Report

	maternal.bp.hap1.p_ctg	maternal.bp.hap2.p_ctg	paternal.bp.hap1.p_ctg	paternal.bp.hap2.p_ctg
# contigs (>= 0 bp)	6762	1772	5305	1740
# contigs (>= 1000 bp)	6762	1772	5305	1740
# contigs (>= 5000 bp)	6762	1772	5305	1740
# contigs (>= 10000 bp)	6751	1769	5298	1739
# contigs (>= 25000 bp)	5576	1595	4449	1586
# contigs (>= 50000 bp)	1686	987	1689	1085
Total length (>= 0 bp)	327886234	140531454	294788904	165666671
Total length (>= 1000 bp)	327886234	140531454	294788904	165666671
Total length (>= 5000 bp)	327886234	140531454	294788904	165666671
Total length (>= 10000 bp)	327791330	140505503	294727266	165657937
Total length (>= 25000 bp)	304327999	137169315	277519216	162555904
Total length (>= 50000 bp)	167250566	114471888	179603743	143740007
# contigs	6762	1772	5305	1740
Largest contig	1993820	1350642	1168112	841958
Total length	327886234	140531454	294788904	165666671
Reference length	152958180	152958180	152958180	152958180
GC (%)	38.49	37.24	38.49	37.04
Reference GC (%)	35.92	35.92	35.92	35.92
N50	51175	102204	62815	136461
NG50	111731	93510	141040	151008
N75	34404	59353	38093	73288
NG75	72727	49637	84338	84557
L50	1621	370	1112	343
LG50	369	434	306	298
L75	3615	820	2645	765
LG75	799	992	660	644
# misassemblies	23771	17435	23087	20173
# misassembled contigs	2638	1305	1788	1202
Misassembled contigs length	169828296	117015430	153324272	137678074
# local misassemblies	42634	31781	43613	38377
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	1342	118	527	44
# unaligned contigs	2203 + 3946 part	256 + 1336 part	2675 + 2344 part	436 + 1148 part
Unaligned length	172024196	40678826	164685672	51571473
Genome fraction (%)	59.215	48.725	62.072	57.174
Duplication ratio	1.721	1.340	1.370	1.305
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	4091.01	3600.84	3726.84	3591.29
# indels per 100 kbp	484.71	419.37	418.58	409.83
# genomic features	399550 + 40029 part	330420 + 33629 part	418958 + 42486 part	391552 + 39415 part
Largest alignment	123551	99514	100818	101121
Total aligned length	153507493	98532328	128653439	112522745
NA50	-	6437	-	6020
NGA50	11190	5065	8860	7327
NGA75	5623	-	2205	-
LA50	-	4934	-	5843
LGA50	3859	6023	4438	4888
LGA75	8474	-	12463	-

