

Report

	maternal.bp.hap1.p_ctg	maternal.bp.hap2.p_ctg
# contigs (>= 0 bp)	236	6
# contigs (>= 1000 bp)	236	6
# contigs (>= 5000 bp)	236	6
# contigs (>= 10000 bp)	236	6
# contigs (>= 25000 bp)	207	4
# contigs (>= 50000 bp)	29	1
Total length (>= 0 bp)	8947302	290950
Total length (>= 1000 bp)	8947302	290950
Total length (>= 5000 bp)	8947302	290950
Total length (>= 10000 bp)	8947302	290950
Total length (>= 25000 bp)	8293490	258832
Total length (>= 50000 bp)	2080599	163655
# contigs	236	6
Largest contig	207945	163655
Total length	8947302	290950
Reference length	152958180	152958180
GC (%)	36.53	41.50
Reference GC (%)	35.92	35.92
N50	37567	163655
N75	30432	32607
L50	85	1
L75	151	3
# misassemblies	1007	8
# misassembled contigs	205	5
Misassembled contigs length	7943237	127295
# local misassemblies	2664	3
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	13	1
# unaligned contigs	0 + 205 part	0 + 1 part
Unaligned length	1899517	118964
Genome fraction (%)	4.238	0.062
Duplication ratio	1.087	1.802
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	3052.82	2279.35
# indels per 100 kbp	428.09	332.06
# genomic features	28478 + 3859 part	239 + 22 part
Largest alignment	63484	24354
Total aligned length	6968487	173916
NA50	8380	4846
NGA50	-	-
NA75	985	-
LA50	267	11
LA75	907	-

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

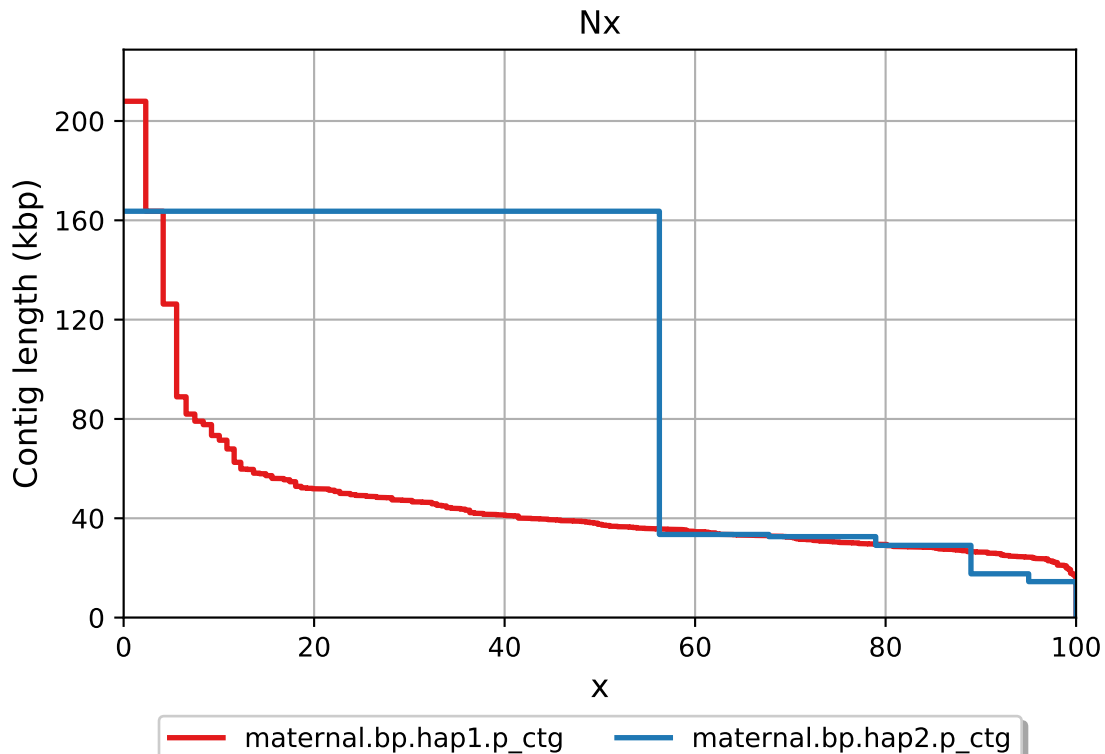
	maternal.bp.hap1.p_ctg	maternal.bp.hap2.p_ctg
# misassemblies	1007	8
# contig misassemblies	1007	8
# c. relocations	436	4
# c. translocations	571	4
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	205	5
Misassembled contigs length	7943237	127295
# local misassemblies	2664	3
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	13	1
# mismatches	197898	2176
# indels	27751	317
# indels (<= 5 bp)	23590	291
# indels (> 5 bp)	4161	26
Indels length	107980	950

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).

