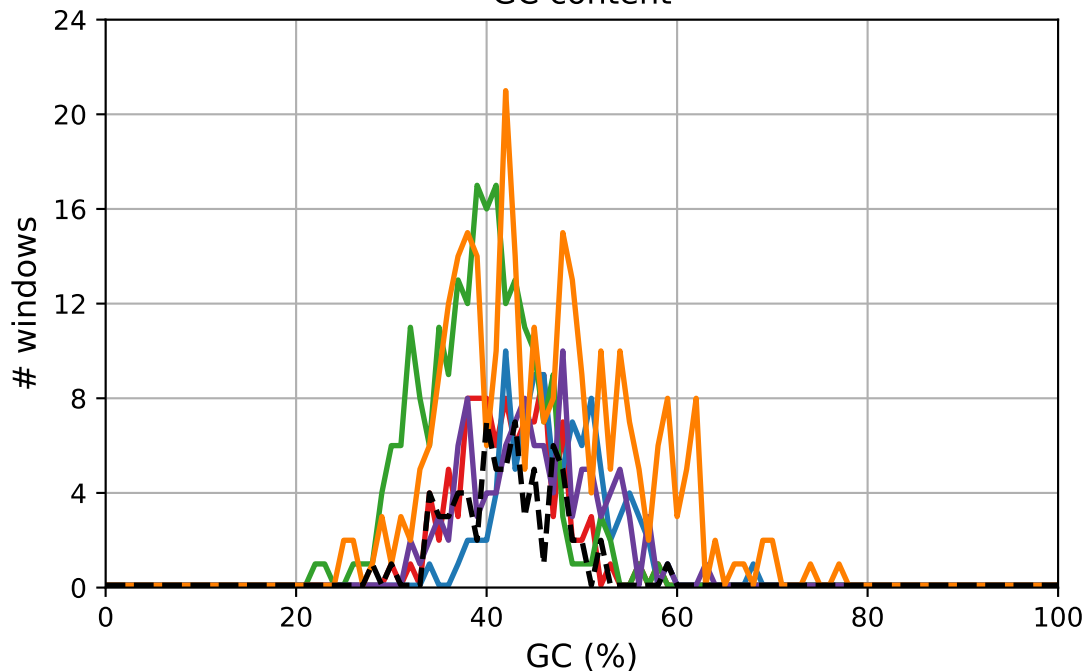


PTA102.scaffolds PTA128.scaffolds PTA132.scaffolds
PTA103.scaffolds PTA127.scaffolds

