Report

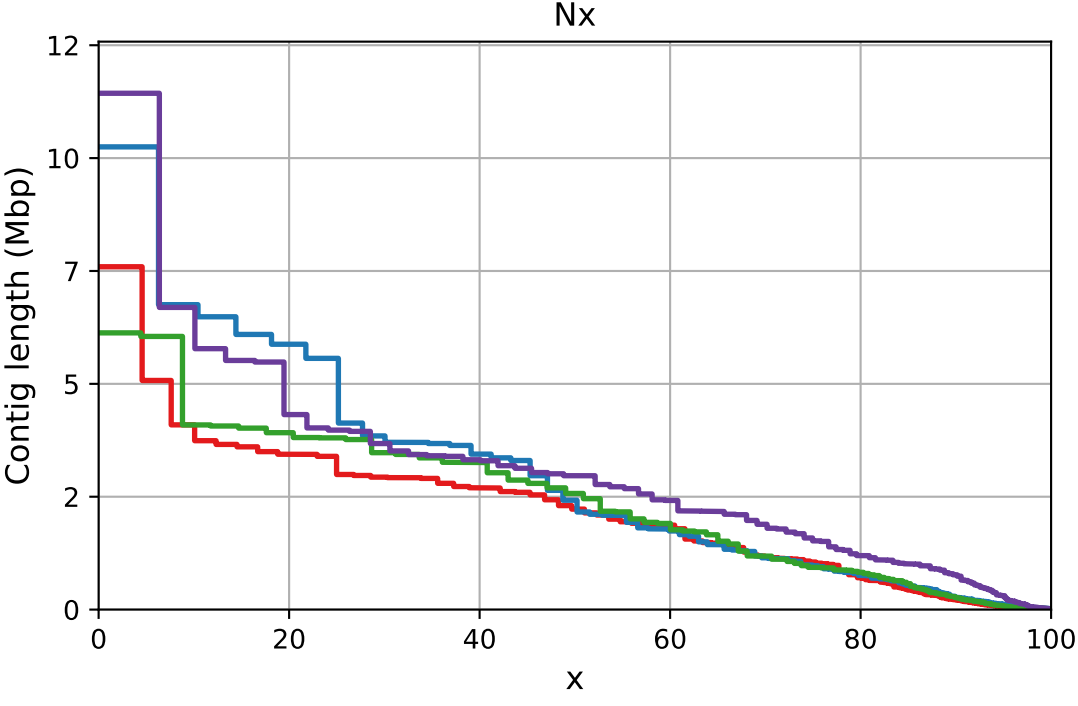
	assemblies_VW4_HiFiasm.asm.11.hic.hap1.p_ctg	assemblies_VW4_HiFiasm.asm.11.hic.hap2.p_ctg	assemblies_VW4_HiFiasm.asm.15.hic.hap1.p_ctg	assemblies_VW4_HiFiasm.asm.15.hic.hap2.p_ctg
# contigs (>= 0 bp)	421	295	315	227
# contigs (>= 1000 bp)	421	295	315	227
# contigs (>= 5000 bp)	421	295	315	227
# contigs (>= 10000 bp)	418	295	315	227
# contigs (>= 25000 bp)	354	272	265	199
# contigs (>= 50000 bp)	204	193	162	142
Total length (>= 0 bp)	166265887	162972331	138348712	179375020
Total length (>= 1000 bp)	166265887	162972331	138348712	179375020
Total length (>= 5000 bp)	166265887	162972331	138348712	179375020
Total length (>= 10000 bp)	166244747	162972331	138348712	179375020
Total length (>= 25000 bp)	164986753	162522872	137347857	178808480
Total length (>= 50000 bp)	159577980	159531474	133774049	176807667
# contigs	421	295	315	227
Largest contig	7593577	10248763	6129226	11436107
Total length	166265887	162972331	138348712	179375020
GC (%)	30.31	30.29	30.30	30.21
N50	2225187	2422397	2572107	2965407
N90	214889	270426	269489	770494
L50	26	18	19	21
L90	104	87	77	66
# total reads	1629080	1567212	1901420	1374343
# left	0	0	0	0
# right	0	0	0	0
Mapped (%)	99.98	99.97	99.95	99.98
Properly paired (%)	0.0	0.0	0.0	0.0
Avg. coverage depth	60	60	70	54
Coverage >= 1x (%)	99.84	99.87	99.92	99.92
# N's per 100 kbp	0.00	0.00	0.00	0.00
# predicted genes (unique)	10656	10789	9188	11720
# predicted genes (>= 0 bp)	12722 + 4 part	12468 + 3 part	10700 + 0 part	13517 + 3 part
# predicted genes (>= 300 bp)	11007 + 4 part	10949 + 3 part	9304 + 0 part	11747 + 3 part
# predicted genes (>= 1500 bp)	5299 + 1 part	5234 + 1 part	4481 + 0 part	5690 + 3 part
# predicted genes (>= 3000 bp)	2487 + 1 part	2440 + 0 part	2080 + 0 part	2649 + 1 part

