

# Report

	maternal.p_ctg	maternal.p_utg
# contigs (>= 0 bp)	235	249
# contigs (>= 1000 bp)	235	249
# contigs (>= 5000 bp)	235	249
# contigs (>= 10000 bp)	235	249
# contigs (>= 25000 bp)	207	213
# contigs (>= 50000 bp)	30	29
Total length (>= 0 bp)	8948377	9210770
Total length (>= 1000 bp)	8948377	9210770
Total length (>= 5000 bp)	8948377	9210770
Total length (>= 10000 bp)	8948377	9210770
Total length (>= 25000 bp)	8319260	8423696
Total length (>= 50000 bp)	2136332	2024991
# contigs	235	249
Largest contig	207945	207945
Total length	8948377	9210770
Reference length	152958180	152958180
GC (%)	36.53	36.81
Reference GC (%)	35.92	35.92
N50	38042	36614
N75	30503	30153
L50	85	90
L75	150	159
# misassemblies	1007	1019
# misassembled contigs	204	214
Misassembled contigs length	7944312	8167737
# local misassemblies	2661	2667
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	13	14
# unaligned contigs	0 + 205 part	0 + 209 part
Unaligned length	1900162	1954182
Genome fraction (%)	4.247	4.239
Duplication ratio	1.085	1.119
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	3052.29	3090.79
# indels per 100 kbp	427.60	433.30
# genomic features	28508 + 3859 part	28487 + 3857 part
Largest alignment	63484	63484
Total aligned length	6978825	7172833
NA50	8380	8430
NGA50	-	-
NA75	990	990
LA50	268	275
LA75	905	923

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

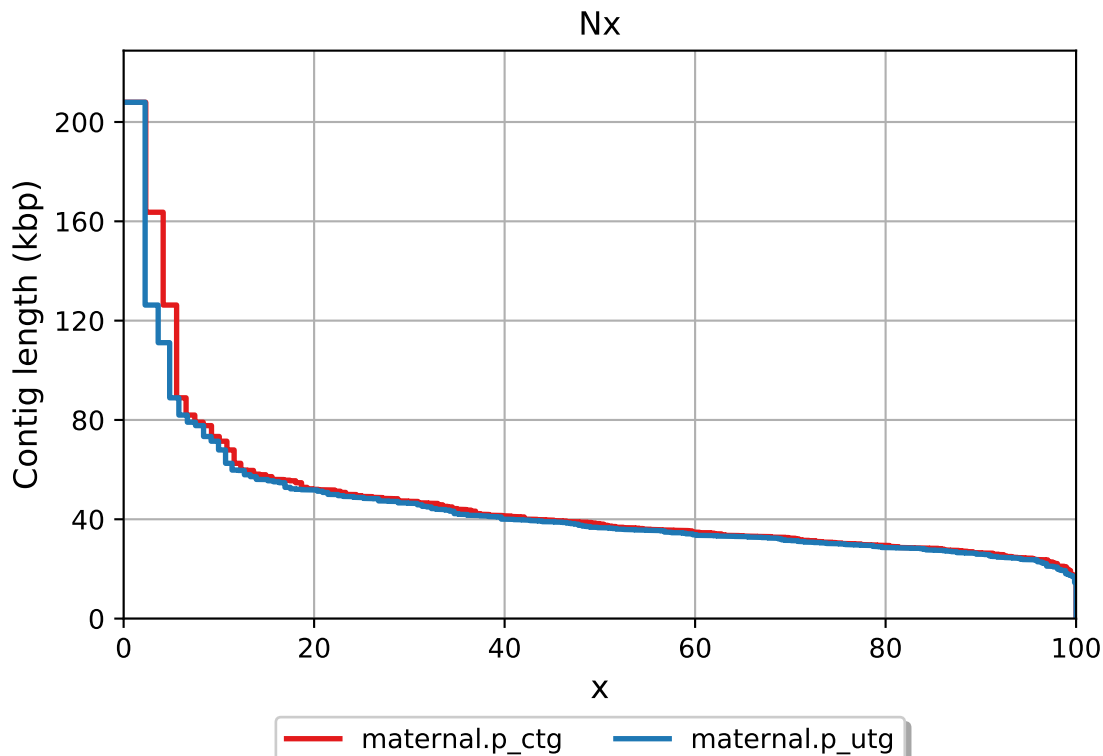
	maternal.p_ctg	maternal.p_utg
# misassemblies	1007	1019
# contig misassemblies	1007	1019
# c. relocations	435	443
# c. translocations	572	576
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	204	214
Misassembled contigs length	7944312	8167737
# local misassemblies	2661	2667
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	13	14
# mismatches	198250	200368
# indels	27773	28090
# indels (<= 5 bp)	23606	23893
# indels (> 5 bp)	4167	4197
Indels length	108215	109396