Cumulative length

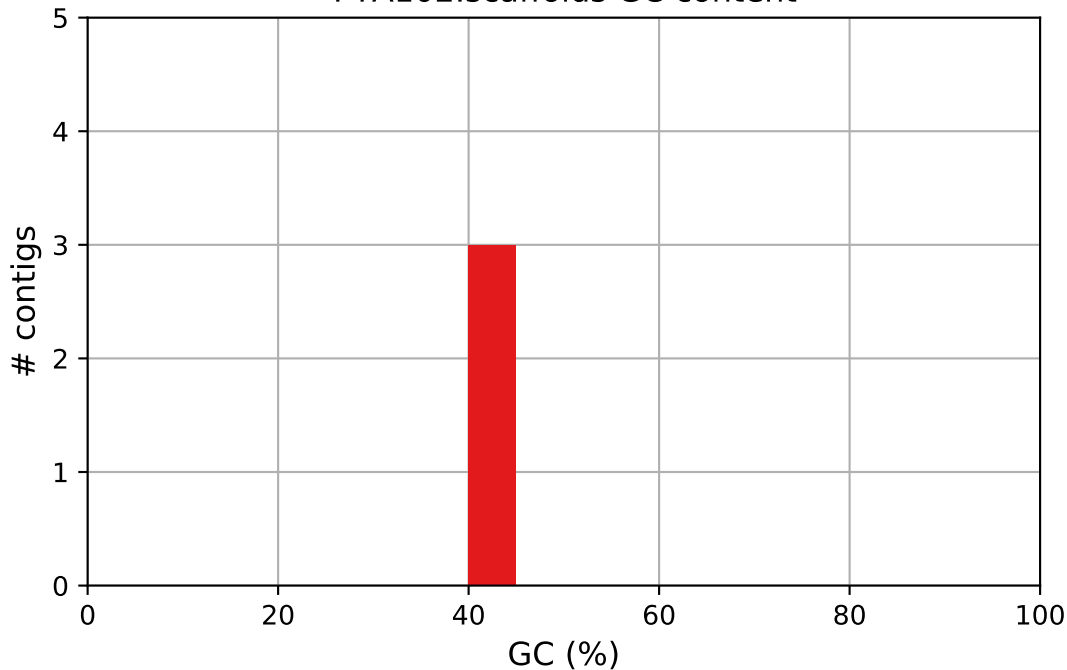


GC content



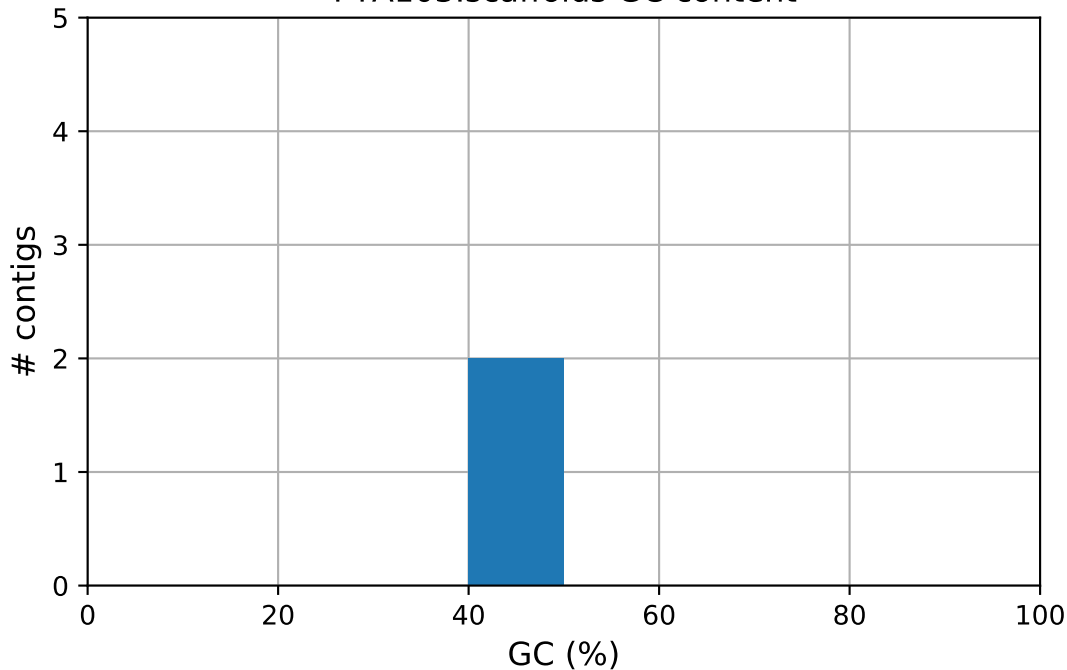
PTA102.scaffolds PTA128.scaffolds PTA132.scaffolds
PTA103.scaffolds PTA127.scaffolds Reference

