Report

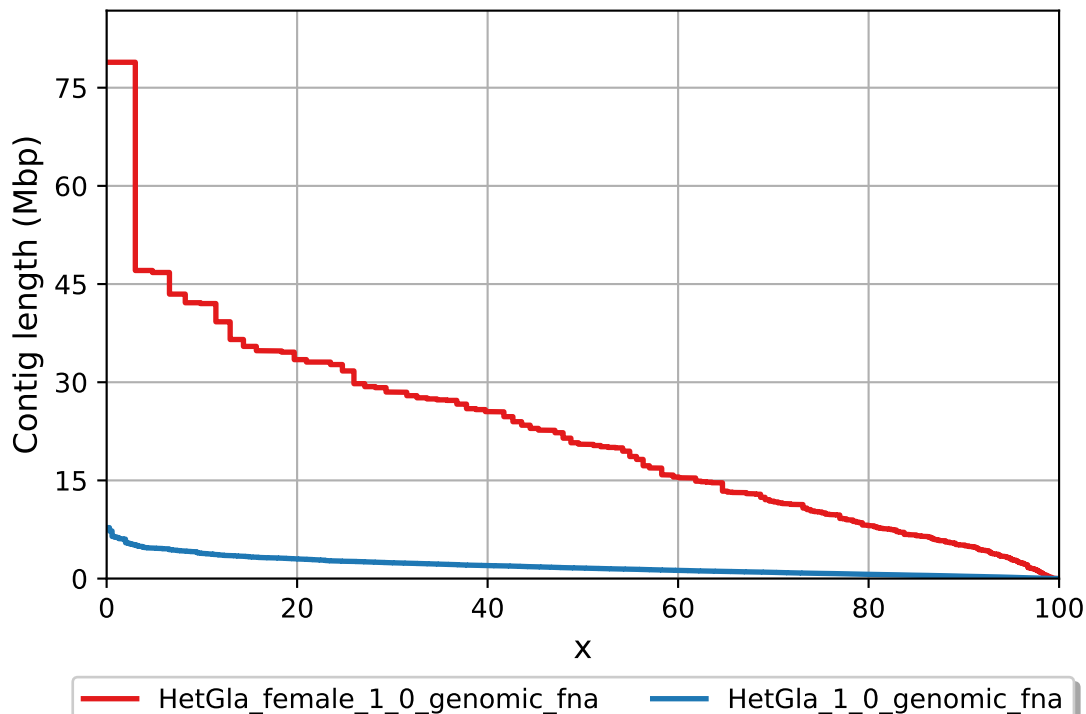|	HetGla_female_1_0_genomic_fna	HetGla_1_0_genomic_fna
# contigs (>= 0 bp)	4229	39267
# contigs (>= 1000 bp)	4229	9182
Total length (>= 0 bp)	2618204639	2643978223
Total length (>= 1000 bp)	2618204639	2632364653
# contigs	4229	16122
Largest contig	78885850	7787482
Total length	2618204639	2637221728
Reference length	2618204639	2618204639
GC (%)	40.21	40.09
Reference GC (%)	40.21	40.21
N50	20532749	1604037
NG50	20532749	1615425
N75	10179728	797993
NG75	10179728	806918
L50	42	500
LG50	42	494
L75	87	1080
LG75	87	1063
# misassemblies	0	73328
# misassembled contigs	0	3940
Misassembled contigs length	0	2601754958
# local misassemblies	0	38172
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	86284	89327
# possible TEs	0	4092
# unaligned mis. contigs	0	177
# unaligned contigs	0 + 0 part	2756 + 4487 part
Unaligned length	0	102139122
Genome fraction (%)	99.999	97.447
Duplication ratio	1.131	1.124
# N's per 100 kbp	11589.37	8111.31
# mismatches per 100 kbp	0.00	143.79
# indels per 100 kbp	0.00	30.10
# genomic features	1775969 + 36736 part	1690655 + 91334 part
Largest alignment	69639376	1225012
Total aligned length	2317183832	2333124718
NA50	15721476	86596
NGA50	15721476	87574
NA75	5894851	30877
NGA75	5894851	32096
LA50	50	8032
LGA50	50	7923
LA75	116	20401
LGA75	116	19948