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).
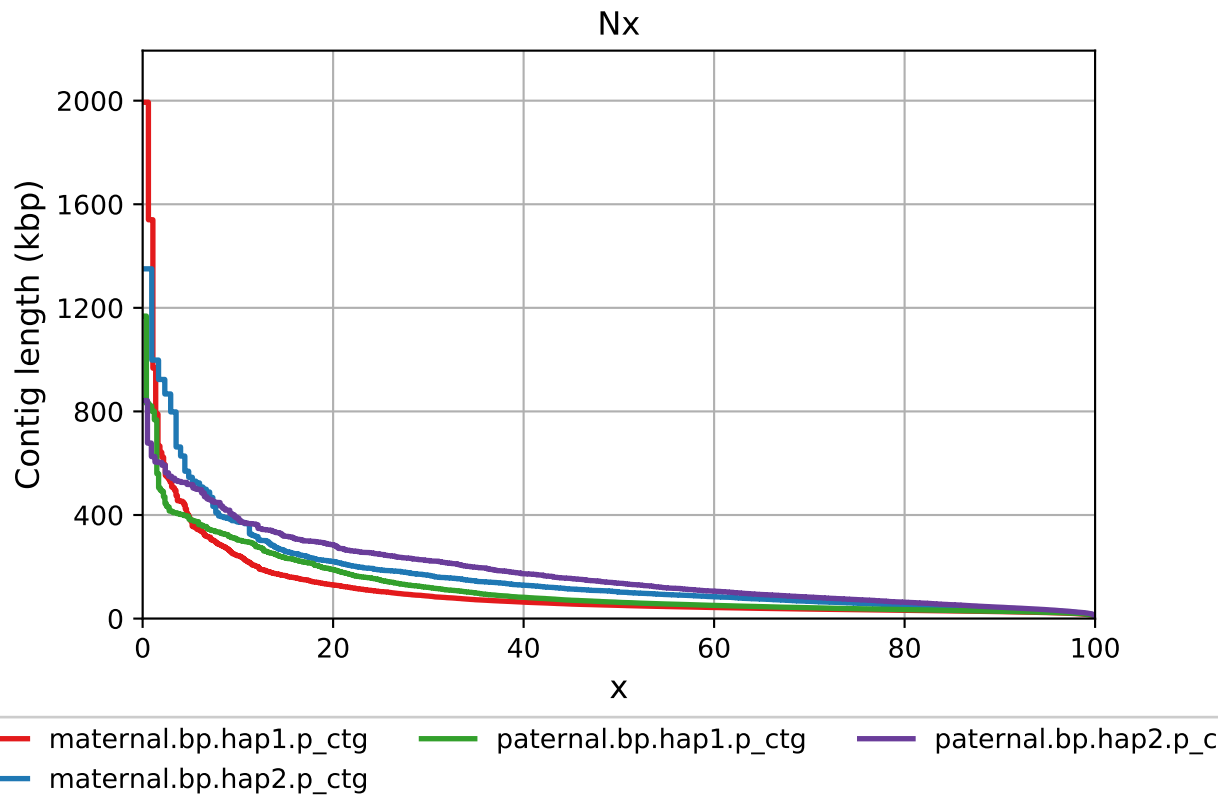
Misassemblies report
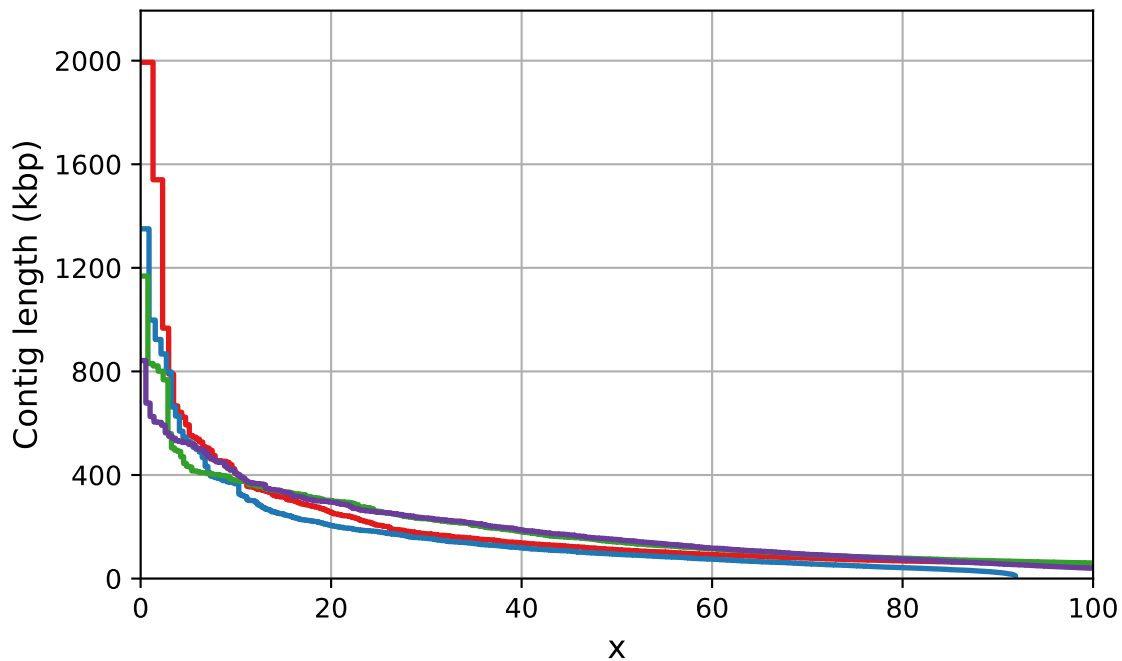
	maternal.bp.hap1.p_ctg	maternal.bp.hap2.p_ctg	paternal.bp.hap1.p_ctg	paternal.bp.hap2.p_ctg
# misassemblies	23771	17435	23087	20173
# contig misassemblies	23771	17435	23087	20173
# c. relocations	10344	7146	9424	8344
# c. translocations	13365	10248	13605	11766
# c. inversions	62	41	58	63
# scaffold misassemblies	0	0	0	0
# s. relocations	0	0	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	2638	1305	1788	1202
Misassembled contigs length	169828296	117015430	153324272	137678074
# local misassemblies	42634	31781	43613	38377
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	1342	118	527	44
# mismatches	3705005	2683396	3538050	3140363
# indels	438977	312520	397375	358368
# indels (<= 5 bp)	361497	253971	319169	288425
# indels (> 5 bp)	77480	58549	78206	69943
Indels length	1918254	1421823	1879566	1680077