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

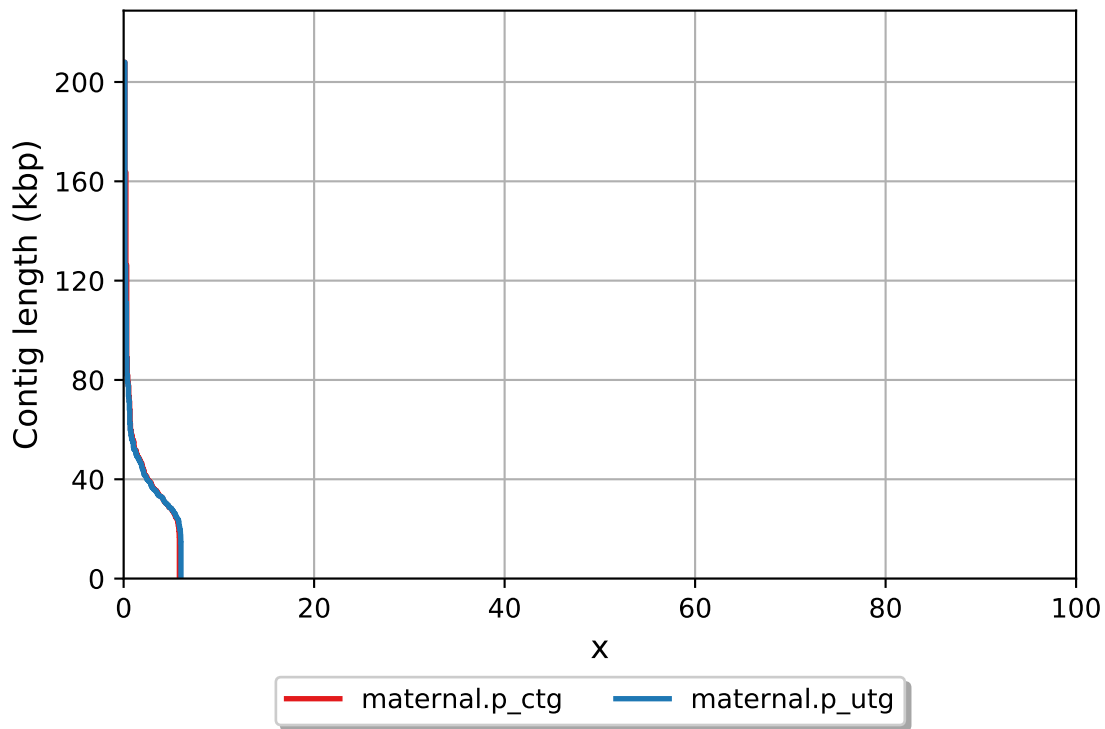
## Unaligned report

	maternal.p_ctg	maternal.p_utg
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	205	209
Partially unaligned length	1900162	1954182
# N's	0	0

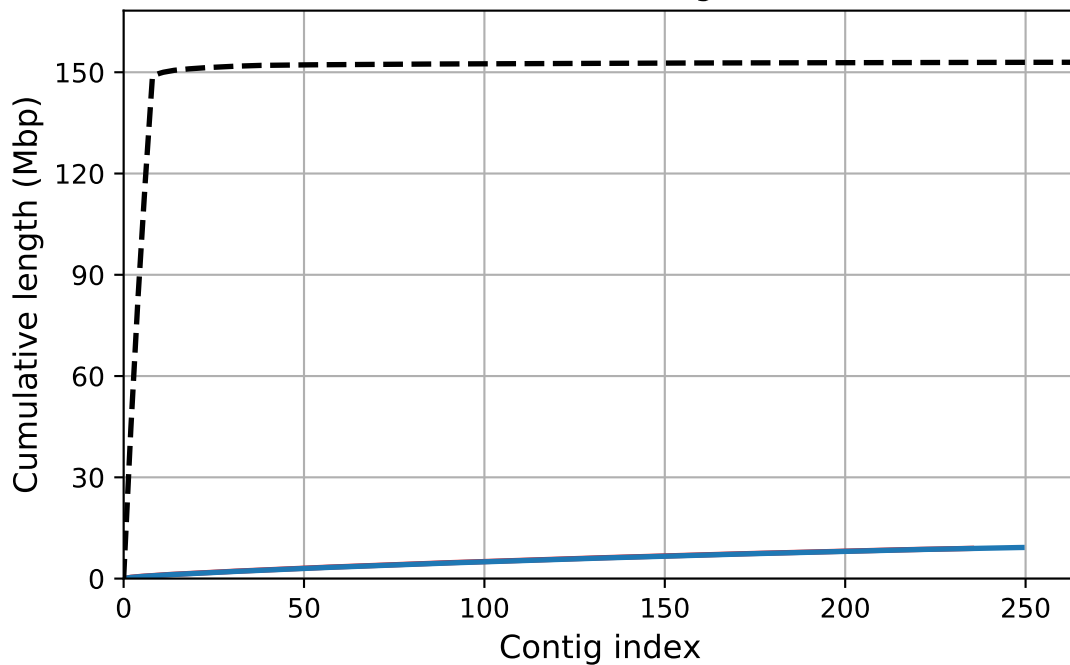
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