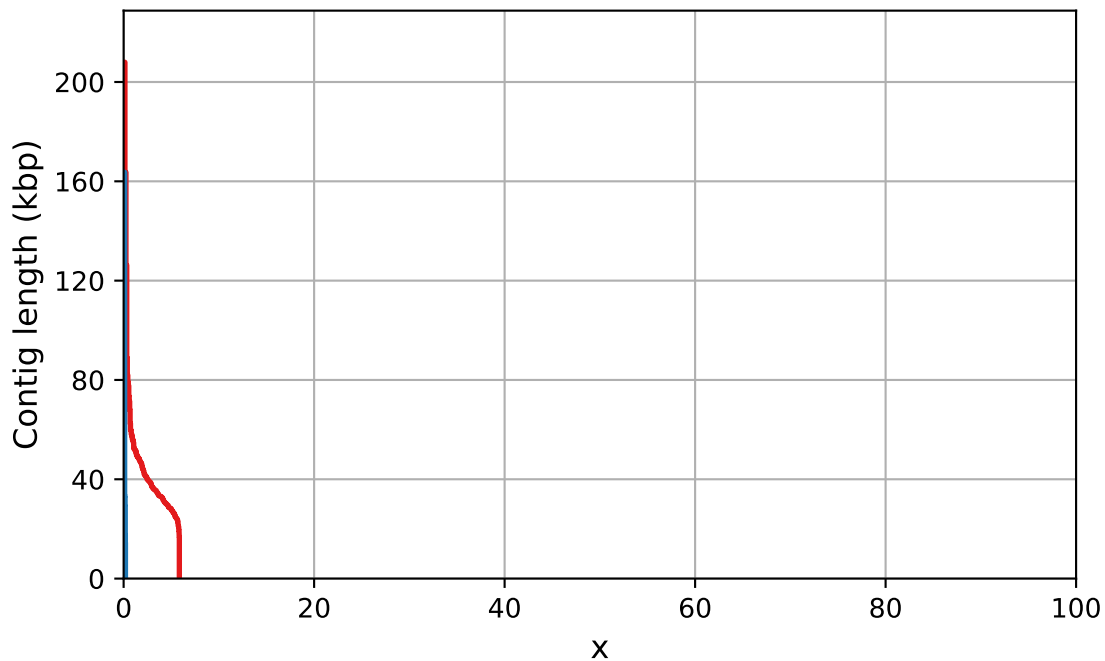
Unaligned report

	maternal.bp.hap1.p_ctg	maternal.bp.hap2.p_ctg
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	205	1
Partially unaligned length	1899517	118964
# 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).

