

# Report

	maternal.p_ctg	paternal.p_ctg	maternal.p_utg	paternal.p_utg
# contigs (>= 0 bp)	6080	4938	9464	7906
# contigs (>= 1000 bp)	6080	4938	9464	7906
# contigs (>= 5000 bp)	6080	4938	9464	7906
# contigs (>= 10000 bp)	6071	4932	9440	7894
# contigs (>= 25000 bp)	5145	4225	7605	6437
# contigs (>= 50000 bp)	1853	1783	2632	2835
Total length (>= 0 bp)	354203527	333664625	480685454	472687125
Total length (>= 1000 bp)	354203527	333664625	480685454	472687125
Total length (>= 5000 bp)	354203527	333664625	480685454	472687125
Total length (>= 10000 bp)	354124291	333612369	480469753	472579661
Total length (>= 25000 bp)	335665158	319222108	443899520	443429310
Total length (>= 50000 bp)	218390382	232411411	266938261	315449455
# contigs	6080	4938	9464	7906
Largest contig	2109571	1601083	1690174	830741
Total length	354203527	333664625	480685454	472687125
Reference length	152958180	152958180	152958180	152958180
GC (%)	38.26	38.41	38.15	38.18
Reference GC (%)	35.92	35.92	35.92	35.92
N50	66996	88539	56259	75080
NG50	215366	285955	172836	236720
N75	38702	43656	35865	41161
NG75	127586	180346	121250	175792
L50	1135	762	2132	1527
LG50	192	167	254	227
L75	2935	2166	4860	3700
LG75	429	336	522	413
# misassemblies	28451	27984	41470	43843
# misassembled contigs	2088	1440	4304	3625
Misassembled contigs length	190038996	181463407	286836951	299064543
# local misassemblies	49935	51191	74973	82962
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	1278	509	1726	584
# unaligned contigs	2287 + 3535 part	2688 + 2069 part	2537 + 5902 part	3154 + 3760 part
Unaligned length	186941794	182916746	221883341	217444586
Genome fraction (%)	64.382	67.110	70.434	74.220
Duplication ratio	1.699	1.469	2.402	2.249
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	4411.57	4059.15	6044.25	6038.60
# indels per 100 kbp	499.16	441.70	705.69	681.15
# genomic features	433613 + 41779 part	451412 + 43864 part	467834 + 35258 part	494060 + 34604 part
Largest alignment	127443	100917	123551	101121
Total aligned length	164723538	148906683	255167454	252183134
NA50	-	-	1257	1415
NGA50	11345	10683	17521	18102
NGA75	6425	4836	12188	12484
LA50	-	-	31853	29528
LGA50	3846	3920	2936	2730
LGA75	8177	9185	5569	5295

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

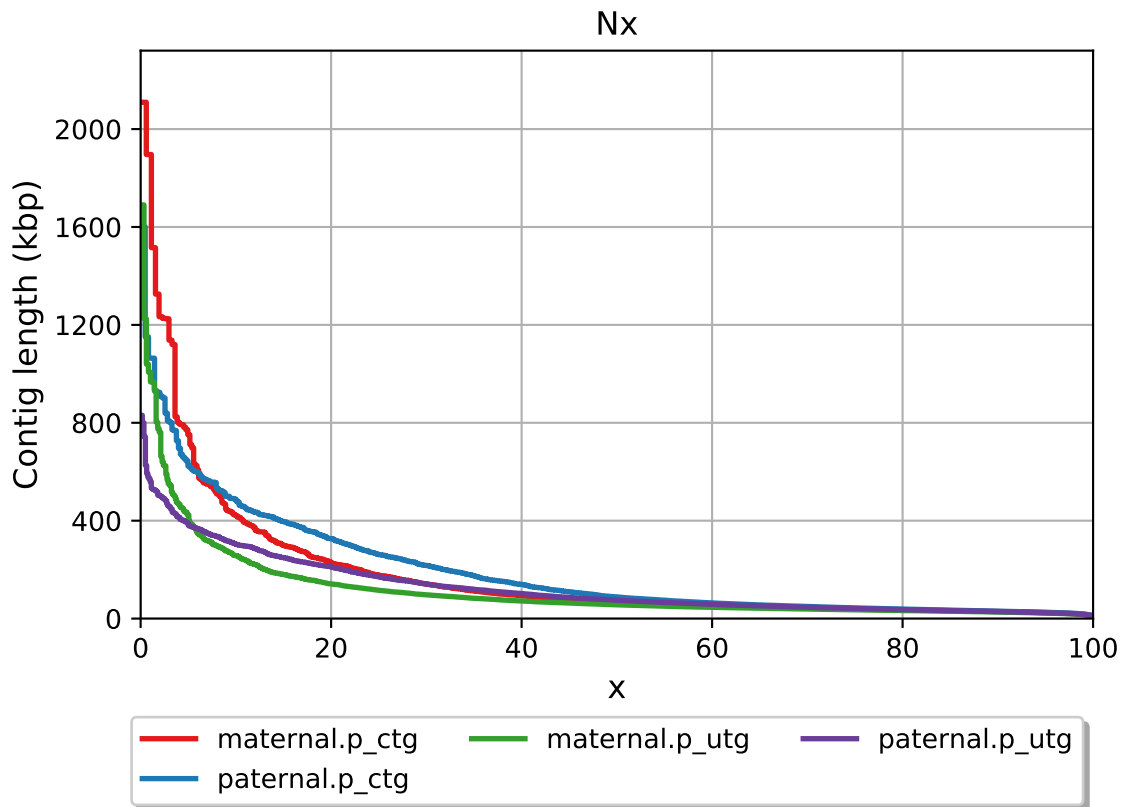
	maternal.p_ctg	paternal.p_ctg	maternal.p_utg	paternal.p_utg
# misassemblies	28451	27984	41470	43843
# contig misassemblies	28451	27984	41470	43843
# c. relocations	11915	11492	17542	18064
# c. translocations	16461	16409	23832	25658
# c. inversions	75	83	96	121
# scaffold misassemblies	0	0	0	0
# s. relocations	0	0	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	2088	1440	4304	3625
Misassembled contigs length	190038996	181463407	286836951	299064543
# local misassemblies	49935	51191	74973	82962
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	1278	509	1726	584
# mismatches	4343975	4166290	6511096	6854690
# indels	491508	453354	760192	773200
# indels (<= 5 bp)	402623	363915	621902	622891
# indels (> 5 bp)	88885	89439	138290	150309
Indels length	2184066	2145311	3409730	3642938

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).