PTA102.scaffolds GC content



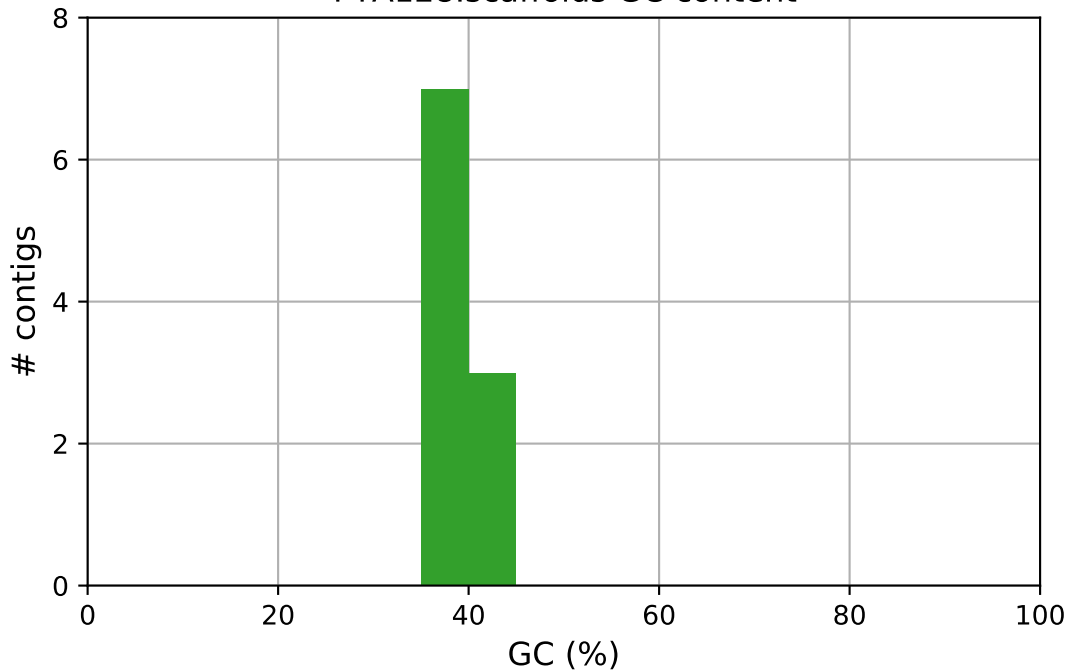
PTA102.scaffolds

PTA103.scaffolds GC content



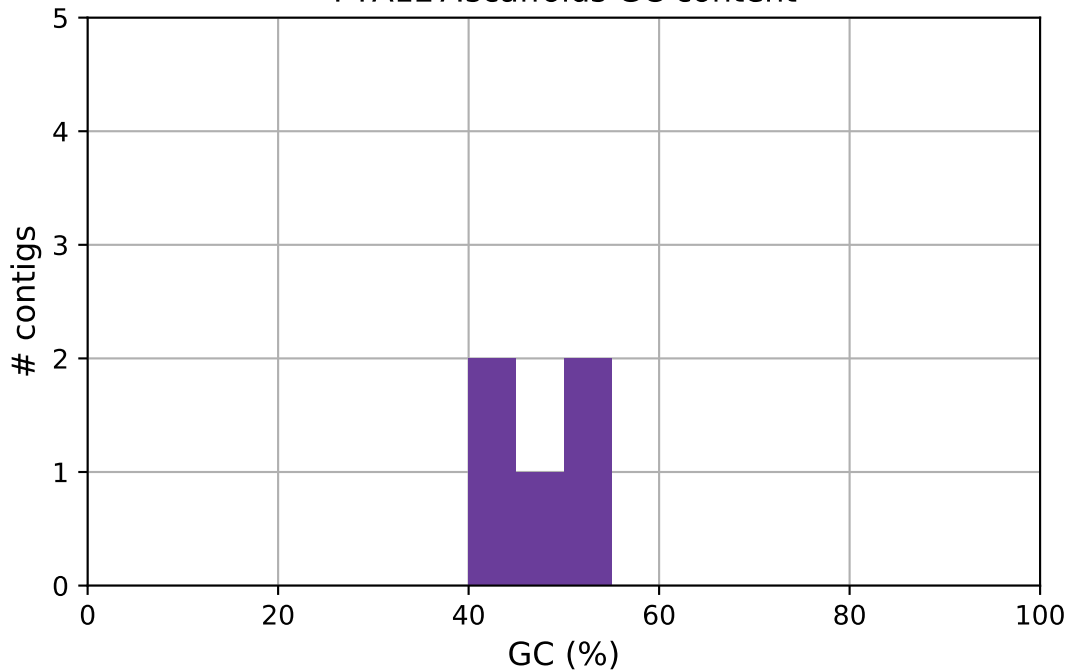
PTA103.scaffolds

PTA128.scaffolds GC content



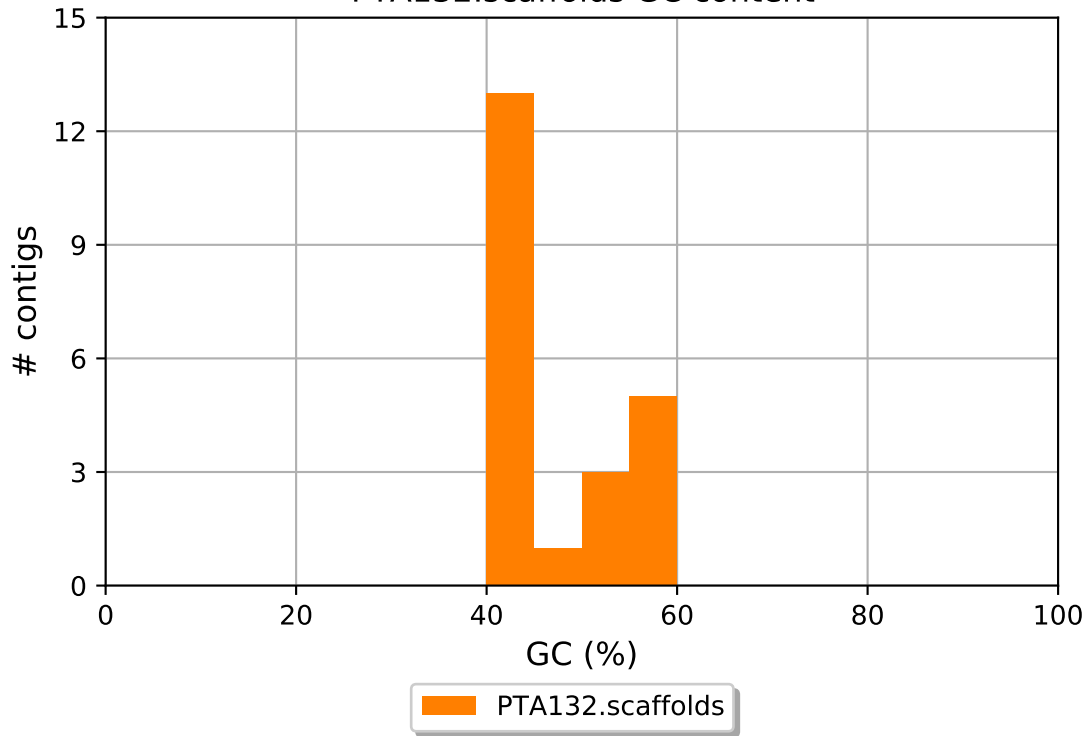
PTA128.scaffolds

PTA127.scaffolds GC content

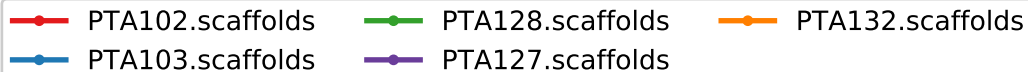
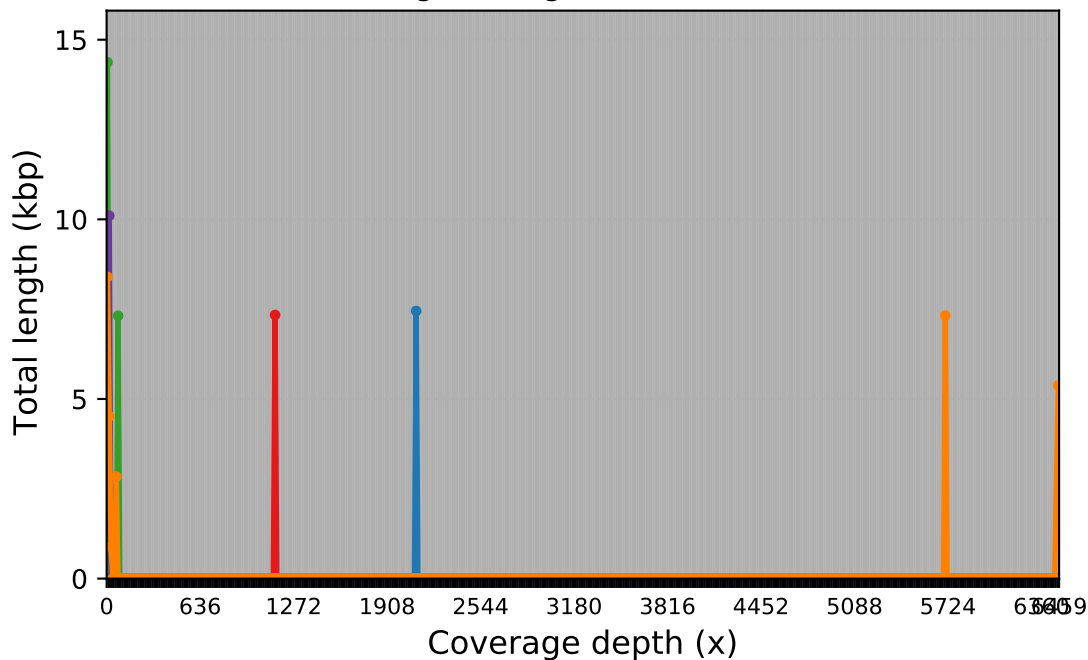