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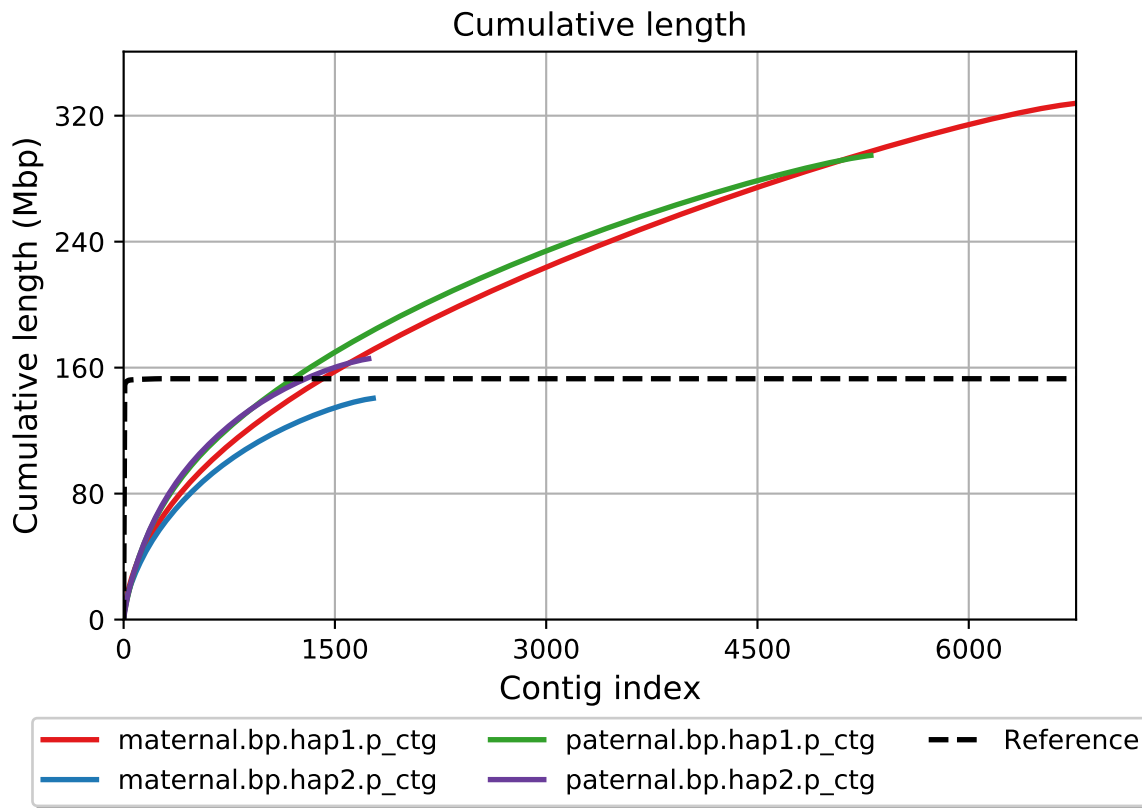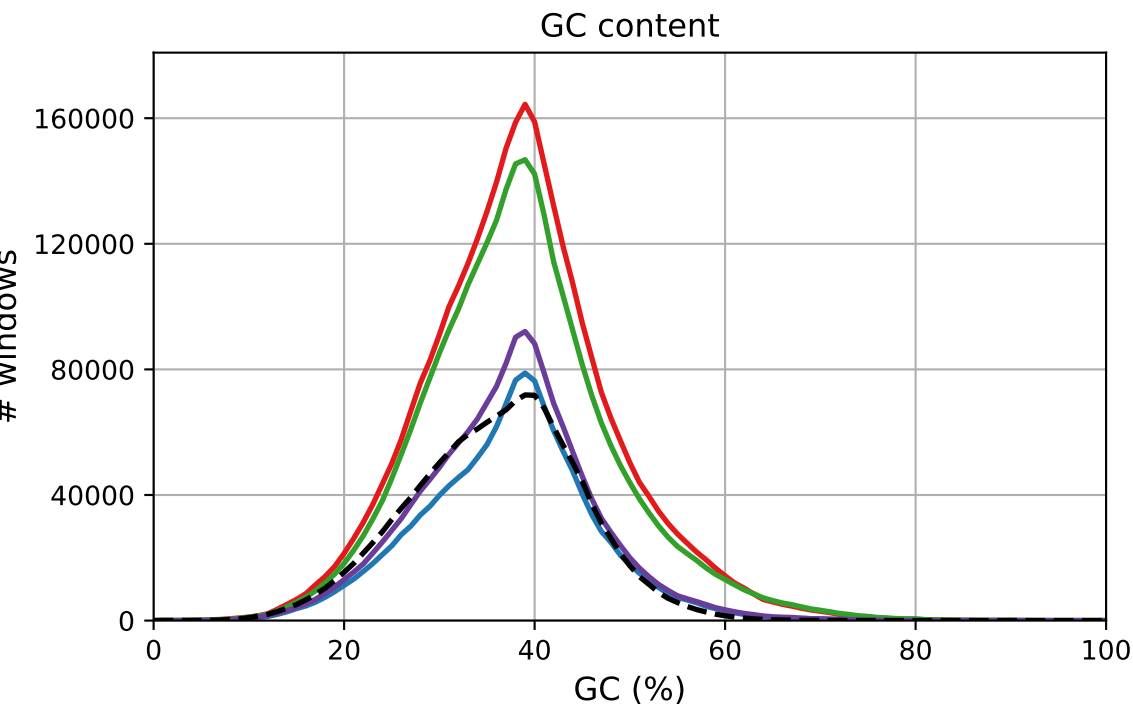(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	maternal.bp.hap1.p_ctg	maternal.bp.hap2.p_ctg	paternal.bp.hap1.p_ctg	paternal.bp.hap2.p_ctg
# fully unaligned contigs	2203	256	2675	436
Fully unaligned length	87867627	12071795	109993941	22257344
# partially unaligned contigs	3946	1336	2344	1148
Partially unaligned length	84156569	28607031	54691731	29314129
# N's	0	0	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).

Nx

maternal.bp.hap1.p_ctg
paternal.bp.hap1.p_ctg
paternal.bp.hap2.p_c
maternal.bp.hap2.p_ctg

NGx

Cumulative length

GC content

Legend:
- maternal.bp.hap1.p_ctg
- maternal.bp.hap2.p_ctg
- paternal.bp.hap1.p_ctg
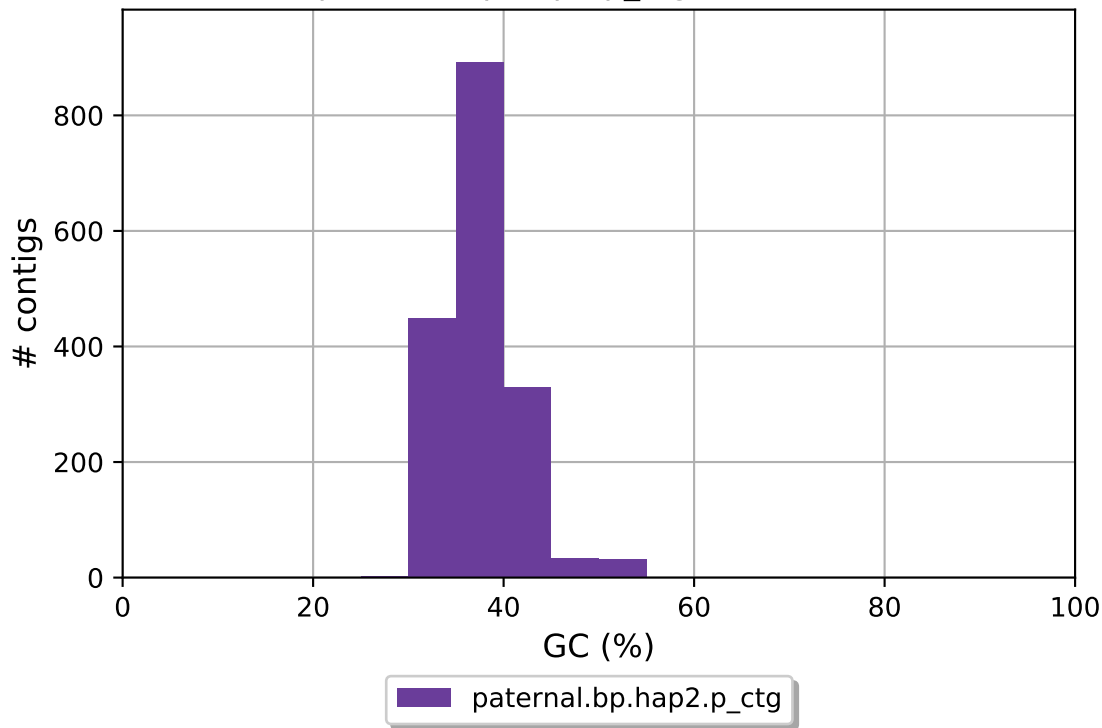- paternal.bp.hap2.p_ctg
- Reference