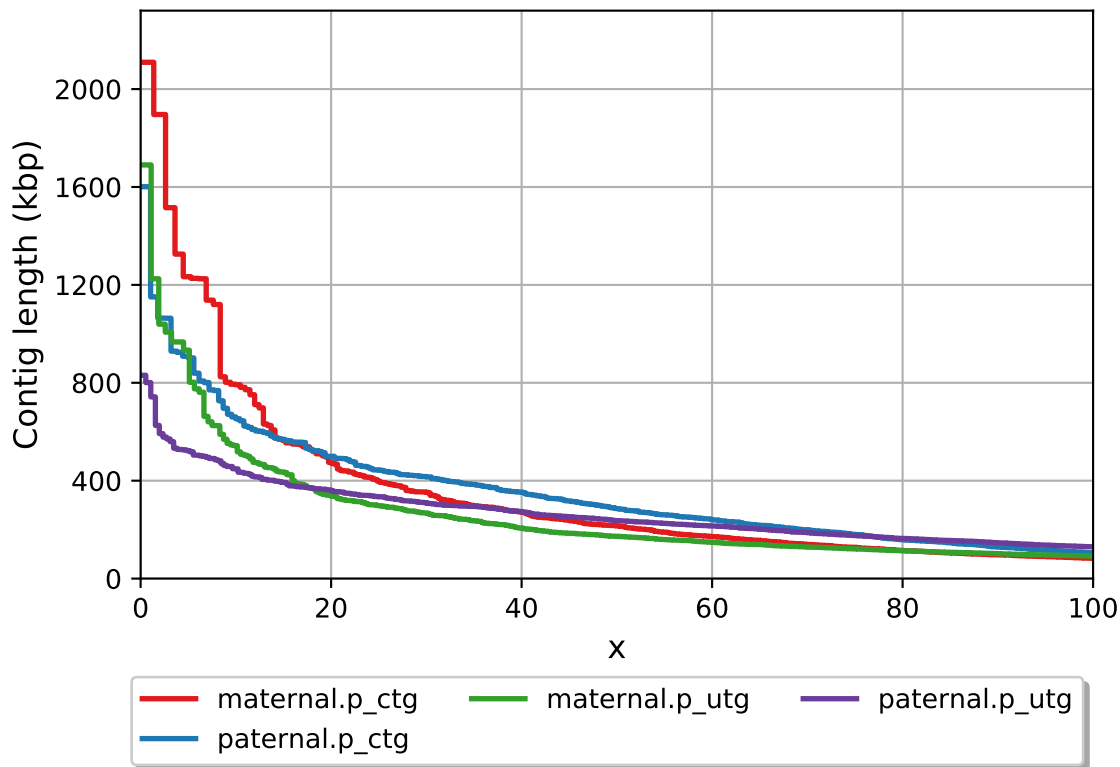
## Unaligned report

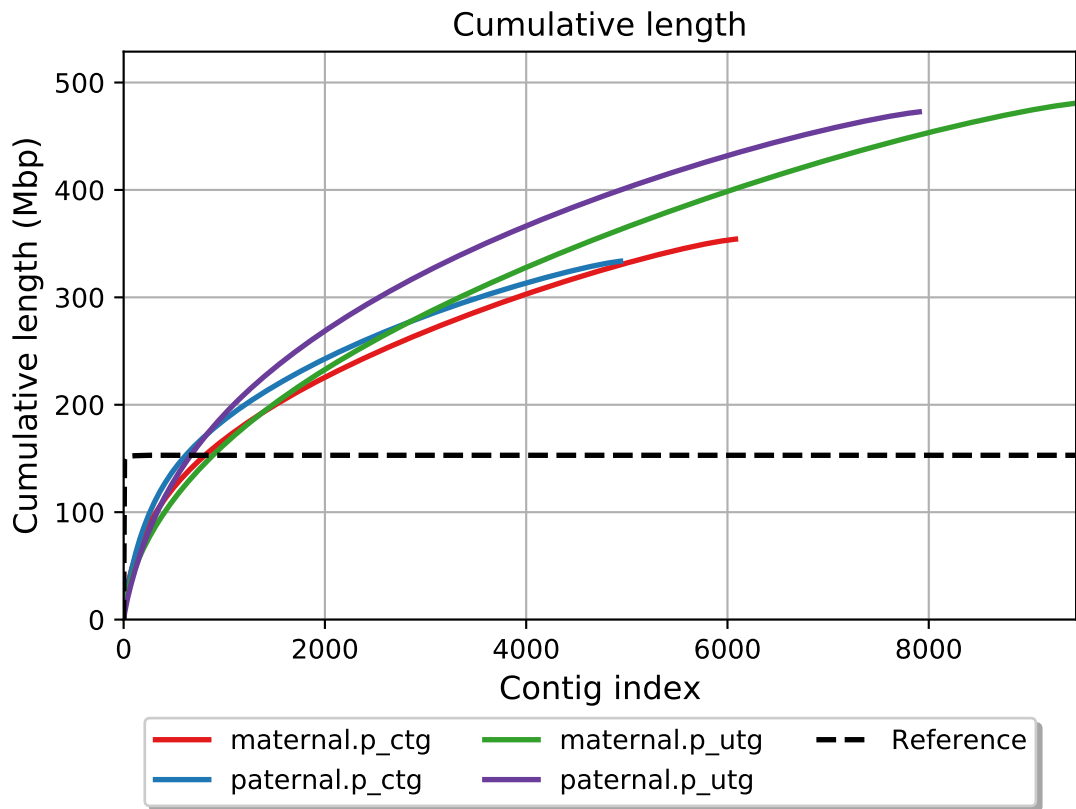
	maternal.p_ctg	paternal.p_ctg	maternal.p_utg	paternal.p_utg
# fully unaligned contigs	2287	2688	2537	3154
Fully unaligned length	94850726	119126432	101568566	132433668
# partially unaligned contigs	3535	2069	5902	3760
Partially unaligned length	92091068	63790314	120314775	85010918
# N's	0	0	0	0