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

	HetGla_female_1_0_genomic_fna	HetGla_1_0_genomic_fna
# misassemblies	0	73328
# contig misassemblies	0	42127
# c. relocations	0	18072
# c. translocations	0	23964
# c. inversions	0	91
# scaffold misassemblies	0	31201
# s. relocations	0	20331
# s. translocations	0	10839
# s. inversions	0	31
# misassembled contigs	0	3940
Misassembled contigs length	0	2601754958
# local misassemblies	0	38172
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	86284	89327
# possible TEs	0	4092
# unaligned mis. contigs	0	177
# mismatches	0	3243447
# indels	0	678997
# indels (<= 5 bp)	0	416565
# indels (> 5 bp)	0	262432
Indels length	0	26734729

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

	HetGla_female_1_0_genomic_fna	HetGla_1_0_genomic_fna
# fully unaligned contigs	0	2756
Fully unaligned length	0	2833563
# partially unaligned contigs	0	4487
Partially unaligned length	0	99305559
# N's	303433536	213913259

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

NGx
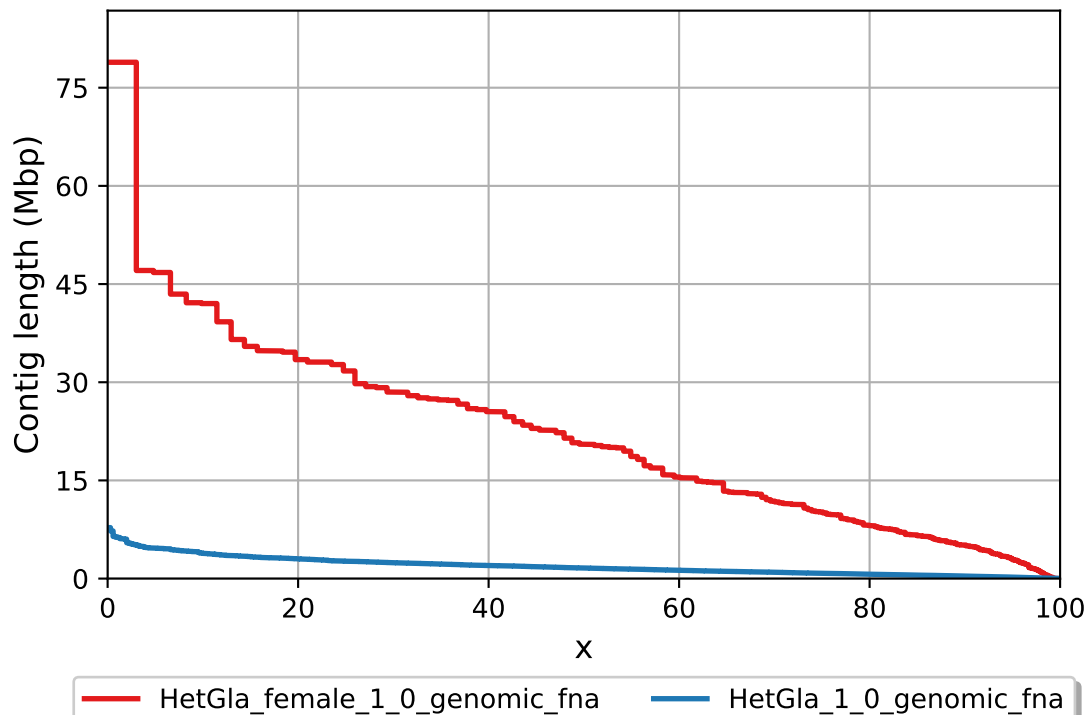
Cumulative length
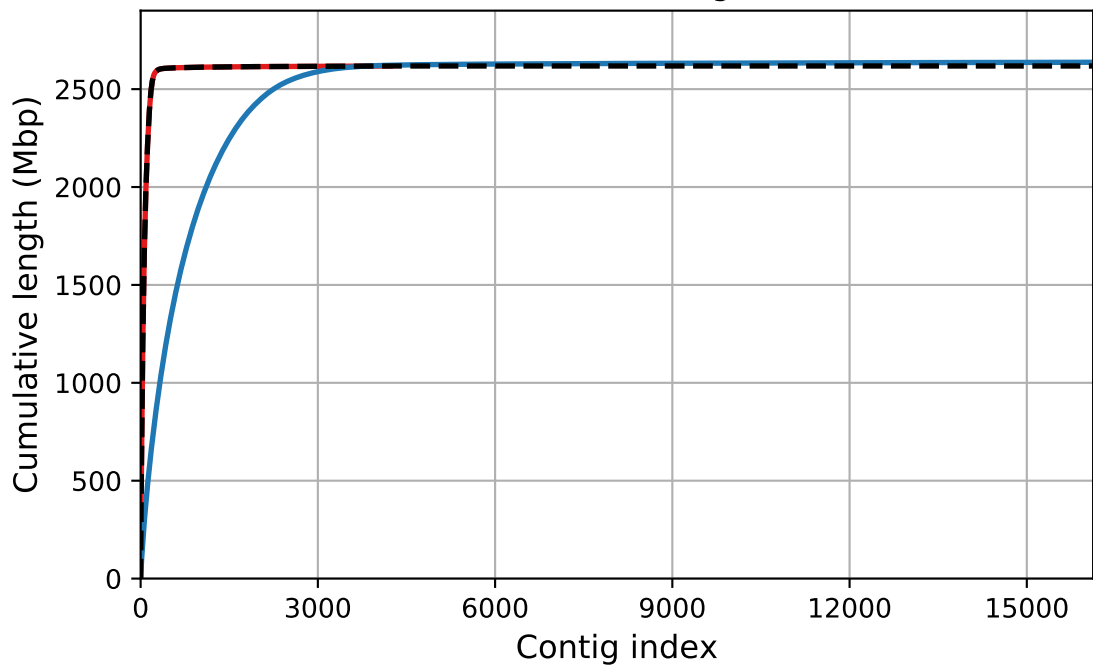
| | HetGla_female_1_0_genomic_fna | HetGla_1_0_genomic_fna | **- -** Reference |