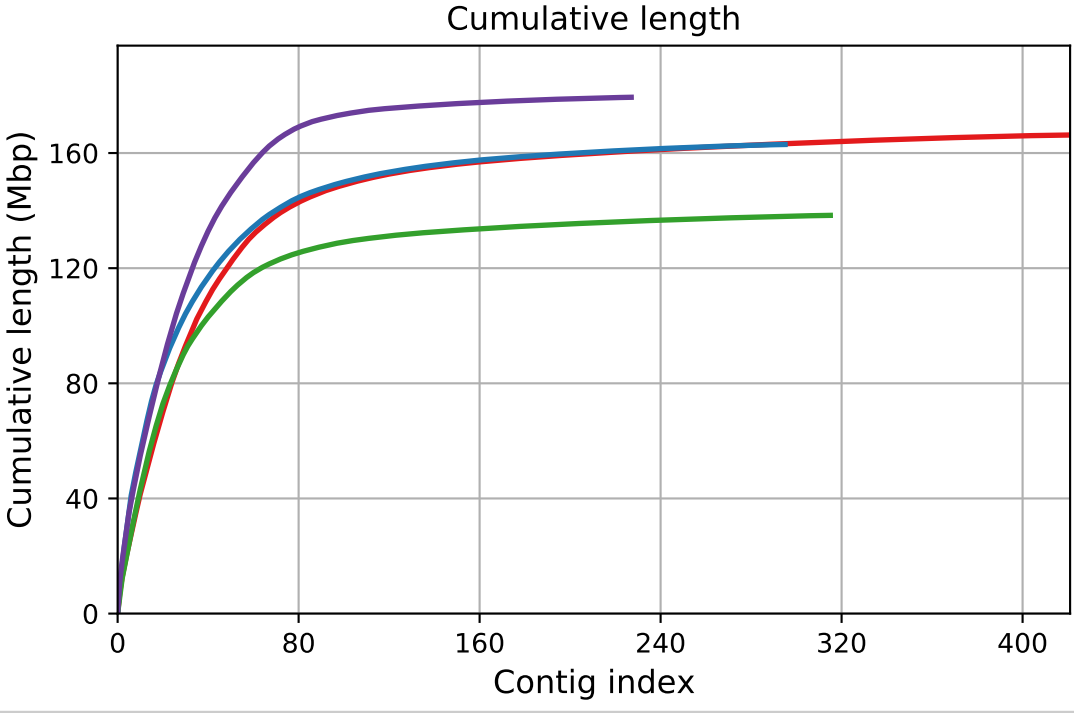
All statistics are based on contigs of size >= 3000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Reads report