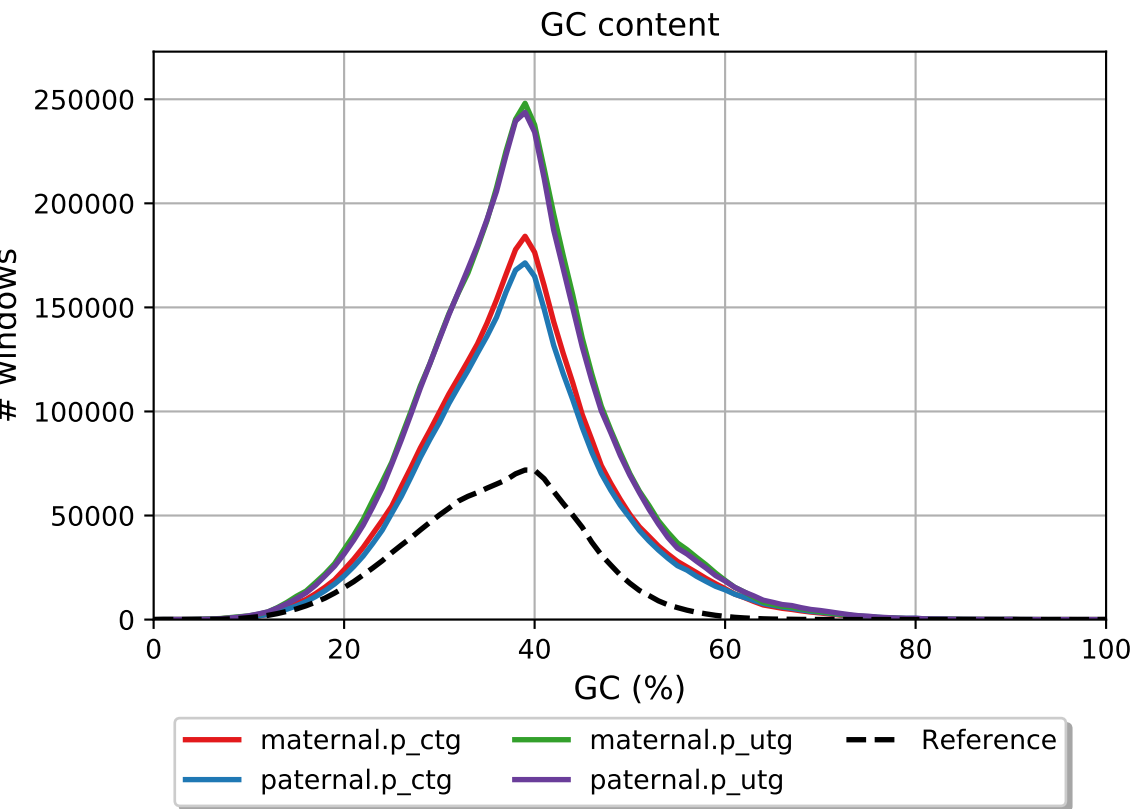
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