# NGx

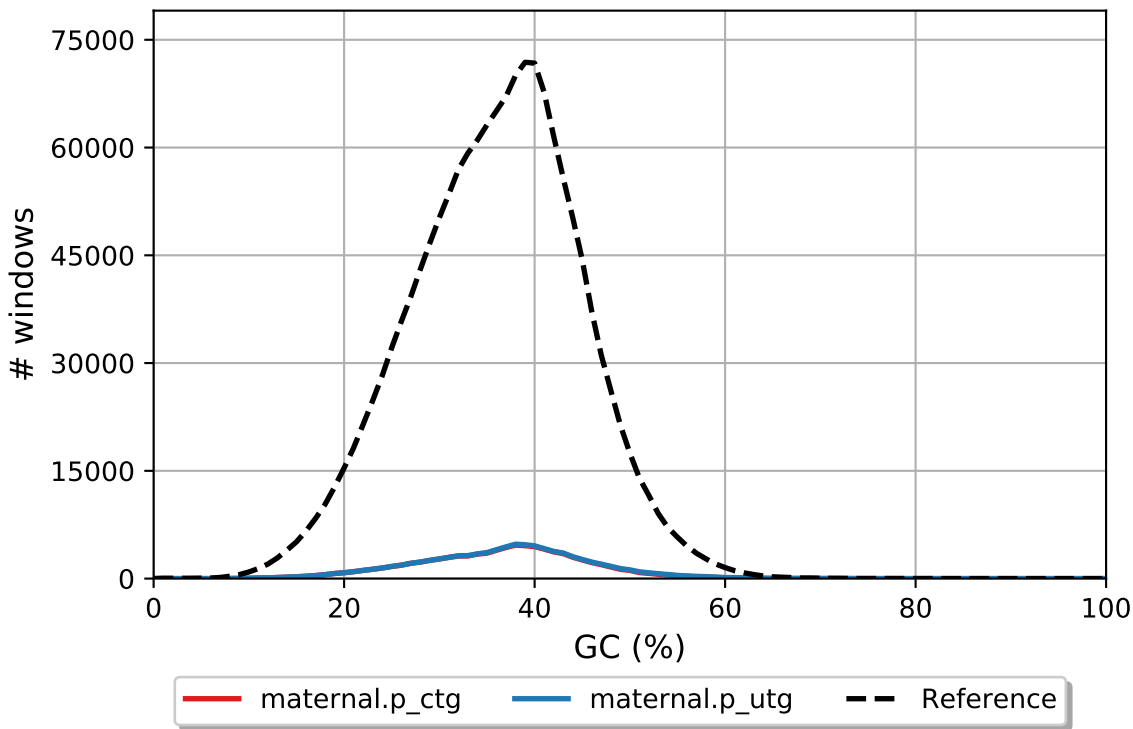


Cumulative length

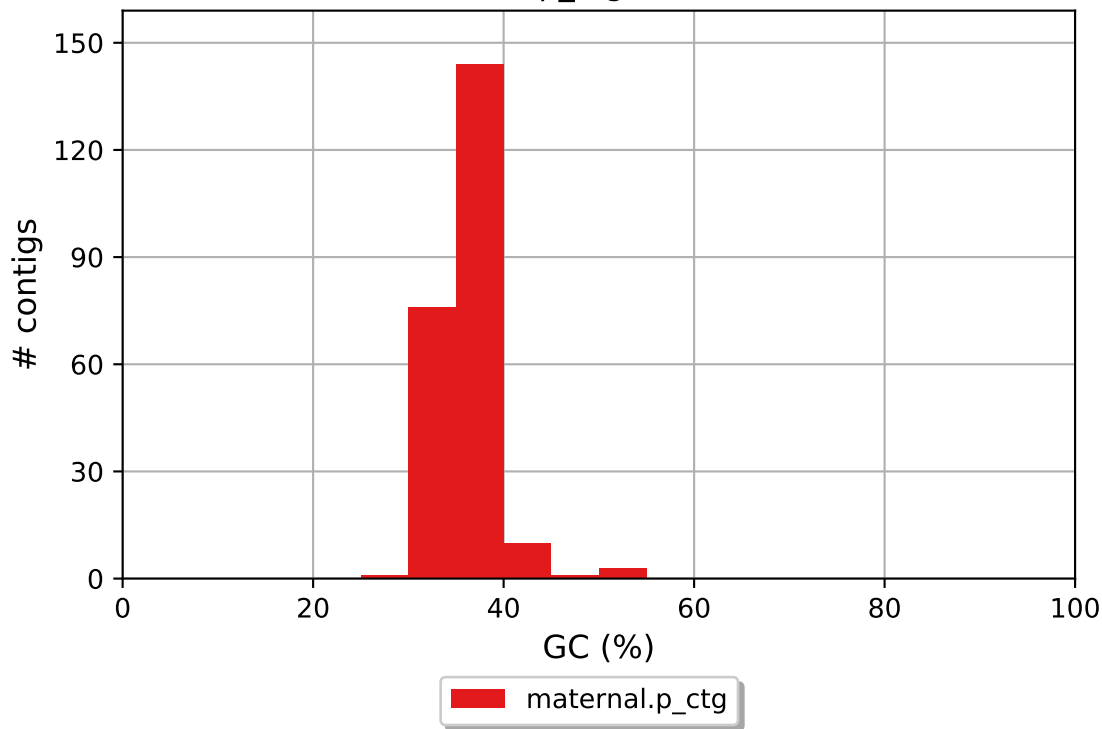


maternal.p\_ctg    maternal.p\_utg    Reference