GC content
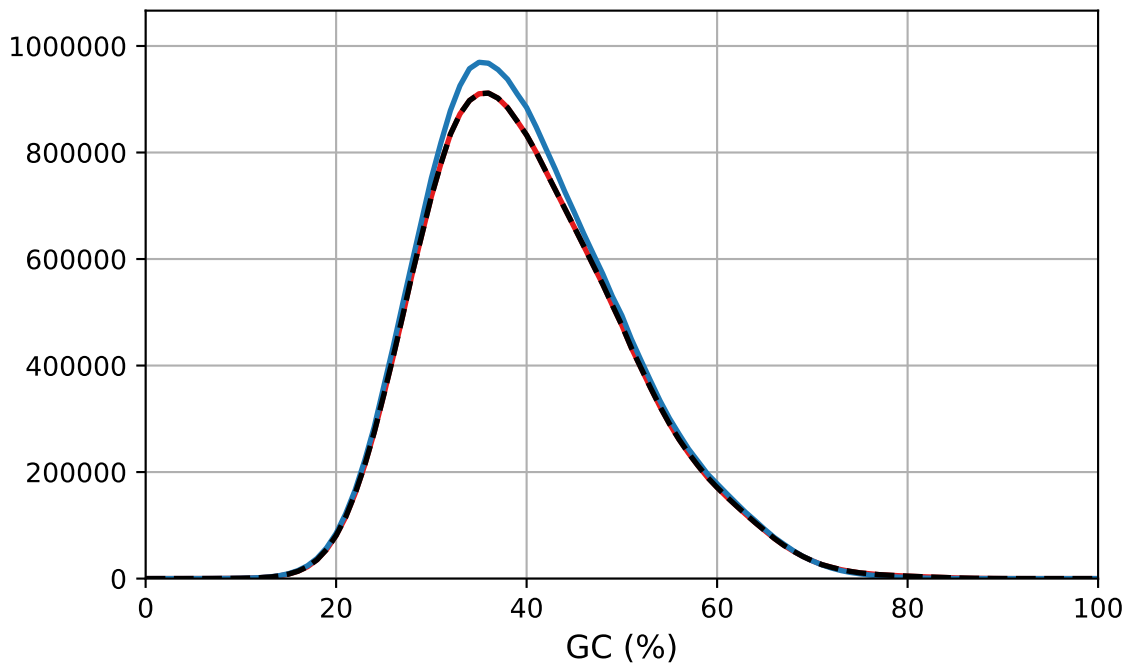
Legend: HetGla_female_1_0_genomic_fna, HetGla_1_0_genomic_fna, Reference