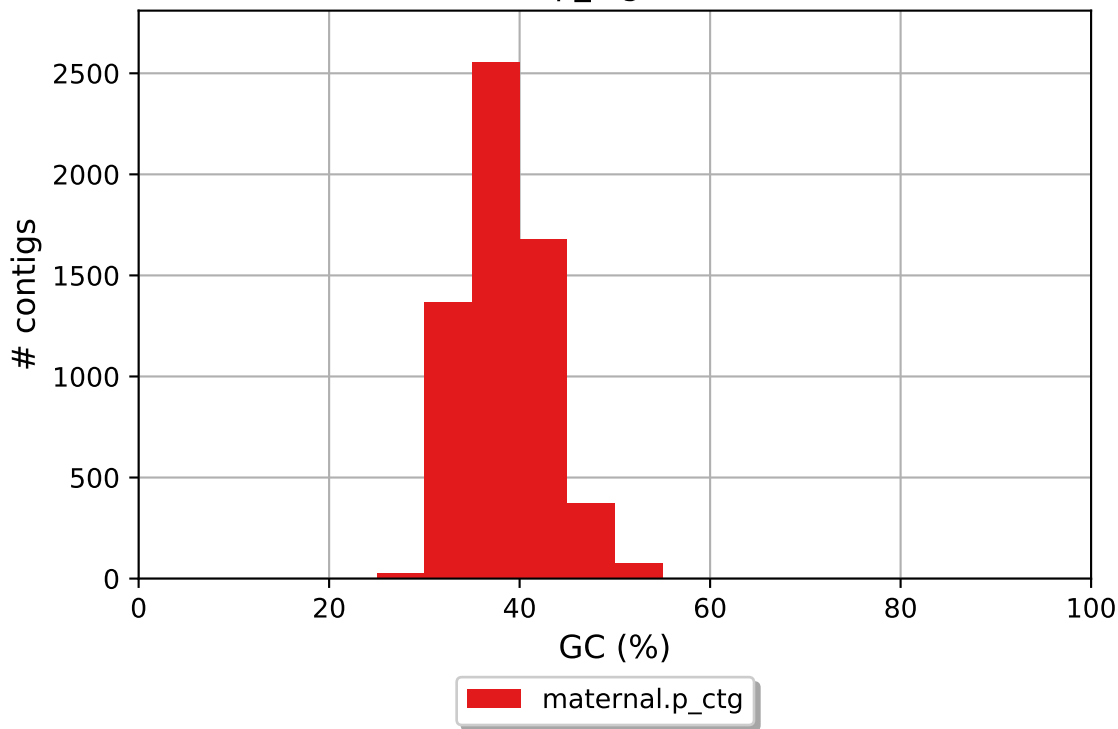
## NGx





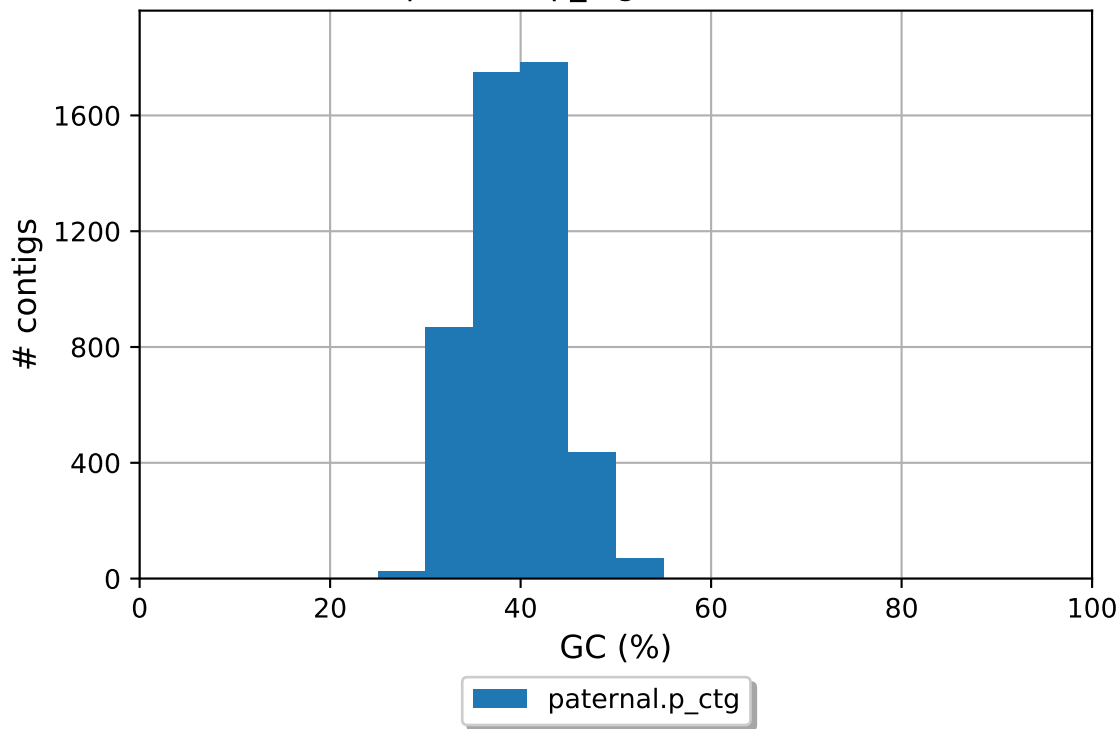


maternal.p\_ctg GC content

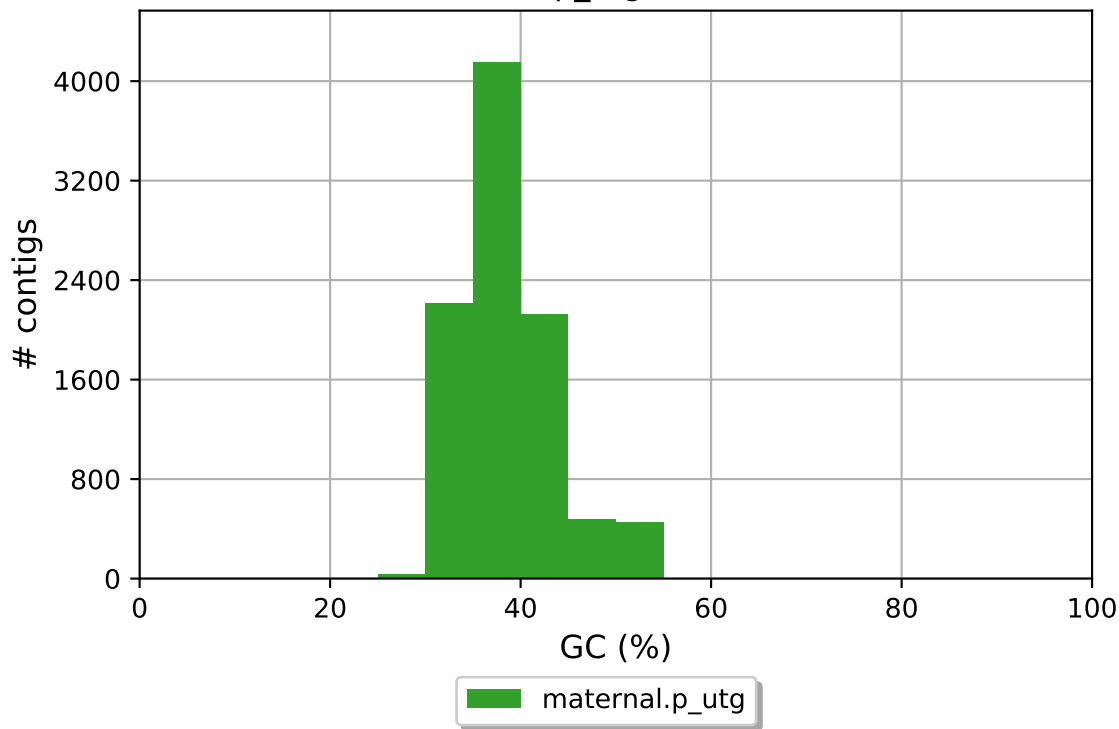




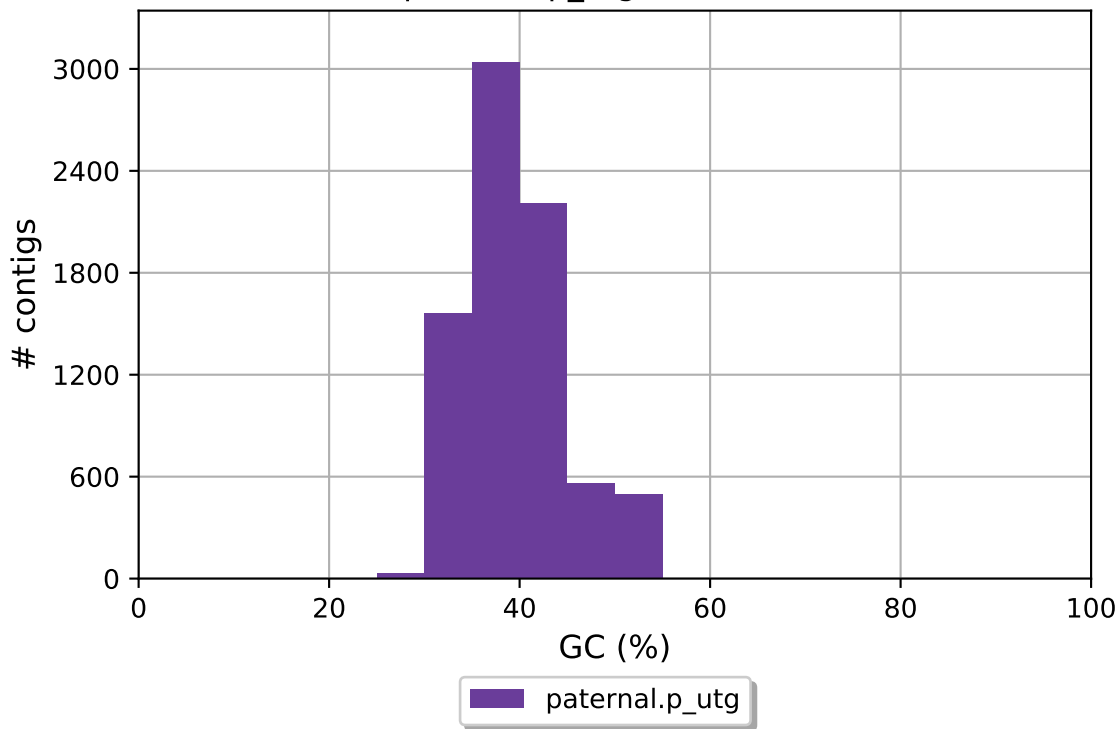