GC content

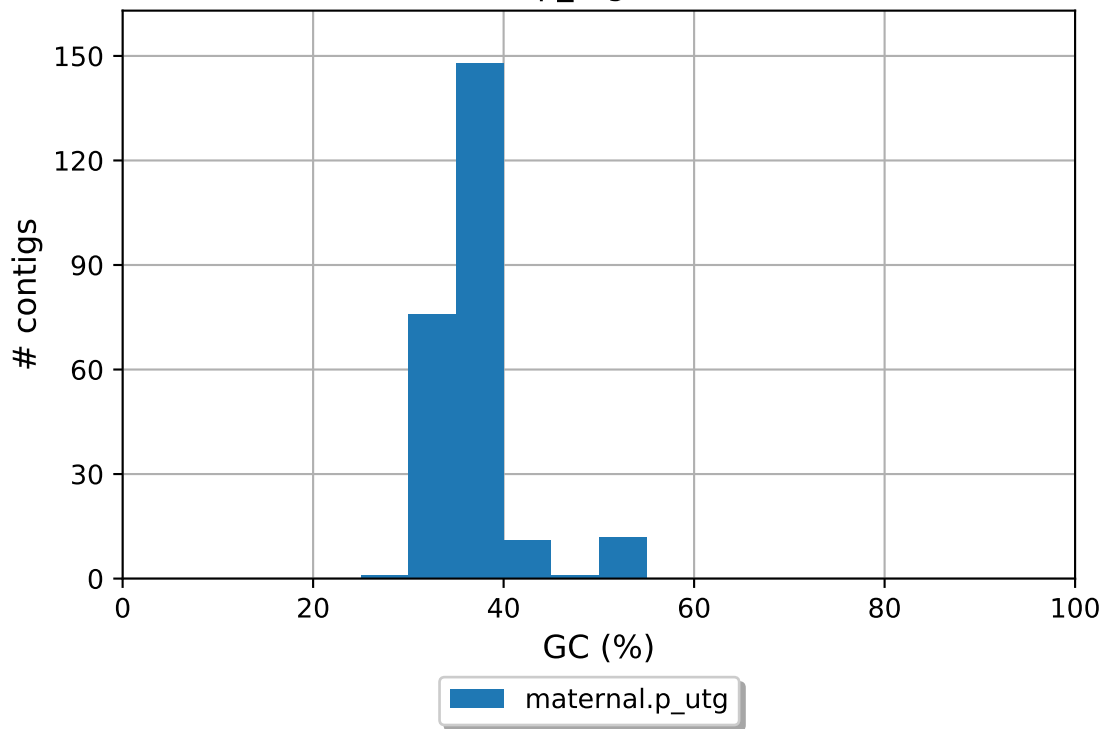


maternal.p\_ctg GC content

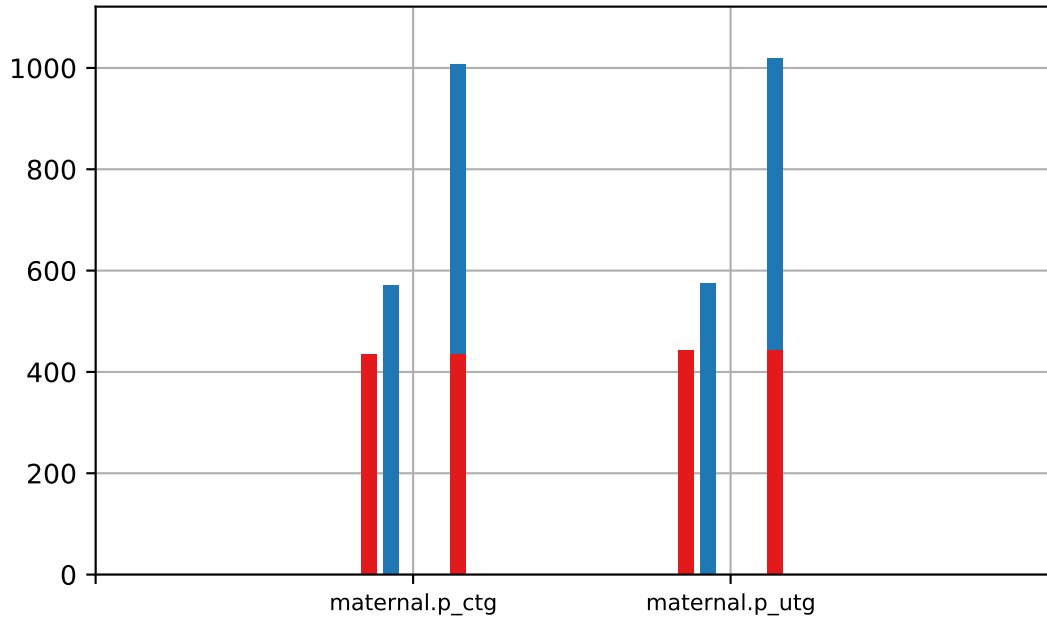




