Report

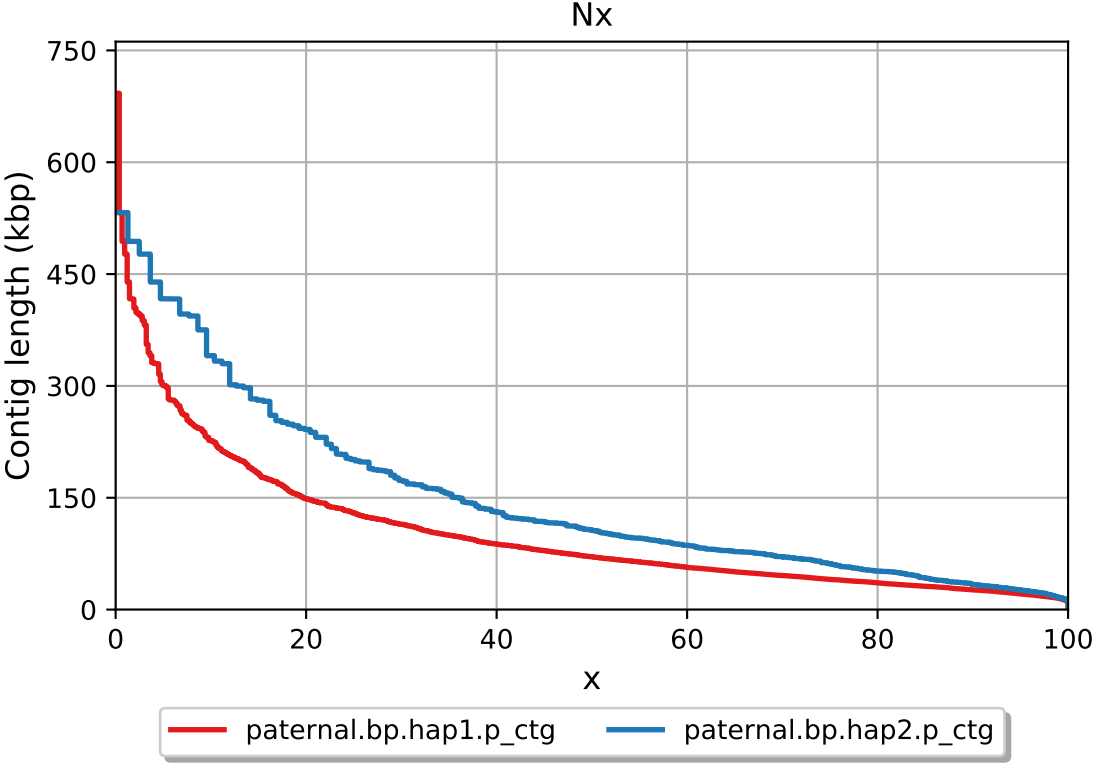
	paternal.bp.hap1.p_ctg	paternal.bp.hap2.p_ctg
# contigs (>= 0 bp)	3302	541
# contigs (>= 1000 bp)	3302	541
# contigs (>= 5000 bp)	3302	541
# contigs (>= 10000 bp)	3291	540
# contigs (>= 25000 bp)	2503	449
# contigs (>= 50000 bp)	1186	286
Total length (>= 0 bp)	181189152	41286925
Total length (>= 1000 bp)	181189152	41286925
Total length (>= 5000 bp)	181189152	41286925
Total length (>= 10000 bp)	181089027	41277876
Total length (>= 25000 bp)	166180516	39525897
Total length (>= 50000 bp)	118968275	33789884
# contigs	3302	541
Largest contig	692509	532462
Total length	181189152	41286925
Reference length	152958180	152958180
GC (%)	35.88	35.78
Reference GC (%)	35.92	35.92
N50	70909	106988
NG50	84564	-
N75	40541	61329
NG75	52845	-
L50	709	107
LG50	526	-
L75	1561	235
LG75	1104	-
# misassemblies	21551	5074
# misassembled contigs	2618	487
Misassembled contigs length	159580710	39566723
# local misassemblies	54446	12363
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	200	17
# unaligned contigs	296 + 2731 part	13 + 484 part
Unaligned length	47476316	8683304
Genome fraction (%)	56.296	18.477
Duplication ratio	1.553	1.154
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	4290.29	3065.03
# indels per 100 kbp	499.26	369.72
# genomic features	397498 + 34342 part	134344 + 13206 part
Largest alignment	125973	99909
Total aligned length	133193379	32460450
NA50	7719	10491
NGA50	10839	-
NA75	-	1161
NGA75	3085	-
LA50	5198	955
LGA50	3657	-
LA75	-	3507
LGA75	9995	-