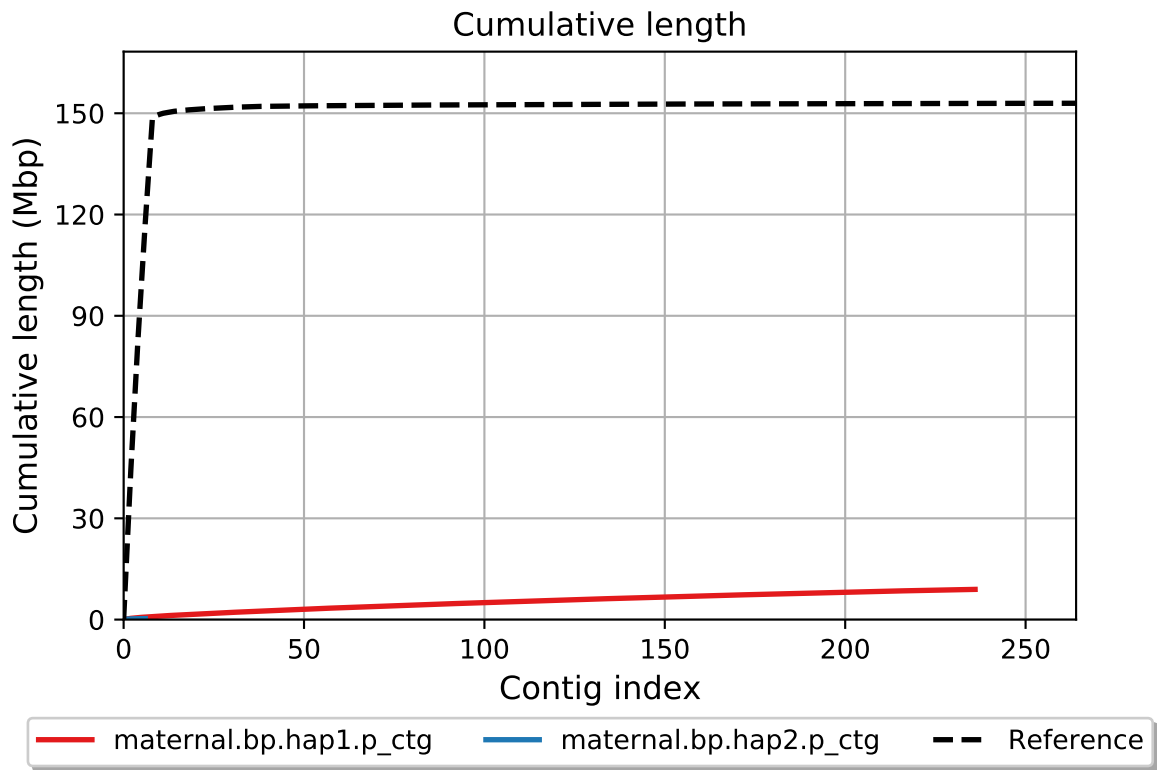


NGx

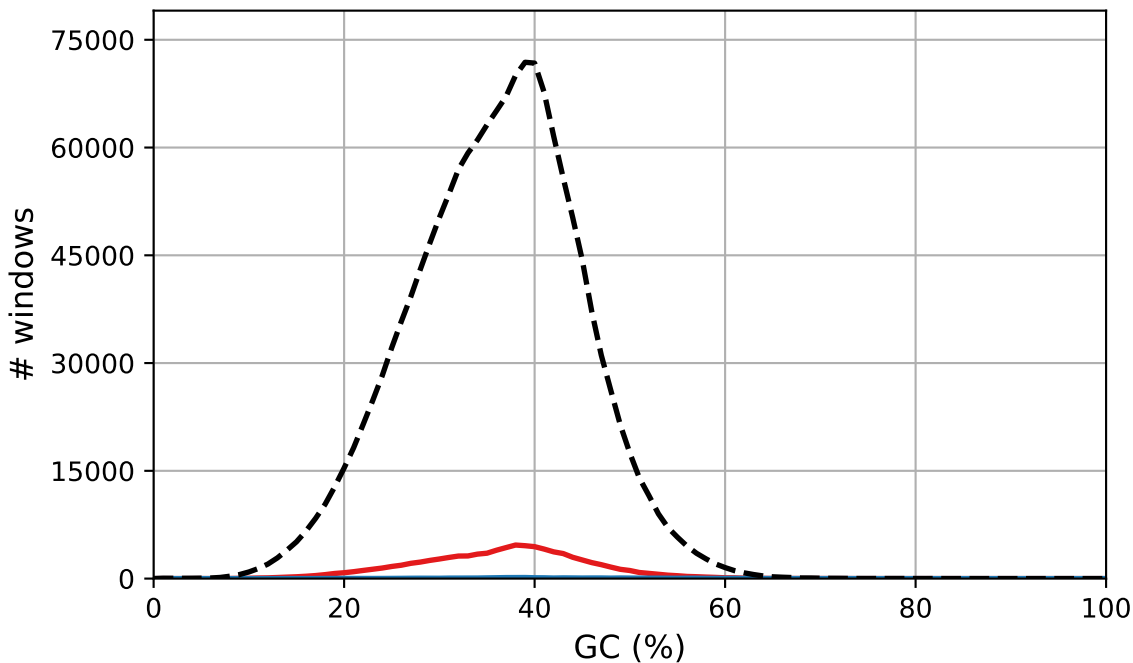


maternal.bp.hap1.p_ctg

maternal.bp.hap2.p_ctg