maternal.p\_utg GC content



## Misassemblies

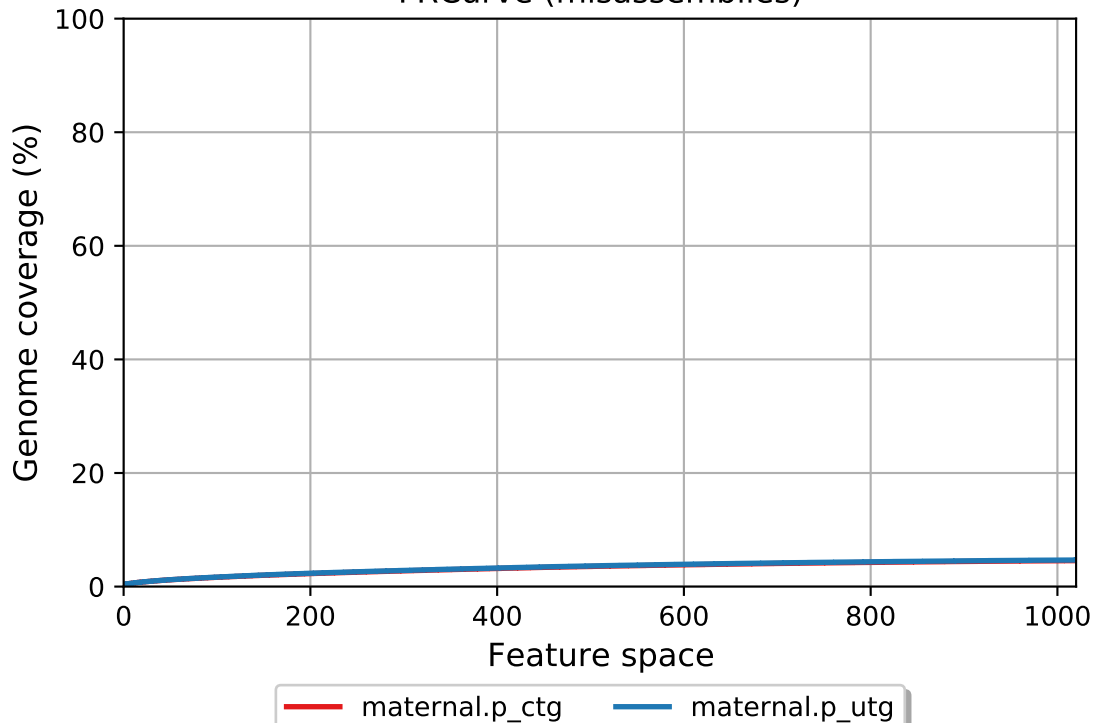


# relocations

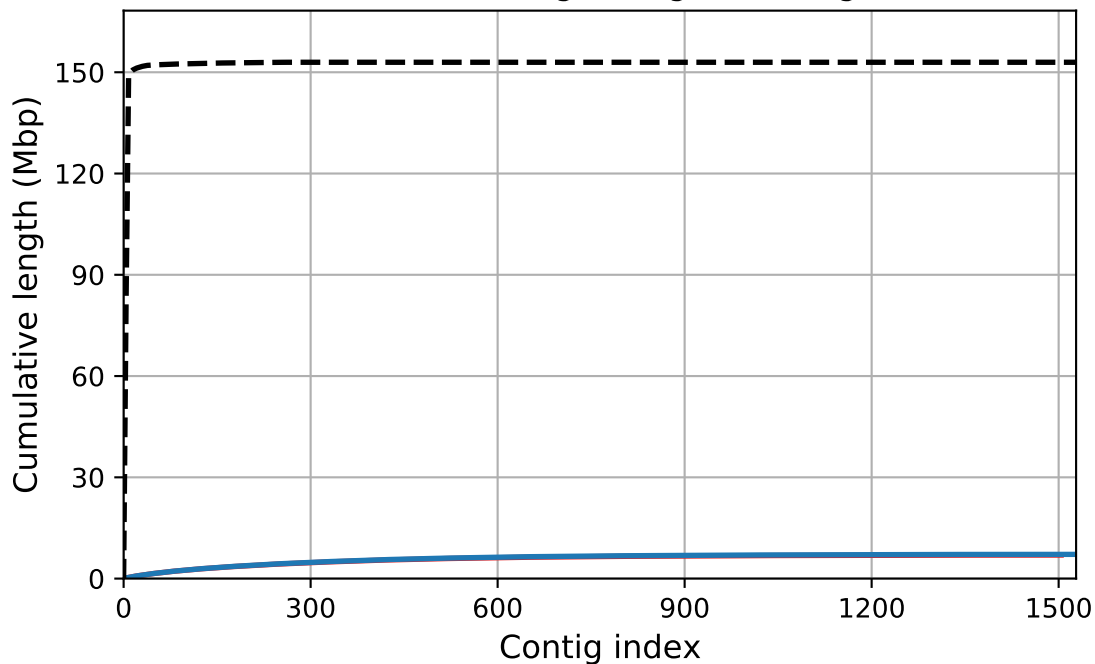