paternal.p\_ctg GC content



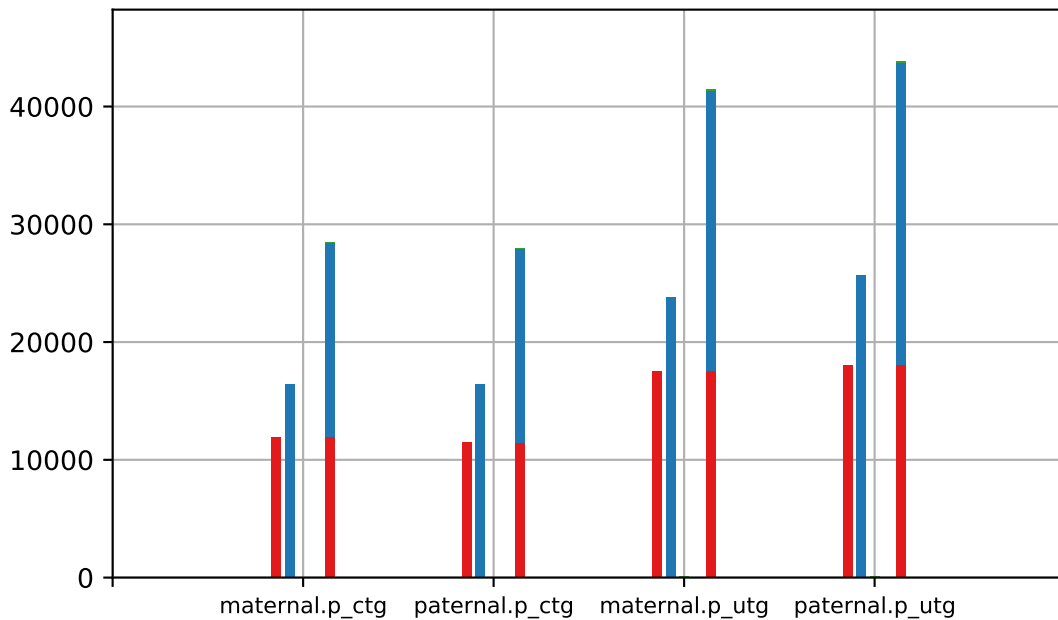
maternal.p\_utg GC content



paternal.p\_utg GC content



## Misassemblies



# relocations

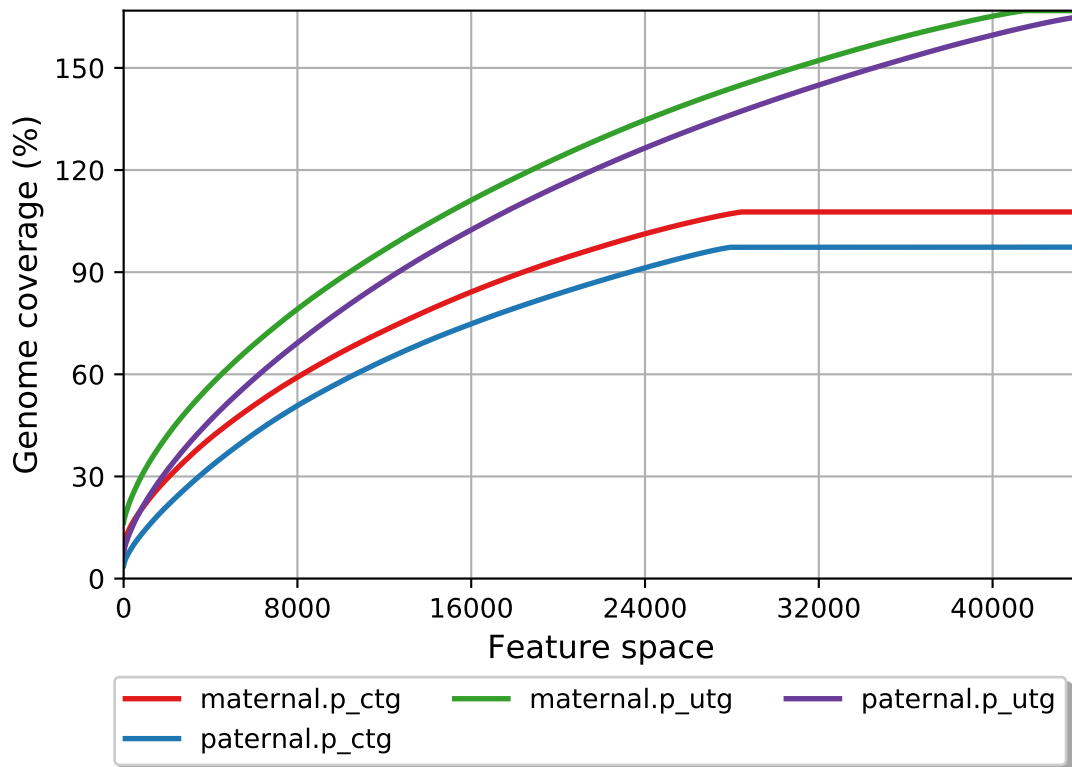