PTA127.scaffolds

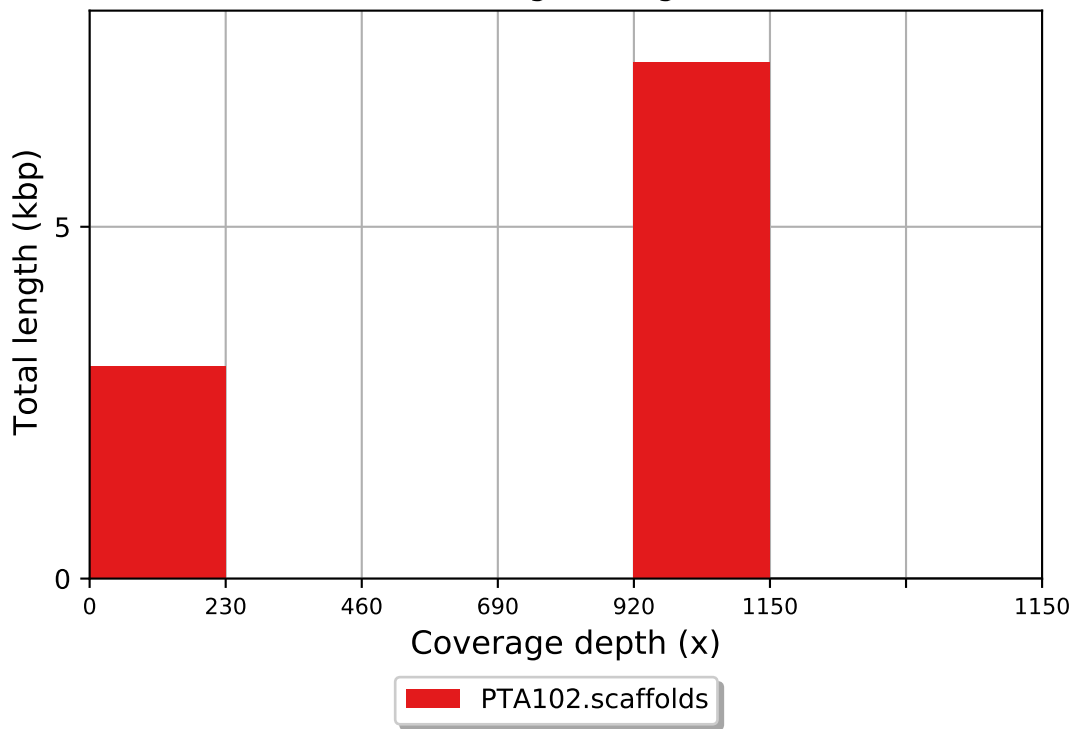
PTA132.scaffolds GC content



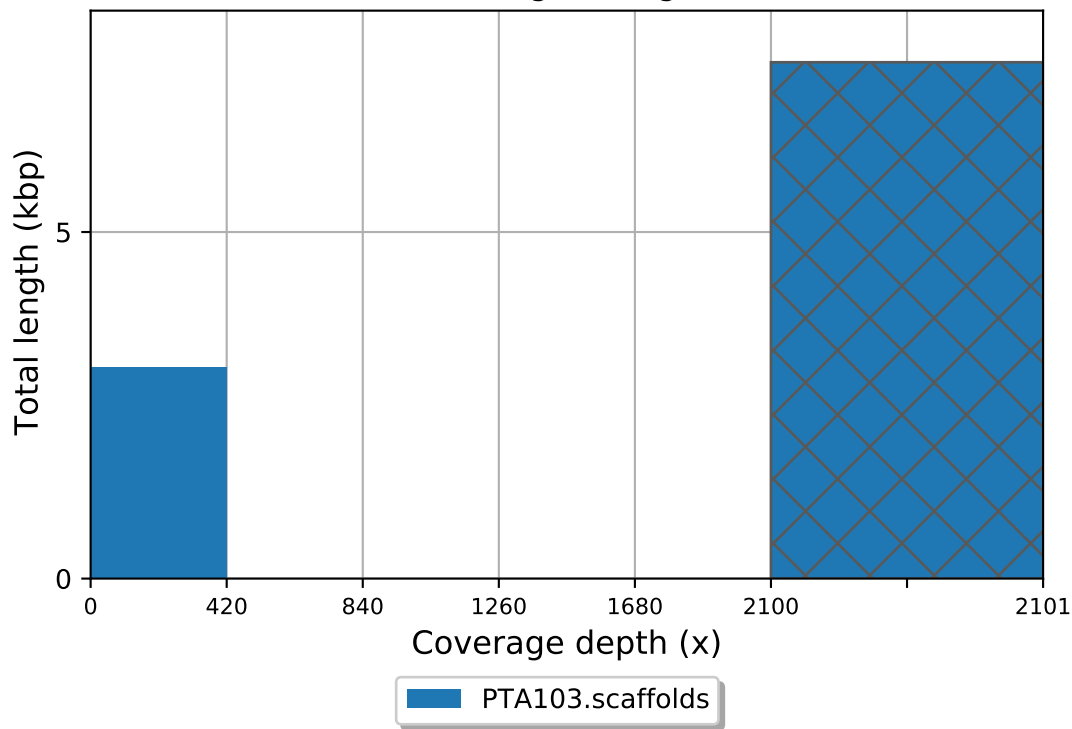
Coverage histogram (bin size: 12x)