# translocations

FRCurve (misassemblies)

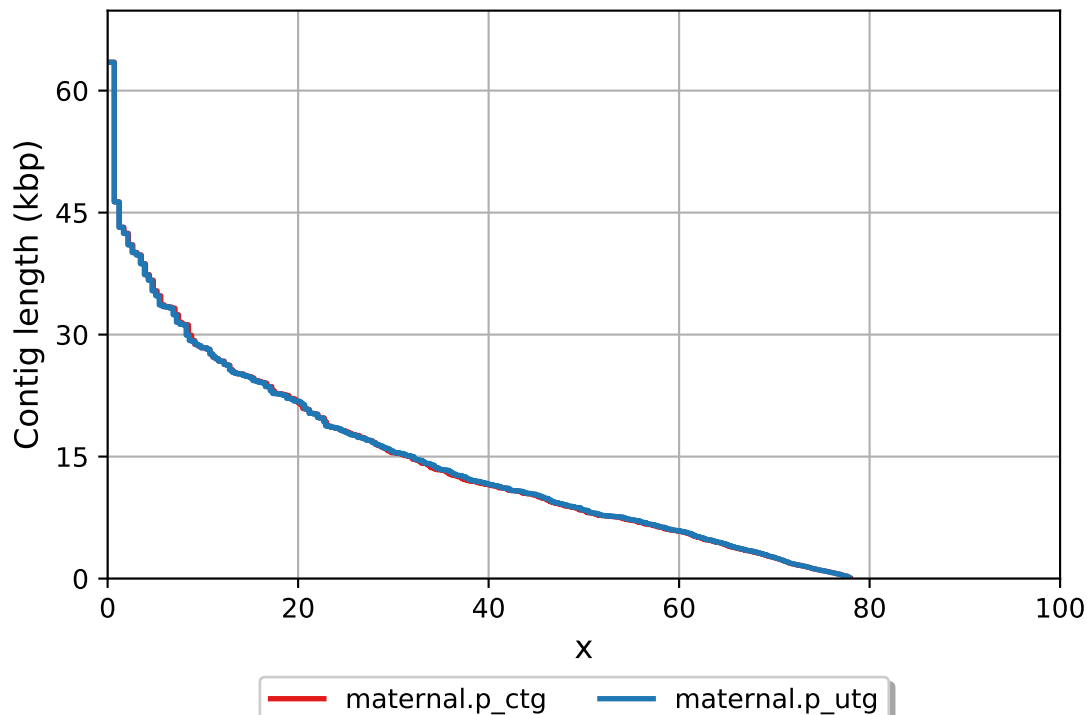


Cumulative length (aligned contigs)