# translocations

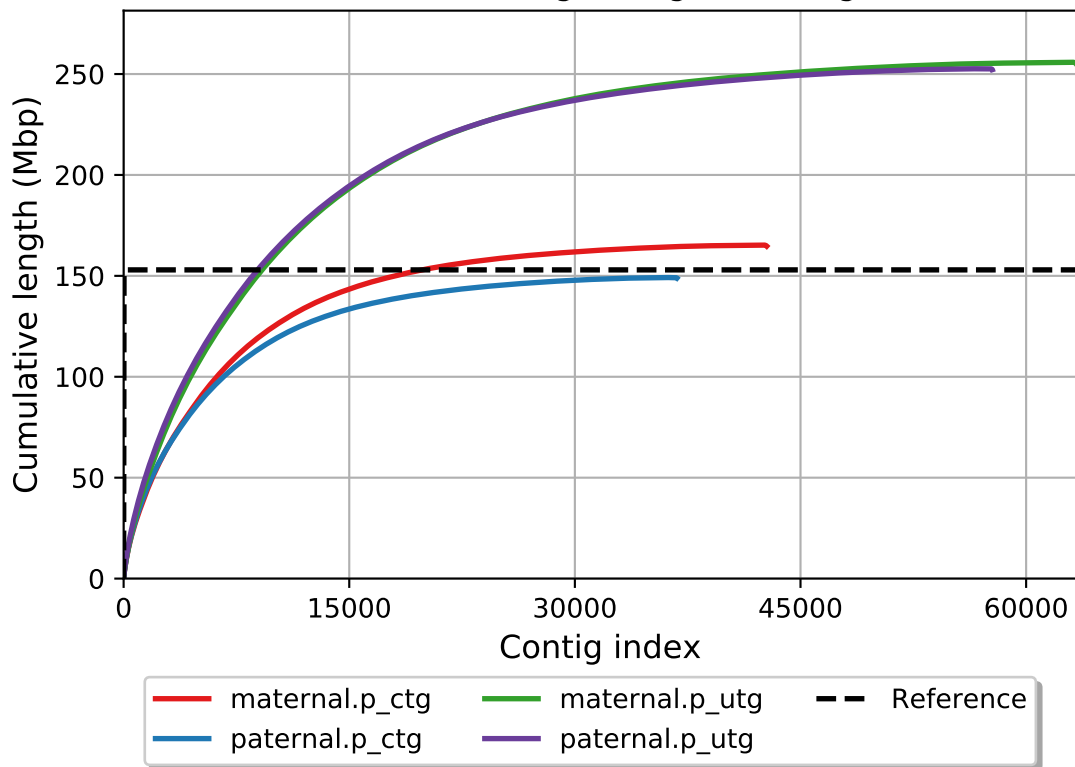


# inversions

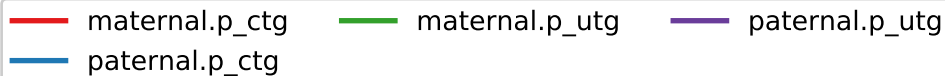
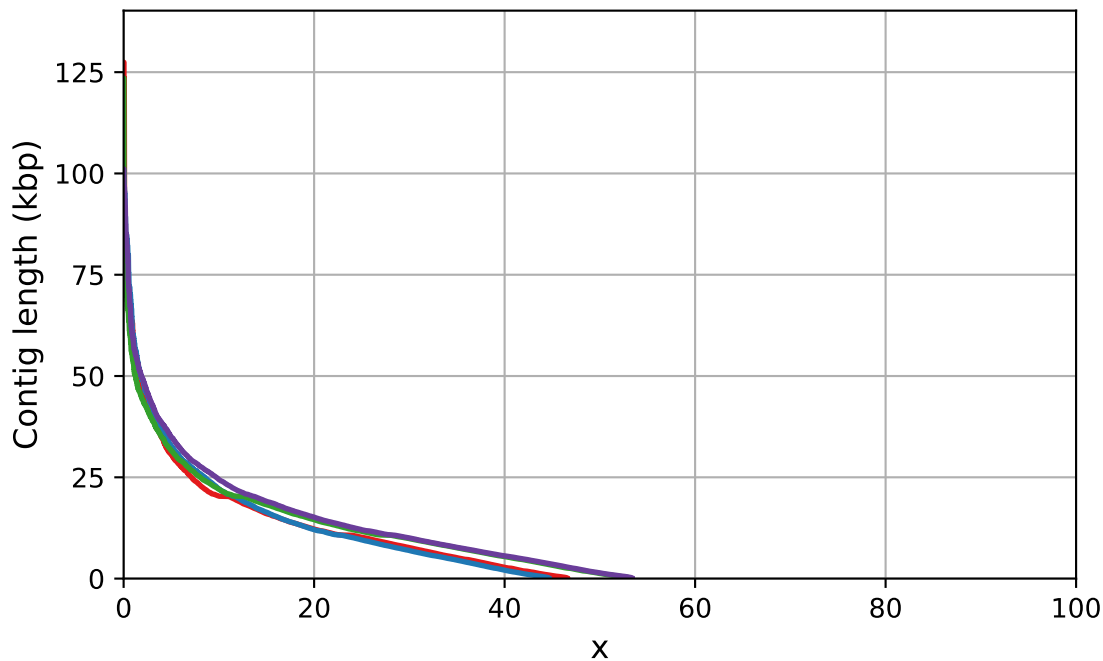
FRCurve (misassemblies)