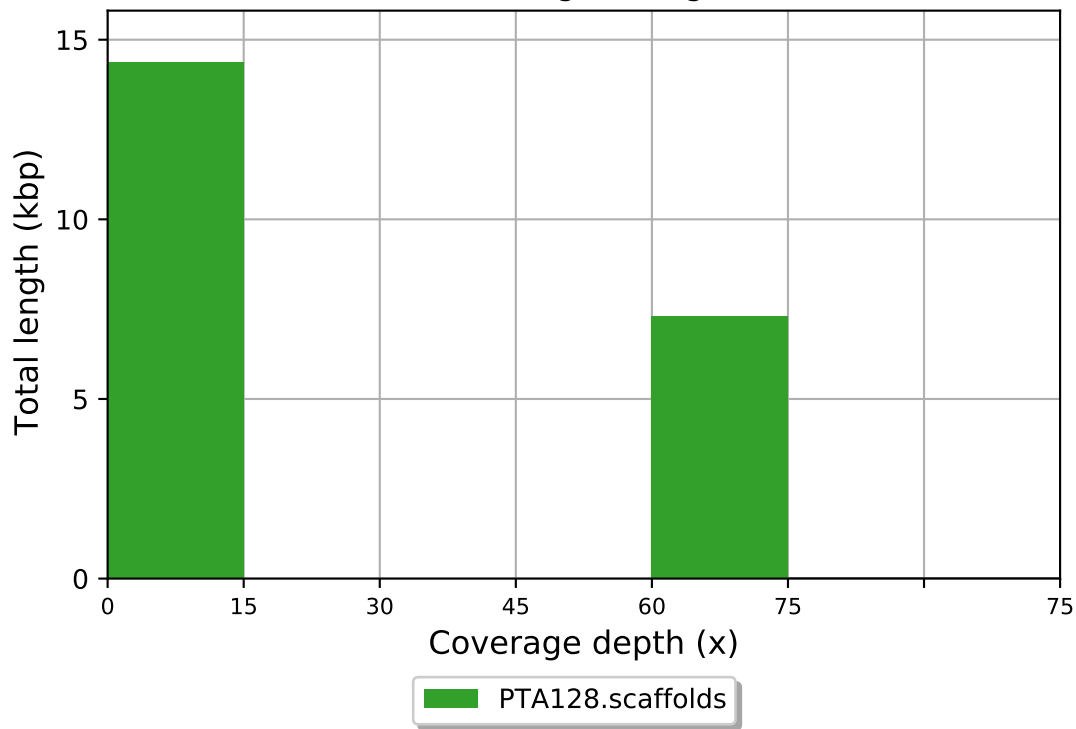
PTA102.scaffolds coverage histogram (bin size: 230x)



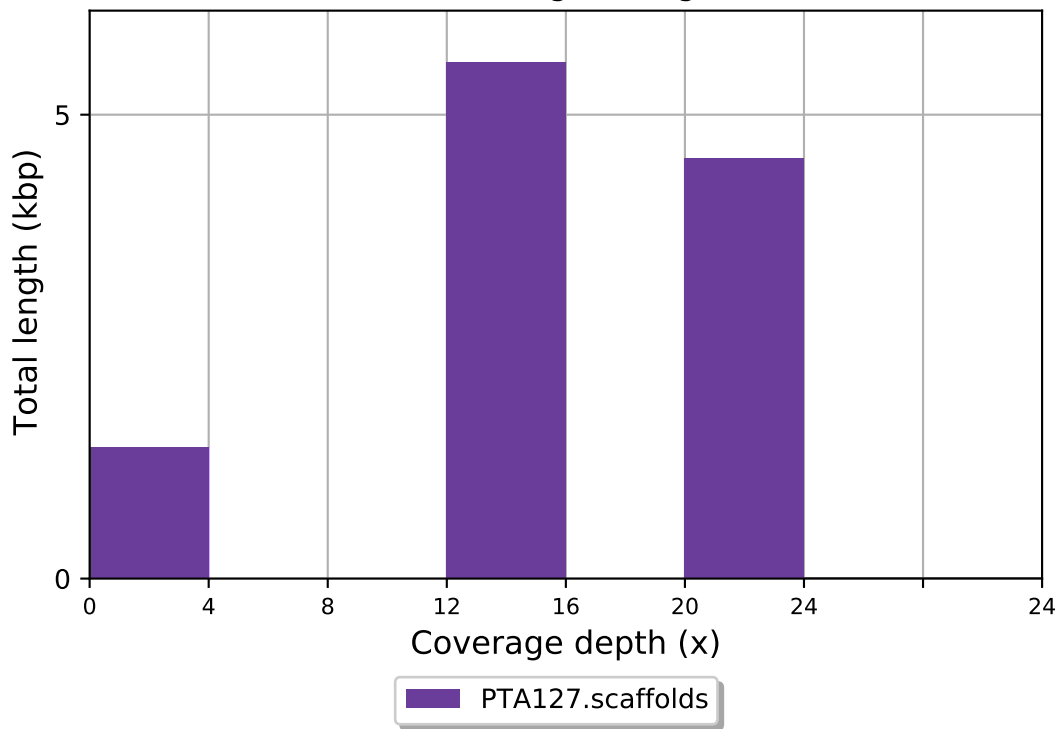
PTA103.scaffolds coverage histogram (bin size: 420x)