HetGla_female_1_0_genomic_fna GC content
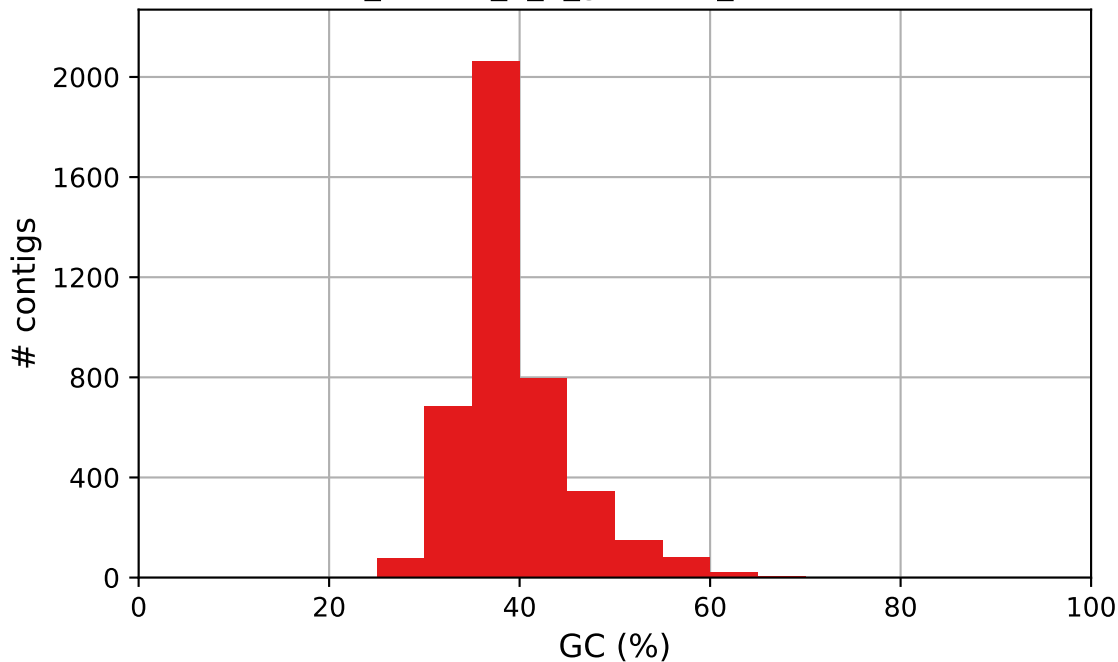
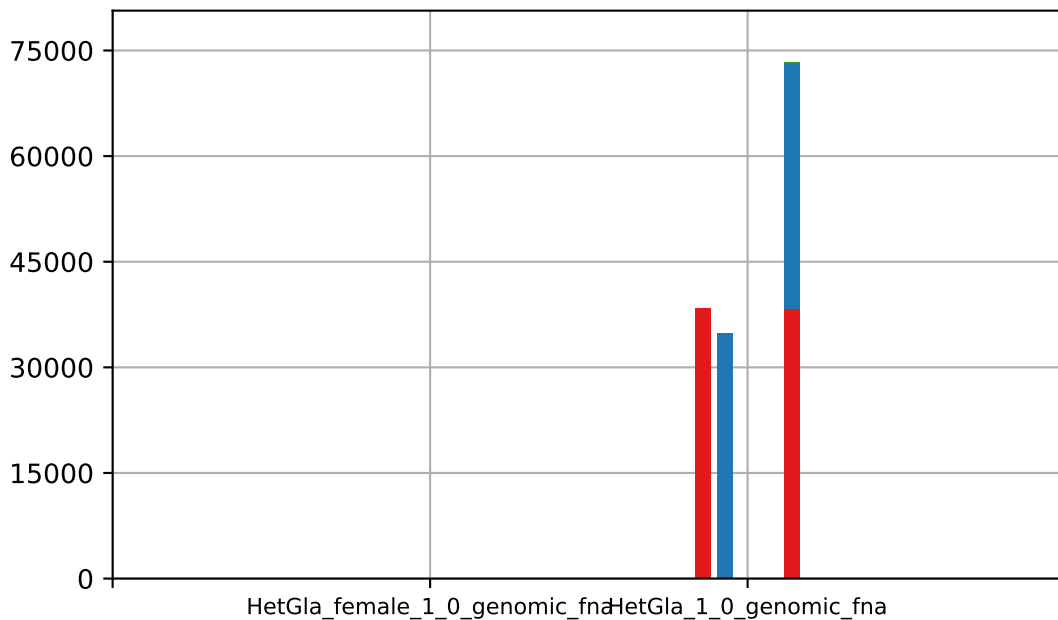