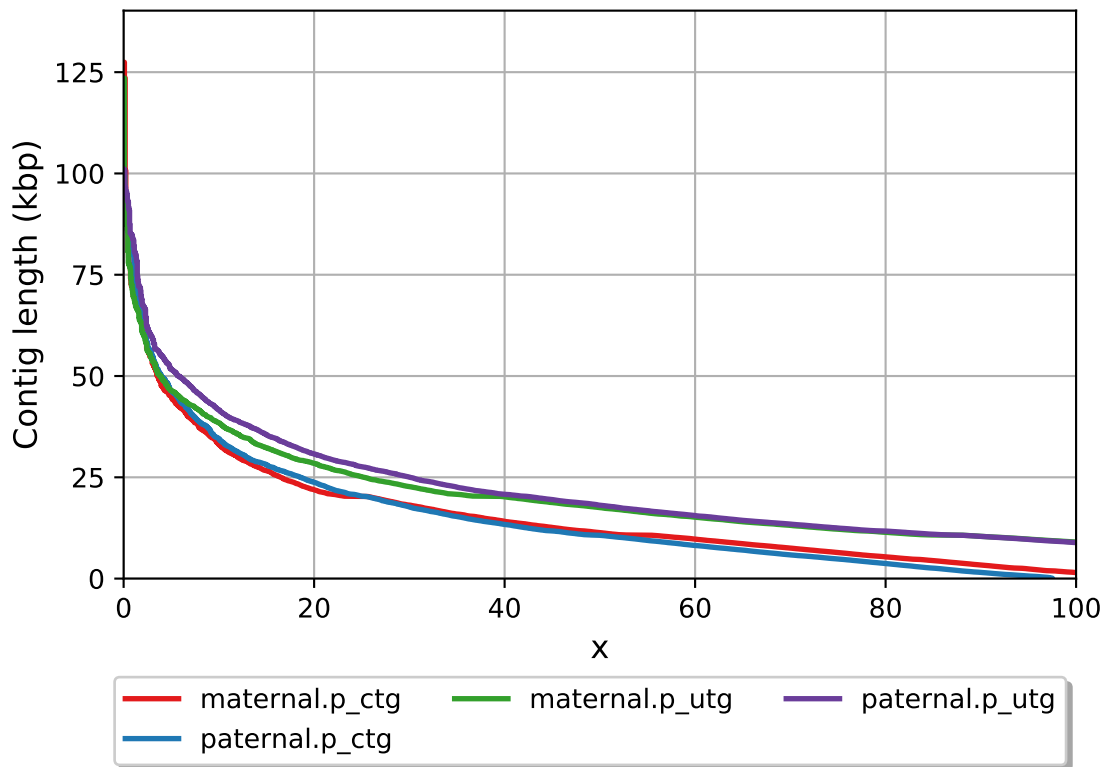
Cumulative length (aligned contigs)