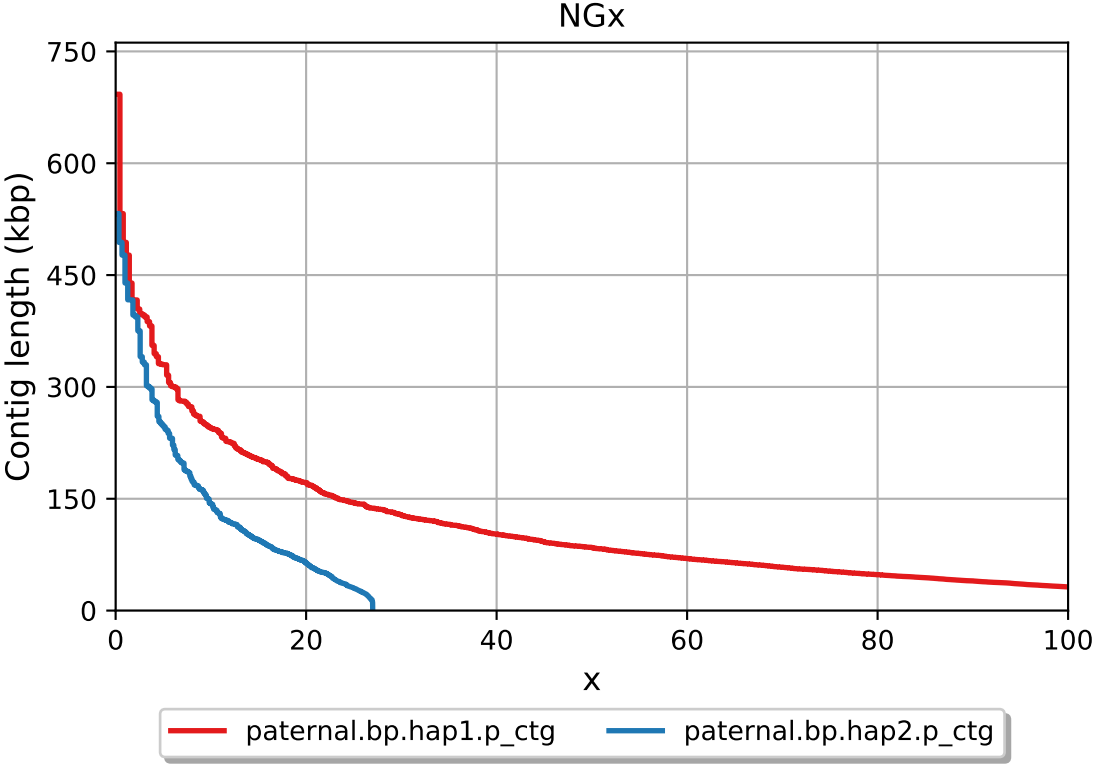
Misassemblies report

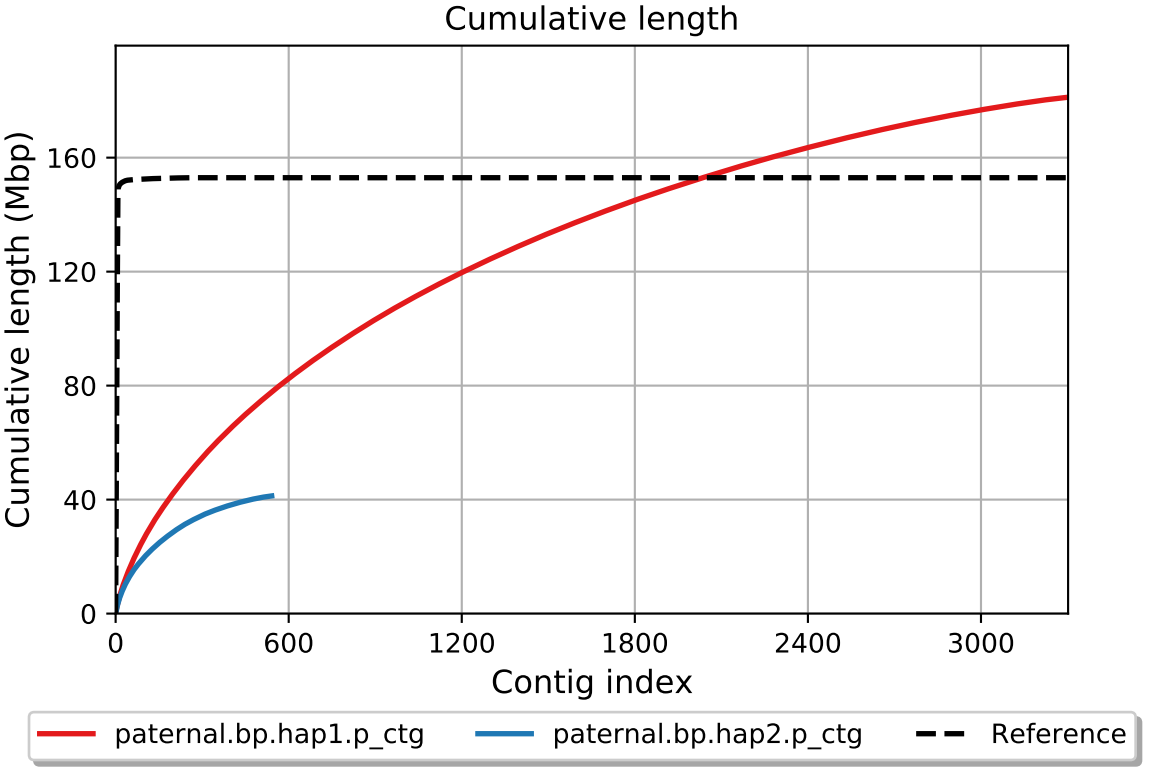
	paternal.bp.hap1.p_ctg	paternal.bp.hap2.p_ctg
# misassemblies	21551	5074
# contig misassemblies	21551	5074
# c. relocations	8937	2138
# c. translocations	12557	2913
# c. inversions	57	23
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	2618	487
Misassembled contigs length	159580710	39566723
# local misassemblies	54446	12363
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	200	17
# mismatches	3694010	866139
# indels	429871	104477
# indels (<= 5 bp)	331049	80255
# indels (> 5 bp)	98822	24222
Indels length	2250173	551992