HetGla_1_0_genomic_fna GC content
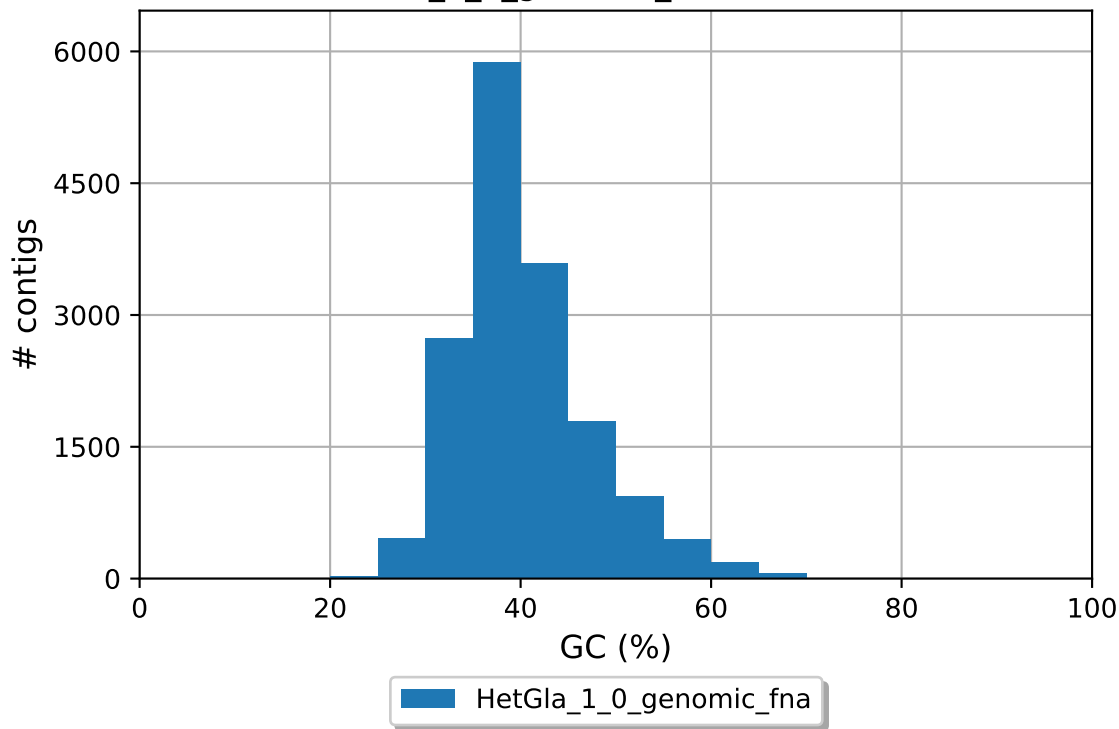
Misassemblies