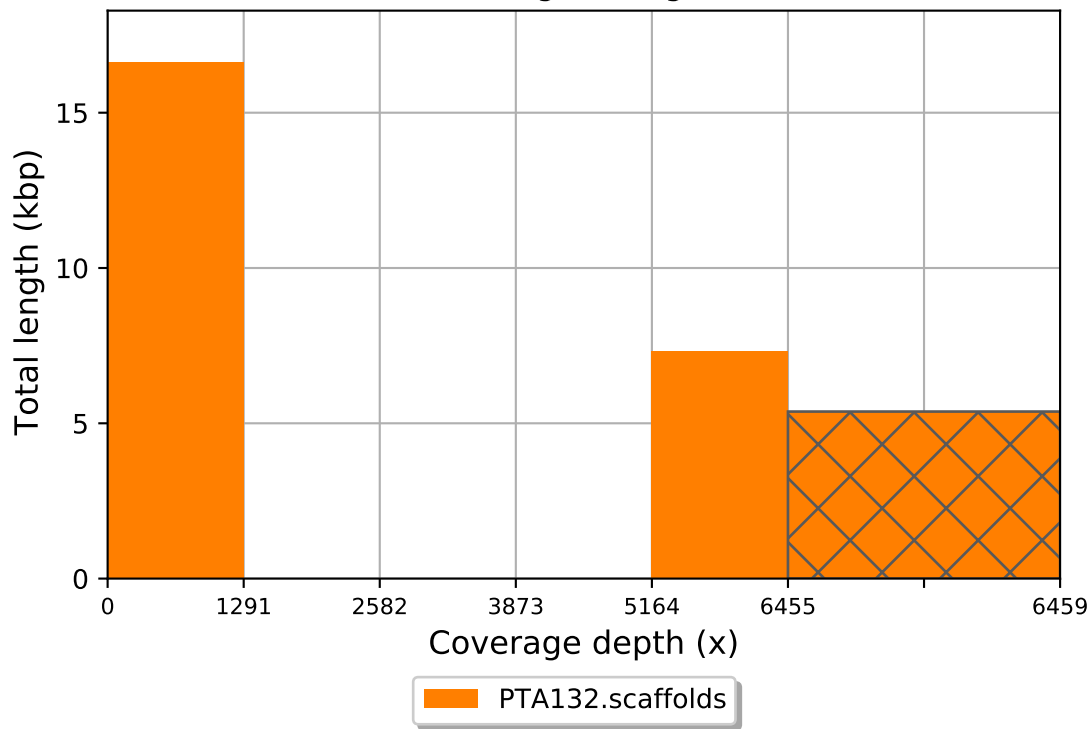
PTA128.scaffolds coverage histogram (bin size: 15x)



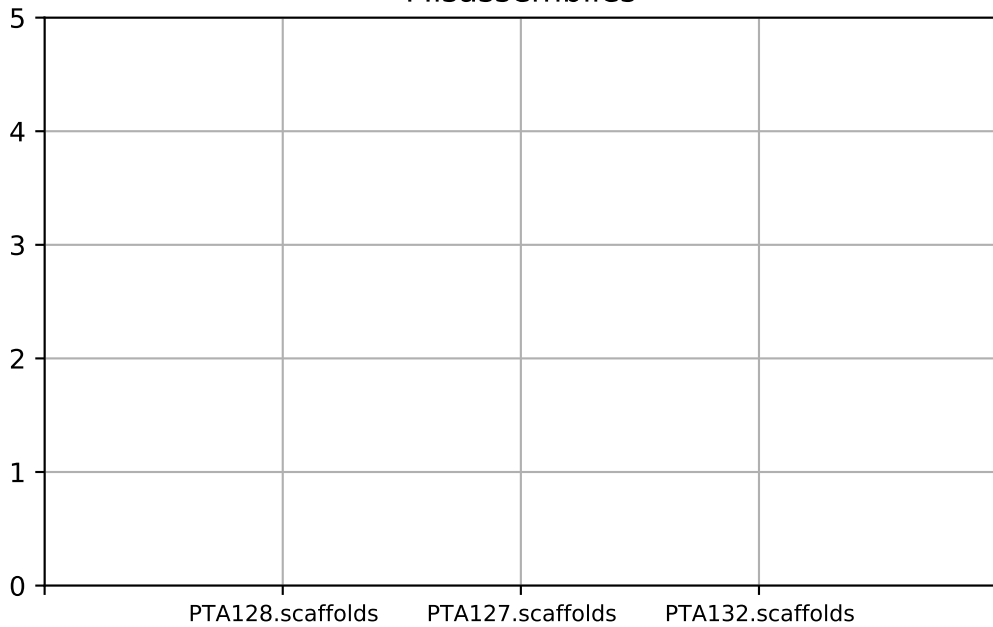
PTA127.scaffolds coverage histogram (bin size: 4x)