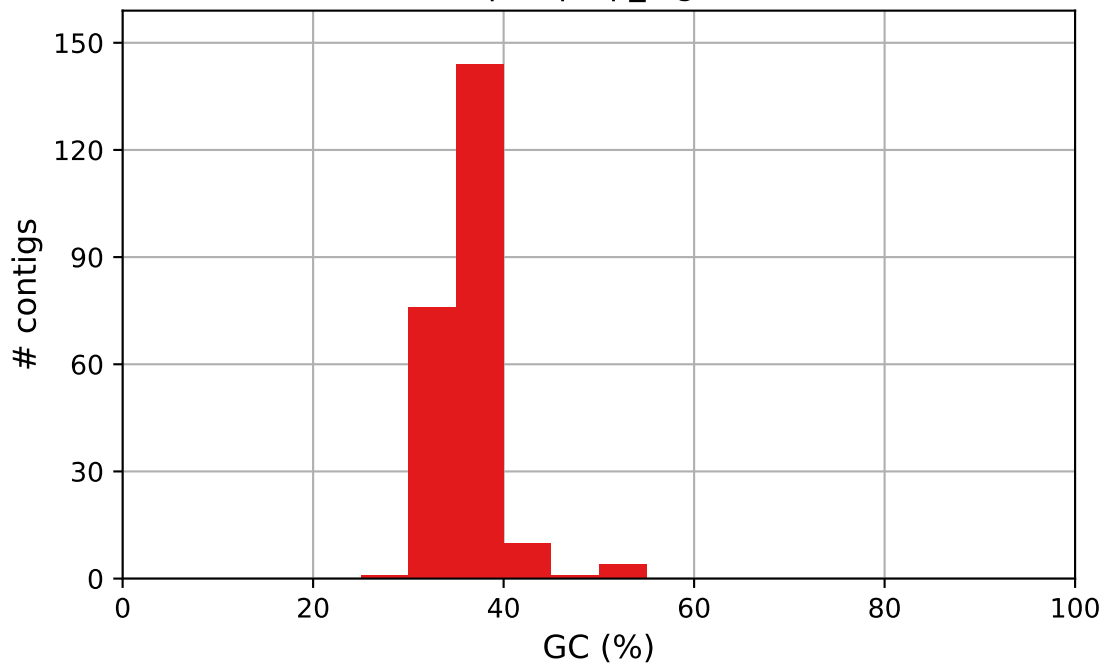


GC content



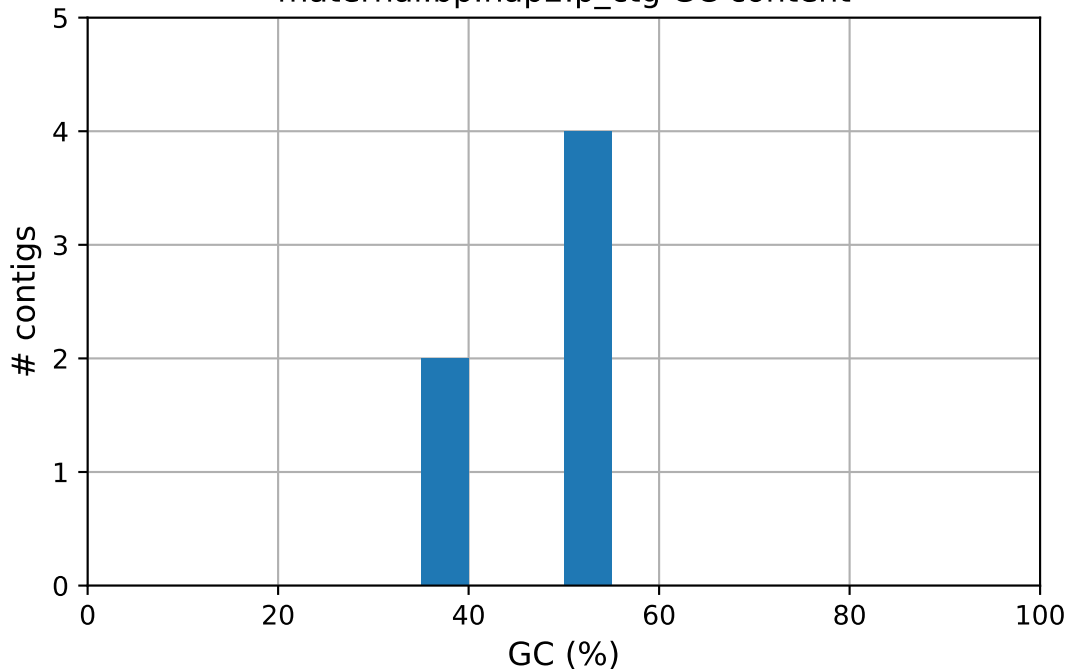
maternal.bp.hap1.p_ctg maternal.bp.hap2.p_ctg -- Reference