FRCurve (misassemblies)

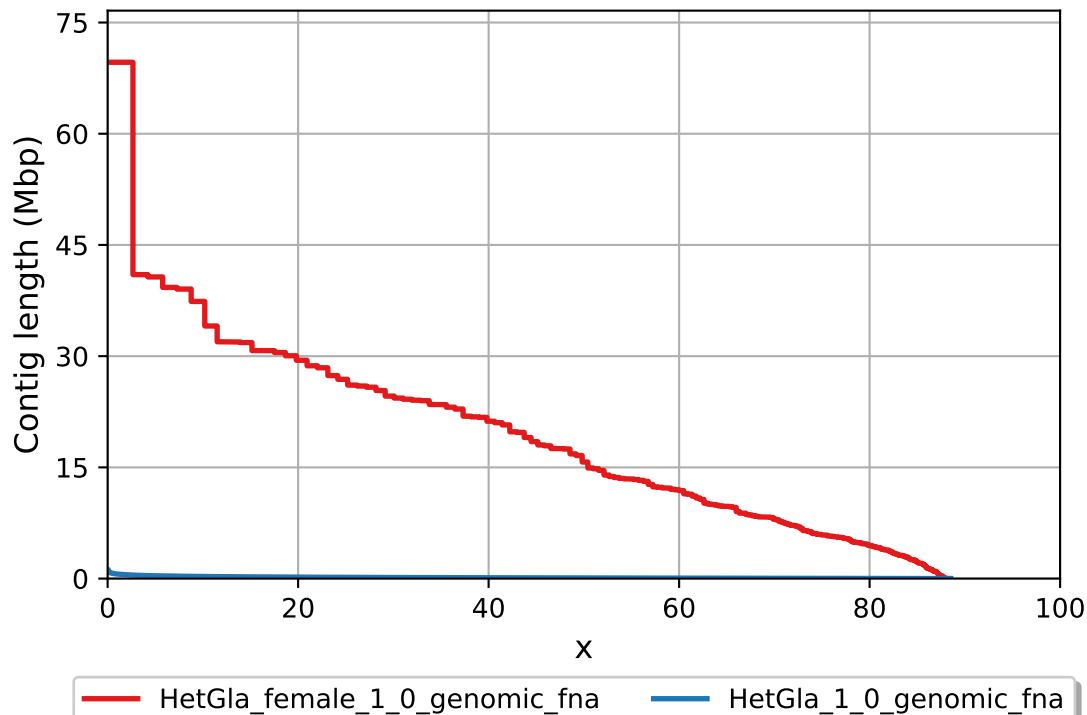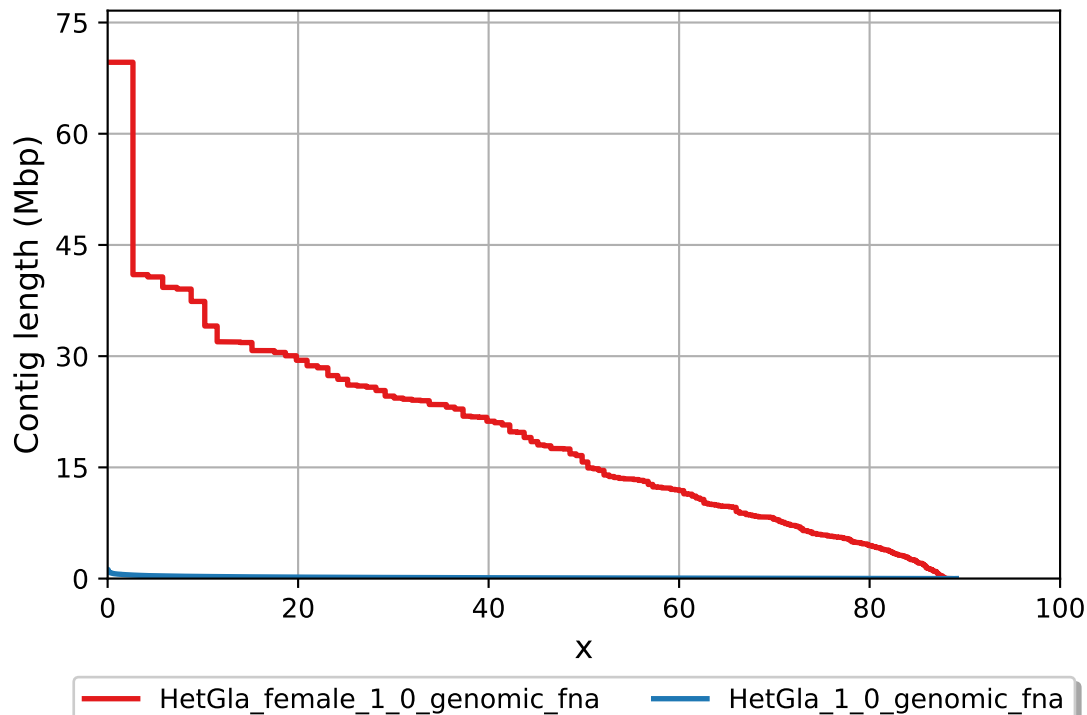Legend: HetGla_female_1_0_genomic_fna, HetGla_1_0_genomic_fna