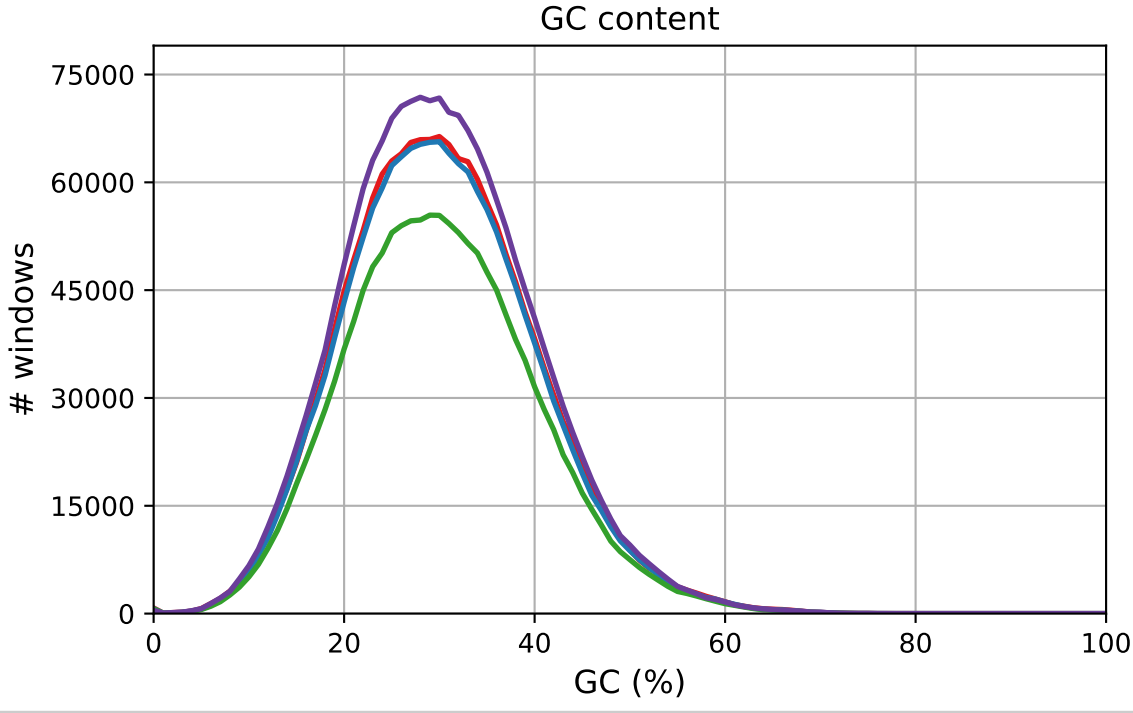
	assemblies_VW4_HiFiasm.asm.11.hic.hap1.p_ctg	assemblies_VW4_HiFiasm.asm.11.hic.hap2.p_ctg	assemblies_VW4_HiFiasm.asm.15.hic.hap1.p_ctg	assemblies_VW4_HiFiasm.asm.15.hic.hap2.p_ctg
# total reads	1629080	1567212	1901420	1374343
# left	0	0	0	0
# right	0	0	0	0
# mapped	1628712	1566786	1900547	1374133
Mapped (%)	99.98	99.97	99.95	99.98
# properly paired	0	0	0	0
Properly paired (%)	0.0	0.0	0.0	0.0
# singletons	0	0	0	0
Singletons (%)	0.0	0.0	0.0	0.0
# misjoint mates	0	0	0	0
Misjoint mates (%)	0.0	0.0	0.0	0.0
Avg. coverage depth	60	60	70	54
Coverage >= 1x (%)	99.84	99.87	99.92	99.92
Coverage >= 5x (%)	99.59	99.71	99.76	99.82
Coverage >= 10x (%)	98.94	99.17	99.36	99.24