maternal.bp.hap1.p_ctg GC content



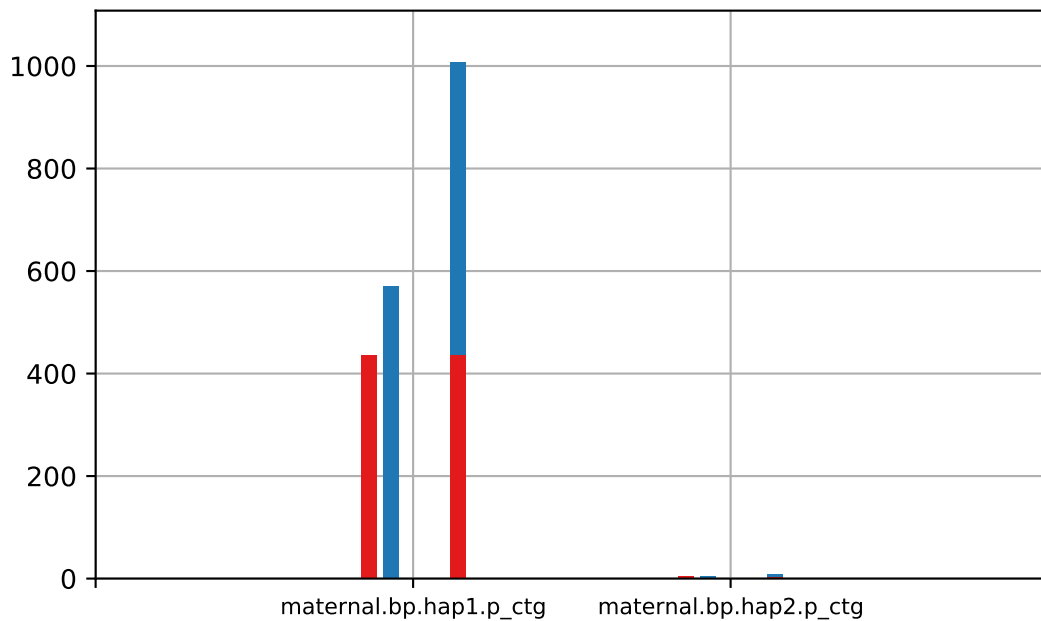
maternal.bp.hap1.p_ctg

maternal.bp.hap2.p_ctg GC content



maternal.bp.hap2.p_ctg

Misassemblies

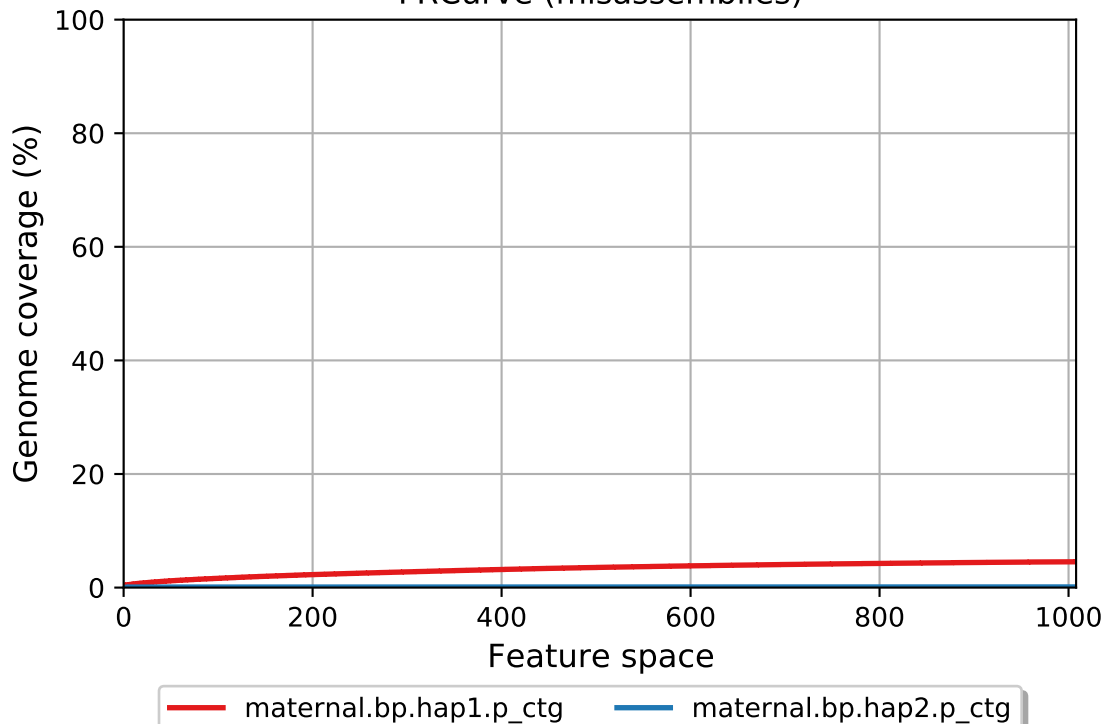


relocations

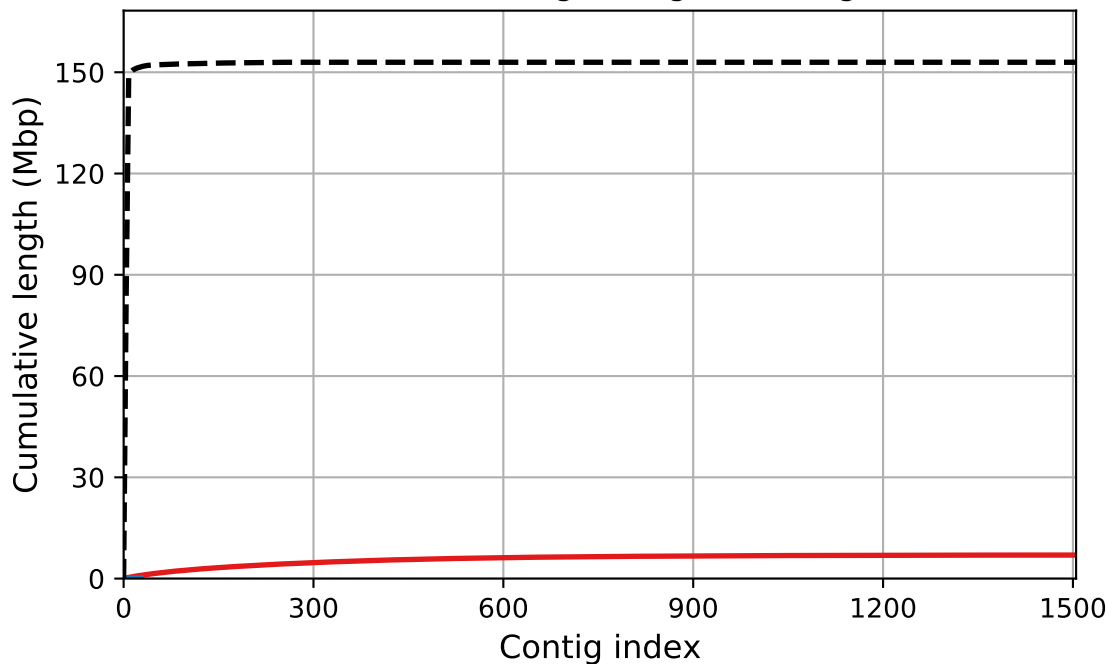


translocations

FRCurve (misassemblies)