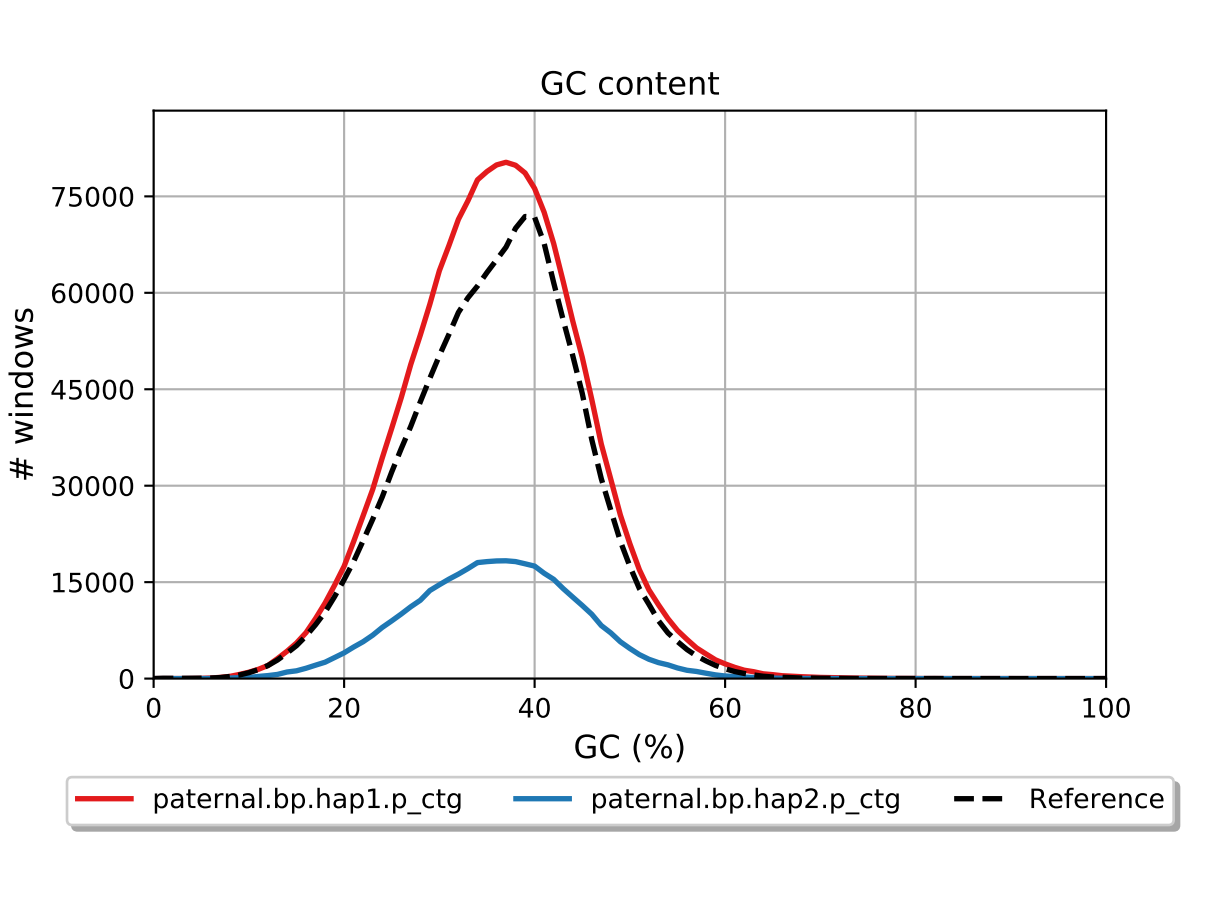
Unaligned report

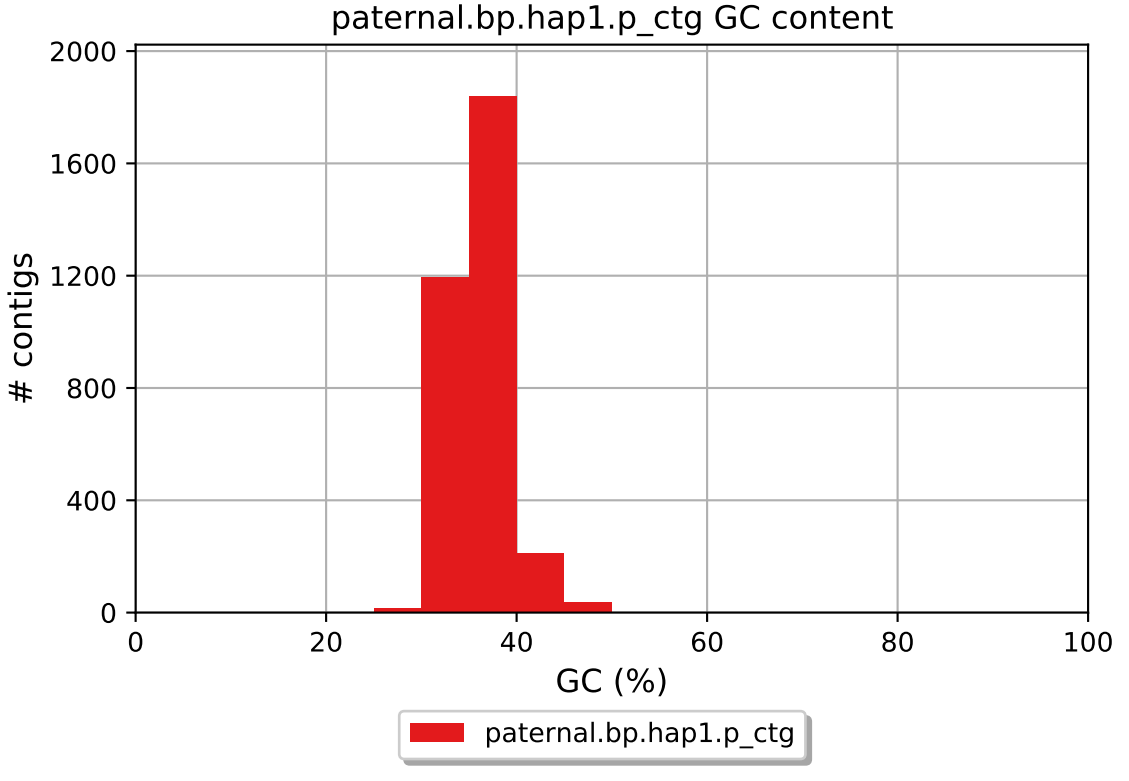
	paternal.bp.hap1.p_ctg	paternal.bp.hap2.p_ctg
# fully unaligned contigs	296	13
Fully unaligned length	9406295	534982
# partially unaligned contigs	2731	484
Partially unaligned length	38070021	8148322
# N's	0	0