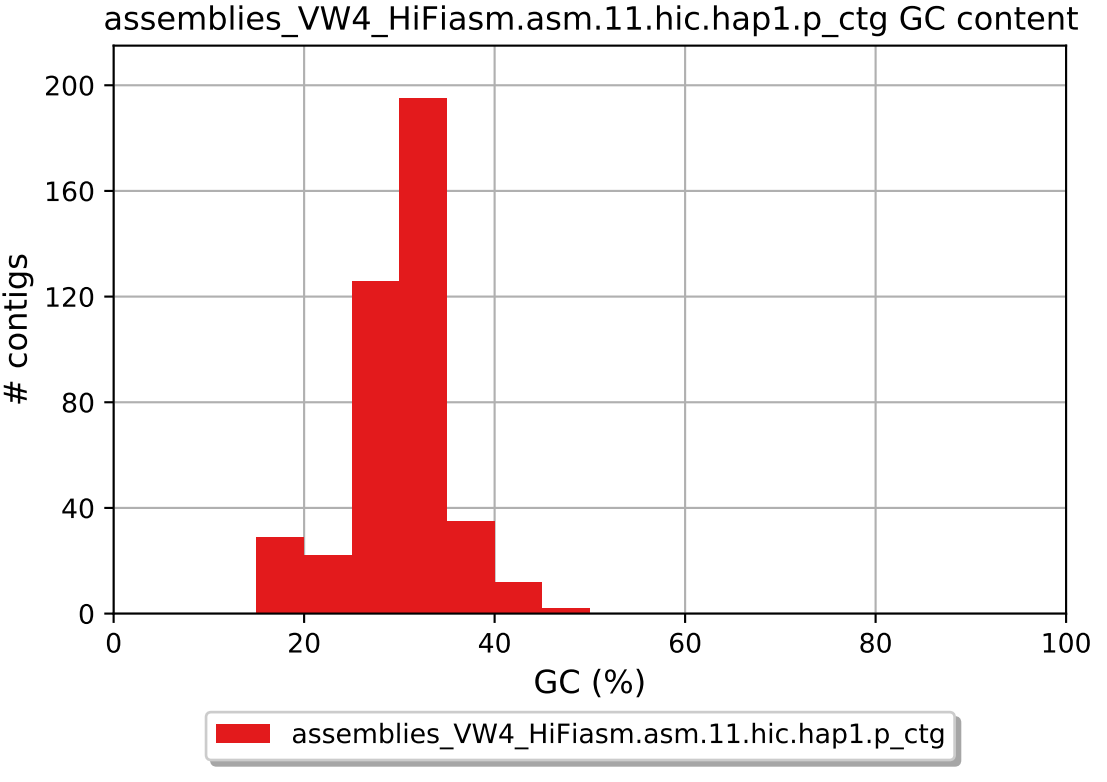
All statistics are based on contigs of size >= 3000 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