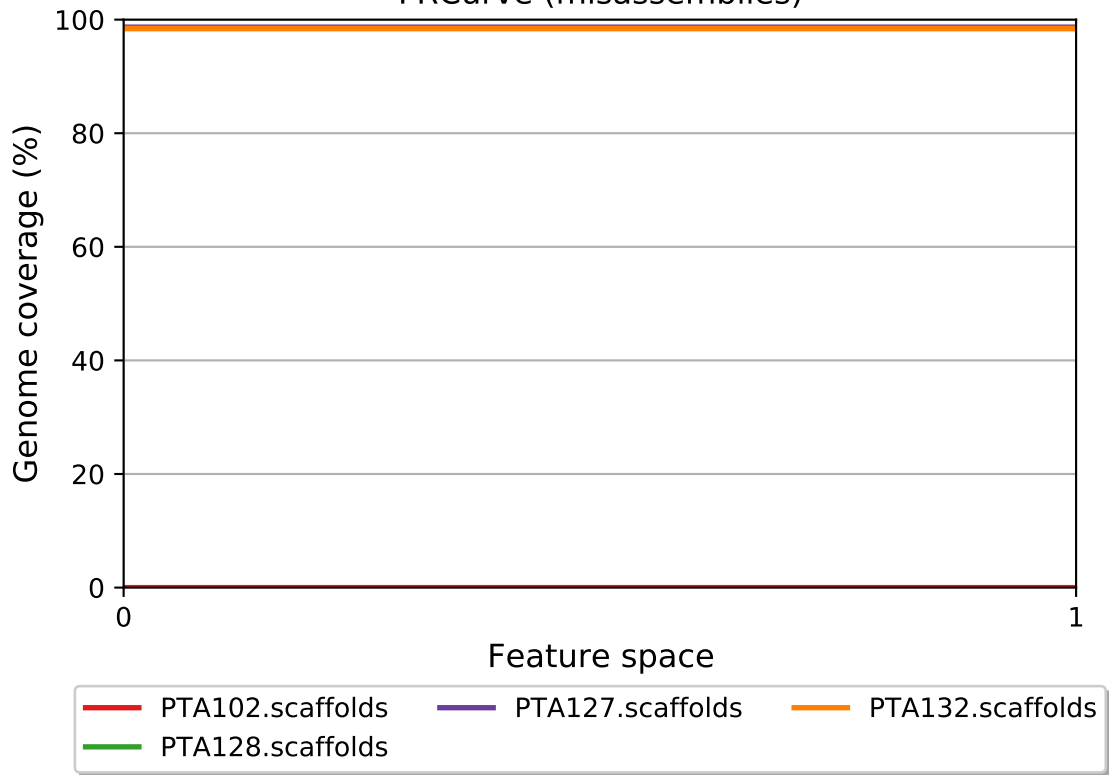
PTA132.scaffolds coverage histogram (bin size: 1291x)