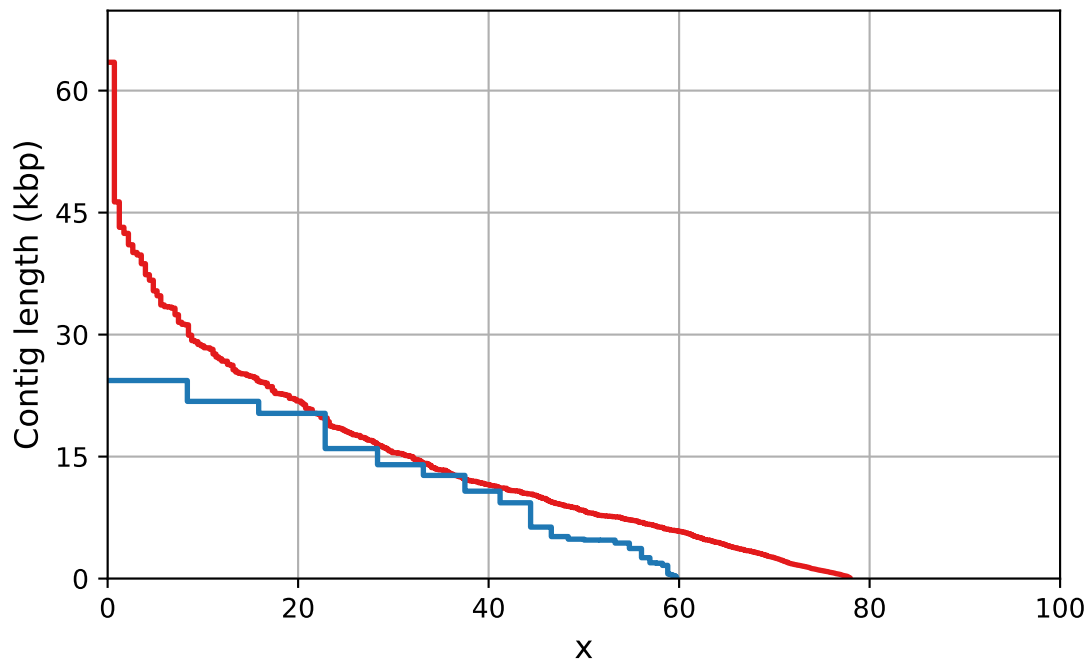


Cumulative length (aligned contigs)