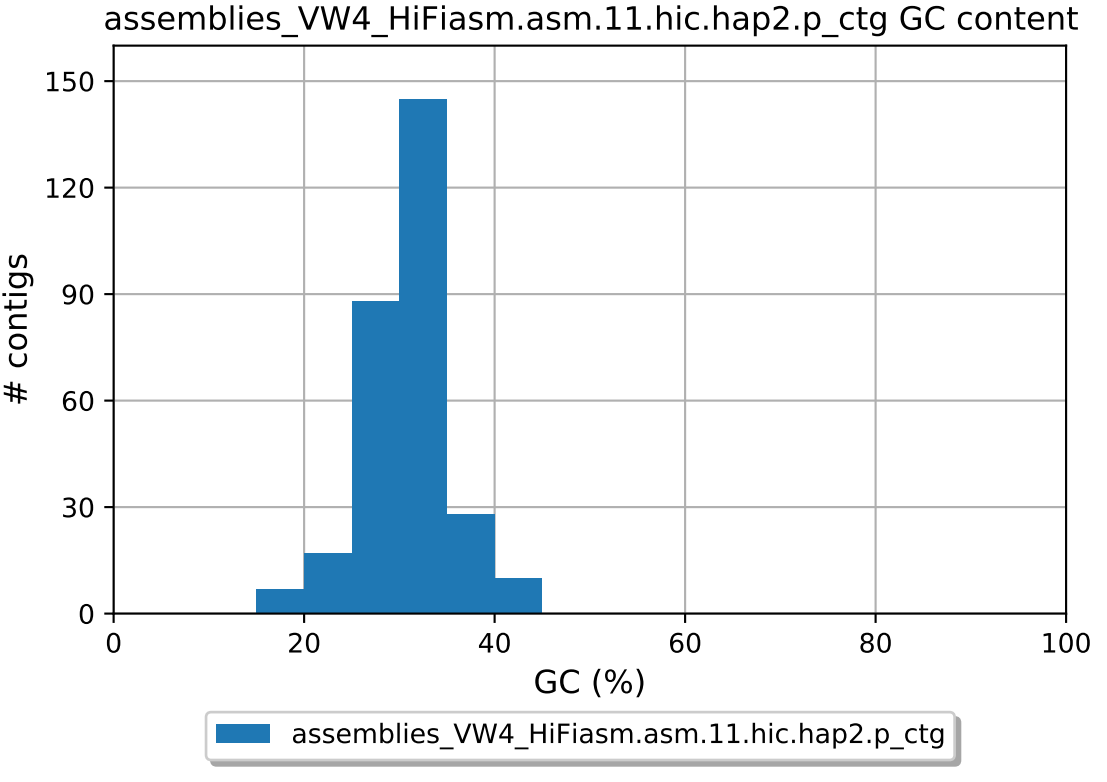

Nx
Contig length (Mbp)
x
0
2
5
7
10
12
0
20
40
60
80
100
.hic.hap1.p_ctg
assemblies_VW4_HiFiasm.asm.15.hic.hap1.p_ctg
assembli
.hic.hap2.p_ctg