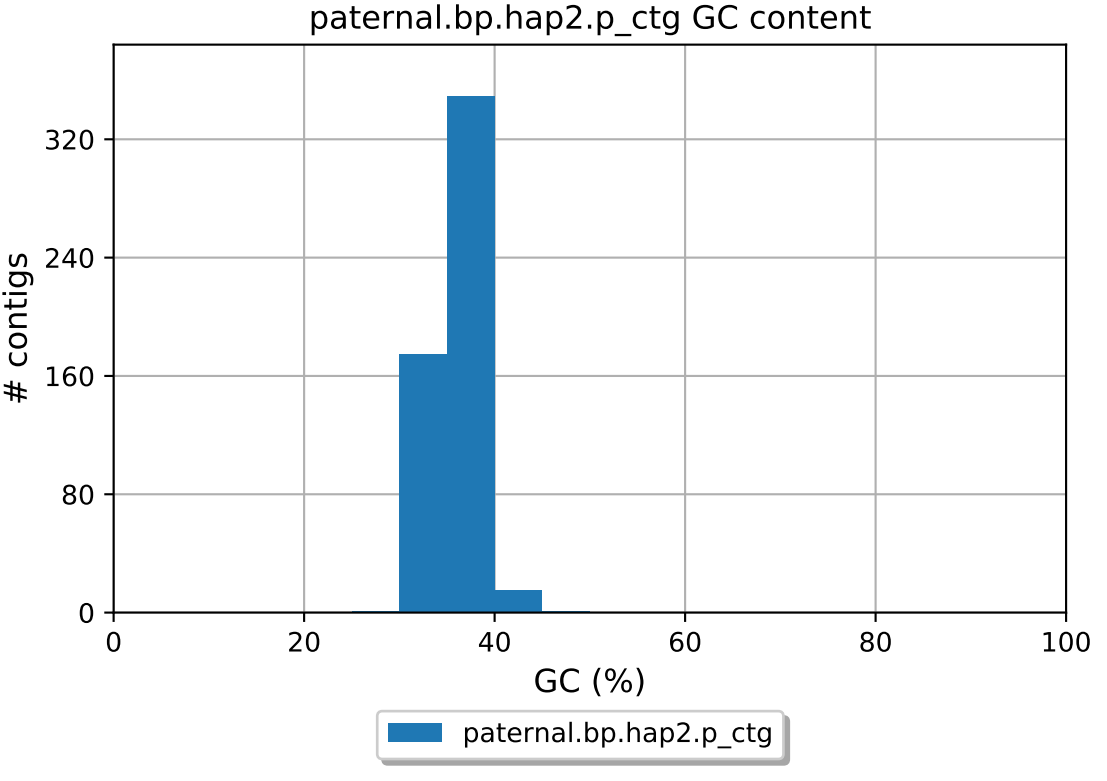

Nx
Contig length (kbp)
750
600
450
300
150
0
0
20
40
60
80
100
x
paternal.bp.hap1.p_ctg
paternal.bp.hap2.p_ctg

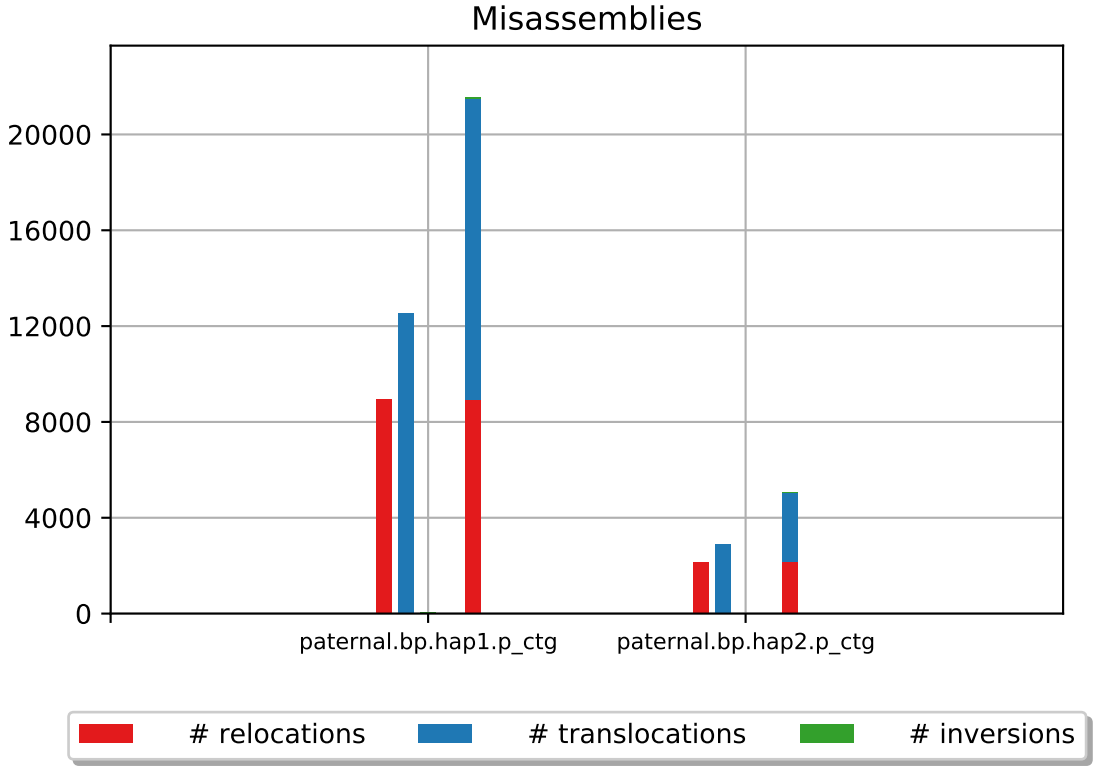

NGx
Contig length (kbp)
750
600
450
300
150
0
0
20
40
60
80
100
x
paternal.bp.hap1.p_ctg
paternal.bp.hap2.p_ctg