maternal.bp.hap1.p_ctg maternal.bp.hap2.p_ctg Reference

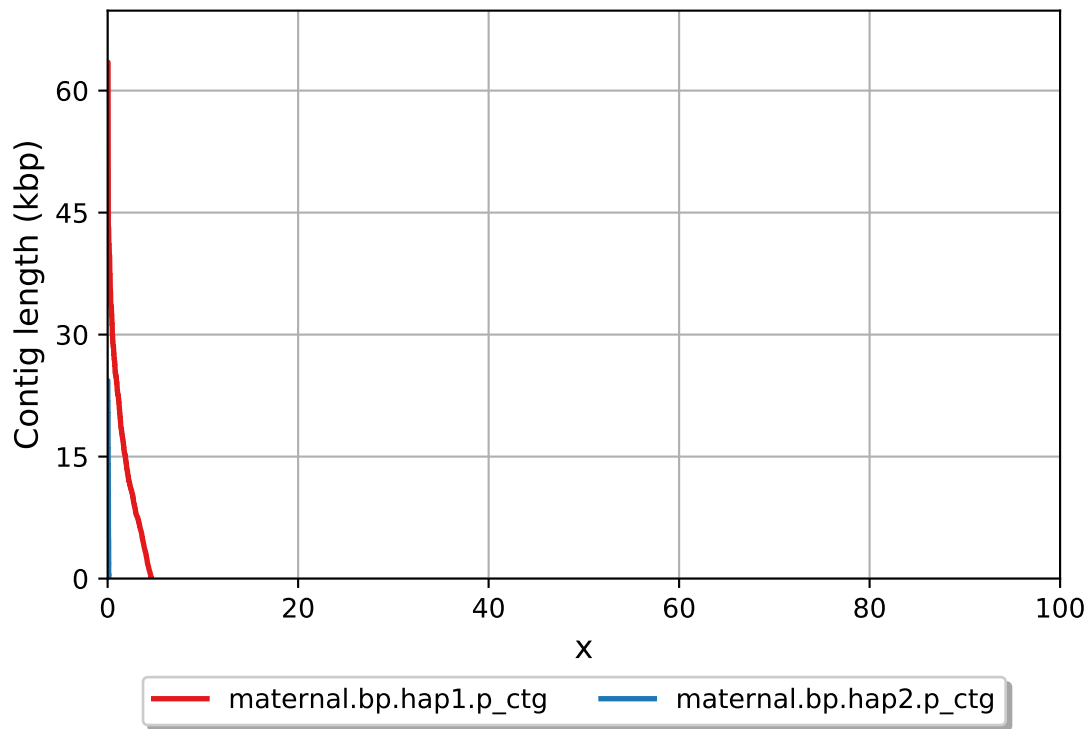
NAx



maternal.bp.hap1.p_ctg

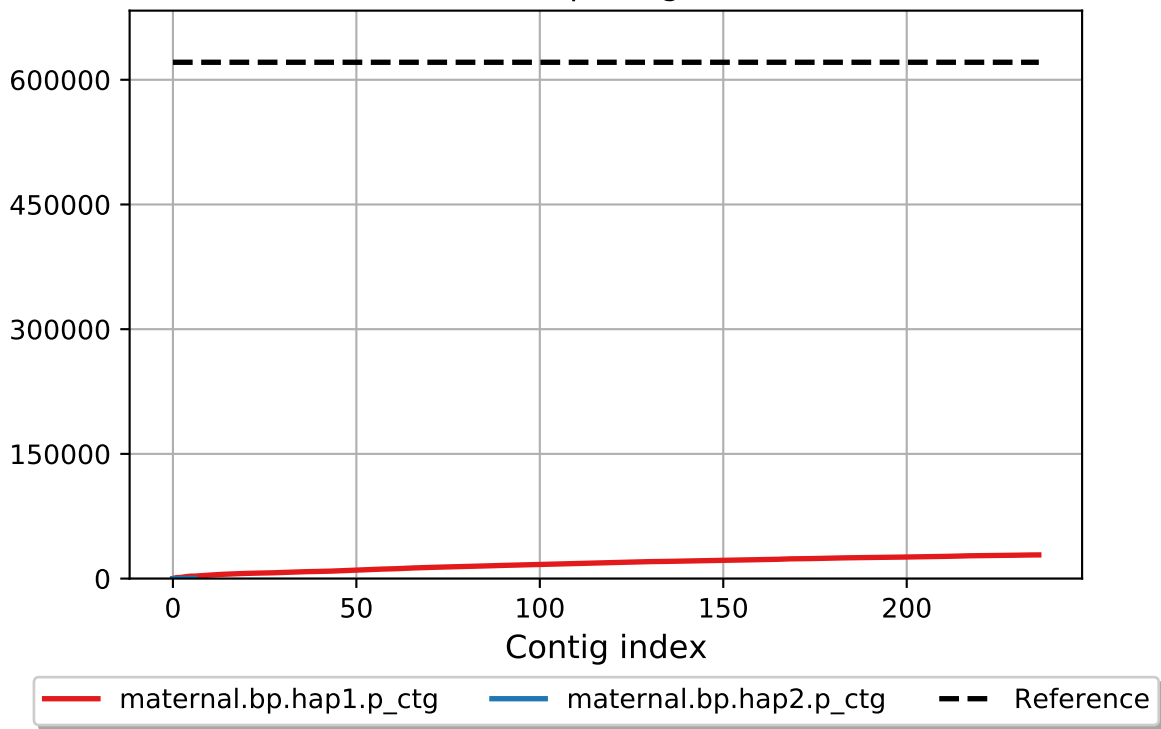
maternal.bp.hap2.p_ctg

NGAx

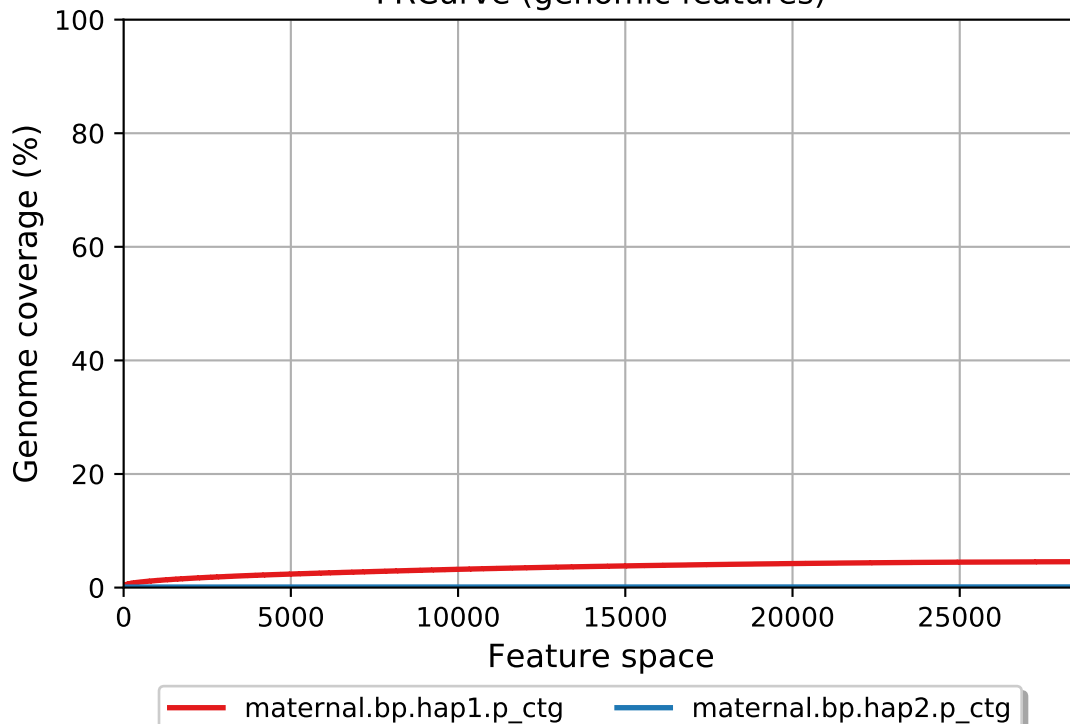


Cumulative # complete genomic features