maternal.bp.hap1.p_ctg GC content
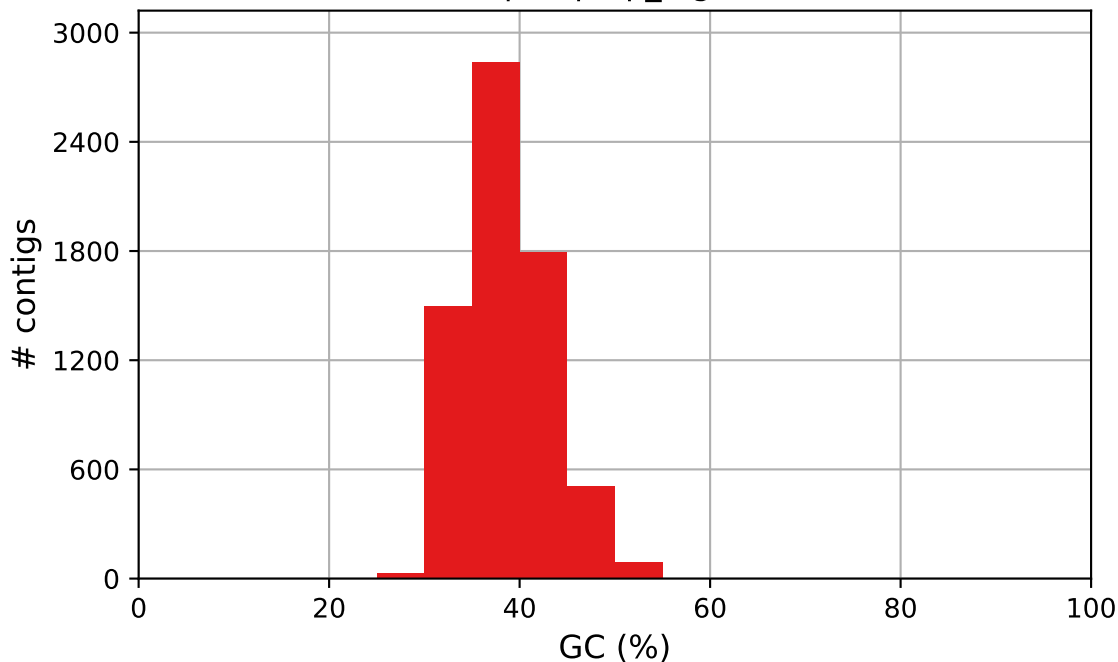
maternal.bp.hap2.p_ctg GC content
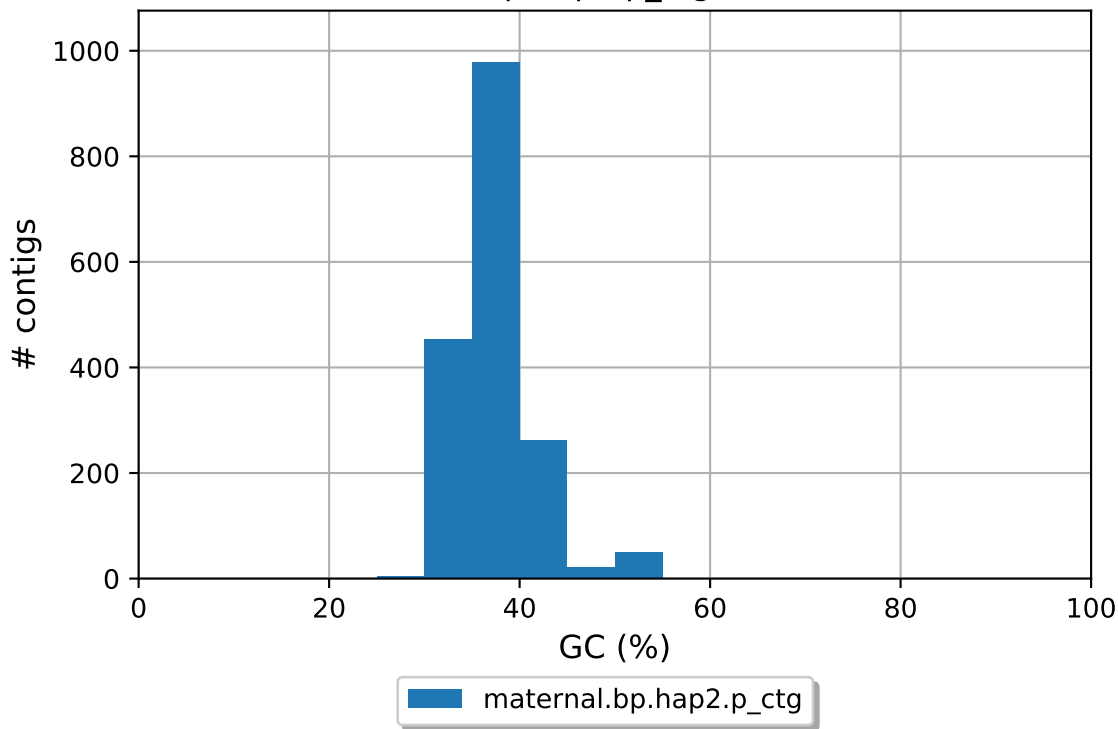