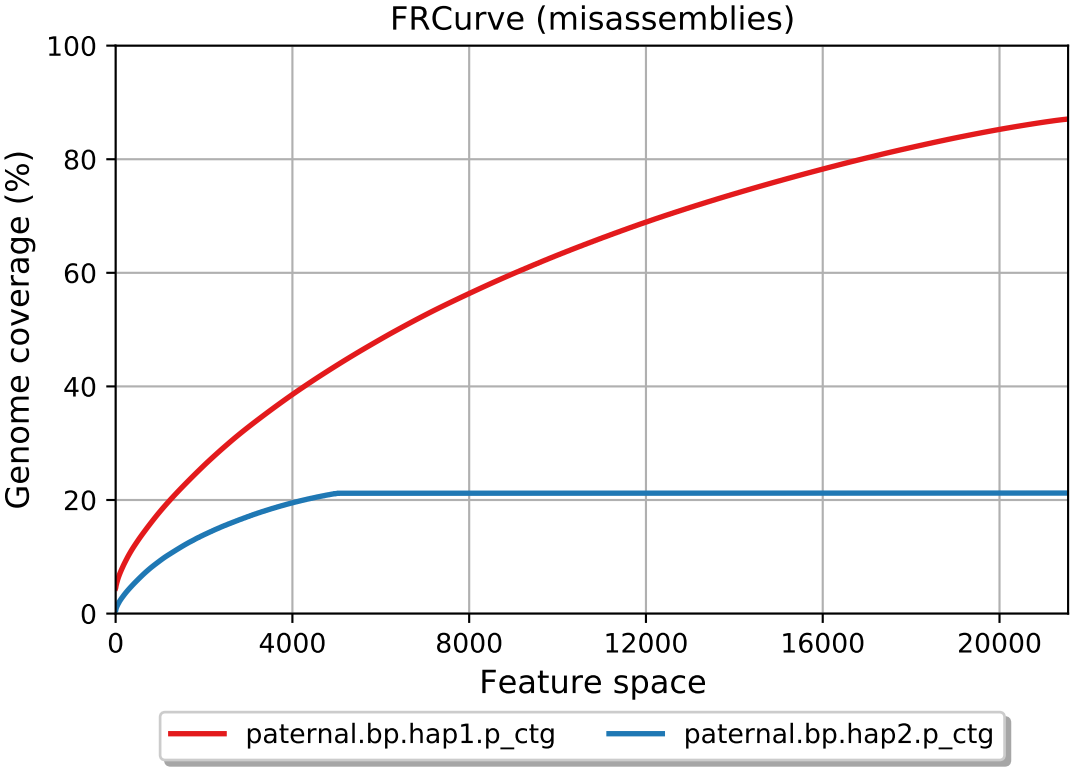

Cumulative length
Cumulative length (Mbp)
0
40
80
120
160
0
600
1200
1800
2400
3000
Contig index
paternal.bp.hap1.p_ctg
paternal.bp.hap2.p_ctg
Reference

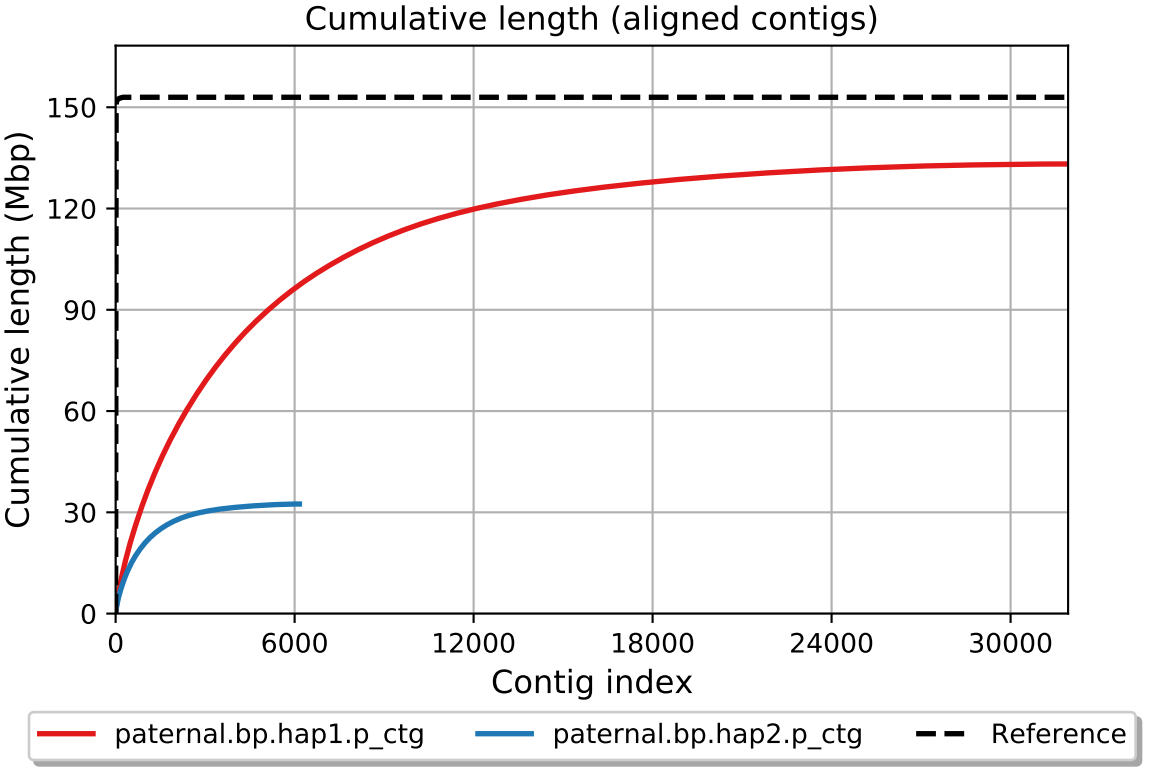

GC content
windows
75000
60000
45000
30000
15000
0
0
20
40
60
80
100
GC (%)
paternal.bp.hap1.p_ctg
paternal.bp.hap2.p_ctg
Reference