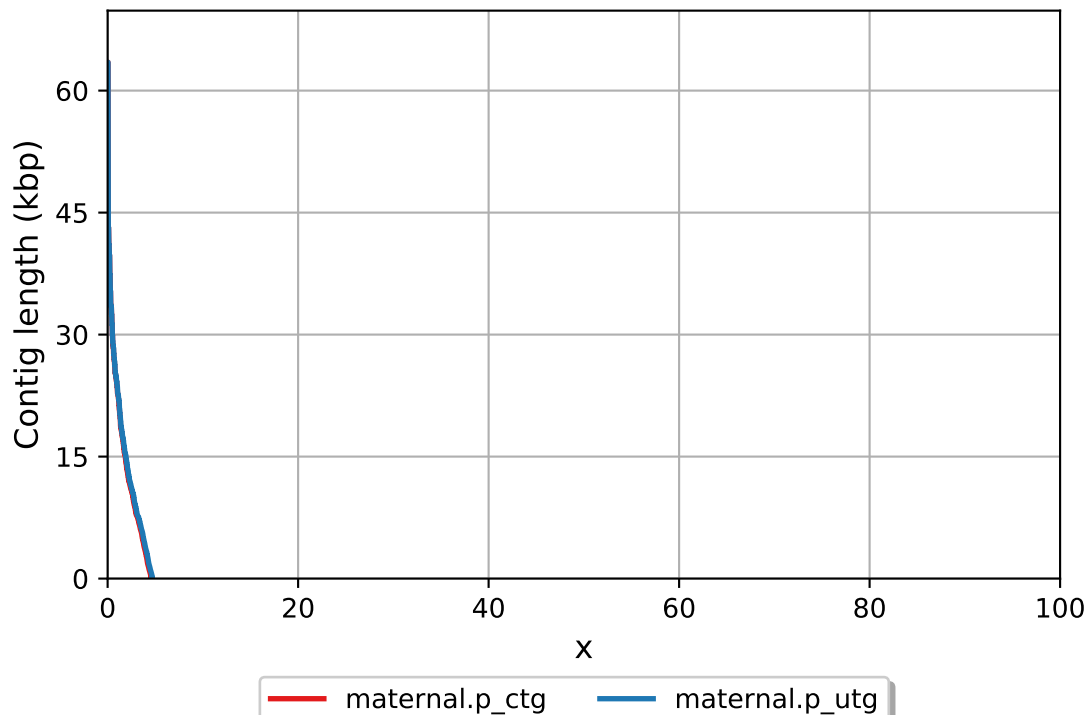


maternal.p\_ctg    maternal.p\_utg    Reference

NAx

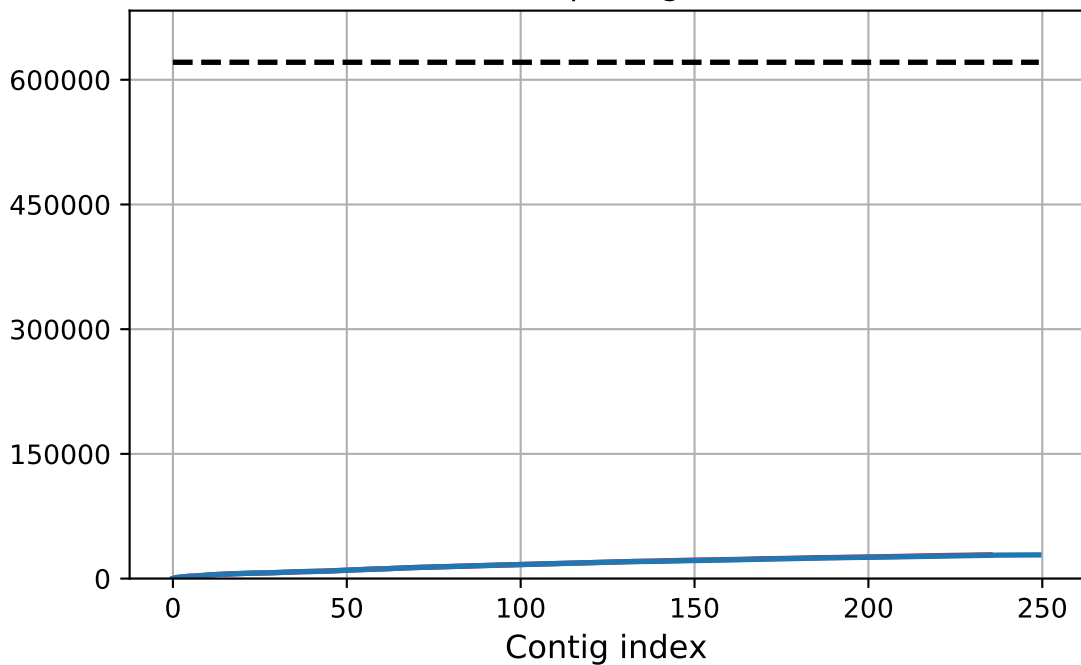


## NGAx



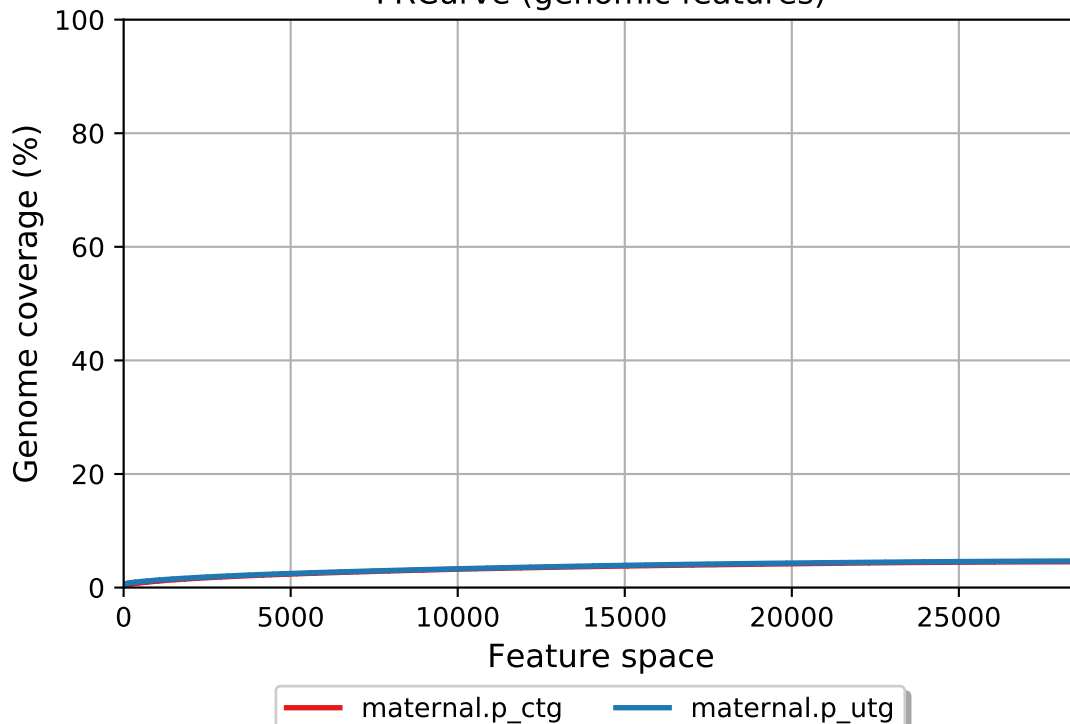
Cumulative # complete genomic features

Cumulative # complete genomic features



