

Report

	Pae21_unmappedregions
# contigs (>= 0 bp)	73
# contigs (>= 1000 bp)	50
# contigs (>= 5000 bp)	5
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	119043
Total length (>= 1000 bp)	107316
Total length (>= 5000 bp)	28777
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	62
Largest contig	7206
Total length	116027
Reference length	6654766
GC (%)	61.48
Reference GC (%)	66.09
N50	1692
N75	1457
L50	14
L75	34
# 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	0 + 0 part
Unaligned length	0
Genome fraction (%)	1.137
Duplication ratio	1.533
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	7206
Total aligned length	116027
NA50	1692
NGA50	-
NA75	1457
LA50	14
LA75	34

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

	Pae21_unmappedregions
# 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	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

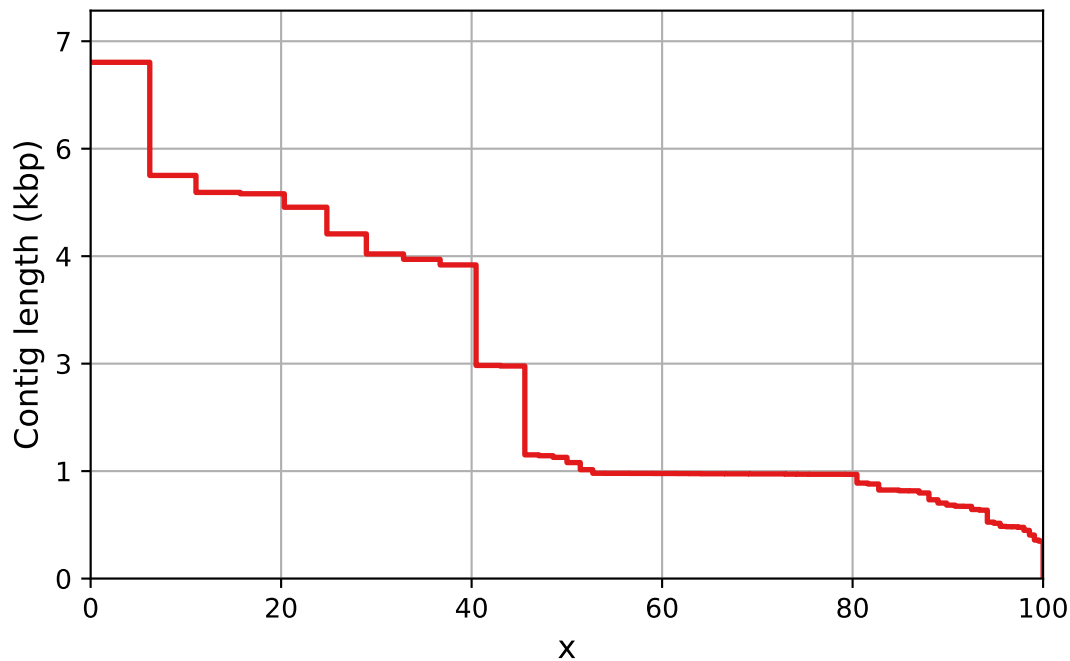
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	Pae21_unmappedregions
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

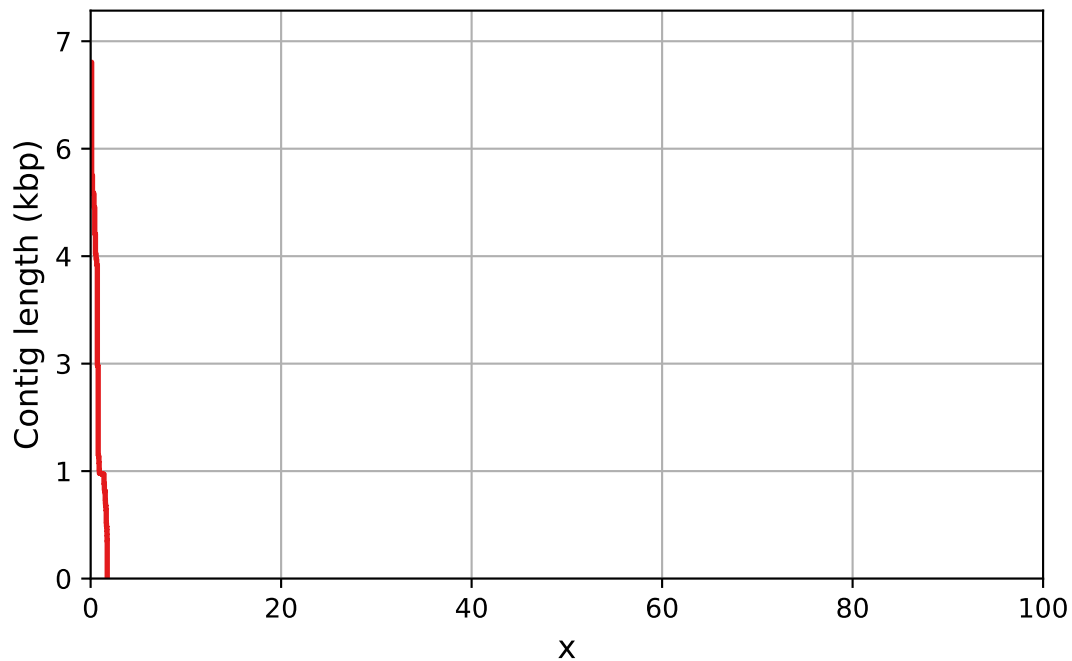
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