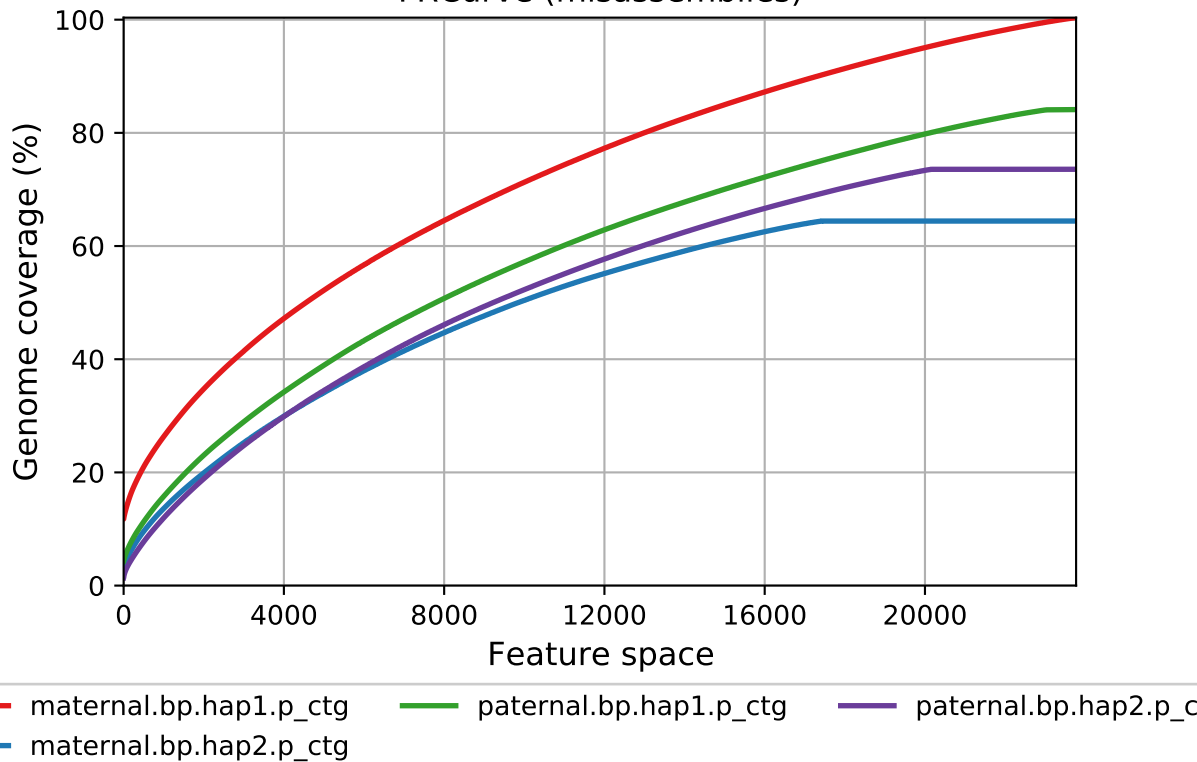paternal.bp.hap1.p_ctg GC content
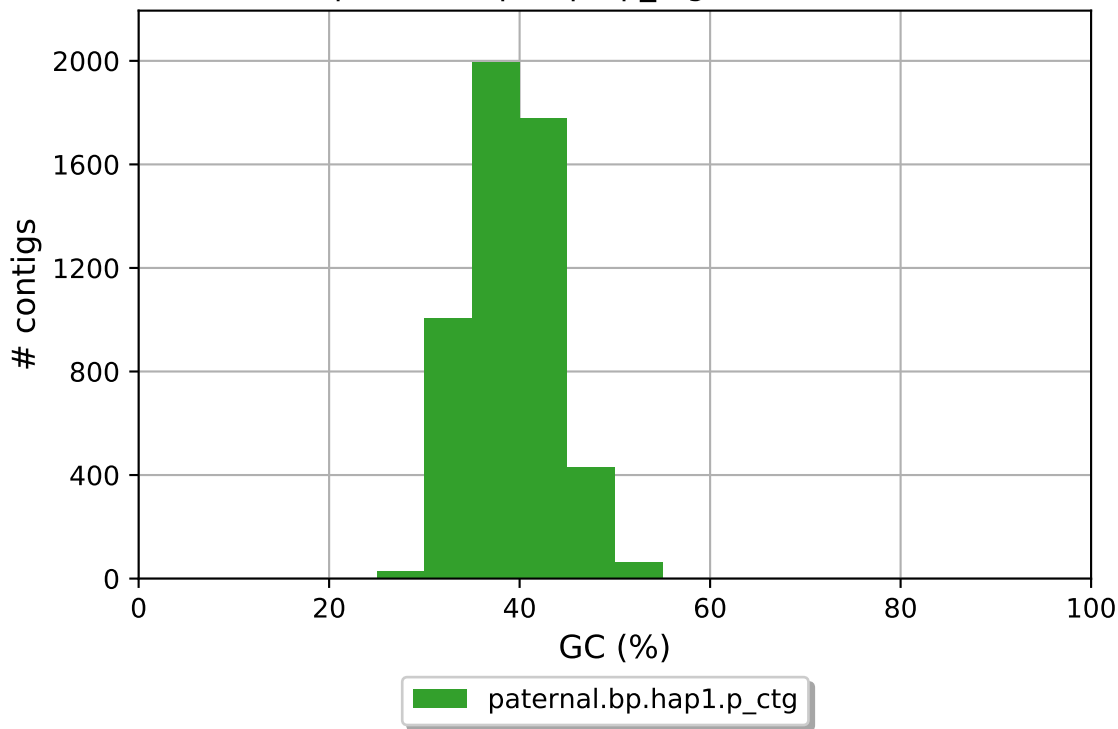