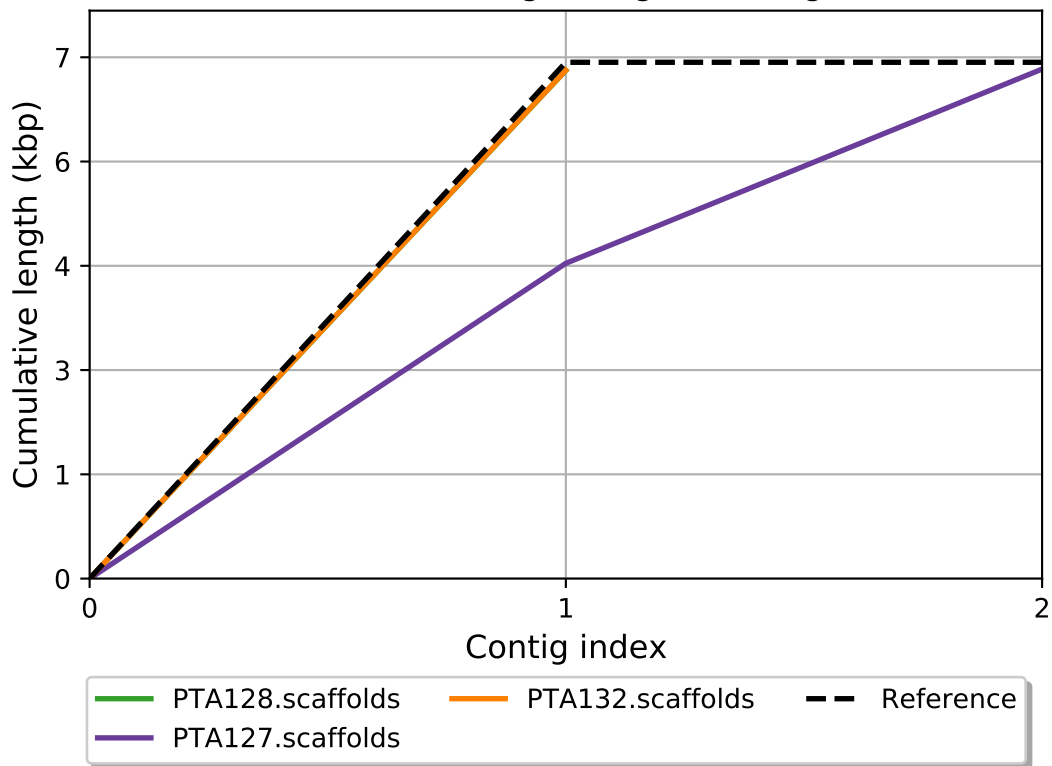
Misassemblies



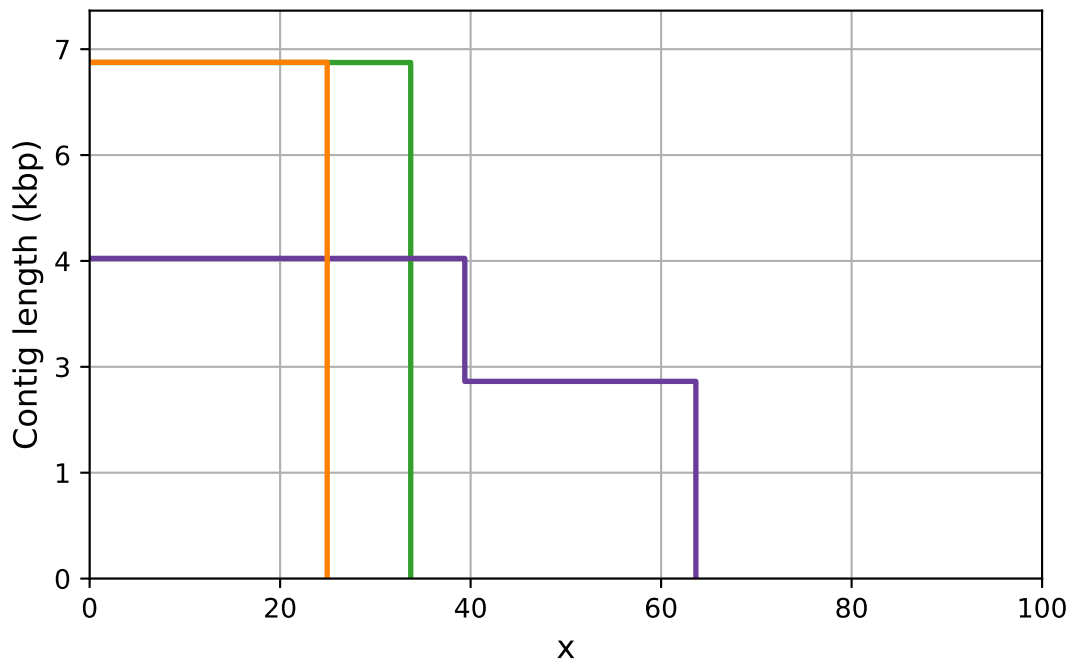
FRCurve (misassemblies)



Cumulative length (aligned contigs)

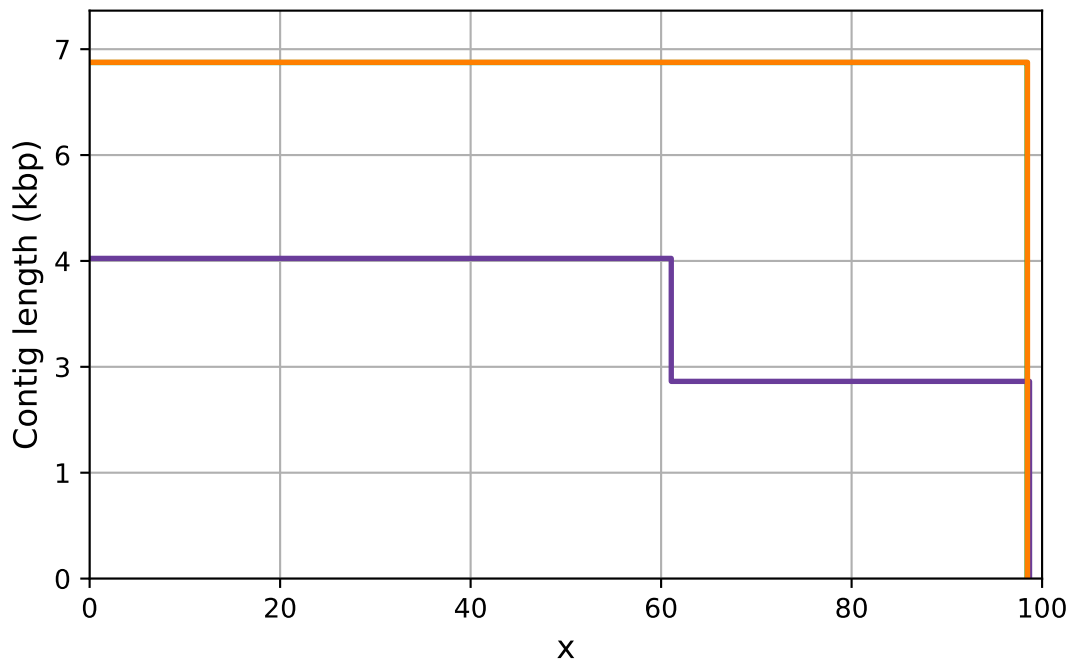


NAx



PTA128.scaffolds PTA127.scaffolds PTA132.scaffolds

NGAx



PTA128.scaffolds PTA127.scaffolds PTA132.scaffolds

Genome fraction, %