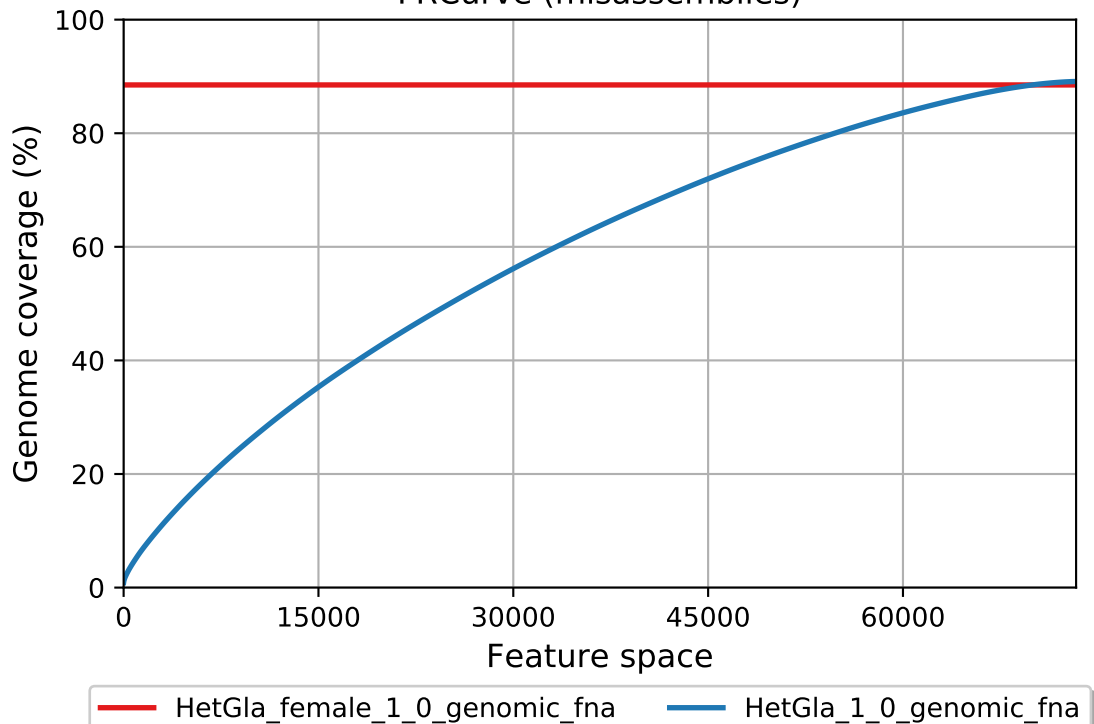
Cumulative length (aligned contigs)
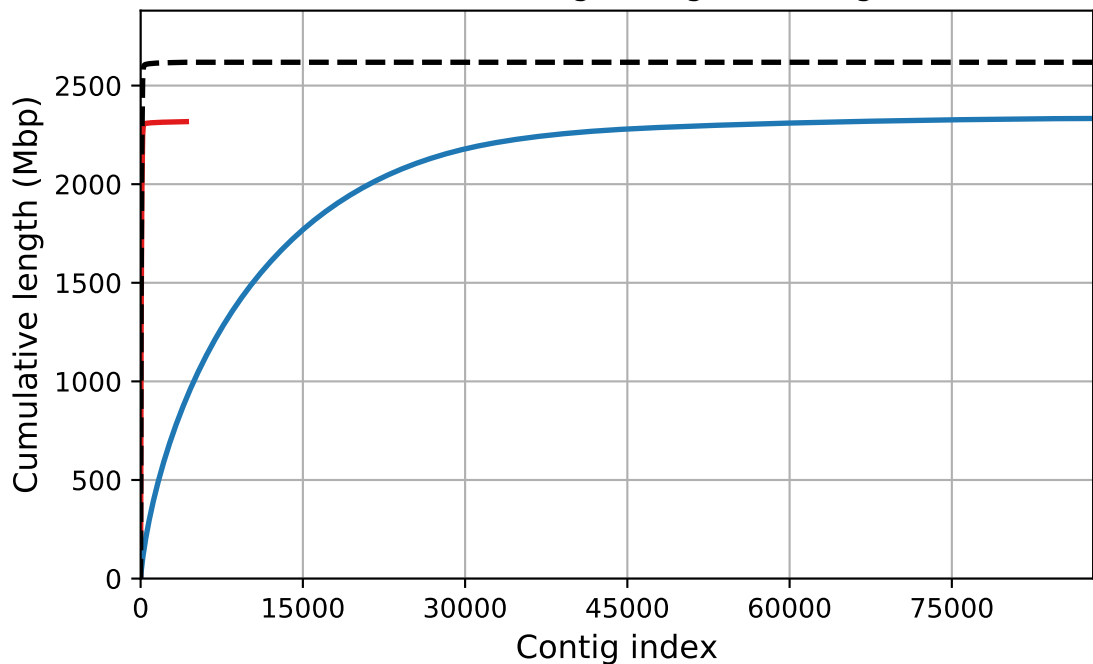
Legend:
- HetGla_female_1_0_genomic_fna
- HetGla_1_0_genomic_fna
- Reference