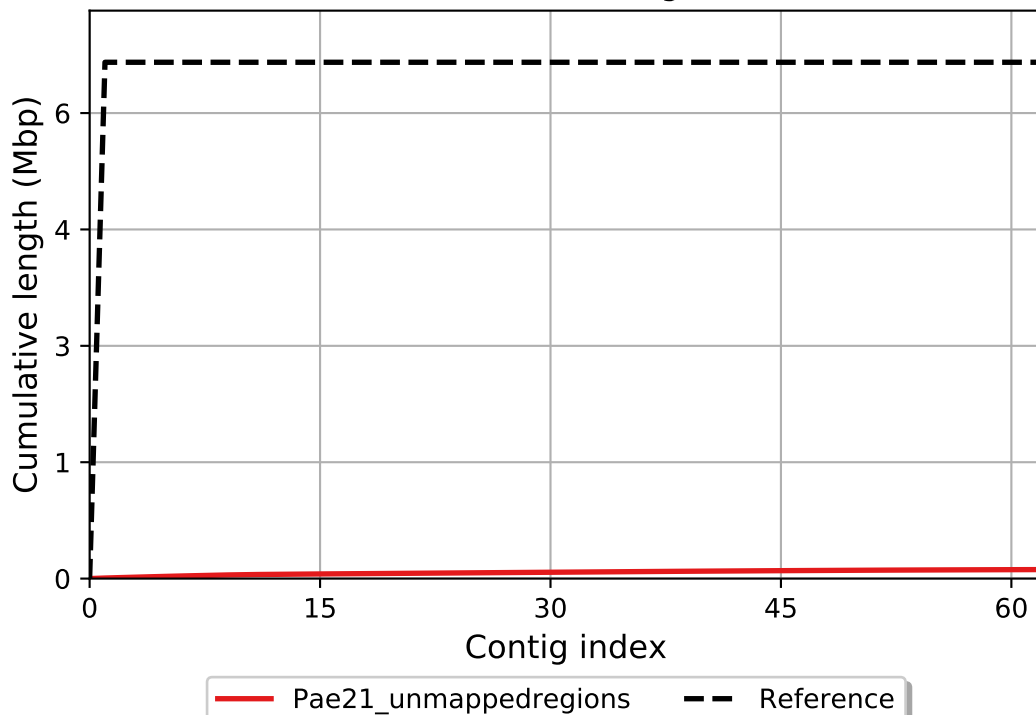
Pae21_unmappedregions

NGx

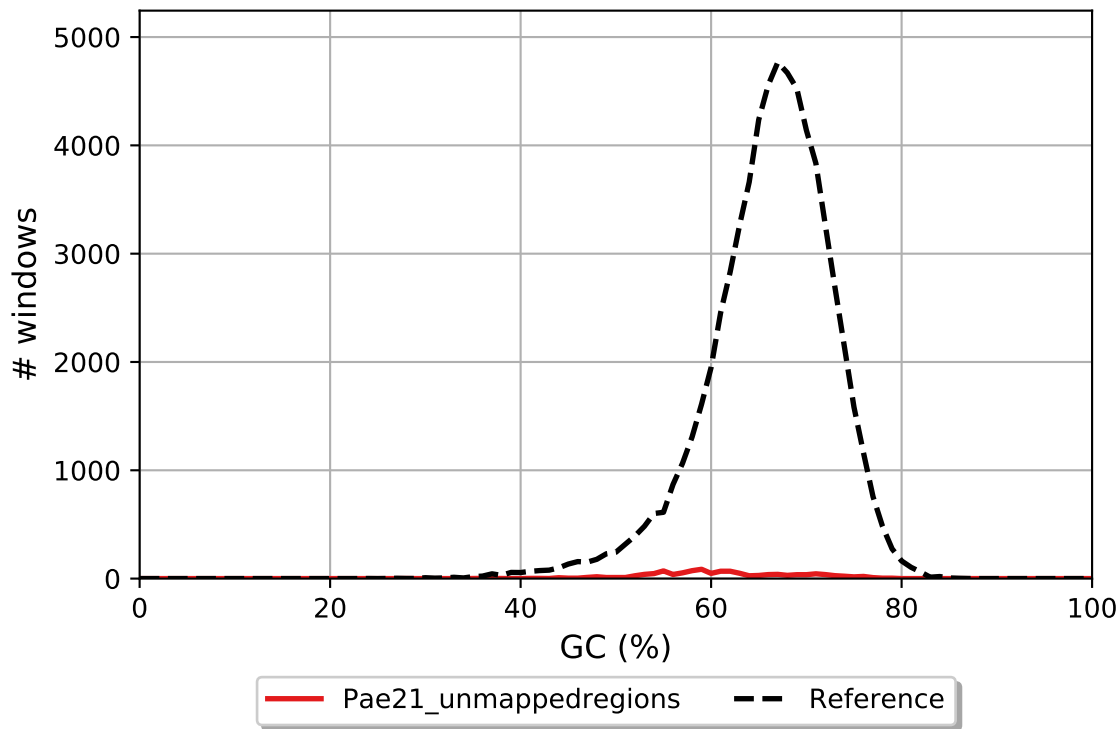


— Pae21_unmappedregions