NAx



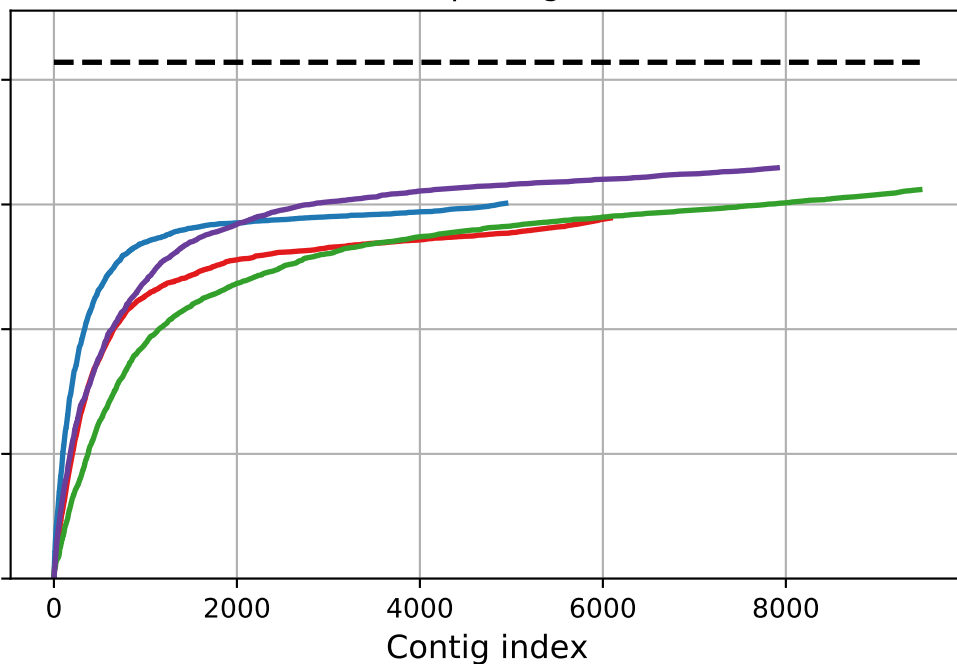
# NGAx





Cumulative # complete genomic features

Cumulative # complete genomic features



maternal.p\_ctg

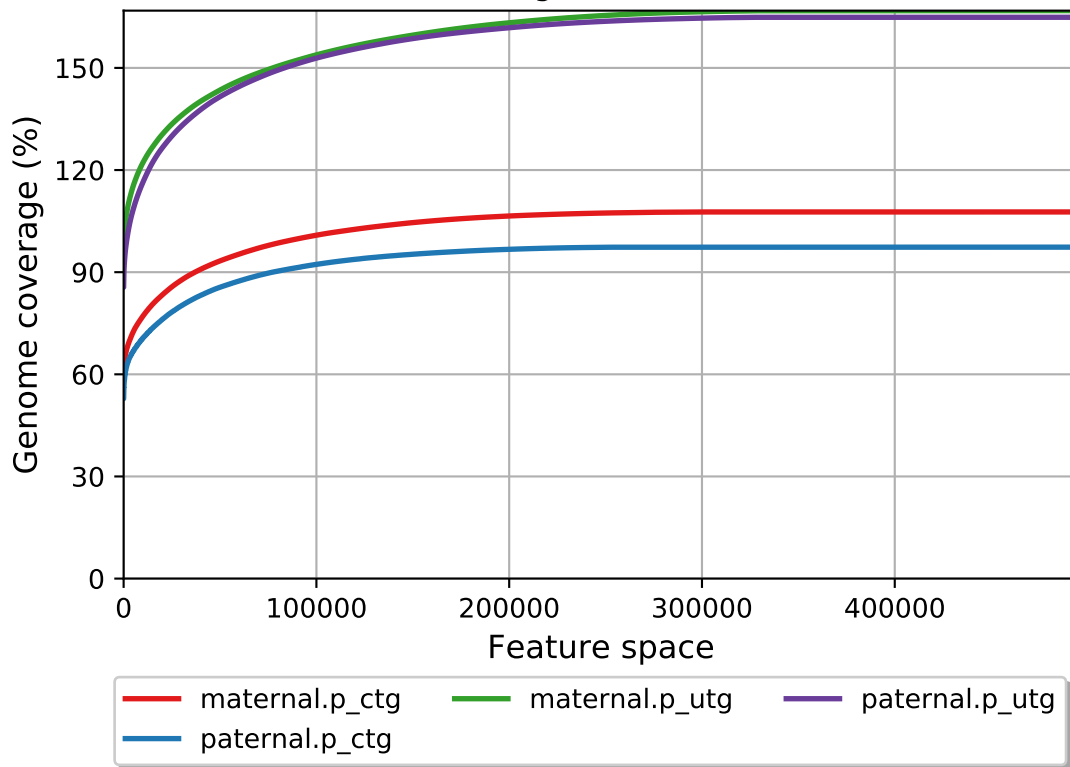
maternal.p\_utg

Reference

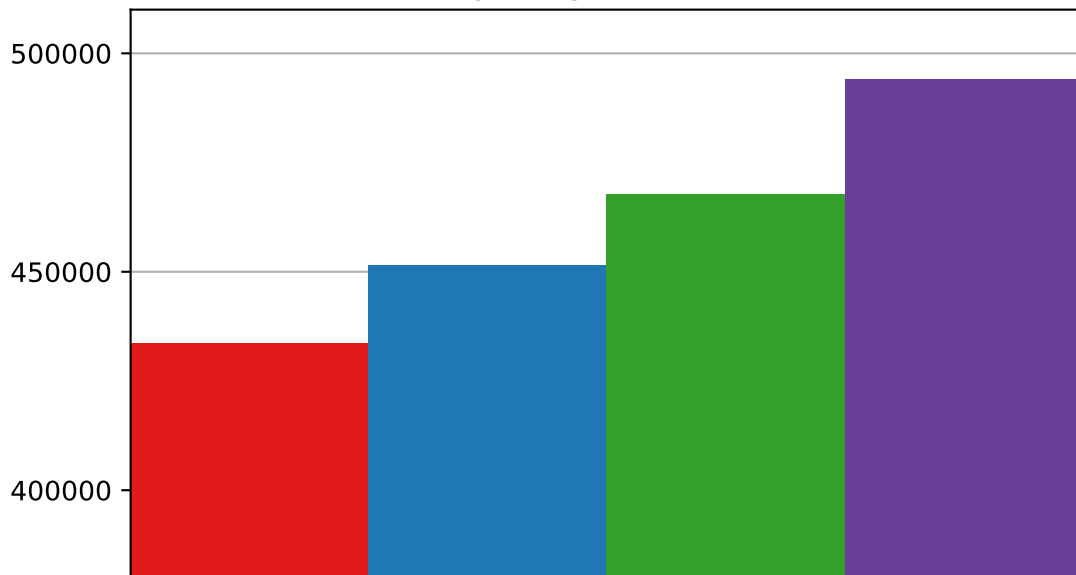
paternal.p\_ctg

paternal.p\_utg

FRCurve (genomic features)



# complete genomic features



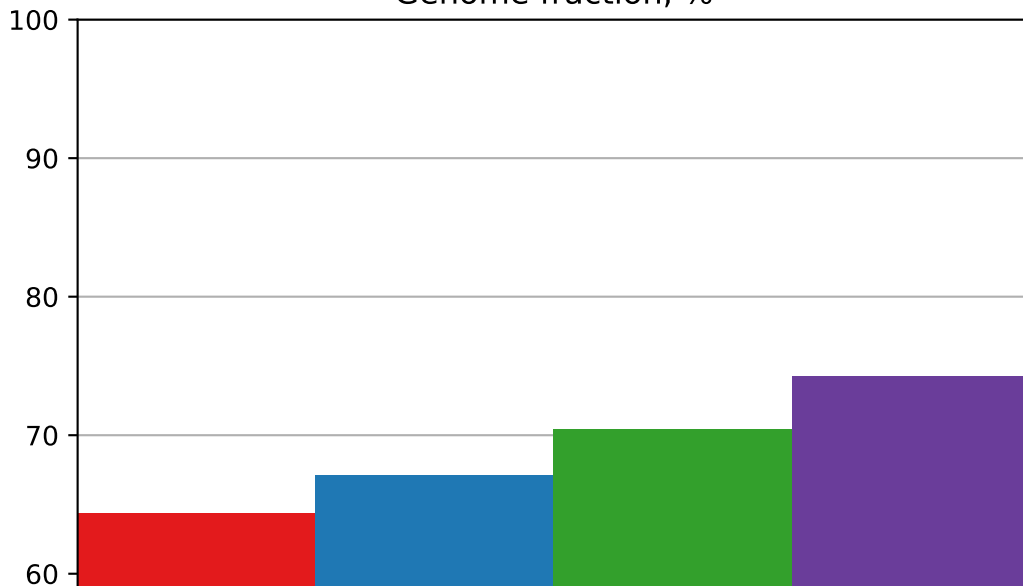
maternal.p\_ctg

maternal.p\_utg

paternal.p\_utg

paternal.p\_ctg

Genome fraction, %



maternal.p\_ctg

maternal.p\_utg

paternal.p\_utg

paternal.p\_ctg