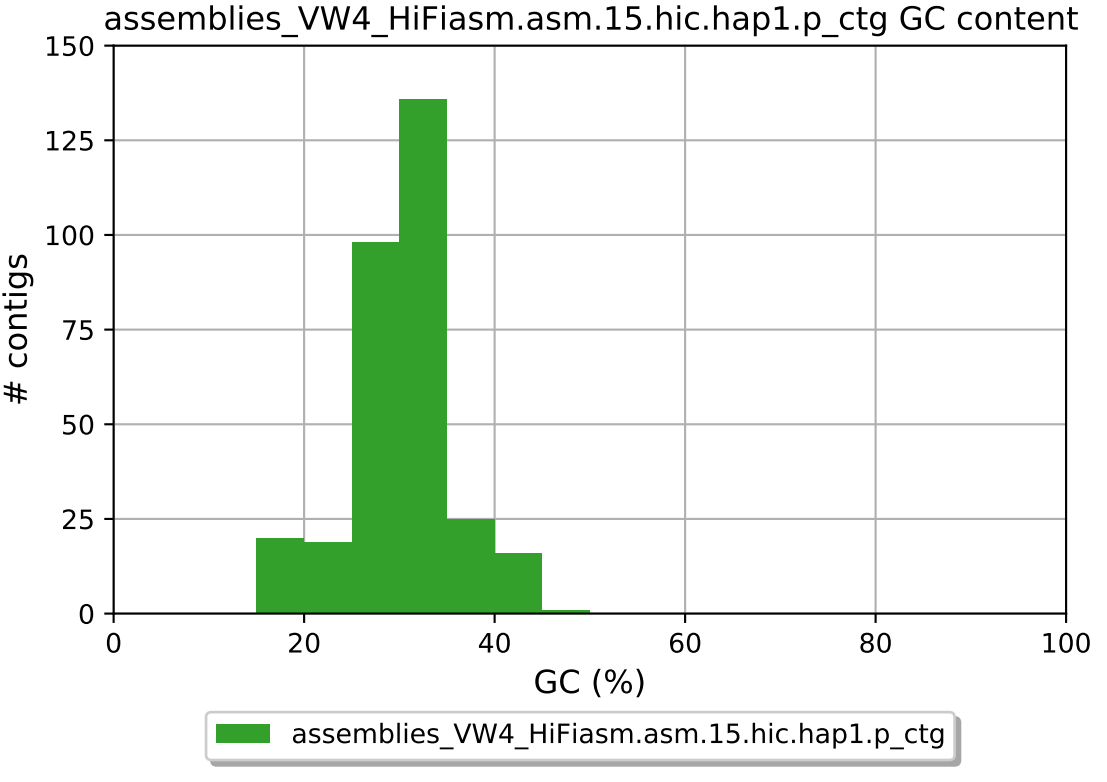


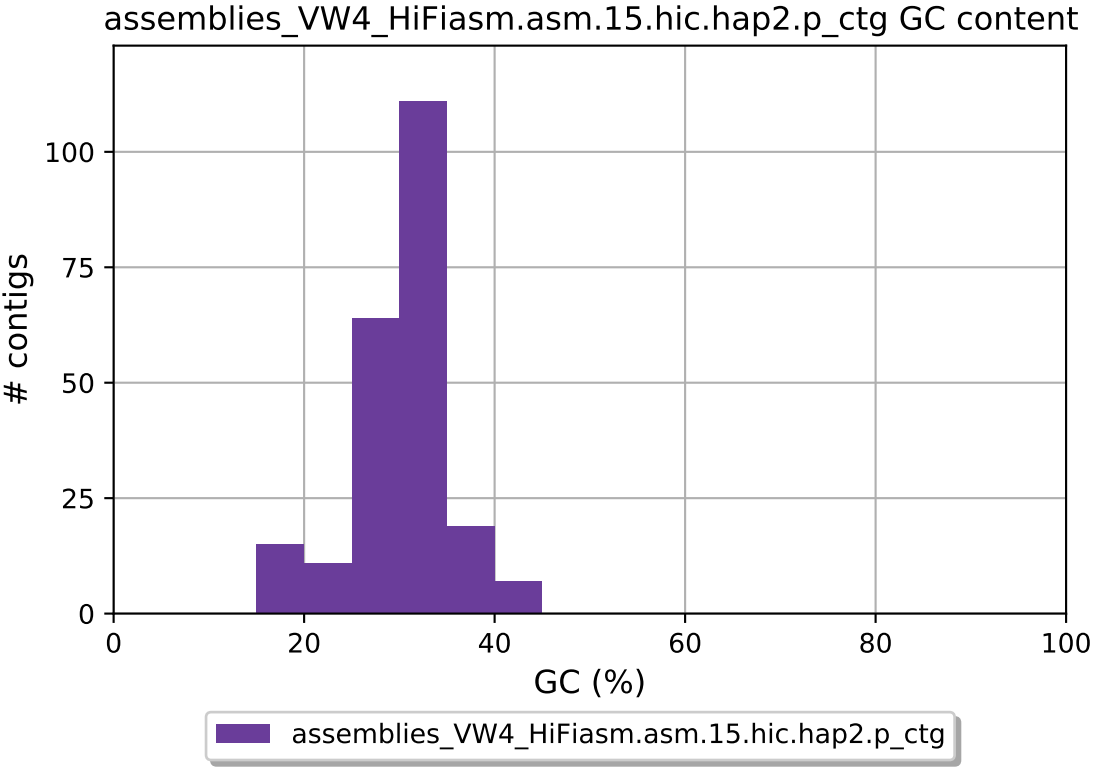
.hic.hap1.p_ctg
.hic.hap2.p_ctg
assemblies_VW4_HiFiasm.asm.15.hic.hap1.p_ctg
assembli


GC content
75000
60000
45000
30000
15000
0
windows
0
20
40
60
80
100
GC (%)
.hic.hap1.p_ctg
.hic.hap2.p_ctg
assemblies_VW4_HiFiasm.asm.15.hic.hap1.p_ctg
assembli


assemblies_VW4_HiFiasm.asm.11.hic.hap1.p_ctg GC content
contigs
GC (%)
0
40
80
120
160
200
0
20
40
60
80
100
assemblies_VW4_HiFiasm.asm.11.hic.hap1.p_ctg


assemblies_VW4_HiFiasm.asm.11.hic.hap2.p_ctg GC content
contigs
GC (%)
0
30
60
90
120
150
0
20
40
60
80
100
assemblies_VW4_HiFiasm.asm.11.hic.hap2.p_ctg


assemblies_VW4_HiFiasm.asm.15.hic.hap1.p_ctg GC content
contigs
GC (%)
0
25
50
75
100
125
150
0
20
40
60
80
100
assemblies_VW4_HiFiasm.asm.15.hic.hap1.p_ctg


assemblies_VW4_HiFiasm.asm.15.hic.hap2.p_ctg GC content
contigs
GC (%)
0
25
50
75
100
0
20
40
60
80
100
assemblies_VW4_HiFiasm.asm.15.hic.hap2.p_ctg