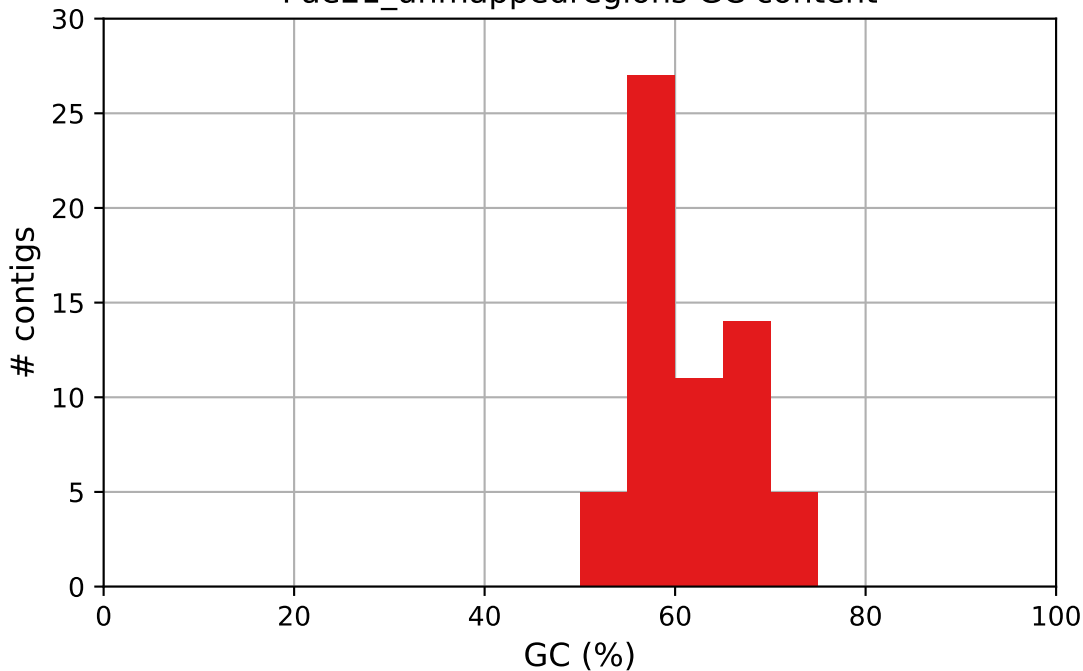
Cumulative length



GC content



Pae21_unmappedregions GC content

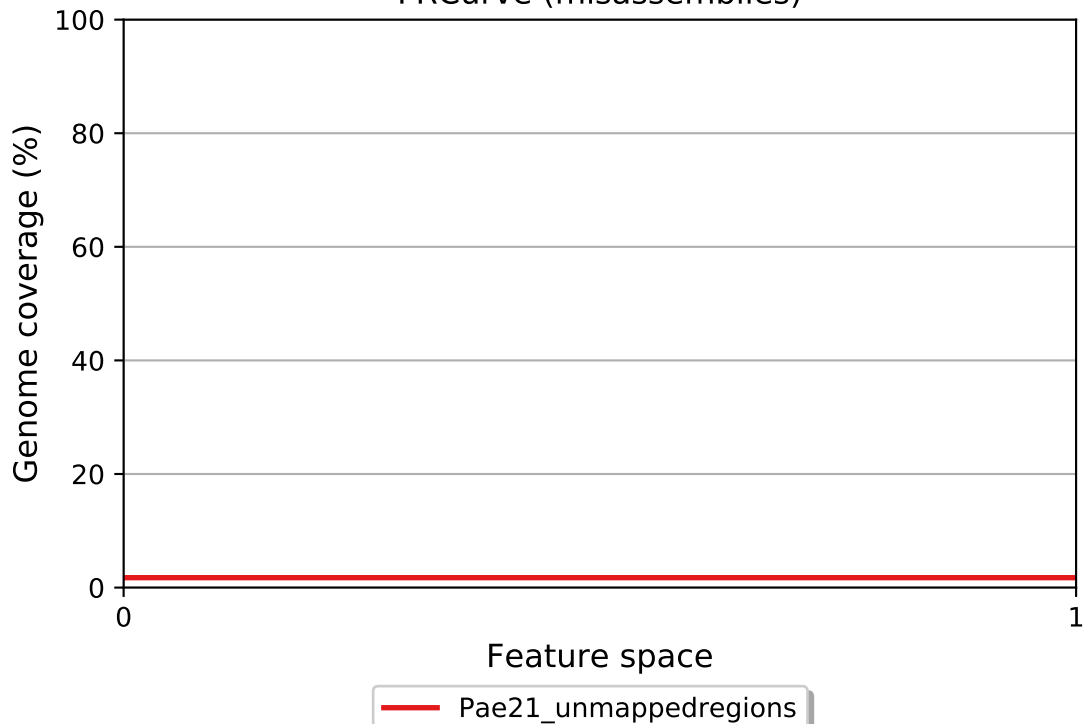