NAx

NGAx

Cumulative # complete genomic features

Legend: HetGla_female_1_0_genomic_fna · HetGla_1_0_genomic_fna · Reference
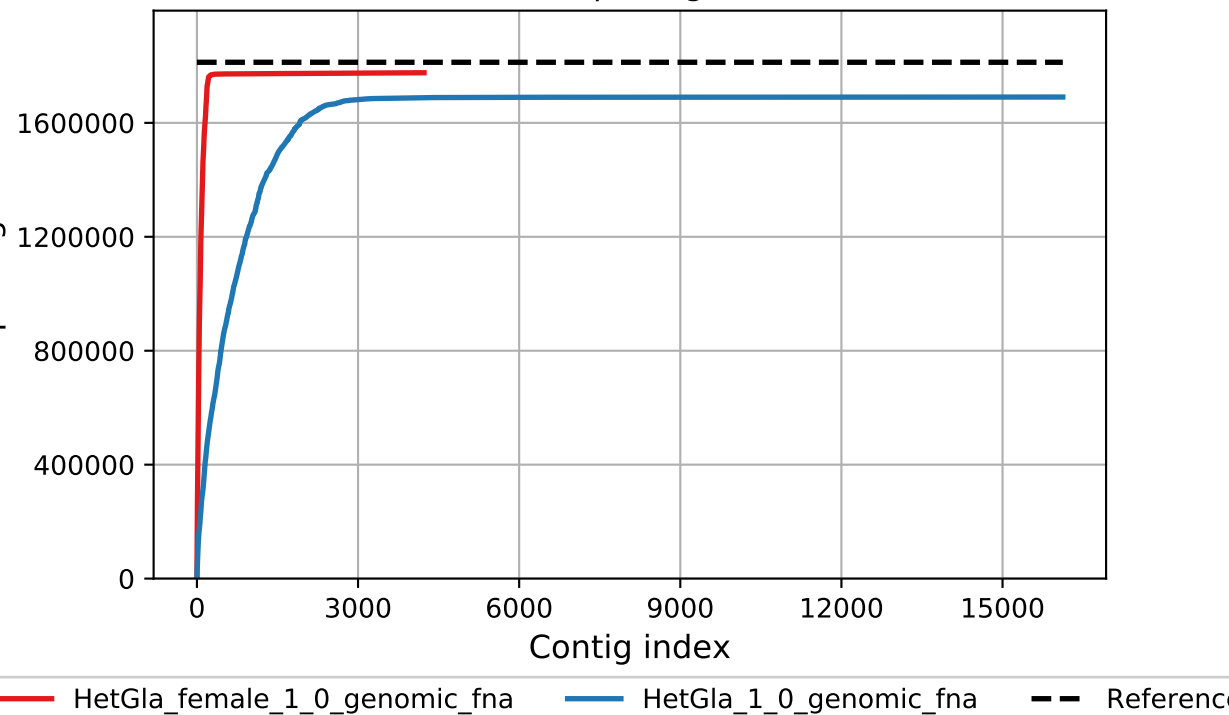
FRCurve (genomic features)

complete genomic features

Genome fraction, %

Legend:
- HetGla_female_1_0_genomic_fna
- HetGla_1_0_genomic_fna