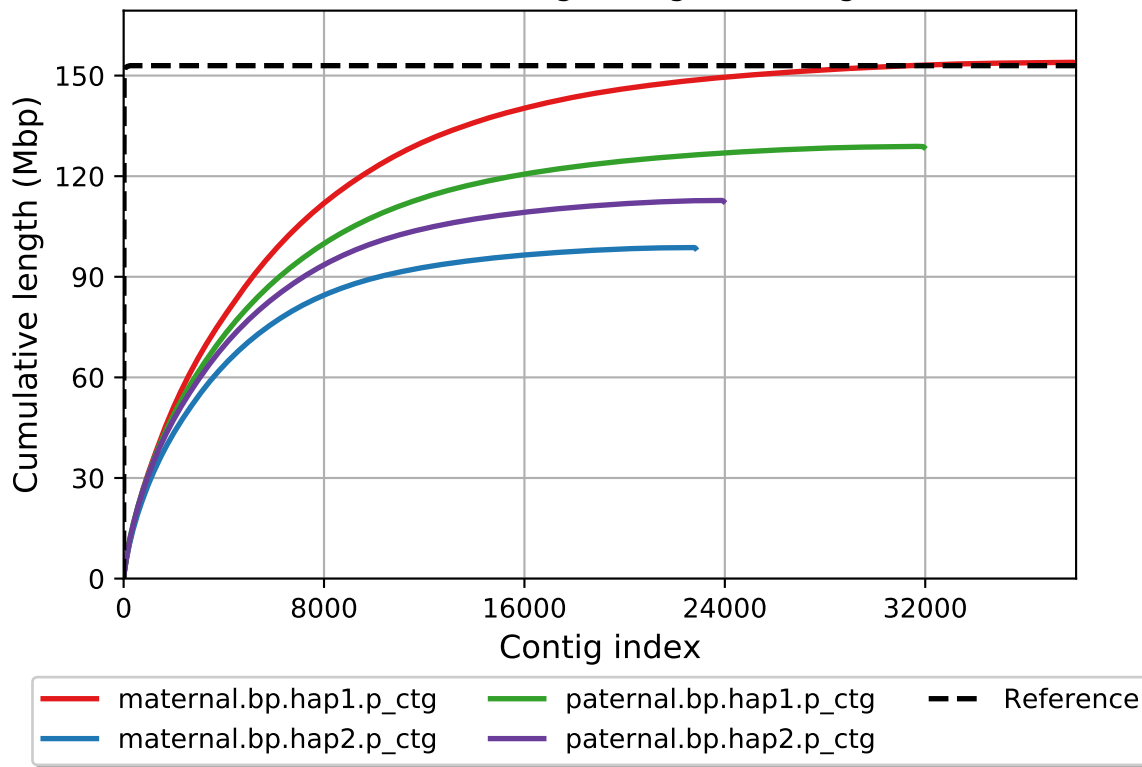
paternal.bp.hap2.p_ctg GC content
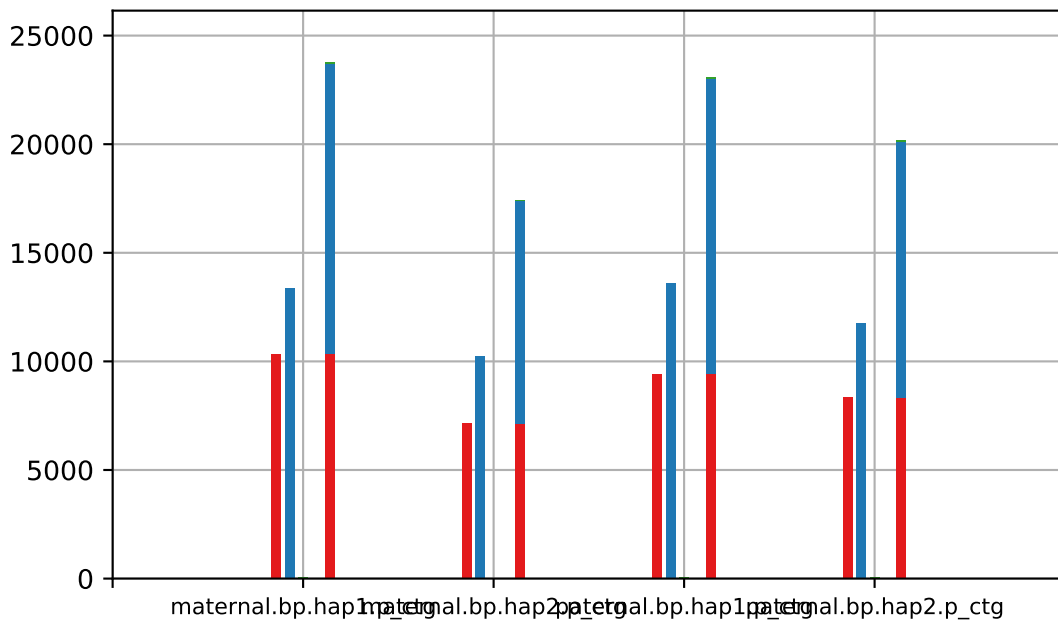
Misassemblies