Pae21_unmappedregions

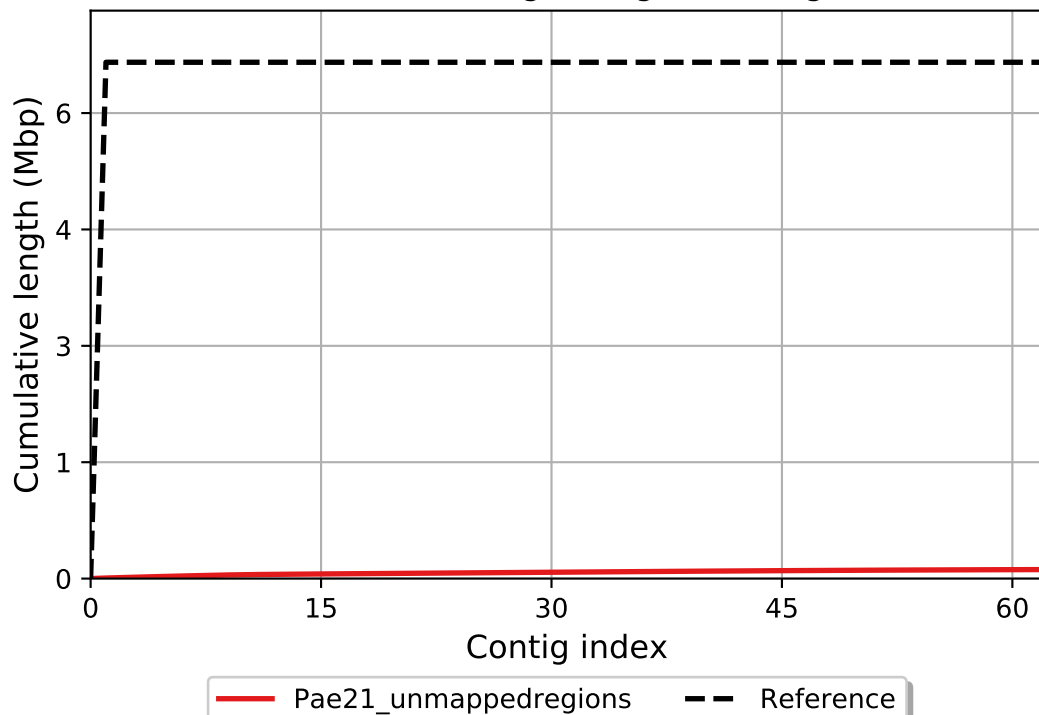
Misassemblies



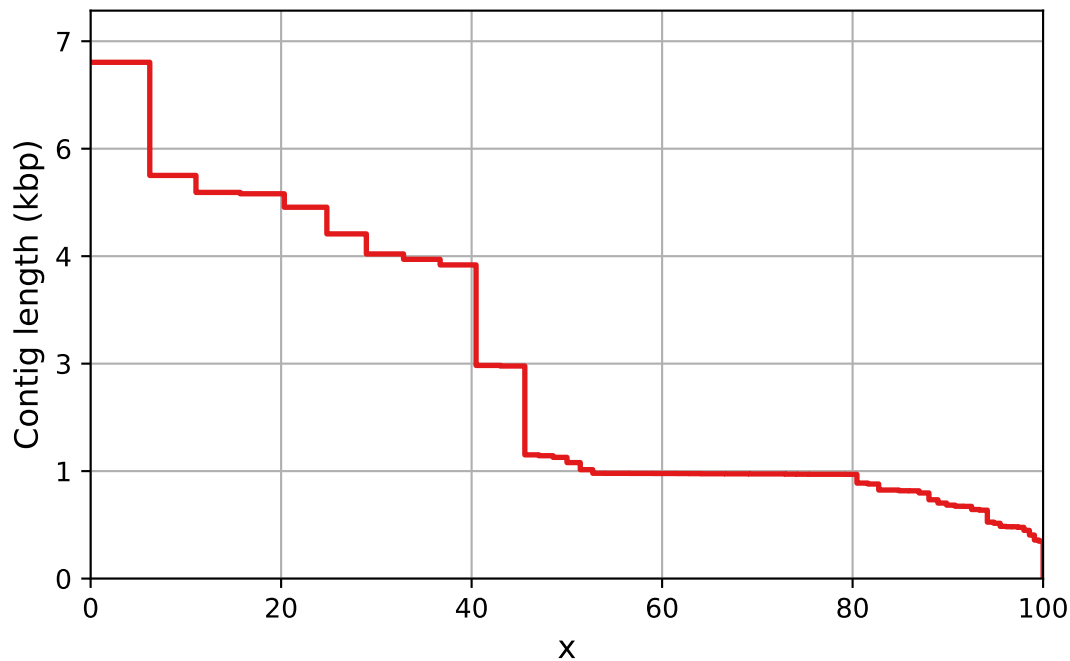
FRCurve (misassemblies)