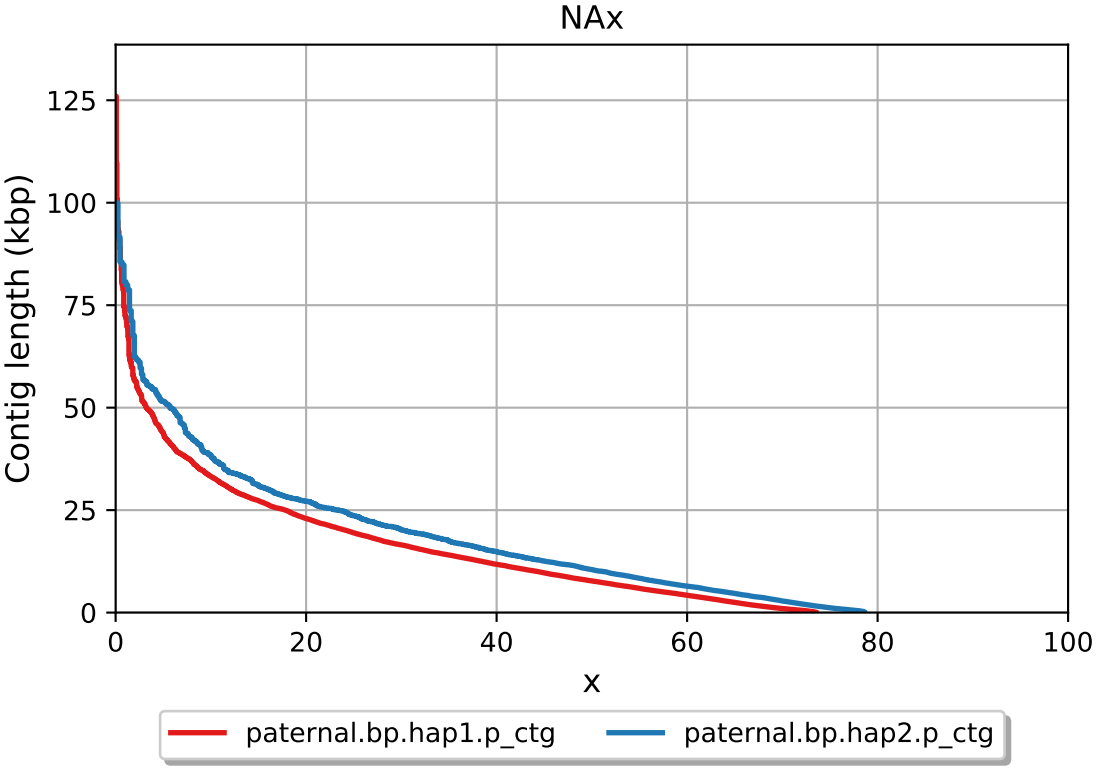

paternal.bp.hap1.p_ctg GC content
2000
1600
1200
800
400
0
contigs
0
20
40
60
80
100
GC (%)
paternal.bp.hap1.p_ctg

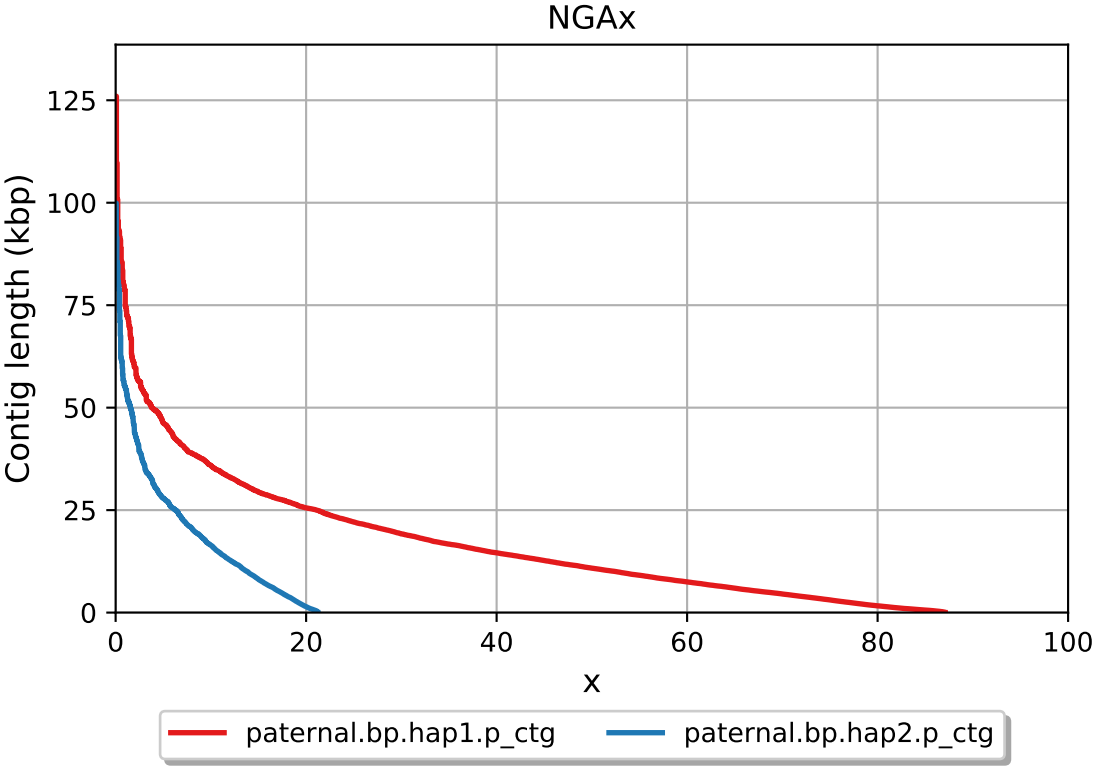

paternal.bp.hap2.p_ctg GC content
contigs
0
80
160
240
320
0
20
40
60
80
100
GC (%)
paternal.bp.hap2.p_ctg