FRCurve (misassemblies)

Legend:
- maternal.bp.hap1.p_ctg
- paternal.bp.hap1.p_ctg
- paternal.bp.hap2.p_c
- maternal.bp.hap2.p_ctg

Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x
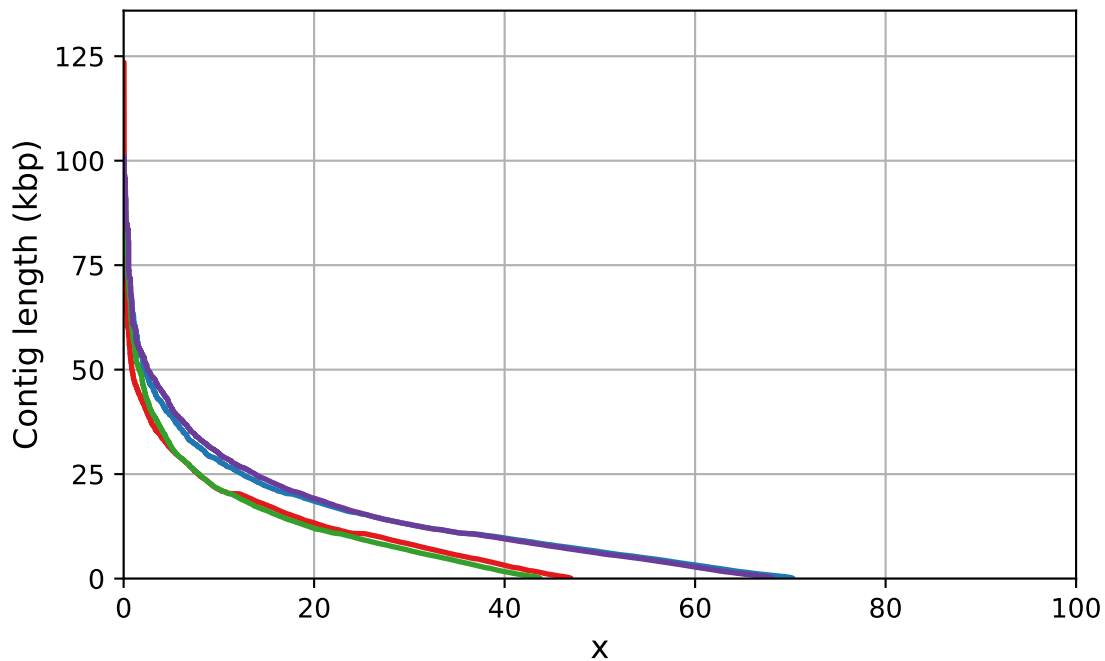
- maternal.bp.hap1.p_ctg
- paternal.bp.hap1.p_ctg
- paternal.bp.hap2.p_c
- maternal.bp.hap2.p_ctg

NGAx
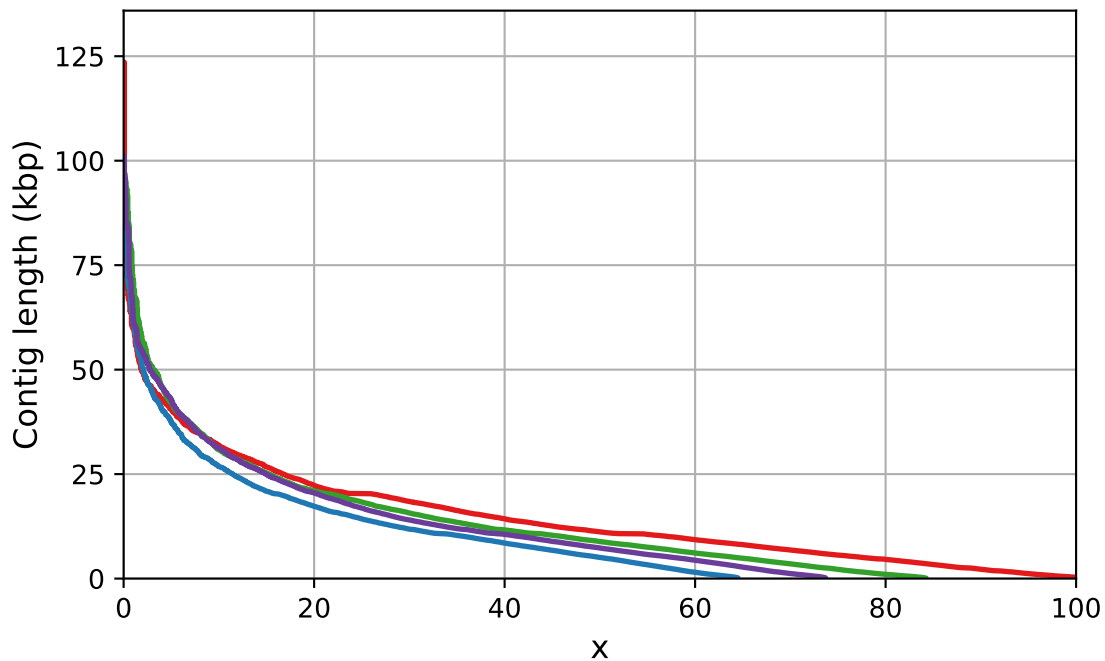
Contig length (kbp)

x

- maternal.bp.hap1.p_ctg
- paternal.bp.hap1.p_ctg
- paternal.bp.hap2.p_c
- maternal.bp.hap2.p_ctg