Cumulative length (aligned contigs)

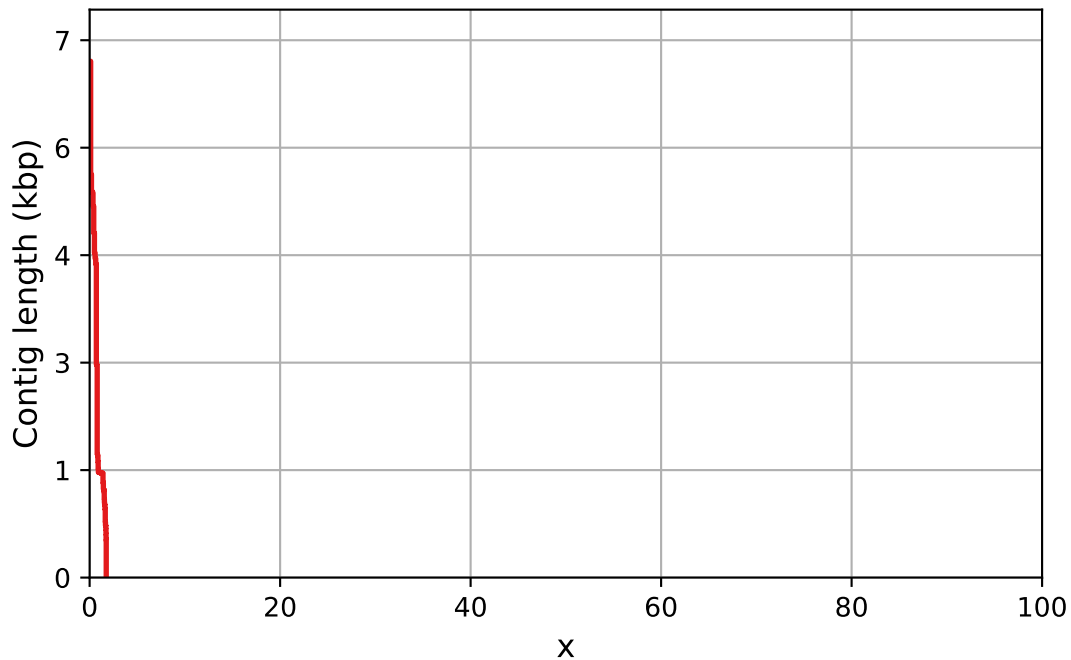


NAx



— Pae21_unmappedregions

NGAx



— Pae21_unmappedregions