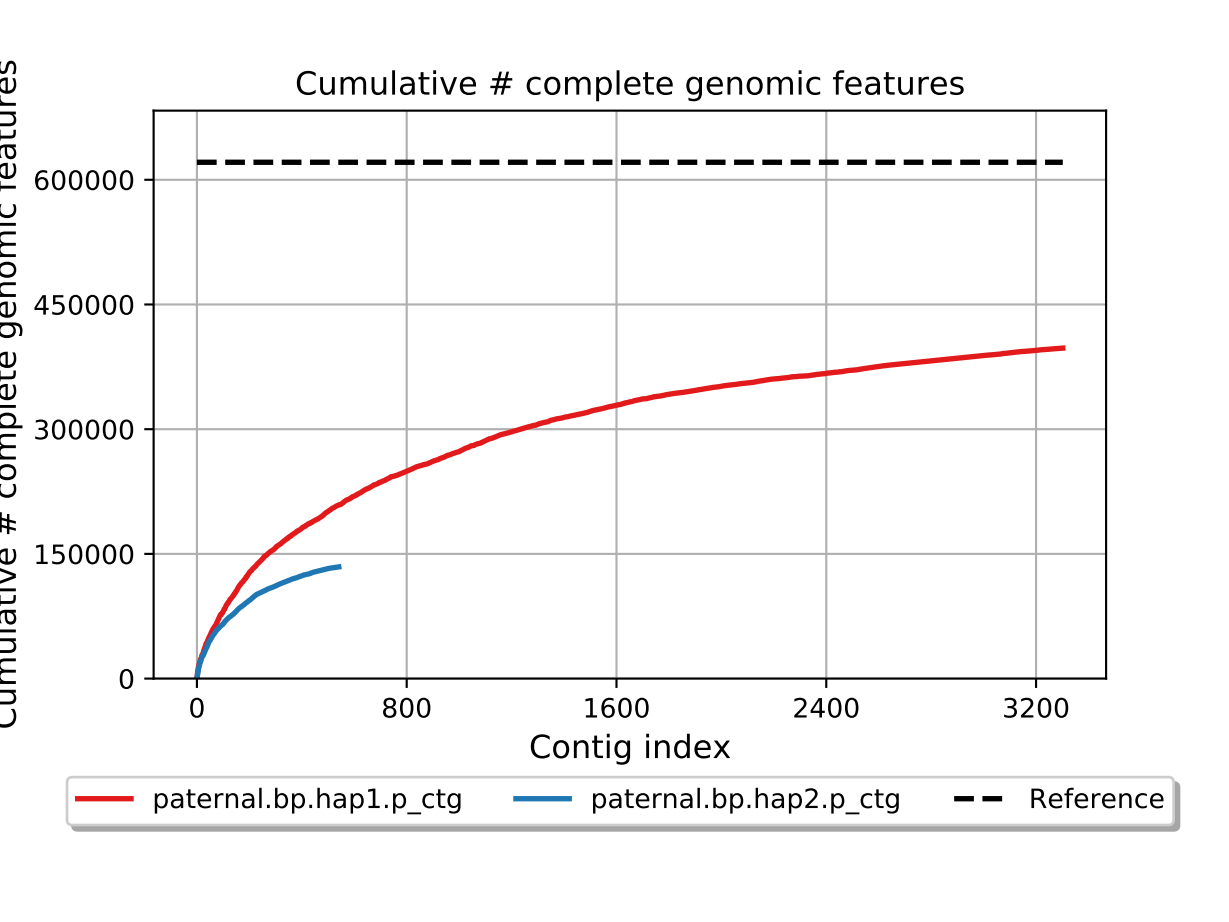

Misassemblies
20000
16000
12000
8000
4000
0
paternal.bp.hap1.p_ctg
paternal.bp.hap2.p_ctg
relocations
translocations
inversions

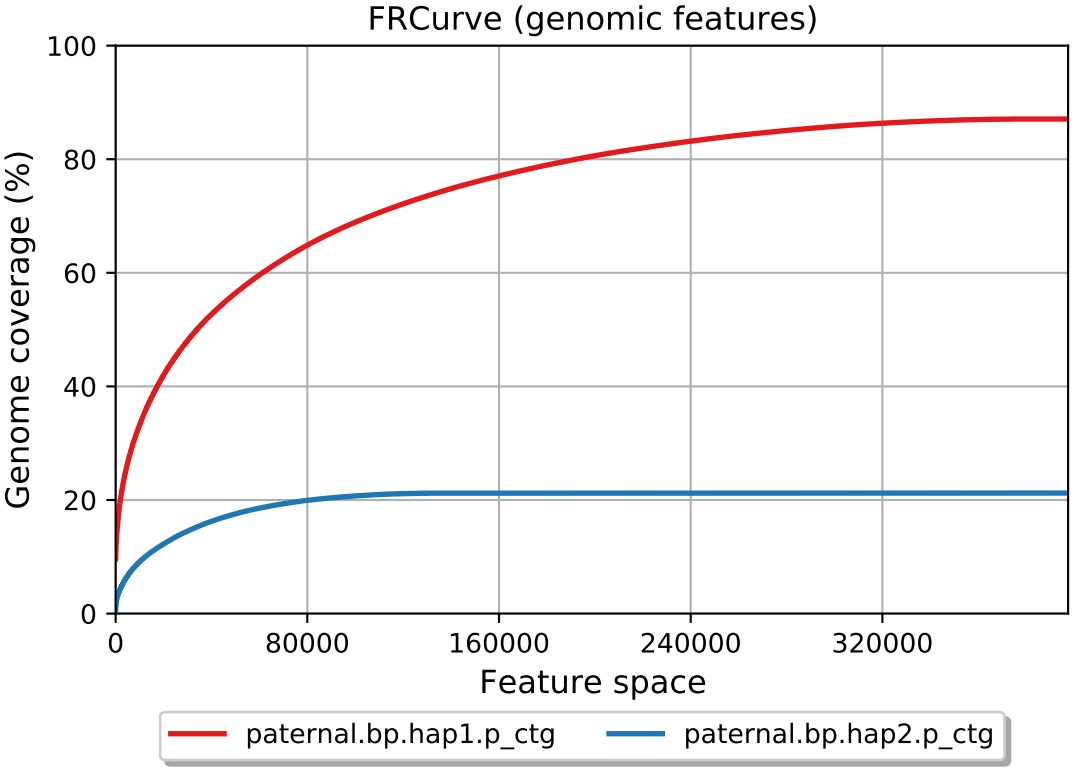

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
4000
8000
12000
16000
20000
Feature space
paternal.bp.hap1.p_ctg
paternal.bp.hap2.p_ctg