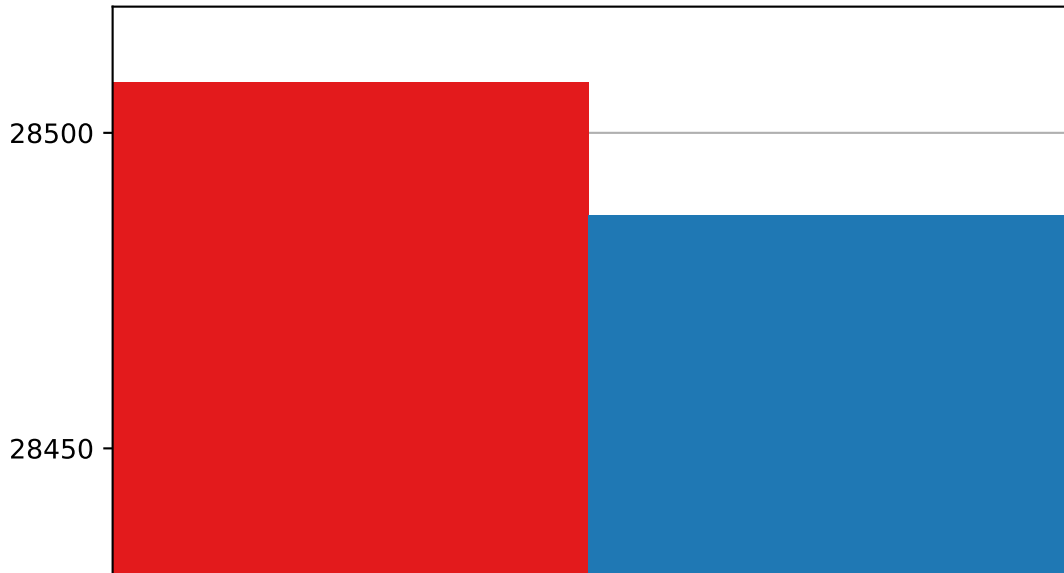
maternal.p\_ctg maternal.p\_utg Reference

FRCurve (genomic features)





# complete genomic features



maternal.p\_ctg



maternal.p\_utg

# Genome fraction, %

100

50



maternal.p\_ctg



maternal.p\_utg