Cumulative # complete genomic features

Legend:
- maternal.bp.hap1.p_ctg
- maternal.bp.hap2.p_ctg
- paternal.bp.hap1.p_ctg
- paternal.bp.hap2.p_ctg
- Reference
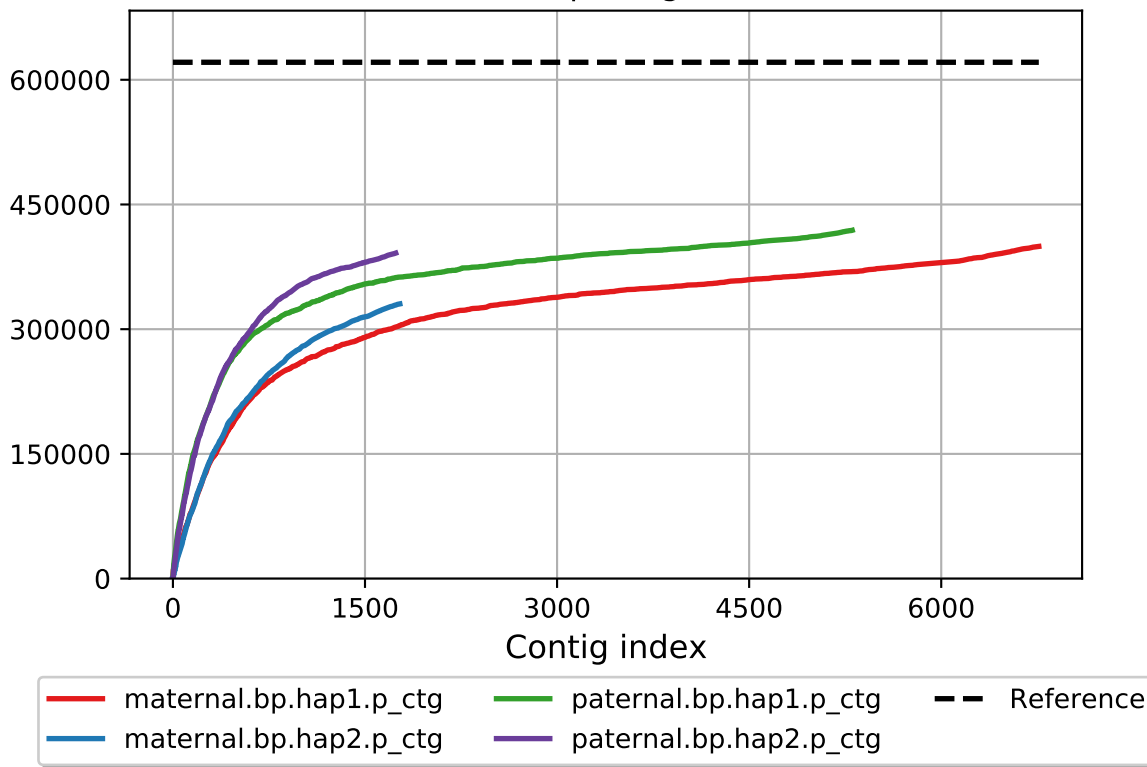
FRCurve (genomic features)

Legend:
- maternal.bp.hap1.p_ctg
- paternal.bp.hap1.p_ctg
- paternal.bp.hap2.p_c
- maternal.bp.hap2.p_ctg

complete genomic features

- maternal.bp.hap1.p_ctg
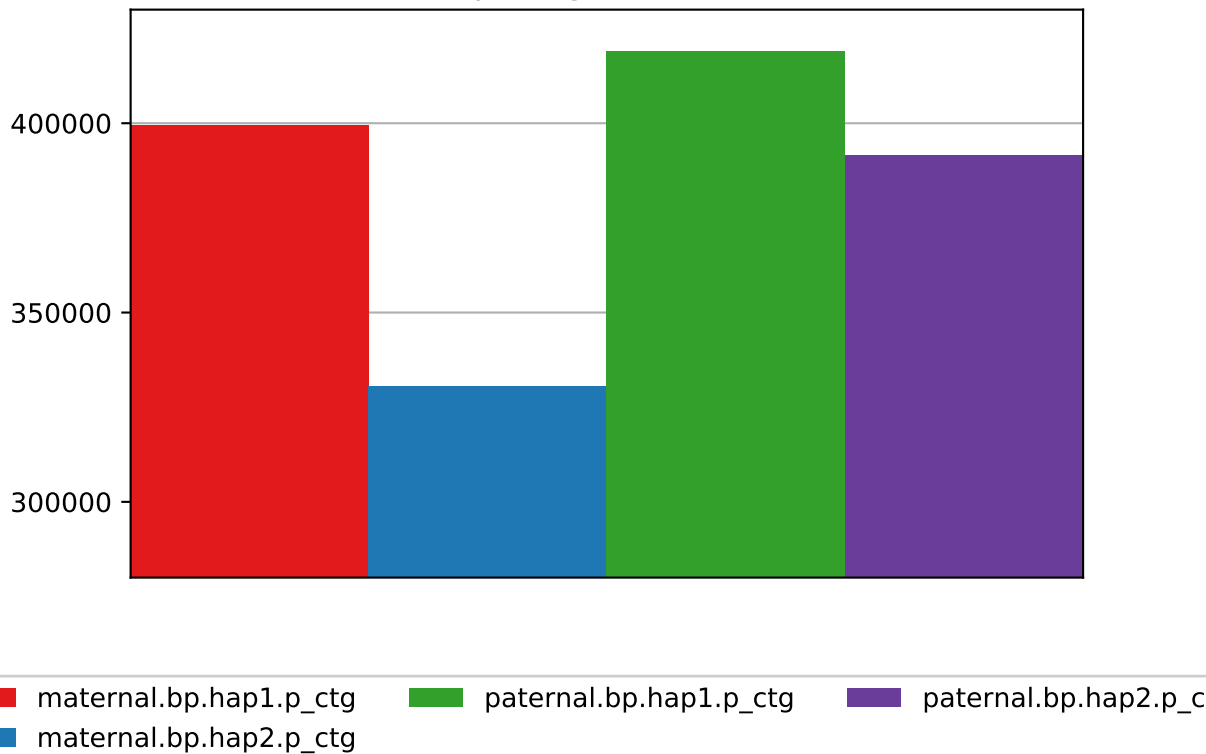- maternal.bp.hap2.p_ctg
- paternal.bp.hap1.p_ctg
- paternal.bp.hap2.p_c

Genome fraction, %

- 🟥 maternal.bp.hap1.p_ctg
- 🟦 maternal.bp.hap2.p_ctg
- 🟩 paternal.bp.hap1.p_ctg
- 🟪 paternal.bp.hap2.p_c