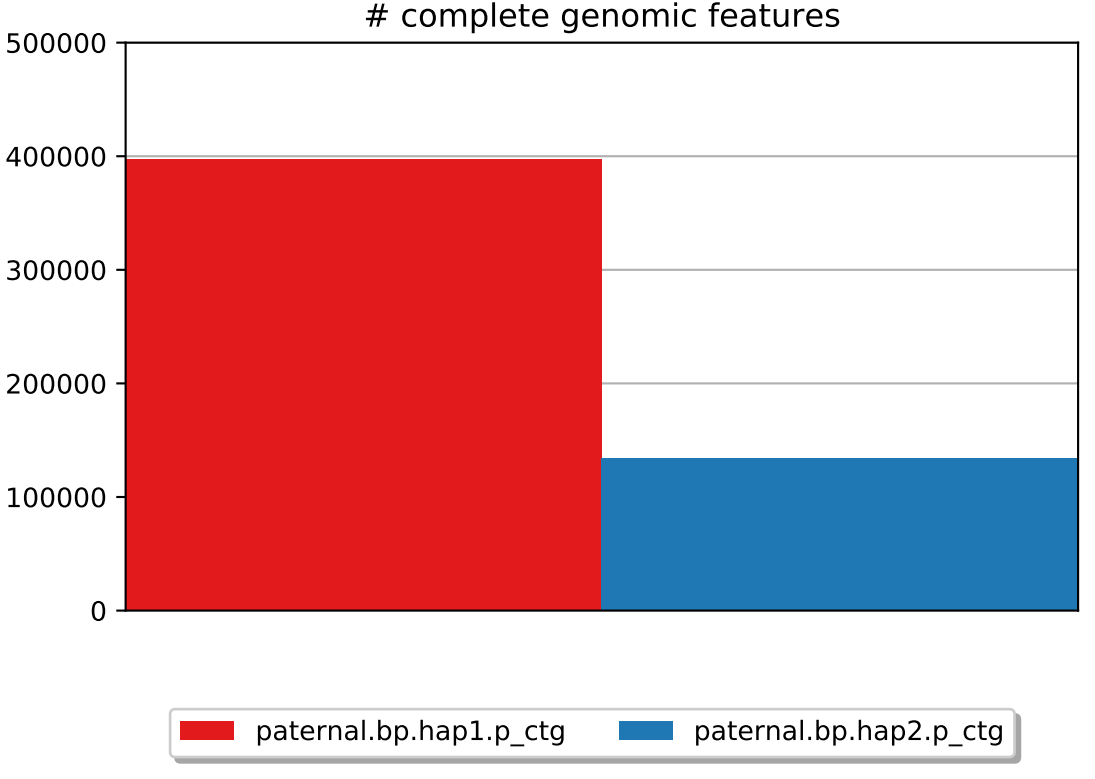

Cumulative length (aligned contigs)
Cumulative length (Mbp)
150
120
90
60
30
0
0
6000
12000
18000
24000
30000
Contig index
paternal.bp.hap1.p_ctg
paternal.bp.hap2.p_ctg
Reference

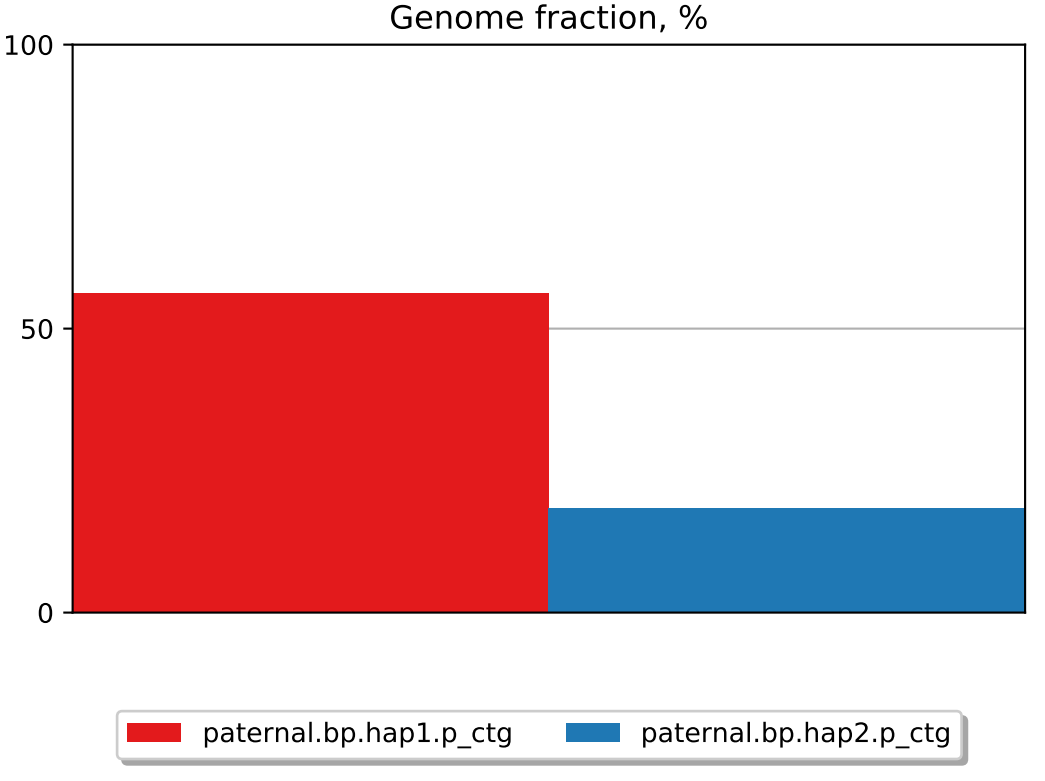

NAx
Contig length (kbp)
125
100
75
50
25
0
0
20
40
60
80
100
x
paternal.bp.hap1.p_ctg
paternal.bp.hap2.p_ctg


NGAx
Contig length (kbp)
125
100
75
50
25
0
0
20
40
60
80
100
x
paternal.bp.hap1.p_ctg
paternal.bp.hap2.p_ctg


Cumulative # complete genomic features
Cumulative # complete genomic features
600000
450000
300000
150000
0
0
800
1600
2400
3200
Contig index
paternal.bp.hap1.p_ctg
paternal.bp.hap2.p_ctg
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
80000
160000
240000
320000
Feature space
paternal.bp.hap1.p_ctg
paternal.bp.hap2.p_ctg


complete genomic features
500000
400000
300000
200000
100000
0
paternal.bp.hap1.p_ctg
paternal.bp.hap2.p_ctg


Genome fraction, %
100
50
0
paternal.bp.hap1.p_ctg
paternal.bp.hap2.p_ctg