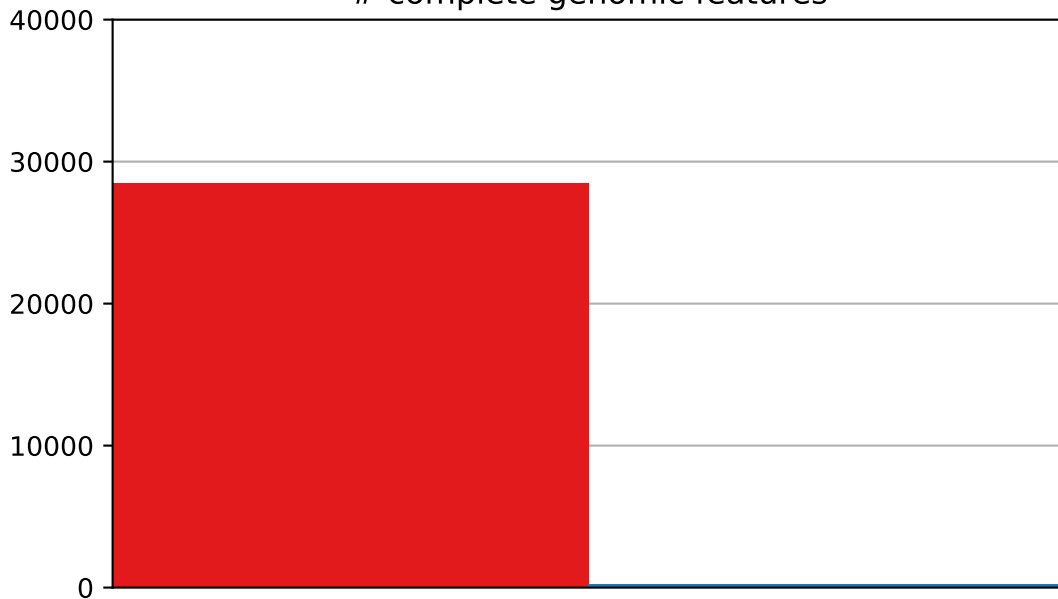
Cumulative # complete genomic features



FRCurve (genomic features)



complete genomic features

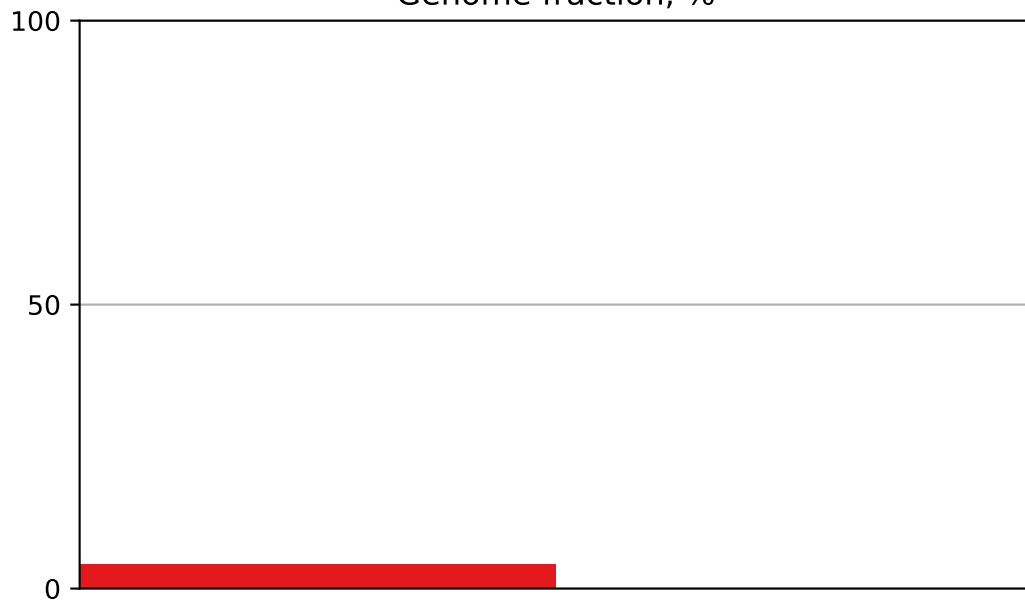


maternal.bp.hap1.p_ctg



maternal.bp.hap2.p_ctg

Genome fraction, %



maternal.bp.hap1.p_ctg



maternal.bp.hap2.p_ctg